



wwPDB EM Validation Summary Report ⓘ

Sep 28, 2024 – 05:44 pm BST

PDB ID : 4V92
EMDB ID : EMD-2604
Title : Kluyveromyces lactis 80S ribosome in complex with CrPV-IRES
Authors : Fernandez, I.S.; Bai, X.; Scheres, S.H.W.; Ramakrishnan, V.
Deposited on : 2014-03-21
Resolution : 3.70 Å(reported)
Based on initial model : 3B31

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:

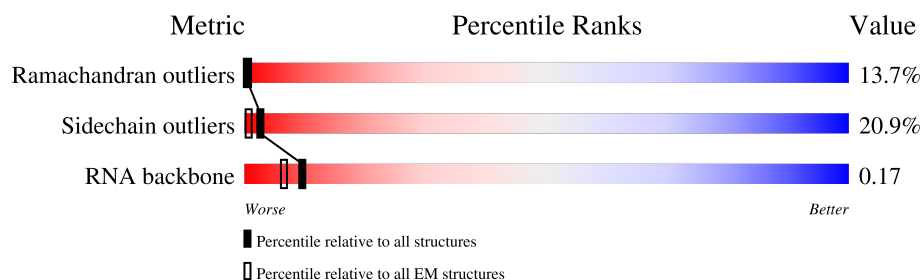
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

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 3.70 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	A2	1767	<div> <div>6%</div> <div>34%</div> <div>43%</div> <div>23%</div> </div>
2	AZ	190	<div> <div>14%</div> <div>18%</div> <div>57%</div> <div>25%</div> </div>
3	BA	206	<div> <div>83%</div> <div>63%</div> <div>26%</div> <div>8%</div> </div>
4	BB	213	<div> <div>63%</div> <div>70%</div> <div>24%</div> <div>6%</div> </div>
5	BC	216	<div> <div>68%</div> <div>81%</div> <div>15%</div> <div>•</div> </div>
6	BD	222	<div> <div>76%</div> <div>76%</div> <div>18%</div> <div>5%</div> </div>
7	BE	260	<div> <div>68%</div> <div>72%</div> <div>25%</div> <div>•</div> </div>
8	BF	206	<div> <div>60%</div> <div>73%</div> <div>20%</div> <div>6%</div> </div>

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Mol	Chain	Length	Quality of chain
9	BG	226	
10	BH	184	
11	BI	187	
12	BJ	179	
13	BK	93	
14	BL	142	
15	BM	120	
16	BN	150	
17	BO	127	
18	BP	115	
19	BQ	140	
20	BR	121	
21	BS	140	
22	BT	142	
23	BU	104	
24	BV	87	
25	BW	129	
26	BX	142	
27	BY	134	
28	BZ	64	
29	Ba	97	
30	Bb	81	
31	Bc	63	
32	Bd	52	
33	Be	55	

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Mol	Chain	Length	Quality of chain
34	Bf	64	<div><div>56%</div><div>61%</div><div>31%</div><div>6%</div><div></div></div>
35	Bg	315	<div><div>63%</div><div>74%</div><div>23%</div><div></div><div></div></div>

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 79002 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A2	1764	Total	C	N	O	P	0	0
			37579	16801	6644	12370	1764		

- Molecule 2 is a RNA chain called RNA OF CRICKET-PARALYSIS-VIRUS-IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AZ	190	Total	C	N	O	P	0	0
			4018	1801	685	1342	190		

- Molecule 3 is a protein called US2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	BA	206	Total	C	N	O	S	0	0
			1577	1014	278	283	2		

- Molecule 4 is a protein called ES1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	BB	213	Total	C	N	O	S	0	0
			1686	1070	302	310	4		

- Molecule 5 is a protein called US5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	BC	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 6 is a protein called US3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	BD	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

- Molecule 7 is a protein called ES4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	BE	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 8 is a protein called US7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	BF	206	Total	C	N	O	S	0	0
			1603	1004	297	299	3		

- Molecule 9 is a protein called ES6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	BG	226	Total	C	N	O	S	0	0
			1790	1123	343	321	3		

- Molecule 10 is a protein called ES7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	BH	184	Total	C	N	O	S	0	0
			1481	951	265	265			

- Molecule 11 is a protein called ES8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	BI	187	Total	C	N	O	S	0	0
			1480	919	296	263	2		

- Molecule 12 is a protein called US4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	BJ	179	Total	C	N	O	S	0	0
			1452	919	282	250	1		

- Molecule 13 is a protein called ES10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BK	93	Total	C	N	O	S	0	0
			765	496	123	144	2		

- Molecule 14 is a protein called US17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	BL	142	Total	C	N	O	S	0	0
			1146	735	217	191	3		

- Molecule 15 is a protein called ES12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BM	120	Total	C	N	O	S	0	0
			870	548	152	168	2		

- Molecule 16 is a protein called US15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BN	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 17 is a protein called US11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BO	127	Total	C	N	O	S	0	0
			905	555	183	165	2		

- Molecule 18 is a protein called US19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BP	115	Total	C	N	O	S	0	0
			914	585	165	157	7		

- Molecule 19 is a protein called US9.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	BQ	140	Total	C	N	O	0	0
			1082	696	193	193		

- Molecule 20 is a protein called ES17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BR	121	Total	C	N	O	S	0	0
			934	583	179	170	2		

- Molecule 21 is a protein called US13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BS	140	Total	C	N	O	S	0	0
			1150	720	223	205	2		

- Molecule 22 is a protein called ES19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BT	142	Total	C	N	O	S	0	0
			1105	689	207	207	2		

- Molecule 23 is a protein called US10.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	BU	104	Total	C	N	O	S	0	0
			829	525	150	153	1		

- Molecule 24 is a protein called ES21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BV	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 25 is a protein called US8.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 26 is a protein called US12.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BX	142	Total	C	N	O	S	0	0
			1101	698	215	186	2		

- Molecule 27 is a protein called ES24.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	BY	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 28 is a protein called ES25.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	BZ	64	Total	C	N	O	0	0
			518	331	95	92		

- Molecule 29 is a protein called ES26.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ba	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 30 is a protein called ES27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Bb	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 31 is a protein called ES28.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Bc	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 32 is a protein called US14.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Bd	52	Total	C	N	O	S	0	0
			433	269	91	69	4		

- Molecule 33 is a protein called ES30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Be	55	Total	C	N	O	S	0	0
			440	277	90	72	1		

- Molecule 34 is a protein called ES31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Bf	64	Total	C	N	O	S	0	0
			458	289	83	82	4		

- Molecule 35 is a protein called RACK1.

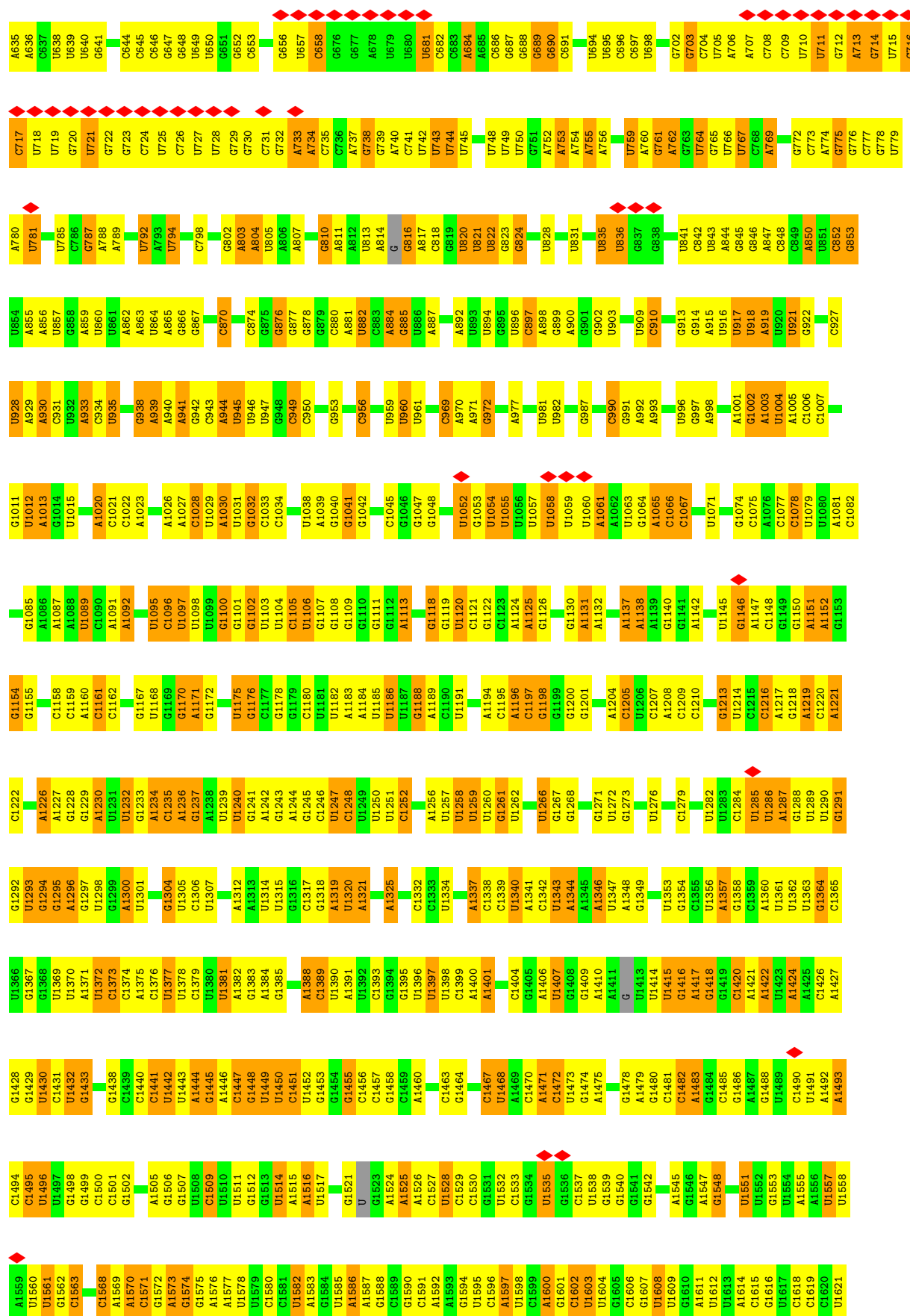
Mol	Chain	Residues	Atoms					AltConf	Trace
35	Bg	315	Total	C	N	O	S	0	0
			2417	1531	414	464	8		

