



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:54 PM UTC

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

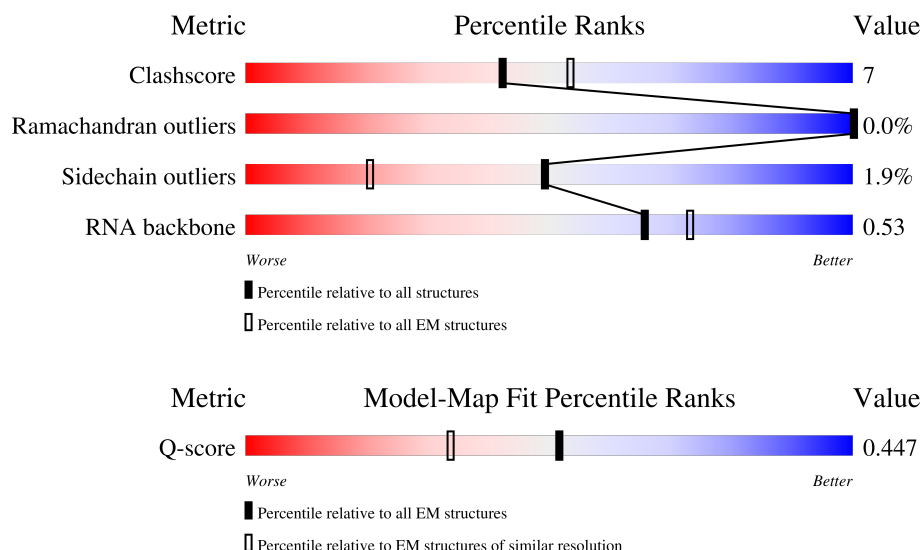
1 Overall quality at a glance

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	

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Mol	Chain	Length	Quality of chain
4	D	297	
5	E	291	
6	F	249	
7	G	319	
8	H	192	
9	I	214	
10	J	178	
11	K	211	
12	L	218	
13	M	204	
14	N	203	
15	O	213	
16	P	188	
17	Q	212	
18	R	224	
19	S	160	
20	T	128	
21	U	140	
22	V	157	
23	W	156	
24	X	145	
25	Y	136	
26	Z	148	
27	AA	245	
28	BA	115	

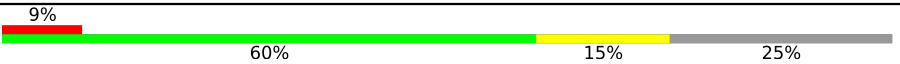

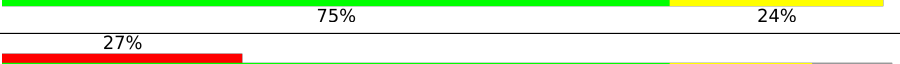
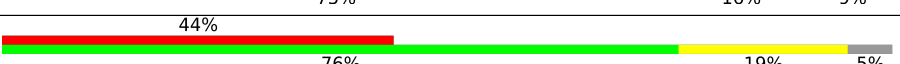


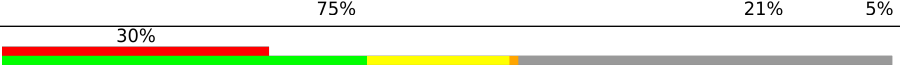
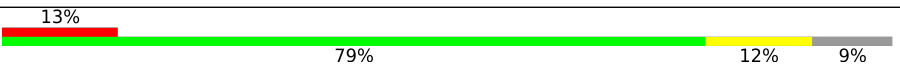
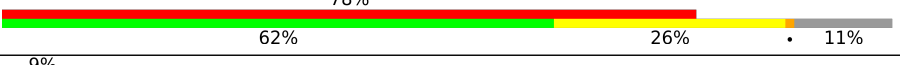

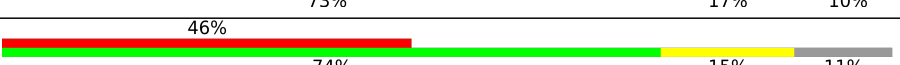


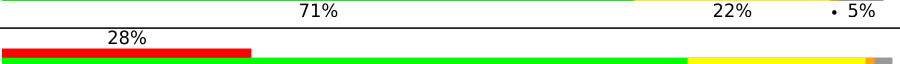
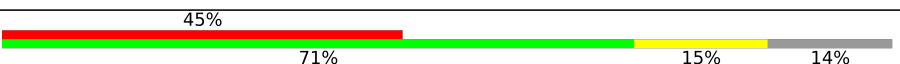


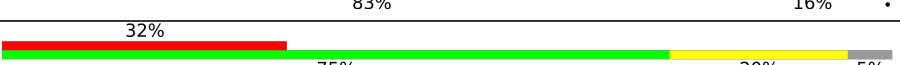
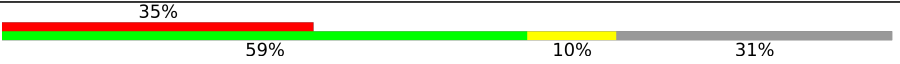




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Mol	Chain	Length	Quality of chain
29	CA	125	
30	DA	135	
31	EA	110	
32	FA	129	
33	GA	123	
34	HA	105	
35	IA	97	
36	JA	70	
37	KA	51	
38	LA	128	
39	MA	25	
40	NA	106	
41	OA	92	
42	PA	137	
43	RA	165	
44	SA	76	
45	TA	76	
46	UA	75	
47	VA	12	
48	WA	3584	
49	XA	120	
50	YA	156	
51	ZA	1869	
52	AB	295	
53	BB	264	

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Mol	Chain	Length	Quality of chain
54	CB	293	
55	DB	281	
56	EB	263	
57	FB	204	
58	GB	249	
59	HB	432	
60	IB	208	
61	JB	194	
62	KB	165	
63	LB	158	
64	MB	132	
65	NB	151	
66	OB	151	
67	PB	145	
68	QB	172	
69	RB	135	
70	SB	152	
71	TB	145	
72	UB	119	
73	VB	83	
74	WB	130	
75	XB	143	
76	YB	131	
77	ZB	124	
78	AC	115	

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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

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
1	A	250	Total	C	N	O	S	0	0
			1914	1199	392	317	6		

- Molecule 2 is a protein called uL3.

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

- Molecule 3 is a protein called uL4.

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

- Molecule 4 is a protein called uL18.

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

- Molecule 5 is a protein called L6.

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

- Molecule 6 is a protein called uL30.

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

- Molecule 7 is a protein called L7A.

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

- Molecule 8 is a protein called L9.

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

- Molecule 9 is a protein called L10.

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

- Molecule 10 is a protein called uL5.

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

- Molecule 11 is a protein called eL13.

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

There are 9 discrepancies between the modelled and reference sequences:

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

- Molecule 12 is a protein called eL14.

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

- Molecule 13 is a protein called eL15.

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

- Molecule 14 is a protein called uL13.

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

- Molecule 15 is a protein called uL22.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 16 is a protein called eL18.

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

There are 12 discrepancies between the modelled and reference sequences:

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

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

- Molecule 17 is a protein called eL19.

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

- Molecule 18 is a protein called eL20.

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

- Molecule 19 is a protein called eL21.

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

- Molecule 20 is a protein called eL22.

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

There are 11 discrepancies between the modelled and reference sequences:

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

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

- Molecule 21 is a protein called L23.

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

- Molecule 22 is a protein called uL24.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 23 is a protein called uL23.

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

- Molecule 24 is a protein called L26.

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

- Molecule 25 is a protein called L27.

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

- Molecule 26 is a protein called uL15.

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

- Molecule 27 is a protein called L29.

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

- Molecule 28 is a protein called eL30.

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

- Molecule 29 is a protein called L31.

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

- Molecule 30 is a protein called L32.

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

- Molecule 31 is a protein called eL33.

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

- Molecule 32 is a protein called L34.

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

- Molecule 33 is a protein called L35.

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

- Molecule 34 is a protein called L36.

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

- Molecule 35 is a protein called L37.

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

- Molecule 36 is a protein called eL38.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 37 is a protein called eL39.

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

- Molecule 38 is a protein called eL40.

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

- Molecule 39 is a protein called eL41.

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

- Molecule 40 is a protein called eL42.

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

- Molecule 41 is a protein called eL43.

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

- Molecule 42 is a protein called L28.

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

- Molecule 43 is a protein called L12.

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

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

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

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

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

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

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

- Molecule 47 is a RNA chain called mRNA.

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

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

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

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

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

There are 7 discrepancies between the modelled and reference sequences:

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

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

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

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

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

- Molecule 52 is a protein called RPSA.

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

- Molecule 53 is a protein called S3A.

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

- Molecule 54 is a protein called eS1.

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

- Molecule 55 is a protein called S3.

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

- Molecule 56 is a protein called S4.

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

There are 4 discrepancies between the modelled and reference sequences:

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

- Molecule 57 is a protein called S5.

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

- Molecule 58 is a protein called eS6.

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

- Molecule 59 is a protein called eS7.

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

- Molecule 60 is a protein called S8.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 61 is a protein called S9.

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

- Molecule 62 is a protein called S10.

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

- Molecule 63 is a protein called S11.

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

- Molecule 64 is a protein called S12.

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

- Molecule 65 is a protein called uS15.

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

- Molecule 66 is a protein called S14.

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

- Molecule 67 is a protein called S15.

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

- Molecule 68 is a protein called uS9.

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

- Molecule 69 is a protein called eS17.

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

- Molecule 70 is a protein called S18.

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

- Molecule 71 is a protein called S19.

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

- Molecule 72 is a protein called uS10.

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

- Molecule 73 is a protein called S21.

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

There are 7 discrepancies between the modelled and reference sequences:

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

- Molecule 74 is a protein called S15A.

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

- Molecule 75 is a protein called S23.

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

- Molecule 76 is a protein called S24.

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

- Molecule 77 is a protein called eS25.

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

- Molecule 78 is a protein called S26.

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

There are 3 discrepancies between the modelled and reference sequences:

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

- Molecule 79 is a protein called S27.

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

- Molecule 80 is a protein called S28.

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

- Molecule 81 is a protein called uS14.

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

- Molecule 82 is a protein called S30.

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

- Molecule 83 is a protein called S27A.

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

- Molecule 84 is a protein called RACK1.

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

- Molecule 85 is a protein called peptide.

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

- Molecule 86 is a protein called RPLP0.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 87 is a protein called RPLP peptide.

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

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

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

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

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

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

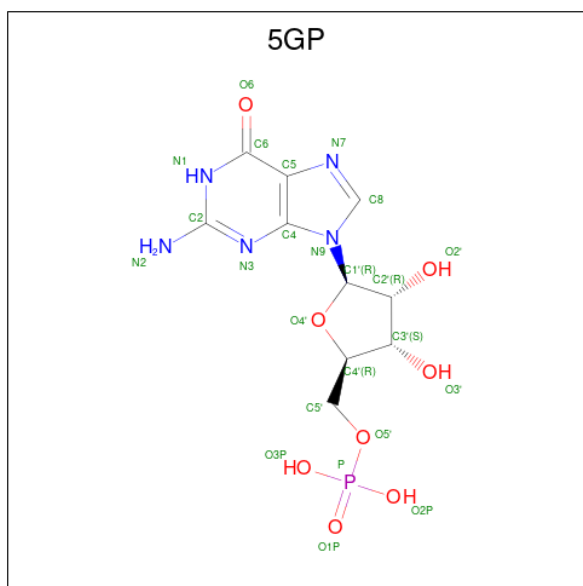
Mol	Chain	Residues	Atoms		AltConf
90	FA	1	Total	Zn	0
			1	1	
90	IA	1	Total	Zn	0
			1	1	

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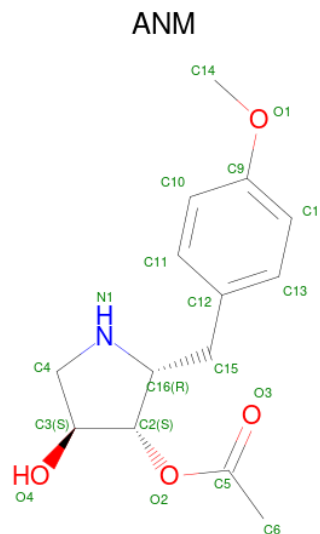
Mol	Chain	Residues	Atoms		AltConf
90	LA	1	Total	Zn	0
			1	1	
90	NA	1	Total	Zn	0
			1	1	
90	OA	1	Total	Zn	0
			1	1	
90	AC	1	Total	Zn	0
			1	1	
90	DC	1	Total	Zn	0
			1	1	
90	FC	1	Total	Zn	0
			1	1	

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



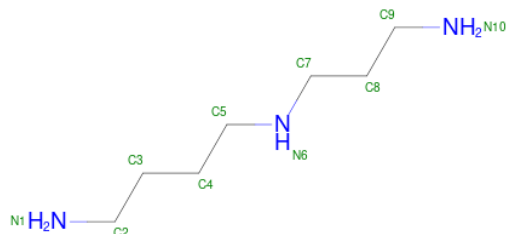
Mol	Chain	Residues	Atoms					AltConf
91	UA	1	Total	C	N	O	P	0
			24	10	5	8	1	

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



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

- Molecule 93 is SPERMIDINE (CCD ID: SPD) (formula: $\text{C}_7\text{H}_{19}\text{N}_3$).



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

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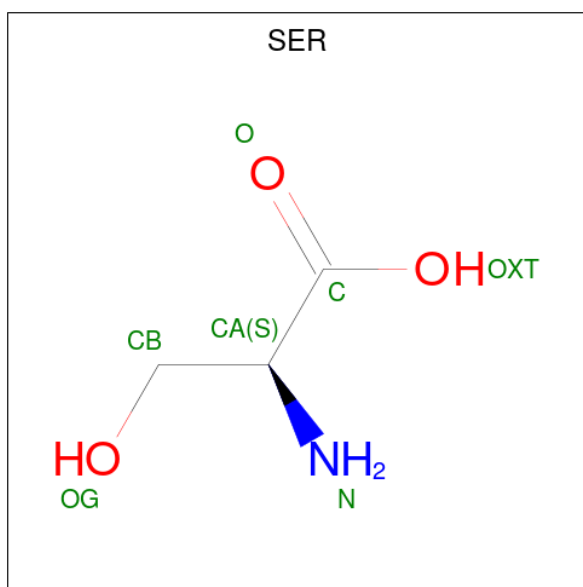
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Mol	Chain	Residues	Atoms			AltConf
93	ZA	1	Total	C	N	0
			10	7	3	

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

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

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




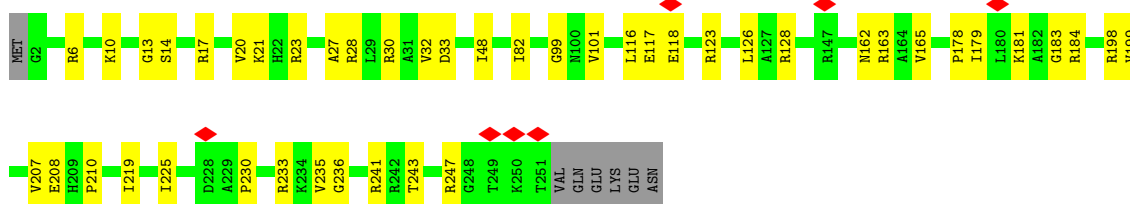
Mol	Chain	Residues	Atoms				AltConf
95	HC	1	Total	C	N	O	0
			6	3	1	2	

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.

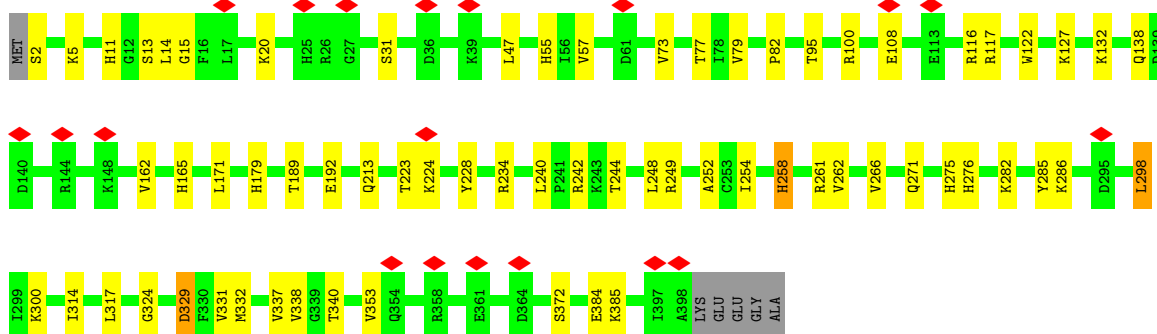
• Molecule 1: uL2

Chain A: 




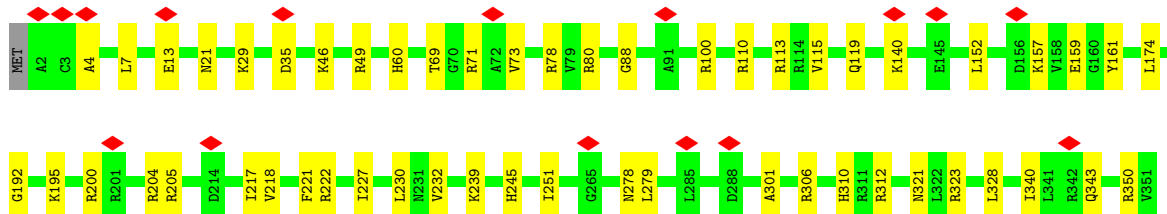
• Molecule 2: uL3

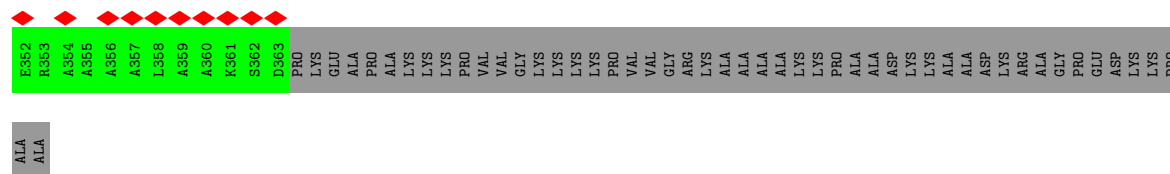
Chain B: 



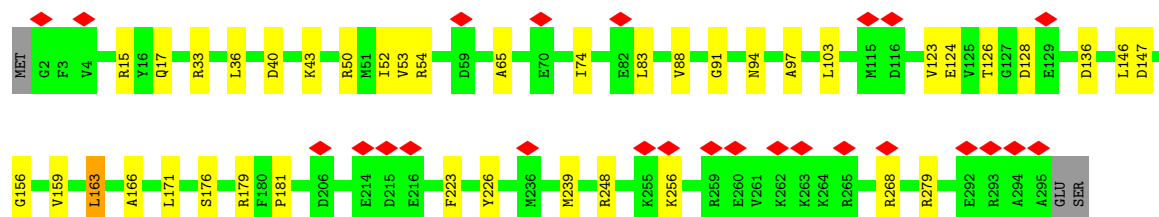
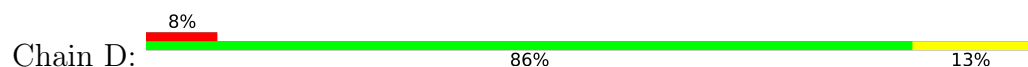
• Molecule 3: uL4

