



wwPDB EM Validation Summary Report ⓘ

Nov 4, 2024 – 05:13 AM JST

PDB ID : 7DVQ
EMDB ID : EMD-30875
Title : Cryo-EM Structure of the Activated Human Minor Spliceosome (minor Bact Complex)
Authors : Bai, R.; Wan, R.; Wang, L.; Xu, K.; Zhang, Q.; Lei, J.; Shi, Y.
Deposited on : 2021-01-14
Resolution : 2.89 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:

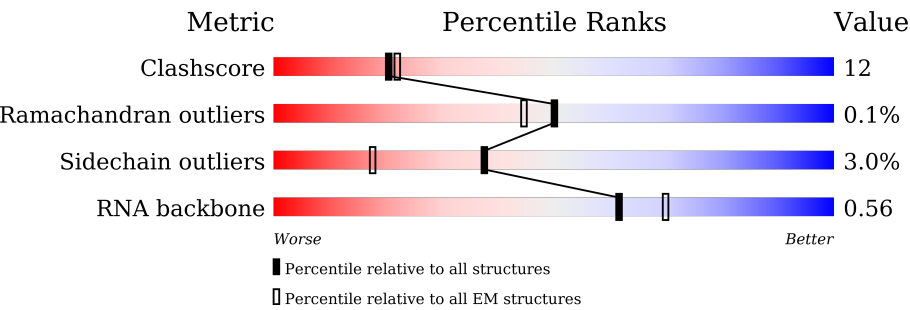
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.89 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	2335	<div><div>11%</div><div>79%</div><div>15%</div><div>• 5%</div></div>
2	B	117	<div><div>24%</div><div>40%</div><div>31%</div><div>6%</div><div>23%</div></div>
3	C	972	<div><div>•</div><div>75%</div><div>17%</div><div>• 7%</div></div>
4	D	2136	<div><div>55%</div><div>78%</div><div>6%</div><div>• 16%</div></div>
5	E	357	<div><div>83%</div><div>53%</div><div>29%</div><div>• 16%</div></div>
6	a	126	<div><div>62%</div><div>64%</div><div>36%</div></div>
6	h	126	<div><div>63%</div><div>63%</div><div>37%</div></div>



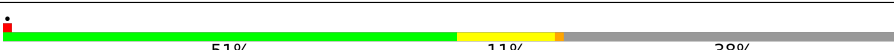


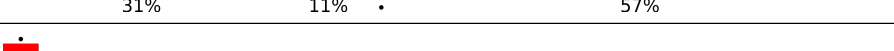
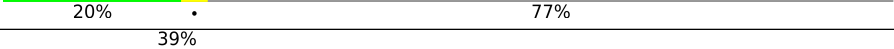



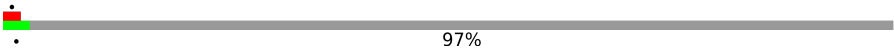
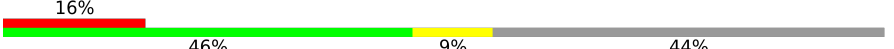
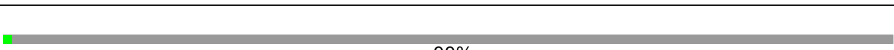

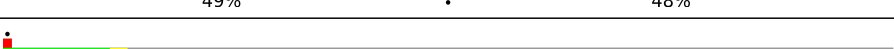
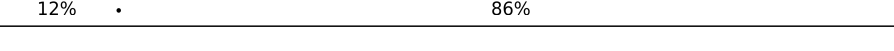

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Mol	Chain	Length	Quality of chain
7	b	240	
7	i	240	
8	c	119	
8	j	119	
9	d	118	
9	k	118	
10	f	86	
10	m	86	
11	e	92	
11	l	92	
12	g	76	
12	n	76	
13	F	124	
14	G	142	
15	H	150	
16	v	230	
17	1	1304	
18	2	895	
19	3	1217	
20	4	424	
21	5	125	
22	6	110	
23	7	86	
24	L	802	
25	J	848	

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Mol	Chain	Length	Quality of chain
26	P	229	
27	R	536	
28	T	514	
29	X	396	
30	Y	322	
31	Z	619	
32	9	520	
33	z	472	
34	x	1041	
35	y	476	
36	M	343	
37	U	2752	
38	V	908	
39	8	904	
40	0	101	
41	I	367	
42	K	198	

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 99906 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 Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2223	Total	C	N	O	S	0	0
			18354	11832	3206	3236	80		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	90	Total	C	N	O	P	0	0
			1898	850	320	638	90		

- Molecule 3 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	902	Total	C	N	O	S	0	0
			7125	4560	1185	1345	35		

- Molecule 4 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	1803	Total	C	N	O	S	0	0
			9215	5522	1841	1851	1		

- Molecule 5 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	299	Total	C	N	O	S	0	0
			2337	1470	409	445	13		

- Molecule 6 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	a	81	Total	C	N	O	0	0
			399	237	81	81		

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Mol	Chain	Residues	Atoms				AltConf	Trace
6	h	80	Total	C	N	O	0	0
			392	233	79	80		

- Molecule 7 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	b	82	Total	C	N	O	0	0
			405	241	82	82		
7	i	86	Total	C	N	O	0	0
			422	250	86	86		

- Molecule 8 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	c	82	Total	C	N	O	0	0
			406	242	82	82		
8	j	82	Total	C	N	O	0	0
			406	242	82	82		

- Molecule 9 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	d	97	Total	C	N	O	0	0
			480	286	97	97		
9	k	85	Total	C	N	O	0	0
			422	252	85	85		

- Molecule 10 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	f	74	Total	C	N	O	0	0
			361	213	74	74		
10	m	74	Total	C	N	O	0	0
			361	213	74	74		

- Molecule 11 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	e	79	Total	C	N	O	0	0
			391	233	79	79		
11	l	79	Total	C	N	O	0	0
			391	233	79	79		

- Molecule 12 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	g	74	Total	C	N	O	0	0
			363	215	74	74		
12	n	68	Total	C	N	O	0	0
			334	198	68	68		

- Molecule 13 is a RNA chain called U6atac snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	60	Total	C	N	O	P	0	0
			1294	577	242	415	60		

- Molecule 14 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	63	Total	C	N	O	P	0	0
			1303	585	197	458	63		

- Molecule 15 is a RNA chain called U12 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	63	Total	C	N	O	P	0	0
			1350	604	247	436	63		

- Molecule 16 is a protein called Sodium channel modifier 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	v	119	Total	C	N	O	S	0	0
			963	601	179	178	5		

- Molecule 17 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	1	986	Total	C	N	O	P	S	0	0
			7879	5035	1361	1435	1	47		

- Molecule 18 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	2	216	Total	C	N	O	S	0	0
			1674	1067	296	305	6		

- Molecule 19 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	3	1193	Total	C	N	O	P	S	
			9352	5932	1590	1784	1	45	
								0	0

- Molecule 20 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	4	78	Total	C	N	O		
			383	227	78	78	0	0

- Molecule 21 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	5	109	Total	C	N	O	S		
			906	582	157	163	4	0	0

- Molecule 22 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	6	105	Total	C	N	O	S		
			811	502	145	151	13	0	0

- Molecule 23 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	7	81	Total	C	N	O	S		
			669	422	117	124	6	0	0

- Molecule 24 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L	101	Total	C	N	O	S		
			843	540	152	147	4	0	0

- Molecule 25 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	J	522	Total	C	N	O	S		
			3457	2153	654	645	5	0	0

- Molecule 26 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	P	44	Total	C	N	O	S	0	0
			384	243	71	68	2		

- Molecule 27 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	R	241	Total	C	N	O	S	0	0
			1923	1191	347	374	11		

- Molecule 28 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	320	Total	C	N	O	S	0	0
			2507	1582	456	462	7		

- Molecule 29 is a protein called Smad nuclear-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	156	Total	C	N	O	S	0	0
			1271	815	227	227	2		

- Molecule 30 is a protein called RNA-binding motif protein, X-linked 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	140	Total	C	N	O	S	0	0
			1095	692	192	206	5		

- Molecule 31 is a protein called BUD13 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	140	Total	C	N	O	S	0	0
			1129	703	214	207	5		

- Molecule 32 is a protein called RING-type E3 ubiquitin-protein ligase PPIL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	9	409	Total	C	N	O	S	0	0
			2691	1672	487	525	7		

- Molecule 33 is a protein called Peptidyl-prolyl cis-trans isomerase CWC27 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	z	177	Total	C	N	O	S	0	0
			1400	883	245	267	5		

- Molecule 34 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	x	599	Total	C	N	O	S	0	0
			3007	1794	607	605	1		

- Molecule 35 is a protein called G-patch domain and KOW motifs-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	y	13	Total	C	N	O	0	0
			105	66	22	17		

- Molecule 36 is a protein called RING finger protein 113A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	M	191	Total	C	N	O	S	0	0
			1572	983	282	295	12		

- Molecule 37 is a protein called Serine/arginine repetitive matrix protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	U	26	Total	C	N	O	S	0	0
			193	120	36	36	1		

- Molecule 38 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	V	468	Total	C	N	O	S	0	0
			3008	1873	548	574	13		

- Molecule 39 is a protein called Serine/arginine repetitive matrix protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	8	126	Total	C	N	O	S	0	0
			1011	652	168	185	6		

- Molecule 40 is a protein called Cysteine-rich PDZ-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	0	100	Total	C	N	O	S	0	0
			770	475	142	144	9		

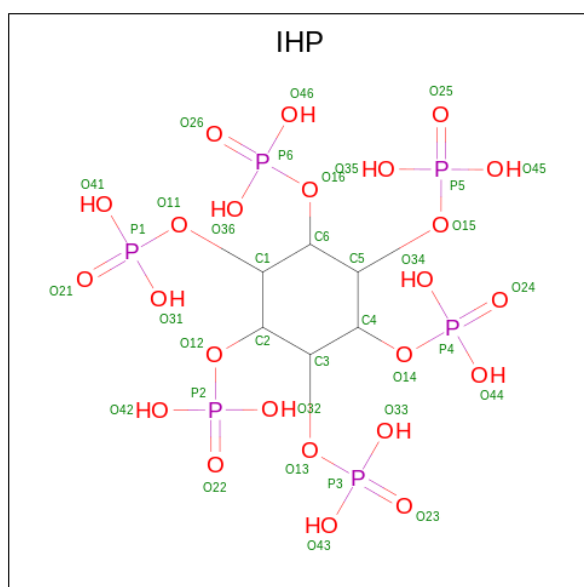
- Molecule 41 is a protein called RNA-binding protein 48.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	I	128	Total	C	N	O	S	0	0
			1062	683	184	190	5		

- Molecule 42 is a protein called Armadillo repeat-containing protein 7.

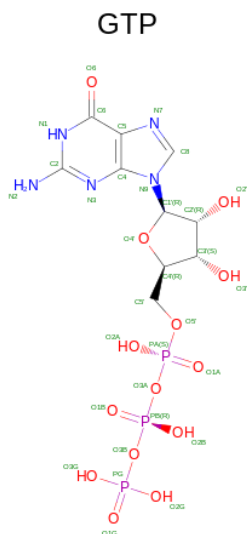
Mol	Chain	Residues	Atoms					AltConf	Trace
42	K	188	Total	C	N	O	S	0	0
			1314	824	229	256	5		

- Molecule 43 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: $C_6H_{18}O_{24}P_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
43	A	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 44 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
44	C	1	Total	C	N	O	P	0
			32	10	5	14	3	

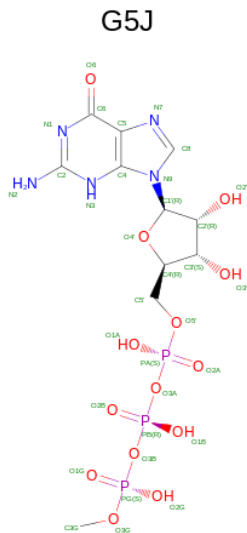
- Molecule 45 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
45	C	1	Total Mg 1 1	0
45	F	4	Total Mg 4 4	0

- Molecule 46 is POTASSIUM ION (three-letter code: K) (formula: K) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
46	F	2	Total 2	K 2	0

- Molecule 47 is 5'-O-[(S)-hydroxy{[(R)-hydroxy{[(S)-hydroxy(methoxy)phosphoryl]oxy}phosphoryl]oxy}phosphoryl]guanosine (three-letter code: G5J) (formula: C₁₁H₁₈N₅O₁₄P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
47	F	1	Total 33	C 11	N 5	O 14	P 3	0

- Molecule 48 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
48	v	1	Total 1	Zn 1	0
48	6	3	Total 3	Zn 3	0
48	M	1	Total 1	Zn 1	0
48	0	2	Total 2	Zn 2	0

- Molecule 49 is water.

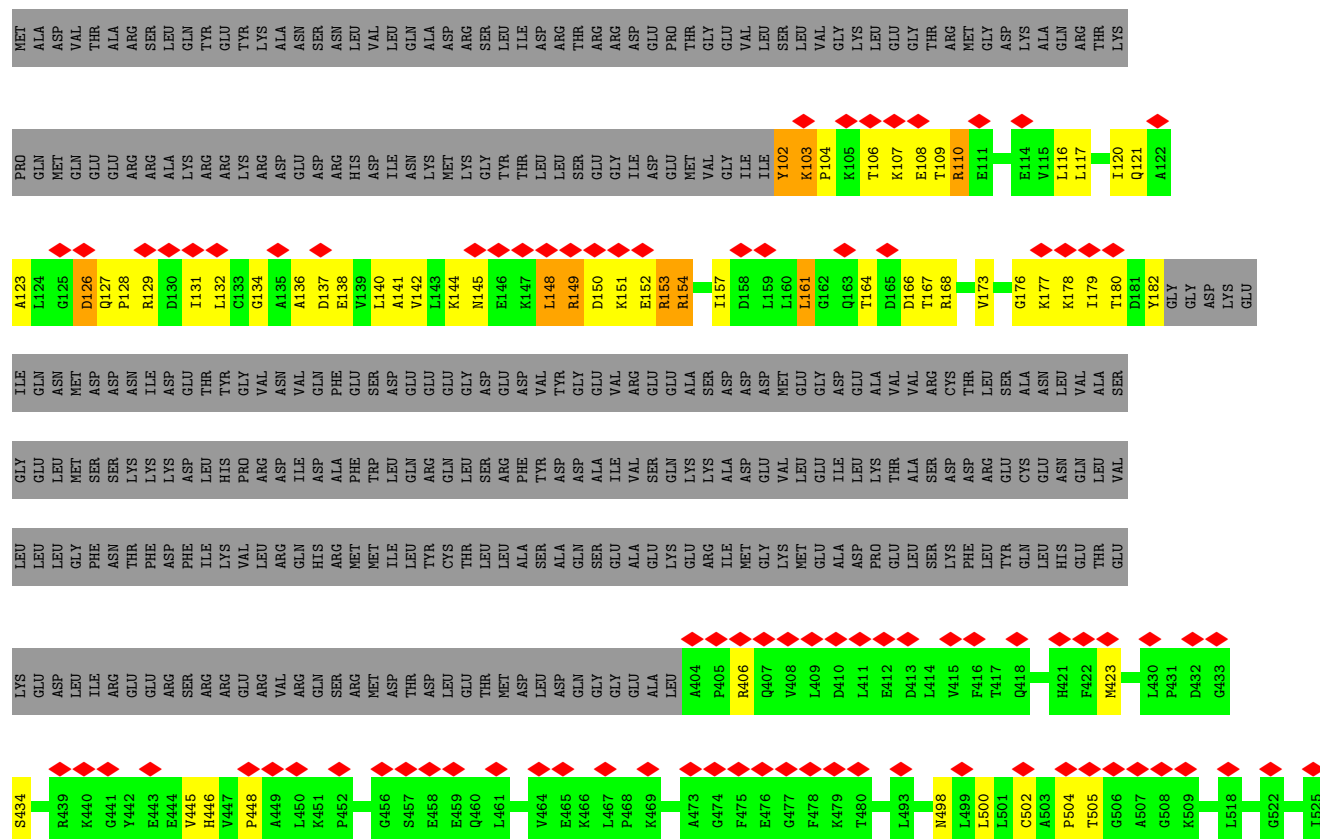
Mol	Chain	Residues	Atoms	AltConf
49	C	3	Total O 3 3	0

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.

