



## wwPDB EM Validation Summary Report ⓘ

Jul 21, 2025 – 08:13 PM EDT

PDB ID : 8VVR / pdb\_00008vvr  
EMDB ID : EMD-43566  
Title : Post-decoding/Post-hydrolysis state obtained from Anisomycin-treated mammalian ribosomes  
Authors : Loerch, S.; Petrossian, E.; Smith, P.R.; Campbell, Z.T.  
Deposited on : 2024-01-31  
Resolution : 3.10 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev118  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0rc1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.44

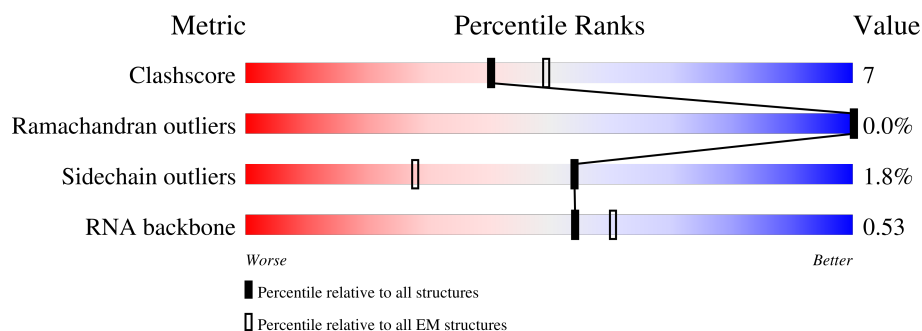
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	A	257	
2	B	403	
3	C	413	
4	D	297	
5	E	291	
6	F	249	
7	G	319	

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Mol	Chain	Length	Quality of chain
8	H	192	
9	I	214	
10	J	178	
11	K	211	
12	L	218	
13	M	204	
14	N	203	
15	O	213	
16	P	188	
17	Q	212	
18	R	224	
19	S	160	
20	T	128	
21	U	140	
22	V	157	
23	W	156	
24	X	145	
25	Y	136	
26	Z	148	
27	AA	245	
28	BA	115	
29	CA	125	
30	DA	135	
31	EA	110	
32	FA	129	

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Mol	Chain	Length	Quality of chain
33	GA	123	
34	HA	105	
35	IA	97	
36	JA	70	
37	KA	51	
38	LA	128	
39	MA	25	
40	NA	106	
41	OA	92	
42	PA	137	
43	RA	165	
44	SA	76	
45	TA	76	
46	UA	75	
47	VA	12	
48	WA	3584	
49	XA	120	
50	YA	156	
51	ZA	1869	
52	AB	295	
53	BB	264	
54	CB	293	
55	DB	281	
56	EB	263	
57	FB	204	

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Mol	Chain	Length	Quality of chain
58	GB	249	
59	HB	432	
60	IB	208	
61	JB	194	
62	KB	165	
63	LB	158	
64	MB	132	
65	NB	151	
66	OB	151	
67	PB	145	
68	QB	172	
69	RB	135	
70	SB	152	
71	TB	145	
72	UB	119	
73	VB	83	
74	WB	130	
75	XB	143	
76	YB	131	
77	ZB	124	
78	AC	115	
79	BC	84	
80	CC	69	
81	DC	56	
82	EC	133	

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Mol	Chain	Length	Quality of chain
83	FC	188	
84	GC	317	
85	IC	4	
86	b	318	
87	c	14	
88	HC	462	

## 2 Entry composition

There are 95 unique types of molecules in this entry. The entry contains 220661 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 uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	250	Total	C	N	O	S	0	0
			1914	1199	392	317	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	397	Total	C	N	O	S	0	0
			3196	2035	603	545	13		

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 4 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	294	Total	C	N	O	S	0	0
			2395	1514	439	428	14		

- Molecule 5 is a protein called L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	228	Total	C	N	O	S	0	0
			1823	1173	349	298	3		

- Molecule 6 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	227	Total	C	N	O	S	0	0
			1897	1217	366	305	9		

- Molecule 7 is a protein called L7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	229	Total	C	N	O	S	0	0
			1850	1181	356	309	4		

- Molecule 8 is a protein called L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 9 is a protein called L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 10 is a protein called uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	171	Total	C	N	O	S	0	0
			1372	867	256	243	6		

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	46	ILE	-	insertion	UNP G1TPV0
K	47	ALA	-	insertion	UNP G1TPV0
K	48	PRO	-	insertion	UNP G1TPV0
K	49	ARG	-	insertion	UNP G1TPV0
K	50	PRO	-	insertion	UNP G1TPV0
K	51	ALA	-	insertion	UNP G1TPV0
K	52	ALA	-	insertion	UNP G1TPV0
K	53	GLY	-	insertion	UNP G1TPV0
K	54	PRO	-	insertion	UNP G1TPV0

- Molecule 12 is a protein called eL14.



Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 13 is a protein called eL15.

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

- Molecule 14 is a protein called uL13.

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

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	156	Total	C	N	O	S	0	0
			1266	793	245	219	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	43	SER	ALA	conflict	UNP G1TVT6

- Molecule 16 is a protein called eL18.

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

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	4	ASP	ASN	conflict	UNP G1TFE0
P	14	ARG	TRP	conflict	UNP G1TFE0
P	53	MET	LEU	conflict	UNP G1TFE0
P	58	ARG	TRP	conflict	UNP G1TFE0
P	75	ARG	GLN	conflict	UNP G1TFE0
P	80	ALA	PRO	conflict	UNP G1TFE0
P	86	VAL	ILE	conflict	UNP G1TFE0

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Chain	Residue	Modelled	Actual	Comment	Reference
P	104	ARG	HIS	conflict	UNP G1TFE0
P	110	ARG	CYS	conflict	UNP G1TFE0
P	137	VAL	GLY	conflict	UNP G1TFE0
P	157	GLY	ARG	conflict	UNP G1TFE0
P	181	ARG	TRP	conflict	UNP G1TFE0

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	101	Total	C	N	O	S	0	0
			826	530	144	150	2		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	18	LEU	VAL	conflict	UNP G1TSG1
T	32	GLY	ARG	conflict	UNP G1TSG1
T	36	ALA	GLU	conflict	UNP G1TSG1
T	39	PHE	SER	conflict	UNP G1TSG1
T	54	GLY	ARG	conflict	UNP G1TSG1
T	60	VAL	ALA	conflict	UNP G1TSG1
T	62	SER	THR	conflict	UNP G1TSG1
T	63	LEU	ILE	conflict	UNP G1TSG1

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Chain	Residue	Modelled	Actual	Comment	Reference
T	97	ARG	HIS	conflict	UNP G1TSG1
T	106	THR	SER	conflict	UNP G1TSG1
T	126	GLU	ASP	conflict	UNP G1TSG1

- Molecule 21 is a protein called L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	135	Total	C	N	O	S	0	0
			1004	631	191	177	5		

- Molecule 22 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	110	Total	C	N	O	S	0	0
			887	555	179	149	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	78	SER	PHE	conflict	UNP G1SE28

- Molecule 23 is a protein called uL23.

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

- Molecule 24 is a protein called L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 25 is a protein called L27.

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

- Molecule 26 is a protein called uL15.

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

- Molecule 27 is a protein called L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AA	107	Total	C	N	O	S	0	0
			873	542	195	133	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BA	99	Total	C	N	O	S	0	0
			769	486	135	141	7		

- Molecule 29 is a protein called L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	CA	108	Total	C	N	O	S	0	0
			893	563	172	156	2		

- Molecule 30 is a protein called L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	DA	129	Total	C	N	O	S	0	0
			1064	673	220	166	5		

- Molecule 31 is a protein called eL33.

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

- Molecule 32 is a protein called L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	FA	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 33 is a protein called L35.

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

- Molecule 34 is a protein called L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	HA	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	IA	87	Total	C	N	O	S	0	0
			716	440	159	112	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	JA	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 37 is a protein called eL39.

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

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LA	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 39 is a protein called eL41.

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

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	NA	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 41 is a protein called eL43.

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

- Molecule 42 is a protein called L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	PA	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 43 is a protein called L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	RA	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 44 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	SA	76	Total	C	N	O	P	0	0
			1622	726	300	521	75		

- Molecule 45 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	TA	76	Total	C	N	O	P	0	0
			1615	722	286	532	75		

- Molecule 46 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	UA	75	Total	C	N	O	P	0	0
			1596	713	285	523	75		

- Molecule 47 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	VA	12	Total	C	N	O	P	0	0
			251	113	41	85	12		

- Molecule 48 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	WA	3578	Total	C	N	O	P	0	0
			76735	34173	14061	24923	3578		

- Molecule 49 is a RNA chain called 5S rRNA.

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

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
XA	2	U	N	conflict	GB X06789.1
XA	36	C	N	conflict	GB X06789.1
XA	102	U	N	conflict	GB X06789.1
XA	112	U	N	conflict	GB X06789.1
XA	114	U	N	conflict	GB X06789.1
XA	119	U	C	conflict	GB X06789.1
XA	120	U	N	conflict	GB X06789.1

- Molecule 50 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	YA	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 51 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	ZA	1716	Total	C	N	O	P	0	0
			36623	16347	6572	11989	1715		

- Molecule 52 is a protein called RPSA.

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

- Molecule 53 is a protein called S3A.

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

- Molecule 54 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	CB	220	Total	C	N	O	S	0	0
			1707	1105	293	300	9		

- Molecule 55 is a protein called S3.

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

- Molecule 56 is a protein called S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	EB	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
EB	25	GLY	SER	conflict	UNP G1TK17
EB	51	ARG	LYS	conflict	UNP G1TK17
EB	78	THR	ALA	conflict	UNP G1TK17
EB	156	VAL	MET	conflict	UNP G1TK17

- Molecule 57 is a protein called S5.

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



- Molecule 58 is a protein called eS6.

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

- Molecule 59 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	HB	185	Total	C	N	O	S	0	0
			1489	952	271	265	1		

- Molecule 60 is a protein called S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	IB	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
IB	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 61 is a protein called S9.

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

- Molecule 62 is a protein called S10.

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

- Molecule 63 is a protein called S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	LB	144	Total	C	N	O	S	0	0
			1180	752	223	199	6		

- Molecule 64 is a protein called S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	MB	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 65 is a protein called uS15.

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

- Molecule 66 is a protein called S14.

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

- Molecule 67 is a protein called S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	PB	129	Total	C	N	O	S	0	0
			1058	670	201	180	7		

- Molecule 68 is a protein called uS9.

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

- Molecule 69 is a protein called eS17.

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

- Molecule 70 is a protein called S18.

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

- Molecule 71 is a protein called S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	TB	142	Total	C	N	O	S	0	0
			1104	693	212	196	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
TB	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 72 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	UB	102	Total	C	N	O	S	0	0
			808	507	154	143	4		

- Molecule 73 is a protein called S21.

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

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
VB	3	ASN	SER	conflict	UNP G1TM82
VB	4	ASP	ASN	conflict	UNP G1TM82
VB	33	GLN	PRO	conflict	UNP G1TM82
VB	50	PHE	SER	conflict	UNP G1TM82
VB	75	ALA	SER	conflict	UNP G1TM82
VB	76	ASP	HIS	conflict	UNP G1TM82
VB	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 74 is a protein called S15A.

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

- Molecule 75 is a protein called S23.

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

- Molecule 76 is a protein called S24.

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

- Molecule 77 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	ZB	85	Total	C	N	O	S	0	0
			683	439	128	115	1		

- Molecule 78 is a protein called S26.

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

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AC	28	ARG	CYS	conflict	UNP G1TFE8
AC	56	ALA	VAL	conflict	UNP G1TFE8
AC	109	ARG	PRO	conflict	UNP G1TFE8

- Molecule 79 is a protein called S27.

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

- Molecule 80 is a protein called S28.

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

- Molecule 81 is a protein called uS14.

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

- Molecule 82 is a protein called S30.

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

- Molecule 83 is a protein called S27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	FC	69	Total	C	N	O	S	0	0
			564	357	105	95	7		

- Molecule 84 is a protein called RACK1.

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

- Molecule 85 is a protein called peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
85	IC	4	Total	C	N	O	0	0
			20	12	4	4		

- Molecule 86 is a protein called RPLP0.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	b	167	Total	C	N	O	S	0	0
			1279	813	228	229	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	82	LEU	ILE	conflict	UNP G1SPK4

- Molecule 87 is a protein called RPLP peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	c	14	Total	C	N	O	S	0	0
			110	66	14	29	1		

- Molecule 88 is a protein called eukaryotic elongation factor 1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	HC	223	Total	C	N	O	S	0	0
			1664	1048	299	308	9		

- Molecule 89 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
89	A	1	Total	Mg	0
			1	1	
89	I	1	Total	Mg	0
			1	1	
89	O	1	Total	Mg	0
			1	1	
89	P	1	Total	Mg	0
			1	1	
89	U	1	Total	Mg	0
			1	1	
89	Z	1	Total	Mg	0
			1	1	
89	FA	1	Total	Mg	0
			1	1	
89	IA	1	Total	Mg	0
			1	1	
89	VA	1	Total	Mg	0
			1	1	
89	WA	142	Total	Mg	0
			142	142	
89	XA	4	Total	Mg	0
			4	4	
89	YA	2	Total	Mg	0
			2	2	
89	ZA	45	Total	Mg	0
			45	45	
89	AC	1	Total	Mg	0
			1	1	
89	HC	1	Total	Mg	0
			1	1	

- Molecule 90 is ZINC ION (CCD ID: ZN) (formula: Zn).

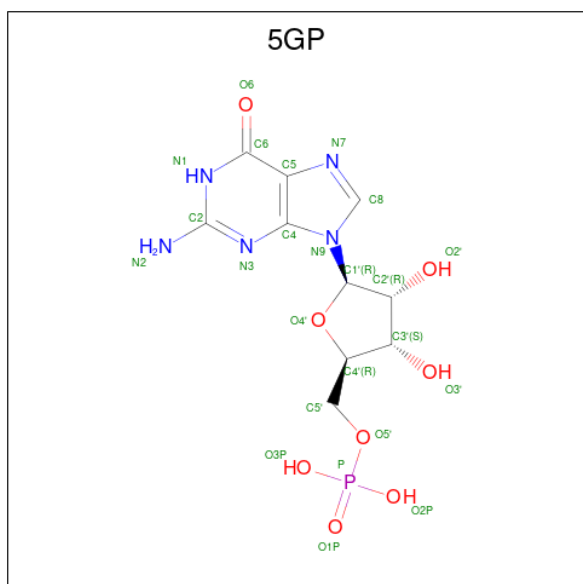
Mol	Chain	Residues	Atoms		AltConf
90	FA	1	Total	Zn	0
			1	1	
90	IA	1	Total	Zn	0
			1	1	

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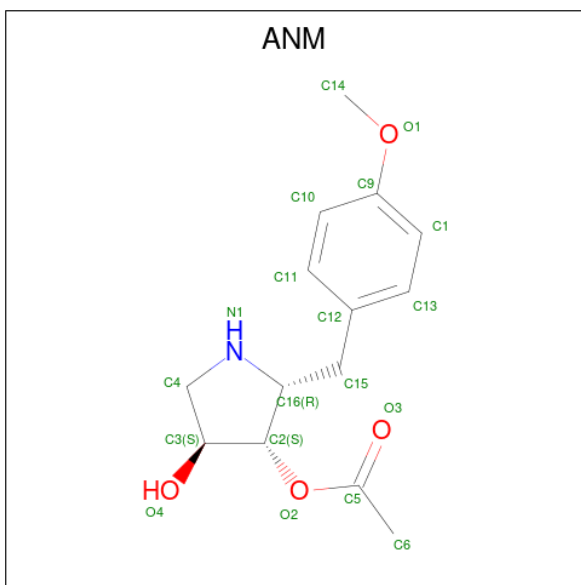
Mol	Chain	Residues	Atoms		AltConf
90	LA	1	Total	Zn	0
			1	1	
90	NA	1	Total	Zn	0
			1	1	
90	OA	1	Total	Zn	0
			1	1	
90	AC	1	Total	Zn	0
			1	1	
90	DC	1	Total	Zn	0
			1	1	
90	FC	1	Total	Zn	0
			1	1	

- Molecule 91 is GUANOSINE-5'-MONOPHOSPHATE (CCD ID: 5GP) (formula:  $C_{10}H_{14}N_5O_8P$ ).



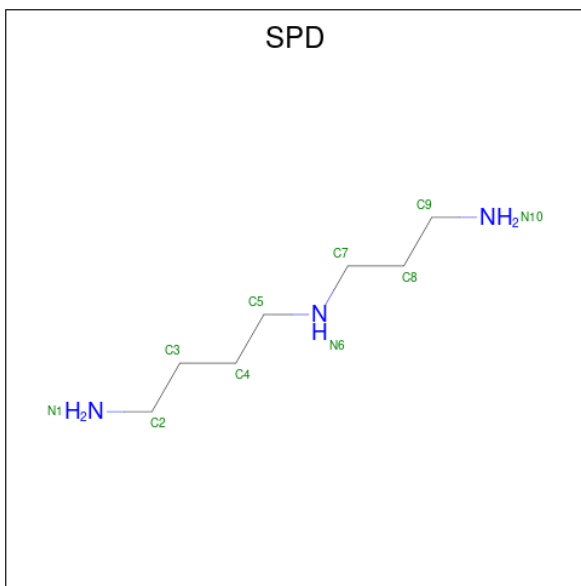
Mol	Chain	Residues	Atoms					AltConf
91	UA	1	Total	C	N	O	P	0
			24	10	5	8	1	

- Molecule 92 is ANISOMYCIN (CCD ID: ANM) (formula:  $C_{14}H_{19}NO_4$ ).



Mol	Chain	Residues	Atoms				AltConf
92	WA	1	Total	C	N	O	0
			19	14	1	4	

- Molecule 93 is SPERMIDINE (CCD ID: SPD) (formula:  $C_7H_{19}N_3$ ).



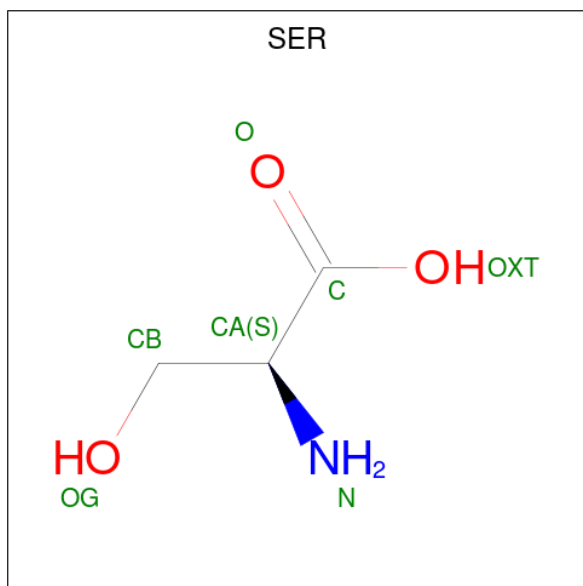
Mol	Chain	Residues	Atoms			AltConf
93	WA	1	Total	C	N	0
			10	7	3	
93	WA	1	Total	C	N	0
			10	7	3	
93	ZA	1	Total	C	N	0
			10	7	3	



- Molecule 94 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms			AltConf
94	WA	1	Total	K		0
			1	1		

- Molecule 95 is SERINE (CCD ID: SER) (formula:  $C_3H_7NO_3$ ).




