



wwPDB EM Validation Summary Report ⓘ

Jul 11, 2022 – 09:04 pm BST

PDB ID : 7OYD
EMDB ID : EMD-13114
Title : Cryo-EM structure of a rabbit 80S ribosome with zebrafish Dap1b
Authors : Leesch, F.; Lorenzo-Orts, L.; Grishkovskaya, I.; Kandolf, S.; Belacic, K.; Meinhart, A.; Haselbach, D.; Pauli, A.
Deposited on : 2021-06-24
Resolution : 2.30 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.dev8
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.29

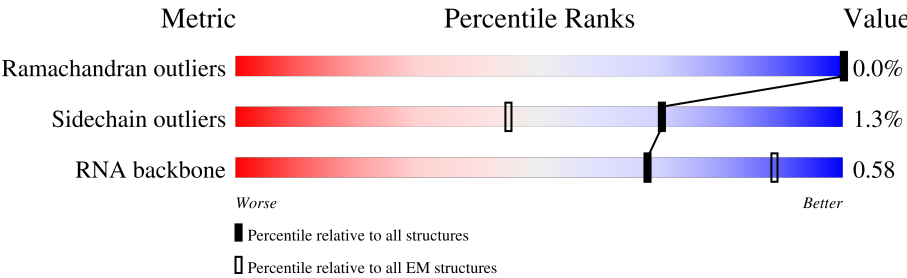
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.30 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	x	217	<div> <div>42%</div> <div>74%</div> <div>25%</div> </div>
2	5	3598	<div> <div>77%</div> <div>16%</div> <div>7%</div> </div>
3	8	151	<div> <div>85%</div> <div>10%</div> <div>5%</div> </div>
4	9	1698	<div> <div>33%</div> <div>70%</div> <div>26%</div> </div>
5	A	257	<div> <div>95%</div> <div>2%</div> </div>
6	AA	295	<div> <div>33%</div> <div>73%</div> <div>26%</div> </div>
7	Aa	115	<div> <div>28%</div> <div>87%</div> <div>12%</div> </div>
8	B	403	<div> <div>97%</div> </div>



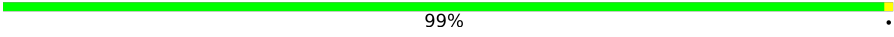
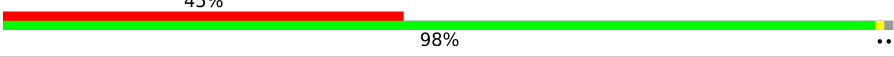
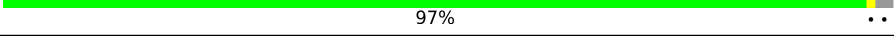


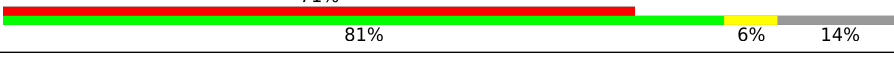
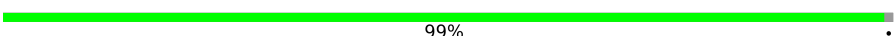
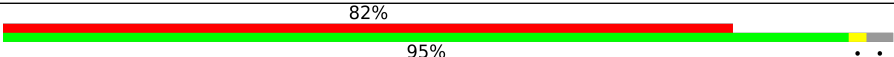
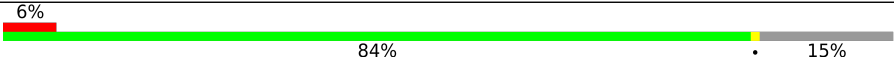
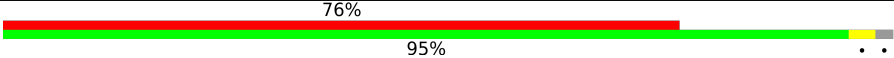

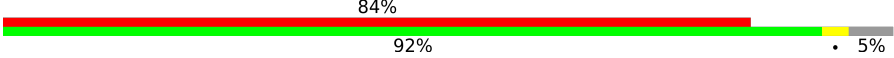
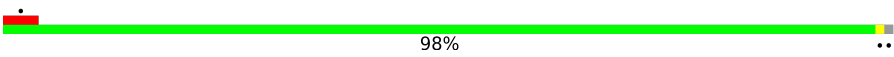
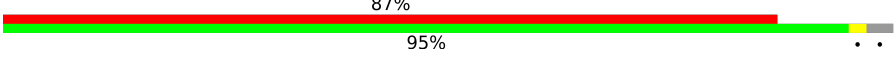


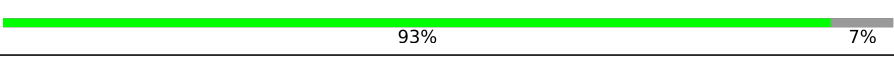
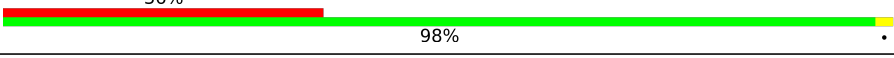

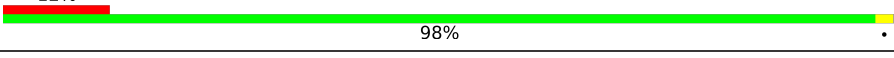

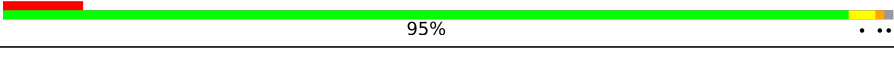
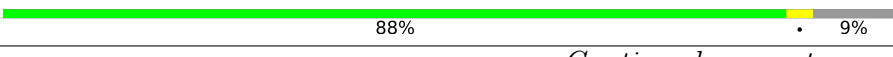
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Mol	Chain	Length	Quality of chain
9	BB	264	
10	Bb	84	
11	C	413	
12	CC	293	
13	Cc	69	
14	D	297	
15	DD	243	
16	Dd	56	
17	E	291	
18	EE	263	
19	Ee	133	
20	F	249	
21	FF	204	
22	G	266	
23	GG	249	
24	Gg	317	
25	H	192	
26	HH	432	
27	I	214	
28	II	208	
29	J	178	
30	JJ	194	
31	K	120	
32	KK	165	
33	L	211	

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Mol	Chain	Length	Quality of chain
34	LL	158	
35	M	218	
36	N	204	
37	NN	151	
38	O	203	
39	OO	151	
40	P	187	
41	PP	145	
42	Q	188	
43	QQ	146	
44	R	196	
45	RR	135	
46	S	224	
47	SS	152	
48	T	160	
49	TT	145	
50	U	141	
51	UU	119	
52	V	140	
53	VV	83	
54	W	157	
55	WW	130	
56	X	156	
57	XX	143	
58	Y	145	

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Mol	Chain	Length	Quality of chain
59	YY	133	
60	Z	136	
61	ZZ	124	
62	a	148	
63	b	245	
64	c	115	
65	d	125	
66	e	157	
67	f	110	
68	g	117	
69	h	123	
70	i	105	
71	j	97	
72	k	70	
73	l	51	
74	m	128	
75	n	25	
76	o	106	
77	p	92	
78	r	137	
79	s	318	
80	s1	109	
81	t	154	
82	v	858	
83	w	407	

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 213014 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Ribosomal protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	x	163	Total	C	N	O	S	0	0
			1291	832	225	228	6		

- Molecule 2 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5	3358	Total	C	N	O	P	0	0
			72165	32204	13226	23377	3358		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	144	Total	C	N	O	P	0	0
			3072	1370	547	1011	144		

- Molecule 4 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	9	1698	Total	C	N	O	P	0	0
			36291	16217	6509	11868	1697		

- Molecule 5 is a protein called Ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	247	Total	C	N	O	S	0	0
			1891	1185	388	312	6		

- Molecule 6 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AA	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AA	114	THR	ALA	conflict	UNP G1TLT8

- Molecule 7 is a protein called RPS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Aa	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 8 is a protein called uL3.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP G1TL06

- Molecule 9 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	BB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 10 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Bb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 11 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	358	Total	C	N	O	S	0	0
			2856	1797	572	473	14		

- Molecule 12 is a protein called RPS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CC	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 13 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Cc	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 14 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	D	289	Total	C	N	O	S	0	0
			2361	1495	431	421	14		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	MET	-	initiating methionine	UNP G1SYJ6

- Molecule 15 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	DD	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 16 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Dd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 17 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	E	213	Total	C	N	O	S	0	0
			1710	1103	325	279	3		

- Molecule 18 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	EE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EE	25	GLY	SER	conflict	UNP G1TK17
EE	51	ARG	LYS	conflict	UNP G1TK17
EE	78	THR	ALA	conflict	UNP G1TK17
EE	156	VAL	MET	conflict	UNP G1TK17

- Molecule 19 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Ee	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 20 is a protein called uL30.

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

- Molecule 21 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	FF	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 22 is a protein called RPL7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	G	215	Total	C	N	O	S	0	0
			1747	1115	337	291	4		

- Molecule 23 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	GG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 24 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Gg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 25 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	H	186	Total	C	N	O	S	0	0
			1484	933	277	268	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	HH	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 27 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	I	202	Total	C	N	O	S	0	0
			1640	1041	317	269	13		

- Molecule 28 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	II	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
II	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 29 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	J	168	Total	C	N	O	S	0	0
			1344	850	251	237	6		

- Molecule 30 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
30	JJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 31 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	K	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

- Molecule 32 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	KK	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 33 is a protein called L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	L	205	Total	C	N	O	S	0	0
			1658	1037	346	271	4		

There are 2 discrepancies between the modelled and reference sequences:

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

- Molecule 34 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LL	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 35 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	M	135	Total	C	N	O	S	0	0
			1117	715	217	178	7		

- Molecule 36 is a protein called Ribosomal protein L15.

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

- Molecule 37 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	NN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 38 is a protein called RPL13A.

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

- Molecule 39 is a protein called RPS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	OO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 40 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	P	152	Total	C	N	O	S	0	0
			1233	772	240	212	9		

- Molecule 41 is a protein called 40S ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	PP	125	Total	C	N	O	S	0	0
			1025	652	192	174	7		

- Molecule 42 is a protein called RPL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

- Molecule 43 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	QQ	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 44 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	R	166	Total	C	N	O	S	0	0
			1383	859	298	217	9		

- Molecule 45 is a protein called 40S ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	RR	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 46 is a protein called RPL18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	S	176	Total	C	N	O	S	0	0
			1456	927	282	236	11		

- Molecule 47 is a protein called 40S ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SS	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 48 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	T	158	Total	C	N	O	S	0	0
			1292	820	251	215	6		

- Molecule 49 is a protein called RPS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	TT	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

- Molecule 50 is a protein called RPL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	U	98	Total	C	N	O	S	0	0
			800	514	139	145	2		

- Molecule 51 is a protein called 40S ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	UU	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 52 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	V	130	Total	C	N	O	S	0	0
			973	615	183	170	5		

- Molecule 53 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	VV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 54 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	W	62	Total	C	N	O	S	0	0
			519	332	101	83	3		

- Molecule 55 is a protein called Ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	WW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 56 is a protein called RPL23A.

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

- Molecule 57 is a protein called RPS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	XX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 58 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Y	132	Total	C	N	O	S	0	0
			1102	692	223	184	3		

- Molecule 59 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	YY	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

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

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

- Molecule 61 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	ZZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 62 is a protein called uL15.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	1	MET	-	initiating methionine	UNP G1SNY0

- Molecule 63 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	b	98	Total	C	N	O	S	0	0
			806	498	182	123	3		

- Molecule 64 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	c	94	Total	C	N	O	S	0	0
			732	464	130	132	6		

- Molecule 65 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	d	106	Total	C	N	O	S	0	0
			879	555	170	152	2		

- Molecule 66 is a protein called eL32.

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

- Molecule 67 is a protein called eL33.

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

- Molecule 68 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	g	111	Total	C	N	O	S	0	0
			882	552	182	142	6		

- Molecule 69 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	h	121	Total	C	N	O	S	0	0
			1008	637	203	167	1		

- Molecule 70 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	i	101	Total	C	N	O	S	0	0
			821	514	174	128	5		

- Molecule 71 is a protein called Ribosomal protein L37.

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

- Molecule 72 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	k	68	Total	C	N	O	S	0	0
			559	360	101	97	1		

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 73 is a protein called eL39.

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

- Molecule 74 is a protein called RPL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	m	51	Total	C	N	O	S	0	0
			420	261	88	65	6		

- Molecule 75 is a protein called 60s ribosomal protein l41.

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

- Molecule 76 is a protein called RPL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	o	102	Total	C	N	O	S	0	0
			834	522	171	135	6		

- Molecule 77 is a protein called eL43.

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

- Molecule 78 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	r	123	Total	C	N	O	S	0	0
			986	611	204	166	5		

- Molecule 79 is a protein called RPLP0.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	s	196	Total	C	N	O	S	0	0
			1501	953	263	276	9		

- Molecule 80 is a protein called Dap1b.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	s1	18	Total	C	N	O	S	0	0
			150	96	30	23	1		

- Molecule 81 is a protein called Eukaryotic translation initiation factor 5A-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	t	126	Total	C	N	O	S	0	0
			961	603	168	182	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t	36	SER	GLY	conflict	UNP P10160

- Molecule 82 is a protein called EEF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	v	726	Total	C	N	O	S	0	0
			5669	3611	972	1046	40		

- Molecule 83 is a protein called SERPINE1 mRNA binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
83	w	32	Total	C	N	O	0	0
			252	148	55	49		

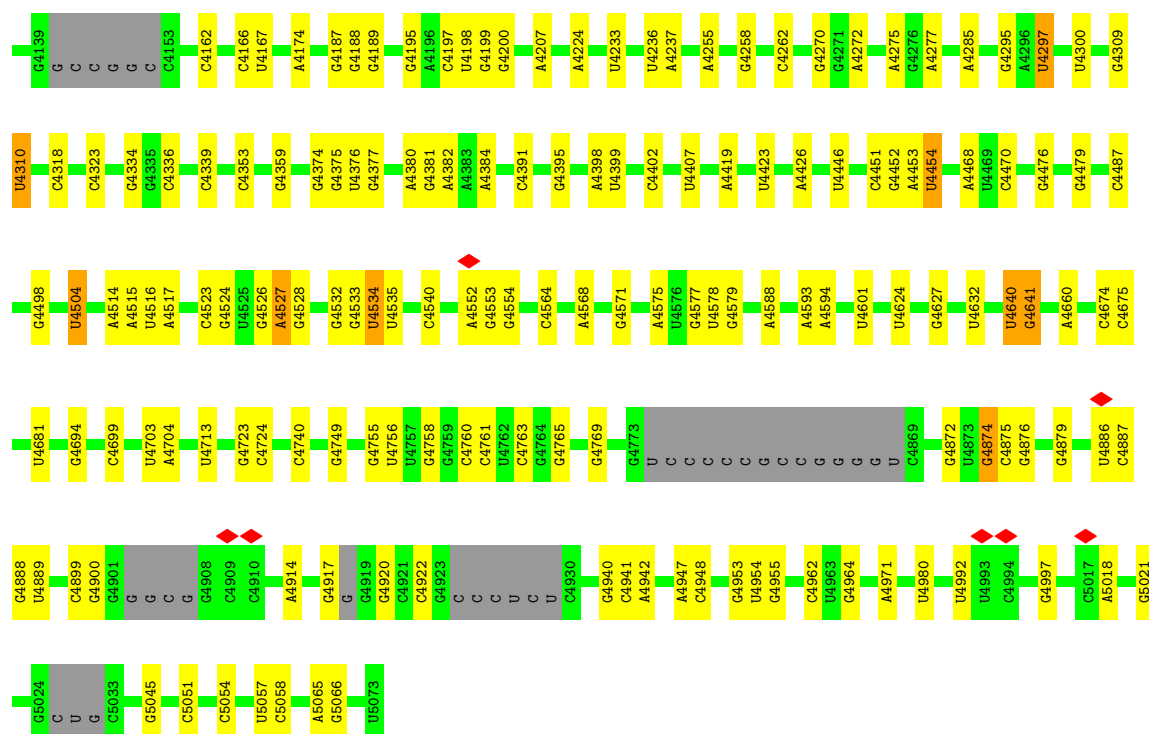
- Molecule 84 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
84	5	195	Total	Mg	0
			195	195	
84	8	2	Total	Mg	0
			2	2	
84	I	1	Total	Mg	0
			1	1	
84	P	1	Total	Mg	0
			1	1	
84	g	1	Total	Mg	0
			1	1	
84	v	1	Total	Mg	0
			1	1	

- Molecule 85 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
85	Aa	1	Total	Zn	0
			1	1	
85	KK	1	Total	Zn	0
			1	1	
85	g	1	Total	Zn	0
			1	1	
85	j	1	Total	Zn	0
			1	1	
85	m	1	Total	Zn	0
			1	1	
85	o	1	Total	Zn	0
			1	1	
85	p	1	Total	Zn	0
			1	1	