Chain C: 

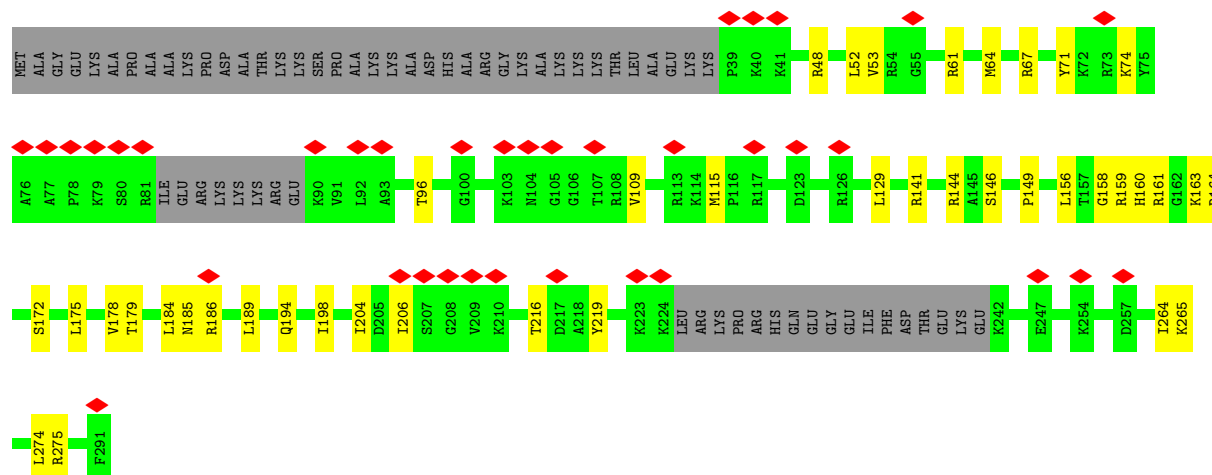




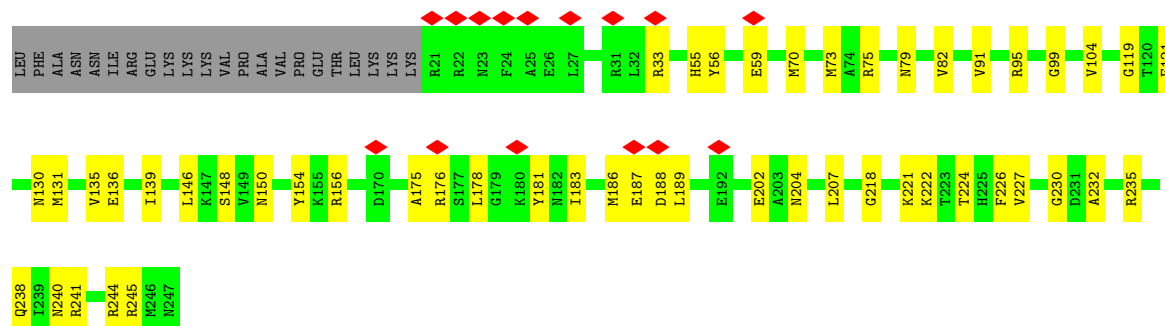
• Molecule 4: uL18



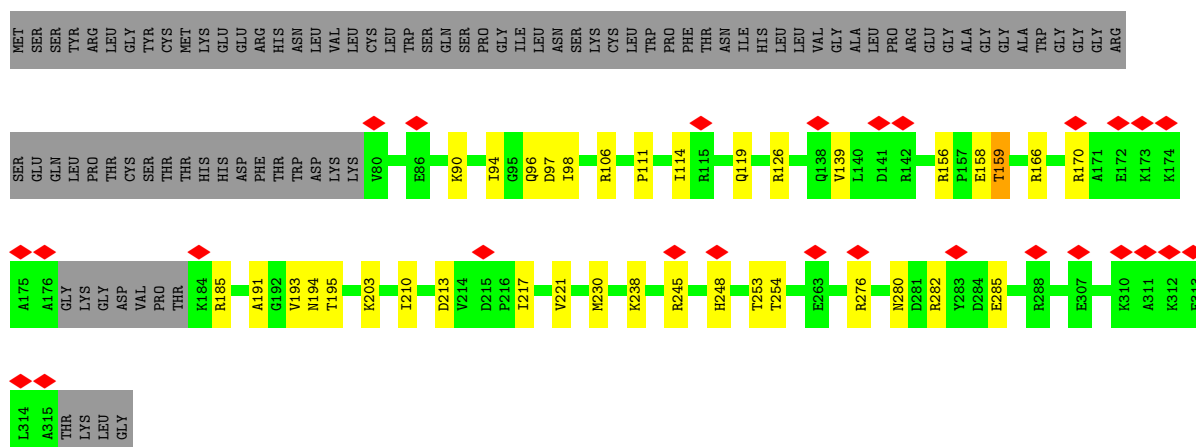
• Molecule 5: L6



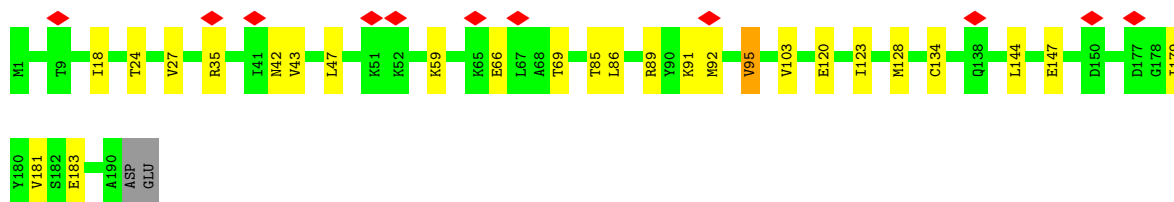
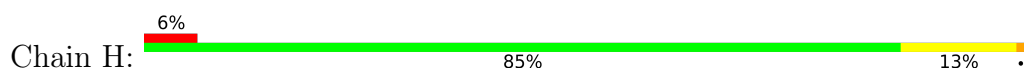
• Molecule 6: uL30



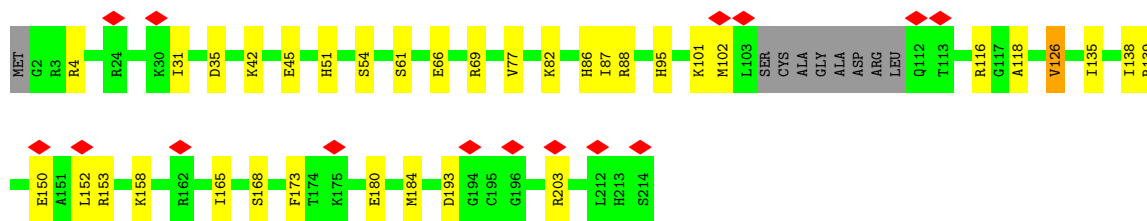
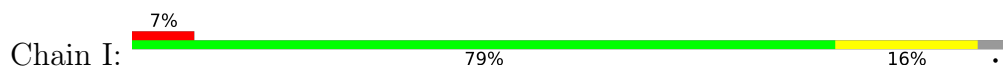
• Molecule 7: L7A



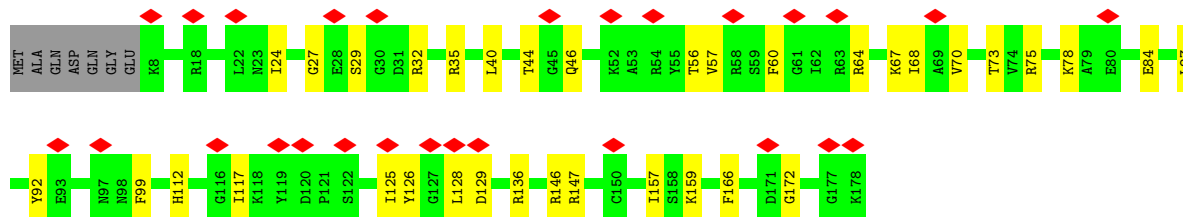
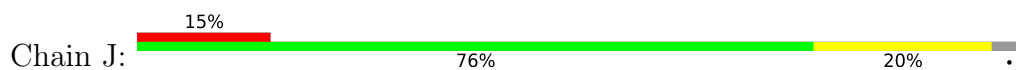
• Molecule 8: L9



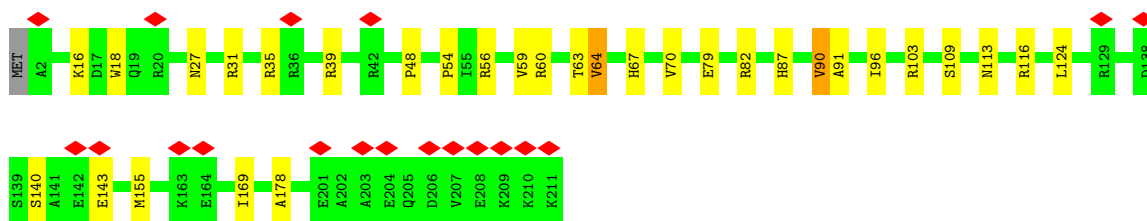
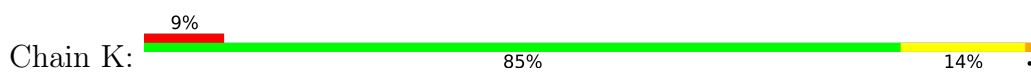
• Molecule 9: L10



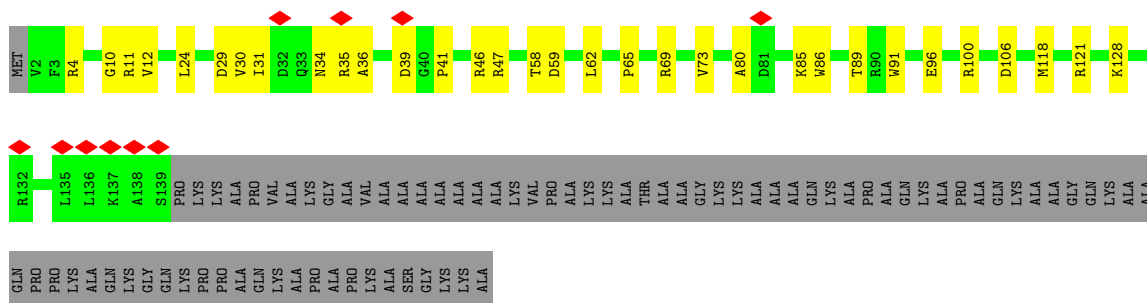
• Molecule 10: uL5



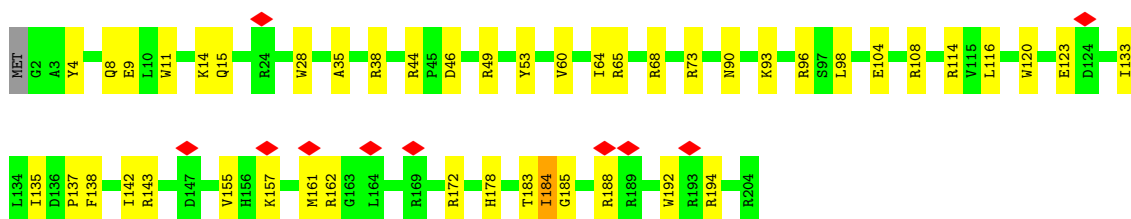
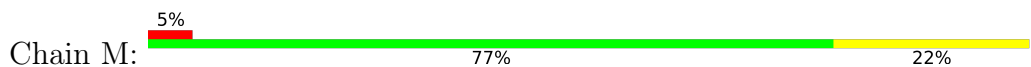
• Molecule 11: eL13



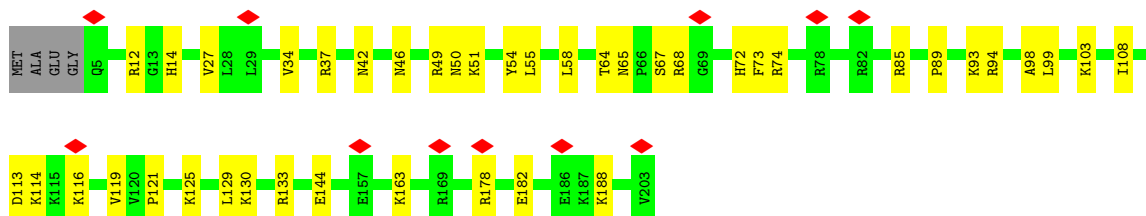
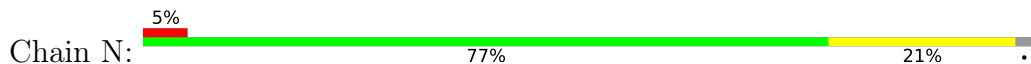
• Molecule 12: eL14



• Molecule 13: eL15

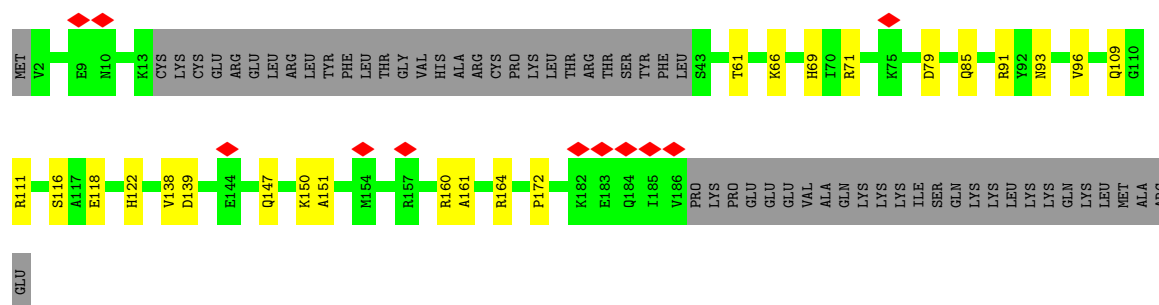


• Molecule 14: uL13

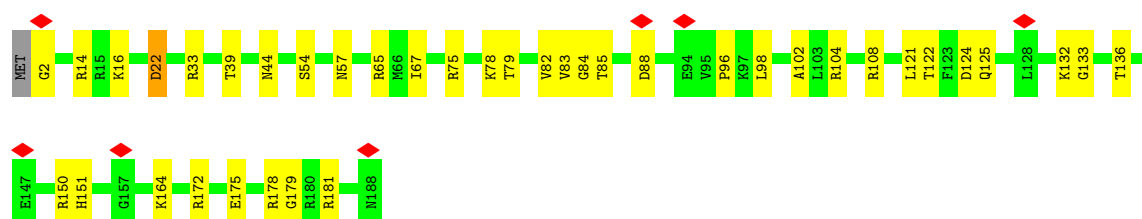
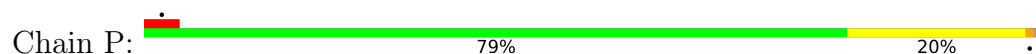


• Molecule 15: uL22

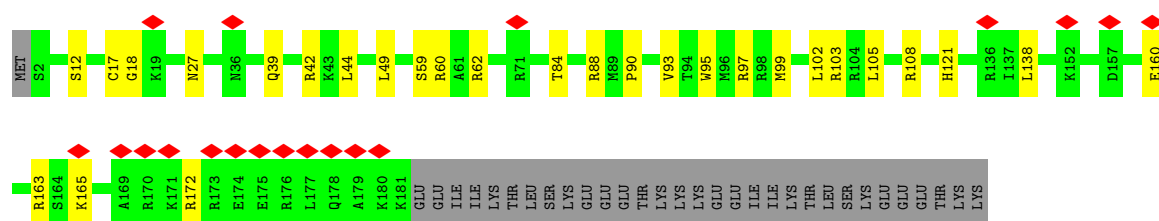




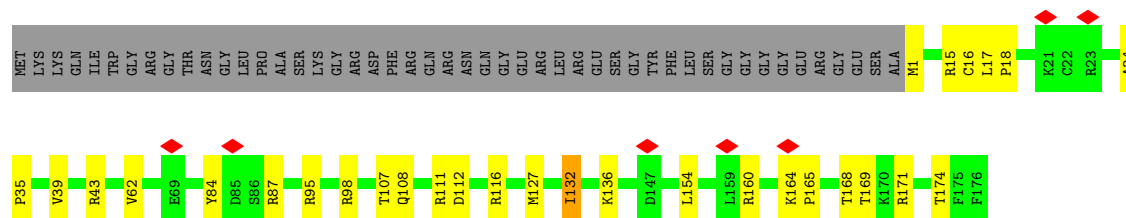
• Molecule 16: eL18



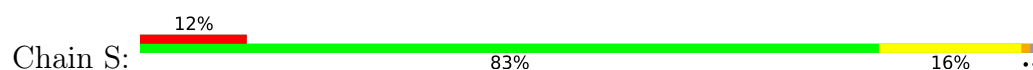
• Molecule 17: eL19



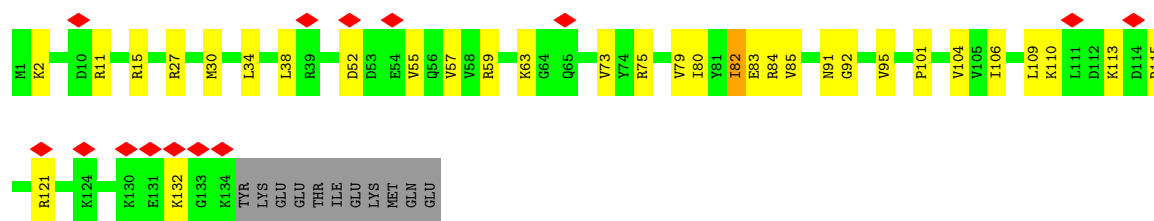
• Molecule 18: eL20



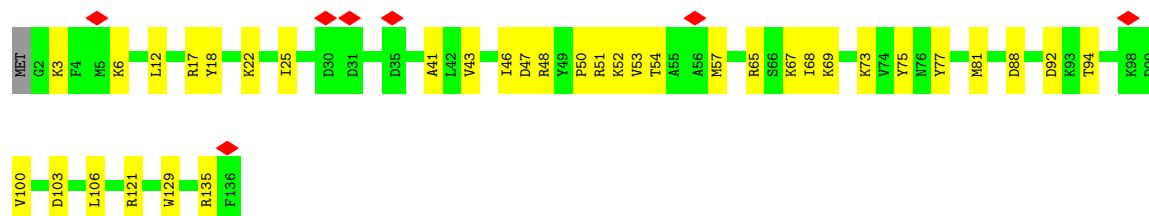
• Molecule 19: eL21



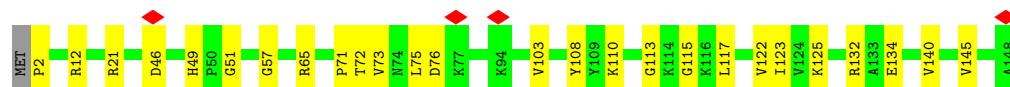
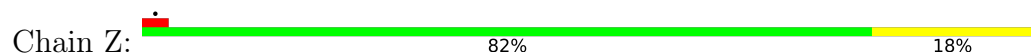




