



wwPDB EM Validation Summary Report ⓘ

Dec 11, 2022 – 09:11 pm GMT

PDB ID : 6SV4
EMDB ID : EMD-10315
Title : The cryo-EM structure of SDD1-stalled collided trisome.
Authors : Tesina, P.; Buschauer, R.; Cheng, J.; Becker, T.; Beckmann, R.
Deposited on : 2019-09-17
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

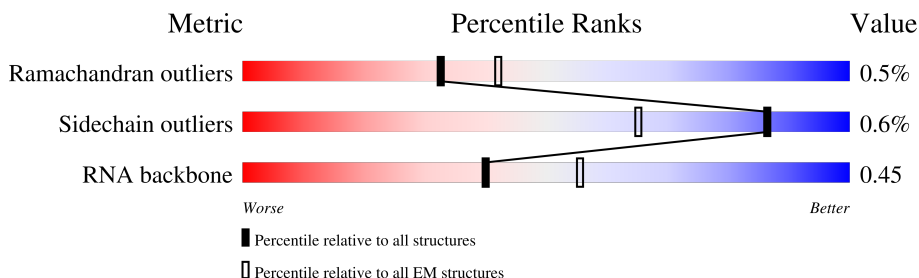
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 Å.

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




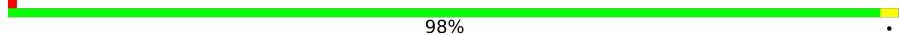
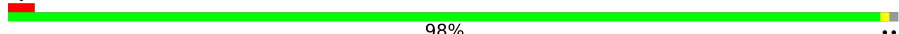
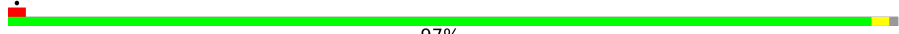


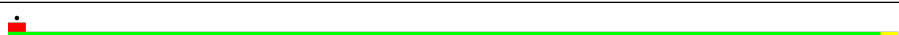
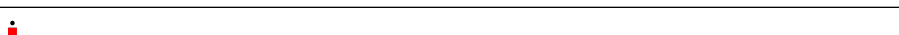
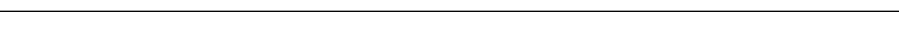
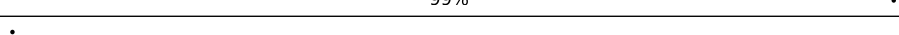
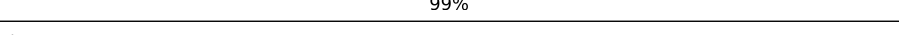
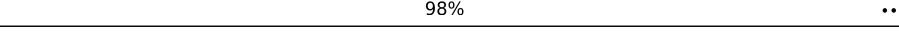
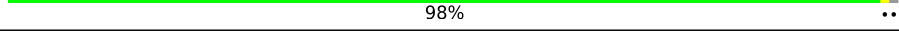
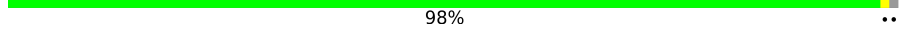










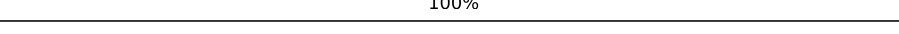
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	BQ	3396	
1	YQ	3396	
1	ZQ	3396	
2	BR	121	
2	YR	121	
2	ZR	121	
3	BS	157	
3	YS	157	

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Mol	Chain	Length	Quality of chain
3	ZS	157	 67% 30%
4	AW	254	 98%
4	XW	254	 98%
4	zW	254	 97%
5	BA	387	 99%
5	YA	387	 99%
5	ZA	387	 98%
6	BE	362	 99%
6	YE	362	 99%
6	ZE	362	 99%
7	BI	297	 98%
7	YI	297	 98%
7	ZI	297	 98%
8	BM	176	 88% 11%
8	YM	176	 89% 11%
8	ZM	176	 5% 89% 11%
9	BO	244	 91% 9%
9	YO	244	 90% 9%
9	ZO	244	 91% 9%
10	AA	256	 90% 10%
10	XA	256	 90% 10%
10	zA	256	 90% 10%
11	AD	190	 100%
11	XD	190	 100%
11	zD	190	 99%




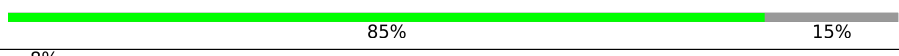
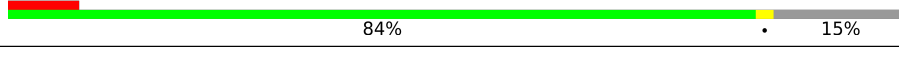
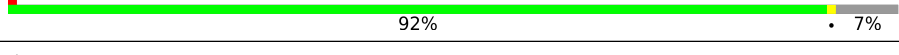
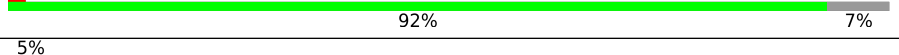
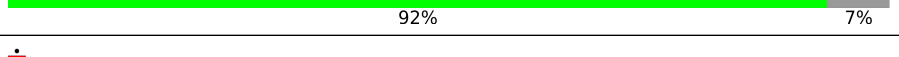
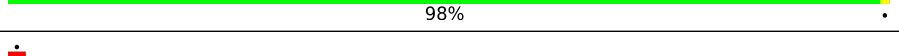
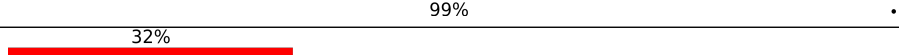
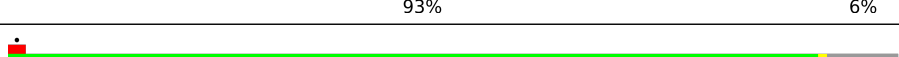
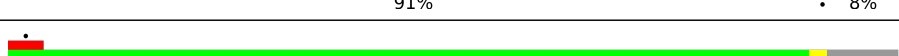
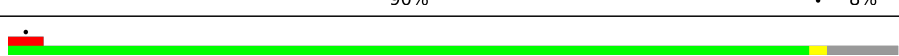
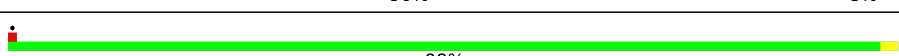
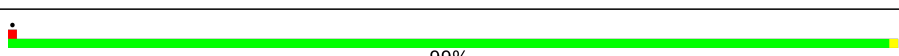
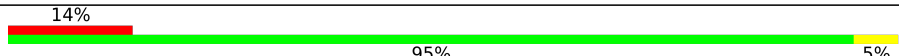
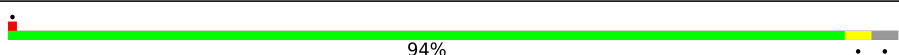
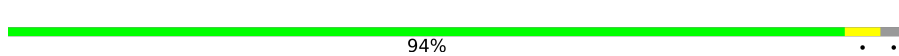
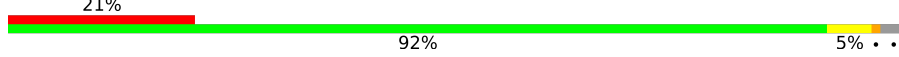
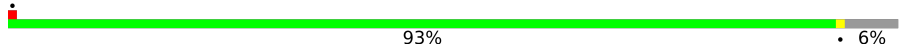
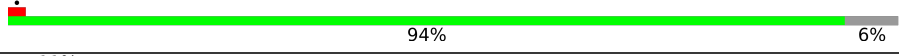
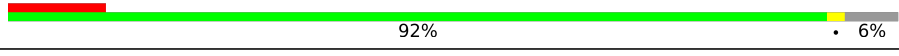
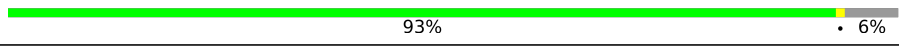
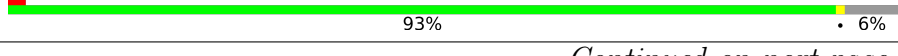

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Mol	Chain	Length	Quality of chain
12	BD	221	94% 5%
12	YD	221	93% 5%
12	ZD	221	93% 5%
13	AG	174	94% ..
13	XG	174	94% ..
13	zG	174	94% ..
14	AJ	199	92% ...
14	XJ	199	92% ...
14	zJ	199	92% ...
15	AM	138	99% .
15	XM	138	99% .
15	zM	138	98% ..
16	AQ	204	98% .
16	XQ	204	99%
16	zQ	204	98% .
17	AU	199	98% ..
17	XU	199	99% .
17	zU	199	99% .
18	2	1800	64% 31% ..
18	2b	1800	66% 30% ..
18	2c	1800	52% 39% 7% .
19	P	252	81% . 18%
19	Pb	252	81% . 18%
19	Pc	252	19% 79% . 18%
20	Q	255	84% 15%

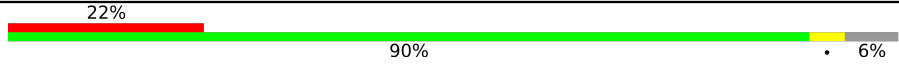
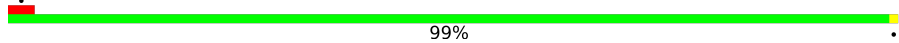
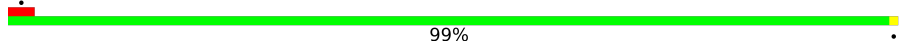
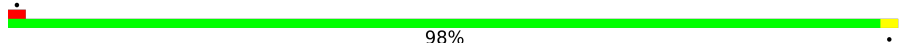




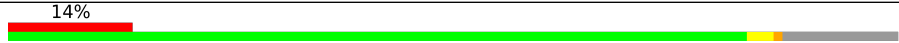

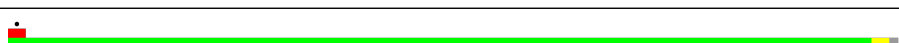

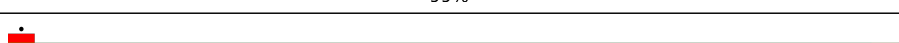
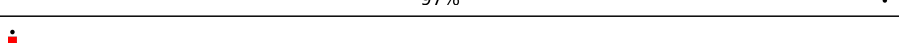
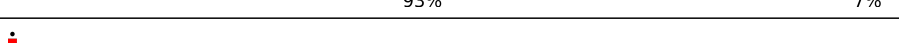
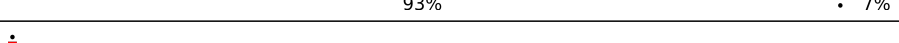
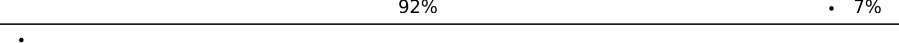
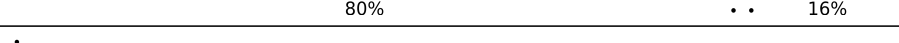
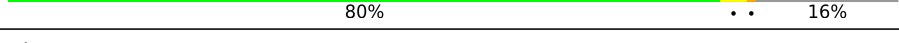

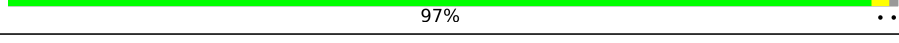
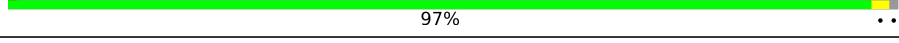
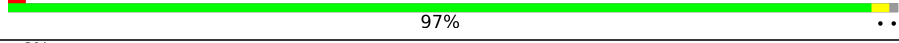
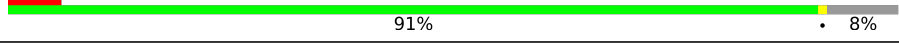

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Mol	Chain	Length	Quality of chain
20	Qb	255	 84% 15%
20	Qc	255	 84% 15%
21	R	254	 83% 15%
21	Rb	254	 85% 15%
21	Rc	254	 84% 15%
22	A	240	 92% 7%
22	Ab	240	 92% 7%
22	Ac	240	 92% 7%
23	S	261	 98%
23	Sb	261	 99%
23	Sc	261	 93% 6%
24	B	225	 91% 8%
24	Bb	225	 90% 8%
24	Bc	225	 90% 8%
25	T	218	 98%
25	Tb	218	 99%
25	Tc	218	 95% 5%
26	U	190	 94%
26	Ub	190	 94%
26	Uc	190	 92% 5%
27	V	200	 93% 6%
27	Vb	200	 94% 6%
27	Vc	200	 92% 6%
28	W	197	 93% 6%
28	Wb	197	 93% 6%

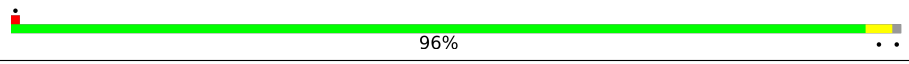
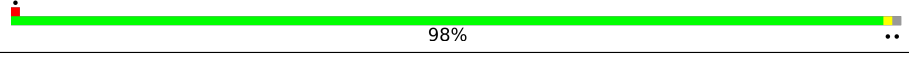
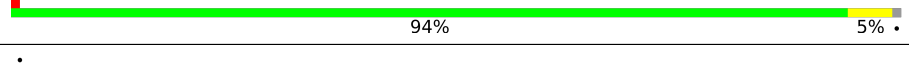
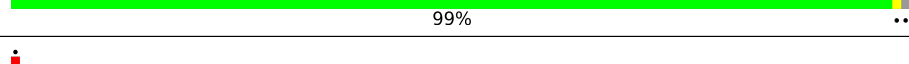
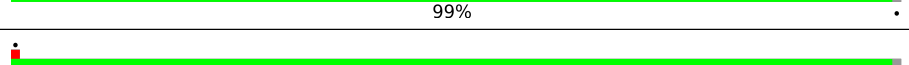
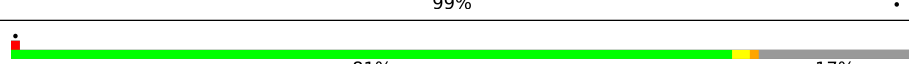
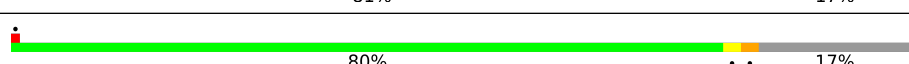
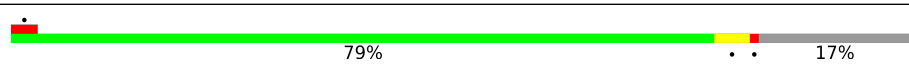
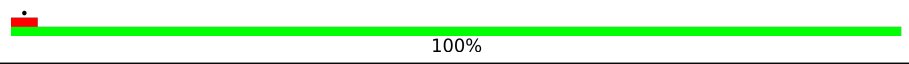
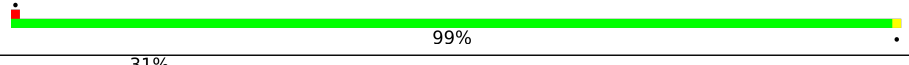
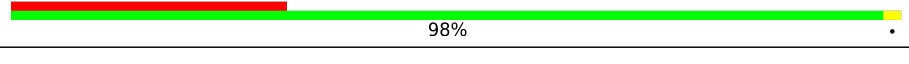
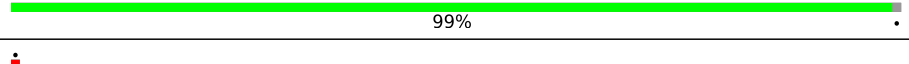
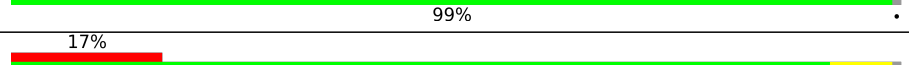
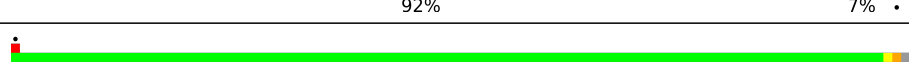
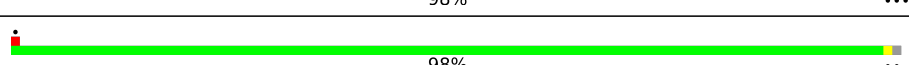
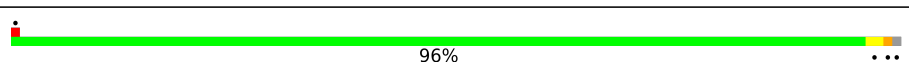
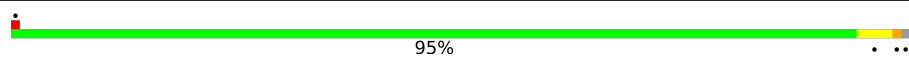
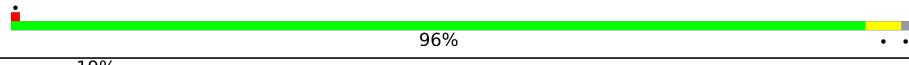
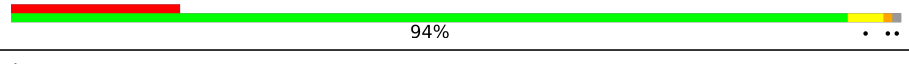






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Mol	Chain	Length	Quality of chain
28	Wc	197	 22% 90% 6%
29	C	92	 99%
29	Cb	92	 99%
29	Cc	92	 98%
30	X	156	 92% 6%
30	Xb	156	 92% 6%
30	Xc	156	 18% 90% 6%
31	D	143	 9% 83% 13%
31	Db	143	 14% 83% 13%
31	Dc	143	 11% 82% 13%
32	Y	151	 97%
32	Yb	151	 99%
32	Yc	151	 97%
33	Z	137	 93% 7%
33	Zb	137	 93% 7%
33	Zc	137	 92% 7%
34	E	142	 80% 16%
34	Eb	142	 80% 16%
34	Ec	142	 79% 16%
35	F	143	 97%
35	Fb	143	 97%
35	Fc	143	 97%
36	G	136	 6% 91% 8%
36	Gb	136	 6% 90% 8%
36	Gc	136	 12% 90% 8%

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Mol	Chain	Length	Quality of chain
37	H	146	 96%
37	Hb	146	 98%
37	Hc	146	 94% 5%
38	I	144	 99%
38	Ib	144	 99%
38	Ic	144	 99%
39	J	121	 81% 17%
39	Jb	121	 80% 17%
39	Jc	121	 79% 17%
40	a	87	 100%
40	ab	87	 99%
40	ac	87	 31% 98%
41	b	130	 99%
41	bb	130	 99%
41	bc	130	 17% 92% 7%
42	c	145	 98%
42	cb	145	 98%
42	cc	145	 96%
43	d	135	 95%
43	db	135	 96%
43	dc	135	 19% 94%
44	K	108	 63% 36%
44	Kb	108	 63% 36%
44	Kc	108	 62% 36%
45	e	119	 79% 18%

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Mol	Chain	Length	Quality of chain
45	eb	119	81% 18%
45	ec	119	79% 18%
46	f	82	95%
46	fb	82	96%
46	fc	82	20% 94% 5%
47	L	67	93% 6%
47	Lb	67	93% 6%
47	Lc	67	94% 6%
48	M	56	20% 88% 7% 5%
48	Mb	56	21% 86% 7% 5%
48	Mc	56	20% 89% 5% 5%
49	g	63	6% 94% 5%
49	gb	63	10% 94% 5%
49	gc	63	11% 92% 5%
50	N	152	46% 52%
50	Nb	152	47% 52%
50	Nc	152	46% 52%
51	O	319	98%
51	Ob	319	5% 98%
51	Oc	319	11% 97%
52	AX	184	94% 5%
52	XX	184	95% 5%
52	zX	184	95% 5%
53	BB	186	99%
53	YB	186	99%

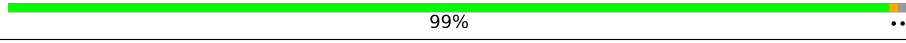
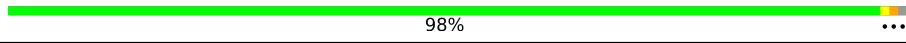
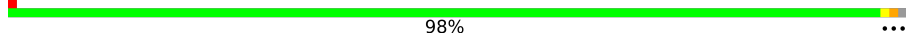
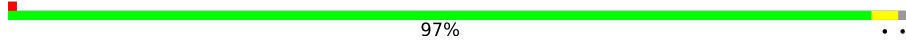
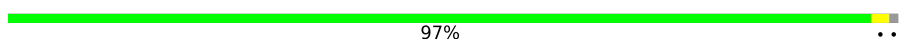
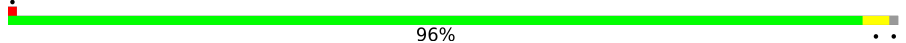

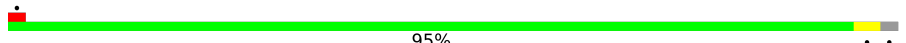
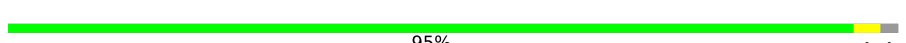
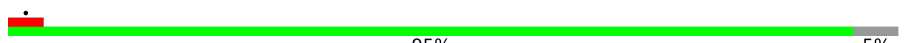
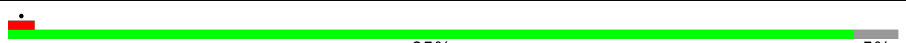
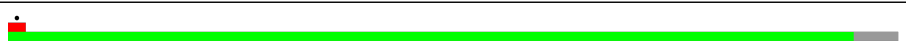



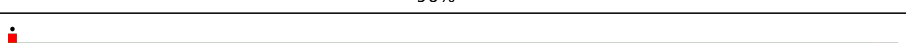
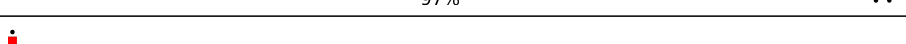
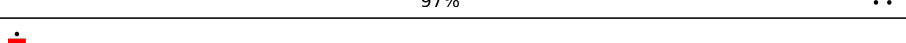
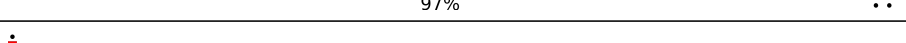
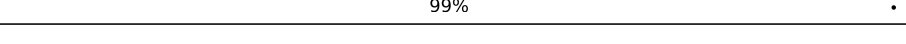
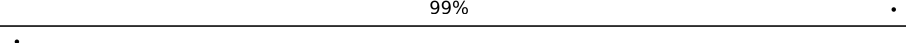
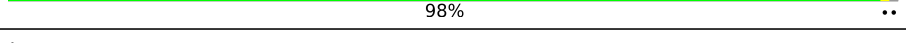
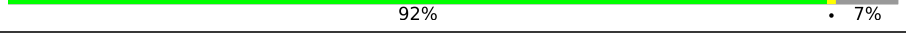

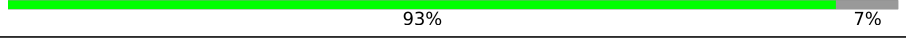
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Mol	Chain	Length	Quality of chain
53	ZB	186	99%
54	BF	189	96%
54	YF	189	98%
54	ZF	189	97%
55	BH	172	100%
55	YH	172	100%
55	ZH	172	100%
56	BJ	160	98%
56	YJ	160	98%
56	ZJ	160	99%
57	BL	121	80% 19%
57	YL	121	80% 19%
57	ZL	121	80% 19%
58	AB	137	96%
58	XB	137	98%
58	zB	137	98%
59	AE	135	48% 97%
59	XE	135	23% 96%
59	zE	135	36% 97%
60	AH	142	84% 15%
60	XH	142	84% 15%
60	zH	142	85% 15%
61	AK	127	97%
61	XK	127	97%
61	zK	127	98%

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Mol	Chain	Length	Quality of chain
62	AN	136	 99% ..
62	XN	136	 98% ...
62	zN	136	 98% ...
63	AR	149	 97% ..
63	XR	149	 97% ..
63	zR	149	 96% ..
64	AV	59	 93% 5% ..
64	XV	59	 95% ..
64	zV	59	 95% ..
65	AY	105	 95% 5% ..
65	XY	105	 95% 5% ..
65	zY	105	 95% 5% ..
66	BC	113	 96% ..
66	YC	113	 96% .
66	ZC	113	 96% ..
67	BG	130	 97% ..
67	YG	130	 97% ..
67	ZG	130	 97% ..
68	BK	107	 99% .
68	YK	107	 99% .
68	ZK	107	 98% ..
69	BN	121	 92% 7% ..
69	YN	121	 91% 7% ..
69	ZN	121	 93% 7% ..
70	BP	120	 99% .

