



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 09:45 AM UTC

PDB ID : 5XJC / pdb_00005xjc
EMDB ID : EMD-6721
Title : Cryo-EM structure of the human spliceosome just prior to exon ligation at 3.6 angstrom
Authors : Zhang, X.; Yan, C.; Hang, J.; Finci, I.L.; Lei, J.; Shi, Y.
Deposited on : 2017-04-30
Resolution : 3.60 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:

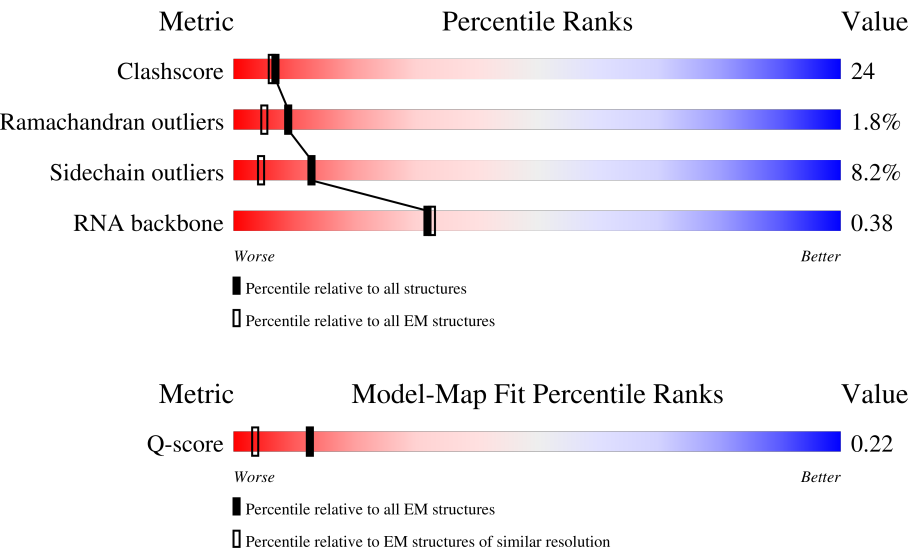
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.60 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	12797 (3.10 - 4.10)

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

Mol	Chain	Length	Quality of chain
1	A	2335	22% 67% 23% 6% .
2	B	117	24% 35% 25% 9% . 28%
3	C	972	26% 54% 27% 7% . 11%

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Mol	Chain	Length	Quality of chain
4	D	2136	
5	E	357	
6	F	107	
7	G	275	
8	H	188	
9	I	855	
10	J	848	
11	K	225	
12	L	802	
13	M	243	
14	N	144	
15	O	420	
16	P	229	
17	Q	1485	
18	R	536	
19	S	166	
20	T	514	
21	U	2752	
22	V	908	
23	W	579	
24	X	184	
25	Y	1220	
26	Z	586	
27	a	126	
27	h	126	

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Mol	Chain	Length	Quality of chain
28	b	231	
28	i	231	
29	c	119	
29	j	119	
30	d	118	
30	k	118	
31	f	86	
31	m	86	
32	e	92	
32	l	92	
33	g	76	
33	n	76	
34	o	255	
35	p	225	
36	q	504	
36	r	504	
36	s	504	
36	t	504	
37	u	411	
38	v	148	
39	w	174	
40	x	703	

2 Entry composition

There are 46 unique types of molecules in this entry. The entry contains 116421 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2253	Total	C	N	O	S	0	0
			18633	11997	3253	3302	81		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	84	Total	C	N	O	P	0	0
			1768	792	295	597	84		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	862	Total	C	N	O	S	0	0
			6798	4347	1138	1281	32		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	1722	Total	C	N	O	S	0	0
			13846	8848	2369	2557	72		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	299	Total	C	N	O	S	0	0
			2338	1470	410	445	13		

- Molecule 6 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	97	Total	C	N	O	P	0	0
			2075	928	381	669	97		

- Molecule 7 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	84	Total	C	N	O	P	0	0
			1551	686	222	560	83		

- Molecule 8 is a RNA chain called Homo sapiens small nuclear RNA (U2) gene.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	140	Total	C	N	O	P	0	0
			2966	1326	510	990	140		

- Molecule 9 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	566	Total	C	N	O	0	0
			2792	1660	566	566		

- Molecule 10 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	571	Total	C	N	O	S	0	0
			3829	2385	720	718	6		

- Molecule 11 is a protein called Pre-mRNA-splicing factor SPF27.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	152	Total	C	N	O	S	0	0
			980	612	177	189	2		

- Molecule 12 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	454	Total	C	N	O	S	0	0
			3205	2001	604	594	6		

- Molecule 13 is a protein called Pre-mRNA-splicing factor SYF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	130	Total	C	N	O	S	0	0
			1098	684	204	208	2		

- Molecule 14 is a protein called Protein BUD31 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	143	Total	C	N	O	S	0	0
			1184	746	217	209	12		

- Molecule 15 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	285	Total	C	N	O	S	0	0
			2296	1442	408	426	20		

- Molecule 16 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	110	Total	C	N	O	S	0	0
			929	569	182	176	2		

- Molecule 17 is a protein called Intron-binding protein aquarius.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	1322	Total	C	N	O	S	4	0
			10885	6989	1879	1963	54		

- Molecule 18 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	261	Total	C	N	O	P S	0	0
			2073	1300	373	386	2 12		

- Molecule 19 is a protein called Peptidyl-prolyl cis-trans isomerase-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	159	Total	C	N	O	S	0	0
			1236	787	215	227	7		

- Molecule 20 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	313	Total	C	N	O	S	0	0
			2461	1554	447	452	8		

- Molecule 21 is a protein called Serine/arginine repetitive matrix protein 2.

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

- Molecule 22 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	452	Total	C	N	O	S	0	0
			3419	2198	593	613	15		

- Molecule 23 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	496	Total	C	N	O	S	0	0
			4023	2560	697	742	24		

- Molecule 24 is a protein called PRKR-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	92	Total	C	N	O	S	0	0
			701	432	133	132	4		

- Molecule 25 is a protein called ATP-dependent RNA helicase DHX8.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	713	Total	C	N	O	S	0	0
			2995	1538	722	734	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	420	THR	ASP	conflict	UNP Q14562

- Molecule 26 is a protein called Pre-mRNA-splicing factor SLU7.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	242	Total	C	N	O	S	0	0
			1999	1260	357	374	8		

- Molecule 27 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	81	Total	C	N	O	S	0	0
			640	401	113	120	6		
27	h	81	Total	C	N	O	S	0	0
			633	397	112	118	6		

- Molecule 28 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	86	Total	C	N	O	S	0	0
			690	434	126	123	7		
28	i	86	Total	C	N	O	S	0	0
			690	434	126	123	7		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	82	Total	C	N	O	S	0	0
			649	413	113	119	4		
29	j	82	Total	C	N	O	S	0	0
			649	413	113	119	4		

- Molecule 30 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	97	Total	C	N	O	S	0	0
			776	488	143	140	5		
30	k	85	Total	C	N	O	S	0	0
			688	432	125	126	5		

- Molecule 31 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	74	Total	C	N	O	S	0	0
			576	373	95	103	5		
31	m	74	Total	C	N	O	S	0	0
			576	373	95	103	5		

- Molecule 32 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	79	Total	C	N	O	S	0	0
			652	412	116	119	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
32	l	79	Total	C	N	O	S	0	0
			652	412	116	119	5		

- Molecule 33 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	74	Total	C	N	O	S	0	0
			577	364	104	103	6		
33	n	69	Total	C	N	O	S	0	0
			542	345	97	94	6		

- Molecule 34 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	o	162	Total	C	N	O	S	0	0
			1282	820	219	240	3		

- Molecule 35 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	p	94	Total	C	N	O	S	0	0
			760	488	135	132	5		

- Molecule 36 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	q	132	Total	C	N	O	S	0	0
			918	581	156	178	3		
36	r	131	Total	C	N	O	S	0	0
			901	572	149	177	3		
36	s	132	Total	C	N	O	S	0	0
			917	581	156	177	3		
36	t	131	Total	C	N	O	S	0	0
			906	575	152	176	3		

- Molecule 37 is a protein called Eukaryotic initiation factor 4A-III.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	u	390	Total	C	N	O	S	0	0
			3130	1976	546	589	19		

- Molecule 38 is a protein called Protein mago nashi homolog 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	v	144	Total	C	N	O	S	0	0
			1196	772	200	221	3		

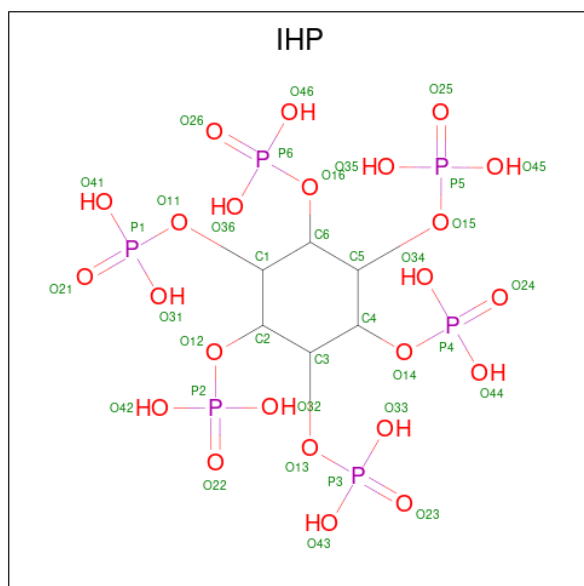
- Molecule 39 is a protein called RNA-binding protein 8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	w	91	Total	C	N	O	S	0	0
			730	463	122	142	3		

- Molecule 40 is a protein called Protein CASC3.

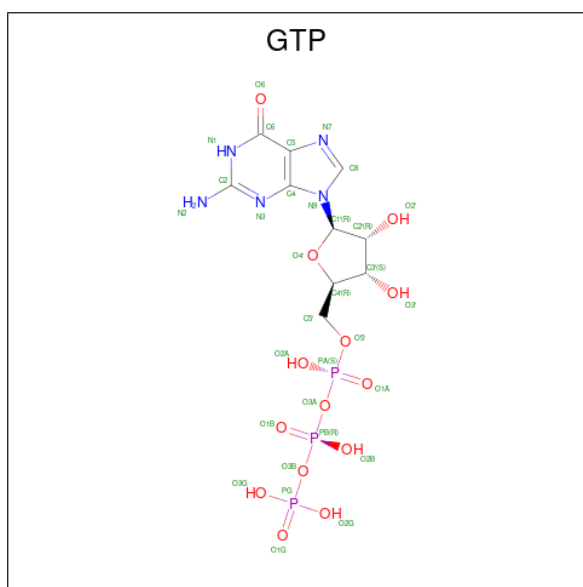
Mol	Chain	Residues	Atoms				AltConf	Trace
40	x	25	Total	C	N	O	0	0
			216	136	39	41		

- Molecule 41 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: $C_6H_{18}O_{24}P_6$).



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

- Molecule 42 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

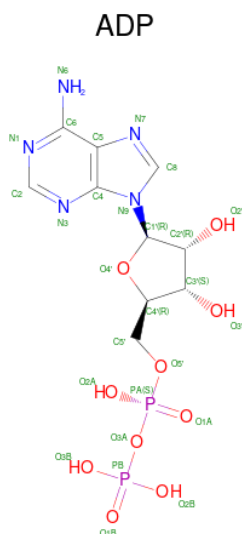


Mol	Chain	Residues	Atoms					AltConf
42	C	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 43 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
43	C	1	Total	Mg	0
			1	1	
43	D	1	Total	Mg	0
			1	1	
43	F	6	Total	Mg	0
			6	6	
43	Q	2	Total	Mg	0
			2	2	
43	u	1	Total	Mg	0
			1	1	

- Molecule 44 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).

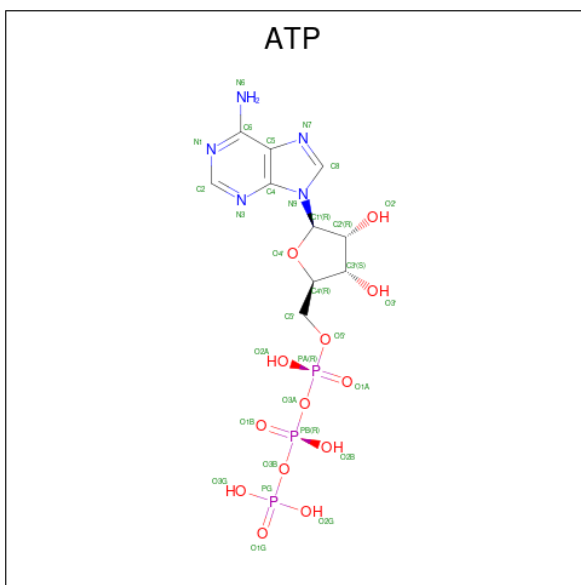


Mol	Chain	Residues	Atoms					AltConf
44	D	1	Total 27	C 10	N 5	O 10	P 2	0
44	D	1	Total 27	C 10	N 5	O 10	P 2	0

- Molecule 45 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
45	N	3	Total Zn 3 3	0
45	O	3	Total Zn 3 3	0
45	Z	1	Total Zn 1 1	0

- Molecule 46 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
46	Q	1	Total 31	C 10	N 5	O 13	P 3	0
46	u	1	Total 31	C 10	N 5	O 13	P 3	0

3 Residue-property plots

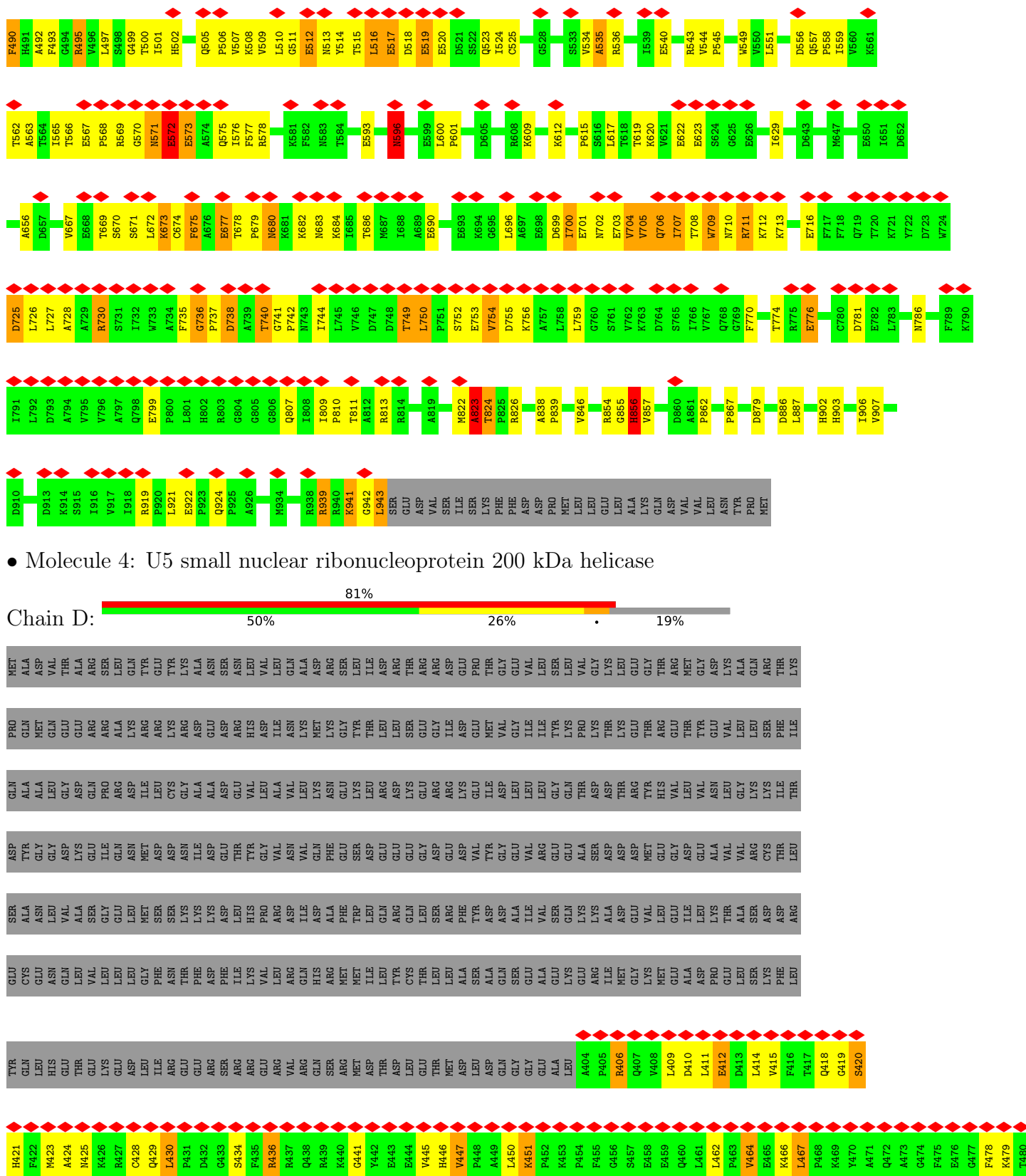
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

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



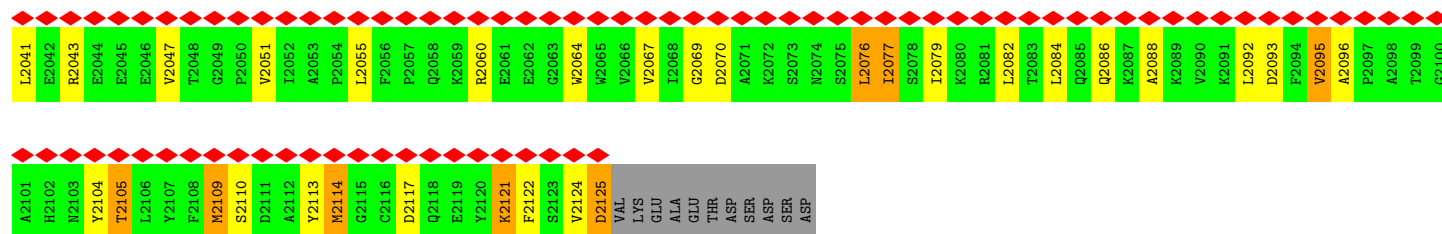
R2143	C2144	I2145	V2146	M2147	V2148	P2149	Q2150	W2151	G2152	T2153	H2154	Q2155	T2156	V2157	H2158	L2159	P2160	G2161	Q2162	L2163	P2164	Q2165	H2166	E2167	Y2168	L2169	K2170	E2171	M2172	E2173	P2174	L2175	G2176	W2177	I2178	H2179	T2180	Q2181	P2182	E2183	S2185	P2186	L2187	L2188	S2189	P2190	Q2191	D2192	V2193	T2194	T2195	H2196	A2197	K2198	I2199	M2200	A2201	D2202	
L2083	H2084	I2085	R2086	T2087	N2088	H2089	T2090	Y2091	W2092	S2093	S2094	D2095	D2096	T2097	K2098	E2099	T2100	G2101	Y2102	T2103	Y2104	I2105	L2106	P2107	K2108	N2109	V2110	L2111	K2112	K2113	F2114	I2115	C2116	I2117	S2118	L2119	L2120	R2121	Q2122	T2123	I2124	A2125	G2126	Y2127	L2128	Y2129	Q2130	V2131	S2132	P2133	P2134	D2135	N2136	P2137	Q2138	V2139	K2140	E2141	I2142
ARG	GLN	GLN	ILE	ALA	GLU	ILE	GLU	LYS	THR	GLN	GLN	SER	GLN	LEU	THR	ALA	THR	GLN	ARG	THR	VAL	ASN	LYS	HIS	GLY	ASP	GLU	ILE	ILE	THR	SER	THR	ASN	GLU	GLN	THR	F2067	S2068	S2069	K2070	T2071	E2072	W2073	R2074	V2075	R2076	A2077	I2078	S2079	A2080	A2081	N2082							
N1946	M1947	R1948	A1949	A1950	K1951	I1952	L1953	L1954	K1955	P1956	D1957	K1958	T1959	T1960	I1961	T1962	E1963	P1964	H1965	H1966	I1967	W1968	P1969	E1974	E1975	E1980	K1984	D1985	L1986	D1990	K1993	N1998	V1999	A2000	S2001	L2002	E2006	I2007	R2008	D2009	L2012	G2013	W2014	E2015	ILE	SER	ALA	PRO	SER	GLN	GLN								
K1838	E1843	E1844	L1848	L1849	R1850	E1855	Q1860	I1861	I1862	V1863	T1864	R1865	M1868	L1869	D1870	P1871	L1872	D1878	F1879	P1880	N1881	I1882	V1883	I1884	K1885	G1886	S1887	E1888	L1889	Q1890	L1891	Q1894	K1898	V1899	A2000	S2001	L2002	E2006	I2007	R2008	D2009	L2012	G2013	W2014	E2015	ILE	SER	ALA	PRO	SER	GLN	GLN							
Y1754	E1757	P1758	T1759	E1760	L1763	S1764	Q1766	N1767	Y1768	G1769	L1770	L1771	N1774	Q1775	I1776	I1777	D1781	D1782	Y1786	R1787	P1788	T1789	H1790	H1791	K1792	T1793	F1794	E1795	G1796	N1797	L1798	T1799	T1800	K1801	P1802	N1811	P1812	R1813	T1814	K1820	W1827	A1828	G1829	Q1830	K1831	R1832	L1833	G1834	Q1835										
M1591	C1594	Q1599	E1600	L1601	D1602	E1607	E1612	T1613	I1614	H1615	P1616	R1617	D1628	R1641	P1642	D1647	S1648	K1649	D1650	V1651	M1652	D1653	S1654	T1657	Q1658	D1663	D1675	R1678	R1681	D1686	D1690	N1691	M1692	S1693	I1694	P1698	K1732	M1737	V1742	L1743	R1744																		
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H1359	E1360	E1361	D1362	Q1363	L1364	I1365	P1366	L1368	Y1369	R1370	Q1373	R1384	V1385	W1386	Y1389	A1390	E1395	A1398	Q1399	N1400	R1401	R1402	L1403	T1404	L1405	E1406	D1407	L1408	E1409	D1410	R1414	G1415	I1416	P1417	Q1424	R1427	W1436	R1437	V1438	R1439	N1451	W1455	R1471	M1474	I1475														
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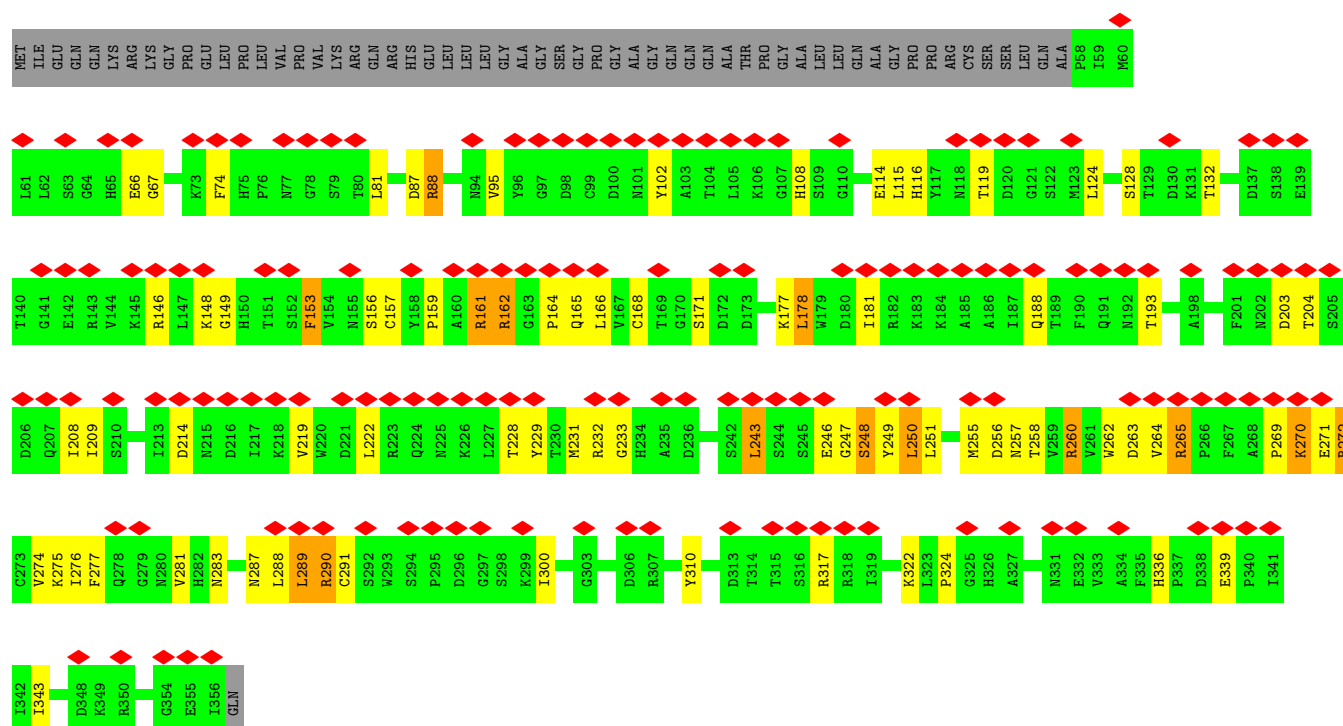
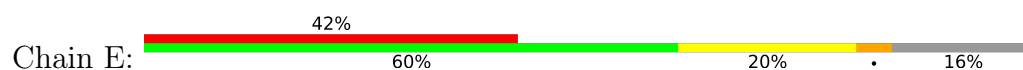