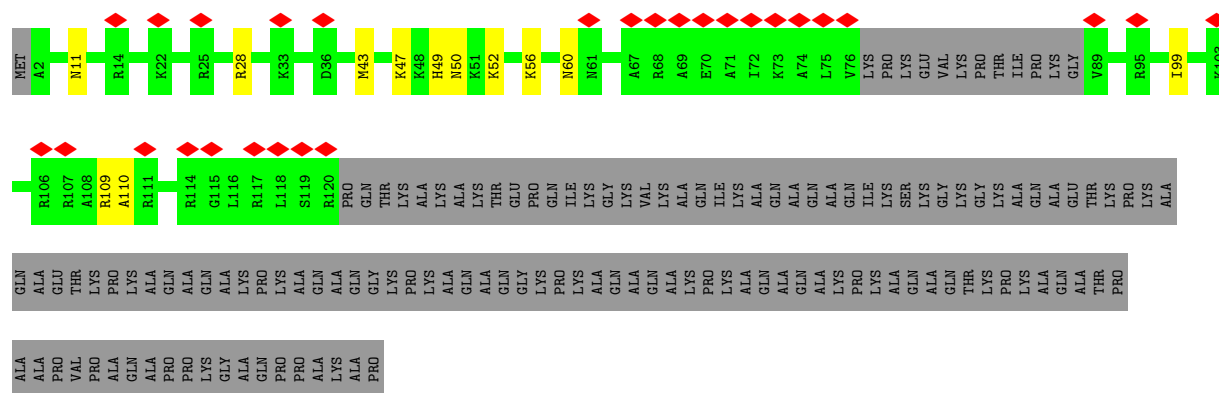
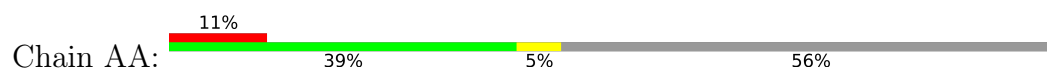
• Molecule 25: L27



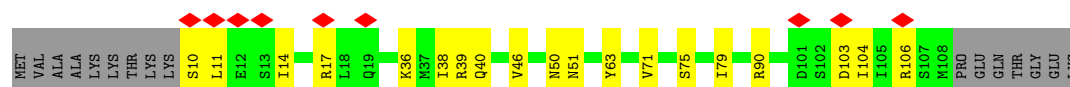
• Molecule 26: uL15



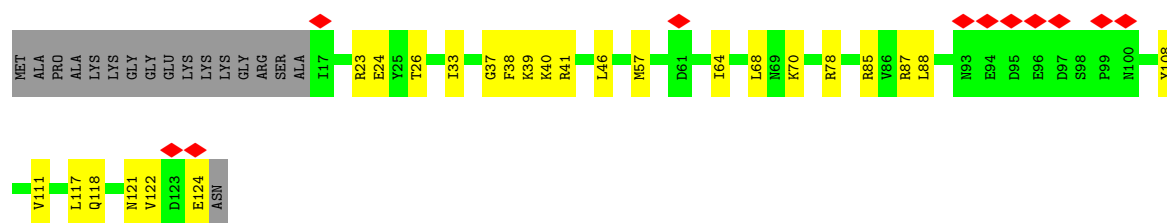
• Molecule 27: L29



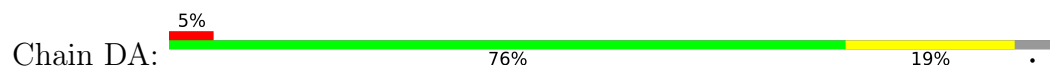
• Molecule 28: eL30



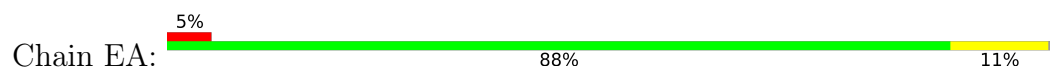
• Molecule 29: L31



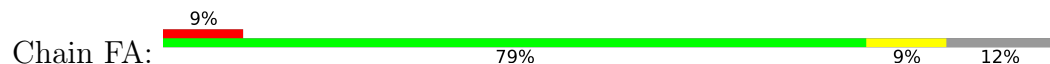
- Molecule 30: L32



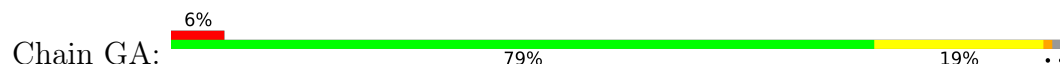
- Molecule 31: eL33



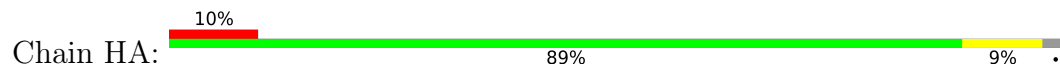
- Molecule 32: L34



- Molecule 33: L35



- Molecule 34: L36

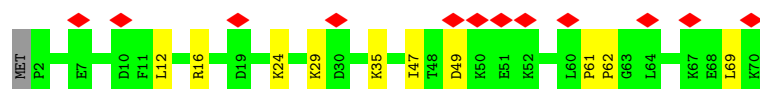
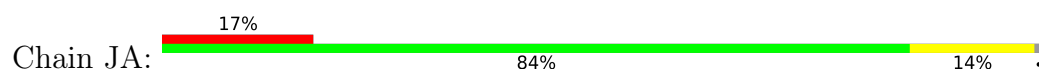


- Molecule 35: L37

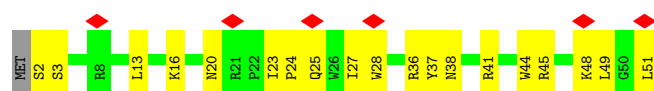




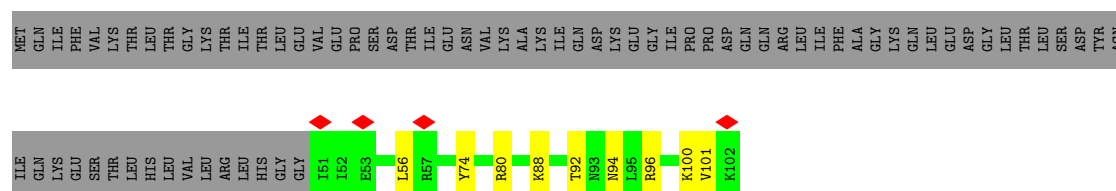
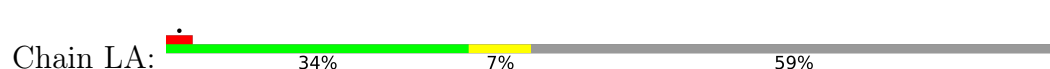
- Molecule 36: eL38



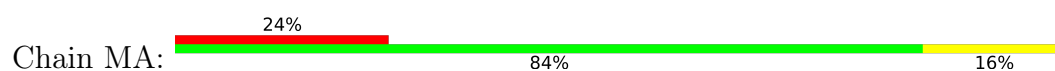
- Molecule 37: eL39



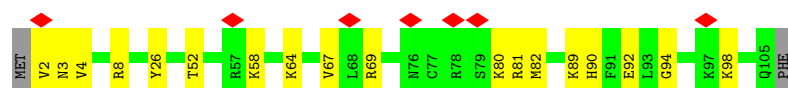
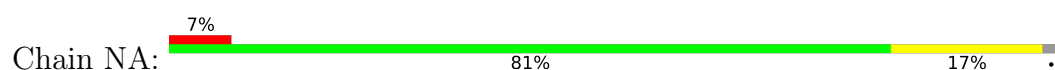
- Molecule 38: eL40



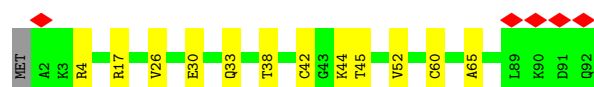
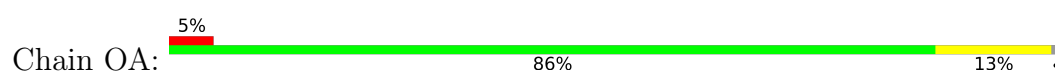
- Molecule 39: eL41



- Molecule 40: eL42

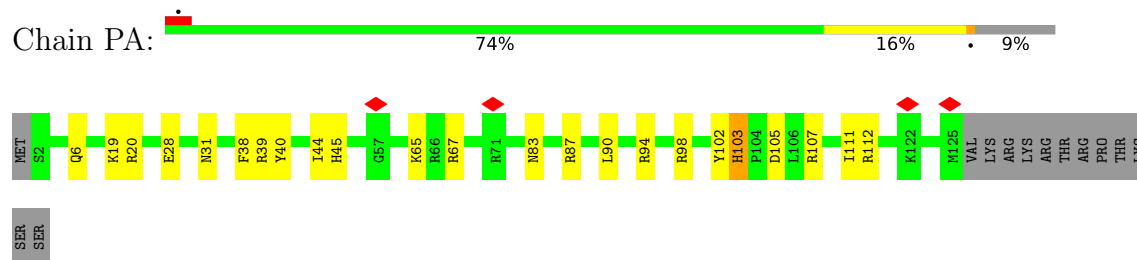


- Molecule 41: eL43



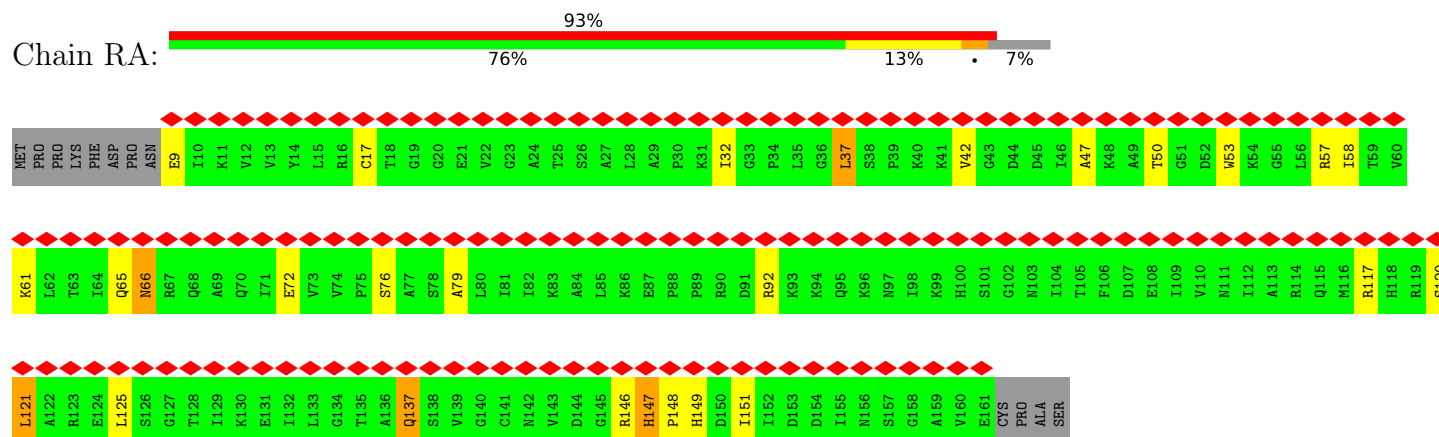
- Molecule 42: L28

Chain PA:



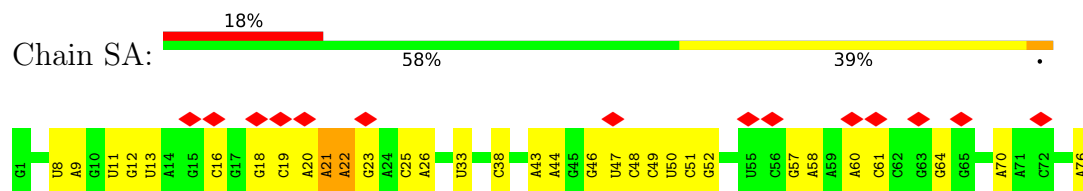
- Molecule 43: L12

Chain RA:



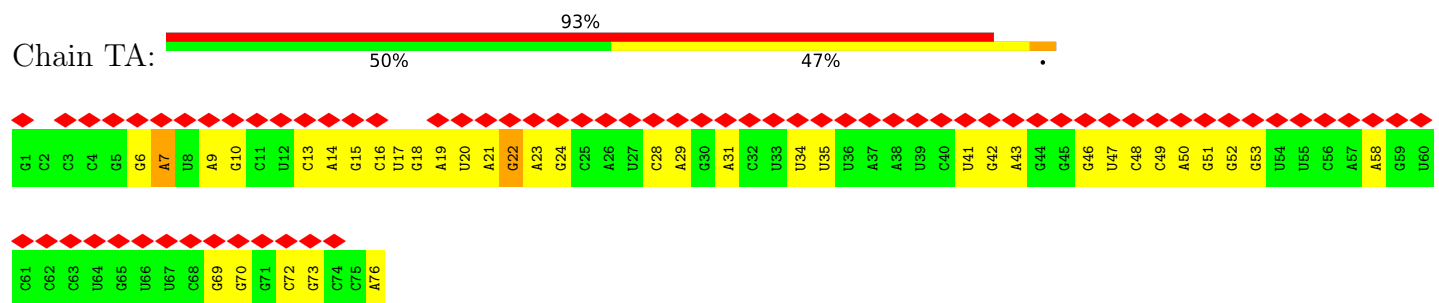
- Molecule 44: P-site tRNA

Chain SA:



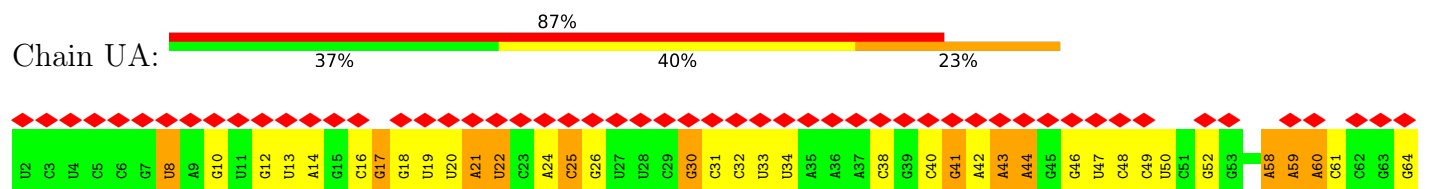
- Molecule 45: E-site tRNA

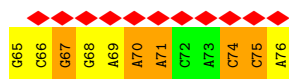
Chain TA:



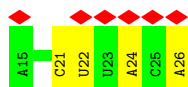
- Molecule 46: A-site tRNA

Chain UA:

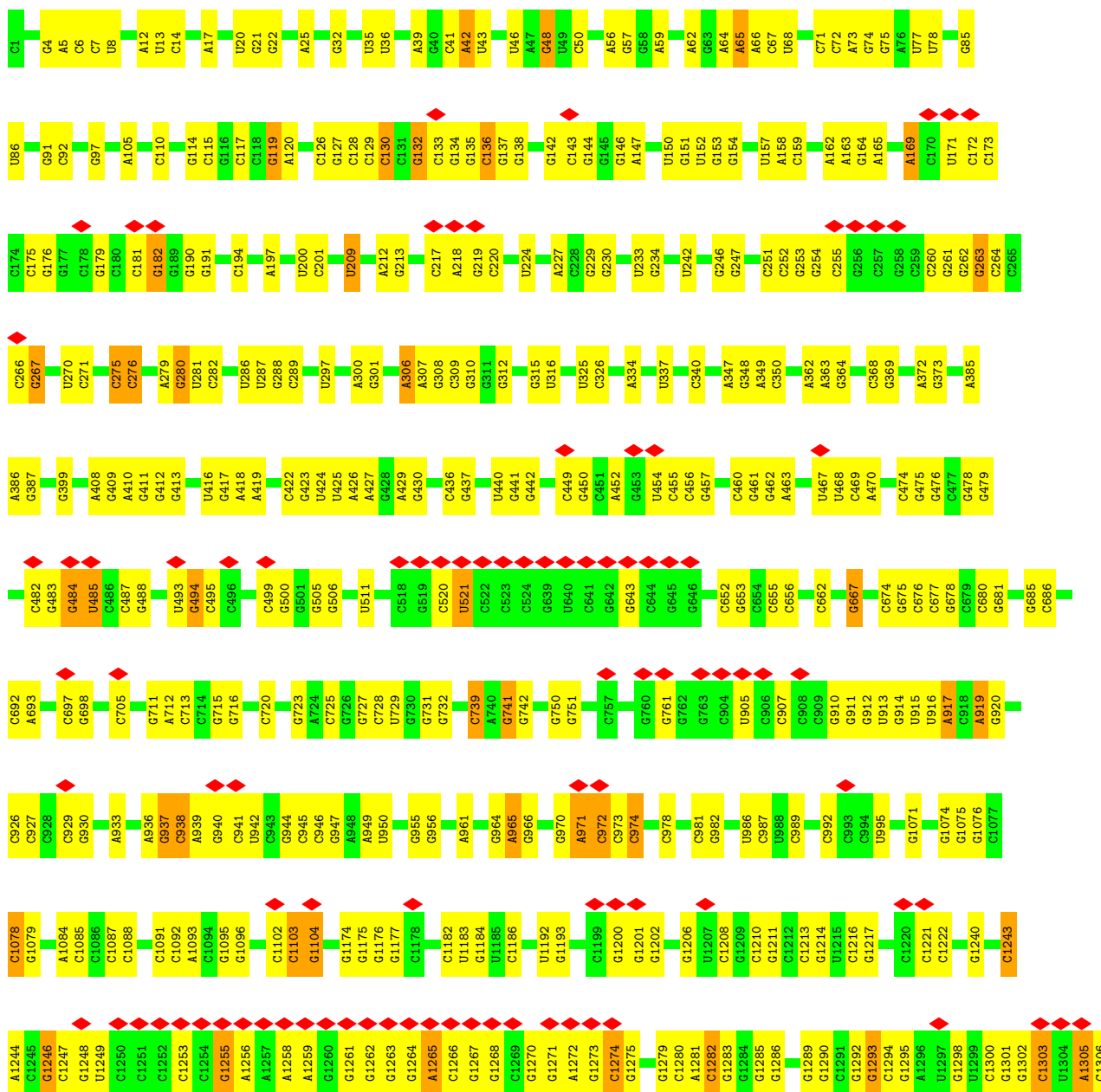




• Molecule 47: mRNA

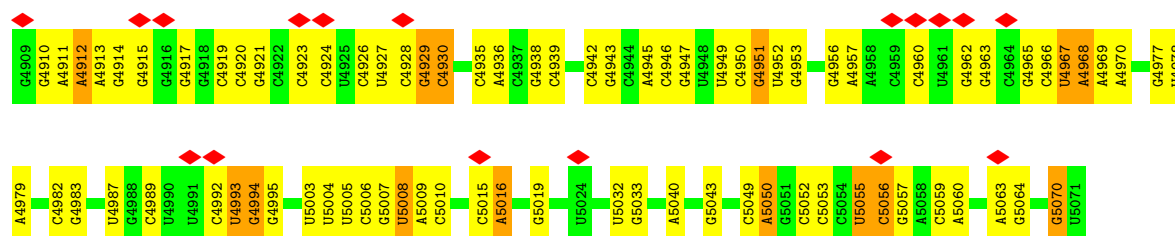


• Molecule 48: 28S rRNA



G2561	G2562	G2563	G2564	G2565	G2566	A2567	G2568	A2575	G2576	G2577	G2578	G2581	A2584	G2585	G2588	A2589	G2590	C2591	G2592	A2515	G2516	G2517	G2518	A2519	G2520	G2521	G2522	G2523	G2524	G2525	G2526	G2527	G2528	A2531	G2532	G2535	A2539	G2540	G2541	G2542	G2543	G2544	A2545	G2546	G2547	G2548	G2549	A2555	G2556	G2557	G2558	G2559	G2560																																																																																																																																																																																																																																																																																																																																																																																																															
U2486	U2487	G2488	G2489	G2490	G2491	U2492	G2493	G2494	G2495	U2496	U2497	G2498	G2499	G2500	G2505	G2506	G2507	G2508	A2509	G2510	G2511	G2512	G2513	G2514	G2515	G2516	G2517	G2518	G2519	G2520	G2521	G2522	G2523	G2524	G2525	G2526	G2527	G2528	G2529	G2530	G2531	G2532	G2533	G2534	G2535	G2536	G2537	G2538	G2539	G2540	G2541	G2542	G2543	G2544	G2545	G2546	G2547	G2548	G2549	G2550	G2551	G2552	G2553	G2554	G2555	G2556	G2557	G2558	G2559	G2560																																																																																																																																																																																																																																																																																																																																																																																														
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G1897	A1898	A1899	C1900	U1908	A1909	G1912	C1916	G1917	G1918	A1919	U1920	G1921	C1922	C1923	G1924	A1925	U1926	U1929	C1930	A1931	U1932	C1933	A1934	G1935	A1936	C1939	C1940	A1941	G1942	A1943	A1944	A1945	G1950	U1951	U1952	G1953	A1960	U1961	A1962	G1963	A1964	C1966	A1969	G1970	G1971	A1972	U1973	G1974	G1975	U1976	G1977	G1978	G1979	G1980	G1981	G1982	G1983	G1984	G1985	G1986	G1987	G1988	G1989	G1990	G1991	G1992	G1993	G1994	G1995	G1996	G1997	G1998	U1999	A2000	A2001	G2002	G2003	A2004	G2005	U2006	G2007	U2008	G2009	U2010	A2011	A2012	C2013	A2014	A2015	C2016	U2017	A2018	A2019	C2020	C2021	U2022	G2023	C2024	C2025	A2027	A2028	G2036	G2048	A2049	U2050	G2054	G2055	G2056	G2057	G2058	G2059	G2060	G2061	G2062	G2063	G2064	G2065	G2066	G2067	G2068	G2069	G2070	G2071	G2072	G2073	G2074	G2075	G2076	G2077	G2078	G2081	U2082	C2083	G2084	C2085	U2086	U2087	G2088	G2089	G2090	G2091	G2092	G2093	G2094	G2095	G2096	A2097	G2098	A2099	G2100	G2101	G2102	A2103	G2104	A2105	A2106	A2107	G2108	A2109	U2113	G2114	G2115	A2116	G2117	C2260	G2261	C2262	G2263	G2264	A2265	G2266	G2267	C2268	U2269	A2270	G2277	G2285	G2286	G2287	G2288	G2289	G2290	G2291	G2292	G2293	G2294	G2295	G2296	G2297	G2298	G2299	G2300	G2301	G2302	G2303	G2304	G2305	G2306	G2307	G2308	G2309	G2310	G2311	G2312	G2313	G2314	G2315	G2316	G2317	G2318	G2319	G2320	G2321	G2322	G2323	G2324	G2325	G2326	G2327	G2328	G2329	G2330	G2331	G2332	G2333	G2334	G2335	G2336	G2337	G2338	G2339	G2340	G2341	G2342	G2343	G2344	G2345	G2346	G2347	G2348	G2349	G2350	G2351	G2352	G2353	G2354	G2355	G2356	G2357	G2358	G2359	G2360	G2361	G2362	G2363	G2364	G2365	G2366	G2367	G2368	G2369	G2370	G2371	G2372	G2373	G2374	G2375	G2376	G2377	G2378	G2379	G2380	G2381	G2382	G2383	G2384	G2385	G2386	G2387	G2388	G2389	G2390	G2391	G2392	G2393	G2394	G2395	G2396	G2397	G2398	G2399	G2400	G2401	G2402	G2403	G2404	G2405	G2406	G2407	G2408	G2409	G2410	G2411	G2412	G2413	G2414	G2415	G2416	G2417	G2418	G2419	G2420	G2421	G2422	G2423	G2424	G2425	G2426	G2427	G2428	G2429	G2430	G2431	G2432	G2433	G2434	G2435	G2436	G2437	G2438	G2439	G2440	G2441	G2442	G2443	G2444	G2445	G2446	G2447	G2448	G2449	G2450	G2451	G2452	G2453	G2454	G2455	G2456	G2457	G2458	G2459	G2460	G2461	G2462	G2463	G2464	G2465	G2466	G2467	G2468	G2469	G2470	G2471	G2472	G2473	G2474	G2475	G2476	G2477	G2478	G2479	G2480	G2481	G2482	G2483	G2484	G2485	G2486	G2487	G2488	G2489	G2490	G2491	G2492	G2493	G2494	G2495	G2496	G2497	G2498	G2499	G2500	G2501	G2502	G2503	G2504	G2505	G2506	G2507	G2508	G2509	G2510	G2511	G2512	G2513	G2514	G2515	G2516	G2517	G2518	G2519	G2520	G2521	G2522	G2523	G2524	G2525	G2526	G2527	G2528	G2529	G2530	G2531	G2532	G2533	G2534	G2535	G2536	G2537	G2538	G2539	G2540	G2541	G2542	G2543	G2544	G2545	G2546	G2547	G2548	G2549	G2550	G2551	G2552	G2553	G2554	G2555	G2556	G2557	G2558	G2559	G2560
C1809	G1812	G1813	C1814	G1817	G1818	G1819	G1820	G1821	U1822	G1823	U1824	G1825	G1826	A1827	C1830	U1836	G1837	G1838	A1839	G1844	G1848	C1849	A1852	G1853	G1857	G1866	G1867	U1868	G1871	C1872	A1873	G1874	U1878	G1879	G1880	C1881	G1882	C1883	U1884	G1885	G1886	G1887	A1890	A1893	A1804	G1805	A1806	A1807	G1808	G1809	G1810	G1811	G1812	G1813	G1814	G1815	G1816	G1817	G1818	G1819	G1820	G1821	G1822	G1823	G1824	G1825	G1826	G1827	G1828	G1829	G1830	G1831	G1832	G1833	G1834	G1835	G1836	G1837	G1838	G1839	G1840	G1841	G1842	G1843	G1844	G1845	G1846	G1847	G1848	G1849	G1850	G1851	G1852	G1853	G1854	G1855	G1856	G1857	G1858	G1859	G1860	G1861	G1862	G1863	G1864	G1865	G1866	G1867	G1868	G1869	G1870	G1871	G1872	G1873	G1874	G1875	G1876	G1877	G1878	G1879	G1880	G1881	G1882	G1883	G1884	G1885	G1886	G1887	G1888	G1889	G1890	G1891	G1892	G1893	G1894	G1895	G1896	G1897	G1898	G1899	G1900	G1901	G1902	G1903	G1904	G1905	G1906	G1907	G1908	G1909	G1910	G1911	G1912	G1913	G1914	G1915	G1916	G1917	G1918	G1919	G1920	G1921	G1922	G1923	G1924	G1925	G1926	G1927	G1928	G1929	G1930	G1931	G1932	G1933	G1934	G1935	G1936	G1937	G1938	G1939	G1940	G1941	G1942	G1943	G1944	G1945	G1946	G1947	G1948	G1949	G1950	G1951	G1952	G1953	G1954	G1955	G1956	G1957	G1958	G1959	G1960	G1961	G1962	G1963	G1964	G1965	G1966	G1967	G1968	G1969	G1970	G1971	G1972	G1973	G1974	G1975	G1976	G1977	G1978	G1979	G1980	G1981	G1982	G1983	G1984	G1985	G1986	G1987	G1988	G1989	G1990	G1991	G1992	G1993	G1994	G1995	G1996	G1997	G1998	G1999	G2000	G2001	G2002	G2003	G2004	G2005	G2006	G2007	G2008	G2009	G2010	G2011	G2012	G2013	G2014	G2015	G2016	G2017	G2018	G2019	G2020	G2021	G2022	G2023	G2024	G2025	G2026	G2027	G2028	G2029	G2030	G2031	G2032	G2033	G2034	G2035	G2036	G2037	G2038	G2039	G2040	G2041	G2042	G2043	G2044	G2045	G2046	G2047	G2048	G2049	G2050	G2051	G2052	G2053	G2054	G2055	G2056	G2057	G2058	G2059	G2060	G2061	G2062	G2063	G2064	G2065	G2066	G2067	G2068	G2069	G2070	G2071	G2072	G2073	G2074	G2075	G2076	G2077	G2078	G2079	G2080	G2081	G2082	G2083	G2084	G2085	G2086	G2087	G2088	G2089	G2090	G2091	G2092	G2093	G2094	G2095	G2096	G2097	G2098	G2099	G2100	G2101	G2102	G2103	G2104	G2105	G2106	G2107	G2108	G2109	G2110	G2111	G2112	G2113	G2114	G2115	G2116	G2117	G2118	G2119	G2120	G2121	G2122	G2123	G2124	G2125	G2126	G2127	G2128	G2129	G2130	G2131	G2132	G2133	G2134	G2135	G2136	G2137	G2138	G2139	G2140	G2141	G2142	G2143	G2144	G2145	G2146	G2147	G2148	G2149	G2150	G2151	G2152	G2153	G2154	G2155	G2156	G2157	G2158	G2159	G2160	G2161	G2162	G2163	G2164	G2165	G2166	G2167	G2168	G2169	G2170	G2171	G2172	G2173	G2174	G2175	G2176	G2177	G2178	G2179	G2180	G2181	G																													





