



## wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 02:47 PM UTC

PDB ID : 7DCO / pdb\_00007dco  
EMDB ID : EMD-30637  
Title : Cryo-EM structure of the activated spliceosome (Bact complex) at an atomic resolution of 2.5 angstrom  
Authors : Bai, R.; Wan, R.; Yan, C.; Qi, J.; Zhang, P.; Lei, J.; Shi, Y.  
Deposited on : 2020-10-26  
Resolution : 2.50 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

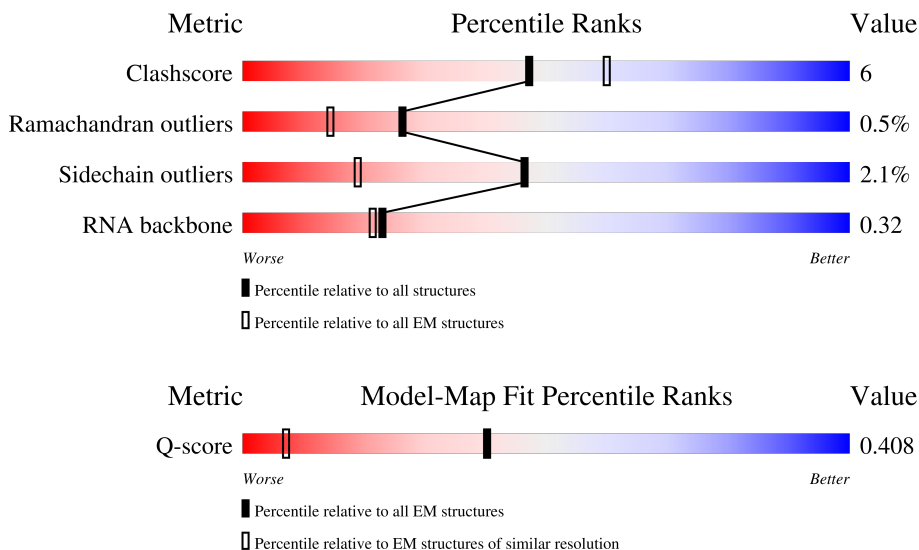
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01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

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 2.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7115 ( 2.00 - 3.00 )

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

Mol	Chain	Length	Quality of chain
1	A	2413	
2	B	214	
3	C	1008	




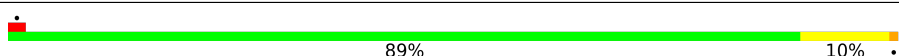

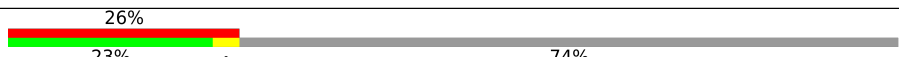
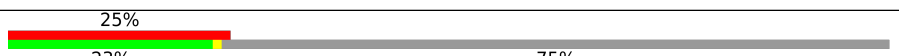


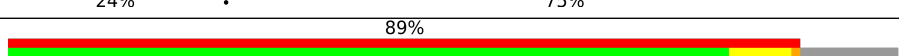
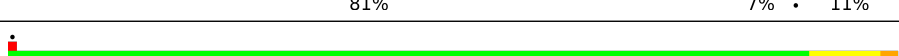
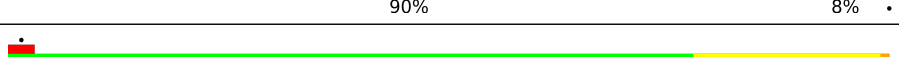

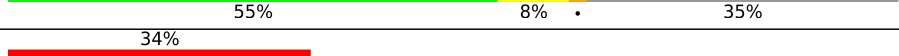
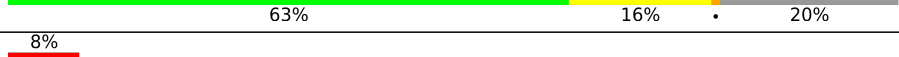




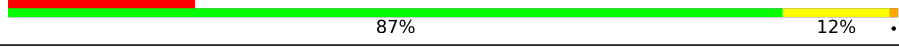
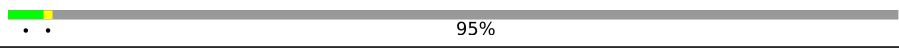
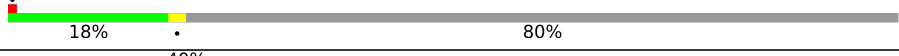



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Mol	Chain	Length	Quality of chain
4	D	2163	44% 74% 10% 15%
5	d	101	40% 78% 22%
6	a	196	18% 37% 63%
6	h	196	40% 27% 13% 60%
7	b	146	36% 51% 47%
7	m	146	56% 44% 12% 44%
8	c	110	66% 80% 18%
8	n	110	59% 44% 15% 41%
9	e	94	69% 77% 23%
9	i	94	80% 57% 22% 20%
10	f	86	76% 81% 19%
10	j	86	81% 69% 13% 19%
11	g	77	83% 91% 9%
11	k	77	90% 74% 16% 10%
12	F	112	12% 62% 24% 5% 8%
13	G	162	31% 30% 28% 7% 35%
14	H	1175	10% 9% 5% 86%
15	o	238	57% 53% 43%
16	p	111	68% 59% 8% 32%
17	l	81	100% 78% 22%
18	u	530	72% 71% 15% 13%
19	w	280	45% 41% 55%
20	v	266	42% 69% 9% 22%
21	1	971	82% 12%
22	2	238	16% 83% 8% 8%




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Mol	Chain	Length	Quality of chain
23	3	1361	
24	4	213	
25	5	107	
26	6	84	
27	L	590	
28	q	503	
28	r	503	
28	s	503	
28	t	503	
29	K	175	
30	N	157	
31	T	337	
32	P	379	
33	Q	364	
34	R	261	
35	S	175	
36	Y	204	
37	X	128	
38	Z	121	
39	W	455	
40	U	135	
41	V	577	
42	M	259	
43	z	301	
44	y	185	

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Mol	Chain	Length	Quality of chain
45	J	687	
46	I	859	
47	x	876	

## 2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 129875 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 PRP8 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	2205	18135	11656	3091	3324	64	0	0

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	179	3795	1699	660	1258	178	0	0

- Molecule 3 is a protein called SNU114 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	918	7328	4725	1218	1355	30	0	0

- Molecule 4 is a protein called BRR2 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	1828	14666	9388	2437	2784	57	0	0

- Molecule 5 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	d	79	316	158	79	79	0	0

- Molecule 6 is a protein called BJ4\_G0014900.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	a	73	292	146	73	73	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	h	78	Total	C	N	O	S	0	0
			610	389	110	108	3		

- Molecule 7 is a protein called SMD1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	b	77	Total	C	N	O	0	0	
			308	154	77	77			
7	m	82	Total	C	N	O	S	0	0
			644	409	110	123	2		

- Molecule 8 is a protein called BJ4\_G0037700.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	c	90	Total	C	N	O	0	0	
			360	180	90	90			
8	n	65	Total	C	N	O	S	0	0
			528	340	102	84	2		

- Molecule 9 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	e	72	Total	C	N	O	0	0	
			288	144	72	72			
9	i	75	Total	C	N	O	S	0	0
			575	379	92	101	3		

- Molecule 10 is a protein called Sm protein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	f	70	Total	C	N	O	0	0	
			280	140	70	70			
10	j	70	Total	C	N	O	S	0	0
			554	355	98	100	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	g	70	Total	C	N	O	0	0	
			280	140	70	70			
11	k	69	Total	C	N	O	S	0	0
			529	337	93	97	2		

- Molecule 12 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
12	F	103	2192	982	391	716	103	0	0

- Molecule 13 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
13	G	105	2099	942	330	723	104	0	0

- Molecule 14 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
14	H	169	3566	1594	595	1208	169	0	0

- Molecule 15 is a protein called HLJ1\_G0053790.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	o	135	841	538	142	161	0	0

- Molecule 16 is a protein called BJ4\_G0027490.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	p	75	476	310	83	83	0	0

- Molecule 17 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	l	81	611	390	106	113	2	0	0

- Molecule 18 is a protein called PRP9 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	u	461	3899	2477	675	732	15	0	0

- Molecule 19 is a protein called Pre-mRNA-splicing factor PRP21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	w	127	Total	C	N	O	S	0	0
			1084	689	193	196	6		

- Molecule 20 is a protein called PRP11 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	v	207	Total	C	N	O	S	0	0
			1621	1014	281	319	7		

- Molecule 21 is a protein called HSH155 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	1	930	Total	C	N	O	S	0	0
			7376	4723	1262	1348	43		

- Molecule 22 is a protein called HLJ1\_G0043010.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	2	220	Total	C	N	O	S	0	0
			1793	1158	311	314	10		

- Molecule 23 is a protein called RSE1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3	1207	Total	C	N	O	S	0	0
			9599	6134	1613	1801	51		

- Molecule 24 is a protein called HSH49 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	4	174	Total	C	N	O	S	0	0
			1433	932	240	259	2		

- Molecule 25 is a protein called BJ4\_G0056610.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	5	103	Total	C	N	O	S	0	0
			814	503	154	143	14		

- Molecule 26 is a protein called RDS3 complex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	6	84	Total	C	N	O	S	0	0
			693	429	130	132	2		

- Molecule 27 is a protein called Pre-mRNA-splicing factor CEF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	L	435	Total	C	N	O	S	0	0
			2901	1799	538	557	7		

- Molecule 28 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	s	124	Total	C	N	O	S	0	0
			819	518	132	167	2		
28	t	128	Total	C	N	O	S	0	0
			843	533	136	172	2		
28	q	129	Total	C	N	O	S	0	0
			850	537	137	174	2		
28	r	125	Total	C	N	O	S	0	0
			823	521	133	167	2		

- Molecule 29 is a protein called SNT309 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	K	155	Total	C	N	O	S	0	0
			920	581	159	179	1		

- Molecule 30 is a protein called BUD31 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	N	157	Total	C	N	O	S	0	0
			1291	808	240	232	11		

- Molecule 31 is a protein called HLJ1\_G0054350.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	T	337	Total	C	N	O	S	0	0
			2646	1669	466	501	10		

- Molecule 32 is a protein called Pre-mRNA-processing protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	P	246	1978	1233	359	380	6	0	0

- Molecule 33 is a protein called Pre-mRNA-splicing factor SLT11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	Q	292	2301	1461	399	426	15	0	0

- Molecule 34 is a protein called Pre-mRNA-splicing factor CWC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	R	261	2089	1320	369	388	12	0	0

- Molecule 35 is a protein called Pre-mRNA-splicing factor CWC15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	S	71	578	361	117	99	1	0	0

- Molecule 36 is a protein called Pre-mRNA leakage protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	Y	174	1386	868	233	275	10	0	0

- Molecule 37 is a protein called SX2\_G0027210.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
37	X	128	1051	662	181	208	0	0

- Molecule 38 is a protein called Pre-mRNA-splicing factor CWC26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	Z	121	920	575	161	182	2	0	0

- Molecule 39 is a protein called CDC40 isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
39	W	23	195	122	41	32	0	0

- Molecule 40 is a protein called Pre-mRNA-splicing factor CWC21.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
40	U	27	190	112	38	40	0	0

- Molecule 41 is a protein called CWC22 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	V	450	3660	2346	605	691	18	0	0

- Molecule 42 is a protein called Pre-mRNA-splicing factor CWC24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	M	176	1360	852	235	260	13	0	0

- Molecule 43 is a protein called CWC27 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	z	150	1224	789	206	223	6	0	0

- Molecule 44 is a protein called Pre-mRNA-splicing factor SPP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	y	73	572	371	93	107	1	0	0

- Molecule 45 is a protein called CLF1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	J	554	3595	2231	680	676	8	0	0

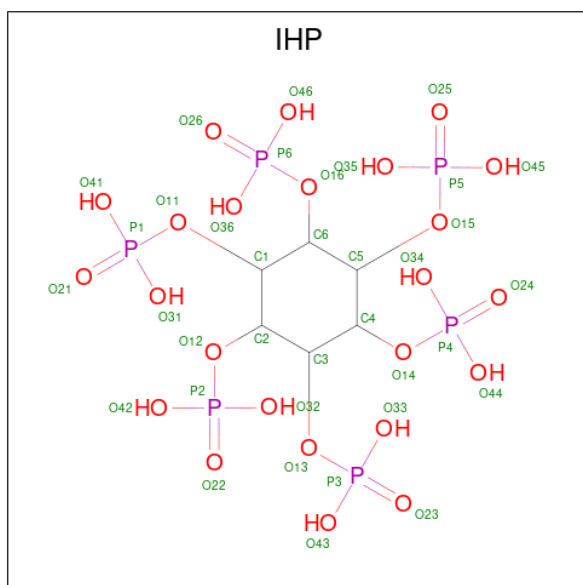
- Molecule 46 is a protein called SYF1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	I	580	3101	1897	590	613	1	0	0

- Molecule 47 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase-like protein PRP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	x	653	5193	3313	891	956	33	0	0

- Molecule 48 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula:  $C_6H_{18}O_{24}P_6$ ) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 49 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula:  $C_{10}H_{16}N_5O_{14}P_3$ ) (labeled as "Ligand of Interest" by depositor).



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Mol	Chain	Residues	Atoms		AltConf
52	v	1	Total 1	Zn 1	0
52	5	3	Total 3	Zn 3	0
52	N	3	Total 3	Zn 3	0
52	Q	2	Total 2	Zn 2	0
52	R	1	Total 1	Zn 1	0
52	M	3	Total 3	Zn 3	0

- Molecule 53 is water.