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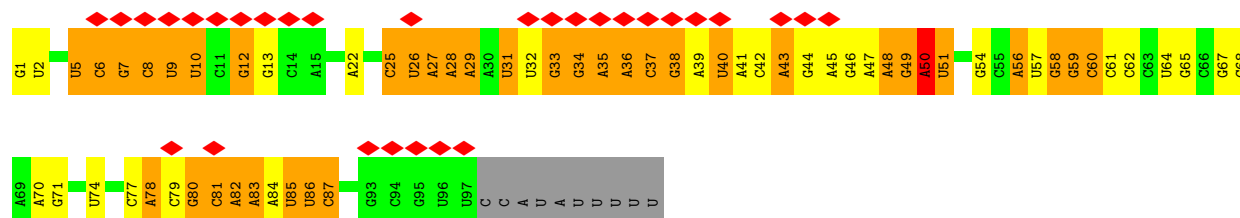
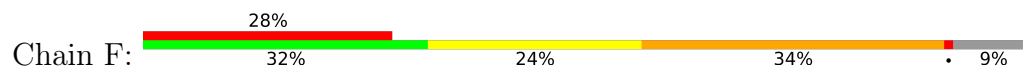
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• Molecule 5: U5 small nuclear ribonucleoprotein 40 kDa protein



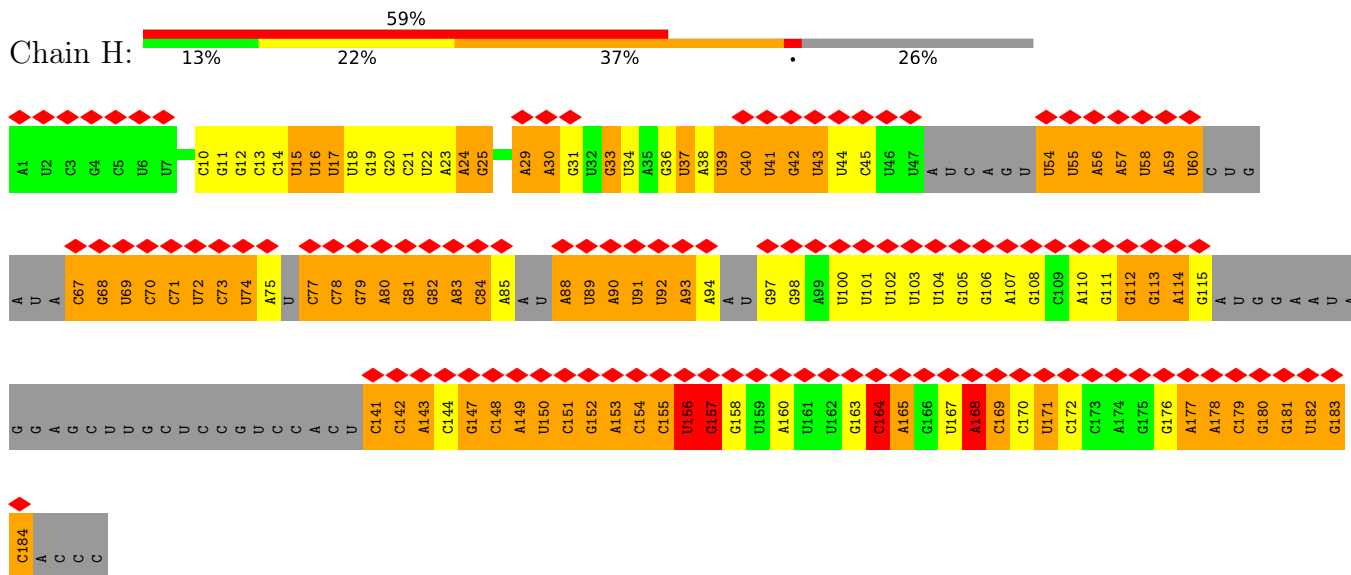
• Molecule 6: U6 snRNA



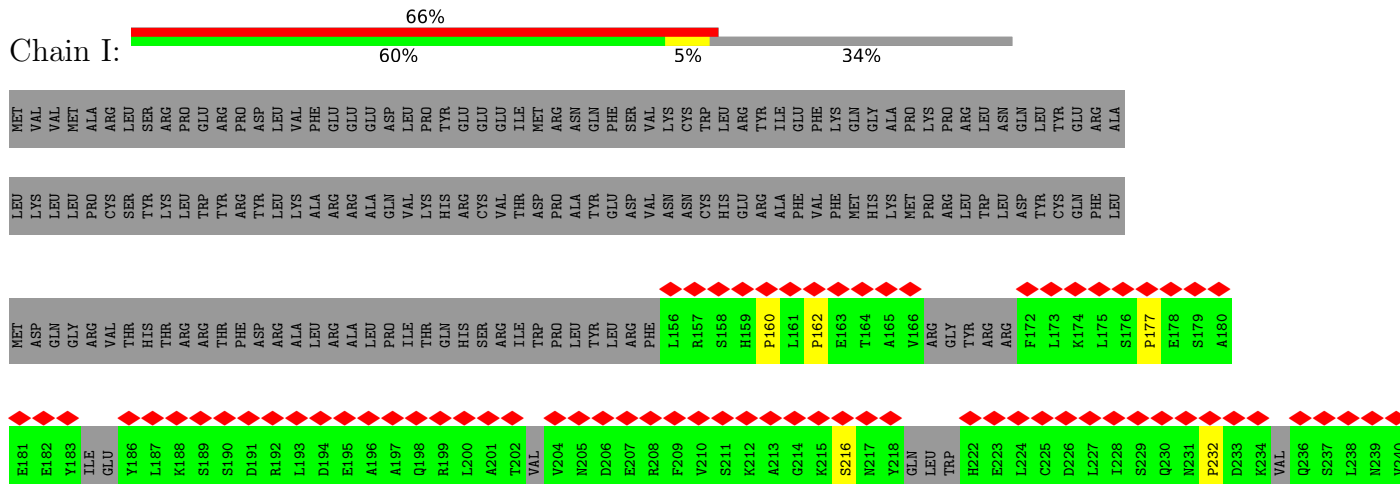
• Molecule 7: pre-mRNA

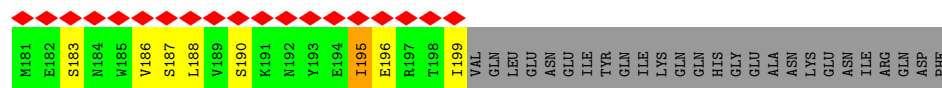


- Molecule 8: Homo sapiens small nuclear RNA (U2) gene

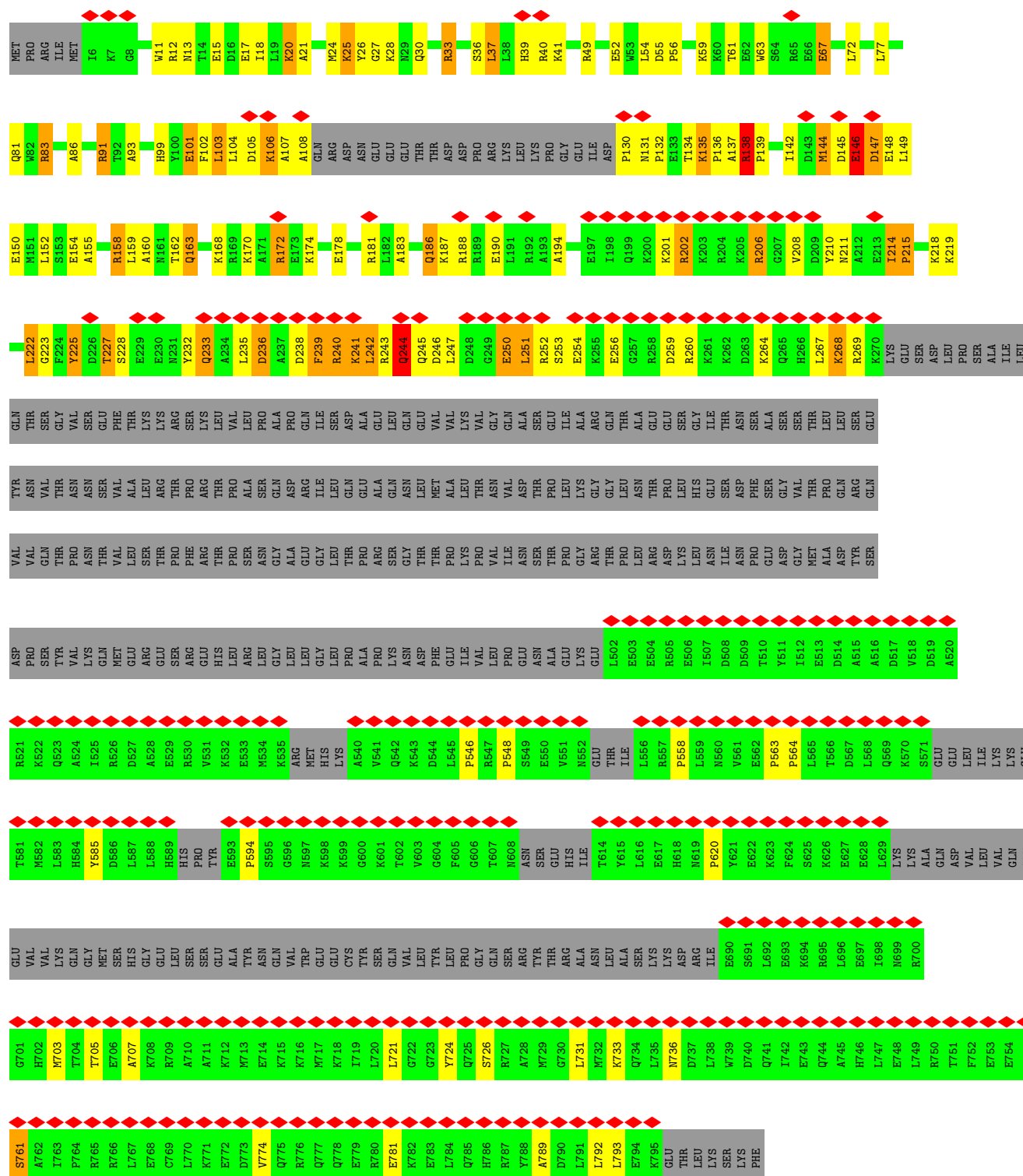
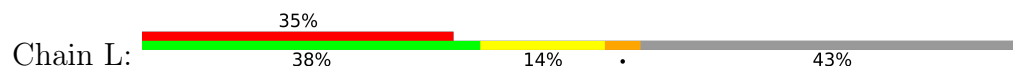


- Molecule 9: Pre-mRNA-splicing factor SYF1

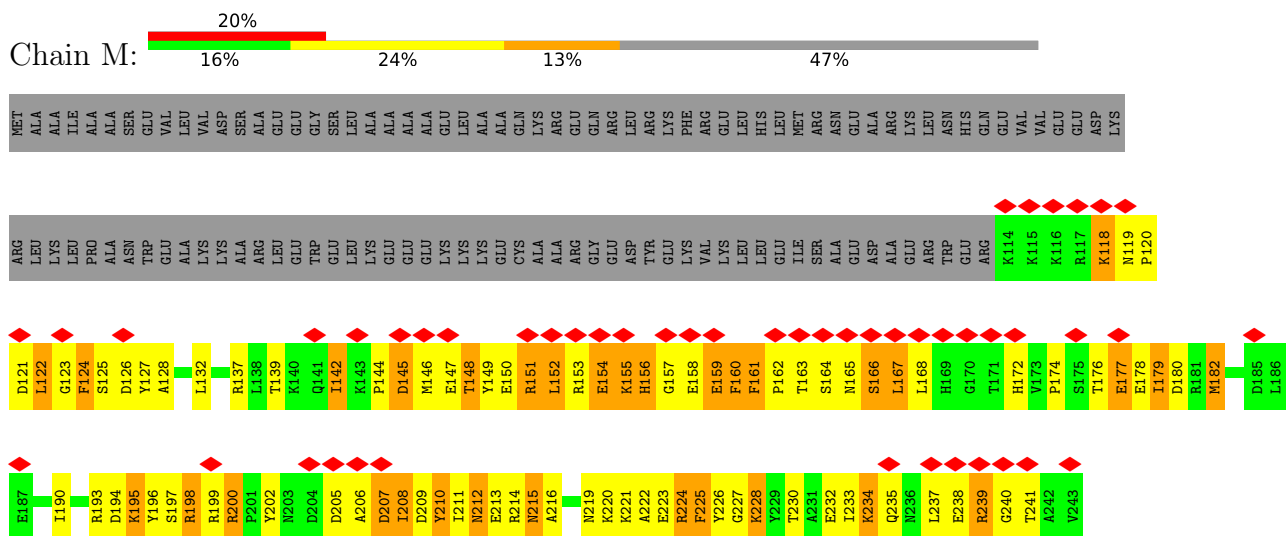




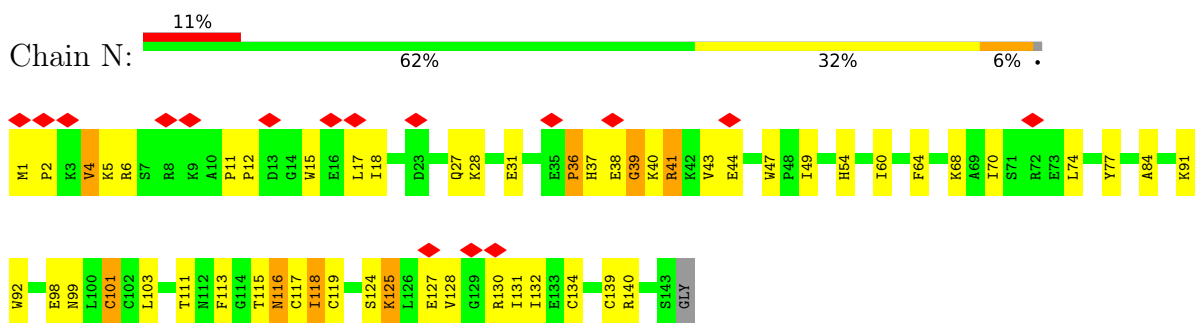
• Molecule 12: Cell division cycle 5-like protein



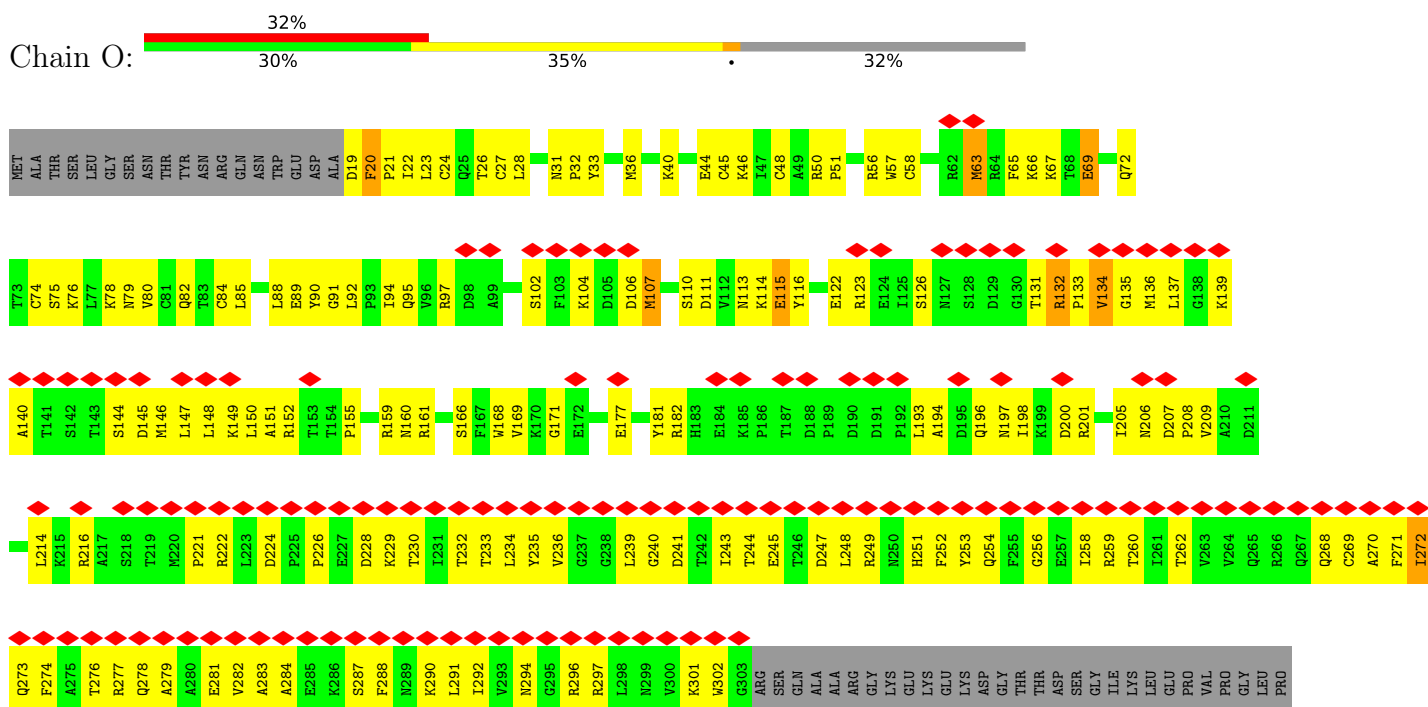
- Molecule 13: Pre-mRNA-splicing factor SYF2