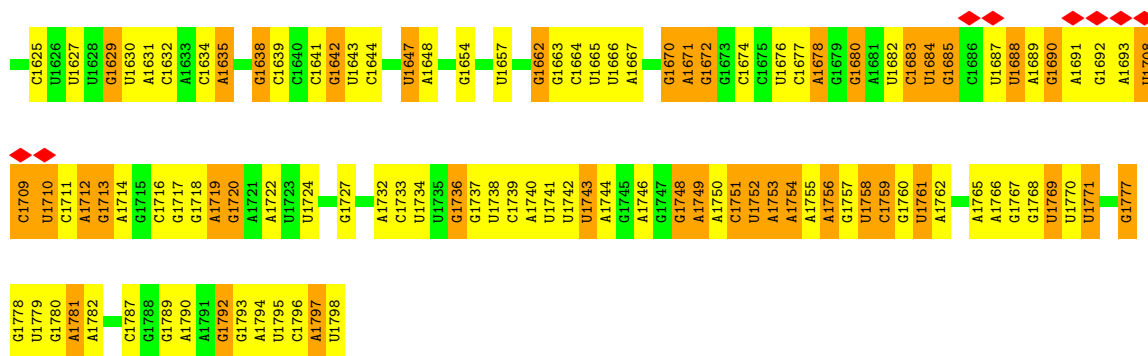
3 Residue-property plots

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

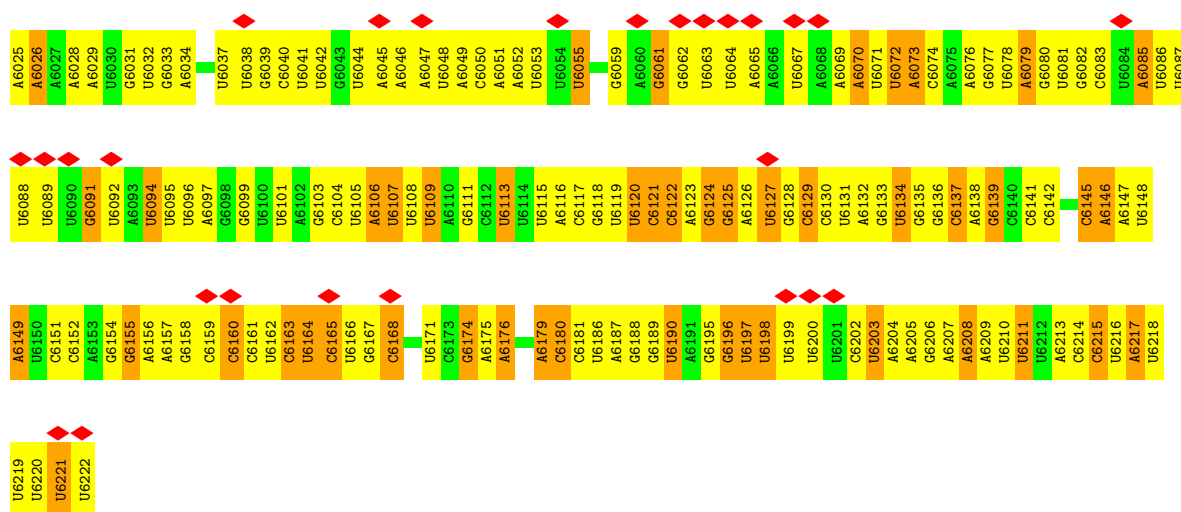
• Molecule 1: 18S RRNA



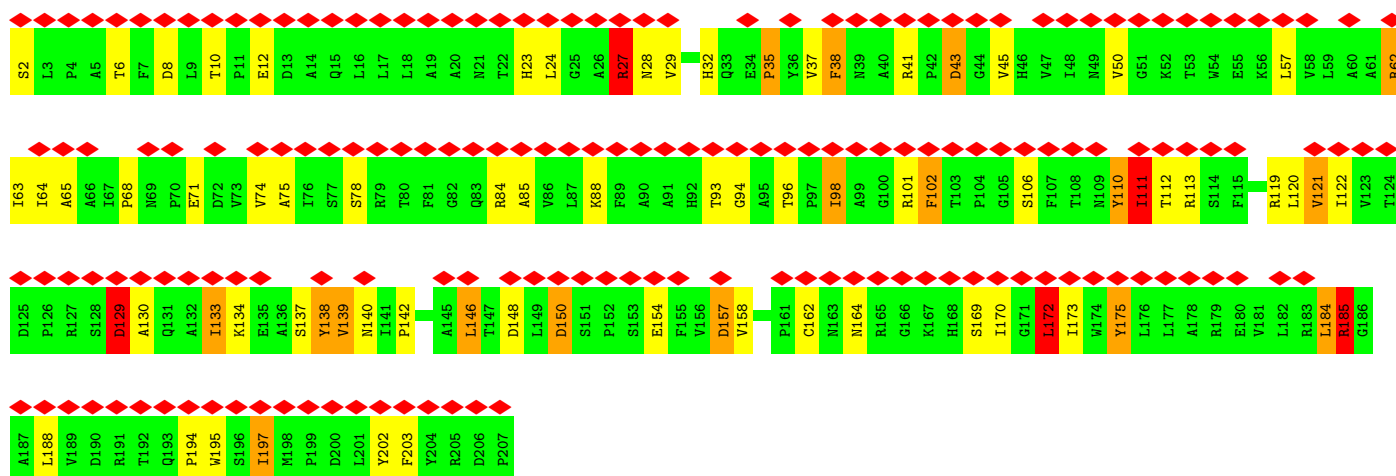
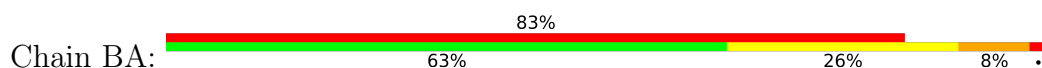




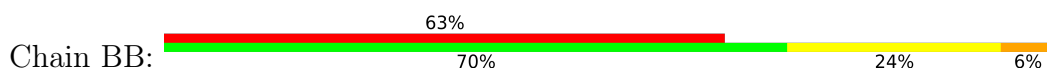
• Molecule 2: RNA OF CRICKET-PARALYSIS-VIRUS-IRES



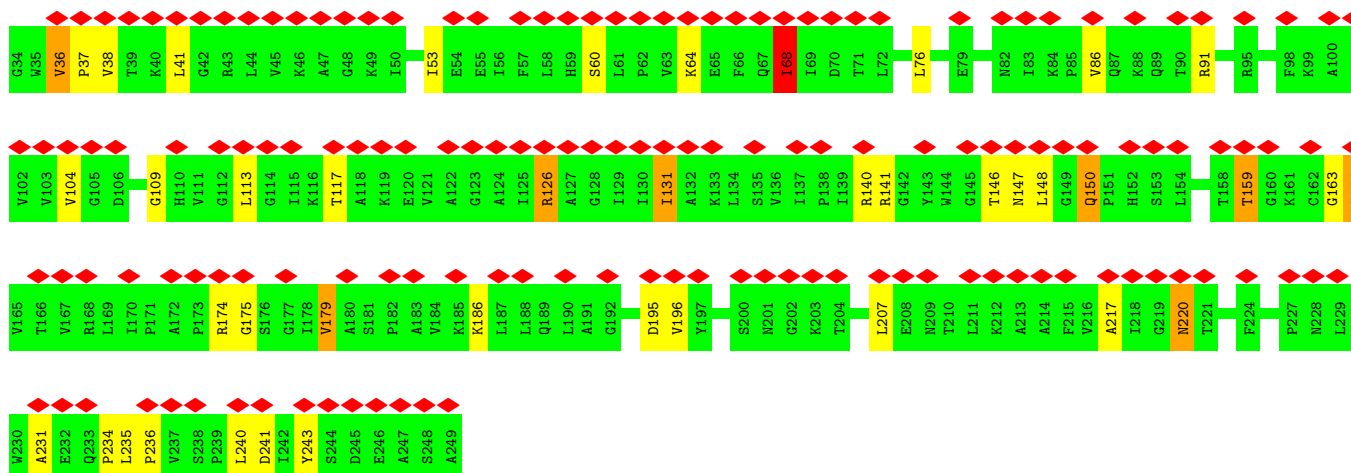
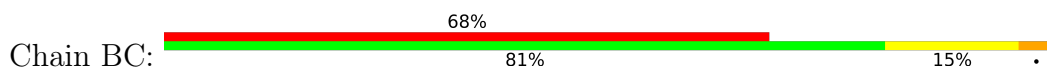
• Molecule 3: US2



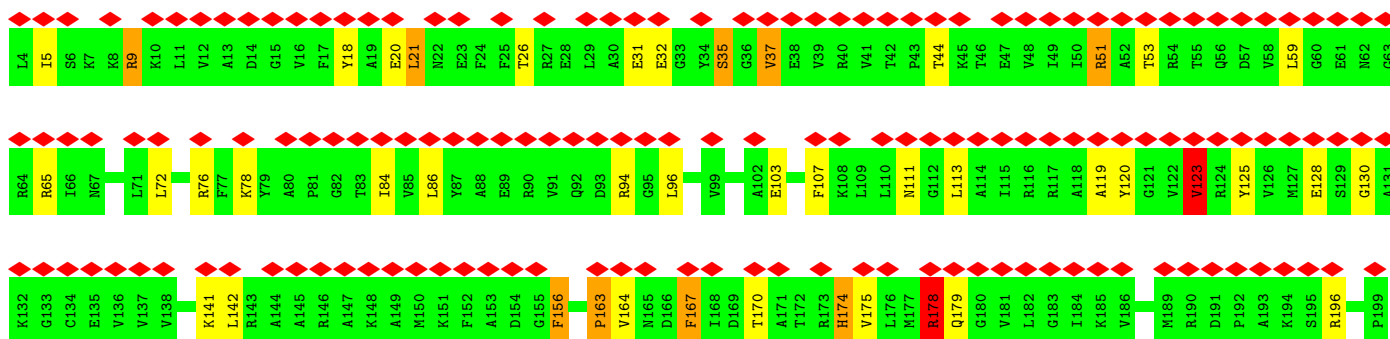
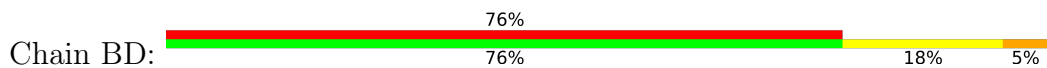
• Molecule 4: ES1

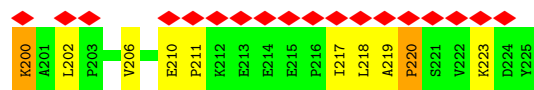


• Molecule 5: US5

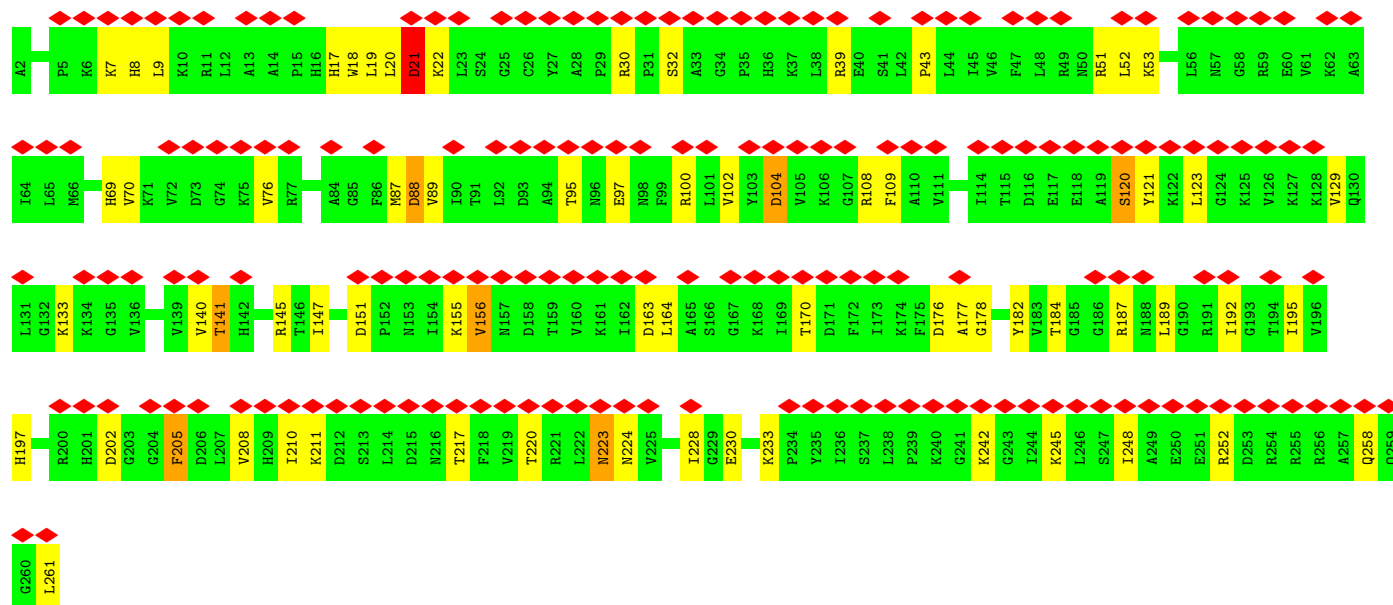
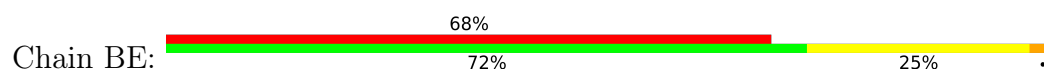


• Molecule 6: US3

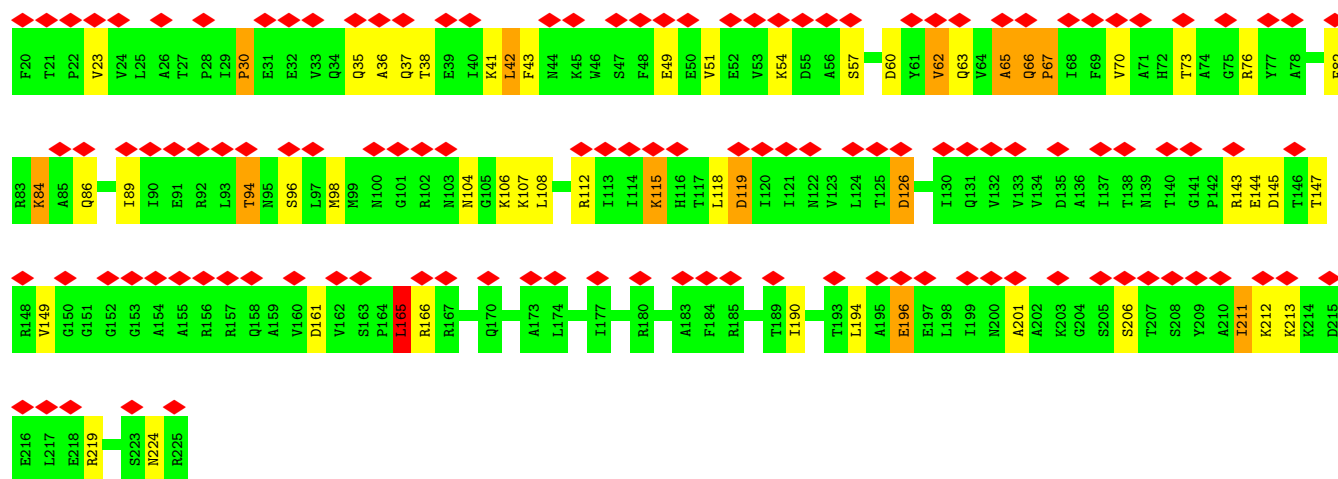
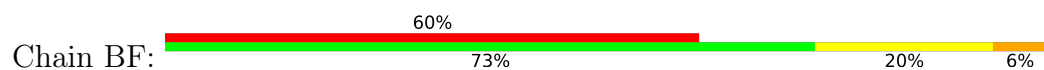




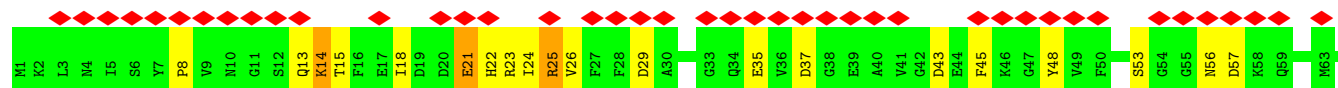
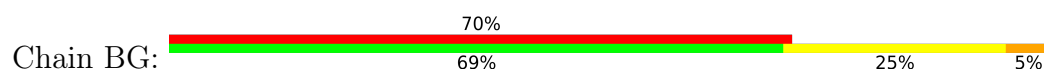
• Molecule 7: ES4