• Molecule 49: 5S rRNA

Chain XA: 71% 23% 5%



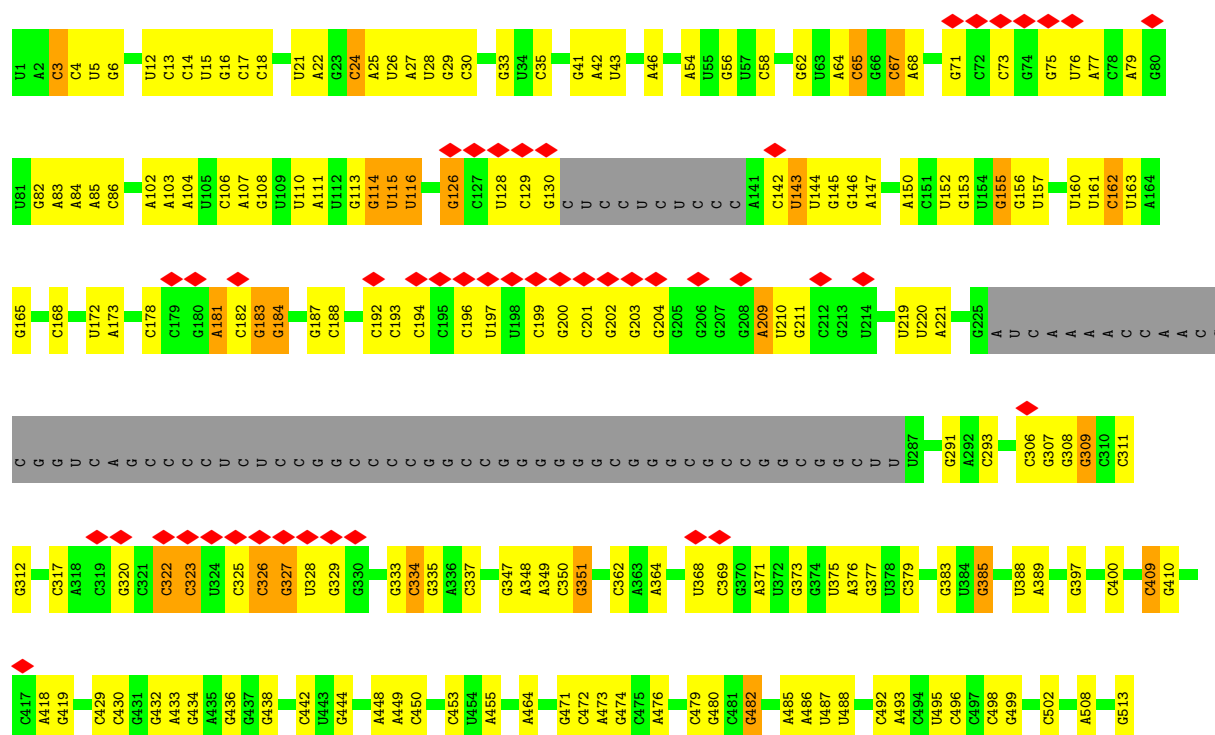
• Molecule 50: 5.8S rRNA

Chain YA: 10% 55% 38% 6%

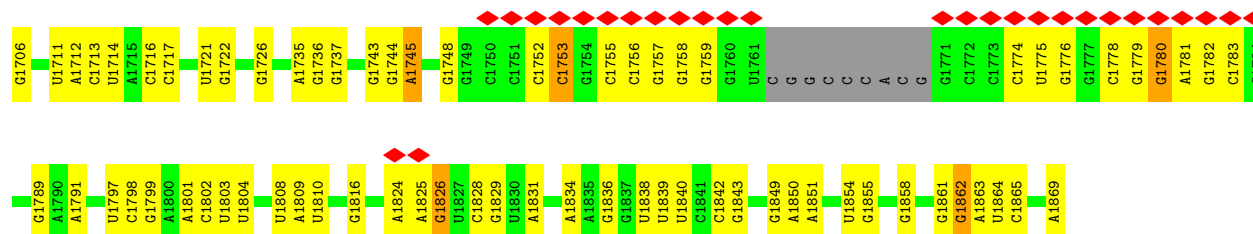


• Molecule 51: 18S rRNA

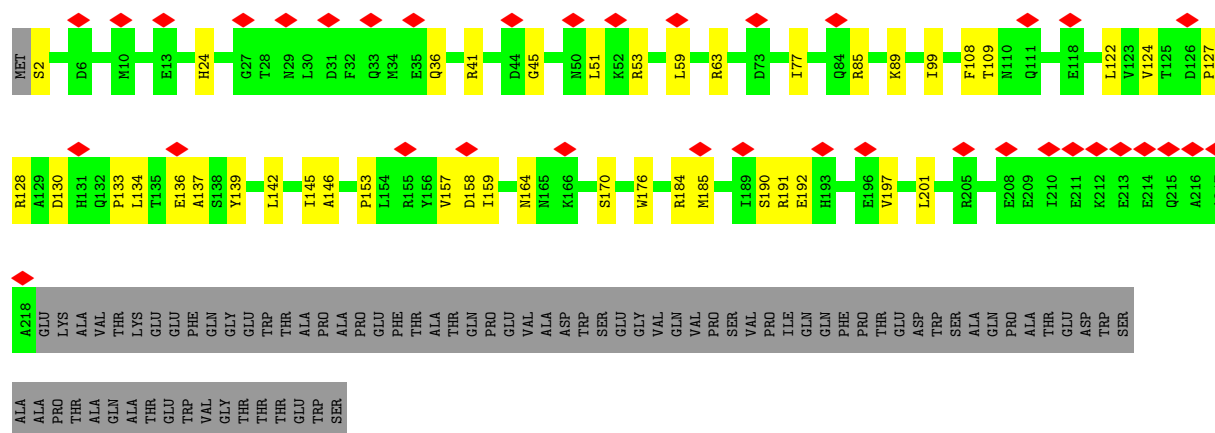
Chain ZA: 10% 51% 36% 6% 8%



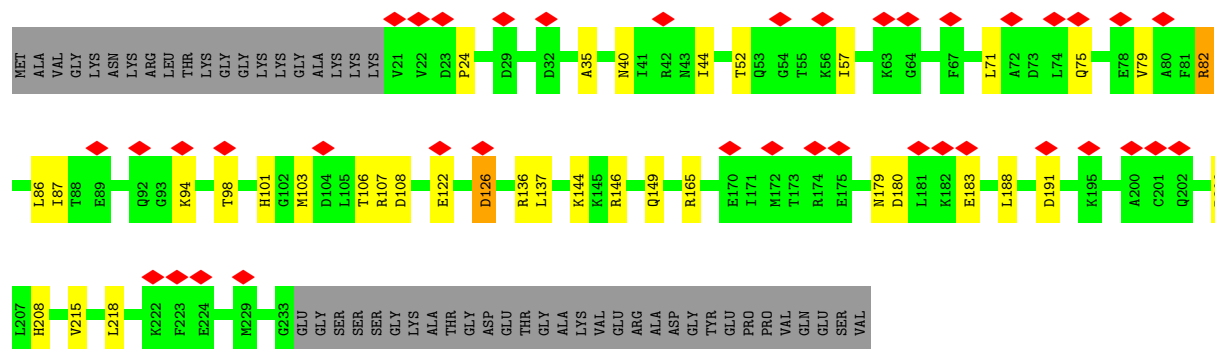




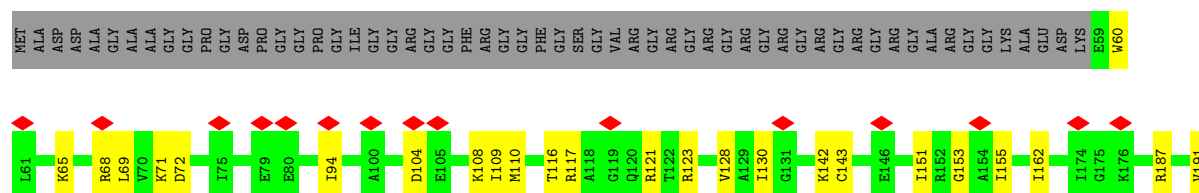
• Molecule 52: RPSA

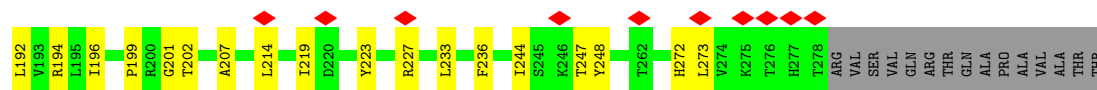


• Molecule 53: S3A

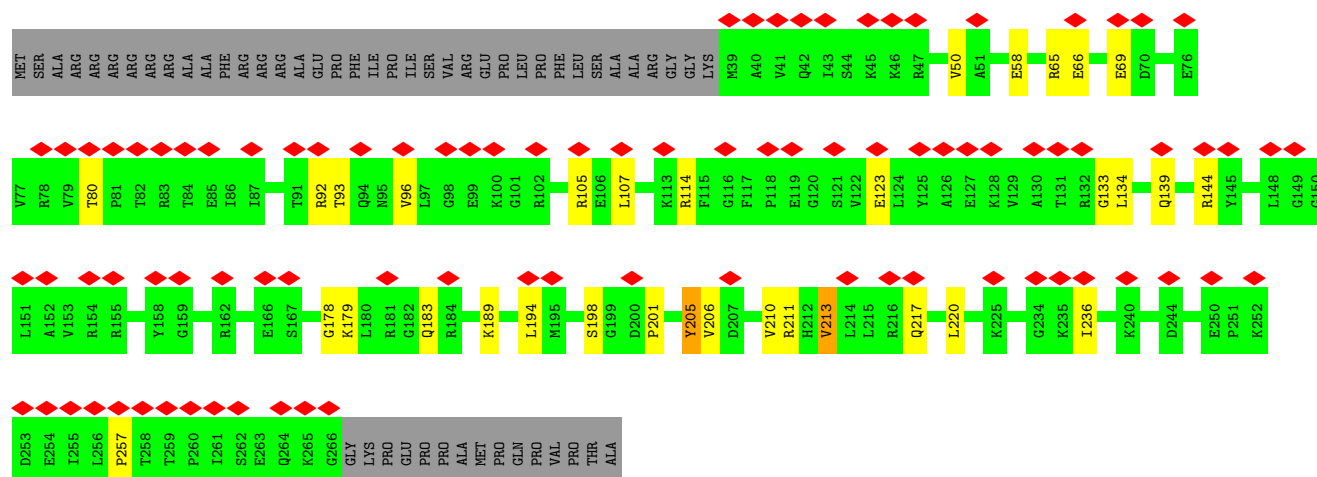


• Molecule 54: eS1

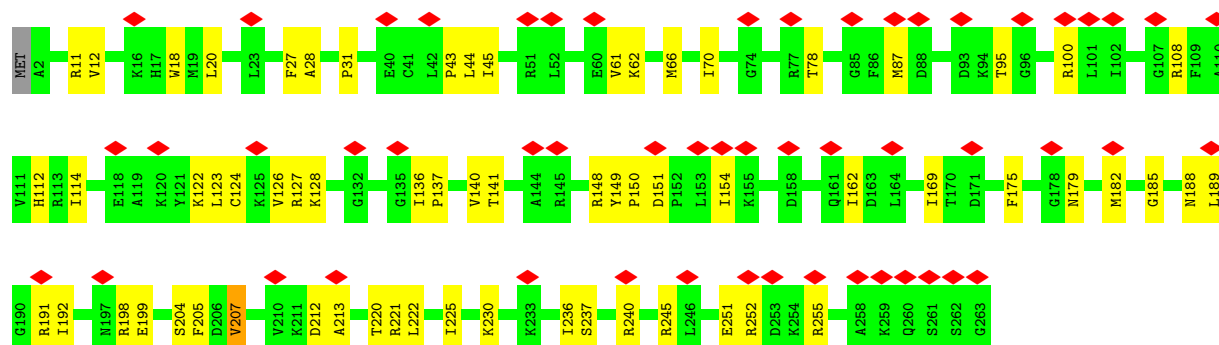
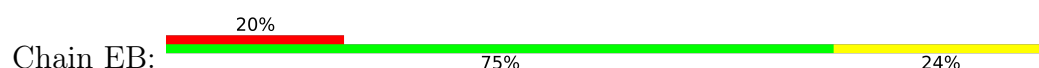




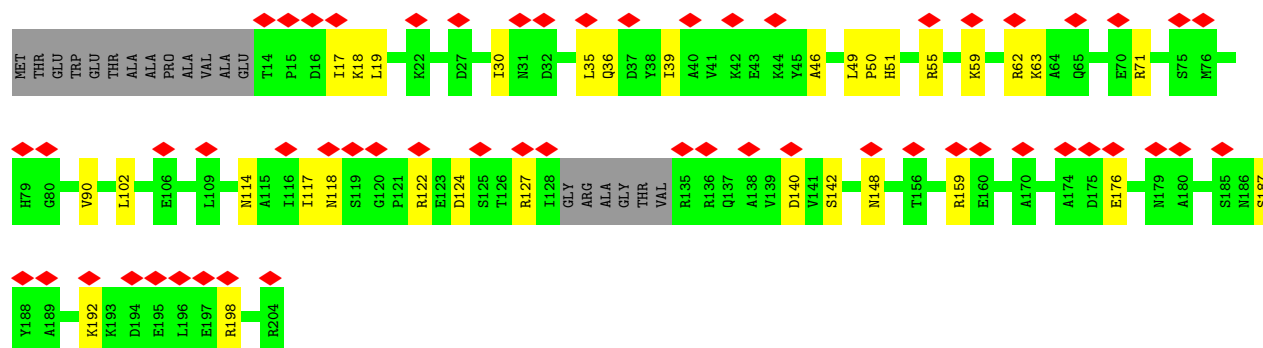
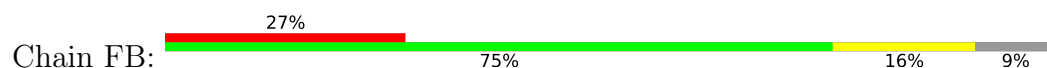
• Molecule 55: S3



• Molecule 56: S4



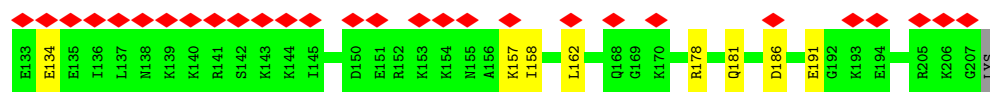
• Molecule 57: S5



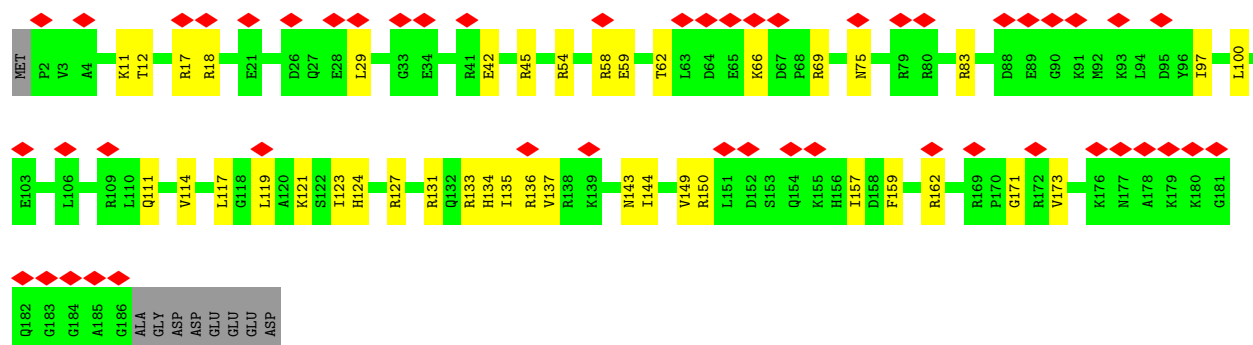
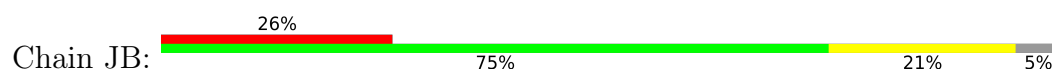
Chain GB:

- Molecule 59: eS7

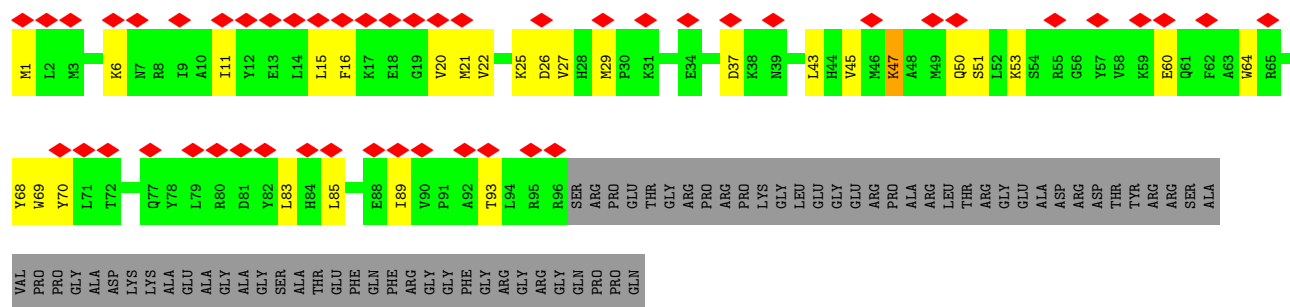
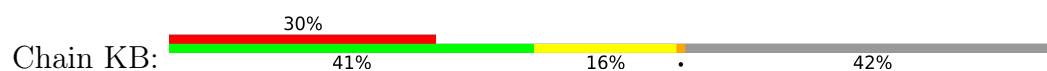
- Molecule 60: S8



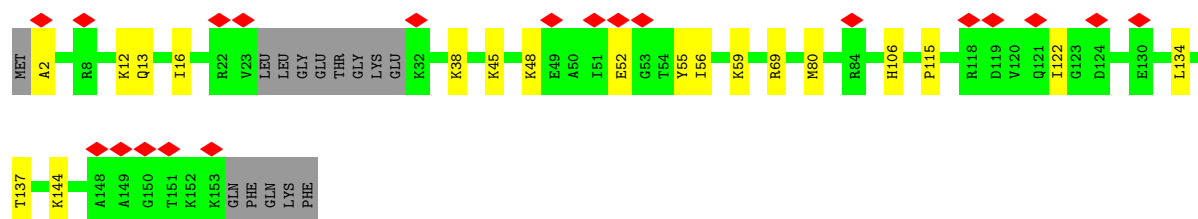
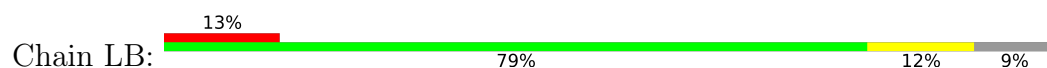
• Molecule 61: S9



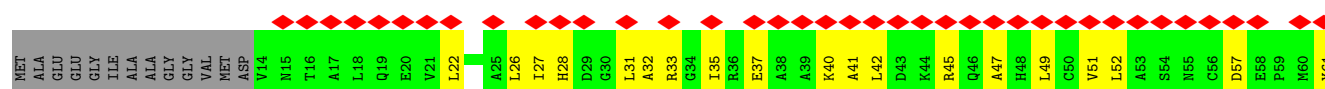
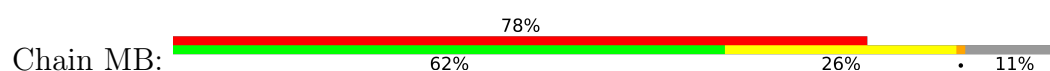
• Molecule 62: S10

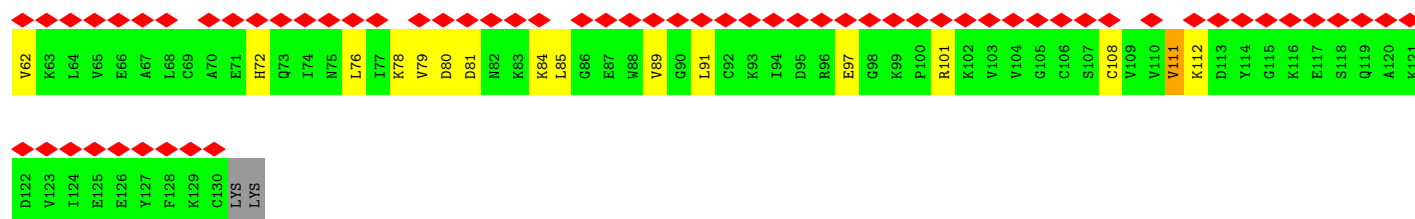


• Molecule 63: S11

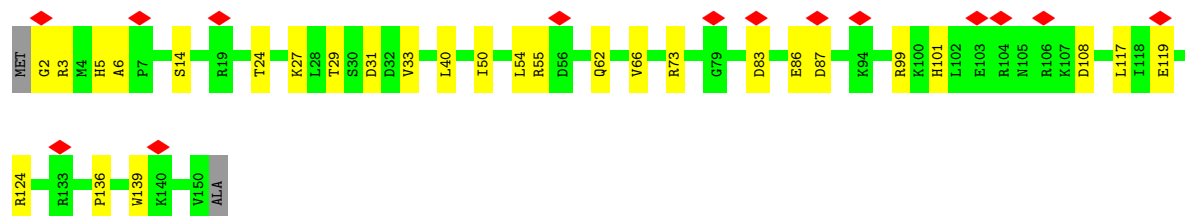
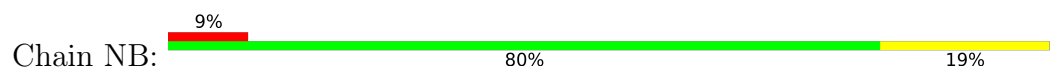


• Molecule 64: S12

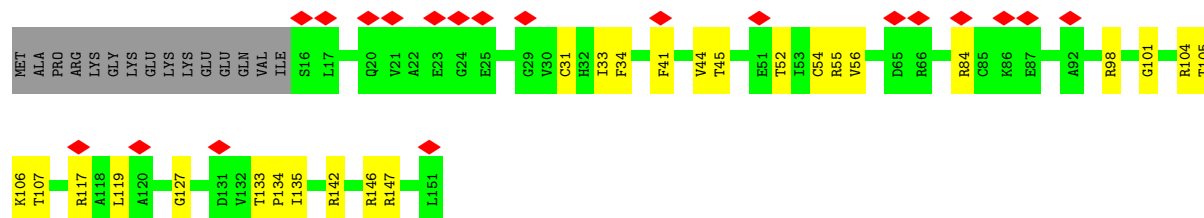
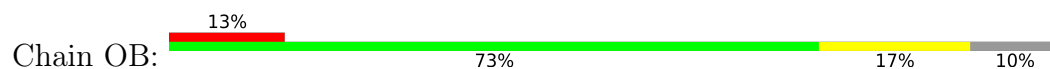




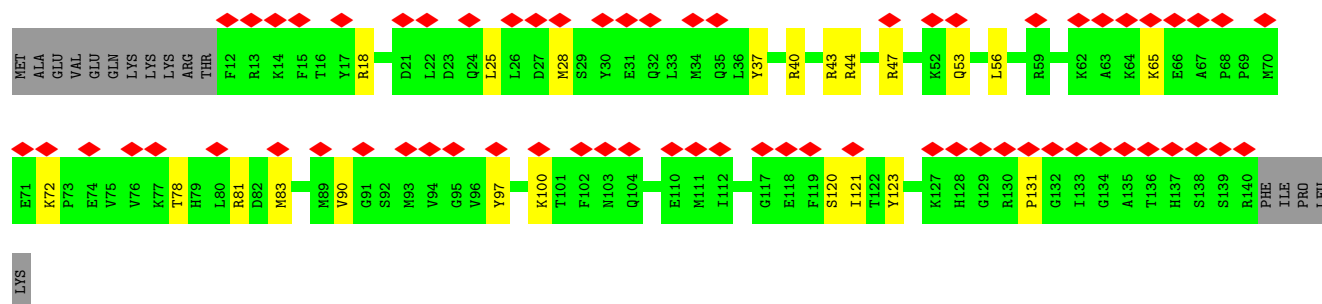
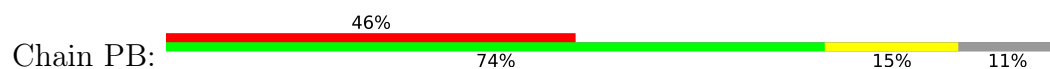
• Molecule 65: uS15



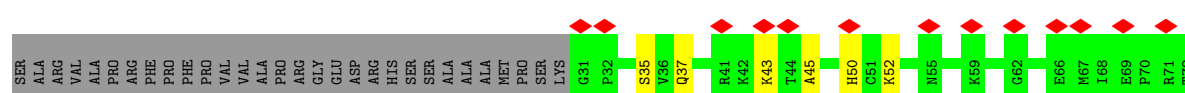
• Molecule 66: S14

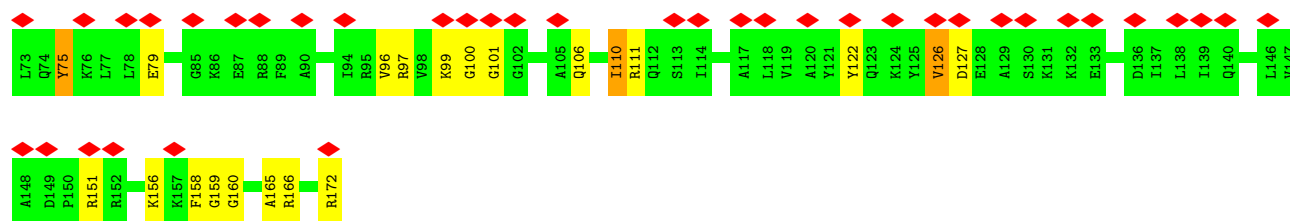


• Molecule 67: S15

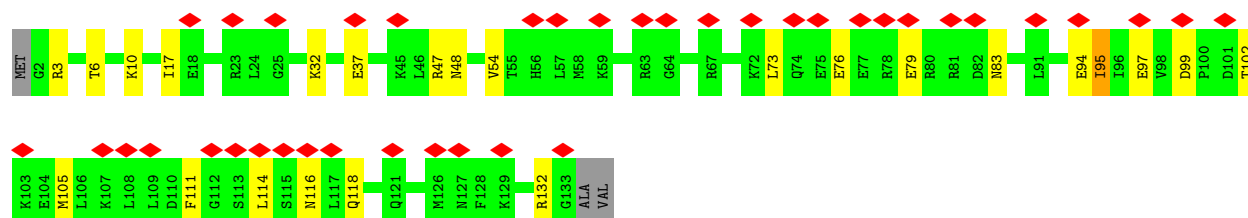
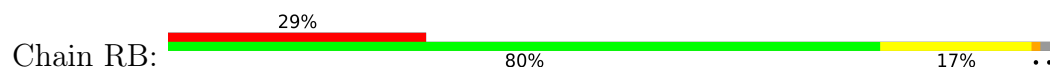


• Molecule 68: uS9

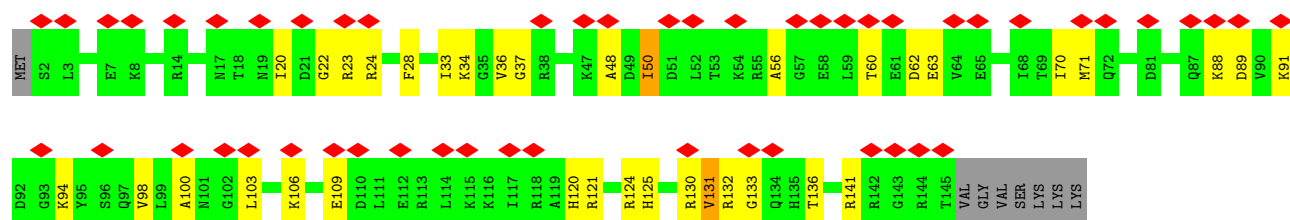
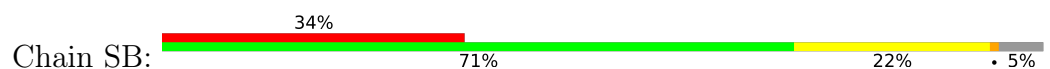