Mol	Chain	Residues	Atoms		AltConf
53	A	582	Total 582	O 582	0
53	B	127	Total 127	O 127	0
53	C	8	Total 8	O 8	0
53	D	2	Total 2	O 2	0
53	F	109	Total 109	O 109	0
53	G	56	Total 56	O 56	0
53	H	70	Total 70	O 70	0
53	v	29	Total 29	O 29	0
53	1	185	Total 185	O 185	0
53	2	51	Total 51	O 51	0
53	3	218	Total 218	O 218	0
53	5	53	Total 53	O 53	0
53	6	42	Total 42	O 42	0

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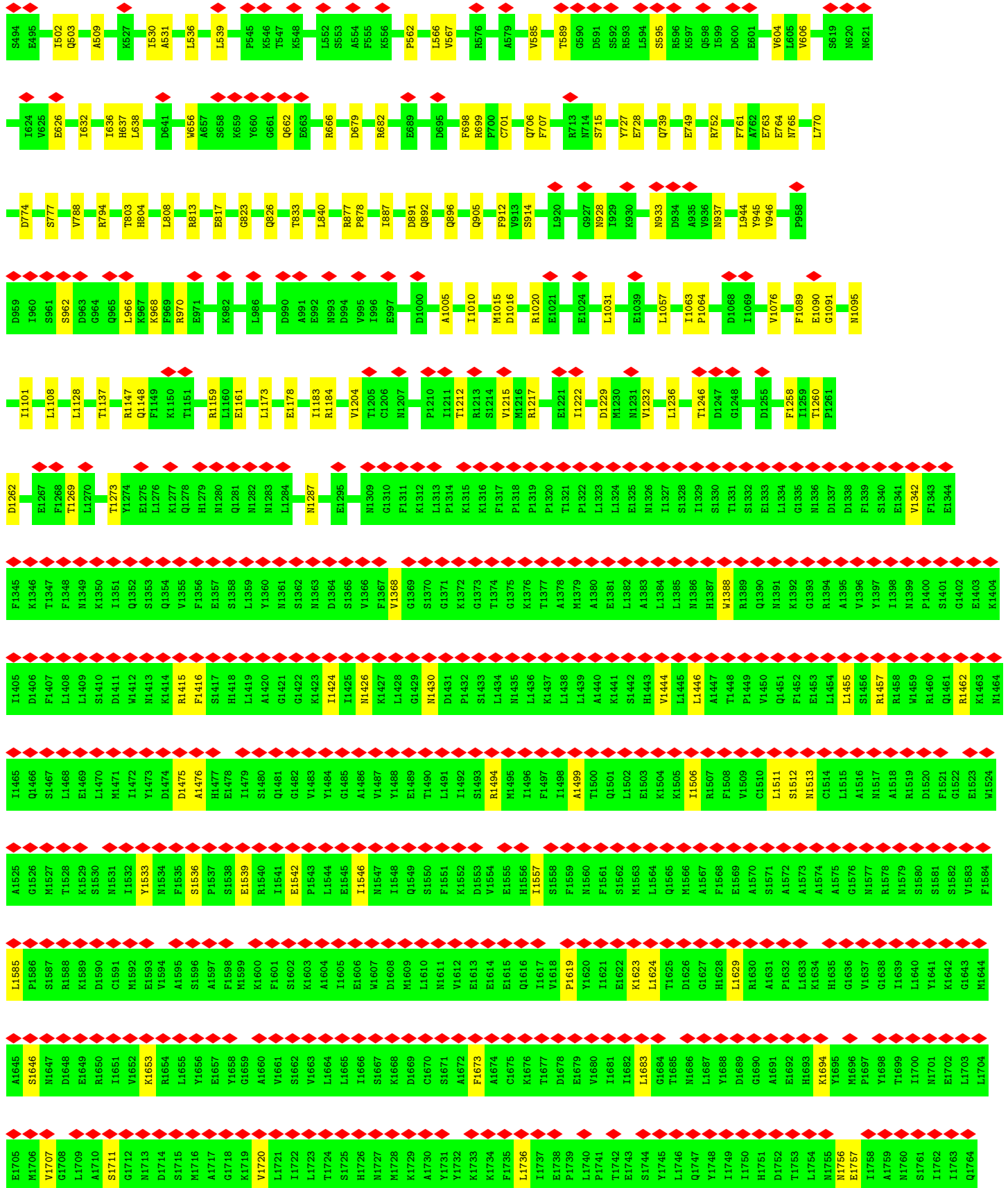
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Mol	Chain	Residues	Atoms		AltConf
53	L	18	Total 18	O 18	0
53	N	12	Total 12	O 12	0
53	T	39	Total 39	O 39	0
53	P	26	Total 26	O 26	0
53	R	8	Total 8	O 8	0
53	S	9	Total 9	O 9	0
53	X	13	Total 13	O 13	0
53	Z	9	Total 9	O 9	0
53	U	6	Total 6	O 6	0
53	V	21	Total 21	O 21	0
53	M	21	Total 21	O 21	0



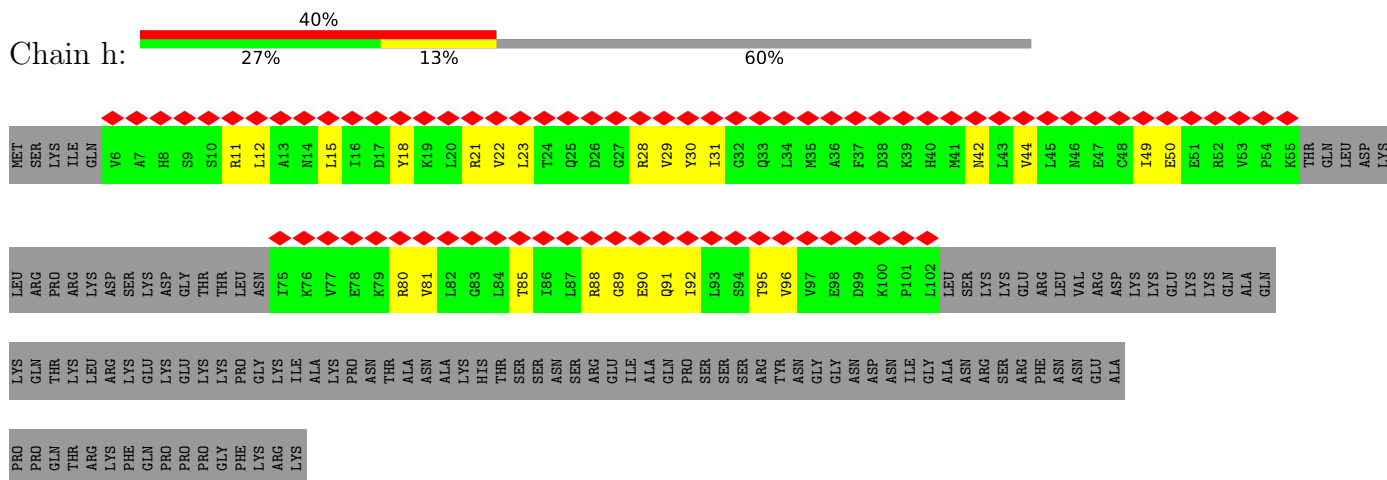




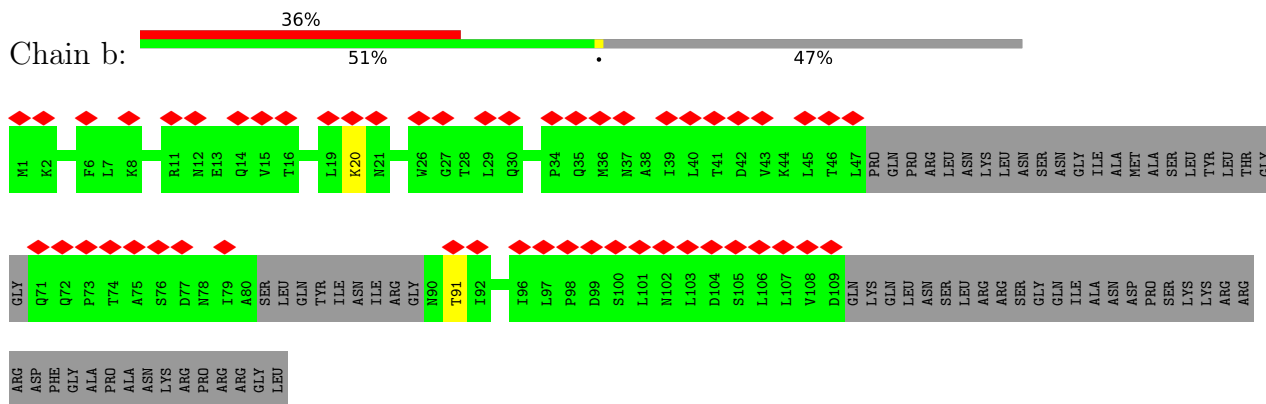




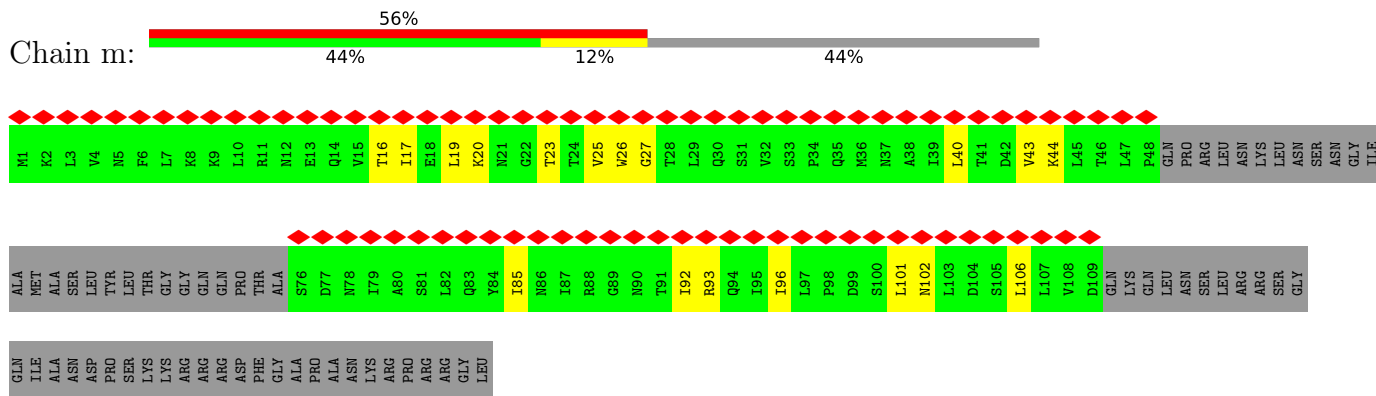
• Molecule 6: BJ4\_G0014900.mRNA.1.CDS.1



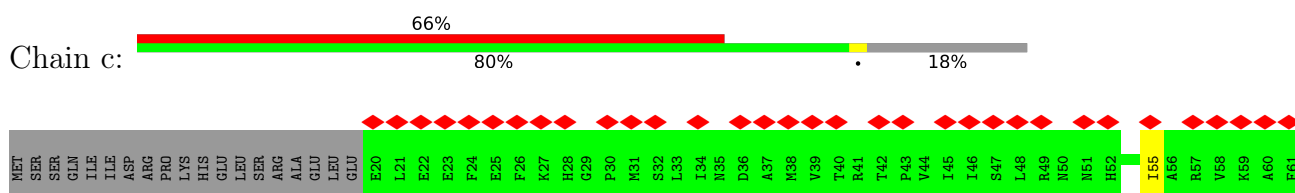
• Molecule 7: SMD1 isoform 1

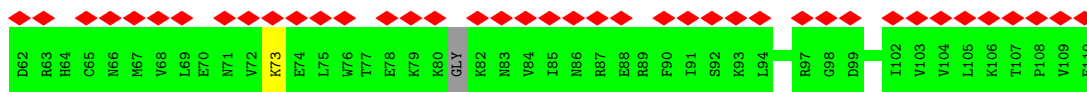


• Molecule 7: SMD1 isoform 1

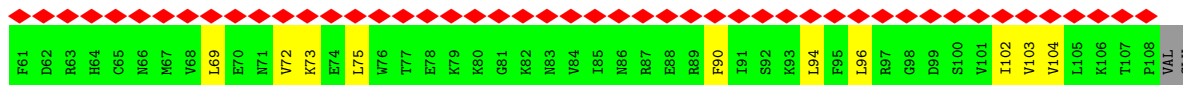
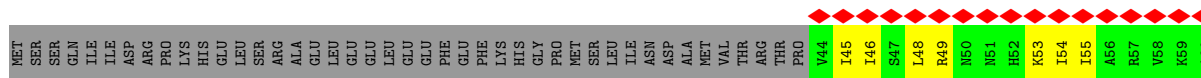
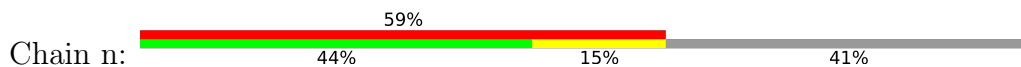


• Molecule 8: BJ4\_G0037700.mRNA.1.CDS.1

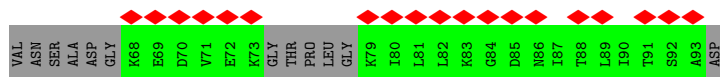
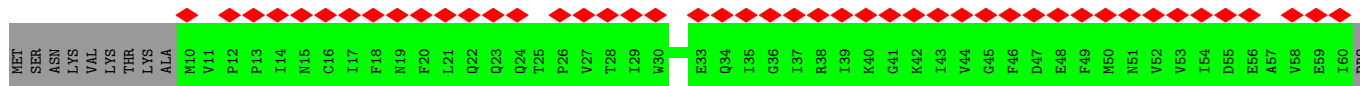
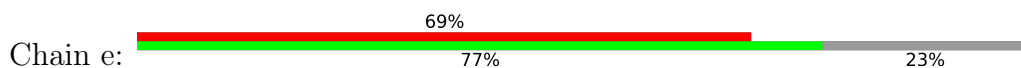




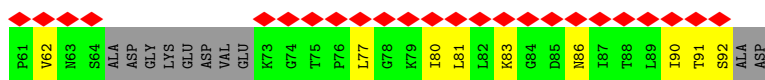
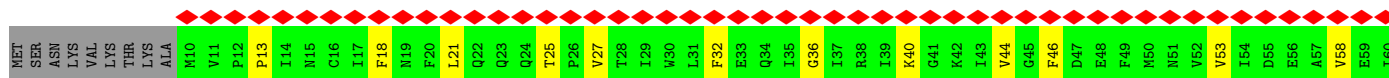
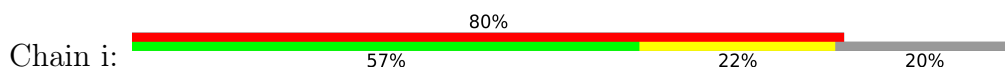
• Molecule 8: BJ4\_G0037700.mRNA.1.CDS.1



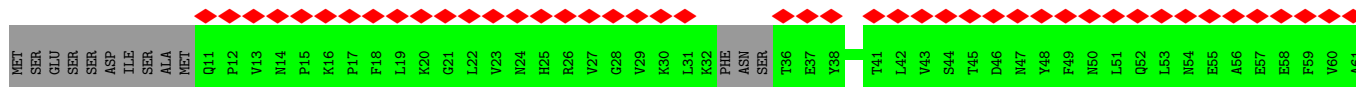
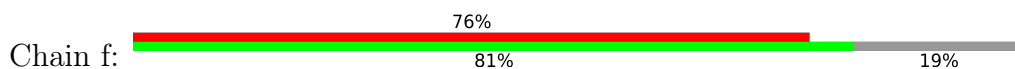
• Molecule 9: Small nuclear ribonucleoprotein E



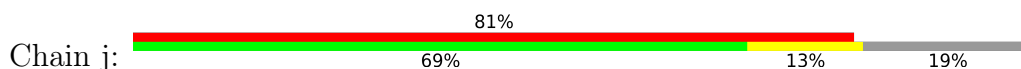
• Molecule 9: Small nuclear ribonucleoprotein E