G3892	G3893	A3722	G2777	A	G2454	G2097	C1935	U1586	A1401	G1248	U968
G3901	G3902	A3727	C2790	G	G2475	A2101	A1943	U1595	A1402	C1249	A969
G3903	G3904	U3733	A2791	C	G2476	G2102	G1944	U1600	G1407	G	C970
A3905	A3906	U3752	U2792	G2573	G2479	C2103	A1945	U1606	C	C	C971
A3909	A3910	G3758	U2794	U2579	G2483	A2105	G1952	U1609	C	C	C972
A3911	A3912	G3759	A2802	C2587	G	G2110	G1955	G1609	C	C	C973
A3913	A3914	G3760	C2808	A2591	G	G2111	A1962	G1616	C	C	U974
A3915	A3916	G3761	C2818	A2605	G	G2112	G1965	A1617	C	C	C975
A3917	A3918	U3762	U2818	A2606	U	G2117	G1968	G1628	C	C	C976
A3919	A3920	A3765	U2830	G2642	G	C	A1988	G1629	C	C	C982
A3921	A3922	C	G2831	U2643	G	G2263	U1978	A1635	C	C	U987
A3923	A3924	U	U2832	G2644	G	C2264	G1979	A1636	C	C	C993
A3925	A3926	U3768	U2833	C2657	C	C2270	U1982	G1637	C	C	G1074
A3927	A3928	C3771	G2846	G2666	U	U2271	A1983	A1638	C	C	G1075
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A3931	A3932	U3778	U2865	C2674	U	C2293	A1988	U1643	C	C	G1077
A3933	A3934	G3781	C2865	U2691	C	G2301	A1989	G1644	C	C	C1083
A3935	A3936	C3786	U2903	A2699	C2503	A2304	U1990	G1645	C	C	C1100
A3937	A3938	A3787	G	A2700	G	G2305	C1991	A1646	C	C	C1101
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A3941	A3942	A3789	U	U	G2507	A2317	A1995	U1663	C	C	U
A3943	A3944	U3790	C	G	G2508	G2320	U2001	U1664	C	C	C1103
A3945	A3946	G3796	C3606	G2718	C2509	G2337	G2005	C1685	C	C	C1172
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A3949	A3950	C3814	C3620	G2720	U2511	C2355	G2007	U1681	C	C	G1174
A3951	A3952	G3815	U3620	C2725	G2512	A2367	C2008	A1682	C	C	G1178
A3953	A3954	C3816	C3621	U2729	A2517	C2368	U2012	G1683	C	C	C1184
A3955	A3956	A3817	C3622	G2730	G2526	C2369	A2030	U1687	C	C	C1197
A3957	A3958	U3818	G3629	U2739	G2527	G2384	G2050	G1700	C	C	G1198
A3959	A3960	A3821	C3630	G2744	A2533	A2399	U2052	C	C	C	G1199
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A3963	A3964	U3823	A3639	U2746	A2547	A2405	C2054	A1733	C	C	G1202
A3965	A3966	A3829	A3652	A2747	G2551	G2425	G2055	G1738	C	C	U1205
A3967	A3968	G3842	A3666	A2748	U	C2426	G2056	A1527	C	C	C1206
A3969	A3970	G3843	C3677	G2758	G	A2427	A2073	A1538	C	C	C1214
A3971	A3972	U3844	C3700	U2767	G2557	U2429	G2088	A1539	C	C	G1215
A3973	A3974	A3871	C3705	A2768	A2562	G2437	U2098	A1551	C	C	G1216
A3975	A3976	G3872	A3715	U2773	C2562	G2445	G2093	U1758	C	C	G1217
A3977	A3978	C3873	U	U2773	G	C	U2094	C	C	C	C1218
A3979	A3980	A3881	A3718	U2773	C	C	G2094	U1758	C	C	C1219
A3981	A3982	G3882	U3719	U2773	C	C	U2094	U1758	C	C	G1238
A3983	A3984	G3883	U3719	U2773	C	C	U2094	U1758	C	C	G1239
A3985	A3986	G3884	U3719	U2773	C	C	U2094	U1758	C	C	C1240
A3987	A3988	C3891	U3719	U2773	C	C	U2094	U1758	C	C	C1241
A3989	A3990	C3891	U3719	U2773	C	C	U2094	U1758	C	C	C1242
A3991	A3992	C3891	U3719	U2773	C	C	U2094	U1758	C	C	C1243
A3993	A3994	C3891	U3719	U2773	C	C	U2094	U1758	C	C	C1244
A3995	A3996	C3891	U3719	U2773	C	C	U2094	U1758	C	C	C1245
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A3999	A4000	C3891	U3719	U2773	C	C	U2094	U1758	C	C	C1247
A4001	A4002	C3891	U3719	U2773	C	C	U2094	U1758	C	C	C1248
A4003	A4004	C3891	U3719	U2773	C	C	U2094	U1758	C	C	C1249
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A4007	A4008	C3891	U3719	U2773	C	C	U2094	U1758	C	C	C1251
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A4013	A4014	C3891	U3719	U2773	C	C	U2094	U1758	C	C	C1254
A4015	A4016	C3891	U3719	U2773	C	C	U2094	U1758	C	C	C1255
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A4019	A4020	C3891	U3719	U2773	C	C	U2094	U1758	C	C	C1257
A4021	A4022	C3891	U3719	U2773	C	C	U2094	U1758	C	C	C1258
A4023	A4024	C3891	U3719	U2773	C	C	U2094	U1758	C	C	C1259
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A4027	A4028	C3891	U3719	U2773	C	C	U2094	U1758	C	C	C1261
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A4031	A4032	C3891	U3719	U2773	C	C	U2094	U1758	C	C	C1263
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A4143	A4144	C3891	U3719	U2773	C						



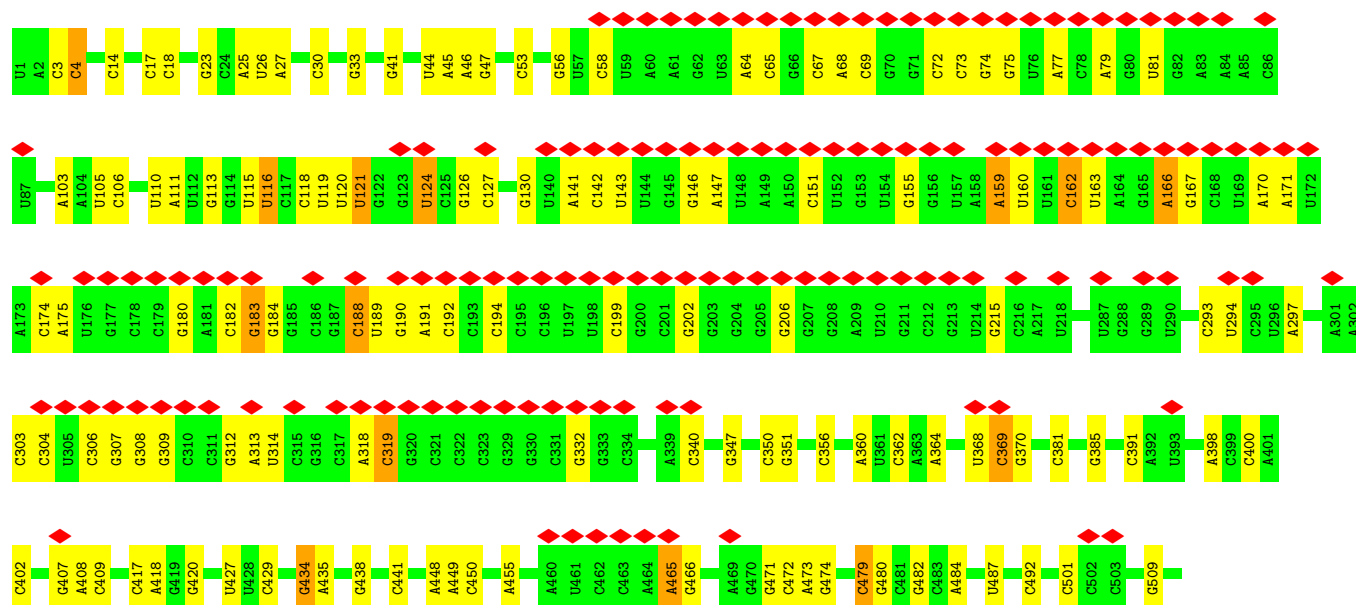
• Molecule 3: 5.8S rRNA

Chain 8: 85% 10% 5%

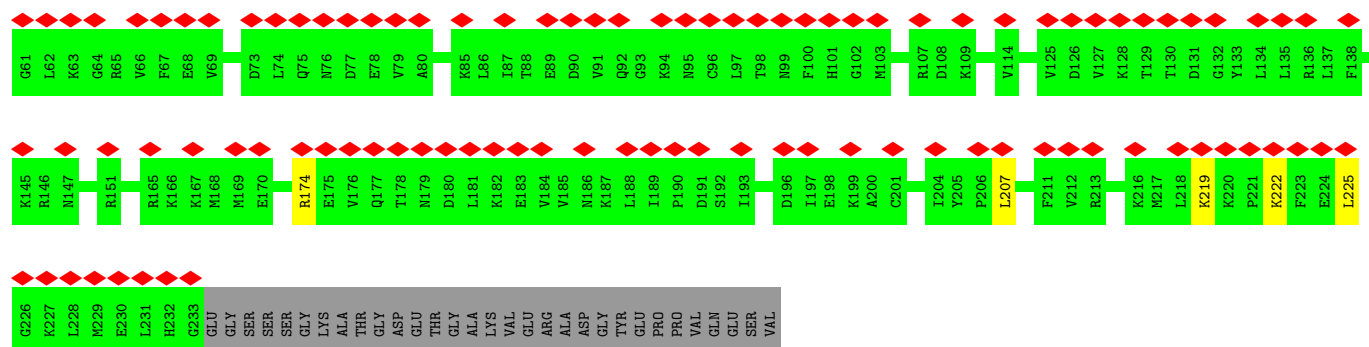


• Molecule 4: 18S rRNA

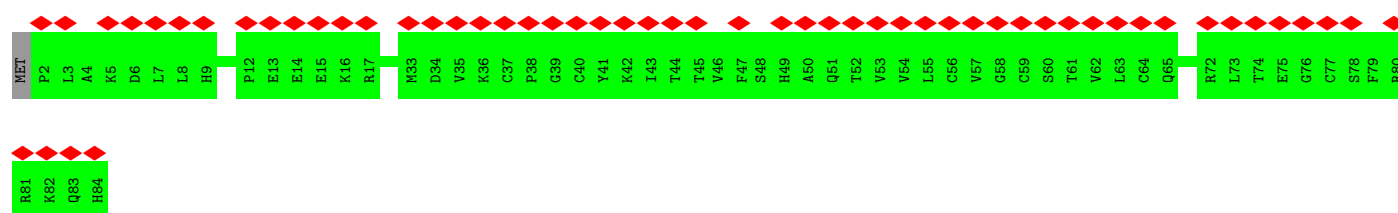
Chain 9: 33% 70% 26%



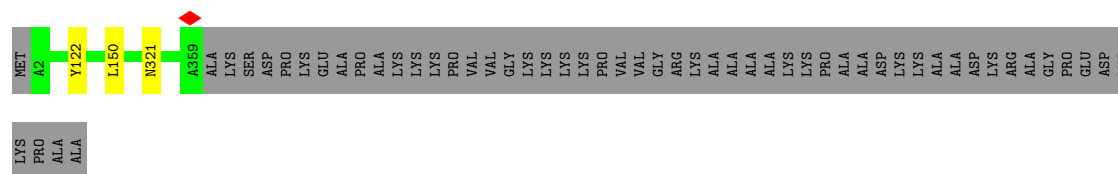
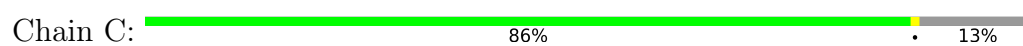




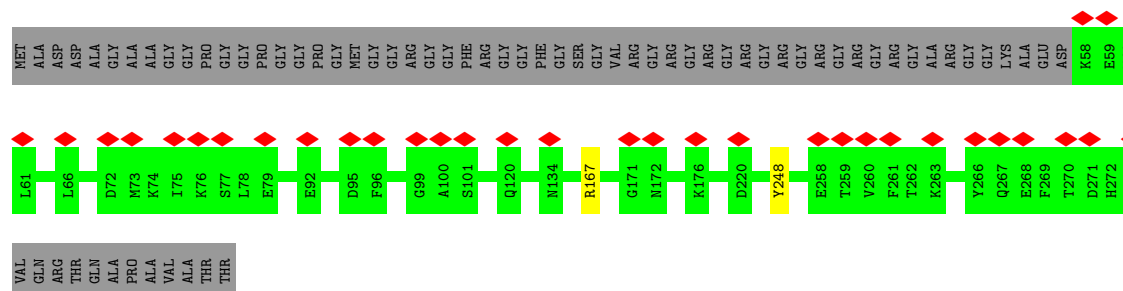
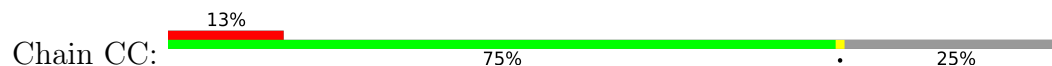
- Molecule 10: 40S ribosomal protein S27



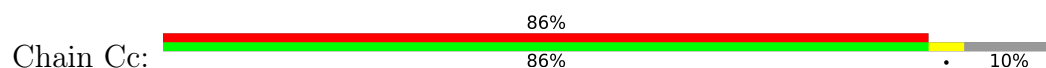
- Molecule 11: 60S ribosomal protein L4

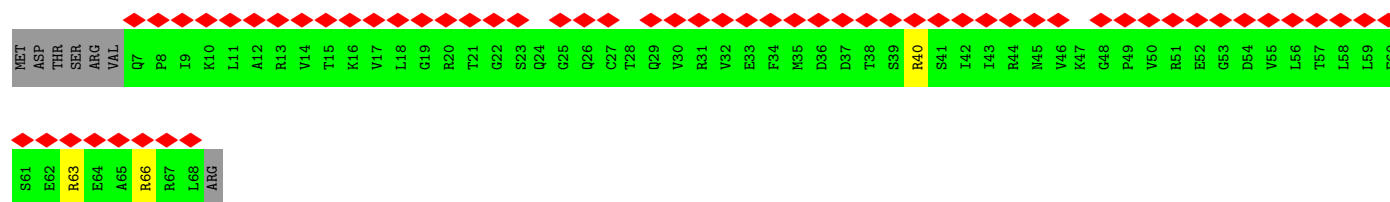


- Molecule 12: RPS2

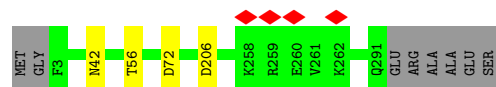


- Molecule 13: Ribosomal protein S28

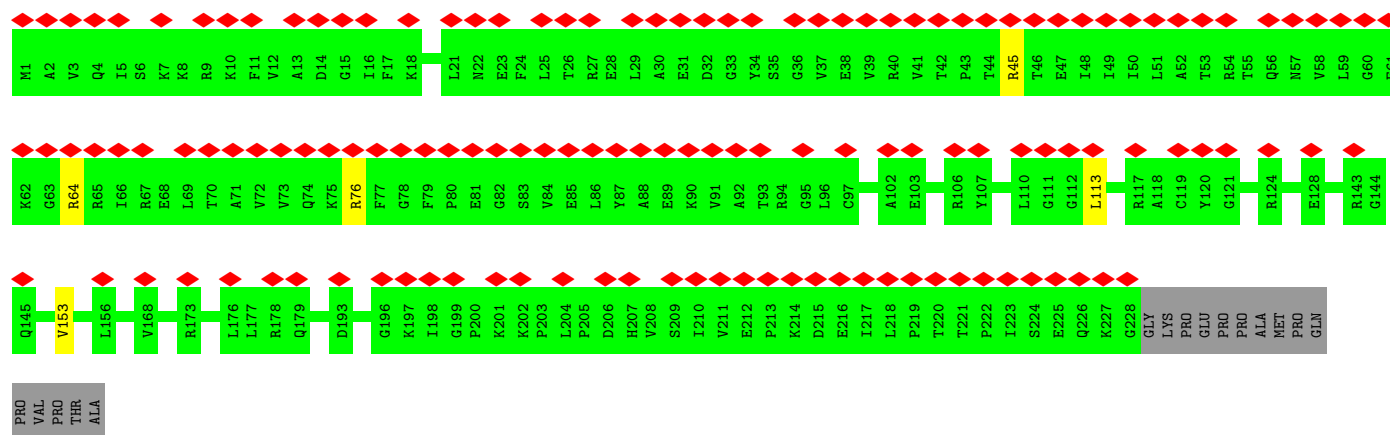




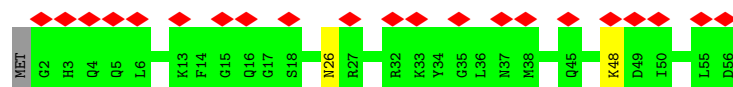
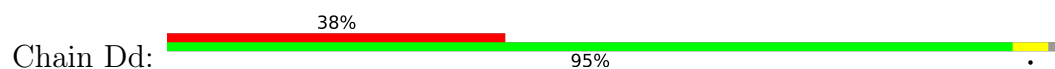
• Molecule 14: 60S ribosomal protein L5