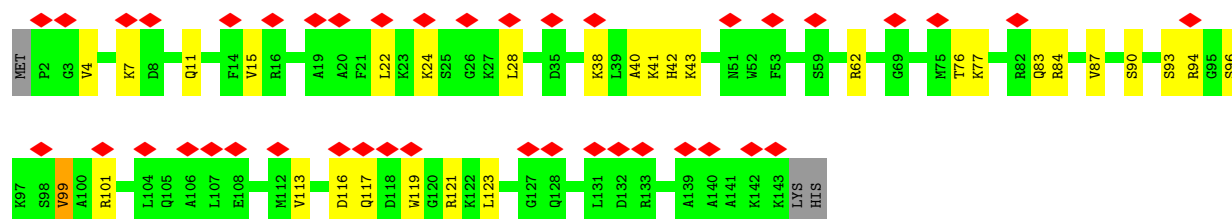
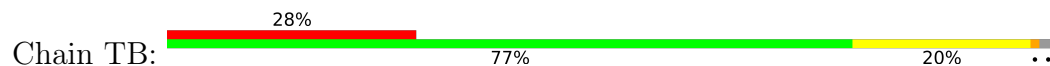
• Molecule 69: eS17



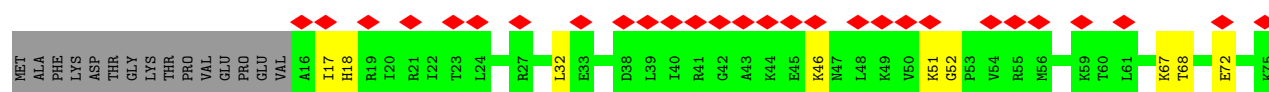
• Molecule 70: S18

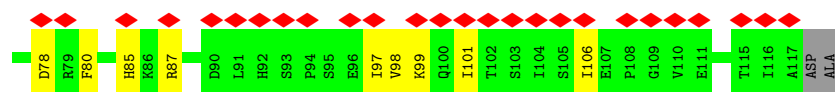


• Molecule 71: S19

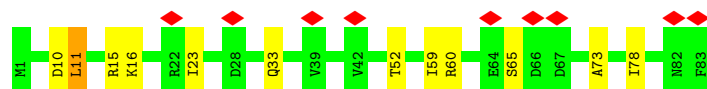
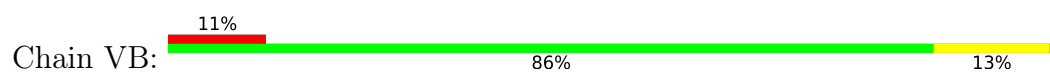


• Molecule 72: uS10

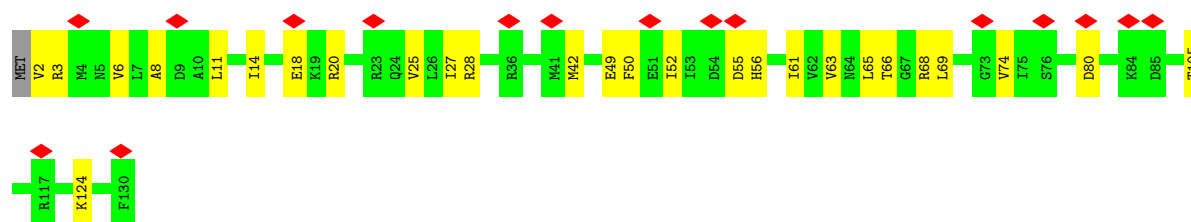
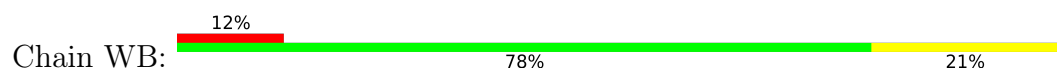




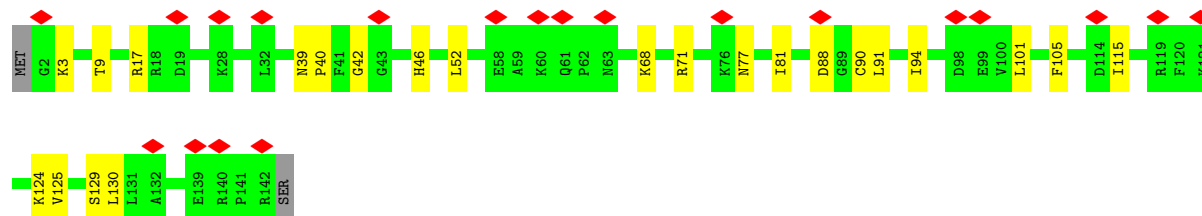
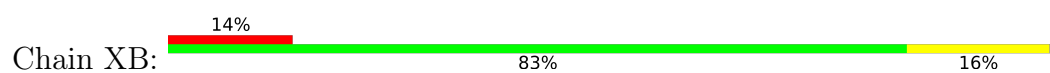
- Molecule 73: S21



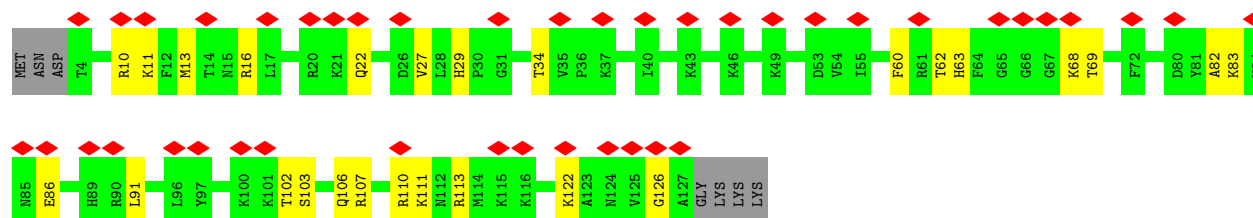
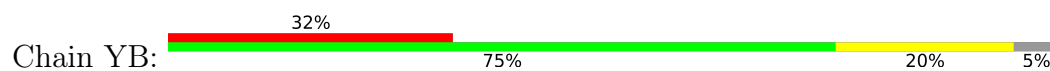
- Molecule 74: S15A



- Molecule 75: S23



- Molecule 76: S24



- Molecule 77: eS25





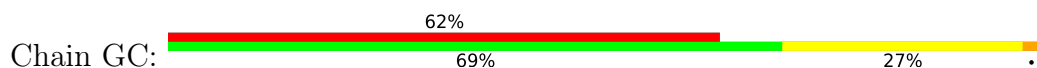
MET
 ALA
 ARG
 HIS
 PRO
 LEU
 TYR
 GLN
 GLY
 SER
 PRO
 ILE
 TRP
 CYS
 GLY
 ARG
 LEU
 ARG
 GLY
 GLY
 ALA
 PHE
 GLY
 ASP
 GLY
 ALA
 GLY
 LYS
 PRO
 ARG
 GLY
 PRO
 ASP
 PHE
 LEU
 PHE
 ASP
 PRO
 SER
 SER
 ALA
 ARG
 ARG
 TRP
 ALA
 ARG
 HIS
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 ASP
 ALA
 ASP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

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

K89
 K90
 N91
 K92
 H93
 K94
 R95
 K96
 K97
 V98
 K99
 L100
 A101
 V102
 L103
 Y104
 Y105
 Y106
 K107
 Y108
 D109
 E110
 N111
 G112
 K113
 T114
 S115
 R116
 L117
 R118
 R119
 E120
 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
 L146
 T147
 Y148

C149
 F150
 ASN
 LYS
 PRO
 GLU
 ASP
 LYS

• Molecule 84: RACK1



MET
 T2
 E3
 Q4
 M5
 T6
 L7
 R8
 G9
 T10
 L11
 G13
 V18
 T19
 Q20
 I21
 A22
 Q26
 F27
 P28
 D29
 G95
 M30
 I31
 L32
 S33
 A34
 S35
 R36
 D37
 K38
 T39
 I40
 I41
 M42
 W43
 K44
 L45
 T46
 R47
 D48
 E49
 T50
 N51
 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
 T86
 L87
 R88
 L89
 W90
 D91
 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
 N117
 R118
 Q119
 I120
 V121
 S122
 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
 N159
 S160
 S161
 N162
 P163
 I164
 I165
 V166
 S167
 C168
 D171
 V174
 K175
 V176
 W177
 N178
 L179
 A180
 N181
 C182
 K183
 L184
 K185
 N186
 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
 W217
 L218
 W219
 D220
 L221
 N222
 E223
 G224
 K225
 H226
 L227
 Y228
 T229
 L230
 D231
 G232
 G233
 D234
 N237
 A238
 L239
 C240
 F241
 S242
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 T252
 G253
 P254
 S255
 I256
 K257
 I258
 W259

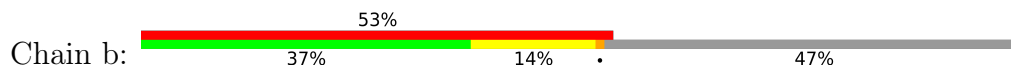
D260
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 K264
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 D268
 E269
 L270
 K271
 Q272
 E273
 V274
 L275
 S276
 T277
 S278
 S279
 K280
 A281
 E282
 C286
 T287
 S288
 L289
 A290
 W291
 S292
 A293
 D294
 G295
 Q296
 T297
 L298
 F299
 A300
 G301
 Y302
 T303
 D304
 N305
 L306
 V307
 R308
 V309
 W310
 Q311
 V312
 T313
 T314
 GLY
 THR
 ARG

• Molecule 85: peptide



A195
 H196
 F197
 D198

• Molecule 86: RPLP0



L421	G422	R423	F424	A425	V426	D427	M428	R429	A430	T432	V433	A434	V435	G436	V437	L438	K439	A440	V441	D442	K443	K444	A445	A446	G447	A448	G449	K450	V451	T452	K453	S454	A455	Q456	K457	A458	Q459	K460	A461	K462																			
L361	D362	C363	H364	T365	A366	H367	L368	A369	C370	K371	F372	A373	E374	L375	K376	E377	K378	L379	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

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 (Å)	686.87994, 686.87994, 686.87994	wwPDB
Map dimensions	648, 648, 648	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: K, MG, 5GP, ZN, ANM, SPD

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

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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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	DB	1768	0	1863	21	0
56	EB	2076	0	2177	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

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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

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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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
65	NB	147/151 (97%)	146 (99%)	1 (1%)	0	100	100
66	OB	134/151 (89%)	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 ⓘ

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

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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

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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 ⓘ

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 ⓘ

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
95	SER	HC	502	-	4,5,6	0.59	0	1,5,7	0.54	0
92	ANM	WA	5243	94	20,20,20	4.07	7 (35%)	24,27,27	1.40	2 (8%)
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
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
91	5GP	UA	101	46	26,26,26	0.98	1 (3%)	39,40,40	1.78	7 (17%)

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
95	SER	HC	502	-	-	1/2/4/6	-
92	ANM	WA	5243	94	-	6/10/23/23	0/2/2/2
93	SPD	WA	5244	-	-	1/7/7/7	-
93	SPD	WA	5245	-	-	1/7/7/7	-
93	SPD	ZA	1944	-	-	1/7/7/7	-
93	SPD	WA	5246	-	-	1/7/7/7	-
91	5GP	UA	101	46	-	5/10/26/26	0/3/3/3

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

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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:

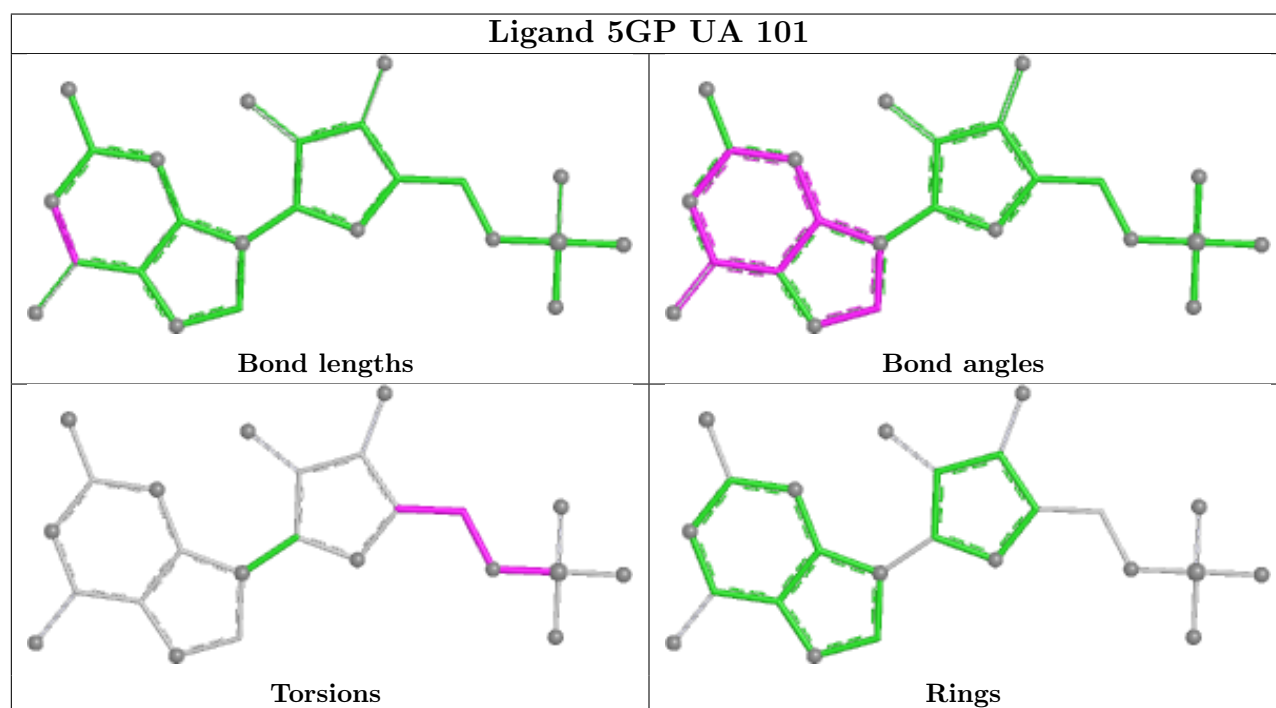
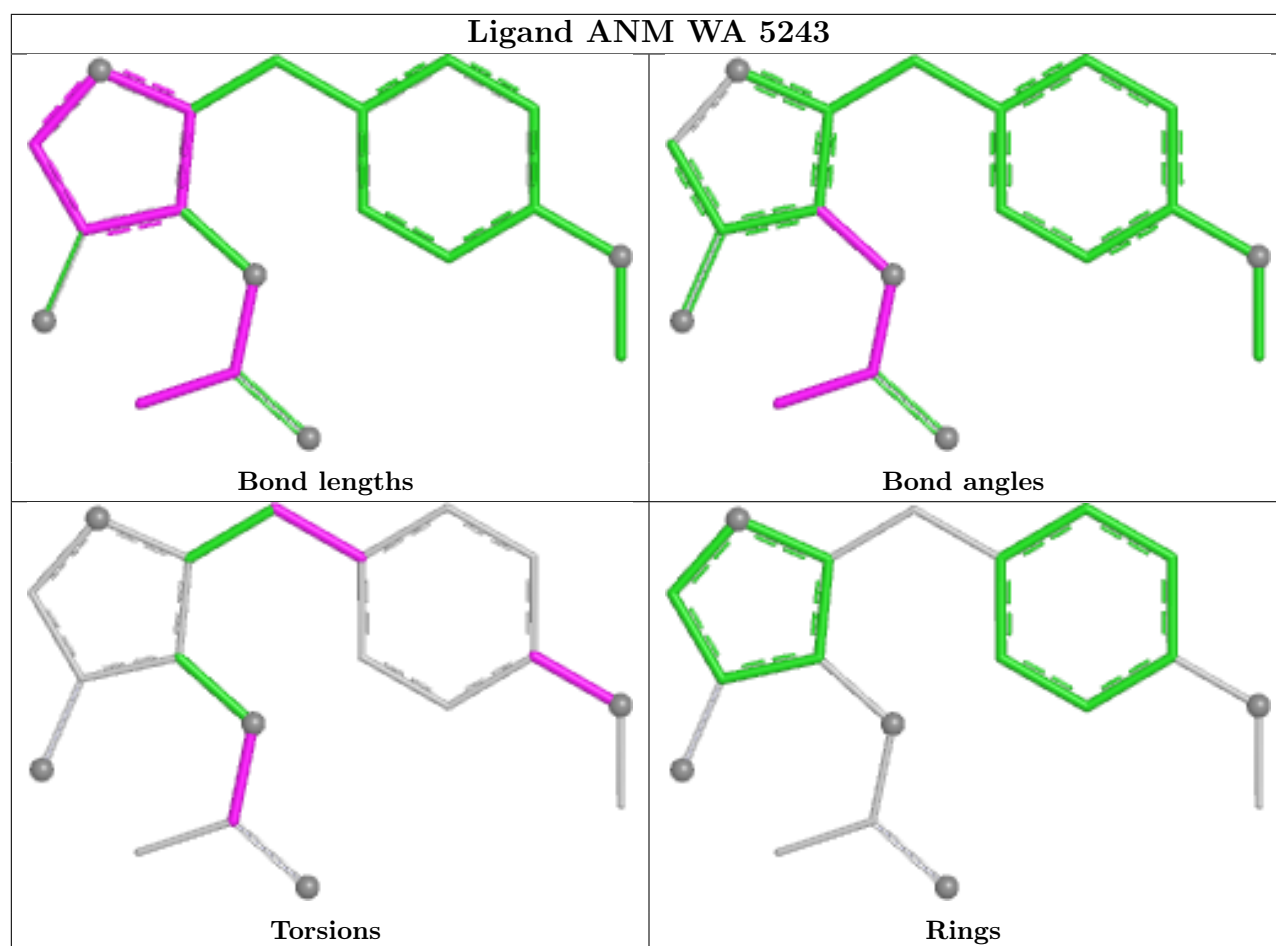
Mol	Chain	Res	Type	Atoms
91	UA	101	5GP	C5'-O5'-P-O1P
92	WA	5243	ANM	C6-C5-O2-C2
92	WA	5243	ANM	O3-C5-O2-C2
92	WA	5243	ANM	C10-C9-O1-C14
92	WA	5243	ANM	C1-C9-O1-C14

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

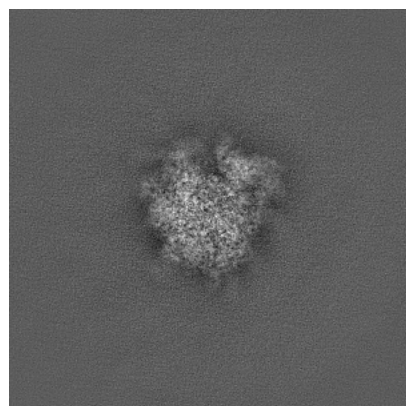
6 Map visualisation [i](#)

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.