• Molecule 10: Sm protein F

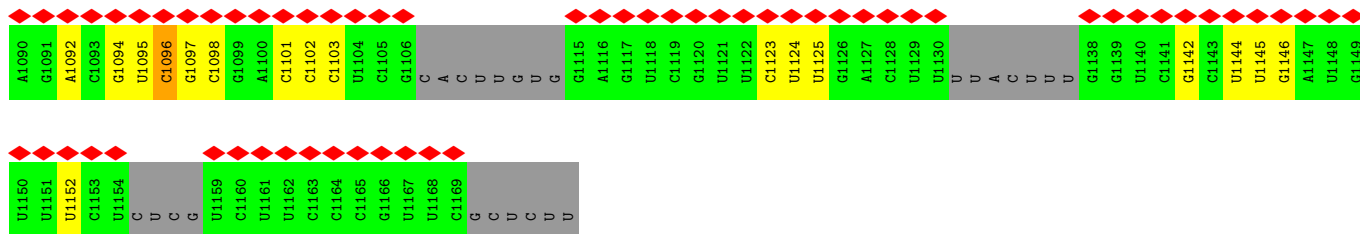


• Molecule 10: Sm protein F

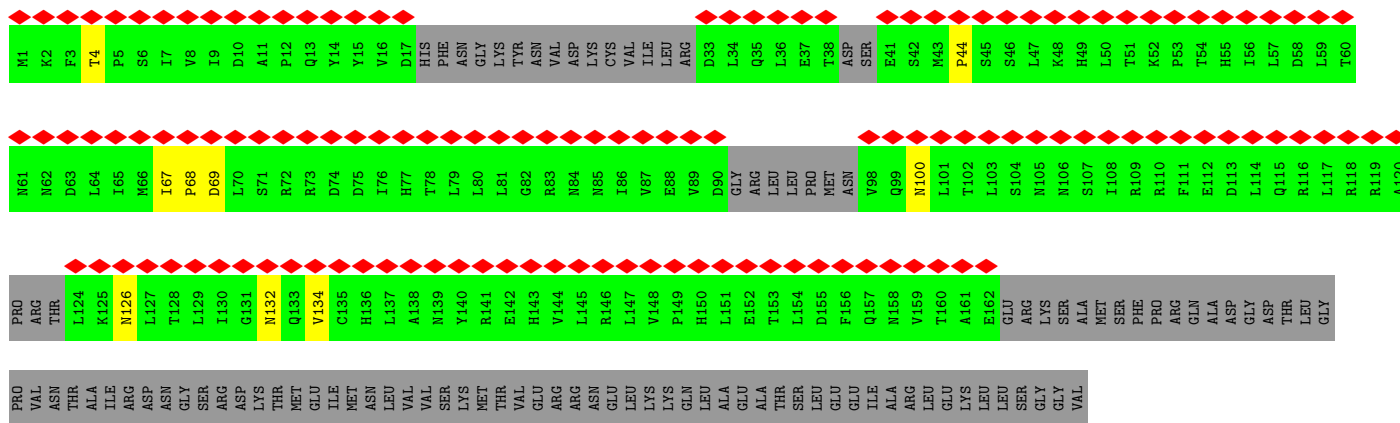




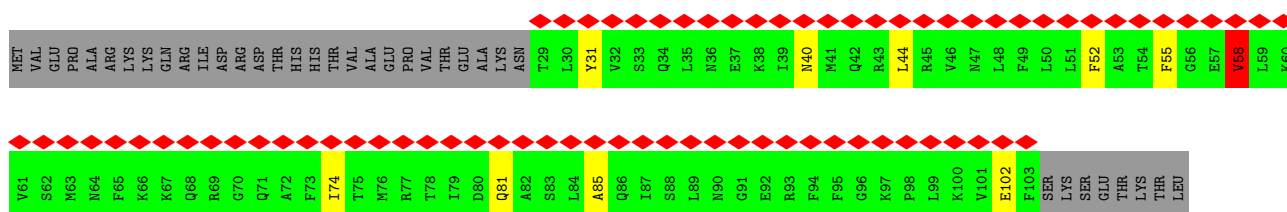




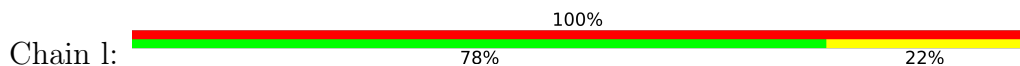
• Molecule 15: HLJ1\_G0053790.mRNA.1.CDS.1



• Molecule 16: BJ4\_G0027490.mRNA.1.CDS.1

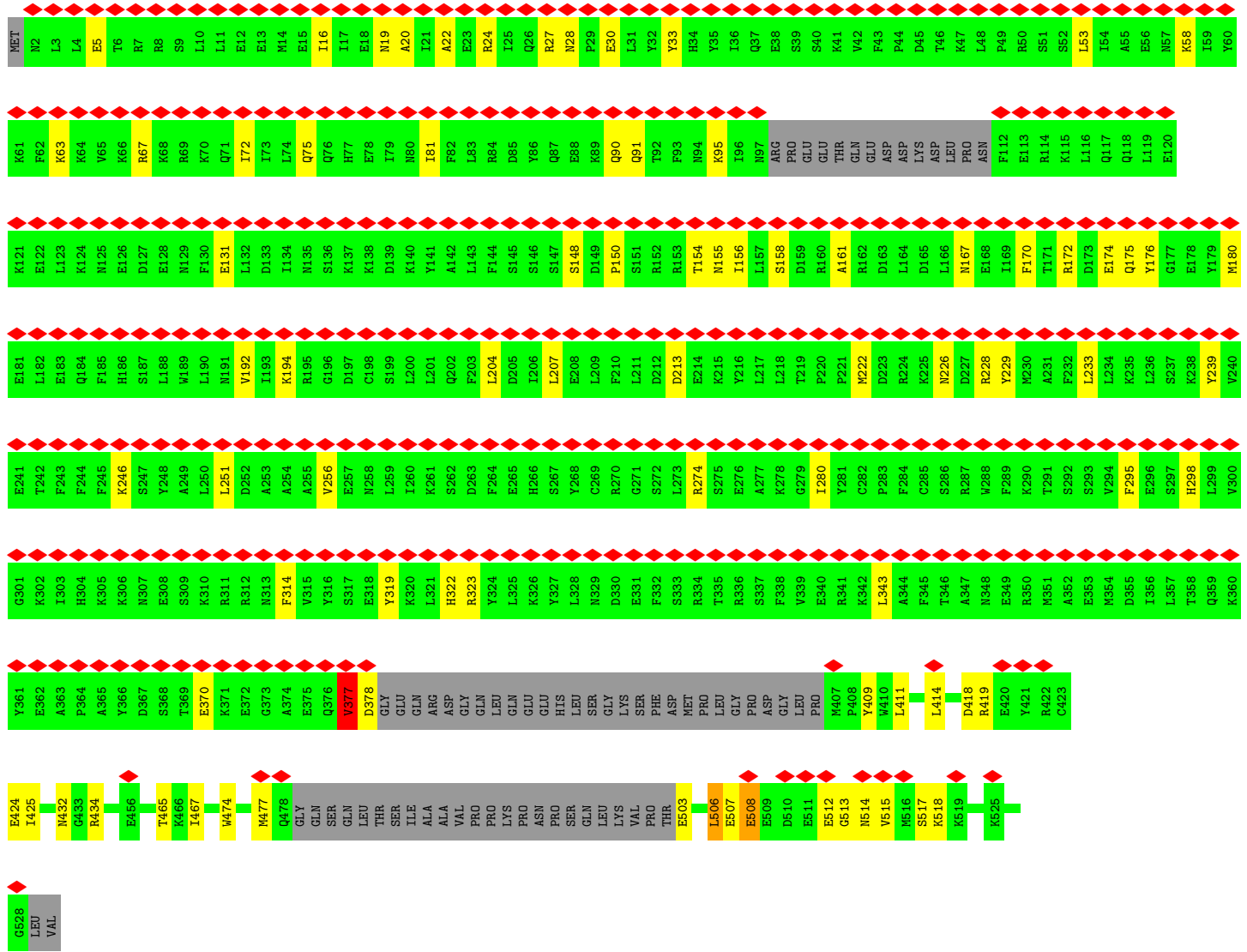


• Molecule 17: Small nuclear ribonucleoprotein Sm D3



• Molecule 18: PRP9 isoform 1

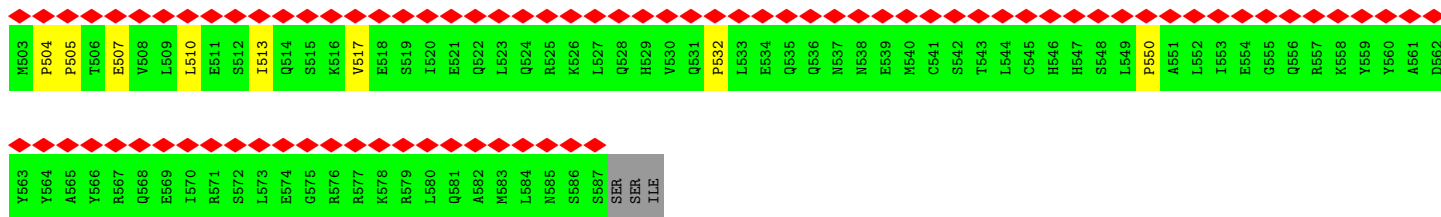




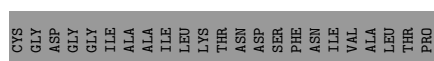
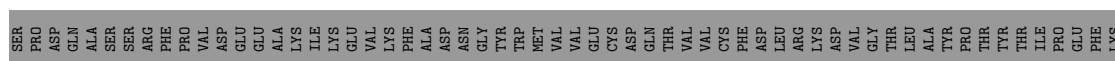
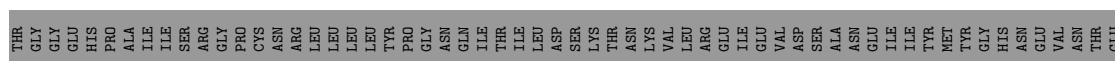
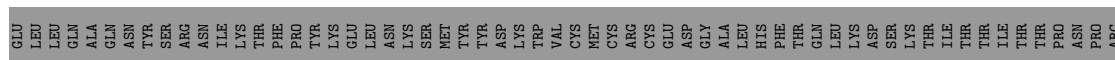
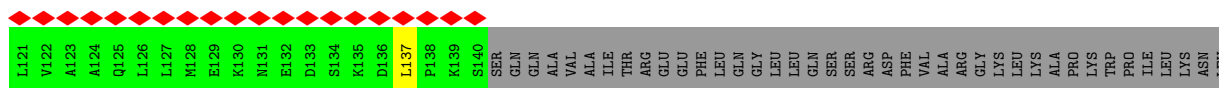
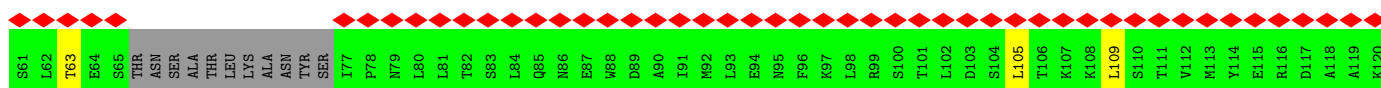




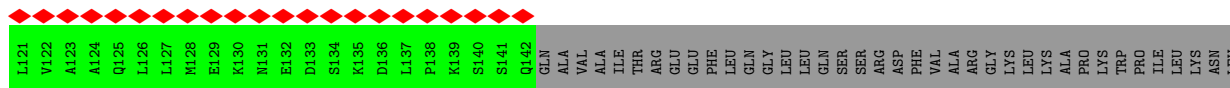
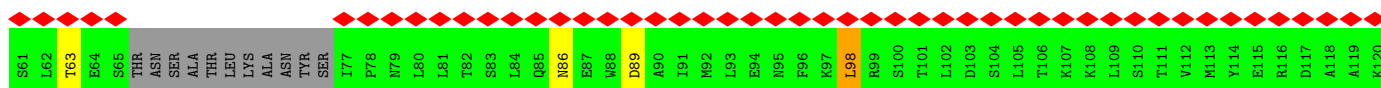
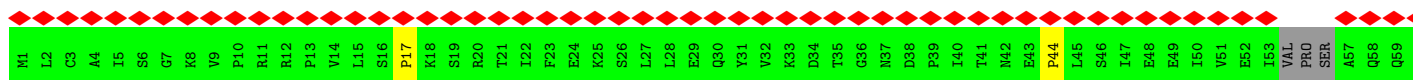




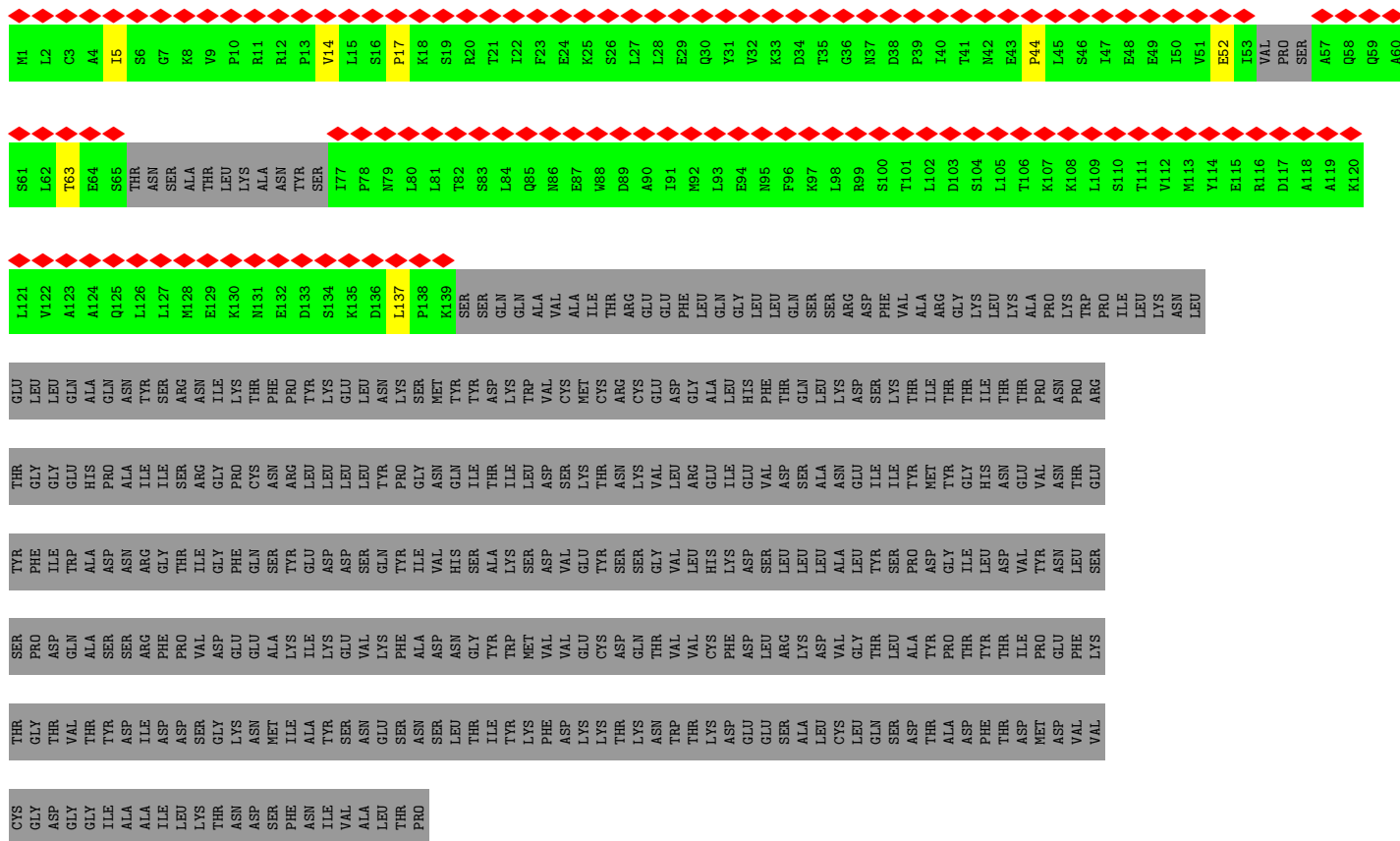
• Molecule 28: Pre-mRNA-processing factor 19