- Molecule 14: Protein BUD31 homolog



- Molecule 15: Pre-mRNA-splicing factor RBM22

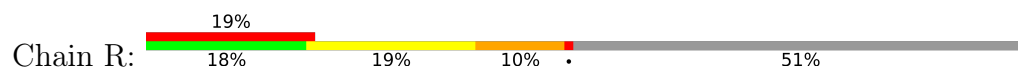




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Q1082	D1022	T962	H842	H782	E722	K662	D602	N542	R482	N422	R362
D1083	R1023	A903	N843	V783	H723	E663	D603	L543	Q483	Q423	E363
G1084	S1024	R904	F844	I784	L724	N664	K604	N544	D484	M424	S364
F1085	R905	R905	P845	P785	K725	N665	G605	V545	I485	P425	L365
S1086	Y1026	I906	E846	N786	A726	F666	R606	R546	E486	L426	V366
R1087	L1027	E907	Q847	R787	S727	K667	V607	D547	D487	Y427	K367
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W1091	E1031	E911	L850	Y790	G730	L670	GLY	D551	E430	E430	P371
I1092	E912	E911	L851	P791	H731	E671	PRO	D551	K431	K431	P371
M1093	Y912	Y912	V852	Y792	N732	T672	GLU	E552	I432	I432	L372
I1094	K913	N793	T853	N793	K733	I673	F614	W553	K493	I433	S373
G1095	R914	Q794	H854	Q794	K734	R674	R615	K494	S374	W434	S374
D1096	L915	P795	S855	P795	V735	N675	F616	W495	N375	D435	N375
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E1010	R949	K829	K890	K829	A774	I709	N650	E529	S409	N469	S409
F1011	K950	T830	K891	T830	K775	A710	E651	N530	R410	F470	R410
Y1012	V951	D831	F892	D831	T776	T711	T652	W531	H411	N471	H411
A1013	K952	V832	F893	V832	L777	L712	F653	P532	E412	L472	E412
S1014	L953	A833	R894	A833	I778	D713	N654	T533	R413	F473	R413
E1015	GLY	V834	Y895	V834	V779	F714	I655	R534	R414	R474	R414
Y1016	SER	Q835	G896	Q835	E780	N715	T656	V535	I415	L475	I415
L1017	THR	I836	R897	I836		D716	M657	R536	S416	E476	S416
R1018	LEU	I837	G897	I837		T717	N658	A537	Q417	S477	Q417
G1137	P959	S838	V898	S838		L718	Q598	D538	I418	T478	I418
A1139	D960	N839	N900	N839		L719	G599	V539	Q419	Y479	Q419
R1140		T840		T840		S720	M600	T540	Q420	E480	Q420

Q1381	THR	S1321	D1261	L1201	A1141
	LEU	Q1322	R1262	G1202	S1142
LEU	L1323	F1263	F1263	E1203	L1143
GLN	T1324	Q1264	Q1264	A1204	C1144
LEU	A1325	G1265	G1265	E1205	M1145
PRO	R1326	Q1266	Q1266	Y1206	L1146
PRO	P1327	Q1267	Q1267	V1207	L1147
ALA	L1328	N1268	N1268	V1208	M1148
MET	H1329	D1269	D1269	A1209	W1149
VAL	GLU	L1330	Y1270	L1210	R1150
GLU	L1330	GLU	Y1270	L1210	R1150
GLY	H1331	H1331	I1271	F1211	Y1151
GLU	I1332	I1332	L1272	M1212	K1152
GLU	L1333	L1333	L1273	Y1213	M1153
VAL	P1334	P1334	S1274	M1214	L1154
GLN	T1335	T1335	L1275	C1215	G1155
GLN	ASN	ASN	L1276	L1216	M1156
GLN	GLN	GLN	V1276	L1217	M1157
GLY	E1336	E1336	R1277	G1218	P1158
THR	PRO	PRO	T1278	Y1219	H1159
THR	PHE	PHE	R1279	P1220	V1160
THR	PRO	PRO	A1280	A1221	Q1161
LEU	T1340	T1340	I1281	D1222	L1162
GLU	T1341	T1341	G1282	K1223	L1163
THR	R1342	R1342	H1283	I1224	P1164
GLU	K1343	K1343	L1284	S1225	E1165
GLU	N1344	N1344	R1285	I1226	F1166
ALA	G1345	G1345	D1286	L1227	S1167
ALA	E1346	E1346	V1287	T1228	T1168
MET	R1347	R1347	R1288	T1229	A1169
THR	P1348	P1348	R1289	Y1230	M1170
ASP	S1349	S1349	L1290	M1231	N1171
ILE	H1350	H1350	V1291	G1232	G1172
ILE	E1351	E1351	V1292	Q1233	L1173
PRO	V1352	V1352	A1293	K1234	L1174
SER	Q1353	Q1353	M1294	H1235	Y1175
THR	I1354	I1354	S1295	L1236	D1176
ASP	T1355	T1355	R1296	I1237	F1177
THR	K1356	K1356	A1297	R1238	Q1178
SER	N1357	N1357	R1298	D1239	L1179
CYS	M1358	M1358	L1299	I1240	M1180
ARG	P1359	P1359	G1300	I1241	M1181
GLN	Q1360	Q1360	L1301	N1242	V1182
GLU	M1361	M1361	Y1302	R1243	E1183
PRO	A1362	A1362	I1303	R1244	D1184
ALA	N1363	N1363	F1304	C1245	F1185
GLN	F1364	F1364	A1305	G1246	Q1186
THR	V1365	V1365	R1306	N1247	G1187
THR	Y1366	Y1366	V1307	P1248	V1188
PRO	M1367	M1367	S1308	P1249	G1189
PRO	M1368	M1368	L1309	L1250	E1190
SER	Y1369	Y1369	F1310	I1251	S1191
THR	H1371	H1371	Q1311	G1252	E1192
GLN	L1372	L1372	M1312	R1253	P1193
THR	I1373	I1373	C1313	P1254	M1194
ASP	Q1374	Q1374	F1314	N1255	P1195
THR	T1375	T1375	E1315	K1256	Y1196
PRO	T1376	T1376	L1316	V1257	F1197
PRO	H1377	H1377	T1317	T1258	Y1198
THR	Y1378	Y1378	P1318	T1259	Q1199
SER	H1380	H1380	A1319	V1260	M1200

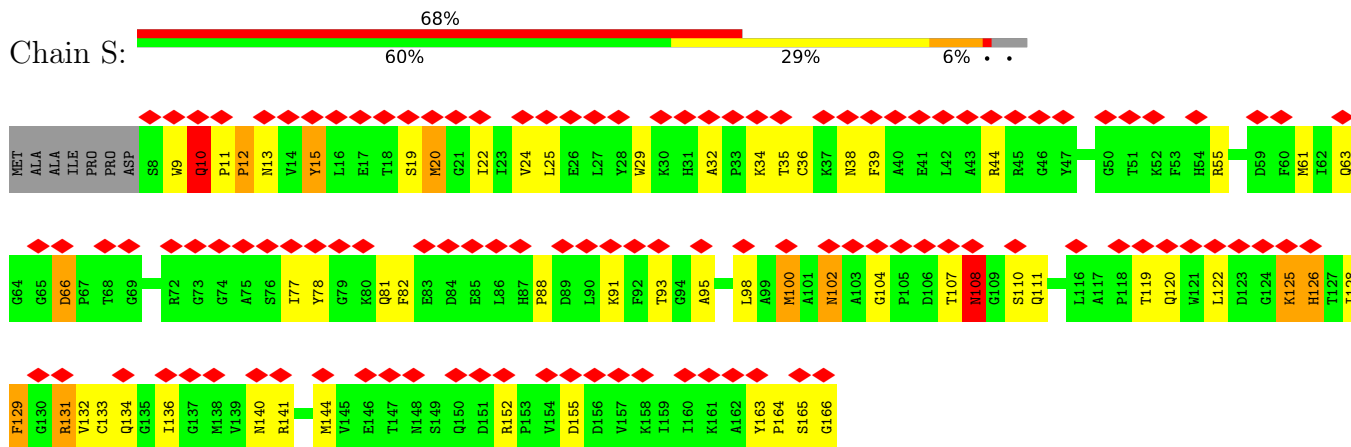
• Molecule 18: SNW domain-containing protein 1



PRO	SER	LYS	ASN	LEU	ASP	LYS	ASP	GLY	TYR	GLY	ASP	ASP	GLN	GLY	THR	ASP	GLN	ARG	GLU	VAL	PRO	ASP	GLY	LYS	GLN	ARG	GLY	GLY	ASP	GLY	ASP	GLY	GLY	ASP	GLY	GLY	ASP	GLY	GLY	ASP	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
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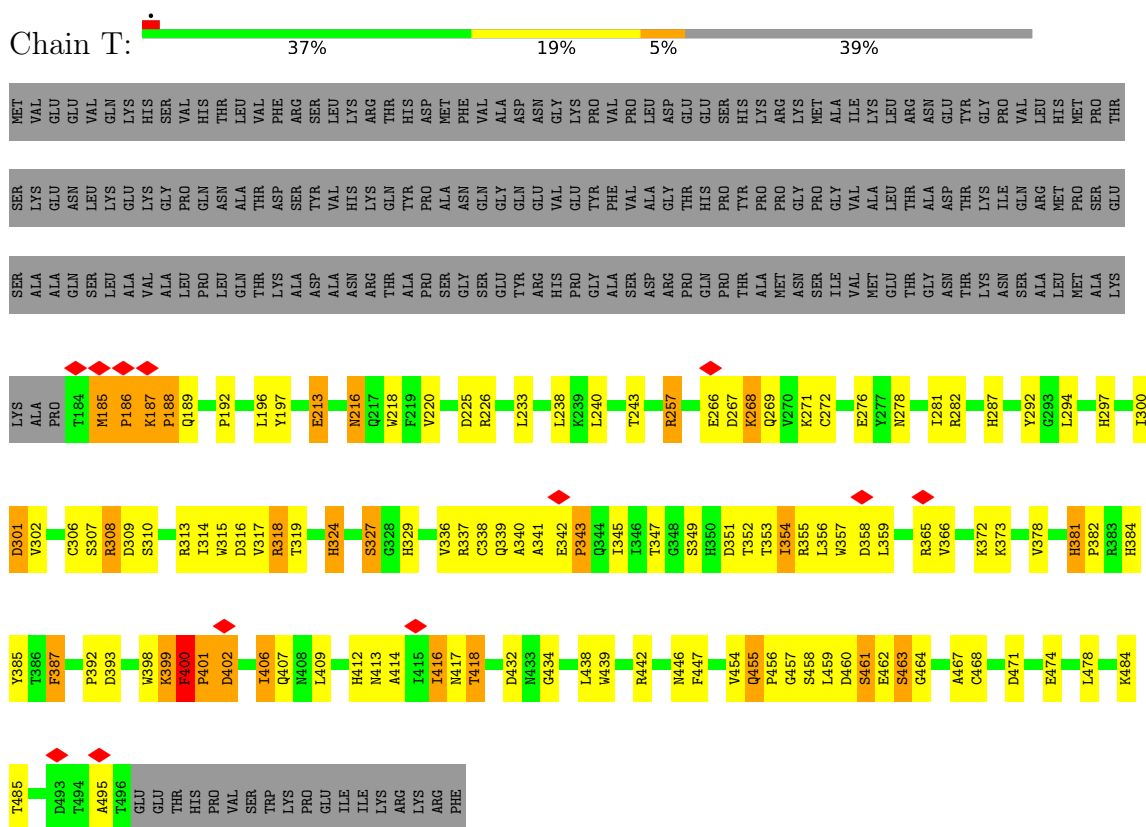
- Molecule 19: Peptidyl-prolyl cis-trans isomerase-like 1

Chain S:



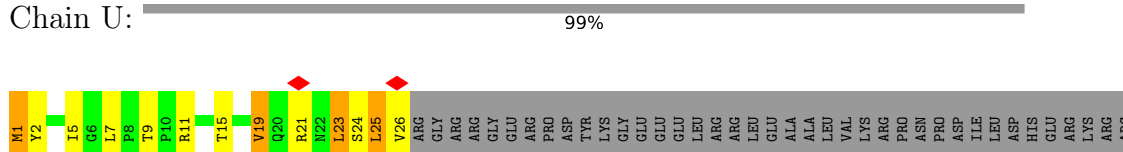
- Molecule 20: Pleiotropic regulator 1

Chain T:



- Molecule 21: Serine/arginine repetitive matrix protein 2

Chain U:

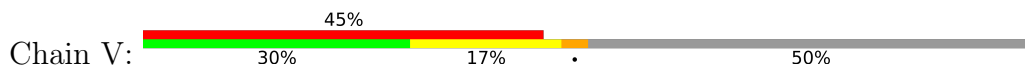






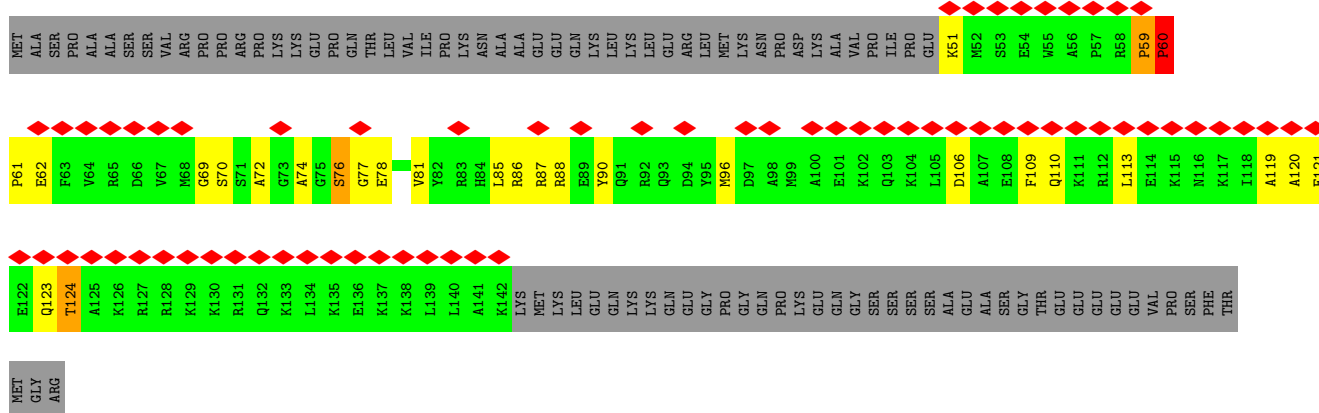
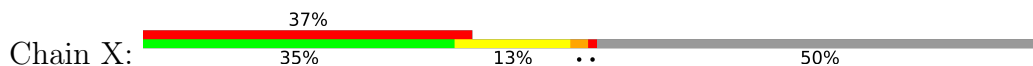
[illegible]

- Molecule 22: Pre-mRNA-splicing factor CWC22 homolog

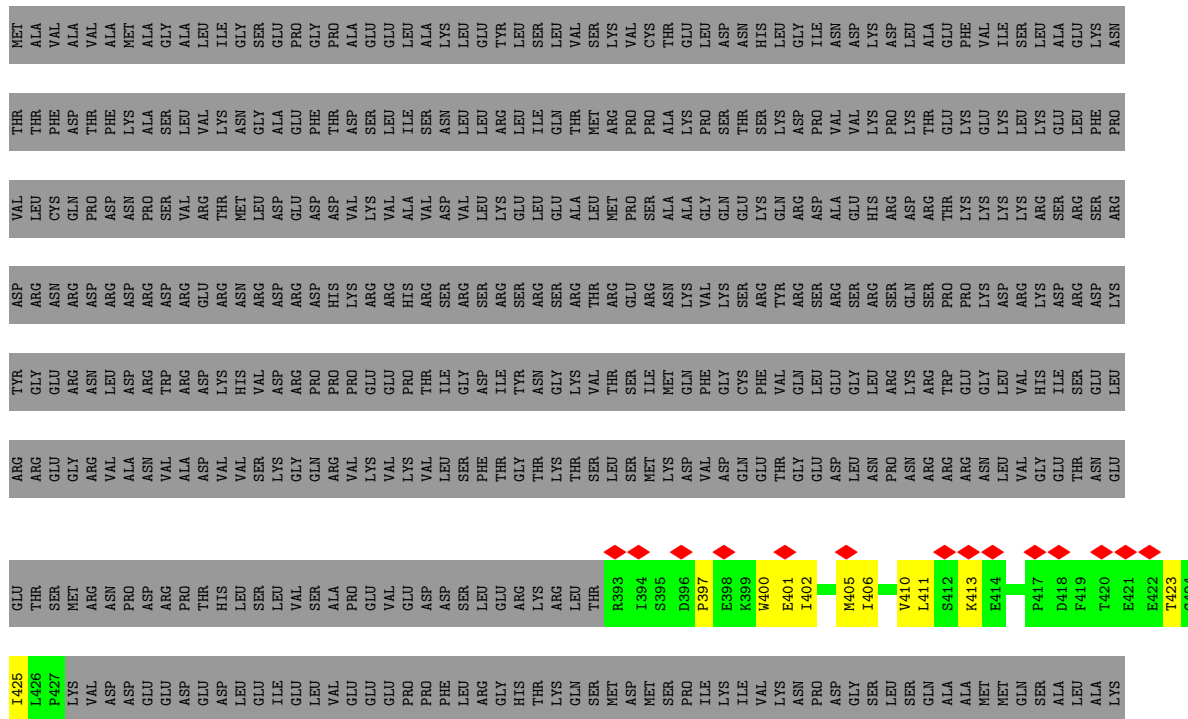


N542	P492	SER	E361	G301	F241	I181	GLU	SER	TYR
K543	E483	SER	E362	L302	R242	I182	LEU	ASP	TYR
L544	S484	GLU	E363	L303	K243	Q183	ASP	PRO	ASP
R545	Q485	ASP	D364	L304	G244	E184	LEU	LEU	SER
N546	T486	GLU	Q365	T305	Y245	L185	THR	MET	MET
F547	K487	GLU	F366	Q306	R246	L186	ARG	GLU	GLU
A548	E488	GLU	T367	S307	R247	Q187	THR	ARG	ILE
K549	L489	GLU	H368	S308	K248	E188	GLY	ASN	ARG
M550	C490	GLU	K369	P309	D249	E189	GLY	SER	PRO
F551	A491	GLU	L370	R310	K250	I190	ALA	ASP	SER
A552	M492	GLY	P371	G311	Q251	I191	TYR	ASP	GLY
H553	L493	GLU	L372	T312	L252	R192	ILE	ARG	HIS
L554	D495	ASP	E373	N313	C253	G193	PRO	LYS	ASP
L555	C496	GLU	D374	A314	L254	R194	ALA	ARG	ARG
Y556	D497	GLY	D375	T315	L255	G195	LYS	GLU	GLU
T557	A498	GLN	Y376	F316	A256	L196	LEU	ARG	ASN
D558	Q499	LYS	N377	E317	S257	L197	ARG	GLU	LEU
S559	Q500	VAL	P378	R318	K258	E198	MET	ASN	ASN
LEU	E501	ILE	E379	R319	F259	R199	THR	THR	TYR
PRO	T502	HIS	D380	L320	V260	S200	GLN	ASP	GLN
Y562	Y503	ASP	V381	N321	A261	S201	ILE	ARG	ARG
S563	E504	LYS	L382	T322	H262	L202	THR	LYS	ASN
F564	K505	T448	L383	L323	L263	Q203	ASP	SER	ASN
L565	F506	E449	N383	H324	T264	A204	GLY	ARG	PRO
E566	F507	L450	V384	E225	Q265	S151	LEU	LYS	GLY
C567	G508	M451	F385	E226	Q266	S152	PRO	ASN	ASP
I568	L509	L452	K386	E327	N267	S206	GLY	TYR	TYR
K569	L510	F455	K387	E328	V268	A153	ARG	GLY	GLY
L570	G512	A456	P388	T328	A269	Q155	GLN	GLU	GLN
S571	R513	R457	D389	D329	H270	S208	ASN	ARG	GLU
E572	F514	T458	N390	K330	E271	P209	ARG	ASN	SER
E573	C515	L459	F391	R331	T211	M157	PRO	GLU	GLU
T574	M516	V460	K392	V332	V272	S158	THR	THR	ARG
T575	L517	L461	E393	Q333	L273	M159	SER	ASP	ASP
T576	K518	L463	N394	Y334	C274	E160	VAL	ARG	ARG
S577	K519	Q464	E395	K335	L275	A161	THR	ASP	ASP
S578	E520	S465	E396	L336	E276	L162	GLN	PHE	SER
S579	Y521	S466	K397	E337	M277	K163	SER	ASP	ASP
R580	M522	L467	Y398	V338	T278	A217	TYR	SER	TYR
F581	E523	D468	K399	N339	L279	L218	ALA	ARG	SER
F582	S524	F469	A400	F340	T290	S165	GLN	SER	ARG
F583	F525	E470	K401	F340	L280	I166	ASP	SER	SER
K584	E526	B471	L401	A341	L281	I167	GLU	ASP	GLU
F585	G527	C472	K402	V342	L282	G168	PRO	TYR	TYR
F586	E528	H474	K403	R343	E283	L169	ALA	GLU	GLU
F587	L529	K475	E404	R344	R284	N223	THR	LYS	LYS
F587	F529	L476	L405	D345	P285	S224	THR	ARG	ARG
Q588	K530	L477	I406	G346	T286	N171	GLY	LYS	GLY
E589	E531	M478	ASP	F347	D287	K172	ASP	GLY	ASP
L590	Q532	E480	GLU	T479	D288	V173	GLU	GLU	ASP
C591	F533	F481	ASP	D349	Q228	S175	ALA	GLU	GLU
E592	D594		THR	R350	I229	S176	THR	LYS	LYS

