



wwPDB EM Validation Summary Report ⓘ

Jun 25, 2026 – 04:12 PM EDT

PDB ID : 8VVS / pdb_00008vvs
EMDB ID : EMD-43567
Title : Post-decoding post-hydrolysis state obtained from merged datasets of elongation inhibitor-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

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:

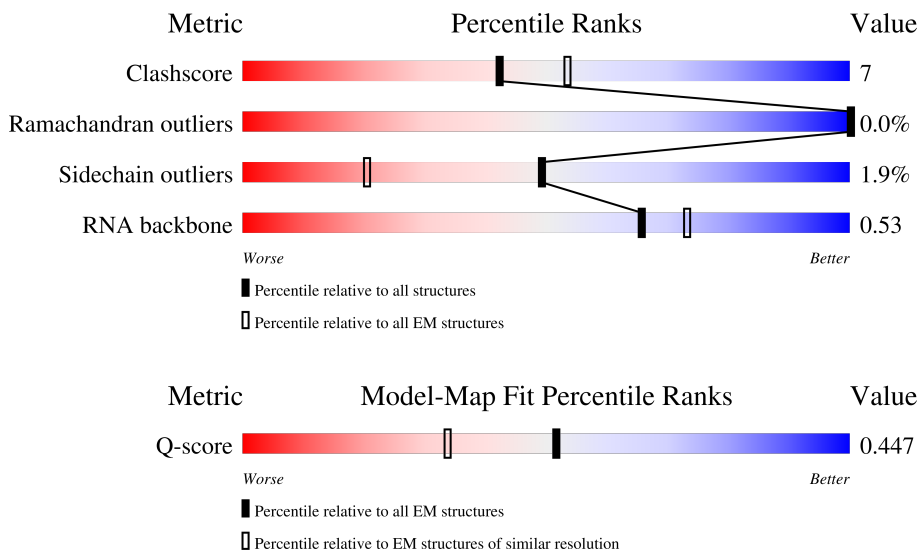
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	A	257	
2	B	403	
3	C	413	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	297	8% 86% 13%
5	E	291	12% 64% 14% 22%
6	F	249	6% 71% 20% 9%
7	G	319	8% 61% 11% 28%
8	H	192	6% 85% 13%
9	I	214	7% 79% 16%
10	J	178	15% 76% 20%
11	K	211	9% 85% 14%
12	L	218	5% 49% 15% 37%
13	M	204	5% 77% 22%
14	N	203	5% 77% 21%
15	O	213	5% 62% 11% 27%
16	P	188	• 79% 20% ••
17	Q	212	9% 72% 13% 15%
18	R	224	• 65% 13% 21%
19	S	160	12% 83% 16% ••
20	T	128	14% 59% 20% 21%
21	U	140	6% 82% 14%
22	V	157	31% 59% 10% • 30%
23	W	156	7% 67% 8% • 24%
24	X	145	10% 70% 21% • 8%
25	Y	136	5% 74% 26%
26	Z	148	• 82% 18% •
27	AA	245	11% 39% 5% 56%
28	BA	115	8% 70% 17% 14%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	CA	125	9% 66% 20% 14%
30	DA	135	5% 76% 19%
31	EA	110	5% 88% 11%
32	FA	129	9% 79% 9% 12%
33	GA	123	6% 79% 19%
34	HA	105	10% 89% 9%
35	IA	97	69% 21% 10%
36	JA	70	17% 84% 14%
37	KA	51	12% 61% 37%
38	LA	128	34% 7% 59%
39	MA	25	24% 84% 16%
40	NA	106	7% 81% 17%
41	OA	92	5% 86% 13%
42	PA	137	74% 16% 9%
43	RA	165	93% 76% 13% 7%
44	SA	76	18% 58% 39%
45	TA	76	93% 50% 47%
46	UA	75	87% 37% 40% 23%
47	VA	12	50% 67% 33%
48	WA	3584	9% 57% 38% 5%
49	XA	120	71% 23% 5%
50	YA	156	10% 55% 38% 6%
51	ZA	1869	10% 51% 36% 6% 8%
52	AB	295	13% 59% 14% 26%
53	BB	264	15% 67% 13% 19%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	CB	293	9% 60% 15% 25%
55	DB	281	32% 69% 11% 19%
56	EB	263	20% 75% 24%
57	FB	204	27% 75% 16% 9%
58	GB	249	44% 76% 19% 5%
59	HB	432	16% 33% 9% 57%
60	IB	208	23% 84% 15%
61	JB	194	26% 75% 21% 5%
62	KB	165	30% 41% 16% 42%
63	LB	158	13% 79% 12% 9%
64	MB	132	78% 62% 26% 11%
65	NB	151	9% 80% 19%
66	OB	151	13% 73% 17% 10%
67	PB	145	46% 74% 15% 11%
68	QB	172	30% 67% 14% 17%
69	RB	135	29% 80% 17%
70	SB	152	34% 71% 22% 5%
71	TB	145	28% 77% 20%
72	UB	119	45% 71% 15% 14%
73	VB	83	11% 86% 13%
74	WB	130	12% 78% 21%
75	XB	143	14% 83% 16%
76	YB	131	32% 75% 20% 5%
77	ZB	124	35% 59% 10% 31%
78	AC	115	15% 70% 17% 12%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
79	BC	84	
80	CC	69	
81	DC	56	
82	EC	133	
83	FC	188	
84	GC	317	
85	IC	4	
86	b	318	
87	c	14	
88	HC	462	

2 Entry composition [i](#)

There are 95 unique types of molecules in this entry. The entry contains 220703 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
			Total	C	N	O	S		
1	A	250	1914	1199	392	317	6	0	0

- Molecule 2 is a protein called uL3.

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

- Molecule 3 is a protein called uL4.

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

- Molecule 4 is a protein called uL18.

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

- Molecule 5 is a protein called L6.

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

- Molecule 6 is a protein called uL30.

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

- Molecule 7 is a protein called L7A.

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

- Molecule 8 is a protein called L9.

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

- Molecule 9 is a protein called L10.

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

- Molecule 10 is a protein called uL5.

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

- Molecule 11 is a protein called eL13.

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

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
			Total	C	N	O	S		
12	L	138	1137	727	221	182	7	0	0

- Molecule 13 is a protein called eL15.

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

- Molecule 14 is a protein called uL13.

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

- Molecule 15 is a protein called uL22.

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

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
			Total	C	N	O	S		
16	P	187	1515	946	315	250	4	0	0

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

Continued on next page...

Continued from previous page...

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
			Total	C	N	O	S		
17	Q	180	1508	933	328	238	9	0	0

- Molecule 18 is a protein called eL20.

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

- Molecule 19 is a protein called eL21.

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

- Molecule 20 is a protein called eL22.

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

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

Continued on next page...

Continued from previous page...

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
			Total	C	N	O	S		
21	U	135	1004	631	191	177	5	0	0

- Molecule 22 is a protein called uL24.

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

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
			Total	C	N	O	S		
23	W	118	967	618	181	167	1	0	0

- Molecule 24 is a protein called L26.

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

- Molecule 25 is a protein called L27.

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

- Molecule 26 is a protein called uL15.

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

- Molecule 27 is a protein called L29.

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

- Molecule 28 is a protein called eL30.

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

- Molecule 29 is a protein called L31.

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

- Molecule 30 is a protein called L32.

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

- Molecule 31 is a protein called eL33.

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

- Molecule 32 is a protein called L34.

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

- Molecule 33 is a protein called L35.

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

- Molecule 34 is a protein called L36.

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

- Molecule 35 is a protein called L37.

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

- Molecule 36 is a protein called eL38.

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

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
			Total	C	N	O	S		
37	KA	50	447	286	96	64	1	0	0

- Molecule 38 is a protein called eL40.

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

- 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
			Total	C	N	O	P		
46	UA	75	1596	713	285	523	75	0	0

- Molecule 47 is a RNA chain called mRNA.

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

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

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

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

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

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
			Total	C	N	O	P		
50	YA	156	3314	1480	585	1094	155	0	0

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

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

- Molecule 52 is a protein called RPSA.

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

- Molecule 53 is a protein called S3A.

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

- Molecule 54 is a protein called eS1.

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

- Molecule 55 is a protein called S3.

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

- Molecule 56 is a protein called S4.

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

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
			Total	C	N	O	S		
57	FB	185	1471	921	277	266	7	0	0

- Molecule 58 is a protein called eS6.

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

- Molecule 59 is a protein called eS7.

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

- Molecule 60 is a protein called S8.

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

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
			Total	C	N	O	S		
61	JB	185	1525	969	306	248	2	0	0

- Molecule 62 is a protein called S10.

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

- Molecule 63 is a protein called S11.

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

- 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
			Total	C	N	O	S		
71	TB	142	1104	693	212	196	3	0	0

- Molecule 72 is a protein called uS10.

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

- Molecule 73 is a protein called S21.

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

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
			Total	C	N	O	S		
74	WB	129	1034	659	193	176	6	0	0

- Molecule 75 is a protein called S23.

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

- Molecule 76 is a protein called S24.

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

- Molecule 77 is a protein called eS25.

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

- Molecule 78 is a protein called S26.

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

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
			Total	C	N	O	S		
79	BC	83	651	408	121	115	7	0	0

- Molecule 80 is a protein called S28.

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

- Molecule 81 is a protein called uS14.

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

- 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 1 A.

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

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

Mol	Chain	Residues	Atoms		AltConf
89	A	1	Total 1	Mg 1	0
89	I	1	Total 1	Mg 1	0
89	O	1	Total 1	Mg 1	0
89	P	1	Total 1	Mg 1	0
89	U	1	Total 1	Mg 1	0
89	Z	2	Total 2	Mg 2	0
89	FA	1	Total 1	Mg 1	0
89	IA	1	Total 1	Mg 1	0
89	SA	1	Total 1	Mg 1	0
89	WA	158	Total 158	Mg 158	0
89	XA	3	Total 3	Mg 3	0
89	YA	2	Total 2	Mg 2	0
89	ZA	61	Total 61	Mg 61	0
89	AC	1	Total 1	Mg 1	0
89	HC	1	Total 1	Mg 1	0

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

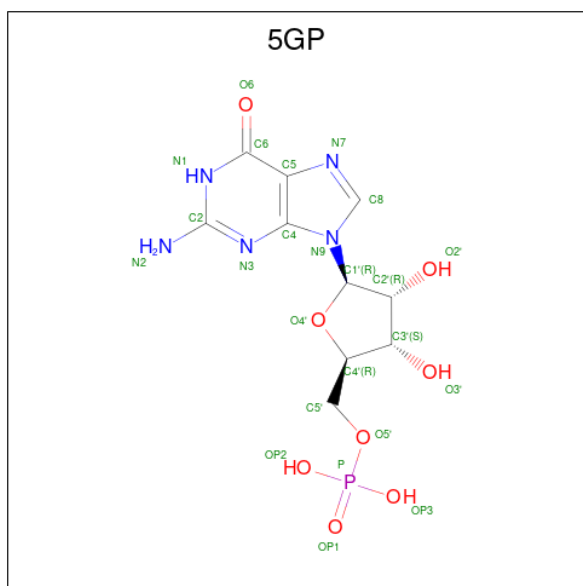
Mol	Chain	Residues	Atoms		AltConf
90	FA	1	Total 1	Zn 1	0
90	IA	1	Total 1	Zn 1	0

Continued on next page...

Continued from previous page...

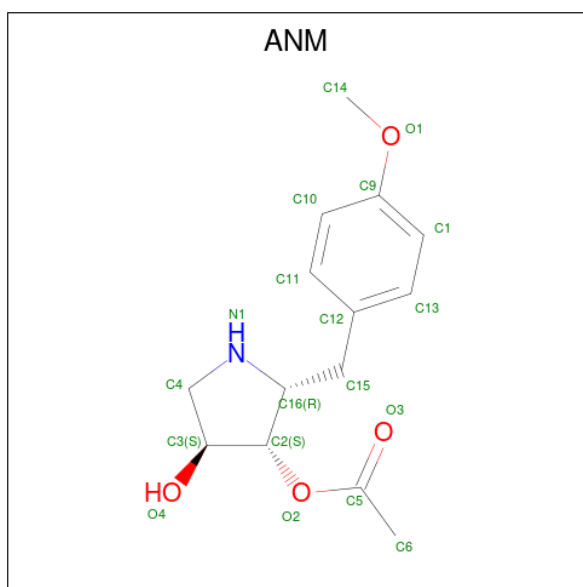
Mol	Chain	Residues	Atoms		AltConf
90	LA	1	Total	Zn	0
			1	1	
90	NA	1	Total	Zn	0
			1	1	
90	OA	1	Total	Zn	0
			1	1	
90	AC	1	Total	Zn	0
			1	1	
90	DC	1	Total	Zn	0
			1	1	
90	FC	1	Total	Zn	0
			1	1	

- Molecule 91 is GUANOSINE-5'-MONOPHOSPHATE (CCD ID: 5GP) (formula: C₁₀H₁₄N₅O₈P).



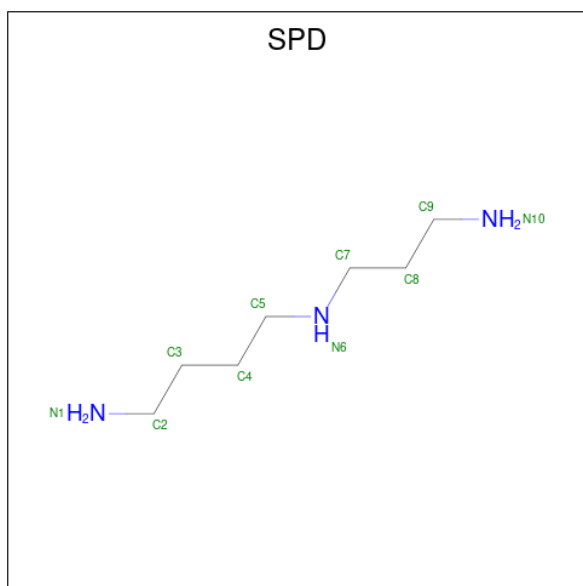
Mol	Chain	Residues	Atoms					AltConf
91	UA	1	Total	C	N	O	P	0
			24	10	5	8	1	

- Molecule 92 is ANISOMYCIN (CCD ID: ANM) (formula: C₁₄H₁₉NO₄).



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

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



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

Continued on next page...

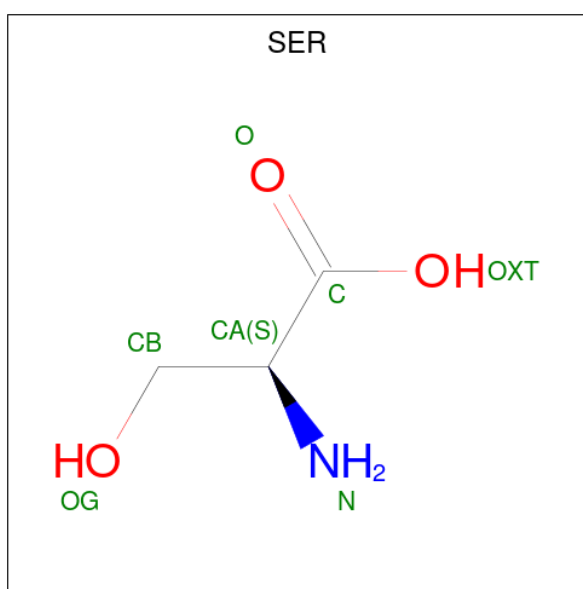
Continued from previous page...

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

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

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

- Molecule 95 is SERINE (CCD ID: SER) (formula: C₃H₇NO₃).




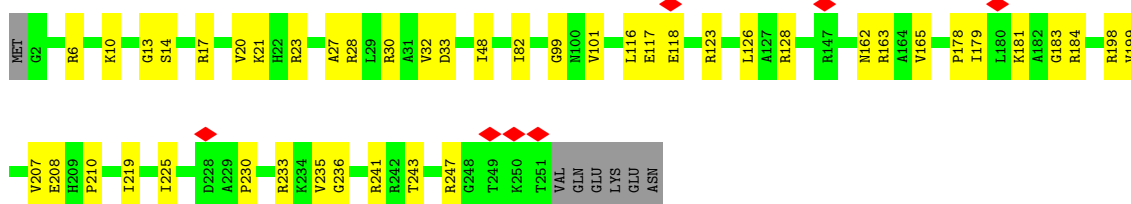
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
95	HC	1	6	3	1	2	0

3 Residue-property plots [i](#)


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

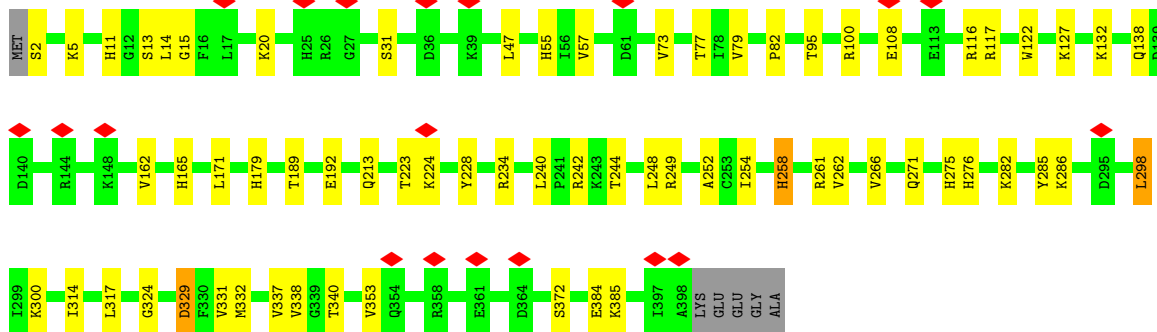
- Molecule 1: uL2

Chain A: 




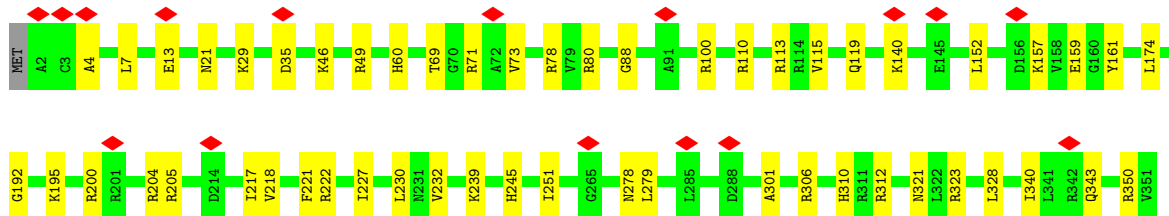
- Molecule 2: uL3

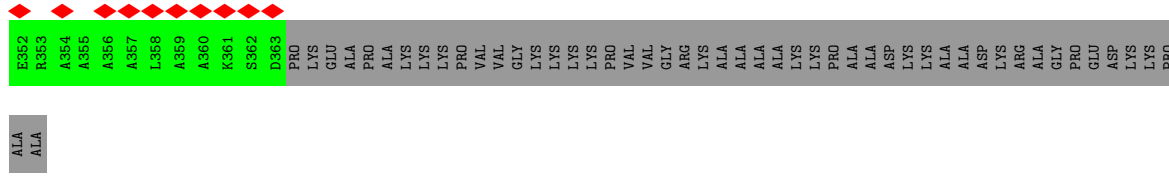
Chain B: 



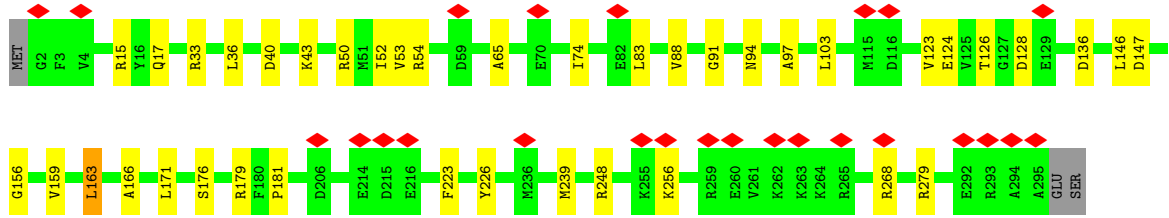
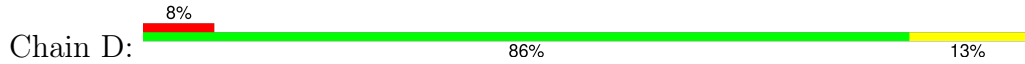
- Molecule 3: uL4

Chain C: 