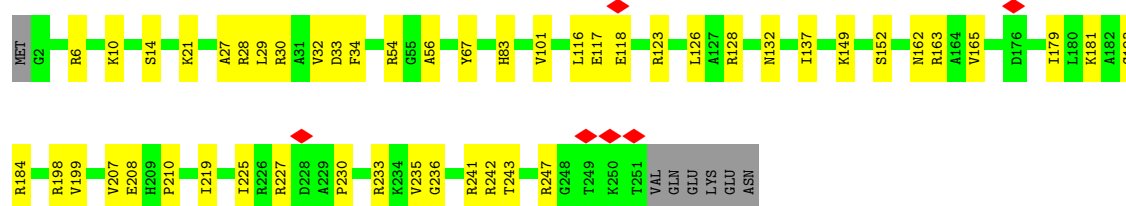
Mol	Chain	Residues	Atoms				AltConf
95	HC	1	Total	C	N	O	0
			6	3	1	2	

### 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.

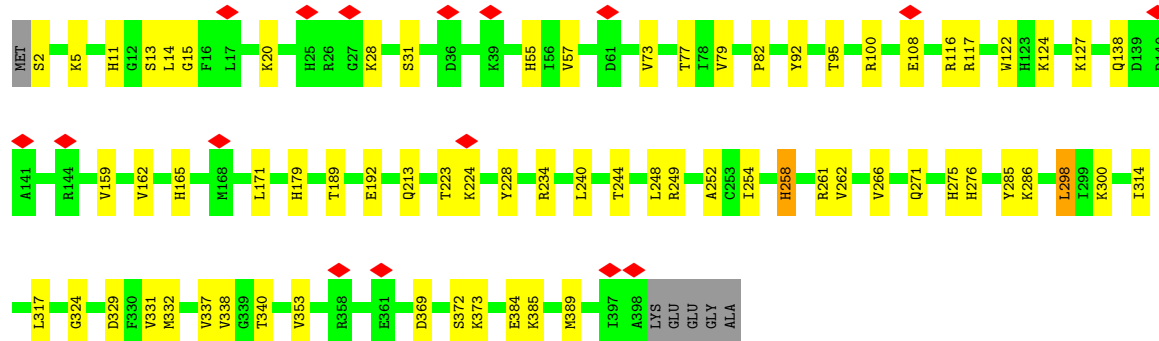
#### • Molecule 1: uL2

Chain A: 




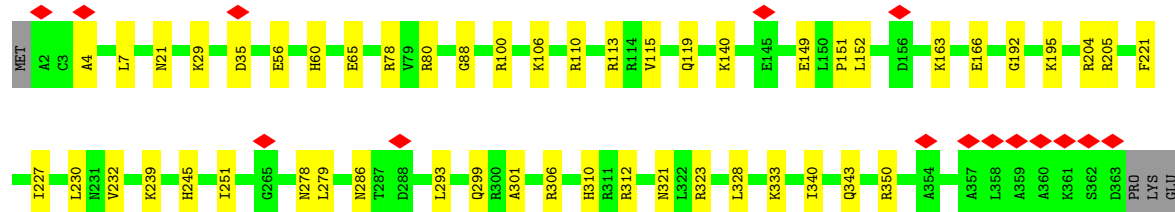
#### • Molecule 2: uL3

Chain B: 



#### • Molecule 3: uL4

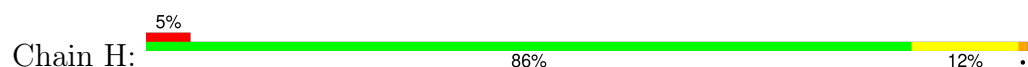
Chain C: 



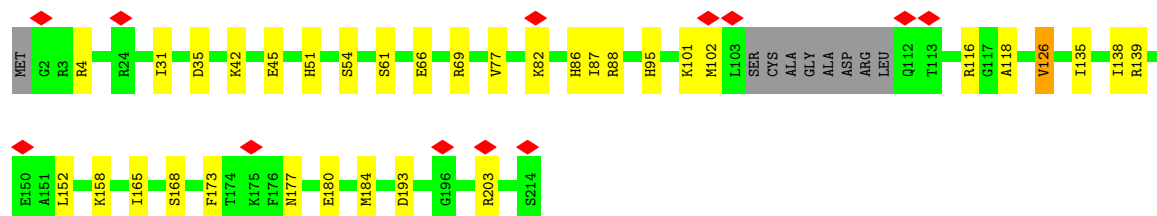
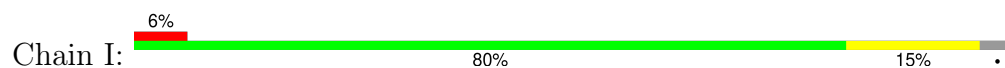




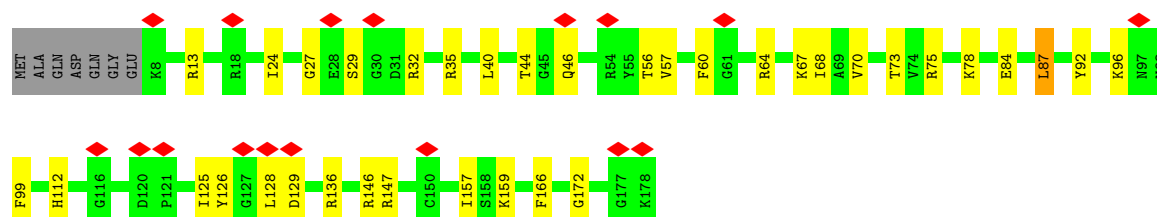
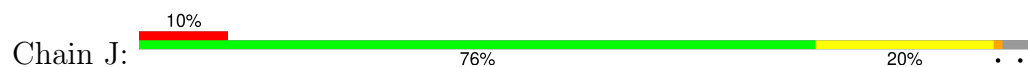
- Molecule 8: L9



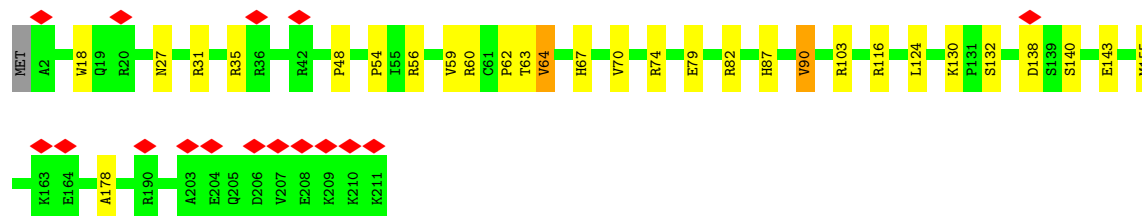
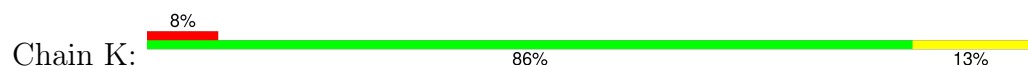
- Molecule 9: L10



- Molecule 10: uL5

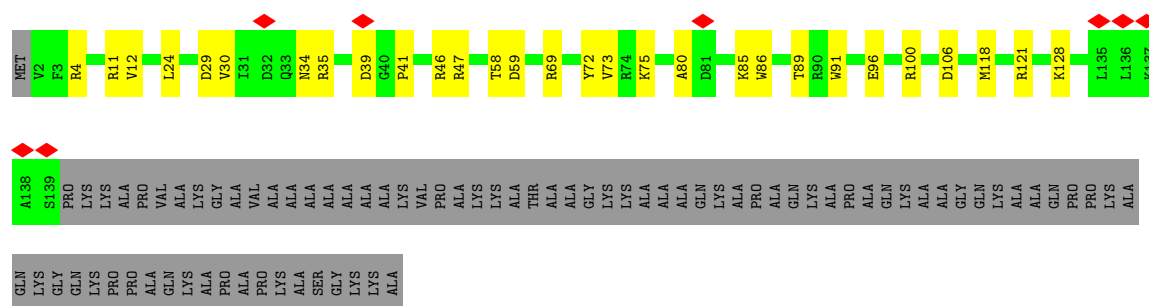


- Molecule 11: eL13




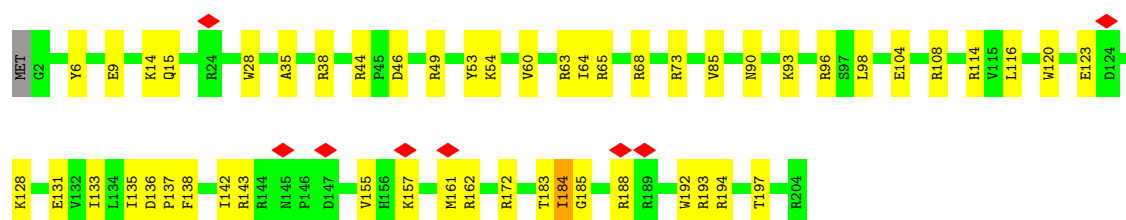
- Molecule 12: eL14

Chain L: 




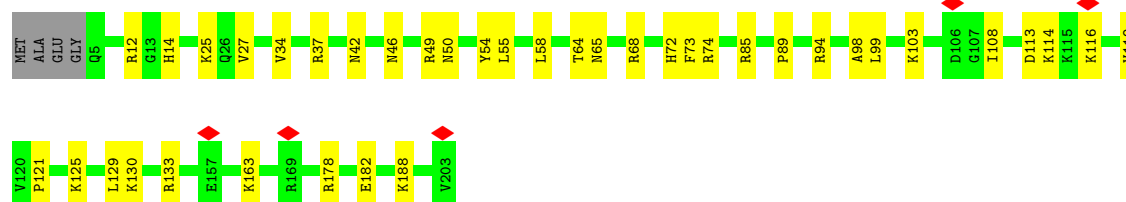
• Molecule 13: eL15

Chain M: 



• Molecule 14: uL13

Chain N: 




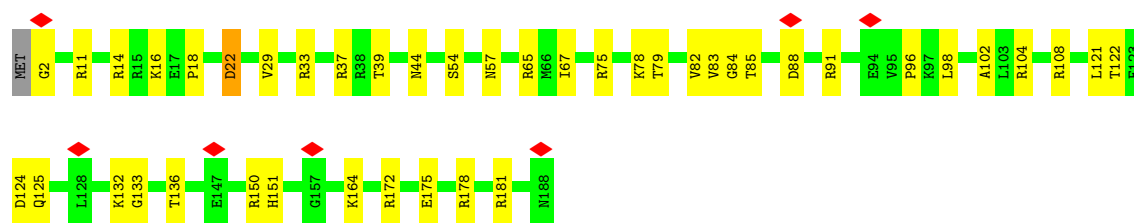
• Molecule 15: uL22

Chain O: 

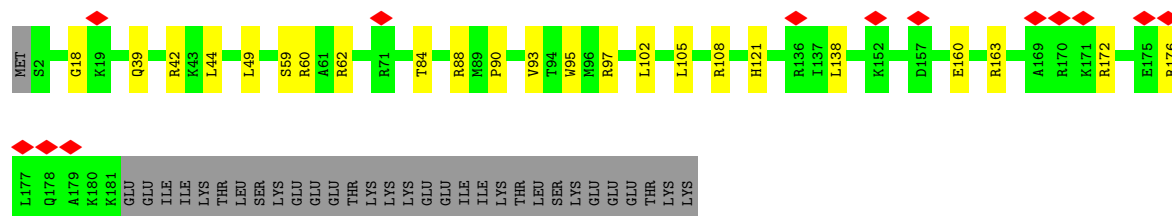
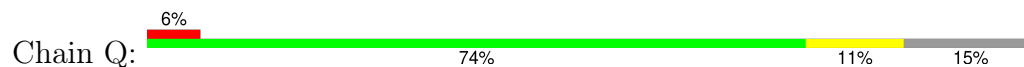


• Molecule 16: eL18

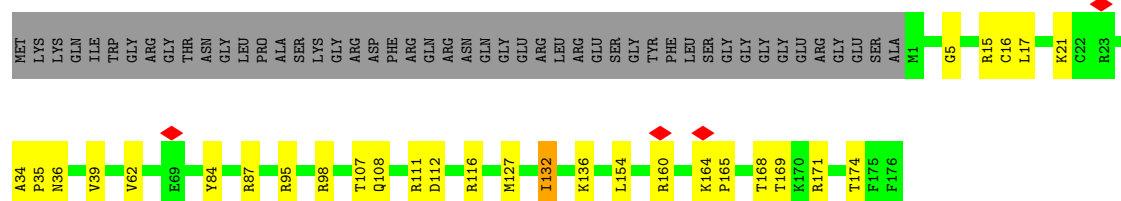
Chain P: 



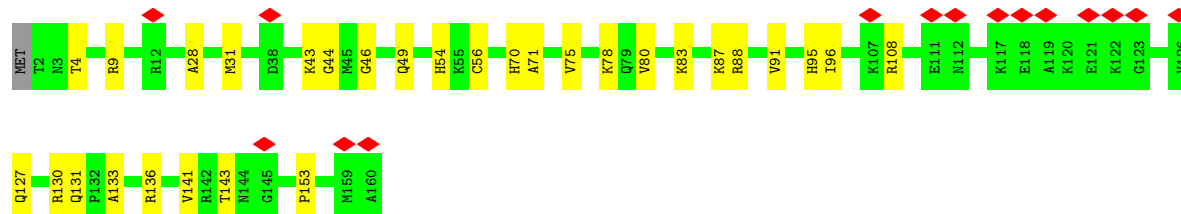
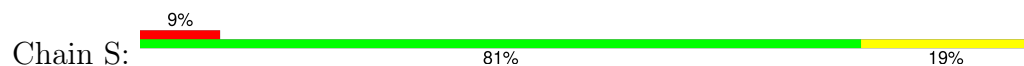
• Molecule 17: eL19



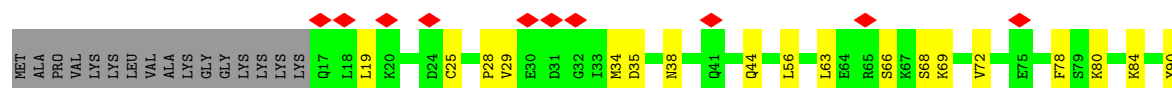
• Molecule 18: eL20



• Molecule 19: eL21

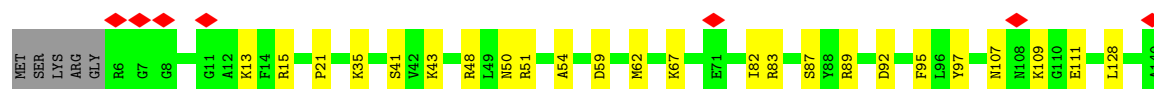
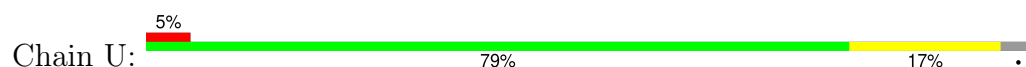


• Molecule 20: eL22

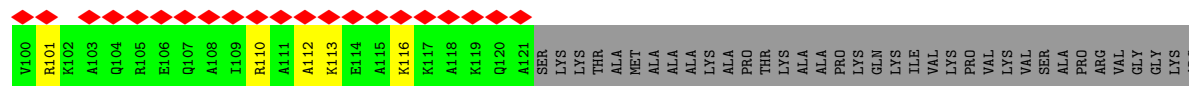
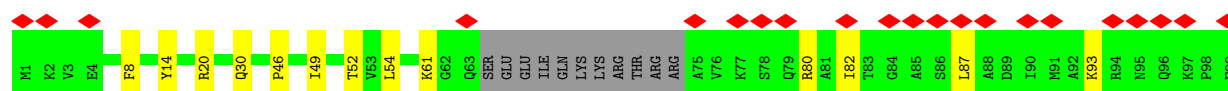




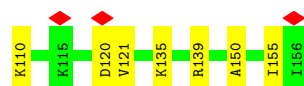
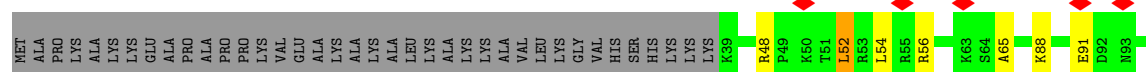
- Molecule 21: L23



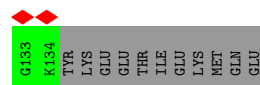
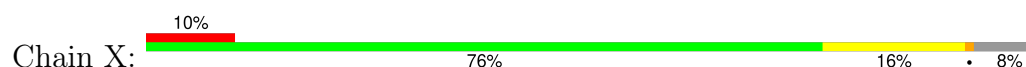
- Molecule 22: uL24



- Molecule 23: uL23



- Molecule 24: L26

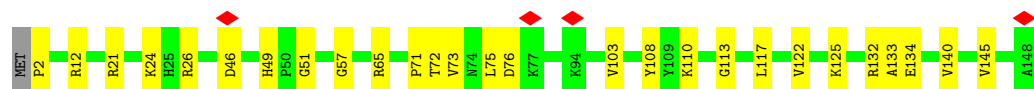
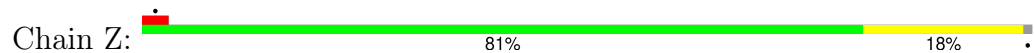


- Molecule 25: L27

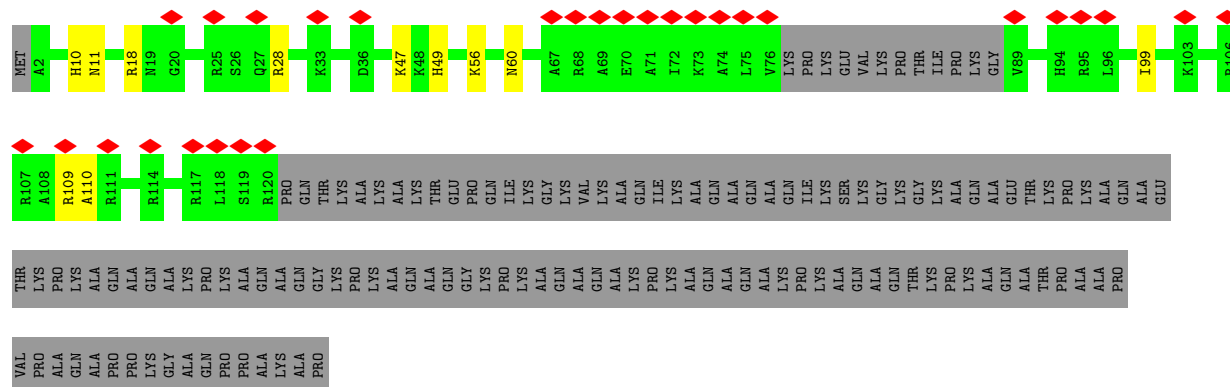
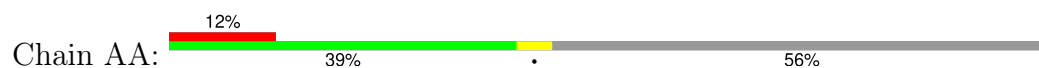




- Molecule 26: uL15



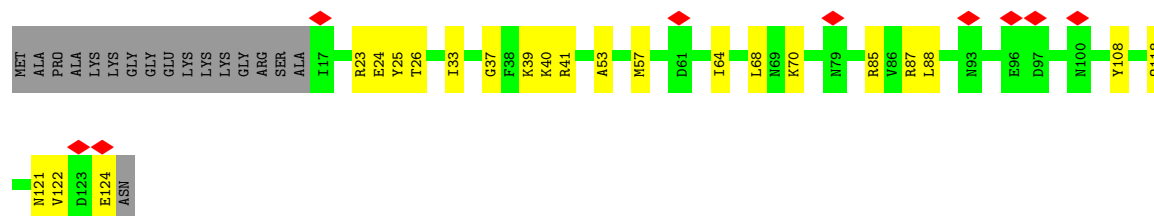
- Molecule 27: L29



- Molecule 28: eL30

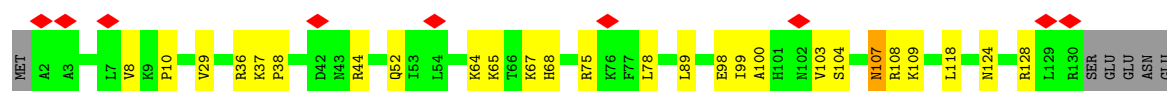
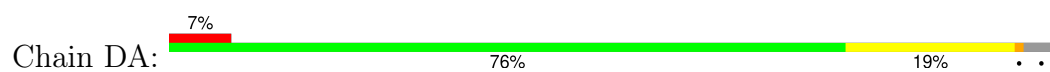


- Molecule 29: L31

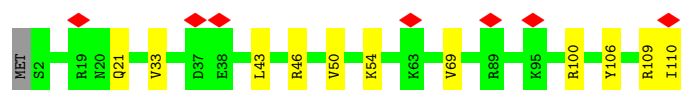
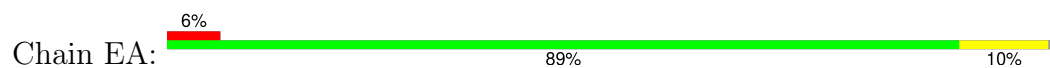