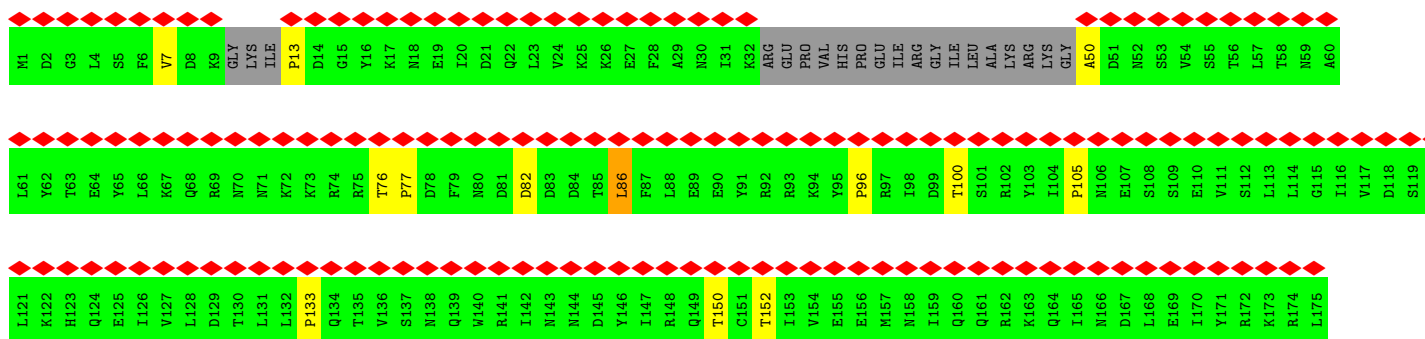
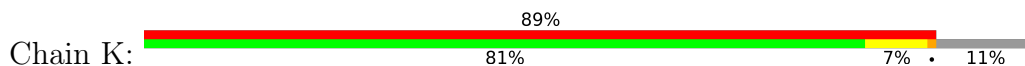
• Molecule 28: Pre-mRNA-processing factor 19



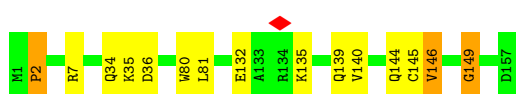




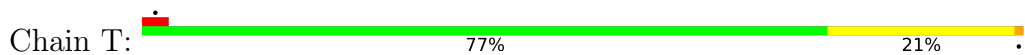
• Molecule 29: SNT309 isoform 1

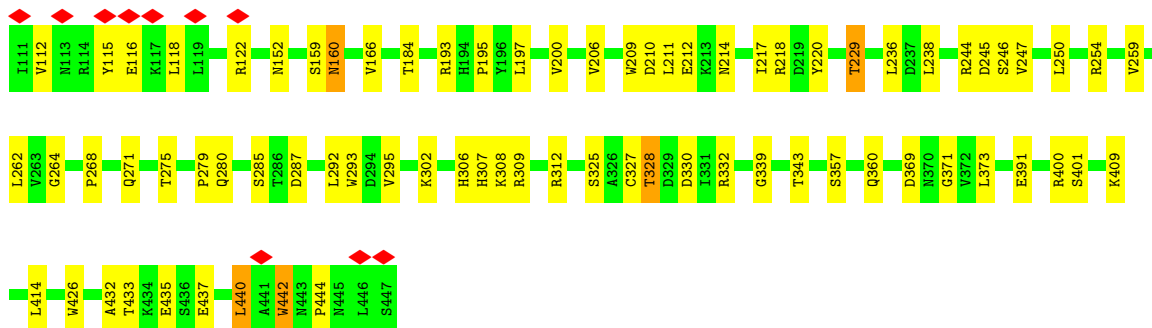


• Molecule 30: BUD31 isoform 1

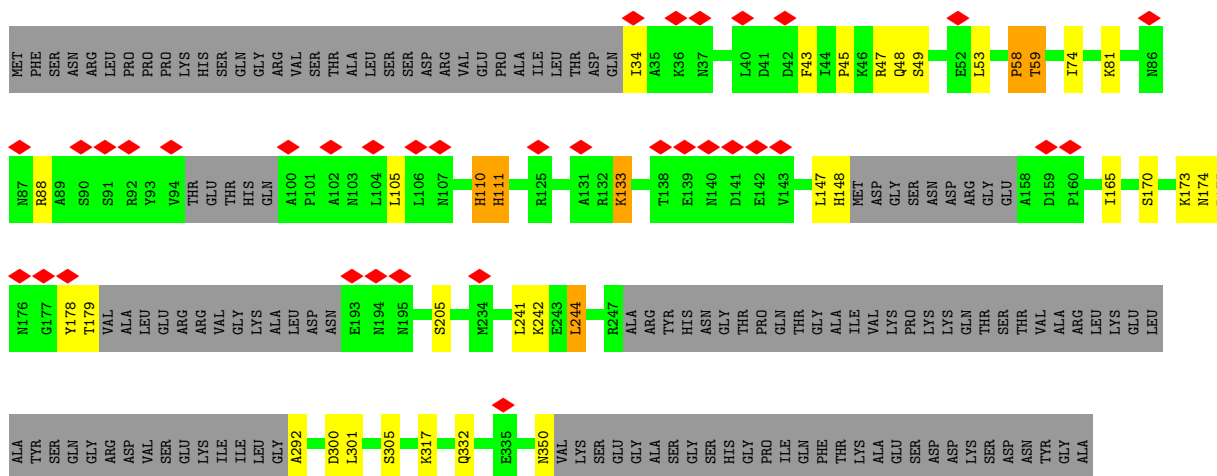


• Molecule 31: HLJ1\_G0054350.mRNA.1.CDS.1

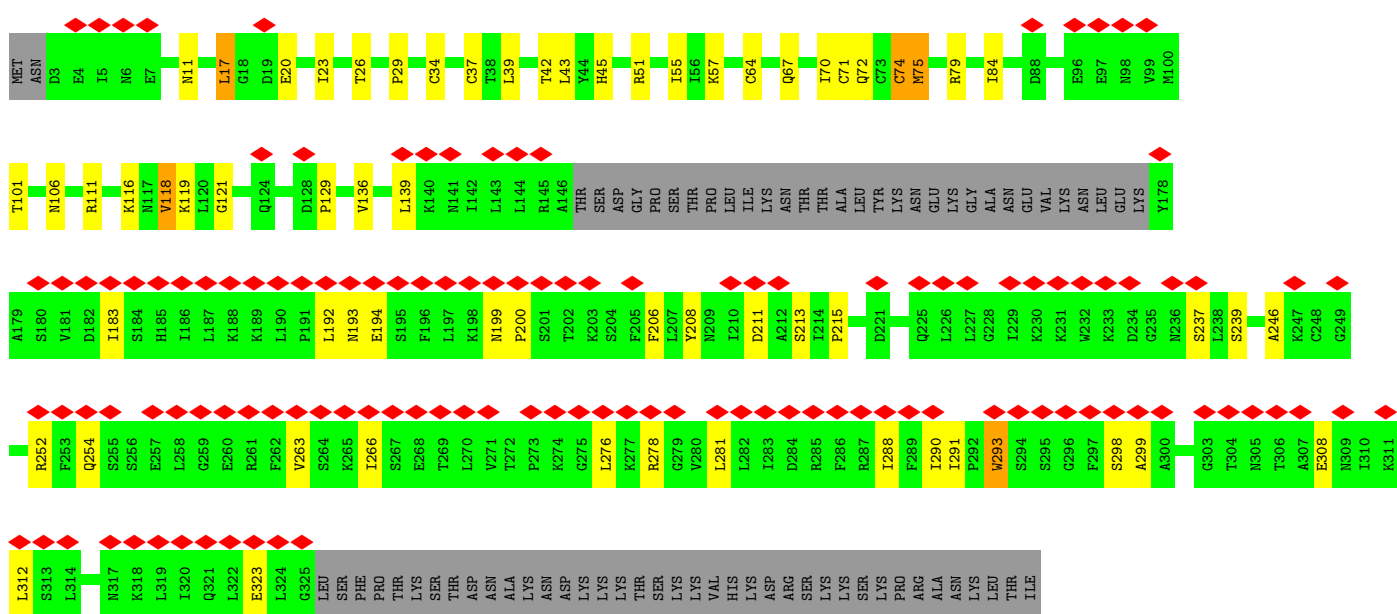




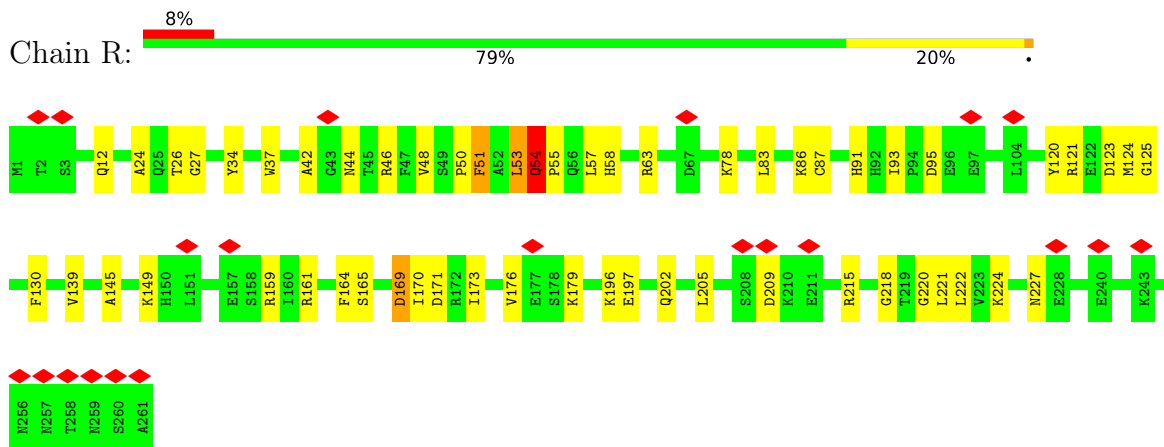
• Molecule 32: Pre-mRNA-processing protein 45



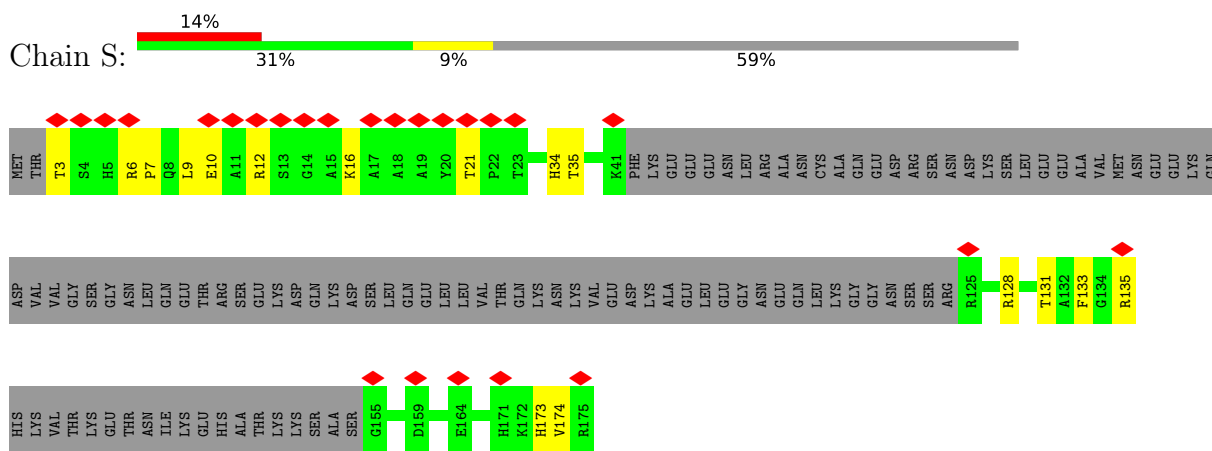
• Molecule 33: Pre-mRNA-splicing factor SLT11



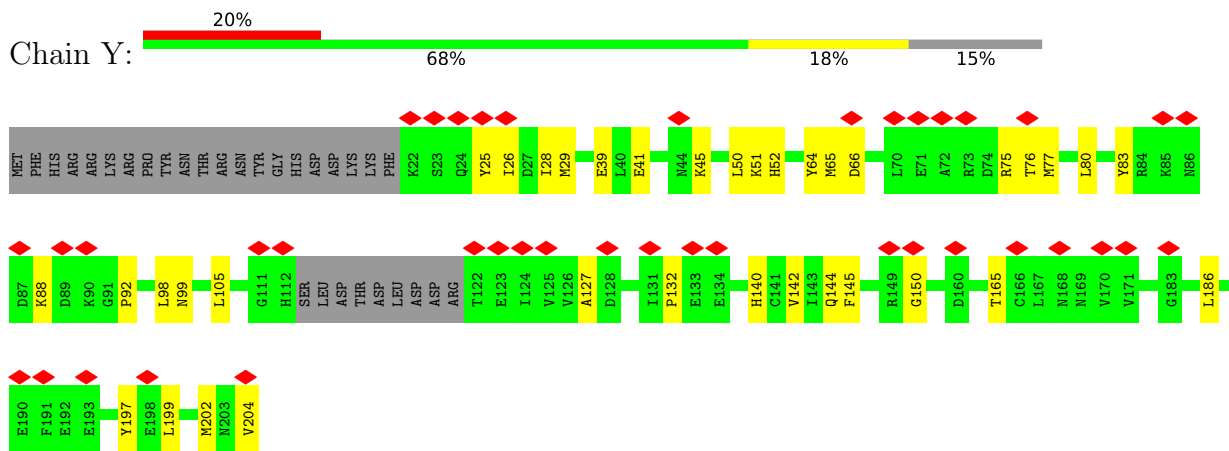
• Molecule 34: Pre-mRNA-splicing factor CWC2