- Molecule 24: PRKR-interacting protein 1



- Molecule 25: ATP-dependent RNA helicase DHX8

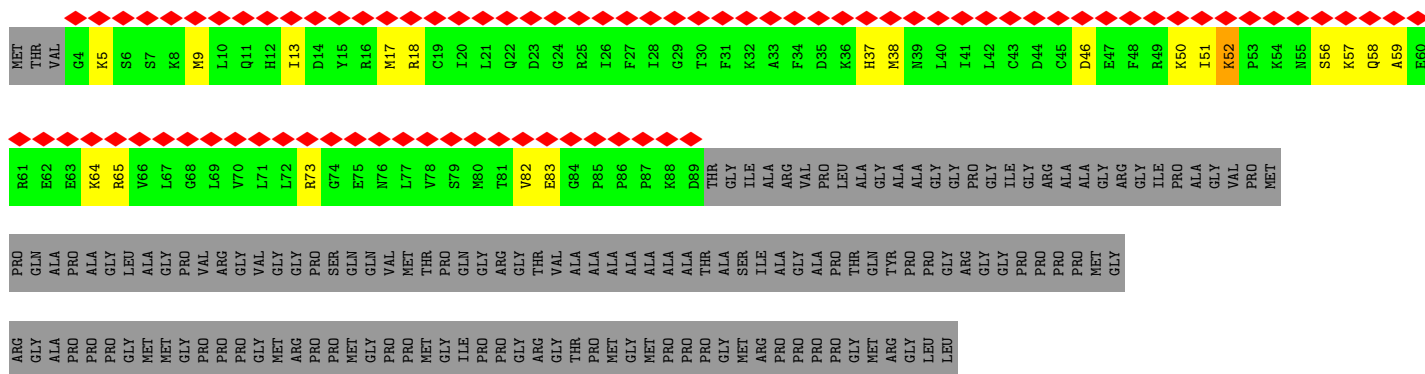


TYR	Q1145	I1085	G965	E905	S945	E785	F725	M665	A605	G545	GLU
GLU	P1146	M1086	A966	R906	L946	I786	S726	L666	G606	N646	ARG
PRO	E1147	D1087	L967	A907	T847	D787	Q727	L667	Y607	K647	GLU
ASN	W1148	R1088	D968	Y908	T848	T788	V728	R668	T608	A648	LEU
ALA	V1149	H1089	D969	R909	D849	A789	V729	E669	S609	S649	LYS
TRP	V1150	K1090	E970	D910	G850	C790	F730	C670	R610	Y550	GLN
ARG	Y1151	L1091	G971	E911	I851	E791	E731	L671	G611	G551	ALA
ILE	H1152	D1092	L972	M912	Y852	I792	A732	I672	K612	K552	GLN
SER	H1153	V1093	L973	L913	T853	L793	P733	D673	L613	K553	ARG
ARG	L1154	V1094	T974	T914	V854	L794	I734	P674	G614	T554	ALA
PHE	V1155	S1095	R975	T915	Y855	E795	F735	D675	C615	Q555	GLU
ARG	L1156	G1096	L976	N916	D656	R796	T736	L676	T616	M556	MET
ARG	T1157	K1097	G977	N917	P657	M797	I737	T677	I617	S557	ASP
ARG	T1158	K1098	R978	P918	G658	K798	P738	Q678	P618	I558	SER
	K1159	S1099	R979	E919	P859	S799	G739	Q679	P619	I559	ILE
	E1160	T1100	M980	I920	V660	L800	R740	E680	R620	E560	PRO
	Y1161	V1101	A981	Q921	K861	G801	T741	I681	Q621	Q561	MET
	R1162	R1102	E982	R922	Q862	P802	V742	I682	A622	R562	GLY
	A1163	V1103	F983	T923	K863	D803	F743	M683	A623	E563	LEU
	E1164	Q1104	P984	N924	V664	E804	V744	L684	M624	S564	ASN
	V1165	K1105	L985	L925	Y865	E805	E745	D685	A624	S564	LYS
	T1166	A1106	E986	A926	N866	E806	I746	E686	V626	P566	TRP
	T1167	I1107	P987	S927	S867	L807	L747	A687	A627	I567	VAL
	I1168	C1108	M988	T928	K868	I808	V748	H688	K628	Y568	D511
	D1169	S1109	L989	V929	T669	I809	T749	E689	R629	K569	P512
	P1170	G1110	C990	L930	G670	L810	K750	R690	V630	L570	L513
	R1171	F1111	K991	S931	I871	P811	E751	T691	S631	K571	P514
	W1172	F1112	M992	L932	D872	V812	F752	I692	E632	E572	D515
	L1173	R1113	K993	A934	Q873	Y813	E753	H693	E633	Q573	A516
	V1174	N1114	I994	A934	L874	S814	T754	T694	F634	L574	E517
	E1175	A1115	M995	M935	V875	A815	D755	D695	G635	V575	G518
	F1176	A1116	S996	G936	V876	L816	V756	V696	C636	Q576	R519
	A1177	K1117	V997	I937	T877	P817	L757	L697	C637	A577	Q520
	P1178	K1118	H998	N938	T878	S818	D758	F698	L638	V578	I521
	A1179	D1119	L999	D939	I879	E819	A759	G699	G639	H579	A522
	F1180	P1120	G1000	L940	S880	M820	S760	L700	D880	D580	A523
	F1181	Q1121	C1001	L941	Q881	Q821	L761	L701	E641	N681	N524
	K1182	I1122	S1002	F943	A882	T822	I762	K702	V642	Q582	M525
	V1183	G1123	E1003	F943	Q883	R823	T763	K703	G643	I583	R526
	S1184	Y1124	E1004	D944	A884	I824	V764	T704	Y644	L584	G527
	D1185	R1125	M1005	F945	K885	F825	M765	V705	T645	I585	I528
	P1186	T1126	L1006	M946	Q886	D826	Q766	Q706	I646	V586	G529
	T1187	L1127	T1007	D947	R887	P827	I767	K707	R647	I587	M530
	K1188	I1128	I1008	A948	A888	A828	H768	R708	F648	E588	M531
LEU	D1129	D1129	V1009	P949	G889	P829	L769	Q709	E649	E589	P532
SER	Q1130	Q1130	S1010	P950	R890	P830	T770	D710	D650	T590	N533
GLN	Q1131	Q1131	M1011	M951	A891	G831	E771	M711	C651	G591	D534
LYS	V1132	V1132	L1012	E952	G892	S832	P772	K712	T652	S592	I535
LYS	V1133	V1133	S1013	T953	R893	R833	F773	L713	S653	G593	E536
GLN	L1134	L1134	L1014	T954	T894	K834	G774	I714	P654	K594	K538
GLN	V1135	V1135	Q1015	I955	G895	V835	D775	V715	E655	T595	K539
ARG	H1136	H1136	N1016	T956	P896	V836	I776	T716	T656	T596	K540
LEU	Q1076	Q1076	N1016	T956	P896	V836	I776	T716	T656	T596	H541
GLU	D1077	D1077	V1017	A957	G897	I837	L777	S717	I657	Q597	A542
PRO	I1078	I1078	F1018	M958	K898	A838	V778	A718	I658	I598	F543
LEU	R1079	R1079	Y1019	E959	C899	T839	F779	T719	K659	T599	G544
TYR	A1140	A1140	K1080	Q960	Y900	N840	L780	L720	Q600	Q600	
ASN	L1141	L1141	P1021	L961	R901	I841	T781	D721	M661	Y601	
ASN	F1142	F1142	K1022	Y962	L902	A842	G782	A722	T662	L602	
ARG	N1143	N1143	D1023	T963	Y903	E843	Q783	V723	D663	A603	
	R1144	R1144	K1024	L964	T904	T844	E784	K724	G664	E604	

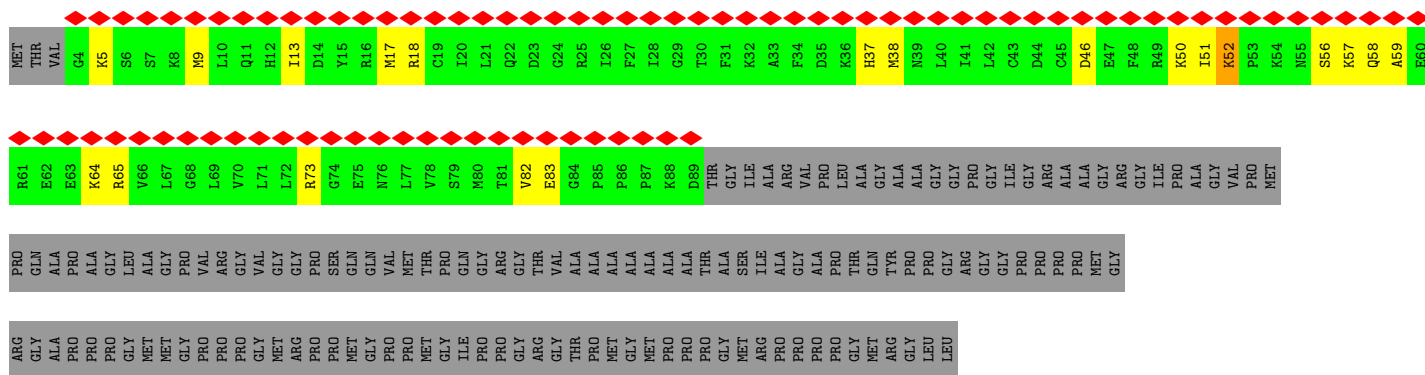
• Molecule 26: Pre-mRNA-splicing factor SLU7



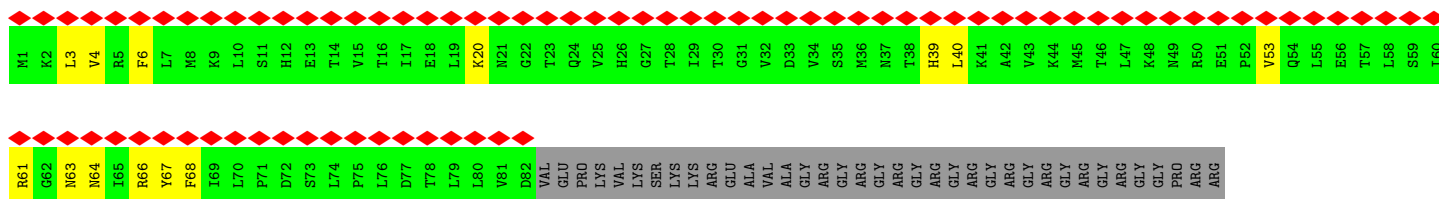
- Molecule 28: Small nuclear ribonucleoprotein-associated proteins B and B'



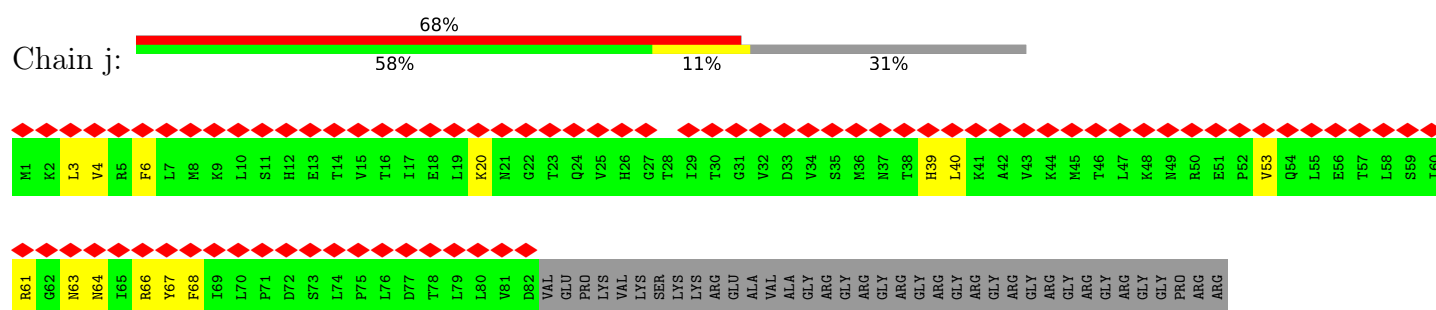
- Molecule 28: Small nuclear ribonucleoprotein-associated proteins B and B'



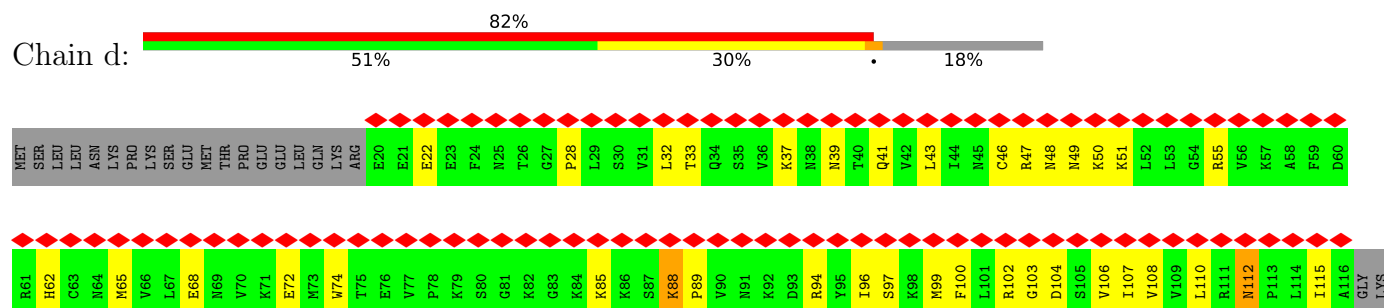
- Molecule 29: Small nuclear ribonucleoprotein Sm D1



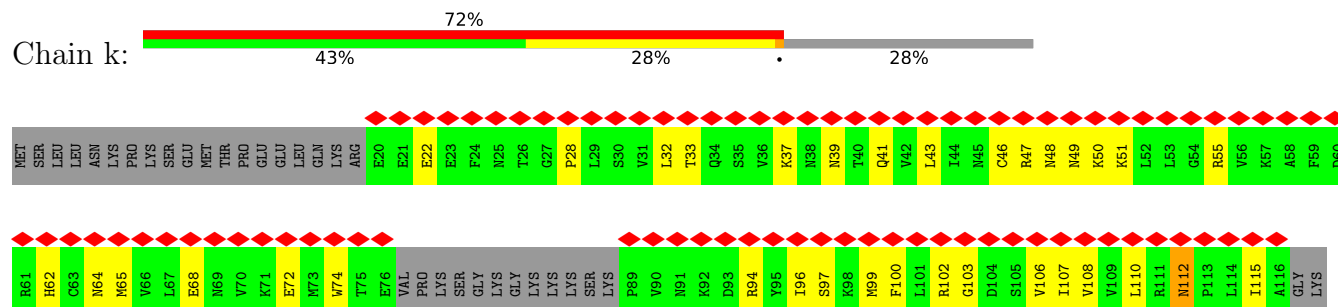
- Molecule 29: Small nuclear ribonucleoprotein Sm D1



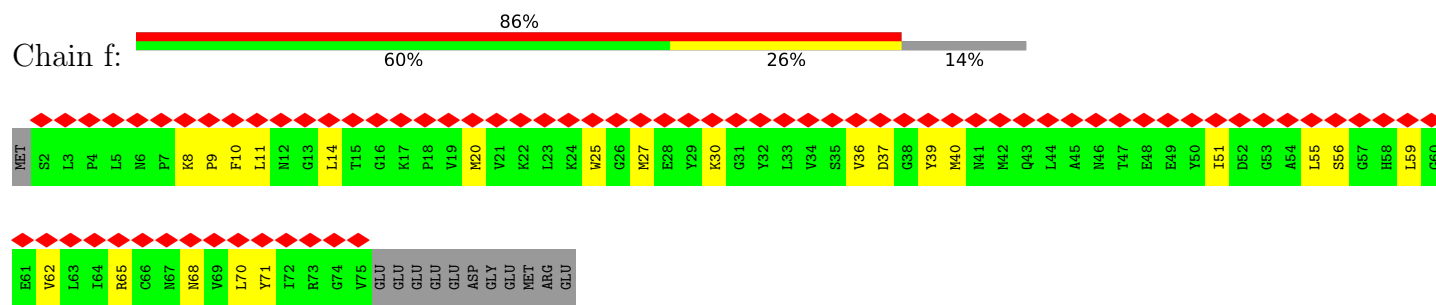
- Molecule 30: Small nuclear ribonucleoprotein Sm D2



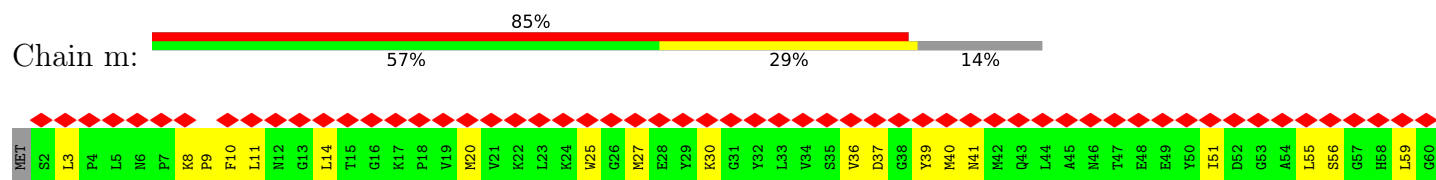
- Molecule 30: Small nuclear ribonucleoprotein Sm D2

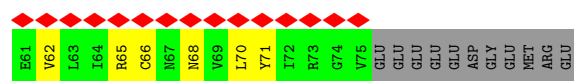


- Molecule 31: Small nuclear ribonucleoprotein F

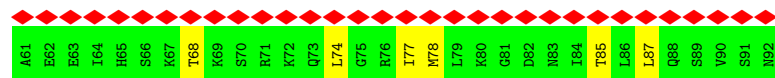
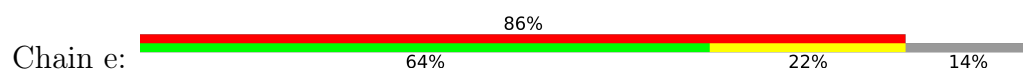


- Molecule 31: Small nuclear ribonucleoprotein F

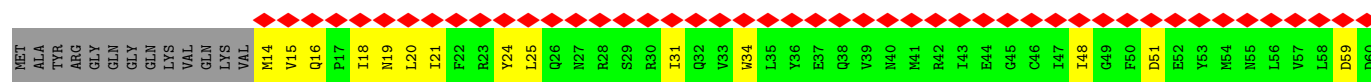
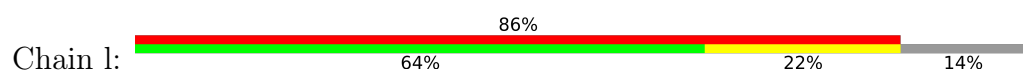




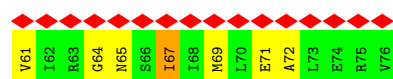
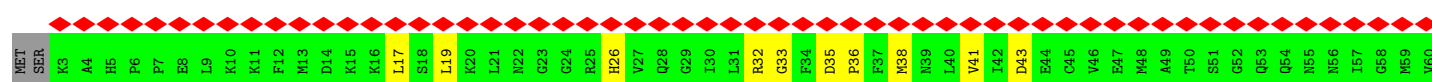
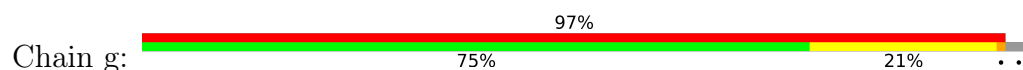
• Molecule 32: Small nuclear ribonucleoprotein E



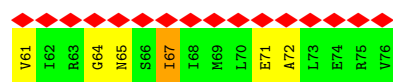
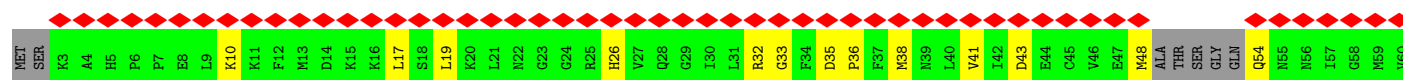
• Molecule 32: Small nuclear ribonucleoprotein E



• Molecule 33: Small nuclear ribonucleoprotein G

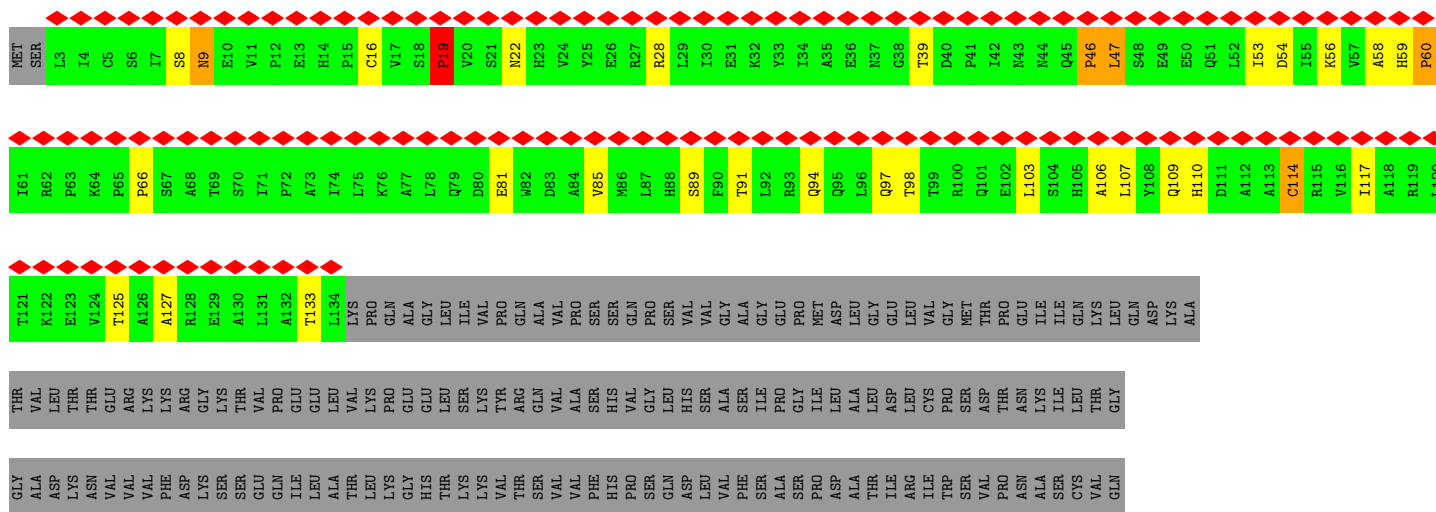


• Molecule 33: Small nuclear ribonucleoprotein G



• Molecule 34: U2 small nuclear ribonucleoprotein A'





[illegible]

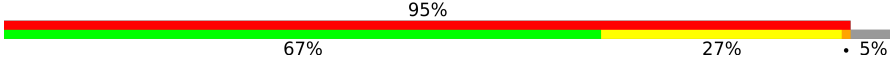
- Molecule 36: Pre-mRNA-processing factor 19