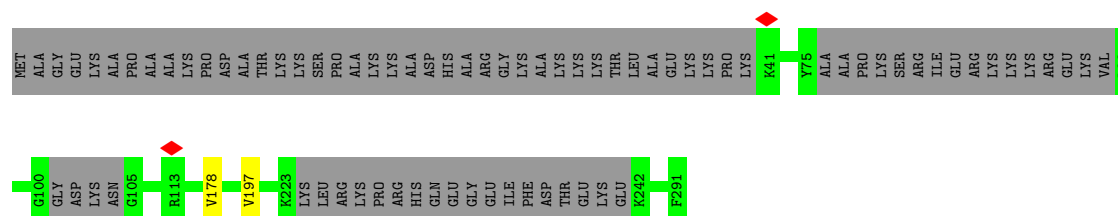
• Molecule 15: Ribosomal protein S3



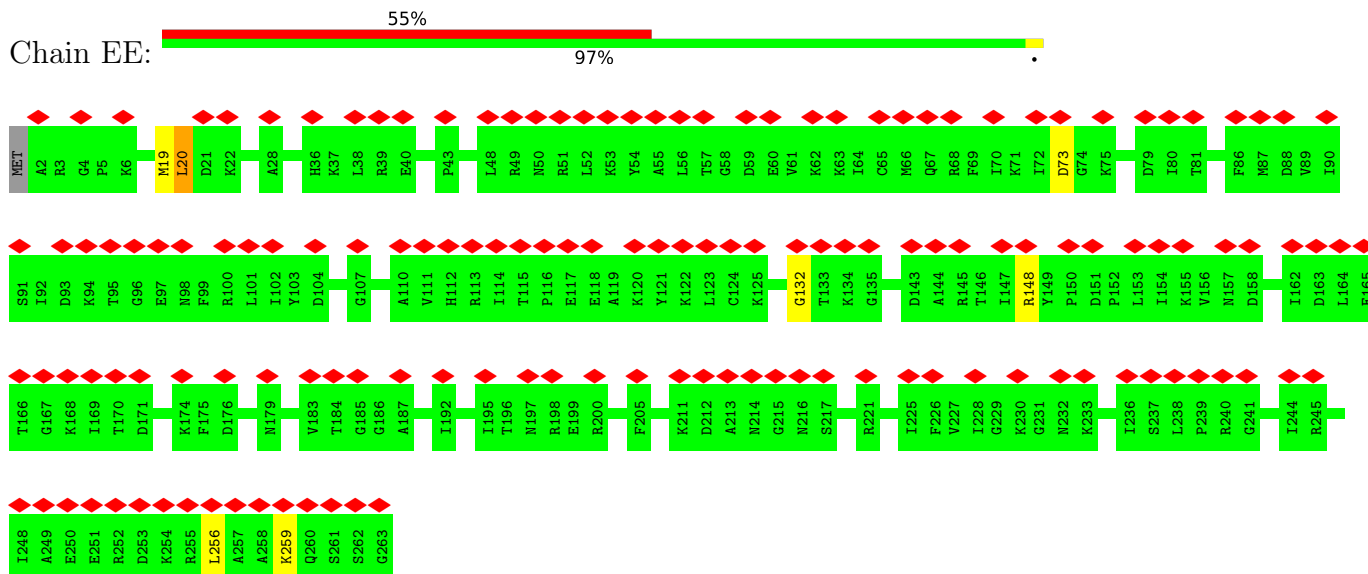
• Molecule 16: uS14



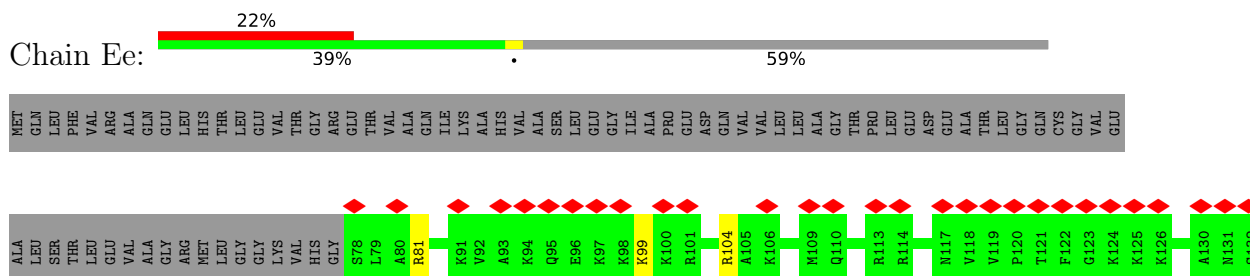
• Molecule 17: 60S ribosomal protein L6



Chain EE:



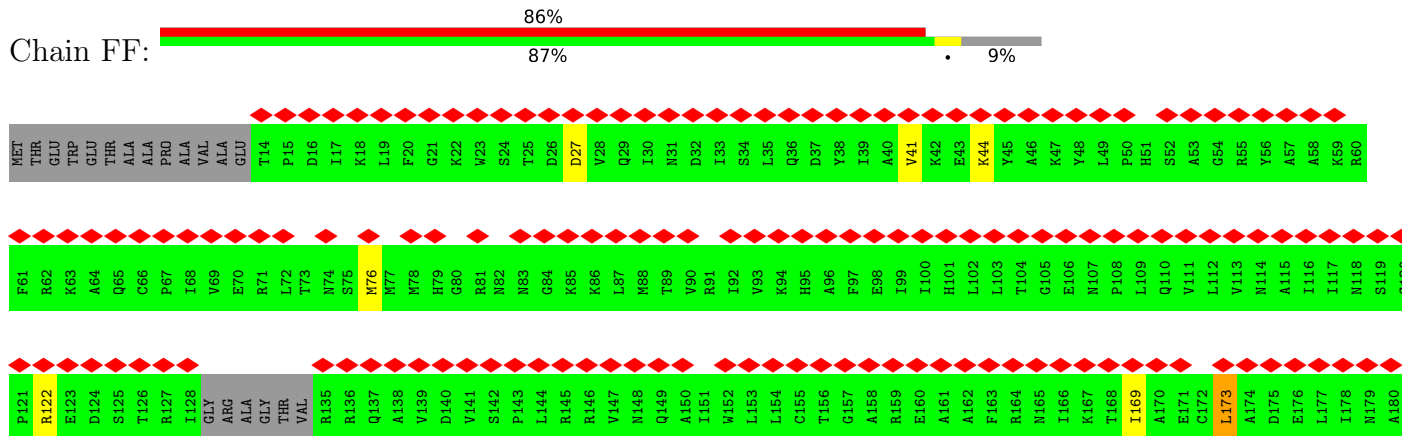
Chain Ee:

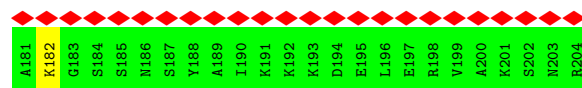


Chain F:

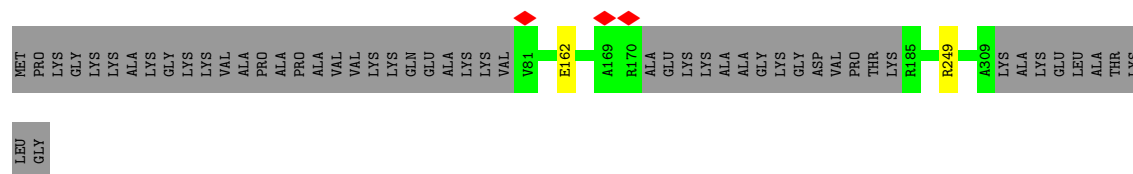
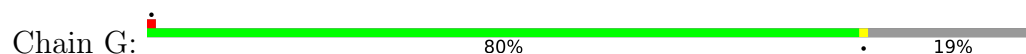


Chain FF:

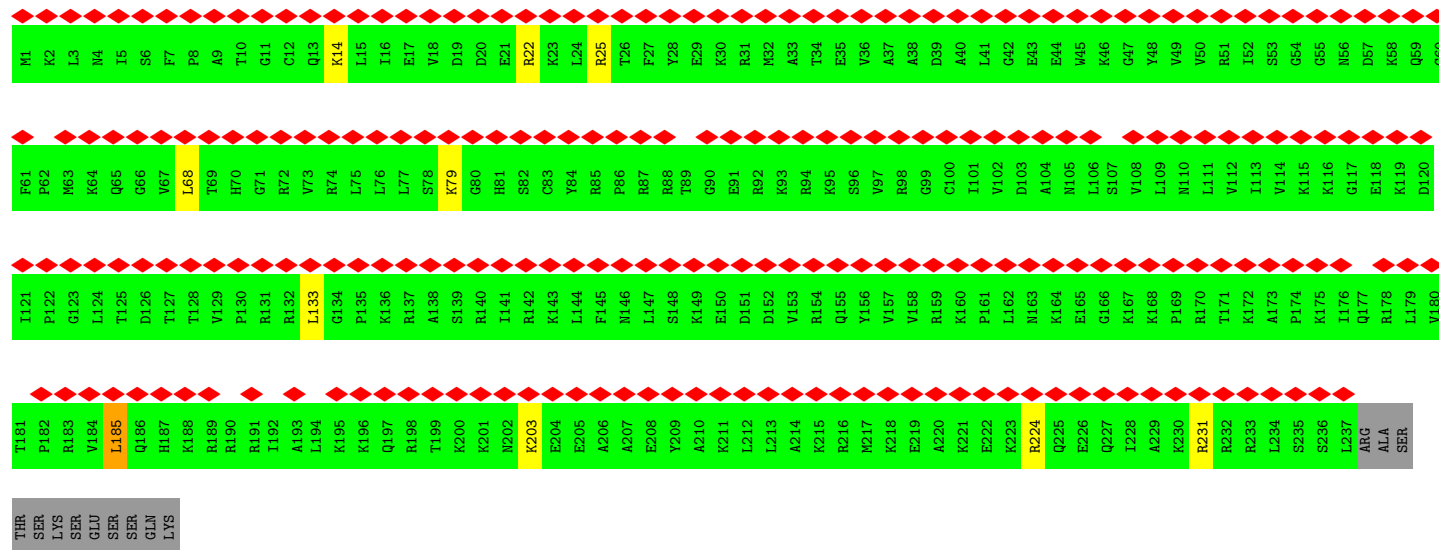




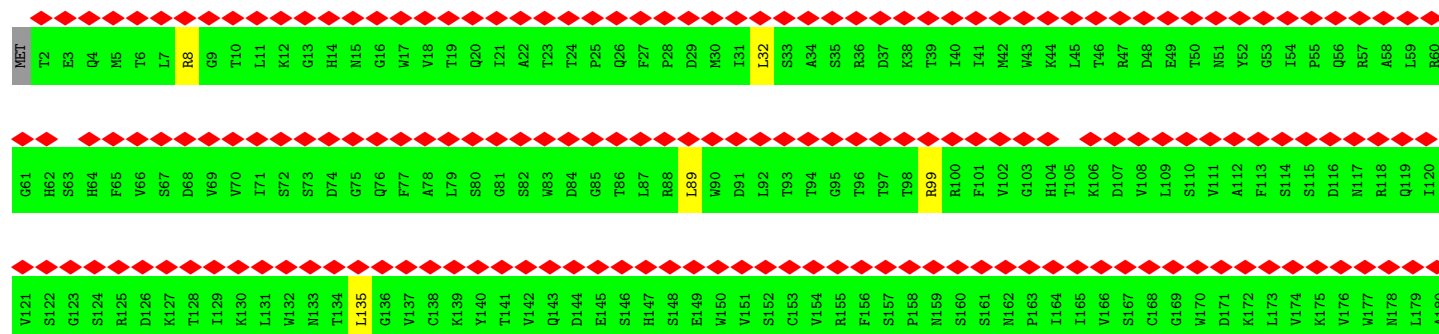
• Molecule 22: RPL7A



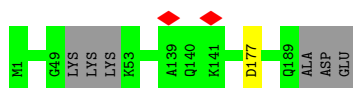
• Molecule 23: 40S ribosomal protein S6



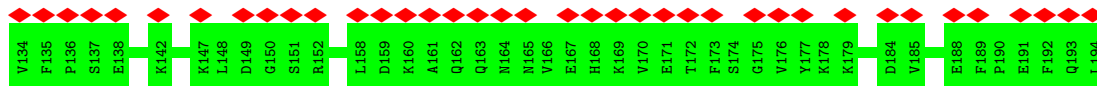
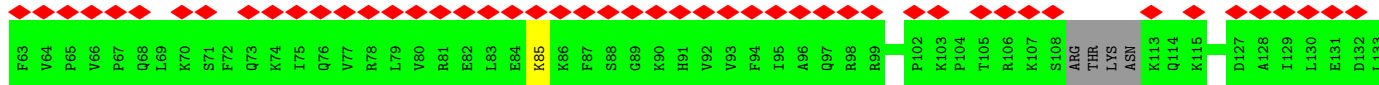
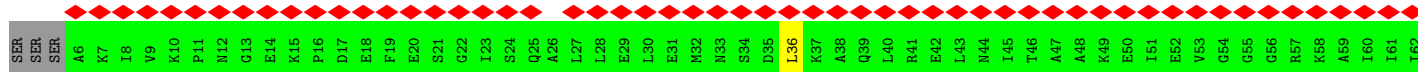
• Molecule 24: RACK1



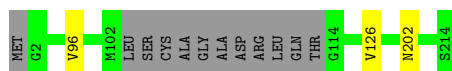
- Molecule 25: 60S ribosomal protein L9



- Molecule 26: 40S ribosomal protein S7

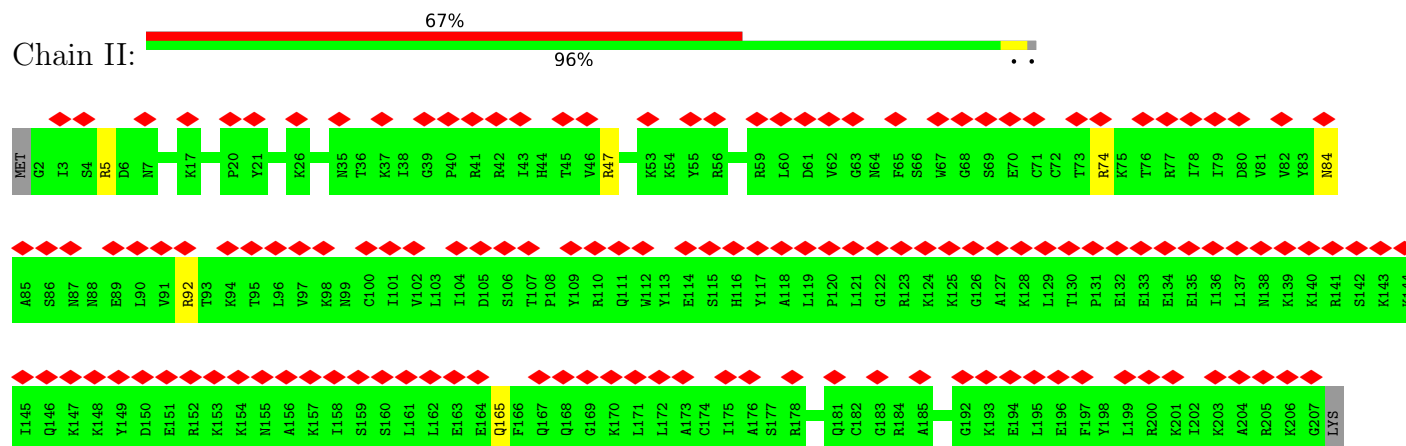


- Molecule 27: 60S ribosomal protein L10



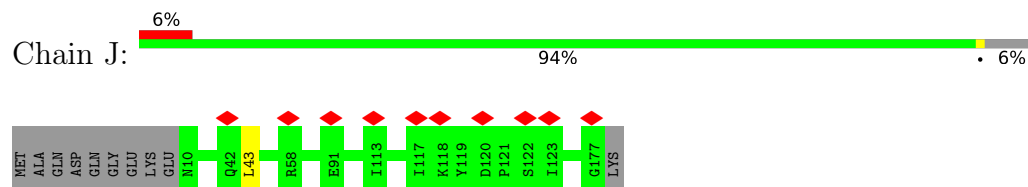
- Molecule 28: 40S ribosomal protein S8

Chain II:



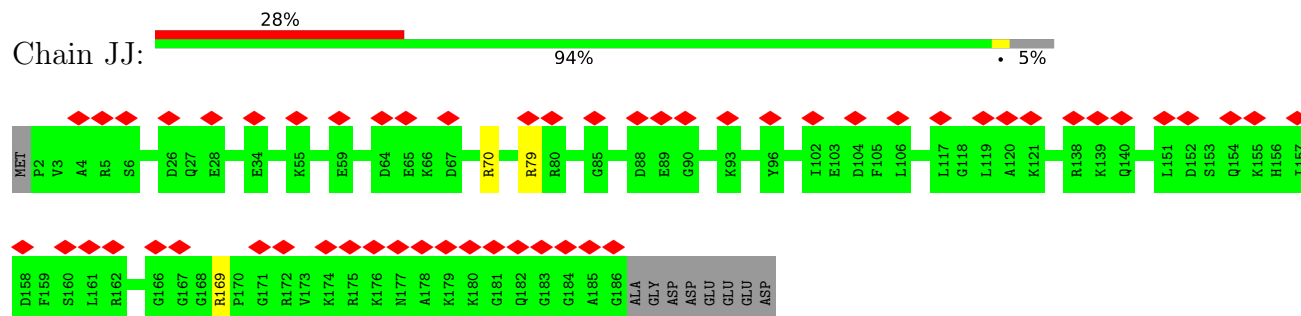
- Molecule 29: Ribosomal protein L11

Chain J:



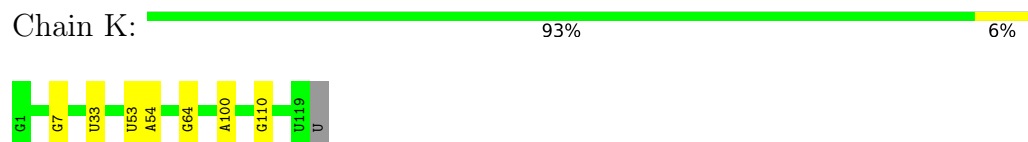
- Molecule 30: Ribosomal protein S9 (Predicted)

Chain JJ:



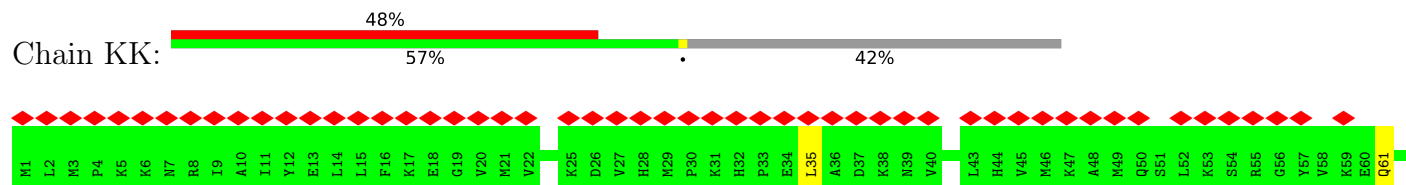
- Molecule 31: 5S rRNA

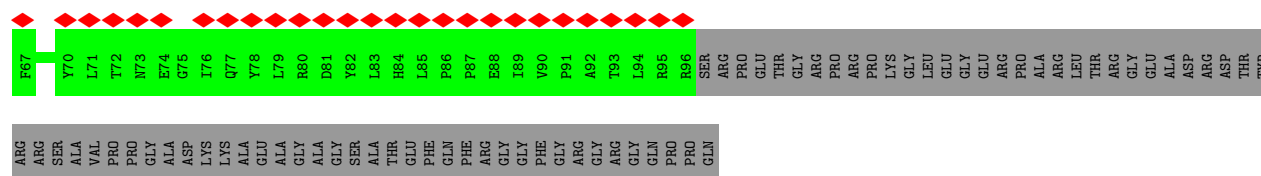
Chain K:



- Molecule 32: eS10

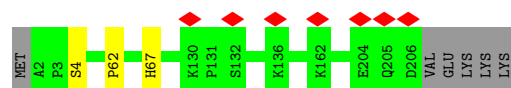
Chain KK:





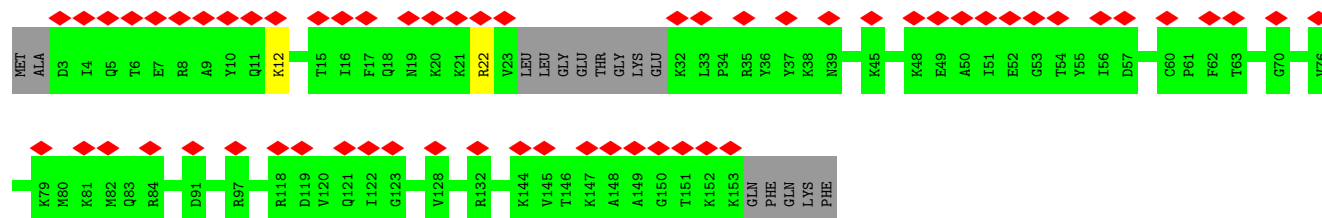
• Molecule 33: L13

Chain L: 96%



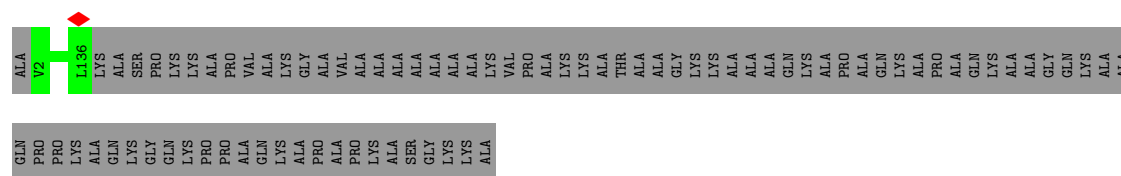
• Molecule 34: 40S ribosomal protein S11

Chain LL: 38% 89% 9%



• Molecule 35: 60S ribosomal protein L14

Chain M: 62% 38%



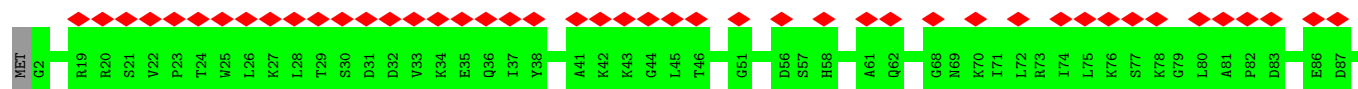
• Molecule 36: Ribosomal protein L15

Chain N: 99%



• Molecule 37: uS15

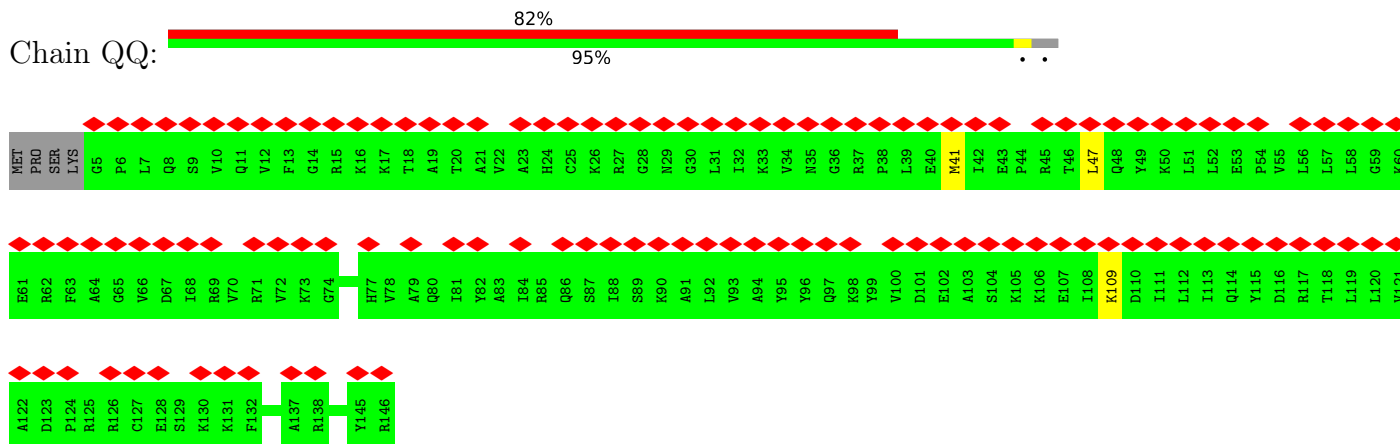
Chain NN: 45% 98% 57%





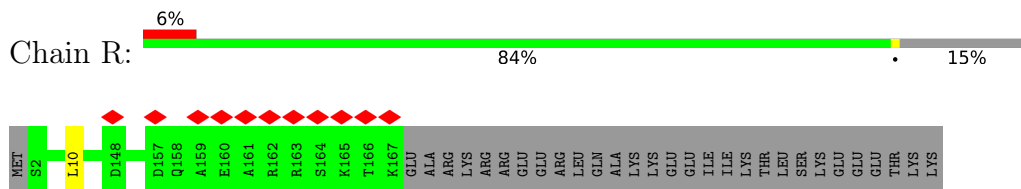
- Molecule 43: Ribosomal protein S16

Chain QQ:



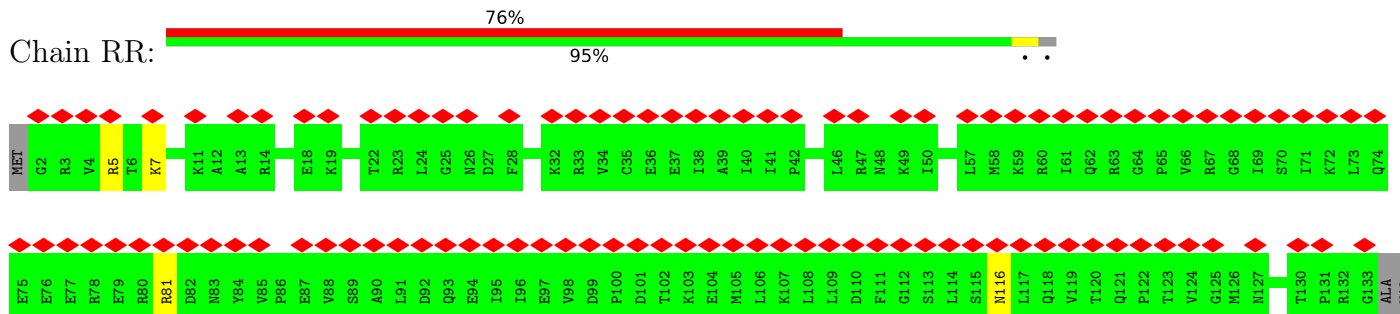
- Molecule 44: 60S ribosomal protein L19

Chain R:



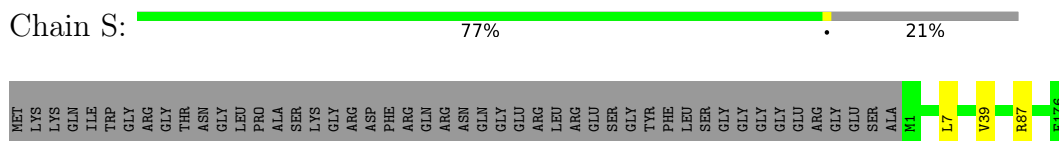
- Molecule 45: 40S ribosomal protein eS17

Chain RR:



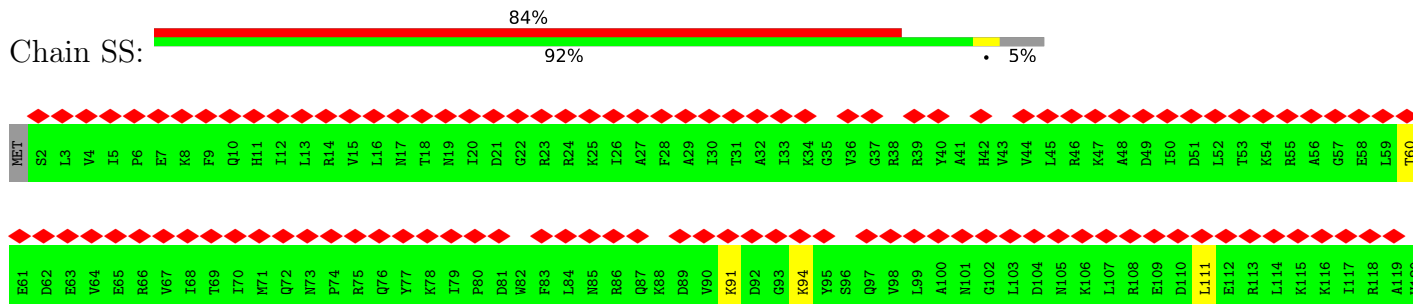
- Molecule 46: RPL18A

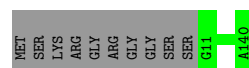
Chain S:



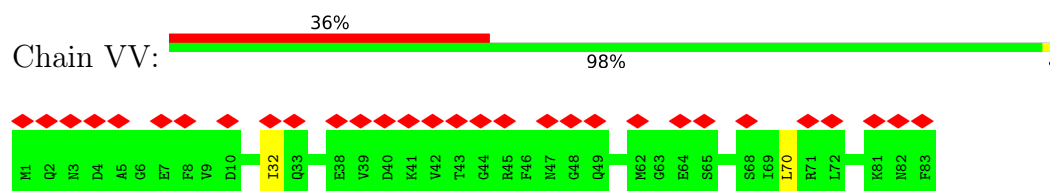
- Molecule 47: 40S ribosomal protein uS13

Chain SS:

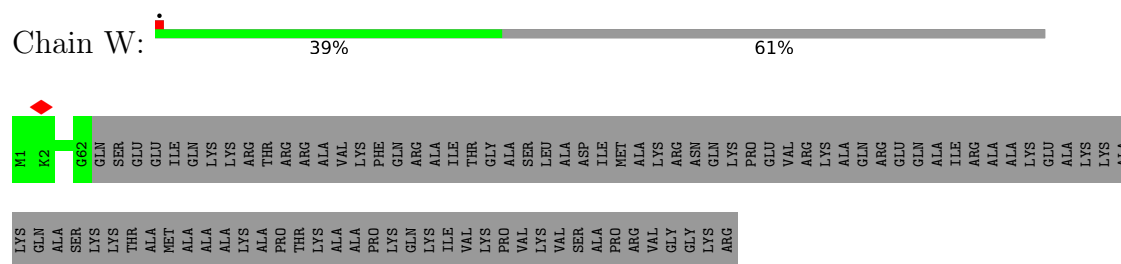




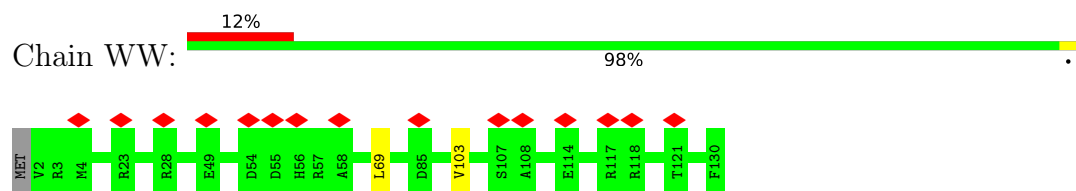
- Molecule 53: 40S ribosomal protein S21



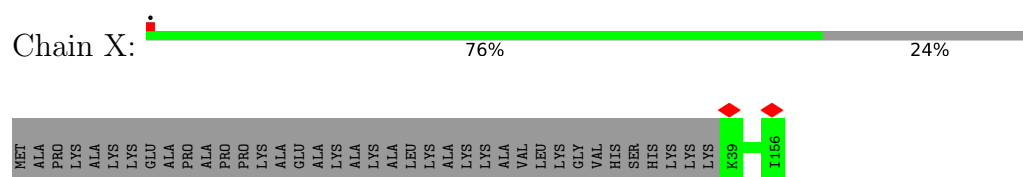
- Molecule 54: eL24



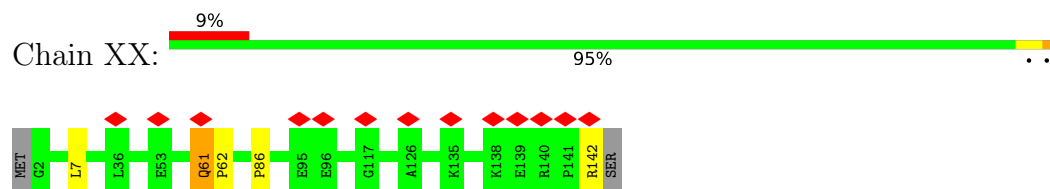
- Molecule 55: Ribosomal protein S15a



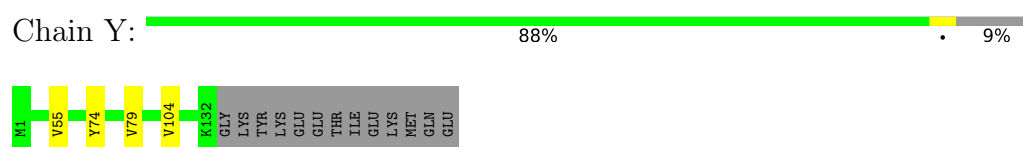
- Molecule 56: RPL23A



- Molecule 57: RPS23



- Molecule 58: Ribosomal protein L26




- Molecule 59: 40S ribosomal protein S24






ALA
LYS
PRO
LYS
LYS
ALA
GLN
GLN
THR
LYS
PRO
LYS
LYS
ALA
GLN
ALA
THR
PRO
ALA
ALA
VAL
PRO
ALA
GLN
GLN
PRO
LYS
GLY
ALA
GLN
PRO
LYS
ALA
ALA
PRO

• Molecule 64: eL30

Chain c:  82% 18%


MET
VAL
ALA
ALA
LYS
LYS
THR
LYS
LYS
SER
LEU
SER
SER
F14
R106
S107
MET
PRO
GLU
GLN
THR
GLY
GLU
LYS

• Molecule 65: eL31

Chain d:  85% 15%

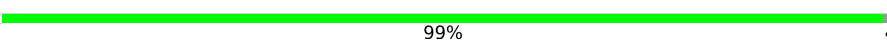
MET
ALA
PRO
ALA
LEU
LYS
GLY
GLY
GLU
LYS
LYS
LYS
GLY
ARG
SER
ALA
N18
E94
D95
E96
D97
D123
GLU
ASN

• Molecule 66: eL32

Chain e:  82% 18%

MET
CYS
LEU
LEU
ILE
SER
PHE
LEU
TYR
LYS
LYS
GLU
LYS
LYS
CYS
ILE
I42
L129
ARG
SER
GLU
GLU
ASN
GLU

• Molecule 67: eL33

Chain f:  99% .

MET
S2
I110

• Molecule 68: 60S ribosomal protein L34

Chain g:  94% . 5%

MET
V2
H73
A111
Q112
SER
GLN
LYS
LYS

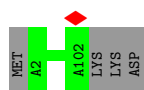
• Molecule 69: uL29

Chain h:  98% .

MET
ALA
K3
A123

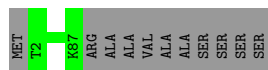
• Molecule 70: 60S ribosomal protein L36

Chain i:  96% .



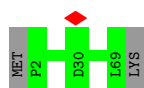
- Molecule 71: Ribosomal protein L37

Chain j: 89% 11%



- Molecule 72: eL38

Chain k: 97% .



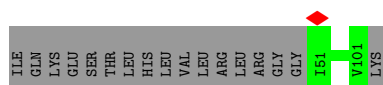
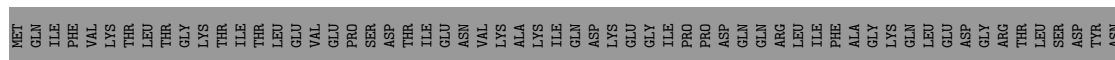
- Molecule 73: eL39

Chain l: 98% .



- Molecule 74: RPL40

Chain m: 40% 60%



- Molecule 75: 60s ribosomal protein l41

Chain n: 100%

There are no outlier residues recorded for this chain.