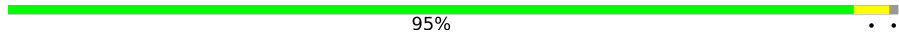








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Mol	Chain	Length	Quality of chain
70	YP	120	99%
70	ZP	120	98%
71	AC	100	98%
71	XC	100	98%
71	zC	100	98%
72	AF	88	91% 7%
72	XF	88	90% 7%
72	zF	88	91% 7%
73	AI	78	97%
73	XI	78	96%
73	zI	78	97%
74	AL	51	98%
74	XL	51	96%
74	zL	51	98%
75	AO	128	40% 59%
75	XO	128	41% 59%
75	zO	128	40% 59%
76	AS	25	100%
76	XS	25	28% 96%
76	zS	25	16% 100%
77	AP	106	98%
77	XP	106	99%
77	zP	106	98%
78	AT	92	97%
78	XT	92	93% 5%

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Mol	Chain	Length	Quality of chain
78	zT	92	 95%
79	BU	312	 15% 44% 56%
79	YU	312	 16% 44% 56%
79	ZU	312	 13% 44% 56%
80	n	76	 71% 29%
81	nb	76	 5% 49% 50%
81	nc	76	 49% 47%
82	mb	77	 78% 21%
82	mc	77	 79% 19%

2 Entry composition [i](#)

There are 82 unique types of molecules in this entry. The entry contains 605489 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	BQ	3127	66891	29878	12066	21820	3127	0	0
1	YQ	3127	66891	29878	12066	21820	3127	0	0
1	ZQ	3127	66891	29878	12066	21820	3127	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	BR	121	2579	1152	461	845	121	0	0
2	YR	121	2579	1152	461	845	121	0	0
2	ZR	121	2579	1152	461	845	121	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	BS	157	3333	1491	584	1101	157	0	0
3	YS	157	3333	1491	584	1101	157	0	0
3	ZS	157	3333	1491	584	1101	157	0	0

- Molecule 4 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	AW	252	1912	1190	388	333	1	0	0
4	XW	252	1912	1190	388	333	1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	zW	252	1912	1190	388	333	1	0	0

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	BA	386	3075	1950	584	533	8	0	0
5	YA	386	3075	1950	584	533	8	0	0
5	ZA	386	3075	1950	584	533	8	0	0

- Molecule 6 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	BI	294	2359	1489	412	456	2	0	0
7	YI	294	2359	1489	412	456	2	0	0
7	ZI	294	2359	1489	412	456	2	0	0

- Molecule 8 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	BM	157	1248	806	224	217	1	0	0
8	YM	157	1248	806	224	217	1	0	0
8	ZM	157	1248	806	224	217	1	0	0

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	BO	223	Total	C	N	O	S	0	0
			1791	1155	325	310	1		
9	YO	223	Total	C	N	O	S	0	0
			1791	1155	325	310	1		
9	ZO	223	Total	C	N	O	S	0	0
			1791	1155	325	310	1		

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AA	231	Total	C	N	O	S	0	0
			1763	1130	316	314	3		
10	XA	231	Total	C	N	O	S	0	0
			1763	1130	316	314	3		
10	zA	231	Total	C	N	O	S	0	0
			1763	1130	316	314	3		

- Molecule 11 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AD	190	Total	C	N	O	S	0	0
			1510	957	273	276	4		
11	XD	190	Total	C	N	O	S	0	0
			1510	957	273	276	4		
11	zD	190	Total	C	N	O	S	0	0
			1510	957	273	276	4		

- Molecule 12 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	BD	209	Total	C	N	O	S	0	0
			1696	1077	321	293	5		
12	YD	209	Total	C	N	O	S	0	0
			1696	1077	321	293	5		
12	ZD	209	Total	C	N	O	S	0	0
			1696	1077	321	293	5		

- Molecule 13 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AG	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		
13	XG	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		
13	zG	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 14 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	AJ	194	Total	C	N	O	0	0
			1548	965	316	267		
14	XJ	194	Total	C	N	O	0	0
			1548	965	316	267		
14	zJ	194	Total	C	N	O	0	0
			1548	965	316	267		

- Molecule 15 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AM	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		
15	XM	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		
15	zM	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

- Molecule 16 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AQ	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		
16	XQ	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		
16	zQ	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AU	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
17	XU	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		
17	zU	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 18 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	2	1758	Total	C	N	O	P	0	0
			37455	16745	6624	12328	1758		
18	2b	1758	Total	C	N	O	P	0	0
			37455	16745	6624	12328	1758		
18	2c	1758	Total	C	N	O	P	0	0
			37455	16745	6624	12328	1758		

- Molecule 19 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	206	Total	C	N	O	S	0	0
			1583	1017	281	283	2		
19	Pb	206	Total	C	N	O	S	0	0
			1583	1017	281	283	2		
19	Pc	206	Total	C	N	O	S	0	0
			1583	1017	281	283	2		

- Molecule 20 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	216	Total	C	N	O	S	0	0
			1722	1091	312	315	4		
20	Qb	216	Total	C	N	O	S	0	0
			1722	1091	312	315	4		
20	Qc	216	Total	C	N	O	S	0	0
			1722	1091	312	315	4		

- Molecule 21 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	R	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		
21	Rb	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

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

- Molecule 22 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	A	223	1734	1101	313	314	6	0	0
22	Ab	223	1734	1101	313	314	6	0	0
22	Ac	223	1734	1101	313	314	6	0	0

- Molecule 23 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	S	260	2068	1316	389	360	3	0	0
23	Sb	260	2068	1316	389	360	3	0	0
23	Sc	260	2068	1316	389	360	3	0	0

- Molecule 24 is a protein called Rps5p.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	B	206	1609	1007	300	299	3	0	0
24	Bb	206	1609	1007	300	299	3	0	0
24	Bc	206	1609	1007	300	299	3	0	0

- Molecule 25 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	T	218	1755	1102	337	313	3	0	0
25	Tb	218	1755	1102	337	313	3	0	0
25	Tc	218	1755	1102	337	313	3	0	0

- Molecule 26 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
26	U	185	Total	C	N	O	0	0
			1486	954	266	266		
26	Ub	185	Total	C	N	O	0	0
			1486	954	266	266		
26	Uc	185	Total	C	N	O	0	0
			1486	954	266	266		

- Molecule 27 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	V	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		
27	Vb	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		
27	Vc	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 28 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	W	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		
28	Wb	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		
28	Wc	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 29 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	C	92	Total	C	N	O	S	0	0
			741	478	121	140	2		
29	Cb	92	Total	C	N	O	S	0	0
			741	478	121	140	2		
29	Cc	92	Total	C	N	O	S	0	0
			741	478	121	140	2		

- Molecule 30 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	X	146	Total	C	N	O	S	0	0
			1168	747	221	197	3		
30	Xb	146	Total	C	N	O	S	0	0
			1168	747	221	197	3		
30	Xc	146	Total	C	N	O	S	0	0
			1168	747	221	197	3		

- Molecule 31 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	D	124	Total	C	N	O	S	0	0
			890	560	156	172	2		
31	Db	124	Total	C	N	O	S	0	0
			890	560	156	172	2		
31	Dc	124	Total	C	N	O	S	0	0
			890	560	156	172	2		

- Molecule 32 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		
32	Yb	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		
32	Yc	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 33 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Z	128	Total	C	N	O	S	0	0
			949	582	188	176	3		
33	Zb	128	Total	C	N	O	S	0	0
			949	582	188	176	3		
33	Zc	128	Total	C	N	O	S	0	0
			949	582	188	176	3		

- Molecule 34 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	E	119	Total	C	N	O	S	0	0
			939	595	176	161	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
34	Eb	119	Total	C	N	O	S	0	0
			939	595	176	161	7		
34	Ec	119	Total	C	N	O	S	0	0
			939	595	176	161	7		

- Molecule 35 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	F	141	Total	C	N	O	0	0
			1105	708	203	194		
35	Fb	141	Total	C	N	O	0	0
			1105	708	203	194		
35	Fc	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 36 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	G	125	Total	C	N	O	S	0	0
			1000	625	188	185	2		
36	Gb	125	Total	C	N	O	S	0	0
			1000	625	188	185	2		
36	Gc	125	Total	C	N	O	S	0	0
			1000	625	188	185	2		

- Molecule 37 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	H	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		
37	Hb	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		
37	Hc	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 38 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	I	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		
38	Ib	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

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

- Molecule 39 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	J	101	Total	C	N	O	S	0	0
			805	512	145	147	1		
39	Jb	101	Total	C	N	O	S	0	0
			805	512	145	147	1		
39	Jc	101	Total	C	N	O	S	0	0
			805	512	145	147	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	a	87	Total	C	N	O	S	0	0
			684	420	125	137	2		
40	ab	87	Total	C	N	O	S	0	0
			684	420	125	137	2		
40	ac	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 41 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	b	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		
41	bb	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		
41	bc	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 42 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	c	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		
42	cb	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		
42	cc	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 43 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	d	134	Total	C	N	O	0	0
			1073	676	208	189		
43	db	134	Total	C	N	O	0	0
			1073	676	208	189		
43	dc	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 44 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	K	69	Total	C	N	O	0	0
			558	357	103	98		
44	Kb	69	Total	C	N	O	0	0
			558	357	103	98		
44	Kc	69	Total	C	N	O	0	0
			558	357	103	98		

- Molecule 45 is a protein called 40S ribosomal protein S26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	e	97	Total	C	N	O	S	0	0
			769	475	160	129	5		
45	eb	97	Total	C	N	O	S	0	0
			769	475	160	129	5		
45	ec	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 46 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	f	81	Total	C	N	O	S	0	0
			610	382	110	113	5		
46	fb	81	Total	C	N	O	S	0	0
			610	382	110	113	5		
46	fc	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 47 is a protein called 40S ribosomal protein S28-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	L	63	Total	C	N	O	S	0	0
			497	306	99	91	1		
47	Lb	63	Total	C	N	O	S	0	0
			497	306	99	91	1		
47	Lc	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 48 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	M	53	Total	C	N	O	S	0	0
			442	274	92	72	4		
48	Mb	53	Total	C	N	O	S	0	0
			442	274	92	72	4		
48	Mc	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 49 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	g	60	Total	C	N	O	S	0	0
			475	299	98	77	1		
49	gb	60	Total	C	N	O	S	0	0
			475	299	98	77	1		
49	gc	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 50 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	N	73	Total	C	N	O	S	0	0
			556	352	105	95	4		
50	Nb	73	Total	C	N	O	S	0	0
			556	352	105	95	4		
50	Nc	73	Total	C	N	O	S	0	0
			556	352	105	95	4		

- Molecule 51 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	O	313	Total	C	N	O	S	0	0
			2403	1521	411	463	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
51	Ob	313	Total	C	N	O	S	0	0
			2403	1521	411	463	8		
51	Oc	313	Total	C	N	O	S	0	0
			2403	1521	411	463	8		

- Molecule 52 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	AX	175	Total	C	N	O	0	0
			1378	856	273	249		
52	XX	175	Total	C	N	O	0	0
			1378	856	273	249		
52	zX	175	Total	C	N	O	0	0
			1378	856	273	249		

- Molecule 53 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BB	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		
53	YB	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		
53	ZB	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 54 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	BF	183	Total	C	N	O	0	0
			1482	911	320	251		
54	YF	188	Total	C	N	O	0	0
			1522	935	326	261		
54	ZF	188	Total	C	N	O	0	0
			1522	935	326	261		

- Molecule 55 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BH	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		
55	YH	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
55	ZH	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 56 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BJ	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		
56	YJ	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		
56	ZJ	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 57 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	BL	98	Total	C	N	O	0	0
			778	505	127	146		
57	YL	98	Total	C	N	O	0	0
			778	505	127	146		
57	ZL	98	Total	C	N	O	0	0
			778	505	127	146		

- Molecule 58 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AB	134	Total	C	N	O	S	0	0
			993	623	187	176	7		
58	XB	134	Total	C	N	O	S	0	0
			993	623	187	176	7		
58	zB	134	Total	C	N	O	S	0	0
			993	623	187	176	7		

- Molecule 59 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AE	135	Total	C	N	O	S	0	0
			1085	679	218	187	1		
59	XE	135	Total	C	N	O	S	0	0
			1089	682	219	187	1		
59	zE	135	Total	C	N	O	S	0	0
			1089	682	219	187	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AH	120	Total	C	N	O	S	0	0
			959	617	168	172	2		
60	XH	120	Total	C	N	O	S	0	0
			959	617	168	172	2		
60	zH	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 61 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	AK	124	Total	C	N	O	0	0
			976	614	190	172		
61	XK	124	Total	C	N	O	0	0
			976	614	190	172		
61	zK	124	Total	C	N	O	0	0
			976	614	190	172		

- Molecule 62 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	AN	135	Total	C	N	O	0	0
			1092	710	202	180		
62	XN	135	Total	C	N	O	0	0
			1092	710	202	180		
62	zN	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 63 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AR	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		
63	XR	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		
63	zR	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 64 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
64	AV	58	Total	C	N	O	0	0
			462	289	100	73		
64	XV	58	Total	C	N	O	0	0
			462	289	100	73		
64	zV	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 65 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AY	100	Total	C	N	O	S	0	0
			767	492	128	146	1		
65	XY	100	Total	C	N	O	S	0	0
			767	492	128	146	1		
65	zY	100	Total	C	N	O	S	0	0
			767	492	128	146	1		

- Molecule 66 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	BC	109	Total	C	N	O	S	0	0
			883	559	167	156	1		
66	YC	109	Total	C	N	O	S	0	0
			883	559	167	156	1		
66	ZC	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 67 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	BG	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		
67	YG	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		
67	ZG	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 68 is a protein called 60S ribosomal protein L33-A.

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

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Mol	Chain	Residues	Atoms					AltConf	Trace
68	YK	106	Total	C	N	O	S	0	0
			850	540	165	144	1		
68	ZK	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 69 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	BN	112	Total	C	N	O	S	0	0
			880	545	179	152	4		
69	YN	112	Total	C	N	O	S	0	0
			880	545	179	152	4		
69	ZN	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 70 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	BP	119	Total	C	N	O	S	0	0
			965	612	185	167	1		
70	YP	119	Total	C	N	O	S	0	0
			965	612	185	167	1		
70	ZP	119	Total	C	N	O	S	0	0
			965	612	185	167	1		

- Molecule 71 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AC	99	Total	C	N	O	S	0	0
			770	481	156	131	2		
71	XC	99	Total	C	N	O	S	0	0
			770	481	156	131	2		
71	zC	99	Total	C	N	O	S	0	0
			770	481	156	131	2		

- Molecule 72 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AF	82	Total	C	N	O	S	0	0
			650	396	142	107	5		
72	XF	82	Total	C	N	O	S	0	0
			650	396	142	107	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	zF	82	650	396	142	107	5	0	0

- Molecule 73 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O			
73	AI	77	608	388	114	106		0	0
73	XI	77	608	388	114	106		0	0
73	zI	77	608	388	114	106		0	0

- Molecule 74 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	AL	50	436	272	97	65	2	0	0
74	XL	50	436	272	97	65	2	0	0
74	zL	50	436	272	97	65	2	0	0

- Molecule 75 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	AO	52	417	259	86	67	5	0	0
75	XO	52	417	259	86	67	5	0	0
75	zO	52	417	259	86	67	5	0	0

- Molecule 76 is a protein called 60S ribosomal protein L41-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	AS	25	233	142	63	27	1	0	0
76	XS	25	233	142	63	27	1	0	0
76	zS	25	233	142	63	27	1	0	0

- Molecule 77 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AP	105	Total	C	N	O	S	0	0
			847	534	170	138	5		
77	XP	105	Total	C	N	O	S	0	0
			847	534	170	138	5		
77	zP	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 78 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	AT	91	Total	C	N	O	S	0	0
			694	429	138	121	6		
78	XT	91	Total	C	N	O	S	0	0
			694	429	138	121	6		
78	zT	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 79 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	BU	138	Total	C	N	O	S	0	0
			1052	672	187	190	3		
79	YU	138	Total	C	N	O	S	0	0
			1052	672	187	190	3		
79	ZU	138	Total	C	N	O	S	0	0
			1052	672	187	190	3		

- Molecule 80 is a RNA chain called tRNA (P/P).

Mol	Chain	Residues	Atoms					AltConf	Trace
80	n	76	Total	C	N	O	P	0	0
			1621	723	291	531	76		

- Molecule 81 is a RNA chain called tRNA (A/P).

Mol	Chain	Residues	Atoms					AltConf	Trace
81	nb	76	Total	C	N	O	P	0	0
			1620	723	290	532	75		
81	nc	76	Total	C	N	O	P	0	0
			1620	723	290	532	75		

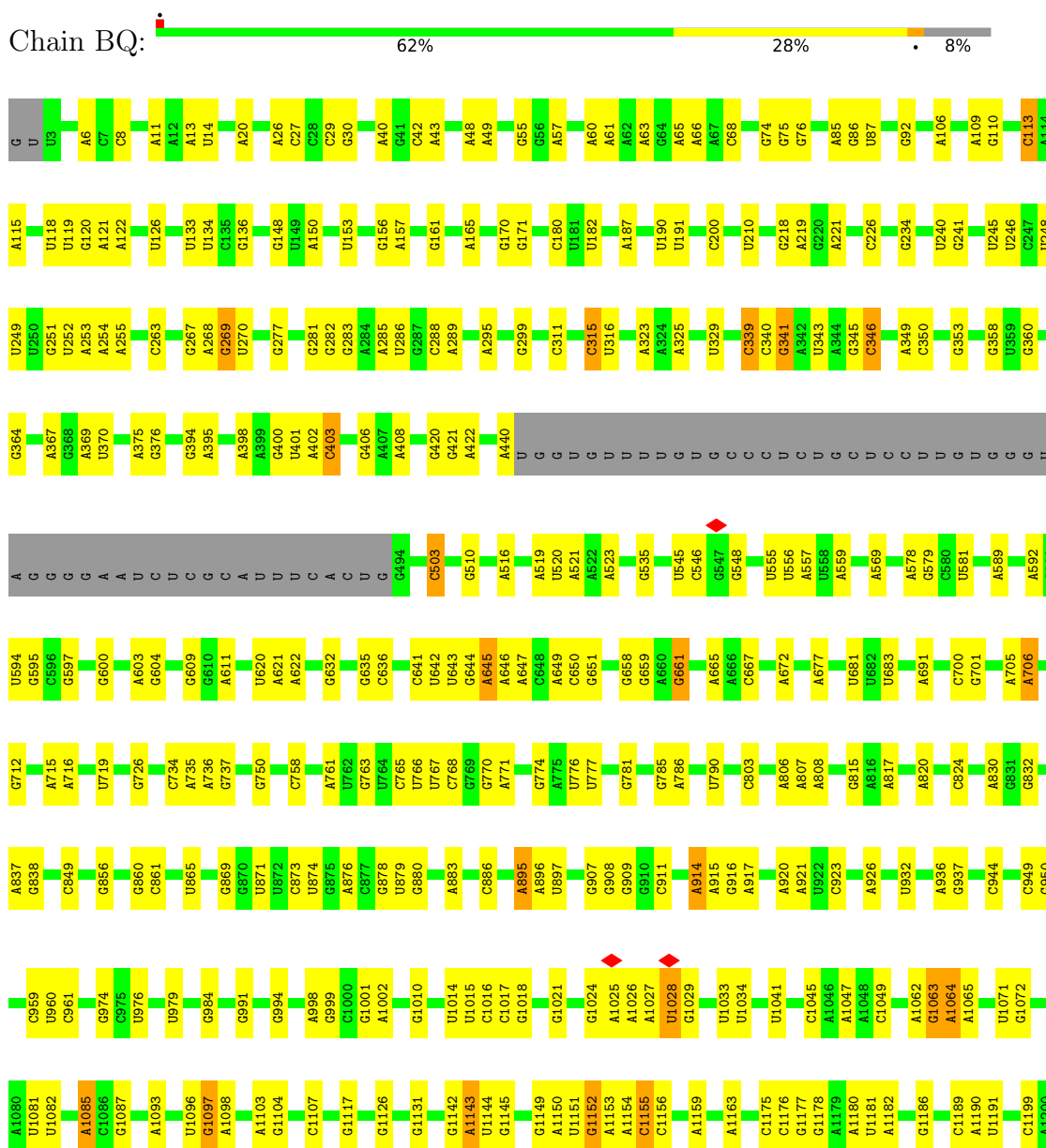
- Molecule 82 is a RNA chain called tRNA (P/E).

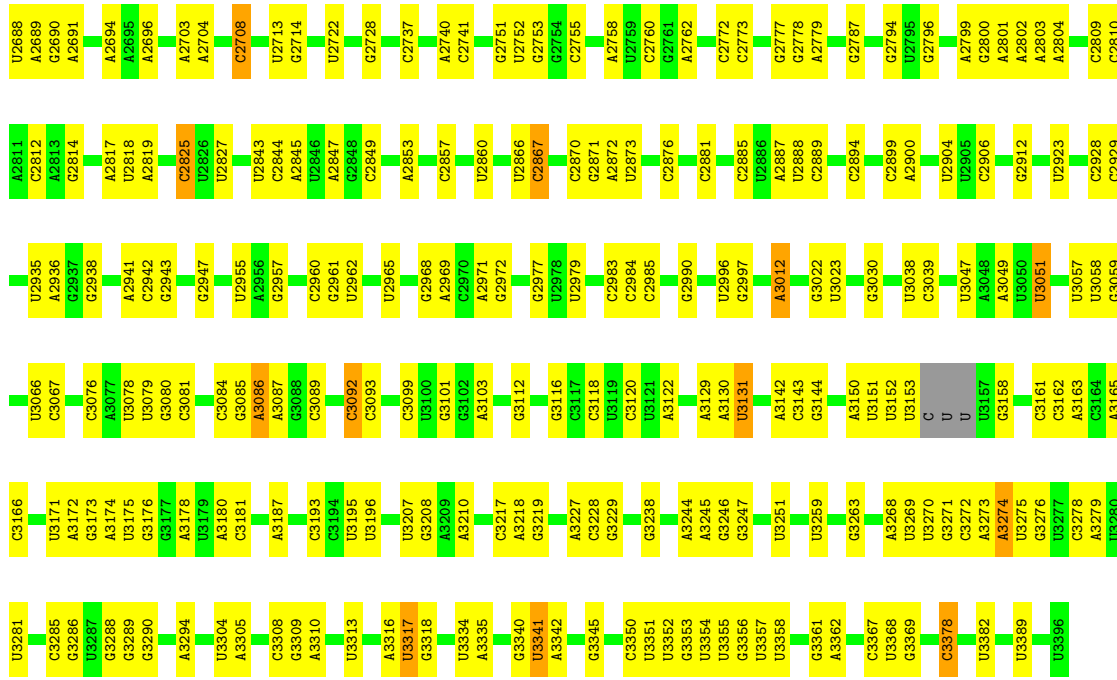
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
82	mb	77	Total	C	N	O	P	0	0
			1644	732	297	538	77		
82	mc	77	Total	C	N	O	P	0	0
			1644	732	297	538	77		

3 Residue-property plots

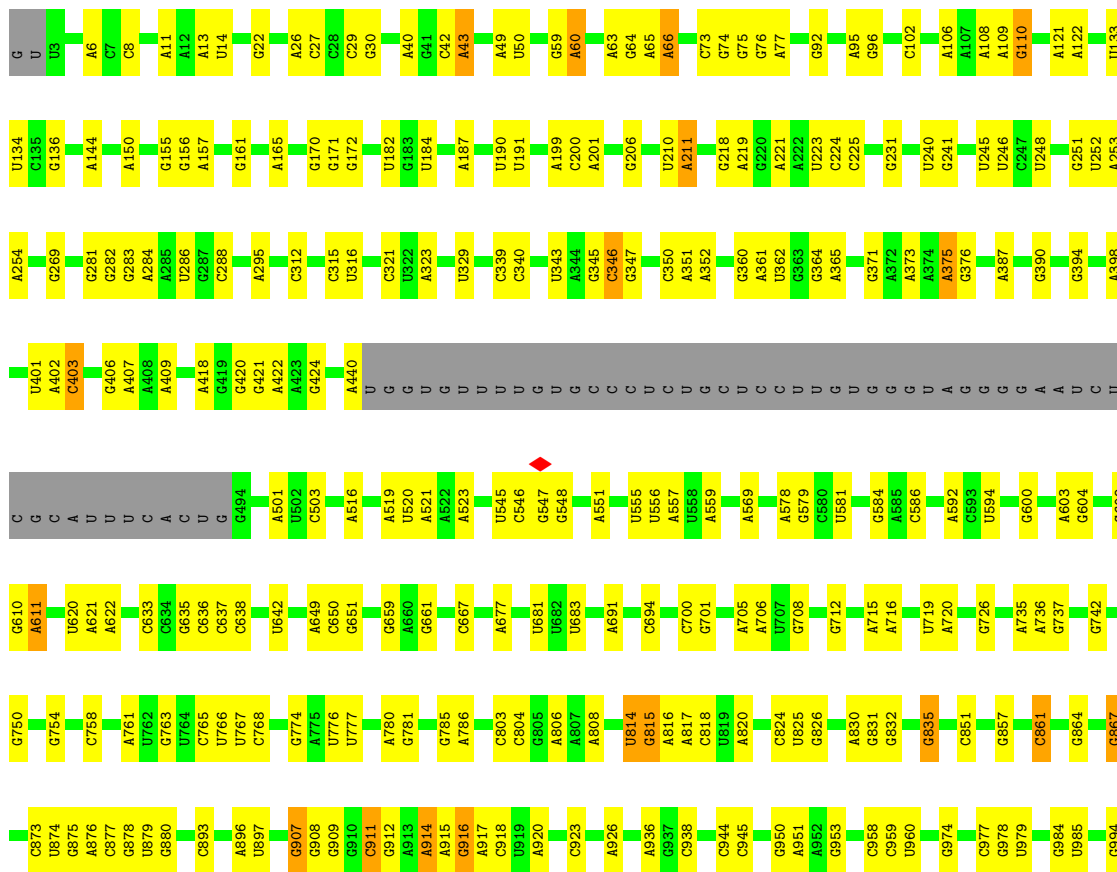
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