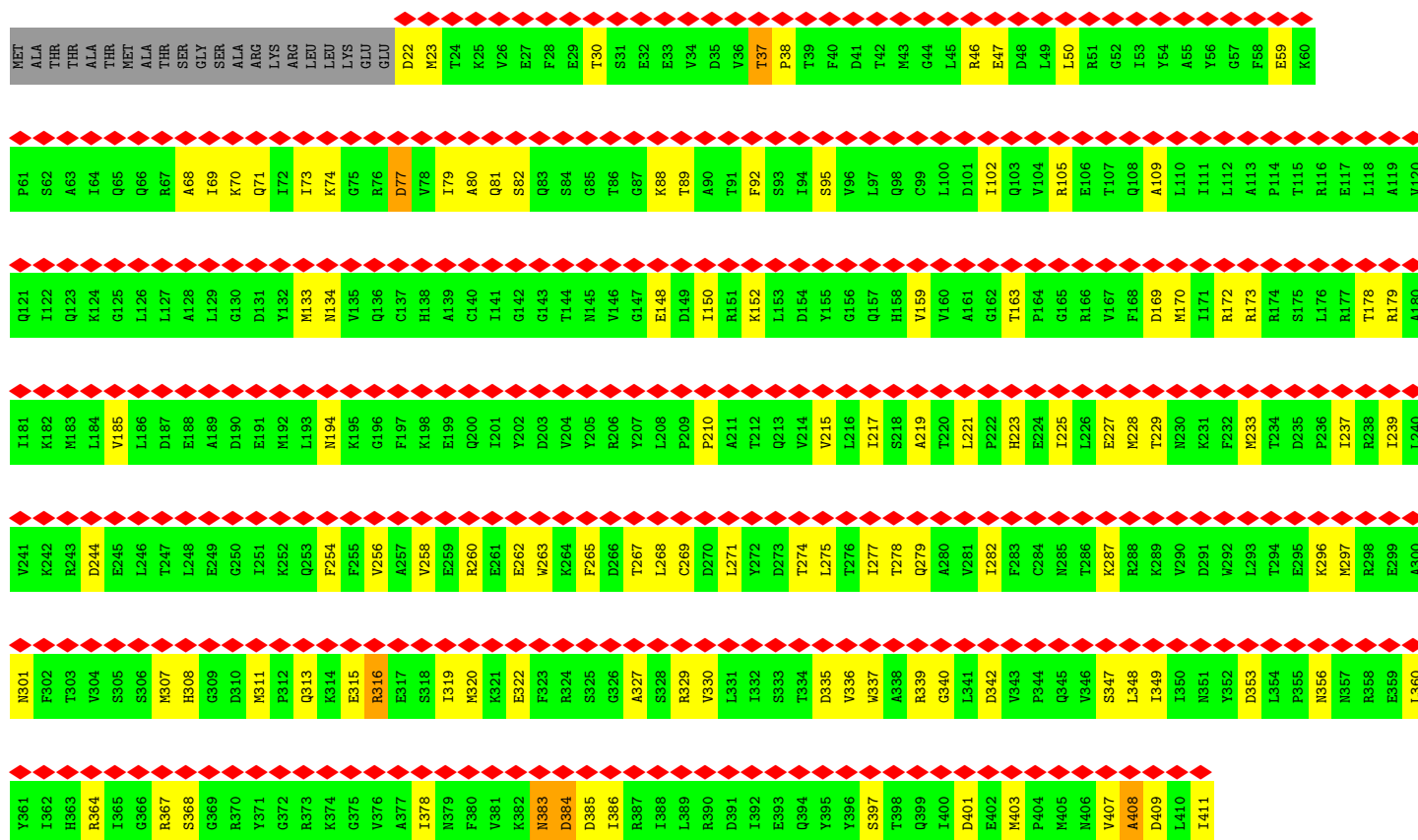
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- Molecule 36: Pre-mRNA-processing factor 19

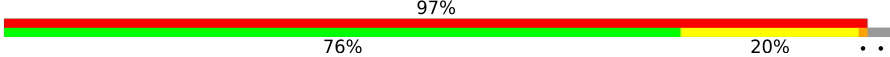


MT	SR	L3	L4	C5	S6	I7	S8	N9	E10	P11	E13	H14	P15	C16	V17	S18	P19	V20	S21	N22	H23	V24	V25	E26	R27	L28	L29	L30	E31	K32	V33	L34	A35	E36	N37	G38	T39	D40	P41	L42	N43	N44	Q45	P46	L47	S48	F49	E50	H10	Q51	L52	S53	D54	S55	K56	V57	A58	H59	P60
I61	R62	P63	K64	P65	P66	S67	A68	T69	S70	I71	P72	A73	I74	L75	K76	L77	L78	Q79	D80	E81	W82	D83	A84	V85	M86	L87	H88	S89	P90	T91	L92	R93	Q94	Q95	L96	Q97	T98	T99	R100	Q101	E102	L103	S104	H105	A106	I107	N108	Q109	H110	D111	A112	A113	C114	R115	V116	I117	A118	R119	L120

Chain u: 



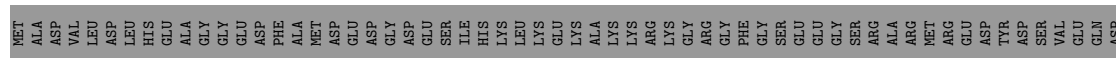
• Molecule 38: Protein mago nashi homolog 2

Chain v: 



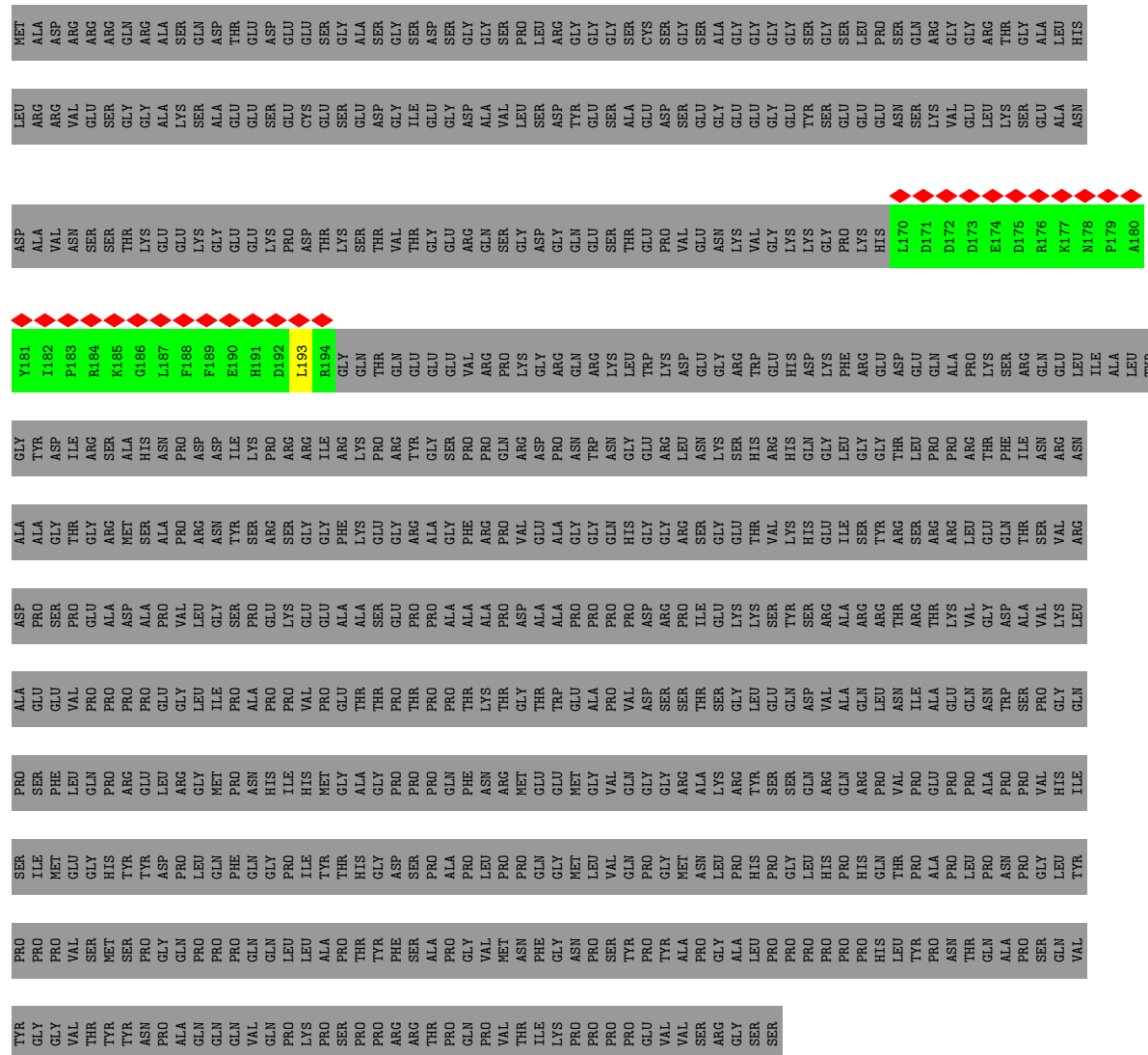
• Molecule 39: RNA-binding protein 8A

Chain w: 



- Molecule 40: Protein CASC3

Chain x:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	100085	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	0.260	Depositor
Minimum map value	-0.149	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.338, 1.338, 1.338	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.90	2/19149 (0.0%)	1.13	103/25983 (0.4%)
2	B	0.60	1/1970 (0.1%)	0.82	6/3060 (0.2%)
3	C	0.76	0/6950	1.14	30/9443 (0.3%)
4	D	0.47	0/14140	0.92	27/19159 (0.1%)
5	E	0.63	1/2392 (0.0%)	0.91	6/3242 (0.2%)
6	F	0.48	0/2323	0.80	1/3619 (0.0%)
7	G	0.62	6/1720 (0.3%)	0.91	6/2664 (0.2%)
8	H	0.84	26/3305 (0.8%)	1.39	58/5130 (1.1%)
9	I	1.83	1/2760 (0.0%)	1.02	21/3790 (0.6%)
10	J	0.73	0/3870	1.09	26/5252 (0.5%)
11	K	1.16	13/982 (1.3%)	1.02	6/1318 (0.5%)
12	L	0.78	4/3236 (0.1%)	1.09	16/4346 (0.4%)
13	M	0.73	0/1119	1.09	3/1497 (0.2%)
14	N	0.73	0/1210	0.89	1/1622 (0.1%)
15	O	0.74	1/2344 (0.0%)	0.89	1/3163 (0.0%)
16	P	0.79	0/943	1.15	5/1255 (0.4%)
17	Q	0.57	71/11155 (0.6%)	0.70	1/15095 (0.0%)
18	R	0.80	1/2091 (0.0%)	1.25	19/2809 (0.7%)
19	S	0.59	0/1268	1.12	12/1714 (0.7%)
20	T	1.11	1/2526 (0.0%)	1.21	15/3443 (0.4%)
21	U	1.05	0/196	1.19	3/265 (1.1%)
22	V	0.63	6/3462 (0.2%)	0.92	16/4651 (0.3%)
23	W	0.73	1/4128 (0.0%)	1.10	30/5572 (0.5%)
24	X	0.59	0/714	1.19	4/959 (0.4%)
25	Y	0.81	0/3000	1.60	19/3777 (0.5%)
26	Z	0.69	0/2049	0.92	5/2757 (0.2%)
27	a	0.65	0/646	0.85	0/867
27	h	0.65	0/639	0.86	0/857
28	b	0.73	0/700	1.03	4/933 (0.4%)
28	i	0.72	0/700	1.03	4/933 (0.4%)
29	c	0.74	0/657	0.98	0/888
29	j	0.74	0/657	0.98	0/888

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	d	0.94	0/786	1.10	2/1053 (0.2%)
30	k	0.95	0/696	1.07	1/935 (0.1%)
31	f	1.04	1/588 (0.2%)	1.08	0/795
31	m	1.03	1/588 (0.2%)	1.08	0/795
32	e	0.85	0/660	1.06	1/886 (0.1%)
32	l	0.84	0/660	1.06	1/886 (0.1%)
33	g	0.71	0/584	0.95	1/779 (0.1%)
33	n	0.70	0/548	0.95	1/729 (0.1%)
34	o	0.81	0/1299	2.05	57/1761 (3.2%)
35	p	0.77	0/774	1.71	13/1035 (1.3%)
36	q	0.98	9/929 (1.0%)	1.00	6/1260 (0.5%)
36	r	0.97	9/912 (1.0%)	1.01	6/1239 (0.5%)
36	s	0.98	10/928 (1.1%)	1.05	7/1258 (0.6%)
36	t	0.98	9/917 (1.0%)	0.96	6/1245 (0.5%)
37	u	0.45	0/3179	1.00	14/4291 (0.3%)
38	v	0.40	0/1225	0.84	3/1648 (0.2%)
39	w	0.40	0/748	0.98	4/1012 (0.4%)
40	x	0.46	0/221	0.92	0/296
All	All	0.78	174/119243 (0.1%)	1.06	571/162854 (0.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
3	C	0	4
4	D	0	1
9	I	0	2
12	L	0	2
14	N	0	2
15	O	0	1
18	R	0	1
20	T	0	2
24	X	0	2
25	Y	0	15
26	Z	0	2
30	d	0	1
30	k	0	1
All	All	0	39

The worst 5 of 174 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	I	283	ILE	C-N	-91.70	0.06	1.33
36	q	47	LEU	CB-CG	14.06	1.81	1.53
36	s	47	LEU	CB-CG	13.99	1.81	1.53
36	r	47	LEU	CB-CG	13.96	1.81	1.53
36	t	47	LEU	CB-CG	13.91	1.81	1.53

The worst 5 of 571 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	283	ILE	CA-C-N	-19.36	80.03	121.45
9	I	283	ILE	C-N-CA	-19.36	80.03	121.45
24	X	59	PRO	CA-C-N	13.75	134.54	120.38
24	X	59	PRO	C-N-CA	13.75	134.54	120.38
34	o	55	ARG	CD-NE-CZ	13.19	142.86	124.40

There are no chirality outliers.

5 of 39 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	166	PHE	Peptide
1	A	81	PHE	Peptide
1	A	941	LYS	Peptide
3	C	622	GLU	Peptide
3	C	88	PRO	Peptide

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	18633	0	18480	846	0
2	B	1768	0	897	54	0
3	C	6798	0	6815	615	0
4	D	13846	0	13985	383	0
5	E	2338	0	2272	149	0
6	F	2075	0	1048	158	0
7	G	1551	0	785	178	0
8	H	2966	0	1505	256	0
9	I	2792	0	1249	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	3829	0	2906	144	0
11	K	980	0	741	11	0
12	L	3205	0	2777	203	0
13	M	1098	0	1080	175	0
14	N	1184	0	1189	62	0
15	O	2296	0	2283	199	0
16	P	929	0	910	100	0
17	Q	10885	0	10852	77	0
18	R	2073	0	2116	289	0
19	S	1236	0	1208	142	0
20	T	2461	0	2420	158	0
21	U	193	0	194	18	0
22	V	3419	0	3300	275	0
23	W	4023	0	3938	879	0
24	X	701	0	631	32	0
25	Y	2995	0	992	14	0
26	Z	1999	0	1951	146	0
27	a	640	0	657	9	0
27	h	633	0	645	15	0
28	b	690	0	712	15	0
28	i	690	0	712	15	0
29	c	649	0	693	10	0
29	j	649	0	693	12	0
30	d	776	0	819	30	0
30	k	688	0	709	31	0
31	f	576	0	589	20	0
31	m	576	0	589	24	0
32	e	652	0	668	20	0
32	l	652	0	668	25	0
33	g	577	0	603	14	0
33	n	542	0	568	28	0
34	o	1282	0	1305	30	0
35	p	760	0	783	11	0
36	q	918	0	801	16	0
36	r	901	0	777	17	0
36	s	917	0	798	13	0
36	t	906	0	785	14	0
37	u	3130	0	3172	131	0
38	v	1196	0	1182	34	0
39	w	730	0	690	26	0
40	x	216	0	202	1	0
41	A	36	0	6	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	C	32	0	12	4	0
43	C	1	0	0	0	0
43	D	1	0	0	0	0
43	F	6	0	0	0	0
43	Q	2	0	0	0	0
43	u	1	0	0	0	0
44	D	54	0	24	3	0
45	N	3	0	0	0	0
45	O	3	0	0	0	0
45	Z	1	0	0	0	0
46	Q	31	0	12	0	0
46	u	31	0	12	2	0
All	All	116421	0	106410	5418	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 24.

The worst 5 of 5418 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:264:PHE:CE1	1:A:459:LEU:HD13	1.13	1.65
1:A:264:PHE:CE1	1:A:459:LEU:CD1	1.79	1.64
11:K:163:LEU:CB	11:K:163:LEU:CG	1.81	1.57
36:q:47:LEU:CB	36:q:47:LEU:CG	1.81	1.55
36:r:47:LEU:CB	36:r:47:LEU:CG	1.81	1.55

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	2247/2335 (96%)	2104 (94%)	107 (5%)	36 (2%)	7	36
3	C	856/972 (88%)	787 (92%)	48 (6%)	21 (2%)	4	28
4	D	1720/2136 (80%)	1632 (95%)	85 (5%)	3 (0%)	43	72
5	E	297/357 (83%)	273 (92%)	17 (6%)	7 (2%)	4	29
9	I	502/855 (59%)	482 (96%)	11 (2%)	9 (2%)	6	34
10	J	530/848 (62%)	482 (91%)	30 (6%)	18 (3%)	3	23
11	K	144/225 (64%)	134 (93%)	6 (4%)	4 (3%)	4	26
12	L	436/802 (54%)	409 (94%)	20 (5%)	7 (2%)	7	36
13	M	128/243 (53%)	118 (92%)	4 (3%)	6 (5%)	2	17
14	N	141/144 (98%)	124 (88%)	13 (9%)	4 (3%)	4	26
15	O	283/420 (67%)	255 (90%)	22 (8%)	6 (2%)	5	31
16	P	104/229 (45%)	91 (88%)	8 (8%)	5 (5%)	2	16
17	Q	1308/1485 (88%)	1283 (98%)	25 (2%)	0	100	100
18	R	255/536 (48%)	229 (90%)	14 (6%)	12 (5%)	2	17
19	S	157/166 (95%)	146 (93%)	8 (5%)	3 (2%)	6	33
20	T	311/514 (60%)	280 (90%)	22 (7%)	9 (3%)	3	26
21	U	24/2752 (1%)	20 (83%)	3 (12%)	1 (4%)	2	19
22	V	444/908 (49%)	418 (94%)	20 (4%)	6 (1%)	9	38
23	W	494/579 (85%)	434 (88%)	31 (6%)	29 (6%)	1	13
24	X	90/184 (49%)	81 (90%)	8 (9%)	1 (1%)	11	43
25	Y	709/1220 (58%)	617 (87%)	60 (8%)	32 (4%)	2	17
26	Z	238/586 (41%)	197 (83%)	30 (13%)	11 (5%)	2	17
27	a	77/126 (61%)	76 (99%)	1 (1%)	0	100	100
27	h	77/126 (61%)	76 (99%)	1 (1%)	0	100	100
28	b	84/231 (36%)	82 (98%)	2 (2%)	0	100	100
28	i	84/231 (36%)	82 (98%)	2 (2%)	0	100	100
29	c	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
29	j	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
30	d	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
30	k	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
31	f	72/86 (84%)	69 (96%)	3 (4%)	0	100	100
31	m	72/86 (84%)	68 (94%)	4 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
32	l	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
33	g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
33	n	65/76 (86%)	63 (97%)	2 (3%)	0	100	100
34	o	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	9	39
35	p	92/225 (41%)	90 (98%)	2 (2%)	0	100	100
36	q	130/504 (26%)	119 (92%)	7 (5%)	4 (3%)	3	25
36	r	129/504 (26%)	118 (92%)	9 (7%)	2 (2%)	7	36
36	s	130/504 (26%)	116 (89%)	7 (5%)	7 (5%)	1	14
36	t	129/504 (26%)	116 (90%)	9 (7%)	4 (3%)	3	25
37	u	388/411 (94%)	376 (97%)	9 (2%)	3 (1%)	16	49
38	v	142/148 (96%)	138 (97%)	4 (3%)	0	100	100
39	w	89/174 (51%)	87 (98%)	1 (1%)	1 (1%)	11	43
40	x	23/703 (3%)	22 (96%)	1 (4%)	0	100	100
All	All	13923/24124 (58%)	12985 (93%)	685 (5%)	253 (2%)	9	34

5 of 253 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	ARG
1	A	308	ILE
1	A	331	TRP
1	A	346	ASP
1	A	365	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	2021/2108 (96%)	1866 (92%)	155 (8%)	12	38
3	C	761/866 (88%)	693 (91%)	68 (9%)	9	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	1541/1908 (81%)	1347 (87%)	194 (13%)	4	22
5	E	256/300 (85%)	243 (95%)	13 (5%)	21	49
10	J	241/751 (32%)	214 (89%)	27 (11%)	6	27
11	K	56/196 (29%)	48 (86%)	8 (14%)	3	19
12	L	229/709 (32%)	184 (80%)	45 (20%)	1	8
13	M	117/209 (56%)	81 (69%)	36 (31%)	0	2
14	N	130/130 (100%)	127 (98%)	3 (2%)	44	64
15	O	255/361 (71%)	250 (98%)	5 (2%)	48	66
16	P	99/203 (49%)	82 (83%)	17 (17%)	2	12
17	Q	1202/1336 (90%)	1197 (100%)	5 (0%)	84	81
18	R	219/457 (48%)	161 (74%)	58 (26%)	0	3
19	S	129/134 (96%)	120 (93%)	9 (7%)	14	41
20	T	269/441 (61%)	253 (94%)	16 (6%)	18	45
21	U	21/2432 (1%)	17 (81%)	4 (19%)	1	9
22	V	327/838 (39%)	306 (94%)	21 (6%)	16	43
23	W	436/502 (87%)	318 (73%)	118 (27%)	0	3
24	X	62/157 (40%)	60 (97%)	2 (3%)	34	58
25	Y	31/1085 (3%)	31 (100%)	0	100	100
26	Z	214/520 (41%)	201 (94%)	13 (6%)	17	45
27	a	72/101 (71%)	72 (100%)	0	100	100
27	h	70/101 (69%)	70 (100%)	0	100	100
28	b	77/169 (46%)	74 (96%)	3 (4%)	28	54
28	i	77/169 (46%)	74 (96%)	3 (4%)	28	54
29	c	77/101 (76%)	75 (97%)	2 (3%)	40	62
29	j	77/101 (76%)	75 (97%)	2 (3%)	40	62
30	d	90/110 (82%)	89 (99%)	1 (1%)	65	74
30	k	80/110 (73%)	79 (99%)	1 (1%)	61	72
31	f	63/74 (85%)	61 (97%)	2 (3%)	34	58
31	m	63/74 (85%)	61 (97%)	2 (3%)	34	58
32	e	74/84 (88%)	74 (100%)	0	100	100
32	l	74/84 (88%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	g	64/66 (97%)	63 (98%)	1 (2%)	55	69
33	n	60/66 (91%)	59 (98%)	1 (2%)	53	69
34	o	139/218 (64%)	133 (96%)	6 (4%)	26	52
35	p	82/195 (42%)	79 (96%)	3 (4%)	30	56
36	q	79/435 (18%)	72 (91%)	7 (9%)	9	33
36	r	77/435 (18%)	66 (86%)	11 (14%)	3	19
36	s	77/435 (18%)	69 (90%)	8 (10%)	7	29
36	t	77/435 (18%)	71 (92%)	6 (8%)	11	38
37	u	345/361 (96%)	338 (98%)	7 (2%)	48	66
38	v	132/134 (98%)	131 (99%)	1 (1%)	73	77
39	w	76/143 (53%)	75 (99%)	1 (1%)	61	72
40	x	23/581 (4%)	23 (100%)	0	100	100
All	All	10741/20425 (53%)	9856 (92%)	885 (8%)	13	36