- Molecule 76: RPL36A

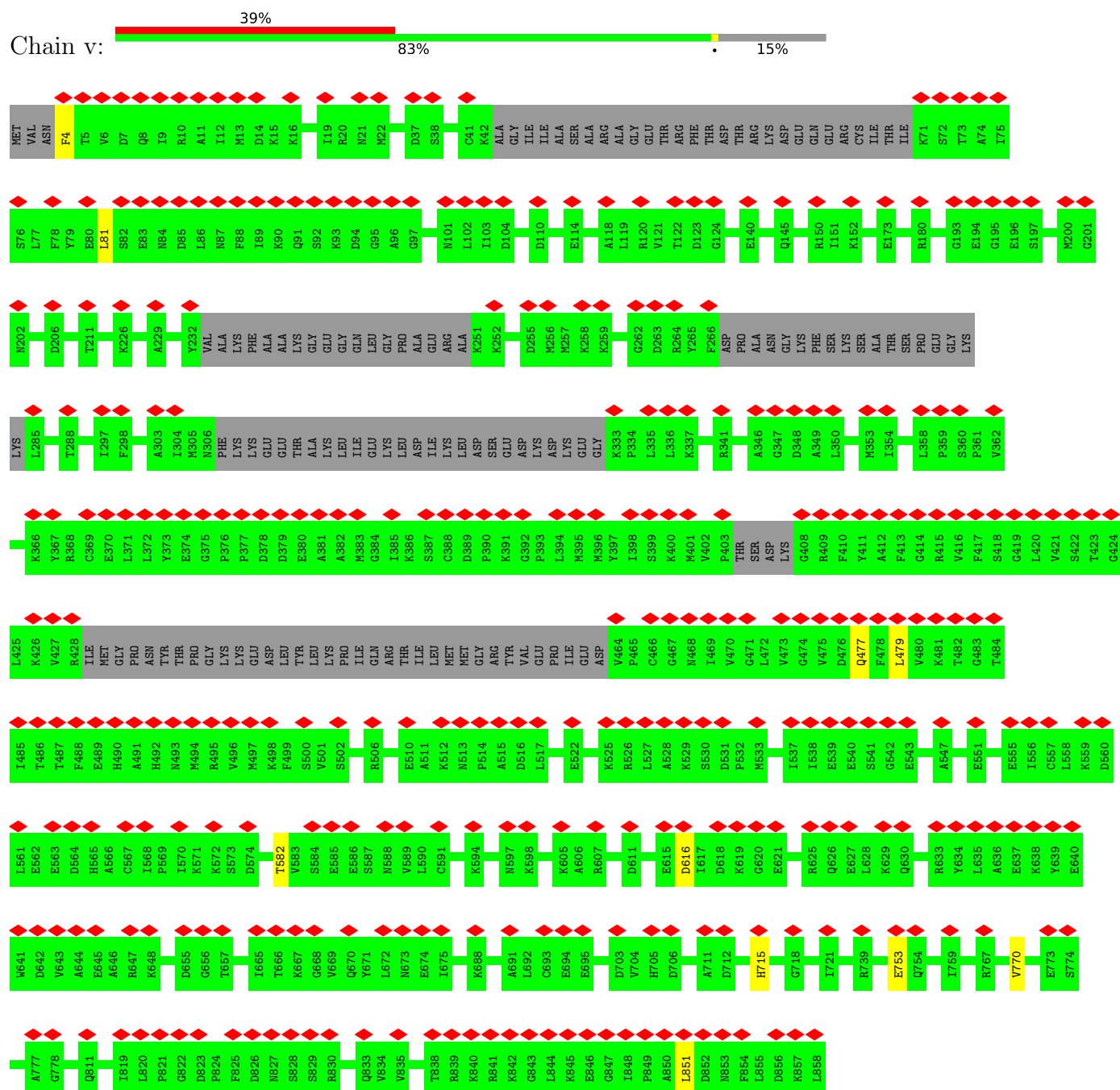
Chain o: 95% . .

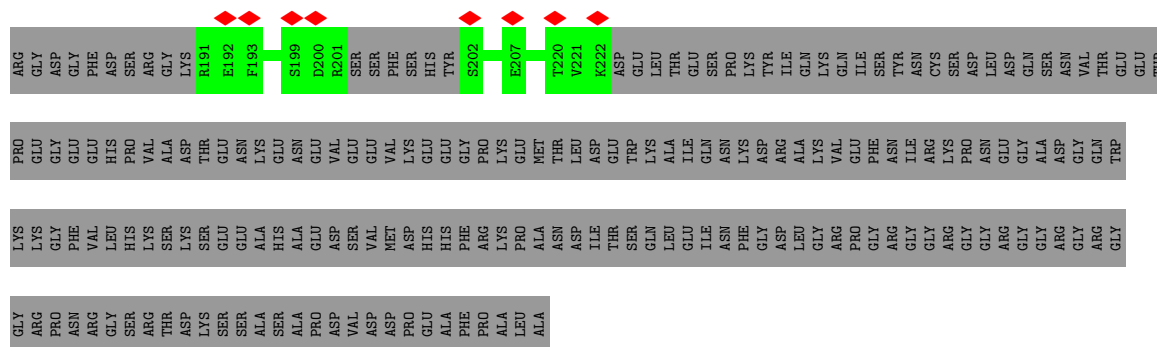


- Molecule 77: eL43

Chain p: 99% .

- Molecule 82: EEF2





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	479754	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	4.432	Depositor
Minimum map value	-1.954	Depositor
Average map value	0.034	Depositor
Map value standard deviation	0.100	Depositor
Recommended contour level	0.38	Depositor
Map size (Å)	508.8, 508.8, 508.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: B8T, 7MG, BGH, 2MG, E7G, DDE, A2M, B8W, 1MA, 5MU, I4U, 4AC, B8Q, UR3, B8N, PSU, OMC, 5MC, 5CT, E6G, 6MZ, E3C, P4U, B8K, MHG, MA6, ZN, OMG, B8H, P7G, OMU, MLZ, B9H, MG, B9B, M7A

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	x	0.30	0/1311	0.44	0/1762
2	5	0.22	0/78172	0.71	7/121809 (0.0%)
3	8	0.21	0/3406	0.69	0/5301
4	9	0.64	0/39723	1.15	275/61870 (0.4%)
5	A	0.25	0/1929	0.44	0/2586
6	AA	0.40	0/1747	0.63	0/2374
7	Aa	0.37	0/828	0.56	0/1109
8	B	0.24	0/3240	0.43	0/4339
9	BB	0.37	0/1756	0.72	4/2350 (0.2%)
10	Bb	0.33	0/665	0.59	0/891
11	C	0.23	0/2899	0.40	0/3895
12	CC	0.47	0/1753	0.64	0/2369
13	Cc	0.32	0/490	0.61	0/656
14	D	0.25	0/2407	0.40	0/3224
15	DD	0.39	0/1796	0.65	0/2417
16	Dd	0.41	0/470	0.61	0/623
17	E	0.24	0/1743	0.42	0/2337
18	EE	0.38	0/2118	0.70	5/2849 (0.2%)
19	Ee	0.36	0/447	0.55	0/587
20	F	0.24	0/1911	0.38	0/2549
21	FF	0.35	0/1492	0.68	2/2005 (0.1%)
22	G	0.23	0/1778	0.39	0/2397
23	GG	0.32	0/1946	0.68	3/2590 (0.1%)
24	Gg	0.32	0/2493	0.64	2/3394 (0.1%)
25	H	0.23	0/1502	0.42	0/2020
26	HH	0.37	0/1510	0.67	1/2022 (0.0%)
27	I	0.24	0/1678	0.40	0/2239
28	II	0.36	0/1715	0.65	0/2287
29	J	0.24	0/1367	0.40	0/1829
30	JJ	0.39	0/1550	0.63	0/2069

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	K	0.19	0/2836	0.68	0/4421
32	KK	0.39	0/834	0.65	1/1125 (0.1%)
33	L	0.23	0/1689	0.41	0/2261
34	LL	0.44	0/1195	0.60	0/1597
35	M	0.24	0/1138	0.38	0/1521
36	N	0.30	0/1746	0.44	0/2338
37	NN	0.36	0/1226	0.58	0/1649
38	O	0.24	0/1662	0.38	0/2222
39	OO	0.33	0/1029	0.63	0/1380
40	P	0.23	0/1259	0.40	0/1688
41	PP	0.34	0/1045	0.66	2/1396 (0.1%)
42	Q	0.24	0/1539	0.42	0/2054
43	QQ	0.33	0/1146	0.66	1/1534 (0.1%)
44	R	0.22	0/1399	0.37	0/1851
45	RR	0.33	0/1082	0.62	0/1452
46	S	0.25	0/1495	0.42	0/2005
47	SS	0.32	0/1208	0.67	0/1618
48	T	0.24	0/1320	0.40	0/1763
49	TT	0.30	0/1115	0.59	0/1493
50	U	0.24	0/814	0.40	0/1092
51	UU	0.33	0/805	0.61	0/1081
52	V	0.25	0/987	0.42	0/1324
53	VV	0.41	0/643	0.61	0/860
54	W	0.25	0/532	0.40	0/708
55	WW	0.48	0/1051	0.69	1/1406 (0.1%)
56	X	0.23	0/984	0.40	0/1323
57	XX	0.46	0/1116	0.64	1/1490 (0.1%)
58	Y	0.23	0/1119	0.40	0/1488
59	YY	0.33	0/1028	0.56	0/1366
60	Z	0.25	0/1130	0.40	0/1507
61	ZZ	0.31	0/604	0.69	0/810
62	a	0.24	0/1191	0.43	0/1590
63	b	0.23	0/819	0.35	0/1081
64	c	0.24	0/742	0.39	0/995
65	d	0.23	0/894	0.41	0/1204
66	e	0.23	0/1071	0.40	0/1429
67	f	0.25	0/895	0.45	0/1198
68	g	0.24	0/892	0.41	0/1189
69	h	0.22	0/1016	0.38	0/1341
70	i	0.23	0/832	0.37	0/1101
71	j	0.24	0/720	0.44	0/952
72	k	0.24	0/565	0.39	0/750
73	l	0.21	0/459	0.41	0/608

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
74	m	0.23	0/415	0.41	0/550
75	n	0.20	0/240	0.32	0/305
76	o	0.28	0/847	0.44	0/1117
77	p	0.23	0/718	0.42	0/953
78	r	0.23	0/1002	0.41	0/1344
79	s	0.24	0/1523	0.42	0/2055
80	s1	0.21	0/154	0.37	0/205
81	t	0.34	0/958	0.60	0/1288
82	v	0.24	0/5758	0.41	0/7779
83	w	0.23	0/257	0.43	0/339
All	All	0.36	0/224586	0.75	305/327945 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	AA	0	2
15	DD	0	1
18	EE	0	1
21	FF	0	1
24	Gg	0	1
28	II	0	1
41	PP	0	1
47	SS	0	1
51	UU	0	1
53	VV	0	1
57	XX	0	1
All	All	0	12

There are no bond length outliers.

The worst 5 of 305 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	9	1116	C	N1-C2-O2	12.77	126.56	118.90
4	9	1116	C	C2-N1-C1'	11.82	131.81	118.80
4	9	501	C	N1-C2-O2	11.01	125.50	118.90
4	9	501	C	C2-N1-C1'	10.28	130.11	118.80
4	9	1116	C	N3-C2-O2	-10.12	114.81	121.90

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	AA	42	LYS	Peptide
6	AA	43	SER	Peptide
15	DD	153	VAL	Peptide
18	EE	132	GLY	Peptide
21	FF	41	VAL	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	x	159/217 (73%)	151 (95%)	8 (5%)	0	100	100
5	A	245/257 (95%)	233 (95%)	12 (5%)	0	100	100
6	AA	215/295 (73%)	206 (96%)	9 (4%)	0	100	100
7	Aa	99/115 (86%)	89 (90%)	10 (10%)	0	100	100
8	B	392/403 (97%)	382 (97%)	10 (3%)	0	100	100
9	BB	211/264 (80%)	203 (96%)	8 (4%)	0	100	100
10	Bb	81/84 (96%)	78 (96%)	3 (4%)	0	100	100
11	C	355/413 (86%)	344 (97%)	11 (3%)	0	100	100
12	CC	219/293 (75%)	205 (94%)	14 (6%)	0	100	100
13	Cc	60/69 (87%)	57 (95%)	3 (5%)	0	100	100
14	D	287/297 (97%)	281 (98%)	6 (2%)	0	100	100
15	DD	226/243 (93%)	216 (96%)	10 (4%)	0	100	100
16	Dd	53/56 (95%)	48 (91%)	5 (9%)	0	100	100
17	E	205/291 (70%)	197 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	EE	260/263 (99%)	244 (94%)	16 (6%)	0	100	100
19	Ee	53/133 (40%)	50 (94%)	3 (6%)	0	100	100
20	F	223/249 (90%)	216 (97%)	7 (3%)	0	100	100
21	FF	181/204 (89%)	162 (90%)	19 (10%)	0	100	100
22	G	211/266 (79%)	208 (99%)	3 (1%)	0	100	100
23	GG	235/249 (94%)	224 (95%)	11 (5%)	0	100	100
24	Gg	311/317 (98%)	281 (90%)	30 (10%)	0	100	100
25	H	182/192 (95%)	179 (98%)	3 (2%)	0	100	100
26	HH	181/432 (42%)	173 (96%)	8 (4%)	0	100	100
27	I	198/214 (92%)	192 (97%)	6 (3%)	0	100	100
28	II	204/208 (98%)	185 (91%)	19 (9%)	0	100	100
29	J	166/178 (93%)	165 (99%)	1 (1%)	0	100	100
30	JJ	183/194 (94%)	180 (98%)	3 (2%)	0	100	100
32	KK	94/165 (57%)	86 (92%)	8 (8%)	0	100	100
33	L	203/211 (96%)	198 (98%)	4 (2%)	1 (0%)	29	35
34	LL	139/158 (88%)	131 (94%)	8 (6%)	0	100	100
35	M	133/218 (61%)	130 (98%)	3 (2%)	0	100	100
36	N	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
37	NN	147/151 (97%)	138 (94%)	9 (6%)	0	100	100
38	O	197/203 (97%)	193 (98%)	4 (2%)	0	100	100
39	OO	134/151 (89%)	123 (92%)	11 (8%)	0	100	100
40	P	150/187 (80%)	147 (98%)	3 (2%)	0	100	100
41	PP	123/145 (85%)	118 (96%)	5 (4%)	0	100	100
42	Q	185/188 (98%)	177 (96%)	8 (4%)	0	100	100
43	QQ	140/146 (96%)	132 (94%)	8 (6%)	0	100	100
44	R	164/196 (84%)	162 (99%)	2 (1%)	0	100	100
45	RR	130/135 (96%)	121 (93%)	9 (7%)	0	100	100
46	S	174/224 (78%)	168 (97%)	6 (3%)	0	100	100
47	SS	142/152 (93%)	135 (95%)	7 (5%)	0	100	100
48	T	156/160 (98%)	151 (97%)	5 (3%)	0	100	100
49	TT	139/145 (96%)	133 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	U	96/141 (68%)	93 (97%)	3 (3%)	0	100	100
51	UU	98/119 (82%)	94 (96%)	4 (4%)	0	100	100
52	V	128/140 (91%)	127 (99%)	1 (1%)	0	100	100
53	VV	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
54	W	60/157 (38%)	59 (98%)	1 (2%)	0	100	100
55	WW	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
56	X	116/156 (74%)	115 (99%)	1 (1%)	0	100	100
57	XX	139/143 (97%)	132 (95%)	4 (3%)	3 (2%)	6	5
58	Y	130/145 (90%)	128 (98%)	2 (2%)	0	100	100
59	YY	122/133 (92%)	120 (98%)	2 (2%)	0	100	100
60	Z	133/136 (98%)	125 (94%)	8 (6%)	0	100	100
61	ZZ	73/124 (59%)	70 (96%)	3 (4%)	0	100	100
62	a	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
63	b	94/245 (38%)	92 (98%)	2 (2%)	0	100	100
64	c	92/115 (80%)	91 (99%)	1 (1%)	0	100	100
65	d	104/125 (83%)	101 (97%)	3 (3%)	0	100	100
66	e	126/157 (80%)	122 (97%)	4 (3%)	0	100	100
67	f	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
68	g	109/117 (93%)	107 (98%)	2 (2%)	0	100	100
69	h	119/123 (97%)	119 (100%)	0	0	100	100
70	i	99/105 (94%)	98 (99%)	1 (1%)	0	100	100
71	j	84/97 (87%)	83 (99%)	1 (1%)	0	100	100
72	k	66/70 (94%)	66 (100%)	0	0	100	100
73	l	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
74	m	48/128 (38%)	47 (98%)	1 (2%)	0	100	100
75	n	23/25 (92%)	23 (100%)	0	0	100	100
76	o	100/106 (94%)	98 (98%)	2 (2%)	0	100	100
77	p	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
78	r	121/137 (88%)	118 (98%)	3 (2%)	0	100	100
79	s	194/318 (61%)	185 (95%)	8 (4%)	1 (0%)	29	35
80	s1	14/109 (13%)	13 (93%)	1 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
81	t	121/154 (79%)	117 (97%)	4 (3%)	0	100	100
82	v	711/858 (83%)	684 (96%)	27 (4%)	0	100	100
83	w	30/407 (7%)	28 (93%)	2 (7%)	0	100	100
All	All	12093/14939 (81%)	11610 (96%)	478 (4%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
57	XX	62	PRO
57	XX	61	GLN
57	XX	86	PRO
79	s	118	PRO
33	L	62	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	x	146/195 (75%)	143 (98%)	3 (2%)	53	70
5	A	189/199 (95%)	187 (99%)	2 (1%)	73	86
6	AA	180/245 (74%)	179 (99%)	1 (1%)	86	94
7	Aa	88/98 (90%)	87 (99%)	1 (1%)	73	86
8	B	342/348 (98%)	338 (99%)	4 (1%)	71	84
9	BB	194/231 (84%)	190 (98%)	4 (2%)	53	70
10	Bb	75/76 (99%)	75 (100%)	0	100	100
11	C	298/336 (89%)	295 (99%)	3 (1%)	76	87
12	CC	187/224 (84%)	185 (99%)	2 (1%)	73	86
13	Cc	55/62 (89%)	52 (94%)	3 (6%)	21	30
14	D	245/250 (98%)	241 (98%)	4 (2%)	62	78
15	DD	190/202 (94%)	186 (98%)	4 (2%)	53	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	Dd	48/49 (98%)	46 (96%)	2 (4%)	30	42
17	E	189/251 (75%)	187 (99%)	2 (1%)	73	86
18	EE	224/225 (100%)	221 (99%)	3 (1%)	69	82
19	Ee	46/106 (43%)	43 (94%)	3 (6%)	17	23
20	F	196/218 (90%)	196 (100%)	0	100	100
21	FF	158/170 (93%)	152 (96%)	6 (4%)	33	47
22	G	188/224 (84%)	186 (99%)	2 (1%)	73	86
23	GG	207/218 (95%)	199 (96%)	8 (4%)	32	46
24	Gg	272/275 (99%)	268 (98%)	4 (2%)	65	79
25	H	166/171 (97%)	165 (99%)	1 (1%)	86	94
26	HH	165/360 (46%)	164 (99%)	1 (1%)	86	94
27	I	172/181 (95%)	169 (98%)	3 (2%)	60	76
28	II	178/180 (99%)	173 (97%)	5 (3%)	43	60
29	J	141/149 (95%)	140 (99%)	1 (1%)	84	92
30	JJ	161/168 (96%)	158 (98%)	3 (2%)	57	73
32	KK	87/136 (64%)	86 (99%)	1 (1%)	73	86
33	L	170/176 (97%)	168 (99%)	2 (1%)	71	84
34	LL	130/142 (92%)	128 (98%)	2 (2%)	65	79
35	M	115/160 (72%)	115 (100%)	0	100	100
36	N	171/172 (99%)	169 (99%)	2 (1%)	71	84
37	NN	130/131 (99%)	129 (99%)	1 (1%)	81	91
38	O	171/174 (98%)	168 (98%)	3 (2%)	59	75
39	OO	106/119 (89%)	105 (99%)	1 (1%)	78	89
40	P	133/165 (81%)	131 (98%)	2 (2%)	65	79
41	PP	111/130 (85%)	106 (96%)	5 (4%)	27	39
42	Q	164/165 (99%)	164 (100%)	0	100	100
43	QQ	117/121 (97%)	115 (98%)	2 (2%)	60	76
44	R	147/175 (84%)	146 (99%)	1 (1%)	84	92
45	RR	119/121 (98%)	115 (97%)	4 (3%)	37	51
46	S	156/192 (81%)	153 (98%)	3 (2%)	57	73
47	SS	125/132 (95%)	122 (98%)	3 (2%)	49	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	T	139/140 (99%)	137 (99%)	2 (1%)	67	81
49	TT	111/115 (96%)	108 (97%)	3 (3%)	44	61
50	U	88/127 (69%)	88 (100%)	0	100	100
51	UU	92/107 (86%)	92 (100%)	0	100	100
52	V	100/107 (94%)	100 (100%)	0	100	100
53	VV	67/67 (100%)	66 (98%)	1 (2%)	65	79
54	W	54/126 (43%)	54 (100%)	0	100	100
55	WW	112/113 (99%)	111 (99%)	1 (1%)	78	89
56	X	106/133 (80%)	106 (100%)	0	100	100
57	XX	113/115 (98%)	112 (99%)	1 (1%)	78	89
58	Y	123/135 (91%)	119 (97%)	4 (3%)	38	53
59	YY	107/115 (93%)	105 (98%)	2 (2%)	57	73
60	Z	117/118 (99%)	117 (100%)	0	100	100
61	ZZ	66/102 (65%)	66 (100%)	0	100	100
62	a	119/120 (99%)	119 (100%)	0	100	100
63	b	80/184 (44%)	79 (99%)	1 (1%)	69	82
64	c	80/98 (82%)	80 (100%)	0	100	100
65	d	97/110 (88%)	97 (100%)	0	100	100
66	e	114/141 (81%)	114 (100%)	0	100	100
67	f	88/89 (99%)	88 (100%)	0	100	100
68	g	95/100 (95%)	94 (99%)	1 (1%)	73	86
69	h	109/110 (99%)	109 (100%)	0	100	100
70	i	85/89 (96%)	85 (100%)	0	100	100
71	j	73/80 (91%)	73 (100%)	0	100	100
72	k	63/65 (97%)	63 (100%)	0	100	100
73	l	47/48 (98%)	47 (100%)	0	100	100
74	m	46/115 (40%)	46 (100%)	0	100	100
75	n	24/24 (100%)	24 (100%)	0	100	100
76	o	90/94 (96%)	89 (99%)	1 (1%)	73	86
77	p	74/75 (99%)	74 (100%)	0	100	100
78	r	107/121 (88%)	106 (99%)	1 (1%)	78	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
79	s	163/258 (63%)	163 (100%)	0	100	100
80	s1	18/97 (19%)	17 (94%)	1 (6%)	21	29
81	t	105/128 (82%)	101 (96%)	4 (4%)	33	47
82	v	619/729 (85%)	610 (98%)	9 (2%)	65	79
83	w	26/327 (8%)	26 (100%)	0	100	100
All	All	10569/12644 (84%)	10430 (99%)	139 (1%)	70	82