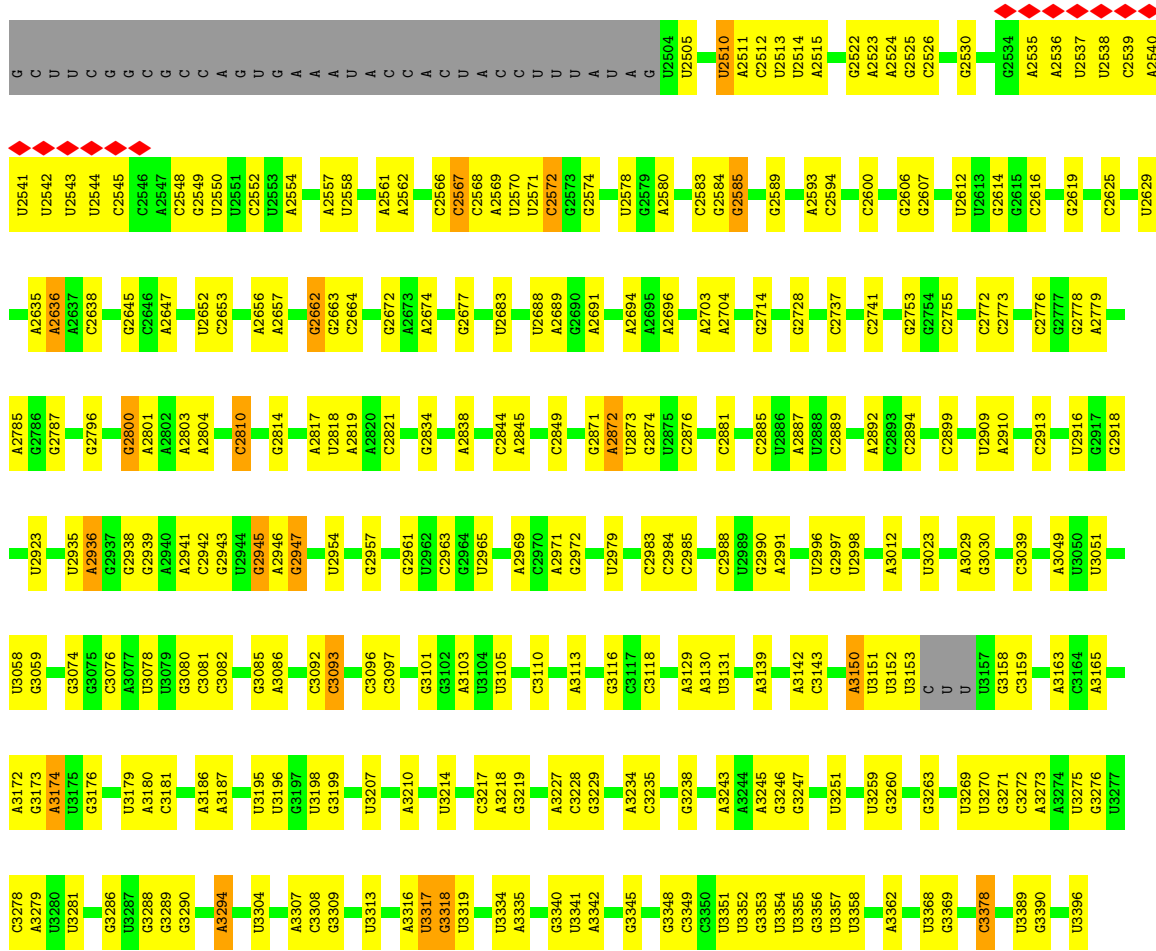
- Molecule 1: 25S rRNA



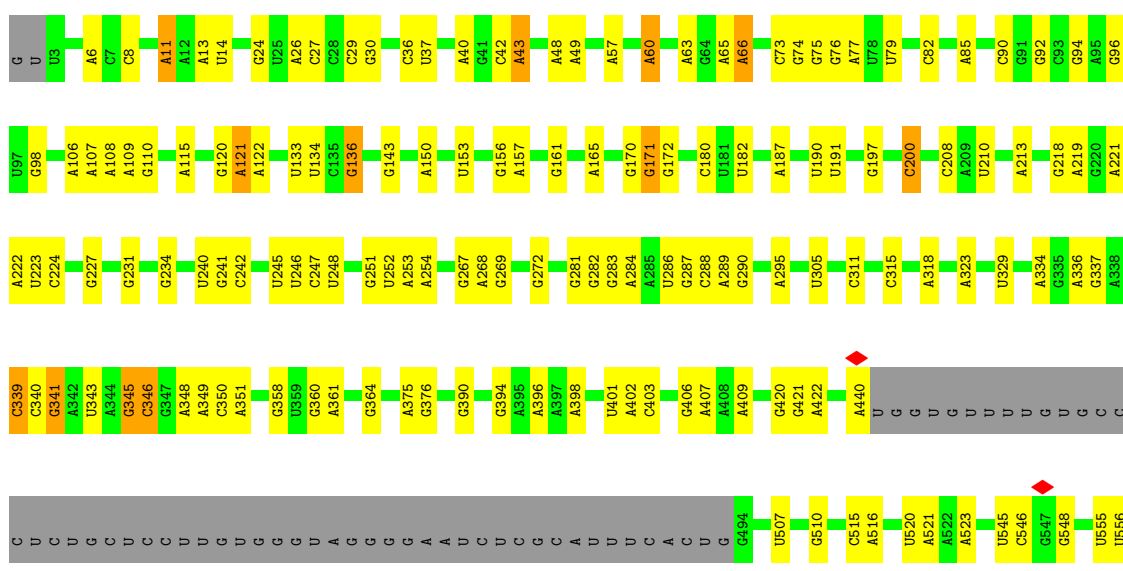


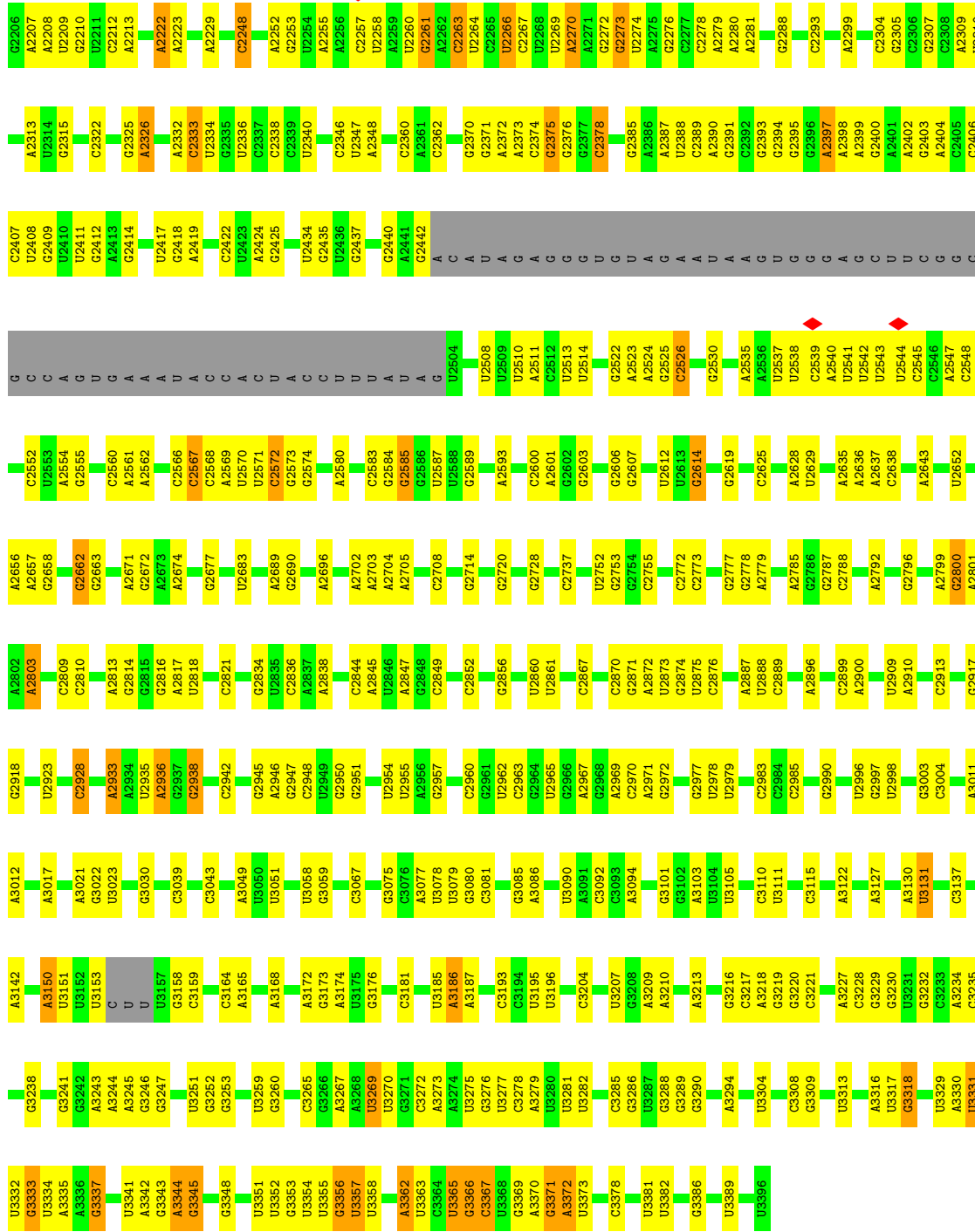
• Molecule 1: 25S rRNA



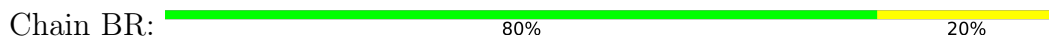


• Molecule 1: 25S rRNA

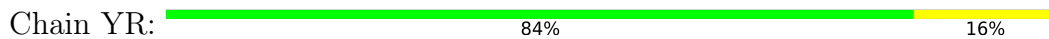




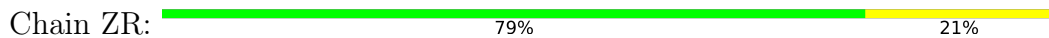
• Molecule 2: 5S rRNA



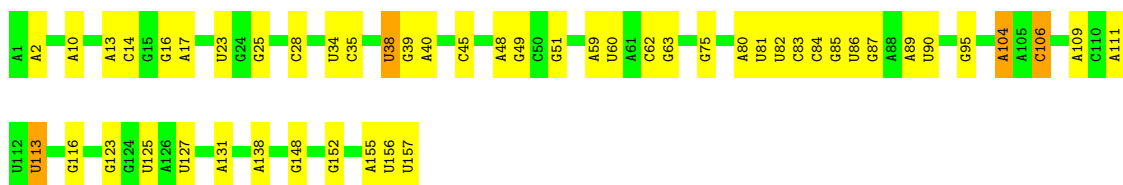
• Molecule 2: 5S rRNA



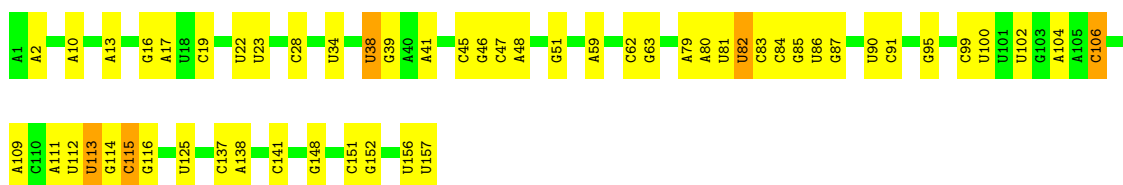
• Molecule 2: 5S rRNA



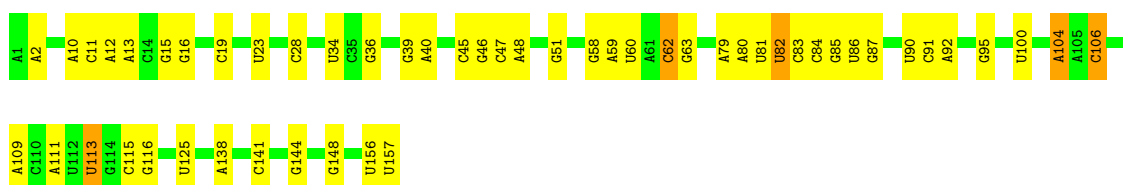
• Molecule 3: 5.8S rRNA



• Molecule 3: 5.8S rRNA



• Molecule 3: 5.8S rRNA

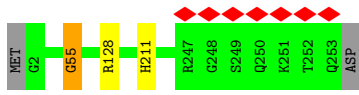


• Molecule 4: 60S ribosomal protein L2-A



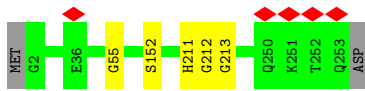
- Molecule 4: 60S ribosomal protein L2-A

Chain XW:  98%



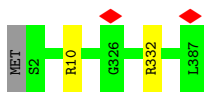
- Molecule 4: 60S ribosomal protein L2-A

Chain zW:  97%



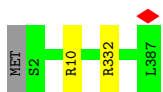
- Molecule 5: 60S ribosomal protein L3

Chain BA:  99%



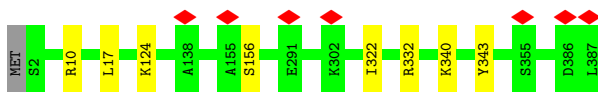
- Molecule 5: 60S ribosomal protein L3

Chain YA:  99%



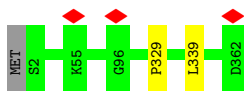
- Molecule 5: 60S ribosomal protein L3

Chain ZA:  98%



- Molecule 6: 60S ribosomal protein L4-A

Chain BE:  99%



- Molecule 6: 60S ribosomal protein L4-A

Chain YE:  99%

- Molecule 11: 60S ribosomal protein L9-A

Chain AD:  100%



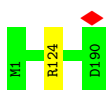
- Molecule 11: 60S ribosomal protein L9-A

Chain XD:  100%



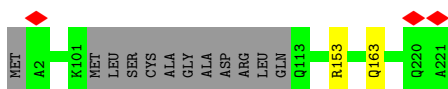
- Molecule 11: 60S ribosomal protein L9-A

Chain zD:  99%



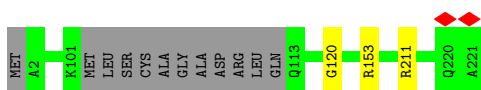
- Molecule 12: 60S ribosomal protein L10

Chain BD:  94% • 5%



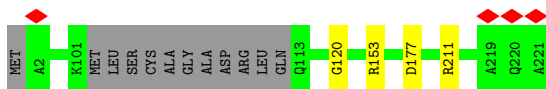
- Molecule 12: 60S ribosomal protein L10

Chain YD:  93% • 5%



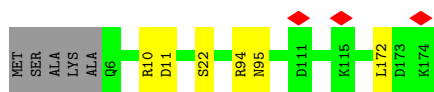
- Molecule 12: 60S ribosomal protein L10

Chain ZD:  93% • 5%

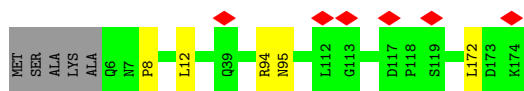


- Molecule 13: 60S ribosomal protein L11-A

Chain AG:  94% • 5%



- Molecule 13: 60S ribosomal protein L11-A



- Molecule 13: 60S ribosomal protein L11-A



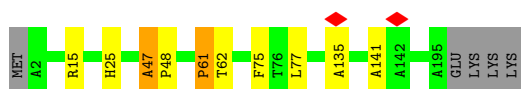
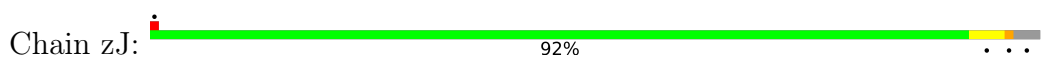
- Molecule 14: 60S ribosomal protein L13-A



- Molecule 14: 60S ribosomal protein L13-A



- Molecule 14: 60S ribosomal protein L13-A



- Molecule 15: 60S ribosomal protein L14-A



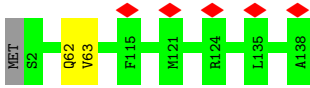
- Molecule 15: 60S ribosomal protein L14-A

Chain XM:  99%



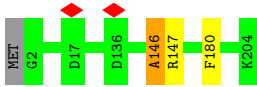
- Molecule 15: 60S ribosomal protein L14-A

Chain zM:  98%



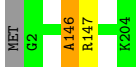
- Molecule 16: 60S ribosomal protein L15-A

Chain AQ:  98%



- Molecule 16: 60S ribosomal protein L15-A

Chain XQ:  99%



- Molecule 16: 60S ribosomal protein L15-A

Chain zQ:  98%



- Molecule 17: 60S ribosomal protein L16-A

Chain AU:  98%

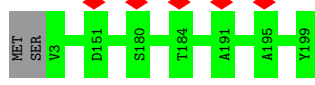


- Molecule 17: 60S ribosomal protein L16-A

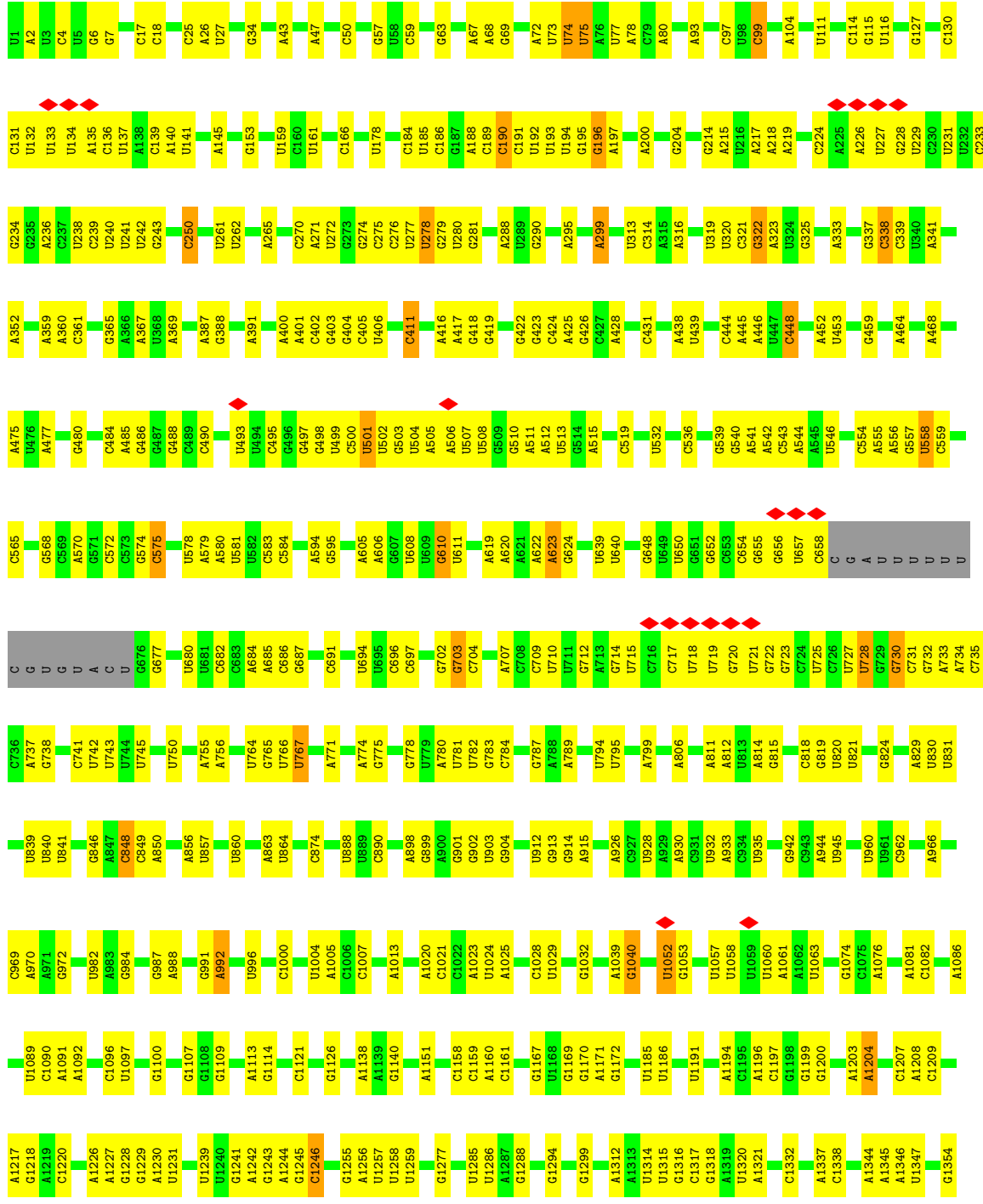
Chain XU:  99%

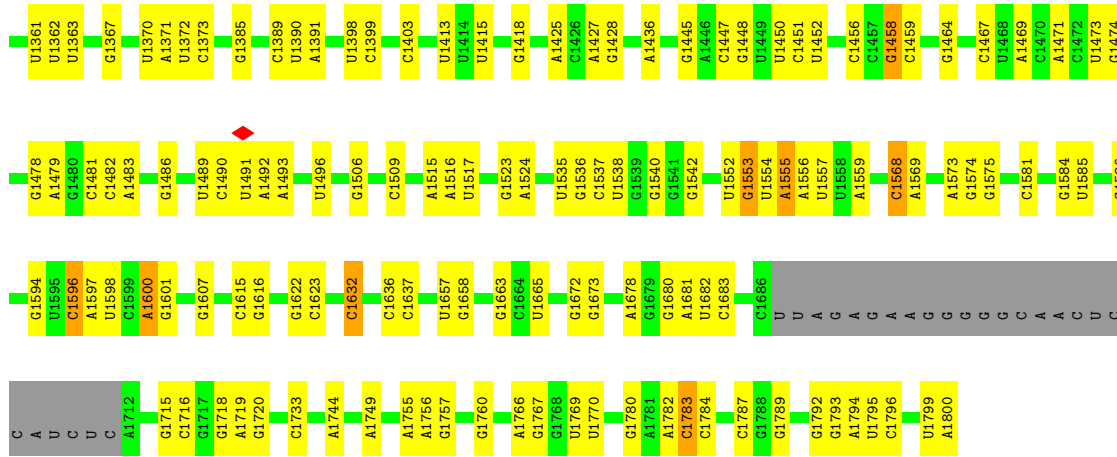


- Molecule 17: 60S ribosomal protein L16-A



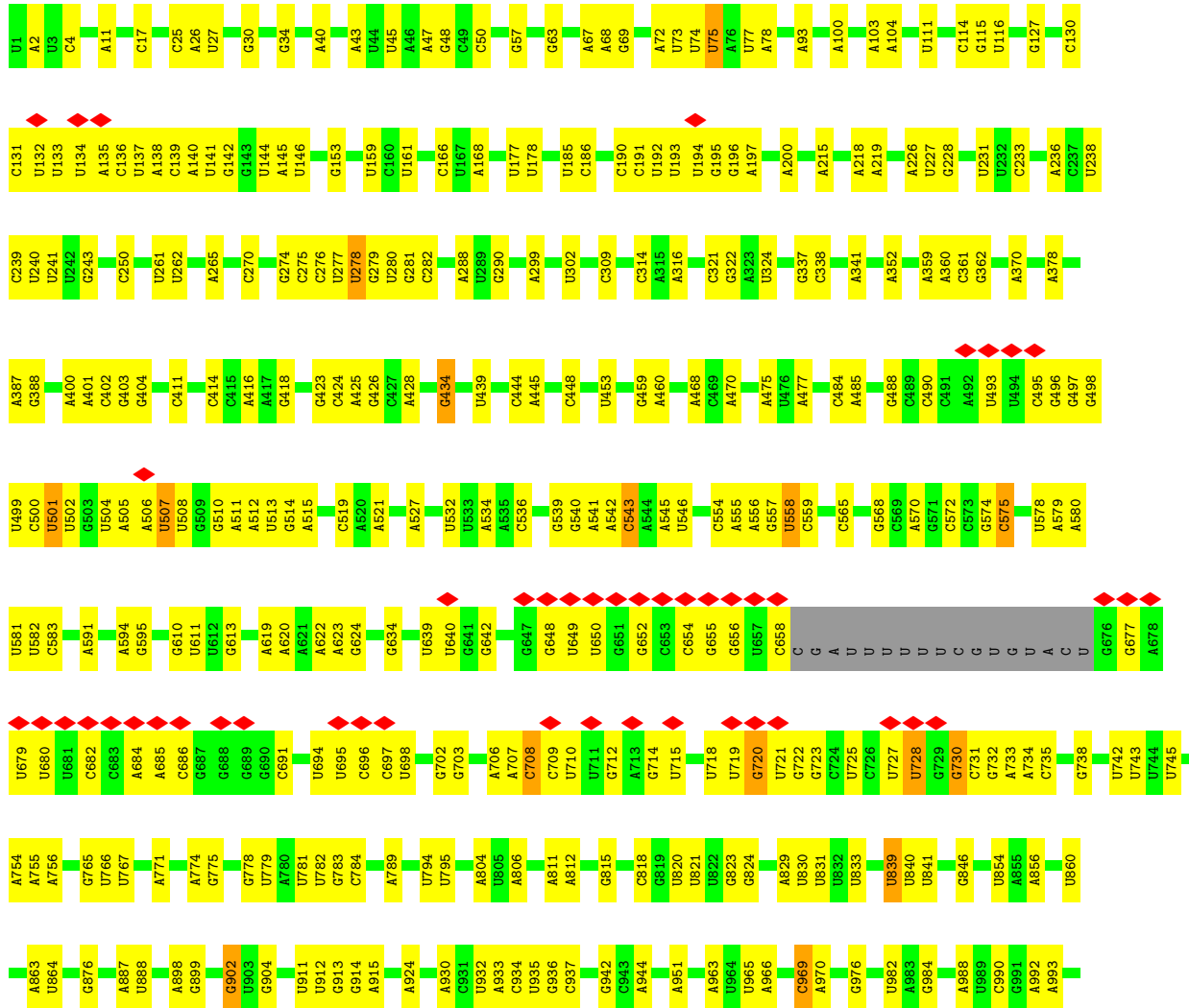
• Molecule 18: 18S rRNA

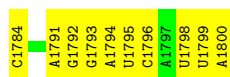




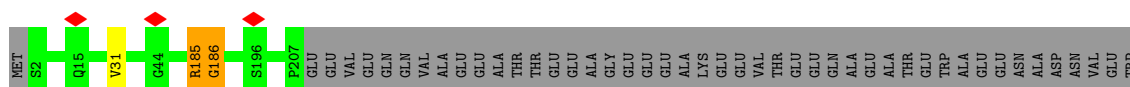
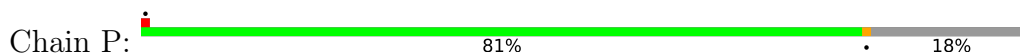
• Molecule 18: 18S rRNA

Chain 2b:

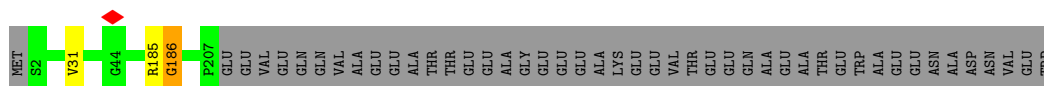
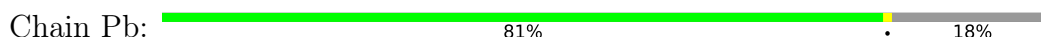




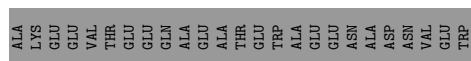
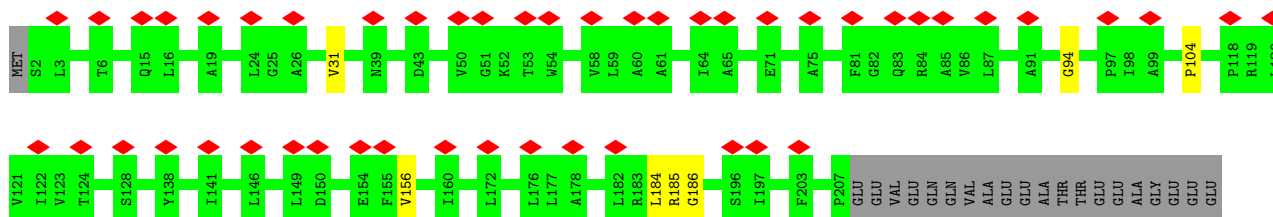
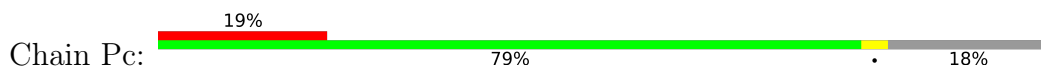
- Molecule 19: 40S ribosomal protein S0-A



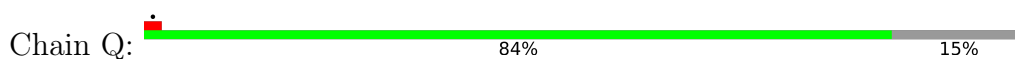
- Molecule 19: 40S ribosomal protein S0-A



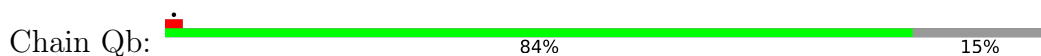
- Molecule 19: 40S ribosomal protein S0-A



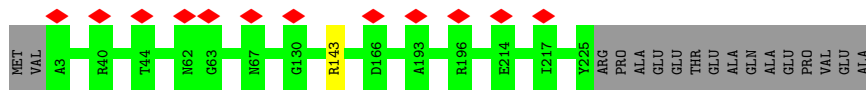
- Molecule 20: 40S ribosomal protein S1-A



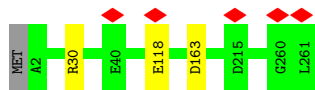
- Molecule 20: 40S ribosomal protein S1-A



- Molecule 20: 40S ribosomal protein S1-A



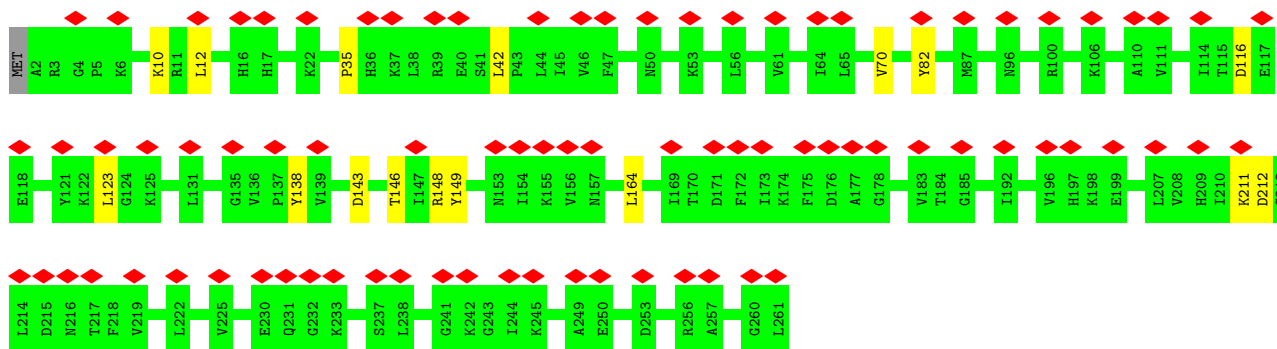
• Molecule 23: 40S ribosomal protein S4-A



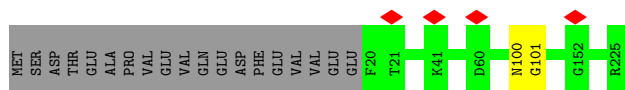
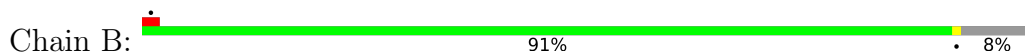
• Molecule 23: 40S ribosomal protein S4-A



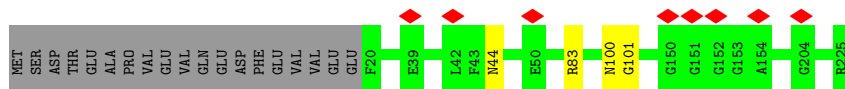
• Molecule 23: 40S ribosomal protein S4-A