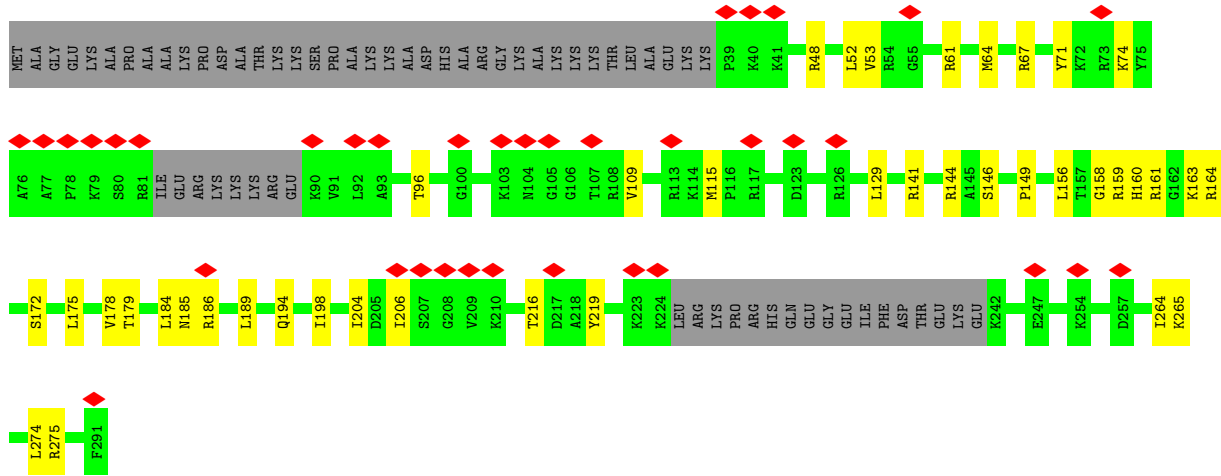




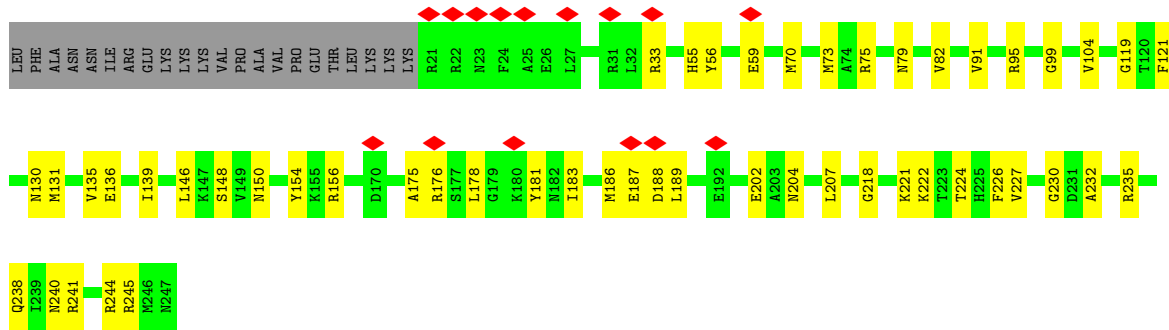
• Molecule 4: uL18



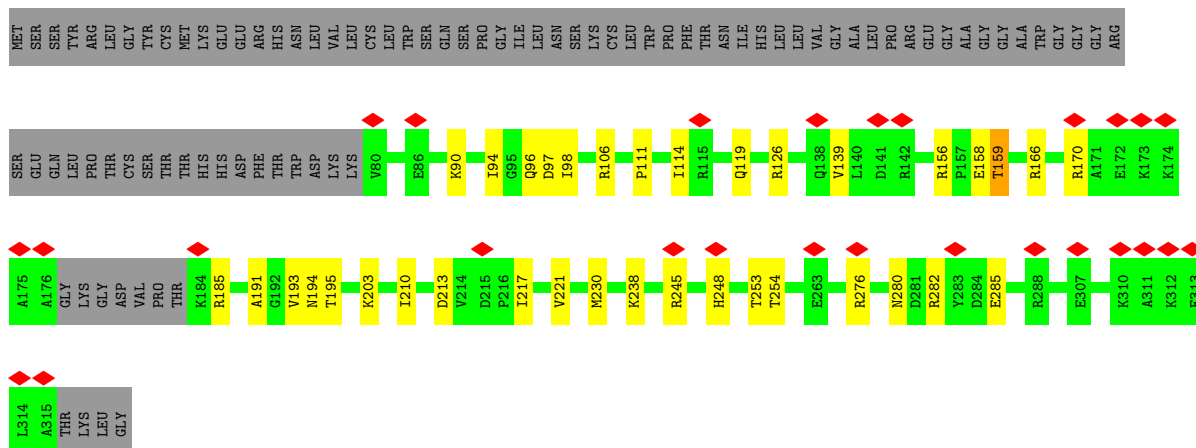
• Molecule 5: L6



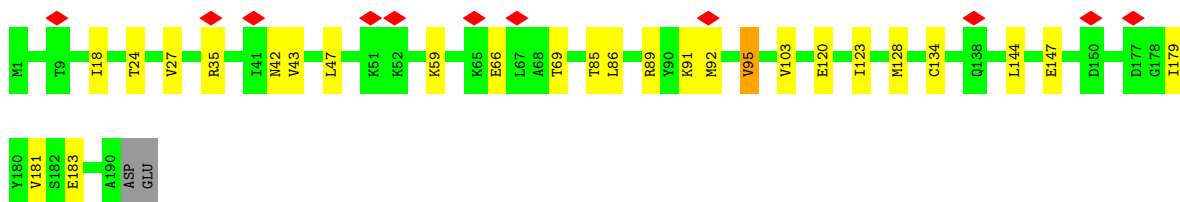
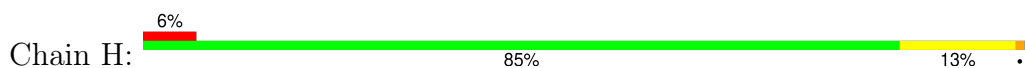
• Molecule 6: uL30



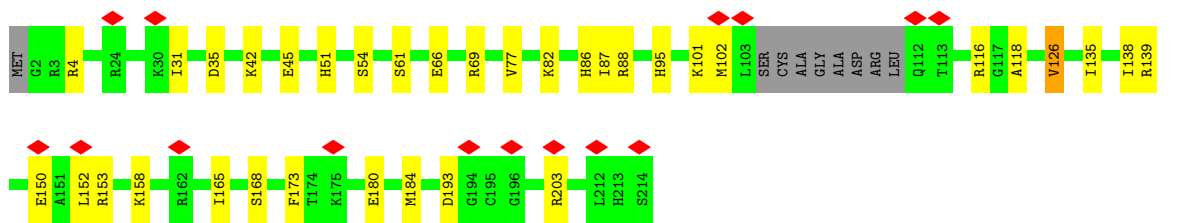
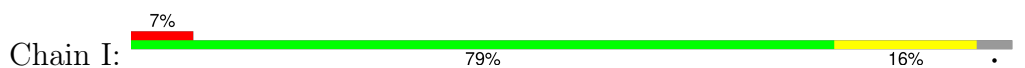
• Molecule 7: L7A



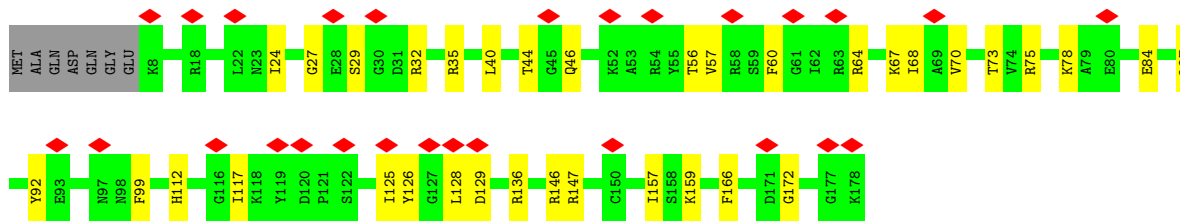
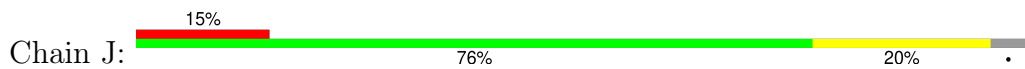
• Molecule 8: L9



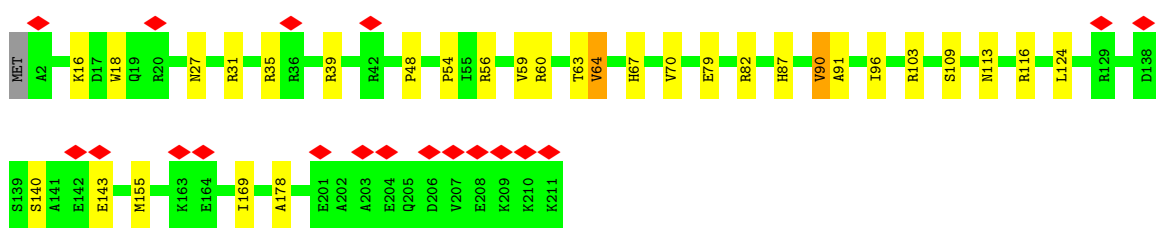
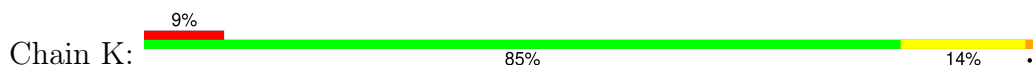
• Molecule 9: L10



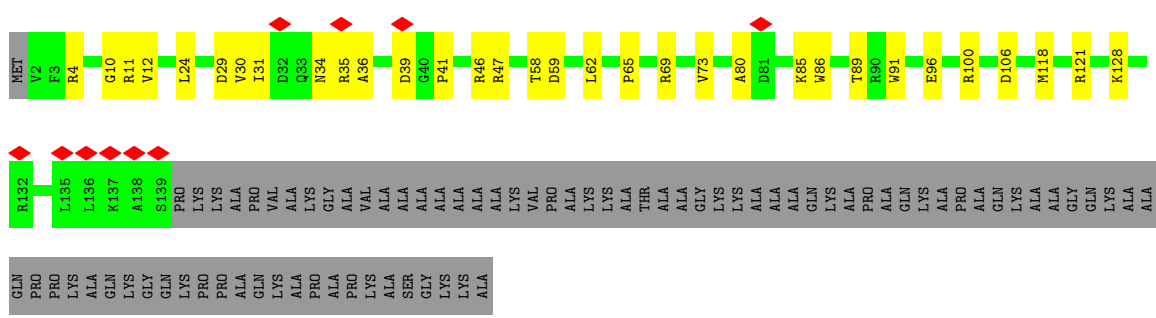
• Molecule 10: uL5



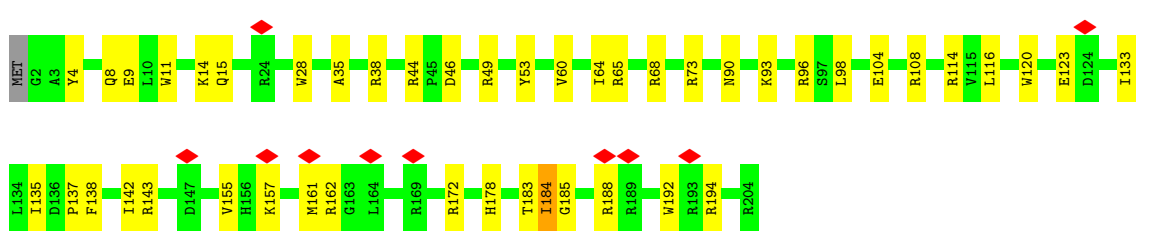
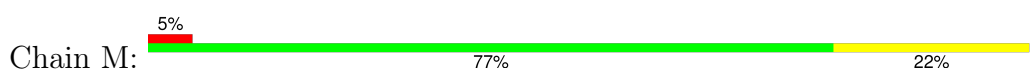
• Molecule 11: eL13



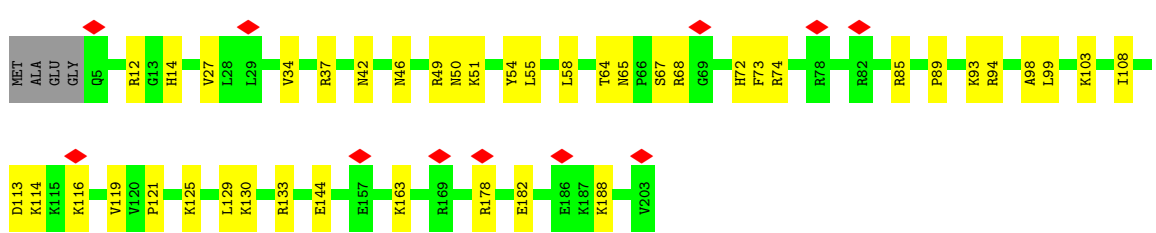
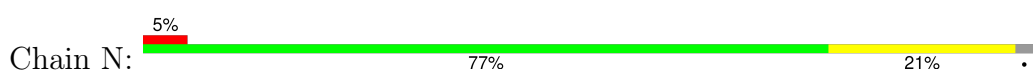
• Molecule 12: eL14



• Molecule 13: eL15

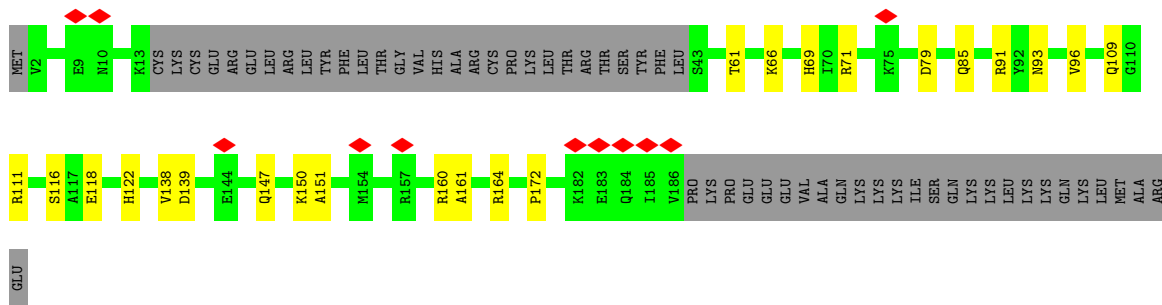


• Molecule 14: uL13

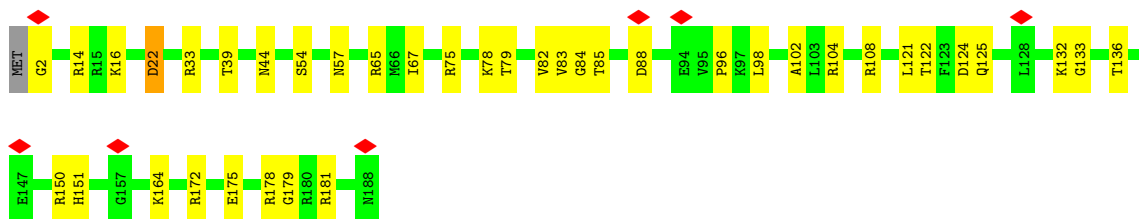
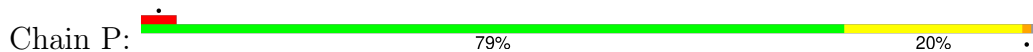


• Molecule 15: uL22

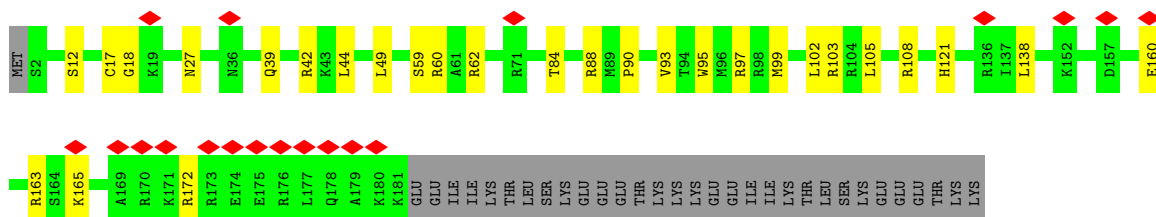




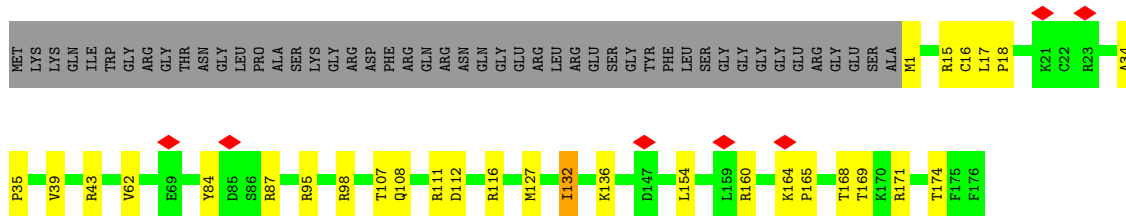
• Molecule 16: eL18



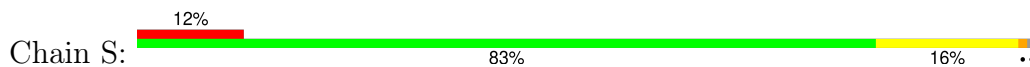
• Molecule 17: eL19



• Molecule 18: eL20

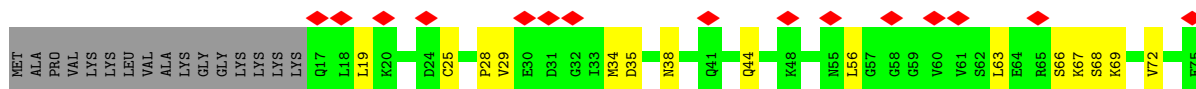


• Molecule 19: eL21

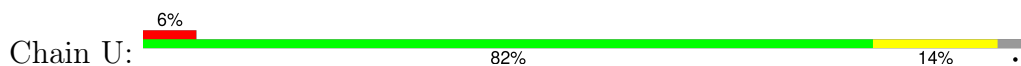




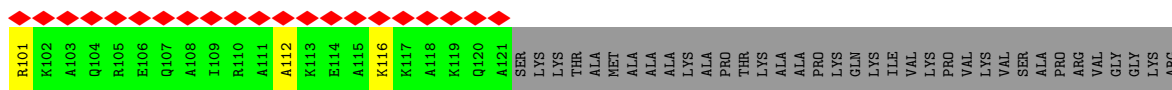
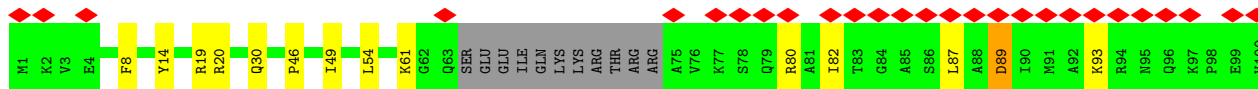
• Molecule 20: eL22



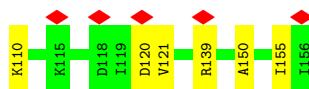
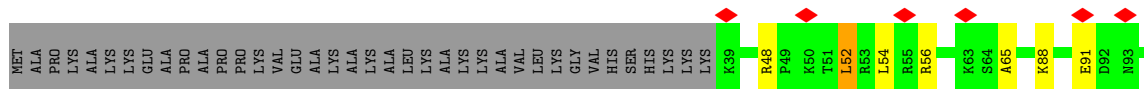
• Molecule 21: L23



• Molecule 22: uL24

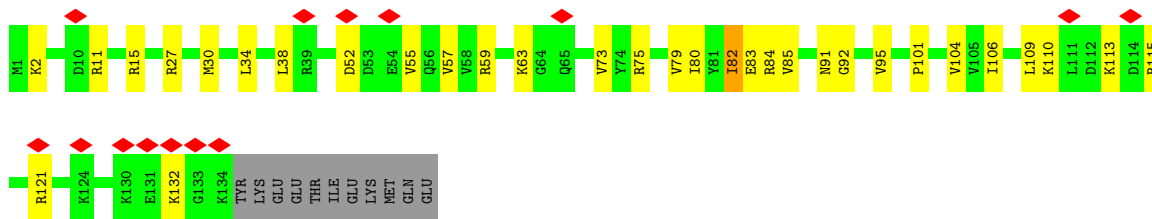


• Molecule 23: uL23

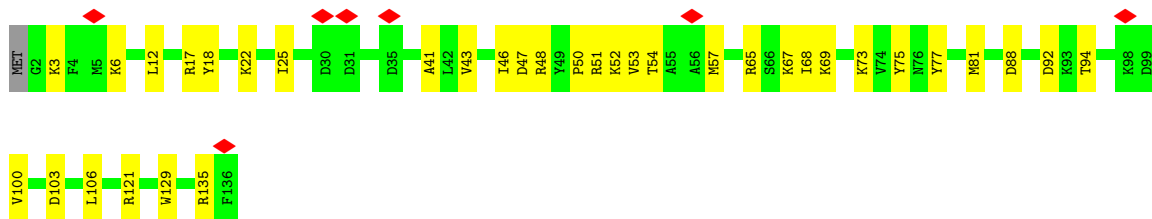
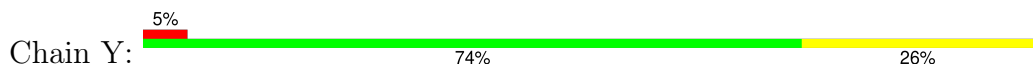


• Molecule 24: L26

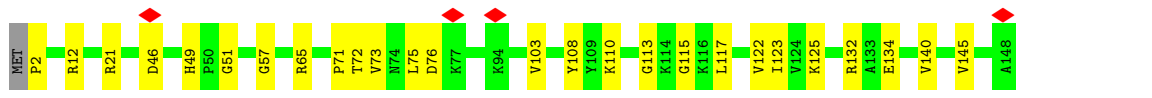
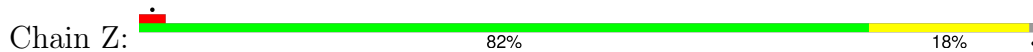