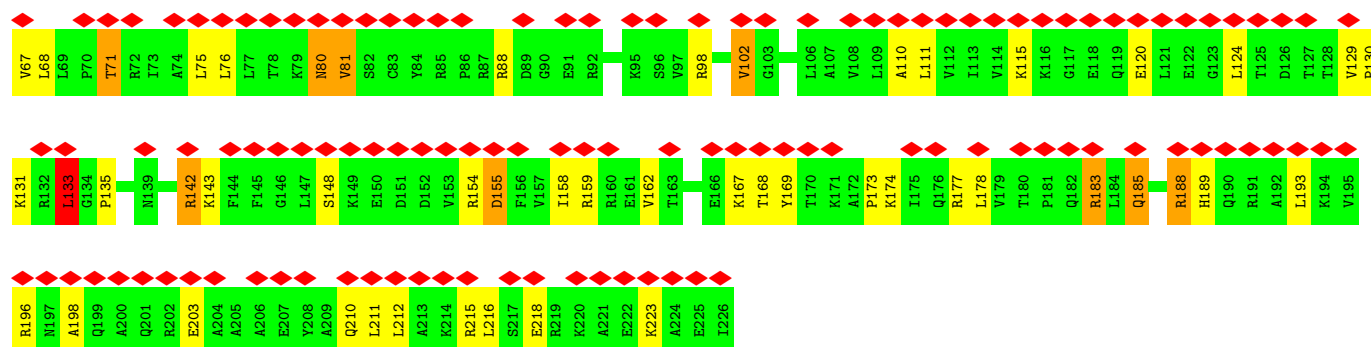


• Molecule 8: US7

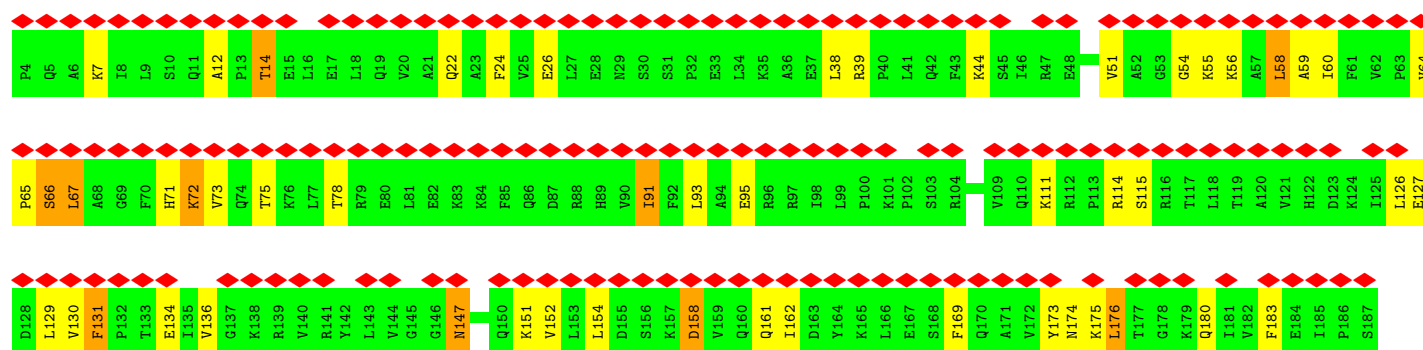
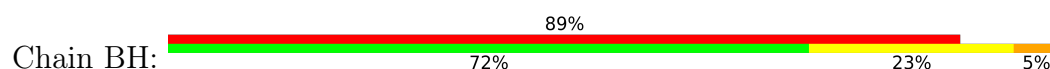


• Molecule 9: ES6

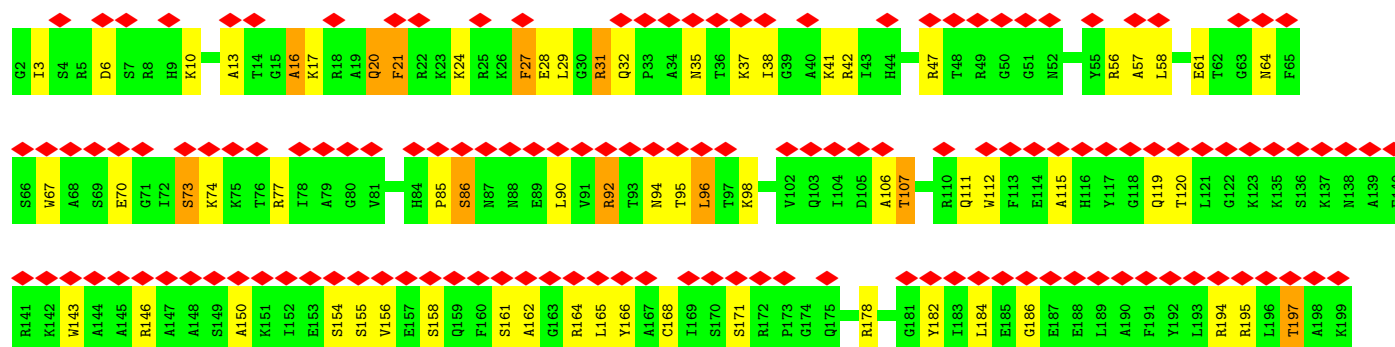
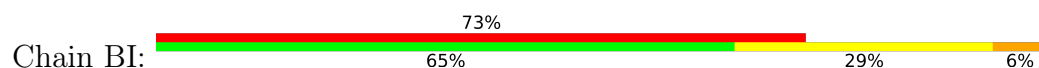




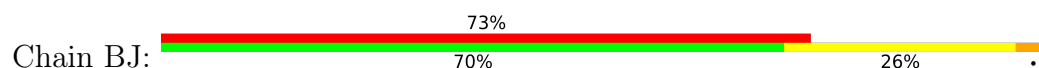
• Molecule 10: ES7



• Molecule 11: ES8

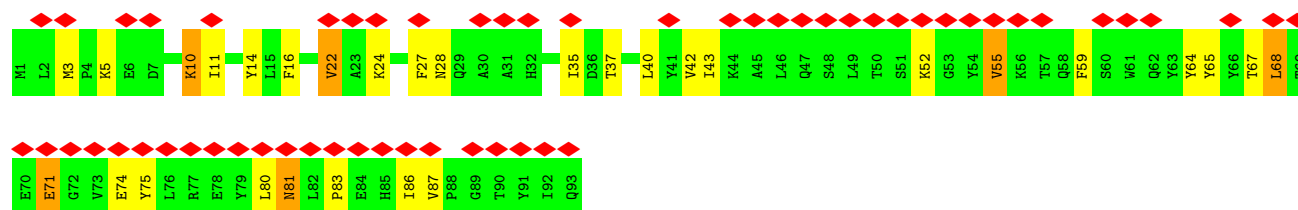


• Molecule 12: US4

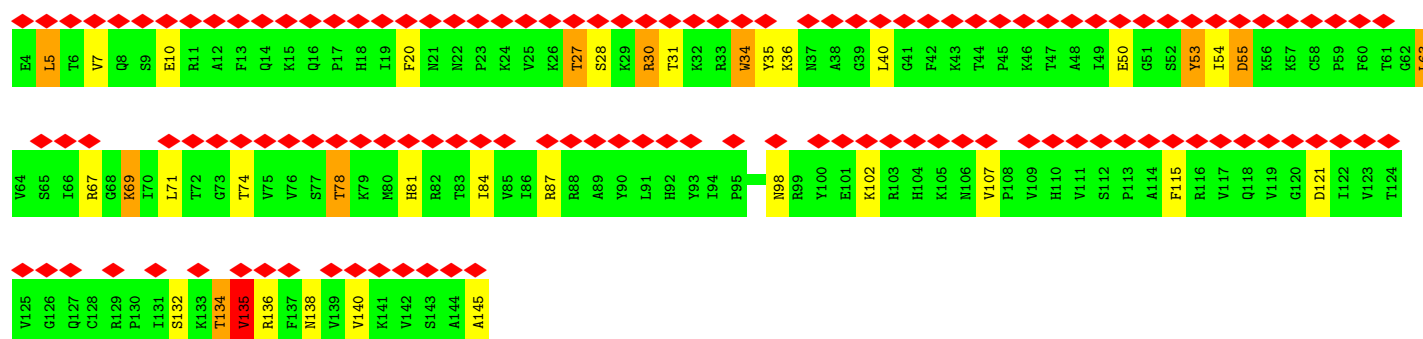
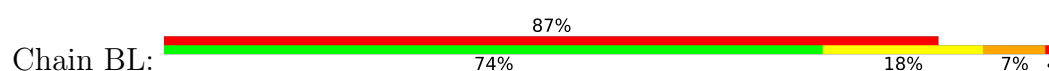




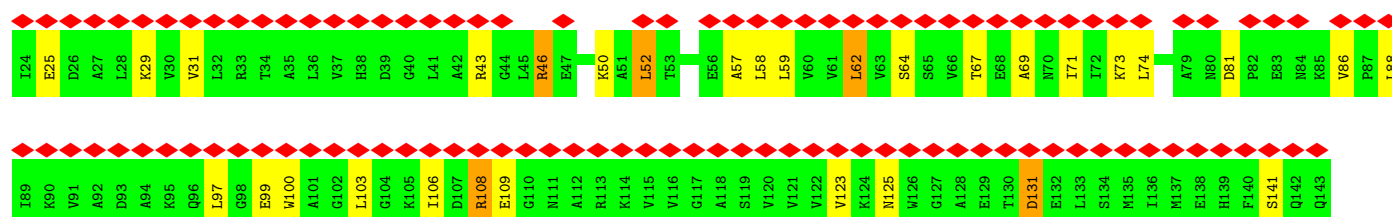
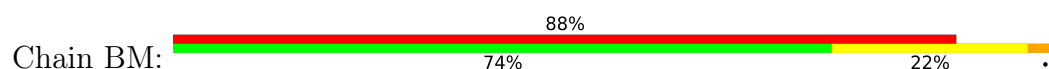
• Molecule 13: ES10



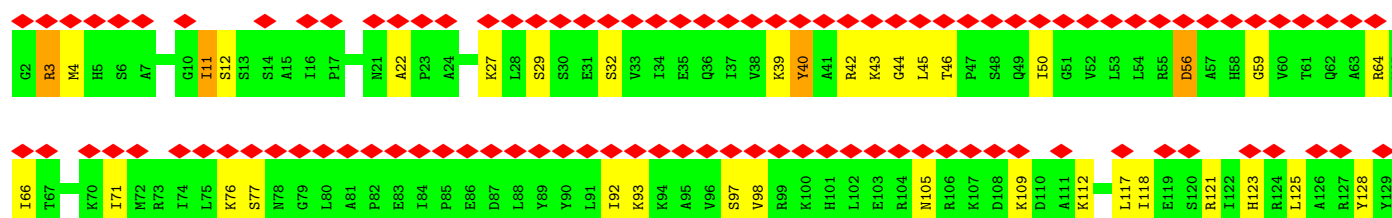
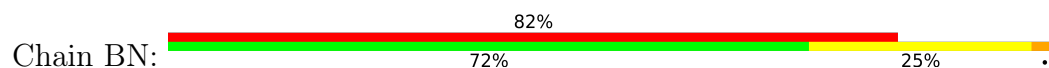
• Molecule 14: US17

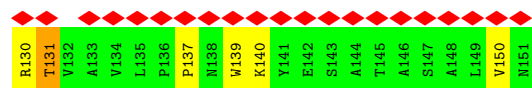


• Molecule 15: ES12

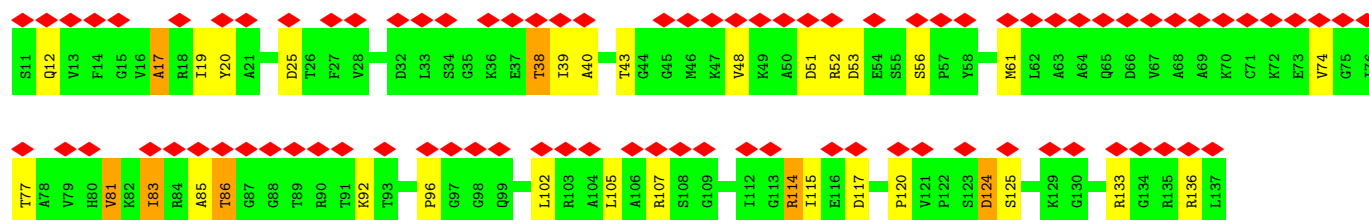
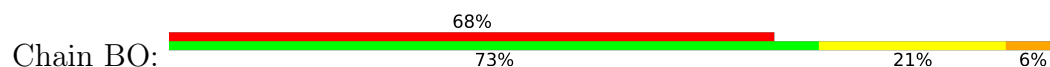