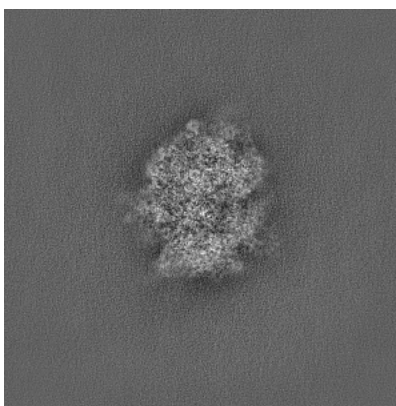
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

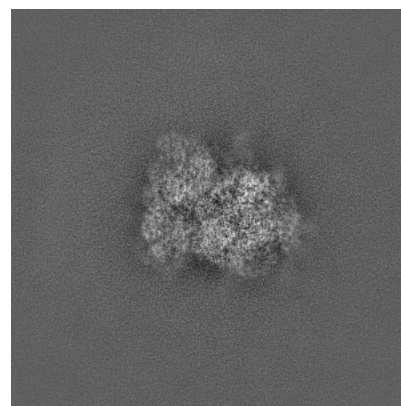
6.1.1 Primary map



X

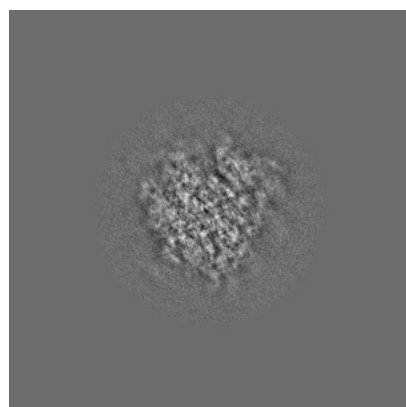


Y

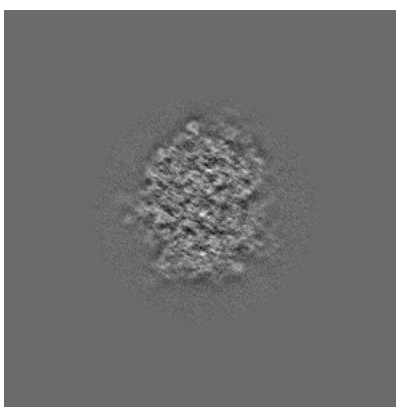


Z

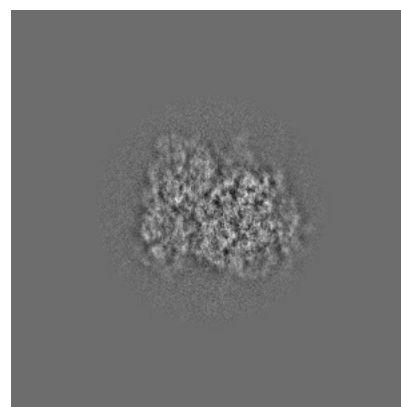
6.1.2 Raw map



X



Y

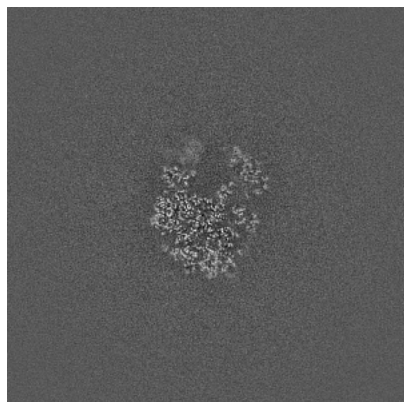


Z

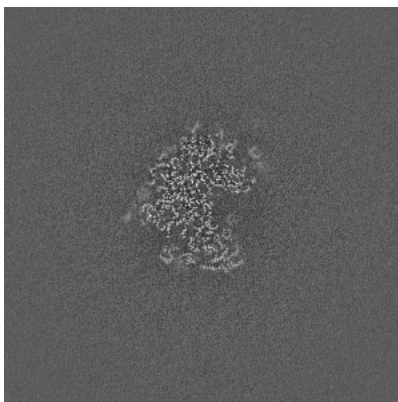
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

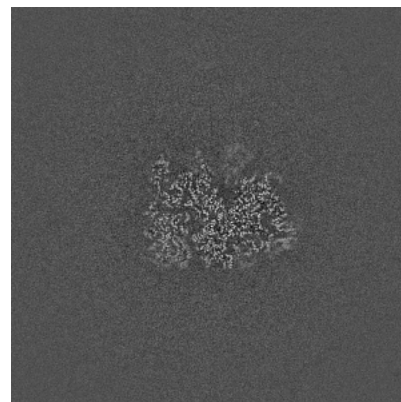
6.2.1 Primary map



X Index: 324

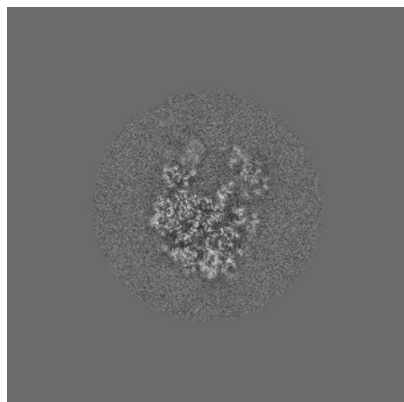


Y Index: 324

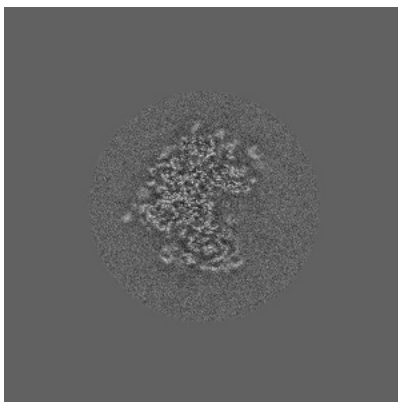


Z Index: 324

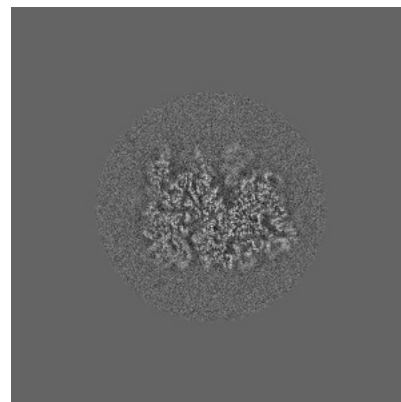
6.2.2 Raw map



X Index: 324



Y Index: 324

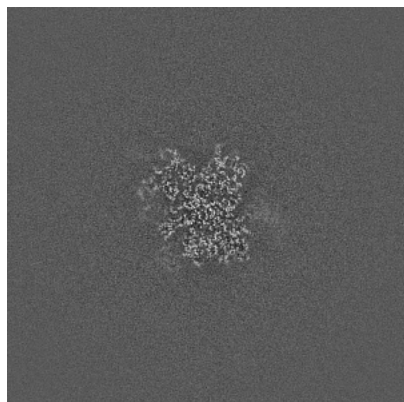


Z Index: 324

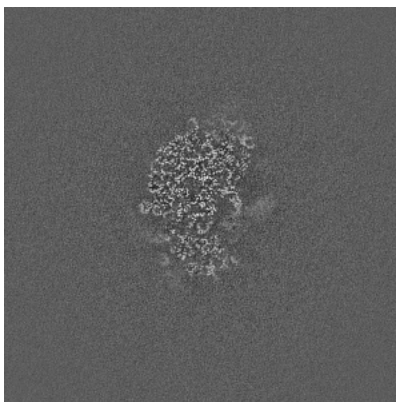
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

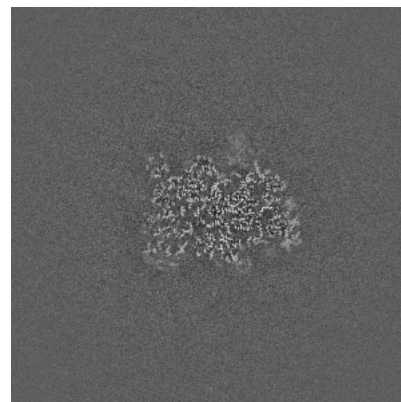
6.3.1 Primary map



X Index: 377

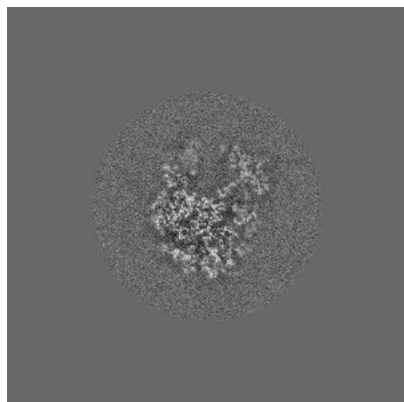


Y Index: 301

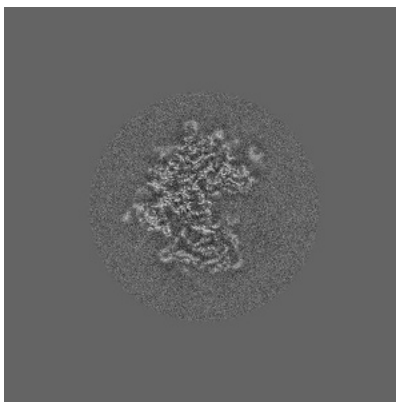


Z Index: 311

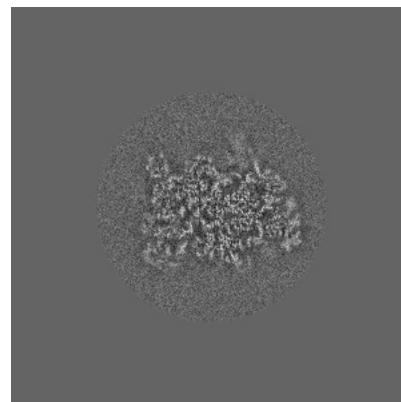
6.3.2 Raw map



X Index: 322



Y Index: 327

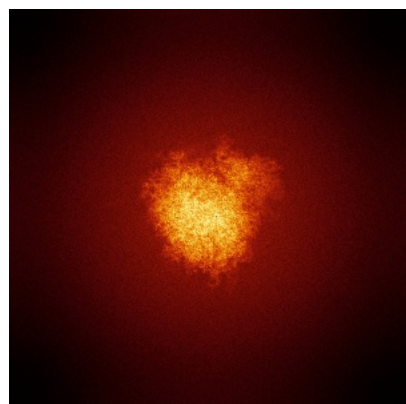


Z Index: 311

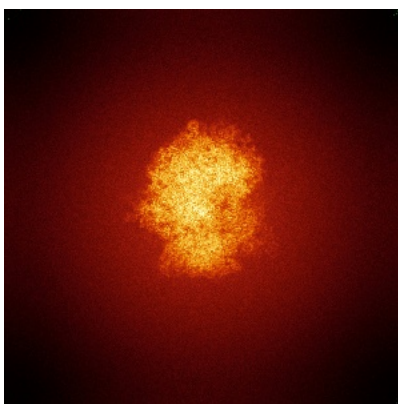
The images above show the largest variance slices of the map in three orthogonal directions.

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

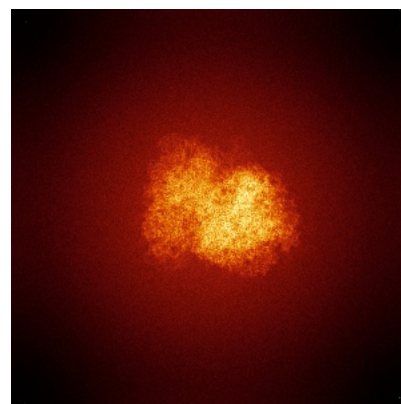
6.4.1 Primary map



X

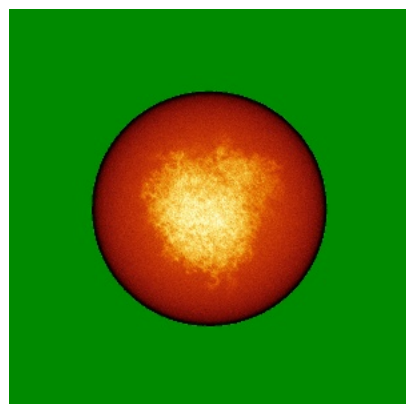


Y

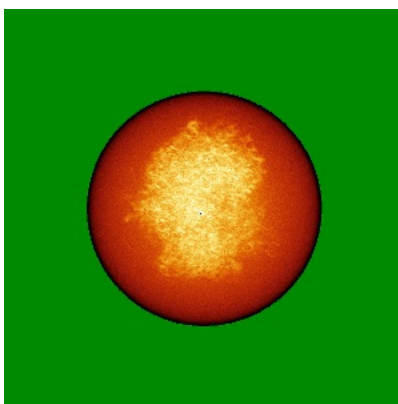


Z

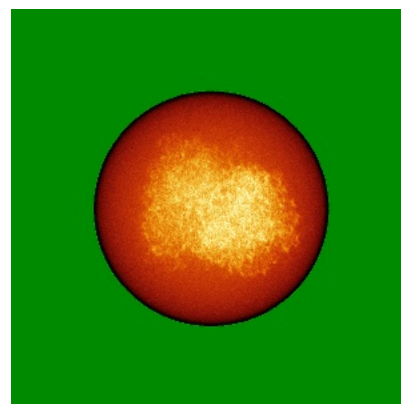
6.4.2 Raw map



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.

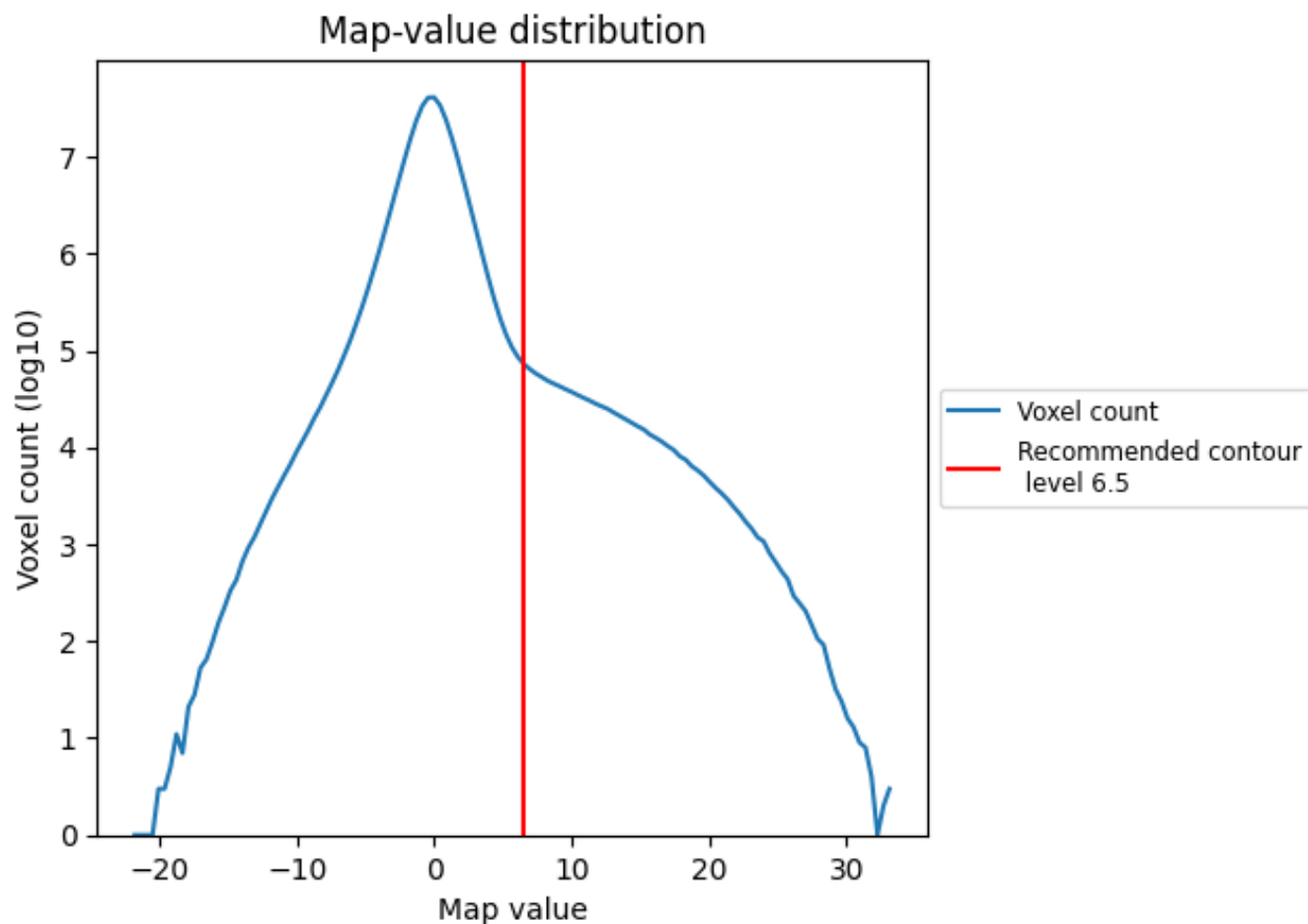
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

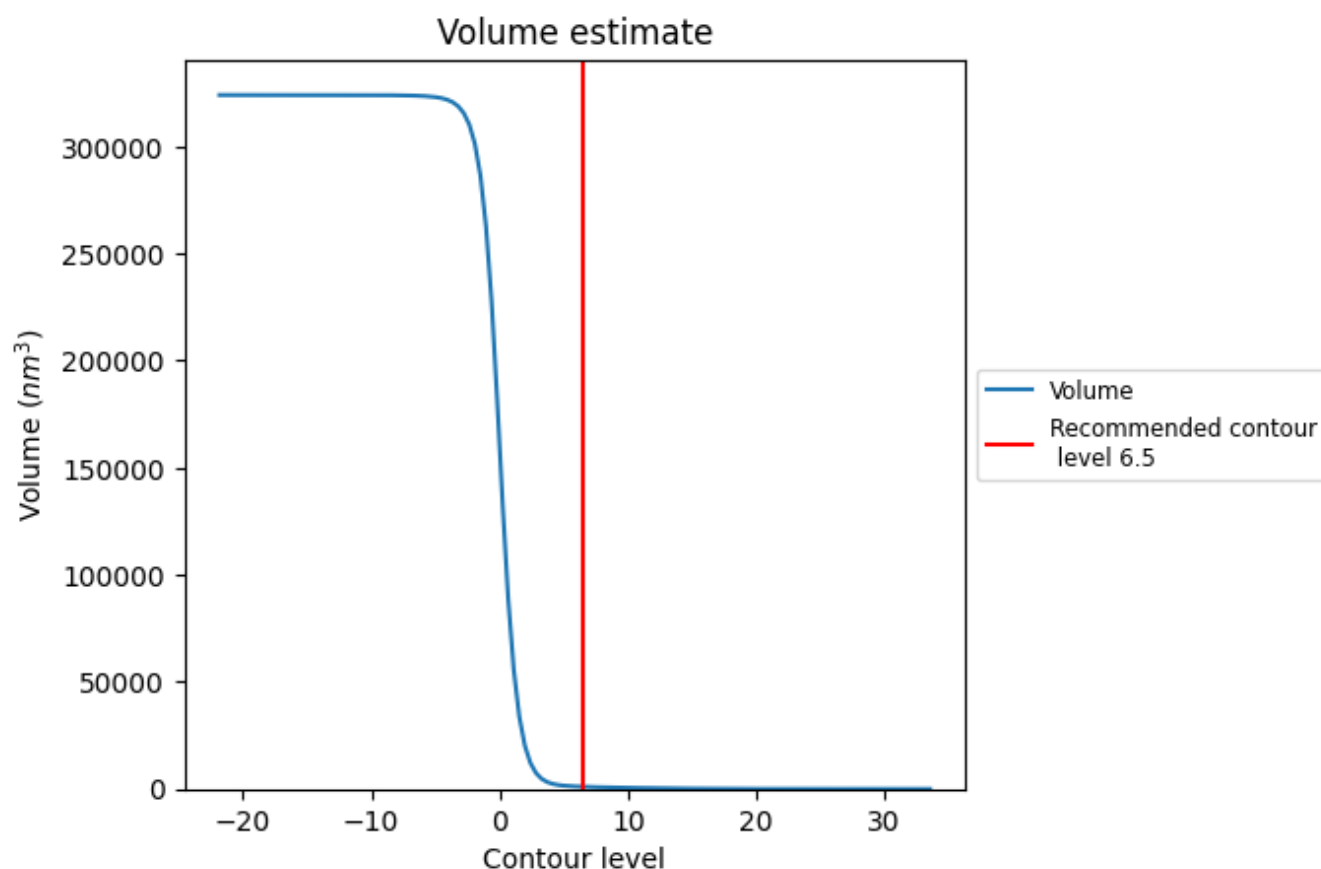
This section contains the results of statistical analysis of the map.