- Molecule 30: L32

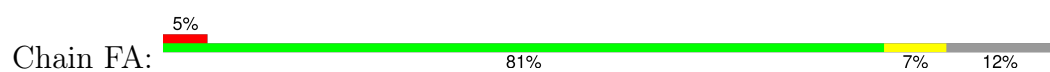




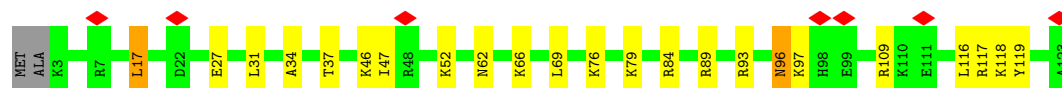
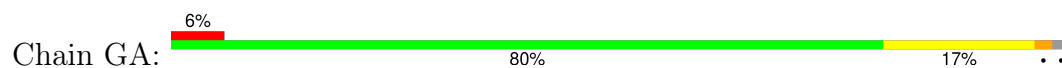
- Molecule 31: eL33



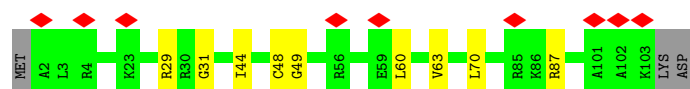
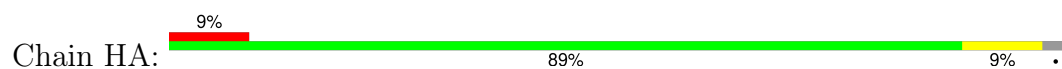
- Molecule 32: L34



- Molecule 33: L35



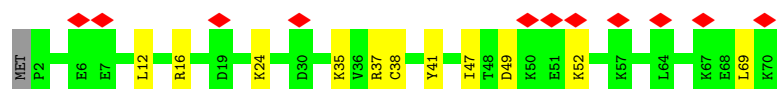
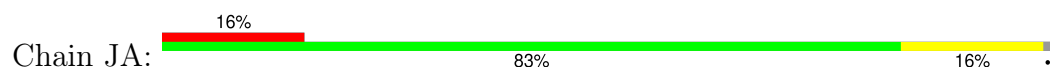
- Molecule 34: L36



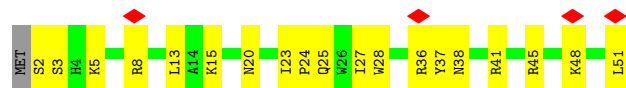
- Molecule 35: L37



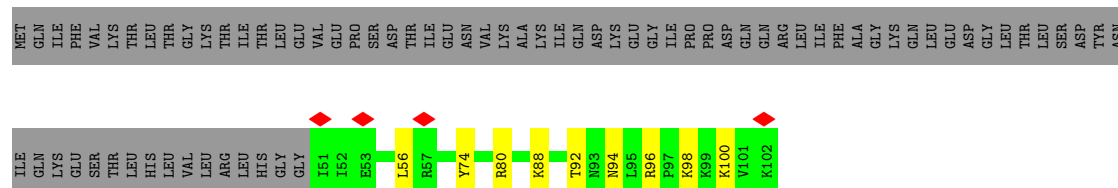
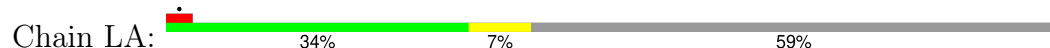
- Molecule 36: eL38



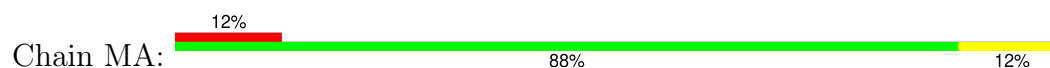
- Molecule 37: eL39



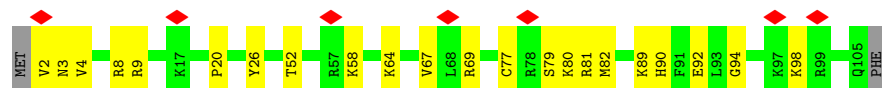
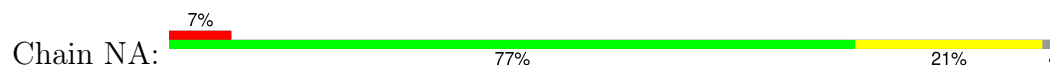
- Molecule 38: eL40



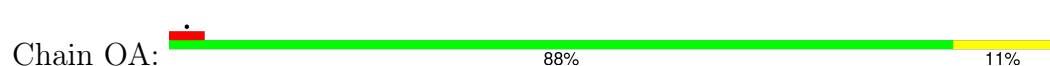
- Molecule 39: eL41



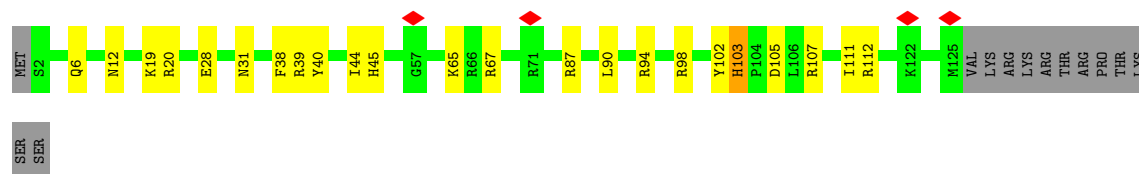
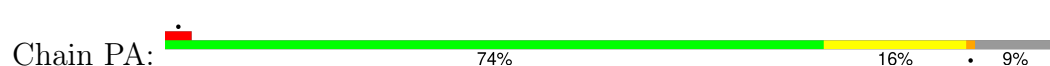
- Molecule 40: eL42



- Molecule 41: eL43

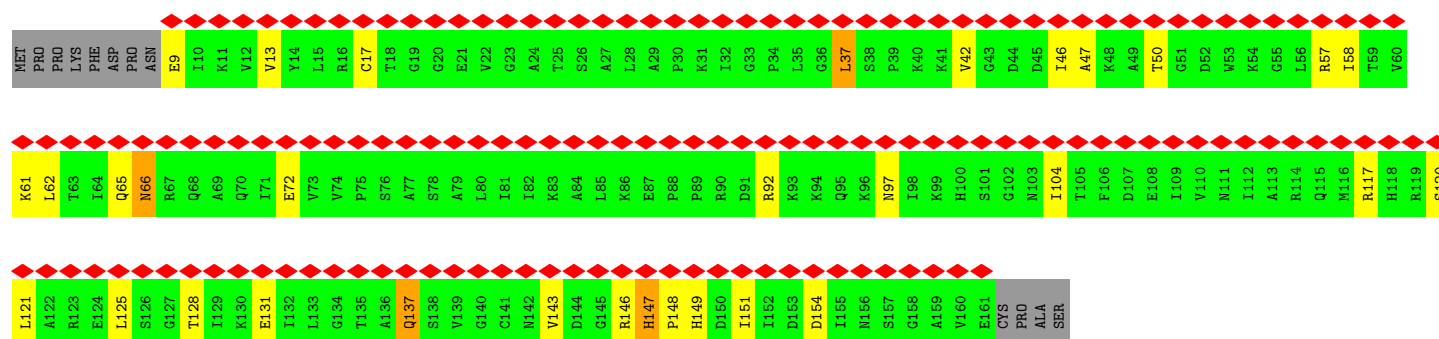


- Molecule 42: L28



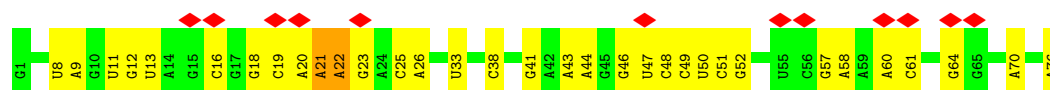
- Molecule 43: L12

Chain RA:



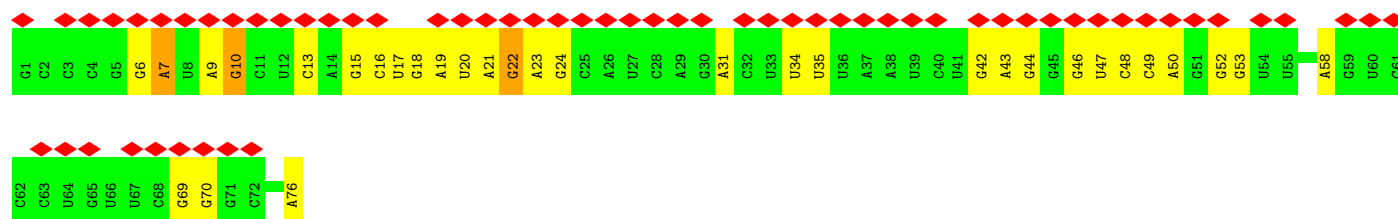
• Molecule 44: P-site tRNA

Chain SA:



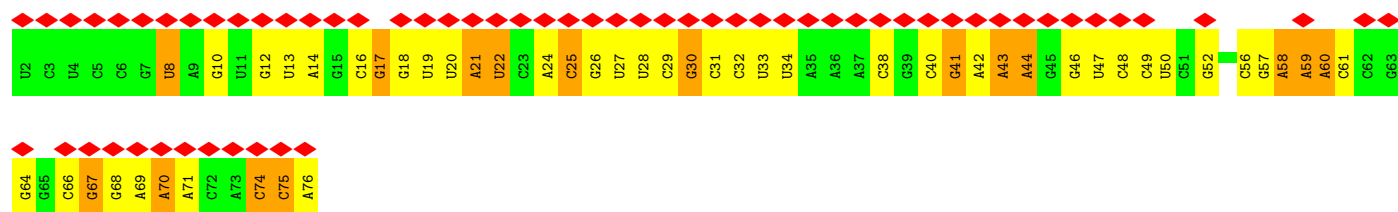
• Molecule 45: E-site tRNA

Chain TA:



• Molecule 46: A-site tRNA

Chain UA:



• Molecule 47: mRNA

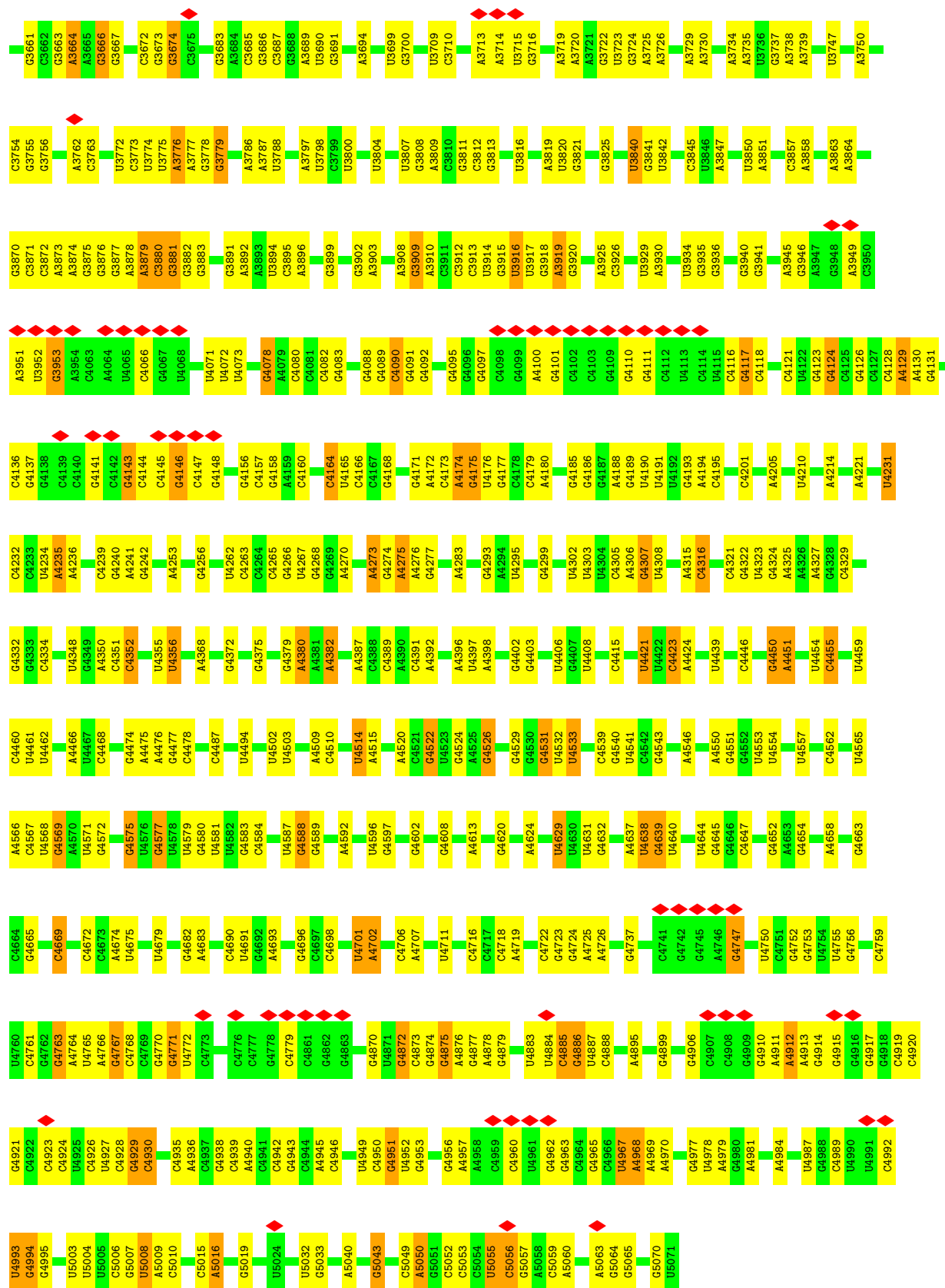
Chain VA:



• Molecule 48: 28S rRNA







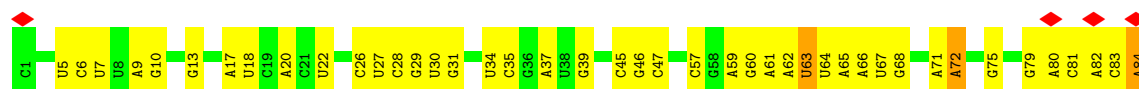
Chain XA: 



U

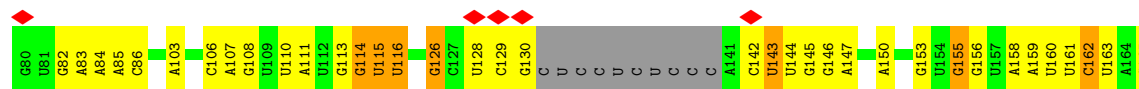
• Molecule 50: 5.8S rRNA

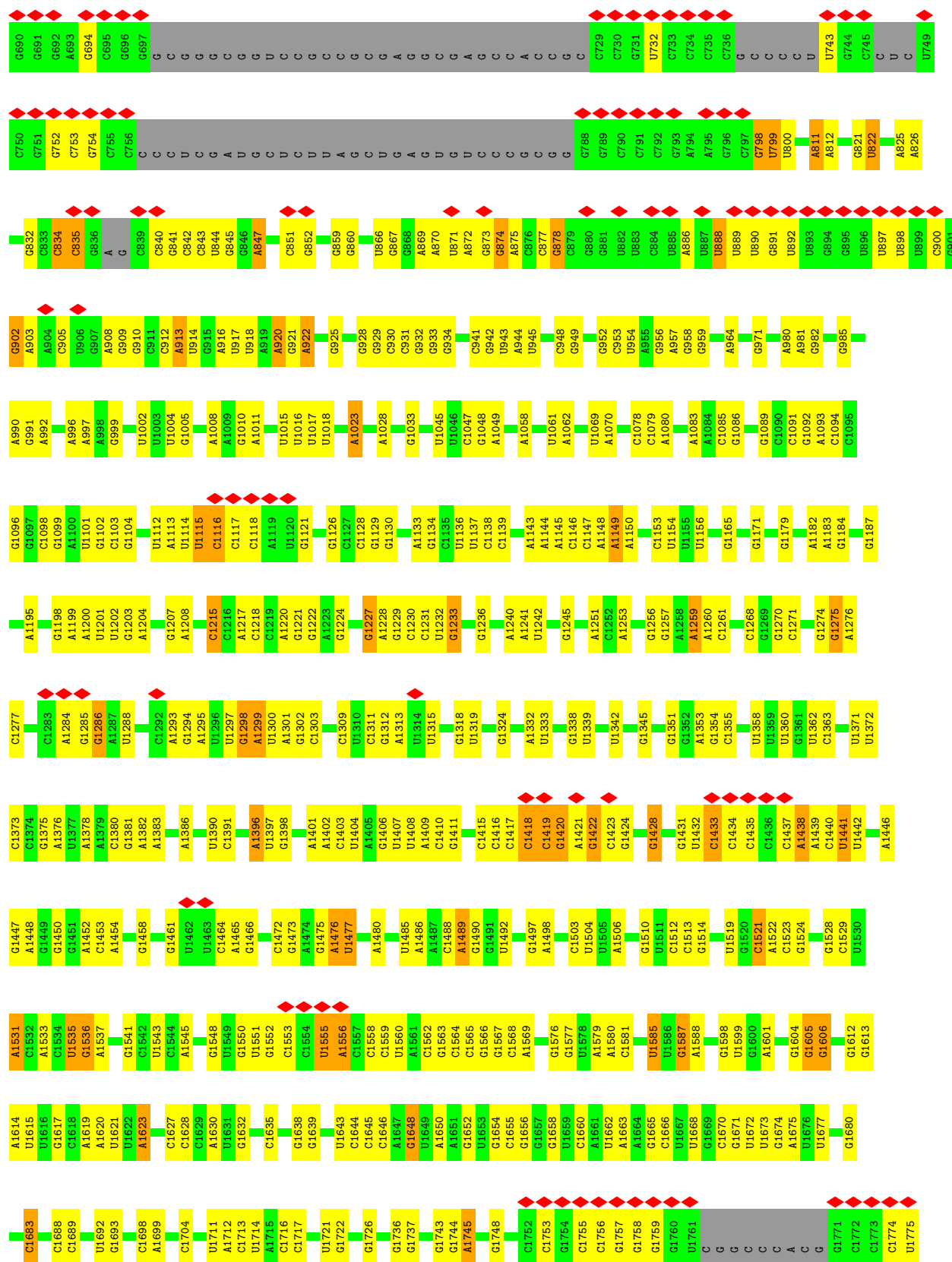
Chain YA: 



• Molecule 51: 18S rRNA

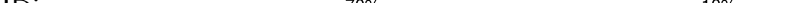
Chain ZA: 

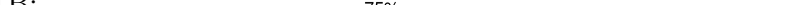


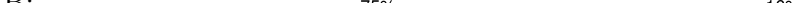







Chain DB: 

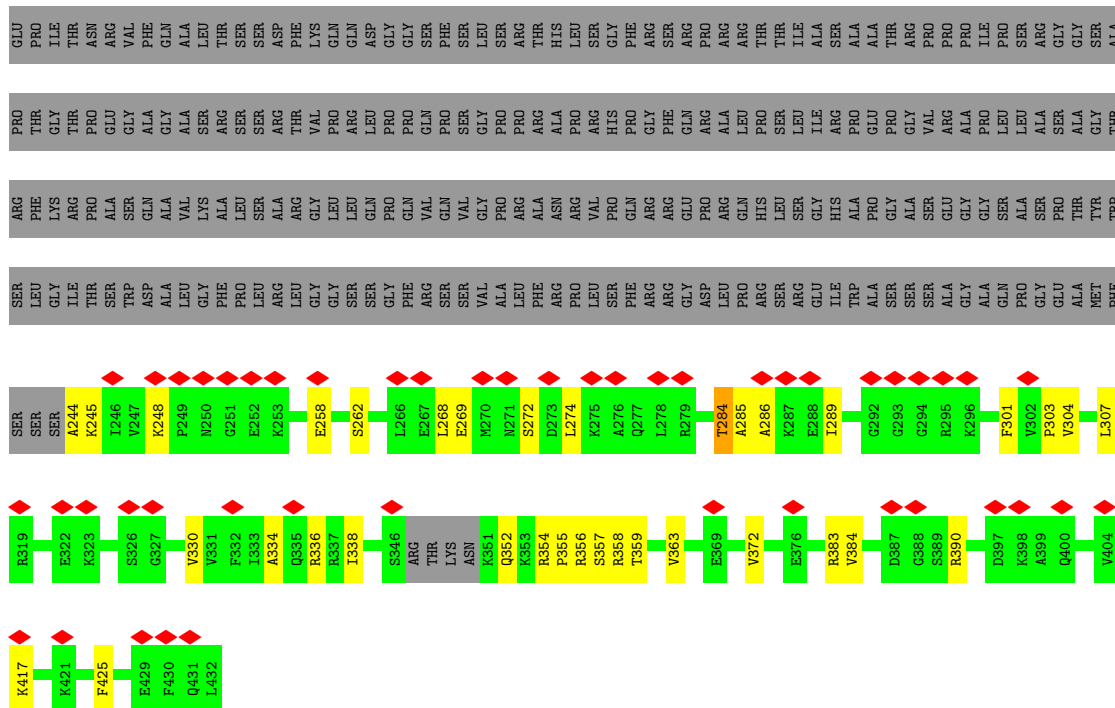
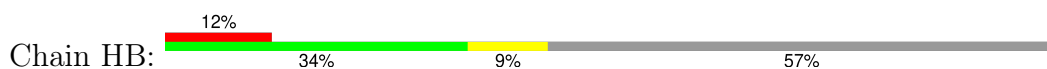
Chain EB: 

