



wwPDB EM Validation Summary Report ⓘ

Mar 22, 2026 – 09:40 PM UTC

PDB ID : 6BK8 / pdb_00006bk8
EMDB ID : EMD-7109
Title : S. cerevisiae spliceosomal post-catalytic P complex
Authors : Liu, S.; Li, X.; Zhou, Z.H.; Zhao, R.
Deposited on : 2017-11-07
Resolution : 3.30 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

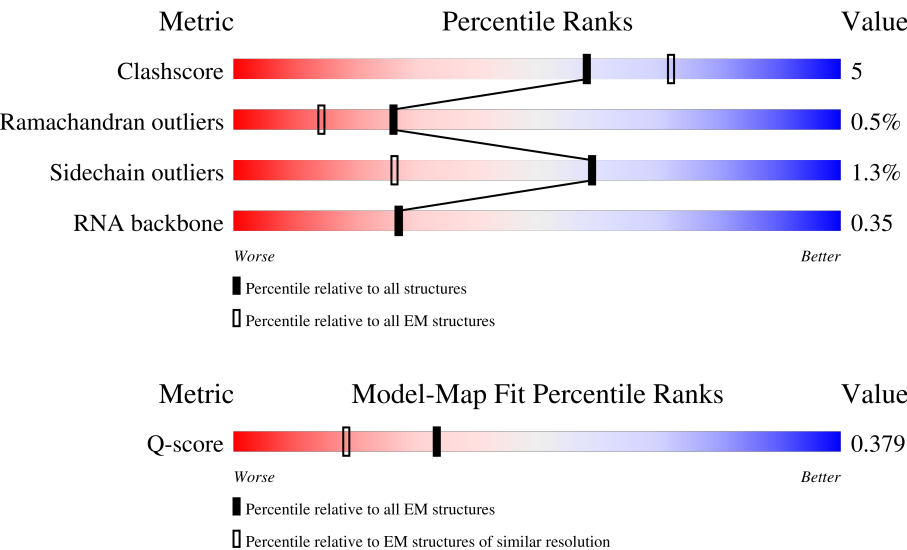
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	2	1175	
2	5	214	
3	6	112	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	e	34	
5	i	59	
6	A	2413	
7	B	1008	
8	D	451	
9	E	379	
10	F	364	
11	G	339	
12	H	175	
13	I	157	
14	K	135	
15	L	577	
16	M	455	
17	N	251	
18	O	382	
19	P	1145	
20	R	215	
21	S	590	
22	T	687	
23	U	859	
24	X	219	
25	Y	16	
26	a	110	
26	q	110	
27	b	86	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
27	m	86	84% 77% 7% 16%
28	c	94	80% 68% 12% 20%
28	l	94	80% 68% 10% 20%
29	d	77	90% 69% 21% 10%
29	n	77	90% 84% 5% 10%
30	f	196	41% 39% 59%
30	k	196	40% 32% 8% 60%
31	g	101	81% 69% 12% 19%
31	o	101	77% 67% 10% 23%
32	h	146	56% 51% 44%
32	p	146	54% 41% 8% 46%
33	r	111	76% 71% 5% 24%
34	s	238	69% 62% 6% 31%
35	u	503	86% 83% 14%
35	v	503	23% 22% 77%
35	w	503	87% 84% 13%
35	x	503	23% 22% 77%
36	y	175	63% 51% 8% 37%

2 Entry composition

There are 40 unique types of molecules in this entry. The entry contains 82745 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	135	Total	C	N	O	P	0	0
			2848	1272	472	969	135		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5	103	Total	C	N	O	P	0	0
			2173	973	367	730	103		

- Molecule 3 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	6	102	Total	C	N	O	P	0	0
			2170	972	386	710	102		

- Molecule 4 is a RNA chain called RNA (34-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	34	Total	C	N	O	P	0	0
			707	319	107	247	34		

- Molecule 5 is a RNA chain called RNA (59-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	i	59	Total	C	N	O	P	0	0
			1239	558	202	420	59		

- Molecule 6 is a protein called Pre-mRNA-splicing factor Prp8.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	1960	Total	C	N	O	S	0	0
			16159	10381	2786	2933	59		

- Molecule 7 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	899	Total	C	N	O	S	0	0
			7179	4638	1191	1321	29		

- Molecule 8 is a protein called Pre-mRNA-splicing factor PRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	359	Total	C	N	O	S	0	0
			2826	1786	497	533	10		

- Molecule 9 is a protein called Pre-mRNA-processing protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	186	Total	C	N	O	S	0	0
			1494	939	276	273	6		

- Molecule 10 is a protein called Pre-mRNA-splicing factor SLT11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	199	Total	C	N	O	S	0	0
			1576	991	277	293	15		

- Molecule 11 is a protein called Pre-mRNA-splicing factor CWC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	255	Total	C	N	O	S	0	0
			2048	1297	362	378	11		

- Molecule 12 is a protein called Pre-mRNA-splicing factor CWC15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	70	Total	C	N	O	S	0	0
			570	357	113	99	1		

- Molecule 13 is a protein called Pre-mRNA-splicing factor BUD31.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	156	Total	C	N	O	S	0	0
			1283	803	239	231	10		

- Molecule 14 is a protein called Pre-mRNA-splicing factor CWC21.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	82	Total	C	N	O	S	0	0
			550	332	106	111	1		

- Molecule 15 is a protein called Pre-mRNA-splicing factor CWC22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	412	Total	C	N	O	S	0	0
			3353	2160	556	620	17		

- Molecule 16 is a protein called Pre-mRNA-processing factor Prp17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	326	Total	C	N	O	S	0	0
			2607	1649	465	485	8		

- Molecule 17 is a protein called Pre-mRNA-splicing factor Prp18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	167	Total	C	N	O	S	0	0
			1326	856	233	233	4		

- Molecule 18 is a protein called Pre-mRNA-splicing factor SLU7.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	229	Total	C	N	O	S	0	0
			1935	1211	347	368	9		

- Molecule 19 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	653	Total	C	N	O	S	0	0
			3872	2393	736	740	3		

- Molecule 20 is a protein called Pre-mRNA-splicing factor SYF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	101	Total	C	N	O	S	0	0
			813	499	150	163	1		

- Molecule 21 is a protein called Pre-mRNA-splicing factor CEF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	238	Total	C	N	O	S	0	0
			1948	1218	355	368	7		

- Molecule 22 is a protein called Pre-mRNA-splicing factor CLF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	483	Total	C	N	O	S	0	0
			3370	2113	624	625	8		

- Molecule 23 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	637	Total	C	N	O	S	0	0
			3625	2226	689	703	7		

- Molecule 24 is a protein called Unknown protein fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	219	Total	C	N	O		0	0
			1095	657	219	219			

- Molecule 25 is a protein called Unknown protein fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	16	Total	C	N	O		0	0
			80	48	16	16			

- Molecule 26 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	94	Total	C	N	O	S	0	0
			741	477	141	119	4		
26	q	93	Total	C	N	O	S	0	0
			726	468	136	118	4		

- Molecule 27 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	72	Total	C	N	O	S	0	0
			573	368	101	103	1		
27	m	72	Total	C	N	O	S	0	0
			573	368	101	103	1		

- Molecule 28 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	75	Total	C	N	O	S	0	0
			575	379	92	101	3		
28	l	75	Total	C	N	O	S	0	0
			575	379	92	101	3		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	69	Total	C	N	O	S	0	0
			529	337	93	97	2		
29	n	69	Total	C	N	O	S	0	0
			526	336	93	95	2		

- Molecule 30 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	80	Total	C	N	O	S	0	0
			631	403	114	111	3		
30	k	78	Total	C	N	O	S	0	0
			610	389	109	109	3		

- Molecule 31 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	g	82	Total	C	N	O	S	0	0
			625	399	109	115	2		
31	o	78	Total	C	N	O	S	0	0
			600	384	104	110	2		

- Molecule 32 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	h	82	Total	C	N	O	S	0	0
			644	409	110	123	2		
32	p	79	Total	C	N	O	S	0	0
			618	393	107	116	2		

- Molecule 33 is a protein called Lea1.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	r	84	Total	C	N	O	0	0
			416	248	84	84		

- Molecule 34 is a protein called Msl1.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	s	164	Total	C	N	O	0	0
			816	488	164	164		

- Molecule 35 is a protein called Pre-mRNA-processing factor Prp19.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	u	435	Total	C	N	O	0	0
			2156	1286	435	435		
35	v	118	Total	C	N	O	0	0
			588	352	118	118		
35	w	438	Total	C	N	O	0	0
			2171	1295	438	438		
35	x	116	Total	C	N	O	0	0
			578	346	116	116		

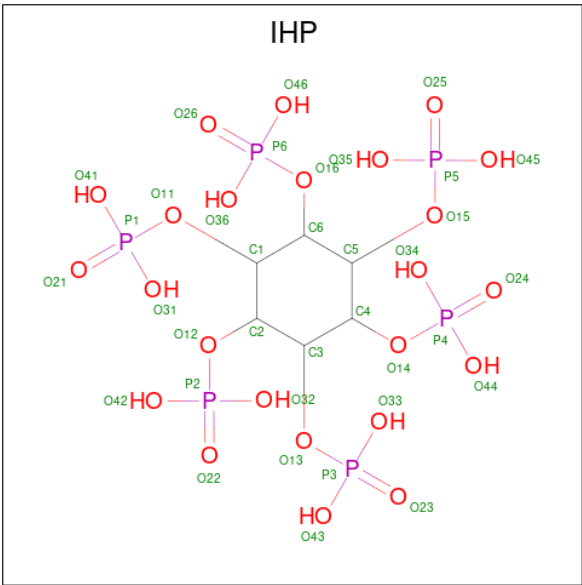
- Molecule 36 is a protein called Pre-mRNA-splicing factor SNT309.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	y	110	Total	C	N	O	0	0
			548	328	110	110		

- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

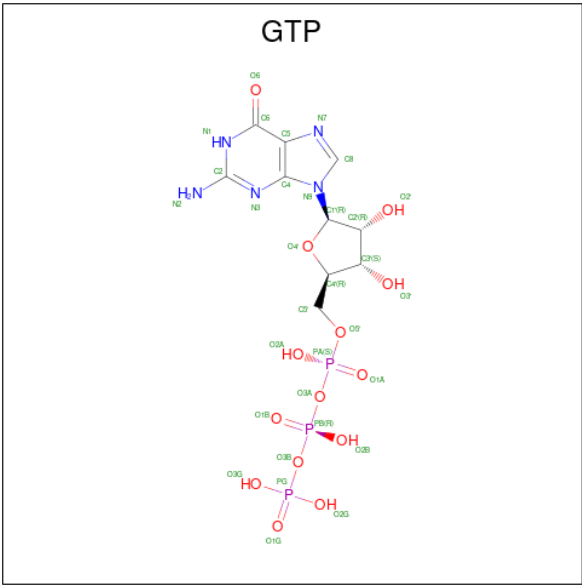
Mol	Chain	Residues	Atoms		AltConf
37	6	4	Total	Mg	0
			4	4	
37	B	1	Total	Mg	0
			1	1	

- Molecule 38 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: C₆H₁₈O₂₄P₆).



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

- Molecule 39 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

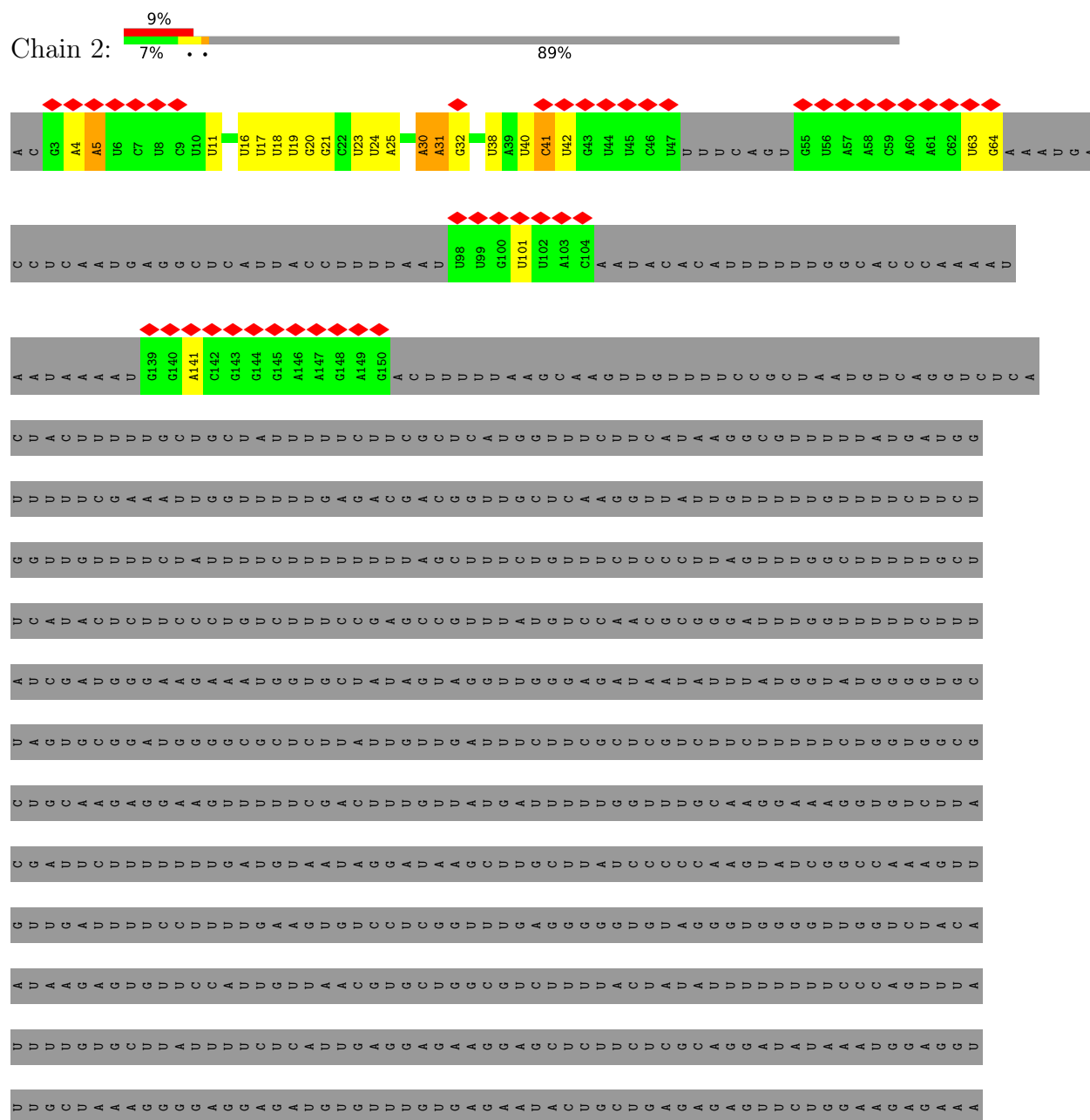
- Molecule 40 is ZINC ION (CCD ID: ZN) (formula: Zn).

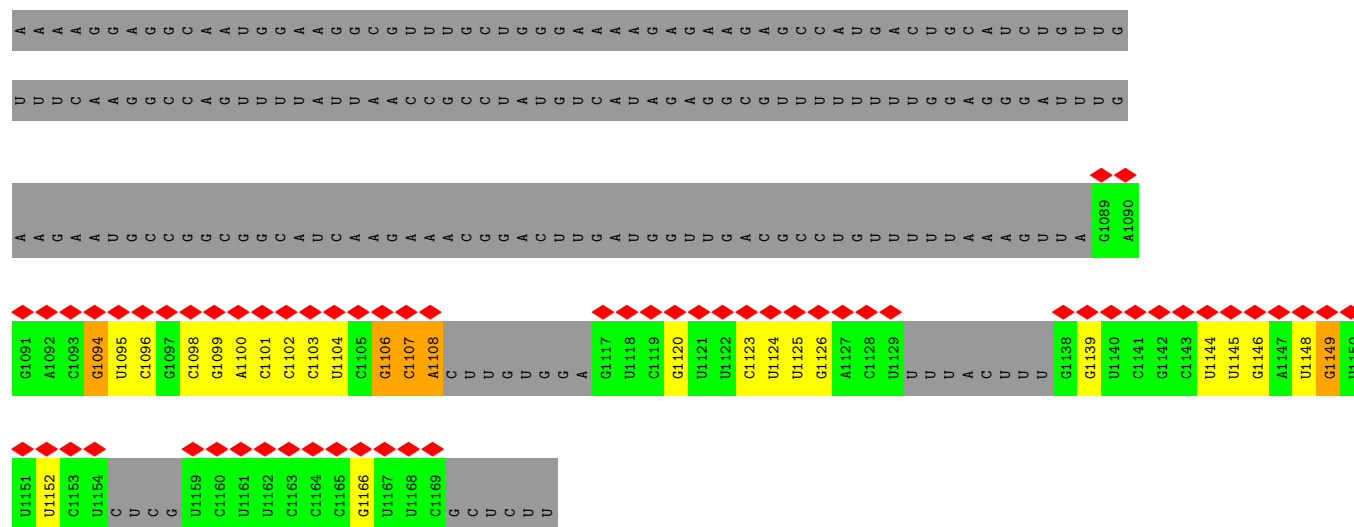
Mol	Chain	Residues	Atoms		AltConf
40	F	2	Total 2	Zn 2	0
40	G	1	Total 1	Zn 1	0
40	I	3	Total 3	Zn 3	0
40	O	1	Total 1	Zn 1	0