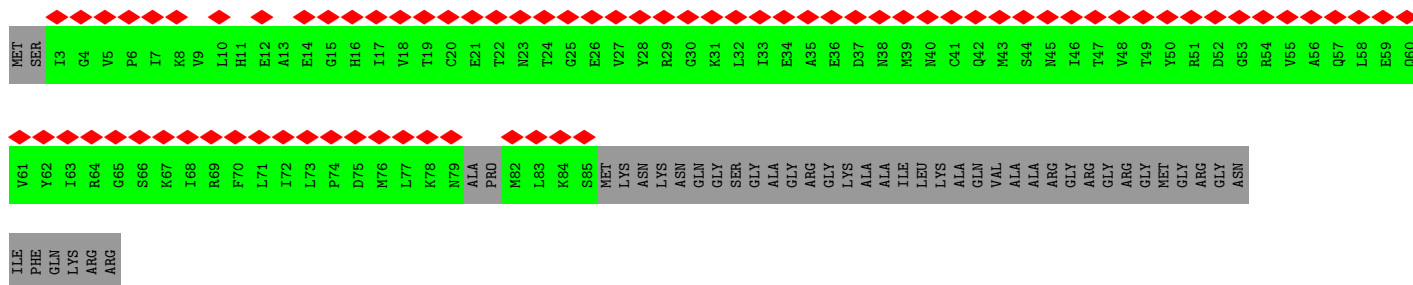
- Molecule 1: Pre-mRNA-processing-splicing factor 8



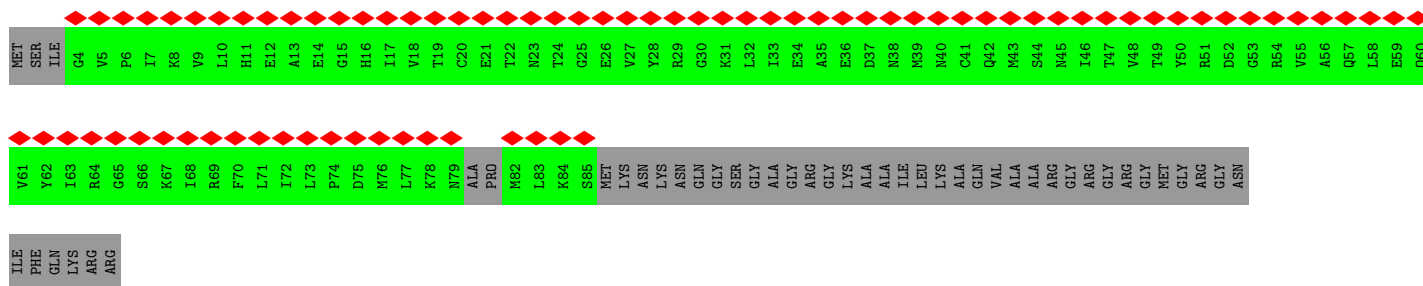




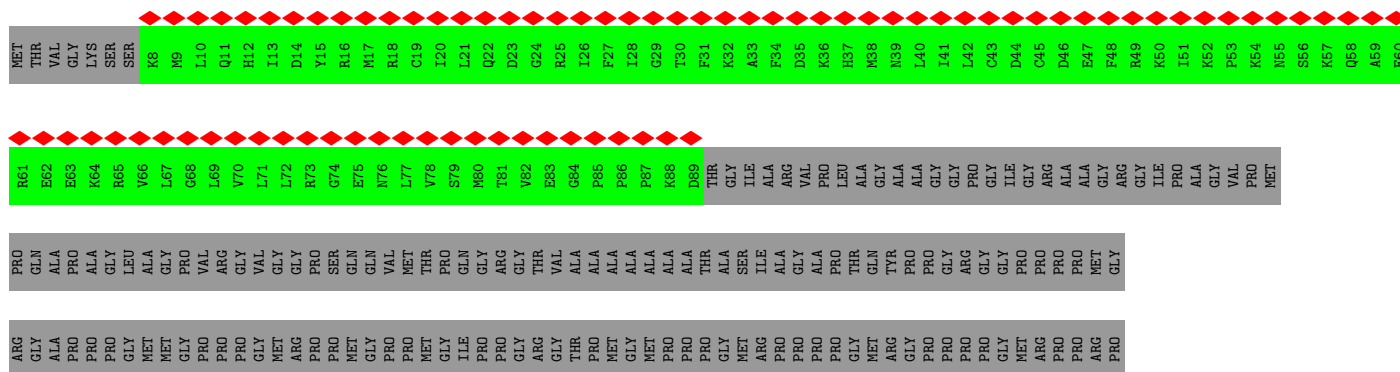
- Molecule 6: Small nuclear ribonucleoprotein Sm D3



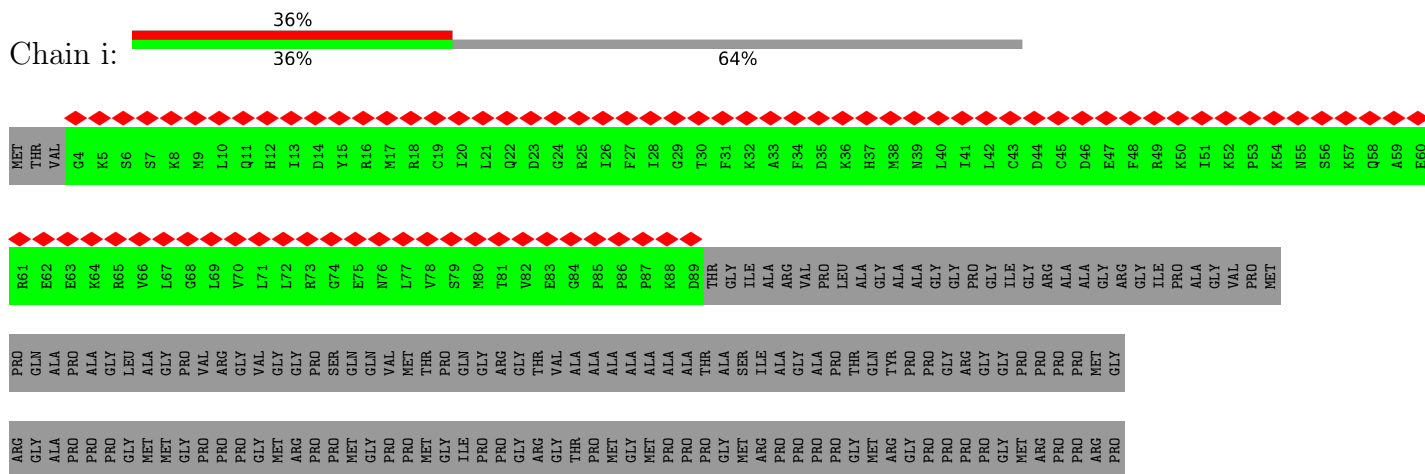
- Molecule 6: Small nuclear ribonucleoprotein Sm D3



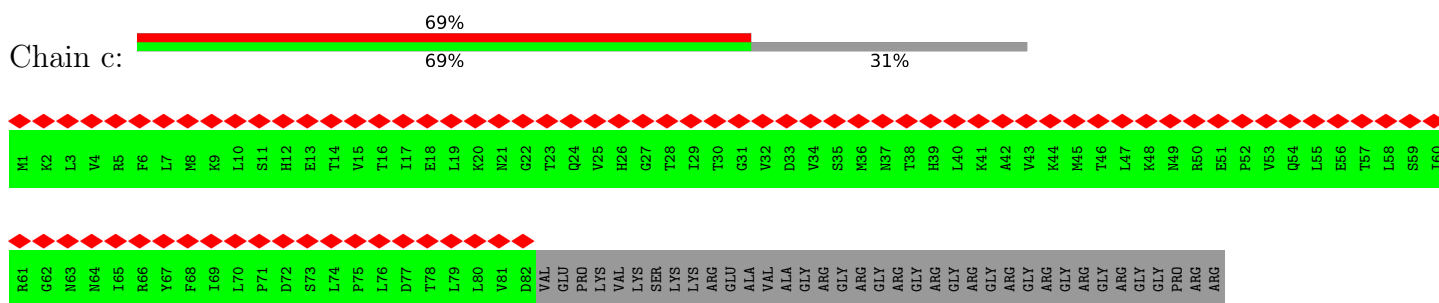
- Molecule 7: Small nuclear ribonucleoprotein-associated proteins B and B'



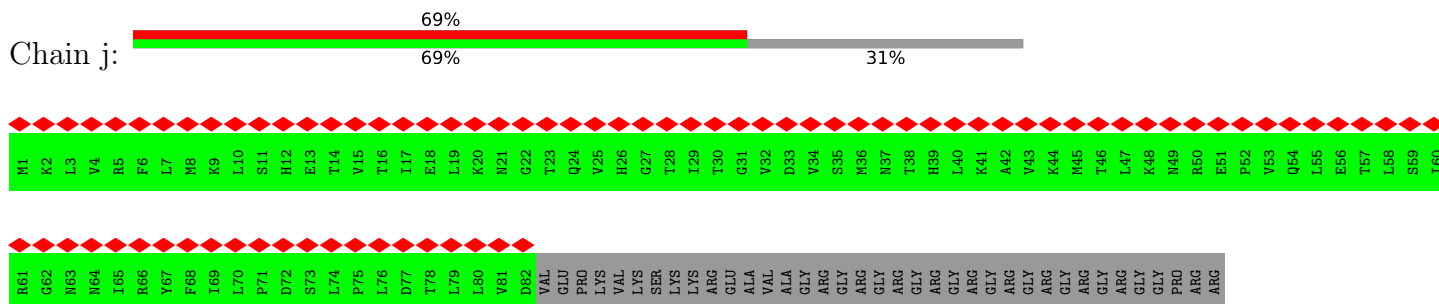
- Molecule 7: Small nuclear ribonucleoprotein-associated proteins B and B'



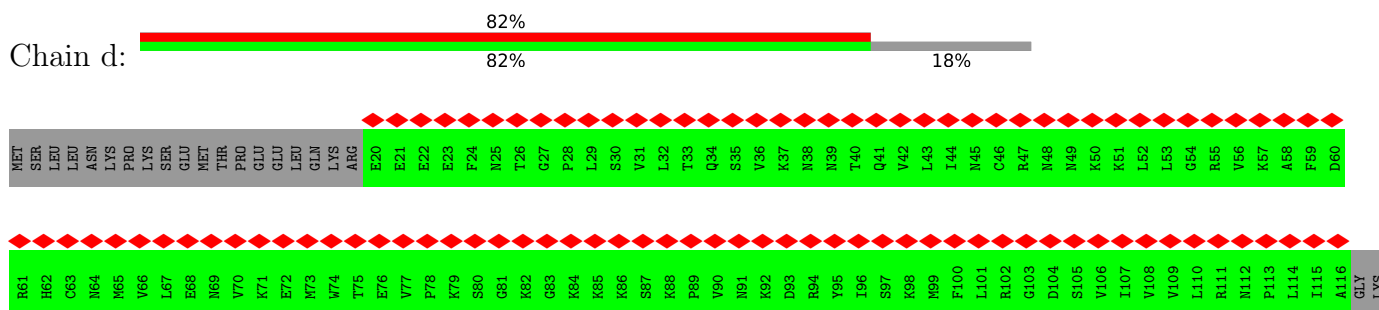
- Molecule 8: Small nuclear ribonucleoprotein Sm D1



- Molecule 8: Small nuclear ribonucleoprotein Sm D1

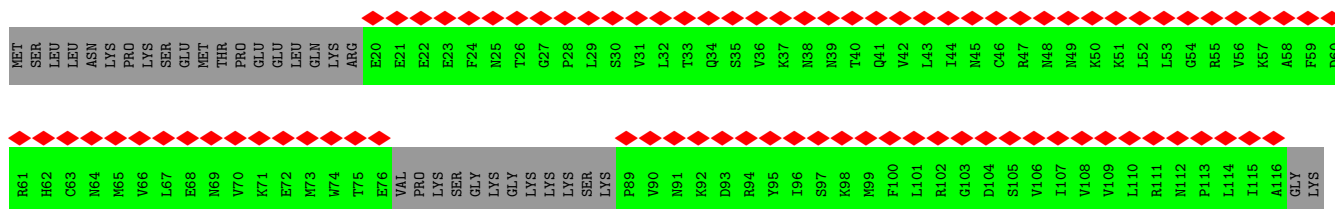


- Molecule 9: Small nuclear ribonucleoprotein Sm D2

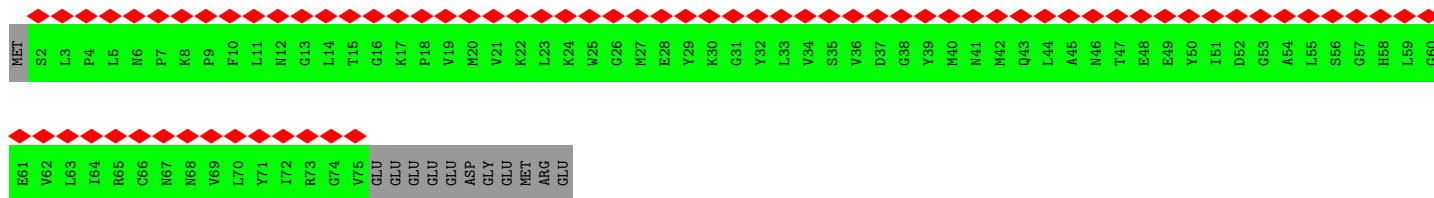
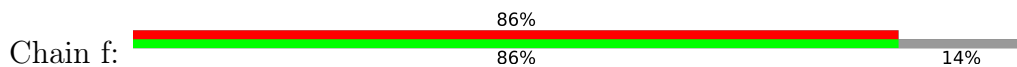