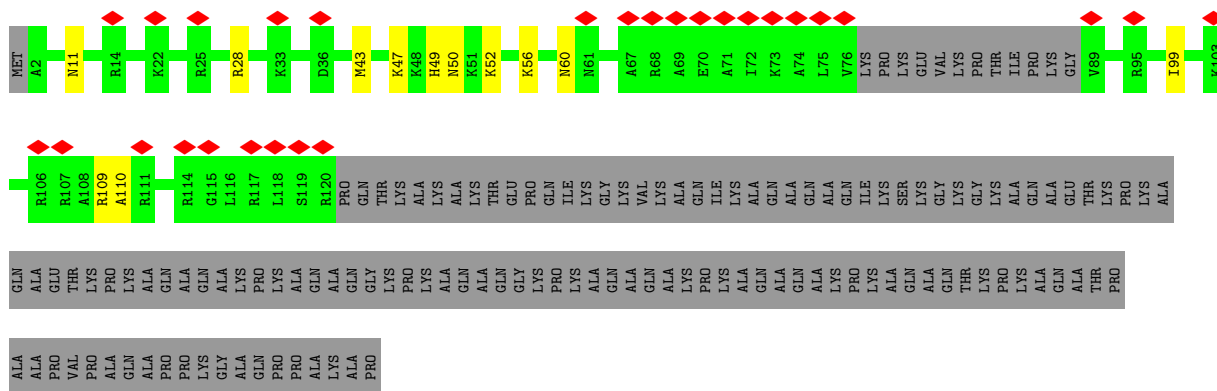
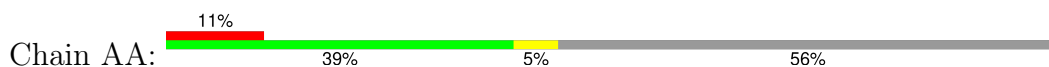
• Molecule 25: L27



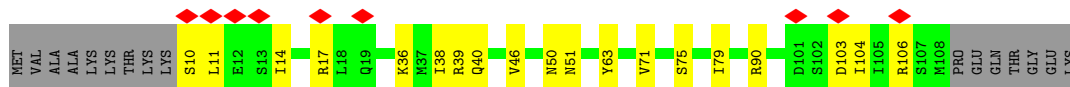
• Molecule 26: uL15



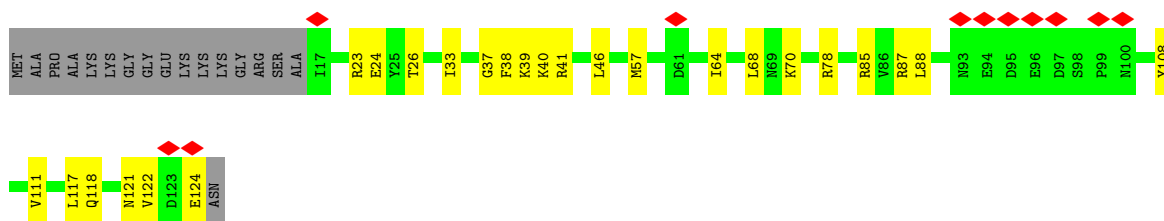
• Molecule 27: L29



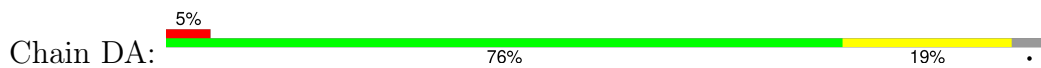
• Molecule 28: eL30



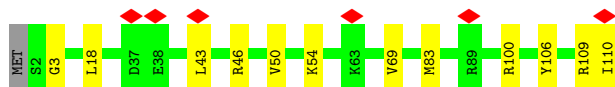
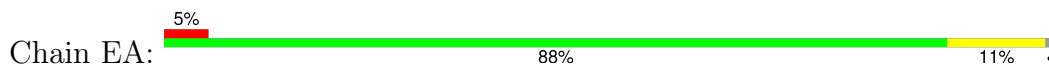
• Molecule 29: L31



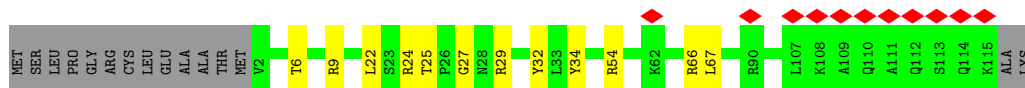
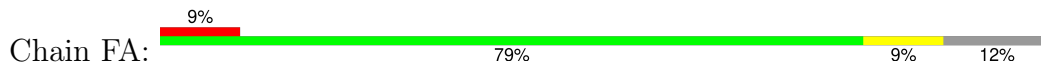
• Molecule 30: L32



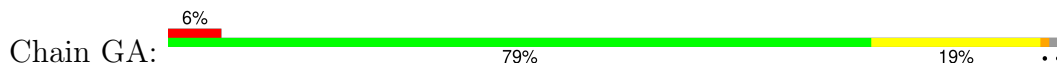
• Molecule 31: eL33



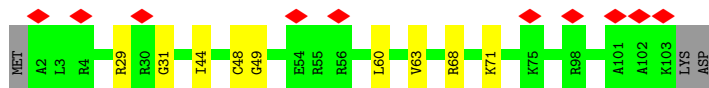
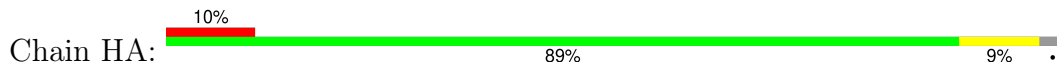
• Molecule 32: L34



• Molecule 33: L35

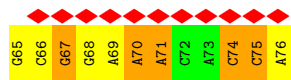


• Molecule 34: L36

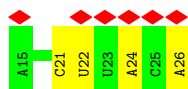


• Molecule 35: L37

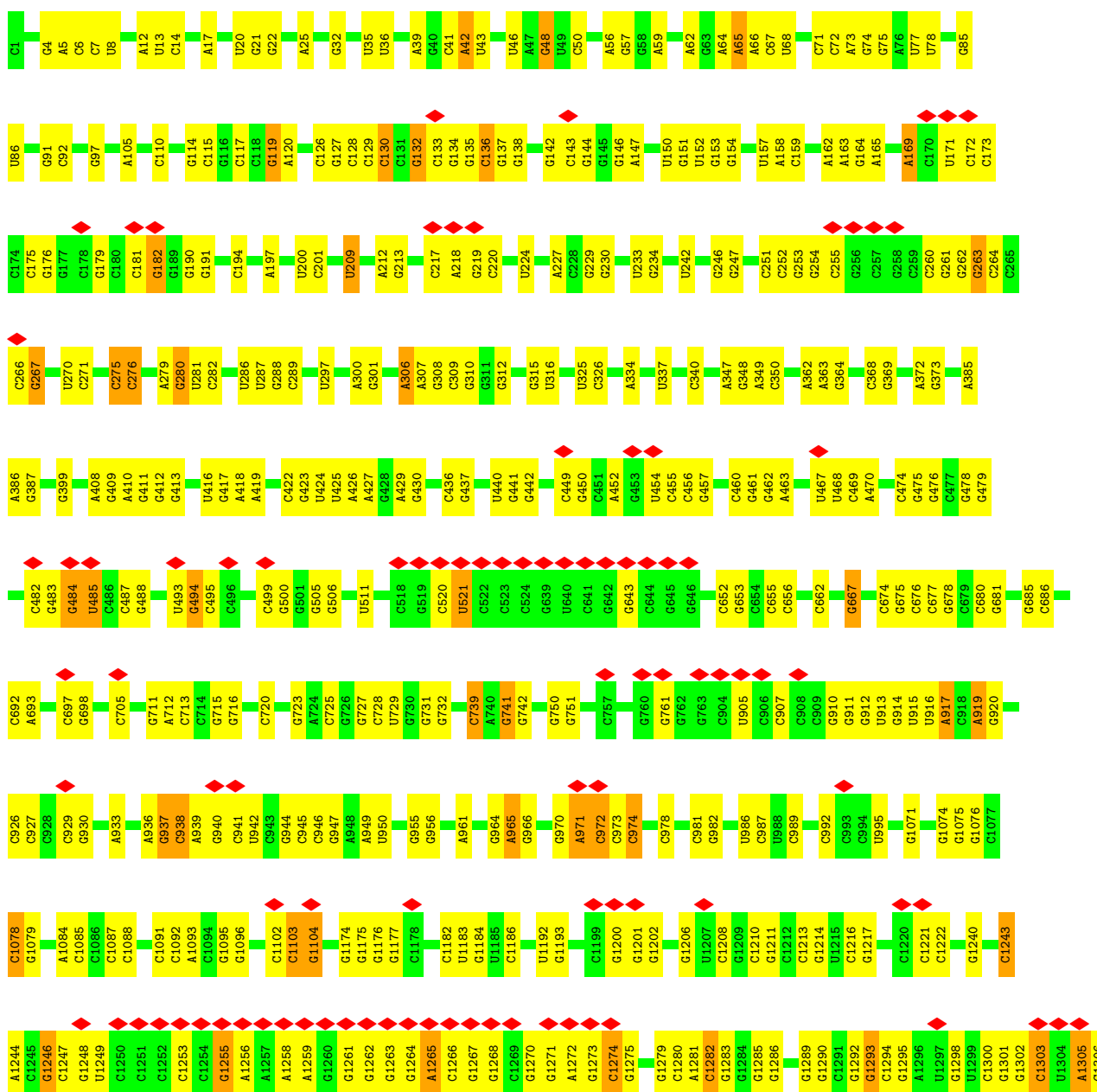


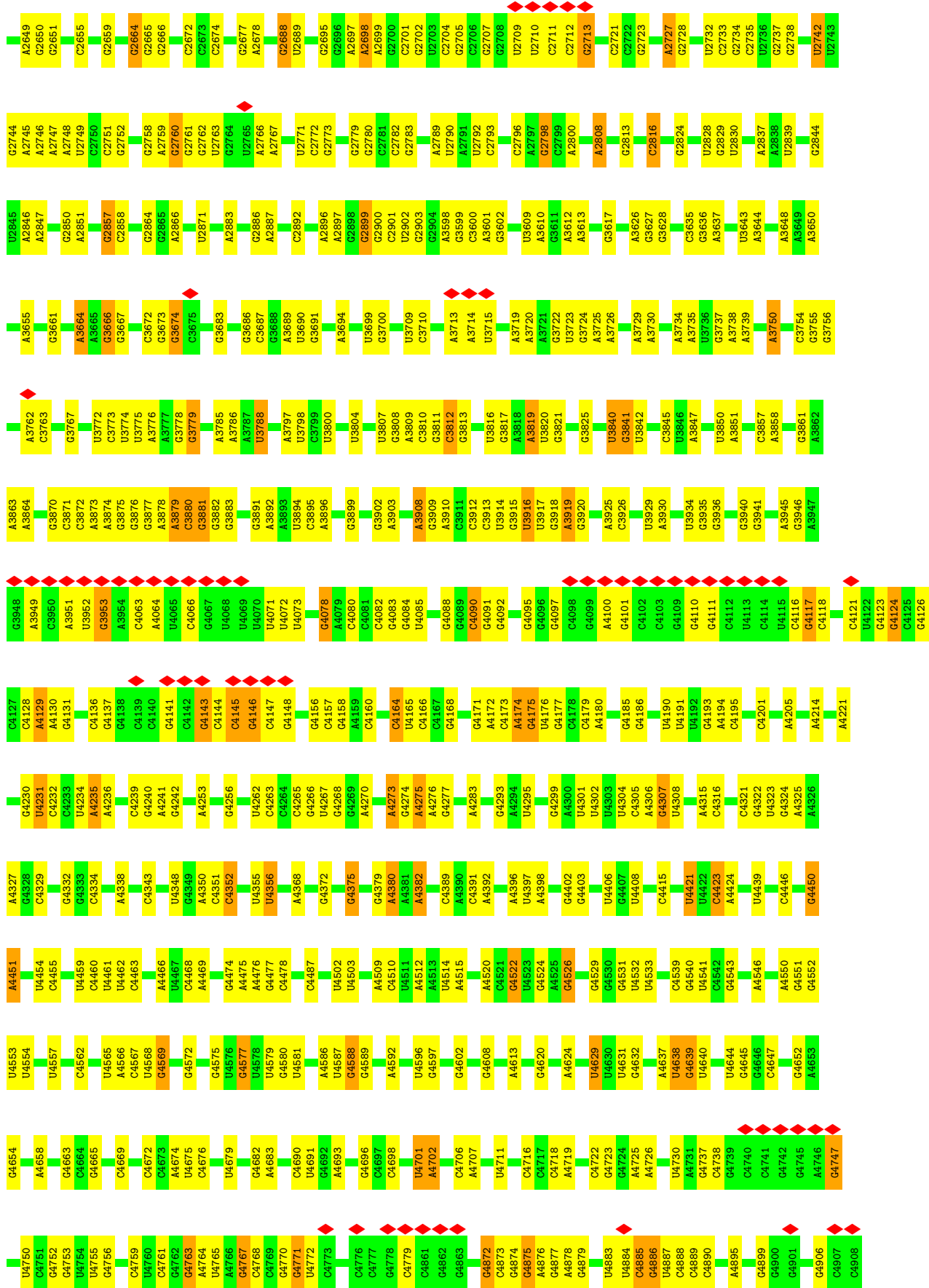


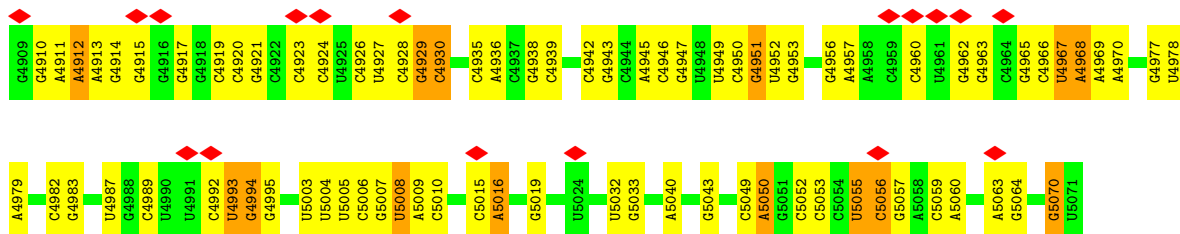
• Molecule 47: mRNA



• Molecule 48: 28S rRNA







• Molecule 49: 5S rRNA

Chain XA:



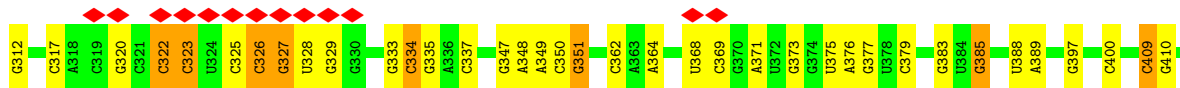
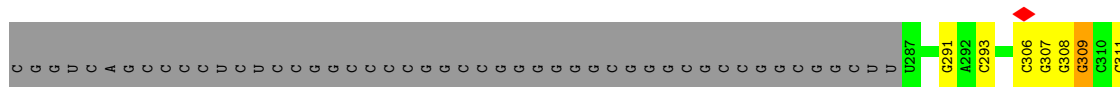
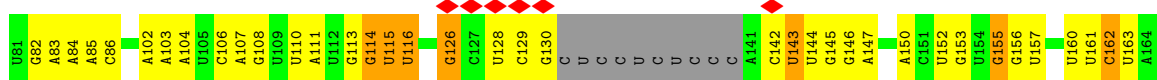
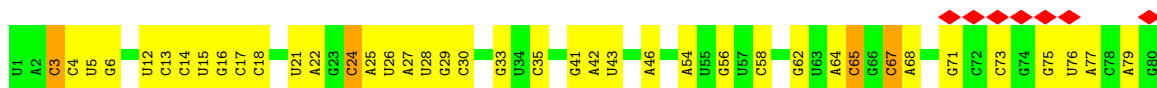
• Molecule 50: 5.8S rRNA

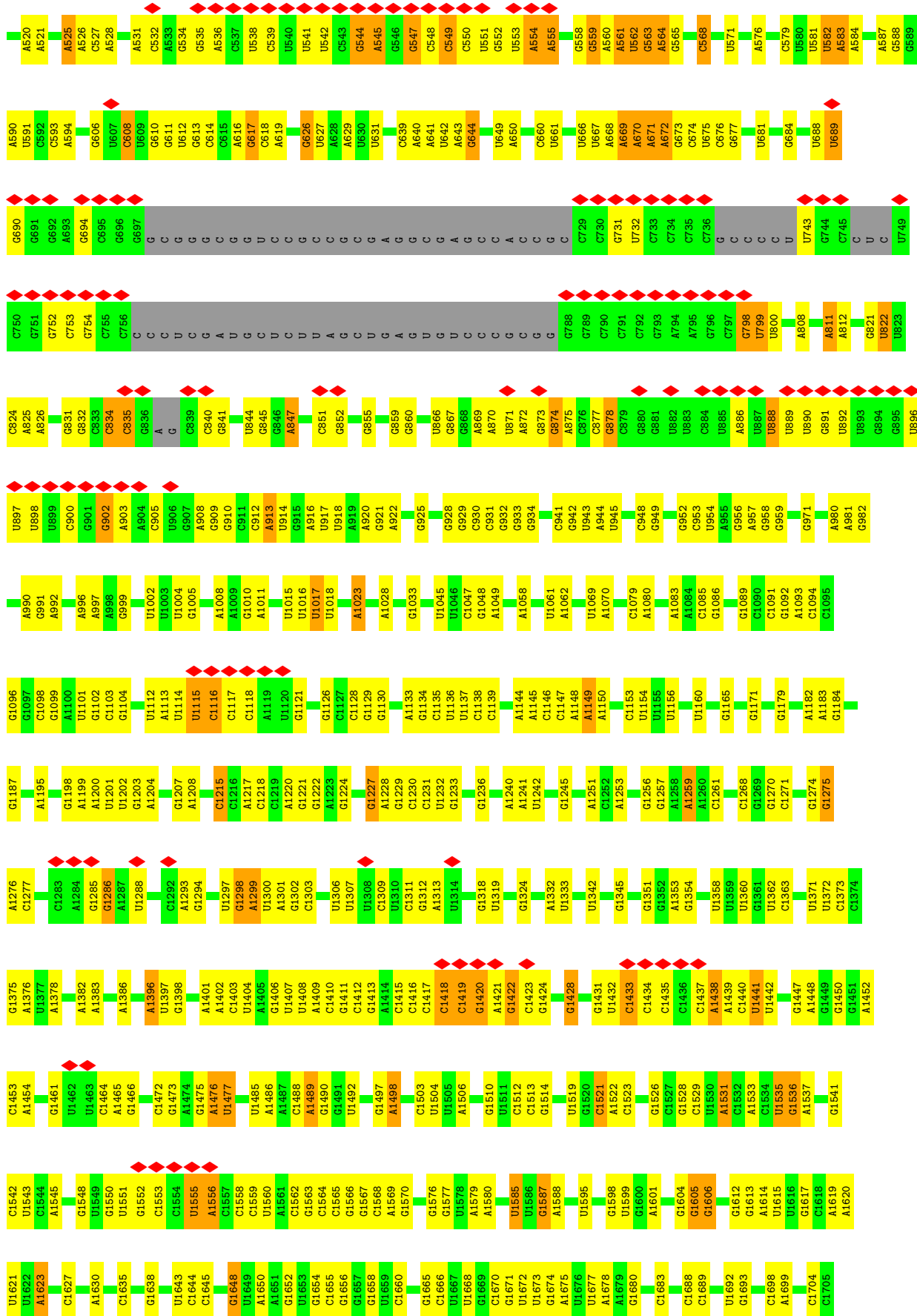
Chain YA:

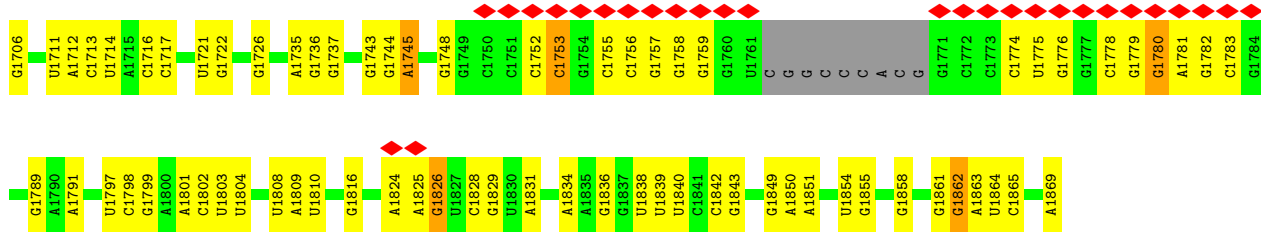


• Molecule 51: 18S rRNA

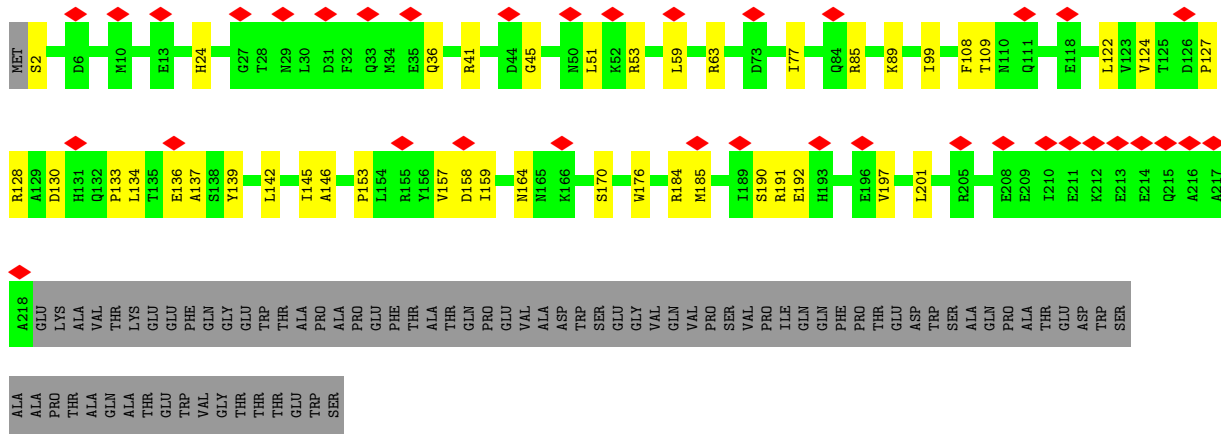
Chain ZA:



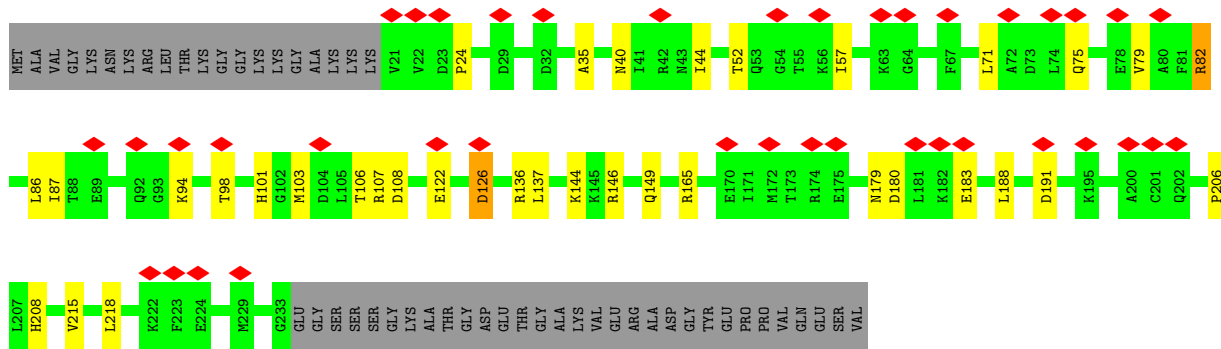




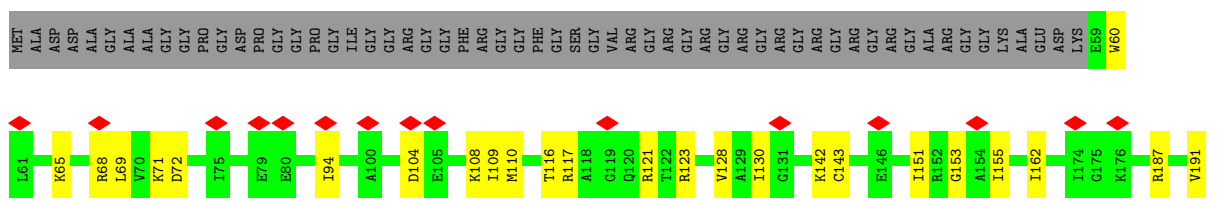
• Molecule 52: RPSA



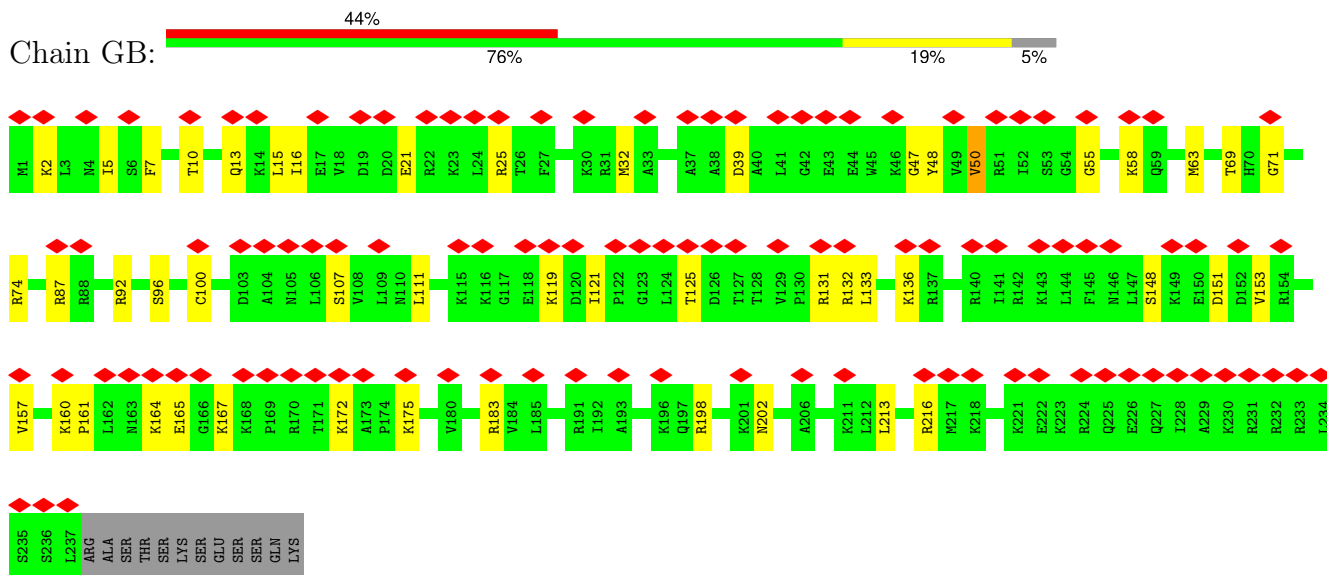
• Molecule 53: S3A



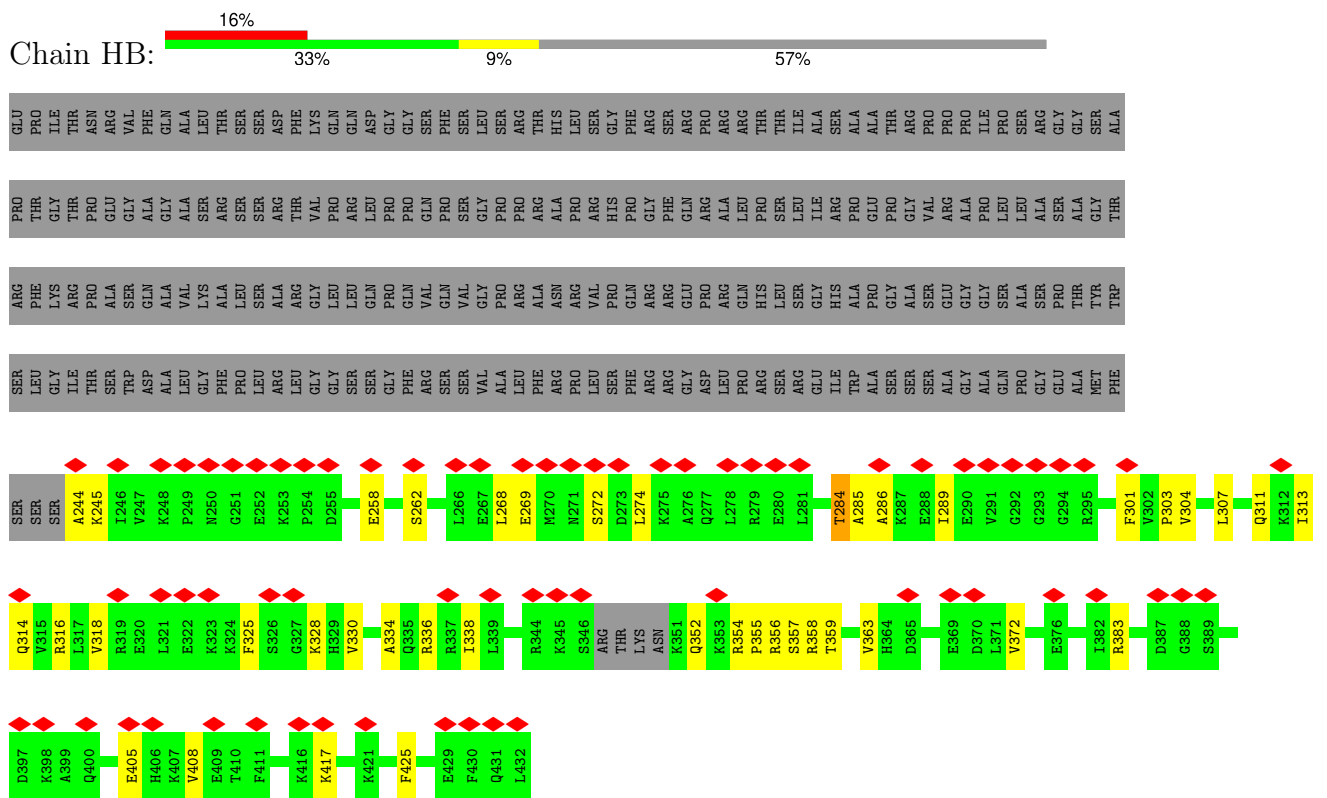
• Molecule 54: eS1



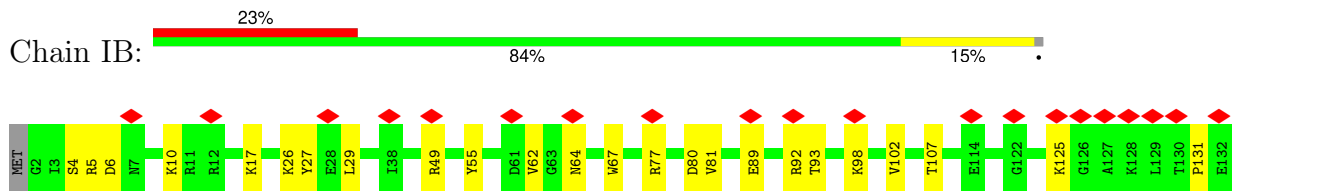
• Molecule 58: eS6



• Molecule 59: eS7

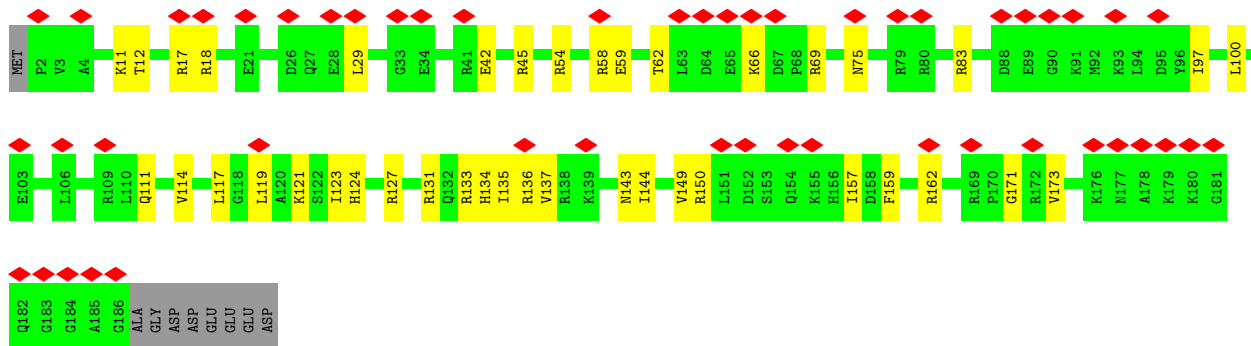
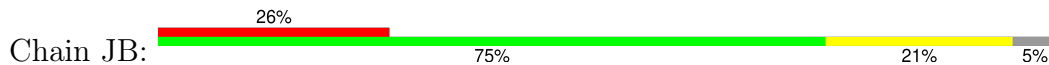


• Molecule 60: S8

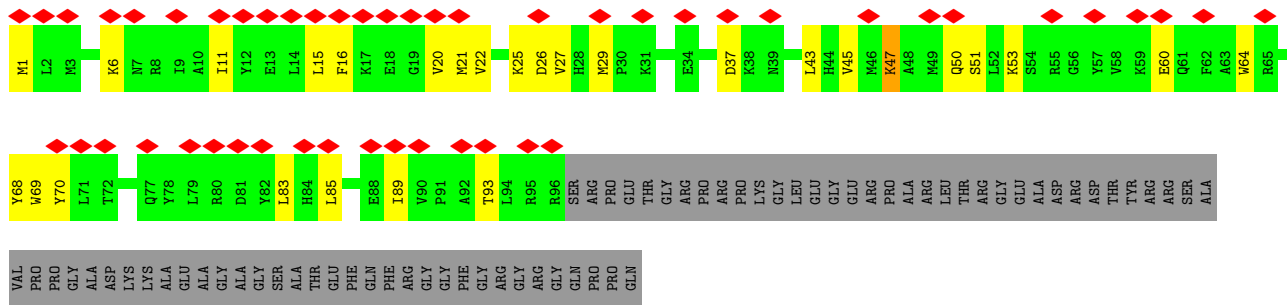




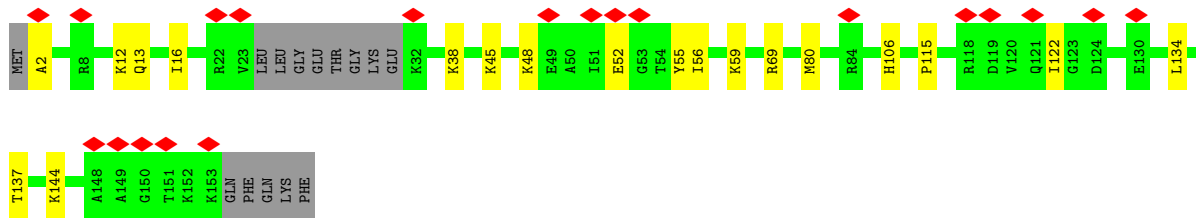
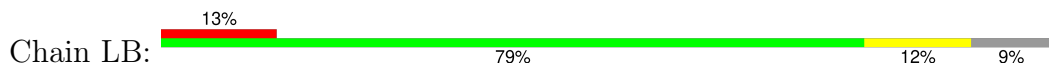
• Molecule 61: S9



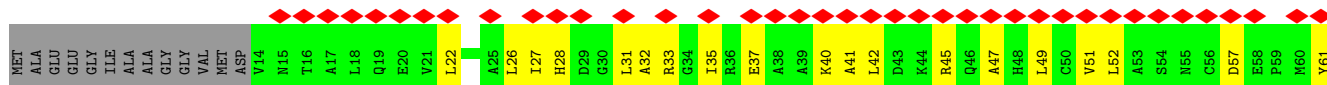
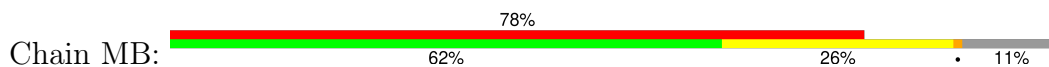
• Molecule 62: S10

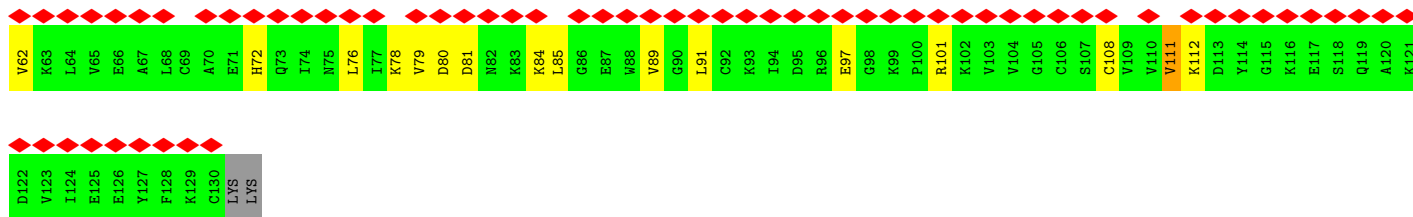


• Molecule 63: S11

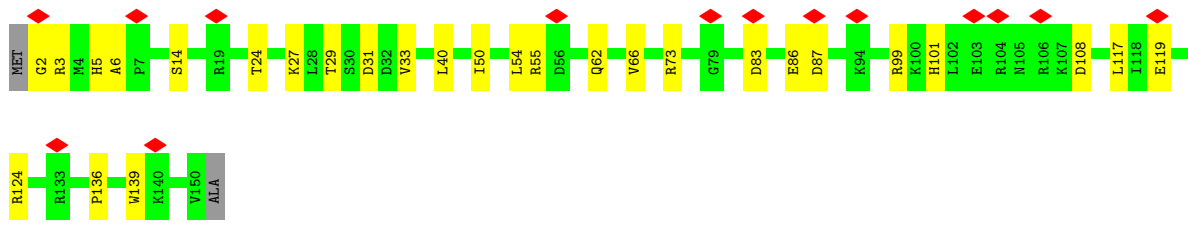
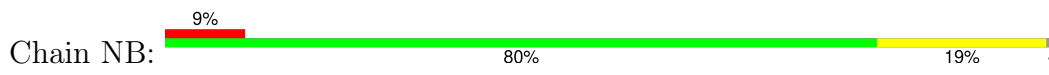


• Molecule 64: S12

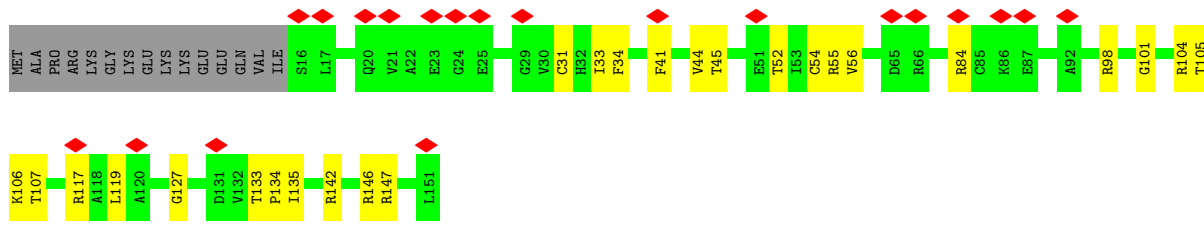
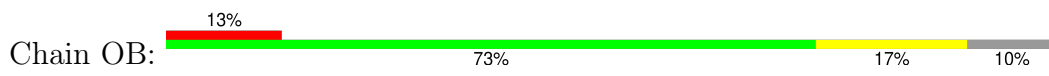




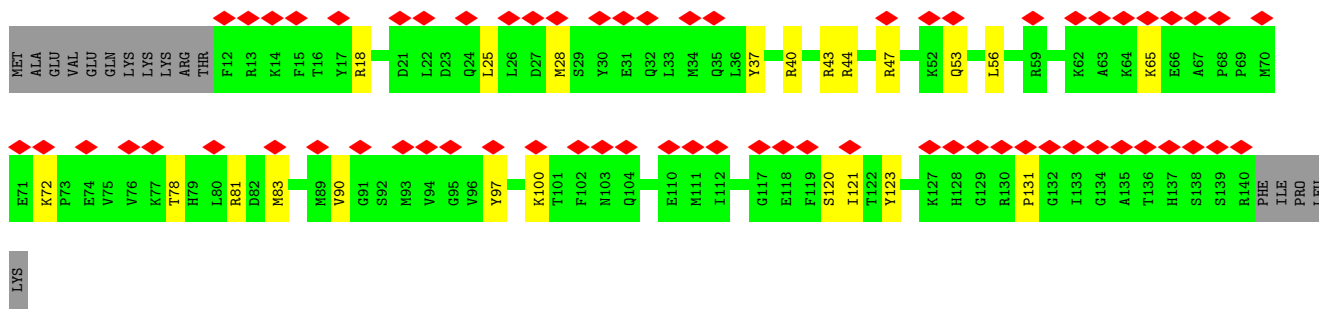
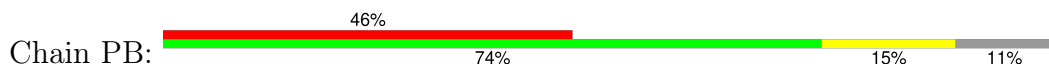
• Molecule 65: uS15



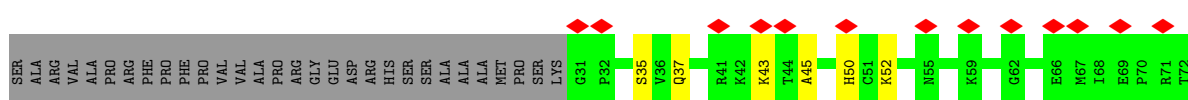
• Molecule 66: S14

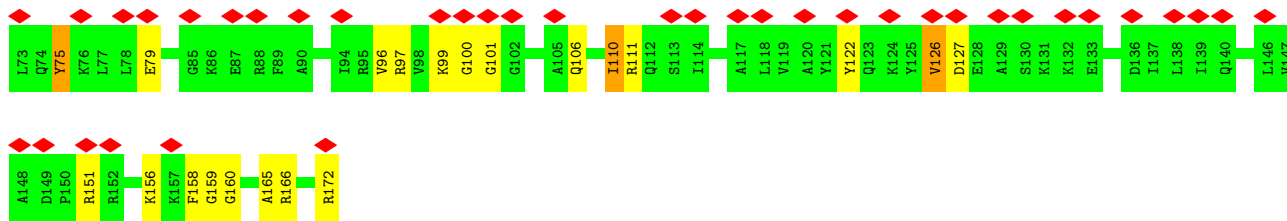


• Molecule 67: S15

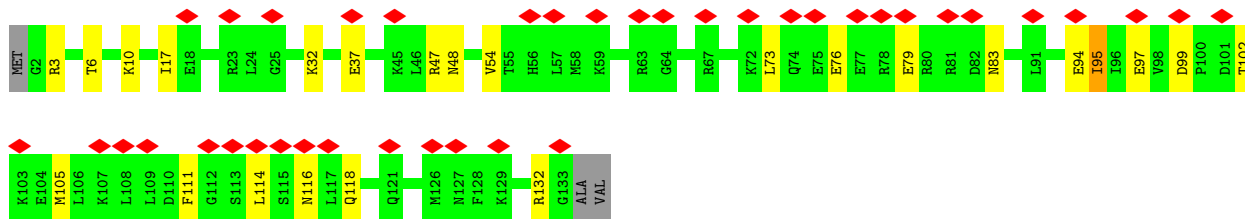
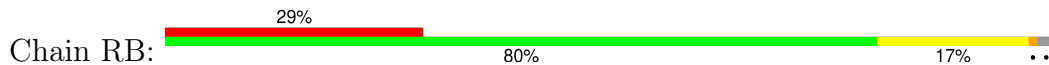