3 Residue-property plots [i](#)

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

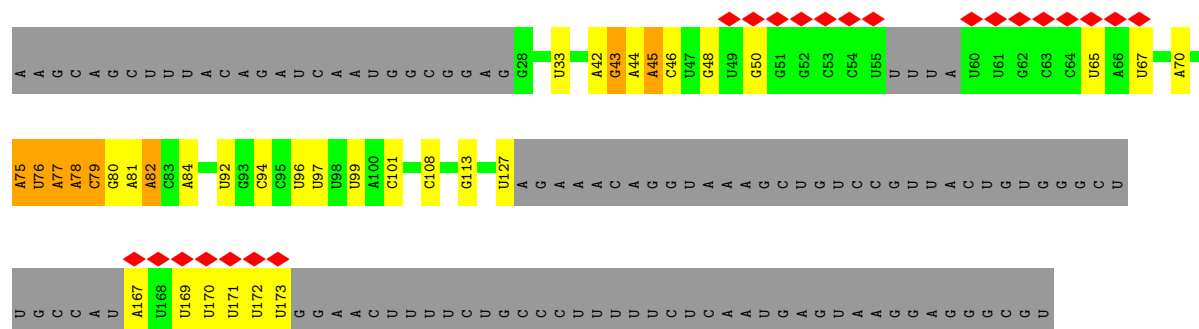
• Molecule 1: U2 snRNA





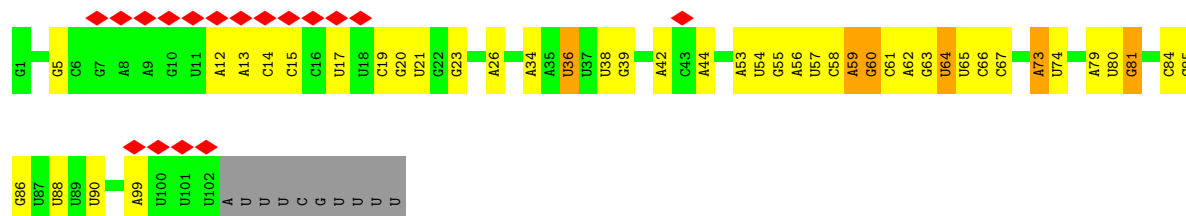
• Molecule 2: U5 snRNA

Chain 5: 10% 32% 13% 52%



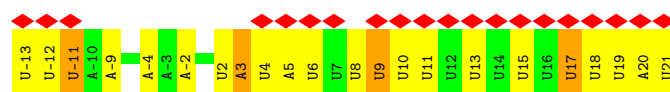
• Molecule 3: U6 snRNA

Chain 6: 15% 53% 33% 5% 9%

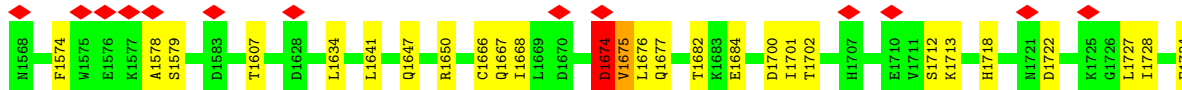


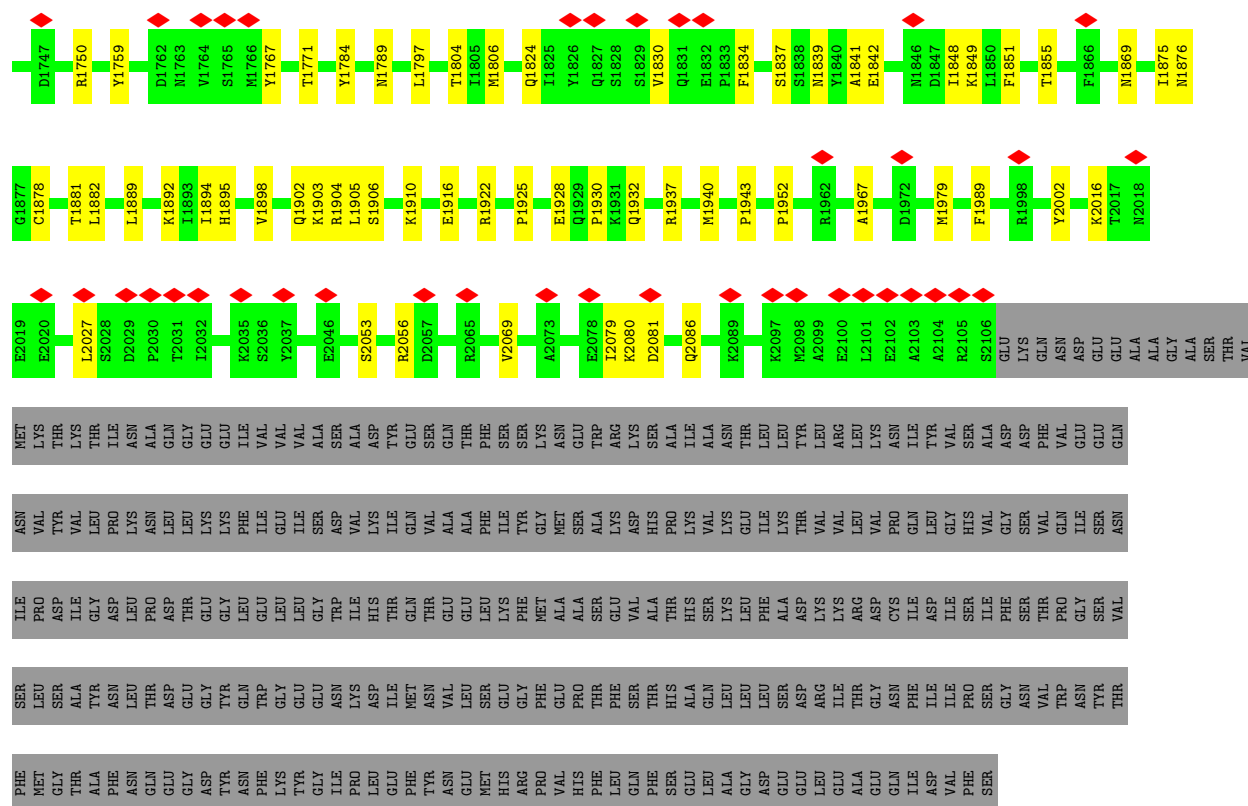
• Molecule 4: RNA (34-MER)

Chain e: 35% 59% 53% 12%

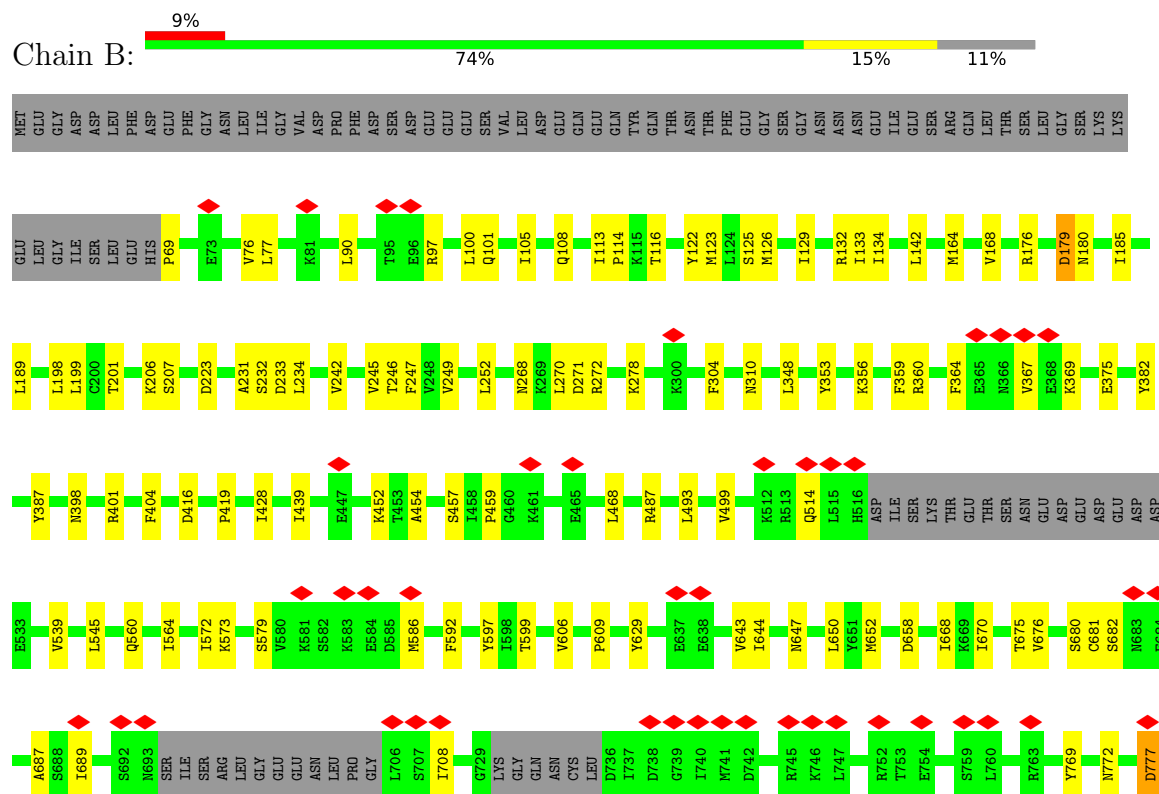


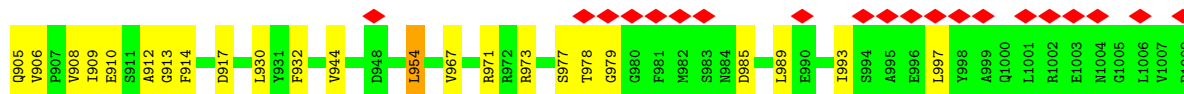
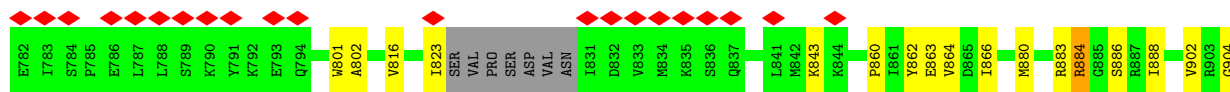
• Molecule 5: RNA (59-MER)



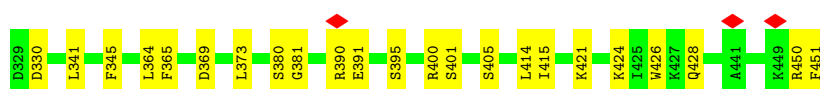
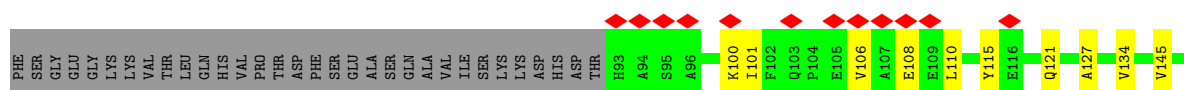


• Molecule 7: Pre-mRNA-splicing factor SNU114

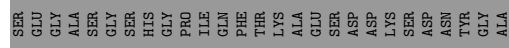
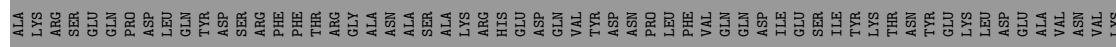
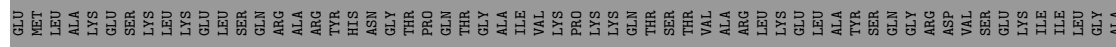
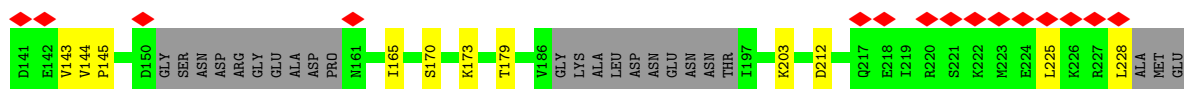
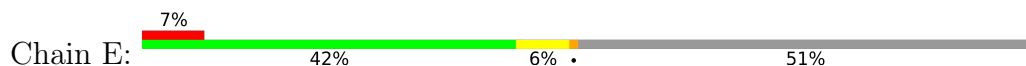




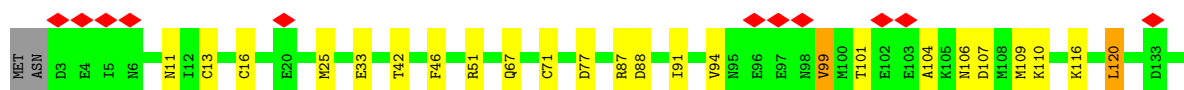
• Molecule 8: Pre-mRNA-splicing factor PRP46

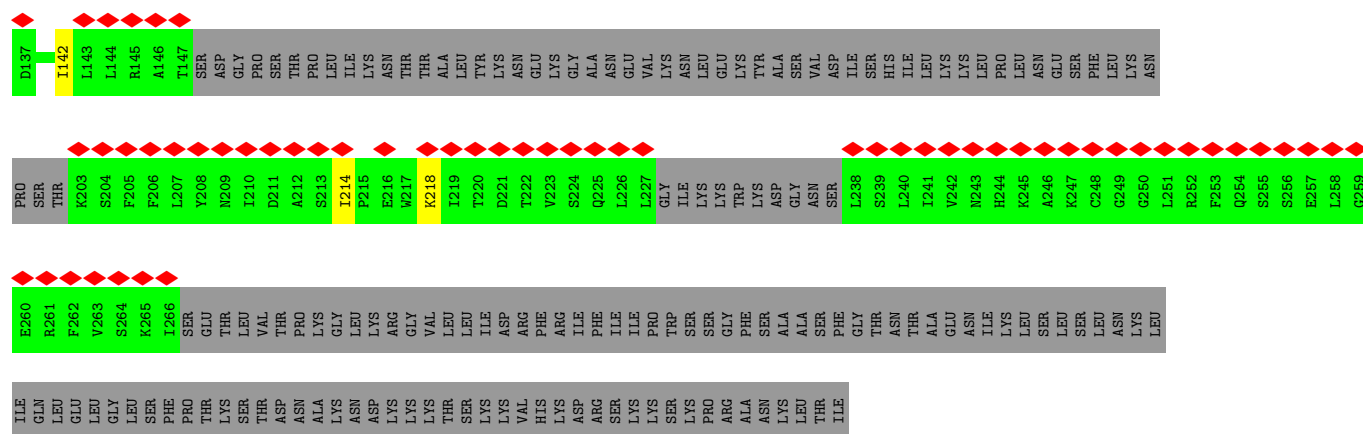


• Molecule 9: Pre-mRNA-processing protein 45

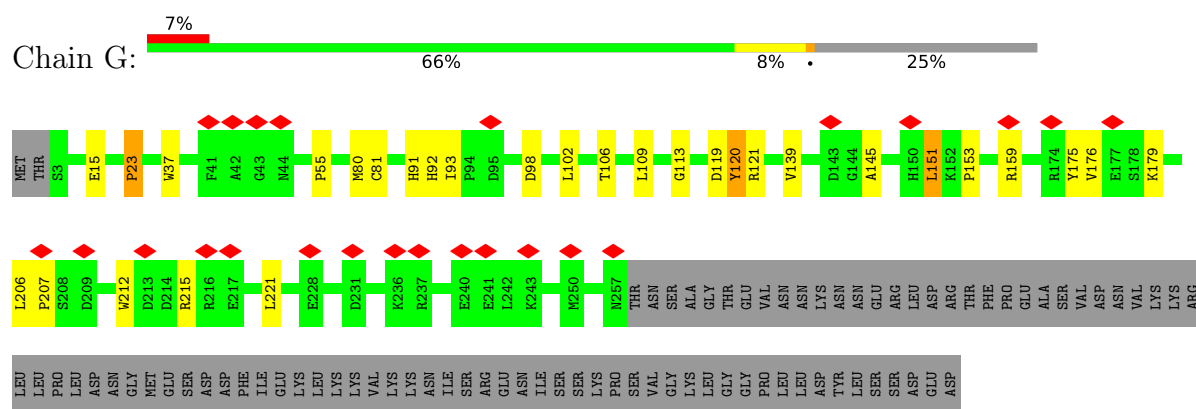


• Molecule 10: Pre-mRNA-splicing factor SLT11

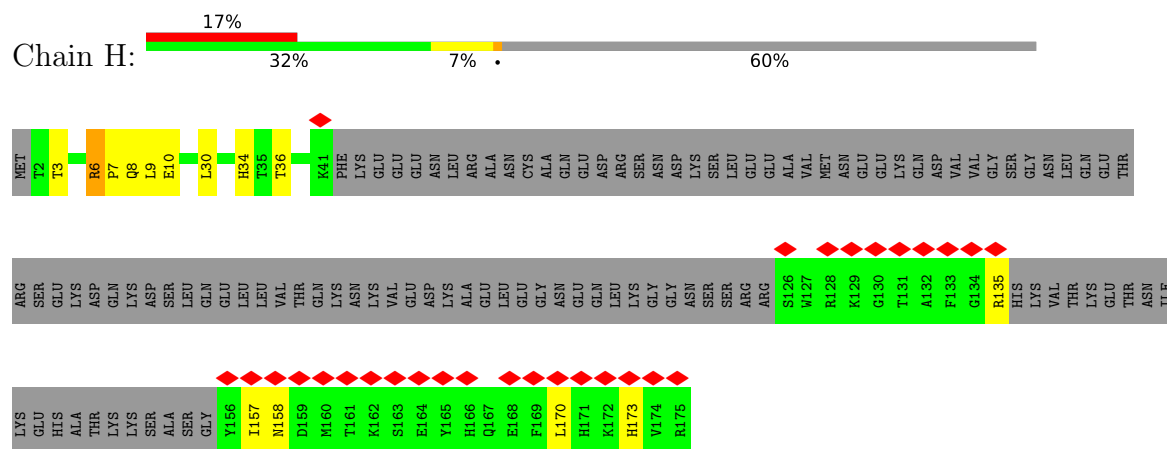




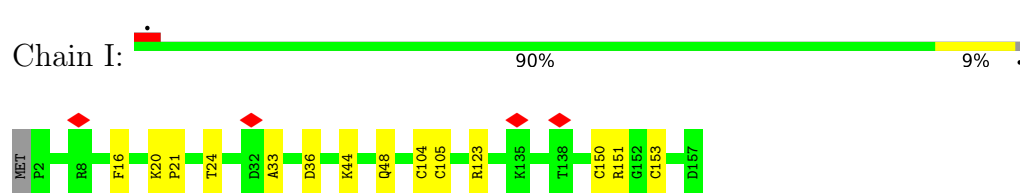
- Molecule 11: Pre-mRNA-splicing factor CWC2