- Molecule 9: Small nuclear ribonucleoprotein Sm D2

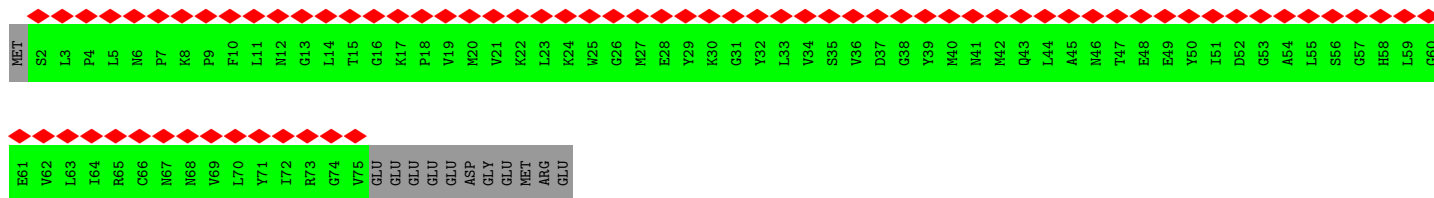
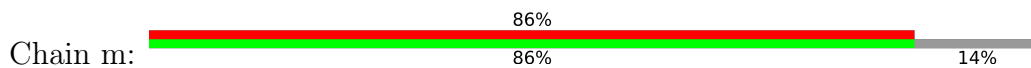




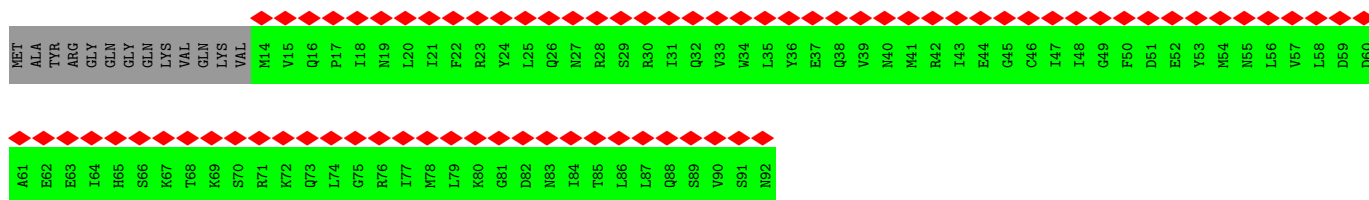
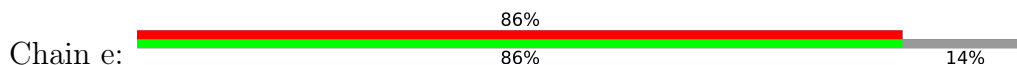
- Molecule 10: Small nuclear ribonucleoprotein F



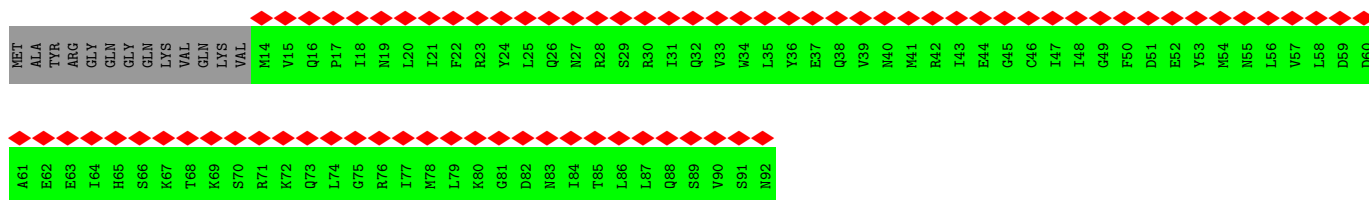
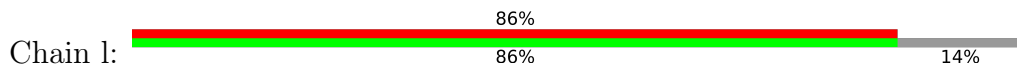
- Molecule 10: Small nuclear ribonucleoprotein F



- Molecule 11: Small nuclear ribonucleoprotein E

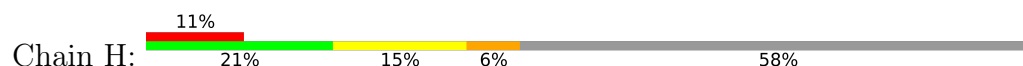
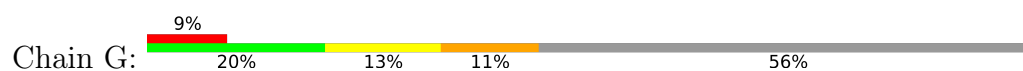
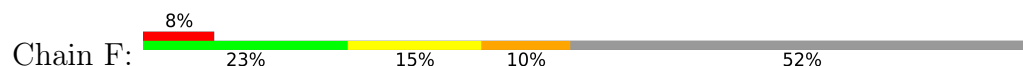


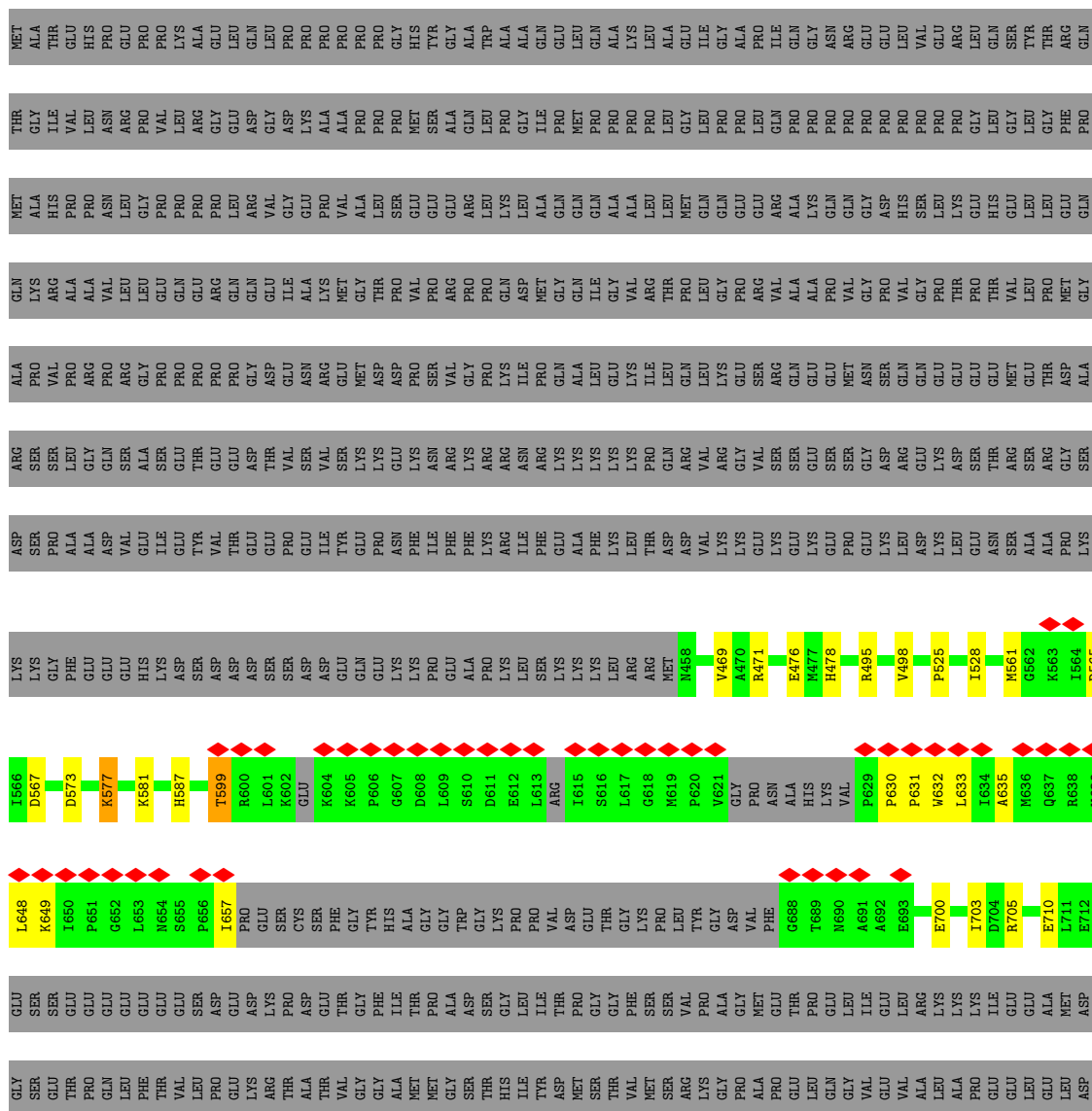
- Molecule 11: Small nuclear ribonucleoprotein E



97%


97%

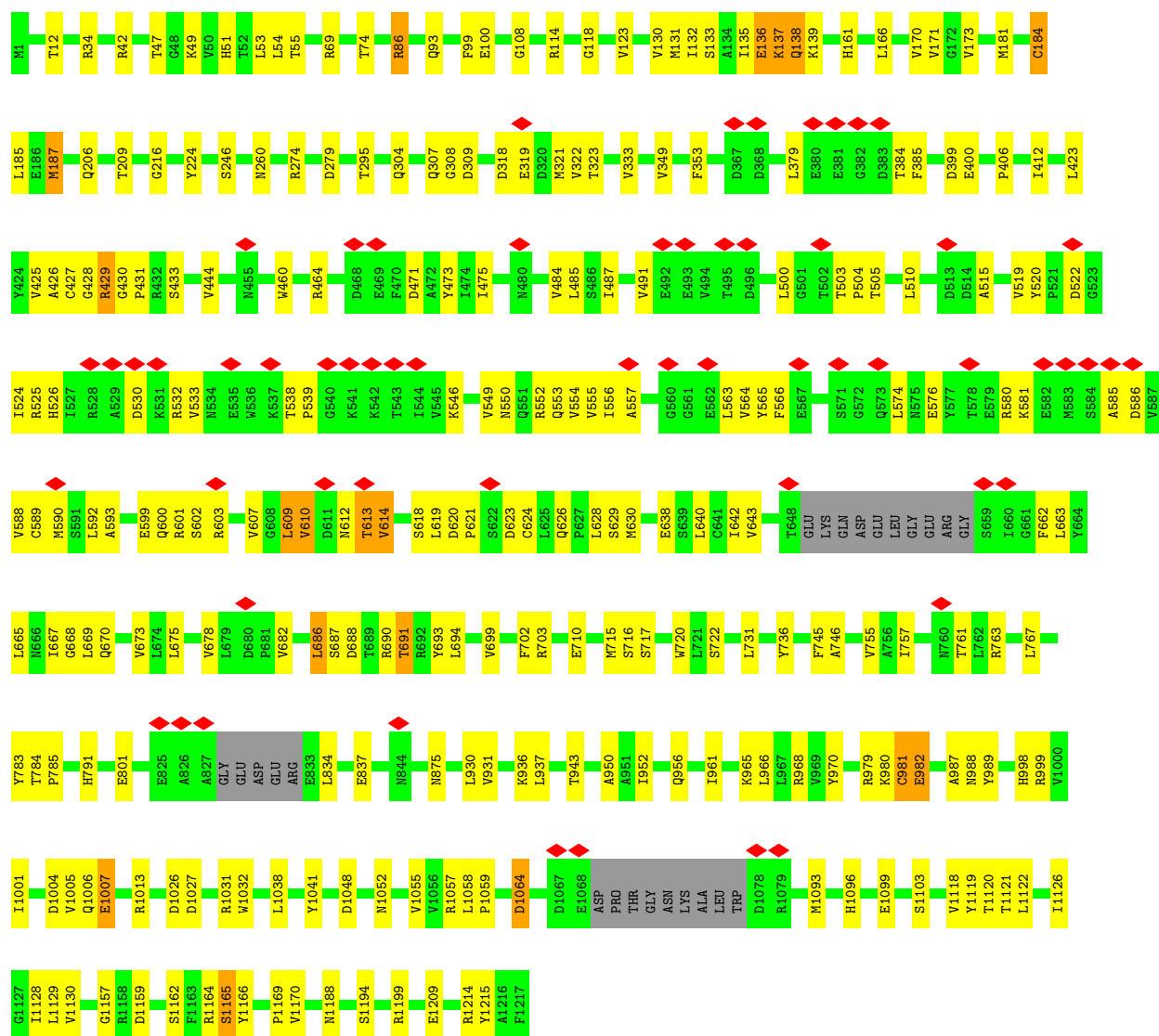




PRO	MEI	ALA	ALA	MET	THR	GLN	LYS	TYR	GLU	GLU	GLU	HIS	VAL	ARG	GLU	GLN	ALA	GLN	VAL	GLU	LYS	GLU	ASP	PHE	SER	ASP	VAL	ALA	GLU	HIS	ALA	ALA	LYS	GLN	LYS	GLN	LYS	LYS	ARG	LYS	LYS	ARG	GLY	GLY	SER	LYS	LYS	TYR	GLY	PHE	PHE
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

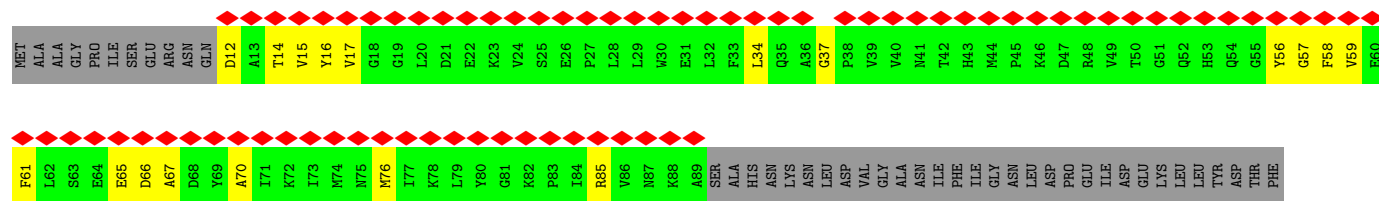
• Molecule 19: Splicing factor 3B subunit 3

Chain 3: 