5 of 139 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
58	Y	55	VAL
59	YY	32	LYS
82	v	4	PHE
22	G	249	ARG
22	G	162	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 119 such sidechains are listed below:

Mol	Chain	Res	Type
38	O	180	GLN
79	s	39	GLN
50	U	44	GLN
78	r	95	HIS
83	w	206	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	5	3290/3598 (91%)	480 (14%)	38 (1%)
3	8	140/151 (92%)	14 (10%)	0
31	K	118/120 (98%)	7 (5%)	0
4	9	1670/1698 (98%)	387 (23%)	18 (1%)
All	All	5218/5567 (93%)	888 (17%)	56 (1%)

5 of 888 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	5	17	A

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Mol	Chain	Res	Type
2	5	25	A
2	5	39	A
2	5	42	A
2	5	56	A

5 of 56 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	5	2506	A
4	9	1664	A
2	5	4888	G
4	9	1637	A
4	9	1137	U

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

138 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	OMG	5	4200	2	18,26,27	2.58	8 (44%)	19,38,41	1.51	4 (21%)
2	5MC	5	4451	2	18,22,23	3.93	7 (38%)	26,32,35	1.05	1 (3%)
4	A2M	9	27	4	18,25,26	4.68	9 (50%)	18,36,39	2.69	4 (22%)
2	PSU	5	4407	2	18,21,22	4.92	7 (38%)	22,30,33	1.76	5 (22%)
2	B8W	5	4476	2	18,26,27	2.03	2 (11%)	21,38,41	2.78	8 (38%)
4	4AC	9	1842	4	21,24,25	3.13	10 (47%)	29,34,37	1.18	4 (13%)
2	B8T	5	4675	2	19,22,23	3.25	8 (42%)	26,31,34	0.91	1 (3%)
2	P4U	5	1352	2	21,24,25	4.09	7 (33%)	27,33,36	0.98	1 (3%)
2	OMG	5	4874	2	18,26,27	2.59	8 (44%)	19,38,41	1.53	4 (21%)
4	A2M	9	166	4	18,25,26	4.79	9 (50%)	18,36,39	2.78	4 (22%)
2	B8T	5	4487	2	19,22,23	3.25	8 (42%)	26,31,34	0.85	1 (3%)
2	PSU	5	4297	2	18,21,22	4.91	7 (38%)	22,30,33	1.86	5 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	OMG	9	683	4	18,26,27	2.48	8 (44%)	19,38,41	1.55	4 (21%)
2	2MG	5	1521	2	18,26,27	2.76	7 (38%)	16,38,41	1.48	4 (25%)
4	OMC	9	517	4	19,22,23	2.84	7 (36%)	26,31,34	0.64	0
2	B9B	5	237	2	21,28,29	1.99	3 (14%)	23,40,43	1.91	5 (21%)
2	PSU	5	3768	2	18,21,22	4.97	7 (38%)	22,30,33	1.71	6 (27%)
2	B8W	5	4533	2,84	18,26,27	2.00	2 (11%)	21,38,41	2.55	7 (33%)
2	A2M	5	4575	2	18,25,26	4.50	7 (38%)	18,36,39	2.83	3 (16%)
2	6MZ	5	4224	2	18,25,26	2.19	3 (16%)	16,36,39	2.05	4 (25%)
2	UR3	5	4534	2	19,22,23	3.20	7 (36%)	26,32,35	1.31	3 (11%)
2	E6G	5	4359	2	20,27,28	2.04	3 (15%)	22,39,42	2.16	7 (31%)
4	OMC	9	1710	4	19,22,23	2.94	7 (36%)	26,31,34	0.92	1 (3%)
2	I4U	5	1663	2	21,24,25	3.63	9 (42%)	27,34,37	0.95	1 (3%)
2	OMG	5	4498	2	18,26,27	2.57	8 (44%)	19,38,41	1.51	4 (21%)
2	B9B	5	2758	2,84	21,28,29	1.98	3 (14%)	23,40,43	1.87	4 (17%)
2	A2M	5	3789	2	18,25,26	4.36	8 (44%)	18,36,39	2.83	3 (16%)
2	BGH	5	3903	2,84	25,29,30	4.62	18 (72%)	31,43,46	2.35	12 (38%)
2	MHG	5	4375	2	29,32,33	3.95	11 (37%)	34,46,49	2.29	10 (29%)
2	B8Q	5	1460	2	17,22,23	2.93	5 (29%)	22,32,35	2.08	4 (18%)
2	OMG	5	2054	2	18,26,27	2.56	8 (44%)	19,38,41	1.54	4 (21%)
3	OMU	8	14	2,3	19,22,23	3.00	8 (42%)	26,31,34	1.69	4 (15%)
4	MA6	9	1850	4	19,26,27	1.03	1 (5%)	18,38,41	2.81	2 (11%)
2	B9B	5	1578	2	21,28,29	1.98	3 (14%)	23,40,43	1.85	5 (21%)
2	A2M	5	398	2	18,25,26	4.49	7 (38%)	18,36,39	2.86	3 (16%)
2	7MG	5	4554	2	22,26,27	3.95	10 (45%)	29,39,42	1.99	9 (31%)
2	A2M	5	1875	2,84	18,25,26	4.51	7 (38%)	18,36,39	2.87	3 (16%)
4	OMU	9	121	4	19,22,23	2.96	8 (42%)	26,31,34	1.77	5 (19%)
2	OMG	5	1526	2	18,26,27	2.58	8 (44%)	19,38,41	1.51	4 (21%)
4	PSU	9	822	4	18,21,22	1.03	2 (11%)	22,30,33	1.93	5 (22%)
4	PSU	9	612	4	18,21,22	0.99	1 (5%)	22,30,33	1.74	4 (18%)
2	1MA	5	1326	2,84	16,25,26	4.04	4 (25%)	18,37,40	1.77	3 (16%)
2	B8K	5	4694	2	24,28,29	3.38	11 (45%)	30,42,45	2.33	11 (36%)
2	7MG	5	1609	2	22,26,27	3.92	10 (45%)	29,39,42	2.03	9 (31%)
4	B8Q	9	1219	4	17,22,23	2.92	4 (23%)	22,32,35	2.34	7 (31%)
2	B8K	5	3901	2	24,28,29	3.30	11 (45%)	30,42,45	2.28	11 (36%)
2	A2M	5	1528	2	18,25,26	4.47	7 (38%)	18,36,39	2.87	3 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	A2M	9	1031	4	18,25,26	4.75	8 (44%)	18,36,39	2.78	4 (22%)
2	5MC	5	3786	2	18,22,23	3.91	7 (38%)	26,32,35	1.03	2 (7%)
2	A2M	5	1538	2,84	18,25,26	4.49	7 (38%)	18,36,39	2.89	3 (16%)
2	P7G	5	3884	2	24,28,29	4.14	11 (45%)	27,41,44	1.60	3 (11%)
2	OMG	5	4641	2	18,26,27	2.57	8 (44%)	19,38,41	1.55	4 (21%)
2	B8H	5	4300	2	19,22,23	6.53	6 (31%)	22,32,35	2.34	5 (22%)
2	A2M	5	2405	2,84	18,25,26	4.48	7 (38%)	18,36,39	2.84	3 (16%)
2	UR3	5	4601	2	19,22,23	3.21	7 (36%)	26,32,35	1.29	2 (7%)
2	OMG	5	2428	2	18,26,27	2.58	8 (44%)	19,38,41	1.48	4 (21%)
2	A2M	5	3722	2	18,25,26	4.49	7 (38%)	18,36,39	2.85	3 (16%)
4	PSU	9	119	4	18,21,22	0.94	1 (5%)	22,30,33	1.60	5 (22%)
4	MA6	9	1851	4	19,26,27	0.99	1 (5%)	18,38,41	2.69	2 (11%)
4	5MU	9	814	4	19,22,23	4.87	7 (36%)	28,32,35	3.59	12 (42%)
2	B8W	5	4189	2	18,26,27	2.04	2 (11%)	21,38,41	2.43	6 (28%)
2	OMC	5	2426	2,84,40	19,22,23	3.35	8 (42%)	26,31,34	0.76	0
2	OMG	5	3796	2	18,26,27	2.57	8 (44%)	19,38,41	1.51	4 (21%)
2	A2M	5	3727	2,70	18,25,26	4.51	7 (38%)	18,36,39	2.84	3 (16%)
2	5MC	5	4339	2	18,22,23	3.92	7 (38%)	26,32,35	1.04	2 (7%)
2	A2M	5	1330	2	18,25,26	4.44	7 (38%)	18,36,39	2.80	3 (16%)
4	A2M	9	159	4	18,25,26	4.83	9 (50%)	18,36,39	2.75	4 (22%)
2	OMG	5	1887	2	18,26,27	2.58	8 (44%)	19,38,41	1.54	4 (21%)
2	OMG	5	2368	2	18,26,27	2.57	8 (44%)	19,38,41	1.55	4 (21%)
2	PSU	5	1586	2	18,21,22	4.95	7 (38%)	22,30,33	1.85	5 (22%)
2	OMG	5	4374	2	18,26,27	2.58	8 (44%)	19,38,41	1.50	4 (21%)
4	E3C	9	568	4	18,23,24	3.37	6 (33%)	21,33,36	2.23	5 (23%)
4	UR3	9	1830	4	19,22,23	2.69	6 (31%)	26,32,35	1.57	4 (15%)
2	I4U	5	4198	2	21,24,25	3.61	8 (38%)	27,34,37	1.00	1 (3%)
4	A2M	9	1678	4	18,25,26	4.81	9 (50%)	18,36,39	2.59	3 (16%)
4	OMG	9	509	4	18,26,27	2.46	8 (44%)	19,38,41	1.46	4 (21%)
2	OMC	5	2865	2	19,22,23	3.33	8 (42%)	26,31,34	0.69	0
2	OMU	5	4310	2	19,22,23	3.03	8 (42%)	26,31,34	1.71	5 (19%)
2	OMG	5	2777	2	18,26,27	2.60	8 (44%)	19,38,41	1.57	4 (21%)
2	PSU	5	3733	2	18,21,22	4.95	7 (38%)	22,30,33	1.82	5 (22%)
2	B8W	5	4133	2	18,26,27	2.06	2 (11%)	21,38,41	2.34	6 (28%)
2	A2M	5	4527	2,84	18,25,26	4.50	7 (38%)	18,36,39	2.81	3 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	2MG	5	4876	2	18,26,27	2.72	7 (38%)	16,38,41	1.55	4 (25%)
2	OMC	5	3705	2,84	19,22,23	3.31	8 (42%)	26,31,34	0.75	0
4	4AC	9	1337	4	21,24,25	3.19	9 (42%)	29,34,37	1.23	3 (10%)
2	B8W	5	2384	2	18,26,27	2.03	2 (11%)	21,38,41	2.23	5 (23%)
2	PSU	5	4535	2	18,21,22	4.93	7 (38%)	22,30,33	1.81	5 (22%)
74	MLZ	m	72	74	8,9,10	0.76	0	4,9,11	0.64	0
2	PSU	5	4504	2	18,21,22	4.95	7 (38%)	22,30,33	1.88	5 (22%)
4	PSU	9	1081	4	18,21,22	1.06	1 (5%)	22,30,33	1.77	5 (22%)
4	A2M	9	668	4	18,25,26	4.68	8 (44%)	18,36,39	2.70	5 (27%)
2	PSU	5	1687	2	18,21,22	4.91	7 (38%)	22,30,33	1.84	5 (22%)
2	PSU	5	4454	2,84	18,21,22	4.95	7 (38%)	22,30,33	1.84	5 (22%)
4	OMC	9	174	4	19,22,23	2.95	7 (36%)	26,31,34	0.81	1 (3%)
2	2MG	5	729	2	18,26,27	2.75	6 (33%)	16,38,41	1.36	3 (18%)
2	E7G	5	1801	2	24,27,28	3.87	11 (45%)	30,40,43	2.22	10 (33%)
2	UR3	5	1870	2	19,22,23	3.20	7 (36%)	26,32,35	1.27	3 (11%)
2	OMC	5	3891	2	19,22,23	3.34	8 (42%)	26,31,34	0.72	0
2	1MA	5	4419	2	16,25,26	4.01	4 (25%)	18,37,40	1.71	3 (16%)
11	MLZ	C	333	11	8,9,10	0.77	0	4,9,11	0.67	0
2	OMC	5	2369	2	19,22,23	3.34	8 (42%)	26,31,34	0.75	0
2	OMC	5	2808	2	19,22,23	3.33	8 (42%)	26,31,34	0.71	0
2	PSU	5	4632	2	18,21,22	4.90	7 (38%)	22,30,33	1.93	5 (22%)
2	PSU	5	2512	2	18,21,22	4.95	7 (38%)	22,30,33	1.88	5 (22%)
2	E7G	5	2301	2	24,27,28	3.86	11 (45%)	30,40,43	2.24	10 (33%)
2	A2M	5	3871	2	18,25,26	4.46	7 (38%)	18,36,39	2.78	3 (16%)
2	B8H	5	1864	2	19,22,23	6.50	6 (31%)	22,32,35	2.35	5 (22%)
4	PSU	9	823	4	18,21,22	1.09	1 (5%)	22,30,33	1.83	4 (18%)
4	OMU	9	116	4	19,22,23	2.88	7 (36%)	26,31,34	1.75	5 (19%)
2	OMG	5	1320	2	18,26,27	2.60	8 (44%)	19,38,41	1.58	5 (26%)
2	A2M	5	2367	2,84	18,25,26	4.49	7 (38%)	18,36,39	2.86	3 (16%)
2	OMC	5	4540	2	19,22,23	3.34	8 (42%)	26,31,34	0.74	0
2	OMG	5	373	2	18,26,27	2.55	8 (44%)	19,38,41	1.56	4 (21%)
2	P7G	5	1913	2	24,28,29	4.23	11 (45%)	27,41,44	1.56	3 (11%)
2	OMG	5	4627	2	18,26,27	2.58	8 (44%)	19,38,41	1.56	4 (21%)
4	B8N	9	1248	4	24,29,30	2.79	6 (25%)	29,42,45	1.75	5 (17%)
4	5MC	9	1374	4	18,22,23	3.69	7 (38%)	26,32,35	1.34	4 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	PSU	9	1243	4	18,21,22	1.06	1 (5%)	22,30,33	1.83	4 (18%)
4	OMC	9	1703	4	19,22,23	2.94	7 (36%)	26,31,34	0.83	1 (3%)
81	5CT	t	51	81	13,14,15	0.66	0	9,15,17	1.20	1 (11%)
2	OMC	5	3913	2	19,22,23	3.34	8 (42%)	26,31,34	0.71	0
2	7MG	5	2526	2	22,26,27	3.92	10 (45%)	29,39,42	2.04	9 (31%)
2	M7A	5	4568	2	20,25,26	2.02	3 (15%)	28,37,40	3.67	8 (28%)
2	OMU	5	4624	2,52	19,22,23	3.00	8 (42%)	26,31,34	1.69	5 (19%)
2	A2M	5	3829	2	18,25,26	4.49	7 (38%)	18,36,39	2.79	3 (16%)
4	OMG	9	644	4	18,26,27	2.47	8 (44%)	19,38,41	1.52	4 (21%)
2	PSU	5	4446	2	18,21,22	4.95	7 (38%)	22,30,33	1.86	5 (22%)
2	PSU	5	1681	2	18,21,22	4.95	8 (44%)	22,30,33	1.88	5 (22%)
2	B9H	5	2790	2	20,25,26	2.95	5 (25%)	22,35,38	1.47	3 (13%)
2	OMG	5	1629	2	18,26,27	2.59	8 (44%)	19,38,41	1.50	4 (21%)
2	PSU	5	4640	2,65	18,21,22	4.96	7 (38%)	22,30,33	1.89	5 (22%)
4	M7A	9	1806	4	20,25,26	2.04	3 (15%)	28,37,40	3.72	8 (28%)
4	A2M	9	484	4	18,25,26	4.71	9 (50%)	18,36,39	2.71	3 (16%)
82	DDE	v	715	82	14,20,21	1.02	1 (7%)	14,28,30	1.09	1 (7%)
4	6MZ	9	1832	4	18,25,26	2.24	3 (16%)	16,36,39	1.53	1 (6%)
2	5MU	5	4087	2	19,22,23	4.98	7 (36%)	28,32,35	3.62	9 (32%)
2	OMC	5	3873	2	19,22,23	3.34	8 (42%)	26,31,34	0.74	0
2	PSU	5	3719	2	18,21,22	4.94	7 (38%)	22,30,33	1.86	5 (22%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMG	5	4200	2	-	0/5/27/28	0/3/3/3
2	5MC	5	4451	2	-	4/7/25/26	0/2/2/2
4	A2M	9	27	4	-	0/5/27/28	0/3/3/3
2	PSU	5	4407	2	-	2/7/25/26	0/2/2/2
2	B8W	5	4476	2	-	2/5/27/28	0/3/3/3
4	4AC	9	1842	4	-	0/11/29/30	0/2/2/2
2	B8T	5	4675	2	-	1/7/27/28	0/2/2/2
2	P4U	5	1352	2	-	3/10/29/30	0/2/2/2
2	OMG	5	4874	2	-	4/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	A2M	9	166	4	-	2/5/27/28	0/3/3/3
2	B8T	5	4487	2	-	0/7/27/28	0/2/2/2
2	PSU	5	4297	2	-	2/7/25/26	0/2/2/2
4	OMG	9	683	4	-	2/5/27/28	0/3/3/3
2	2MG	5	1521	2	-	0/5/27/28	0/3/3/3
4	OMC	9	517	4	-	2/9/27/28	0/2/2/2
2	B9B	5	237	2	-	2/7/29/30	0/3/3/3
2	PSU	5	3768	2	-	4/7/25/26	0/2/2/2
2	B8W	5	4533	2,84	-	2/5/27/28	0/3/3/3
2	A2M	5	4575	2	-	0/5/27/28	0/3/3/3
2	6MZ	5	4224	2	-	0/5/27/28	0/3/3/3
2	UR3	5	4534	2	-	2/7/25/26	0/2/2/2
2	E6G	5	4359	2	-	2/6/28/29	0/3/3/3
4	OMC	9	1710	4	-	0/9/27/28	0/2/2/2
2	I4U	5	1663	2	-	1/9/29/30	0/2/2/2
2	OMG	5	4498	2	-	0/5/27/28	0/3/3/3
2	B9B	5	2758	2,84	-	2/7/29/30	0/3/3/3
2	A2M	5	3789	2	-	2/5/27/28	0/3/3/3
2	BGH	5	3903	2,84	-	2/13/43/44	0/3/3/3
2	MHG	5	4375	2	-	7/16/46/47	0/3/3/3
2	B8Q	5	1460	2	-	0/7/42/43	0/2/2/2
2	OMG	5	2054	2	-	0/5/27/28	0/3/3/3
3	OMU	8	14	2,3	-	1/9/27/28	0/2/2/2
4	MA6	9	1850	4	-	1/7/29/30	0/3/3/3
2	B9B	5	1578	2	-	2/7/29/30	0/3/3/3
2	A2M	5	398	2	-	2/5/27/28	0/3/3/3
2	7MG	5	4554	2	-	0/7/37/38	0/3/3/3
2	A2M	5	1875	2,84	-	0/5/27/28	0/3/3/3
4	OMU	9	121	4	-	2/9/27/28	0/2/2/2
2	OMG	5	1526	2	-	0/5/27/28	0/3/3/3
4	PSU	9	822	4	-	2/7/25/26	0/2/2/2
4	PSU	9	612	4	-	0/7/25/26	0/2/2/2
2	1MA	5	1326	2,84	-	0/3/25/26	0/3/3/3
2	B8K	5	4694	2	-	0/11/41/42	0/3/3/3
2	7MG	5	1609	2	-	0/7/37/38	0/3/3/3
4	B8Q	9	1219	4	-	0/7/42/43	0/2/2/2
2	B8K	5	3901	2	-	3/11/41/42	0/3/3/3
2	A2M	5	1528	2	-	1/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	A2M	9	1031	4	-	0/5/27/28	0/3/3/3
2	5MC	5	3786	2	-	0/7/25/26	0/2/2/2
2	A2M	5	1538	2,84	-	2/5/27/28	0/3/3/3
2	P7G	5	3884	2	-	2/10/40/41	0/3/3/3
2	OMG	5	4641	2	-	3/5/27/28	0/3/3/3
2	B8H	5	4300	2	-	0/7/25/26	0/2/2/2
2	A2M	5	2405	2,84	-	2/5/27/28	0/3/3/3
2	UR3	5	4601	2	-	0/7/25/26	0/2/2/2
2	OMG	5	2428	2	-	2/5/27/28	0/3/3/3
2	A2M	5	3722	2	-	0/5/27/28	0/3/3/3
4	PSU	9	119	4	-	2/7/25/26	0/2/2/2
4	MA6	9	1851	4	-	3/7/29/30	0/3/3/3
4	5MU	9	814	4	-	0/7/25/26	0/2/2/2
2	B8W	5	4189	2	-	2/5/27/28	0/3/3/3
2	OMC	5	2426	2,84,40	-	1/9/27/28	0/2/2/2
2	OMG	5	3796	2	-	2/5/27/28	0/3/3/3
2	A2M	5	3727	2,70	-	1/5/27/28	0/3/3/3
2	5MC	5	4339	2	-	0/7/25/26	0/2/2/2
2	A2M	5	1330	2	-	1/5/27/28	0/3/3/3
4	A2M	9	159	4	-	3/5/27/28	0/3/3/3
2	OMG	5	1887	2	-	0/5/27/28	0/3/3/3
2	OMG	5	2368	2	-	2/5/27/28	0/3/3/3
2	PSU	5	1586	2	-	0/7/25/26	0/2/2/2
2	OMG	5	4374	2	-	0/5/27/28	0/3/3/3
4	E3C	9	568	4	-	4/9/44/45	0/2/2/2
4	UR3	9	1830	4	-	4/7/25/26	0/2/2/2
2	I4U	5	4198	2	-	2/9/29/30	0/2/2/2
4	A2M	9	1678	4	-	0/5/27/28	0/3/3/3
4	OMG	9	509	4	-	0/5/27/28	0/3/3/3
2	OMC	5	2865	2	-	0/9/27/28	0/2/2/2
2	OMU	5	4310	2	-	0/9/27/28	0/2/2/2
2	OMG	5	2777	2	-	1/5/27/28	0/3/3/3
2	PSU	5	3733	2	-	2/7/25/26	0/2/2/2
2	B8W	5	4133	2	-	2/5/27/28	0/3/3/3
2	A2M	5	4527	2,84	-	3/5/27/28	0/3/3/3
2	2MG	5	4876	2	-	0/5/27/28	0/3/3/3
2	OMC	5	3705	2,84	-	4/9/27/28	0/2/2/2
4	4AC	9	1337	4	-	0/11/29/30	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	B8W	5	2384	2	-	4/5/27/28	0/3/3/3
2	PSU	5	4535	2	-	2/7/25/26	0/2/2/2
74	MLZ	m	72	74	-	0/7/8/10	-
2	PSU	5	4504	2	-	3/7/25/26	0/2/2/2
4	PSU	9	1081	4	-	3/7/25/26	0/2/2/2
4	A2M	9	668	4	-	4/5/27/28	0/3/3/3
2	PSU	5	1687	2	-	0/7/25/26	0/2/2/2
2	PSU	5	4454	2,84	-	3/7/25/26	0/2/2/2
4	OMC	9	174	4	-	0/9/27/28	0/2/2/2
2	2MG	5	729	2	-	1/5/27/28	0/3/3/3
2	E7G	5	1801	2	-	2/9/39/40	0/3/3/3
2	UR3	5	1870	2	-	0/7/25/26	0/2/2/2
2	OMC	5	3891	2	-	0/9/27/28	0/2/2/2
2	1MA	5	4419	2	-	2/3/25/26	0/3/3/3
11	MLZ	C	333	11	-	0/7/8/10	-
2	OMC	5	2369	2	-	0/9/27/28	0/2/2/2
2	OMC	5	2808	2	-	0/9/27/28	0/2/2/2
2	PSU	5	4632	2	-	0/7/25/26	0/2/2/2
2	PSU	5	2512	2	-	0/7/25/26	0/2/2/2
2	E7G	5	2301	2	-	1/9/39/40	0/3/3/3
2	A2M	5	3871	2	-	3/5/27/28	0/3/3/3
2	B8H	5	1864	2	-	0/7/25/26	0/2/2/2
4	PSU	9	823	4	-	0/7/25/26	0/2/2/2
4	OMU	9	116	4	-	3/9/27/28	0/2/2/2
2	OMG	5	1320	2	-	0/5/27/28	0/3/3/3
2	A2M	5	2367	2,84	-	1/5/27/28	0/3/3/3
2	OMC	5	4540	2	-	0/9/27/28	0/2/2/2
2	OMG	5	373	2	-	1/5/27/28	0/3/3/3
2	P7G	5	1913	2	-	2/10/40/41	0/3/3/3
2	OMG	5	4627	2	-	0/5/27/28	0/3/3/3
4	B8N	9	1248	4	-	3/16/34/35	0/2/2/2
4	5MC	9	1374	4	-	0/7/25/26	0/2/2/2
4	PSU	9	1243	4	-	2/7/25/26	0/2/2/2
4	OMC	9	1703	4	-	2/9/27/28	0/2/2/2
81	5CT	t	51	81	-	5/13/14/16	-
2	OMC	5	3913	2	-	0/9/27/28	0/2/2/2
2	7MG	5	2526	2	-	0/7/37/38	0/3/3/3
2	M7A	5	4568	2	-	0/7/37/38	0/3/3/3
2	OMU	5	4624	2,52	-	1/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	A2M	5	3829	2	-	0/5/27/28	0/3/3/3
4	OMG	9	644	4	-	1/5/27/28	0/3/3/3
2	PSU	5	4446	2	-	0/7/25/26	0/2/2/2
2	PSU	5	1681	2	-	2/7/25/26	0/2/2/2
2	B9H	5	2790	2	-	1/12/47/48	0/2/2/2
2	OMG	5	1629	2	-	0/5/27/28	0/3/3/3
2	PSU	5	4640	2,65	-	3/7/25/26	0/2/2/2
4	M7A	9	1806	4	-	0/7/37/38	0/3/3/3
4	A2M	9	484	4	-	0/5/27/28	0/3/3/3
82	DDE	v	715	82	-	16/20/21/23	0/1/1/1
4	6MZ	9	1832	4	-	2/5/27/28	0/3/3/3
2	5MU	5	4087	2	-	0/7/25/26	0/2/2/2
2	OMC	5	3873	2	-	0/9/27/28	0/2/2/2
2	PSU	5	3719	2	-	0/7/25/26	0/2/2/2