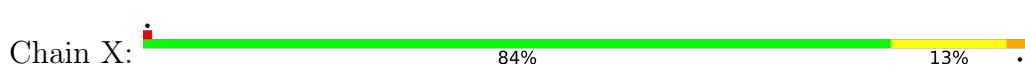
• Molecule 35: Pre-mRNA-splicing factor CWC15



• Molecule 36: Pre-mRNA leakage protein 1



• Molecule 37: SX2\_G0027210.mRNA.1.CDS.1













A421	I422	T423	T424	I425	F426	Q427	I428	H429	T430	T431	Q432	S433	L434	P435	G436	D437	I438	L439	V440	F441	L442	T443	G444	Q445	E446	E447	I448	E449	R450	T451	K452	T453	K454	L455	E456	E457	I458	M459	S460	K461	L462	G463	S464	R465	T466	K467	Q468	M469	I470	I471	T472	P473	I474	Y475	A476	N477	L478	P479	Q480
E481	Q482	Q483	L484	K485	I486	F487	Q488	P489	T490	P491	E492	M493	C494	R495	K496	V497	V498	L499	A500	T501	N502	I503	A504	E505	T506	S507	L508	T509	I510	D511	G512	I513	R514	Y515	V516	I517	D518	P519	G520	F521	V522	K523	E524	N525	S526	Y527	S530	T531	G532	M533	T534	Q535	L536	L537	T538	V539	F540	C541	
S542	R543	A544	S545	V546	D547	Q548	R549	A550	G551	R552	A553	G554	R555	V556	G557	P558	G559	K560	C561	T562	R563	I564	F565	T566	W568	S569	Y570	L571	H572	E573	L574	E575	L576	M577	P578	K579	P580	E581	I582	T583	R584	T585	N586	L587	S588	N589	T590	T591	G592	L592	L593	L594	L595	S596	L597	G598	V599	T600	D601
L602	I603	K604	F605	P606	L607	M608	D609	K610	P611	S612	I613	P614	T615	L616	R617	K618	S619	L620	E621	N622	L623	Y624	I625	L626	G627	A628	L629	N630	S631	K632	G633	T634	I635	T636	R637	L638	G639	K640	M641	M642	C643	E644	F645	P646	C647	E648	P649	E650	F651	A652	K653	V654	L655	Y656	T657	A658	A659	T660	H661
E662	Q663	C664	Q665	G666	V667	L668	E669	E670	C671	L672	T673	S676	M677	L678	H679	E680	T681	P682	S683	L684	F685	I686	Q688	K689	R690	D691	A692	A693	A694	S695	V696	L697	S698	E699	V700	E701	S702	D703	L706	Y707	L708	E709	I710	F711	N712	Q713	M714	R715	N716	S717	K718	F719	S720	R721	S722	W723			
C724	Q725	D726	H727	K728	I729	Q730	F731	K732	C671	L672	T673	L735	R736	N739	I740	R741	N742	Q743	L744	F745	R746	C747	S748	E749	K750	V751	G752	L753	V754	E755	K756	N757	D758	Q759	A760	R761	M762	K763	I764	G765	N766	I767	A768	G769	Y770	I771	M772	A773	R774	R777	P784	M785	I793	M798	G799				
R800	S801	S802	L805	R806	Y807	T812	S813	I814	W817	N818	H819	K820	E821	Q824	Y832	Q833	Q834	L835	R836	L837	T838	S839	K840	E841	F842	I843	R844	D845	K851	E852	E853	M854	M858	V859	I862	F863	R864	D865	L866	I867	ASP	ASP	LYS	THR	ASN	ARG	GLY	ARG	ARG										

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	705371	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 K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.251	Depositor
Minimum map value	-0.119	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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: ZN, GTP, CA, MG, IHP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.58	0/18595	0.72	4/25207 (0.0%)
2	B	0.37	0/4239	0.52	3/6598 (0.0%)
3	C	0.36	0/7484	0.64	5/10135 (0.0%)
4	D	0.26	0/14978	0.52	1/20302 (0.0%)
5	d	0.15	0/315	0.37	0/392
6	a	0.16	0/290	0.34	0/359
6	h	0.24	0/615	0.62	0/829
7	b	0.14	0/305	0.34	0/376
7	m	0.24	0/649	0.49	0/880
8	c	0.14	0/358	0.31	0/444
8	n	0.27	0/535	0.60	0/717
9	e	0.14	0/285	0.31	0/351
9	i	0.27	0/585	0.58	0/795
10	f	0.16	0/278	0.50	0/344
10	j	0.28	0/564	0.68	0/761
11	g	0.14	0/277	0.38	0/341
11	k	0.23	0/532	0.53	0/715
12	F	0.37	0/2452	0.54	0/3817
13	G	0.35	0/2338	0.57	1/3621 (0.0%)
14	H	0.29	0/3969	0.45	0/6159
15	o	0.20	0/839	0.57	1/1127 (0.1%)
16	p	0.20	0/478	0.58	1/640 (0.2%)
17	l	0.27	0/620	0.58	0/841
18	u	0.26	0/3976	0.56	0/5327
19	w	0.21	0/1105	0.46	0/1475
20	v	0.47	0/1647	0.69	0/2213
21	1	0.58	0/7522	0.79	5/10203 (0.0%)
22	2	0.51	0/1840	0.67	0/2484
23	3	0.55	1/9789 (0.0%)	0.77	5/13273 (0.0%)
24	4	0.27	0/1457	0.55	0/1959
25	5	0.65	0/827	0.84	1/1105 (0.1%)
26	6	0.70	0/702	0.81	0/939

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
27	L	0.38	0/2924	0.75	14/3954 (0.4%)
28	q	0.21	0/856	0.55	0/1155
28	r	0.19	0/828	0.47	1/1117 (0.1%)
28	s	0.18	0/824	0.43	0/1111
28	t	0.19	0/848	0.42	0/1143
29	K	0.20	0/918	0.54	0/1236
30	N	0.52	0/1315	0.73	2/1759 (0.1%)
31	T	0.54	0/2704	0.73	0/3676
32	P	0.44	0/2008	0.72	5/2703 (0.2%)
33	Q	0.35	0/2339	0.79	4/3154 (0.1%)
34	R	0.37	0/2135	0.66	2/2871 (0.1%)
35	S	0.40	0/592	0.76	0/790
36	Y	0.28	0/1408	0.58	0/1900
37	X	0.52	0/1071	0.79	1/1445 (0.1%)
38	Z	0.47	0/936	0.63	0/1264
39	W	0.33	0/200	0.64	0/264
40	U	0.46	0/191	0.69	0/254
41	V	0.40	0/3720	0.63	0/5016
42	M	0.48	0/1385	0.68	3/1862 (0.2%)
43	z	0.35	0/1252	0.65	0/1692
44	y	0.36	0/577	0.65	0/765
45	J	0.31	0/3635	0.68	8/4962 (0.2%)
46	I	0.31	0/3095	0.82	23/4242 (0.5%)
47	x	0.49	0/5290	0.59	0/7155
All	All	0.43	1/131496 (0.0%)	0.65	90/180219 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	3	528	PRO	CA-C	5.21	1.54	1.51

The worst 5 of 90 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	L	417	PRO	N-CA-CB	8.57	111.40	103.08
23	3	435	ASN	N-CA-C	7.84	120.43	110.24
2	B	27	G	C2'-C3'-O3'	7.81	121.21	109.50
46	I	773	PRO	N-CA-CB	7.75	110.60	103.08
27	L	432	PRO	N-CA-CB	7.74	110.55	103.20

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

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	18135	0	18054	199	0
2	B	3795	0	1919	67	0
3	C	7328	0	7505	105	0
4	D	14666	0	14661	122	0
5	d	316	0	86	0	0
6	a	292	0	78	0	0
6	h	610	0	640	26	0
7	b	308	0	78	1	0
7	m	644	0	686	13	0
8	c	360	0	89	1	0
8	n	528	0	573	12	0
9	e	288	0	74	0	0
9	i	575	0	597	20	0
10	f	280	0	77	0	0
10	j	554	0	556	8	0
11	g	280	0	79	0	0
11	k	529	0	557	17	0
12	F	2192	0	1106	20	0
13	G	2099	0	1055	43	0
14	H	3566	0	1809	56	0
15	o	841	0	614	2	0
16	p	476	0	378	11	0
17	l	611	0	627	22	0
18	u	3899	0	3826	63	0
19	w	1084	0	1081	9	0
20	v	1621	0	1596	20	0
21	1	7376	0	7521	83	0
22	2	1793	0	1827	18	0
23	3	9599	0	9679	158	0
24	4	1433	0	1461	16	0
25	5	814	0	809	5	0
26	6	693	0	705	12	0
27	L	2901	0	2325	29	0
28	q	850	0	682	6	0
28	r	823	0	654	2	0
28	s	819	0	657	3	0
28	t	843	0	672	2	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	K	920	0	603	5	0
30	N	1291	0	1312	8	0
31	T	2646	0	2639	54	0
32	P	1978	0	1981	37	0
33	Q	2301	0	2366	46	0
34	R	2089	0	2053	52	0
35	S	578	0	565	26	0
36	Y	1386	0	1353	27	0
37	X	1051	0	1015	23	0
38	Z	920	0	841	15	0
39	W	195	0	198	3	0
40	U	190	0	186	3	0
41	V	3660	0	3706	40	0
42	M	1360	0	1280	18	0
43	z	1224	0	1217	28	0
44	y	572	0	597	9	0
45	J	3595	0	2639	39	0
46	I	3101	0	1639	32	0
47	x	5193	0	5347	60	0
48	A	36	0	6	2	0
49	C	32	0	12	2	0
50	3	1	0	0	0	0
50	C	1	0	0	0	0
50	F	4	0	0	0	0
51	C	1	0	0	0	0
52	5	3	0	0	0	0
52	M	3	0	0	0	0
52	N	3	0	0	0	0
52	Q	2	0	0	0	0
52	R	1	0	0	0	0
52	u	2	0	0	0	0
52	v	1	0	0	0	0
53	1	185	0	0	4	0
53	2	51	0	0	1	0
53	3	218	0	0	7	0
53	5	53	0	0	0	0
53	6	42	0	0	1	0
53	A	582	0	0	9	0
53	B	127	0	0	2	0
53	C	8	0	0	0	0
53	D	2	0	0	0	0
53	F	109	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	G	56	0	0	1	0
53	H	70	0	0	0	0
53	L	18	0	0	0	0
53	M	21	0	0	0	0
53	N	12	0	0	0	0
53	P	26	0	0	2	0
53	R	8	0	0	0	0
53	S	9	0	0	0	0
53	T	39	0	0	0	0
53	U	6	0	0	0	0
53	V	21	0	0	1	0
53	X	13	0	0	1	0
53	Z	9	0	0	0	0
53	v	29	0	0	0	0
All	All	129875	0	116948	1450	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 6.

The worst 5 of 1450 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)
1:A:784:GLN:HG2	14:H:19:U:C5	1.67	1.28
18:u:506:LEU:CD2	18:u:518:LYS:HD2	1.64	1.26
46:I:466:ALA:CB	46:I:470:TRP:CB	2.20	1.19
27:L:224:MET:SD	27:L:225:PRO:HD3	1.82	1.19
27:L:224:MET:SD	27:L:225:PRO:CD	2.33	1.17

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	2199/2413 (91%)	2127 (97%)	68 (3%)	4 (0%)	43	63
3	C	912/1008 (90%)	877 (96%)	33 (4%)	2 (0%)	43	63
4	D	1820/2163 (84%)	1759 (97%)	60 (3%)	1 (0%)	48	68
5	d	77/101 (76%)	69 (90%)	8 (10%)	0	100	100
6	a	69/196 (35%)	64 (93%)	5 (7%)	0	100	100
6	h	74/196 (38%)	70 (95%)	4 (5%)	0	100	100
7	b	71/146 (49%)	69 (97%)	2 (3%)	0	100	100
7	m	78/146 (53%)	77 (99%)	1 (1%)	0	100	100
8	c	86/110 (78%)	79 (92%)	7 (8%)	0	100	100
8	n	63/110 (57%)	57 (90%)	6 (10%)	0	100	100
9	e	66/94 (70%)	63 (96%)	3 (4%)	0	100	100
9	i	71/94 (76%)	70 (99%)	1 (1%)	0	100	100
10	f	66/86 (77%)	59 (89%)	7 (11%)	0	100	100
10	j	66/86 (77%)	65 (98%)	1 (2%)	0	100	100
11	g	64/77 (83%)	61 (95%)	3 (5%)	0	100	100
11	k	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
15	o	125/238 (52%)	115 (92%)	8 (6%)	2 (2%)	7	14
16	p	73/111 (66%)	73 (100%)	0	0	100	100
17	l	79/81 (98%)	73 (92%)	6 (8%)	0	100	100
18	u	453/530 (86%)	423 (93%)	29 (6%)	1 (0%)	43	63
19	w	123/280 (44%)	117 (95%)	6 (5%)	0	100	100
20	v	201/266 (76%)	185 (92%)	16 (8%)	0	100	100
21	1	926/971 (95%)	898 (97%)	23 (2%)	5 (0%)	24	43
22	2	214/238 (90%)	208 (97%)	4 (2%)	2 (1%)	14	27
23	3	1193/1361 (88%)	1124 (94%)	65 (5%)	4 (0%)	36	55
24	4	166/213 (78%)	161 (97%)	5 (3%)	0	100	100
25	5	101/107 (94%)	99 (98%)	2 (2%)	0	100	100
26	6	82/84 (98%)	81 (99%)	0	1 (1%)	10	20
27	L	427/590 (72%)	391 (92%)	26 (6%)	10 (2%)	5	8
28	q	125/503 (25%)	116 (93%)	9 (7%)	0	100	100
28	r	119/503 (24%)	114 (96%)	5 (4%)	0	100	100
28	s	118/503 (24%)	114 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	t	122/503 (24%)	118 (97%)	4 (3%)	0	100	100
29	K	149/175 (85%)	140 (94%)	7 (5%)	2 (1%)	9	18
30	N	155/157 (99%)	148 (96%)	6 (4%)	1 (1%)	21	38
31	T	335/337 (99%)	317 (95%)	14 (4%)	4 (1%)	10	20
32	P	236/379 (62%)	228 (97%)	5 (2%)	3 (1%)	9	18
33	Q	288/364 (79%)	265 (92%)	20 (7%)	3 (1%)	12	24
34	R	259/261 (99%)	241 (93%)	17 (7%)	1 (0%)	30	49
35	S	65/175 (37%)	61 (94%)	4 (6%)	0	100	100
36	Y	170/204 (83%)	163 (96%)	6 (4%)	1 (1%)	21	38
37	X	126/128 (98%)	122 (97%)	4 (3%)	0	100	100
38	Z	119/121 (98%)	117 (98%)	2 (2%)	0	100	100
39	W	21/455 (5%)	20 (95%)	1 (5%)	0	100	100
40	U	25/135 (18%)	24 (96%)	1 (4%)	0	100	100
41	V	446/577 (77%)	427 (96%)	19 (4%)	0	100	100
42	M	172/259 (66%)	163 (95%)	8 (5%)	1 (1%)	21	38
43	z	146/301 (48%)	126 (86%)	18 (12%)	2 (1%)	9	17
44	y	63/185 (34%)	57 (90%)	6 (10%)	0	100	100
45	J	528/687 (77%)	493 (93%)	31 (6%)	4 (1%)	16	31
46	I	544/859 (63%)	491 (90%)	36 (7%)	17 (3%)	3	5
47	x	651/876 (74%)	617 (95%)	33 (5%)	1 (0%)	43	63
All	All	14992/20820 (72%)	14260 (95%)	660 (4%)	72 (0%)	26	43