• Molecule 16: US15

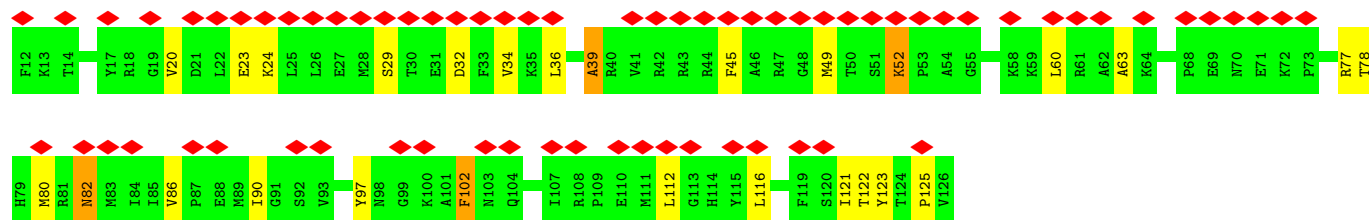
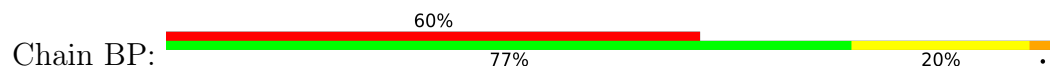




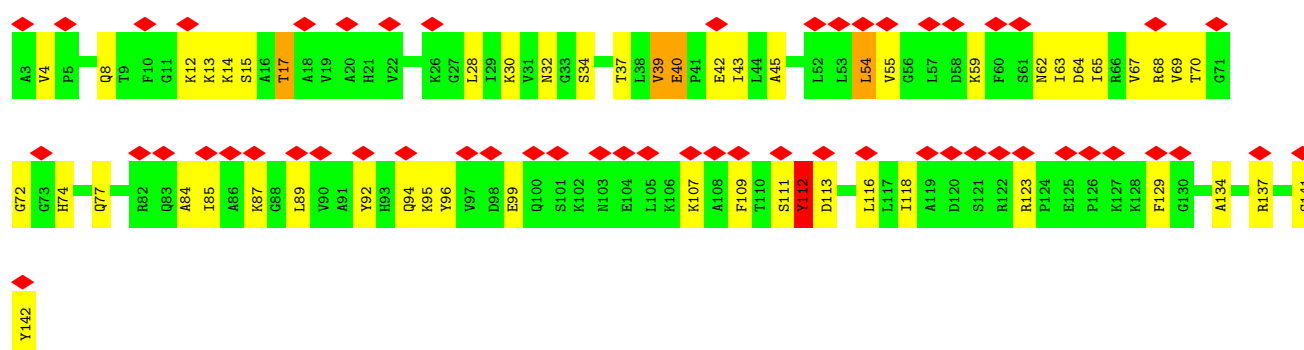
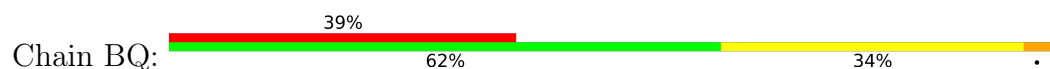
• Molecule 17: US11



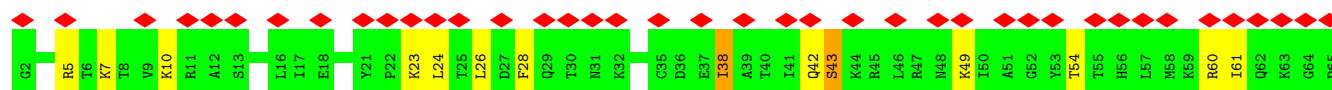
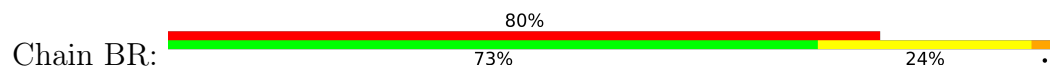
• Molecule 18: US19



• Molecule 19: US9

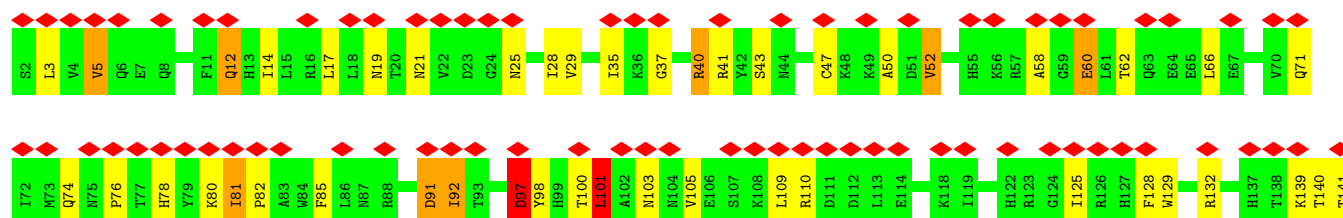


• Molecule 20: ES17

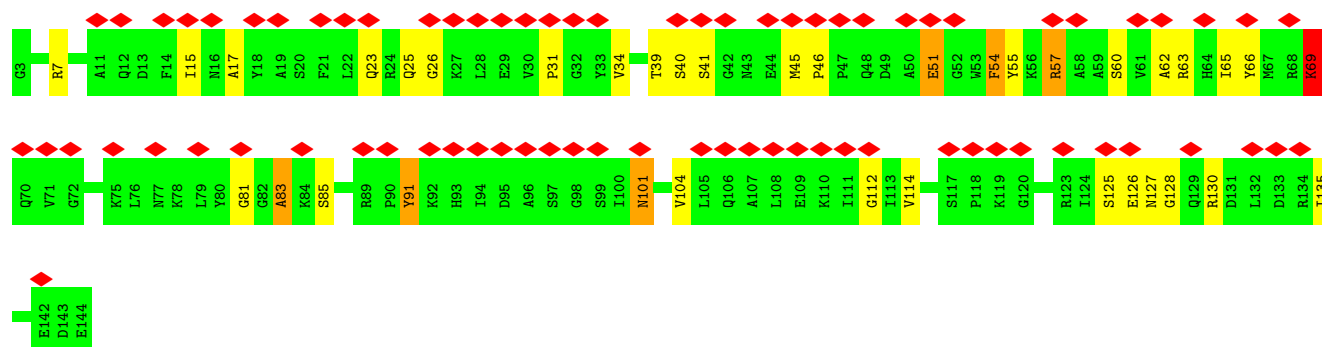
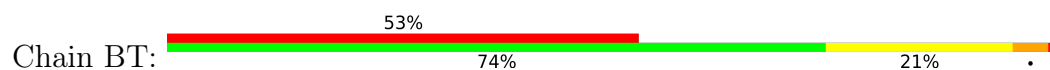




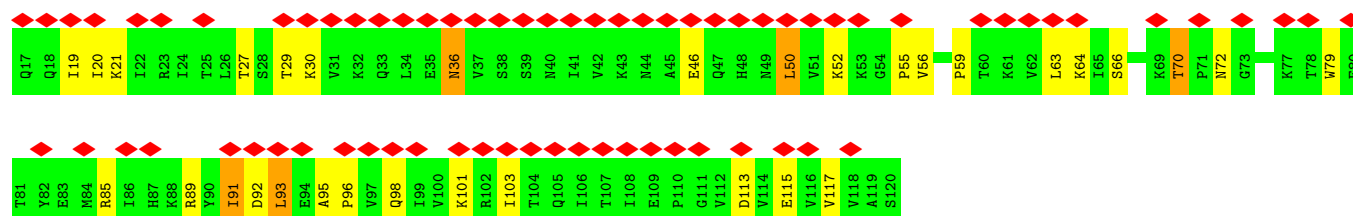
• Molecule 21: US13



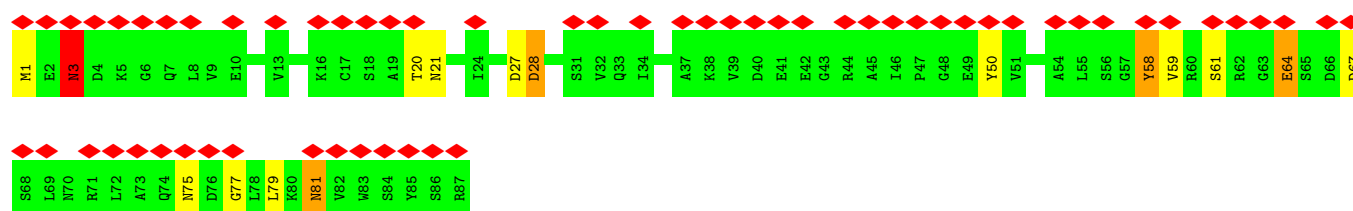
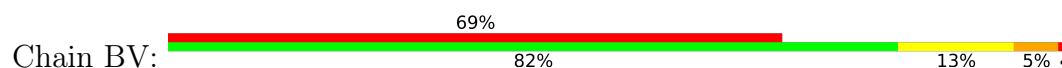
• Molecule 22: ES19