The worst 5 of 920 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	9	166	A2M	O4'-C1'	16.42	1.64	1.41
4	9	159	A2M	O4'-C1'	16.40	1.64	1.41
4	9	1678	A2M	O4'-C1'	16.34	1.63	1.41
2	5	1875	A2M	O4'-C1'	16.24	1.63	1.41
2	5	4527	A2M	O4'-C1'	16.22	1.63	1.41

The worst 5 of 558 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	9	1806	M7A	C5-C6-N6	12.77	145.55	123.74
2	5	4568	M7A	C5-C6-N6	12.30	144.75	123.74
2	5	4087	5MU	C5-C4-N3	12.06	125.61	115.31
4	9	814	5MU	C5-C4-N3	11.64	125.25	115.31
4	9	1806	M7A	N6-C6-N1	-10.95	94.37	118.35

There are no chirality outliers.

5 of 187 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
81	t	51	5CT	NZ-C1-C2-C3
2	5	237	B9B	C5-C6-O6-C61
2	5	237	B9B	N1-C6-O6-C61
2	5	1352	P4U	N3-C4-O4-C41

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Mol	Chain	Res	Type	Atoms
2	5	1352	P4U	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 208 ligands modelled in this entry, 208 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	9	18
2	5	11
3	8	1

The worst 5 of 30 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	1223:G	O3'	1237:G	P	24.58

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	9	1761:U	O3'	1771:G	P	18.12
1	9	834:C	O3'	841:G	P	17.65
1	9	697:G	O3'	729:C	P	17.13
1	9	756:C	O3'	788:G	P	17.02

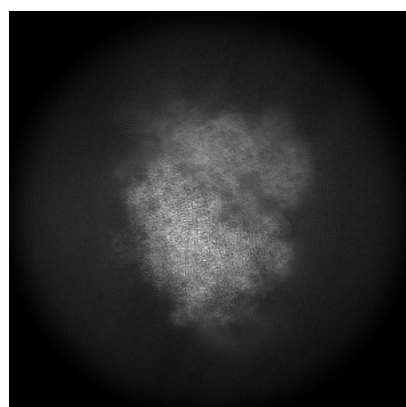
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13114. These allow visual inspection of the internal detail of the map and identification of artifacts.

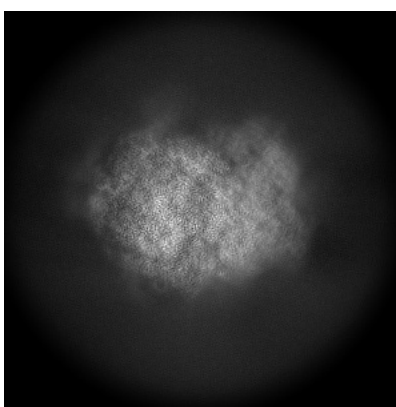
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

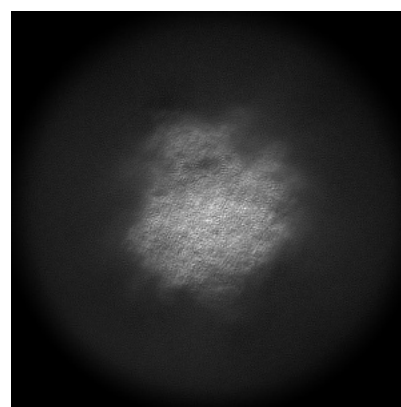
6.1.1 Primary map



X



Y

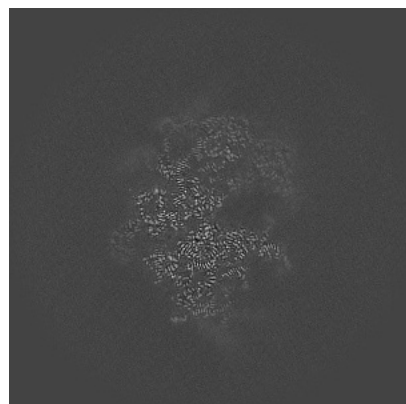


Z

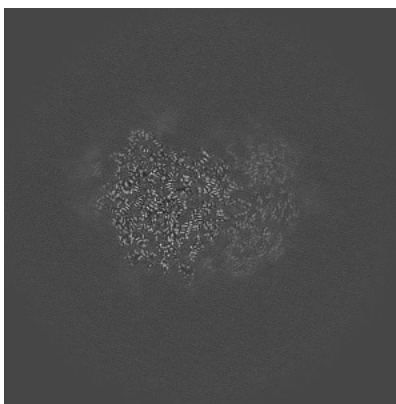
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

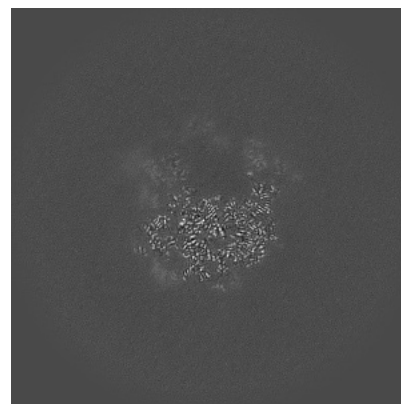
6.2.1 Primary map



X Index: 240



Y Index: 240

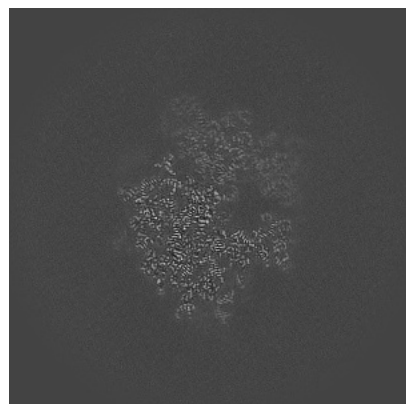


Z Index: 240

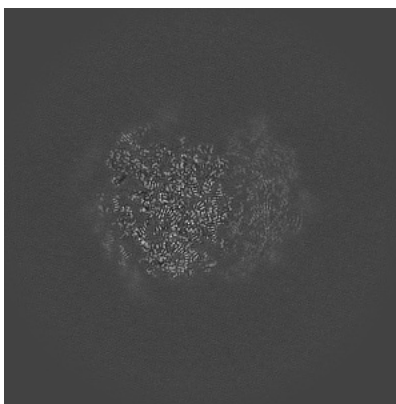
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