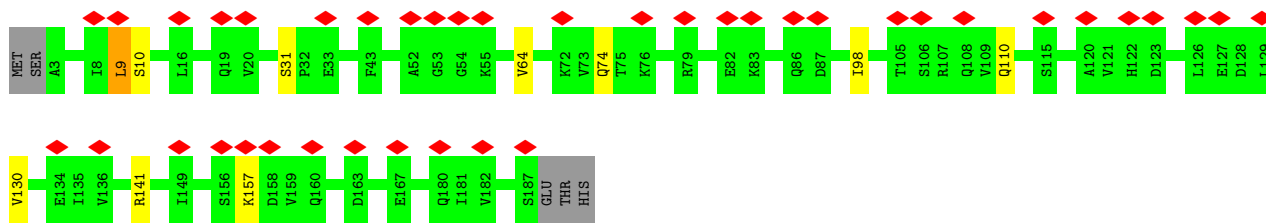
• Molecule 24: Rps5p



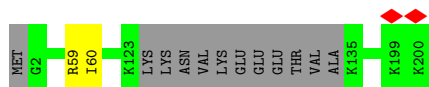
• Molecule 24: Rps5p



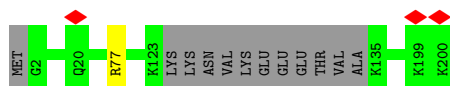
• Molecule 24: Rps5p



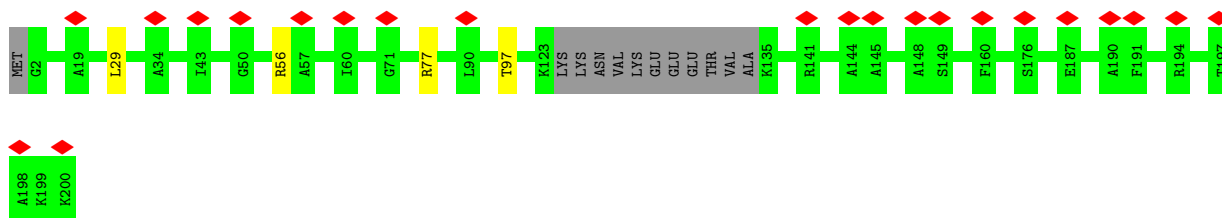
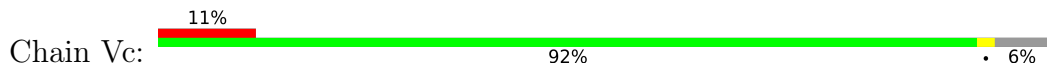
- Molecule 27: 40S ribosomal protein S8-A



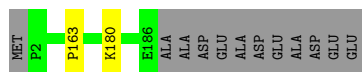
- Molecule 27: 40S ribosomal protein S8-A



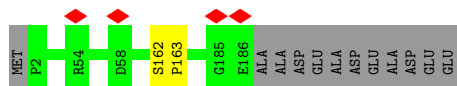
- Molecule 27: 40S ribosomal protein S8-A



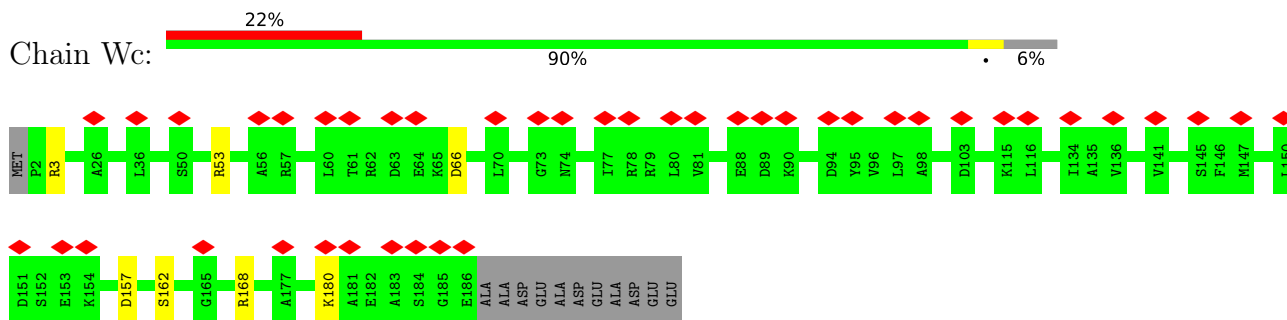
- Molecule 28: 40S ribosomal protein S9-A



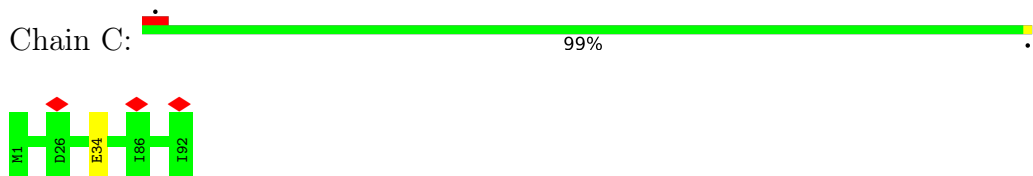
- Molecule 28: 40S ribosomal protein S9-A



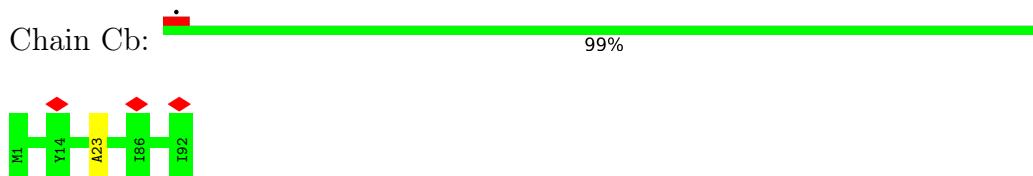
- Molecule 28: 40S ribosomal protein S9-A



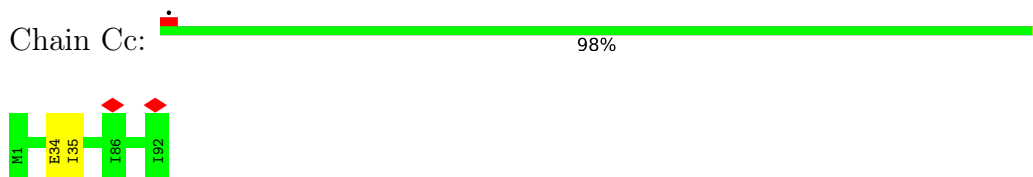
• Molecule 29: 40S ribosomal protein S10-A



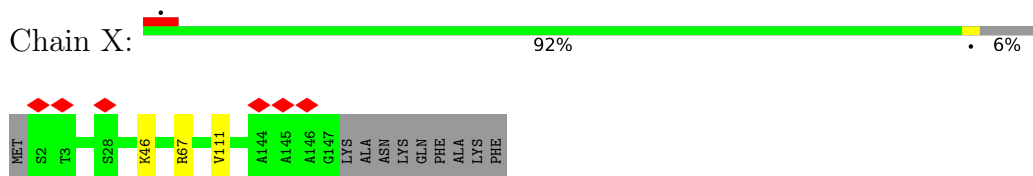
• Molecule 29: 40S ribosomal protein S10-A



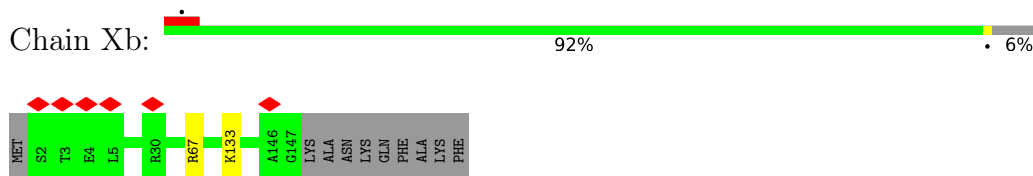
• Molecule 29: 40S ribosomal protein S10-A



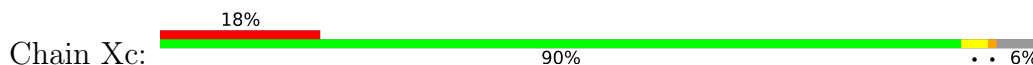
• Molecule 30: 40S ribosomal protein S11-A

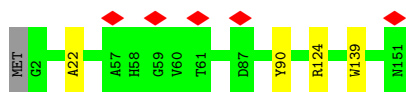


• Molecule 30: 40S ribosomal protein S11-A

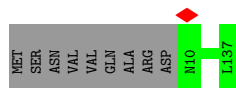


• Molecule 30: 40S ribosomal protein S11-A

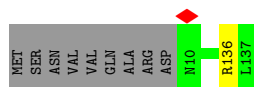




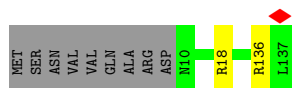
- Molecule 33: 40S ribosomal protein S14-A



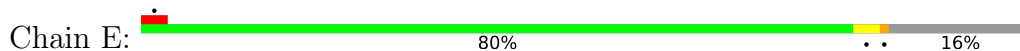
- Molecule 33: 40S ribosomal protein S14-A



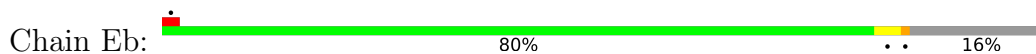
- Molecule 33: 40S ribosomal protein S14-A



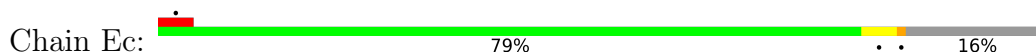
- Molecule 34: 40S ribosomal protein S15



- Molecule 34: 40S ribosomal protein S15

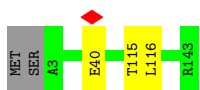


- Molecule 34: 40S ribosomal protein S15



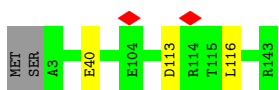
- Molecule 35: 40S ribosomal protein S16-A

Chain F:  97%



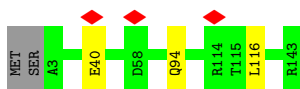
- Molecule 35: 40S ribosomal protein S16-A

Chain Fb:  97%

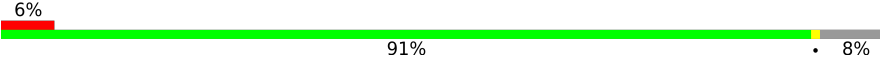


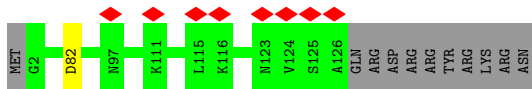
- Molecule 35: 40S ribosomal protein S16-A

Chain Fc:  97%



- Molecule 36: 40S ribosomal protein S17-B

Chain G:  91% 6% 8%

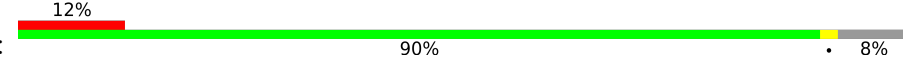


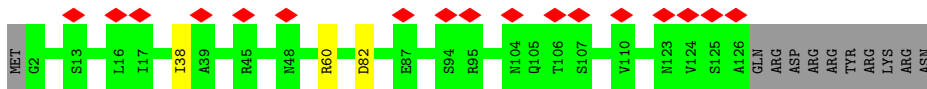
- Molecule 36: 40S ribosomal protein S17-B

Chain Gb:  90% 6% 8%



- Molecule 36: 40S ribosomal protein S17-B

Chain Gc:  90% 12% 8%

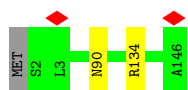


- Molecule 37: 40S ribosomal protein S18-A

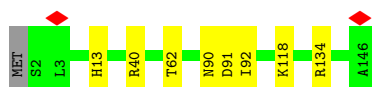
Chain H:  96%



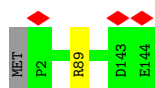
- Molecule 37: 40S ribosomal protein S18-A



- Molecule 37: 40S ribosomal protein S18-A



- Molecule 38: 40S ribosomal protein S19-A



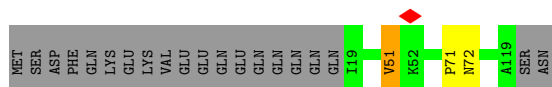
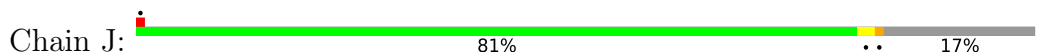
- Molecule 38: 40S ribosomal protein S19-A



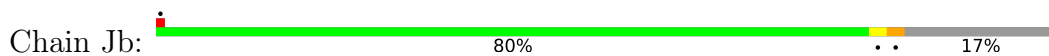
- Molecule 38: 40S ribosomal protein S19-A

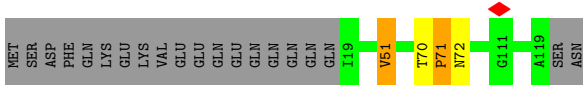


- Molecule 39: 40S ribosomal protein S20

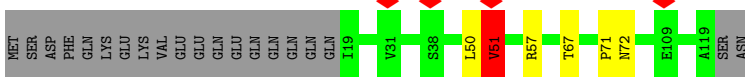
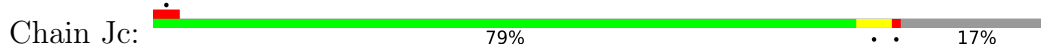


- Molecule 39: 40S ribosomal protein S20

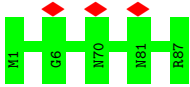




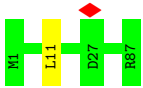
• Molecule 39: 40S ribosomal protein S20



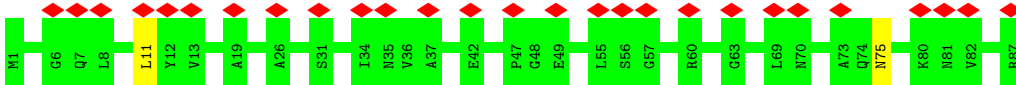
• Molecule 40: 40S ribosomal protein S21-A



• Molecule 40: 40S ribosomal protein S21-A



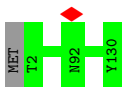
• Molecule 40: 40S ribosomal protein S21-A



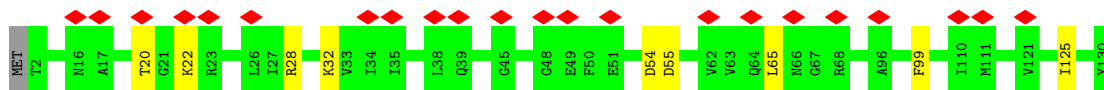
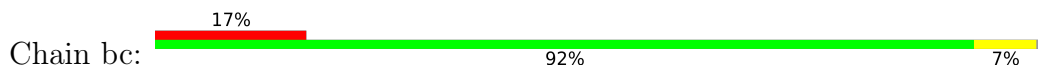
• Molecule 41: 40S ribosomal protein S22-A



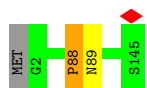
• Molecule 41: 40S ribosomal protein S22-A



• Molecule 41: 40S ribosomal protein S22-A



• Molecule 42: 40S ribosomal protein S23-A



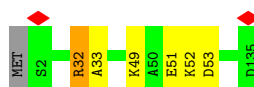
• Molecule 42: 40S ribosomal protein S23-A



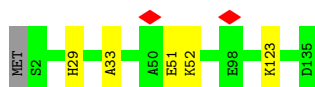
• Molecule 42: 40S ribosomal protein S23-A



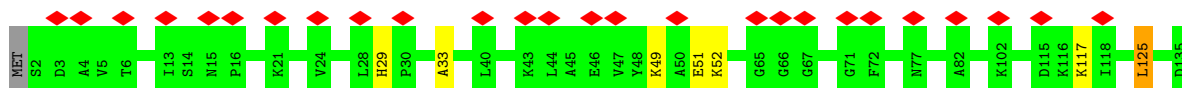
• Molecule 43: 40S ribosomal protein S24-A

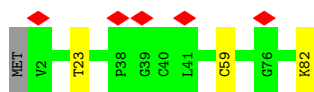


• Molecule 43: 40S ribosomal protein S24-A



• Molecule 43: 40S ribosomal protein S24-A

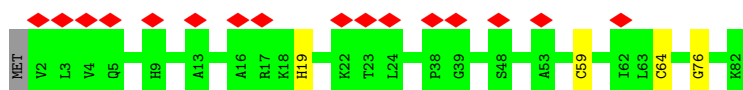




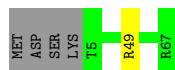
- Molecule 46: 40S ribosomal protein S27-A



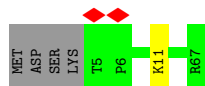
- Molecule 46: 40S ribosomal protein S27-A



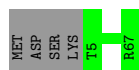
- Molecule 47: 40S ribosomal protein S28-B



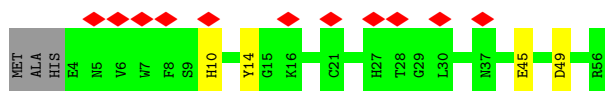
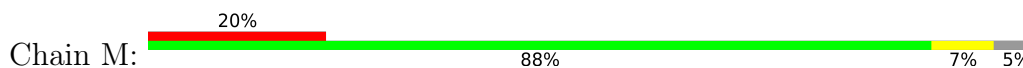
- Molecule 47: 40S ribosomal protein S28-B



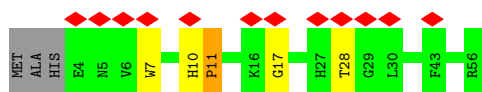
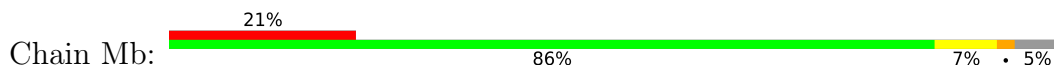
- Molecule 47: 40S ribosomal protein S28-B



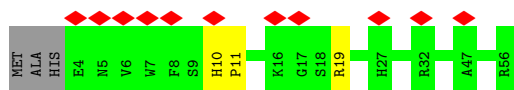
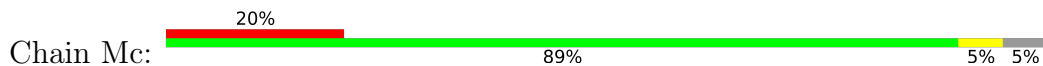
- Molecule 48: 40S ribosomal protein S29-A



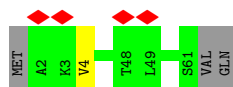
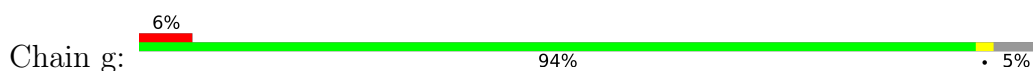
- Molecule 48: 40S ribosomal protein S29-A



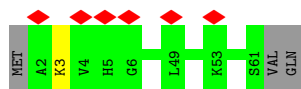
• Molecule 48: 40S ribosomal protein S29-A



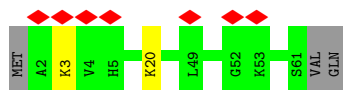
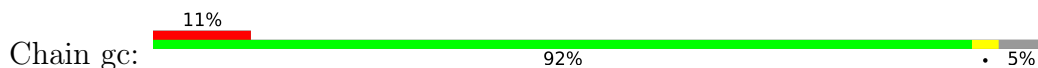
• Molecule 49: 40S ribosomal protein S30-A



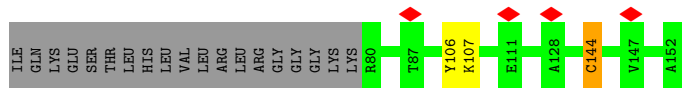
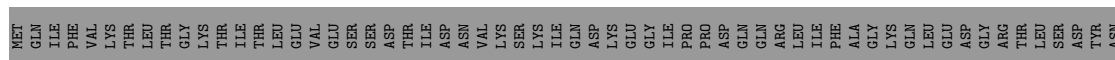
• Molecule 49: 40S ribosomal protein S30-A



• Molecule 49: 40S ribosomal protein S30-A

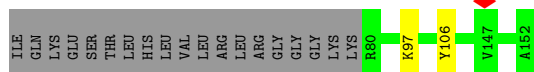
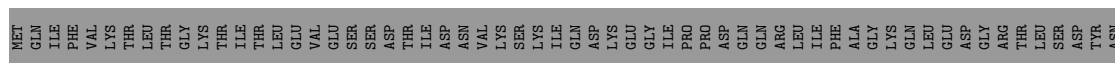


• Molecule 50: Ubiquitin-40S ribosomal protein S31

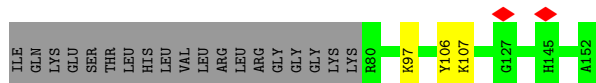
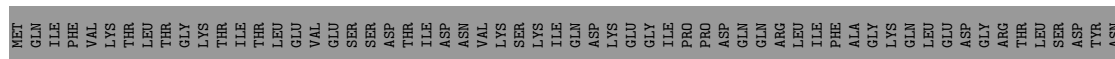


• Molecule 50: Ubiquitin-40S ribosomal protein S31

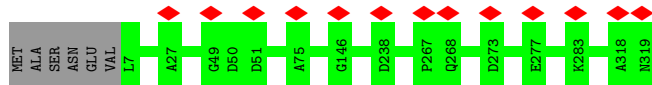




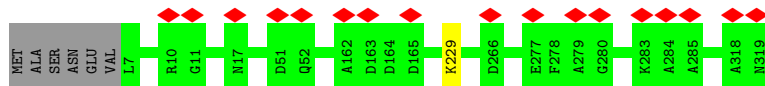
• Molecule 50: Ubiquitin-40S ribosomal protein S31



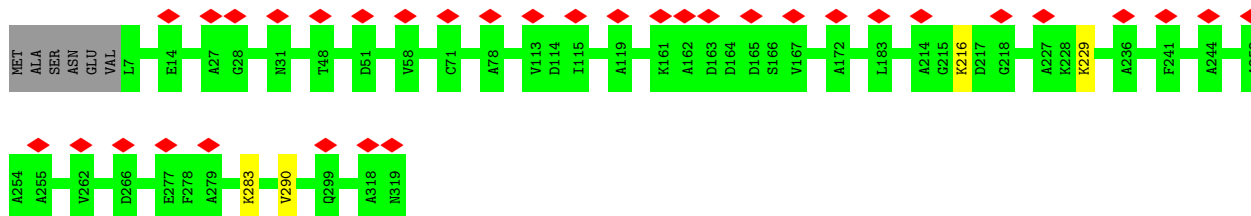
• Molecule 51: Guanine nucleotide-binding protein subunit beta-like protein



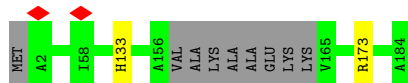
• Molecule 51: Guanine nucleotide-binding protein subunit beta-like protein



• Molecule 51: Guanine nucleotide-binding protein subunit beta-like protein

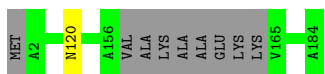


• Molecule 52: 60S ribosomal protein L17-A



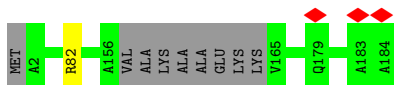
- Molecule 52: 60S ribosomal protein L17-A

Chain XX:  95% • 5%



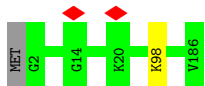
- Molecule 52: 60S ribosomal protein L17-A

Chain zX:  95% • 5%



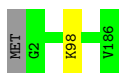
- Molecule 53: 60S ribosomal protein L18-A

Chain BB:  99% ..



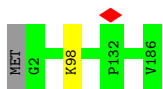
- Molecule 53: 60S ribosomal protein L18-A

Chain YB:  99% ..



- Molecule 53: 60S ribosomal protein L18-A

Chain ZB:  99% ..



- Molecule 54: 60S ribosomal protein L19-A

Chain BF:  96% ..



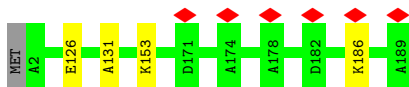
- Molecule 54: 60S ribosomal protein L19-A

Chain YF:  98% ..



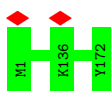
- Molecule 54: 60S ribosomal protein L19-A

Chain ZF: 97%



- Molecule 55: 60S ribosomal protein L20-A

Chain BH: 100%



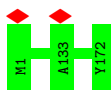
- Molecule 55: 60S ribosomal protein L20-A

Chain YH: 100%



- Molecule 55: 60S ribosomal protein L20-A

Chain ZH: 100%



- Molecule 56: 60S ribosomal protein L21-A

Chain BJ: 98%

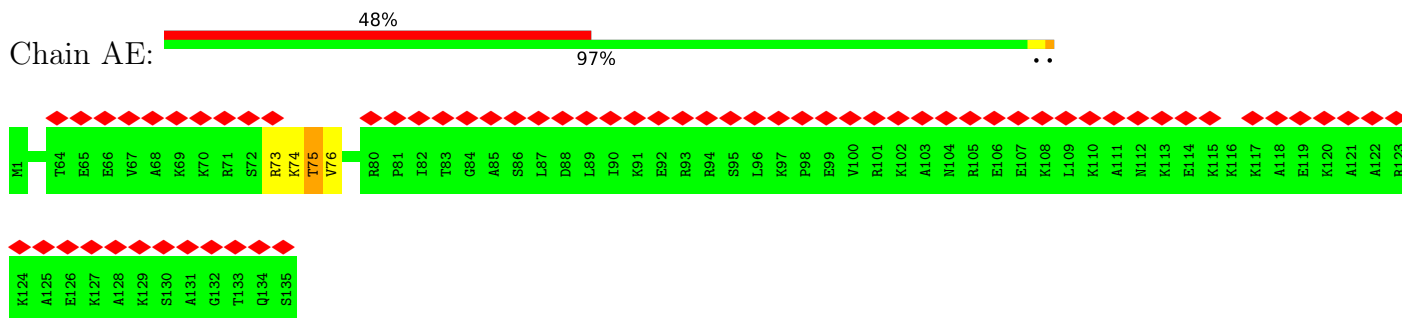


- Molecule 56: 60S ribosomal protein L21-A

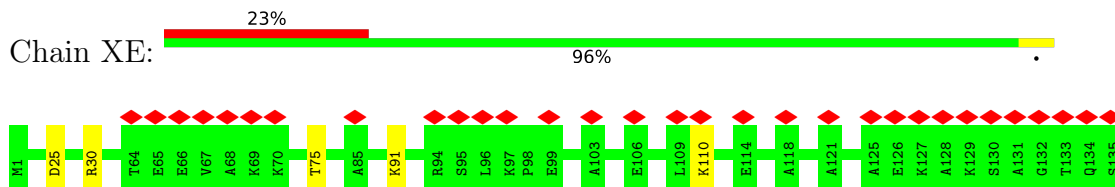
Chain YJ: 98%



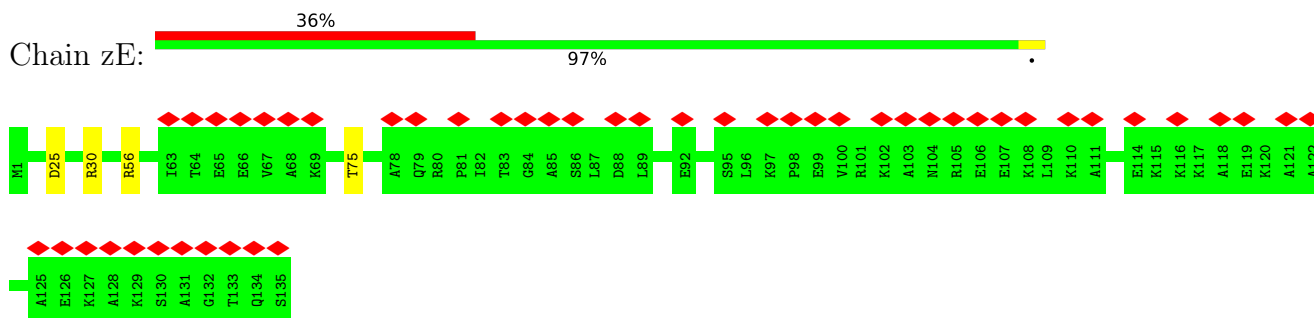
- Molecule 56: 60S ribosomal protein L21-A



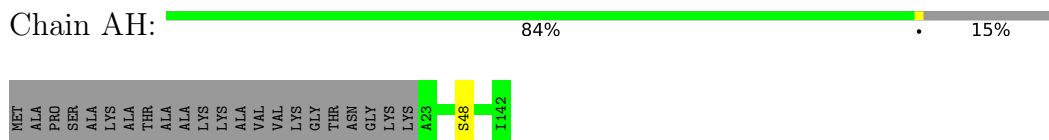
- Molecule 59: 60S ribosomal protein L24-A



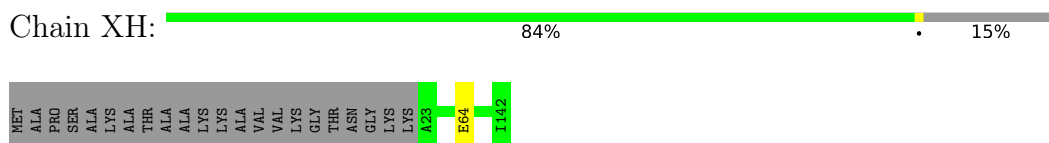
- Molecule 59: 60S ribosomal protein L24-A



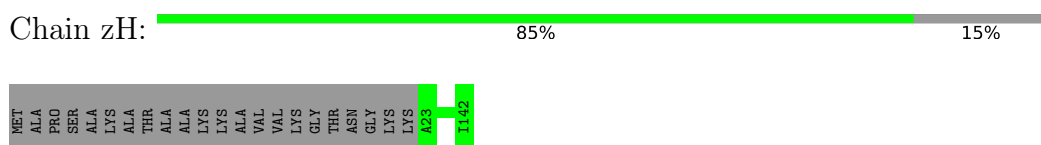
- Molecule 60: 60S ribosomal protein L25



- Molecule 60: 60S ribosomal protein L25

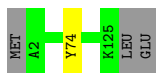


- Molecule 60: 60S ribosomal protein L25



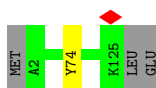
- Molecule 61: 60S ribosomal protein L26-A

Chain AK:  97% ..