• Molecule 68: uS9

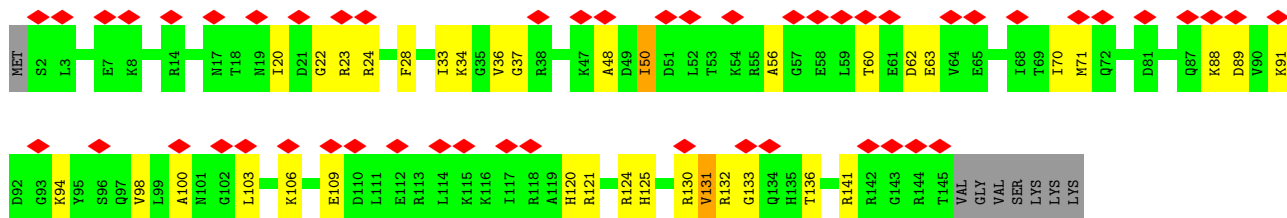
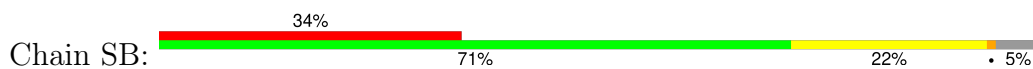




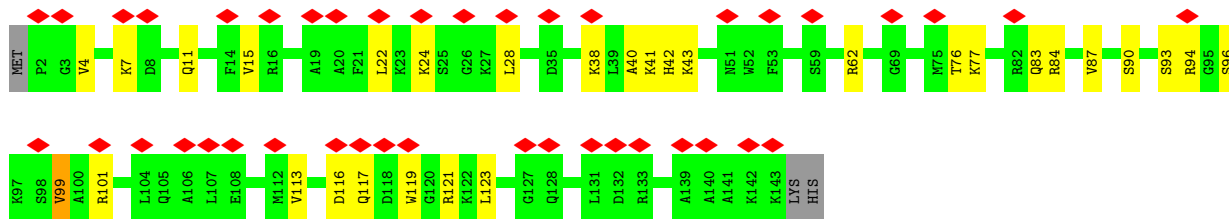
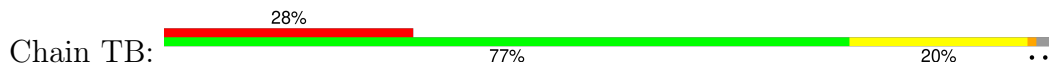
• Molecule 69: eS17



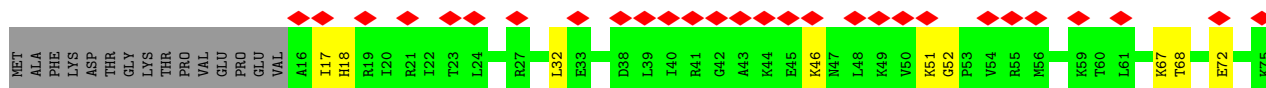
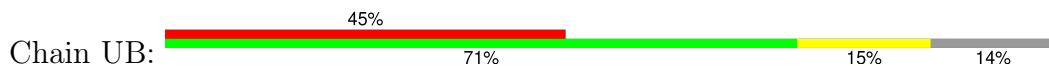
• Molecule 70: S18

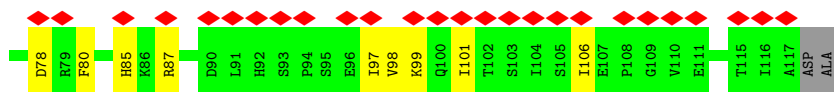


• Molecule 71: S19

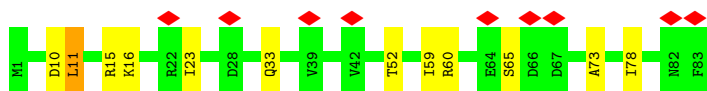
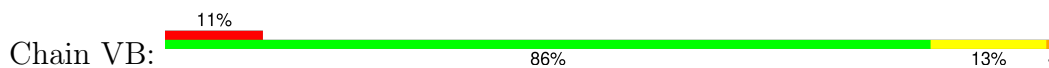


• Molecule 72: uS10

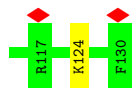
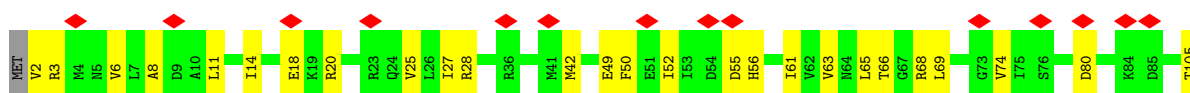
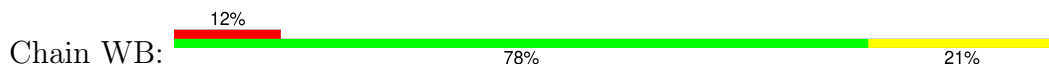




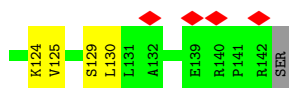
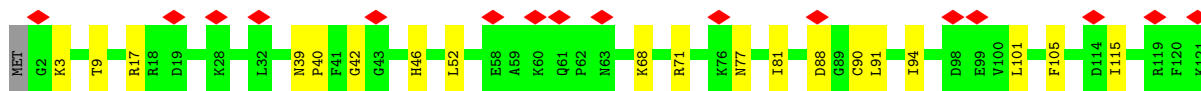
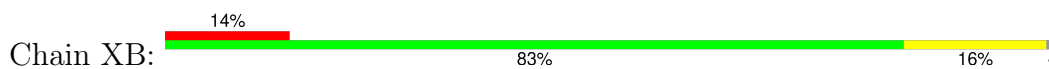
• Molecule 73: S21



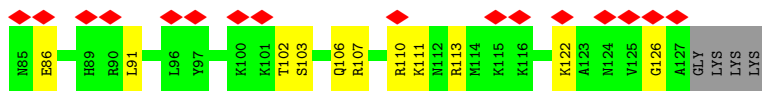
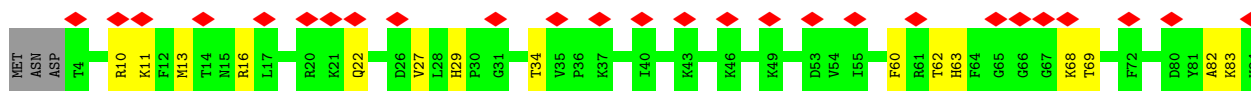
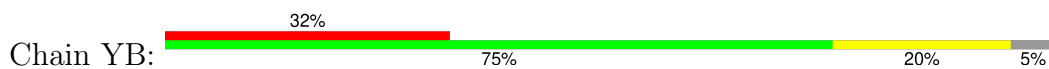
• Molecule 74: S15A



• Molecule 75: S23

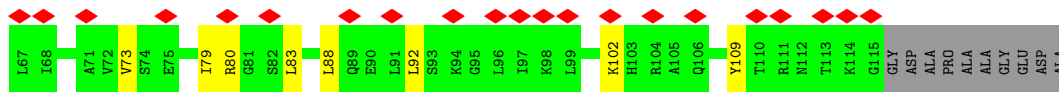


• Molecule 76: S24

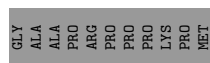
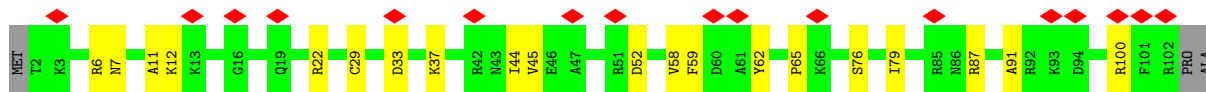
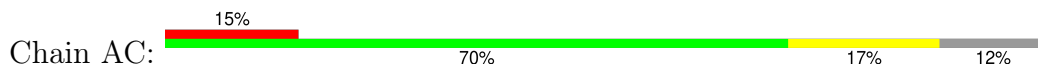


• Molecule 77: eS25

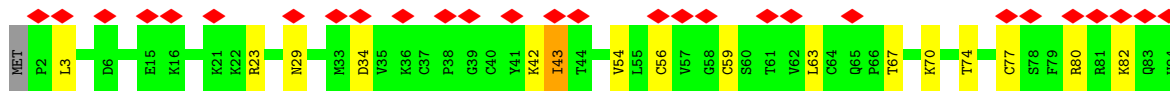
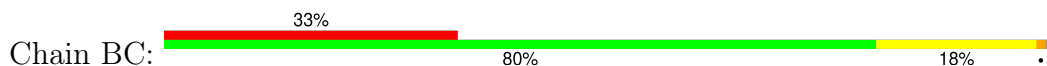




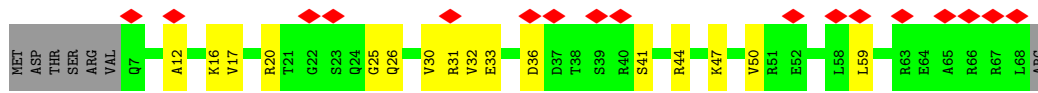
• Molecule 78: S26



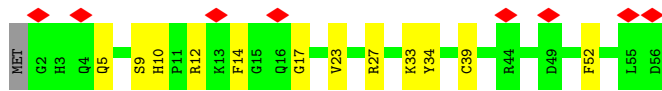
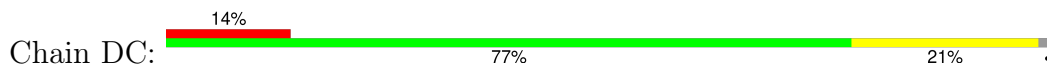
• Molecule 79: S27



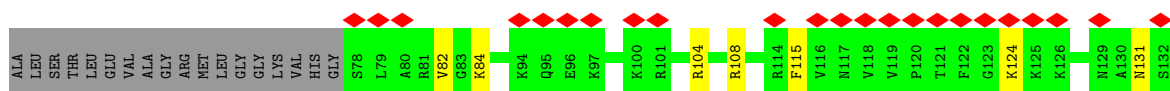
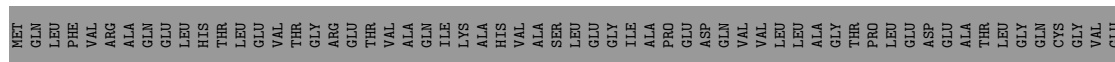
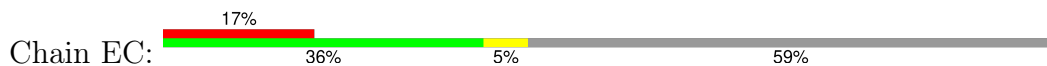
• Molecule 80: S28



• Molecule 81: uS14



• Molecule 82: S30



• Molecule 83: S27A



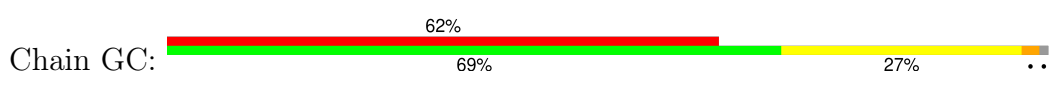
MET ALA ARG HIS PRO LEU TYR GLN SER ILE TRP CYS GLY ARG LEU ARG LEU GLY ALA THR PRO LEU PHE LEU PHE ASP PRO SER SER ALA ARG TRP ARG HIS GLN ASP ALA LEU ARG ASP LEU ARG ASN PRO TYR GLY

GLU ASP HIS HIS ALA ARG GLY ILE PRO PRO ASP ASP GLN ARG ARG LEU PHE LEU ALA GLY LYS LEU ALA GLN LEU ASP GLY ARG THR HIS VAL LEU ARG LEU ARG GLY ALA ALA LYS LYS LYS K82 K83 S84 Y85 T86 T87 P88

K89 K90 N91 K92 H93 K94 R95 K96 K97 V98 K99 L100 A101 V102 L103 K104 Y105 Y106 K107 V108 D109 E110 M111 M112 K113 I114 S115 R116 L117 R118 R119 C121 P122 S123 D124 E125 C126 G127 A128 G129 V130 F131 M132 A133 S134 H135 F136 D137 R138 H139 Y140 C141 G142 K143 C144 C145 T146 Y148

C149 F150 ASN PRO GLU ASP LYS

• Molecule 84: RACK1



MET T2 E3 Q4 M5 T6 L7 R8 G9 T10 L11 K12 G13 V18 T19 Q20 I21 A22 Q26 F27 P28 D29 M30 I31 L32 S33 A34 R36 D37 K38 T39 I40 I41 M42 W43 K44 L45 T46 R47 D48 E49 T50 M51 Y52 G53 I54 R57 R60 G61 H62 S63 S67 D68 V69

V70 I71 S72 D73 D74 G75 F76 F77 A78 L79 S82 W83 D84 G85 L87 R88 L89 W90 L92 T93 T94 G95 T96 T97 T98 R99 R100 F101 V102 G103 H104 T105 K106 D107 V108 L109 S110 V111 A112 F113 S114 S115 D116 M117 R118 Q119 I120 V121 G122 G123 S124 R125 D126 K127 T128 I129 K130

L131 W132 N133 T134 L135 G136 V137 C138 K139 Y140 T141 V142 Q143 D144 E145 W150 V151 S152 R155 F156 S157 P158 M159 S160 S161 N162 P163 I164 I165 V166 S167 C168 D171 V174 K175 V176 W177 N178 L179 A180 M181 C182 K183 L184 K185 T186 N187 H188 I189 G190 H191 T192 G193 Y194 L195 N196

T197 V198 T199 V200 S201 P202 D203 G204 S205 L206 C207 A208 S209 G210 D213 G214 Q215 A216 M217 L218 W219 D220 L221 L222 M222 E223 G224 K225 H226 L227 Y228 T229 L230 D231 G232 G233 D234 N237 A238 L239 C240 F241 S242 P243 M244 R245 Y246 W247 L248 A251 T252 G253 P254 S255 I256 K257 I258 W259

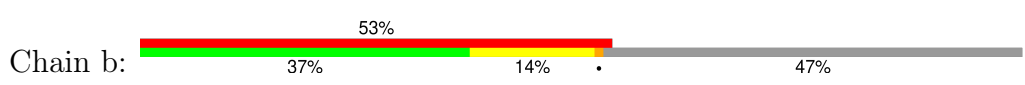
D260 L261 E262 G263 K264 I265 I266 V267 D268 E269 L270 K271 Q272 E273 V274 L275 S276 T277 S278 S279 K280 A281 E282 C286 T287 S288 L289 A290 W291 S292 A293 D294 G295 Q296 T297 L298 F299 A300 G301 Y302 T303 D304 N305 L306 W307 R308 V309 W310 Q311 V312 T313 I314 GLY THR ARG

• Molecule 85: peptide



A195 H196 F197 D198

• Molecule 86: RPLP0



L361	D362	C363	H364	T365	A366	H367	I368	A369	C370	K371	F372	A373	E374	L375	K376	E377	K378	I379	D380	R381	R382	S383	G384	K385	K386	L387	E388	D389	G390	P391	K392	F393	L394	K395	S396	G397	D398	A399	A400	I401	V402	D403	M404	V405	P406	G407	K408	P409	M410	C411	V412	E413	S414	F415	S416	D417	Y418	P419	P420
L421	G422	R423	F424	A425	V426	R427	D428	M429	R430	Q431	T432	V433	A434	V435	G436	V437	I438	K439	A440	V441	D442	K443	K444	A445	A446	G447	A448	G449	K450	V451	T452	K453	S454	A455	Q456	K457	A458	Q459	K460	A461	K462																		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6359	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	33.575	Depositor
Minimum map value	-21.832	Depositor
Average map value	0.004	Depositor
Map value standard deviation	1.513	Depositor
Recommended contour level	6.5	Depositor
Map size (\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 (\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, MG, ANM, 5GP, SPD, K

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	0.11	0/1859	0.26	0/2491
6	F	0.12	0/1933	0.26	0/2577
7	G	0.11	0/1881	0.25	0/2532
8	H	0.11	0/1535	0.27	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	0.24	0/2316
12	L	0.11	0/1158	0.25	0/1547
13	M	0.12	0/1746	0.27	0/2338
14	N	0.13	0/1662	0.29	0/2222
15	O	0.12	0/1292	0.28	0/1733
16	P	0.11	0/1539	0.29	0/2054
17	Q	0.11	0/1524	0.25	0/2013
18	R	0.12	0/1501	0.29	0/2012
19	S	0.11	0/1326	0.24	0/1770
20	T	0.11	0/840	0.31	0/1127
21	U	0.12	0/1018	0.28	0/1364
22	V	0.11	0/900	0.26	0/1194
23	W	0.11	0/984	0.26	0/1323
24	X	0.10	0/1132	0.23	0/1504
25	Y	0.11	0/1130	0.23	0/1507
26	Z	0.11	0/1191	0.26	0/1590
27	AA	0.09	0/886	0.20	0/1171
28	BA	0.10	0/779	0.22	0/1044
29	CA	0.12	0/908	0.28	0/1223
30	DA	0.10	0/1082	0.24	0/1443
31	EA	0.12	0/895	0.27	0/1198
32	FA	0.11	0/916	0.26	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	GA	0.09	0/1016	0.23	0/1341
34	HA	0.09	0/841	0.23	0/1112
35	IA	0.12	0/731	0.27	0/966
36	JA	0.10	0/575	0.26	0/761
37	KA	0.11	0/459	0.27	0/608
38	LA	0.10	0/435	0.28	0/575
39	MA	0.10	0/240	0.19	0/305
40	NA	0.11	0/864	0.24	0/1140
41	OA	0.12	0/718	0.32	0/953
42	PA	0.12	0/1010	0.29	0/1354
43	RA	0.12	0/1174	0.32	0/1582
44	SA	0.10	0/1815	0.24	0/2828
45	TA	0.09	0/1804	0.22	0/2810
46	UA	0.13	0/1783	0.32	0/2776
47	VA	0.09	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	0.23	0/5766
51	ZA	0.11	0/40949	0.24	0/63819
52	AB	0.10	0/1747	0.25	0/2374
53	BB	0.10	0/1756	0.25	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	0.11	0/1511	0.28	0/2022
60	IB	0.11	0/1715	0.26	0/2287
61	JB	0.10	0/1550	0.27	0/2069
62	KB	0.11	0/834	0.28	0/1125
63	LB	0.11	0/1200	0.26	0/1604
64	MB	0.10	0/918	0.27	0/1233
65	NB	0.10	0/1226	0.23	0/1649
66	OB	0.11	0/1029	0.27	0/1380
67	PB	0.12	0/1079	0.28	0/1441
68	QB	0.12	0/1146	0.29	0/1534
69	RB	0.10	0/1082	0.25	0/1452
70	SB	0.10	0/1208	0.29	0/1618
71	TB	0.11	0/1123	0.25	0/1504
72	UB	0.11	0/818	0.28	0/1099
73	VB	0.10	0/643	0.25	0/860
74	WB	0.12	0/1051	0.30	0/1406
75	XB	0.10	0/1116	0.24	0/1490