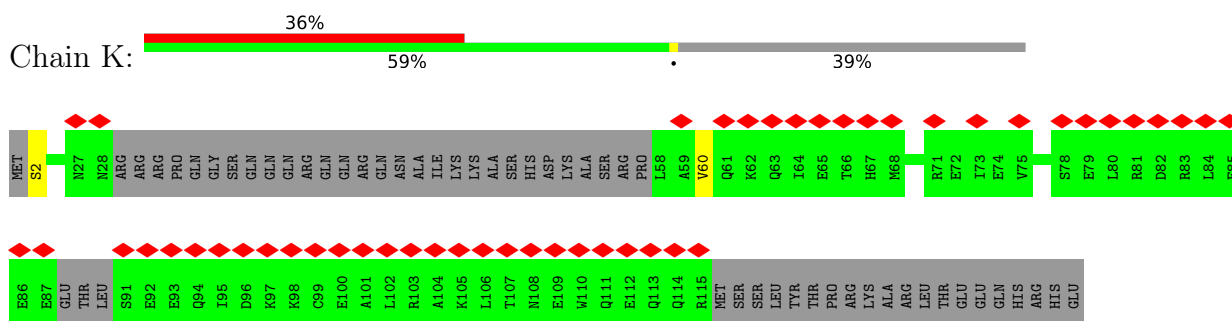
- Molecule 12: Pre-mRNA-splicing factor CWC15



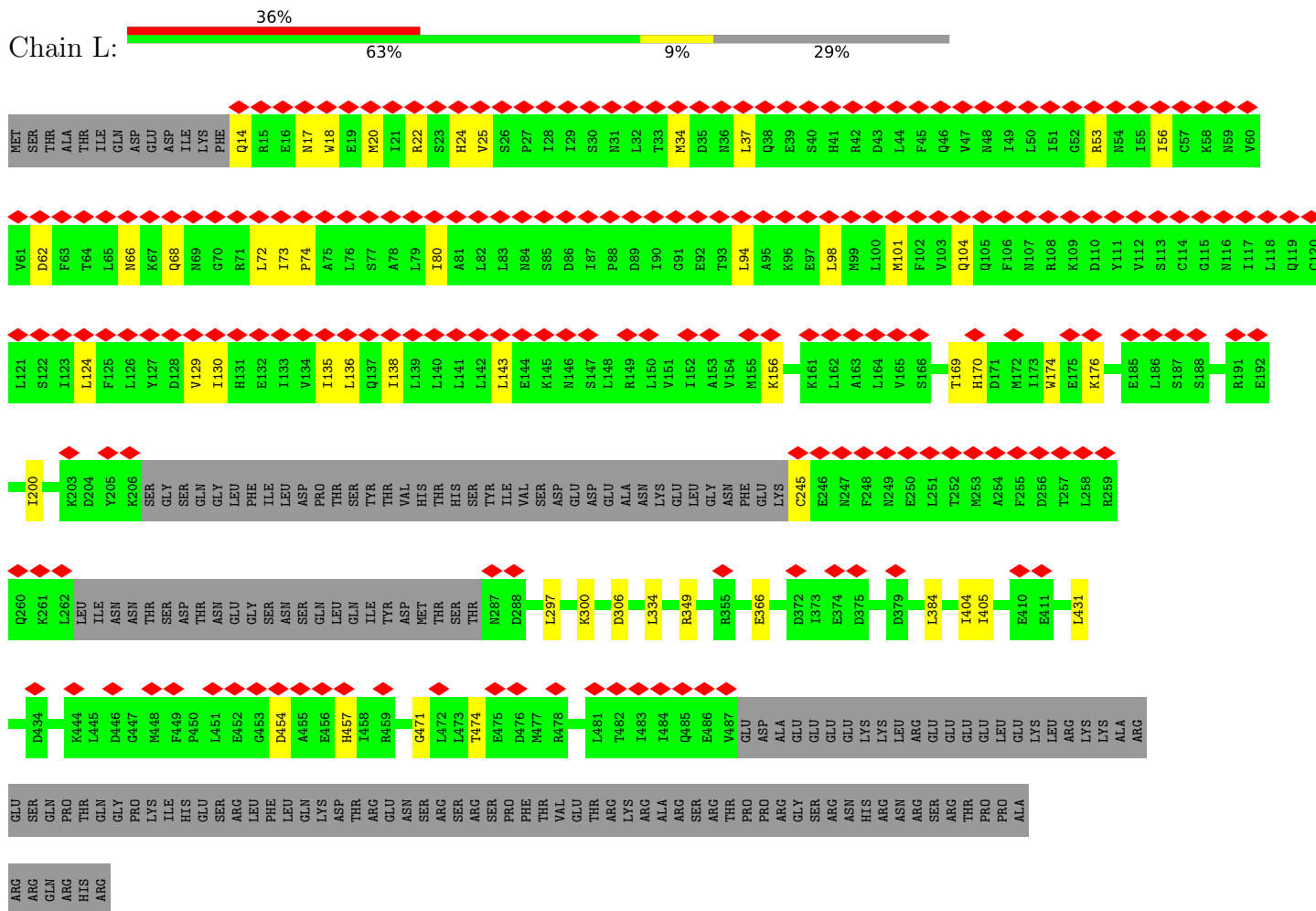
- Molecule 13: Pre-mRNA-splicing factor BUD31



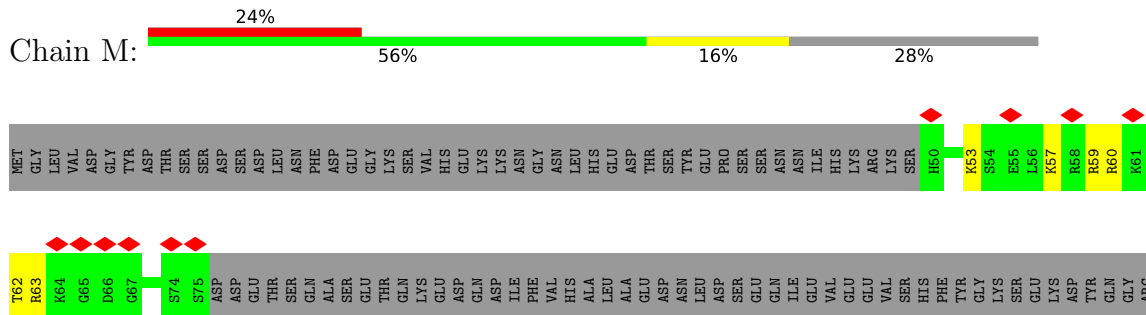
- Molecule 14: Pre-mRNA-splicing factor CWC21

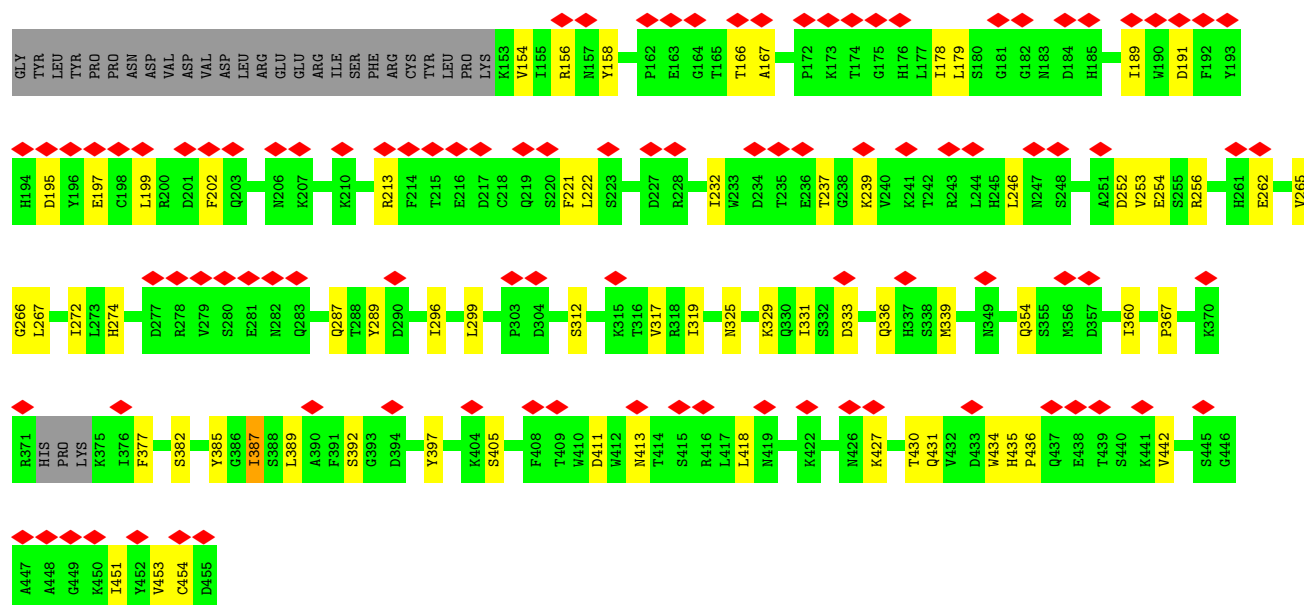


- Molecule 15: Pre-mRNA-splicing factor CWC22

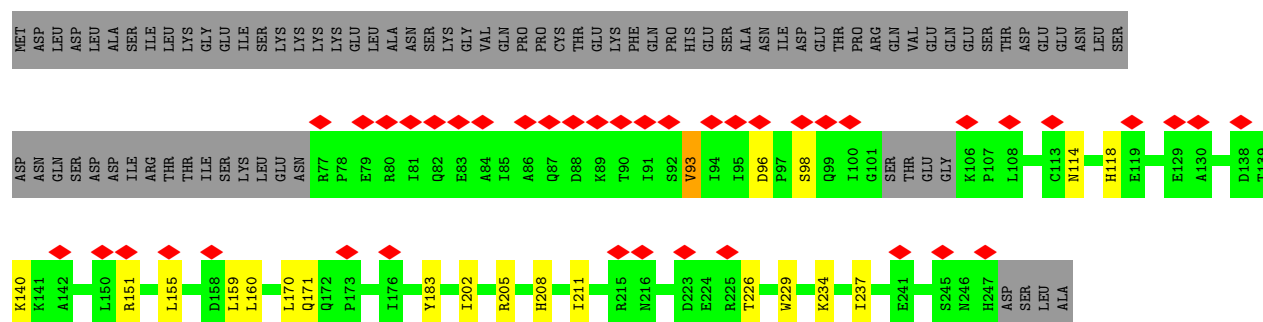


- Molecule 16: Pre-mRNA-processing factor Prp17

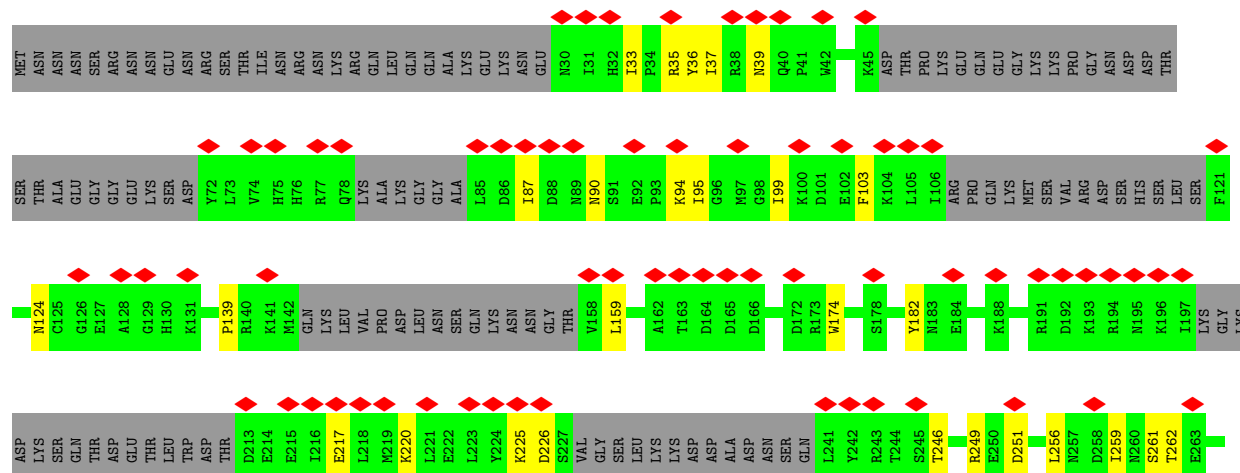




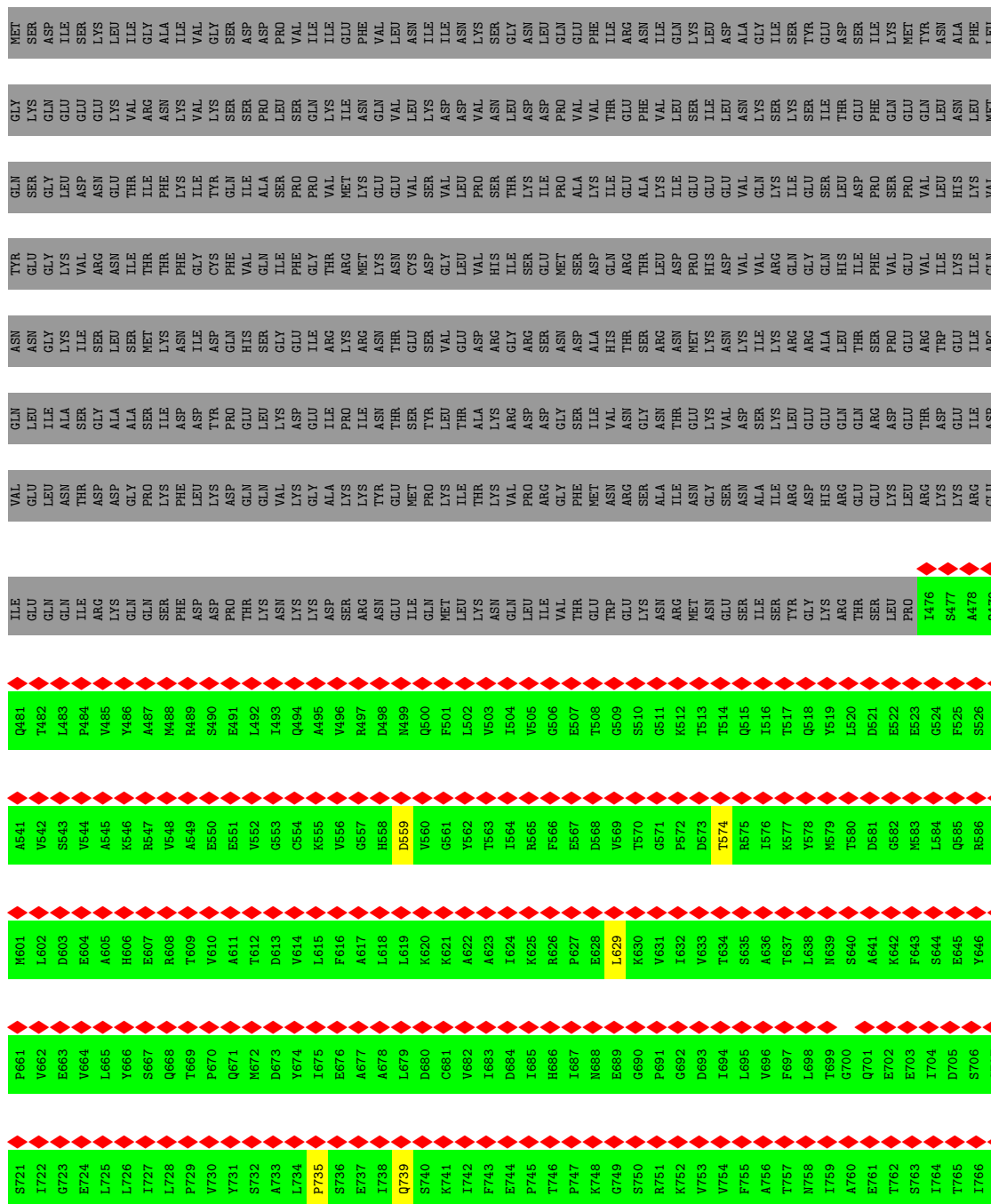
• Molecule 17: Pre-mRNA-splicing factor Prp18