5 of 885 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	K	171	GLN
17	Q	960	ASP
37	u	194	ASN
23	W	554	ILE
12	L	135	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 187 such sidechains are listed below:

Mol	Chain	Res	Type
18	R	68	HIS
23	W	162	ASN
18	R	106	GLN
20	T	297	HIS
23	W	388	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	82/117 (70%)	17 (20%)	4 (4%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
6	F	96/107 (89%)	45 (46%)	14 (14%)
7	G	82/275 (29%)	53 (64%)	10 (12%)
8	H	133/188 (70%)	33 (24%)	8 (6%)
All	All	393/687 (57%)	148 (37%)	36 (9%)

5 of 148 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	12	U
2	B	13	C
2	B	19	A
2	B	20	G
2	B	21	A

5 of 36 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	H	15	U
8	H	168	A
8	H	29	A
8	H	40	C
6	F	50	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
18	SEP	R	224	18	8,9,10	0.71	0	7,12,14	1.26	0
18	SEP	R	232	18	8,9,10	0.85	0	7,12,14	1.23	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
18	SEP	R	224	18	-	0/6/8/10	-
18	SEP	R	232	18	-	2/6/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
18	R	232	SEP	N-CA-CB-OG
18	R	232	SEP	C-CA-CB-OG

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
18	R	224	SEP	2	0
18	R	232	SEP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 18 are monoatomic - leaving 6 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	$\# Z > 2$
46	ATP	u	702	43	32,33,33	1.22	4 (12%)	48,52,52	1.84	8 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
44	ADP	D	2201	-	28,29,29	1.45	5 (17%)	43,45,45	1.78	7 (16%)
41	IHP	A	3000	-	36,36,36	0.80	0	60,60,60	1.34	7 (11%)
42	GTP	C	1500	43	33,34,34	1.18	4 (12%)	50,54,54	1.97	9 (18%)
44	ADP	D	2202	43	28,29,29	1.37	4 (14%)	43,45,45	1.86	9 (20%)
46	ATP	Q	1501	43	32,33,33	2.05	8 (25%)	48,52,52	1.88	16 (33%)

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
46	ATP	u	702	43	-	0/22/38/38	0/3/3/3
44	ADP	D	2201	-	-	8/16/32/32	0/3/3/3
41	IHP	A	3000	-	-	8/30/54/54	0/1/1/1
42	GTP	C	1500	43	-	7/22/38/38	0/3/3/3
44	ADP	D	2202	43	-	2/16/32/32	0/3/3/3
46	ATP	Q	1501	43	-	4/22/38/38	0/3/3/3

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	Q	1501	ATP	PB-O3B	7.29	1.67	1.59
44	D	2201	ADP	C5-C4	4.74	1.47	1.39
46	Q	1501	ATP	C6-N6	4.68	1.46	1.34
44	D	2202	ADP	C5-C4	4.46	1.47	1.39
42	C	1500	GTP	C6-N1	-3.36	1.32	1.38

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	C	1500	GTP	C5-C4-N3	-6.50	118.04	128.39
44	D	2202	ADP	C5-C4-N3	-6.37	117.95	126.72
46	u	702	ATP	C5-C4-N3	-6.36	117.96	126.72
44	D	2201	ADP	C5-C4-N3	-5.85	118.67	126.72
42	C	1500	GTP	N9-C4-N3	5.70	137.36	125.95

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

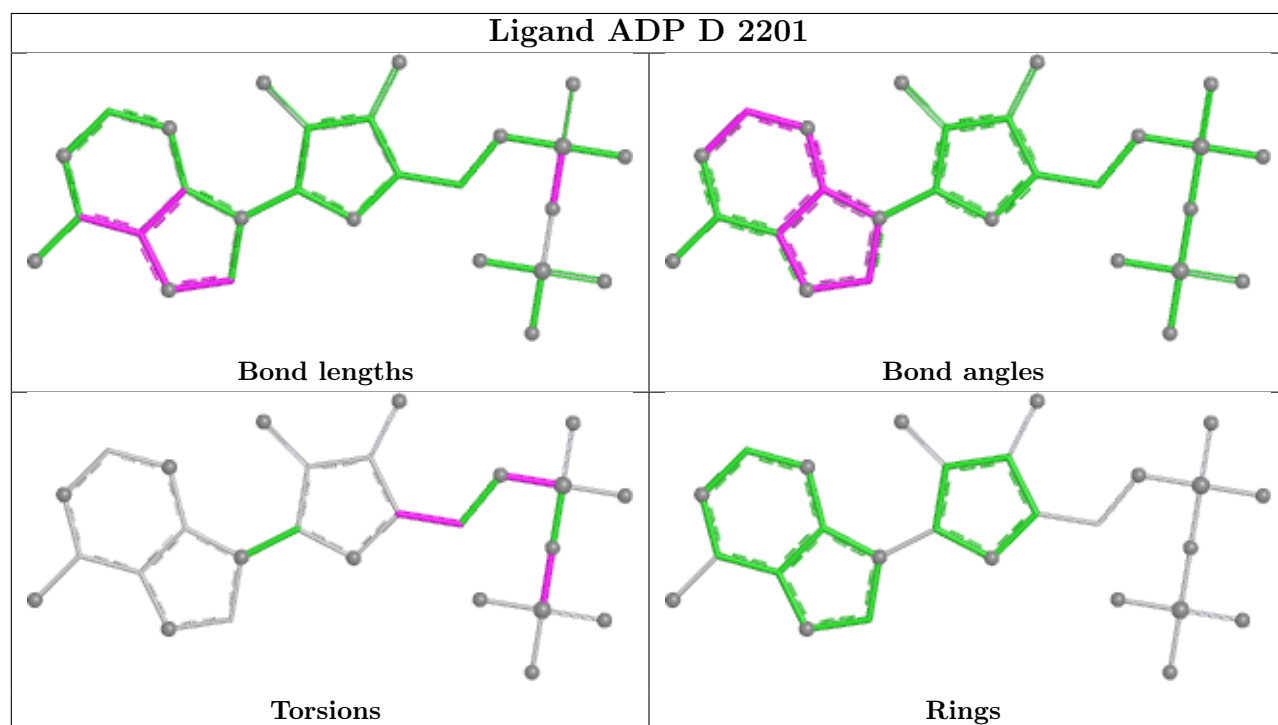
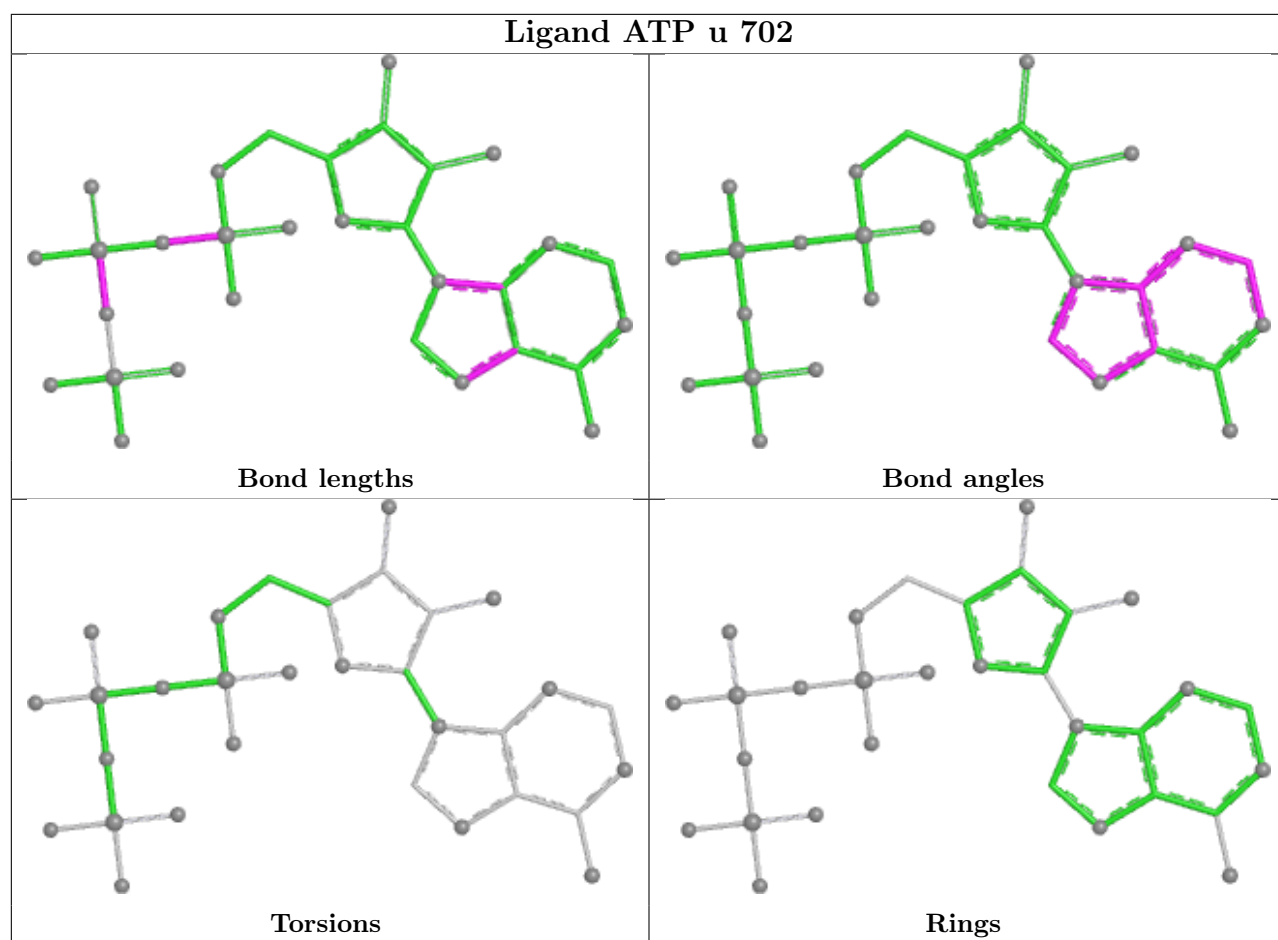
Mol	Chain	Res	Type	Atoms
41	A	3000	IHP	C4-C5-O15-P5
41	A	3000	IHP	C6-C5-O15-P5
42	C	1500	GTP	C5'-O5'-PA-O3A
42	C	1500	GTP	C5'-O5'-PA-O1A
42	C	1500	GTP	C5'-O5'-PA-O2A

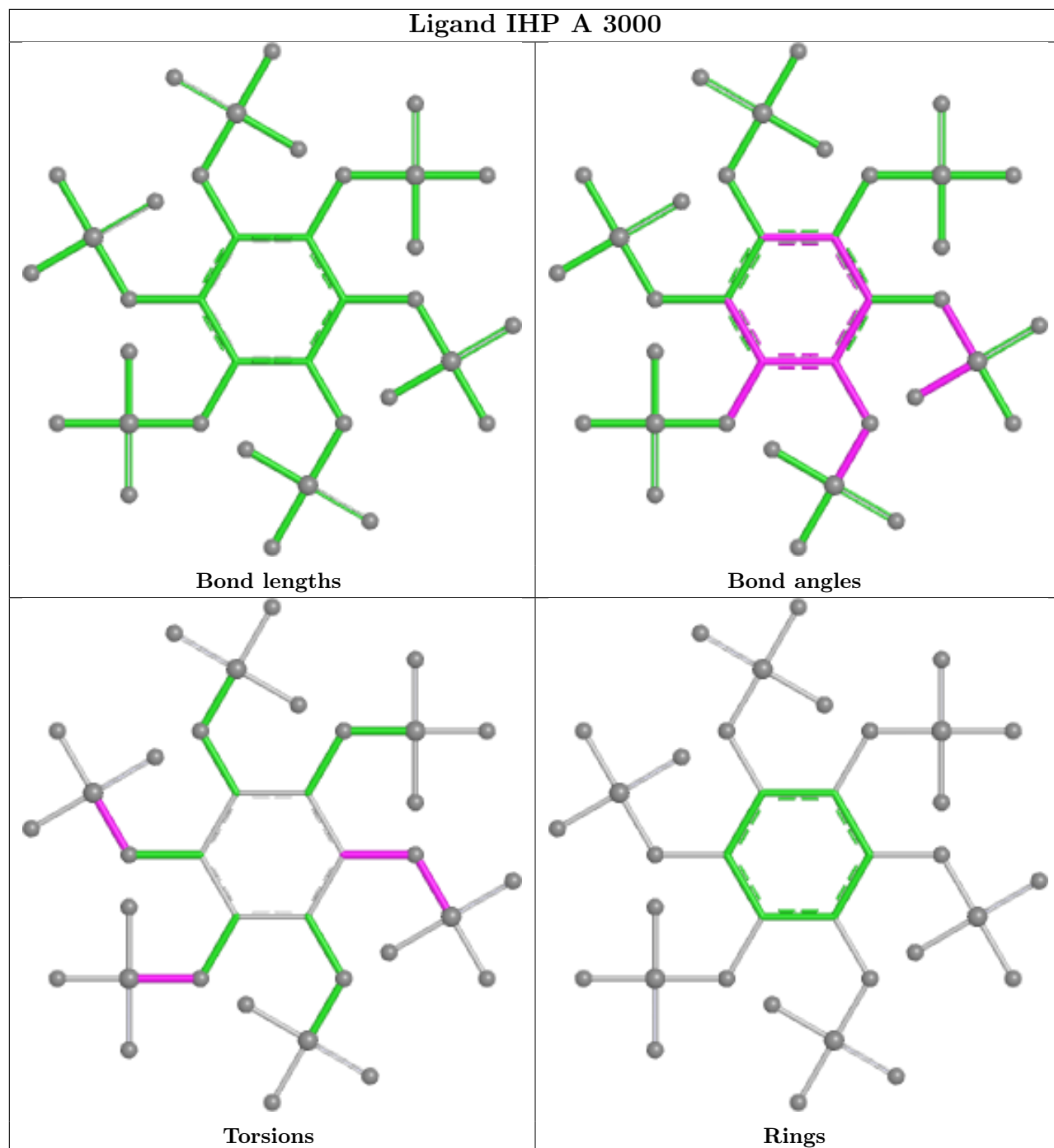
There are no ring outliers.

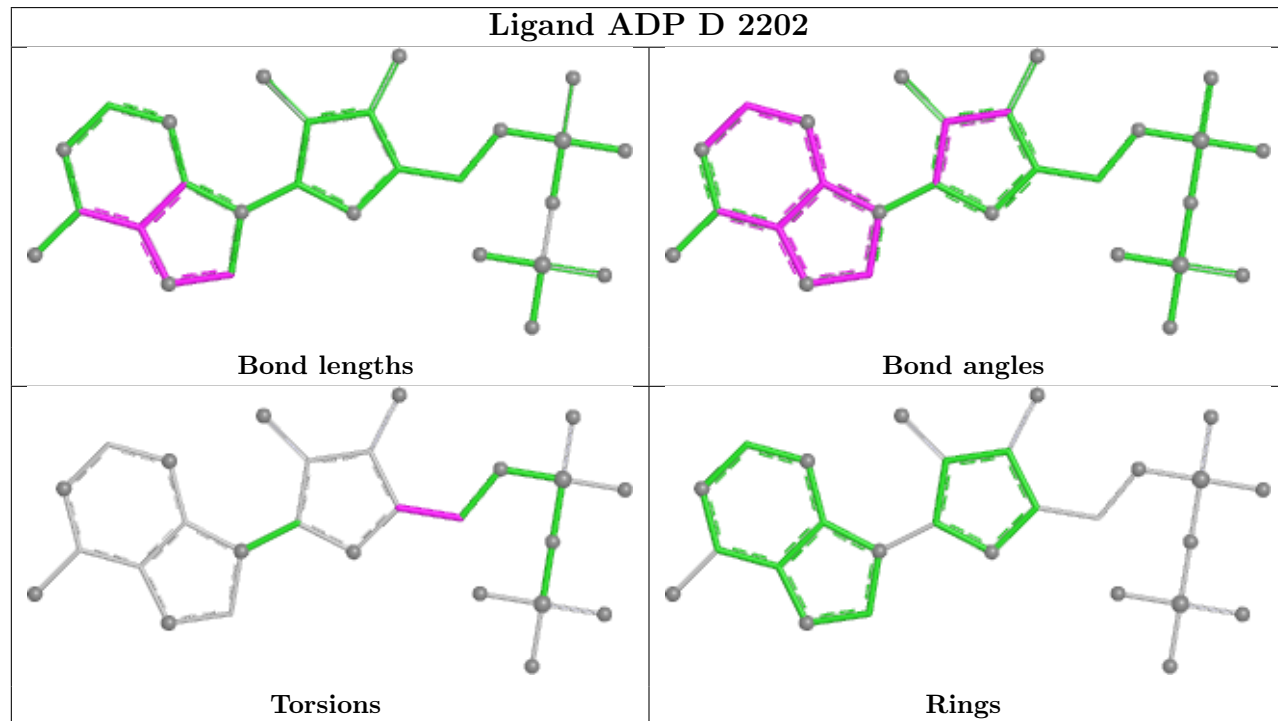
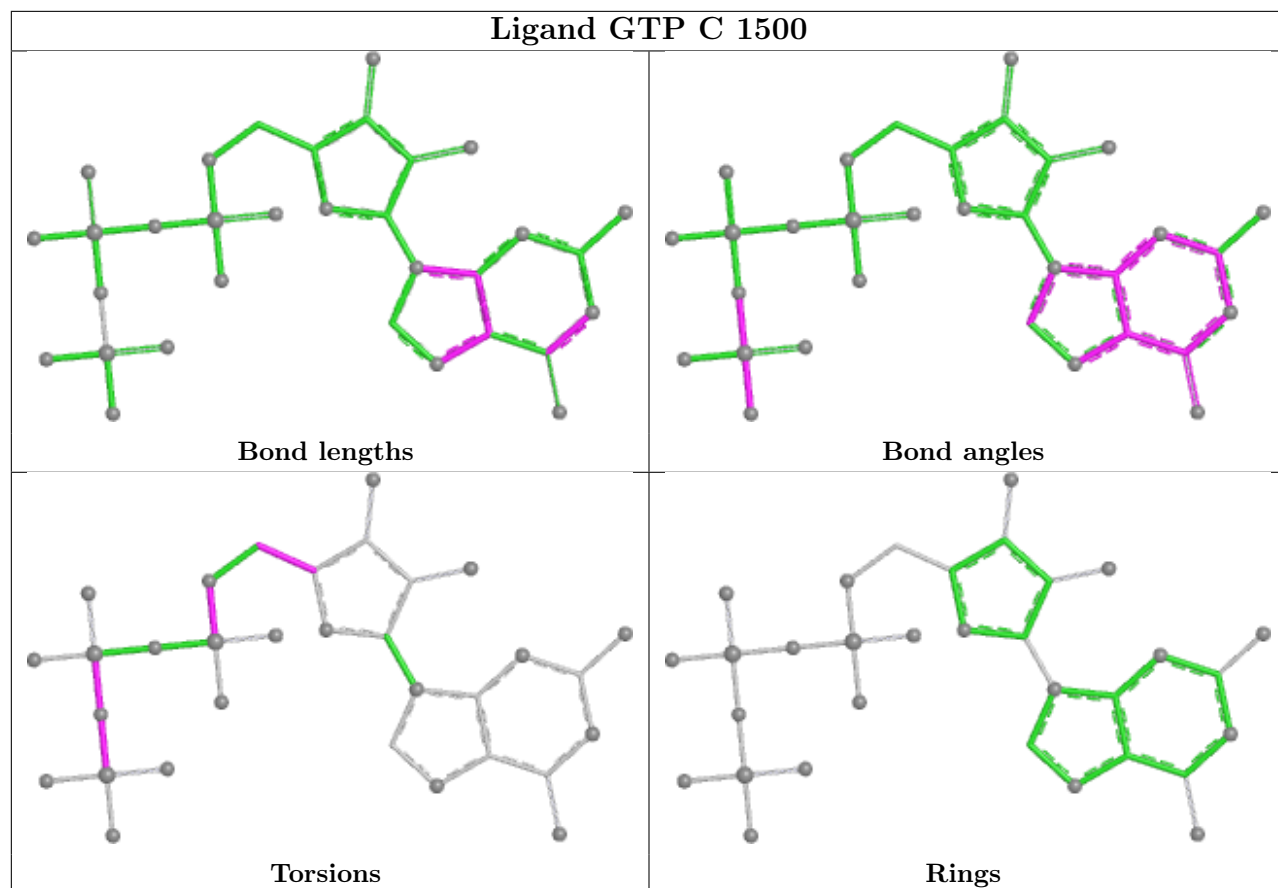
4 monomers are involved in 13 short contacts:

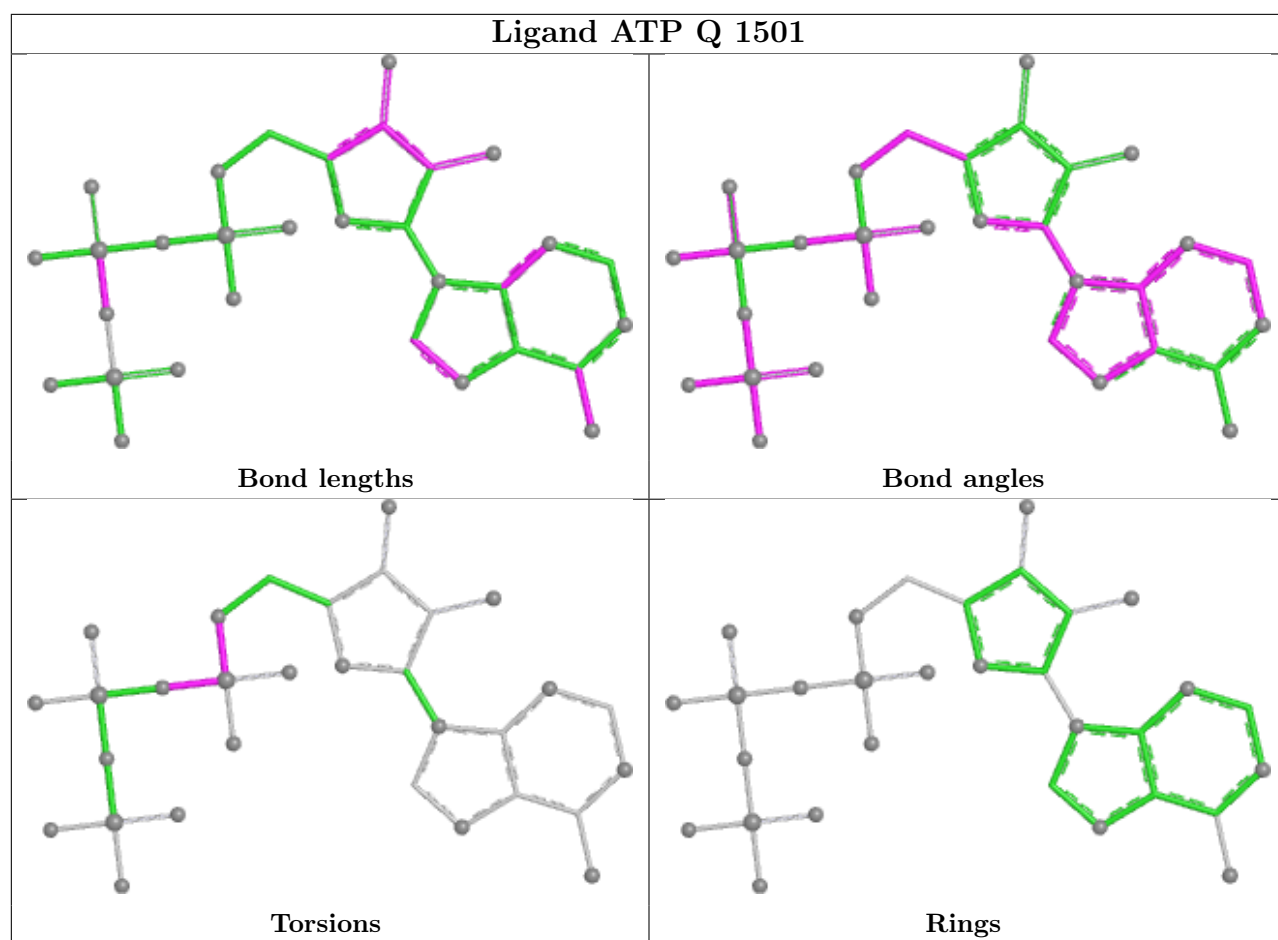
Mol	Chain	Res	Type	Clashes	Symm-Clashes
46	u	702	ATP	2	0
44	D	2201	ADP	3	0
41	A	3000	IHP	4	0
42	C	1500	GTP	4	0

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.

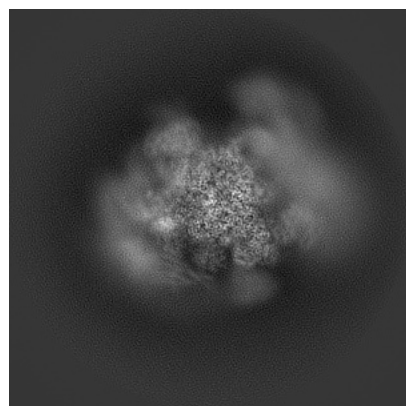
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6721. These allow visual inspection of the internal detail of the map and identification of artifacts.

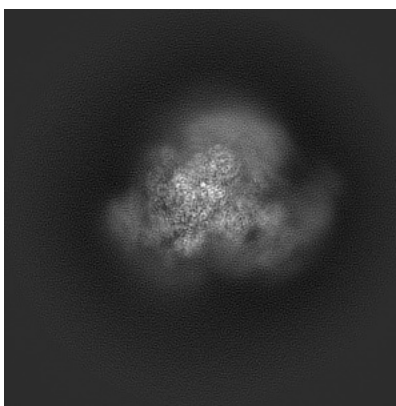
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

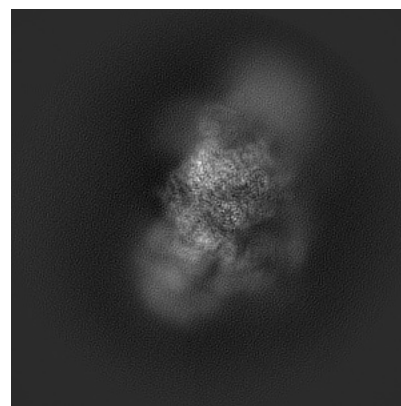
6.1.1 Primary map



X

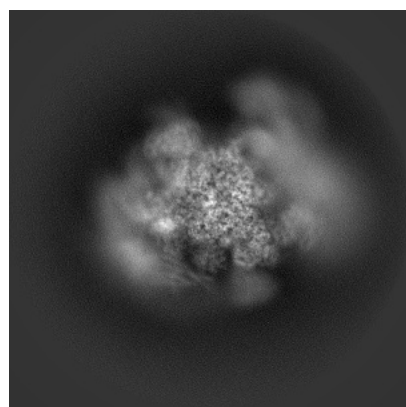


Y

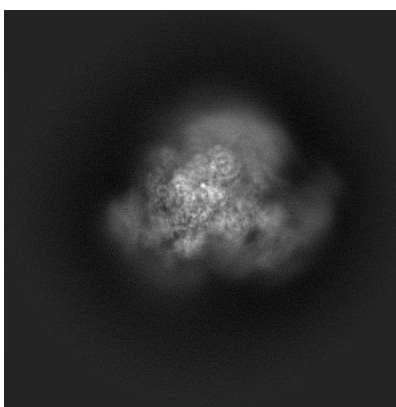


Z

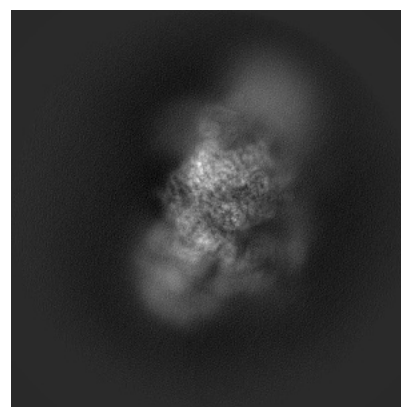
6.1.2 Raw map



X



Y

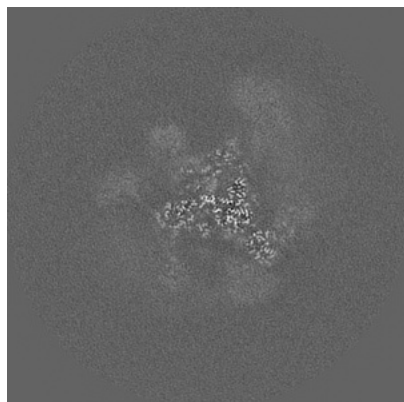


Z

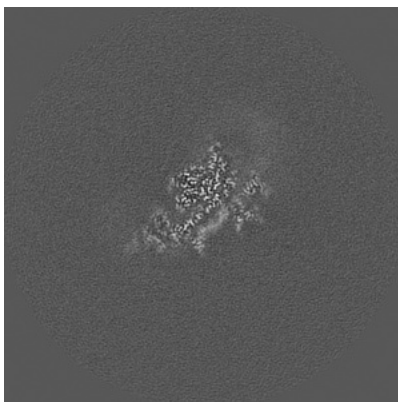
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

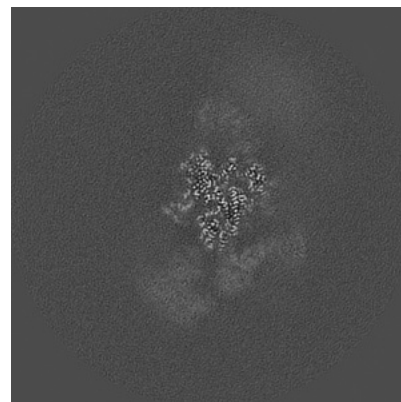
6.2.1 Primary map



X Index: 200

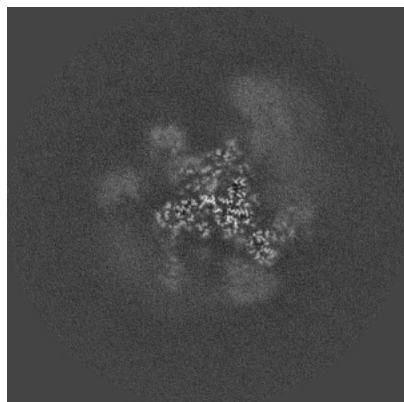


Y Index: 200

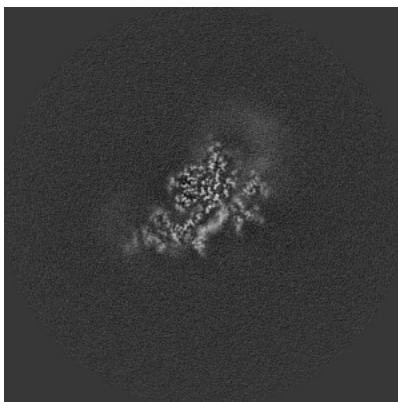


Z Index: 200

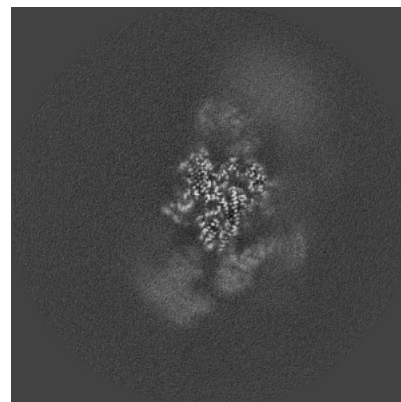
6.2.2 Raw map



X Index: 200



Y Index: 200

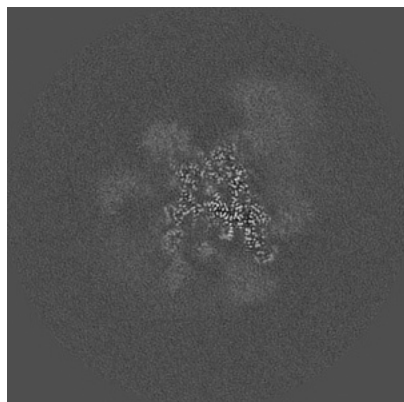


Z Index: 200

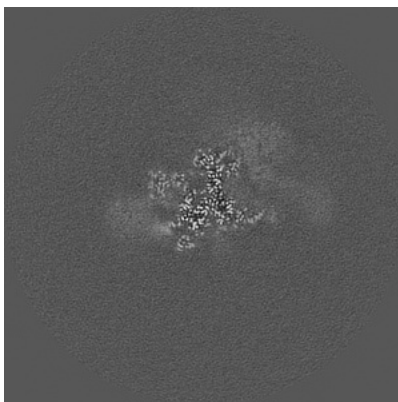
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

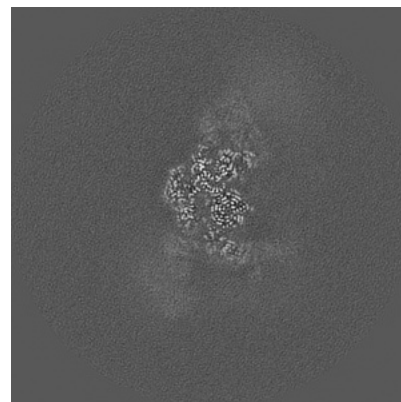
6.3.1 Primary map



X Index: 194

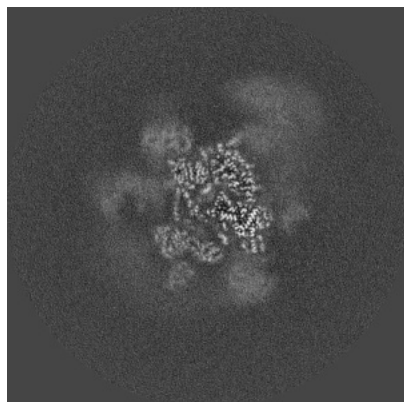


Y Index: 229

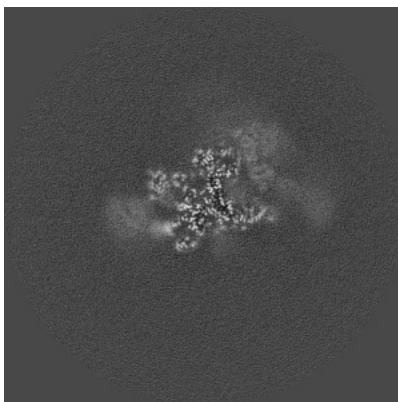


Z Index: 182

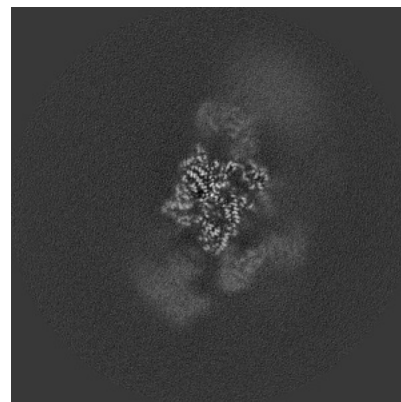
6.3.2 Raw map



X Index: 188



Y Index: 228

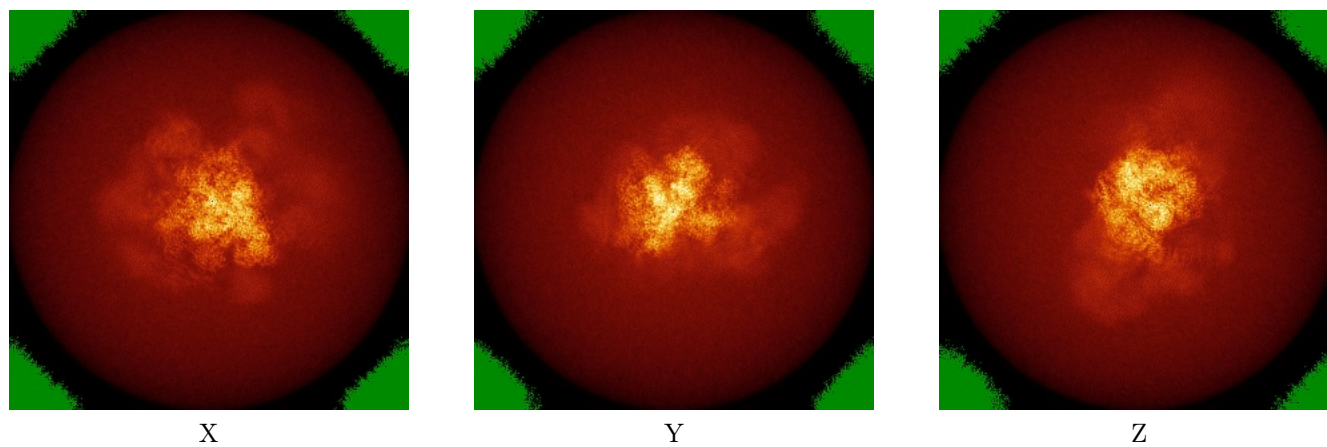


Z Index: 197

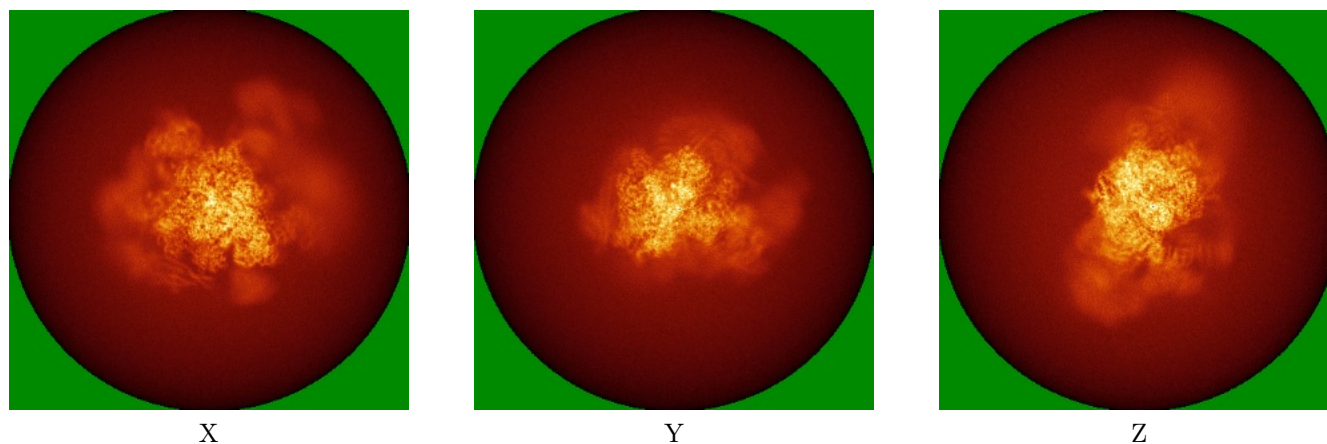
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

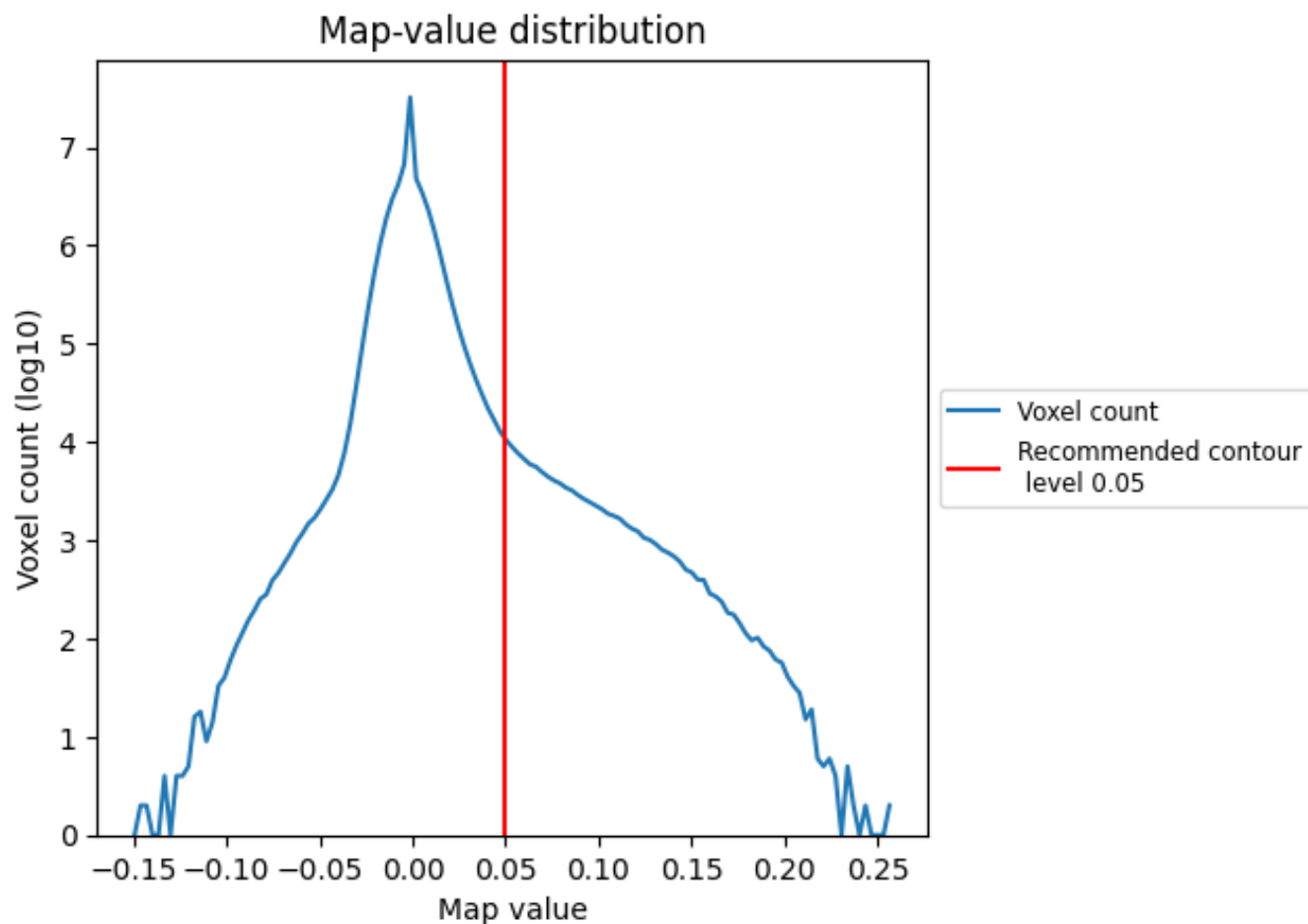
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