5 of 72 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	91	VAL
22	2	268	ASP
23	3	585	GLN
27	L	367	VAL
27	L	417	PRO

### 5.3.2 Protein sidechains [i](#)

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1997/2182 (92%)	1954 (98%)	43 (2%)	45	73
3	C	828/910 (91%)	815 (98%)	13 (2%)	55	79
4	D	1651/1955 (84%)	1646 (100%)	5 (0%)	86	94
6	h	67/176 (38%)	67 (100%)	0	100	100
7	m	77/129 (60%)	77 (100%)	0	100	100
8	n	59/103 (57%)	59 (100%)	0	100	100
9	i	65/83 (78%)	65 (100%)	0	100	100
10	j	61/77 (79%)	61 (100%)	0	100	100
11	k	58/66 (88%)	57 (98%)	1 (2%)	53	78
15	o	44/219 (20%)	42 (96%)	2 (4%)	24	49
16	p	23/100 (23%)	22 (96%)	1 (4%)	26	51
17	l	67/70 (96%)	67 (100%)	0	100	100
18	u	426/492 (87%)	422 (99%)	4 (1%)	70	87
19	w	118/259 (46%)	118 (100%)	0	100	100
20	v	182/236 (77%)	181 (100%)	1 (0%)	81	92
21	1	817/867 (94%)	785 (96%)	32 (4%)	28	55
22	2	197/212 (93%)	194 (98%)	3 (2%)	57	80
23	3	1113/1244 (90%)	1070 (96%)	43 (4%)	28	55
24	4	154/189 (82%)	153 (99%)	1 (1%)	78	91
25	5	93/97 (96%)	91 (98%)	2 (2%)	45	73
26	6	76/76 (100%)	76 (100%)	0	100	100
27	L	195/525 (37%)	186 (95%)	9 (5%)	24	48
28	q	65/451 (14%)	61 (94%)	4 (6%)	16	34
28	r	59/451 (13%)	56 (95%)	3 (5%)	21	43
28	s	61/451 (14%)	58 (95%)	3 (5%)	22	45
28	t	62/451 (14%)	58 (94%)	4 (6%)	15	32
29	K	37/165 (22%)	27 (73%)	10 (27%)	0	1
30	N	141/141 (100%)	137 (97%)	4 (3%)	38	66
31	T	295/295 (100%)	288 (98%)	7 (2%)	43	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	P	218/328 (66%)	215 (99%)	3 (1%)	59	81
33	Q	265/332 (80%)	263 (99%)	2 (1%)	73	88
34	R	224/224 (100%)	220 (98%)	4 (2%)	51	77
35	S	58/151 (38%)	58 (100%)	0	100	100
36	Y	156/186 (84%)	156 (100%)	0	100	100
37	X	114/114 (100%)	107 (94%)	7 (6%)	17	35
38	Z	88/107 (82%)	87 (99%)	1 (1%)	65	84
39	W	20/413 (5%)	20 (100%)	0	100	100
40	U	21/121 (17%)	21 (100%)	0	100	100
41	V	416/538 (77%)	409 (98%)	7 (2%)	53	78
42	M	145/237 (61%)	143 (99%)	2 (1%)	59	81
43	z	134/273 (49%)	131 (98%)	3 (2%)	45	73
44	y	63/167 (38%)	58 (92%)	5 (8%)	11	24
45	J	215/633 (34%)	215 (100%)	0	100	100
46	I	58/786 (7%)	54 (93%)	4 (7%)	14	30
47	x	586/789 (74%)	575 (98%)	11 (2%)	50	76
All	All	11869/18071 (66%)	11625 (98%)	244 (2%)	46	74

5 of 244 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	3	380	LEU
43	z	103	VAL
23	3	1171	ILE
42	M	134	THR
47	x	271	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 232 such sidechains are listed below:

Mol	Chain	Res	Type
21	1	776	GLN
45	J	117	HIS
23	3	754	HIS
43	z	115	ASN
40	U	4	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	F	102/112 (91%)	19 (18%)	1 (0%)
13	G	99/162 (61%)	45 (45%)	4 (4%)
14	H	161/1175 (13%)	40 (24%)	1 (0%)
2	B	177/214 (82%)	58 (32%)	6 (3%)
All	All	539/1663 (32%)	162 (30%)	12 (2%)

5 of 162 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	9	U
2	B	12	C
2	B	13	A
2	B	14	G
2	B	18	A

5 of 12 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
13	G	109	A
13	G	472	A
14	H	36	A
13	G	480	A
2	B	130	A

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 22 are monoatomic - leaving 2 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
49	GTP	C	1101	50	33,34,34	0.90	1 (3%)	50,54,54	1.58	9 (18%)
48	IHP	A	3000	-	36,36,36	0.77	0	60,60,60	0.93	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
49	GTP	C	1101	50	-	7/22/38/38	0/3/3/3
48	IHP	A	3000	-	-	4/30/54/54	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	C	1101	GTP	C5-N7	-2.03	1.35	1.39

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	C	1101	GTP	C5-C4-N3	-4.51	121.22	128.39
49	C	1101	GTP	C2-N3-C4	4.46	119.98	112.30
49	C	1101	GTP	C2-N1-C6	-2.90	119.86	125.11
49	C	1101	GTP	N9-C8-N7	-2.84	108.14	113.40
49	C	1101	GTP	N9-C4-N3	2.60	131.15	125.95

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

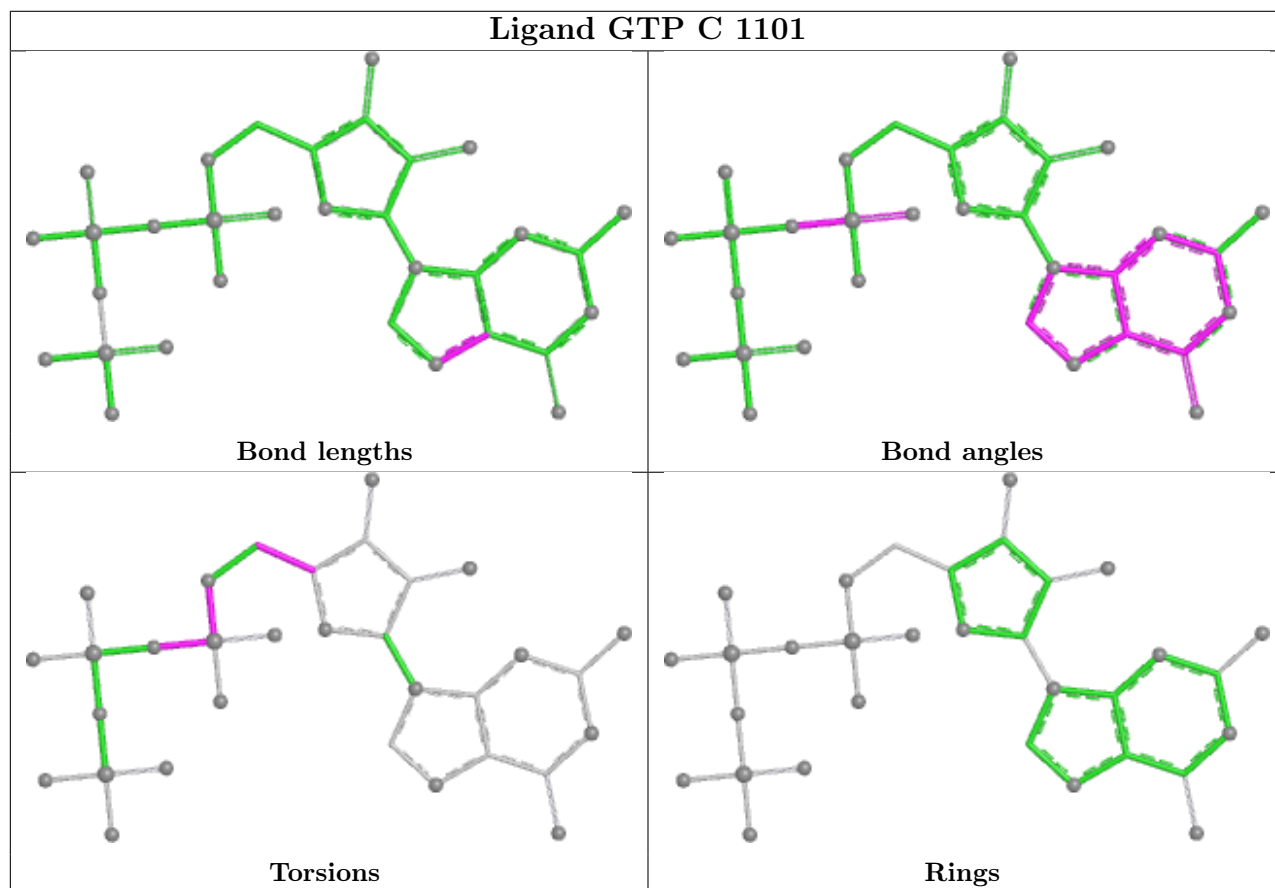
Mol	Chain	Res	Type	Atoms
49	C	1101	GTP	C5'-O5'-PA-O3A
49	C	1101	GTP	C5'-O5'-PA-O2A
49	C	1101	GTP	O4'-C4'-C5'-O5'
49	C	1101	GTP	C3'-C4'-C5'-O5'
48	A	3000	IHP	C2-O12-P2-O22

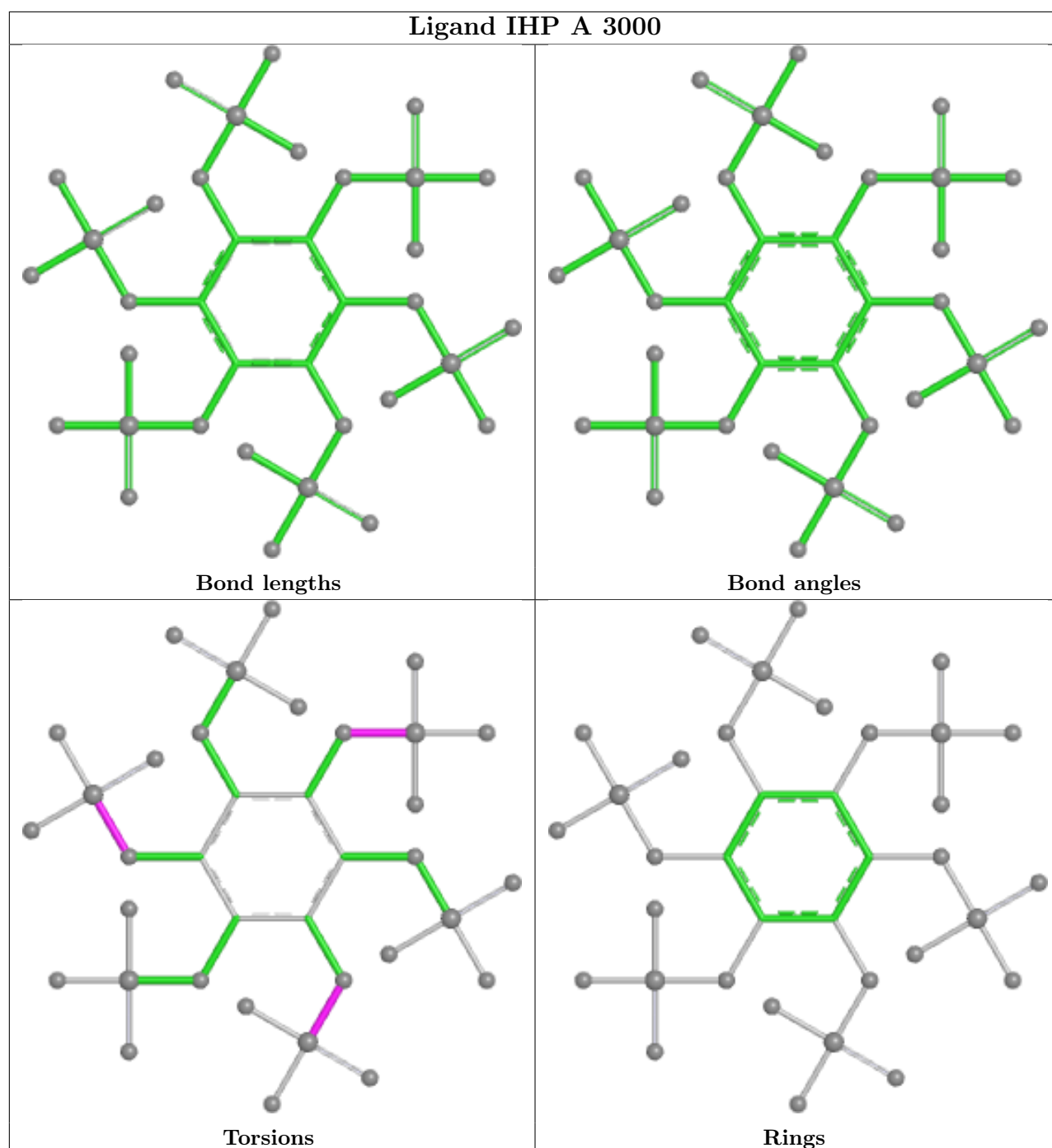
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
49	C	1101	GTP	2	0
48	A	3000	IHP	2	0

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





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

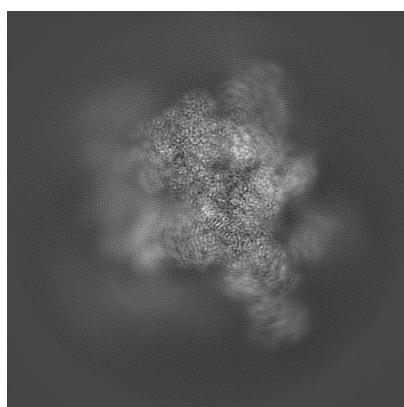
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30637. These allow visual inspection of the internal detail of the map and identification of artifacts.