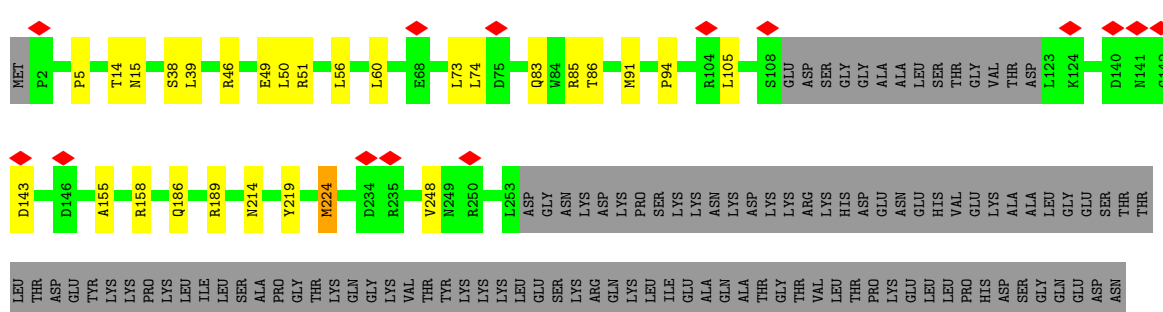
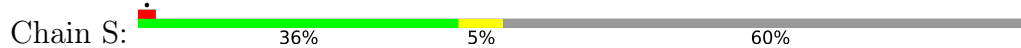
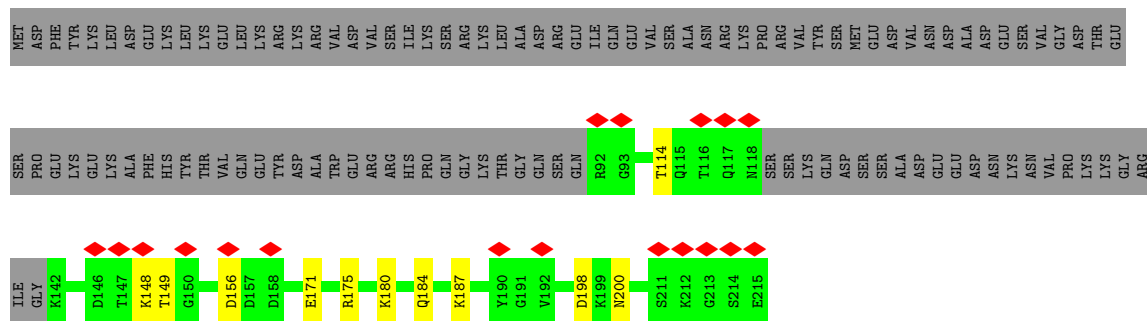
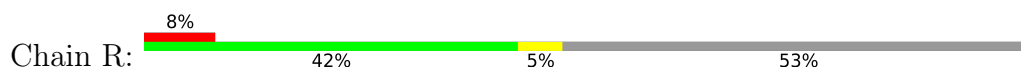
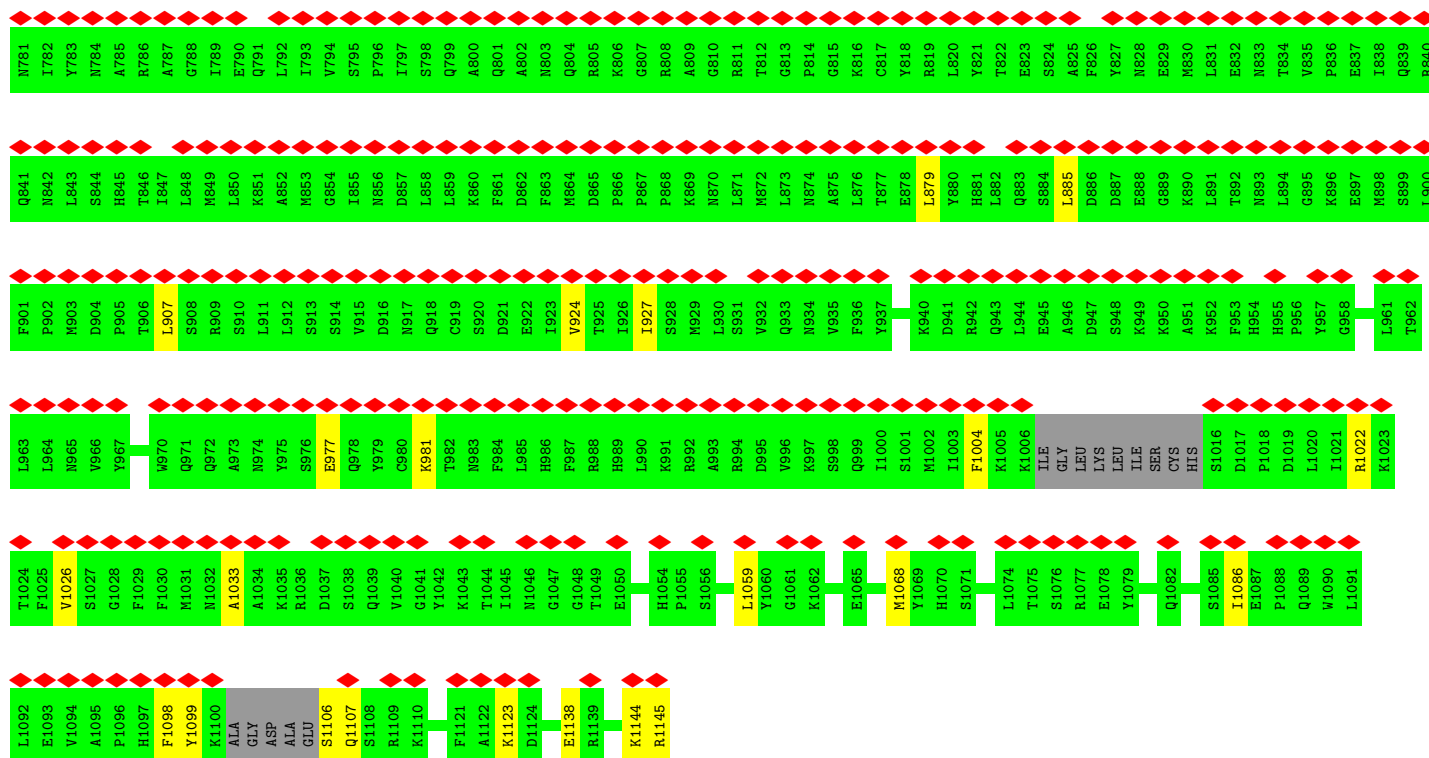


• Molecule 18: Pre-mRNA-splicing factor SLU7



- Molecule 19: Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP22



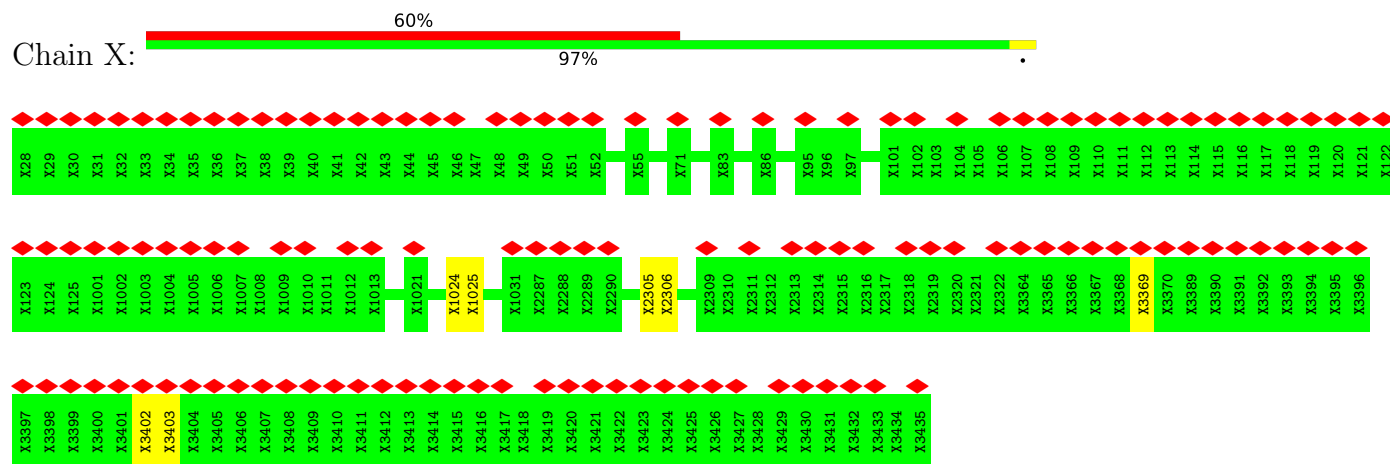




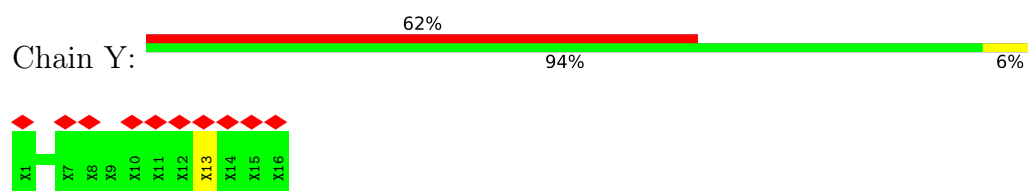
MET	SER	GLN	ALA	TYR	ILE	ALA	LEU	MET	GLY	LYS	VAL	ILE	THR	ASN	VAL	ASP	GLU	ASN	ILE	ARG	ASN	D21	E22	E23	D24	A25	F26	E27	E28	E29	I30	Q31	K32	T33	P34	Q35	K36	I37	L38	T39	W40	K41	R42	Y43	I44	E45	Y46	W47	K48	GLU	GLU	GLY	ARG	THR	D54	K55	Q56	I57	R58	W59	L60
V61	E62	R63	F64	C65	S66	Q67	F68	V69	T70	D71	T72	S73	I74	W75	E76	Y77	D78	I79	R80	W81	E82	S83	THR	LYS	GLU	VAL	VAL	E89	T90	S91	R92	I93	F94	W95	L96	F97	VAL	Q98	R99	C100	L101	K102	S103	C104	V105	D106	C108	D109	R110	I111	C112	L113	S114	Y115	L116	E117	L118	A119	I120		
E121	GLN	TYR	ASP	LEU	ALA	M127	I128	R129	H130	A131	L132	A133	S134	S135	L136	M137	K138	M139	E140	ARG	GLU	M143	GLY	SER	GLY	H144	R145	K146	V147	W148	D149	P150	V151	I152	K153	F154	V155	E156	E157	K158	V159	LEU	PRO	THR	GLN	GLU	ASP	GLU	E174	S175	T176	D177	E178	A179	E180						
L181	I182	M183	V184	L185	W186	V187	K188	G189	F190	T191	LYS	GLY	GLY	PHE	ILE	SER	GLY	GLU	ILE	SER	GLU	ASN	GLY	SER	GLY	ARG	GLY	ASP	I209	W210	S211	S212	T213	T214	L215	E216	R217	Y218	LYS	VAL	ALA	PRO	Q224	Q225	K226	R227	N228	E229	S230	L231	A232	T233	L234	A235	L236	THR	ARG	ASP	I240		
I241	T242	I243	K244	S245	V246	Y247	E248	K249	Y250	L251	PRO	GLN	ASP	GLU	ASN	SER	GLY	TYR	LEU	PRO	SER	S321	C322	G323	D324	L325	L326	K327	N271	F272	N273	Y274	L275	A276	S277	E278	E279	L281	Q282	LEU	D284	N285	Q286	Y287	E288	E289	F290	M291	R292	Q293	M294	N295	G296	ILE	TYR	P299	D300				
K301	W302	L303	F304	L305	I306	L307	S308	L309	A310	K311	Y312	Y313	I314	SER	ARG	G317	R318	L319	D320	S321	C322	G323	D324	L325	L326	K327	N328	S329	L330	Y331	Y332	D333	THR	LEU	ARG	TYR	SER	ASP	F339	D340	R341	I342	Y343	N344	F345	Y346	L347	L348	E409	E410	W411	M412	K413	S344	Q355	F356	I357	L358	G359	K360	
L361	K362	E363	N364	D365	SER	LYS	PHE	PHE	ASN	GLN	D373	W374	T375	E376	K377	L378	Q379	A380	H381	M382	A383	T384	F385	E386	S387	L388	I389	N390	L391	Y392	D393	I394	Y395	L396	N397	D398	V399	A400	L401	R402	Q403	D404	S405	ASN	L407	V408	E409	T410	W411	M412	K413	R414	V415	S416	L417	Q418	K419	S420			
A421	A422	E423	K424	C425	M426	V427	Y428	S429	E430	A431	I432	L433	L434	A435	D436	P437	R438	K439	V440	G441	P442	P443	G444	S445	F446	G447	R448	L449	W450	C451	S452	Y453	G454	D455	L456	Y457	W458	R459	S460	M461	A462	I463	S464	T465	A466	R467	E468	L469	W470	T471	Q472	S473	L474	K475	V476	P477	Y478	F479	Y480		
I481	E482	D483	L484	E485	E486	I487	Y488	L489	M490	W491	A492	D493	R494	E495	L496	D497	LYS	GLU	GLY	V501	E502	R503	A504	F505	S506	I507	L508	E509	D510	A511	L512	H513	V514	P515	T516	M517	P518	E519	I520	L521	L522	E523	TYR	LYS	ASN	GLY	HIS	N590	F591	A592	L593	F594	L595	Q596	N597	H598	TYR	GLU			
S541	L542	R543	I544	W545	S546	K547	Y548	I549	D550	Y551	L552	E553	A554	Y555	CYS	PRO	LYS	ASP	ALA	ASN	SER	ASP	LYS	I566	F567	N568	K569	T570	K571	M572	A573	Y574	N575	T576	V577	I578	D579	L580	R581	LEU	ILE	THR	P585	A586	M587	A588	E589	N590	F591	A592	L593	F594	L595	Q596	N597	H598	TYR	GLU			
V601	M602	E603	S604	F605	Q606	V607	Y608	E609	K610	T611	I612	P613	L614	F615	P616	P617	E618	I619	Q620	Y621	L622	L623	W624	I625	E626	Y627	L628	E629	V630	A631	T632	S633	GLN	LEU	SER	SER	SER	LEU	P641	E642	H643	I644	R645	F646	L647	F648	E649	K650	A651	L652	K653	N654	L655	C656	SER	ASN	GLY	ILE			
ASP	C662	K663	T664	I665	F666	I667	A668	Y669	S670	V671	F672	E673	E674	R675	ILE	SER	GLY	ILE	S681	K682	S683	I684	E685	I686	L687	R688	B689	G690	A691	V692	I693	GLY	THR	VAL	VAL	SER	VAL	SER	THR	HIS	L702	E703	S704	R705	L706	Q707	L708	W709	R710	M711	C712	I713	S714	K715	A716	E717	S718	T719	L720		
G721	P722	S723	V724	T725	R726	E727	L728	Y729	Q730	E731	C732	I733	Q734	I735	L736	P737	N738	S739	K740	A741	V742	E743	F744	W745	F748	S749	D750	F751	E752	V753	S754	I755	G756	E757	T758	I759	R760	A761	R762	E763	I764	L765	A766	V767	G768	A769	K770	L771	L772	P773	P774	S775	R776	N777	T778	E779	W781				
D782	S783	F784	E785	I786	F787	E788	L789	K790	H791	G792	D793	E794	E795	T796	Y797	K798	D799	M800	L801	K802	M803	K804	K805	V806	L807	E808	S809	ASN	MET	LEU	ILE	ASP	SER	ALA	VAL	SER	HIS	GLU	GLY	ASN	ILE	ASN	PHE	VAL	ALA	ALA	ALA	THR	SER	HIS	PRO	ASN	SER	HIS	THR	LEU					

THR
GLN
SER
THR
SER
SER
TVR
SER
ILE
ASN
PRO
ASP
GLU
ILE
GLU
LEU
ASP
ILE

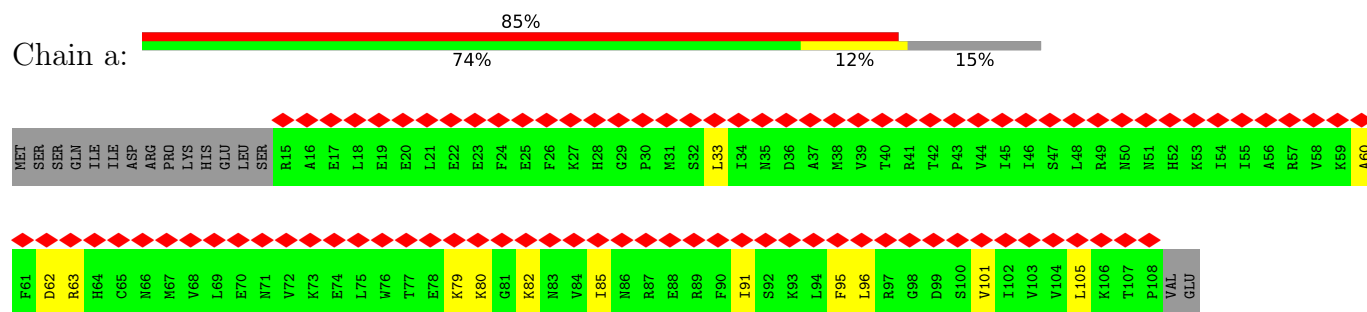
• Molecule 24: Unknown protein fragment



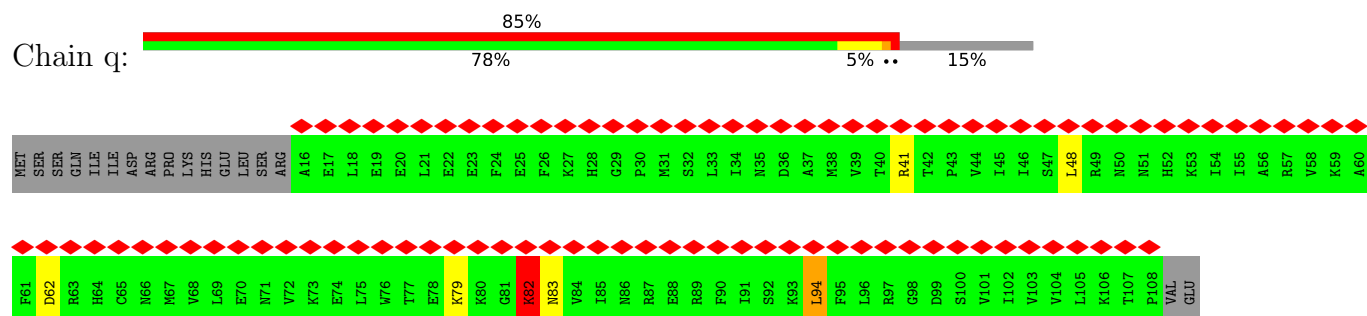
• Molecule 25: Unknown protein fragment



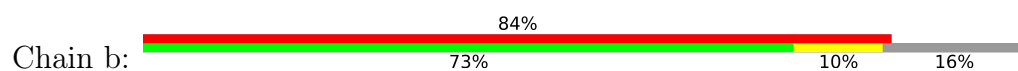
• Molecule 26: Small nuclear ribonucleoprotein Sm D2

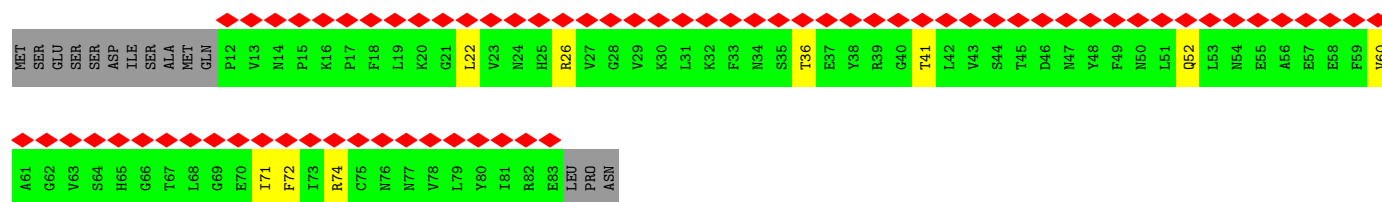


• Molecule 26: Small nuclear ribonucleoprotein Sm D2

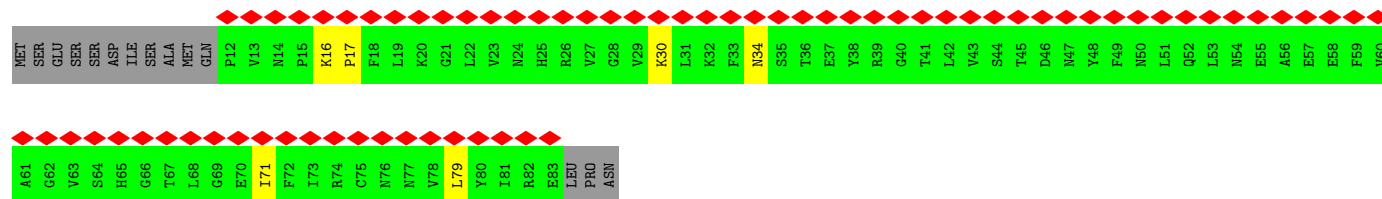
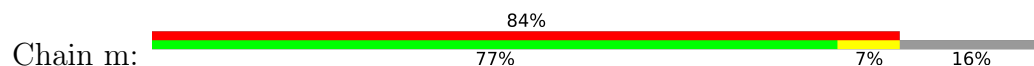