Chain FB: 

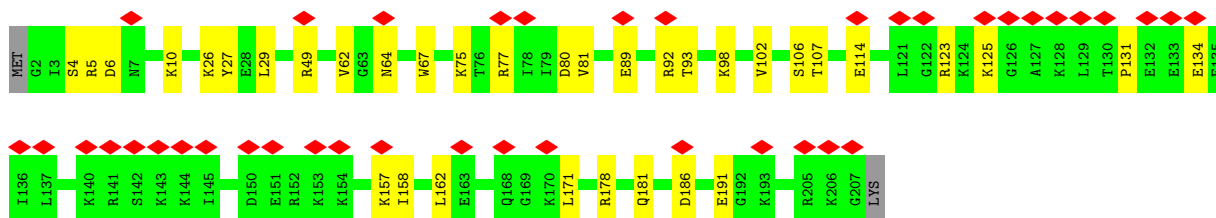
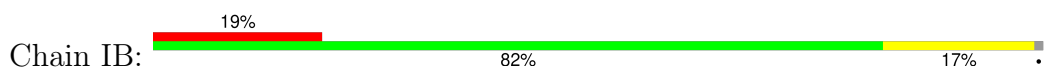
Chain GB: 



• Molecule 59: eS7

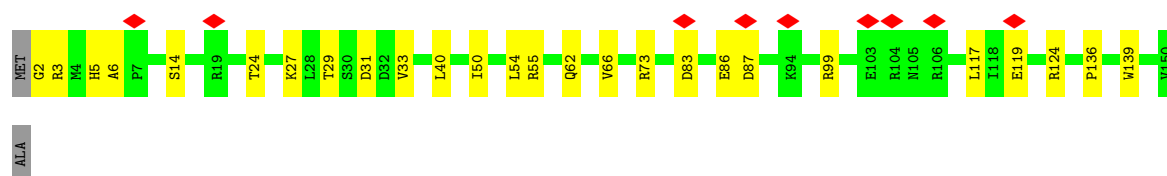
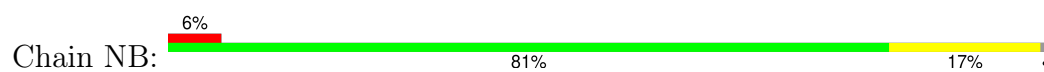


• Molecule 60: S8

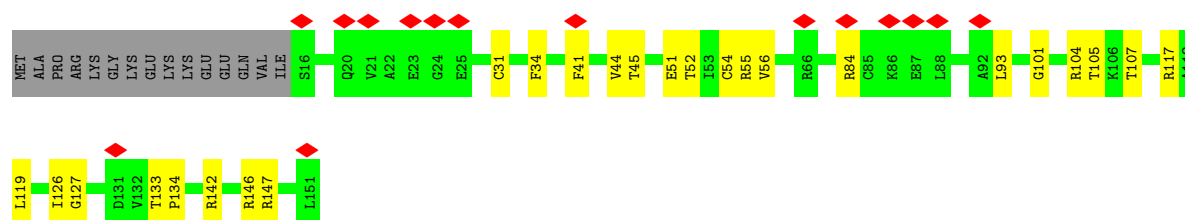
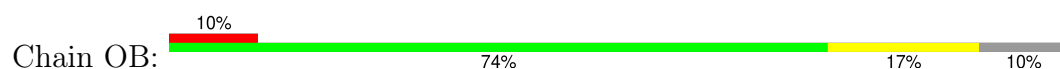


• Molecule 61: S9

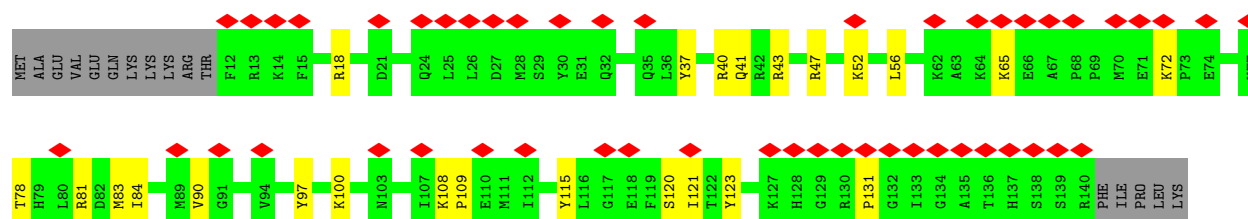
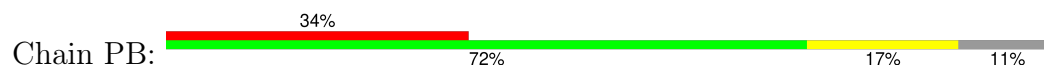




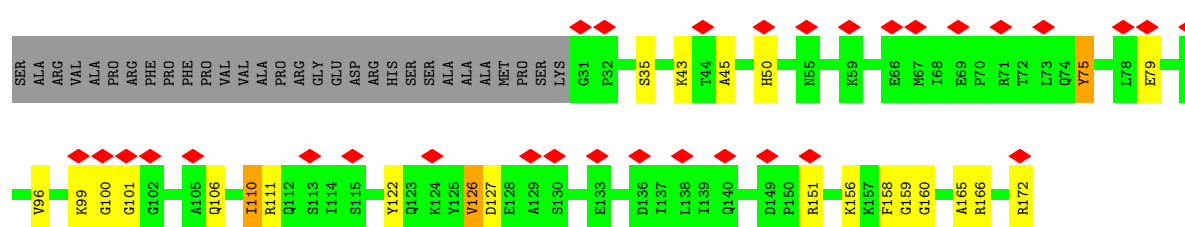
- Molecule 66: S14



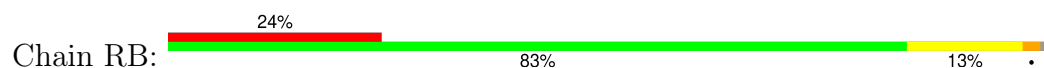
- Molecule 67: S15

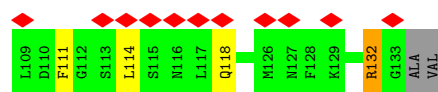


- Molecule 68: uS9



- Molecule 69: eS17

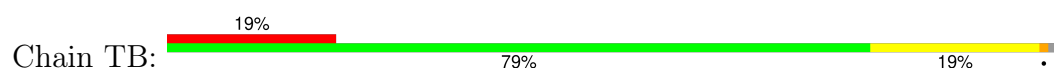




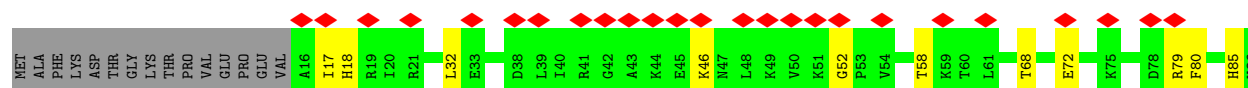
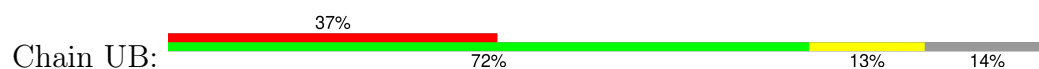
• Molecule 70: S18



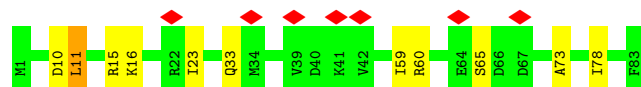
• Molecule 71: S19



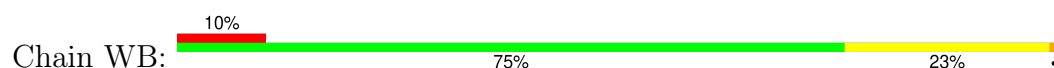
• Molecule 72: uS10

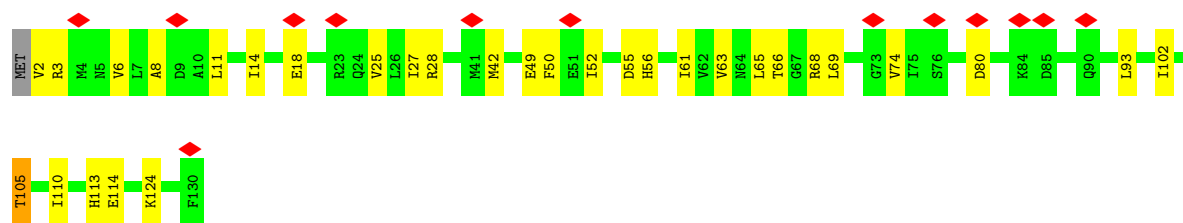


• Molecule 73: S21

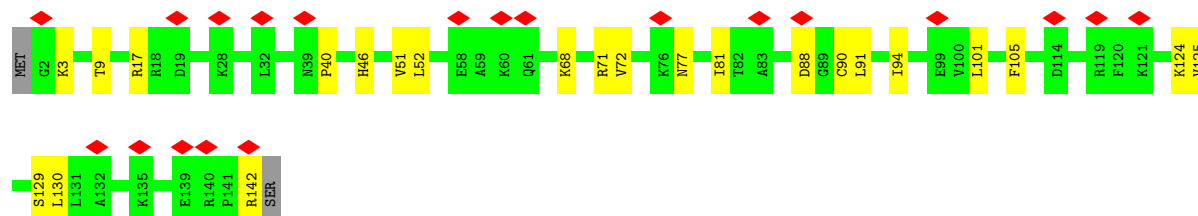
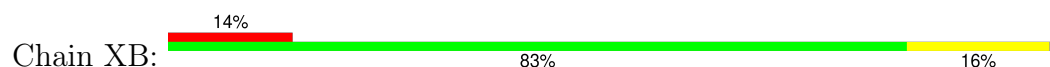


• Molecule 74: S15A

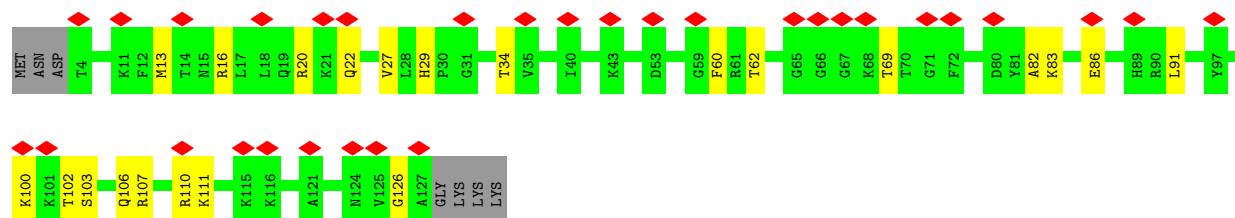
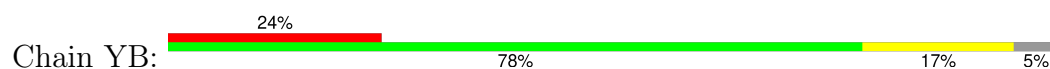




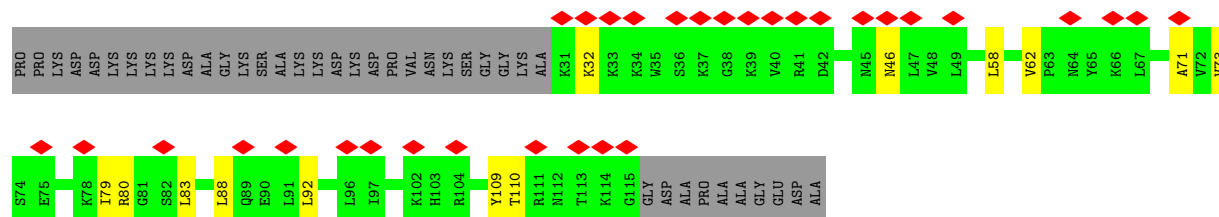
• Molecule 75: S23



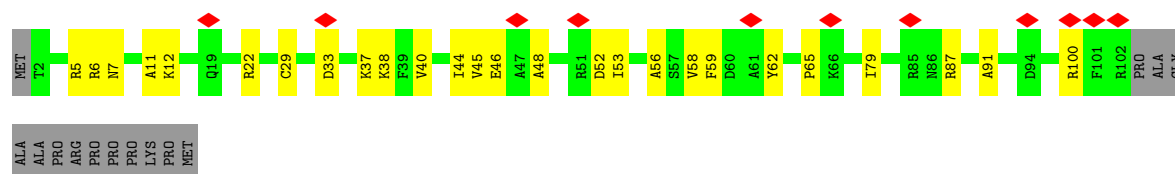
• Molecule 76: S24



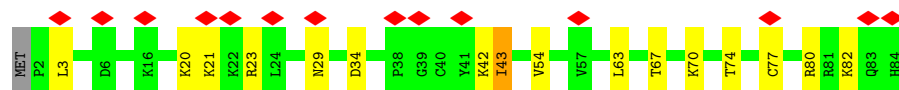
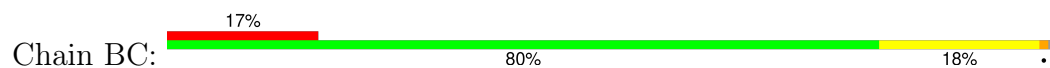
• Molecule 77: eS25



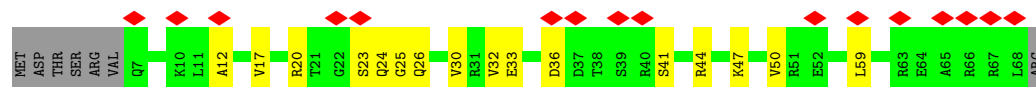
• Molecule 78: S26



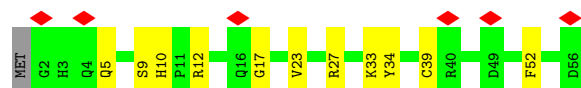
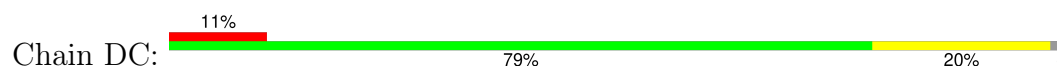
- Molecule 79: S27



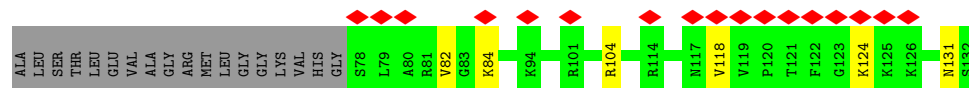
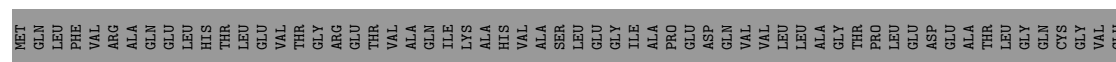
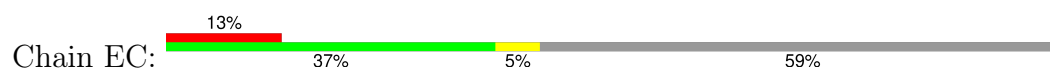
- Molecule 80: S28



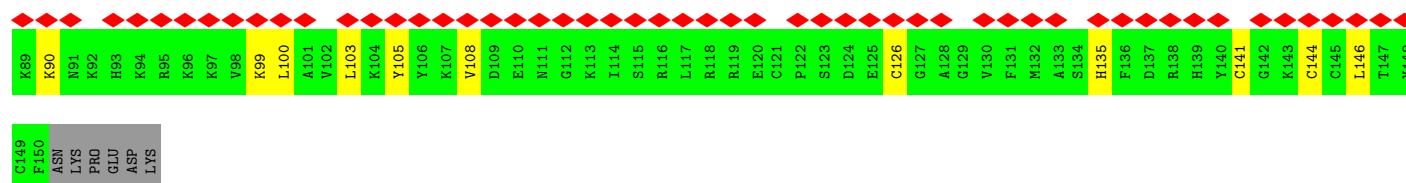
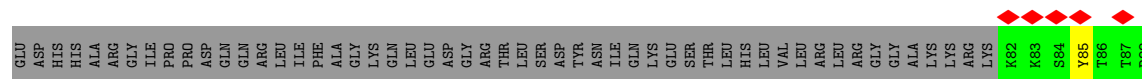
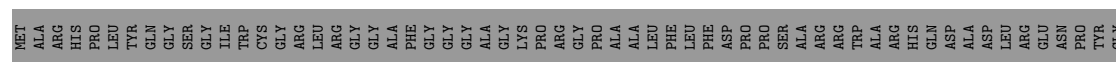
- Molecule 81: uS14



- Molecule 82: S30



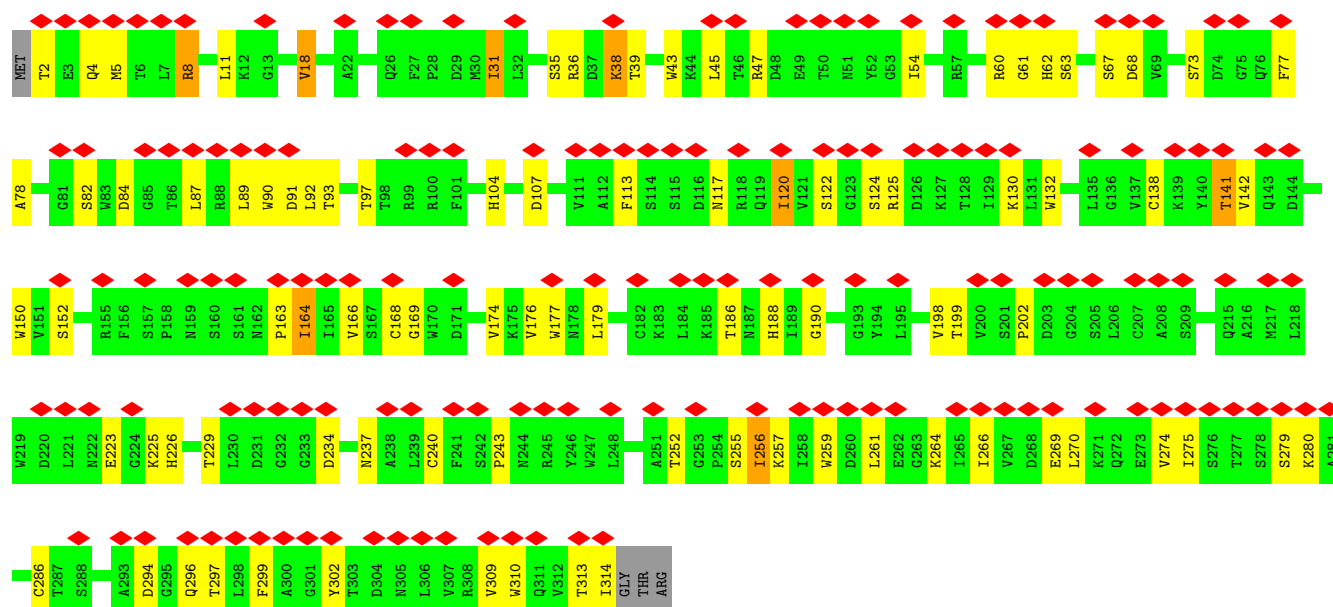
- Molecule 83: S27A




- Molecule 84: RACK1



Chain GC: 