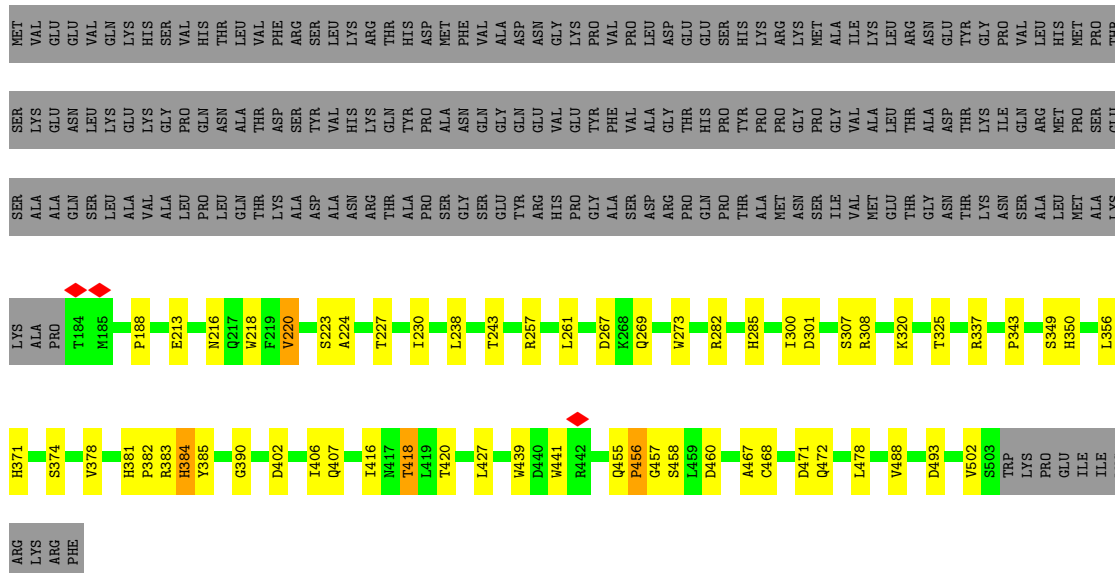


• Molecule 20: Splicing factor 3B subunit 4

Chain 4: 



- Molecule 28: Pleiotropic regulator 1



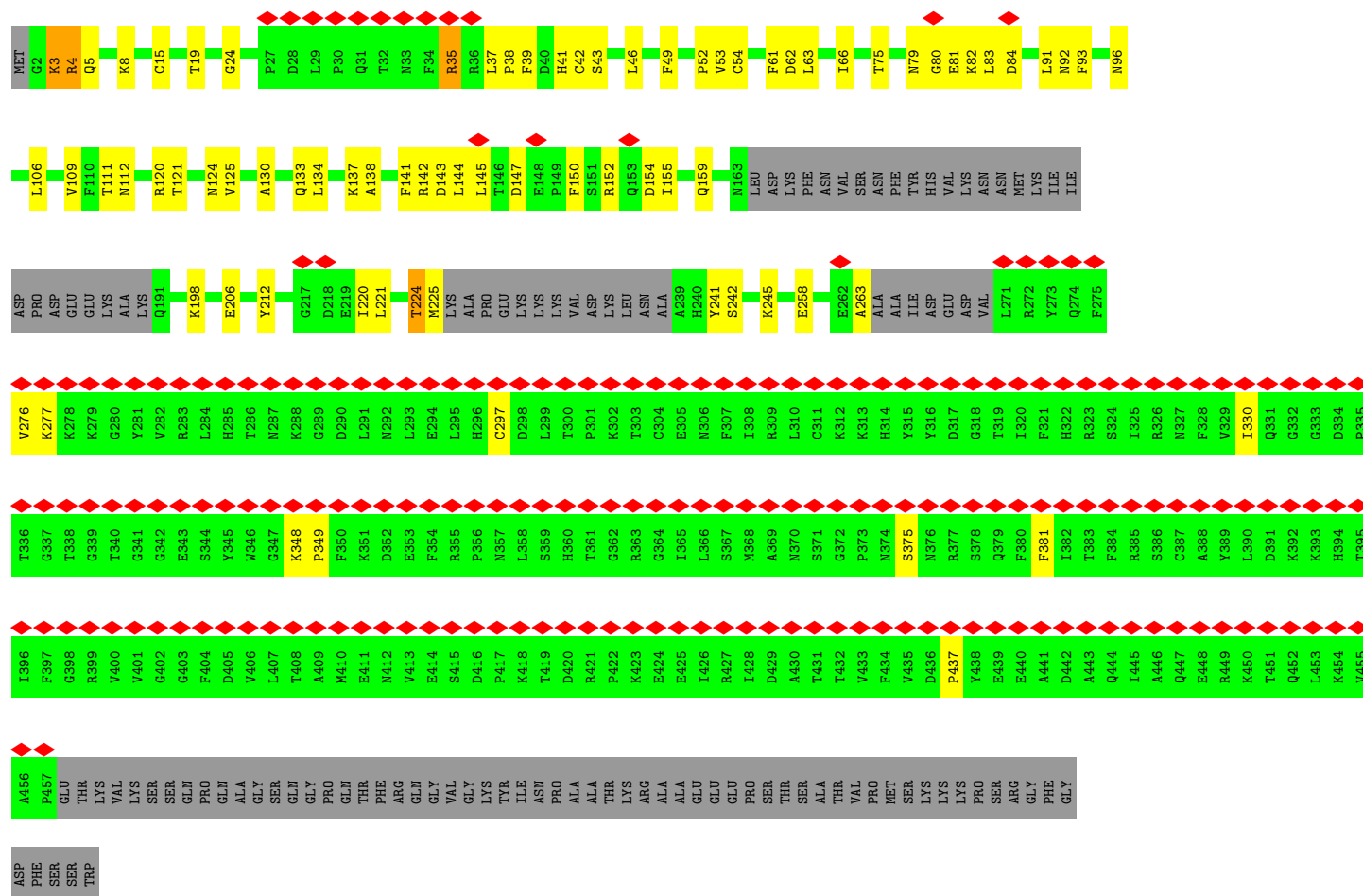
- Molecule 29: Smad nuclear-interacting protein 1





- Molecule 32: RING-type E3 ubiquitin-protein ligase PPIL2

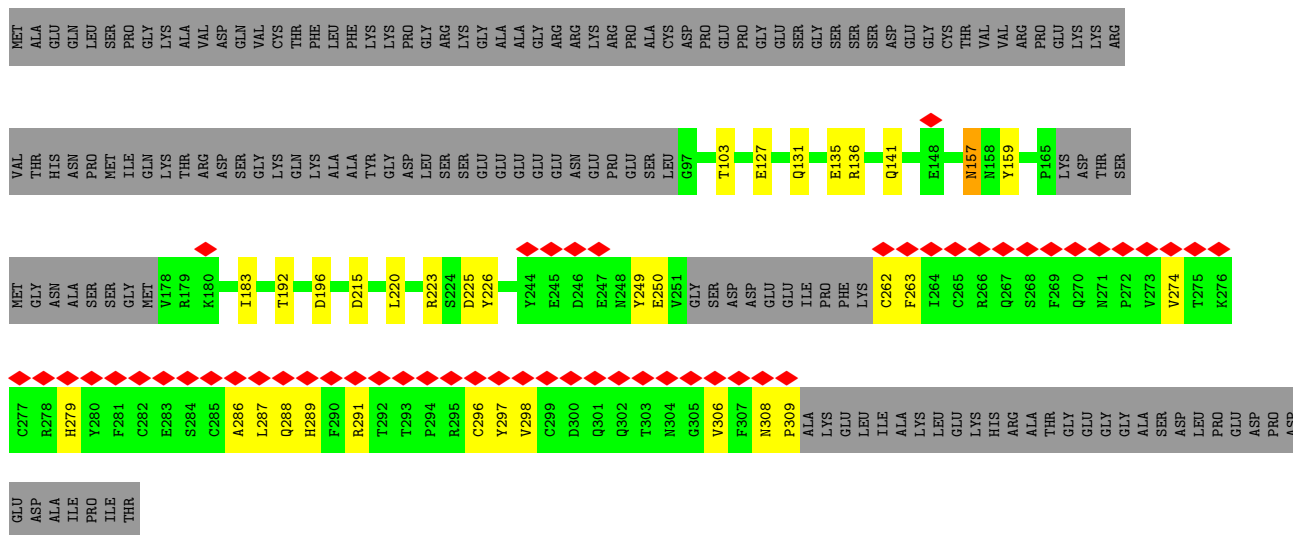
Chain 9: 39% 63% 14% 21%



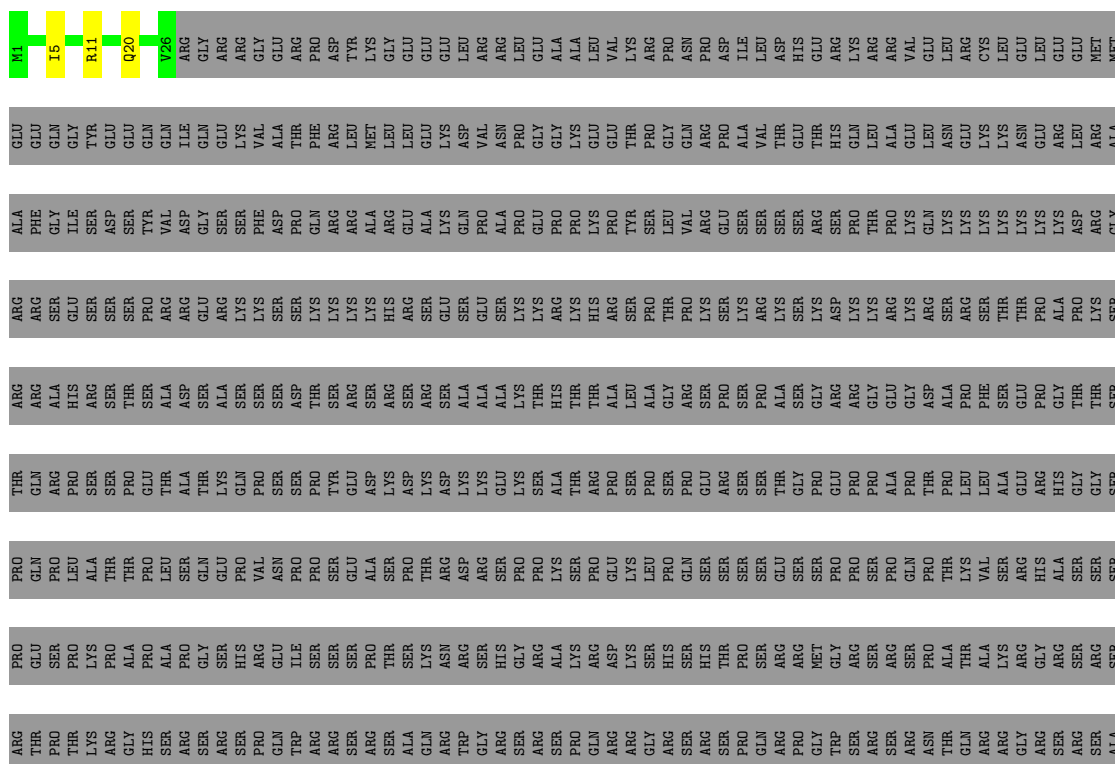
- Molecule 33: Peptidyl-prolyl cis-trans isomerase CWC27 homolog

Chain z: 38% 62%

- Molecule 36: RING finger protein 113A



- Molecule 37: Serine/arginine repetitive matrix protein 2



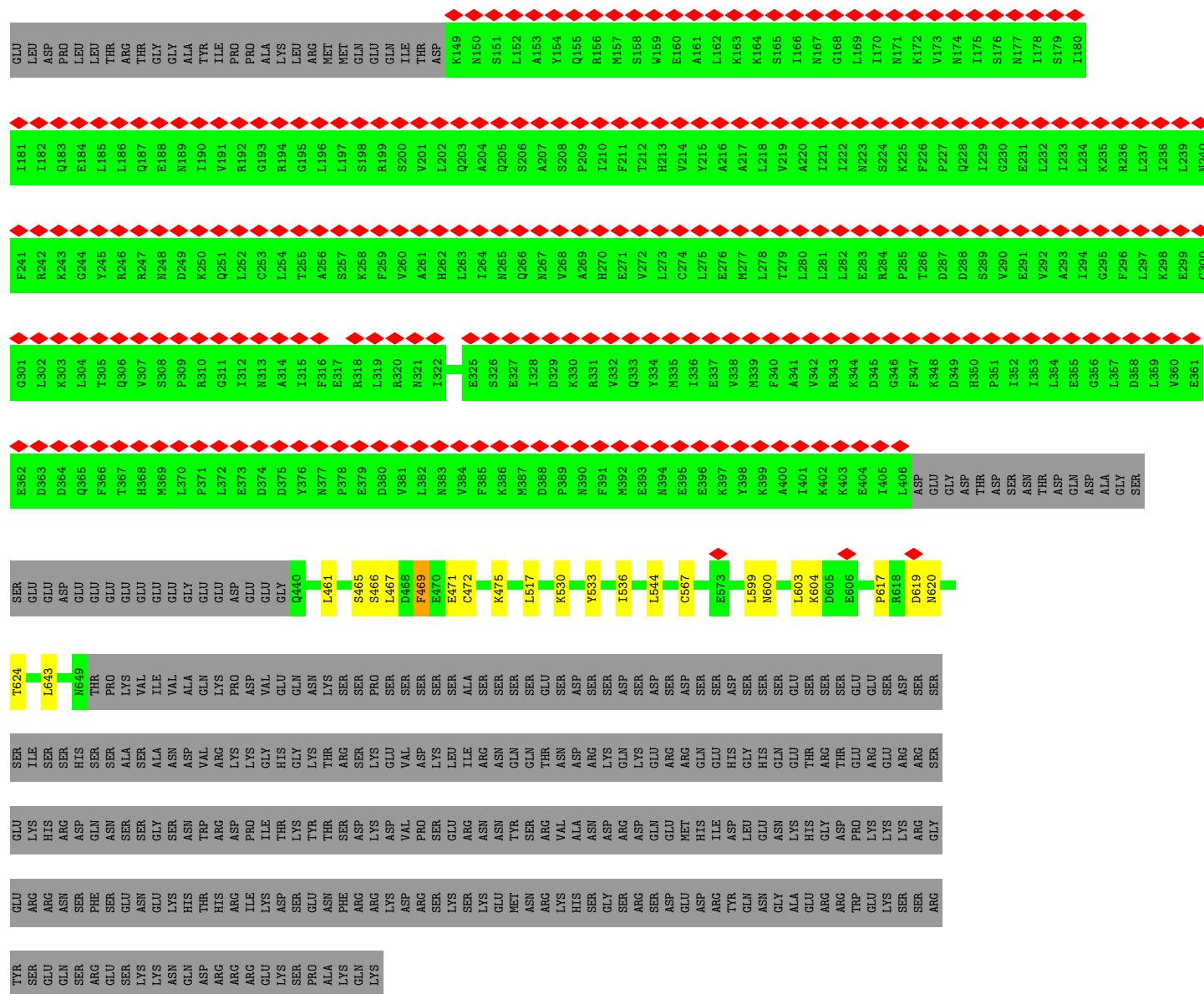


[illegible]