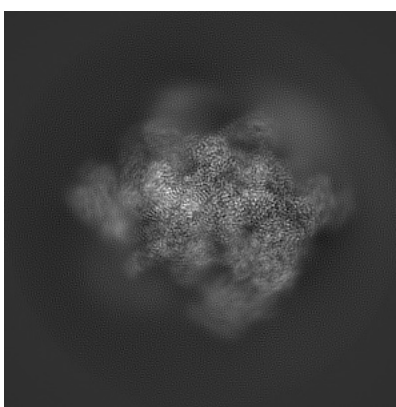
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

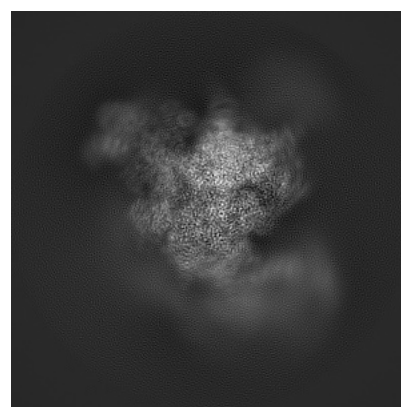
#### 6.1.1 Primary map



X



Y

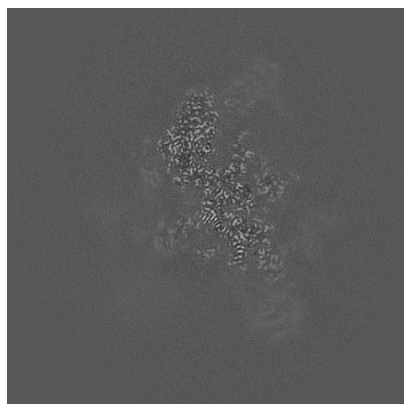


Z

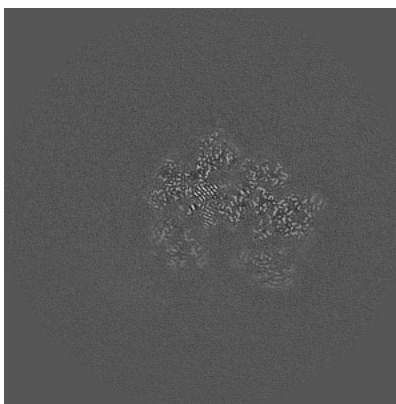
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

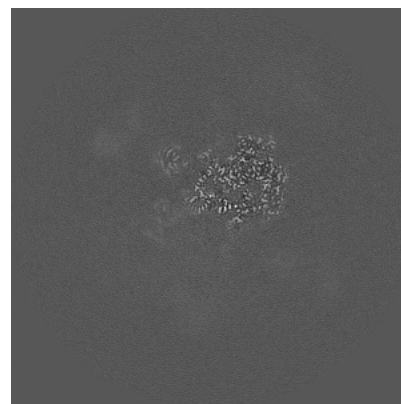
#### 6.2.1 Primary map



X Index: 200



Y Index: 200

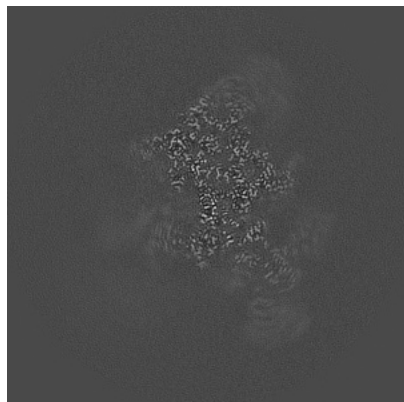


Z Index: 200

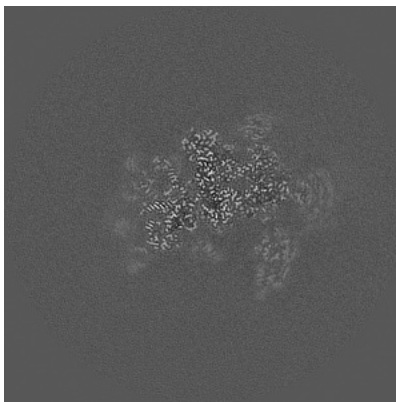
The images above show central slices of the map in three orthogonal directions.

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

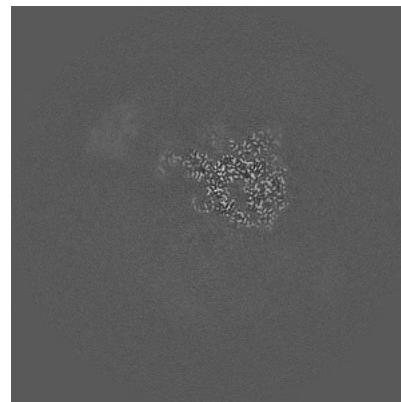
### 6.3.1 Primary map



X Index: 211



Y Index: 233

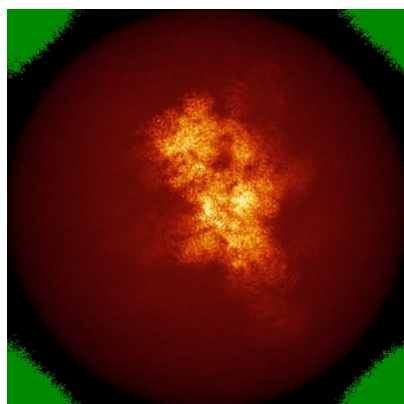


Z Index: 209

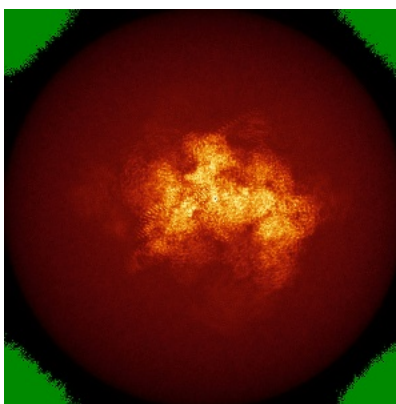
The images above show the largest variance slices of the map in three orthogonal directions.

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

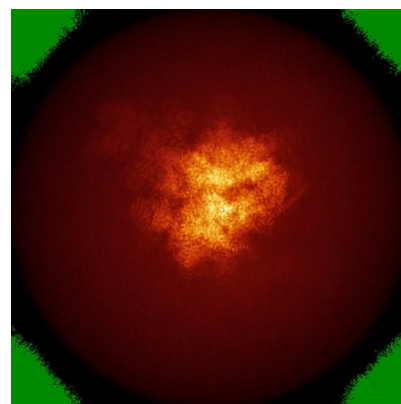
### 6.4.1 Primary map



X



Y

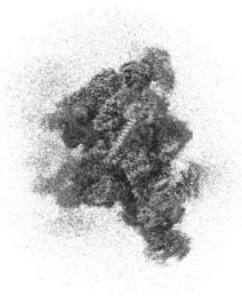


Z

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](#)

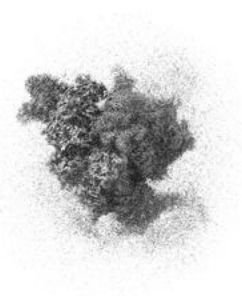
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

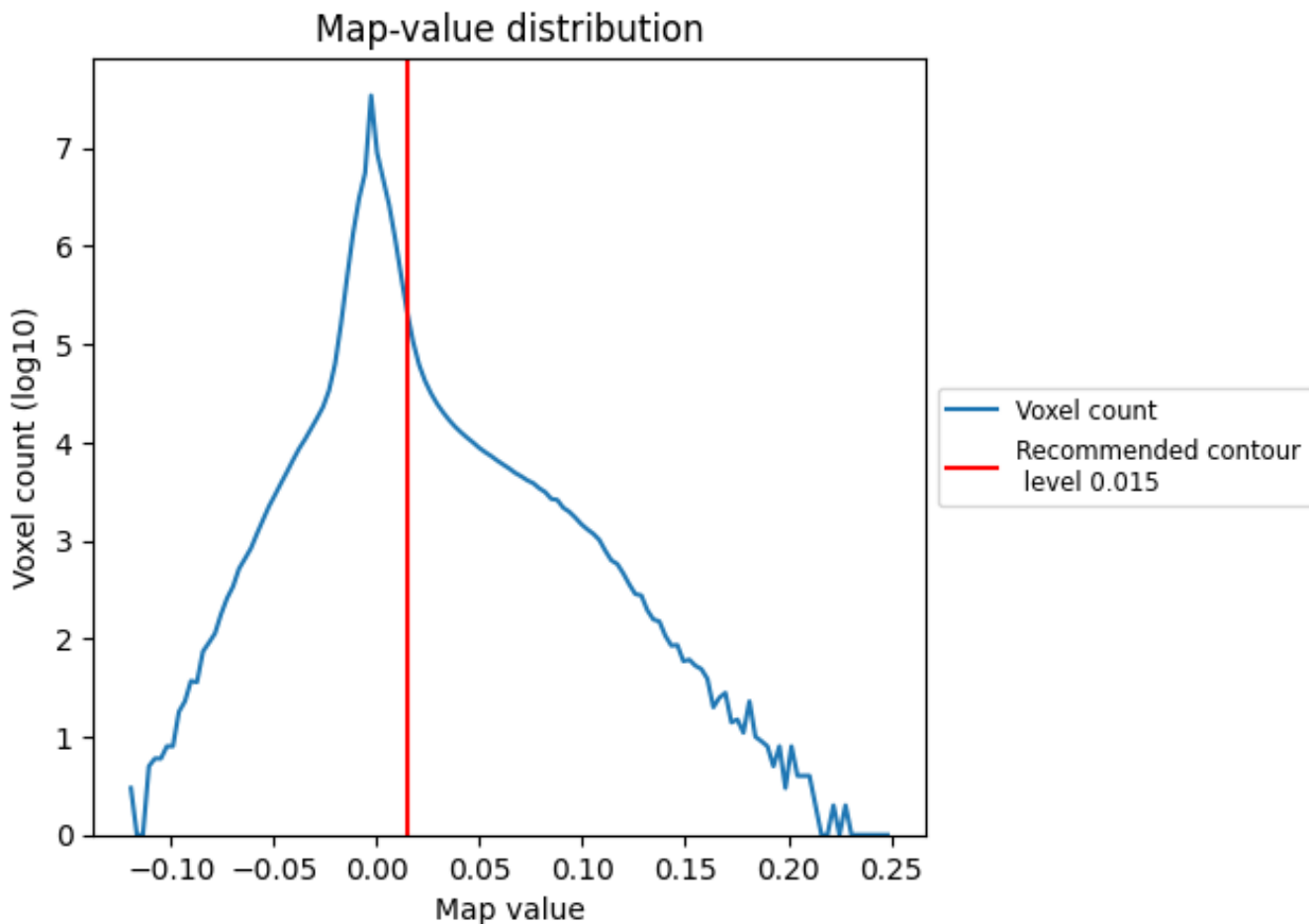
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

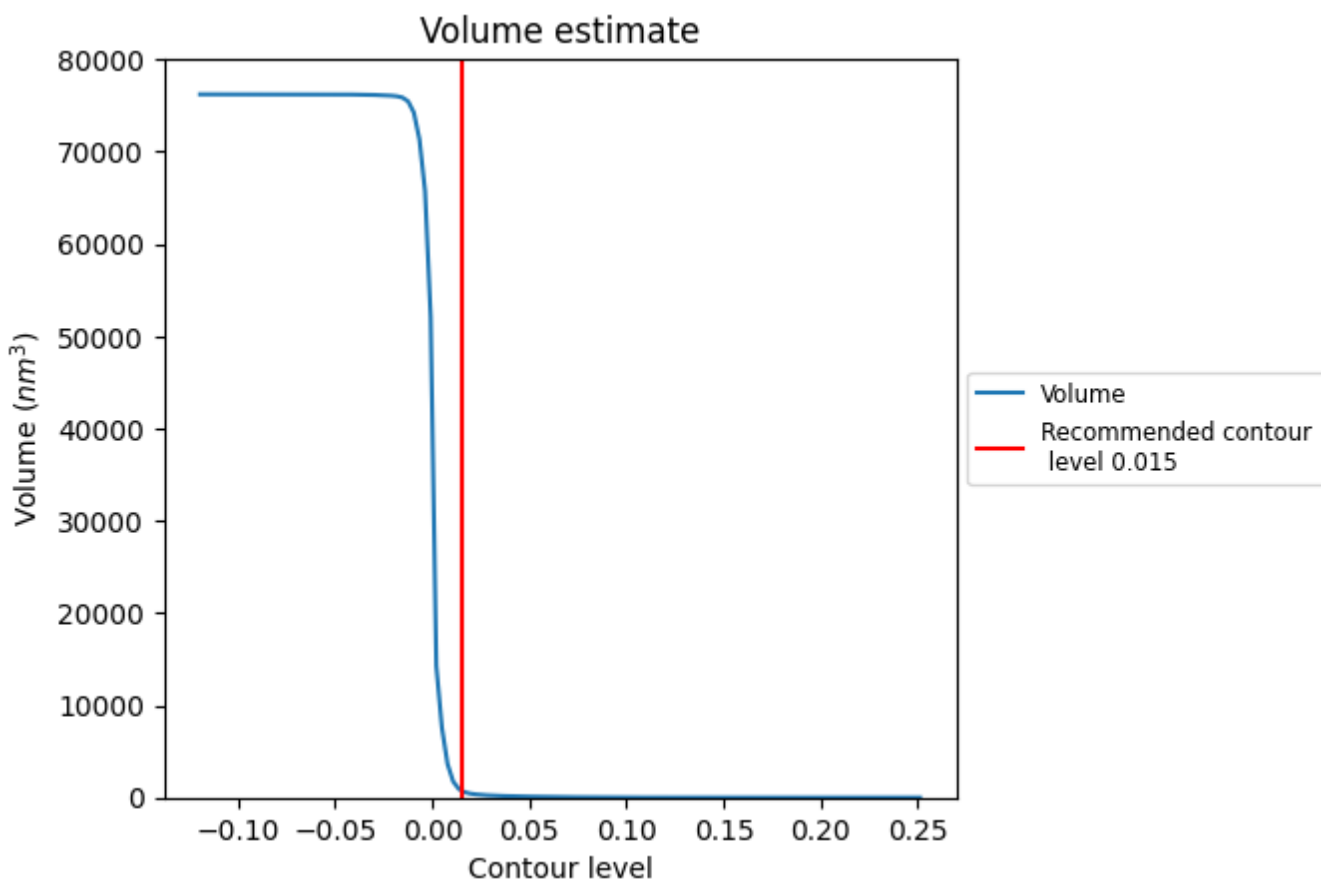
This section contains the results of statistical analysis of the map.