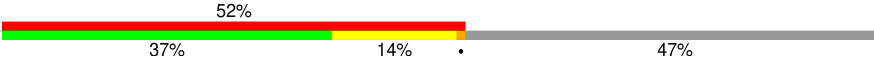


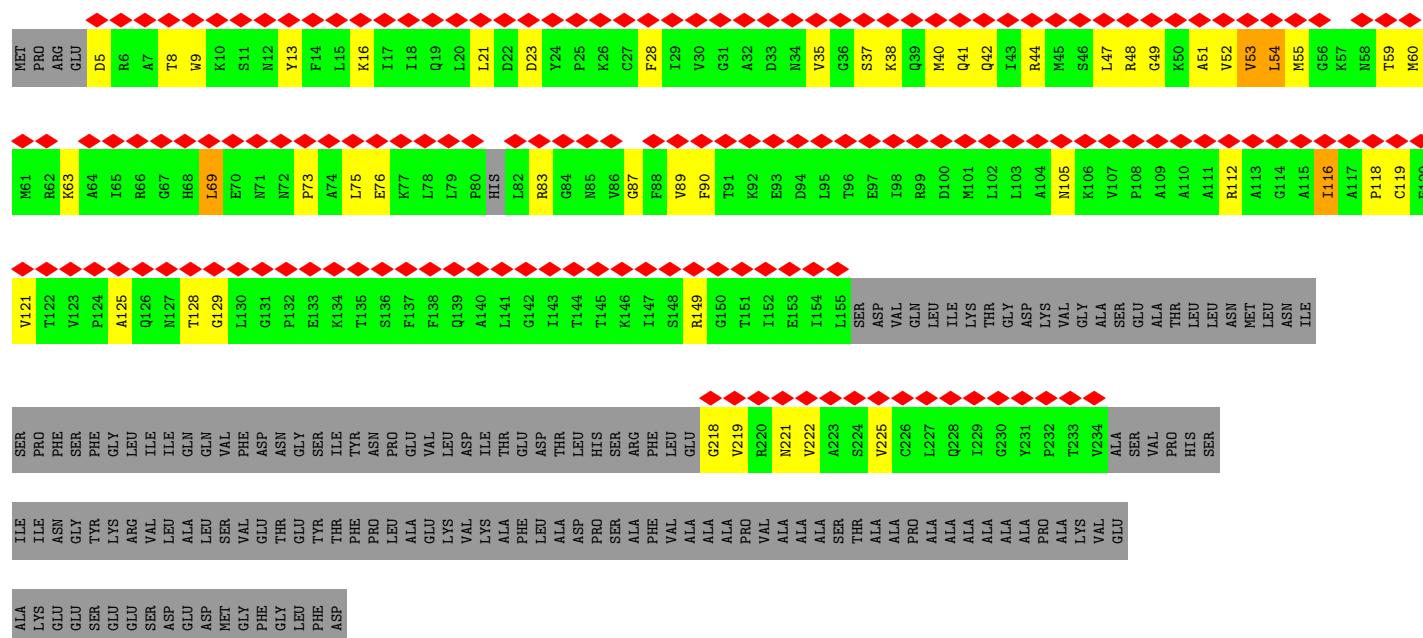
• Molecule 85: peptide

Chain IC: 



• Molecule 86: RPLP0

Chain b: 



Chain c:

100%

50%

50%

S241  
E242  
E243  
S244  
D245  
E246  
D247  
M248  
G249  
F250  
G251  
L252  
F253  
D254

Chain HC:

The figure displays the sequence and structural context of Chain HC. The top section shows a sequence logo with a 45% coverage bar. The central part is a sequence alignment with amino acid codes (e.g., MET, GLY, LYS, ASP, etc.) and their corresponding positions (e.g., 1, 2, 3, etc.). The bottom section features a series of colored blocks (yellow, green, orange) and diamond markers, likely representing specific residues or mutations of interest.

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	5498	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 ( $e^-/\text{\AA}^2$ )	75	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	33.748	Depositor
Minimum map value	-22.021	Depositor
Average map value	0.004	Depositor
Map value standard deviation	1.548	Depositor
Recommended contour level	6	Depositor
Map size ( $\text{\AA}$ )	686.87994, 686.87994, 686.87994	wwPDB
Map dimensions	648, 648, 648	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	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: ZN, SPD, MG, 5GP, K, ANM

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.12	0/1952	0.28	0/2617
2	B	0.12	0/3264	0.28	0/4371
3	C	0.11	0/2937	0.25	0/3946
4	D	0.10	0/2441	0.24	0/3269
5	E	0.10	0/1859	0.26	0/2491
6	F	0.11	0/1933	0.27	0/2577
7	G	0.11	0/1881	0.26	0/2532
8	H	0.11	0/1535	0.28	0/2063
9	I	0.11	0/1702	0.24	0/2272
10	J	0.10	0/1395	0.28	0/1863
11	K	0.10	0/1733	0.25	0/2316
12	L	0.11	0/1158	0.26	0/1547
13	M	0.12	0/1746	0.27	0/2338
14	N	0.12	0/1662	0.28	0/2222
15	O	0.11	0/1292	0.29	0/1733
16	P	0.11	0/1539	0.28	0/2054
17	Q	0.10	0/1524	0.25	0/2013
18	R	0.11	0/1501	0.28	0/2012
19	S	0.10	0/1326	0.24	0/1770
20	T	0.11	0/840	0.31	0/1127
21	U	0.12	0/1018	0.27	0/1364
22	V	0.11	0/900	0.27	0/1194
23	W	0.10	0/984	0.25	0/1323
24	X	0.10	0/1132	0.23	0/1504
25	Y	0.11	0/1130	0.24	0/1507
26	Z	0.11	0/1191	0.26	0/1590
27	AA	0.08	0/886	0.20	0/1171
28	BA	0.10	0/779	0.23	0/1044
29	CA	0.11	0/908	0.27	0/1223
30	DA	0.11	0/1082	0.24	0/1443
31	EA	0.12	0/895	0.27	0/1198
32	FA	0.11	0/916	0.28	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	GA	0.09	0/1016	0.24	0/1341
34	HA	0.09	0/841	0.23	0/1112
35	IA	0.11	0/731	0.26	0/966
36	JA	0.09	0/575	0.26	0/761
37	KA	0.11	0/459	0.27	0/608
38	LA	0.10	0/435	0.26	0/575
39	MA	0.09	0/240	0.19	0/305
40	NA	0.10	0/864	0.23	0/1140
41	OA	0.12	0/718	0.32	0/953
42	PA	0.12	0/1010	0.30	0/1354
43	RA	0.12	0/1174	0.32	0/1582
44	SA	0.10	0/1815	0.23	0/2828
45	TA	0.09	0/1804	0.23	0/2810
46	UA	0.13	0/1783	0.32	0/2776
47	VA	0.08	0/279	0.21	0/431
48	WA	0.12	0/85839	0.25	0/133881
49	XA	0.11	0/2836	0.20	0/4421
50	YA	0.11	0/3701	0.24	0/5766
51	ZA	0.11	0/40949	0.25	0/63819
52	AB	0.11	0/1747	0.26	0/2374
53	BB	0.10	0/1756	0.26	0/2350
54	CB	0.12	0/1744	0.29	0/2358
55	DB	0.10	0/1796	0.25	0/2417
56	EB	0.11	0/2118	0.30	0/2849
57	FB	0.11	0/1492	0.29	0/2005
58	GB	0.10	0/1946	0.25	0/2590
59	HB	0.10	0/1511	0.27	0/2022
60	IB	0.11	0/1715	0.27	0/2287
61	JB	0.10	0/1550	0.27	0/2069
62	KB	0.10	0/834	0.28	0/1125
63	LB	0.10	0/1200	0.25	0/1604
64	MB	0.10	0/918	0.29	0/1233
65	NB	0.10	0/1226	0.23	0/1649
66	OB	0.11	0/1029	0.28	0/1380
67	PB	0.13	0/1079	0.29	0/1441
68	QB	0.12	0/1146	0.30	0/1534
69	RB	0.10	0/1082	0.26	0/1452
70	SB	0.10	0/1208	0.28	0/1618
71	TB	0.10	0/1123	0.25	0/1504
72	UB	0.10	0/818	0.28	0/1099
73	VB	0.10	0/643	0.27	0/860
74	WB	0.11	0/1051	0.31	0/1406
75	XB	0.10	0/1116	0.26	0/1490

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	YB	0.10	0/1028	0.28	0/1366
77	ZB	0.10	0/691	0.25	0/922
78	AC	0.11	0/828	0.27	0/1109
79	BC	0.08	0/665	0.23	0/891
80	CC	0.09	0/490	0.25	0/656
81	DC	0.09	0/470	0.24	0/623
82	EC	0.08	0/447	0.23	0/587
83	FC	0.10	0/576	0.27	0/764
84	GC	0.11	0/2493	0.31	0/3394
85	IC	0.05	0/19	0.15	0/25
86	b	0.14	0/1296	0.32	0/1745
87	c	0.12	0/111	0.30	0/145
88	HC	0.11	0/1694	0.29	0/2287
All	All	0.11	0/236766	0.25	0/347573

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1914	0	2013	40	0
2	B	3196	0	3339	53	0
3	C	2883	0	3053	32	0
4	D	2395	0	2427	29	0
5	E	1823	0	1995	29	0
6	F	1897	0	2021	33	0
7	G	1850	0	1991	25	0
8	H	1516	0	1597	13	0
9	I	1664	0	1712	22	0
10	J	1372	0	1412	23	0
11	K	1702	0	1820	25	0
12	L	1137	0	1211	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	M	1701	0	1749	37	0
14	N	1630	0	1778	30	0
15	O	1266	0	1302	15	0
16	P	1515	0	1634	35	0
17	Q	1508	0	1664	20	0
18	R	1462	0	1508	25	0
19	S	1298	0	1366	24	0
20	T	826	0	852	14	0
21	U	1004	0	1063	15	0
22	V	887	0	935	11	0
23	W	967	0	1040	11	0
24	X	1115	0	1205	16	0
25	Y	1107	0	1182	24	0
26	Z	1162	0	1209	24	0
27	AA	873	0	949	10	0
28	BA	769	0	803	11	0
29	CA	893	0	932	15	0
30	DA	1064	0	1160	20	0
31	EA	876	0	912	10	0
32	FA	906	0	998	5	0
33	GA	1008	0	1142	22	0
34	HA	830	0	916	6	0
35	IA	716	0	750	16	0
36	JA	569	0	637	9	0
37	KA	447	0	480	14	0
38	LA	429	0	465	7	0
39	MA	239	0	289	3	0
40	NA	851	0	920	15	0
41	OA	708	0	757	7	0
42	PA	994	0	1051	18	0
43	RA	1160	0	1218	18	0
44	SA	1622	0	825	15	0
45	TA	1615	0	820	14	0
46	UA	1596	0	810	19	0
47	VA	251	0	128	2	0
48	WA	76735	0	38762	941	0
49	XA	2538	0	1286	28	0
50	YA	3314	0	1683	40	0
51	ZA	36623	0	18504	475	0
52	AB	1710	0	1711	23	0
53	BB	1729	0	1803	23	0
54	CB	1707	0	1793	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	DB	1768	0	1863	21	0
56	EB	2076	0	2177	36	0
57	FB	1471	0	1522	24	0
58	GB	1923	0	2089	38	0
59	HB	1489	0	1582	25	0
60	IB	1686	0	1772	23	0
61	JB	1525	0	1640	27	0
62	KB	810	0	836	21	0
63	LB	1180	0	1254	14	0
64	MB	908	0	939	19	0
65	NB	1202	0	1289	18	0
66	OB	1016	0	1039	20	0
67	PB	1058	0	1104	17	0
68	QB	1128	0	1195	17	0
69	RB	1068	0	1121	15	0
70	SB	1190	0	1249	30	0
71	TB	1104	0	1140	20	0
72	UB	808	0	878	13	0
73	VB	636	0	637	8	0
74	WB	1034	0	1080	22	0
75	XB	1098	0	1167	15	0
76	YB	1011	0	1083	19	0
77	ZB	683	0	761	9	0
78	AC	814	0	864	19	0
79	BC	651	0	672	9	0
80	CC	488	0	514	12	0
81	DC	459	0	449	8	0
82	EC	443	0	492	7	0
83	FC	564	0	577	7	0
84	GC	2436	0	2393	49	0
85	IC	20	0	10	1	0
86	b	1279	0	1343	34	0
87	c	110	0	83	4	0
88	HC	1664	0	1721	31	0
89	A	1	0	0	0	0
89	AC	1	0	0	0	0
89	FA	1	0	0	0	0
89	HC	1	0	0	0	0
89	I	1	0	0	0	0
89	IA	1	0	0	0	0
89	O	1	0	0	0	0
89	P	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
89	U	1	0	0	0	0
89	VA	1	0	0	0	0
89	WA	142	0	0	0	0
89	XA	4	0	0	0	0
89	YA	2	0	0	0	0
89	Z	1	0	0	0	0
89	ZA	45	0	0	0	0
90	AC	1	0	0	0	0
90	DC	1	0	0	0	0
90	FA	1	0	0	0	0
90	FC	1	0	0	0	0
90	IA	1	0	0	0	0
90	LA	1	0	0	0	0
90	NA	1	0	0	0	0
90	OA	1	0	0	0	0
91	UA	24	0	11	0	0
92	WA	19	0	18	1	0
93	WA	20	0	38	1	0
93	ZA	10	0	19	0	0
94	WA	1	0	0	0	0
95	HC	6	0	4	0	0
All	All	220661	0	164207	2523	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 2523 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:2847:A:H61	48:WA:3845:C:N4	1.54	1.04
48:WA:2847:A:N6	48:WA:3845:C:H42	1.58	1.00
51:ZA:197:U:H3	51:ZA:202:G:H1	1.04	1.00
48:WA:1249:U:H3	48:WA:1268:G:H1	1.03	0.96
51:ZA:1743:G:N2	51:ZA:1791:A:H62	1.64	0.95

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	248/257 (96%)	236 (95%)	12 (5%)	0	100	100
2	B	395/403 (98%)	383 (97%)	12 (3%)	0	100	100
3	C	360/413 (87%)	348 (97%)	12 (3%)	0	100	100
4	D	292/297 (98%)	286 (98%)	6 (2%)	0	100	100
5	E	222/291 (76%)	217 (98%)	5 (2%)	0	100	100
6	F	225/249 (90%)	219 (97%)	6 (3%)	0	100	100
7	G	225/319 (70%)	220 (98%)	5 (2%)	0	100	100
8	H	188/192 (98%)	182 (97%)	6 (3%)	0	100	100
9	I	201/214 (94%)	196 (98%)	5 (2%)	0	100	100
10	J	169/178 (95%)	167 (99%)	2 (1%)	0	100	100
11	K	208/211 (99%)	202 (97%)	6 (3%)	0	100	100
12	L	136/218 (62%)	132 (97%)	4 (3%)	0	100	100
13	M	201/204 (98%)	198 (98%)	3 (2%)	0	100	100
14	N	197/203 (97%)	195 (99%)	2 (1%)	0	100	100
15	O	154/213 (72%)	151 (98%)	3 (2%)	0	100	100
16	P	185/188 (98%)	181 (98%)	4 (2%)	0	100	100
17	Q	178/212 (84%)	174 (98%)	4 (2%)	0	100	100
18	R	174/224 (78%)	166 (95%)	8 (5%)	0	100	100
19	S	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
20	T	99/128 (77%)	96 (97%)	3 (3%)	0	100	100
21	U	133/140 (95%)	129 (97%)	4 (3%)	0	100	100
22	V	106/157 (68%)	104 (98%)	2 (2%)	0	100	100
23	W	116/156 (74%)	115 (99%)	1 (1%)	0	100	100
24	X	132/145 (91%)	128 (97%)	4 (3%)	0	100	100
25	Y	133/136 (98%)	131 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	Z	145/148 (98%)	141 (97%)	4 (3%)	0	100	100
27	AA	103/245 (42%)	101 (98%)	2 (2%)	0	100	100
28	BA	97/115 (84%)	95 (98%)	2 (2%)	0	100	100
29	CA	106/125 (85%)	104 (98%)	2 (2%)	0	100	100
30	DA	127/135 (94%)	124 (98%)	3 (2%)	0	100	100
31	EA	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
32	FA	112/129 (87%)	111 (99%)	1 (1%)	0	100	100
33	GA	119/123 (97%)	117 (98%)	2 (2%)	0	100	100
34	HA	100/105 (95%)	93 (93%)	7 (7%)	0	100	100
35	IA	85/97 (88%)	84 (99%)	1 (1%)	0	100	100
36	JA	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
37	KA	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
38	LA	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
39	MA	23/25 (92%)	23 (100%)	0	0	100	100
40	NA	102/106 (96%)	98 (96%)	4 (4%)	0	100	100
41	OA	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
42	PA	122/137 (89%)	119 (98%)	3 (2%)	0	100	100
43	RA	151/165 (92%)	140 (93%)	11 (7%)	0	100	100
52	AB	215/295 (73%)	213 (99%)	2 (1%)	0	100	100
53	BB	211/264 (80%)	207 (98%)	4 (2%)	0	100	100
54	CB	218/293 (74%)	213 (98%)	5 (2%)	0	100	100
55	DB	226/281 (80%)	225 (100%)	1 (0%)	0	100	100
56	EB	260/263 (99%)	251 (96%)	9 (4%)	0	100	100
57	FB	181/204 (89%)	175 (97%)	6 (3%)	0	100	100
58	GB	235/249 (94%)	231 (98%)	4 (2%)	0	100	100
59	HB	181/432 (42%)	176 (97%)	5 (3%)	0	100	100
60	IB	204/208 (98%)	201 (98%)	3 (2%)	0	100	100
61	JB	183/194 (94%)	179 (98%)	4 (2%)	0	100	100
62	KB	94/165 (57%)	92 (98%)	2 (2%)	0	100	100
63	LB	140/158 (89%)	136 (97%)	4 (3%)	0	100	100
64	MB	115/132 (87%)	109 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
65	NB	147/151 (97%)	146 (99%)	1 (1%)	0	100	100
66	OB	134/151 (89%)	130 (97%)	4 (3%)	0	100	100
67	PB	127/145 (88%)	125 (98%)	2 (2%)	0	100	100
68	QB	140/172 (81%)	136 (97%)	4 (3%)	0	100	100
69	RB	130/135 (96%)	127 (98%)	3 (2%)	0	100	100
70	SB	142/152 (93%)	139 (98%)	3 (2%)	0	100	100
71	TB	140/145 (97%)	135 (96%)	5 (4%)	0	100	100
72	UB	100/119 (84%)	97 (97%)	3 (3%)	0	100	100
73	VB	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
74	WB	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
75	XB	139/143 (97%)	135 (97%)	4 (3%)	0	100	100
76	YB	122/131 (93%)	120 (98%)	2 (2%)	0	100	100
77	ZB	83/124 (67%)	82 (99%)	1 (1%)	0	100	100
78	AC	99/115 (86%)	96 (97%)	3 (3%)	0	100	100
79	BC	81/84 (96%)	79 (98%)	2 (2%)	0	100	100
80	CC	60/69 (87%)	60 (100%)	0	0	100	100
81	DC	53/56 (95%)	53 (100%)	0	0	100	100
82	EC	53/133 (40%)	51 (96%)	2 (4%)	0	100	100
83	FC	67/188 (36%)	63 (94%)	4 (6%)	0	100	100
84	GC	311/317 (98%)	301 (97%)	10 (3%)	0	100	100
85	IC	2/4 (50%)	2 (100%)	0	0	100	100
86	b	162/318 (51%)	152 (94%)	9 (6%)	1 (1%)	22	53
87	c	12/14 (86%)	12 (100%)	0	0	100	100
88	HC	221/462 (48%)	209 (95%)	12 (5%)	0	100	100
All	All	11783/14293 (82%)	11469 (97%)	313 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
86	b	225	VAL