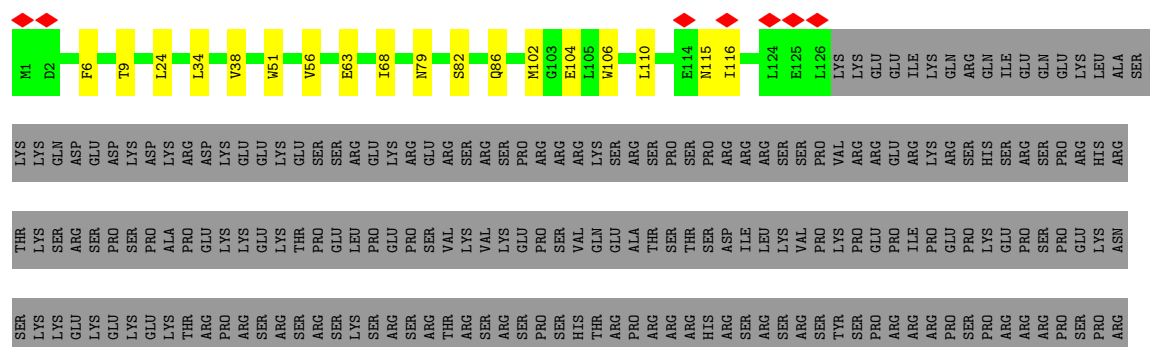
- Molecule 38: Pre-mRNA-splicing factor CWC22 homolog

Chain V:  28% 49% 48%

[illegible]

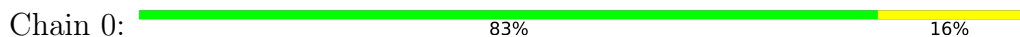


● Molecule 39: Serine/arginine repetitive matrix protein 1

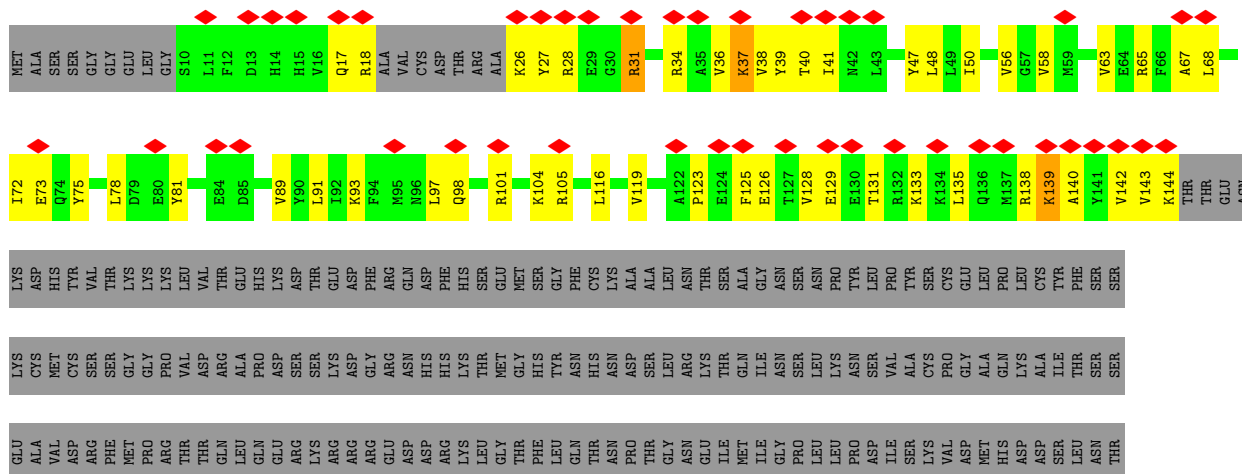


[illegible]

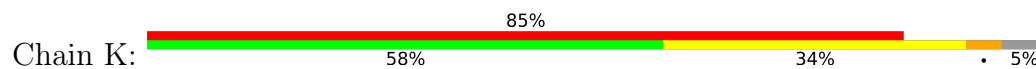
- Molecule 40: Cysteine-rich PDZ-binding protein



- Molecule 41: RNA-binding protein 48



- Molecule 42: Armadillo repeat-containing protein 7



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	101443	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.134	Depositor
Minimum map value	-0.056	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.014	Depositor
Map size (\AA)	644.52, 644.52, 644.52	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.0742, 1.0742, 1.0742	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, K, TPO, SEP, IHP, GTP, G5J

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	1.19	1/18863 (0.0%)	0.77	0/25599
2	B	0.51	0/2115	0.92	0/3284
3	C	1.03	1/7287 (0.0%)	0.79	0/9902
4	D	0.32	0/9225	0.58	0/12826
5	E	0.60	0/2390	0.75	0/3238
6	a	0.43	0/397	0.58	0/549
6	h	0.47	0/390	0.62	0/539
7	b	0.50	0/404	0.72	0/561
7	i	0.50	0/421	0.73	0/583
8	c	0.58	0/405	0.73	0/563
8	j	0.57	0/405	0.73	0/563
9	d	0.66	0/479	0.82	0/666
9	k	0.67	0/420	0.81	0/583
10	f	0.75	0/360	0.82	0/497
10	m	0.75	0/360	0.81	0/497
11	e	0.65	0/390	0.80	0/542
11	l	0.64	0/390	0.81	0/542
12	g	0.54	0/362	0.71	0/501
12	n	0.54	0/332	0.73	0/458
13	F	0.43	0/1449	0.77	0/2257
14	G	0.31	0/1445	0.71	0/2238
15	H	0.45	0/1511	0.72	0/2351
16	v	0.94	0/984	0.66	0/1326
17	1	1.13	0/8025	0.79	0/10859
18	2	1.01	0/1710	0.70	0/2306
19	3	1.03	0/9531	0.74	0/12931
20	4	0.60	0/382	0.70	0/529
21	5	0.88	0/925	0.71	0/1247
22	6	1.15	0/825	0.77	0/1106
23	7	1.29	0/688	0.85	0/930
24	L	1.26	0/864	0.78	0/1165
25	J	0.35	0/3494	0.52	0/4743

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	P	1.18	0/391	0.72	0/517
27	R	0.78	0/1954	0.58	0/2622
28	T	1.28	0/2574	0.84	0/3511
29	X	0.31	0/1304	0.52	0/1760
30	Y	1.05	0/1113	0.72	0/1501
31	Z	1.08	0/1153	0.70	0/1548
32	9	0.57	0/2732	0.60	0/3733
33	z	1.09	0/1434	0.76	0/1941
34	x	0.37	0/2996	0.49	0/4142
35	y	0.25	0/107	0.47	0/141
36	M	1.03	0/1609	0.70	0/2164
37	U	0.91	0/196	0.66	0/265
38	V	0.88	0/3042	0.70	0/4152
39	8	0.95	0/1028	0.75	0/1379
40	0	1.01	0/782	0.68	0/1043
41	I	0.42	0/1083	0.53	0/1454
42	K	0.29	0/1333	0.50	0/1826
All	All	0.91	2/102059 (0.0%)	0.72	0/140180

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	204	ASP	C-N	-5.74	1.20	1.34
1	A	279	PHE	C-N	-5.65	1.21	1.34

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	18354	0	18178	381	0
2	B	1898	0	963	36	0
3	C	7125	0	7130	122	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	9215	0	4458	170	0
5	E	2337	0	2272	194	0
6	a	399	0	173	0	0
6	h	392	0	168	0	0
7	b	405	0	170	0	0
7	i	422	0	177	0	0
8	c	406	0	170	0	0
8	j	406	0	170	0	0
9	d	480	0	200	0	0
9	k	422	0	175	0	0
10	f	361	0	158	0	0
10	m	361	0	158	0	0
11	e	391	0	163	0	0
11	l	391	0	163	0	0
12	g	363	0	160	0	0
12	n	334	0	143	0	0
13	F	1294	0	650	41	0
14	G	1303	0	667	46	0
15	H	1350	0	679	30	0
16	v	963	0	945	0	0
17	1	7879	0	8044	165	0
18	2	1674	0	1580	23	0
19	3	9352	0	9273	220	0
20	4	383	0	173	24	0
21	5	906	0	913	31	0
22	6	811	0	788	20	0
23	7	669	0	631	6	0
24	L	843	0	852	15	0
25	J	3457	0	2537	157	0
26	P	384	0	382	10	0
27	R	1923	0	1889	117	0
28	T	2507	0	2451	41	0
29	X	1271	0	1252	92	0
30	Y	1095	0	1083	59	0
31	Z	1129	0	1077	20	0
32	9	2691	0	2121	91	0
33	z	1400	0	1344	0	0
34	x	3007	0	1453	0	0
35	y	105	0	107	0	0
36	M	1572	0	1483	36	0
37	U	193	0	196	3	0
38	V	3008	0	2291	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
39	8	1011	0	1035	17	0
40	0	770	0	778	28	0
41	I	1062	0	1067	67	0
42	K	1314	0	1177	100	0
43	A	36	0	6	0	0
44	C	32	0	12	3	0
45	C	1	0	0	0	0
45	F	4	0	0	0	0
46	F	2	0	0	0	0
47	F	33	0	0	3	0
48	0	2	0	0	0	0
48	6	3	0	0	0	0
48	M	1	0	0	0	0
48	v	1	0	0	0	0
49	C	3	0	0	0	0
All	All	99906	0	84285	2086	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 12.

The worst 5 of 2086 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)
17:1:641:ILE:HD11	17:1:675:MET:CE	1.58	1.34
20:4:14:THR:HA	20:4:59:VAL:O	1.32	1.30
25:J:337:MET:HE2	25:J:346:TRP:CH2	1.69	1.26
5:E:62:LEU:HD12	5:E:351:LEU:CD1	1.66	1.26
5:E:62:LEU:CD1	5:E:351:LEU:HD12	1.68	1.23

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	2213/2335 (95%)	2146 (97%)	66 (3%)	1 (0%)	100	100
3	C	900/972 (93%)	862 (96%)	38 (4%)	0	100	100
4	D	1799/2136 (84%)	1710 (95%)	84 (5%)	5 (0%)	37	66
5	E	297/357 (83%)	278 (94%)	19 (6%)	0	100	100
6	a	77/126 (61%)	76 (99%)	1 (1%)	0	100	100
6	h	76/126 (60%)	74 (97%)	2 (3%)	0	100	100
7	b	80/240 (33%)	78 (98%)	2 (2%)	0	100	100
7	i	84/240 (35%)	82 (98%)	2 (2%)	0	100	100
8	c	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
8	j	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
9	d	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
9	k	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
10	f	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
10	m	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
11	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
11	l	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
12	g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
12	n	64/76 (84%)	62 (97%)	2 (3%)	0	100	100
16	v	115/230 (50%)	113 (98%)	2 (2%)	0	100	100
17	1	977/1304 (75%)	961 (98%)	16 (2%)	0	100	100
18	2	206/895 (23%)	198 (96%)	8 (4%)	0	100	100
19	3	1184/1217 (97%)	1136 (96%)	48 (4%)	0	100	100
20	4	76/424 (18%)	71 (93%)	5 (7%)	0	100	100
21	5	107/125 (86%)	104 (97%)	3 (3%)	0	100	100
22	6	103/110 (94%)	98 (95%)	5 (5%)	0	100	100
23	7	79/86 (92%)	78 (99%)	1 (1%)	0	100	100
24	L	99/802 (12%)	93 (94%)	6 (6%)	0	100	100
25	J	483/848 (57%)	447 (92%)	36 (8%)	0	100	100
26	P	42/229 (18%)	37 (88%)	5 (12%)	0	100	100
27	R	229/536 (43%)	219 (96%)	10 (4%)	0	100	100
28	T	318/514 (62%)	310 (98%)	8 (2%)	0	100	100
29	X	154/396 (39%)	137 (89%)	16 (10%)	1 (1%)	22	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	Y	138/322 (43%)	135 (98%)	3 (2%)	0	100	100
31	Z	138/619 (22%)	137 (99%)	1 (1%)	0	100	100
32	9	401/520 (77%)	382 (95%)	18 (4%)	1 (0%)	44	73
33	z	175/472 (37%)	169 (97%)	6 (3%)	0	100	100
34	x	575/1041 (55%)	554 (96%)	21 (4%)	0	100	100
35	y	11/476 (2%)	11 (100%)	0	0	100	100
36	M	185/343 (54%)	172 (93%)	13 (7%)	0	100	100
37	U	24/2752 (1%)	24 (100%)	0	0	100	100
38	V	464/908 (51%)	457 (98%)	7 (2%)	0	100	100
39	8	124/904 (14%)	124 (100%)	0	0	100	100
40	0	98/101 (97%)	98 (100%)	0	0	100	100
41	I	124/367 (34%)	120 (97%)	4 (3%)	0	100	100
42	K	186/198 (94%)	183 (98%)	2 (1%)	1 (0%)	25	56
All	All	13111/24253 (54%)	12617 (96%)	485 (4%)	9 (0%)	50	77

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	1584	ILE
4	D	1864	GLU
1	A	1092	ILE
29	X	263	PRO
42	K	127	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1979/2108 (94%)	1924 (97%)	55 (3%)	38	73
3	C	798/866 (92%)	787 (99%)	11 (1%)	62	86
4	D	76/1908 (4%)	62 (82%)	14 (18%)	1	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	255/300 (85%)	245 (96%)	10 (4%)	27	62
16	v	104/199 (52%)	99 (95%)	5 (5%)	21	54
17	1	854/1103 (77%)	820 (96%)	34 (4%)	27	61
18	2	163/776 (21%)	158 (97%)	5 (3%)	35	70
19	3	1031/1050 (98%)	997 (97%)	34 (3%)	33	68
21	5	97/109 (89%)	96 (99%)	1 (1%)	73	91
22	6	90/95 (95%)	87 (97%)	3 (3%)	33	68
23	7	72/77 (94%)	72 (100%)	0	100	100
24	L	87/709 (12%)	86 (99%)	1 (1%)	70	90
25	J	203/751 (27%)	197 (97%)	6 (3%)	36	71
26	P	42/203 (21%)	41 (98%)	1 (2%)	44	76
27	R	206/459 (45%)	194 (94%)	12 (6%)	17	46
28	T	273/441 (62%)	268 (98%)	5 (2%)	54	82
29	X	134/349 (38%)	127 (95%)	7 (5%)	19	50
30	Y	117/291 (40%)	113 (97%)	4 (3%)	32	67
31	Z	110/545 (20%)	108 (98%)	2 (2%)	54	82
32	9	195/456 (43%)	190 (97%)	5 (3%)	41	74
33	z	152/416 (36%)	152 (100%)	0	100	100
34	x	14/897 (2%)	13 (93%)	1 (7%)	12	36
35	y	11/397 (3%)	11 (100%)	0	100	100
36	M	168/294 (57%)	165 (98%)	3 (2%)	54	82
37	U	21/2432 (1%)	20 (95%)	1 (5%)	21	54
38	V	193/838 (23%)	190 (98%)	3 (2%)	58	84
39	8	111/831 (13%)	111 (100%)	0	100	100
40	0	86/87 (99%)	84 (98%)	2 (2%)	45	77
41	I	112/326 (34%)	108 (96%)	4 (4%)	30	65
42	K	119/171 (70%)	108 (91%)	11 (9%)	7	24
All	All	7873/19484 (40%)	7633 (97%)	240 (3%)	37	71

5 of 240 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	1	1127	THR

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Mol	Chain	Res	Type
38	V	469	PHE
19	3	295	THR
37	U	20	GLN
42	K	136	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
40	0	98	GLN
39	8	88	ASN
19	3	51	HIS
30	Y	66	ASN
17	1	1252	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	F	58/124 (46%)	14 (24%)	3 (5%)
14	G	62/142 (43%)	22 (35%)	5 (8%)
15	H	61/150 (40%)	14 (22%)	0
2	B	87/117 (74%)	21 (24%)	2 (2%)
All	All	268/533 (50%)	71 (26%)	10 (3%)