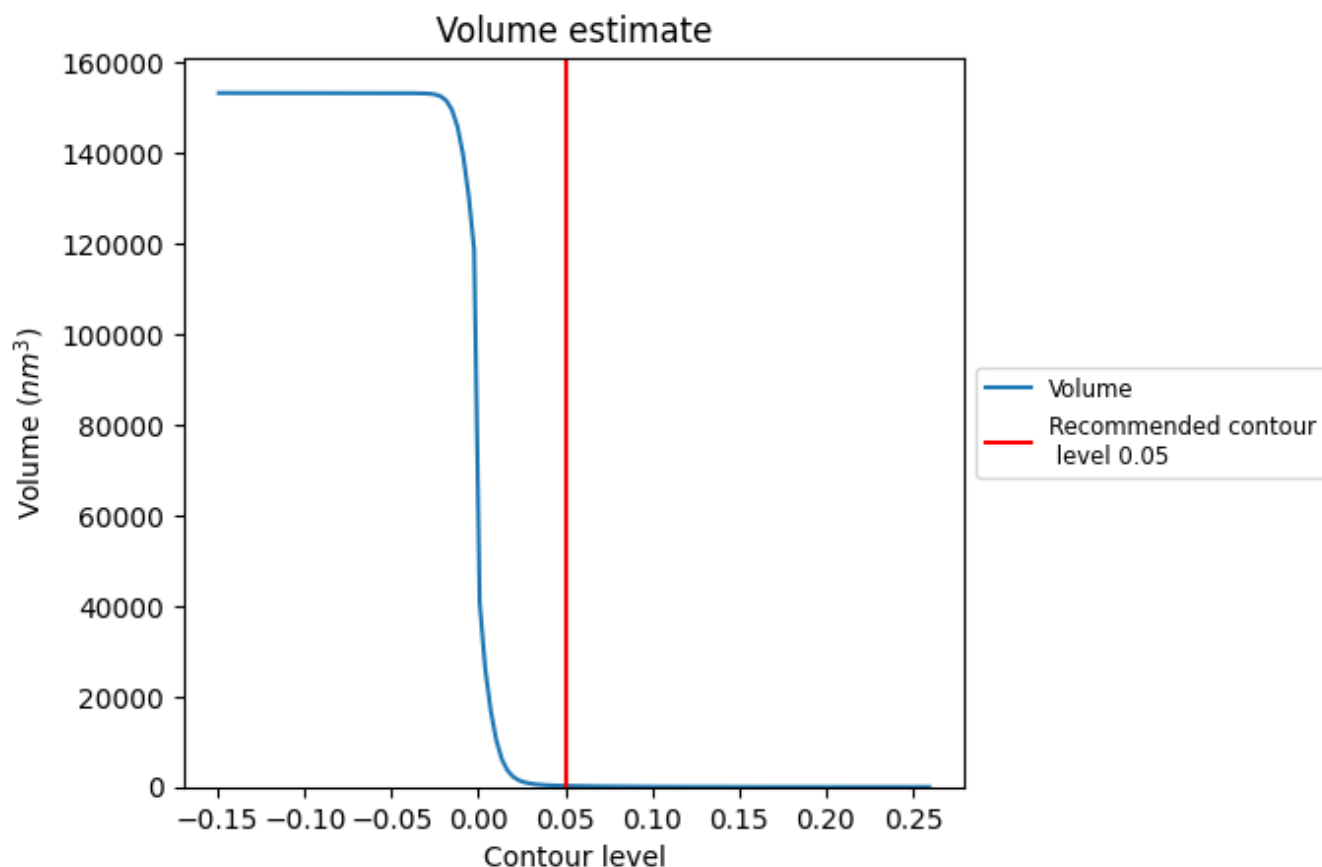
This section contains the results of statistical analysis of the map.

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.

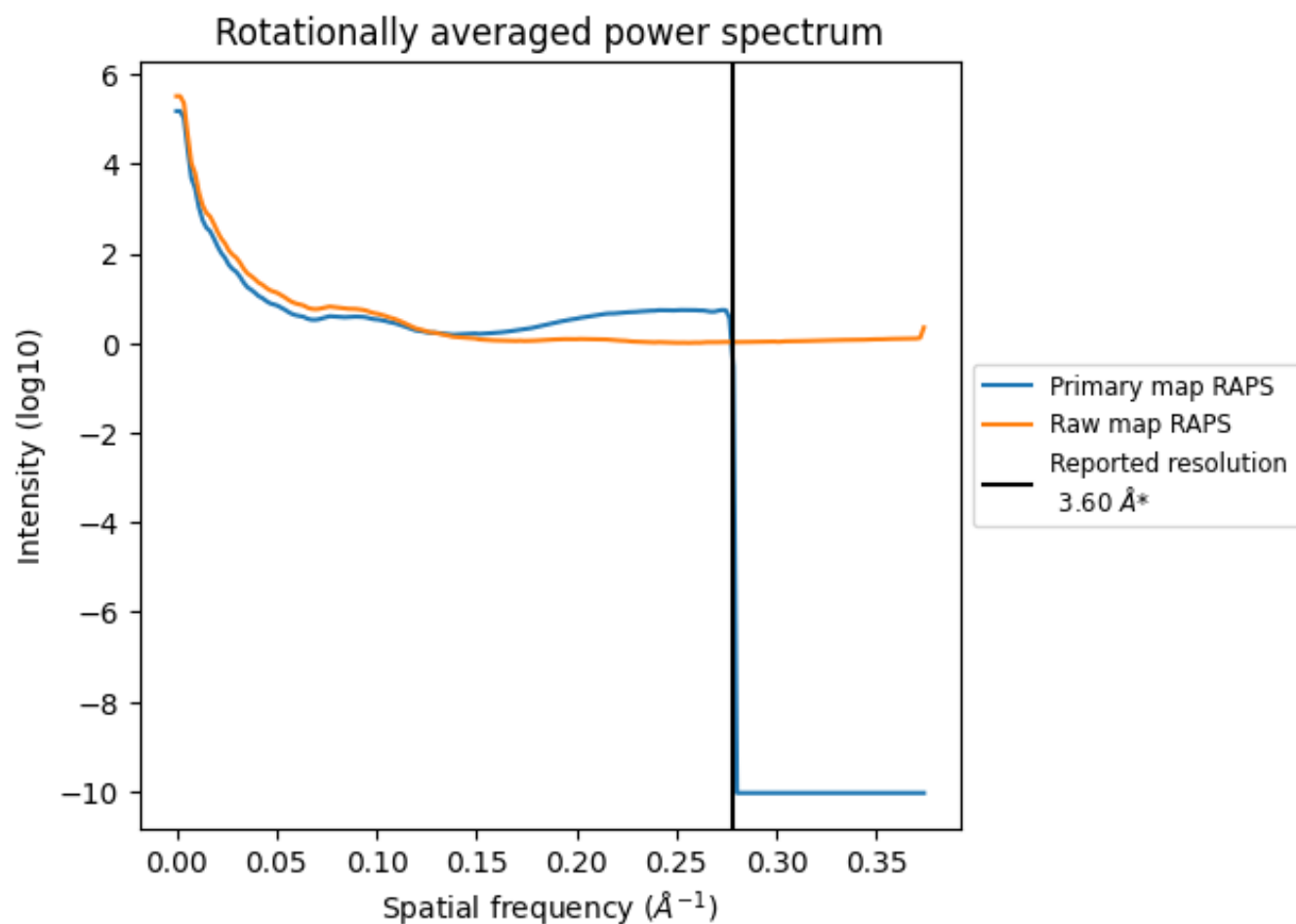
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 243 nm³; this corresponds to an approximate mass of 220 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 ⓘ

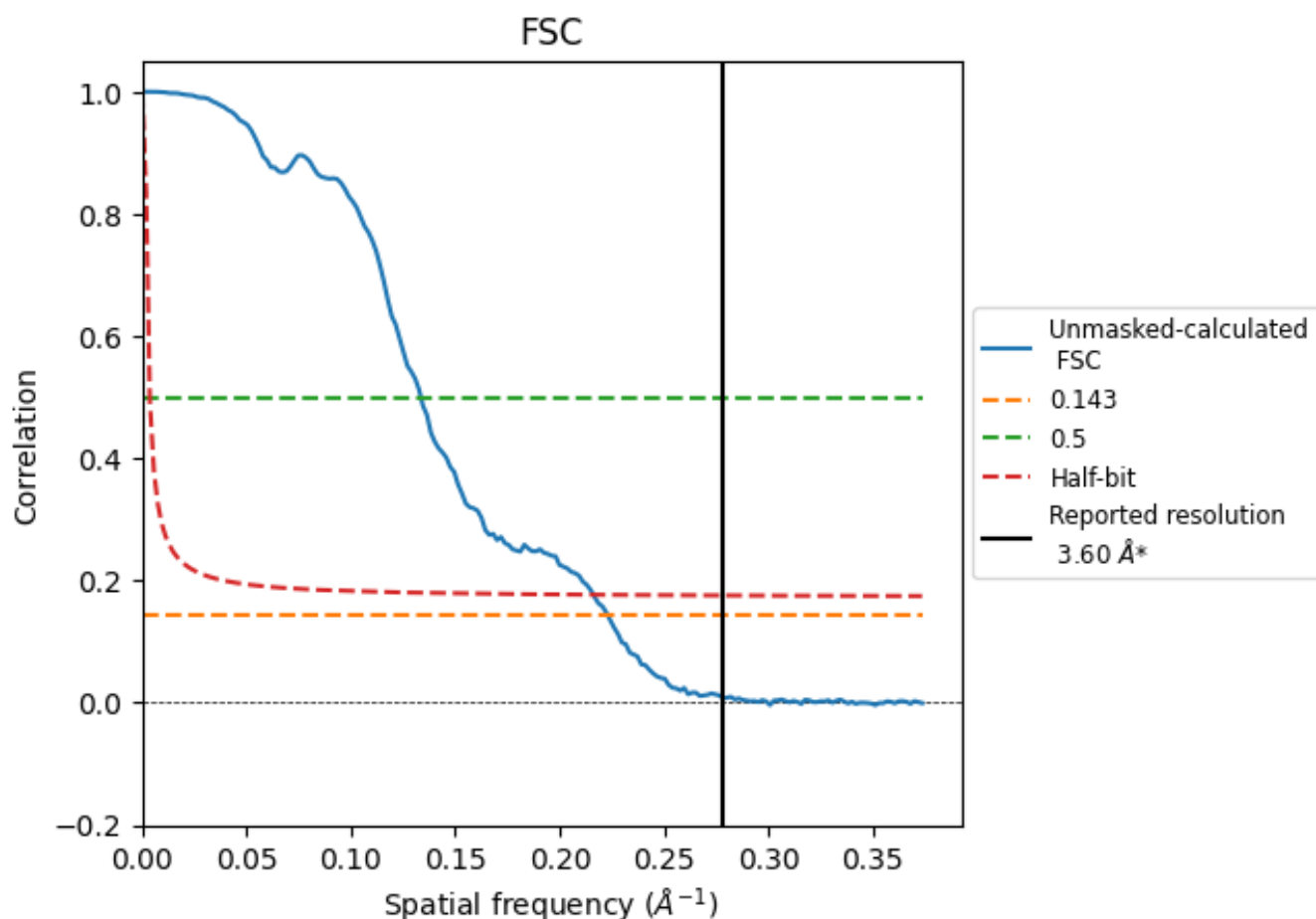


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.278 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

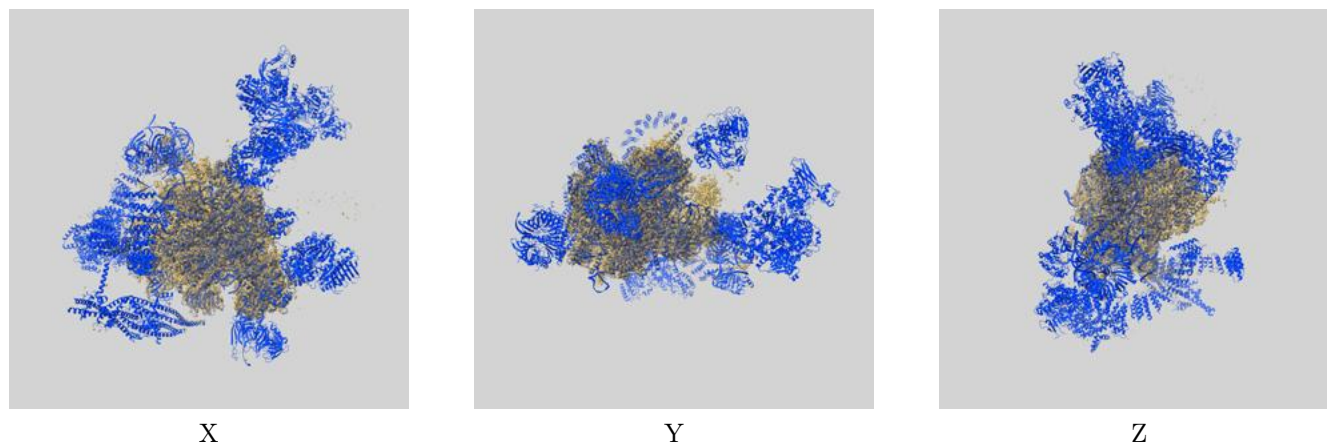
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.48	7.49	4.63

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.48 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

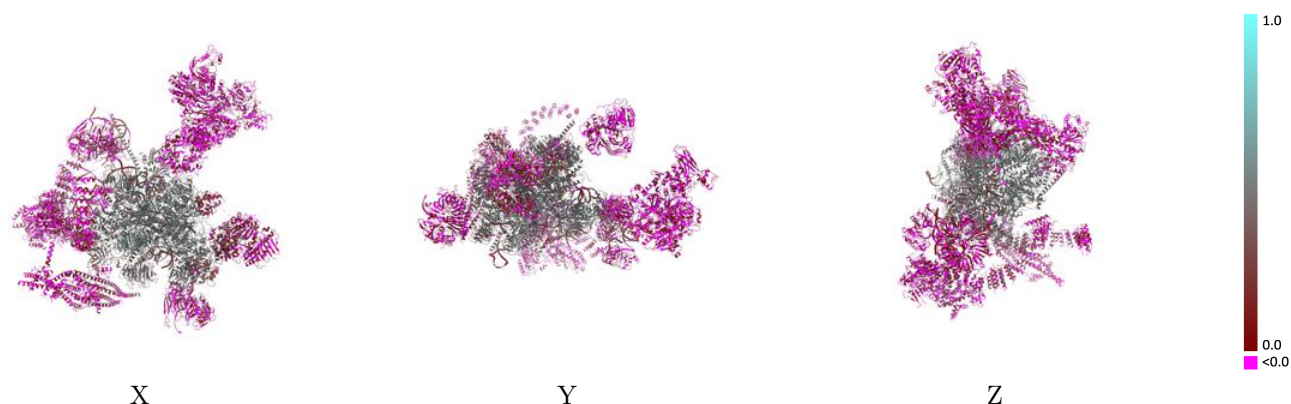
This section contains information regarding the fit between EMDB map EMD-6721 and PDB model 5XJC. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



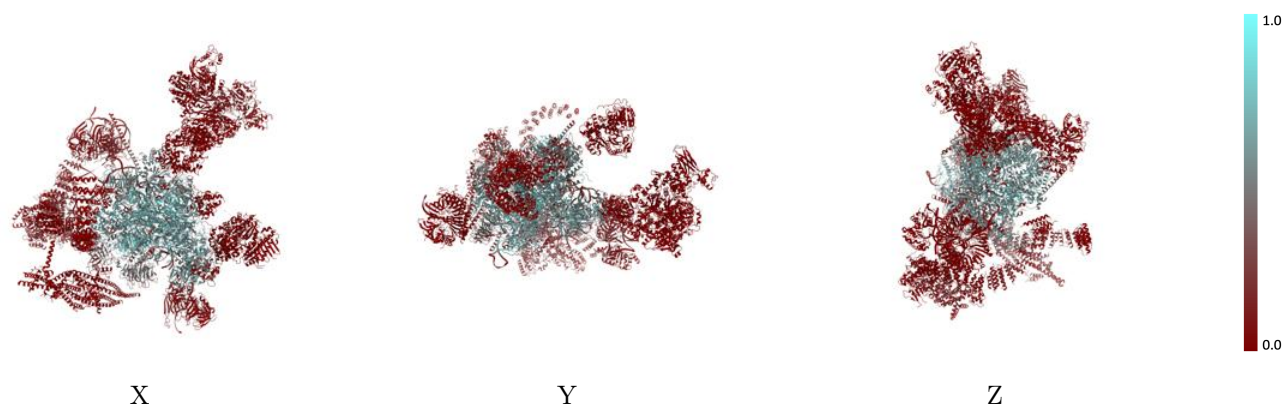
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



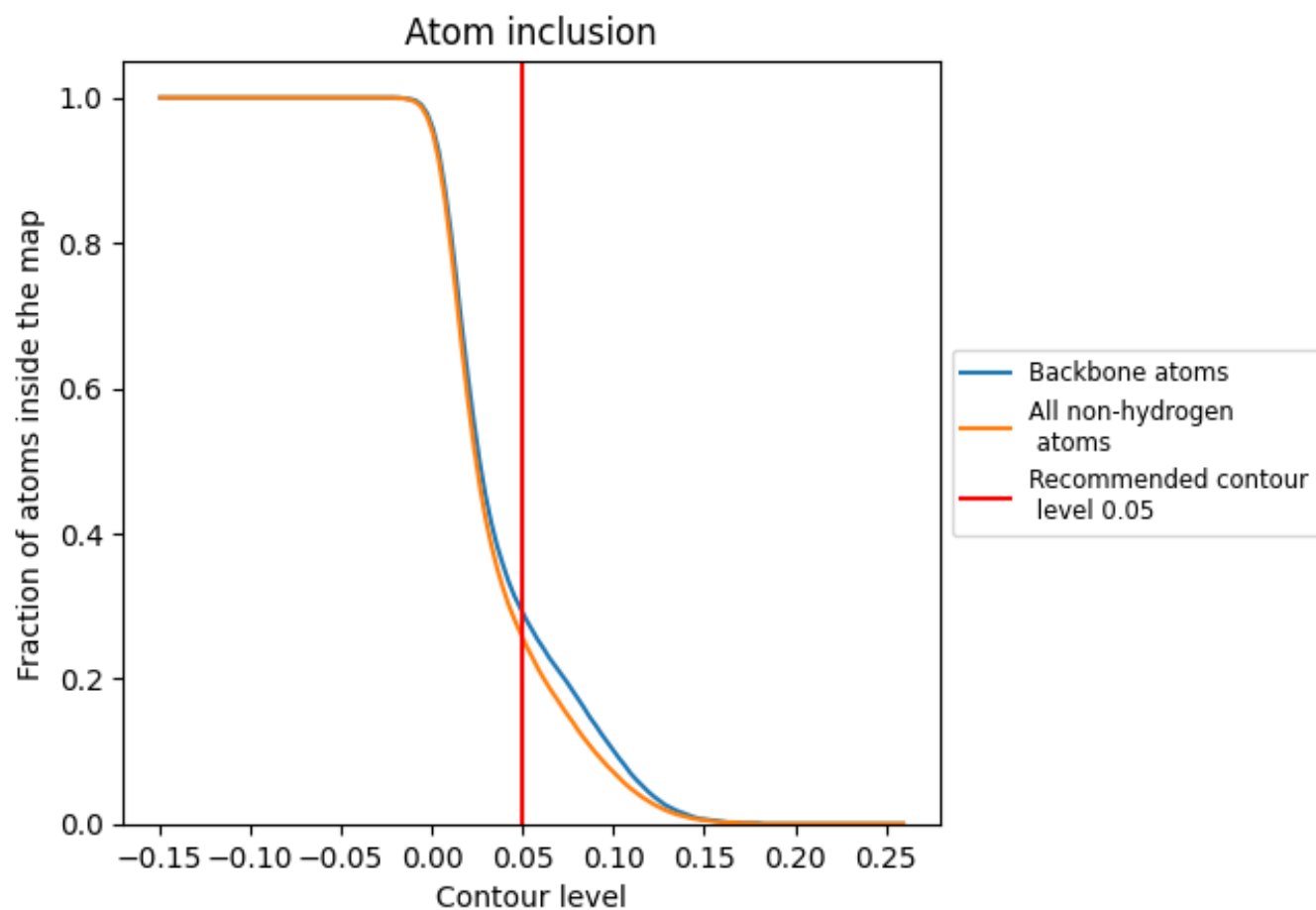
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 29% of all backbone atoms, 26% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.2560	 0.2200
A	 0.5640	 0.4190
B	 0.5240	 0.3110
C	 0.5120	 0.4170
D	 0.0000	 0.0040
E	 0.3880	 0.4040
F	 0.6060	 0.3820
G	 0.3400	 0.2520
H	 0.2000	 0.1500
I	 0.0060	 0.0560
J	 0.3380	 0.2840
K	 0.0030	 0.1110
L	 0.3250	 0.2780
M	 0.4910	 0.4280
N	 0.6470	 0.4810
O	 0.4250	 0.4380
P	 0.4330	 0.4200
Q	 0.0000	 0.0010
R	 0.4730	 0.4290
S	 0.2880	 0.3640
T	 0.7080	 0.5000
U	 0.7010	 0.5090
V	 0.0960	 0.1920
W	 0.4500	 0.4070
X	 0.2420	 0.3880
Y	 0.0400	 0.0400
Z	 0.4240	 0.4540
a	 0.0000	 0.0300
b	 0.0000	 0.0130
c	 0.0000	 -0.0140
d	 0.0000	 0.0020
e	 0.0000	 0.0320
f	 0.0000	 0.0120
g	 0.0000	 0.0170
h	 0.0110	 0.0680



Continued on next page...

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Chain	Atom inclusion	Q-score
i	 0.0040	 0.0110
j	 0.0090	 -0.0050
k	 0.0040	 0.0070
l	 0.0050	 -0.0070
m	 0.0160	 0.0990
n	 0.0190	 0.0720
o	 0.0010	 0.0030
p	 0.0010	 0.0030
q	 0.0000	 -0.0090
r	 0.0000	 0.0390
s	 0.0000	 0.0600
t	 0.0000	 0.0090
u	 0.0060	 0.1250
v	 0.0010	 0.0320
w	 0.0000	 0.0570
x	 0.0000	 0.0030