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	192/199 (96%)	191 (100%)	1 (0%)	86	92
2	B	344/348 (99%)	337 (98%)	7 (2%)	50	74
3	C	302/337 (90%)	300 (99%)	2 (1%)	81	90
4	D	247/250 (99%)	246 (100%)	1 (0%)	89	94
5	E	201/251 (80%)	199 (99%)	2 (1%)	73	86
6	F	198/218 (91%)	198 (100%)	0	100	100
7	G	197/273 (72%)	194 (98%)	3 (2%)	60	80
8	H	169/171 (99%)	165 (98%)	4 (2%)	44	70
9	I	175/181 (97%)	173 (99%)	2 (1%)	70	84
10	J	144/149 (97%)	142 (99%)	2 (1%)	62	81
11	K	175/176 (99%)	171 (98%)	4 (2%)	45	70
12	L	117/161 (73%)	117 (100%)	0	100	100
13	M	171/172 (99%)	167 (98%)	4 (2%)	45	70
14	N	171/173 (99%)	171 (100%)	0	100	100
15	O	137/190 (72%)	137 (100%)	0	100	100
16	P	164/165 (99%)	162 (99%)	2 (1%)	67	83
17	Q	159/191 (83%)	159 (100%)	0	100	100
18	R	157/192 (82%)	153 (98%)	4 (2%)	42	69
19	S	139/140 (99%)	137 (99%)	2 (1%)	62	81
20	T	91/114 (80%)	91 (100%)	0	100	100
21	U	103/107 (96%)	101 (98%)	2 (2%)	52	75
22	V	89/126 (71%)	88 (99%)	1 (1%)	70	84
23	W	106/134 (79%)	105 (99%)	1 (1%)	75	88
24	X	124/135 (92%)	120 (97%)	4 (3%)	34	63
25	Y	117/118 (99%)	116 (99%)	1 (1%)	75	88
26	Z	119/120 (99%)	118 (99%)	1 (1%)	79	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	AA	87/184 (47%)	87 (100%)	0	100	100
28	BA	85/98 (87%)	83 (98%)	2 (2%)	44	70
29	CA	98/110 (89%)	98 (100%)	0	100	100
30	DA	115/121 (95%)	114 (99%)	1 (1%)	75	88
31	EA	88/89 (99%)	88 (100%)	0	100	100
32	FA	98/109 (90%)	95 (97%)	3 (3%)	35	63
33	GA	109/110 (99%)	106 (97%)	3 (3%)	38	66
34	HA	86/89 (97%)	86 (100%)	0	100	100
35	IA	74/80 (92%)	73 (99%)	1 (1%)	62	81
36	JA	64/65 (98%)	64 (100%)	0	100	100
37	KA	47/48 (98%)	46 (98%)	1 (2%)	48	72
38	LA	48/116 (41%)	47 (98%)	1 (2%)	48	72
39	MA	24/24 (100%)	24 (100%)	0	100	100
40	NA	92/94 (98%)	92 (100%)	0	100	100
41	OA	74/75 (99%)	73 (99%)	1 (1%)	62	81
42	PA	108/121 (89%)	107 (99%)	1 (1%)	75	88
43	RA	126/137 (92%)	117 (93%)	9 (7%)	12	39
52	AB	180/244 (74%)	179 (99%)	1 (1%)	84	91
53	BB	194/231 (84%)	192 (99%)	2 (1%)	73	86
54	CB	186/225 (83%)	185 (100%)	1 (0%)	86	92
55	DB	190/232 (82%)	189 (100%)	1 (0%)	86	92
56	EB	224/225 (100%)	219 (98%)	5 (2%)	47	71
57	FB	158/170 (93%)	156 (99%)	2 (1%)	65	82
58	GB	207/218 (95%)	203 (98%)	4 (2%)	52	75
59	HB	165/360 (46%)	161 (98%)	4 (2%)	44	70
60	IB	178/180 (99%)	176 (99%)	2 (1%)	70	84
61	JB	161/168 (96%)	160 (99%)	1 (1%)	84	91
62	KB	87/136 (64%)	86 (99%)	1 (1%)	70	84
63	LB	130/142 (92%)	128 (98%)	2 (2%)	60	80
64	MB	99/108 (92%)	93 (94%)	6 (6%)	15	43
65	NB	130/131 (99%)	129 (99%)	1 (1%)	79	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	OB	106/119 (89%)	105 (99%)	1 (1%)	75	88
67	PB	115/130 (88%)	111 (96%)	4 (4%)	31	61
68	QB	117/140 (84%)	114 (97%)	3 (3%)	41	68
69	RB	119/121 (98%)	115 (97%)	4 (3%)	32	62
70	SB	125/132 (95%)	123 (98%)	2 (2%)	58	79
71	TB	112/115 (97%)	109 (97%)	3 (3%)	40	67
72	UB	93/107 (87%)	90 (97%)	3 (3%)	34	63
73	VB	67/67 (100%)	66 (98%)	1 (2%)	60	80
74	WB	112/113 (99%)	111 (99%)	1 (1%)	75	88
75	XB	113/115 (98%)	110 (97%)	3 (3%)	40	67
76	YB	107/113 (95%)	107 (100%)	0	100	100
77	ZB	75/102 (74%)	74 (99%)	1 (1%)	65	82
78	AC	88/98 (90%)	87 (99%)	1 (1%)	70	84
79	BC	75/76 (99%)	73 (97%)	2 (3%)	40	67
80	CC	55/62 (89%)	55 (100%)	0	100	100
81	DC	48/49 (98%)	47 (98%)	1 (2%)	48	72
82	EC	46/106 (43%)	44 (96%)	2 (4%)	25	55
83	FC	62/154 (40%)	59 (95%)	3 (5%)	21	51
84	GC	272/275 (99%)	252 (93%)	20 (7%)	11	36
86	b	138/258 (54%)	128 (93%)	10 (7%)	12	38
87	c	12/12 (100%)	12 (100%)	0	100	100
88	HC	179/379 (47%)	163 (91%)	16 (9%)	8	29
All	All	10256/12074 (85%)	10069 (98%)	187 (2%)	54	76

5 of 187 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
69	RB	95	ILE
84	GC	18	VAL
70	SB	131	VAL
75	XB	105	PHE
84	GC	141	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 88 such sidechains are listed below:

Mol	Chain	Res	Type
60	IB	22	HIS
70	SB	10	GLN
60	IB	155	ASN
65	NB	49	GLN
75	XB	61	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
44	SA	75/76 (98%)	16 (21%)	3 (4%)
45	TA	75/76 (98%)	16 (21%)	0
46	UA	74/75 (98%)	38 (51%)	1 (1%)
47	VA	11/12 (91%)	3 (27%)	0
48	WA	3556/3584 (99%)	610 (17%)	20 (0%)
49	XA	118/120 (98%)	10 (8%)	0
50	YA	155/156 (99%)	32 (20%)	0
51	ZA	1707/1869 (91%)	327 (19%)	9 (0%)
All	All	5771/5968 (96%)	1052 (18%)	33 (0%)

5 of 1052 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
44	SA	9	A
44	SA	16	C
44	SA	18	G
44	SA	19	C
44	SA	20	A

5 of 33 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	ZA	752	G
51	ZA	870	A
51	ZA	1433	C
48	WA	1806	A
48	WA	1677	C

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

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



## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 219 ligands modelled in this entry, 213 are monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
92	ANM	WA	5228	94	20,20,20	4.08	7 (35%)	24,27,27	1.38	2 (8%)
91	5GP	UA	101	46	22,26,26	1.23	2 (9%)	24,40,40	1.28	4 (16%)
95	SER	HC	502	-	4,5,6	0.57	0	1,5,7	0.58	0
93	SPD	WA	5230	-	9,9,9	0.28	0	8,8,8	0.29	0
93	SPD	WA	5229	-	9,9,9	0.28	0	8,8,8	0.33	0
93	SPD	ZA	1933	-	9,9,9	0.26	0	8,8,8	0.30	0

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
92	ANM	WA	5228	94	-	6/10/23/23	0/2/2/2
91	5GP	UA	101	46	-	5/6/26/26	0/3/3/3
95	SER	HC	502	-	-	0/2/4/6	-
93	SPD	WA	5230	-	-	1/7/7/7	-
93	SPD	WA	5229	-	-	0/7/7/7	-
93	SPD	ZA	1933	-	-	1/7/7/7	-

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
92	WA	5228	ANM	C3-C2	-11.79	1.32	1.53
92	WA	5228	ANM	C16-N1	-8.89	1.30	1.47
92	WA	5228	ANM	C2-C16	7.41	1.68	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
91	UA	101	5GP	C5-C6	-4.13	1.39	1.47
92	WA	5228	ANM	C4-C3	3.97	1.58	1.53

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
92	WA	5228	ANM	O2-C5-C6	5.04	120.08	111.09
91	UA	101	5GP	C8-N7-C5	2.91	107.50	102.55
91	UA	101	5GP	C5-C6-N1	2.88	119.57	114.07
91	UA	101	5GP	C2-N1-C6	-2.31	120.88	125.11
92	WA	5228	ANM	C2-O2-C5	-2.28	114.17	117.72

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

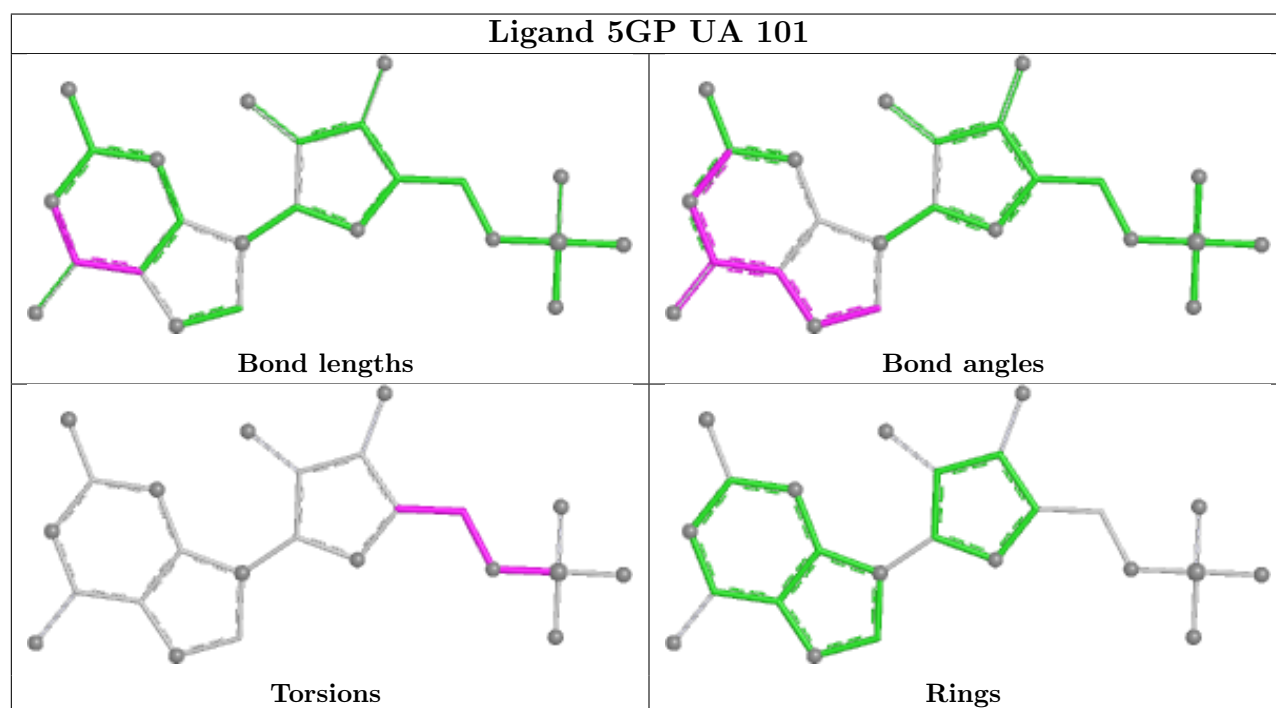
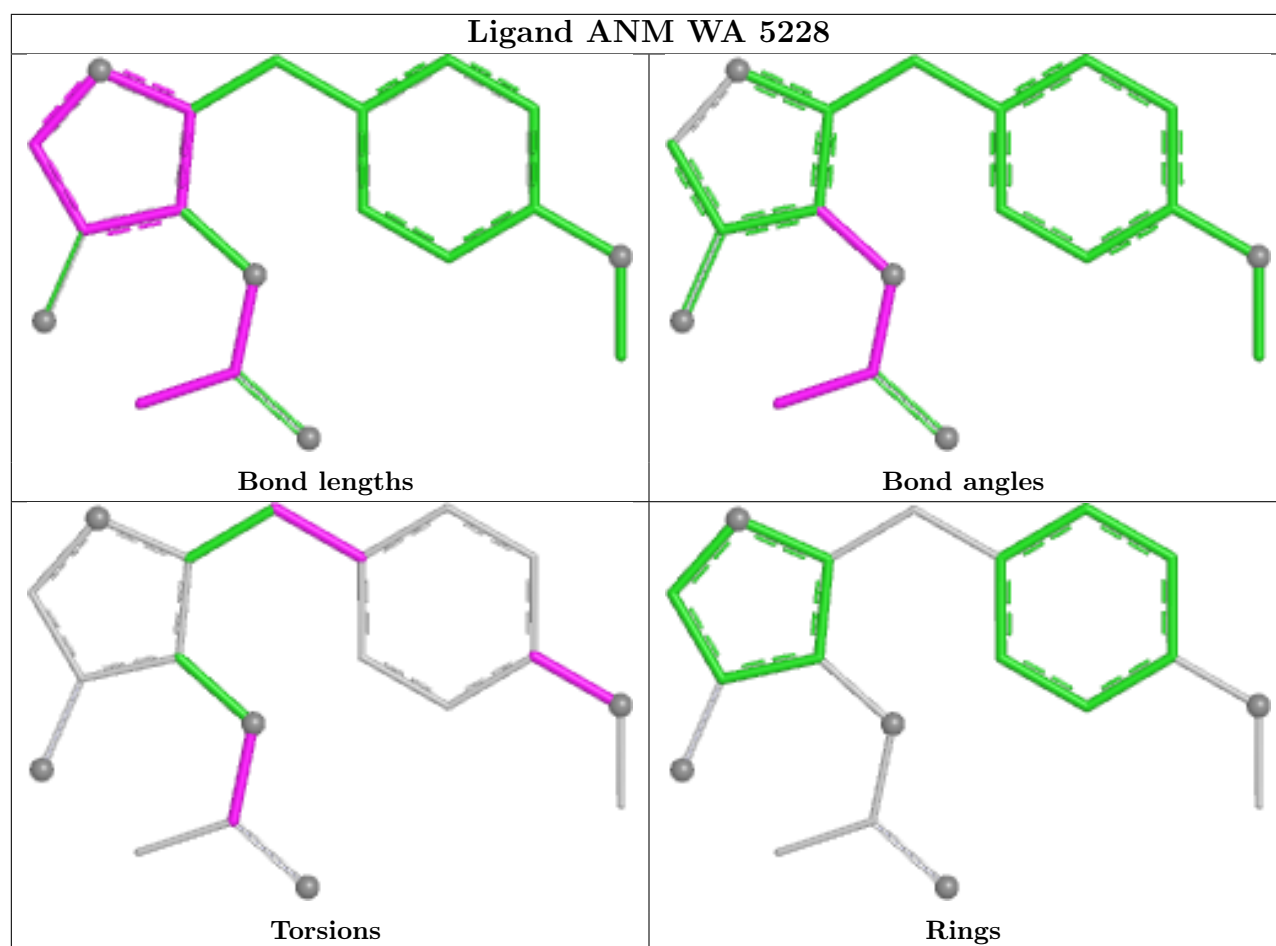
Mol	Chain	Res	Type	Atoms
92	WA	5228	ANM	C6-C5-O2-C2
92	WA	5228	ANM	O3-C5-O2-C2
92	WA	5228	ANM	C1-C9-O1-C14
92	WA	5228	ANM	C10-C9-O1-C14
91	UA	101	5GP	O4'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
92	WA	5228	ANM	1	0
93	WA	5229	SPD	1	0

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



## 5.7 Other polymers [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
48	WA	21
86	b	2

The worst 5 of 23 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	WA	2118:C	O3'	2260:C	P	37.14
1	WA	1225:G	O3'	1239:G	P	20.72
1	WA	996:C	O3'	1070:G	P	17.81
1	WA	4779:C	O3'	4861:C	P	17.44
1	WA	524:C	O3'	639:G	P	16.85

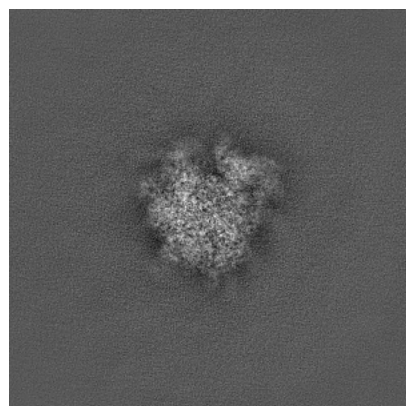
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43566. These allow visual inspection of the internal detail of the map and identification of artifacts.

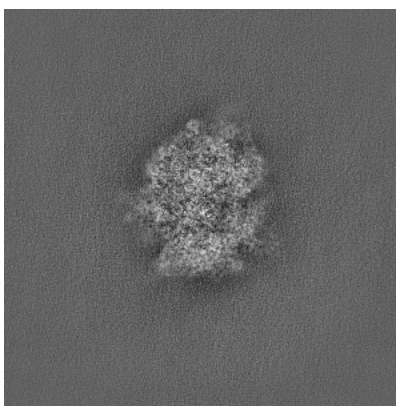
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

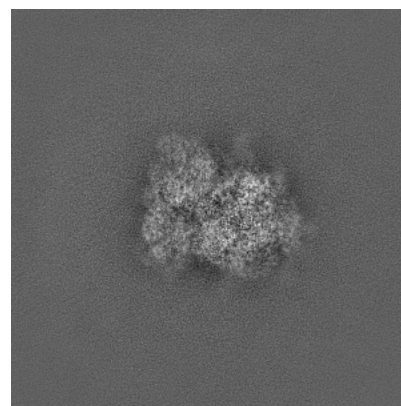
#### 6.1.1 Primary map



X

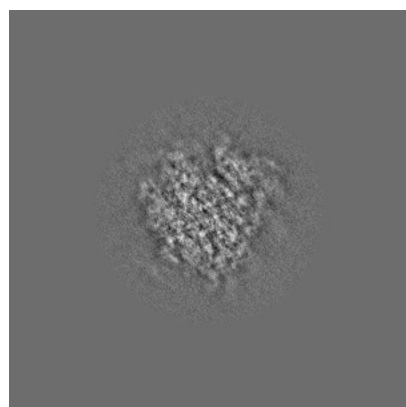


Y

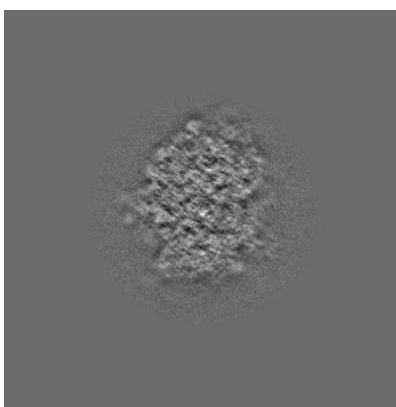


Z

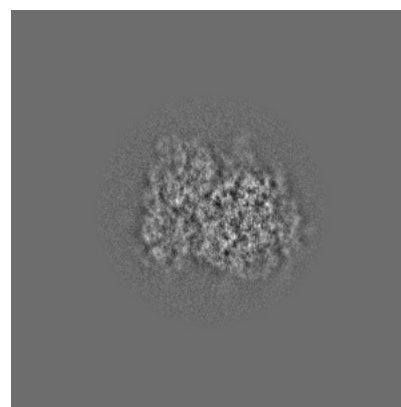
#### 6.1.2 Raw map



X



Y

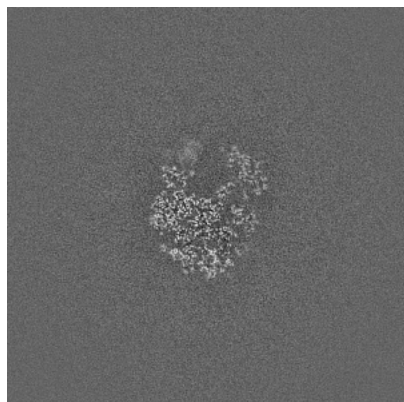


Z

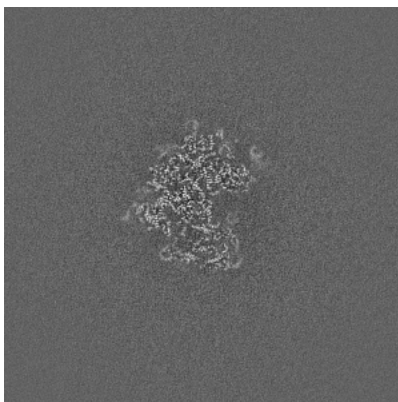
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