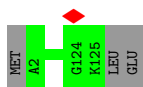
- Molecule 61: 60S ribosomal protein L26-A

Chain XK:  97% ..



- Molecule 61: 60S ribosomal protein L26-A

Chain zK:  98% .



- Molecule 62: 60S ribosomal protein L27-A

Chain AN:  99% ..



- Molecule 62: 60S ribosomal protein L27-A

Chain XN:  98% ...



- Molecule 62: 60S ribosomal protein L27-A

Chain zN:  98% ...



- Molecule 63: 60S ribosomal protein L28

Chain AR:  97% ..



- Molecule 63: 60S ribosomal protein L28

Chain XR:  97%



- Molecule 63: 60S ribosomal protein L28

Chain zR:  96%



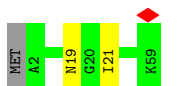
- Molecule 64: 60S ribosomal protein L29

Chain AV:  93%



- Molecule 64: 60S ribosomal protein L29

Chain XV:  95%



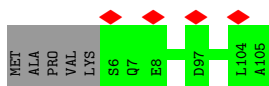
- Molecule 64: 60S ribosomal protein L29

Chain zV:  95%



- Molecule 65: 60S ribosomal protein L30

Chain AY:  95%



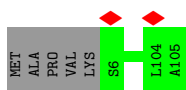
- Molecule 65: 60S ribosomal protein L30

Chain XY:  95%



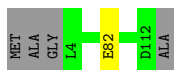
- Molecule 65: 60S ribosomal protein L30

Chain zY:  95% 5%



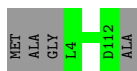
- Molecule 66: 60S ribosomal protein L31-A

Chain BC:  96% ..



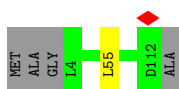
- Molecule 66: 60S ribosomal protein L31-A

Chain YC:  96% .



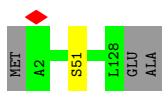
- Molecule 66: 60S ribosomal protein L31-A

Chain ZC:  96% ..



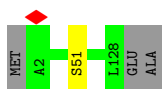
- Molecule 67: 60S ribosomal protein L32

Chain BG:  97% ..



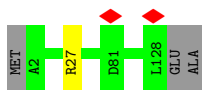
- Molecule 67: 60S ribosomal protein L32

Chain YG:  97% ..

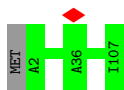


- Molecule 67: 60S ribosomal protein L32

Chain ZG:  97% ..



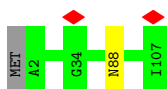
- Molecule 68: 60S ribosomal protein L33-A



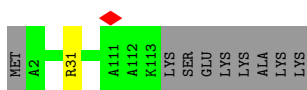
- Molecule 68: 60S ribosomal protein L33-A



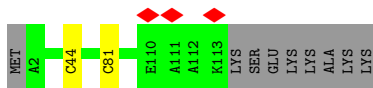
- Molecule 68: 60S ribosomal protein L33-A



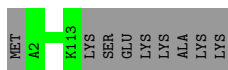
- Molecule 69: 60S ribosomal protein L34-A



- Molecule 69: 60S ribosomal protein L34-A



- Molecule 69: 60S ribosomal protein L34-A



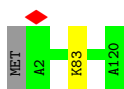
- Molecule 70: 60S ribosomal protein L35-A



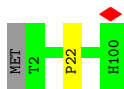
- Molecule 70: 60S ribosomal protein L35-A



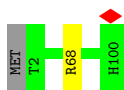
- Molecule 70: 60S ribosomal protein L35-A



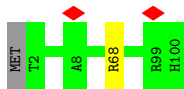
- Molecule 71: 60S ribosomal protein L36-A



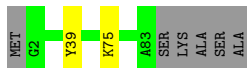
- Molecule 71: 60S ribosomal protein L36-A



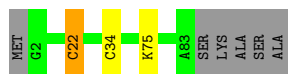
- Molecule 71: 60S ribosomal protein L36-A



- Molecule 72: 60S ribosomal protein L37-A



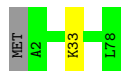
- Molecule 72: 60S ribosomal protein L37-A



- Molecule 72: 60S ribosomal protein L37-A



- Molecule 73: 60S ribosomal protein L38



- Molecule 73: 60S ribosomal protein L38



- Molecule 73: 60S ribosomal protein L38



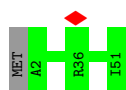
- Molecule 74: 60S ribosomal protein L39



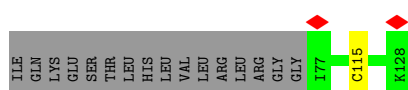
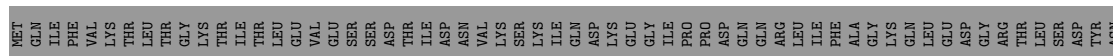
- Molecule 74: 60S ribosomal protein L39



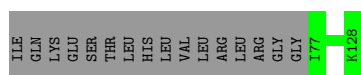
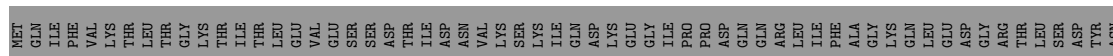
• Molecule 74: 60S ribosomal protein L39



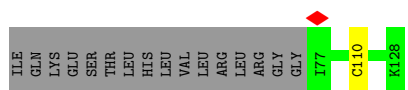
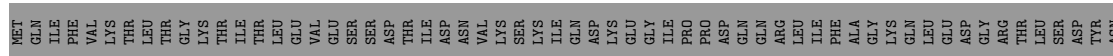
• Molecule 75: Ubiquitin-60S ribosomal protein L40



• Molecule 75: Ubiquitin-60S ribosomal protein L40



• Molecule 75: Ubiquitin-60S ribosomal protein L40

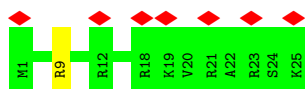


• Molecule 76: 60S ribosomal protein L41-B

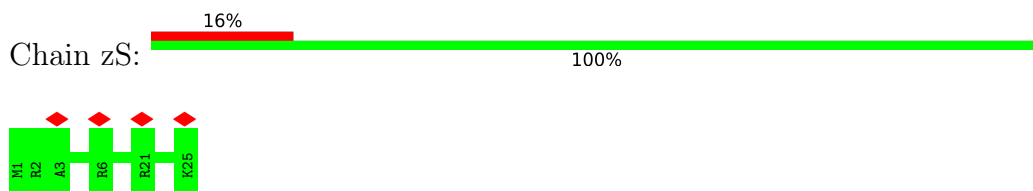


There are no outlier residues recorded for this chain.

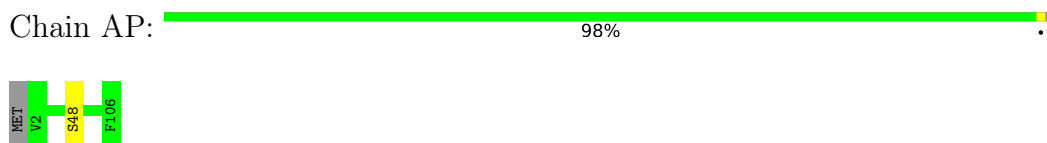
• Molecule 76: 60S ribosomal protein L41-B



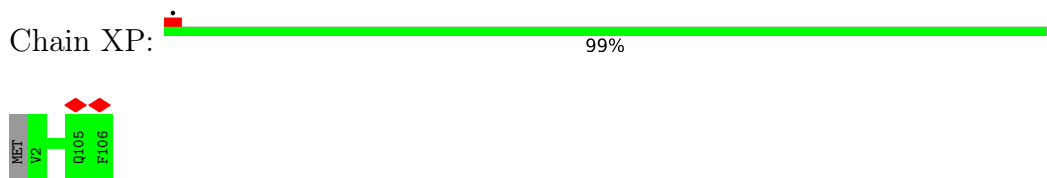
- Molecule 76: 60S ribosomal protein L41-B



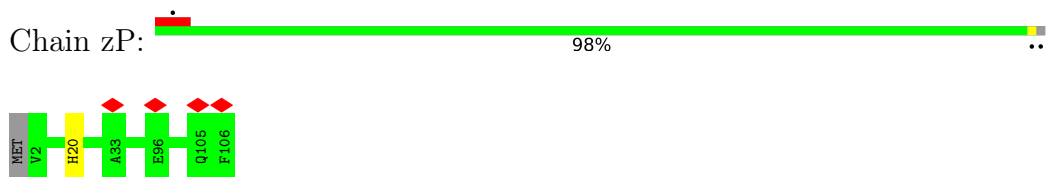
- Molecule 77: 60S ribosomal protein L42-A



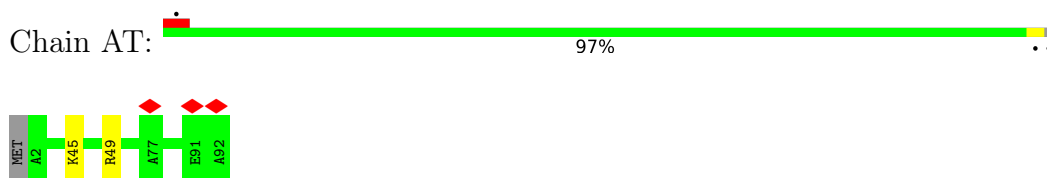
- Molecule 77: 60S ribosomal protein L42-A



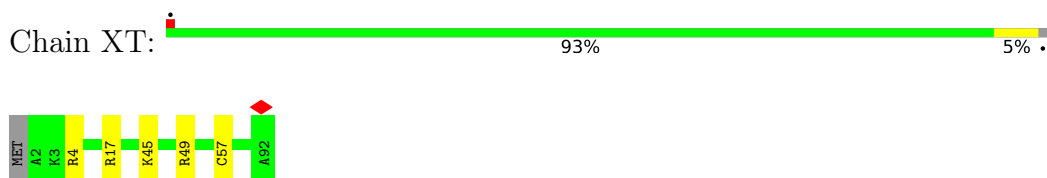
- Molecule 77: 60S ribosomal protein L42-A



- Molecule 78: 60S ribosomal protein L43-A



- Molecule 78: 60S ribosomal protein L43-A

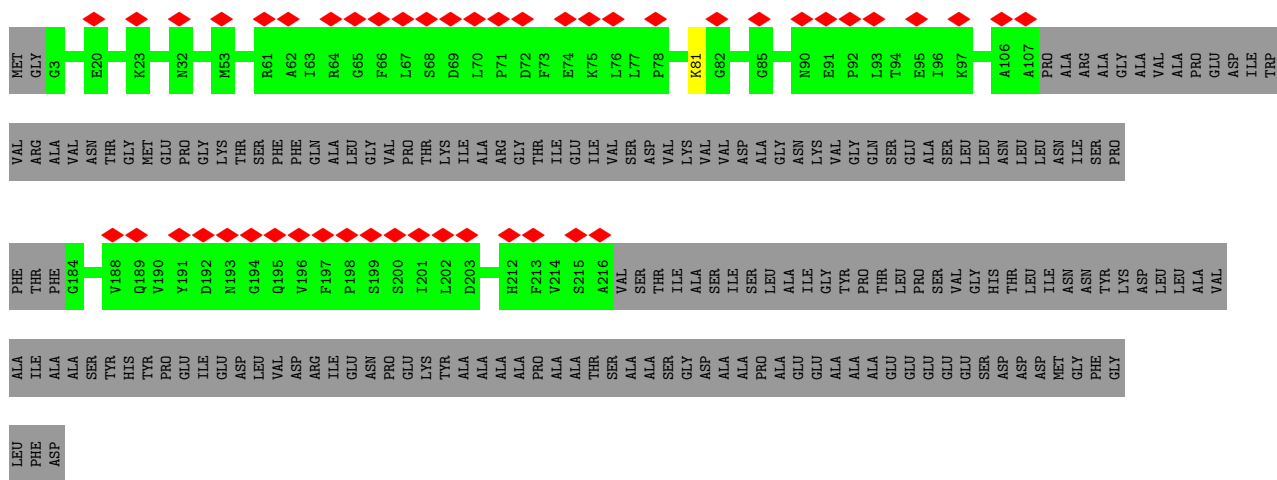


- Molecule 78: 60S ribosomal protein L43-A

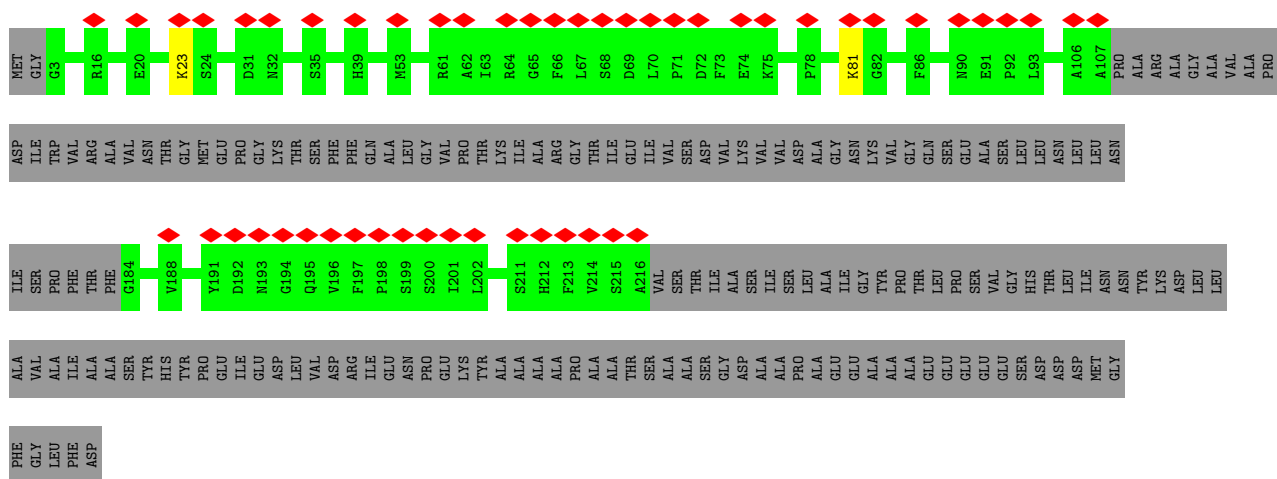




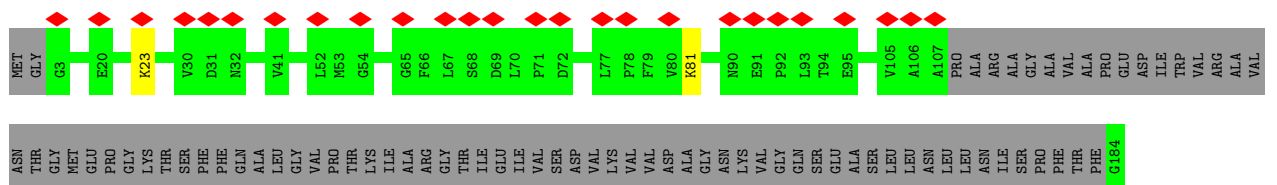
• Molecule 79: 60S acidic ribosomal protein P0

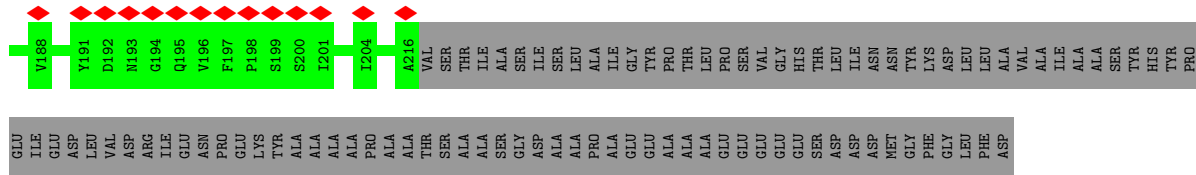


• Molecule 79: 60S acidic ribosomal protein P0

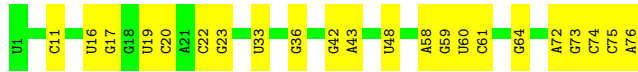


• Molecule 79: 60S acidic ribosomal protein P0

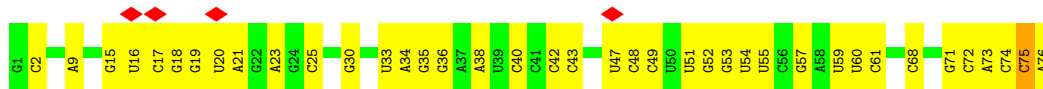




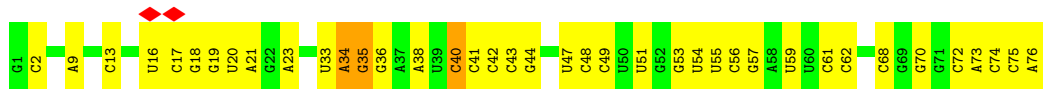
• Molecule 80: tRNA (P/P)



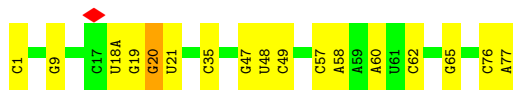
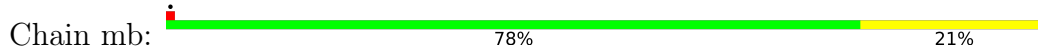
• Molecule 81: tRNA (A/P)



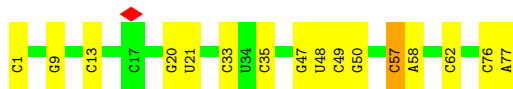
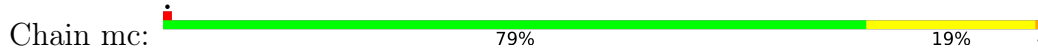
• Molecule 81: tRNA (A/P)



• Molecule 82: tRNA (P/E)



• Molecule 82: tRNA (P/E)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	69054	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	0.367	Depositor
Minimum map value	-0.023	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	542.0, 542.0, 542.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality i

5.1 Standard geometry i

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	BQ	1.23	59/74873 (0.1%)	1.27	372/116727 (0.3%)
1	YQ	1.33	83/74873 (0.1%)	1.28	424/116727 (0.4%)
1	ZQ	1.38	136/74873 (0.2%)	1.34	534/116727 (0.5%)
2	BR	1.00	0/2883	1.19	9/4491 (0.2%)
2	YR	1.11	0/2883	1.21	8/4491 (0.2%)
2	ZR	1.12	0/2883	1.20	14/4491 (0.3%)
3	BS	1.28	1/3724 (0.0%)	1.28	20/5798 (0.3%)
3	YS	1.38	4/3724 (0.1%)	1.32	30/5798 (0.5%)
3	ZS	1.40	7/3724 (0.2%)	1.31	27/5798 (0.5%)
4	AW	0.76	0/1946	0.69	0/2614
4	XW	0.83	0/1946	0.74	1/2614 (0.0%)
4	zW	0.79	0/1946	0.74	0/2614
5	BA	0.74	0/3146	0.64	0/4228
5	YA	0.76	0/3146	0.65	0/4228
5	ZA	0.76	0/3146	0.70	1/4228 (0.0%)
6	BE	0.71	0/2800	0.64	0/3790
6	YE	0.76	0/2800	0.64	0/3790
6	ZE	0.79	0/2800	0.66	0/3790
7	BI	0.51	0/2408	0.57	0/3248
7	YI	0.59	0/2408	0.59	0/3248
7	ZI	0.61	0/2408	0.62	0/3248
8	BM	0.56	0/1269	0.61	1/1705 (0.1%)
8	YM	0.59	1/1269 (0.1%)	0.58	0/1705
8	ZM	0.57	0/1269	0.73	1/1705 (0.1%)
9	BO	0.69	0/1828	0.61	0/2461
9	YO	0.74	0/1828	0.63	1/2461 (0.0%)
9	ZO	0.80	0/1828	0.68	0/2461
10	AA	0.61	0/1795	0.58	0/2429
10	XA	0.71	0/1795	0.59	0/2429
10	zA	0.66	0/1795	0.61	0/2429
11	AD	0.56	0/1531	0.59	0/2062
11	XD	0.64	0/1531	0.57	0/2062
11	zD	0.66	0/1531	0.64	0/2062
12	BD	0.62	0/1732	0.61	0/2323

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
12	YD	0.71	1/1732 (0.1%)	0.62	0/2323
12	ZD	0.73	1/1732 (0.1%)	0.64	0/2323
13	AG	0.45	0/1374	0.68	0/1842
13	XG	0.51	0/1374	0.61	0/1842
13	zG	0.57	0/1374	0.67	0/1842
14	AJ	0.61	0/1573	0.70	0/2113
14	XJ	0.75	1/1573 (0.1%)	0.75	0/2113
14	zJ	0.75	1/1573 (0.1%)	0.74	0/2113
15	AM	0.58	0/1074	0.58	0/1446
15	XM	0.64	0/1074	0.61	0/1446
15	zM	0.66	1/1074 (0.1%)	0.71	0/1446
16	AQ	0.80	0/1757	0.68	0/2354
16	XQ	0.94	0/1757	0.73	0/2354
16	zQ	0.93	0/1757	0.74	0/2354
17	AU	0.73	0/1585	0.63	0/2128
17	XU	0.81	0/1585	0.66	0/2128
17	zU	0.81	0/1585	0.69	0/2128
18	2	1.12	13/41891 (0.0%)	1.20	151/65273 (0.2%)
18	2b	0.97	5/41891 (0.0%)	1.16	122/65273 (0.2%)
18	2c	1.07	34/41891 (0.1%)	1.45	633/65273 (1.0%)
19	P	0.53	0/1623	0.60	0/2222
19	Pb	0.49	0/1623	0.58	0/2222
19	Pc	0.45	0/1623	0.72	0/2222
20	Q	0.51	0/1748	0.57	0/2352
20	Qb	0.52	0/1748	0.60	0/2352
20	Qc	0.59	0/1748	0.68	0/2352
21	R	0.64	1/1665 (0.1%)	0.59	0/2263
21	Rb	0.60	0/1665	0.60	0/2263
21	Rc	0.60	0/1665	0.78	1/2263 (0.0%)
22	A	0.49	0/1759	0.58	0/2368
22	Ab	0.47	0/1759	0.58	0/2368
22	Ac	0.45	0/1759	0.63	0/2368
23	S	0.62	0/2109	0.62	0/2839
23	Sb	0.49	0/2109	0.59	0/2839
23	Sc	0.52	1/2109 (0.0%)	0.78	3/2839 (0.1%)
24	B	0.50	0/1629	0.58	0/2202
24	Bb	0.49	0/1629	0.61	1/2202 (0.0%)
24	Bc	0.50	0/1629	0.64	1/2202 (0.0%)
25	T	0.48	0/1779	0.63	1/2379 (0.0%)
25	Tb	0.41	0/1779	0.62	0/2379
25	Tc	0.51	1/1779 (0.1%)	0.81	5/2379 (0.2%)
26	U	0.51	0/1511	0.59	0/2036
26	Ub	0.46	0/1511	0.59	0/2036

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	Uc	0.48	0/1511	0.73	2/2036 (0.1%)
27	V	0.66	0/1514	0.63	0/2021
27	Vb	0.49	0/1514	0.59	0/2021
27	Vc	0.48	0/1514	0.71	1/2021 (0.0%)
28	W	0.57	0/1519	0.64	0/2035
28	Wb	0.47	0/1519	0.59	0/2035
28	Wc	0.51	0/1519	0.73	1/2035 (0.0%)
29	C	0.43	0/757	0.57	0/1022
29	Cb	0.47	0/757	0.51	0/1022
29	Cc	0.47	0/757	0.64	0/1022
30	X	0.80	1/1194 (0.1%)	0.64	0/1610
30	Xb	0.60	0/1194	0.63	0/1610
30	Xc	0.58	0/1194	0.76	0/1610
31	D	0.33	0/898	0.58	0/1220
31	Db	0.32	0/898	0.57	0/1220
31	Dc	0.31	0/898	0.60	0/1220
32	Y	0.71	0/1215	0.60	0/1638
32	Yb	0.58	0/1215	0.56	0/1638
32	Yc	0.57	0/1215	0.71	2/1638 (0.1%)
33	Z	0.61	0/960	0.66	0/1290
33	Zb	0.63	0/960	0.77	2/1290 (0.2%)
33	Zc	0.67	0/960	0.76	1/1290 (0.1%)
34	E	0.42	0/959	0.59	0/1288
34	Eb	0.46	0/959	0.60	0/1288
34	Ec	0.53	0/959	0.65	0/1288
35	F	0.55	0/1125	0.59	0/1510
35	Fb	0.54	0/1125	0.62	0/1510
35	Fc	0.56	0/1125	0.67	0/1510
36	G	0.47	0/1010	0.60	0/1355
36	Gb	0.46	0/1010	0.60	0/1355
36	Gc	0.46	0/1010	0.67	0/1355
37	H	0.41	0/1211	0.60	0/1628
37	Hb	0.43	0/1211	0.60	0/1628
37	Hc	0.48	0/1211	0.63	0/1628
38	I	0.47	0/1130	0.56	0/1517
38	Ib	0.48	0/1130	0.59	0/1517
38	Ic	0.55	0/1130	0.63	0/1517
39	J	0.50	0/815	0.59	0/1102
39	Jb	0.48	0/815	0.61	0/1102
39	Jc	0.49	0/815	0.67	0/1102
40	a	0.61	0/693	0.65	0/935
40	ab	0.54	0/693	0.68	0/935
40	ac	0.52	0/693	0.81	0/935