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.

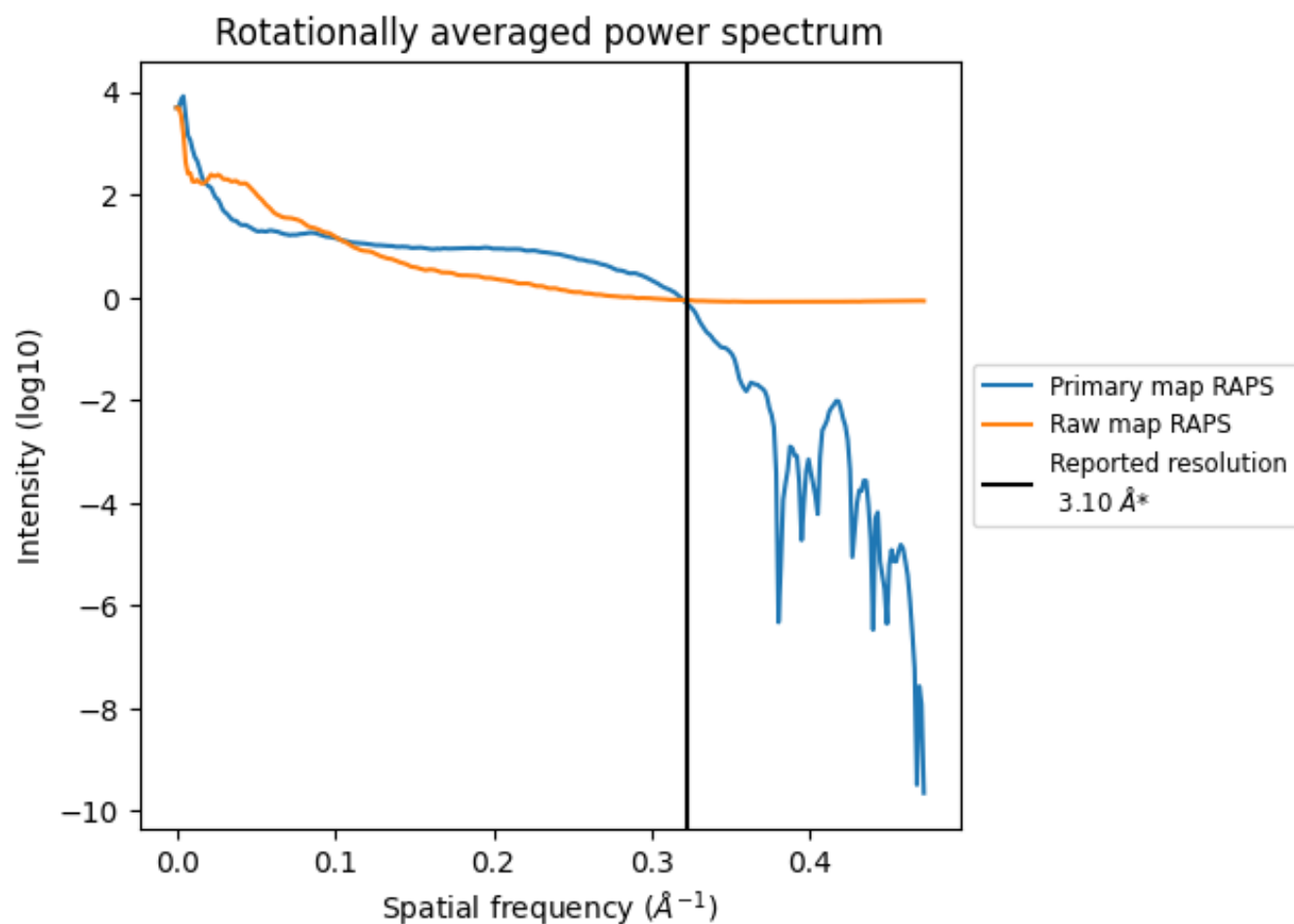
7.2 Volume estimate [i](#)



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 ⓘ

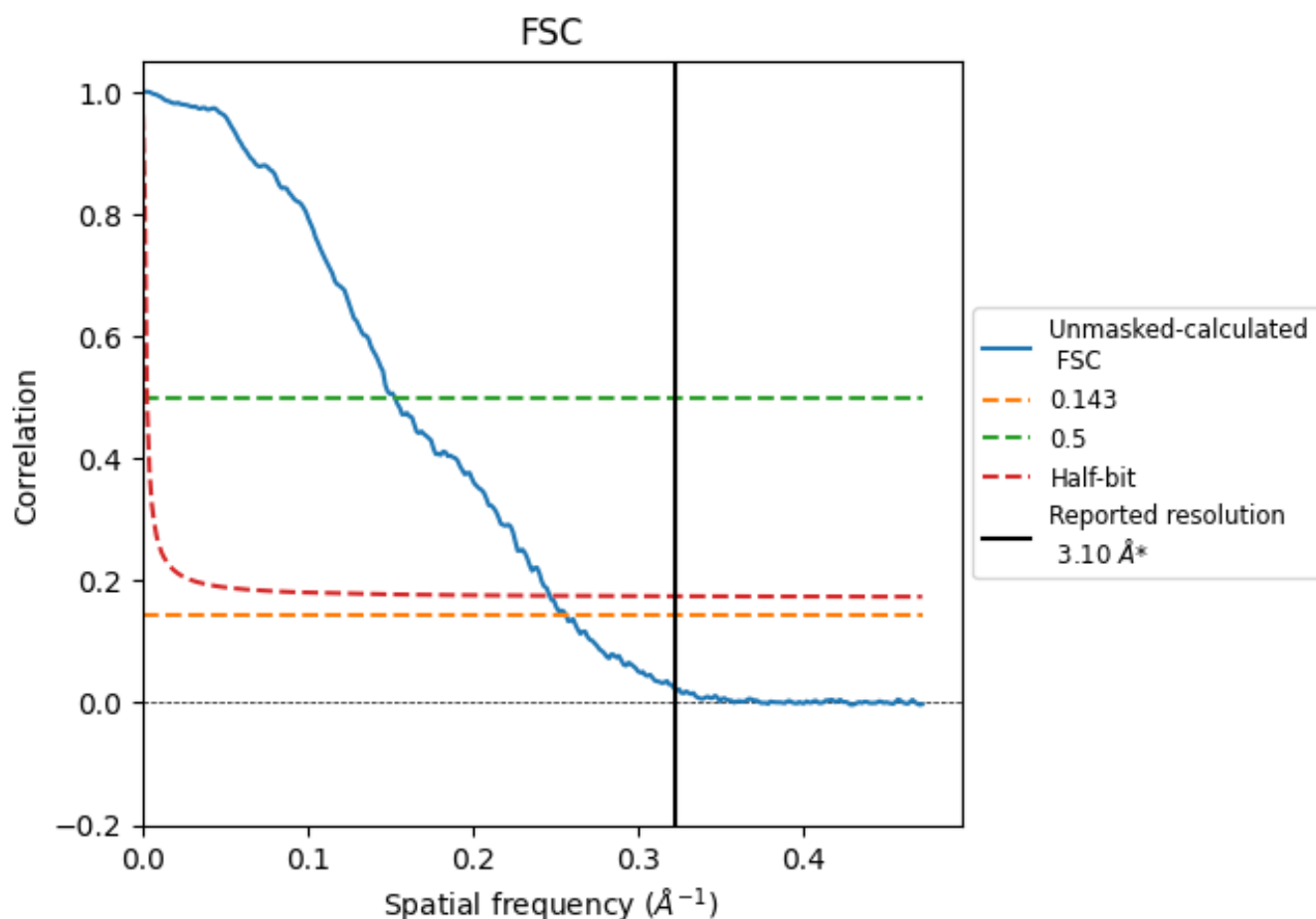


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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](#)

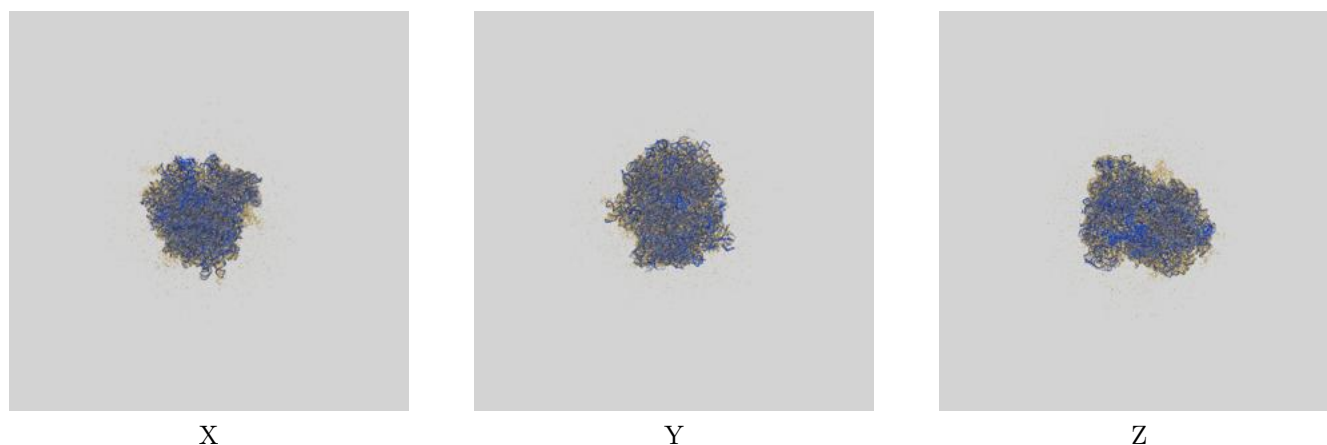
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.90	6.55	4.06

*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](#)

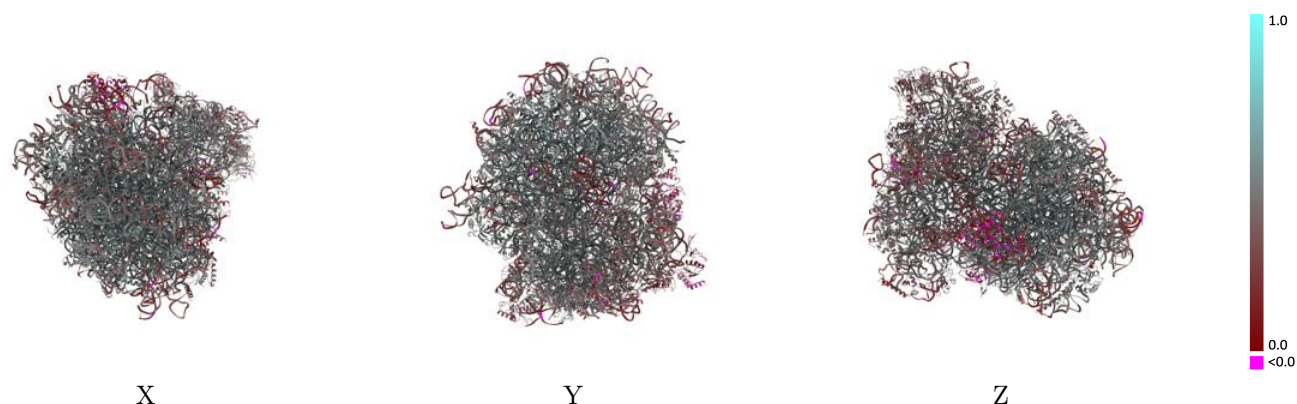
This section contains information regarding the fit between EMDB map EMD-43567 and PDB model 8VVS. Per-residue inclusion information can be found in section [3](#) on page [26](#).

9.1 Map-model overlay [i](#)



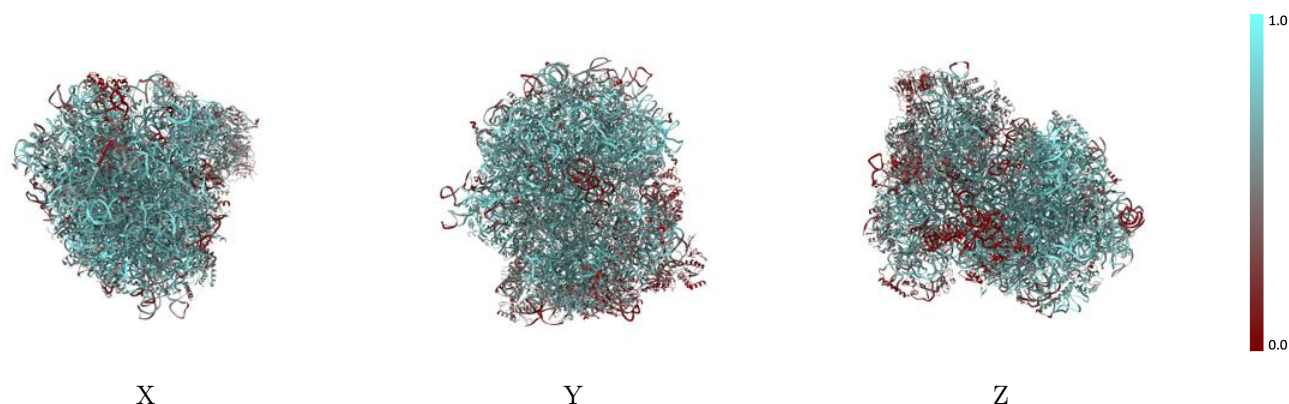
The images above show the 3D surface view of the map at the recommended contour level 6.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



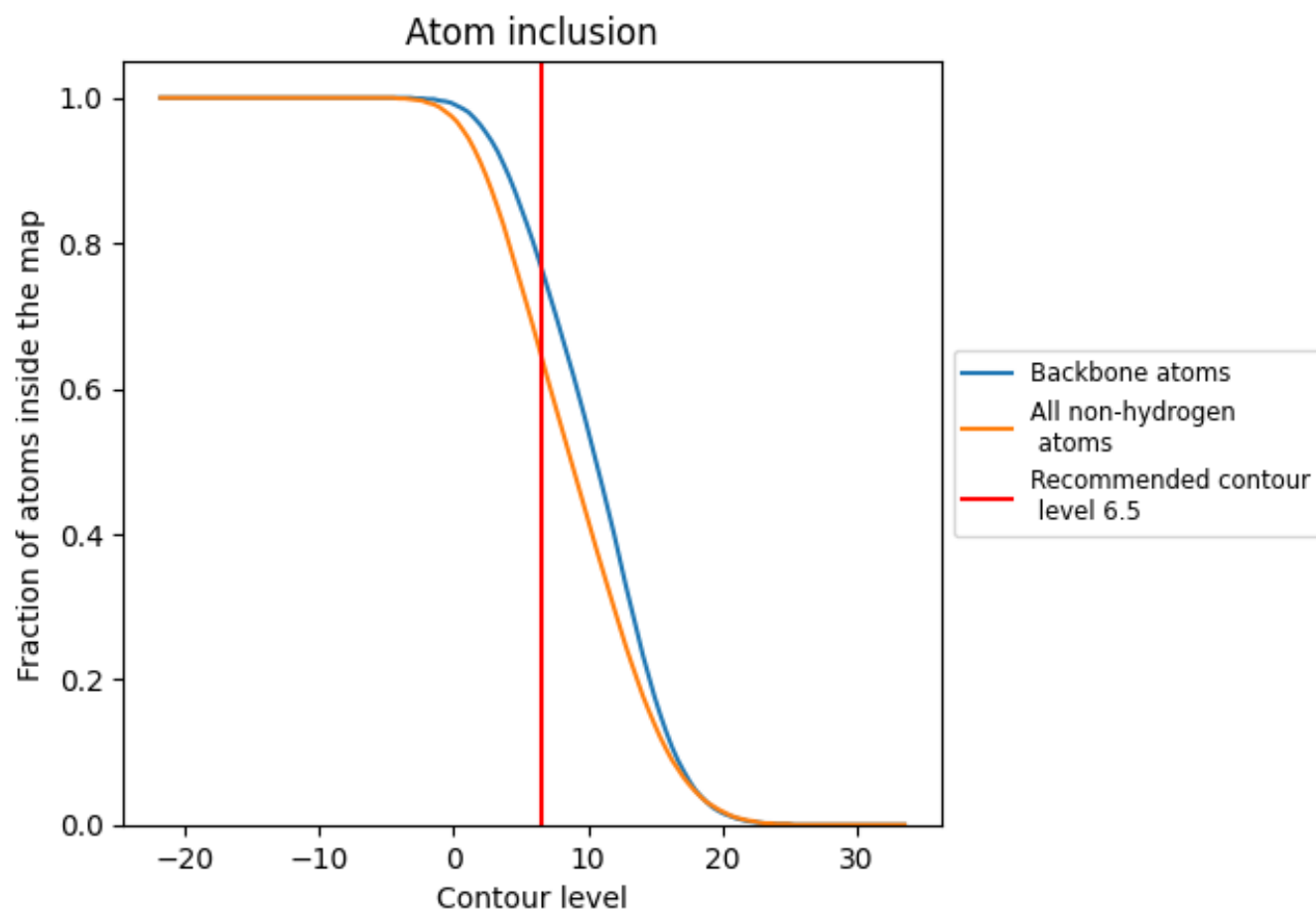
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



























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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

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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