• Molecule 27: Small nuclear ribonucleoprotein F

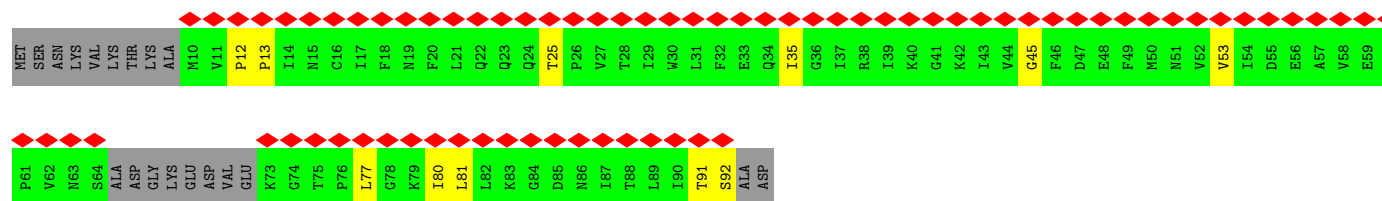
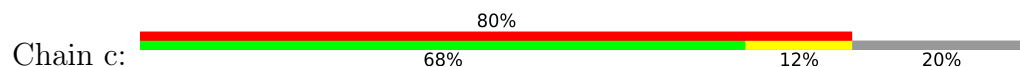




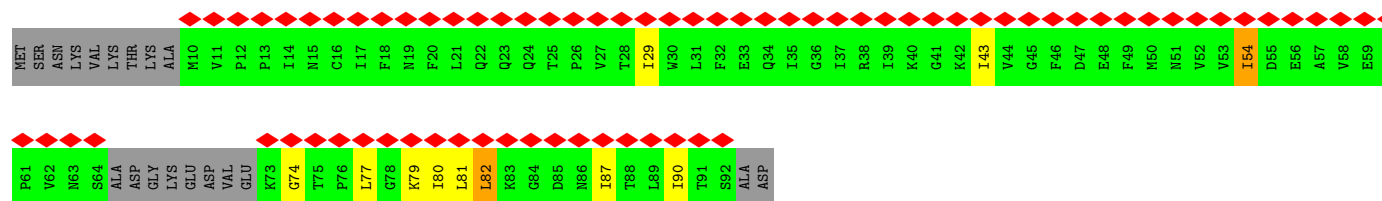
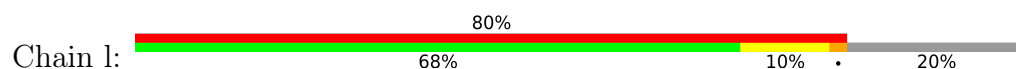
• Molecule 27: Small nuclear ribonucleoprotein F



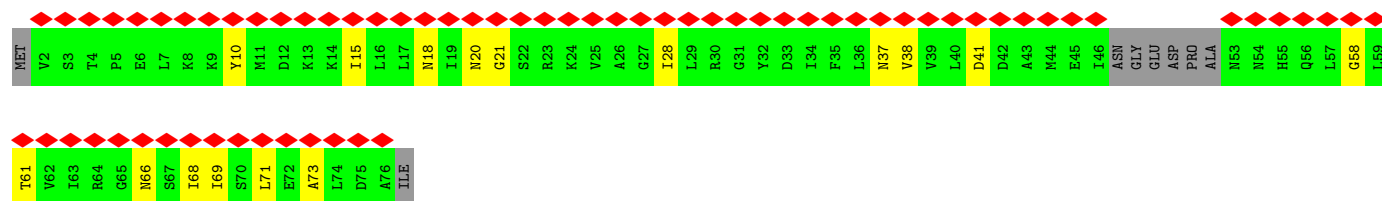
• Molecule 28: Small nuclear ribonucleoprotein E



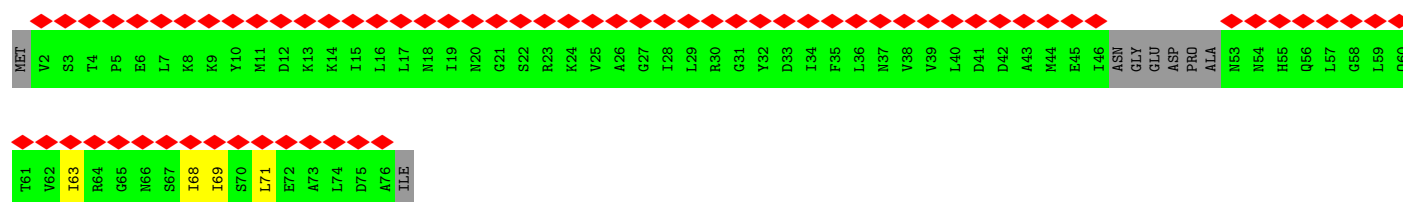
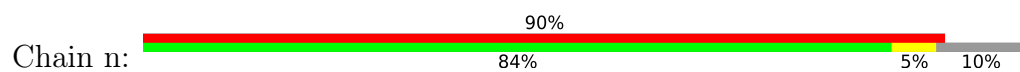
• Molecule 28: Small nuclear ribonucleoprotein E



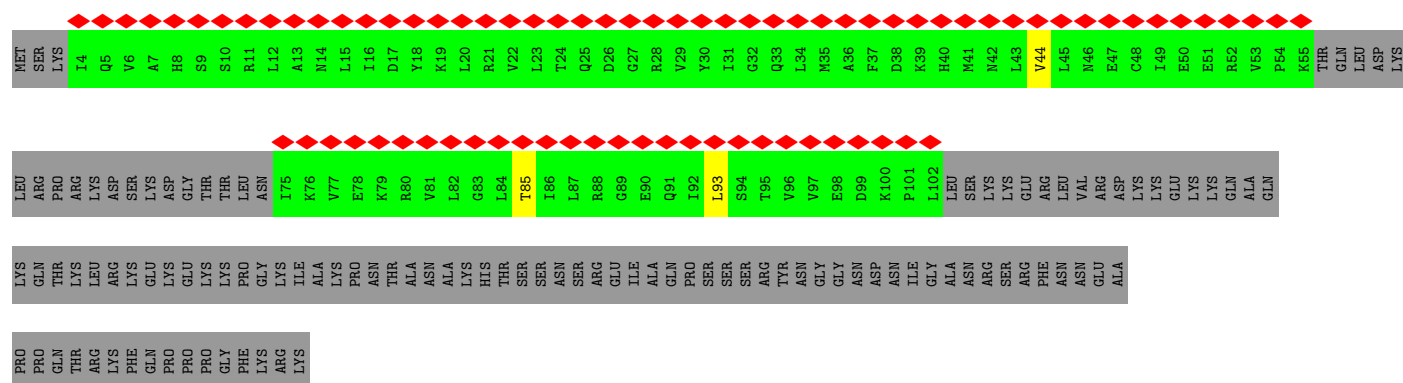
• Molecule 29: Small nuclear ribonucleoprotein G



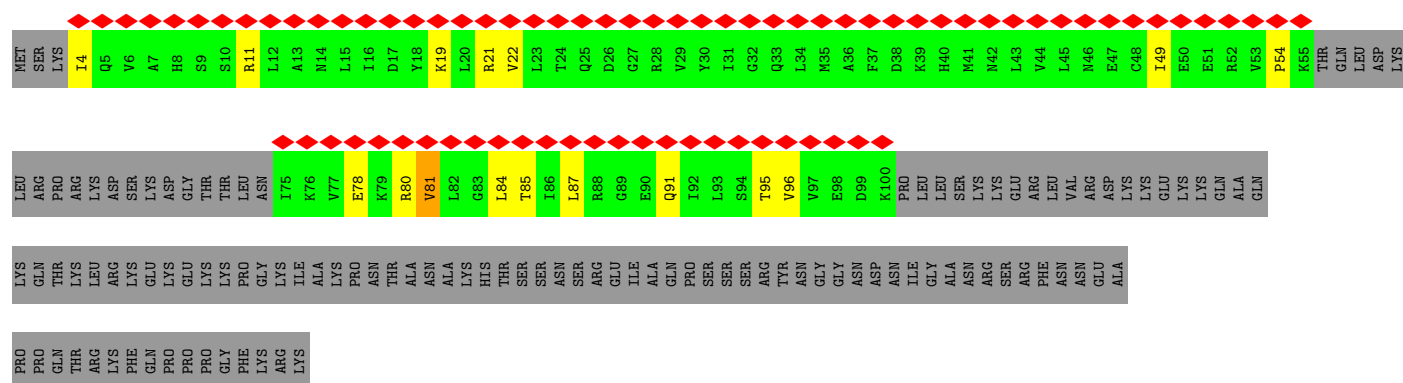
• Molecule 29: Small nuclear ribonucleoprotein G



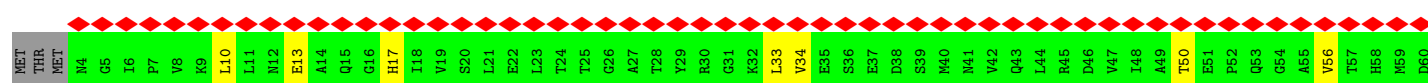
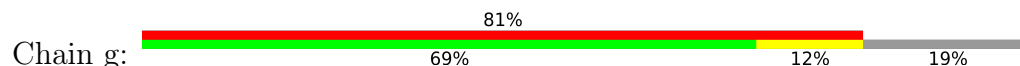
• Molecule 30: Small nuclear ribonucleoprotein-associated protein B

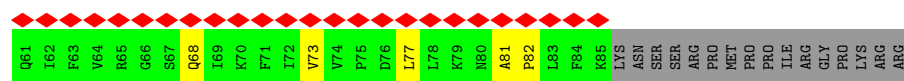


• Molecule 30: Small nuclear ribonucleoprotein-associated protein B

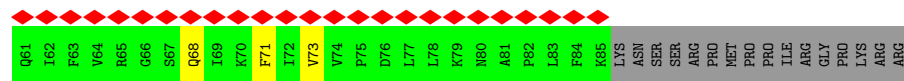
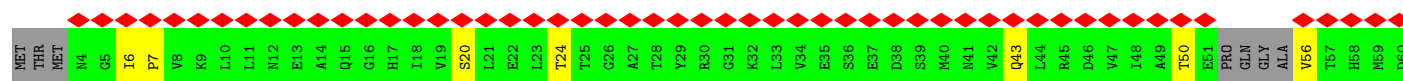
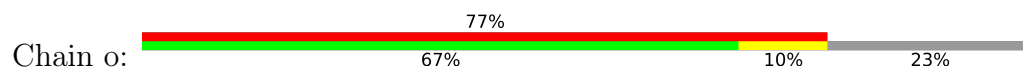


• Molecule 31: Small nuclear ribonucleoprotein Sm D3

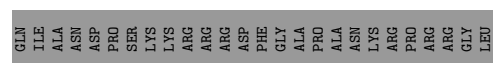
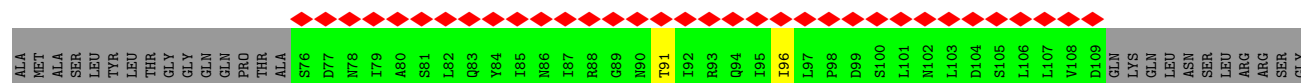
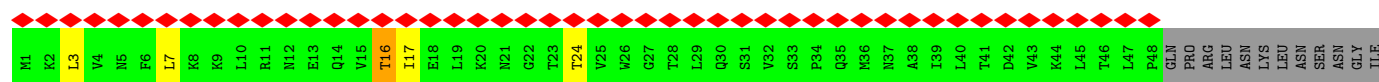




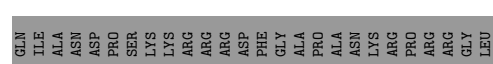
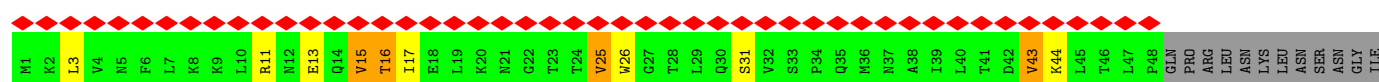
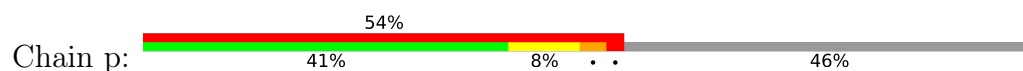
• Molecule 31: Small nuclear ribonucleoprotein Sm D3



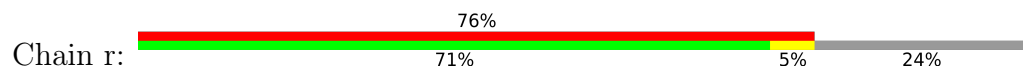
• Molecule 32: Small nuclear ribonucleoprotein Sm D1

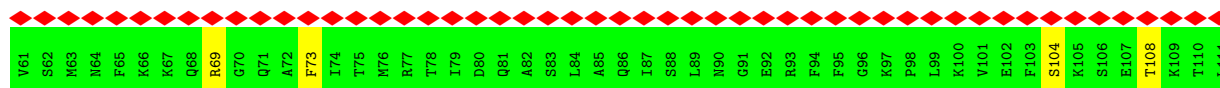


• Molecule 32: Small nuclear ribonucleoprotein Sm D1

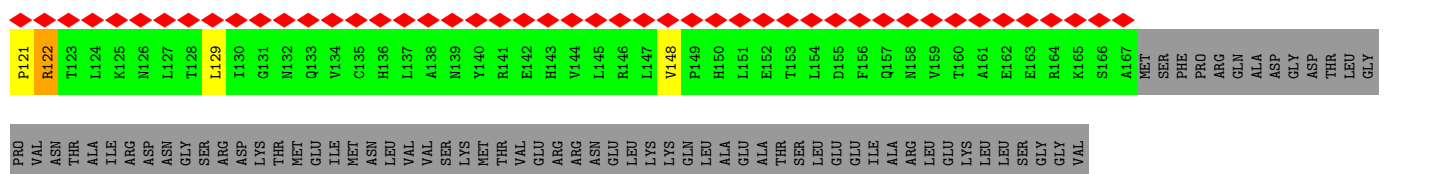


• Molecule 33: Lea1

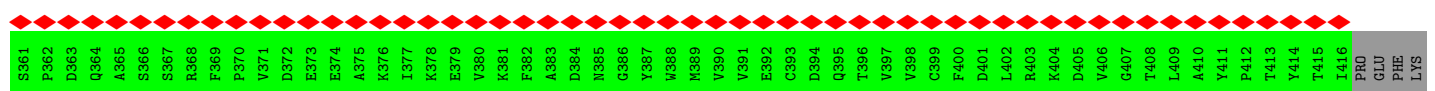
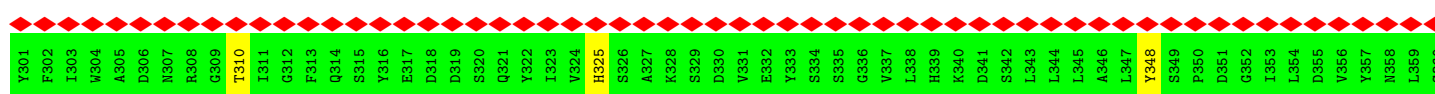
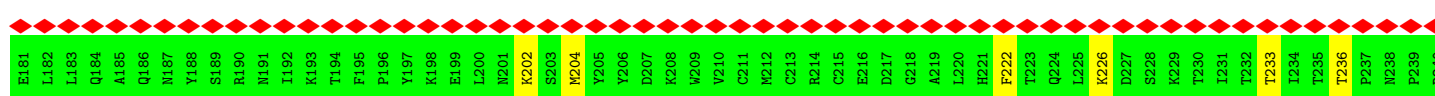
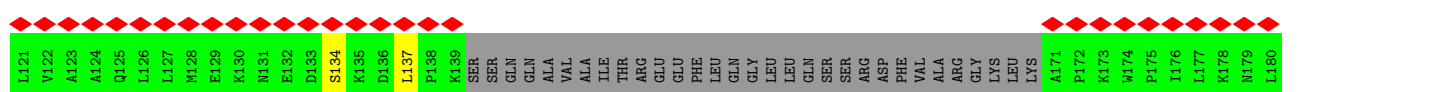
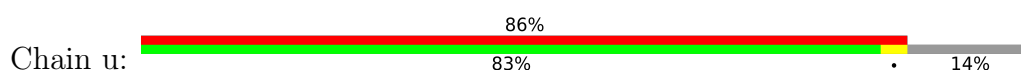