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
41	b	0.74	0/1038	0.64	0/1395
41	bb	0.68	0/1038	0.63	0/1395
41	bc	0.64	0/1038	0.91	1/1395 (0.1%)
42	c	0.63	0/1139	0.63	0/1518
42	cb	0.62	0/1139	0.64	0/1518
42	cc	0.72	1/1139 (0.1%)	0.75	0/1518
43	d	0.56	0/1087	0.65	0/1449
43	db	0.44	0/1087	0.60	0/1449
43	dc	0.47	0/1087	0.77	1/1449 (0.1%)
44	K	0.42	0/566	0.52	0/761
44	Kb	0.46	0/566	0.57	0/761
44	Kc	0.47	0/566	0.62	1/761 (0.1%)
45	e	0.64	0/782	0.71	0/1047
45	eb	0.64	0/782	0.69	0/1047
45	ec	0.74	0/782	0.81	2/1047 (0.2%)
46	f	0.62	0/620	0.65	0/838
46	fb	0.49	0/620	0.61	0/838
46	fc	0.50	0/620	0.79	0/838
47	L	0.63	1/499 (0.2%)	0.74	0/670
47	Lb	0.49	0/499	0.71	0/670
47	Lc	0.49	0/499	0.73	0/670
48	M	0.49	0/452	0.81	0/600
48	Mb	0.69	0/452	0.98	0/600
48	Mc	0.65	0/452	0.93	0/600
49	g	0.48	0/483	0.59	0/643
49	gb	0.47	0/483	0.62	0/643
49	gc	0.51	0/483	0.66	0/643
50	N	0.43	0/567	0.64	0/764
50	Nb	0.38	0/567	0.62	0/764
50	Nc	0.35	0/567	0.63	0/764
51	O	0.37	0/2456	0.55	0/3343
51	Ob	0.37	0/2456	0.55	0/3343
51	Oc	0.41	0/2456	0.63	0/3343
52	AX	0.75	0/1400	0.65	0/1882
52	XX	0.81	0/1400	0.67	0/1882
52	zX	0.81	0/1400	0.76	0/1882
53	BB	0.67	0/1465	0.67	0/1965
53	YB	0.71	0/1465	0.68	0/1965
53	ZB	0.72	0/1465	0.71	0/1965
54	BF	0.66	0/1499	0.66	0/1998
54	YF	0.71	0/1539	0.64	0/2050
54	ZF	0.71	0/1539	0.69	0/2050
55	BH	0.66	0/1481	0.64	0/1990

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
55	YH	0.76	0/1481	0.63	0/1990
55	ZH	0.78	0/1481	0.67	0/1990
56	BJ	0.65	0/1300	0.62	0/1743
56	YJ	0.73	0/1300	0.63	0/1743
56	ZJ	0.75	0/1300	0.68	0/1743
57	BL	0.54	0/794	0.55	0/1076
57	YL	0.61	0/794	0.57	0/1076
57	ZL	0.61	0/794	0.59	0/1076
58	AB	0.69	0/1008	0.62	0/1356
58	XB	0.74	0/1008	0.68	0/1356
58	zB	0.75	0/1008	0.67	0/1356
59	AE	0.56	0/1099	0.63	0/1454
59	XE	0.61	0/1103	0.61	0/1458
59	zE	0.59	0/1103	0.68	1/1458 (0.1%)
60	AH	0.71	0/974	0.59	0/1314
60	XH	0.76	0/974	0.64	0/1314
60	zH	0.77	0/974	0.63	0/1314
61	AK	0.69	1/987 (0.1%)	0.63	0/1318
61	XK	0.74	0/987	0.72	1/1318 (0.1%)
61	zK	0.71	0/987	0.66	0/1318
62	AN	0.65	0/1118	0.59	0/1497
62	XN	0.77	0/1118	0.62	0/1497
62	zN	0.72	0/1118	0.63	0/1497
63	AR	0.70	0/1204	0.66	0/1612
63	XR	0.78	0/1204	0.70	2/1612 (0.1%)
63	zR	0.84	0/1204	0.77	2/1612 (0.1%)
64	AV	0.55	0/473	0.63	0/629
64	XV	0.60	0/473	0.61	0/629
64	zV	0.61	0/473	0.71	0/629
65	AY	0.70	0/775	0.62	0/1040
65	XY	0.71	0/775	0.54	0/1040
65	zY	0.67	0/775	0.59	0/1040
66	BC	0.70	0/897	0.63	0/1205
66	YC	0.81	0/897	0.66	0/1205
66	ZC	0.74	0/897	0.66	0/1205
67	BG	0.73	1/1041 (0.1%)	0.66	0/1394
67	YG	0.74	1/1041 (0.1%)	0.62	0/1394
67	ZG	0.75	0/1041	0.70	1/1394 (0.1%)
68	BK	0.81	0/868	0.64	0/1168
68	YK	0.87	0/868	0.67	0/1168
68	ZK	0.85	0/868	0.70	0/1168
69	BN	0.73	0/890	0.69	1/1189 (0.1%)
69	YN	0.82	0/890	0.64	0/1189

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
69	ZN	0.83	0/890	0.68	0/1189
70	BP	0.62	0/974	0.58	0/1297
70	YP	0.69	0/974	0.59	0/1297
70	ZP	0.72	0/974	0.67	0/1297
71	AC	0.61	1/777 (0.1%)	0.61	0/1033
71	XC	0.61	0/777	0.66	0/1033
71	zC	0.63	0/777	0.69	0/1033
72	AF	0.79	0/665	0.74	1/882 (0.1%)
72	XF	0.97	2/665 (0.3%)	0.72	0/882
72	zF	0.96	1/665 (0.2%)	0.81	1/882 (0.1%)
73	AI	0.58	0/614	0.60	0/822
73	XI	0.64	0/614	0.62	0/822
73	zI	0.64	0/614	0.67	0/822
74	AL	0.78	0/443	0.67	0/588
74	XL	0.81	1/443 (0.2%)	0.67	0/588
74	zL	0.80	0/443	0.70	0/588
75	AO	0.55	0/423	0.71	0/562
75	XO	0.62	0/423	0.66	0/562
75	zO	0.64	0/423	0.68	0/562
76	AS	0.41	0/234	0.70	0/300
76	XS	0.43	0/234	0.67	0/300
76	zS	0.49	0/234	0.76	0/300
77	AP	0.63	0/860	0.65	0/1136
77	XP	0.71	0/860	0.66	0/1136
77	zP	0.76	0/860	0.67	0/1136
78	AT	0.81	1/701 (0.1%)	0.67	0/934
78	XT	0.89	1/701 (0.1%)	0.69	2/934 (0.2%)
78	zT	0.90	1/701 (0.1%)	0.74	0/934
79	BU	0.31	0/1067	0.53	0/1439
79	YU	0.30	0/1067	0.51	0/1439
79	ZU	0.31	0/1067	0.55	0/1439
80	n	0.77	0/1811	1.14	3/2821 (0.1%)
81	nb	0.52	0/1810	1.03	4/2821 (0.1%)
81	nc	0.60	0/1810	1.17	10/2821 (0.4%)
82	mb	0.70	1/1836 (0.1%)	1.00	4/2859 (0.1%)
82	mc	0.79	1/1836 (0.1%)	1.01	4/2859 (0.1%)
All	All	1.02	367/650387 (0.1%)	1.09	2412/955438 (0.3%)

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
4	AW	0	1
4	XW	0	2
4	zW	0	1
5	ZA	0	2
6	BE	0	1
6	YE	0	1
7	BI	0	1
13	AG	0	4
13	XG	0	2
13	zG	0	2
14	AJ	0	5
14	XJ	0	4
14	zJ	0	4
15	zM	0	1
16	AQ	0	1
16	XQ	0	1
16	zQ	0	1
19	P	0	1
19	Pb	0	1
19	Pc	0	4
21	R	0	3
21	Rb	0	1
21	Rc	0	2
22	A	0	1
23	S	0	1
23	Sb	0	1
23	Sc	0	4
24	B	0	1
24	Bb	0	2
24	Bc	0	1
25	T	0	2
25	Tb	0	1
25	Tc	0	2
26	U	0	4
26	Ub	0	5
26	Uc	0	5
27	V	0	1
29	Cb	0	1
30	Xc	0	1
31	D	0	3
31	Db	0	3
31	Dc	0	2
32	Y	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
32	Yc	0	1
34	E	0	2
34	Eb	0	3
34	Ec	0	3
35	F	0	2
35	Fb	0	2
35	Fc	0	1
36	Gc	0	1
37	H	0	1
37	Hb	0	2
37	Hc	0	3
39	J	0	1
39	Jb	0	3
39	Jc	0	2
41	bc	0	3
42	c	0	1
42	cc	0	2
43	d	0	3
43	db	0	3
43	dc	0	4
44	Kc	0	1
45	e	0	2
45	eb	0	1
45	ec	0	1
48	M	0	2
48	Mb	0	4
48	Mc	0	2
49	g	0	1
49	gb	0	1
49	gc	0	1
50	N	0	2
50	Nb	0	2
50	Nc	0	2
53	BB	0	1
53	YB	0	1
53	ZB	0	1
57	BL	0	1
57	YL	0	1
57	ZL	0	1
58	AB	0	1
59	AE	0	3
59	XE	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
59	zE	0	2
60	XH	0	1
62	AN	0	1
62	XN	0	1
62	zN	0	1
63	AR	0	1
63	XR	0	1
63	zR	0	1
64	AV	0	2
64	XV	0	2
64	zV	0	2
70	ZP	0	1
78	AT	0	1
78	XT	0	1
All	All	0	182

The worst 5 of 367 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	2	74	U	C2-N3	40.22	1.66	1.37
18	2	74	U	N1-C2	32.77	1.68	1.38
18	2	74	U	N1-C6	31.91	1.66	1.38
18	2	74	U	N3-C4	30.82	1.66	1.38
18	2	74	U	C4-C5	27.17	1.68	1.43

The worst 5 of 2412 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	2c	871	G	N3-C4-N9	13.70	134.22	126.00
18	2c	1555	A	C2-N3-C4	13.52	117.36	110.60
18	2c	47	A	N1-C6-N6	-13.51	110.49	118.60
18	2c	1102	G	N3-C2-N2	12.11	128.38	119.90
18	2c	15	U	C5-C6-N1	12.05	128.73	122.70

There are no chirality outliers.

5 of 182 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	AG	10	ARG	Peptide
13	AG	11	ASP	Peptide
4	AW	214	GLY	Peptide

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Mol	Chain	Res	Type	Group
6	BE	329	PRO	Peptide
7	BI	270	LYS	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AW	250/254 (98%)	208 (83%)	41 (16%)	1 (0%)	34	66
4	XW	250/254 (98%)	211 (84%)	38 (15%)	1 (0%)	34	66
4	zW	250/254 (98%)	213 (85%)	34 (14%)	3 (1%)	13	42
5	BA	384/387 (99%)	338 (88%)	46 (12%)	0	100	100
5	YA	384/387 (99%)	341 (89%)	43 (11%)	0	100	100
5	ZA	384/387 (99%)	331 (86%)	52 (14%)	1 (0%)	41	71
6	BE	359/362 (99%)	315 (88%)	43 (12%)	1 (0%)	41	71
6	YE	359/362 (99%)	310 (86%)	48 (13%)	1 (0%)	41	71
6	ZE	359/362 (99%)	299 (83%)	59 (16%)	1 (0%)	41	71
7	BI	292/297 (98%)	260 (89%)	32 (11%)	0	100	100
7	YI	292/297 (98%)	258 (88%)	34 (12%)	0	100	100
7	ZI	292/297 (98%)	258 (88%)	34 (12%)	0	100	100
8	BM	153/176 (87%)	137 (90%)	16 (10%)	0	100	100
8	YM	153/176 (87%)	140 (92%)	13 (8%)	0	100	100
8	ZM	153/176 (87%)	132 (86%)	21 (14%)	0	100	100
9	BO	221/244 (91%)	204 (92%)	15 (7%)	2 (1%)	17	48
9	YO	221/244 (91%)	202 (91%)	16 (7%)	3 (1%)	11	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	ZO	221/244 (91%)	204 (92%)	16 (7%)	1 (0%)	29	61
10	AA	229/256 (90%)	197 (86%)	32 (14%)	0	100	100
10	XA	229/256 (90%)	191 (83%)	38 (17%)	0	100	100
10	zA	229/256 (90%)	193 (84%)	36 (16%)	0	100	100
11	AD	188/190 (99%)	169 (90%)	19 (10%)	0	100	100
11	XD	188/190 (99%)	174 (93%)	14 (7%)	0	100	100
11	zD	188/190 (99%)	177 (94%)	11 (6%)	0	100	100
12	BD	205/221 (93%)	183 (89%)	22 (11%)	0	100	100
12	YD	205/221 (93%)	180 (88%)	25 (12%)	0	100	100
12	ZD	205/221 (93%)	189 (92%)	15 (7%)	1 (0%)	29	61
13	AG	167/174 (96%)	130 (78%)	35 (21%)	2 (1%)	13	42
13	XG	167/174 (96%)	134 (80%)	31 (19%)	2 (1%)	13	42
13	zG	167/174 (96%)	131 (78%)	34 (20%)	2 (1%)	13	42
14	AJ	192/199 (96%)	155 (81%)	30 (16%)	7 (4%)	3	20
14	XJ	192/199 (96%)	156 (81%)	30 (16%)	6 (3%)	4	23
14	zJ	192/199 (96%)	154 (80%)	32 (17%)	6 (3%)	4	23
15	AM	135/138 (98%)	117 (87%)	18 (13%)	0	100	100
15	XM	135/138 (98%)	120 (89%)	15 (11%)	0	100	100
15	zM	135/138 (98%)	124 (92%)	11 (8%)	0	100	100
16	AQ	201/204 (98%)	179 (89%)	20 (10%)	2 (1%)	15	46
16	XQ	201/204 (98%)	183 (91%)	16 (8%)	2 (1%)	15	46
16	zQ	201/204 (98%)	176 (88%)	23 (11%)	2 (1%)	15	46
17	AU	195/199 (98%)	175 (90%)	20 (10%)	0	100	100
17	XU	195/199 (98%)	178 (91%)	17 (9%)	0	100	100
17	zU	195/199 (98%)	181 (93%)	14 (7%)	0	100	100
19	P	204/252 (81%)	169 (83%)	32 (16%)	3 (2%)	10	38
19	Pb	204/252 (81%)	164 (80%)	38 (19%)	2 (1%)	15	46
19	Pc	204/252 (81%)	163 (80%)	38 (19%)	3 (2%)	10	38
20	Q	214/255 (84%)	187 (87%)	26 (12%)	1 (0%)	29	61
20	Qb	214/255 (84%)	190 (89%)	24 (11%)	0	100	100
20	Qc	214/255 (84%)	190 (89%)	24 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	R	215/254 (85%)	176 (82%)	38 (18%)	1 (0%)	29	61
21	Rb	215/254 (85%)	179 (83%)	34 (16%)	2 (1%)	17	48
21	Rc	215/254 (85%)	176 (82%)	39 (18%)	0	100	100
22	A	221/240 (92%)	185 (84%)	35 (16%)	1 (0%)	29	61
22	Ab	221/240 (92%)	196 (89%)	25 (11%)	0	100	100
22	Ac	221/240 (92%)	186 (84%)	35 (16%)	0	100	100
23	S	258/261 (99%)	219 (85%)	38 (15%)	1 (0%)	34	66
23	Sb	258/261 (99%)	222 (86%)	35 (14%)	1 (0%)	34	66
23	Sc	258/261 (99%)	204 (79%)	53 (20%)	1 (0%)	34	66
24	B	204/225 (91%)	179 (88%)	24 (12%)	1 (0%)	29	61
24	Bb	204/225 (91%)	181 (89%)	22 (11%)	1 (0%)	29	61
24	Bc	204/225 (91%)	162 (79%)	41 (20%)	1 (0%)	29	61
25	T	216/218 (99%)	176 (82%)	38 (18%)	2 (1%)	17	48
25	Tb	216/218 (99%)	194 (90%)	21 (10%)	1 (0%)	29	61
25	Tc	216/218 (99%)	189 (88%)	25 (12%)	2 (1%)	17	48
26	U	183/190 (96%)	148 (81%)	34 (19%)	1 (0%)	29	61
26	Ub	183/190 (96%)	155 (85%)	26 (14%)	2 (1%)	14	45
26	Uc	183/190 (96%)	142 (78%)	38 (21%)	3 (2%)	9	36
27	V	184/200 (92%)	158 (86%)	26 (14%)	0	100	100
27	Vb	184/200 (92%)	167 (91%)	17 (9%)	0	100	100
27	Vc	184/200 (92%)	164 (89%)	20 (11%)	0	100	100
28	W	183/197 (93%)	158 (86%)	24 (13%)	1 (0%)	29	61
28	Wb	183/197 (93%)	150 (82%)	31 (17%)	2 (1%)	14	45
28	Wc	183/197 (93%)	150 (82%)	32 (18%)	1 (0%)	29	61
29	C	90/92 (98%)	68 (76%)	21 (23%)	1 (1%)	14	45
29	Cb	90/92 (98%)	66 (73%)	24 (27%)	0	100	100
29	Cc	90/92 (98%)	72 (80%)	16 (18%)	2 (2%)	6	30
30	X	144/156 (92%)	113 (78%)	31 (22%)	0	100	100
30	Xb	144/156 (92%)	118 (82%)	25 (17%)	1 (1%)	22	54
30	Xc	144/156 (92%)	117 (81%)	25 (17%)	2 (1%)	11	38
31	D	122/143 (85%)	84 (69%)	34 (28%)	4 (3%)	4	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	Db	122/143 (85%)	87 (71%)	31 (25%)	4 (3%)	4	22
31	Dc	122/143 (85%)	81 (66%)	35 (29%)	6 (5%)	2	14
32	Y	148/151 (98%)	128 (86%)	19 (13%)	1 (1%)	22	54
32	Yb	148/151 (98%)	130 (88%)	18 (12%)	0	100	100
32	Yc	148/151 (98%)	120 (81%)	27 (18%)	1 (1%)	22	54
33	Z	126/137 (92%)	107 (85%)	19 (15%)	0	100	100
33	Zb	126/137 (92%)	107 (85%)	19 (15%)	0	100	100
33	Zc	126/137 (92%)	108 (86%)	18 (14%)	0	100	100
34	E	117/142 (82%)	93 (80%)	20 (17%)	4 (3%)	3	22
34	Eb	117/142 (82%)	98 (84%)	16 (14%)	3 (3%)	5	27
34	Ec	117/142 (82%)	101 (86%)	12 (10%)	4 (3%)	3	22
35	F	139/143 (97%)	122 (88%)	16 (12%)	1 (1%)	22	54
35	Fb	139/143 (97%)	118 (85%)	20 (14%)	1 (1%)	22	54
35	Fc	139/143 (97%)	121 (87%)	17 (12%)	1 (1%)	22	54
36	G	123/136 (90%)	103 (84%)	19 (15%)	1 (1%)	19	51
36	Gb	123/136 (90%)	105 (85%)	17 (14%)	1 (1%)	19	51
36	Gc	123/136 (90%)	102 (83%)	20 (16%)	1 (1%)	19	51
37	H	143/146 (98%)	123 (86%)	18 (13%)	2 (1%)	11	38
37	Hb	143/146 (98%)	122 (85%)	21 (15%)	0	100	100
37	Hc	143/146 (98%)	122 (85%)	18 (13%)	3 (2%)	7	31
38	I	141/144 (98%)	127 (90%)	14 (10%)	0	100	100
38	Ib	141/144 (98%)	132 (94%)	9 (6%)	0	100	100
38	Ic	141/144 (98%)	122 (86%)	19 (14%)	0	100	100
39	J	99/121 (82%)	85 (86%)	11 (11%)	3 (3%)	4	24
39	Jb	99/121 (82%)	80 (81%)	16 (16%)	3 (3%)	4	24
39	Jc	99/121 (82%)	83 (84%)	13 (13%)	3 (3%)	4	24
40	a	85/87 (98%)	75 (88%)	10 (12%)	0	100	100
40	ab	85/87 (98%)	73 (86%)	11 (13%)	1 (1%)	13	42
40	ac	85/87 (98%)	72 (85%)	12 (14%)	1 (1%)	13	42
41	b	127/130 (98%)	110 (87%)	17 (13%)	0	100	100
41	bb	127/130 (98%)	109 (86%)	18 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	bc	127/130 (98%)	99 (78%)	26 (20%)	2 (2%)	9	36
42	c	142/145 (98%)	126 (89%)	14 (10%)	2 (1%)	11	38
42	cb	142/145 (98%)	122 (86%)	18 (13%)	2 (1%)	11	38
42	cc	142/145 (98%)	119 (84%)	21 (15%)	2 (1%)	11	38
43	d	132/135 (98%)	109 (83%)	19 (14%)	4 (3%)	4	24
43	db	132/135 (98%)	113 (86%)	18 (14%)	1 (1%)	19	51
43	dc	132/135 (98%)	107 (81%)	23 (17%)	2 (2%)	10	38
44	K	67/108 (62%)	62 (92%)	5 (8%)	0	100	100
44	Kb	67/108 (62%)	61 (91%)	6 (9%)	0	100	100
44	Kc	67/108 (62%)	56 (84%)	11 (16%)	0	100	100
45	e	95/119 (80%)	75 (79%)	19 (20%)	1 (1%)	14	45
45	eb	95/119 (80%)	76 (80%)	19 (20%)	0	100	100
45	ec	95/119 (80%)	78 (82%)	17 (18%)	0	100	100
46	f	79/82 (96%)	62 (78%)	17 (22%)	0	100	100
46	fb	79/82 (96%)	65 (82%)	13 (16%)	1 (1%)	12	40
46	fc	79/82 (96%)	62 (78%)	16 (20%)	1 (1%)	12	40
47	L	61/67 (91%)	51 (84%)	10 (16%)	0	100	100
47	Lb	61/67 (91%)	51 (84%)	10 (16%)	0	100	100
47	Lc	61/67 (91%)	52 (85%)	9 (15%)	0	100	100
48	M	51/56 (91%)	38 (74%)	13 (26%)	0	100	100
48	Mb	51/56 (91%)	34 (67%)	17 (33%)	0	100	100
48	Mc	51/56 (91%)	35 (69%)	16 (31%)	0	100	100
49	g	58/63 (92%)	50 (86%)	8 (14%)	0	100	100
49	gb	58/63 (92%)	47 (81%)	11 (19%)	0	100	100
49	gc	58/63 (92%)	47 (81%)	11 (19%)	0	100	100
50	N	71/152 (47%)	48 (68%)	22 (31%)	1 (1%)	11	38
50	Nb	71/152 (47%)	46 (65%)	25 (35%)	0	100	100
50	Nc	71/152 (47%)	50 (70%)	20 (28%)	1 (1%)	11	38
51	O	311/319 (98%)	291 (94%)	20 (6%)	0	100	100
51	Ob	311/319 (98%)	283 (91%)	28 (9%)	0	100	100
51	Oc	311/319 (98%)	274 (88%)	37 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	AX	171/184 (93%)	151 (88%)	19 (11%)	1 (1%)	25	57
52	XX	171/184 (93%)	155 (91%)	16 (9%)	0	100	100
52	zX	171/184 (93%)	154 (90%)	17 (10%)	0	100	100
53	BB	183/186 (98%)	165 (90%)	18 (10%)	0	100	100
53	YB	183/186 (98%)	164 (90%)	19 (10%)	0	100	100
53	ZB	183/186 (98%)	159 (87%)	24 (13%)	0	100	100
54	BF	181/189 (96%)	169 (93%)	12 (7%)	0	100	100
54	YF	186/189 (98%)	168 (90%)	17 (9%)	1 (0%)	29	61
54	ZF	186/189 (98%)	176 (95%)	9 (5%)	1 (0%)	29	61
55	BH	170/172 (99%)	154 (91%)	16 (9%)	0	100	100
55	YH	170/172 (99%)	152 (89%)	18 (11%)	0	100	100
55	ZH	170/172 (99%)	157 (92%)	13 (8%)	0	100	100
56	BJ	157/160 (98%)	140 (89%)	16 (10%)	1 (1%)	25	57
56	YJ	157/160 (98%)	135 (86%)	21 (13%)	1 (1%)	25	57
56	ZJ	157/160 (98%)	133 (85%)	23 (15%)	1 (1%)	25	57
57	BL	96/121 (79%)	83 (86%)	13 (14%)	0	100	100
57	YL	96/121 (79%)	84 (88%)	12 (12%)	0	100	100
57	ZL	96/121 (79%)	90 (94%)	6 (6%)	0	100	100
58	AB	132/137 (96%)	122 (92%)	10 (8%)	0	100	100
58	XB	132/137 (96%)	115 (87%)	17 (13%)	0	100	100
58	zB	132/137 (96%)	119 (90%)	13 (10%)	0	100	100
59	AE	133/135 (98%)	109 (82%)	22 (16%)	2 (2%)	10	38
59	XE	133/135 (98%)	112 (84%)	21 (16%)	0	100	100
59	zE	133/135 (98%)	115 (86%)	18 (14%)	0	100	100
60	AH	118/142 (83%)	102 (86%)	15 (13%)	1 (1%)	19	51
60	XH	118/142 (83%)	107 (91%)	11 (9%)	0	100	100
60	zH	118/142 (83%)	106 (90%)	12 (10%)	0	100	100
61	AK	122/127 (96%)	114 (93%)	8 (7%)	0	100	100
61	XK	122/127 (96%)	104 (85%)	18 (15%)	0	100	100
61	zK	122/127 (96%)	108 (88%)	14 (12%)	0	100	100
62	AN	133/136 (98%)	115 (86%)	17 (13%)	1 (1%)	19	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	XN	133/136 (98%)	113 (85%)	18 (14%)	2 (2%)	10	38
62	zN	133/136 (98%)	107 (80%)	24 (18%)	2 (2%)	10	38
63	AR	146/149 (98%)	120 (82%)	23 (16%)	3 (2%)	7	31
63	XR	146/149 (98%)	114 (78%)	31 (21%)	1 (1%)	22	54
63	zR	146/149 (98%)	115 (79%)	28 (19%)	3 (2%)	7	31
64	AV	56/59 (95%)	45 (80%)	11 (20%)	0	100	100
64	XV	56/59 (95%)	42 (75%)	14 (25%)	0	100	100
64	zV	56/59 (95%)	43 (77%)	13 (23%)	0	100	100
65	AY	98/105 (93%)	89 (91%)	9 (9%)	0	100	100
65	XY	98/105 (93%)	92 (94%)	6 (6%)	0	100	100
65	zY	98/105 (93%)	90 (92%)	8 (8%)	0	100	100
66	BC	107/113 (95%)	94 (88%)	12 (11%)	1 (1%)	17	48
66	YC	107/113 (95%)	92 (86%)	15 (14%)	0	100	100
66	ZC	107/113 (95%)	94 (88%)	13 (12%)	0	100	100
67	BG	125/130 (96%)	112 (90%)	13 (10%)	0	100	100
67	YG	125/130 (96%)	108 (86%)	17 (14%)	0	100	100
67	ZG	125/130 (96%)	112 (90%)	13 (10%)	0	100	100
68	BK	104/107 (97%)	91 (88%)	13 (12%)	0	100	100
68	YK	104/107 (97%)	93 (89%)	11 (11%)	0	100	100
68	ZK	104/107 (97%)	89 (86%)	14 (14%)	1 (1%)	15	46
69	BN	110/121 (91%)	104 (94%)	6 (6%)	0	100	100
69	YN	110/121 (91%)	100 (91%)	10 (9%)	0	100	100
69	ZN	110/121 (91%)	101 (92%)	9 (8%)	0	100	100
70	BP	117/120 (98%)	105 (90%)	12 (10%)	0	100	100
70	YP	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
70	ZP	117/120 (98%)	110 (94%)	7 (6%)	0	100	100
71	AC	97/100 (97%)	84 (87%)	13 (13%)	0	100	100
71	XC	97/100 (97%)	86 (89%)	11 (11%)	0	100	100
71	zC	97/100 (97%)	88 (91%)	9 (9%)	0	100	100
72	AF	80/88 (91%)	63 (79%)	17 (21%)	0	100	100
72	XF	80/88 (91%)	65 (81%)	15 (19%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	zF	80/88 (91%)	68 (85%)	12 (15%)	0	100	100
73	AI	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
73	XI	75/78 (96%)	72 (96%)	2 (3%)	1 (1%)	12	40
73	zI	75/78 (96%)	67 (89%)	7 (9%)	1 (1%)	12	40
74	AL	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
74	XL	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
74	zL	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
75	AO	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
75	XO	50/128 (39%)	46 (92%)	4 (8%)	0	100	100
75	zO	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
76	AS	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
76	XS	23/25 (92%)	21 (91%)	2 (9%)	0	100	100
76	zS	23/25 (92%)	23 (100%)	0	0	100	100
77	AP	103/106 (97%)	91 (88%)	11 (11%)	1 (1%)	15	46
77	XP	103/106 (97%)	95 (92%)	8 (8%)	0	100	100
77	zP	103/106 (97%)	88 (85%)	15 (15%)	0	100	100
78	AT	89/92 (97%)	78 (88%)	11 (12%)	0	100	100
78	XT	89/92 (97%)	75 (84%)	14 (16%)	0	100	100
78	zT	89/92 (97%)	76 (85%)	13 (15%)	0	100	100
79	BU	134/312 (43%)	122 (91%)	12 (9%)	0	100	100
79	YU	134/312 (43%)	121 (90%)	13 (10%)	0	100	100
79	ZU	134/312 (43%)	125 (93%)	9 (7%)	0	100	100
All	All	33256/36420 (91%)	28677 (86%)	4397 (13%)	182 (0%)	32	61