5 of 71 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	20	G
2	B	21	A
2	B	22	U
2	B	24	G
2	B	25	C

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
14	G	213	C
14	G	217	U
14	G	219	U
13	F	31	U
13	F	51	G

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
17	SEP	1	129	17	8,9,10	1.07	1 (12%)	8,12,14	1.70	3 (37%)
19	TPO	3	613	19	8,10,11	0.89	0	10,14,16	1.61	2 (20%)

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
17	SEP	1	129	17	-	4/5/8/10	-
19	TPO	3	613	19	-	2/9/11/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	1	129	SEP	P-O1P	2.12	1.57	1.50

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	3	613	TPO	P-OG1-CB	-4.43	109.83	123.21
17	1	129	SEP	P-OG-CB	-2.83	110.49	118.30
19	3	613	TPO	O-C-CA	-2.22	118.95	124.78
17	1	129	SEP	O3P-P-OG	2.17	112.52	106.73
17	1	129	SEP	OG-CB-CA	2.09	110.18	108.14

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	1	129	SEP	N-CA-CB-OG
17	1	129	SEP	CB-OG-P-O1P
17	1	129	SEP	CB-OG-P-O2P
17	1	129	SEP	CB-OG-P-O3P
19	3	613	TPO	O-C-CA-CB

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	1	129	SEP	2	0
19	3	613	TPO	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 14 are monoatomic - leaving 3 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
44	GTP	C	1500	45	26,34,34	2.33	11 (42%)	32,54,54	1.91	9 (28%)
47	G5J	F	207	13	25,35,35	0.92	1 (4%)	31,55,55	1.41	3 (9%)
43	IHP	A	3000	-	36,36,36	1.12	3 (8%)	54,60,60	1.06	3 (5%)

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
44	GTP	C	1500	45	-	4/18/38/38	0/3/3/3
47	G5J	F	207	13	-	6/21/41/41	0/3/3/3
43	IHP	A	3000	-	-	1/30/54/54	0/1/1/1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	C	1500	GTP	C5-C6	-6.29	1.34	1.47
44	C	1500	GTP	C5-C4	-3.87	1.33	1.43
44	C	1500	GTP	C2'-C1'	-3.54	1.48	1.53
44	C	1500	GTP	O4'-C4'	-2.59	1.39	1.45
44	C	1500	GTP	C6-N1	-2.44	1.34	1.37

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C	1500	GTP	C5-C6-N1	4.60	122.07	113.95
47	F	207	G5J	PG-O3B-PB	-4.55	117.21	132.83
44	C	1500	GTP	C2-N1-C6	-4.29	117.20	125.10
47	F	207	G5J	PB-O3A-PA	-3.93	119.34	132.83
43	A	3000	IHP	C5-C6-C1	-3.74	102.23	110.41

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
44	C	1500	GTP	O4'-C4'-C5'-O5'
47	F	207	G5J	C5'-O5'-PA-O3A
47	F	207	G5J	O4'-C4'-C5'-O5'
47	F	207	G5J	C3'-C4'-C5'-O5'
44	C	1500	GTP	C3'-C4'-C5'-O5'

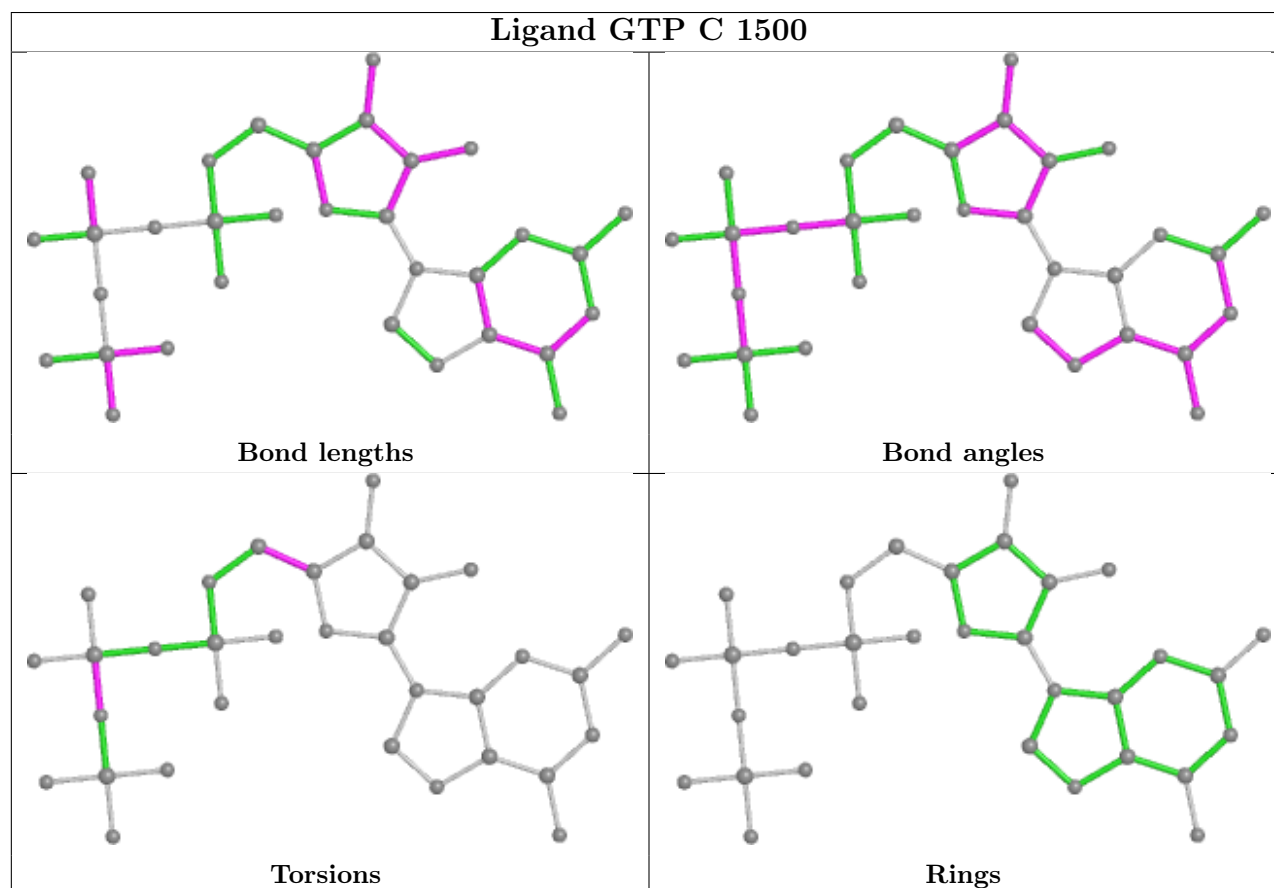
There are no ring outliers.

2 monomers are involved in 6 short contacts:

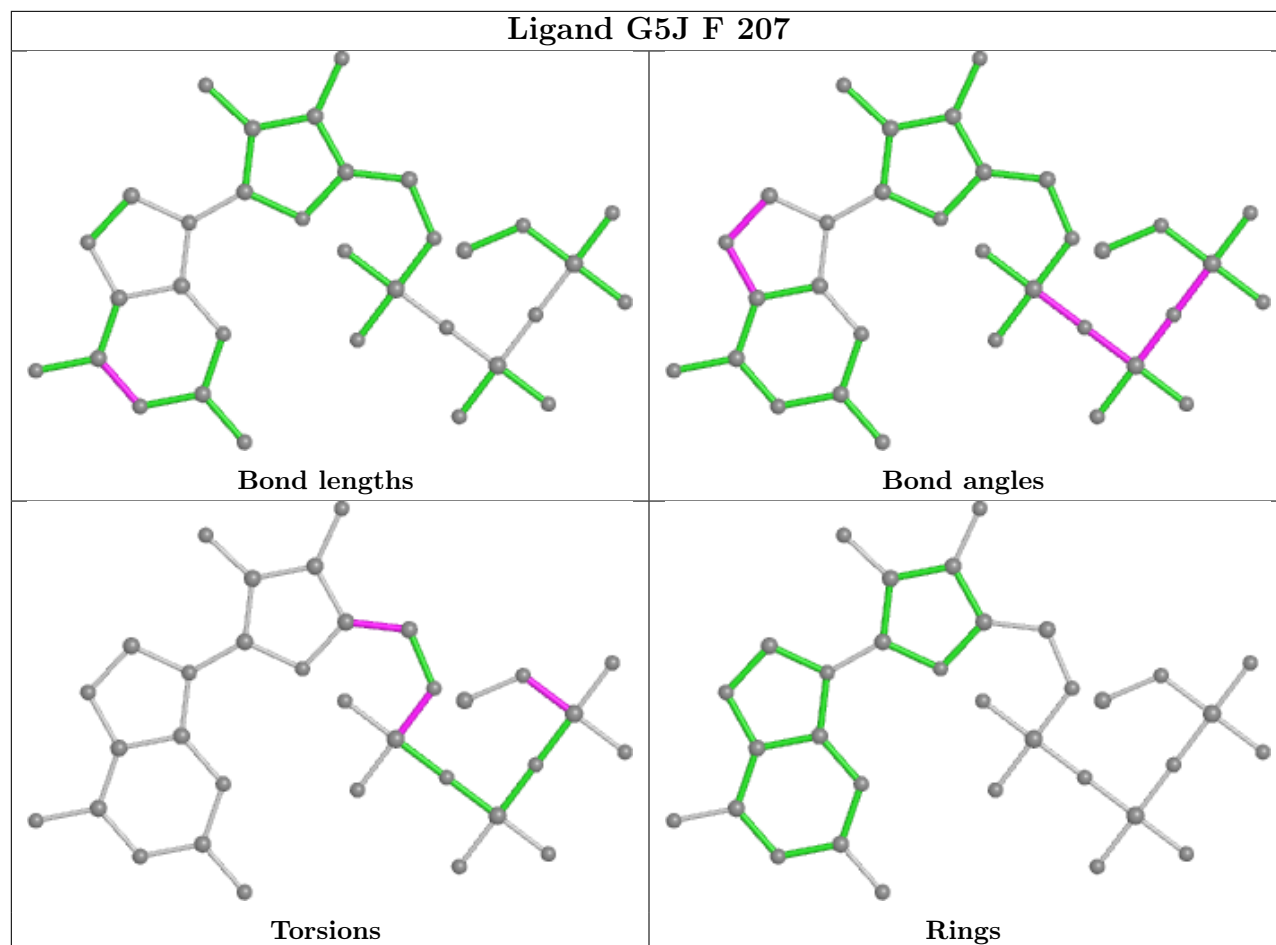
Mol	Chain	Res	Type	Clashes	Symm-Clashes
44	C	1500	GTP	3	0
47	F	207	G5J	3	0

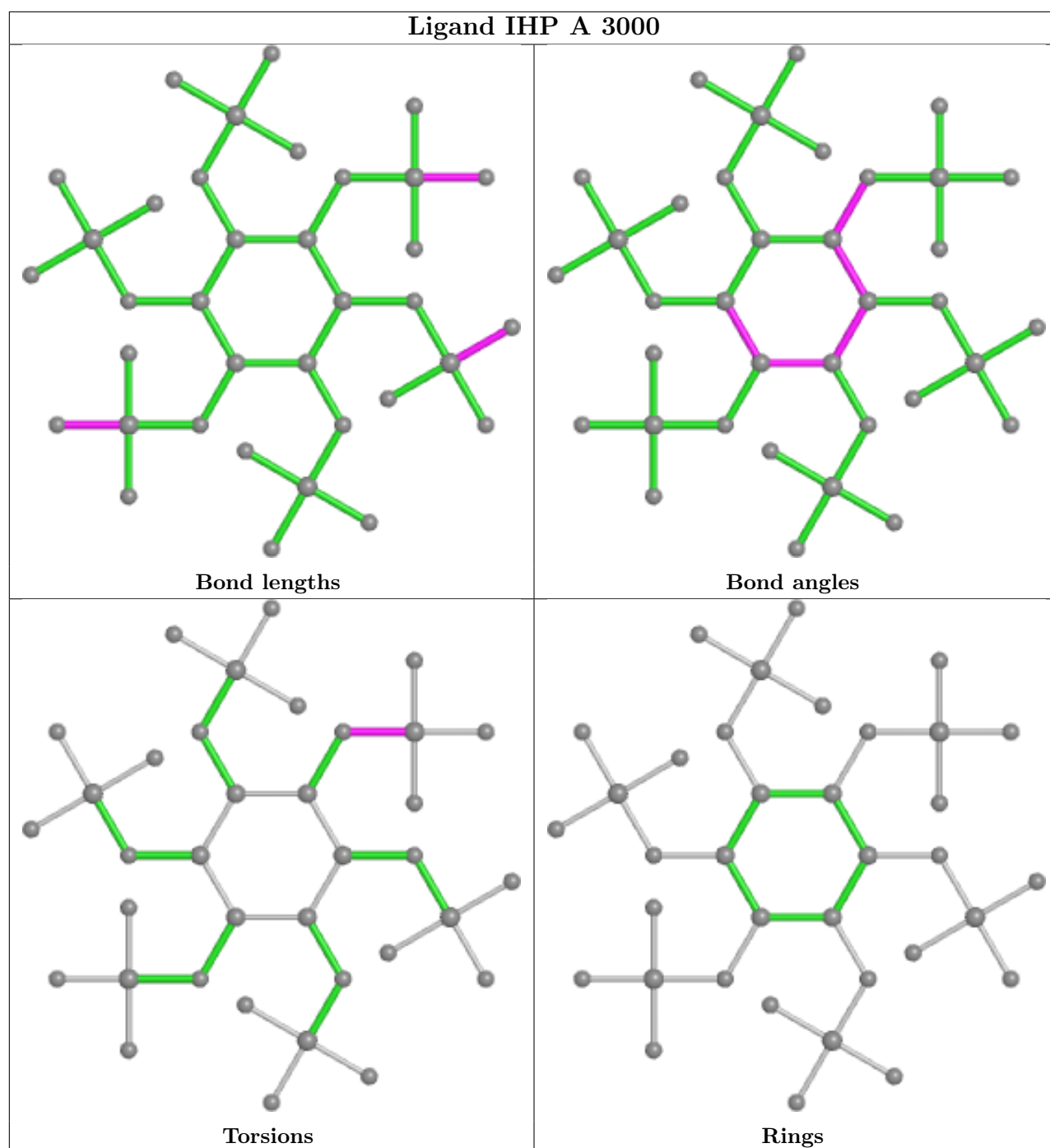
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

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.



Ligand G5J F 207





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

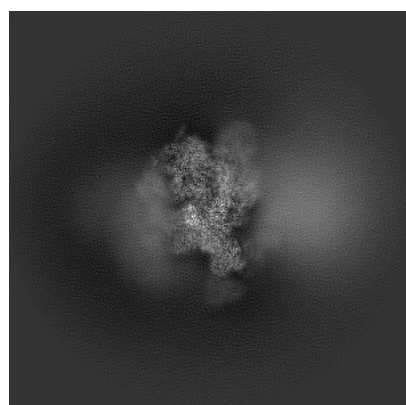
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30875. These allow visual inspection of the internal detail of the map and identification of artifacts.