### 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.

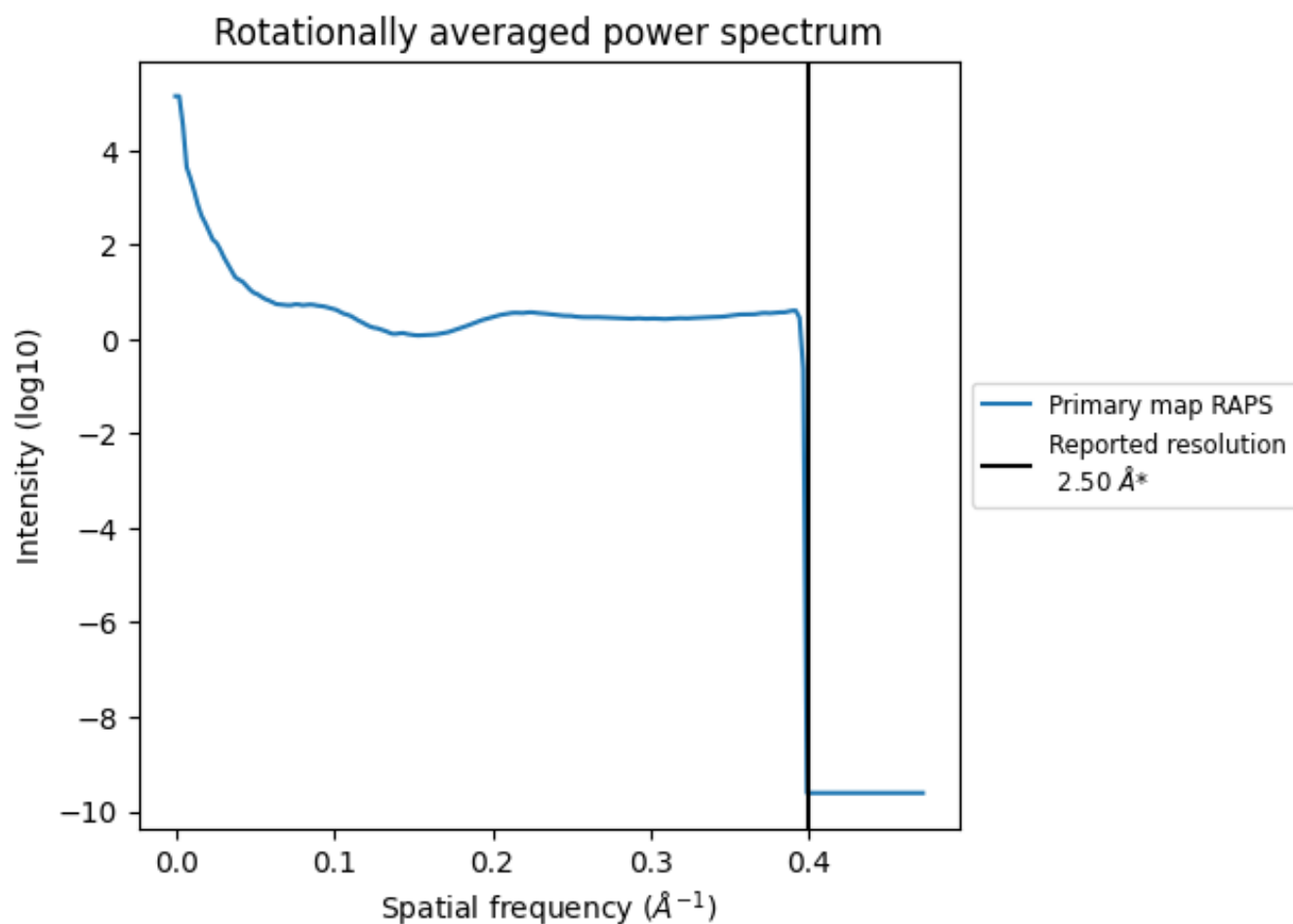
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 787  $\text{nm}^3$ ; this corresponds to an approximate mass of 711 kDa.

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

### 7.3 Rotationally averaged power spectrum [i](#)



\*Reported resolution corresponds to spatial frequency of  $0.400 \text{\AA}^{-1}$

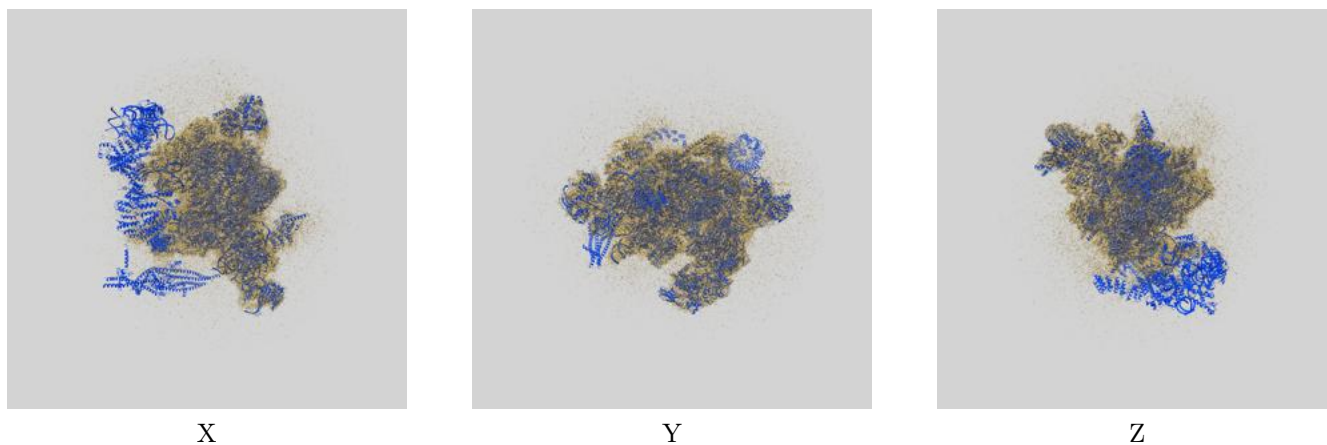
## 8 Fourier-Shell correlation

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

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

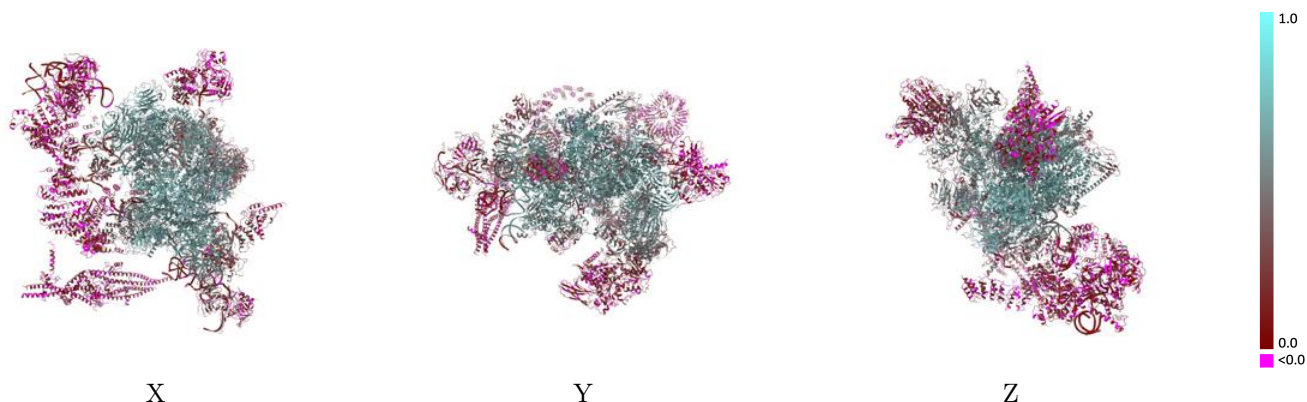
This section contains information regarding the fit between EMDB map EMD-30637 and PDB model 7DCO. Per-residue inclusion information can be found in section [3](#) on page [17](#).

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



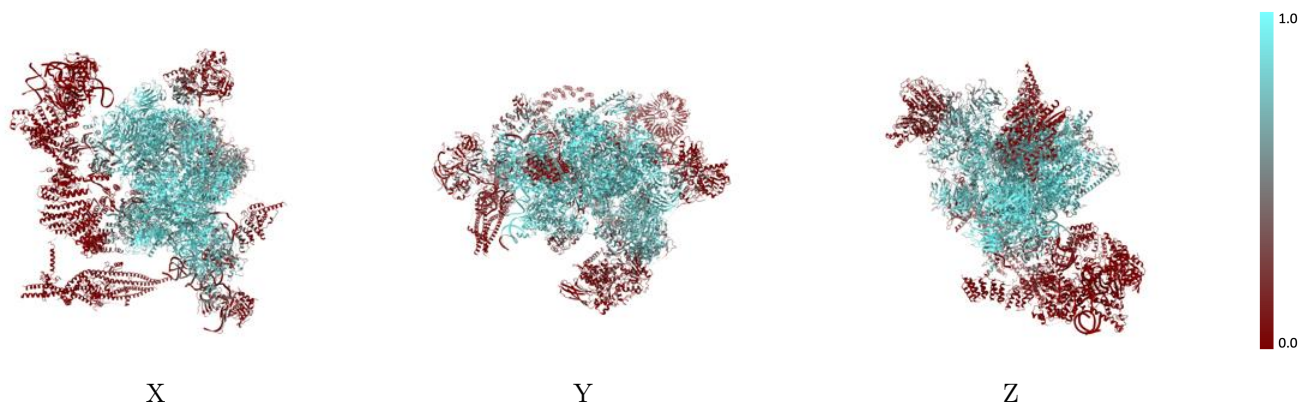
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



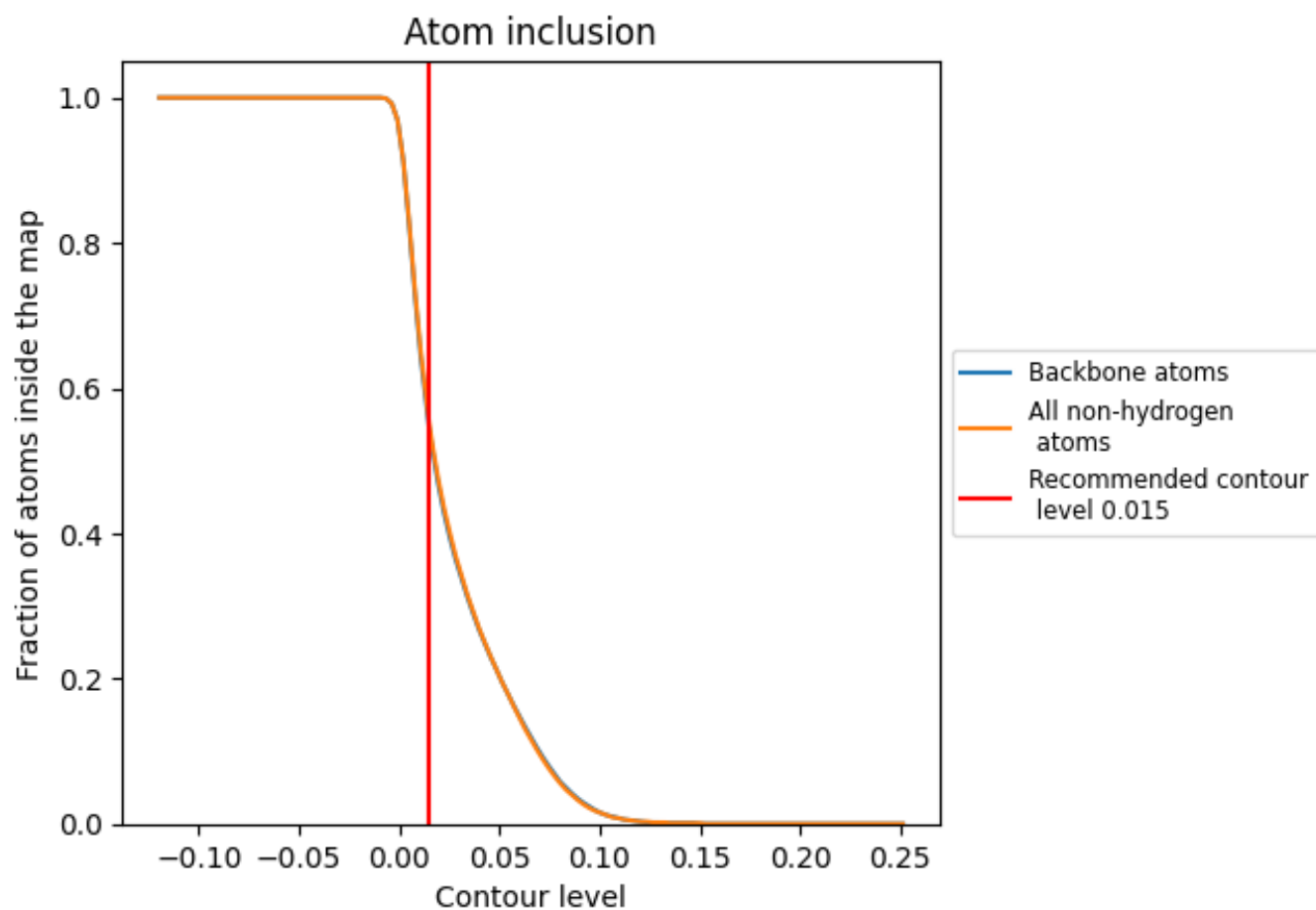
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 55% of all backbone atoms, 55% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5530	 0.4080
1	 0.9220	 0.6380
2	 0.7810	 0.5440
3	 0.8940	 0.6140
4	 0.3420	 0.2650
5	 0.9540	 0.6630
6	 0.9480	 0.6510
A	 0.8840	 0.6170
B	 0.5340	 0.3560
C	 0.7090	 0.4860
D	 0.4180	 0.3250
F	 0.8190	 0.5270
G	 0.5350	 0.3840
H	 0.2790	 0.2360
I	 0.0170	 0.1150
J	 0.2970	 0.2660
K	 0.0020	 0.0860
L	 0.3340	 0.3050
M	 0.6130	 0.4670
N	 0.8920	 0.5960
P	 0.7290	 0.5100
Q	 0.5000	 0.3620
R	 0.7500	 0.5030
S	 0.5910	 0.4930
T	 0.9080	 0.6170
U	 0.8660	 0.6060
V	 0.4750	 0.3730
W	 0.7890	 0.4970
X	 0.8940	 0.6040
Y	 0.6090	 0.4020
Z	 0.7450	 0.5220
a	 0.3660	 0.2980
b	 0.2730	 0.2640
c	 0.1780	 0.2200
d	 0.3990	 0.2990



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Chain	Atom inclusion	Q-score
e	 0.1290	 0.2060
f	 0.1210	 0.1970
g	 0.1110	 0.1900
h	 0.0020	 0.1030
i	 0.0040	 0.0620
j	 0.0020	 0.1110
k	 0.0020	 0.0870
l	 0.0050	 0.1030
m	 0.0020	 0.0930
n	 0.0040	 0.0790
o	 0.0040	 0.1290
p	 0.0110	 0.1330
q	 0.0040	 0.1050
r	 0.0020	 0.1400
s	 0.0050	 0.1100
t	 0.0020	 0.1190
u	 0.1370	 0.1700
v	 0.4320	 0.3700
w	 0.0030	 0.0800
x	 0.1680	 0.0830
y	 0.2280	 0.1810
z	 0.6640	 0.4540