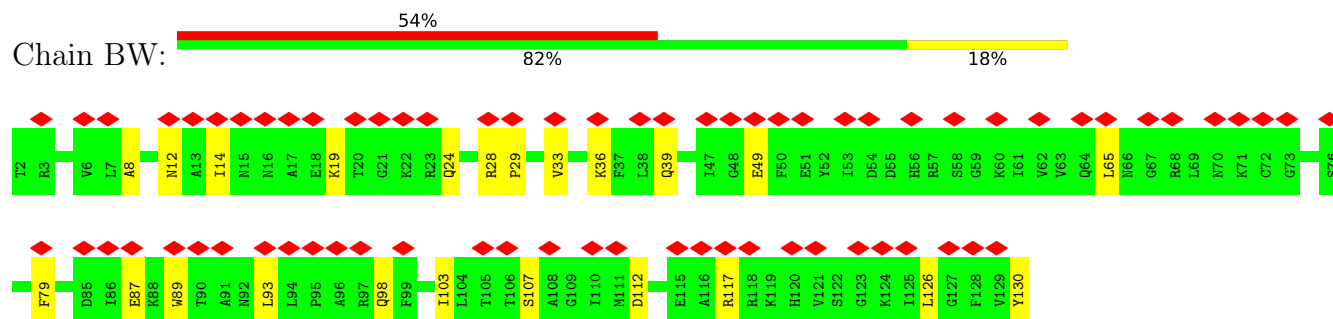
• Molecule 23: US10



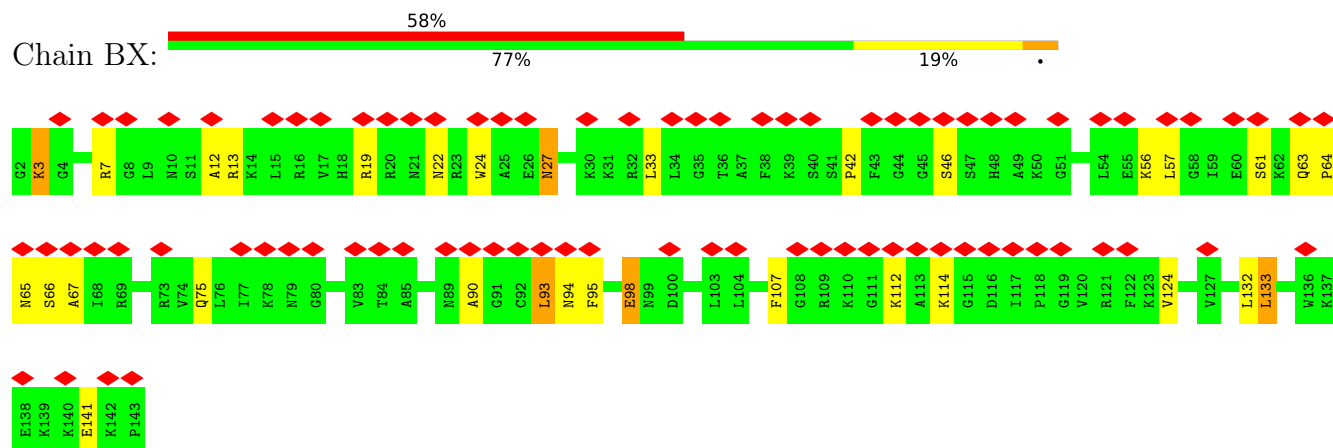
• Molecule 24: ES21



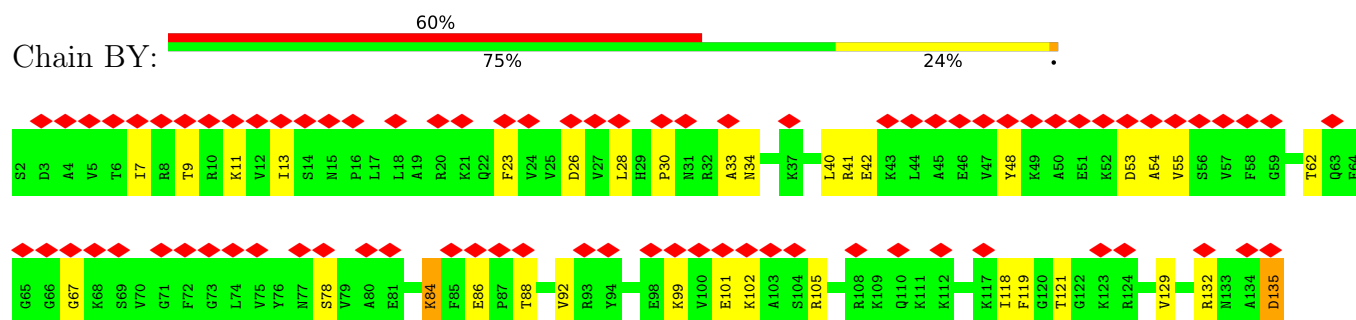
- Molecule 25: US8



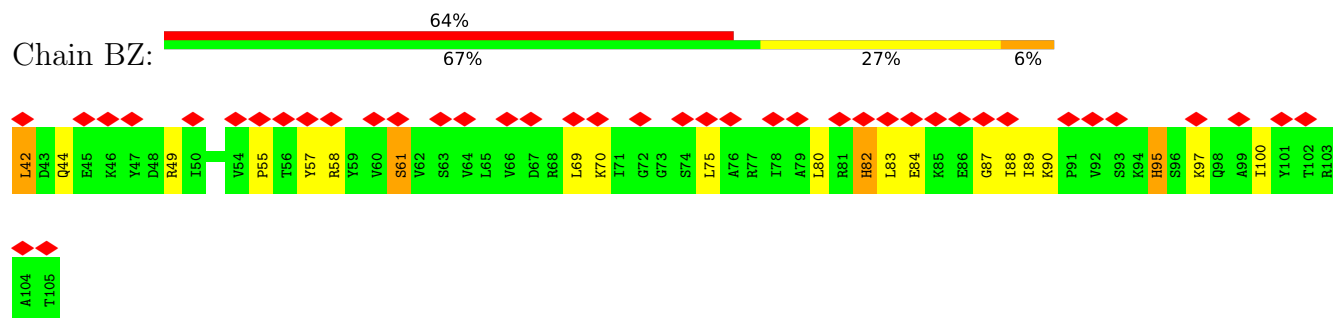
- Molecule 26: US12



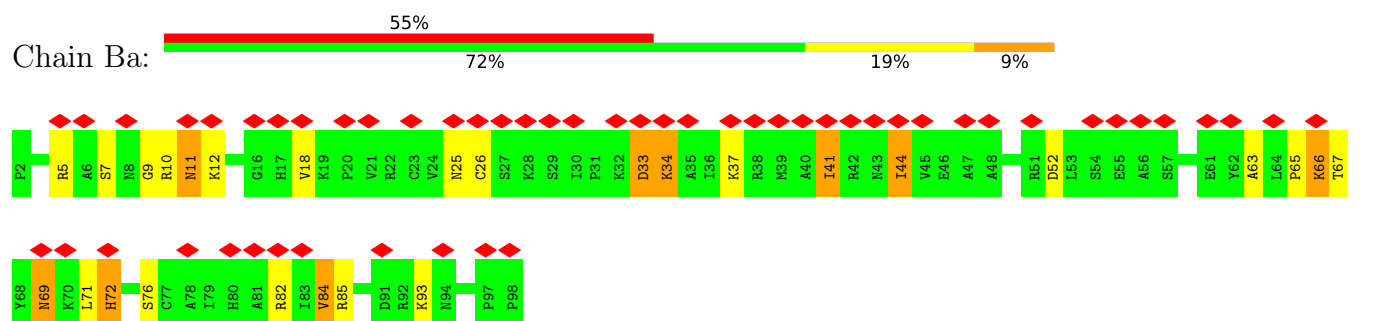
- Molecule 27: ES24



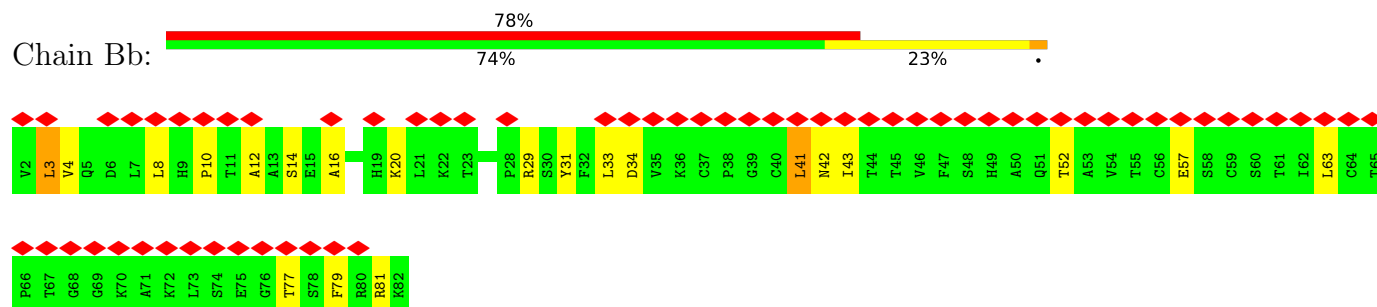
- Molecule 28: ES25



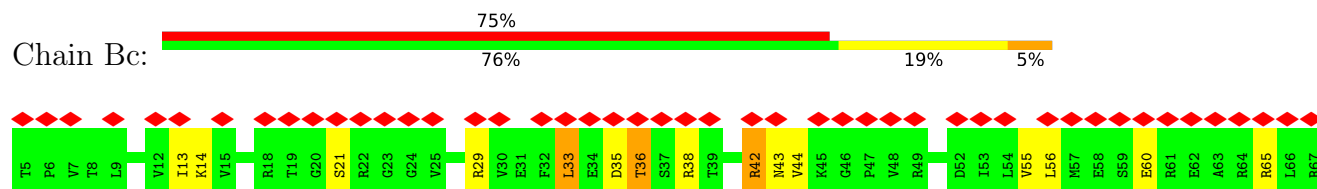
- Molecule 29: ES26



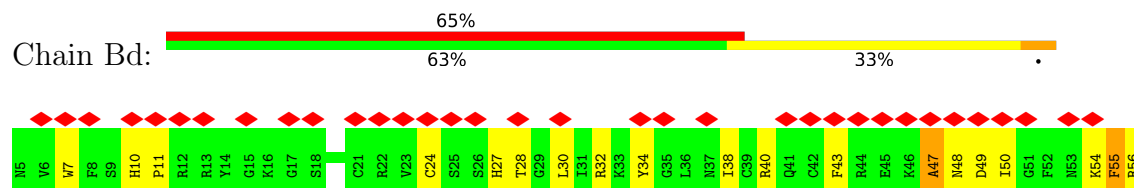
- Molecule 30: ES27



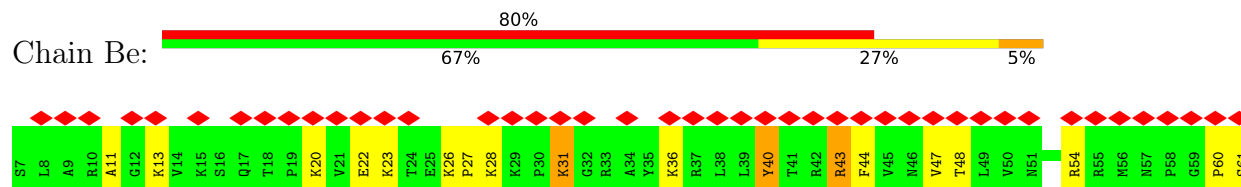
- Molecule 31: ES28



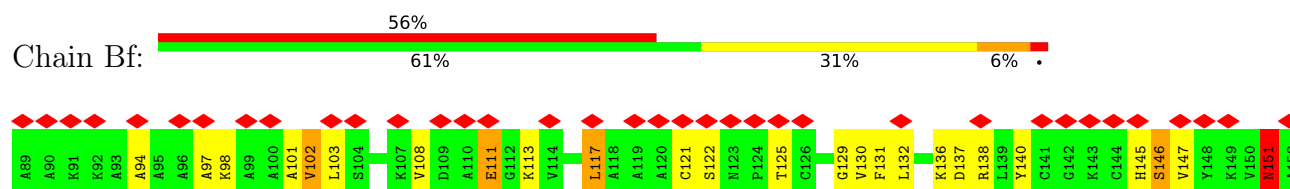
- Molecule 32: US14



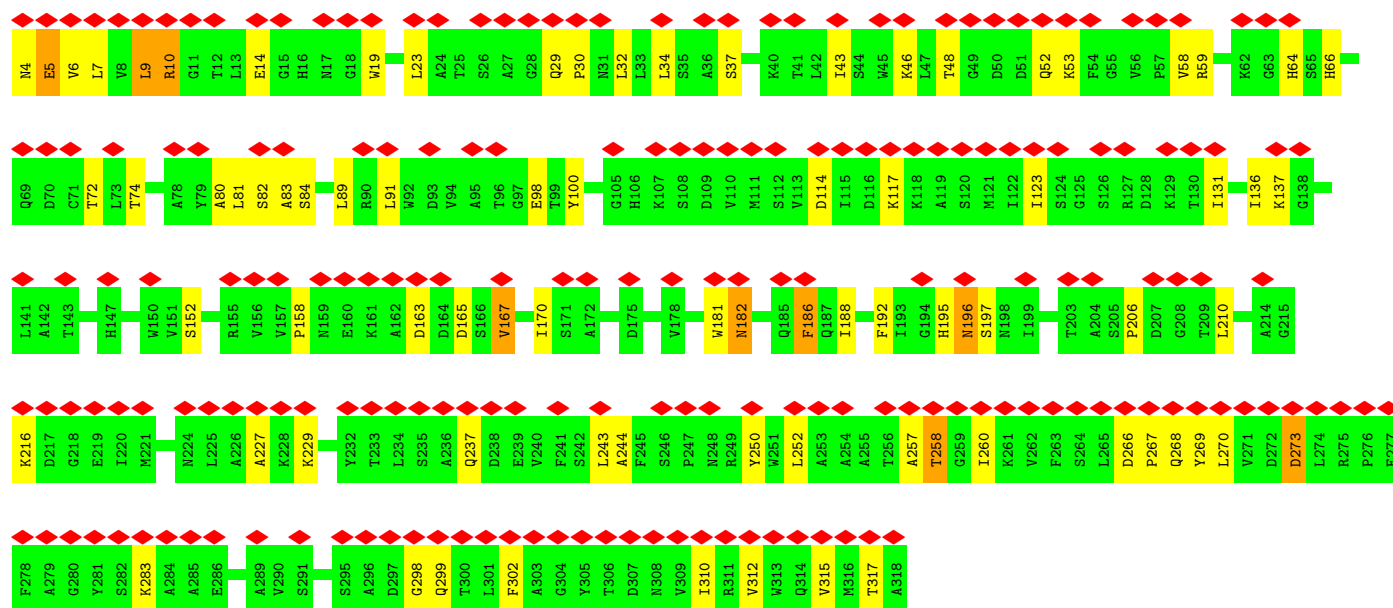
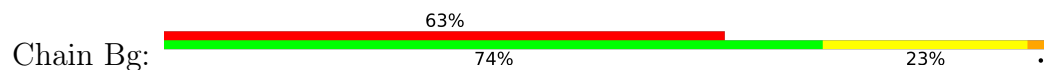
- Molecule 33: ES30



- Molecule 34: ES31



● Molecule 35: RACK1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	18132	Depositor
Resolution determination method	Not provided	
CTF correction method	EACH PARTICLE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1.8	Depositor
Maximum defocus (nm)	3	Depositor
Magnification	47000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.990	Depositor
Minimum map value	-0.618	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.07	Depositor
Map size (\AA)	428.80002, 428.80002, 428.80002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.34, 1.34, 1.34	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	A2	1.00	25/41655 (0.1%)	1.31	1105/63991 (1.7%)
2	AZ	0.91	5/4449 (0.1%)	1.28	113/6827 (1.7%)
3	BA	0.95	2/1574 (0.1%)	1.25	26/2086 (1.2%)
4	BB	0.50	0/1661	1.06	16/2154 (0.7%)
5	BC	0.40	0/1610	0.99	14/2113 (0.7%)
6	BD	0.46	0/1692	1.06	19/2175 (0.9%)
7	BE	0.42	1/2045 (0.0%)	0.99	23/2647 (0.9%)
8	BF	0.53	0/1571	1.00	14/2039 (0.7%)
9	BG	0.49	1/1767 (0.1%)	1.06	13/2288 (0.6%)
10	BH	0.43	0/1455	1.04	17/1875 (0.9%)
11	BI	0.53	0/1448	1.18	19/1839 (1.0%)
12	BJ	0.40	0/1435	0.99	18/1854 (1.0%)
13	BK	0.56	0/759	1.07	8/988 (0.8%)
14	BL	0.52	1/1140 (0.1%)	1.12	15/1484 (1.0%)
15	BM	0.70	0/845	1.03	8/1093 (0.7%)
16	BN	0.45	0/1186	1.04	12/1551 (0.8%)
17	BO	0.39	0/893	0.96	9/1167 (0.8%)
18	BP	0.66	1/903 (0.1%)	1.09	8/1162 (0.7%)
19	BQ	0.63	1/1072 (0.1%)	1.15	13/1392 (0.9%)
20	BR	0.44	0/908	1.02	10/1159 (0.9%)
21	BS	0.69	0/1140	1.18	11/1487 (0.7%)
22	BT	0.92	3/1083 (0.3%)	1.16	15/1389 (1.1%)
23	BU	0.57	0/812	1.06	9/1053 (0.9%)
24	BV	0.47	0/675	0.89	4/881 (0.5%)
25	BW	0.42	0/999	0.91	4/1278 (0.3%)
26	BX	0.38	0/1079	0.97	11/1372 (0.8%)
27	BY	0.50	0/1056	1.15	14/1356 (1.0%)
28	BZ	0.73	0/511	1.11	5/663 (0.8%)
29	Ba	0.43	0/758	1.06	7/975 (0.7%)
30	Bb	0.41	0/596	1.05	6/766 (0.8%)
31	Bc	0.42	0/485	1.03	5/628 (0.8%)
32	Bd	0.51	0/427	1.04	5/540 (0.9%)
33	Be	0.47	0/436	1.16	6/562 (1.1%)
34	Bf	0.71	0/456	1.07	5/599 (0.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Bg	0.55	0/2390	1.01	23/3123 (0.7%)
All	All	0.83	40/82971 (0.0%)	1.21	1610/118556 (1.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A2	98	0
2	AZ	8	0
3	BA	8	3
4	BB	11	2
5	BC	8	1
6	BD	6	1
7	BE	8	0
8	BF	6	1
9	BG	10	3
10	BH	7	2
11	BI	12	2
12	BJ	5	1
13	BK	2	0
14	BL	8	0
15	BM	2	0
16	BN	6	0
17	BO	4	1
18	BP	4	0
19	BQ	8	2
20	BR	5	0
21	BS	6	4
22	BT	6	0
23	BU	1	1
24	BV	2	1
25	BW	3	0
26	BX	5	2
27	BY	6	0
28	BZ	1	0
29	Ba	4	1
30	Bb	5	0
31	Bc	2	0
32	Bd	3	1
33	Be	3	0