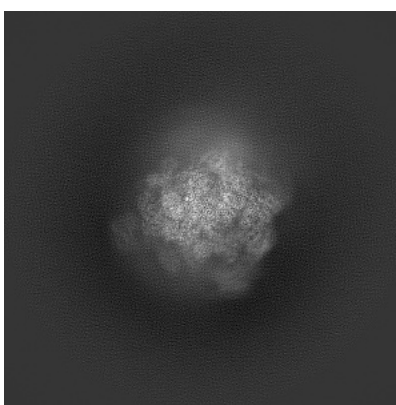
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

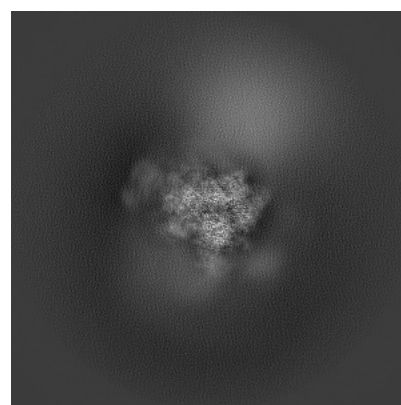
6.1.1 Primary map



X



Y

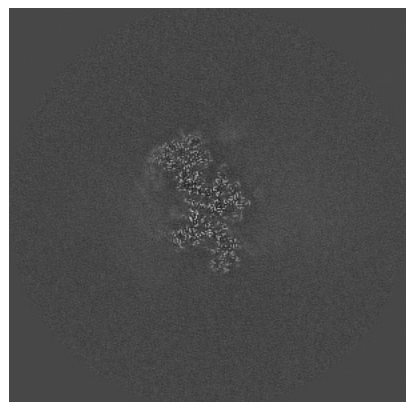


Z

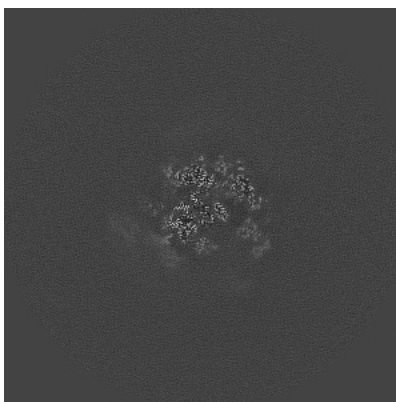
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

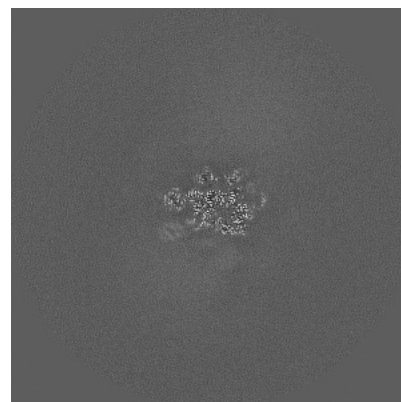
6.2.1 Primary map



X Index: 300



Y Index: 300

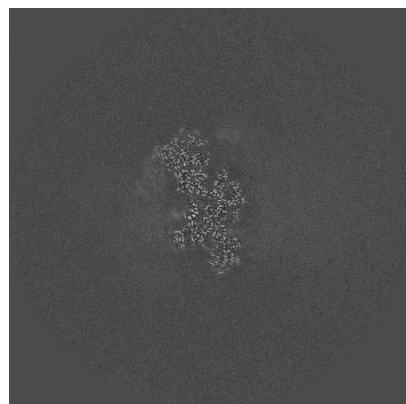


Z Index: 300

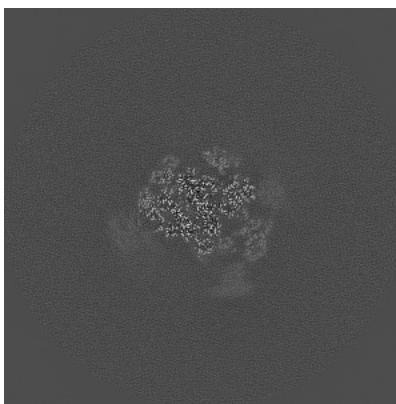
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 304



Y Index: 316

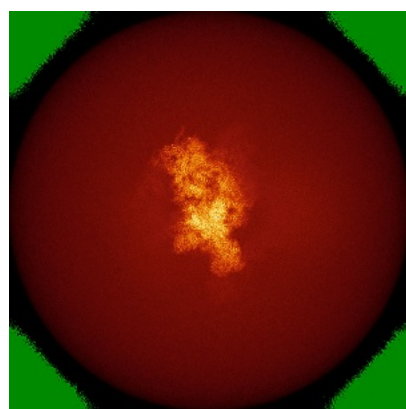


Z Index: 284

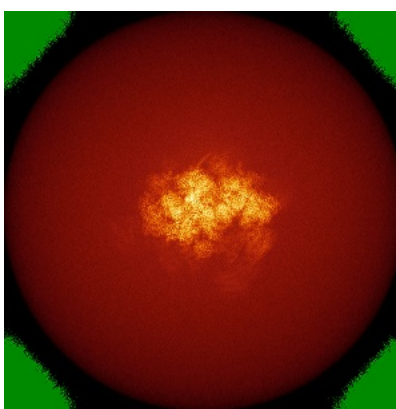
The images above show the largest variance slices of the map in three orthogonal directions.

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

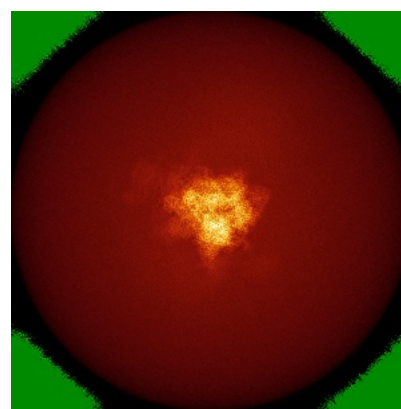
6.4.1 Primary map



X



Y

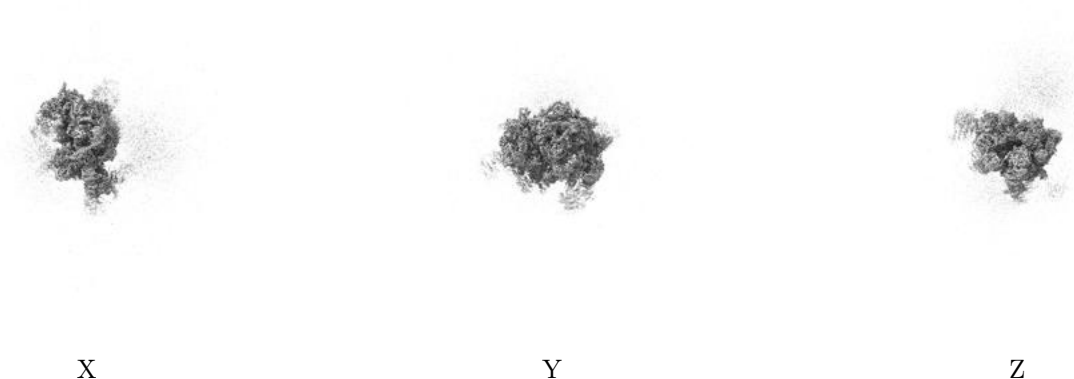


Z

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 0.014. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

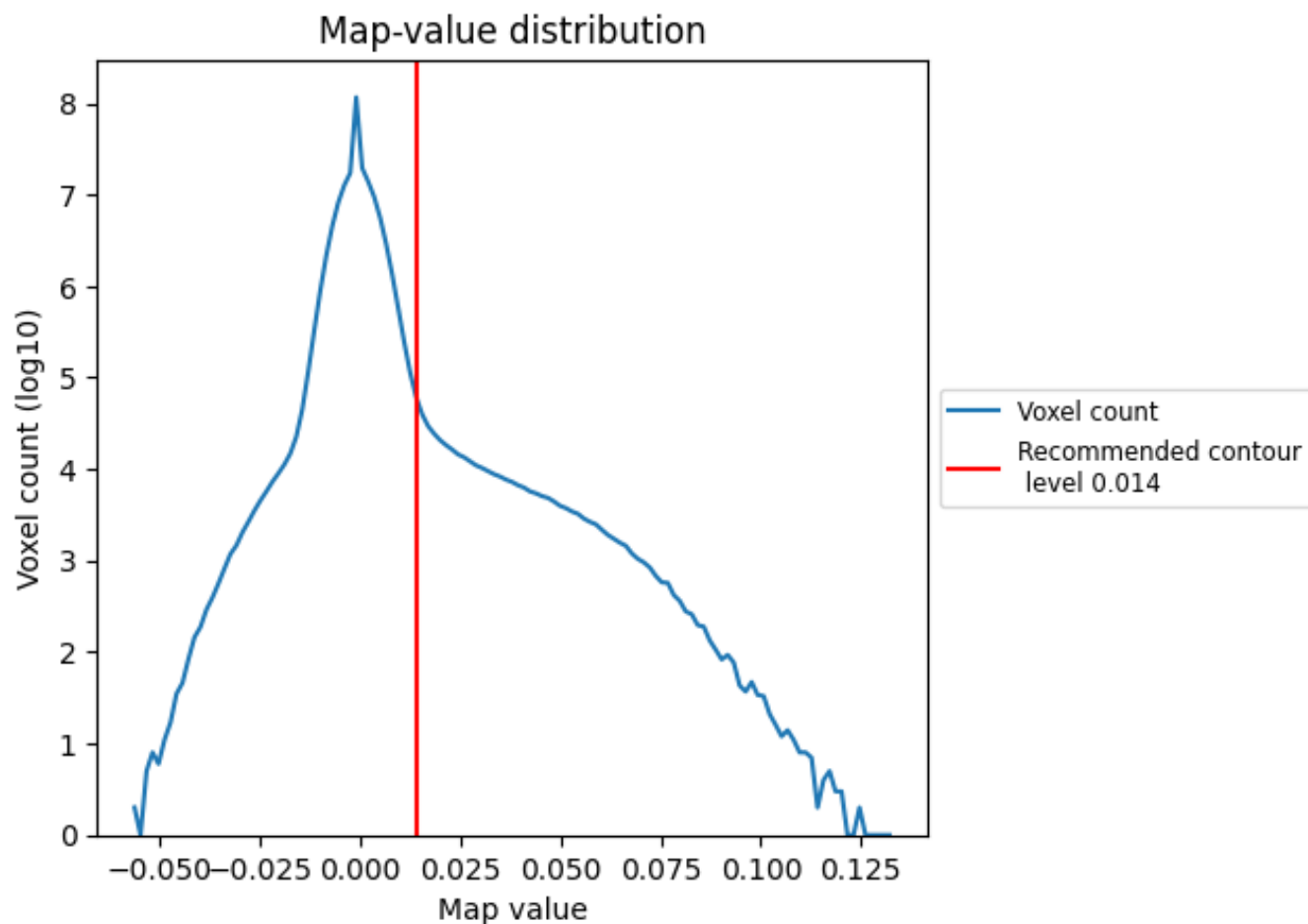
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

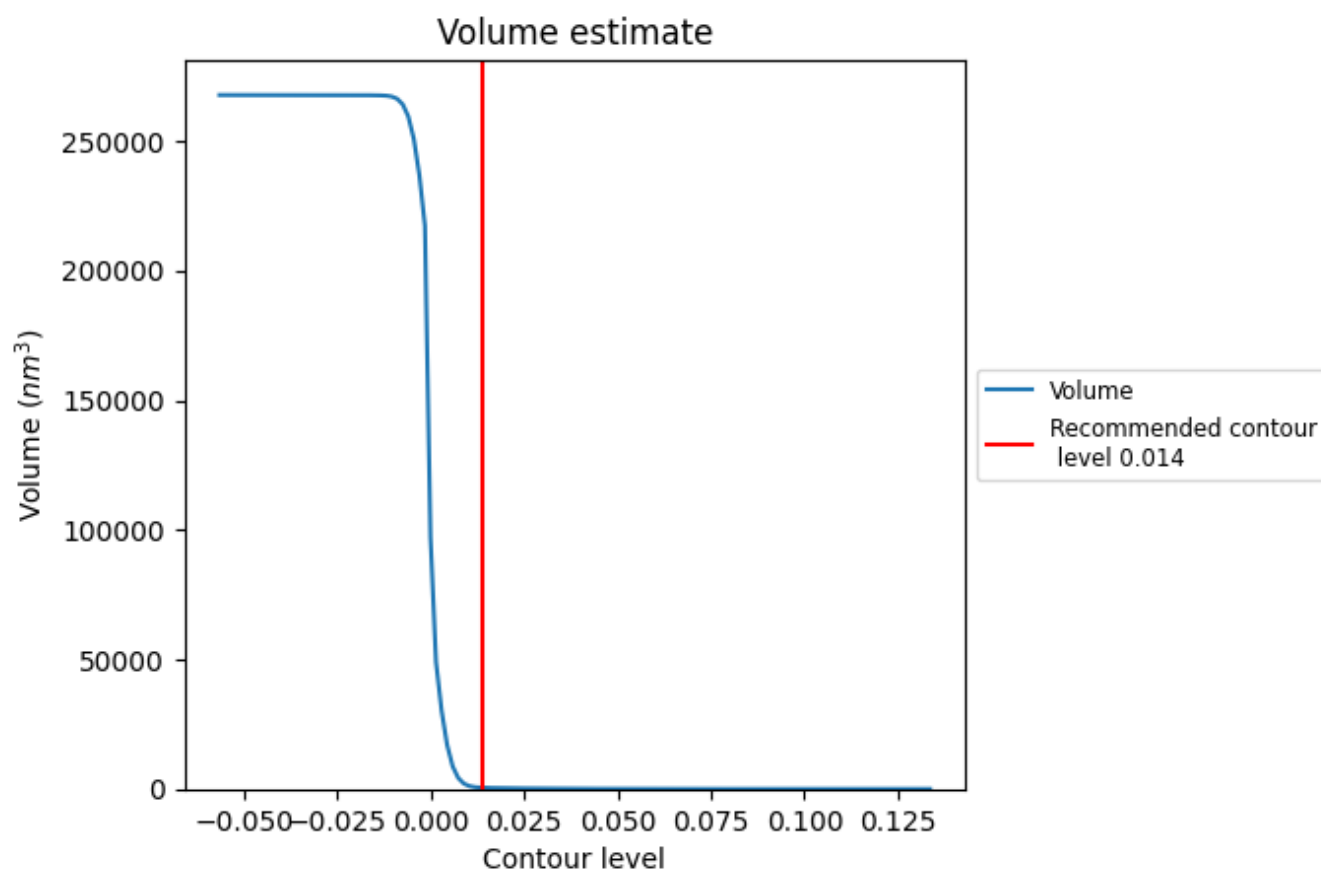
This section contains the results of statistical analysis of the map.