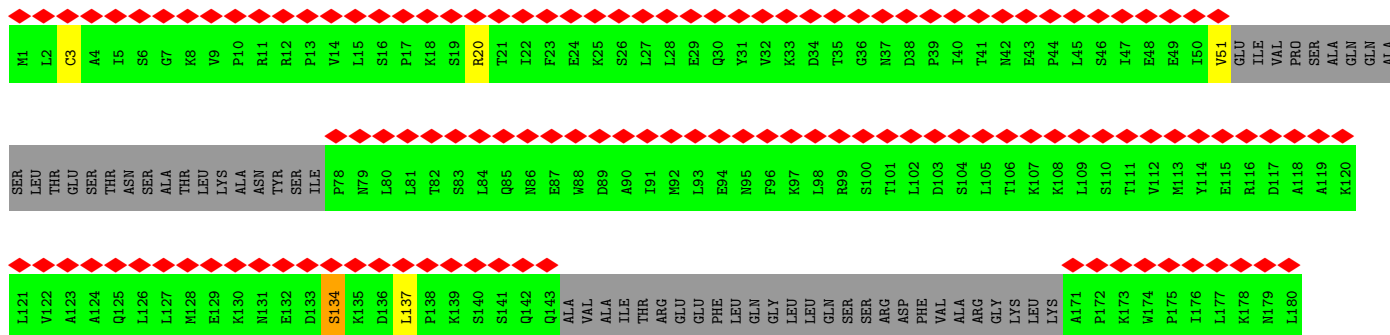


• Molecule 34: Msl1

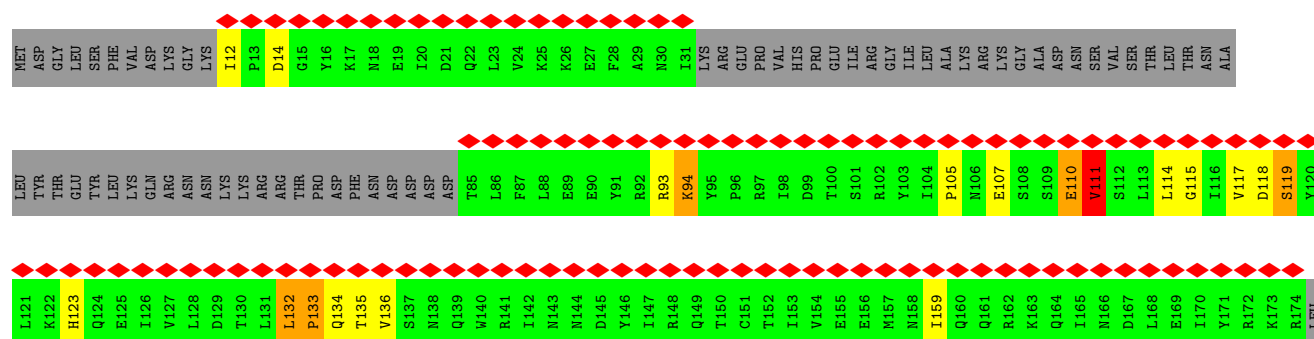


• Molecule 35: Pre-mRNA-processing factor Prp19





Chain y:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	212219	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 ($e^-/\text{\AA}^2$)	2.0	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	0.404	Depositor
Minimum map value	-0.197	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	544.0, 544.0, 544.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.36, 1.36, 1.36	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, ZN, 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	2	0.40	0/3167	0.68	0/4911
2	5	0.45	0/2422	0.51	0/3762
3	6	0.45	0/2427	0.52	1/3778 (0.0%)
4	e	0.59	4/787 (0.5%)	0.67	1/1219 (0.1%)
5	i	0.30	0/1379	0.50	0/2131
6	A	0.48	0/16570	0.77	11/22456 (0.0%)
7	B	0.45	0/7331	0.76	4/9926 (0.0%)
8	D	0.52	0/2889	0.82	1/3924 (0.0%)
9	E	0.41	0/1517	0.73	0/2043
10	F	0.42	0/1598	0.78	4/2151 (0.2%)
11	G	0.42	0/2094	0.70	0/2815
12	H	0.43	0/584	0.89	1/781 (0.1%)
13	I	0.43	0/1307	0.71	0/1748
14	K	0.33	0/552	0.66	0/746
15	L	0.33	0/3406	0.67	0/4592
16	M	0.32	0/2678	0.70	1/3619 (0.0%)
17	N	0.34	0/1354	0.66	1/1838 (0.1%)
18	O	0.31	0/1967	0.71	0/2624
19	P	0.22	0/3918	0.56	0/5386
20	R	0.34	0/817	0.64	0/1083
21	S	0.41	0/1978	0.73	3/2655 (0.1%)
22	T	0.38	0/3411	0.61	2/4632 (0.0%)
23	U	0.21	0/3625	0.56	1/4963 (0.0%)
26	a	0.54	0/753	0.80	0/1013
26	q	0.57	0/738	0.87	1/995 (0.1%)
27	b	0.59	0/585	0.76	0/791
27	m	0.56	0/585	0.83	0/791
28	c	0.68	1/585 (0.2%)	0.84	0/795
28	l	0.62	0/585	0.79	0/795
29	d	0.70	2/532 (0.4%)	0.80	0/715
29	n	0.54	0/529	0.68	0/711
30	f	0.55	0/636	0.75	0/856

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	k	0.56	0/614	0.66	0/826
31	g	0.54	0/634	0.77	0/859
31	o	0.54	0/607	0.76	0/820
32	h	0.57	0/649	0.78	0/880
32	p	0.62	0/623	0.88	4/844 (0.5%)
33	r	0.50	0/415	1.08	0/577
34	s	0.50	0/814	1.19	10/1134 (0.9%)
35	u	0.76	0/2150	1.12	9/2989 (0.3%)
35	v	1.03	2/586 (0.3%)	1.56	7/816 (0.9%)
35	w	0.77	0/2165	1.20	12/3010 (0.4%)
35	x	0.96	1/576 (0.2%)	1.34	3/802 (0.4%)
36	y	0.98	1/546 (0.2%)	1.45	11/760 (1.4%)
All	All	0.48	11/83685 (0.0%)	0.77	88/115562 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	A	0	6
7	B	0	9
8	D	0	2
9	E	0	3
10	F	0	1
11	G	0	2
15	L	0	1
18	O	0	1
30	k	0	1
35	u	0	1
35	v	0	1
35	w	0	2
36	y	0	2
All	All	0	32

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	v	109	LEU	C-N	8.14	1.44	1.33
4	e	9	U	C1'-N1	7.24	1.59	1.48
4	e	-13	U	C1'-N1	7.01	1.58	1.48
4	e	-11	U	C1'-N1	6.25	1.57	1.48

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	v	134	SER	C-O	-5.79	1.17	1.24

The worst 5 of 88 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	w	134	SER	CA-C-O	-16.70	103.49	120.70
35	v	134	SER	CA-C-O	-11.57	108.16	120.42
35	v	137	LEU	CA-C-N	10.19	130.36	119.05
35	v	137	LEU	C-N-CA	10.19	130.36	119.05
36	y	132	LEU	CA-C-N	10.15	132.53	119.84

There are no chirality outliers.

5 of 32 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	A	1325	SER	Peptide
6	A	405	ASN	Peptide
6	A	542	HIS	Peptide
6	A	774	ILE	Peptide
6	A	775	ARG	Peptide

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	2	2848	0	1445	36	0
2	5	2173	0	1102	13	0
3	6	2170	0	1095	15	0
4	e	707	0	354	3	0
5	i	1239	0	624	6	0
6	A	16159	0	16162	193	0
7	B	7179	0	7361	87	0
8	D	2826	0	2816	48	0
9	E	1494	0	1540	22	0
10	F	1576	0	1607	15	0
11	G	2048	0	2011	18	0
12	H	570	0	556	11	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	I	1283	0	1301	11	0
14	K	550	0	454	2	0
15	L	3353	0	3421	28	0
16	M	2607	0	2512	43	0
17	N	1326	0	1367	15	0
18	O	1935	0	1894	34	0
19	P	3872	0	2618	17	0
20	R	813	0	837	7	0
21	S	1948	0	1979	22	0
22	T	3370	0	2727	24	0
23	U	3625	0	2248	16	0
24	X	1095	0	231	9	0
25	Y	80	0	18	1	0
26	a	741	0	778	16	0
26	q	726	0	754	5	0
27	b	573	0	572	7	0
27	m	573	0	572	2	0
28	c	575	0	597	9	0
28	l	575	0	597	4	0
29	d	529	0	557	9	0
29	n	526	0	555	2	0
30	f	631	0	670	3	0
30	k	610	0	638	23	0
31	g	625	0	647	14	0
31	o	600	0	623	9	0
32	h	644	0	686	10	0
32	p	618	0	660	43	0
33	r	416	0	182	14	0
34	s	816	0	341	5	0
35	u	2156	0	938	3	0
35	v	588	0	250	12	0
35	w	2171	0	945	4	0
35	x	578	0	246	3	0
36	y	548	0	219	17	0
37	6	4	0	0	0	0
37	B	1	0	0	0	0
38	A	36	0	6	3	0
39	B	32	0	12	0	0
40	F	2	0	0	0	0
40	G	1	0	0	0	0
40	I	3	0	0	0	0
40	O	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	82745	0	70325	715	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 5.

The worst 5 of 715 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)
35:v:78:PRO:N	36:y:123:HIS:HA	1.46	1.26
32:p:16:THR:C	32:p:96:ILE:HD11	1.60	1.26
32:p:16:THR:CA	32:p:96:ILE:HD11	1.66	1.24
32:p:16:THR:HG22	32:p:96:ILE:CD1	1.67	1.24
9:E:212:ASP:OD2	24:X:1024:UNK:O	1.57	1.22

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	
6	A	1954/2413 (81%)	1813 (93%)	126 (6%)	15 (1%)	16	45
7	B	889/1008 (88%)	830 (93%)	55 (6%)	4 (0%)	30	60
8	D	357/451 (79%)	329 (92%)	28 (8%)	0	100	100
9	E	176/379 (46%)	164 (93%)	11 (6%)	1 (1%)	21	52
10	F	193/364 (53%)	173 (90%)	19 (10%)	1 (0%)	24	55
11	G	253/339 (75%)	229 (90%)	23 (9%)	1 (0%)	30	60
12	H	64/175 (37%)	55 (86%)	8 (12%)	1 (2%)	7	31
13	I	154/157 (98%)	140 (91%)	14 (9%)	0	100	100
14	K	76/135 (56%)	72 (95%)	4 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	L	406/577 (70%)	380 (94%)	26 (6%)	0	100	100
16	M	320/455 (70%)	302 (94%)	18 (6%)	0	100	100
17	N	163/251 (65%)	157 (96%)	6 (4%)	0	100	100
18	O	215/382 (56%)	196 (91%)	19 (9%)	0	100	100
19	P	645/1145 (56%)	610 (95%)	35 (5%)	0	100	100
20	R	97/215 (45%)	94 (97%)	3 (3%)	0	100	100
21	S	234/590 (40%)	223 (95%)	11 (5%)	0	100	100
22	T	451/687 (66%)	442 (98%)	9 (2%)	0	100	100
23	U	587/859 (68%)	555 (94%)	30 (5%)	2 (0%)	36	65
26	a	92/110 (84%)	83 (90%)	9 (10%)	0	100	100
26	q	91/110 (83%)	84 (92%)	7 (8%)	0	100	100
27	b	70/86 (81%)	61 (87%)	9 (13%)	0	100	100
27	m	70/86 (81%)	65 (93%)	5 (7%)	0	100	100
28	c	71/94 (76%)	62 (87%)	9 (13%)	0	100	100
28	l	71/94 (76%)	66 (93%)	4 (6%)	1 (1%)	9	33
29	d	65/77 (84%)	63 (97%)	2 (3%)	0	100	100
29	n	65/77 (84%)	57 (88%)	8 (12%)	0	100	100
30	f	76/196 (39%)	74 (97%)	2 (3%)	0	100	100
30	k	74/196 (38%)	66 (89%)	7 (10%)	1 (1%)	9	33
31	g	80/101 (79%)	73 (91%)	7 (9%)	0	100	100
31	o	74/101 (73%)	70 (95%)	4 (5%)	0	100	100
32	h	78/146 (53%)	71 (91%)	7 (9%)	0	100	100
32	p	75/146 (51%)	65 (87%)	8 (11%)	2 (3%)	4	22
33	r	82/111 (74%)	76 (93%)	6 (7%)	0	100	100
34	s	160/238 (67%)	117 (73%)	35 (22%)	8 (5%)	1	11
35	u	423/503 (84%)	413 (98%)	8 (2%)	2 (0%)	24	55
35	v	114/503 (23%)	108 (95%)	3 (3%)	3 (3%)	4	23
35	w	426/503 (85%)	417 (98%)	9 (2%)	0	100	100
35	x	112/503 (22%)	104 (93%)	8 (7%)	0	100	100
36	y	106/175 (61%)	92 (87%)	8 (8%)	6 (6%)	1	9
All	All	9709/14738 (66%)	9051 (93%)	610 (6%)	48 (0%)	26	55

5 of 48 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	A	1905	LEU
12	H	9	LEU
23	U	37	ILE
34	s	76	ILE
36	y	94	LYS

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	
6	A	1778/2182 (82%)	1761 (99%)	17 (1%)	68	76
7	B	809/910 (89%)	796 (98%)	13 (2%)	55	72
8	D	313/397 (79%)	310 (99%)	3 (1%)	68	76
9	E	168/328 (51%)	166 (99%)	2 (1%)	63	75
10	F	183/332 (55%)	182 (100%)	1 (0%)	81	83
11	G	219/296 (74%)	218 (100%)	1 (0%)	81	83
12	H	58/151 (38%)	55 (95%)	3 (5%)	21	49
13	I	140/141 (99%)	140 (100%)	0	100	100
14	K	44/121 (36%)	44 (100%)	0	100	100
15	L	379/538 (70%)	378 (100%)	1 (0%)	86	86
16	M	288/413 (70%)	285 (99%)	3 (1%)	68	76
17	N	144/225 (64%)	144 (100%)	0	100	100
18	O	210/346 (61%)	208 (99%)	2 (1%)	68	76
19	P	178/1029 (17%)	176 (99%)	2 (1%)	65	76
20	R	90/193 (47%)	90 (100%)	0	100	100
21	S	208/525 (40%)	208 (100%)	0	100	100
22	T	248/633 (39%)	247 (100%)	1 (0%)	84	84
23	U	131/786 (17%)	127 (97%)	4 (3%)	35	60
26	a	79/103 (77%)	79 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	q	77/103 (75%)	73 (95%)	4 (5%)	21	49
27	b	63/77 (82%)	63 (100%)	0	100	100
27	m	63/77 (82%)	60 (95%)	3 (5%)	23	52
28	c	65/83 (78%)	63 (97%)	2 (3%)	35	60
28	l	65/83 (78%)	60 (92%)	5 (8%)	12	37
29	d	58/66 (88%)	57 (98%)	1 (2%)	53	71
29	n	57/66 (86%)	56 (98%)	1 (2%)	51	70
30	f	70/176 (40%)	70 (100%)	0	100	100
30	k	67/176 (38%)	66 (98%)	1 (2%)	57	72
31	g	69/89 (78%)	69 (100%)	0	100	100
31	o	67/89 (75%)	65 (97%)	2 (3%)	36	61
32	h	77/129 (60%)	76 (99%)	1 (1%)	61	74
32	p	73/129 (57%)	63 (86%)	10 (14%)	3	16
All	All	6538/10992 (60%)	6455 (99%)	83 (1%)	59	74

5 of 83 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	k	19	LYS
32	p	16	THR
28	l	77	LEU
27	m	79	LEU
32	p	95	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 128 such sidechains are listed below:

Mol	Chain	Res	Type
23	U	777	ASN
28	c	86	ASN
7	B	180	ASN
7	B	112	ASN
31	g	17	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	127/1175 (10%)	44 (34%)	4 (3%)
2	5	100/214 (46%)	25 (25%)	2 (2%)
3	6	101/112 (90%)	28 (27%)	3 (2%)
4	e	33/34 (97%)	19 (57%)	0
5	i	54/59 (91%)	18 (33%)	0
All	All	415/1594 (26%)	134 (32%)	9 (2%)

5 of 134 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	5	A
1	2	11	U
1	2	16	U
1	2	17	U
1	2	18	U

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	6	56	A
3	6	64	U
1	2	1145	U
2	5	78	A
2	5	81	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 14 ligands modelled in this entry, 12 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	$\# Z > 2$
38	IHP	A	3001	-	36,36,36	0.88	0	60,60,60	1.67	12 (20%)
39	GTP	B	2001	37	33,34,34	0.97	1 (3%)	50,54,54	1.60	10 (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
38	IHP	A	3001	-	-	7/30/54/54	0/1/1/1
39	GTP	B	2001	37	-	5/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	B	2001	GTP	O4'-C4'	-2.14	1.40	1.45

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	B	2001	GTP	C2-N3-C4	4.62	120.25	112.30
39	B	2001	GTP	C5-C4-N3	-4.21	121.69	128.39
38	A	3001	IHP	C4-C3-C2	3.66	118.45	110.43
38	A	3001	IHP	C5-C6-C1	3.62	118.38	110.43
38	A	3001	IHP	O15-C5-C6	3.61	116.44	108.76

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

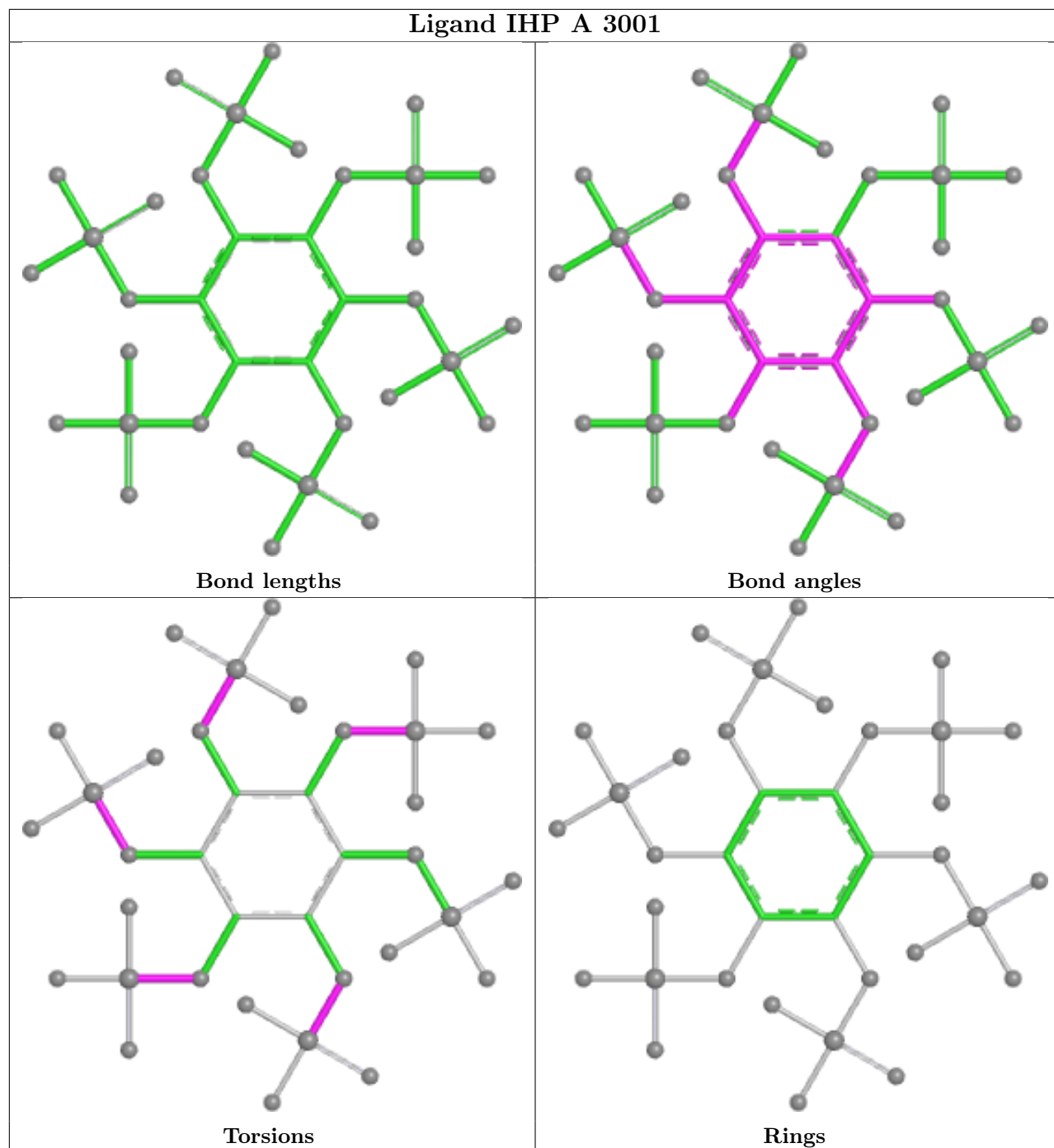
Mol	Chain	Res	Type	Atoms
39	B	2001	GTP	PB-O3B-PG-O2G
38	A	3001	IHP	C1-O11-P1-O21
39	B	2001	GTP	C5'-O5'-PA-O3A
39	B	2001	GTP	C5'-O5'-PA-O1A
39	B	2001	GTP	C5'-O5'-PA-O2A