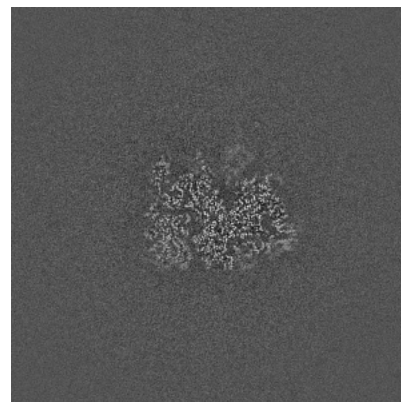
### 6.2.1 Primary map



X Index: 324

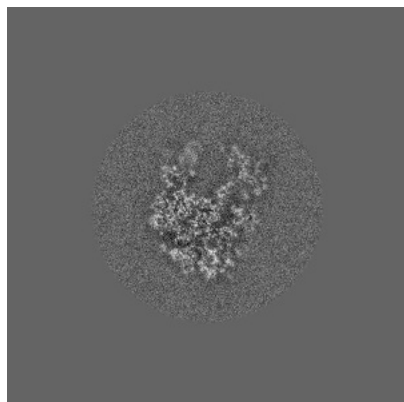


Y Index: 324

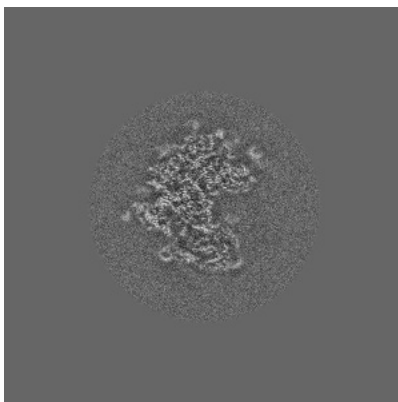


Z Index: 324

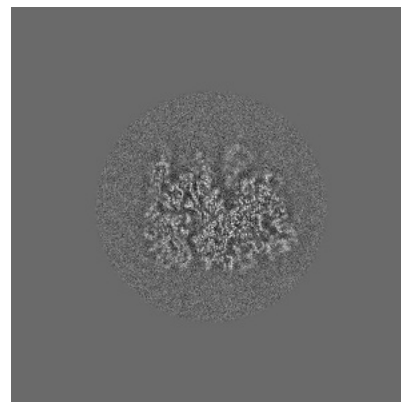
### 6.2.2 Raw map



X Index: 324



Y Index: 324



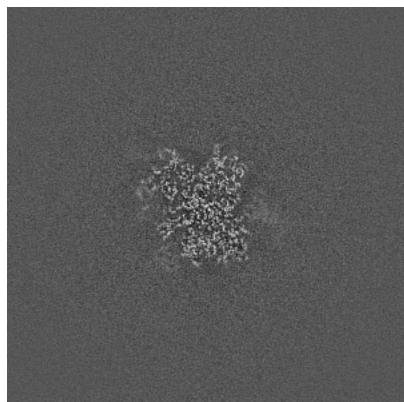
Z Index: 324

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

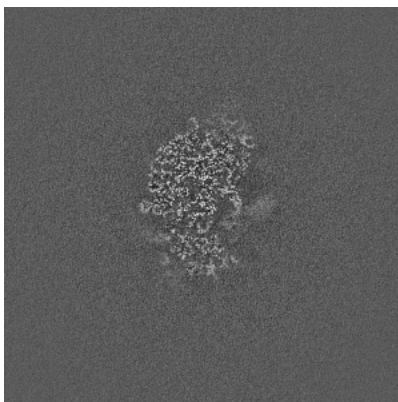


## 6.3 Largest variance slices [i](#)

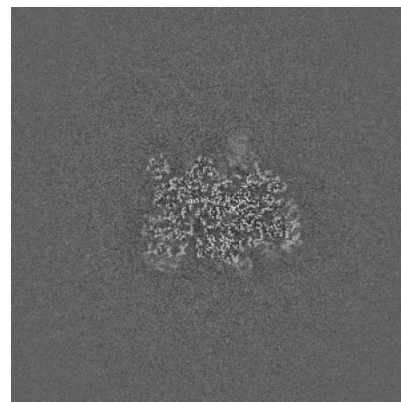
### 6.3.1 Primary map



X Index: 378

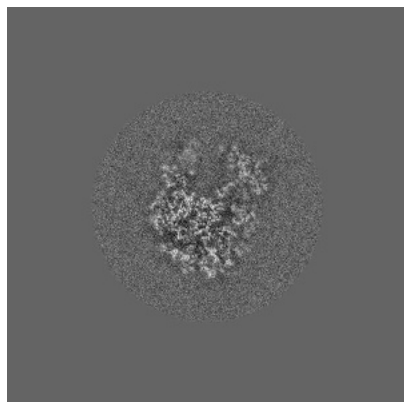


Y Index: 299

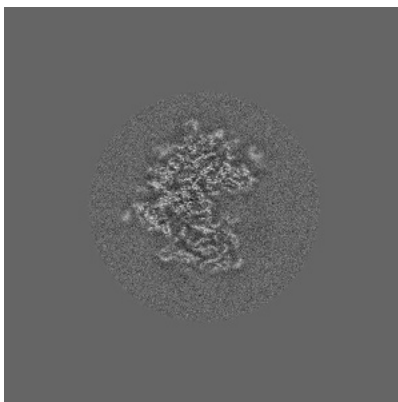


Z Index: 312

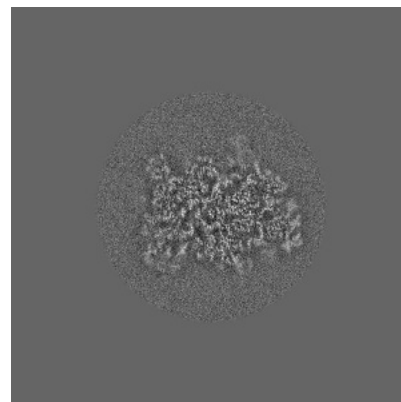
### 6.3.2 Raw map



X Index: 323



Y Index: 325

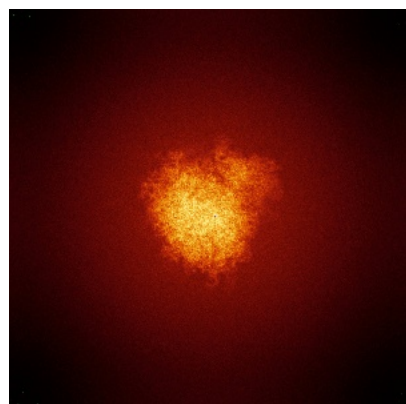


Z Index: 311

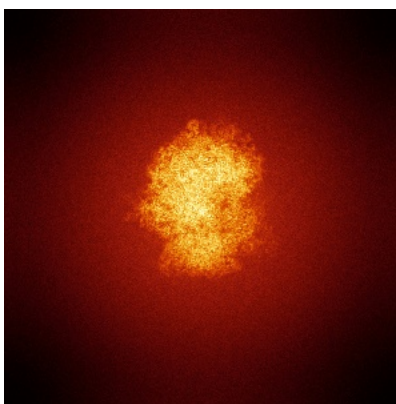
The images above show the largest variance slices of the map in three orthogonal directions.

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

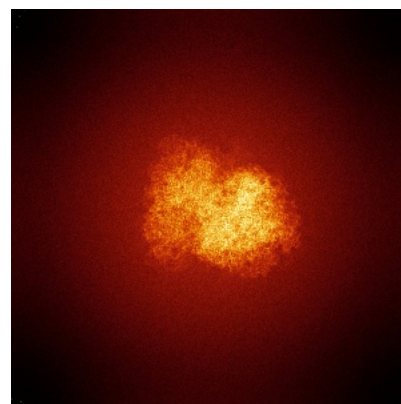
### 6.4.1 Primary map



X

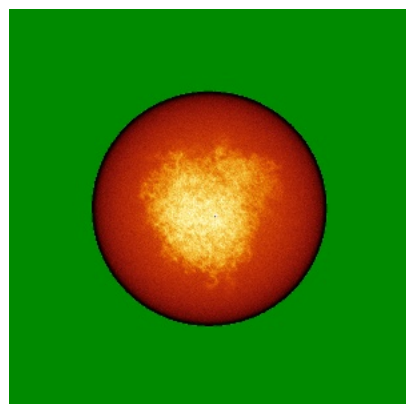


Y

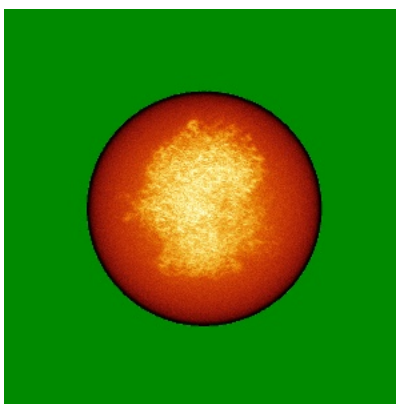


Z

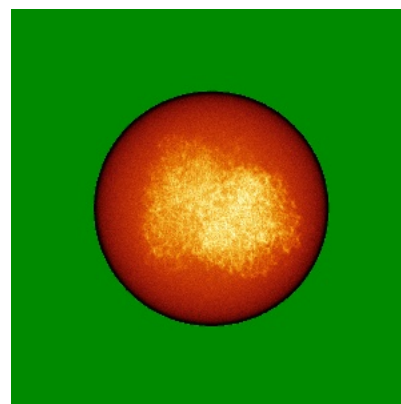
### 6.4.2 Raw map



X



Y



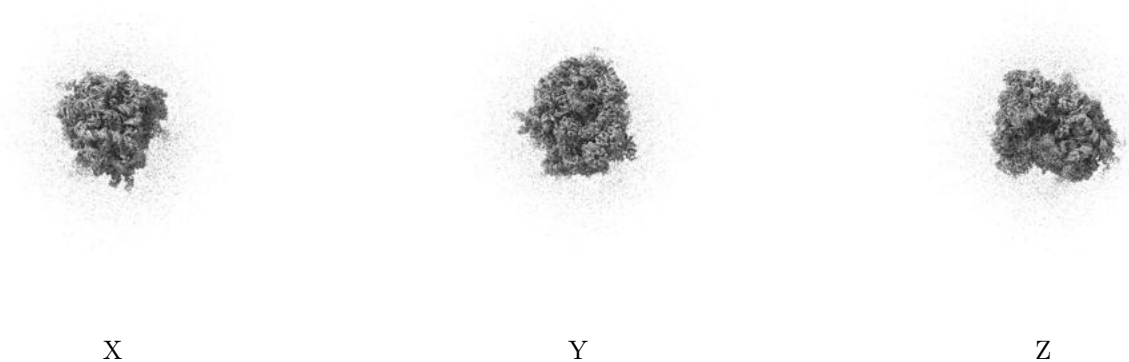
Z

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



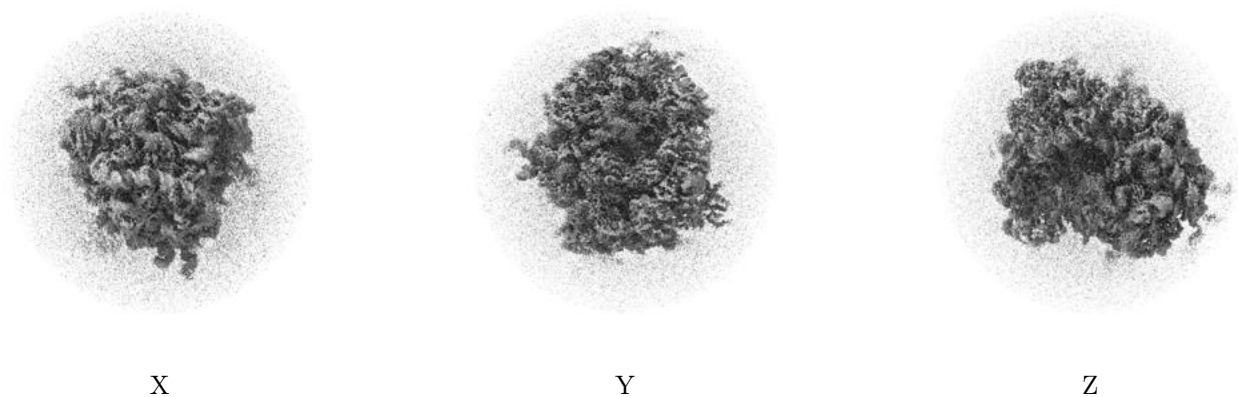
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 6.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



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

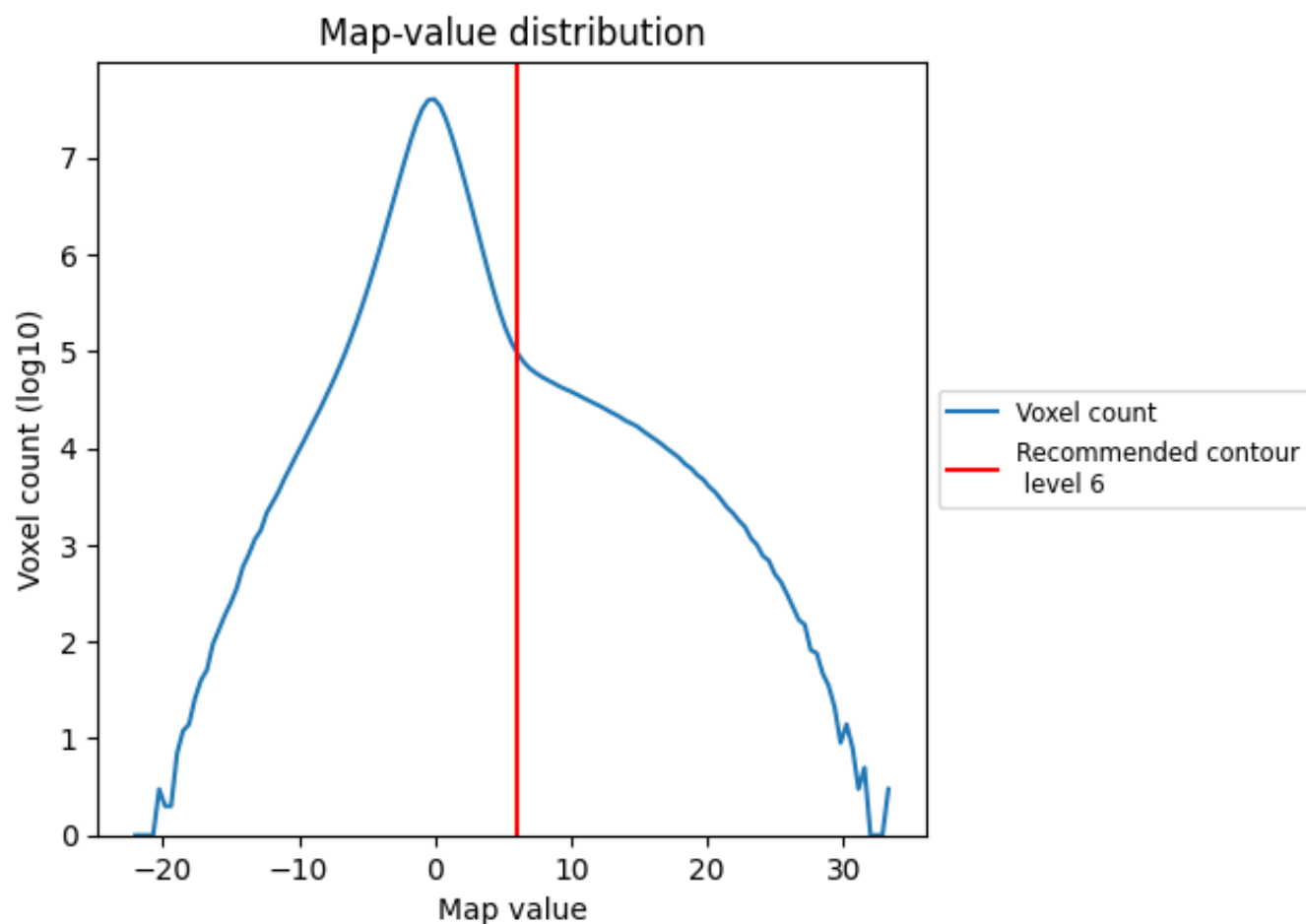
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

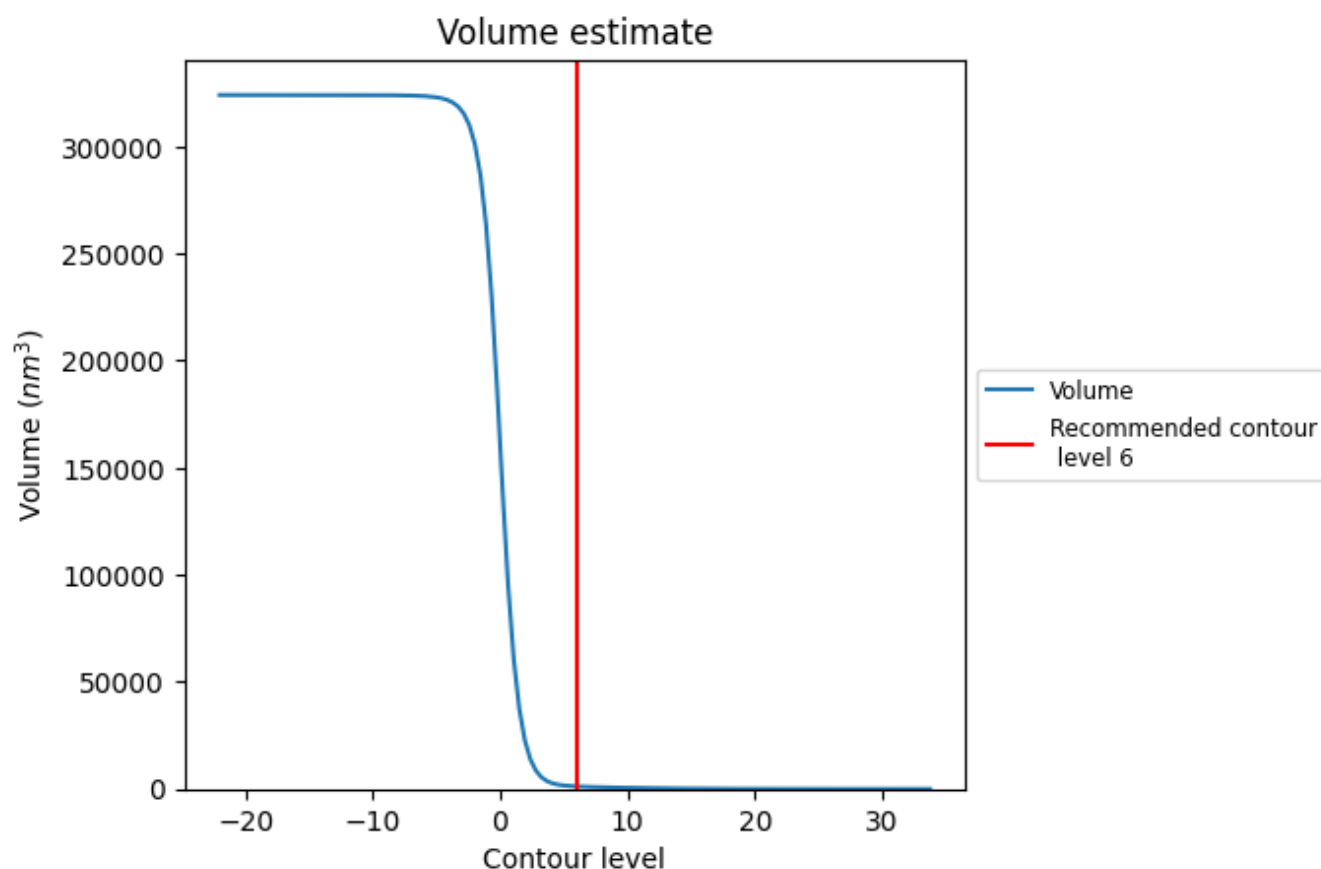
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