5 of 182 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	BE	339	LEU
13	AG	95	ASN
14	AJ	48	PRO
14	AJ	62	THR
16	AQ	147	ARG

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	AW	192/196 (98%)	190 (99%)	2 (1%)	76	86
4	XW	192/196 (98%)	192 (100%)	0	100	100
4	zW	192/196 (98%)	191 (100%)	1 (0%)	88	93
5	BA	318/323 (98%)	316 (99%)	2 (1%)	86	91
5	YA	318/323 (98%)	316 (99%)	2 (1%)	86	91
5	ZA	318/323 (98%)	314 (99%)	4 (1%)	69	82
6	BE	288/289 (100%)	288 (100%)	0	100	100
6	YE	288/289 (100%)	287 (100%)	1 (0%)	92	96
6	ZE	288/289 (100%)	288 (100%)	0	100	100
7	BI	243/245 (99%)	242 (100%)	1 (0%)	91	95
7	YI	243/245 (99%)	240 (99%)	3 (1%)	71	83
7	ZI	243/245 (99%)	239 (98%)	4 (2%)	62	79
8	BM	135/153 (88%)	133 (98%)	2 (2%)	65	81
8	YM	135/153 (88%)	135 (100%)	0	100	100
8	ZM	135/153 (88%)	135 (100%)	0	100	100
9	BO	187/205 (91%)	187 (100%)	0	100	100
9	YO	187/205 (91%)	187 (100%)	0	100	100
9	ZO	187/205 (91%)	187 (100%)	0	100	100
10	AA	177/208 (85%)	176 (99%)	1 (1%)	86	91
10	XA	177/208 (85%)	177 (100%)	0	100	100
10	zA	177/208 (85%)	176 (99%)	1 (1%)	86	91
11	AD	170/170 (100%)	170 (100%)	0	100	100
11	XD	170/170 (100%)	170 (100%)	0	100	100
11	zD	170/170 (100%)	169 (99%)	1 (1%)	86	91
12	BD	177/187 (95%)	175 (99%)	2 (1%)	73	85
12	YD	177/187 (95%)	175 (99%)	2 (1%)	73	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	ZD	177/187 (95%)	175 (99%)	2 (1%)	73	85
13	AG	147/150 (98%)	147 (100%)	0	100	100
13	XG	147/150 (98%)	146 (99%)	1 (1%)	84	90
13	zG	147/150 (98%)	146 (99%)	1 (1%)	84	90
14	AJ	154/159 (97%)	153 (99%)	1 (1%)	86	91
14	XJ	154/159 (97%)	153 (99%)	1 (1%)	86	91
14	zJ	154/159 (97%)	153 (99%)	1 (1%)	86	91
15	AM	108/109 (99%)	108 (100%)	0	100	100
15	XM	108/109 (99%)	108 (100%)	0	100	100
15	zM	108/109 (99%)	108 (100%)	0	100	100
16	AQ	175/176 (99%)	174 (99%)	1 (1%)	86	91
16	XQ	175/176 (99%)	175 (100%)	0	100	100
16	zQ	175/176 (99%)	174 (99%)	1 (1%)	86	91
17	AU	160/162 (99%)	158 (99%)	2 (1%)	69	82
17	XU	160/162 (99%)	160 (100%)	0	100	100
17	zU	160/162 (99%)	160 (100%)	0	100	100
19	P	165/210 (79%)	164 (99%)	1 (1%)	86	91
19	Pb	165/210 (79%)	164 (99%)	1 (1%)	86	91
19	Pc	165/210 (79%)	165 (100%)	0	100	100
20	Q	192/224 (86%)	192 (100%)	0	100	100
20	Qb	192/224 (86%)	191 (100%)	1 (0%)	88	93
20	Qc	192/224 (86%)	190 (99%)	2 (1%)	76	86
21	R	176/205 (86%)	175 (99%)	1 (1%)	86	91
21	Rb	176/205 (86%)	176 (100%)	0	100	100
21	Rc	176/205 (86%)	175 (99%)	1 (1%)	86	91
22	A	182/195 (93%)	181 (100%)	1 (0%)	88	93
22	Ab	182/195 (93%)	181 (100%)	1 (0%)	88	93
22	Ac	182/195 (93%)	181 (100%)	1 (0%)	88	93
23	S	221/222 (100%)	220 (100%)	1 (0%)	88	93
23	Sb	221/222 (100%)	221 (100%)	0	100	100
23	Sc	221/222 (100%)	214 (97%)	7 (3%)	39	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	B	173/191 (91%)	173 (100%)	0	100	100
24	Bb	173/191 (91%)	173 (100%)	0	100	100
24	Bc	173/191 (91%)	172 (99%)	1 (1%)	86	91
25	T	187/187 (100%)	187 (100%)	0	100	100
25	Tb	187/187 (100%)	186 (100%)	1 (0%)	88	93
25	Tc	187/187 (100%)	185 (99%)	2 (1%)	73	85
26	U	165/170 (97%)	164 (99%)	1 (1%)	86	91
26	Ub	165/170 (97%)	165 (100%)	0	100	100
26	Uc	165/170 (97%)	164 (99%)	1 (1%)	86	91
27	V	150/161 (93%)	149 (99%)	1 (1%)	84	90
27	Vb	150/161 (93%)	149 (99%)	1 (1%)	84	90
27	Vc	150/161 (93%)	147 (98%)	3 (2%)	55	76
28	W	158/166 (95%)	157 (99%)	1 (1%)	86	91
28	Wb	158/166 (95%)	158 (100%)	0	100	100
28	Wc	158/166 (95%)	153 (97%)	5 (3%)	39	67
29	C	73/85 (86%)	73 (100%)	0	100	100
29	Cb	73/85 (86%)	73 (100%)	0	100	100
29	Cc	73/85 (86%)	73 (100%)	0	100	100
30	X	129/137 (94%)	127 (98%)	2 (2%)	62	79
30	Xb	129/137 (94%)	128 (99%)	1 (1%)	81	89
30	Xc	129/137 (94%)	126 (98%)	3 (2%)	50	73
31	D	88/119 (74%)	88 (100%)	0	100	100
31	Db	88/119 (74%)	88 (100%)	0	100	100
31	Dc	88/119 (74%)	88 (100%)	0	100	100
32	Y	127/128 (99%)	126 (99%)	1 (1%)	81	89
32	Yb	127/128 (99%)	126 (99%)	1 (1%)	81	89
32	Yc	127/128 (99%)	126 (99%)	1 (1%)	81	89
33	Z	97/105 (92%)	97 (100%)	0	100	100
33	Zb	97/105 (92%)	97 (100%)	0	100	100
33	Zc	97/105 (92%)	96 (99%)	1 (1%)	76	86
34	E	98/118 (83%)	98 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	Eb	98/118 (83%)	98 (100%)	0	100	100
34	Ec	98/118 (83%)	97 (99%)	1 (1%)	76	86
35	F	117/119 (98%)	117 (100%)	0	100	100
35	Fb	117/119 (98%)	117 (100%)	0	100	100
35	Fc	117/119 (98%)	116 (99%)	1 (1%)	78	87
36	G	113/124 (91%)	113 (100%)	0	100	100
36	Gb	113/124 (91%)	112 (99%)	1 (1%)	78	87
36	Gc	113/124 (91%)	112 (99%)	1 (1%)	78	87
37	H	128/129 (99%)	126 (98%)	2 (2%)	62	79
37	Hb	128/129 (99%)	128 (100%)	0	100	100
37	Hc	128/129 (99%)	126 (98%)	2 (2%)	62	79
38	I	115/116 (99%)	114 (99%)	1 (1%)	78	87
38	Ib	115/116 (99%)	115 (100%)	0	100	100
38	Ic	115/116 (99%)	115 (100%)	0	100	100
39	J	94/114 (82%)	94 (100%)	0	100	100
39	Jb	94/114 (82%)	94 (100%)	0	100	100
39	Jc	94/114 (82%)	91 (97%)	3 (3%)	39	67
40	a	74/74 (100%)	74 (100%)	0	100	100
40	ab	74/74 (100%)	74 (100%)	0	100	100
40	ac	74/74 (100%)	73 (99%)	1 (1%)	67	82
41	b	110/111 (99%)	110 (100%)	0	100	100
41	bb	110/111 (99%)	110 (100%)	0	100	100
41	bc	110/111 (99%)	107 (97%)	3 (3%)	44	71
42	c	119/120 (99%)	119 (100%)	0	100	100
42	cb	119/120 (99%)	119 (100%)	0	100	100
42	cc	119/120 (99%)	117 (98%)	2 (2%)	60	78
43	d	112/113 (99%)	112 (100%)	0	100	100
43	db	112/113 (99%)	111 (99%)	1 (1%)	78	87
43	dc	112/113 (99%)	111 (99%)	1 (1%)	78	87
44	K	61/89 (68%)	60 (98%)	1 (2%)	62	79
44	Kb	61/89 (68%)	60 (98%)	1 (2%)	62	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	Kc	61/89 (68%)	61 (100%)	0	100	100
45	e	83/101 (82%)	83 (100%)	0	100	100
45	eb	83/101 (82%)	83 (100%)	0	100	100
45	ec	83/101 (82%)	83 (100%)	0	100	100
46	f	70/71 (99%)	67 (96%)	3 (4%)	29	59
46	fb	70/71 (99%)	69 (99%)	1 (1%)	67	82
46	fc	70/71 (99%)	67 (96%)	3 (4%)	29	59
47	L	56/60 (93%)	56 (100%)	0	100	100
47	Lb	56/60 (93%)	55 (98%)	1 (2%)	59	78
47	Lc	56/60 (93%)	56 (100%)	0	100	100
48	M	47/49 (96%)	45 (96%)	2 (4%)	29	59
48	Mb	47/49 (96%)	45 (96%)	2 (4%)	29	59
48	Mc	47/49 (96%)	46 (98%)	1 (2%)	53	75
49	g	51/54 (94%)	51 (100%)	0	100	100
49	gb	51/54 (94%)	51 (100%)	0	100	100
49	gc	51/54 (94%)	50 (98%)	1 (2%)	55	76
50	N	56/135 (42%)	55 (98%)	1 (2%)	59	78
50	Nb	56/135 (42%)	56 (100%)	0	100	100
50	Nc	56/135 (42%)	56 (100%)	0	100	100
51	O	255/262 (97%)	255 (100%)	0	100	100
51	Ob	255/262 (97%)	254 (100%)	1 (0%)	91	95
51	Oc	255/262 (97%)	251 (98%)	4 (2%)	62	79
52	AX	139/146 (95%)	138 (99%)	1 (1%)	84	90
52	XX	139/146 (95%)	138 (99%)	1 (1%)	84	90
52	zX	139/146 (95%)	138 (99%)	1 (1%)	84	90
53	BB	150/151 (99%)	150 (100%)	0	100	100
53	YB	150/151 (99%)	150 (100%)	0	100	100
53	ZB	150/151 (99%)	150 (100%)	0	100	100
54	BF	149/154 (97%)	148 (99%)	1 (1%)	84	90
54	YF	153/154 (99%)	151 (99%)	2 (1%)	69	82
54	ZF	153/154 (99%)	150 (98%)	3 (2%)	55	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	BH	156/156 (100%)	156 (100%)	0	100	100
55	YH	156/156 (100%)	156 (100%)	0	100	100
55	ZH	156/156 (100%)	156 (100%)	0	100	100
56	BJ	136/137 (99%)	135 (99%)	1 (1%)	84	90
56	YJ	136/137 (99%)	135 (99%)	1 (1%)	84	90
56	ZJ	136/137 (99%)	136 (100%)	0	100	100
57	BL	85/107 (79%)	85 (100%)	0	100	100
57	YL	85/107 (79%)	85 (100%)	0	100	100
57	ZL	85/107 (79%)	85 (100%)	0	100	100
58	AB	103/105 (98%)	102 (99%)	1 (1%)	76	86
58	XB	103/105 (98%)	103 (100%)	0	100	100
58	zB	103/105 (98%)	103 (100%)	0	100	100
59	AE	113/114 (99%)	113 (100%)	0	100	100
59	XE	114/114 (100%)	110 (96%)	4 (4%)	36	64
59	zE	114/114 (100%)	113 (99%)	1 (1%)	78	87
60	AH	104/118 (88%)	104 (100%)	0	100	100
60	XH	104/118 (88%)	104 (100%)	0	100	100
60	zH	104/118 (88%)	104 (100%)	0	100	100
61	AK	107/110 (97%)	107 (100%)	0	100	100
61	XK	107/110 (97%)	107 (100%)	0	100	100
61	zK	107/110 (97%)	107 (100%)	0	100	100
62	AN	115/116 (99%)	115 (100%)	0	100	100
62	XN	115/116 (99%)	115 (100%)	0	100	100
62	zN	115/116 (99%)	115 (100%)	0	100	100
63	AR	118/119 (99%)	118 (100%)	0	100	100
63	XR	118/119 (99%)	118 (100%)	0	100	100
63	zR	118/119 (99%)	118 (100%)	0	100	100
64	AV	46/47 (98%)	45 (98%)	1 (2%)	52	74
64	XV	46/47 (98%)	46 (100%)	0	100	100
64	zV	46/47 (98%)	46 (100%)	0	100	100
65	AY	84/88 (96%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
65	XY	84/88 (96%)	84 (100%)	0	100	100
65	zY	84/88 (96%)	84 (100%)	0	100	100
66	BC	94/97 (97%)	94 (100%)	0	100	100
66	YC	94/97 (97%)	94 (100%)	0	100	100
66	ZC	94/97 (97%)	93 (99%)	1 (1%)	73	85
67	BG	109/111 (98%)	109 (100%)	0	100	100
67	YG	109/111 (98%)	109 (100%)	0	100	100
67	ZG	109/111 (98%)	109 (100%)	0	100	100
68	BK	90/91 (99%)	90 (100%)	0	100	100
68	YK	90/91 (99%)	90 (100%)	0	100	100
68	ZK	90/91 (99%)	90 (100%)	0	100	100
69	BN	95/103 (92%)	95 (100%)	0	100	100
69	YN	95/103 (92%)	93 (98%)	2 (2%)	53	75
69	ZN	95/103 (92%)	95 (100%)	0	100	100
70	BP	103/105 (98%)	103 (100%)	0	100	100
70	YP	103/105 (98%)	103 (100%)	0	100	100
70	ZP	103/105 (98%)	103 (100%)	0	100	100
71	AC	80/82 (98%)	80 (100%)	0	100	100
71	XC	80/82 (98%)	79 (99%)	1 (1%)	69	82
71	zC	80/82 (98%)	79 (99%)	1 (1%)	69	82
72	AF	67/71 (94%)	66 (98%)	1 (2%)	65	81
72	XF	67/71 (94%)	65 (97%)	2 (3%)	41	68
72	zF	67/71 (94%)	66 (98%)	1 (2%)	65	81
73	AI	67/69 (97%)	66 (98%)	1 (2%)	65	81
73	XI	67/69 (97%)	66 (98%)	1 (2%)	65	81
73	zI	67/69 (97%)	67 (100%)	0	100	100
74	AL	45/46 (98%)	45 (100%)	0	100	100
74	XL	45/46 (98%)	45 (100%)	0	100	100
74	zL	45/46 (98%)	45 (100%)	0	100	100
75	AO	47/116 (40%)	46 (98%)	1 (2%)	53	75
75	XO	47/116 (40%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
75	zO	47/116 (40%)	46 (98%)	1 (2%)	53	75
76	AS	23/23 (100%)	23 (100%)	0	100	100
76	XS	23/23 (100%)	22 (96%)	1 (4%)	29	59
76	zS	23/23 (100%)	23 (100%)	0	100	100
77	AP	90/91 (99%)	90 (100%)	0	100	100
77	XP	90/91 (99%)	90 (100%)	0	100	100
77	zP	90/91 (99%)	89 (99%)	1 (1%)	73	85
78	AT	71/72 (99%)	71 (100%)	0	100	100
78	XT	71/72 (99%)	69 (97%)	2 (3%)	43	70
78	zT	71/72 (99%)	68 (96%)	3 (4%)	30	60
79	BU	105/254 (41%)	104 (99%)	1 (1%)	76	86
79	YU	105/254 (41%)	103 (98%)	2 (2%)	57	77
79	ZU	105/254 (41%)	103 (98%)	2 (2%)	57	77
All	All	28102/30585 (92%)	27932 (99%)	170 (1%)	86	91

5 of 170 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	Ec	72	LYS
5	ZA	343	TYR
37	Hc	118	LYS
46	fc	19	HIS
12	ZD	153	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 260 such sidechains are listed below:

Mol	Chain	Res	Type
12	ZD	92	HIS
53	ZB	126	GLN
34	Eb	70	ASN
30	Xb	16	GLN
61	zK	4	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	BQ	3120/3396 (91%)	777 (24%)	65 (2%)
1	YQ	3120/3396 (91%)	711 (22%)	59 (1%)
1	ZQ	3120/3396 (91%)	780 (25%)	60 (1%)
18	2	1755/1800 (97%)	520 (29%)	58 (3%)
18	2b	1755/1800 (97%)	511 (29%)	0
18	2c	1755/1800 (97%)	669 (38%)	0
2	BR	120/121 (99%)	18 (15%)	0
2	YR	120/121 (99%)	12 (10%)	0
2	ZR	120/121 (99%)	16 (13%)	0
3	BS	156/157 (99%)	41 (26%)	1 (0%)
3	YS	156/157 (99%)	40 (25%)	3 (1%)
3	ZS	156/157 (99%)	36 (23%)	2 (1%)
80	n	75/76 (98%)	20 (26%)	0
81	nb	75/76 (98%)	37 (49%)	0
81	nc	75/76 (98%)	36 (48%)	0
82	mb	76/77 (98%)	15 (19%)	0
82	mc	76/77 (98%)	13 (17%)	0
All	All	15830/16804 (94%)	4252 (26%)	248 (1%)

5 of 4252 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	BQ	6	A
1	BQ	11	A
1	BQ	14	U
1	BQ	26	A
1	BQ	30	G

5 of 248 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
18	2	1537	C
1	ZQ	1878	G
1	YQ	1096	U
1	ZQ	1815	U
1	ZQ	3195	U

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
71	AC	1
12	YD	1
67	YG	1
12	ZD	1
30	X	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AC	22:PRO	C	23:ALA	N	1.19
1	YD	120:GLY	C	121:LYS	N	1.17
1	YG	51:SER	C	52:GLN	N	1.17
1	ZD	120:GLY	C	121:LYS	N	1.13
1	X	111:VAL	C	112:SER	N	1.12

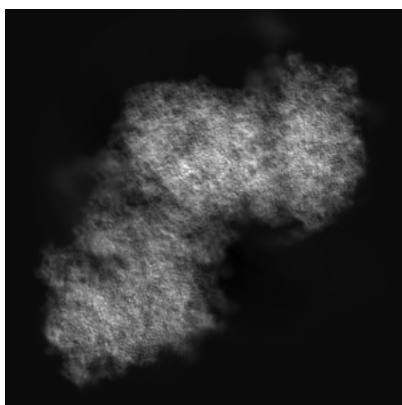
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10315. These allow visual inspection of the internal detail of the map and identification of artifacts.

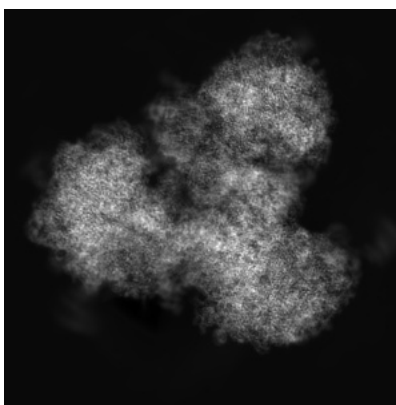
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

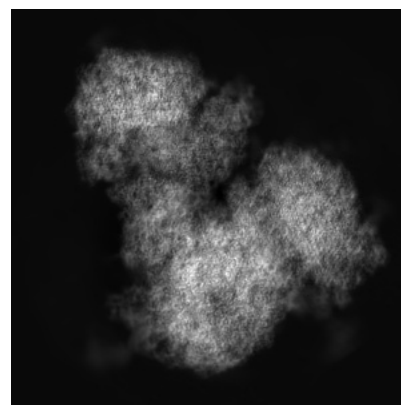
6.1.1 Primary map



X



Y

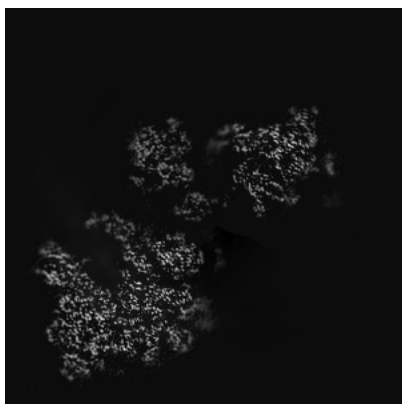


Z

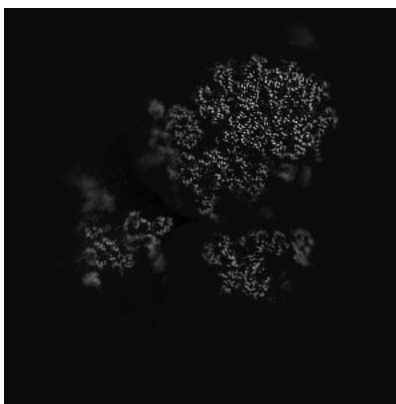
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

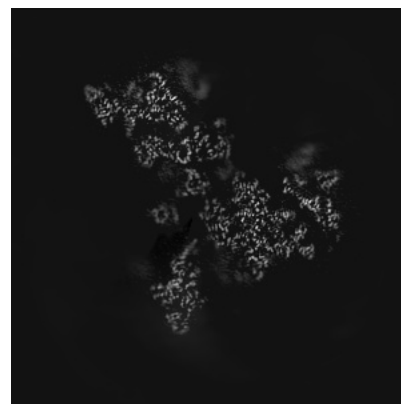
6.2.1 Primary map



X Index: 250



Y Index: 250

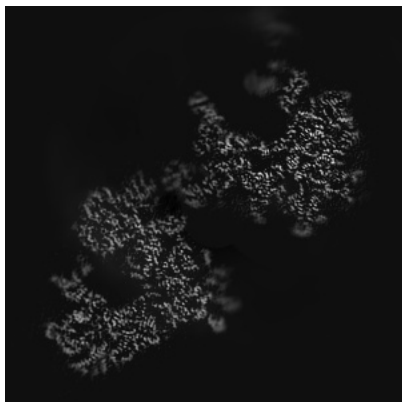


Z Index: 250

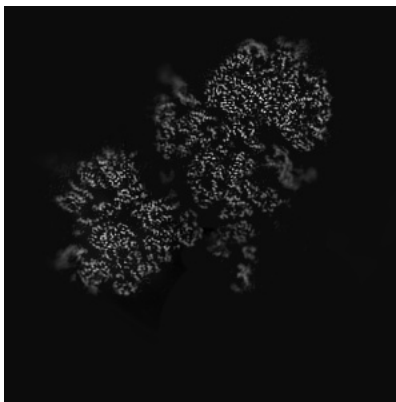
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