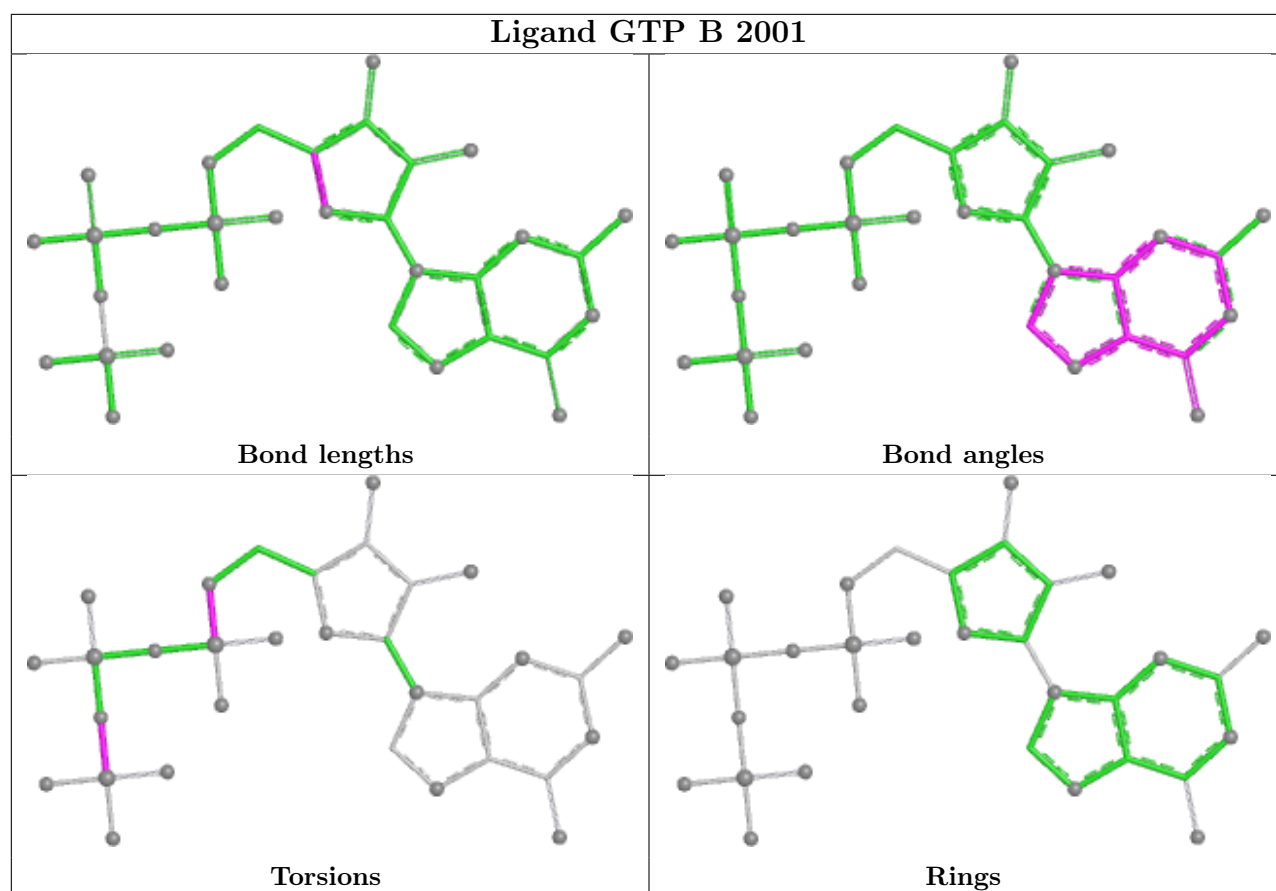
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	A	3001	IHP	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.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
5	i	4
24	X	4

The worst 5 of 8 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	i	15:U	O3'	501:A	P	58.05
1	X	3370:UNK	C	3389:UNK	N	35.33
1	X	1031:UNK	C	2287:UNK	N	34.77
1	X	125:UNK	C	1001:UNK	N	25.13
1	X	2322:UNK	C	3364:UNK	N	19.85

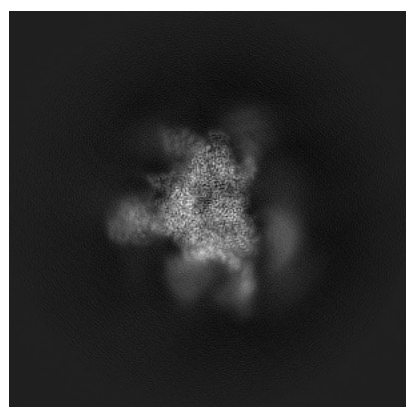
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7109. These allow visual inspection of the internal detail of the map and identification of artifacts.

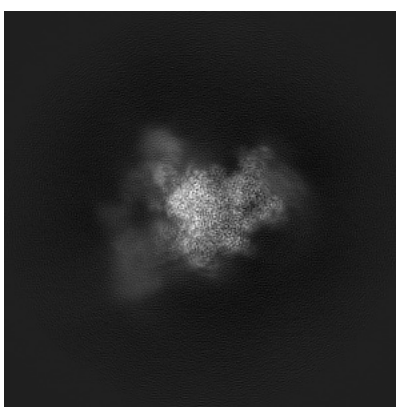
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

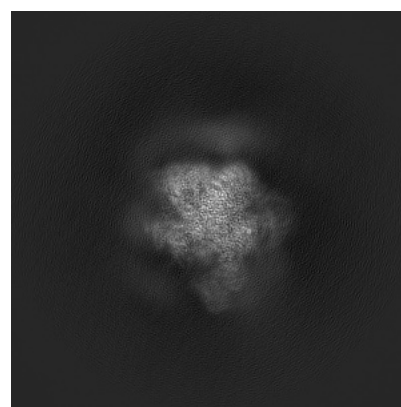
6.1.1 Primary map



X



Y

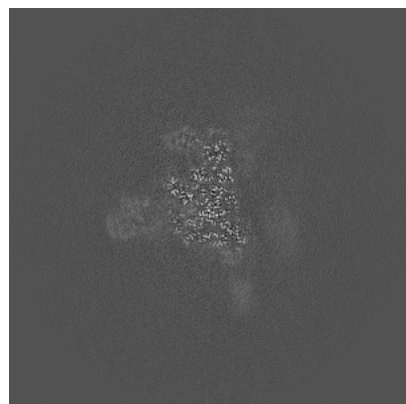


Z

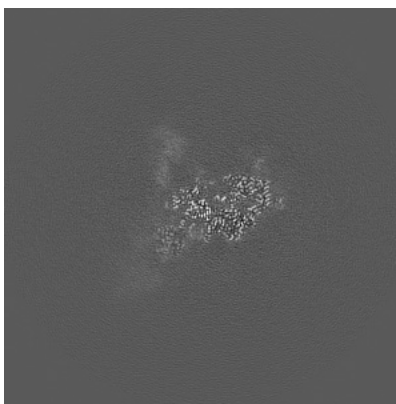
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

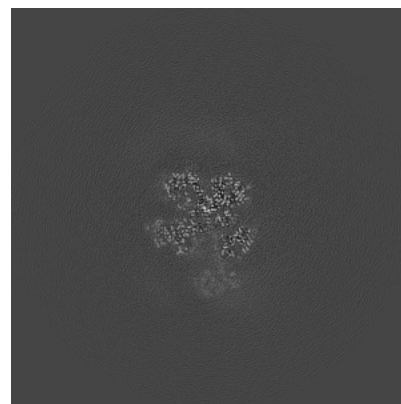
6.2.1 Primary map



X Index: 200



Y Index: 200

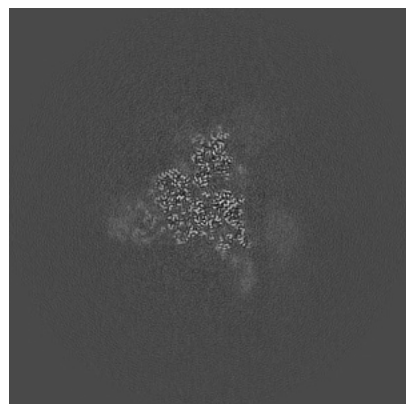


Z Index: 200

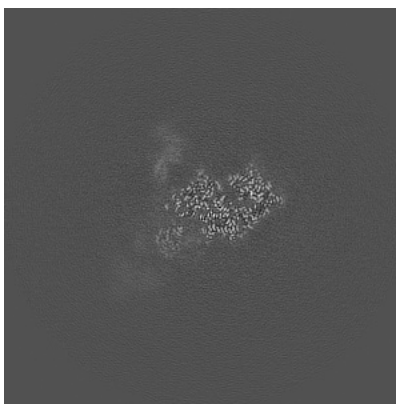
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

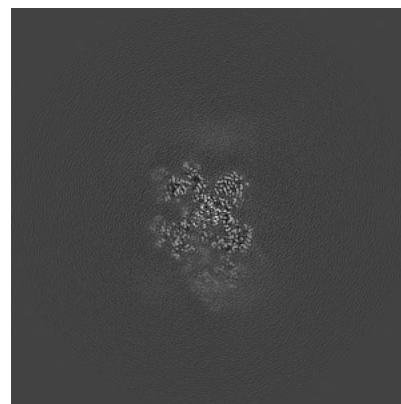
6.3.1 Primary map



X Index: 212



Y Index: 204

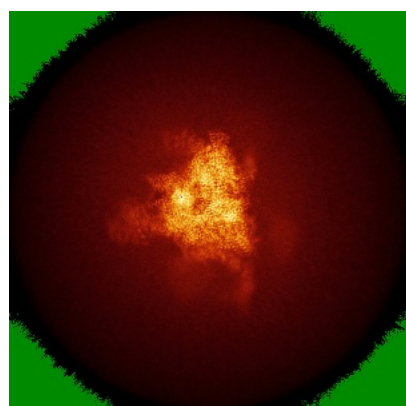


Z Index: 191

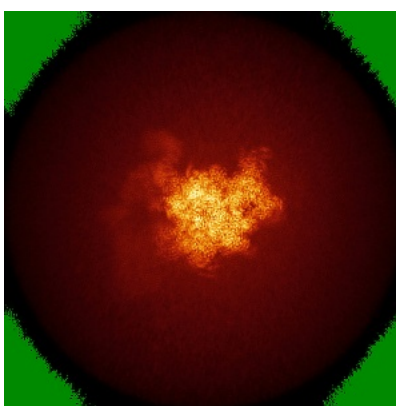
The images above show the largest variance slices of the map in three orthogonal directions.

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

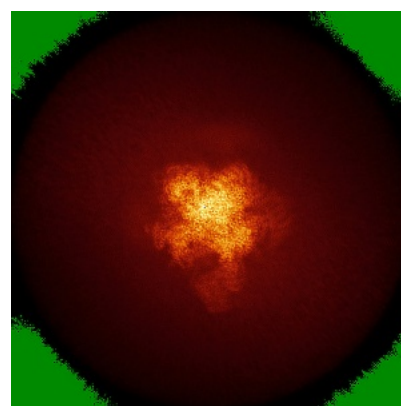
6.4.1 Primary map



X



Y

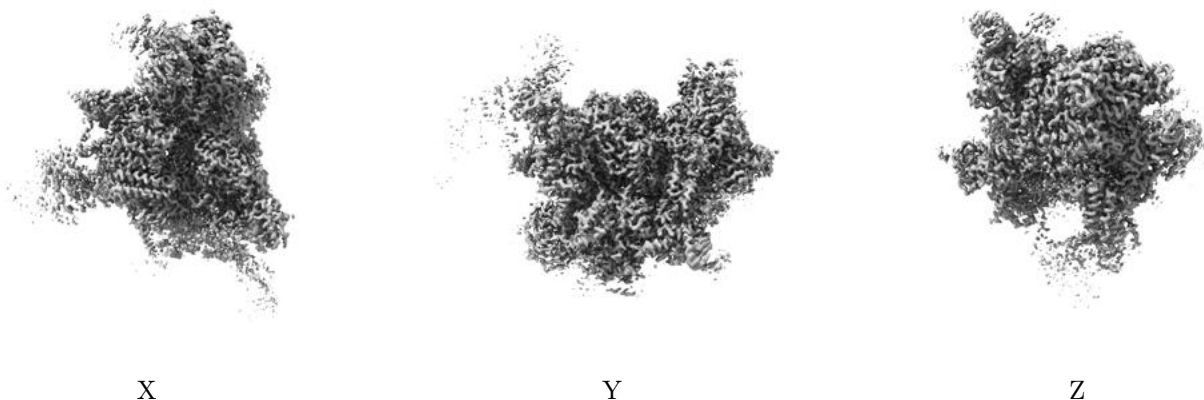


Z

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

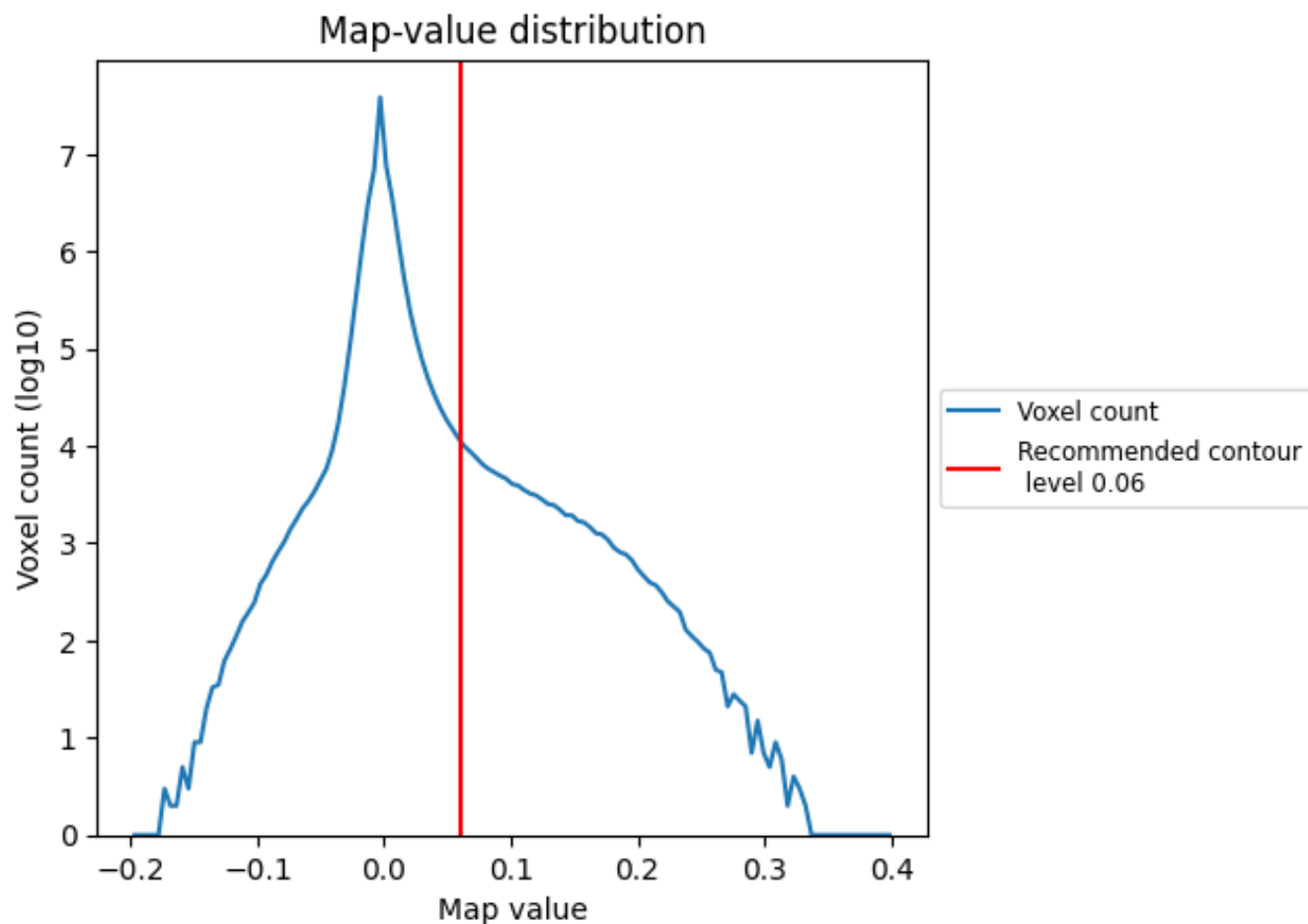
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