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Mol	Chain	#Chirality outliers	#Planarity outliers
34	Bf	2	1
35	Bg	9	1
All	All	284	31

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A2	897	C	O3'-P	48.97	2.19	1.61
1	A2	633	U	O3'-P	48.70	2.19	1.61
1	A2	1797	A	O3'-P	47.72	2.18	1.61
1	A2	1388	A	O3'-P	46.19	2.16	1.61
1	A2	388	G	O3'-P	45.98	2.16	1.61

The worst 5 of 1610 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	104	A	P-O3'-C3'	41.97	170.06	119.70
1	A2	56	U	P-O3'-C3'	36.36	163.33	119.70
1	A2	1797	A	O3'-P-O5'	29.86	160.74	104.00
1	A2	862	A	P-O3'-C3'	26.83	151.90	119.70
1	A2	960	U	P-O3'-C3'	-25.06	89.62	119.70

5 of 284 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A2	7	G	C3'
1	A2	41	A	C3'
1	A2	67	A	C3'
1	A2	102	U	C3'
1	A2	124	A	C2'

5 of 31 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	BA	138	TYR	Peptide
3	BA	35	PRO	Peptide
3	BA	62	ARG	Peptide
4	BB	177	GLN	Peptide
4	BB	178	GLY	Peptide

5.2 Too-close contacts

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

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	
3	BA	129/206 (63%)	60 (46%)	39 (30%)	30 (23%)	0	0
4	BB	118/213 (55%)	88 (75%)	17 (14%)	13 (11%)	0	5
5	BC	136/216 (63%)	84 (62%)	31 (23%)	21 (15%)	0	3
6	BD	116/222 (52%)	83 (72%)	17 (15%)	16 (14%)	0	3
7	BE	143/260 (55%)	100 (70%)	26 (18%)	17 (12%)	0	4
8	BF	116/206 (56%)	81 (70%)	20 (17%)	15 (13%)	0	4
9	BG	141/226 (62%)	88 (62%)	32 (23%)	21 (15%)	0	3
10	BH	100/184 (54%)	61 (61%)	22 (22%)	17 (17%)	0	2
11	BI	87/187 (46%)	51 (59%)	22 (25%)	14 (16%)	0	2
12	BJ	101/179 (56%)	58 (57%)	27 (27%)	16 (16%)	0	2
13	BK	48/93 (52%)	29 (60%)	9 (19%)	10 (21%)	0	1
14	BL	85/142 (60%)	53 (62%)	25 (29%)	7 (8%)	1	9
15	BM	63/120 (52%)	36 (57%)	20 (32%)	7 (11%)	0	5
16	BN	97/150 (65%)	62 (64%)	22 (23%)	13 (13%)	0	3
17	BO	84/127 (66%)	58 (69%)	16 (19%)	10 (12%)	0	4
18	BP	60/115 (52%)	40 (67%)	14 (23%)	6 (10%)	0	7
19	BQ	85/140 (61%)	56 (66%)	19 (22%)	10 (12%)	0	4
20	BR	59/121 (49%)	45 (76%)	9 (15%)	5 (8%)	0	9
21	BS	89/140 (64%)	61 (68%)	13 (15%)	15 (17%)	0	2
22	BT	72/142 (51%)	47 (65%)	14 (19%)	11 (15%)	0	3
23	BU	57/104 (55%)	38 (67%)	12 (21%)	7 (12%)	0	4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	BV	53/87 (61%)	38 (72%)	10 (19%)	5 (9%)	0	8
25	BW	58/129 (45%)	41 (71%)	11 (19%)	6 (10%)	0	6
26	BX	70/142 (49%)	49 (70%)	12 (17%)	9 (13%)	0	4
27	BY	77/134 (58%)	55 (71%)	15 (20%)	7 (9%)	0	8
28	BZ	37/64 (58%)	22 (60%)	9 (24%)	6 (16%)	0	2
29	Ba	51/97 (53%)	29 (57%)	12 (24%)	10 (20%)	0	1
30	Bb	38/81 (47%)	24 (63%)	11 (29%)	3 (8%)	1	10
31	Bc	38/63 (60%)	29 (76%)	7 (18%)	2 (5%)	1	18
32	Bd	25/52 (48%)	15 (60%)	8 (32%)	2 (8%)	1	10
33	Be	33/55 (60%)	16 (48%)	12 (36%)	5 (15%)	0	3
34	Bf	45/64 (70%)	18 (40%)	14 (31%)	13 (29%)	0	0
35	Bg	170/315 (54%)	115 (68%)	38 (22%)	17 (10%)	0	7
All	All	2681/4776 (56%)	1730 (64%)	585 (22%)	366 (14%)	0	3

5 of 366 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	BA	27	ARG
3	BA	43	ASP
3	BA	50	VAL
3	BA	121	VAL
3	BA	122	ILE

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	
3	BA	164/173 (95%)	117 (71%)	47 (29%)	0	2
4	BB	187/187 (100%)	142 (76%)	45 (24%)	0	4
5	BC	175/175 (100%)	156 (89%)	19 (11%)	5	24
6	BD	182/182 (100%)	148 (81%)	34 (19%)	1	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	BE	221/221 (100%)	178 (80%)	43 (20%)	1	7
8	BF	172/172 (100%)	131 (76%)	41 (24%)	0	4
9	BG	185/191 (97%)	138 (75%)	47 (25%)	0	4
10	BH	165/165 (100%)	138 (84%)	27 (16%)	2	12
11	BI	149/149 (100%)	105 (70%)	44 (30%)	0	2
12	BJ	154/154 (100%)	126 (82%)	28 (18%)	1	9
13	BK	80/84 (95%)	62 (78%)	18 (22%)	1	5
14	BL	127/127 (100%)	100 (79%)	27 (21%)	1	6
15	BM	88/97 (91%)	67 (76%)	21 (24%)	0	4
16	BN	127/127 (100%)	104 (82%)	23 (18%)	1	9
17	BO	84/96 (88%)	62 (74%)	22 (26%)	0	3
18	BP	97/97 (100%)	81 (84%)	16 (16%)	2	12
19	BQ	114/114 (100%)	80 (70%)	34 (30%)	0	2
20	BR	94/109 (86%)	71 (76%)	23 (24%)	0	4
21	BS	125/125 (100%)	96 (77%)	29 (23%)	0	5
22	BT	114/114 (100%)	94 (82%)	20 (18%)	1	10
23	BU	97/97 (100%)	77 (79%)	20 (21%)	1	6
24	BV	74/74 (100%)	62 (84%)	12 (16%)	2	12
25	BW	110/110 (100%)	97 (88%)	13 (12%)	4	21
26	BX	116/116 (100%)	101 (87%)	15 (13%)	3	19
27	BY	112/112 (100%)	94 (84%)	18 (16%)	2	13
28	BZ	57/57 (100%)	42 (74%)	15 (26%)	0	3
29	Ba	83/83 (100%)	65 (78%)	18 (22%)	1	6
30	Bb	70/70 (100%)	56 (80%)	14 (20%)	1	7
31	Bc	56/56 (100%)	44 (79%)	12 (21%)	1	6
32	Bd	46/46 (100%)	33 (72%)	13 (28%)	0	2
33	Be	48/48 (100%)	38 (79%)	10 (21%)	1	6
34	Bf	43/43 (100%)	31 (72%)	12 (28%)	0	2
35	Bg	257/259 (99%)	208 (81%)	49 (19%)	1	8
All	All	3973/4030 (99%)	3144 (79%)	829 (21%)	2	6

5 of 829 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	BN	150	VAL
21	BS	81	ILE
35	Bg	89	LEU
17	BO	86	THR
16	BN	140	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 96 such sidechains are listed below:

Mol	Chain	Res	Type
20	BR	31	ASN
24	BV	75	ASN
20	BR	83	GLN
22	BT	70	GLN
25	BW	56	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A2	1459/1767 (82%)	899 (61%)	316 (21%)
2	AZ	160/190 (84%)	128 (80%)	43 (26%)
All	All	1619/1957 (82%)	1027 (63%)	359 (22%)

5 of 1027 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A2	2	A
1	A2	3	U
1	A2	4	C
1	A2	6	G
1	A2	7	G

5 of 359 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A2	1340	U
1	A2	1647	U
1	A2	1399	C
1	A2	1491	U
1	A2	1743	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A2	393
35	Bg	80
7	BE	64
6	BD	62
11	BI	58
8	BF	52
10	BH	51
4	BB	51
9	BG	47
5	BC	46
3	BA	43
12	BJ	42
2	AZ	40
26	BX	40
22	BT	39
25	BW	39
20	BR	36
15	BM	33
14	BL	32
18	BP	31

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Mol	Chain	Number of breaks
27	BY	31
19	BQ	30
21	BS	29
16	BN	29
23	BU	27
13	BK	25
30	Bb	24
29	Ba	24
17	BO	23
24	BV	18
32	Bd	16
28	BZ	14
31	Bc	14
33	Be	11
34	Bf	9

The worst 5 of 1603 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	1693:A	O3'	1708:U	P	22.38
1	A2	658:C	O3'	676:G	P	18.27
1	BI	123:LYS	C	135:LYS	N	16.74
1	BA	190:ASP	C	191:ARG	N	10.15
1	BR	124:VAL	C	125:SER	N	8.71

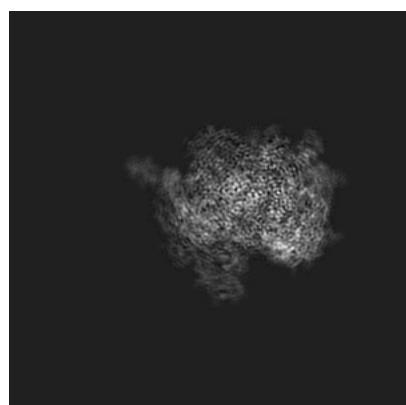
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2604. These allow visual inspection of the internal detail of the map and identification of artifacts.

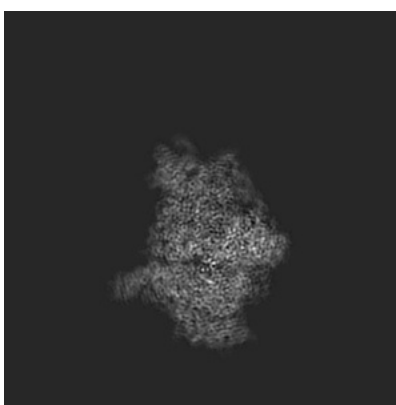
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

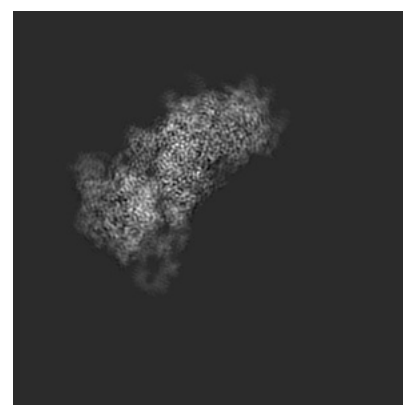
6.1.1 Primary map



X



Y

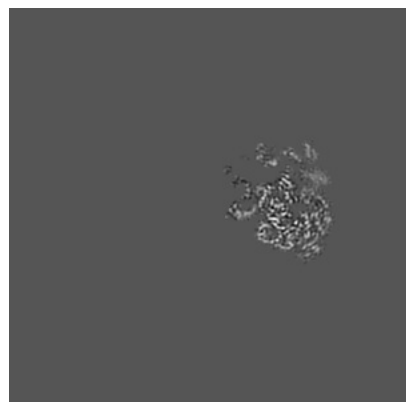


Z

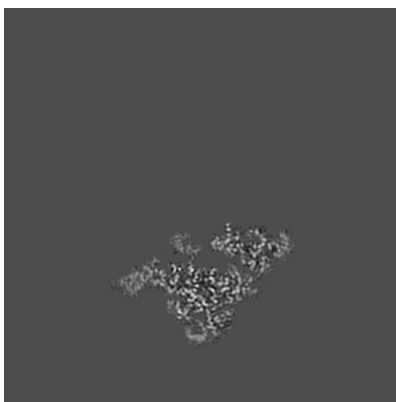
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