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	YB	0.11	0/1028	0.28	0/1366
77	ZB	0.11	0/691	0.32	0/922
78	AC	0.10	0/828	0.27	0/1109
79	BC	0.09	0/665	0.23	0/891
80	CC	0.10	0/490	0.26	0/656
81	DC	0.10	0/470	0.25	0/623
82	EC	0.08	0/447	0.24	0/587
83	FC	0.09	0/576	0.23	0/764
84	GC	0.11	0/2493	0.32	0/3394
85	IC	0.06	0/19	0.14	0/25
86	b	0.14	0/1296	0.31	0/1745
87	c	0.12	0/111	0.29	0/145
88	HC	0.11	0/1694	0.30	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	35	0
2	B	3196	0	3339	51	0
3	C	2883	0	3053	37	0
4	D	2395	0	2427	30	0
5	E	1823	0	1995	31	0
6	F	1897	0	2021	36	0
7	G	1850	0	1991	23	0
8	H	1516	0	1597	15	0
9	I	1664	0	1712	23	0
10	J	1372	0	1412	21	0
11	K	1702	0	1820	26	0
12	L	1137	0	1211	24	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	M	1701	0	1749	34	0
14	N	1630	0	1778	32	0
15	O	1266	0	1302	16	0
16	P	1515	0	1634	30	0
17	Q	1508	0	1664	24	0
18	R	1462	0	1508	24	0
19	S	1298	0	1366	21	0
20	T	826	0	852	17	0
21	U	1004	0	1063	15	0
22	V	887	0	935	11	0
23	W	967	0	1040	10	0
24	X	1115	0	1205	19	0
25	Y	1107	0	1182	22	0
26	Z	1162	0	1209	23	0
27	AA	873	0	949	8	0
28	BA	769	0	803	11	0
29	CA	893	0	932	16	0
30	DA	1064	0	1160	21	0
31	EA	876	0	912	12	0
32	FA	906	0	998	7	0
33	GA	1008	0	1142	18	0
34	HA	830	0	916	6	0
35	IA	716	0	750	17	0
36	JA	569	0	637	8	0
37	KA	447	0	480	13	0
38	LA	429	0	465	6	0
39	MA	239	0	289	4	0
40	NA	851	0	920	13	0
41	OA	708	0	757	9	0
42	PA	994	0	1051	16	0
43	RA	1160	0	1218	15	0
44	SA	1622	0	825	12	0
45	TA	1615	0	820	18	0
46	UA	1596	0	810	17	0
47	VA	251	0	128	1	0
48	WA	76735	0	38762	933	0
49	XA	2538	0	1286	27	0
50	YA	3314	0	1683	35	0
51	ZA	36623	0	18504	464	0
52	AB	1710	0	1711	26	0
53	BB	1729	0	1803	21	0
54	CB	1707	0	1793	29	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	DB	1768	0	1863	21	0
56	EB	2076	0	2177	37	0
57	FB	1471	0	1522	23	0
58	GB	1923	0	2089	38	0
59	HB	1489	0	1582	25	0
60	IB	1686	0	1772	21	0
61	JB	1525	0	1640	34	0
62	KB	810	0	836	20	0
63	LB	1180	0	1254	14	0
64	MB	908	0	939	19	0
65	NB	1202	0	1289	19	0
66	OB	1016	0	1039	20	0
67	PB	1058	0	1104	15	0
68	QB	1128	0	1195	20	0
69	RB	1068	0	1121	16	0
70	SB	1190	0	1249	28	0
71	TB	1104	0	1138	21	0
72	UB	808	0	878	14	0
73	VB	636	0	637	8	0
74	WB	1034	0	1080	20	0
75	XB	1098	0	1167	15	0
76	YB	1011	0	1083	18	0
77	ZB	683	0	761	8	0
78	AC	814	0	864	16	0
79	BC	651	0	672	8	0
80	CC	488	0	514	11	0
81	DC	459	0	449	9	0
82	EC	443	0	492	8	0
83	FC	564	0	577	7	0
84	GC	2436	0	2393	47	0
85	IC	20	0	10	0	0
86	b	1279	0	1343	29	0
87	c	110	0	83	4	0
88	HC	1664	0	1721	27	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

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
89	SA	1	0	0	0	0
89	U	1	0	0	0	0
89	WA	158	0	0	0	0
89	XA	3	0	0	0	0
89	YA	2	0	0	0	0
89	Z	2	0	0	0	0
89	ZA	61	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	0	0
93	WA	30	0	57	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	220703	0	164224	2507	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 2507 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)
46:UA:8:U:H3	46:UA:14:A:H62	1.07	1.03
48:WA:1446:G:H1	48:WA:2113:U:H3	1.02	1.00
48:WA:2847:A:H61	48:WA:3845:C:N4	1.57	1.00
48:WA:1249:U:H3	48:WA:1268:G:H1	1.07	0.99
51:ZA:197:U:H3	51:ZA:202:G:H1	0.98	0.97

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%)	385 (98%)	10 (2%)	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%)	183 (97%)	5 (3%)	0	100	100
9	I	201/214 (94%)	196 (98%)	5 (2%)	0	100	100
10	J	169/178 (95%)	168 (99%)	1 (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%)	196 (98%)	5 (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%)	180 (97%)	5 (3%)	0	100	100
17	Q	178/212 (84%)	175 (98%)	3 (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%)	95 (96%)	4 (4%)	0	100	100
21	U	133/140 (95%)	128 (96%)	5 (4%)	0	100	100
22	V	106/157 (68%)	103 (97%)	3 (3%)	0	100	100
23	W	116/156 (74%)	114 (98%)	2 (2%)	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

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	Z	145/148 (98%)	143 (99%)	2 (1%)	0	100	100
27	AA	103/245 (42%)	101 (98%)	2 (2%)	0	100	100
28	BA	97/115 (84%)	96 (99%)	1 (1%)	0	100	100
29	CA	106/125 (85%)	104 (98%)	2 (2%)	0	100	100
30	DA	127/135 (94%)	122 (96%)	5 (4%)	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%)	95 (95%)	5 (5%)	0	100	100
35	IA	85/97 (88%)	83 (98%)	2 (2%)	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%)	50 (100%)	0	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%)	85 (96%)	4 (4%)	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%)	211 (98%)	4 (2%)	0	100	100
53	BB	211/264 (80%)	207 (98%)	4 (2%)	0	100	100
54	CB	218/293 (74%)	214 (98%)	4 (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%)	174 (96%)	7 (4%)	0	100	100
58	GB	235/249 (94%)	233 (99%)	2 (1%)	0	100	100
59	HB	181/432 (42%)	175 (97%)	6 (3%)	0	100	100
60	IB	204/208 (98%)	201 (98%)	3 (2%)	0	100	100
61	JB	183/194 (94%)	180 (98%)	3 (2%)	0	100	100
62	KB	94/165 (57%)	92 (98%)	2 (2%)	0	100	100
63	LB	140/158 (89%)	138 (99%)	2 (1%)	0	100	100
64	MB	115/132 (87%)	109 (95%)	6 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
65	NB	147/151 (97%)	146 (99%)	1 (1%)	0	100	100
66	OB	134/151 (89%)	128 (96%)	6 (4%)	0	100	100
67	PB	127/145 (88%)	123 (97%)	4 (3%)	0	100	100
68	QB	140/172 (81%)	135 (96%)	5 (4%)	0	100	100
69	RB	130/135 (96%)	126 (97%)	4 (3%)	0	100	100
70	SB	142/152 (93%)	139 (98%)	3 (2%)	0	100	100
71	TB	140/145 (97%)	135 (96%)	4 (3%)	1 (1%)	18	49
72	UB	100/119 (84%)	96 (96%)	4 (4%)	0	100	100
73	VB	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
74	WB	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
75	XB	139/143 (97%)	136 (98%)	3 (2%)	0	100	100
76	YB	122/131 (93%)	119 (98%)	3 (2%)	0	100	100
77	ZB	83/124 (67%)	83 (100%)	0	0	100	100
78	AC	99/115 (86%)	96 (97%)	3 (3%)	0	100	100
79	BC	81/84 (96%)	80 (99%)	1 (1%)	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%)	150 (93%)	11 (7%)	1 (1%)	21	52
87	c	12/14 (86%)	11 (92%)	1 (8%)	0	100	100
88	HC	221/462 (48%)	209 (95%)	12 (5%)	0	100	100
All	All	11783/14293 (82%)	11464 (97%)	317 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
71	TB	119	TRP
86	b	225	VAL

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	192/199 (96%)	191 (100%)	1 (0%)	81	85
2	B	344/348 (99%)	336 (98%)	8 (2%)	44	70
3	C	302/337 (90%)	300 (99%)	2 (1%)	76	82
4	D	247/250 (99%)	246 (100%)	1 (0%)	84	86
5	E	201/251 (80%)	199 (99%)	2 (1%)	68	79
6	F	198/218 (91%)	198 (100%)	0	100	100
7	G	197/273 (72%)	194 (98%)	3 (2%)	57	75
8	H	169/171 (99%)	166 (98%)	3 (2%)	51	73
9	I	175/181 (97%)	173 (99%)	2 (1%)	65	78
10	J	144/149 (97%)	143 (99%)	1 (1%)	76	82
11	K	175/176 (99%)	171 (98%)	4 (2%)	44	70
12	L	117/161 (73%)	117 (100%)	0	100	100
13	M	171/172 (99%)	167 (98%)	4 (2%)	44	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%)	63	78
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%)	59	76
20	T	91/114 (80%)	91 (100%)	0	100	100
21	U	103/107 (96%)	102 (99%)	1 (1%)	68	79
22	V	89/126 (71%)	87 (98%)	2 (2%)	45	71
23	W	106/134 (79%)	105 (99%)	1 (1%)	70	80
24	X	124/135 (92%)	120 (97%)	4 (3%)	34	64
25	Y	117/118 (99%)	116 (99%)	1 (1%)	70	80
26	Z	119/120 (99%)	118 (99%)	1 (1%)	73	81

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	AA	87/184 (47%)	86 (99%)	1 (1%)	65	78
28	BA	85/98 (87%)	83 (98%)	2 (2%)	43	69
29	CA	98/110 (89%)	97 (99%)	1 (1%)	68	79
30	DA	115/121 (95%)	115 (100%)	0	100	100
31	EA	88/89 (99%)	88 (100%)	0	100	100
32	FA	98/109 (90%)	95 (97%)	3 (3%)	35	64
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%)	59	76
36	JA	64/65 (98%)	64 (100%)	0	100	100
37	KA	47/48 (98%)	46 (98%)	1 (2%)	47	71
38	LA	48/116 (41%)	46 (96%)	2 (4%)	26	58
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%)	59	76
42	PA	108/121 (89%)	106 (98%)	2 (2%)	50	73
43	RA	126/137 (92%)	118 (94%)	8 (6%)	16	45
52	AB	180/244 (74%)	180 (100%)	0	100	100
53	BB	194/231 (84%)	192 (99%)	2 (1%)	68	79
54	CB	186/225 (83%)	185 (100%)	1 (0%)	81	85
55	DB	190/232 (82%)	186 (98%)	4 (2%)	47	71
56	EB	224/225 (100%)	219 (98%)	5 (2%)	45	71
57	FB	158/170 (93%)	157 (99%)	1 (1%)	78	83
58	GB	207/218 (95%)	203 (98%)	4 (2%)	50	73
59	HB	165/360 (46%)	161 (98%)	4 (2%)	43	69
60	IB	178/180 (99%)	176 (99%)	2 (1%)	65	78
61	JB	161/168 (96%)	159 (99%)	2 (1%)	63	78
62	KB	87/136 (64%)	86 (99%)	1 (1%)	65	78
63	LB	130/142 (92%)	128 (98%)	2 (2%)	57	75
64	MB	99/108 (92%)	93 (94%)	6 (6%)	17	46
65	NB	130/131 (99%)	129 (99%)	1 (1%)	73	81

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	OB	106/119 (89%)	105 (99%)	1 (1%)	70	80
67	PB	115/130 (88%)	111 (96%)	4 (4%)	32	62
68	QB	117/140 (84%)	114 (97%)	3 (3%)	40	68
69	RB	119/121 (98%)	116 (98%)	3 (2%)	42	69
70	SB	125/132 (95%)	123 (98%)	2 (2%)	55	75
71	TB	112/116 (97%)	109 (97%)	3 (3%)	39	67
72	UB	93/107 (87%)	90 (97%)	3 (3%)	34	64
73	VB	67/67 (100%)	65 (97%)	2 (3%)	36	65
74	WB	112/113 (99%)	111 (99%)	1 (1%)	70	80
75	XB	113/115 (98%)	109 (96%)	4 (4%)	32	62
76	YB	107/113 (95%)	107 (100%)	0	100	100
77	ZB	75/102 (74%)	74 (99%)	1 (1%)	61	77
78	AC	88/98 (90%)	87 (99%)	1 (1%)	65	78
79	BC	75/76 (99%)	73 (97%)	2 (3%)	39	67
80	CC	55/62 (89%)	55 (100%)	0	100	100
81	DC	48/49 (98%)	47 (98%)	1 (2%)	47	71
82	EC	46/106 (43%)	45 (98%)	1 (2%)	45	71
83	FC	62/154 (40%)	59 (95%)	3 (5%)	23	54
84	GC	272/275 (99%)	250 (92%)	22 (8%)	11	36
86	b	138/258 (54%)	126 (91%)	12 (9%)	9	34
87	c	12/12 (100%)	12 (100%)	0	100	100
88	HC	179/379 (47%)	164 (92%)	15 (8%)	10	35
All	All	10256/12075 (85%)	10063 (98%)	193 (2%)	49	73

5 of 193 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
68	QB	110	ILE
83	FC	135	HIS
69	RB	99	ASP
74	WB	105	THR
84	GC	54	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 80 such sidechains are listed below:

Mol	Chain	Res	Type
64	MB	75	ASN
78	AC	72	HIS
68	QB	37	GLN
75	XB	61	GLN
84	GC	222	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
44	SA	75/76 (98%)	16 (21%)	3 (4%)
45	TA	75/76 (98%)	15 (20%)	0
46	UA	74/75 (98%)	37 (50%)	1 (1%)
47	VA	11/12 (91%)	3 (27%)	0
48	WA	3556/3584 (99%)	603 (16%)	20 (0%)
49	XA	118/120 (98%)	9 (7%)	0
50	YA	155/156 (99%)	33 (21%)	0
51	ZA	1707/1869 (91%)	326 (19%)	8 (0%)
All	All	5771/5968 (96%)	1042 (18%)	32 (0%)

5 of 1042 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 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	ZA	870	A
51	ZA	890	U
48	WA	1806	A
48	WA	1677	C
51	ZA	1137	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 252 ligands modelled in this entry, 245 are monoatomic - leaving 7 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
91	5GP	UA	101	46	26,26,26	0.98	1 (3%)	39,40,40	1.78	7 (17%)
93	SPD	WA	5244	-	9,9,9	0.27	0	8,8,8	0.34	0
93	SPD	WA	5245	-	9,9,9	0.28	0	8,8,8	0.30	0
92	ANM	WA	5243	94	20,20,20	4.07	7 (35%)	24,27,27	1.40	2 (8%)
95	SER	HC	502	-	4,5,6	0.59	0	1,5,7	0.54	0
93	SPD	ZA	1944	-	9,9,9	0.26	0	8,8,8	0.29	0
93	SPD	WA	5246	-	9,9,9	0.26	0	8,8,8	0.29	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
91	5GP	UA	101	46	-	5/10/26/26	0/3/3/3
93	SPD	WA	5244	-	-	1/7/7/7	-
93	SPD	WA	5245	-	-	1/7/7/7	-
92	ANM	WA	5243	94	-	6/10/23/23	0/2/2/2
95	SER	HC	502	-	-	1/2/4/6	-
93	SPD	ZA	1944	-	-	1/7/7/7	-
93	SPD	WA	5246	-	-	1/7/7/7	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
92	WA	5243	ANM	C3-C2	-11.79	1.32	1.53

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
92	WA	5243	ANM	C16-N1	-8.84	1.30	1.47
92	WA	5243	ANM	C2-C16	7.40	1.68	1.53
92	WA	5243	ANM	C4-C3	4.00	1.58	1.53
92	WA	5243	ANM	C4-N1	3.87	1.60	1.47

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
91	UA	101	5GP	C5-C4-N3	-6.07	118.72	128.39
92	WA	5243	ANM	O2-C5-C6	5.19	120.35	111.09
91	UA	101	5GP	C2-N3-C4	4.77	120.51	112.30
91	UA	101	5GP	N9-C4-N3	3.89	133.73	125.95
91	UA	101	5GP	C5-C6-N1	2.48	119.57	113.25

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

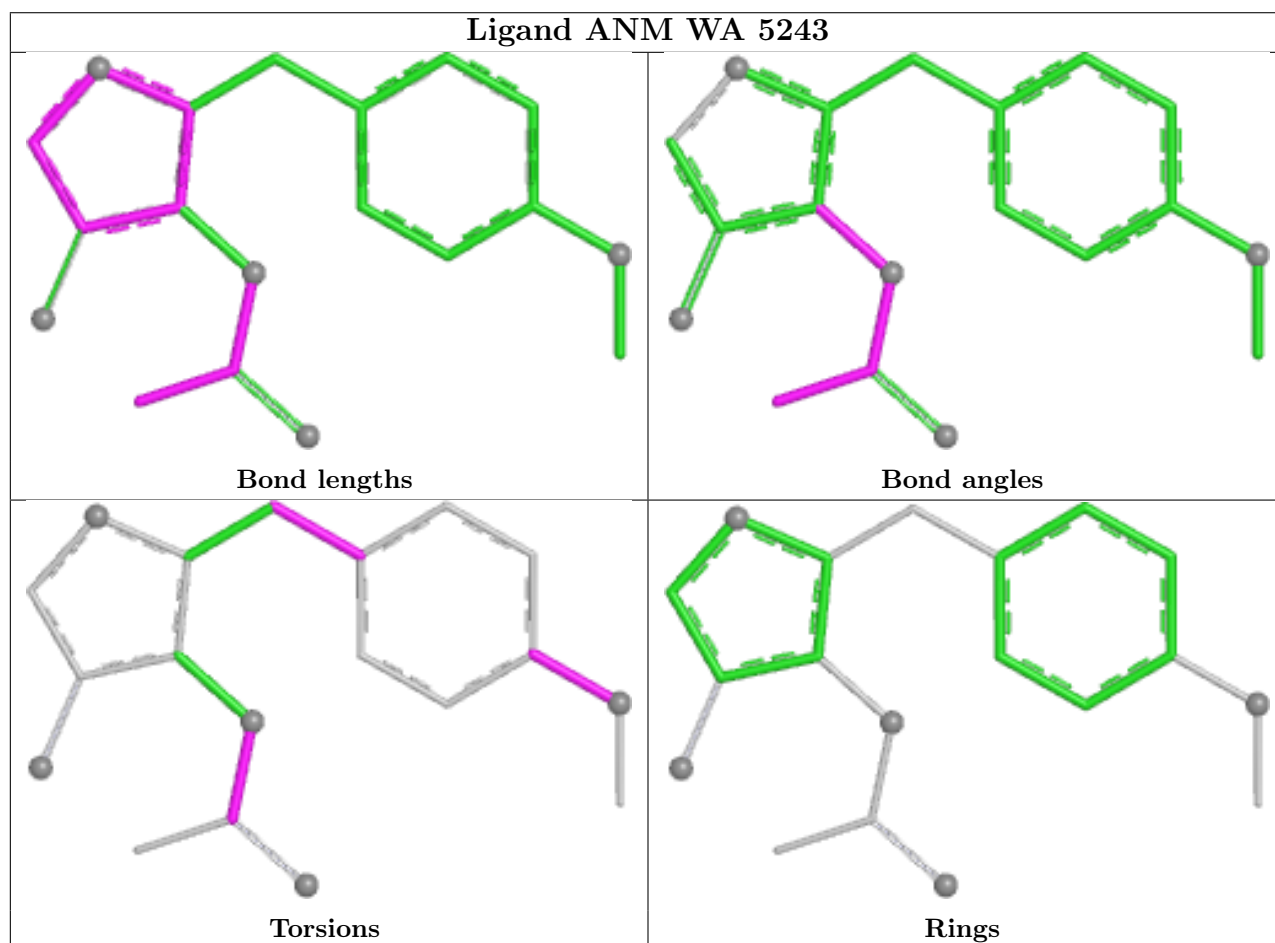
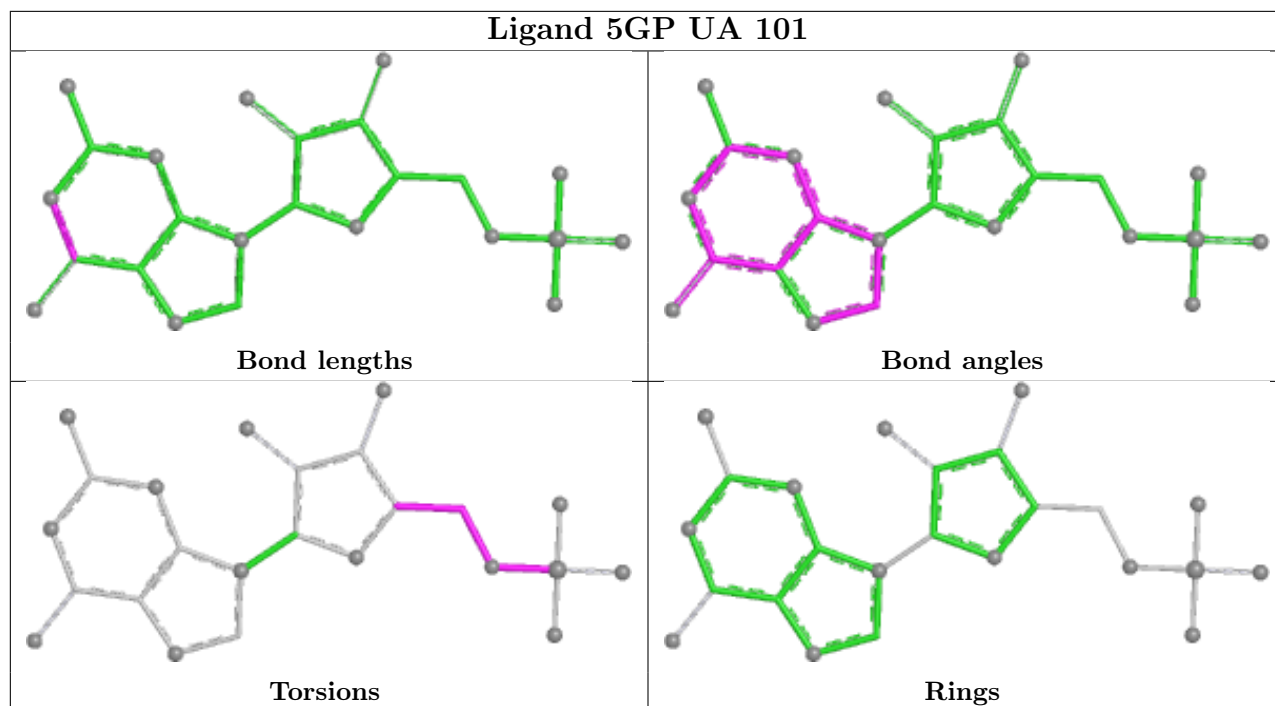
Mol	Chain	Res	Type	Atoms
91	UA	101	5GP	C5'-O5'-P-OP1
92	WA	5243	ANM	C6-C5-O2-C2
92	WA	5243	ANM	O3-C5-O2-C2
92	WA	5243	ANM	C10-C9-O1-C14
92	WA	5243	ANM	C1-C9-O1-C14

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
93	WA	5244	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	37.06
1	WA	1225:G	O3'	1239:G	P	20.73
1	WA	996:C	O3'	1070:G	P	17.80
1	WA	4779:C	O3'	4861:C	P	17.50
1	WA	763:G	O3'	904:C	P	16.92

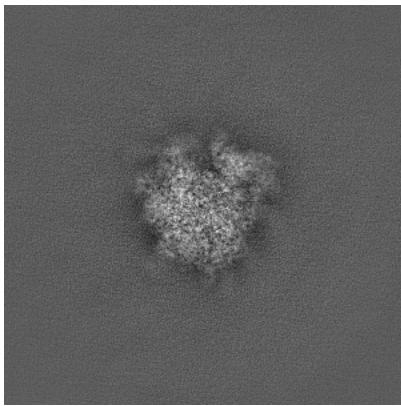
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43567. These allow visual inspection of the internal detail of the map and identification of artifacts.