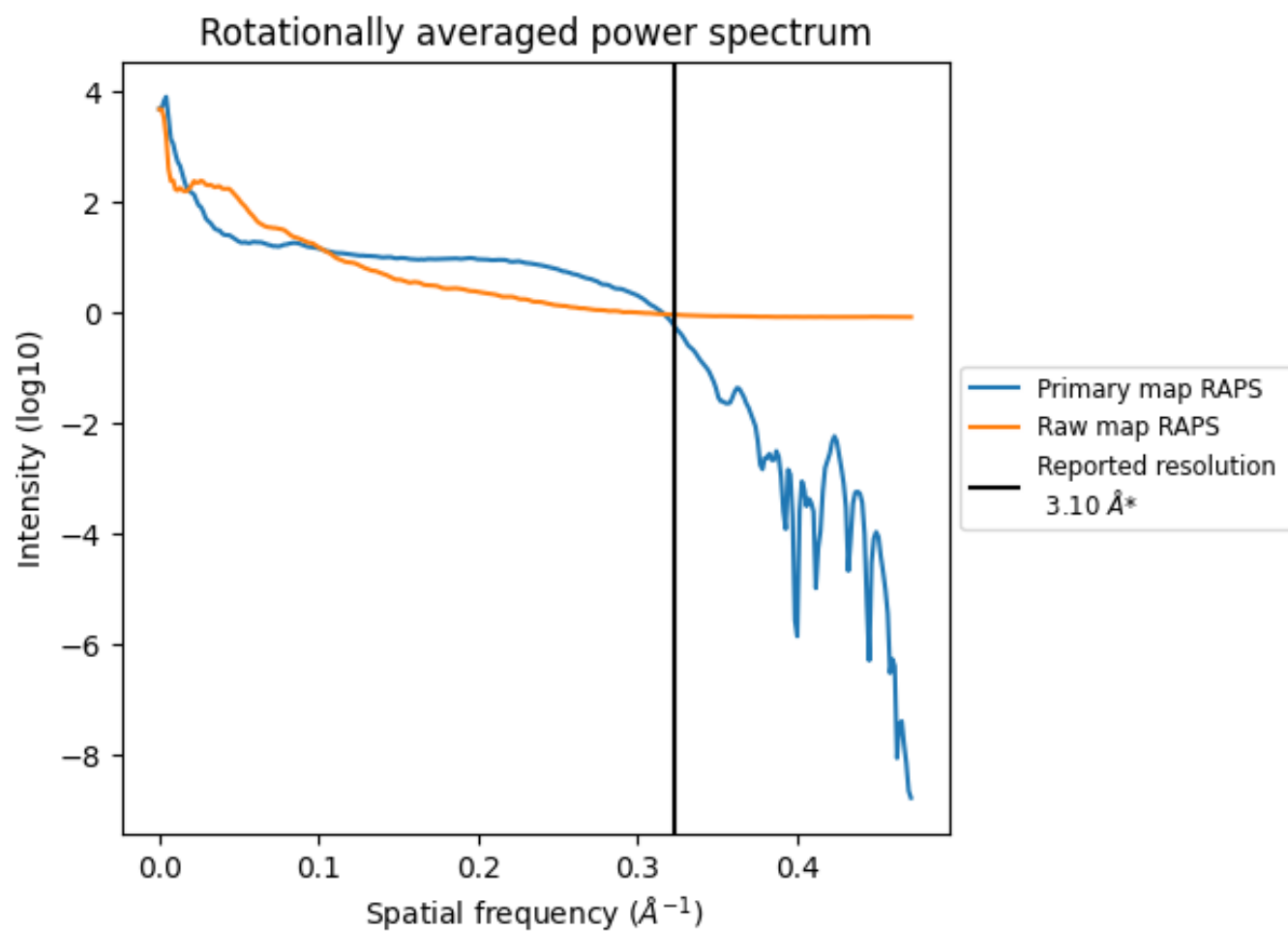
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1186  $\text{nm}^3$ ; this corresponds to an approximate mass of 1072 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 ⓘ

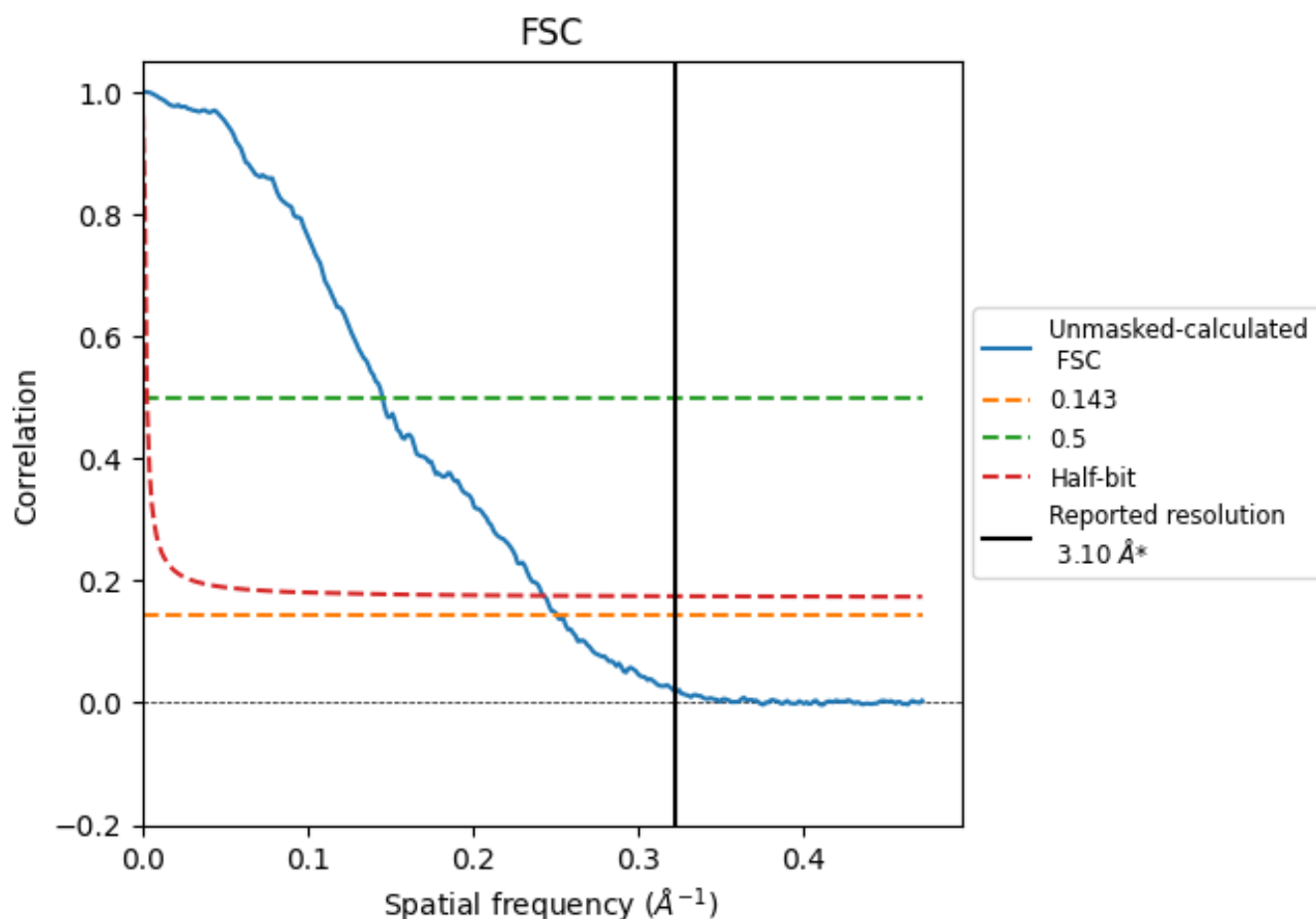


\*Reported resolution corresponds to spatial frequency of 0.323 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.323 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

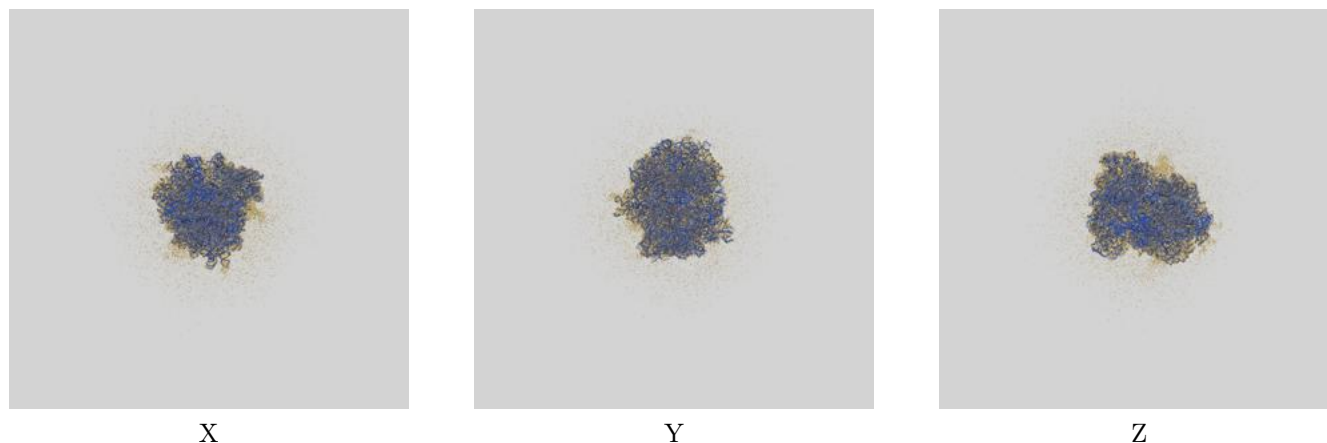
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.99	6.89	4.12

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.99 differs from the reported value 3.1 by more than 10 %

## 9 Map-model fit [i](#)

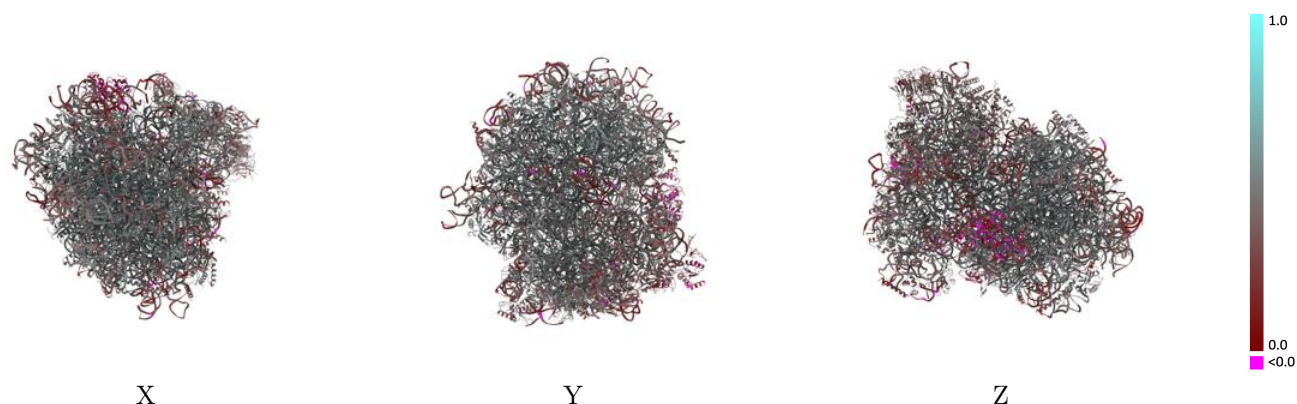
This section contains information regarding the fit between EMDB map EMD-43566 and PDB model 8VVR. Per-residue inclusion information can be found in [section 3](#) on [page 26](#).

### 9.1 Map-model overlay [i](#)



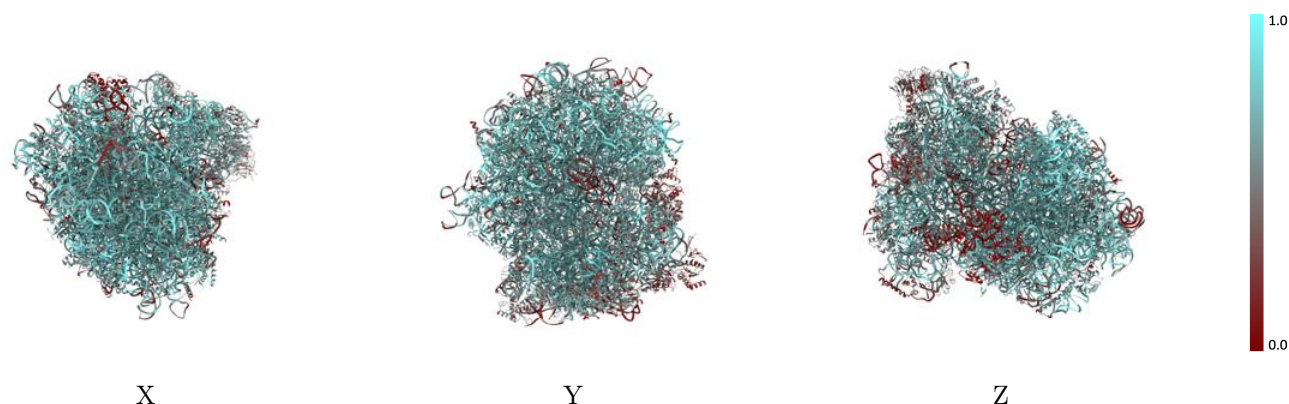
The images above show the 3D surface view of the map at the recommended contour level 6.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

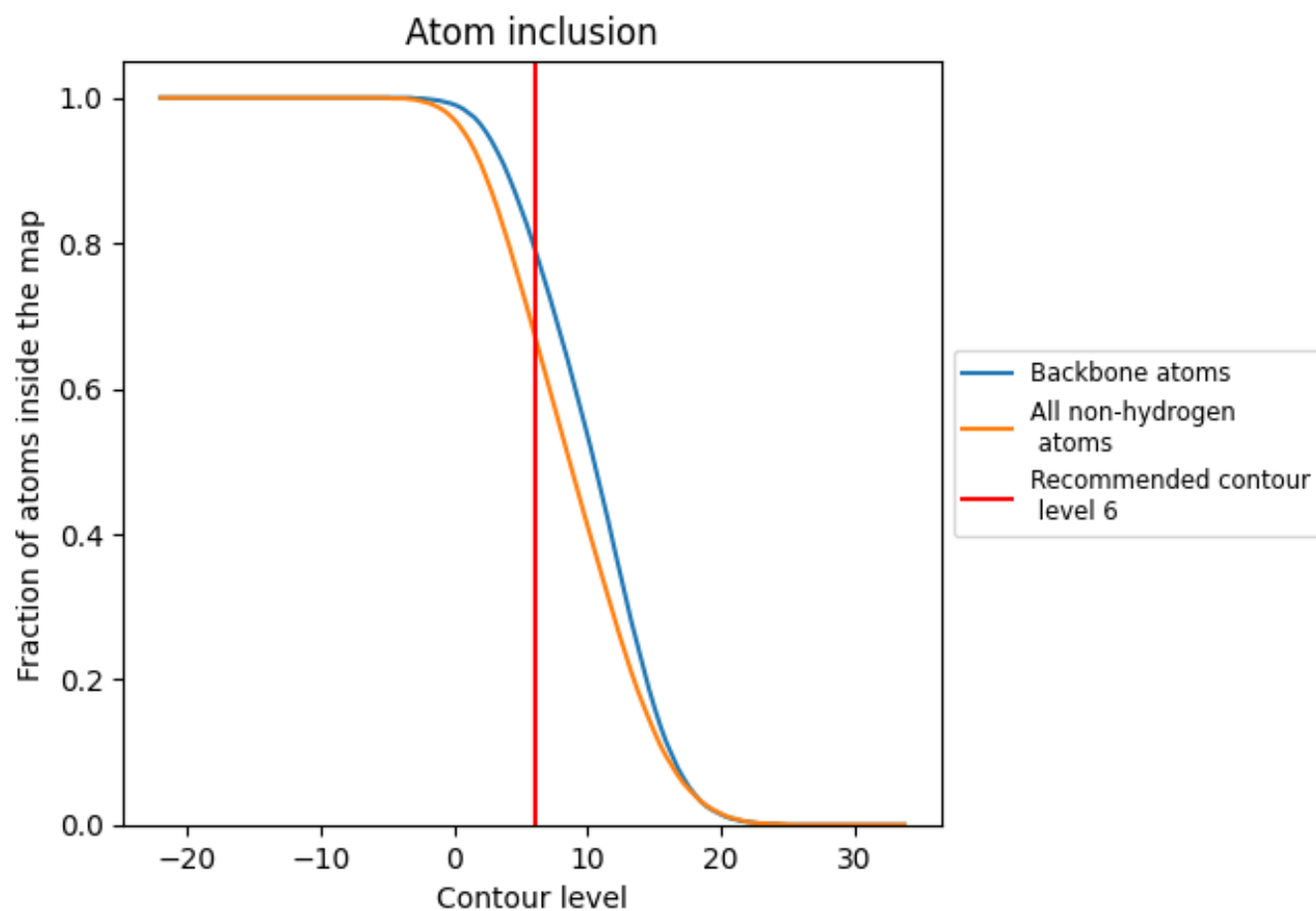
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (6).









































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 68% 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 (6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6750	 0.4410
A	 0.7060	 0.5200
AA	 0.5450	 0.4210
AB	 0.5990	 0.4410
AC	 0.6220	 0.4750
B	 0.6880	 0.4930
BA	 0.6640	 0.4640
BB	 0.5780	 0.4560
BC	 0.5540	 0.4340
C	 0.6780	 0.4980
CA	 0.6660	 0.4830
CB	 0.6130	 0.4630
CC	 0.5080	 0.4150
D	 0.6790	 0.4540
DA	 0.6810	 0.5090
DB	 0.4850	 0.3960
DC	 0.5910	 0.4400
E	 0.6230	 0.4470
EA	 0.6760	 0.5190
EB	 0.5700	 0.4510
EC	 0.4860	 0.3880
F	 0.6670	 0.4910
FA	 0.6590	 0.4870
FB	 0.5380	 0.4110
FC	 0.2160	 0.2470
G	 0.6390	 0.4380
GA	 0.6530	 0.4700
GB	 0.4720	 0.3630
GC	 0.3960	 0.3440
H	 0.6500	 0.4630
HA	 0.6510	 0.4520
HB	 0.5010	 0.3870
HC	 0.1340	 0.2910
I	 0.6900	 0.4970
IA	 0.7070	 0.5150



























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Chain	Atom inclusion	Q-score
IB	 0.5690	 0.4410
IC	 0.4500	 0.4380
J	 0.6210	 0.4360
JA	 0.5730	 0.4280
JB	 0.5880	 0.4320
K	 0.6560	 0.4800
KA	 0.6350	 0.4850
KB	 0.4820	 0.3660
L	 0.6510	 0.4610
LA	 0.7090	 0.4940
LB	 0.6240	 0.4810
M	 0.7110	 0.5170
MA	 0.6470	 0.4830
MB	 0.2220	 0.2090
N	 0.6930	 0.4880
NA	 0.6740	 0.5080
NB	 0.6420	 0.4630
O	 0.6750	 0.4990
OA	 0.6700	 0.5030
OB	 0.6030	 0.4530
P	 0.6930	 0.5050
PA	 0.6880	 0.4970
PB	 0.4600	 0.3640
Q	 0.6680	 0.4640
QB	 0.5400	 0.4130
R	 0.6790	 0.4910
RA	 0.0400	 0.0950
RB	 0.5420	 0.4090
S	 0.6650	 0.4890
SA	 0.6200	 0.3980
SB	 0.5400	 0.3980
T	 0.6020	 0.4290
TA	 0.2320	 0.2320
TB	 0.5440	 0.4010
U	 0.6690	 0.5050
UA	 0.2220	 0.2550
UB	 0.4550	 0.3760
V	 0.5090	 0.3860
VA	 0.5440	 0.4210
VB	 0.6220	 0.4440
W	 0.6510	 0.4700
WA	 0.7710	 0.4530

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Chain	Atom inclusion	Q-score
WB	 0.6230	 0.4740
X	 0.6600	 0.4770
XA	 0.8620	 0.4890
XB	 0.6020	 0.4740
Y	 0.6940	 0.4730
YA	 0.7790	 0.4620
YB	 0.5050	 0.3960
Z	 0.7280	 0.5100
ZA	 0.7230	 0.4300
ZB	 0.4480	 0.3710
b	 0.0650	 0.1310
c	 0.0180	 0.1630