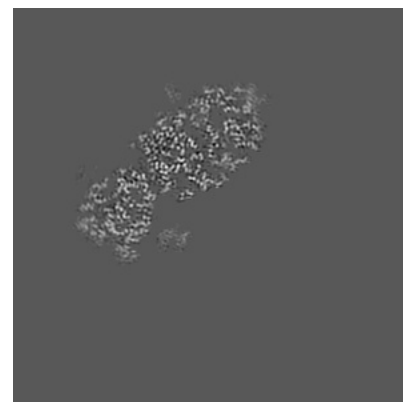
6.2.1 Primary map



X Index: 160



Y Index: 160

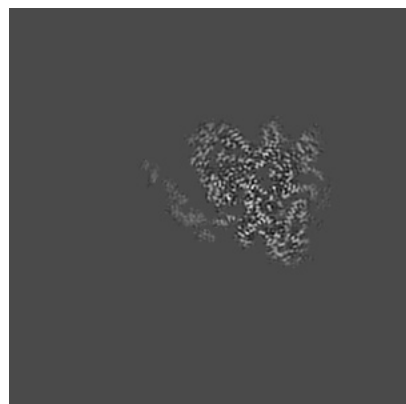


Z Index: 160

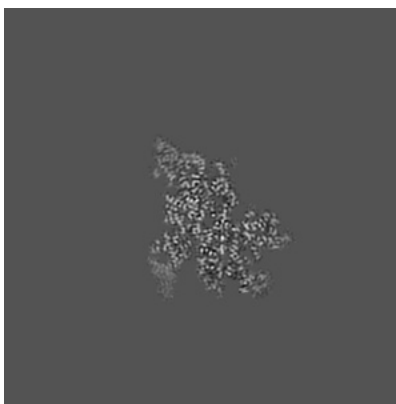
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

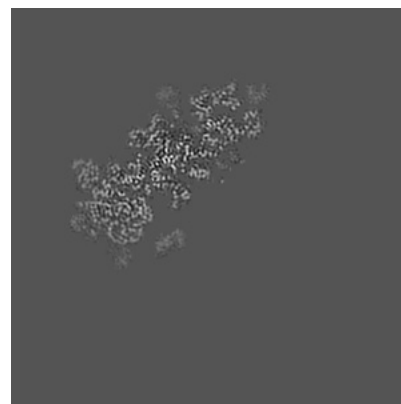
6.3.1 Primary map



X Index: 132



Y Index: 215

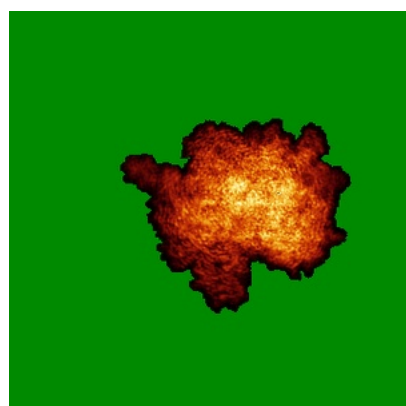


Z Index: 166

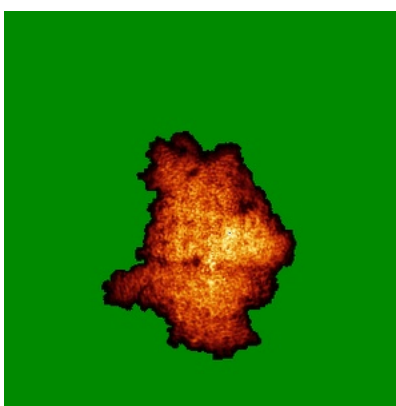
The images above show the largest variance slices of the map in three orthogonal directions.

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

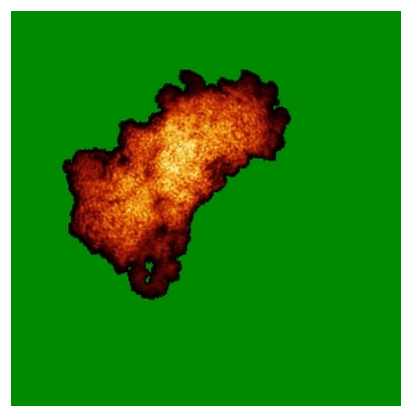
6.4.1 Primary map



X



Y

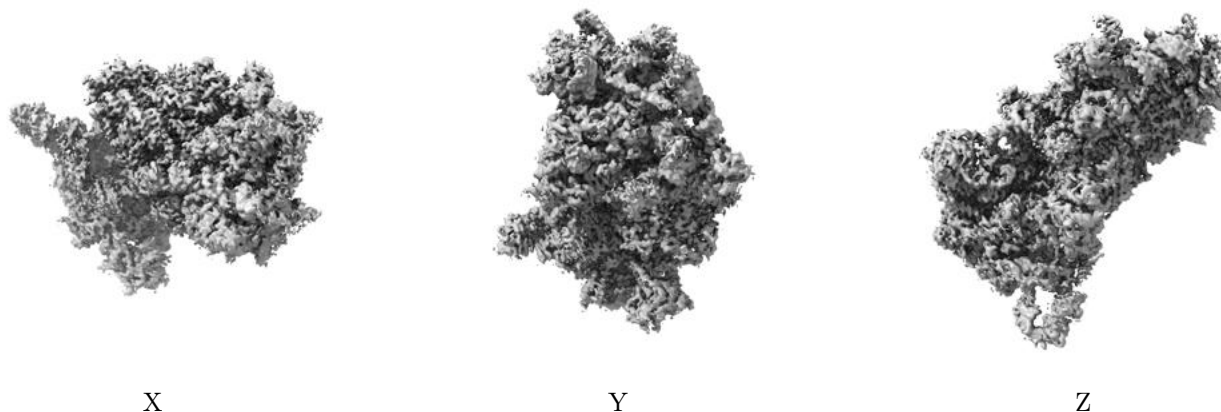


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

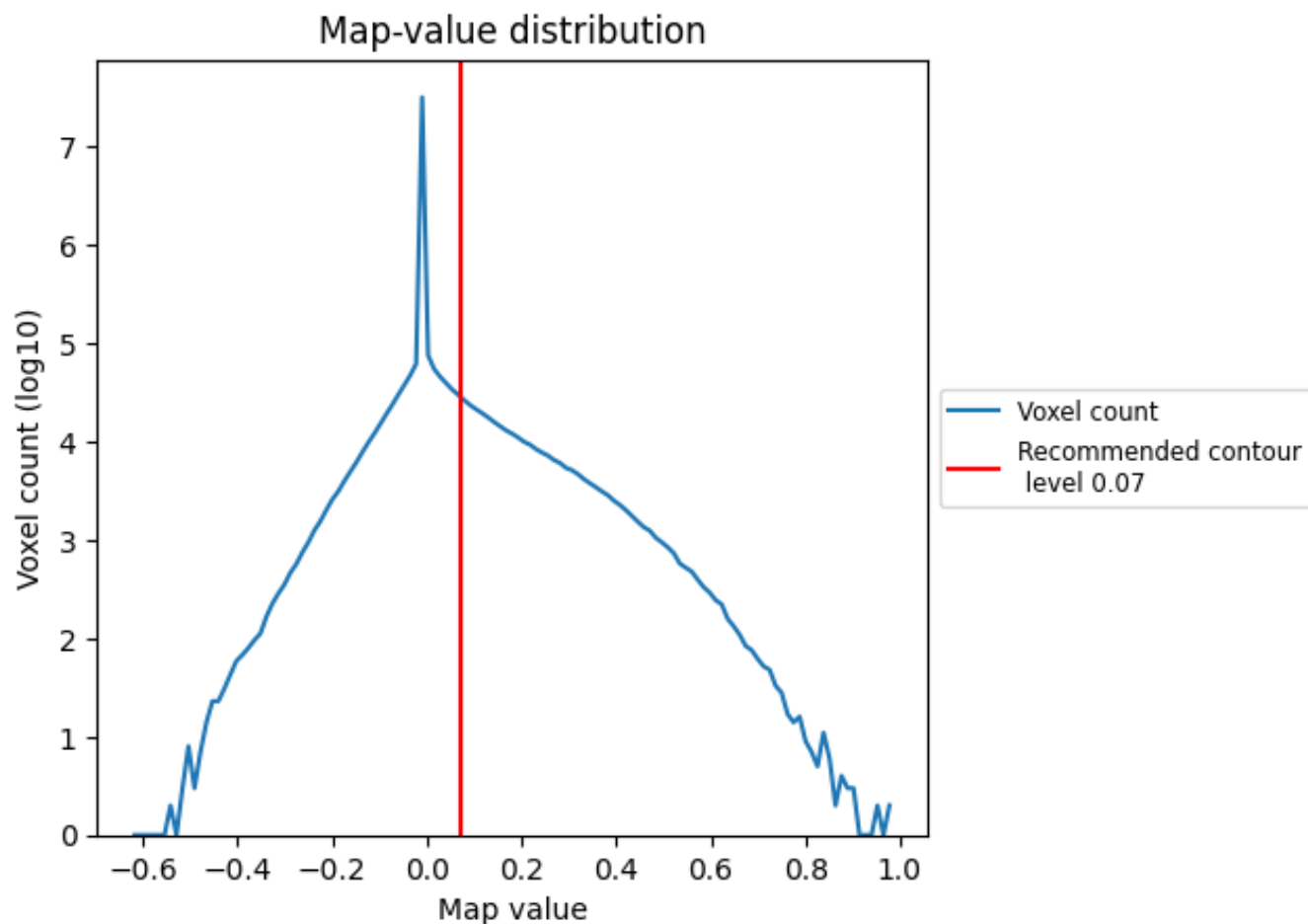
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

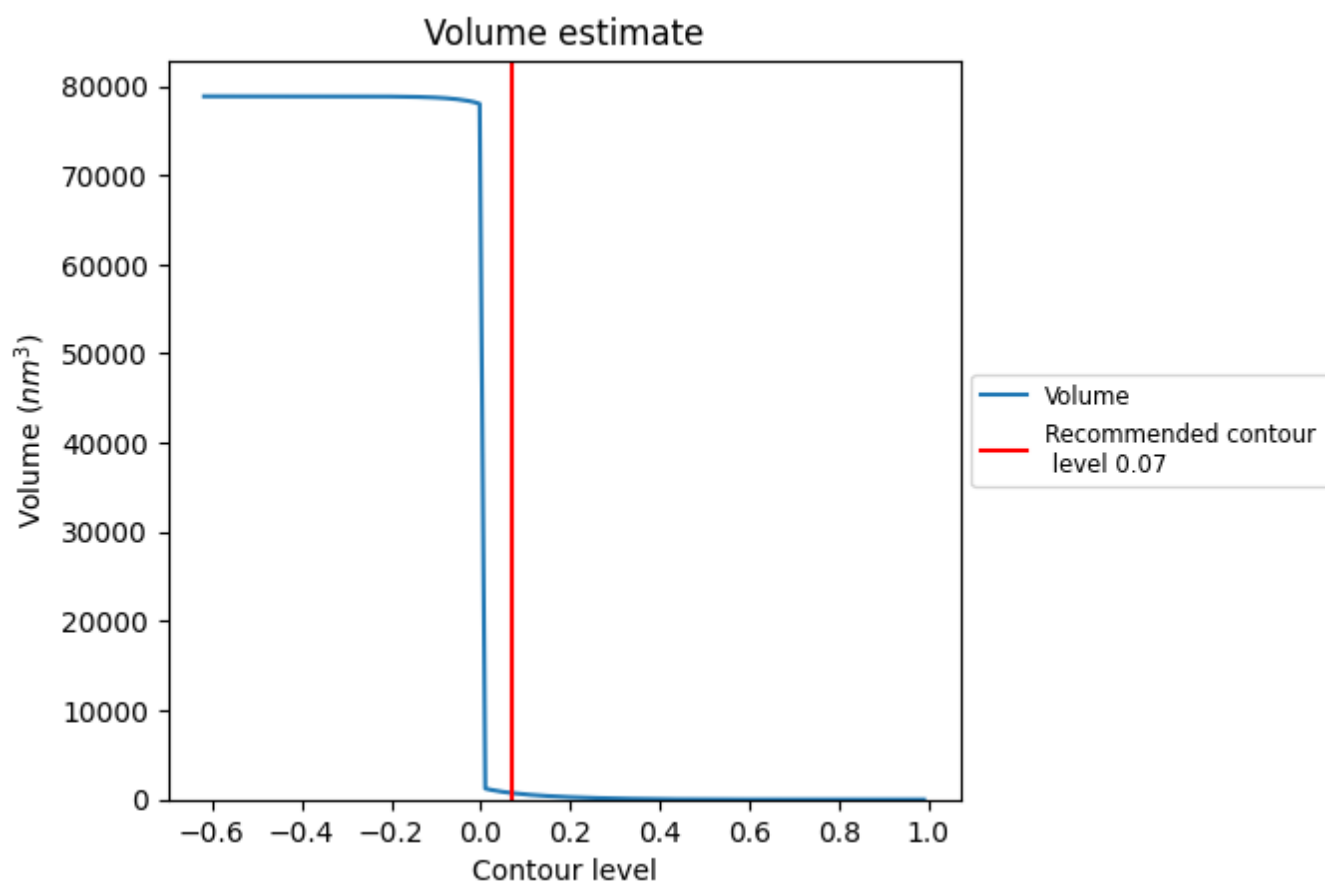
This section contains the results of statistical analysis of the map.

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.