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.

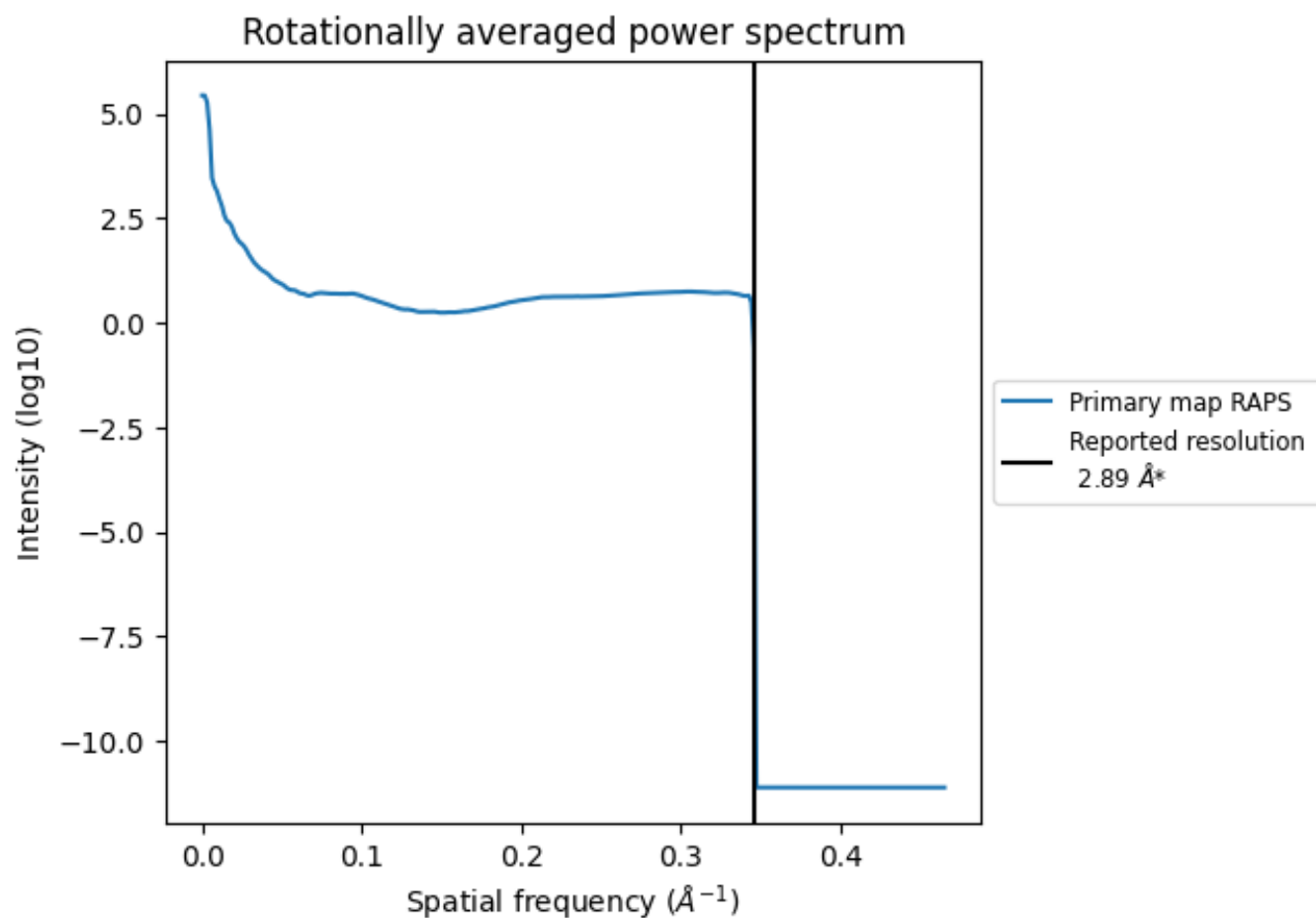
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 486 nm^3 ; this corresponds to an approximate mass of 439 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 0.346 \AA^{-1}

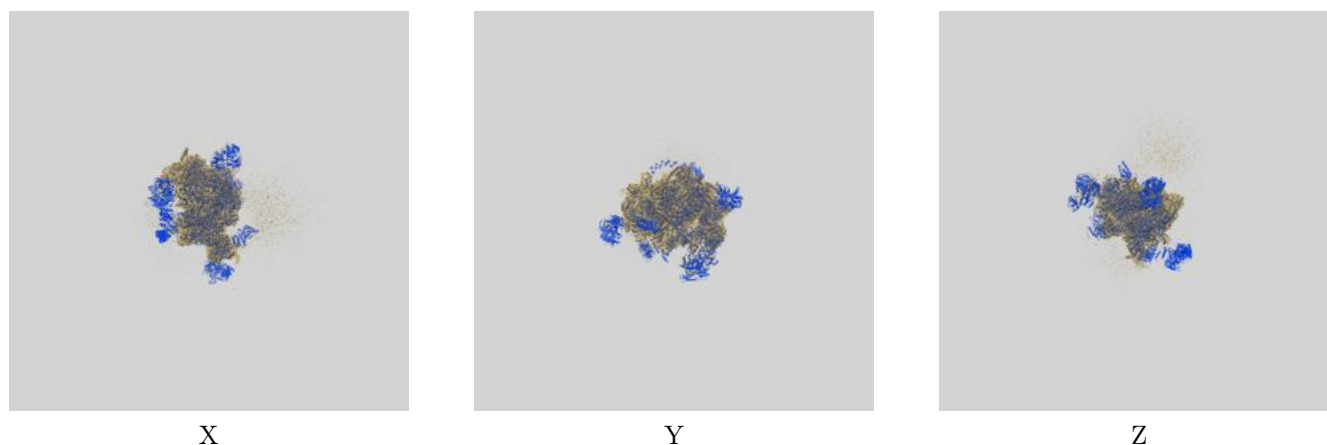
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

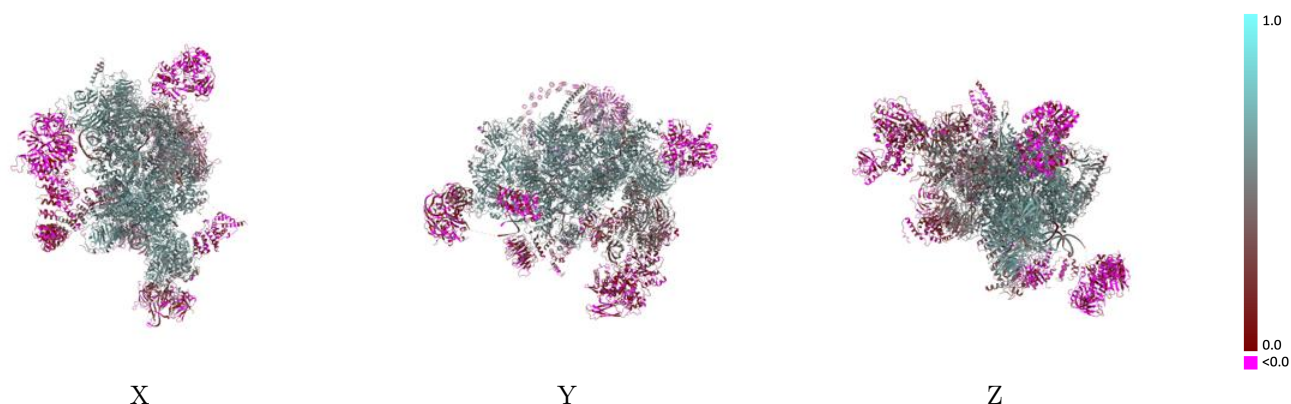
This section contains information regarding the fit between EMDB map EMD-30875 and PDB model 7DVQ. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



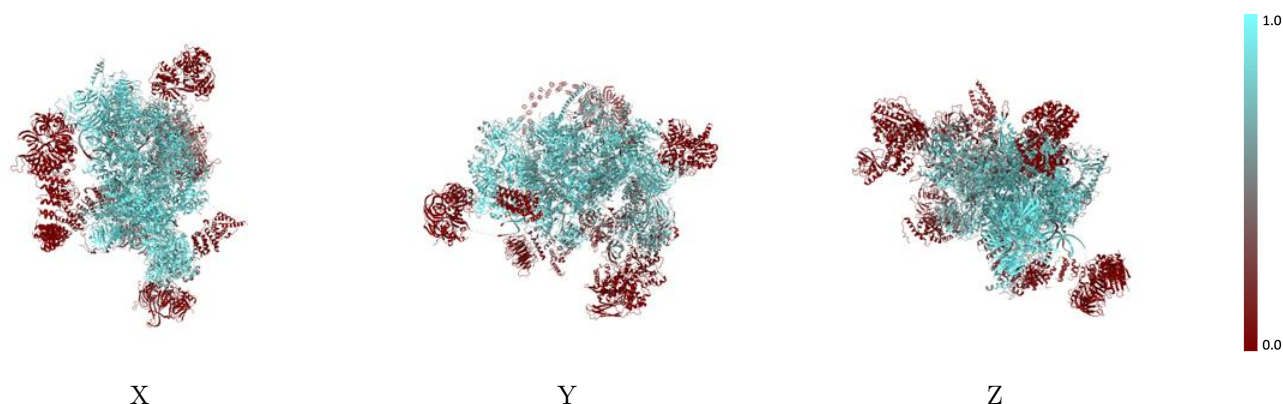
The images above show the 3D surface view of the map at the recommended contour level 0.014 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



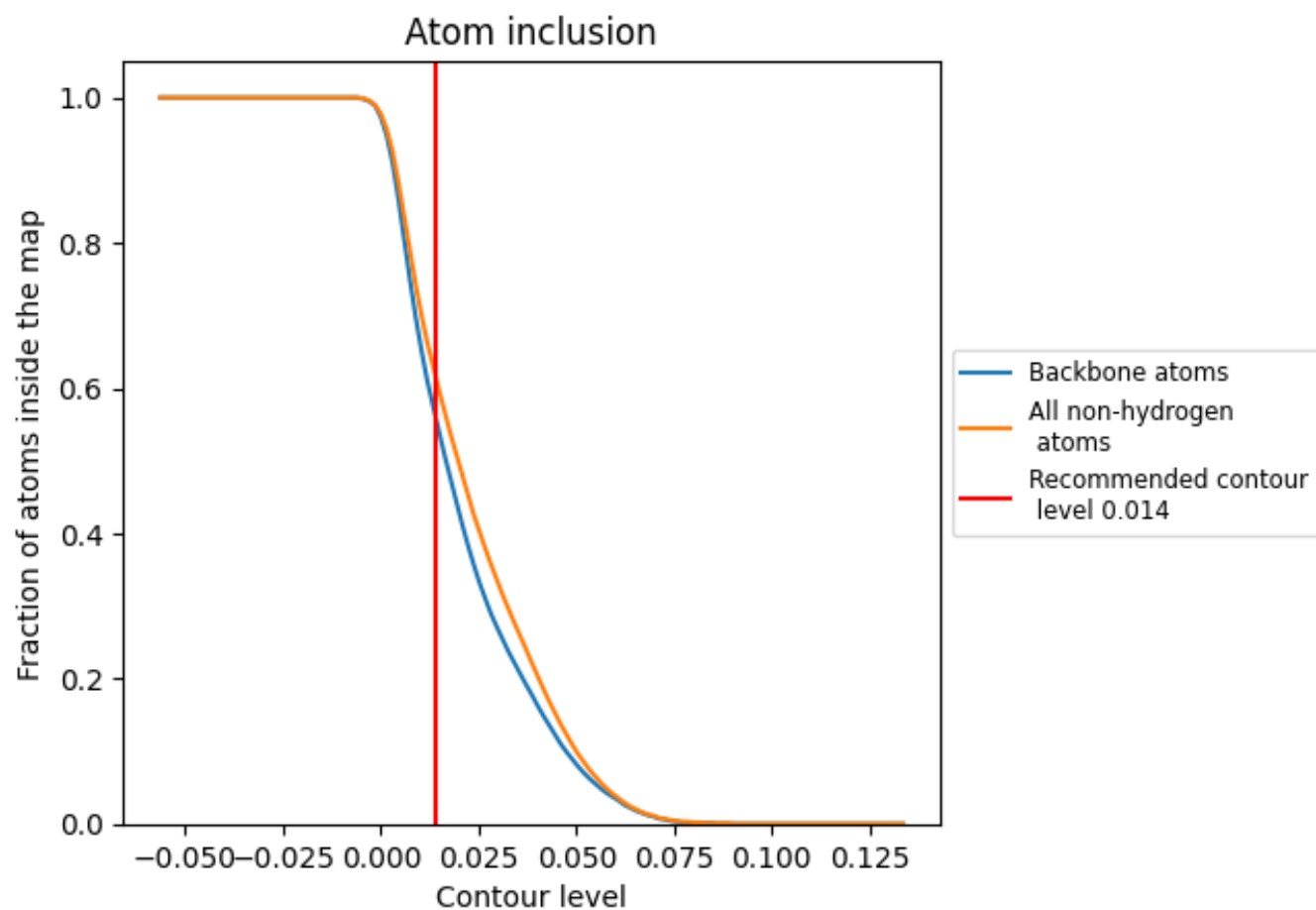
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.014).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 56% of all backbone atoms, 62% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6160	 0.4320
0	 0.8640	 0.6050
1	 0.8840	 0.5900
2	 0.7180	 0.5030
3	 0.8240	 0.5400
4	 0.0500	 0.0180
5	 0.7480	 0.5010
6	 0.9240	 0.6120
7	 0.8850	 0.5890
8	 0.8130	 0.5490
9	 0.5000	 0.3510
A	 0.8240	 0.5630
B	 0.6310	 0.4010
C	 0.8440	 0.5630
D	 0.3160	 0.2360
E	 0.0330	 0.1220
F	 0.7790	 0.4750
G	 0.7180	 0.4570
H	 0.6700	 0.4050
I	 0.4980	 0.3360
J	 0.0750	 0.2170
K	 0.1660	 0.1400
L	 0.8980	 0.5950
M	 0.6270	 0.4630
P	 0.7410	 0.5350
R	 0.6330	 0.5000
T	 0.9430	 0.6110
U	 0.9250	 0.6080
V	 0.4990	 0.3300
X	 0.6770	 0.4420
Y	 0.8180	 0.5610
Z	 0.7390	 0.5420
a	 0.0880	 0.2650
b	 0.0320	 0.1610
c	 0.0200	 0.0820



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Chain	Atom inclusion	Q-score
d	 0.0150	 0.0700
e	 0.0080	 0.0930
f	 0.0050	 0.0620
g	 0.0140	 0.1750
h	 0.0000	 -0.0340
i	 0.0020	 -0.0230
j	 0.0000	 0.0510
k	 0.0020	 0.0090
l	 0.0030	 -0.0030
m	 0.0030	 0.0080
n	 0.0030	 -0.0330
v	 0.8140	 0.5130
x	 0.0320	 0.0370
y	 0.3030	 0.2890
z	 0.8920	 0.5800