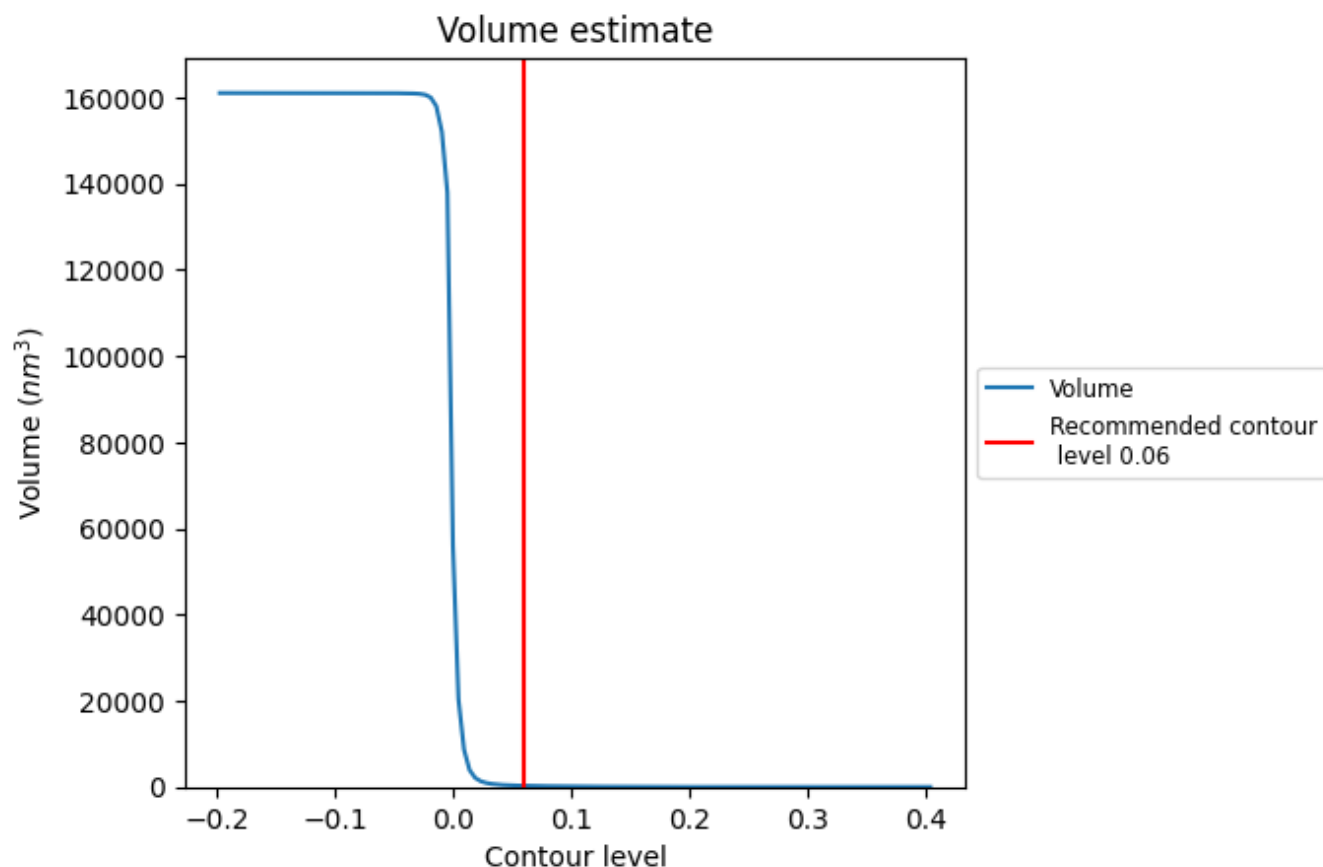
This section contains the results of statistical analysis of the map.

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.

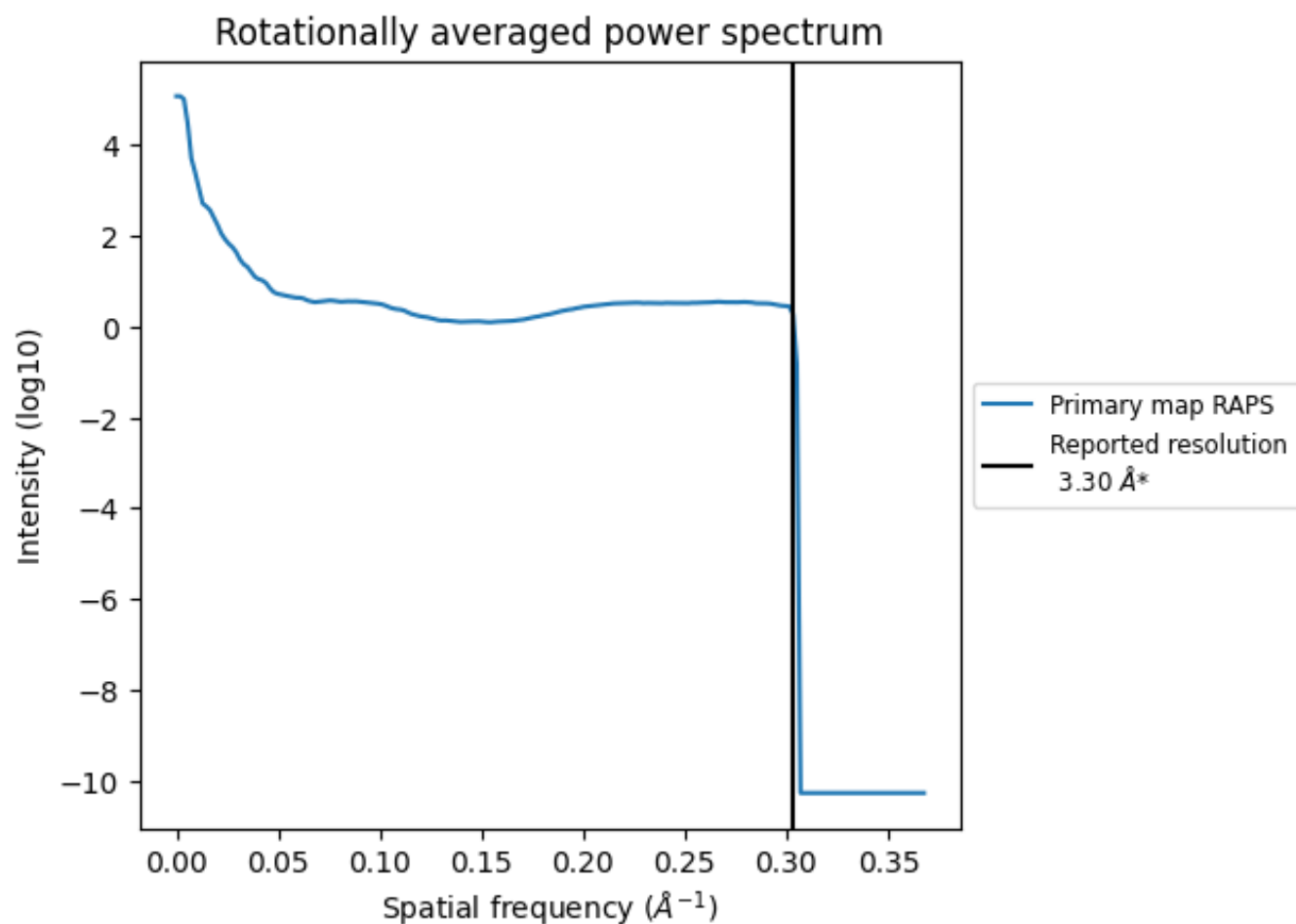
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 272 nm^3 ; this corresponds to an approximate mass of 246 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 0.303 Å⁻¹

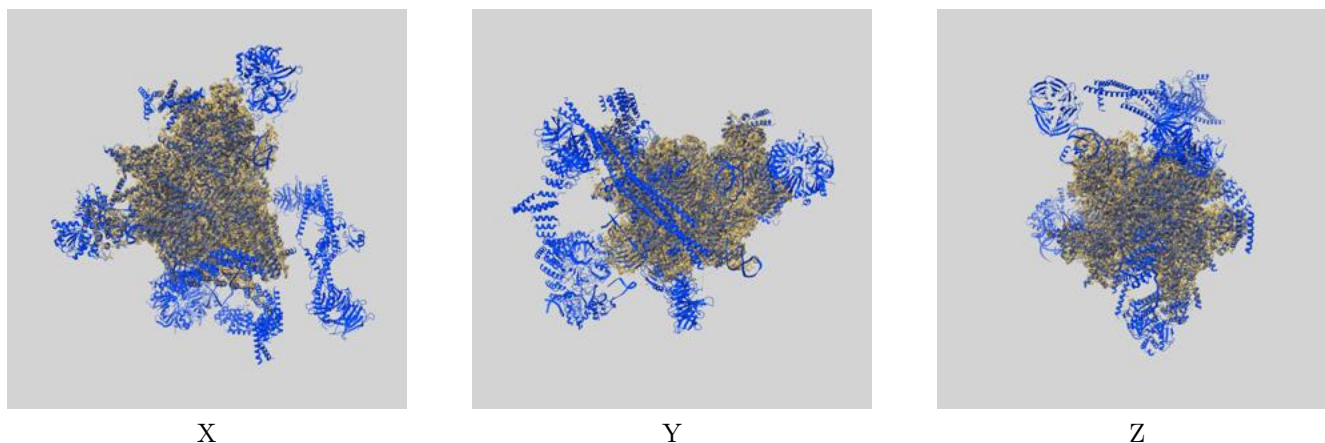
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

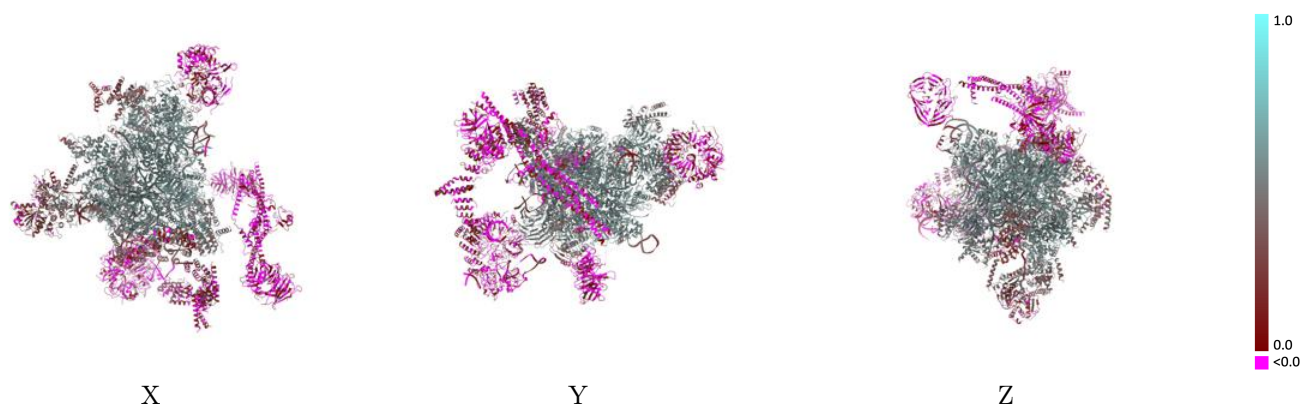
This section contains information regarding the fit between EMDB map EMD-7109 and PDB model 6BK8. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



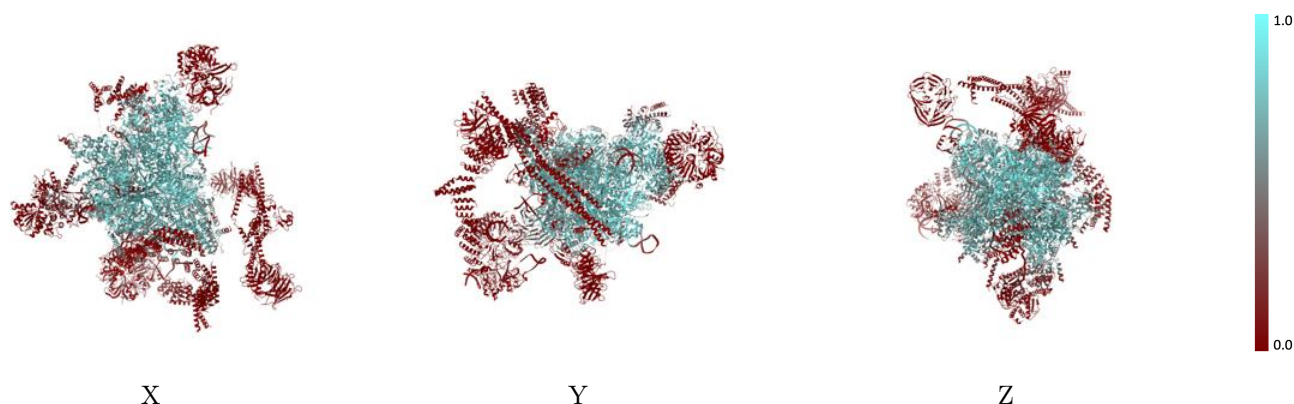
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



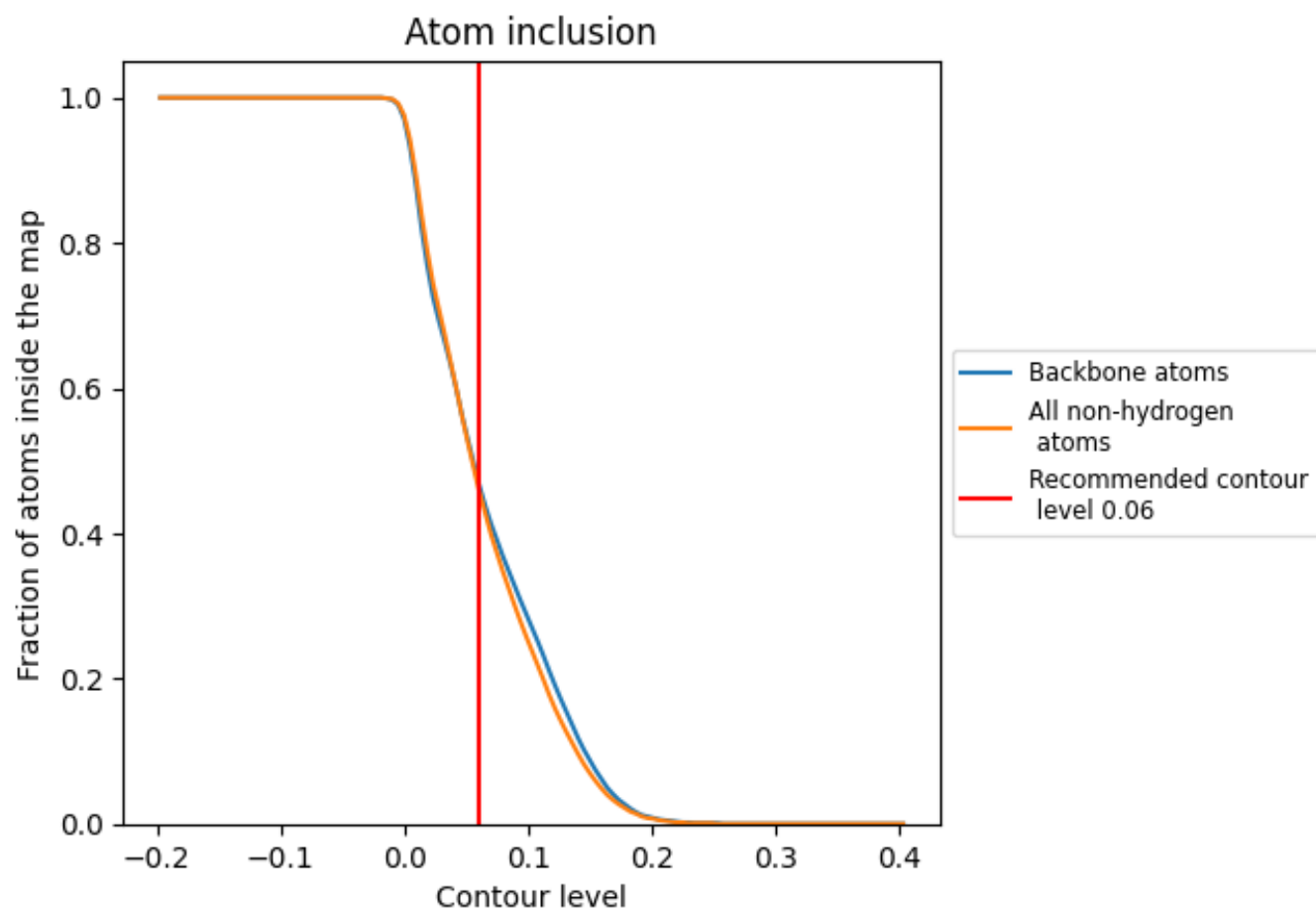
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 47% of all backbone atoms, 46% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4630	 0.3790
2	 0.2020	 0.1350
5	 0.7190	 0.4800
6	 0.7540	 0.5110
A	 0.7660	 0.5480
B	 0.7220	 0.5340
D	 0.7990	 0.5590
E	 0.6660	 0.5200
F	 0.5400	 0.4790
G	 0.6930	 0.5240
H	 0.5260	 0.5260
I	 0.7560	 0.5480
K	 0.3800	 0.4500
L	 0.4030	 0.3920
M	 0.5040	 0.5000
N	 0.5580	 0.4770
O	 0.4720	 0.4870
P	 0.1570	 0.3460
R	 0.6000	 0.5230
S	 0.7020	 0.5300
T	 0.5060	 0.4260
U	 0.0770	 0.2040
X	 0.4060	 0.4340
Y	 0.3380	 0.3790
a	 0.0000	 0.0440
b	 0.0000	 0.0190
c	 0.0000	 0.0250
d	 0.0000	 0.0920
e	 0.4160	 0.4330
f	 0.0000	 0.0780
g	 0.0000	 0.1650
h	 0.0000	 0.0050
i	 0.4260	 0.3650
k	 0.0000	 0.0040
l	 0.0000	 0.0130



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
m	 0.0000	 0.0240
n	 0.0000	 0.0090
o	 0.0000	 0.0240
p	 0.0000	 0.0100
q	 0.0000	 0.0120
r	 0.0000	 0.0330
s	 0.0000	 0.0040
u	 0.0000	 -0.0080
v	 0.0000	 -0.0290
w	 0.0000	 -0.0040
x	 0.0000	 -0.0220
y	 0.0000	 -0.0290