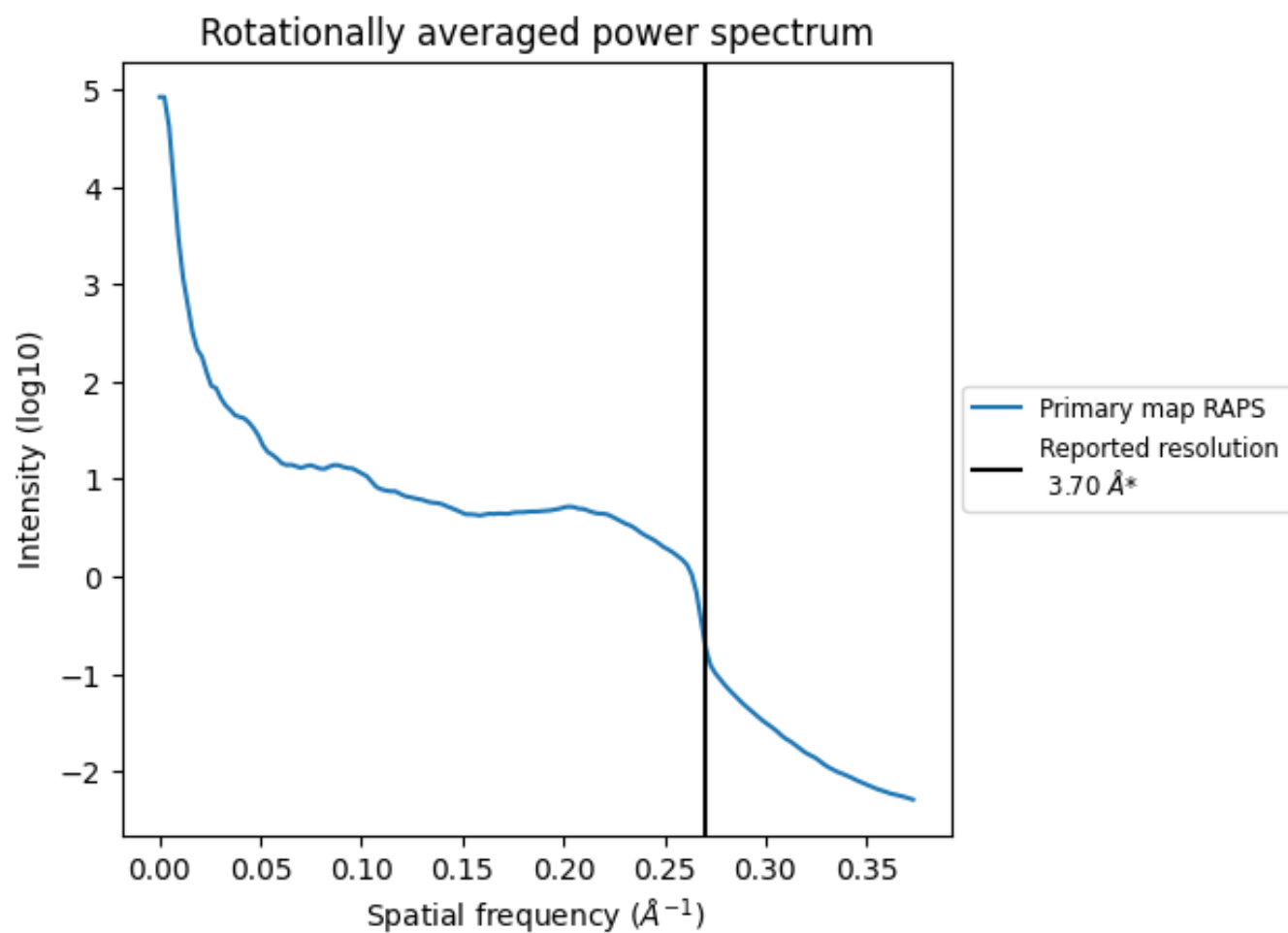
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 732 nm³; this corresponds to an approximate mass of 661 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 0.270 Å⁻¹

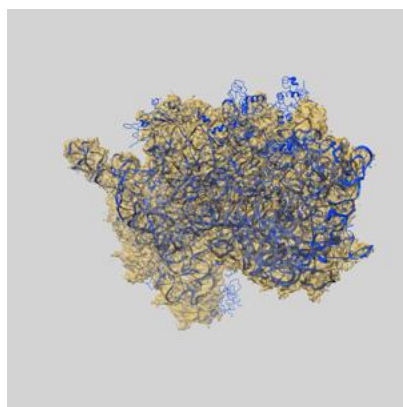
8 Fourier-Shell correlation ⓘ

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

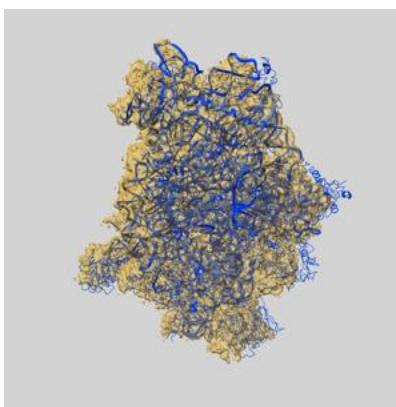
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2604 and PDB model 4V92. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

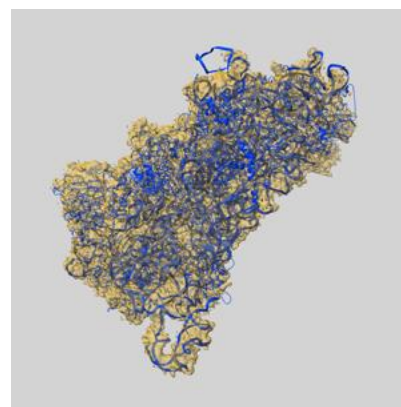
9.1 Map-model overlay [i](#)



X



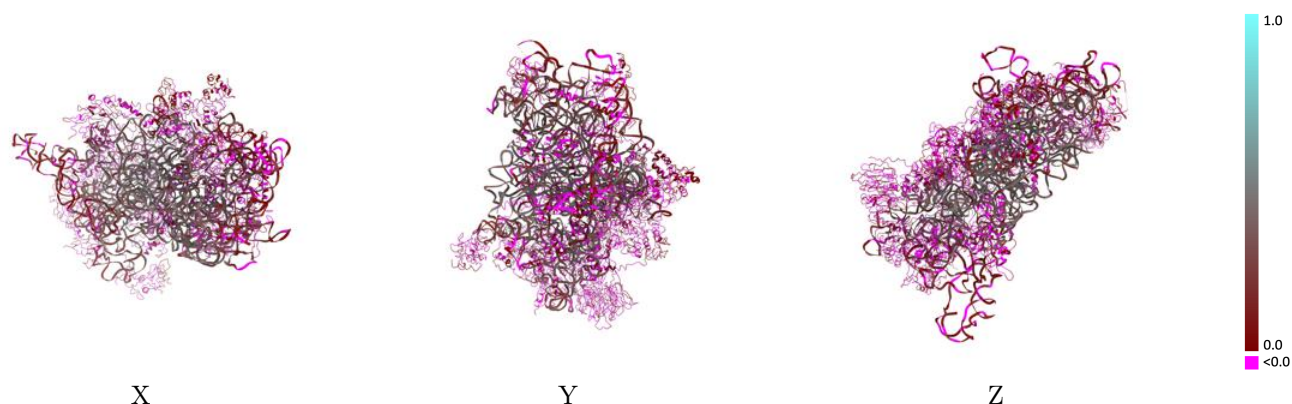
Y



Z

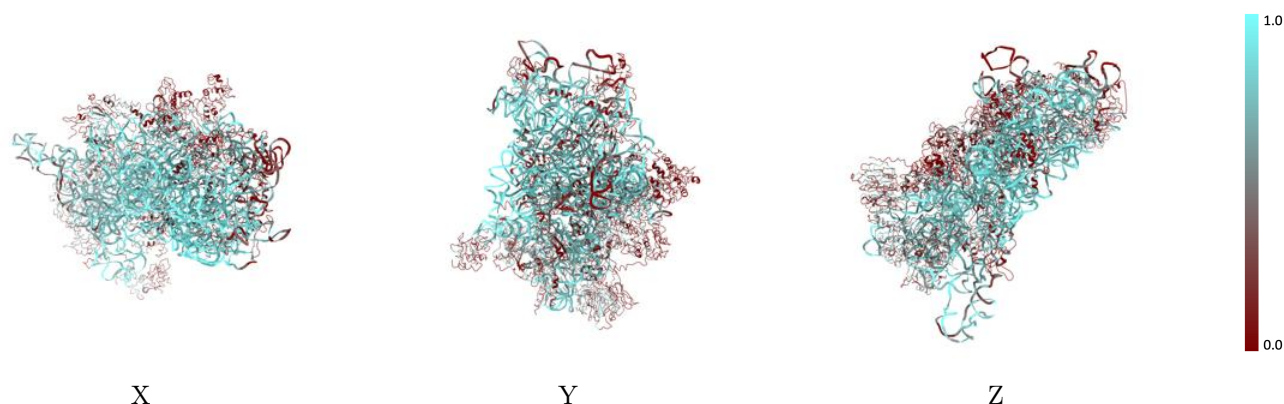
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



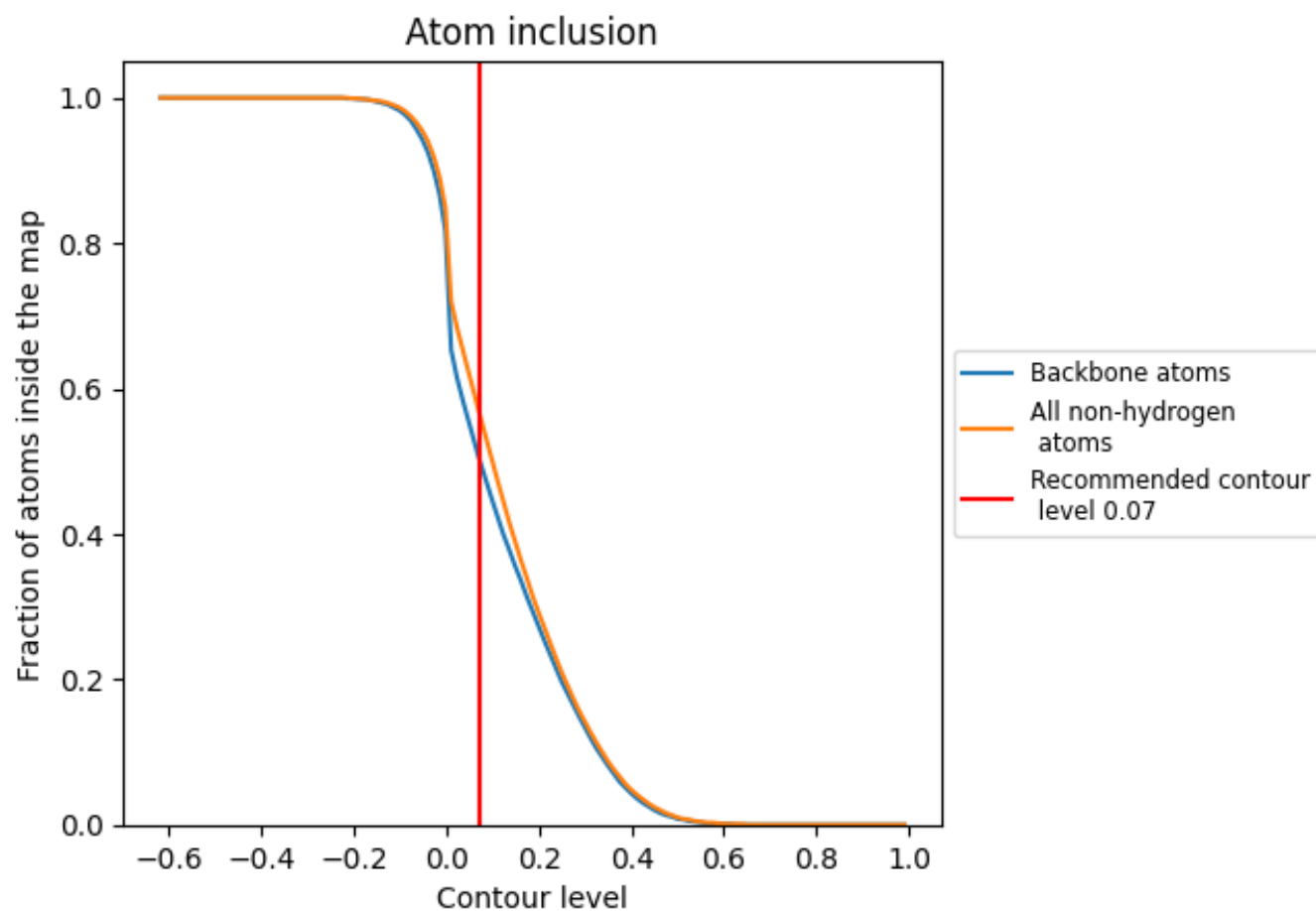
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.07).









































































9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 57% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5690	 0.1590
A2	 0.8410	 0.3170
AZ	 0.6810	 0.1240
BA	 0.1470	 -0.0090
BB	 0.3000	 0.0170
BC	 0.2880	 0.0070
BD	 0.2120	 -0.0100
BE	 0.2780	 0.0090
BF	 0.3500	 -0.0310
BG	 0.2790	 0.0230
BH	 0.1180	 0.0020
BI	 0.2240	 -0.0060
BJ	 0.2530	 0.0090
BK	 0.3050	 -0.0070
BL	 0.1120	 0.0110
BM	 0.1190	 -0.0300
BN	 0.1840	 0.0090
BO	 0.3120	 0.0220
BP	 0.3540	 0.0130
BQ	 0.4810	 0.0470
BR	 0.1720	 -0.0160
BS	 0.3780	 0.0120
BT	 0.4070	 -0.0030
BU	 0.2490	 0.0000
BV	 0.2350	 0.0060
BW	 0.3910	 0.0410
BX	 0.3360	 0.0340
BY	 0.3310	 0.0280
BZ	 0.3330	 -0.0250
Ba	 0.3710	 0.0150
Bb	 0.1850	 0.0230
Bc	 0.2330	 -0.0630
Bd	 0.2990	 -0.0060
Be	 0.1890	 0.0050
Bf	 0.3940	 -0.0050
Bg	 0.3250	 -0.0060