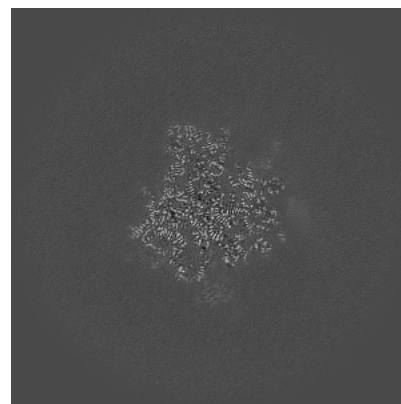
6.3.1 Primary map



X Index: 225



Y Index: 228



Z Index: 194

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

6.4 Orthogonal surface views [i](#)

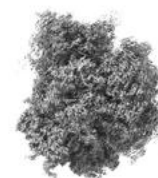
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.38. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

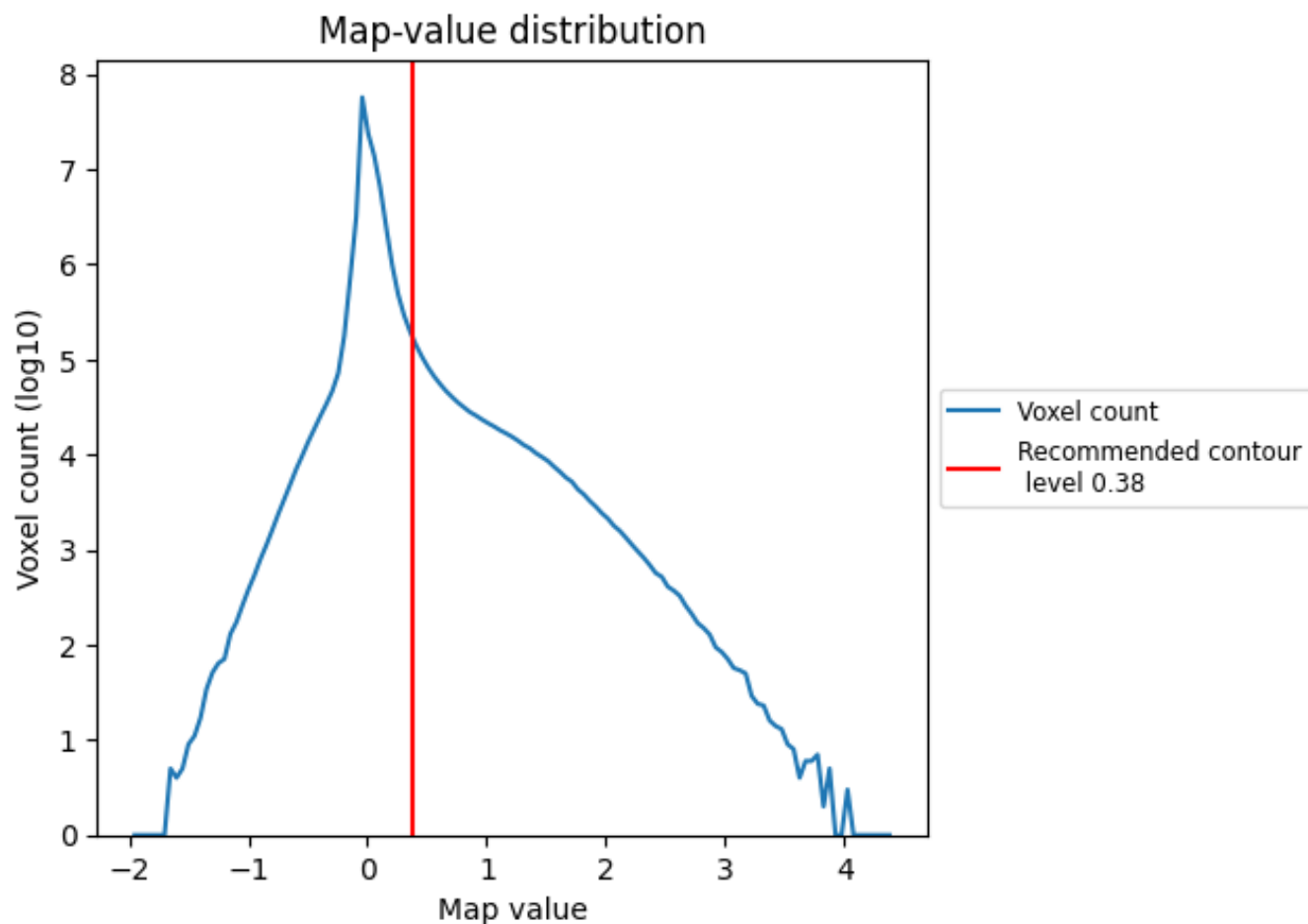
6.5 Mask visualisation

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

7 Map analysis [i](#)

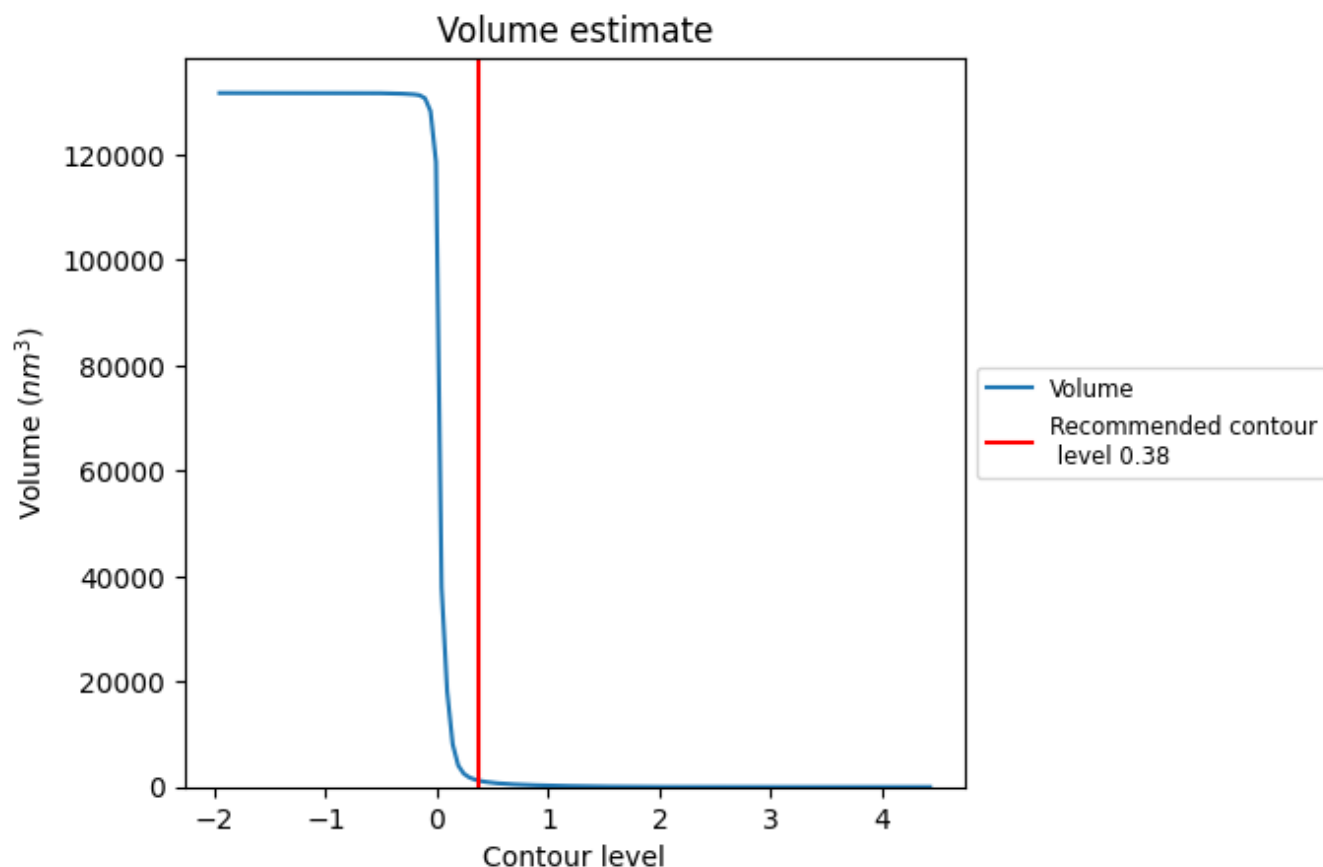
This section contains the results of statistical analysis of the map.

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.

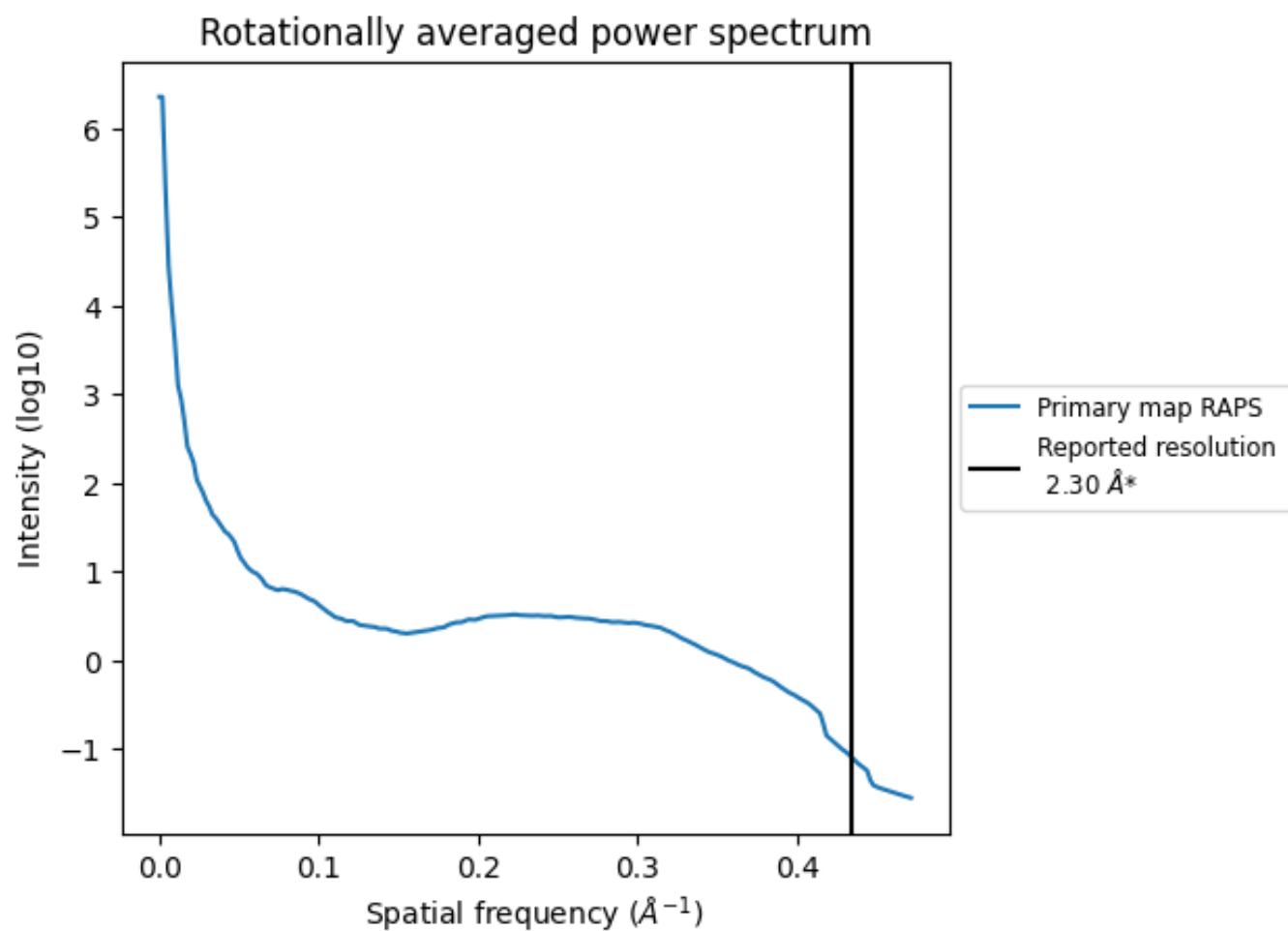
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1197 nm^3 ; this corresponds to an approximate mass of 1081 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.435 Å⁻¹

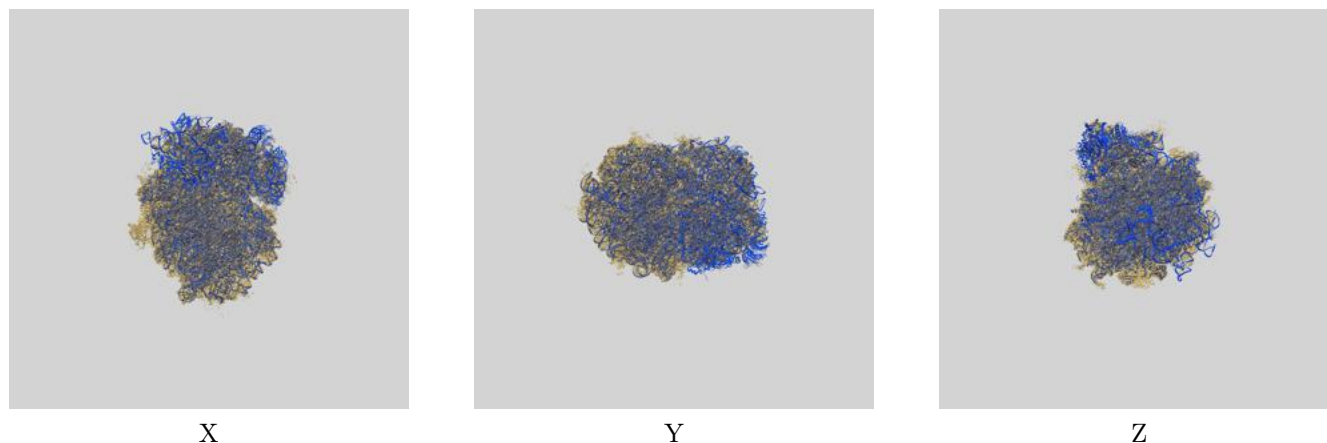
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

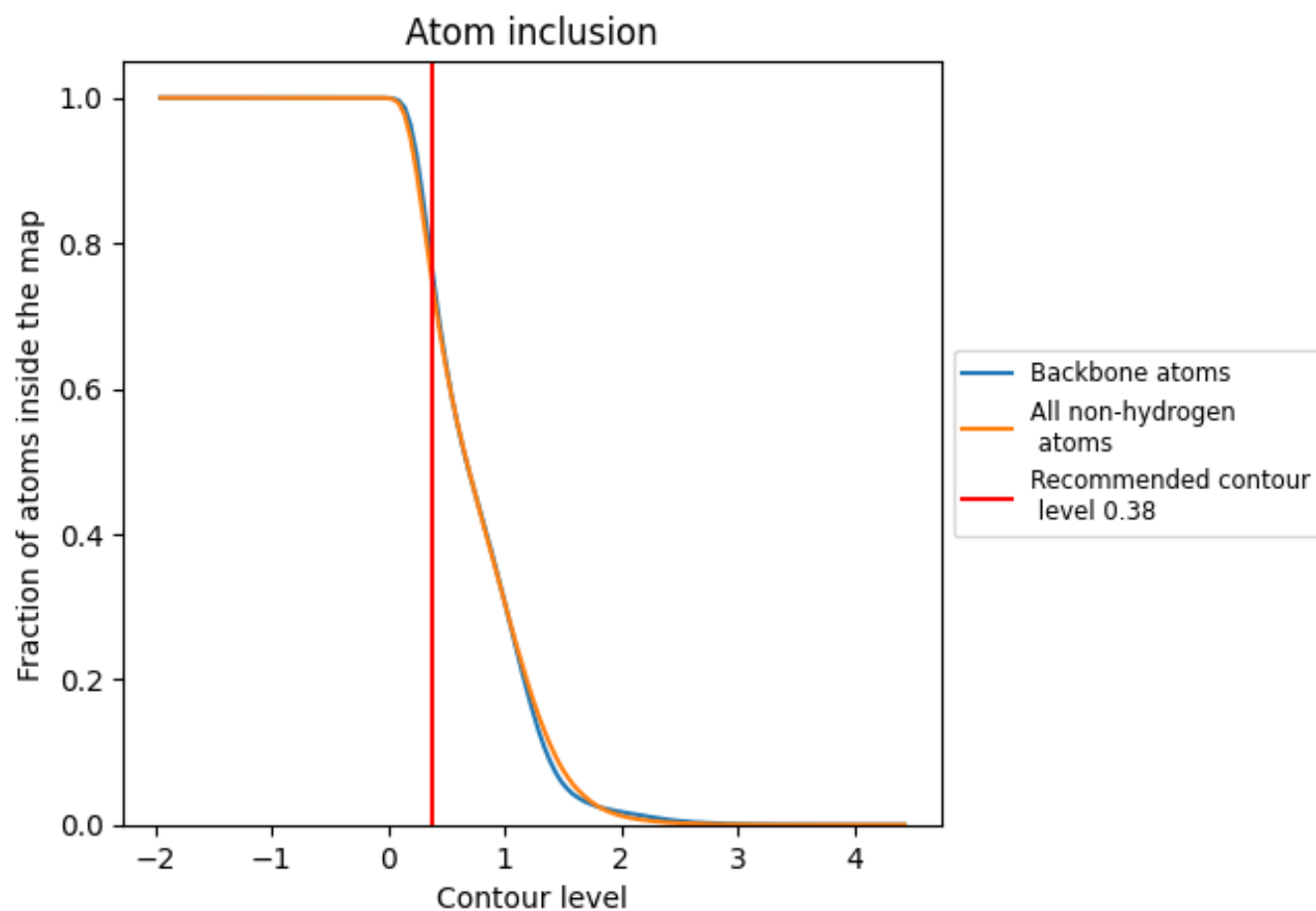
This section contains information regarding the fit between EMDB map EMD-13114 and PDB model 7OYD. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.38 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 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 74% of all non-hydrogen atoms, are inside the map.