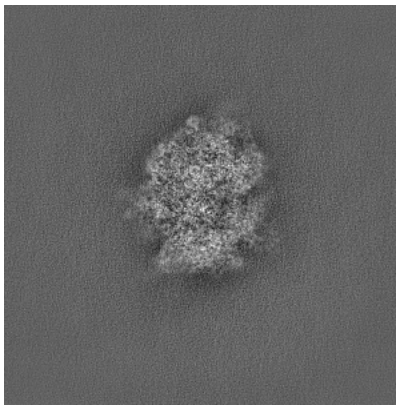
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

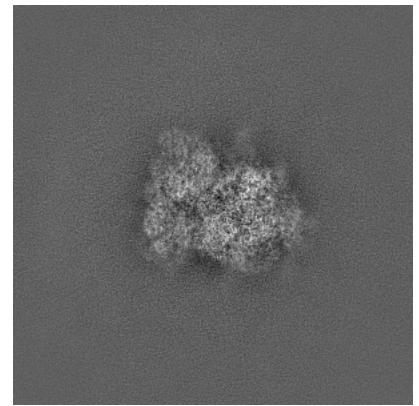
6.1.1 Primary map



X

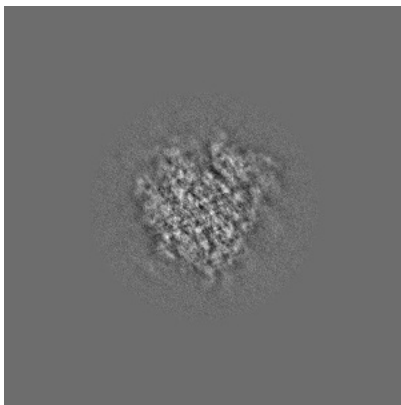


Y

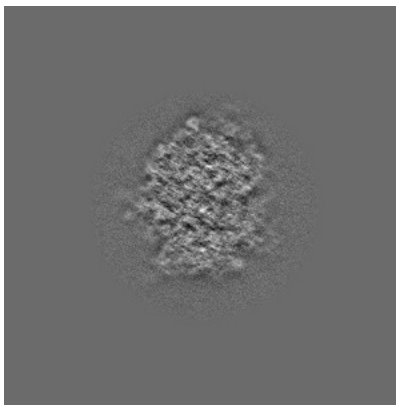


Z

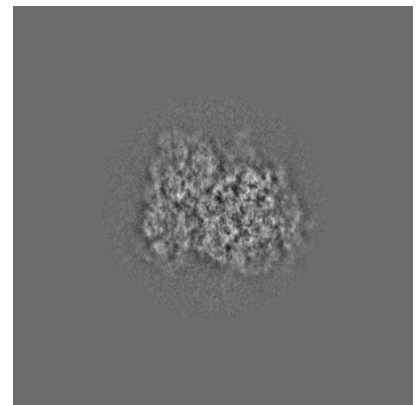
6.1.2 Raw map



X



Y

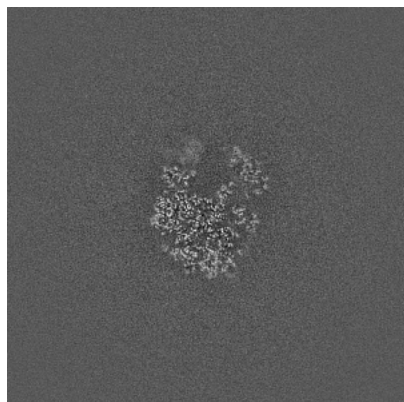


Z

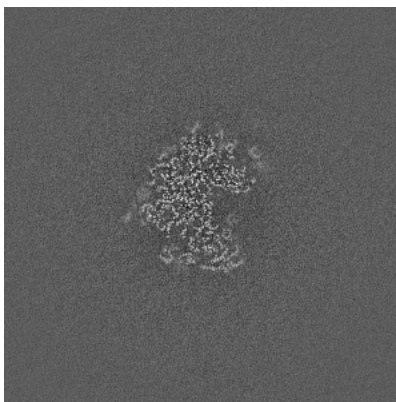
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

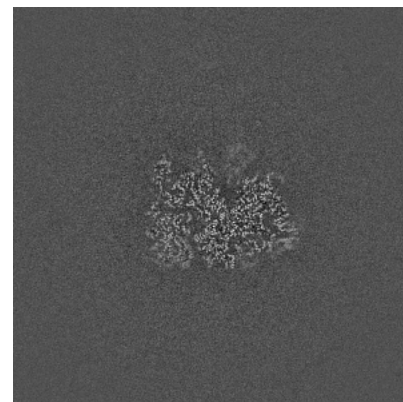
6.2.1 Primary map



X Index: 324

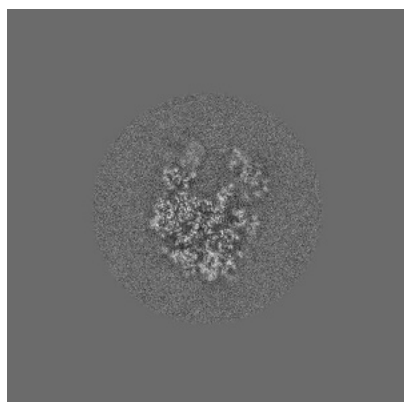


Y Index: 324

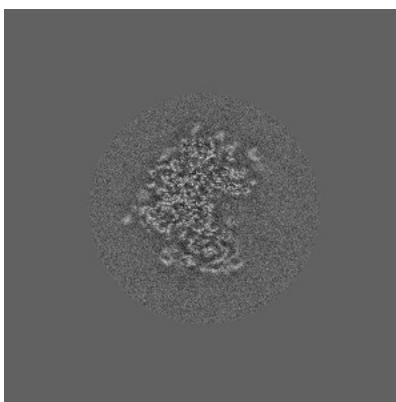


Z Index: 324

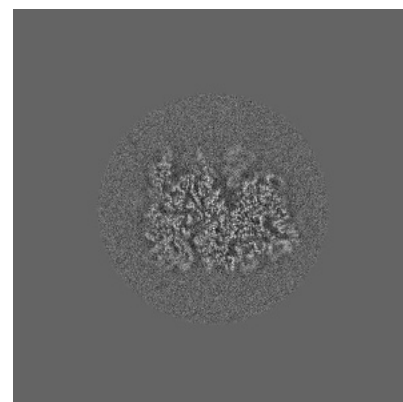
6.2.2 Raw map



X Index: 324



Y Index: 324

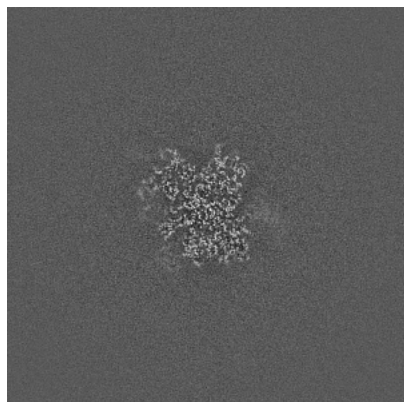


Z Index: 324

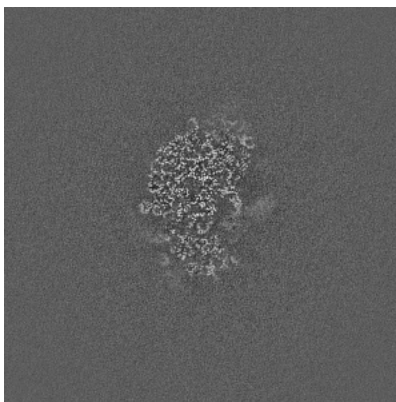
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

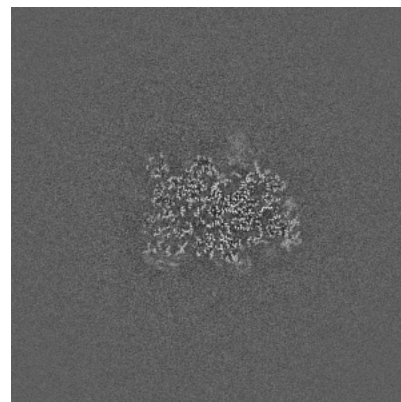
6.3.1 Primary map



X Index: 377

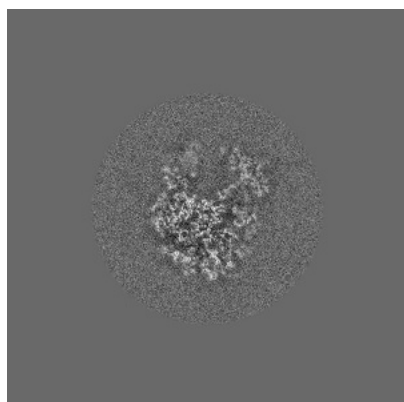


Y Index: 301

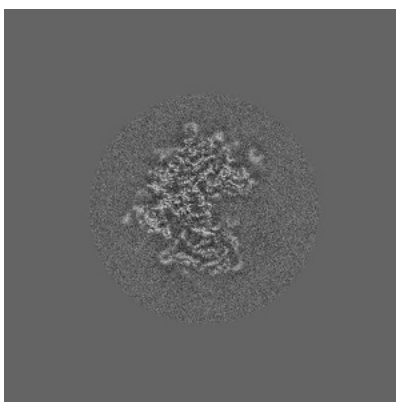


Z Index: 311

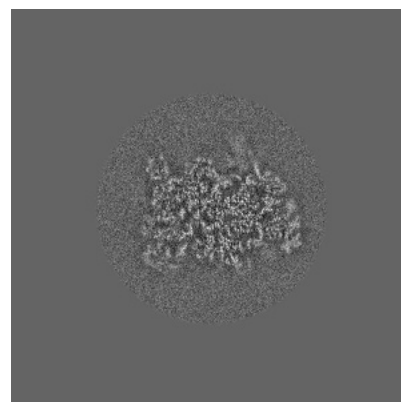
6.3.2 Raw map



X Index: 322



Y Index: 327

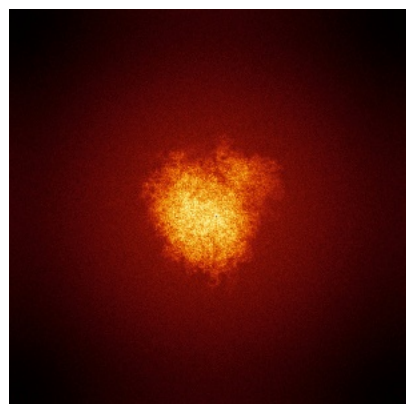


Z Index: 311

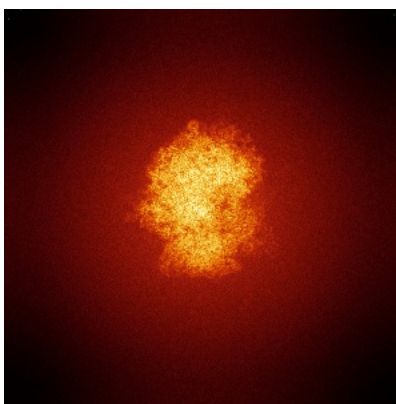
The images above show the largest variance slices of the map in three orthogonal directions.

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

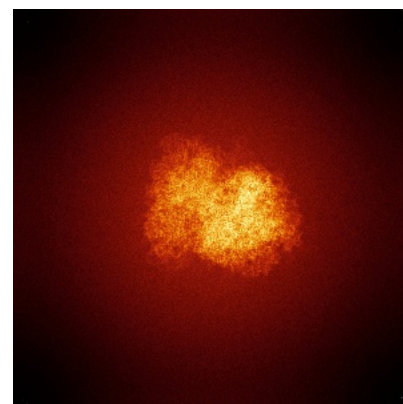
6.4.1 Primary map



X

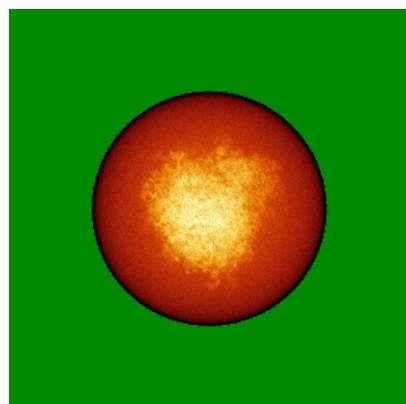


Y

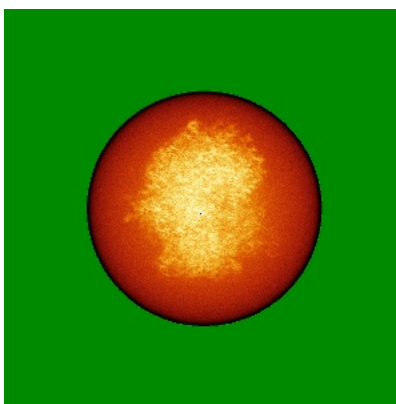


Z

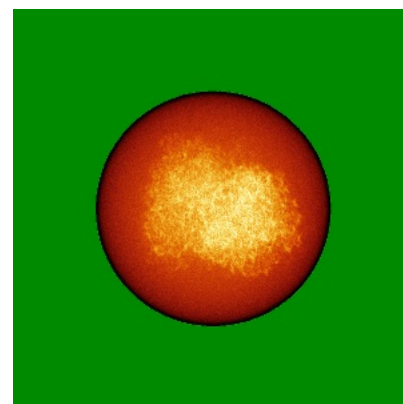
6.4.2 Raw map



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](#)

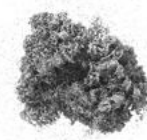
6.5.1 Primary map



X



Y



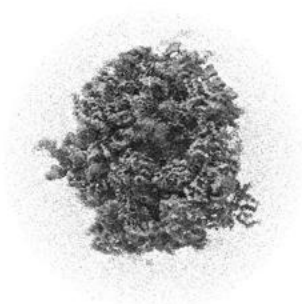
Z

The images above show the 3D surface view of the map at the recommended contour level 6.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

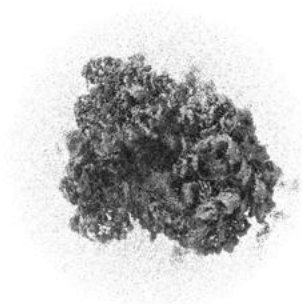
6.5.2 Raw map



X



Y



Z

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

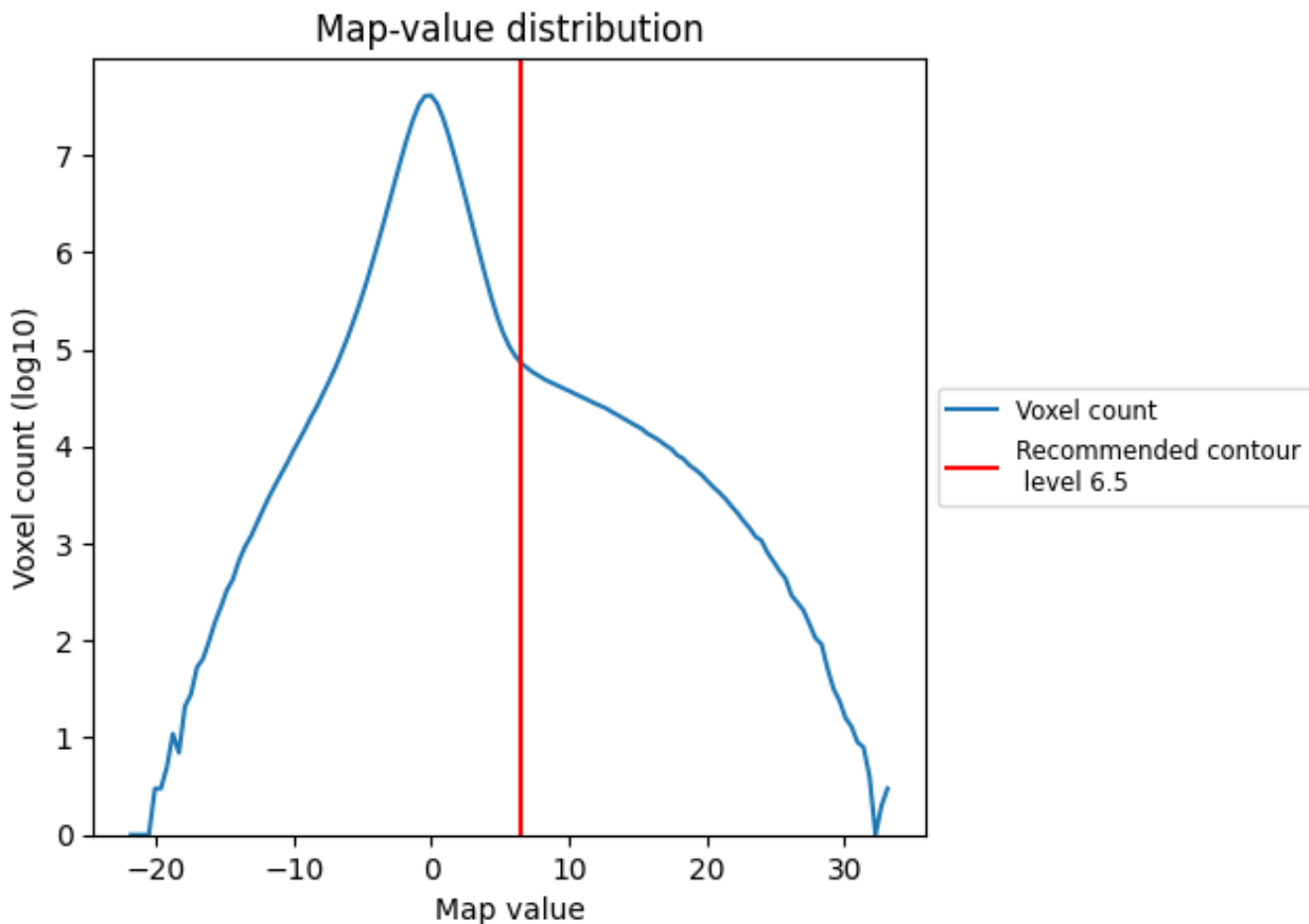
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

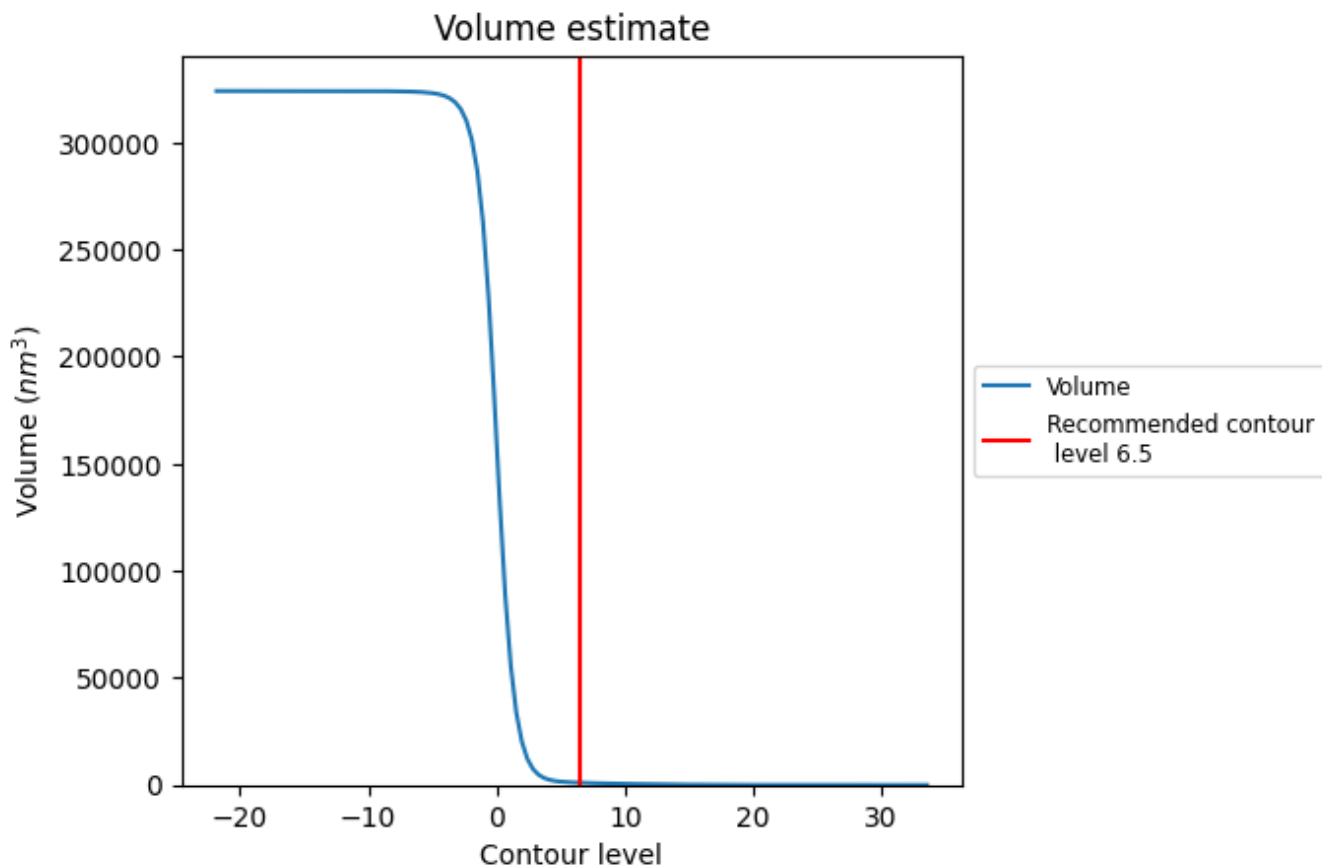
This section contains the results of statistical analysis of the map.