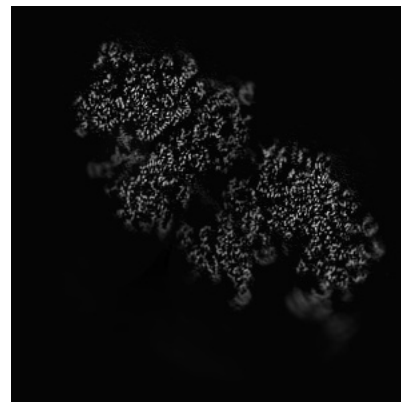
6.3.1 Primary map



X Index: 205



Y Index: 221



Z Index: 308

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

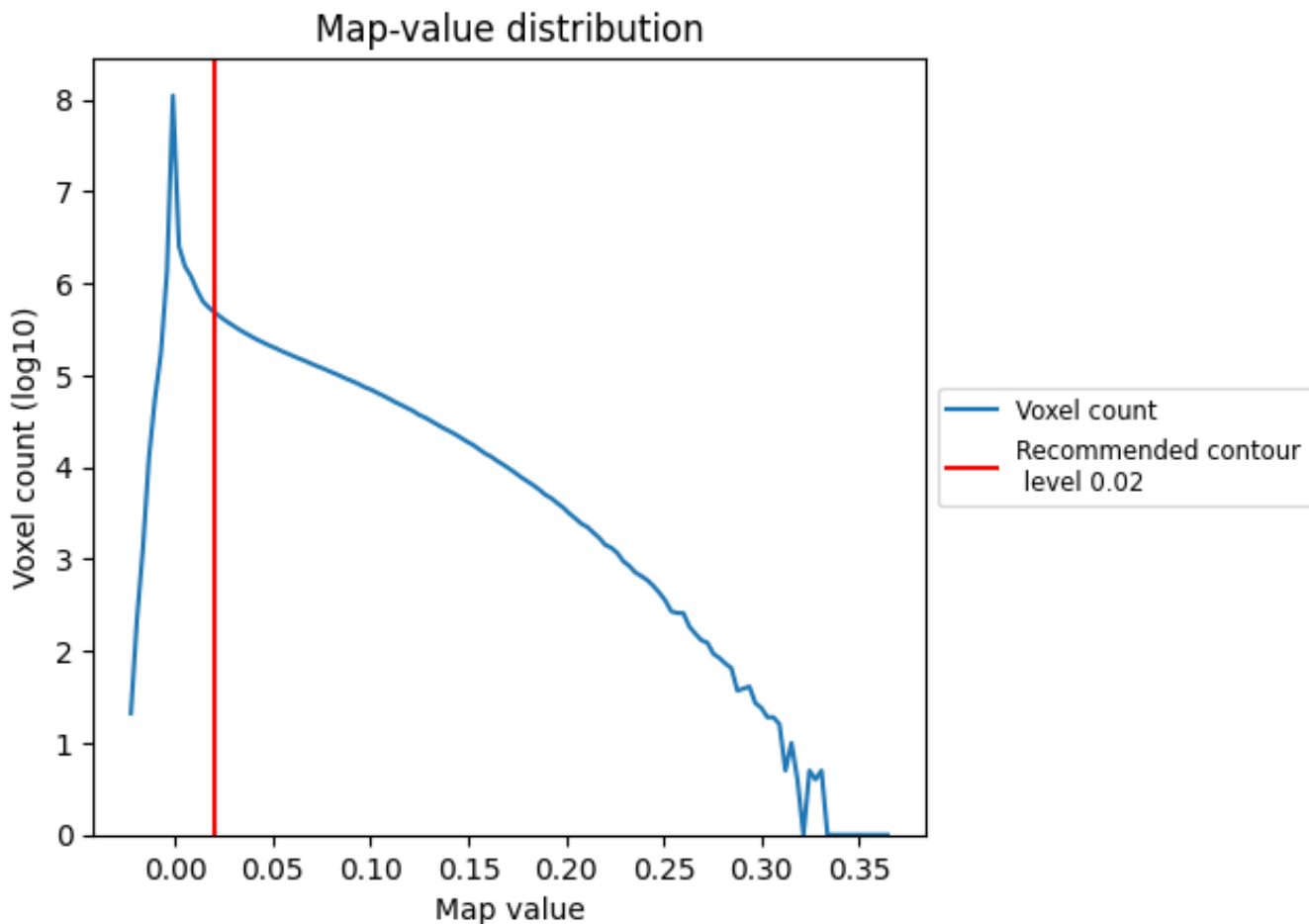
6.5 Mask visualisation

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

7 Map analysis [i](#)

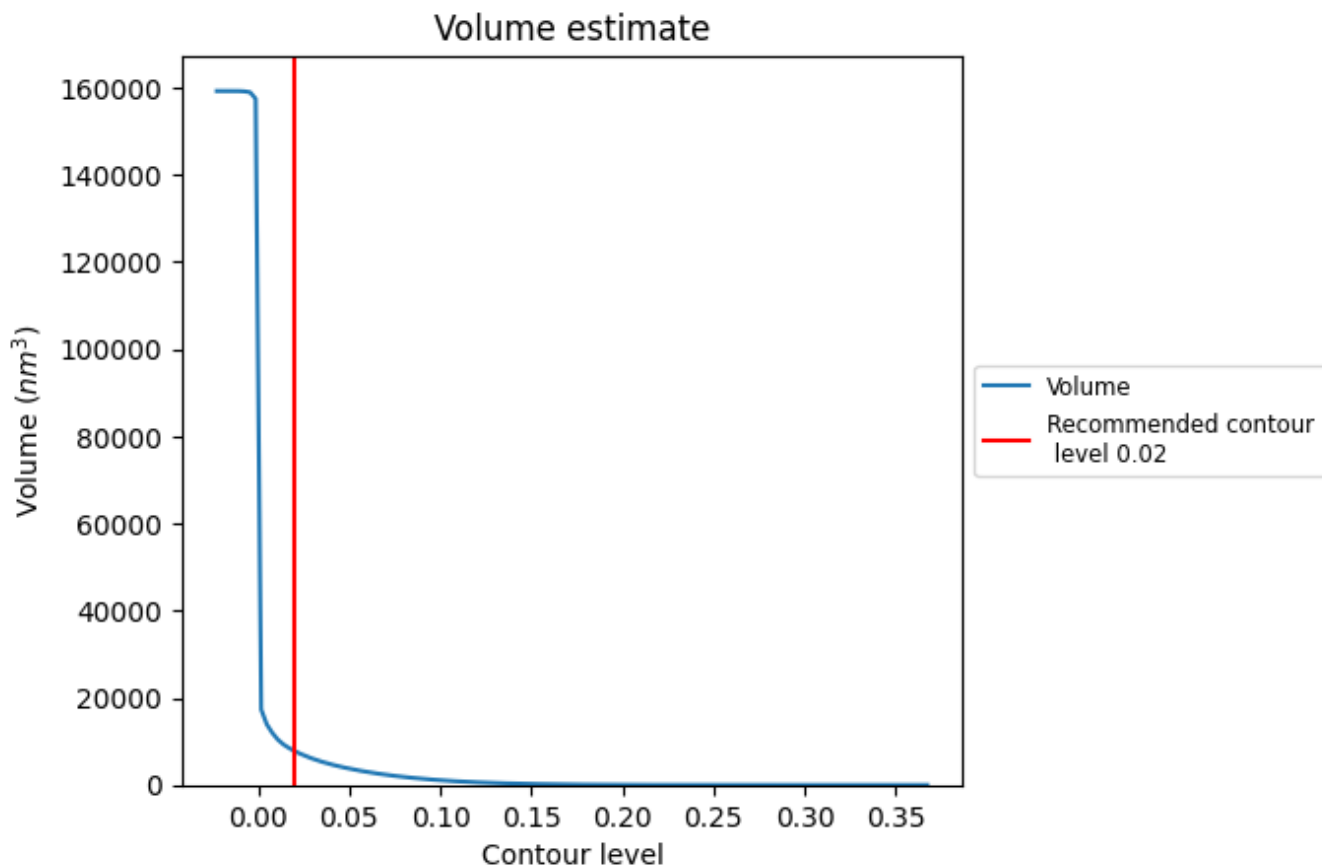
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

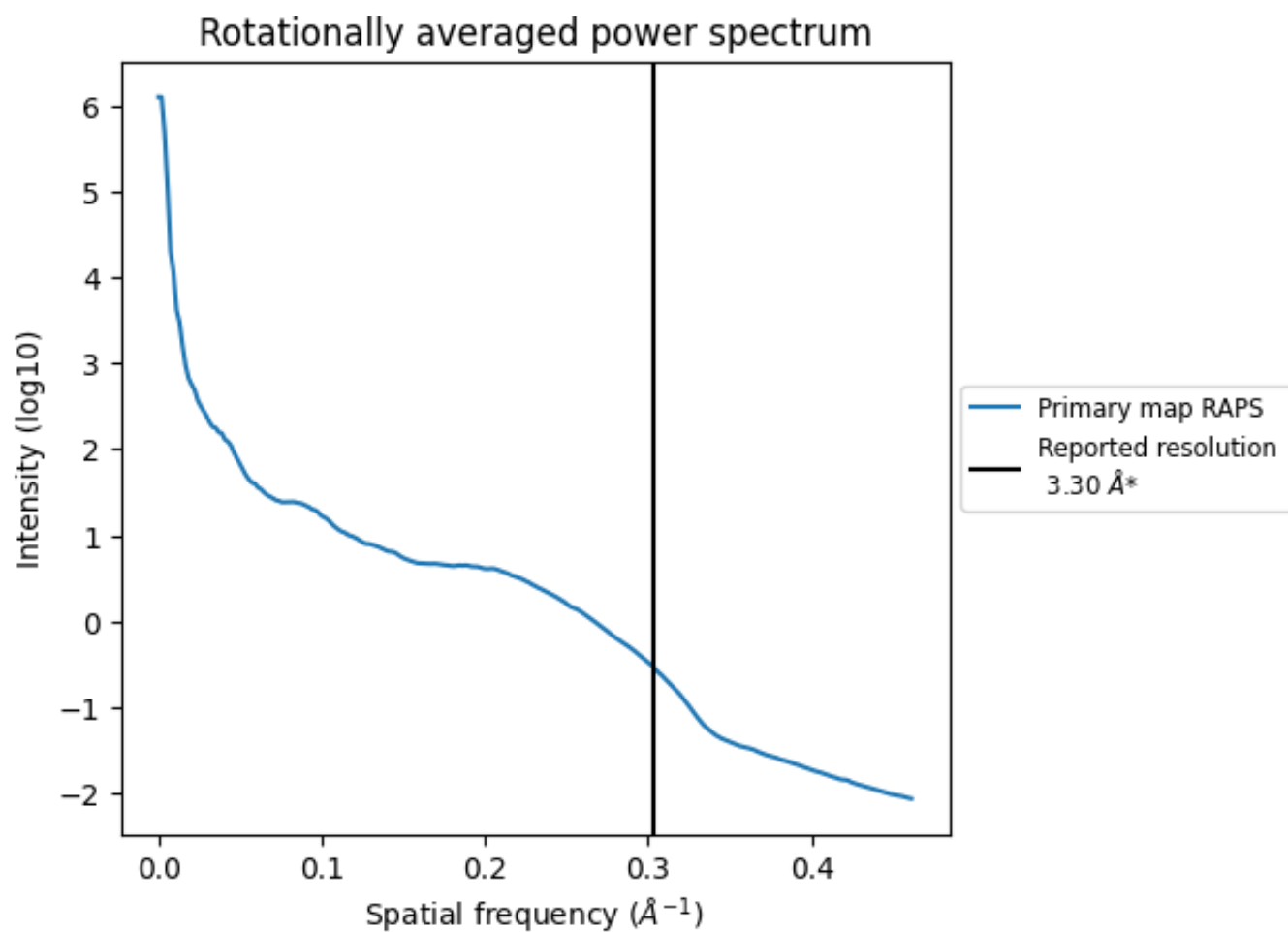
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 7800 nm^3 ; this corresponds to an approximate mass of 7046 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

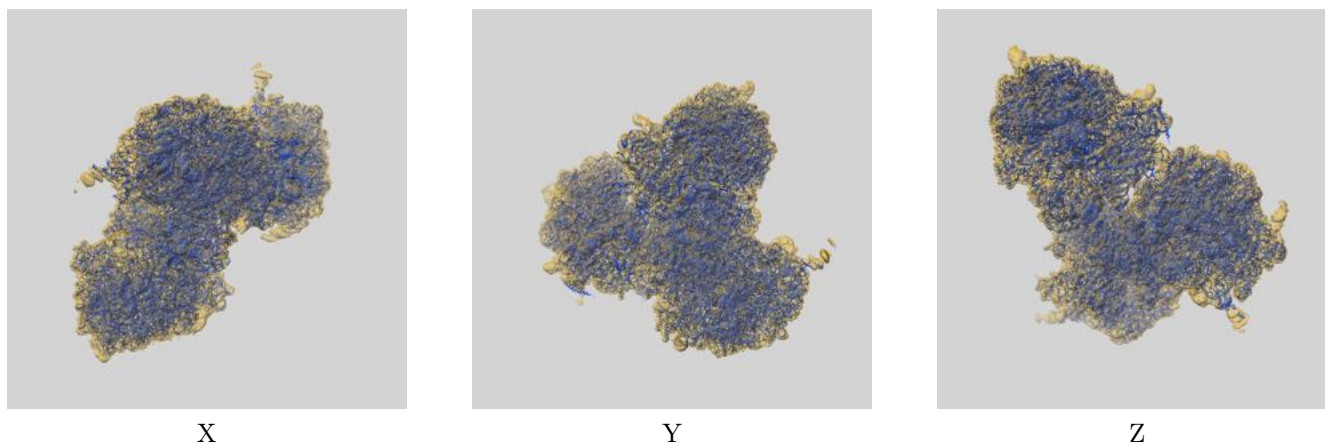
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

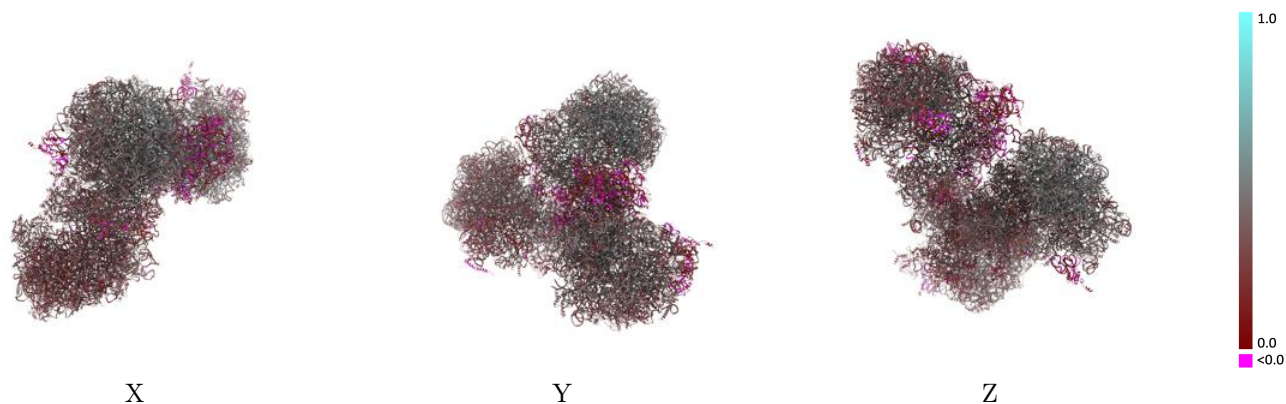
This section contains information regarding the fit between EMDB map EMD-10315 and PDB model 6SV4. Per-residue inclusion information can be found in section 3 on page 33.

9.1 Map-model overlay [i](#)



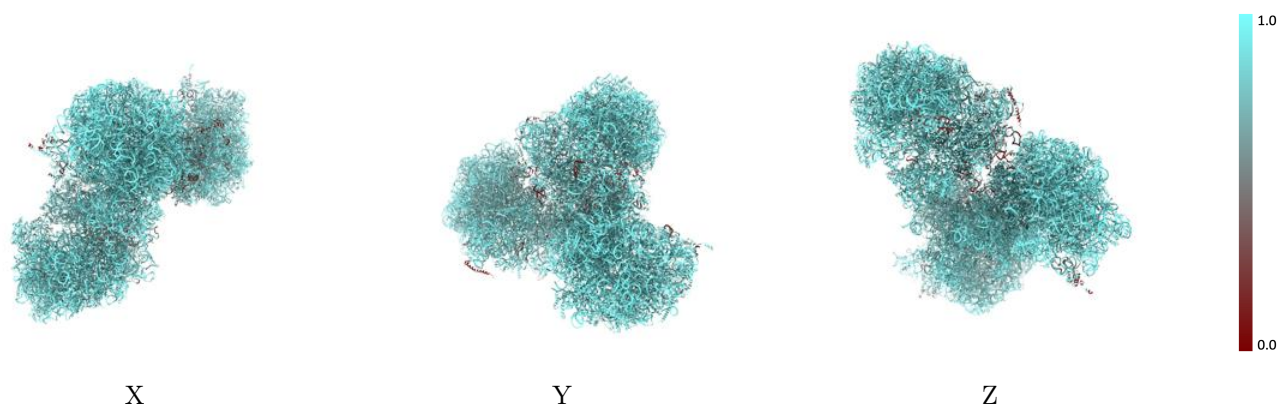
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



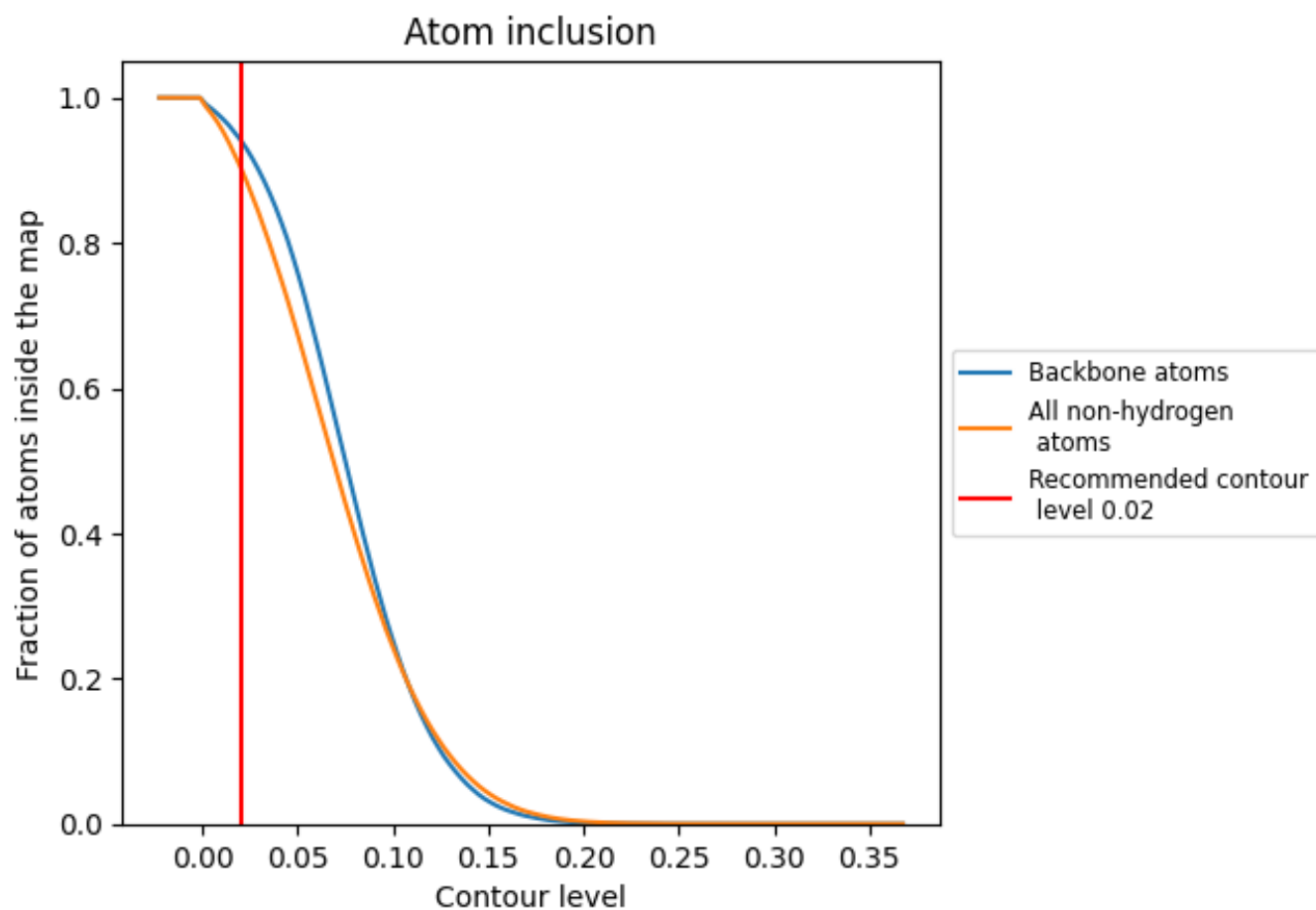
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9038	 0.3260
2	 0.9404	 0.2930
2b	 0.9262	 0.3530
2c	 0.8942	 0.2870
A	 0.8650	 0.2980
AA	 0.8667	 0.2990
AB	 0.8194	 0.2580
AC	 0.8602	 0.2680
AD	 0.8839	 0.2620
AE	 0.4682	 0.1160
AF	 0.9151	 0.2770
AG	 0.8745	 0.2730
AH	 0.8858	 0.2880
AI	 0.9193	 0.2970
AJ	 0.9082	 0.2690
AK	 0.8978	 0.2790
AL	 0.8771	 0.2640
AM	 0.9147	 0.2760
AN	 0.8889	 0.3270
AO	 0.8660	 0.2610
AP	 0.8720	 0.2970
AQ	 0.8870	 0.2720
AR	 0.8923	 0.2690
AS	 0.7783	 0.2970
AT	 0.8386	 0.2690
AU	 0.8653	 0.2300
AV	 0.8739	 0.2680
AW	 0.8494	 0.2870
AX	 0.8778	 0.2780
AY	 0.8093	 0.2790
Ab	 0.8313	 0.3210
Ac	 0.8129	 0.3020
B	 0.8797	 0.2730
BA	 0.8656	 0.2610
BB	 0.8860	 0.2820























































































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Chain	Atom inclusion	Q-score
BC	 0.8565	 0.2720
BD	 0.8801	 0.2730
BE	 0.8902	 0.2710
BF	 0.8711	 0.2450
BG	 0.8501	 0.2650
BH	 0.8488	 0.2620
BI	 0.9094	 0.2830
BJ	 0.8911	 0.2700
BK	 0.8343	 0.2330
BL	 0.9306	 0.3210
BM	 0.8903	 0.2610
BN	 0.8672	 0.2890
BO	 0.8754	 0.2650
BP	 0.8850	 0.2830
BQ	 0.9343	 0.2750
BR	 0.9639	 0.3090
BS	 0.9508	 0.2820
BU	 0.6039	 0.0400
Bb	 0.8160	 0.3190
Bc	 0.8638	 0.3150
C	 0.8349	 0.2450
Cb	 0.7923	 0.3180
Cc	 0.8212	 0.3190
D	 0.8250	 0.1530
Db	 0.7568	 0.1570
Dc	 0.7670	 0.1610
E	 0.8771	 0.2410
Eb	 0.8957	 0.3500
Ec	 0.8628	 0.3350
F	 0.8638	 0.2680
Fb	 0.8563	 0.3510
Fc	 0.8647	 0.3370
G	 0.8138	 0.2520
Gb	 0.8086	 0.3140
Gc	 0.7469	 0.2030
H	 0.8596	 0.2250
Hb	 0.8640	 0.3460
Hc	 0.8518	 0.3100
I	 0.8853	 0.2210
Ib	 0.8927	 0.3610
Ic	 0.8881	 0.3560
J	 0.8684	 0.2660





















































































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Chain	Atom inclusion	Q-score
Jb	 0.8557	 0.3230
Jc	 0.8051	 0.2740
K	 0.8635	 0.2280
Kb	 0.8339	 0.3130
Kc	 0.8708	 0.3180
L	 0.8826	 0.3100
Lb	 0.8428	 0.3500
Lc	 0.9140	 0.3310
M	 0.6856	 0.0730
Mb	 0.6643	 0.1240
Mc	 0.6501	 0.1090
N	 0.9006	 0.1780
Nb	 0.9006	 0.2390
Nc	 0.8895	 0.2340
O	 0.8161	 0.2610
Ob	 0.8017	 0.2960
Oc	 0.7607	 0.1710
P	 0.8487	 0.3070
Pb	 0.8668	 0.3560
Pc	 0.6535	 0.0690
Q	 0.8044	 0.3100
Qb	 0.8191	 0.3700
Qc	 0.8783	 0.3550
R	 0.8731	 0.2870
Rb	 0.8700	 0.3600
Rc	 0.7643	 0.2580
S	 0.8635	 0.2920
Sb	 0.8590	 0.3250
Sc	 0.5626	 0.0510
T	 0.8772	 0.2280
Tb	 0.8801	 0.3190
Tc	 0.7227	 0.1080
U	 0.8277	 0.2840
Ub	 0.8806	 0.3190
Uc	 0.6960	 0.0920
V	 0.8997	 0.2750
Vb	 0.9130	 0.3500
Vc	 0.7709	 0.1230
W	 0.8641	 0.2830
Wb	 0.8350	 0.3040
Wc	 0.6789	 0.1460
X	 0.8232	 0.2810





















































































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Chain	Atom inclusion	Q-score
XA	 0.9025	 0.4040
XB	 0.8411	 0.3900
XC	 0.9167	 0.4210
XD	 0.9103	 0.3800
XE	 0.6831	 0.2380
XF	 0.9327	 0.4640
XG	 0.8639	 0.3230
XH	 0.9306	 0.4350
XI	 0.9361	 0.3820
XJ	 0.9377	 0.4210
XK	 0.9410	 0.4380
XL	 0.9181	 0.4530
XM	 0.9603	 0.3840
XN	 0.9113	 0.3910
XO	 0.8983	 0.3810
XP	 0.8780	 0.4210
XQ	 0.9285	 0.4760
XR	 0.9229	 0.4420
XS	 0.6085	 0.3200
XT	 0.8640	 0.4020
XU	 0.9247	 0.4020
XV	 0.8850	 0.3650
XW	 0.8817	 0.4240
XX	 0.9348	 0.4400
XY	 0.8450	 0.3870
Xb	 0.8769	 0.3760
Xc	 0.6825	 0.1740
Y	 0.8563	 0.3180
YA	 0.9114	 0.4110
YB	 0.9376	 0.4480
YC	 0.9160	 0.4160
YD	 0.9075	 0.3750
YE	 0.9367	 0.4410
YF	 0.9164	 0.3970
YG	 0.9245	 0.4570
YH	 0.9016	 0.4090
YI	 0.9194	 0.3550
YJ	 0.9331	 0.4270
YK	 0.9147	 0.4340
YL	 0.9437	 0.3840
YM	 0.9223	 0.3820
YN	 0.8895	 0.4290

















































































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Chain	Atom inclusion	Q-score
YO	 0.9337	 0.4120
YP	 0.9063	 0.4280
YQ	 0.9617	 0.4240
YR	 0.9860	 0.4140
YS	 0.9787	 0.4650
YU	 0.5961	 0.0390
Yb	 0.8459	 0.3710
Yc	 0.8398	 0.3210
Z	 0.8716	 0.3140
ZA	 0.8742	 0.3490
ZB	 0.8789	 0.3300
ZC	 0.9020	 0.3830
ZD	 0.8898	 0.3460
ZE	 0.9002	 0.3330
ZF	 0.8822	 0.3420
ZG	 0.8773	 0.3590
ZH	 0.9044	 0.3560
ZI	 0.9016	 0.2770
ZJ	 0.8855	 0.3530
ZK	 0.8648	 0.3560
ZL	 0.9228	 0.3390
ZM	 0.7995	 0.1800
ZN	 0.8837	 0.3740
ZO	 0.8897	 0.3320
ZP	 0.9116	 0.3490
ZQ	 0.9520	 0.3690
ZR	 0.9732	 0.3590
ZS	 0.9628	 0.3810
ZU	 0.6369	 0.0800
Zb	 0.8803	 0.3660
Zc	 0.9075	 0.3750
a	 0.8253	 0.3070
ab	 0.8298	 0.3360
ac	 0.5828	 0.0440
b	 0.8848	 0.3160
bb	 0.8878	 0.3790
bc	 0.6964	 0.1420
c	 0.8702	 0.2800
cb	 0.8812	 0.3870
cc	 0.9031	 0.3930
d	 0.8972	 0.2860
db	 0.8405	 0.2900

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Chain	Atom inclusion	Q-score
dc	 0.6484	 0.0910
e	 0.8579	 0.3040
eb	 0.8742	 0.3750
ec	 0.9256	 0.4030
f	 0.8236	 0.3150
fb	 0.8735	 0.3620
fc	 0.7521	 0.1740
g	 0.8279	 0.2510
gb	 0.7756	 0.3080
gc	 0.7712	 0.3150
mb	 0.9276	 0.3260
mc	 0.9501	 0.3120
n	 0.9624	 0.2750
nb	 0.8685	 0.2540
nc	 0.8741	 0.2660
zA	 0.8909	 0.3410
zB	 0.8627	 0.3950
zC	 0.8871	 0.3050
zD	 0.9008	 0.3290
zE	 0.5894	 0.1920
zF	 0.9359	 0.3890
zG	 0.8783	 0.3190
zH	 0.9082	 0.3740
zI	 0.9227	 0.3740
zJ	 0.8948	 0.3210
zK	 0.9125	 0.3480
zL	 0.8843	 0.3660
zM	 0.8643	 0.2590
zN	 0.8973	 0.3780
zO	 0.9007	 0.3910
zP	 0.8563	 0.3410
zQ	 0.8998	 0.3470
zR	 0.8940	 0.3420
zS	 0.6792	 0.3040
zT	 0.8939	 0.3720
zU	 0.8752	 0.3430
zV	 0.9004	 0.3460
zW	 0.8920	 0.3900
zX	 0.8958	 0.3740
zY	 0.8596	 0.3510