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.

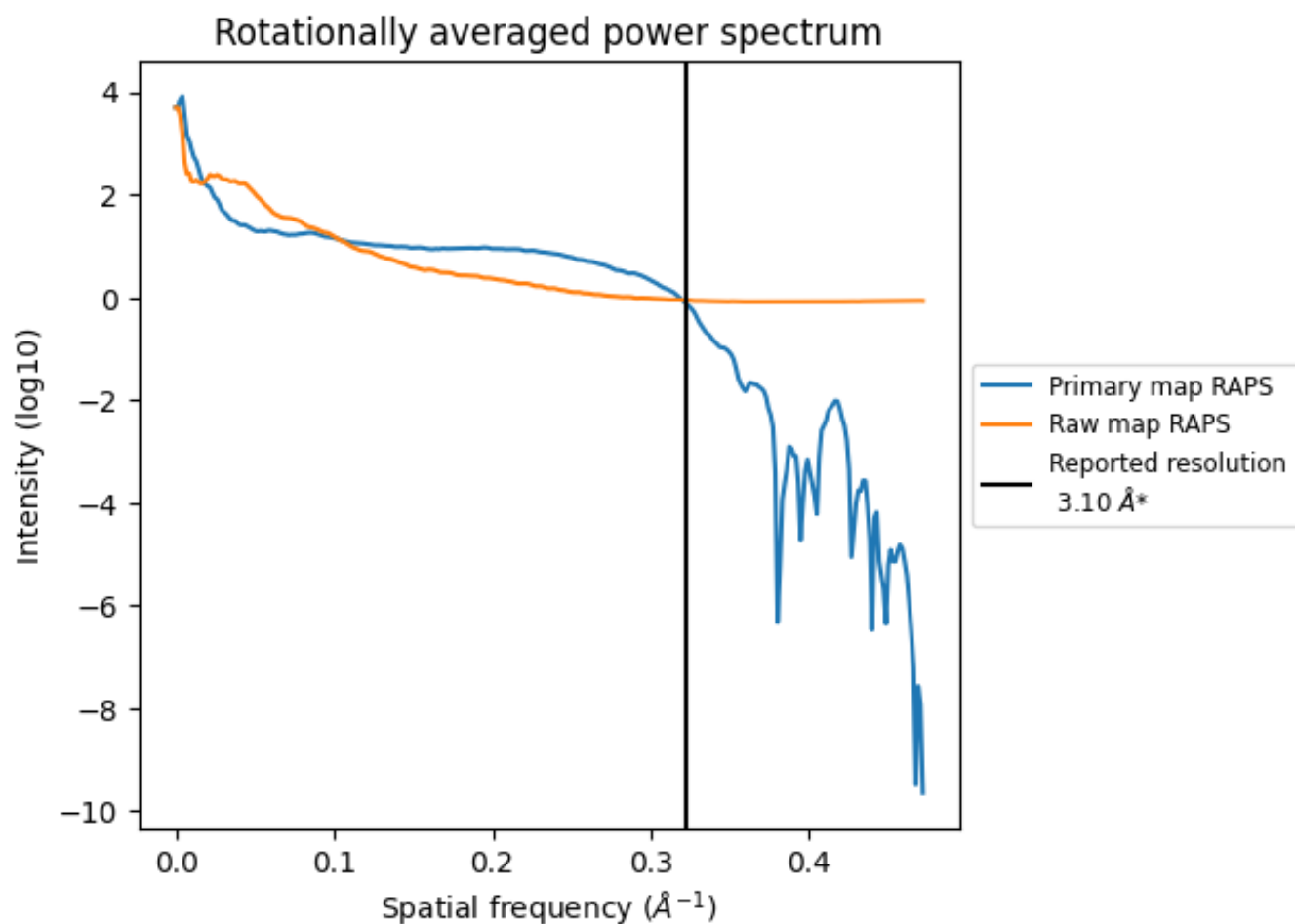
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1042 nm^3 ; this corresponds to an approximate mass of 941 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

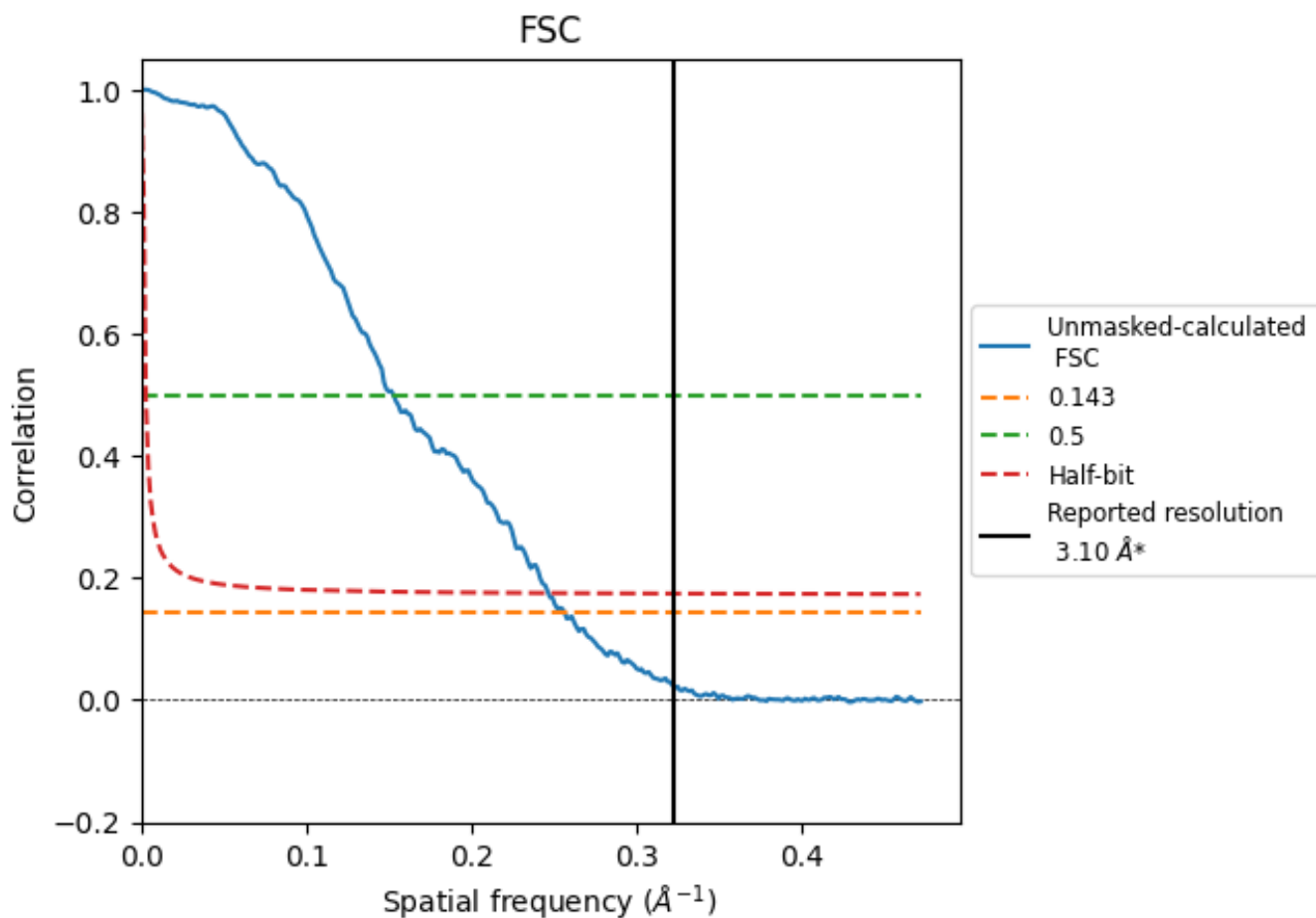


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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

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

8.1 FSC [\(i\)](#)



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

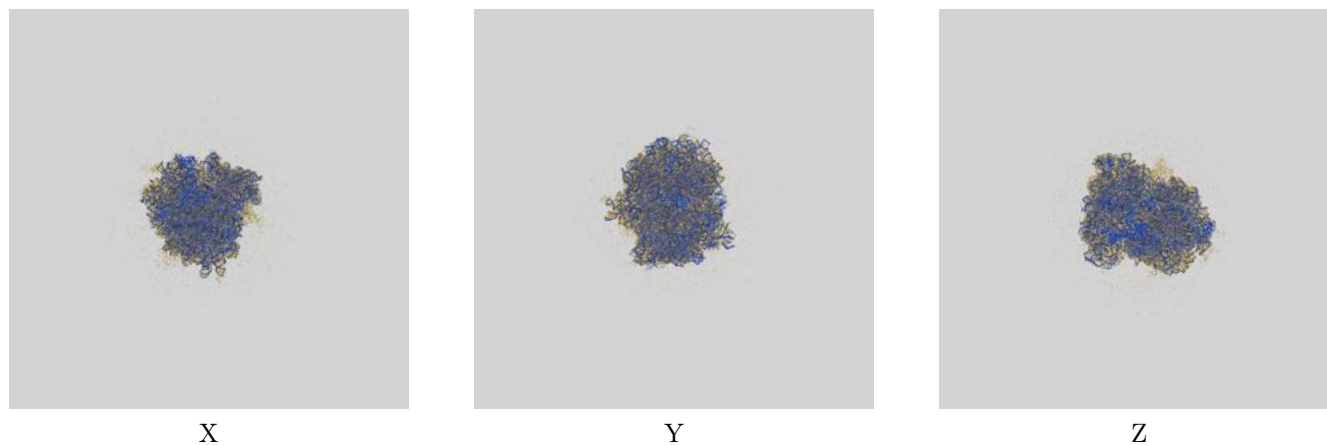
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.90	6.55	4.06

*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 3.90 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

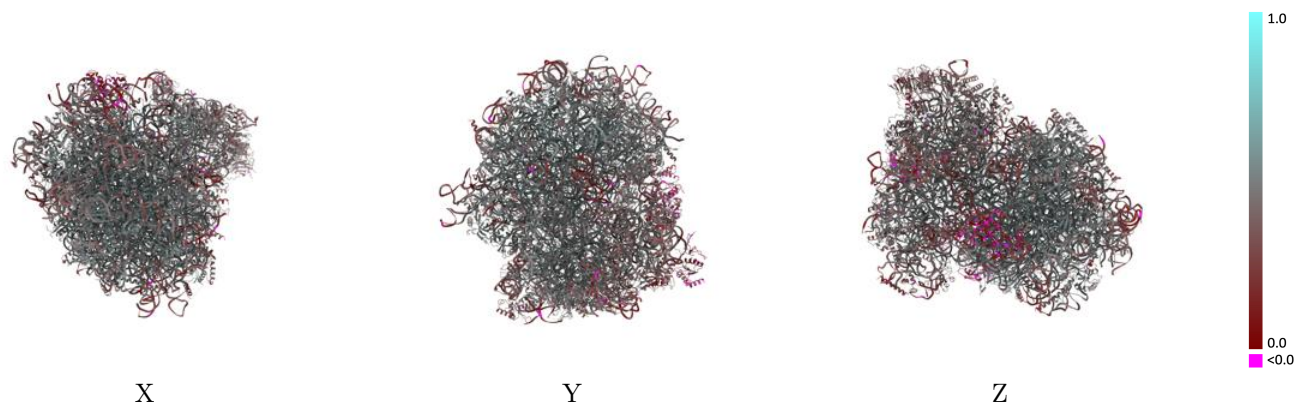
This section contains information regarding the fit between EMDB map EMD-43567 and PDB model 8VVS. Per-residue inclusion information can be found in section 3 on page 26.

9.1 Map-model overlay [i](#)



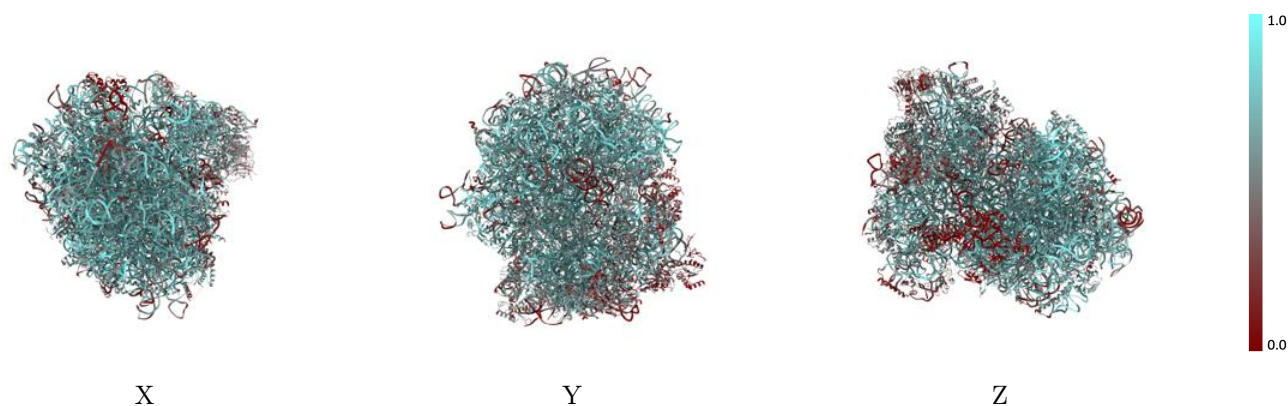
The images above show the 3D surface view of the map at the recommended contour level 6.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



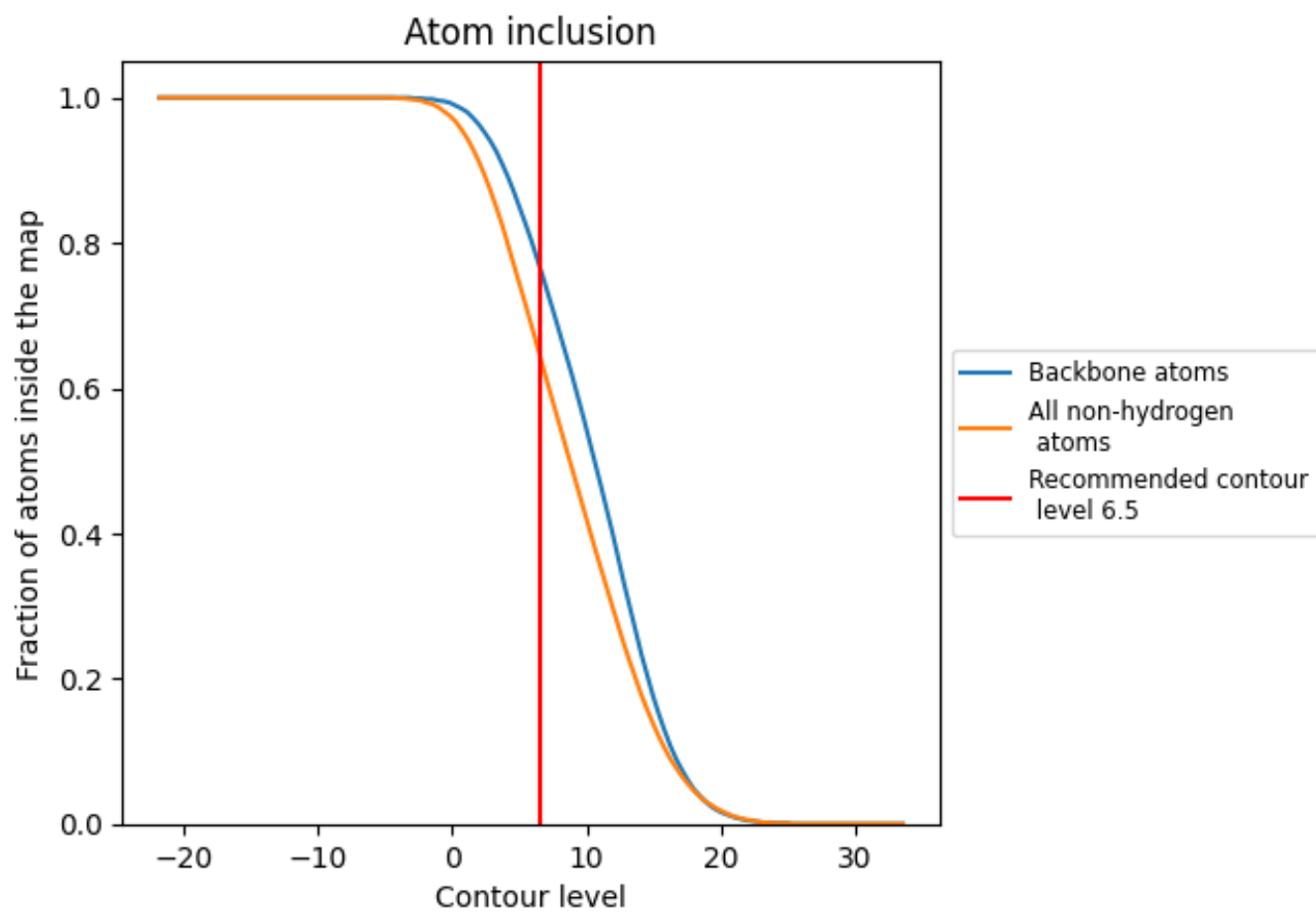
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (6.5).







































































9.4 Atom inclusion [i](#)

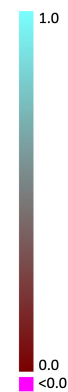


At the recommended contour level, 77% of all backbone atoms, 65% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (6.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6460	 0.4470
A	 0.6850	 0.5250
AA	 0.5240	 0.4290
AB	 0.5640	 0.4480
AC	 0.5950	 0.4800
B	 0.6640	 0.5000
BA	 0.6370	 0.4740
BB	 0.5470	 0.4620
BC	 0.4960	 0.4430
C	 0.6580	 0.5050
CA	 0.6370	 0.4870
CB	 0.5790	 0.4700
CC	 0.4830	 0.4270
D	 0.6490	 0.4570
DA	 0.6690	 0.5140
DB	 0.4440	 0.4000
DC	 0.5360	 0.4510
E	 0.5860	 0.4560
EA	 0.6590	 0.5230
EB	 0.5430	 0.4600
EC	 0.4440	 0.3890
F	 0.6400	 0.4970
FA	 0.6370	 0.4940
FB	 0.4920	 0.4150
FC	 0.1510	 0.2610
G	 0.5960	 0.4450
GA	 0.6280	 0.4750
GB	 0.4160	 0.3710
GC	 0.3270	 0.3460
H	 0.6140	 0.4700
HA	 0.6240	 0.4600
HB	 0.4550	 0.3990
HC	 0.0940	 0.2990
I	 0.6600	 0.5050
IA	 0.6960	 0.5230



























Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
IB	0.5400	0.4470
IC	0.4500	0.4450
J	0.5850	0.4410
JA	0.5550	0.4330
JB	0.5490	0.4390
K	0.6270	0.4870
KA	0.6230	0.4920
KB	0.4160	0.3740
L	0.6270	0.4650
LA	0.6710	0.5040
LB	0.5980	0.4910
M	0.6990	0.5240
MA	0.6190	0.4880
MB	0.1710	0.2180
N	0.6630	0.4960
NA	0.6490	0.5150
NB	0.6130	0.4650
O	0.6530	0.5080
OA	0.6490	0.5070
OB	0.5720	0.4590
P	0.6760	0.5120
PA	0.6630	0.5020
PB	0.4030	0.3730
Q	0.6320	0.4700
QB	0.4780	0.4160
R	0.6550	0.4970
RA	0.0190	0.1040
RB	0.4910	0.4190
S	0.6370	0.4920
SA	0.5680	0.4020
SB	0.4790	0.4040
T	0.5610	0.4300
TA	0.1550	0.2340
TB	0.4980	0.4050
U	0.6480	0.5110
UA	0.1610	0.2630
UB	0.4050	0.3770
V	0.4820	0.3960
VA	0.4820	0.4170
VB	0.5850	0.4520
W	0.6310	0.4740
WA	0.7500	0.4610

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
WB	 0.6060	 0.4800
X	 0.6350	 0.4820
XA	 0.8460	 0.4940
XB	 0.5810	 0.4850
Y	 0.6570	 0.4800
YA	 0.7580	 0.4690
YB	 0.4740	 0.4100
Z	 0.7070	 0.5150
ZA	 0.6920	 0.4370
ZB	 0.3880	 0.3790
b	 0.0410	 0.1270
c	 0.0090	 0.1480