



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 01:47 AM UTC

PDB ID : 7W5B / pdb_00007w5b
EMDB ID : EMD-32321
Title : The cryo-EM structure of human C* complex
Authors : Zhan, X.; Lu, Y.; Shi, Y.
Deposited on : 2021-11-29
Resolution : 4.30 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:

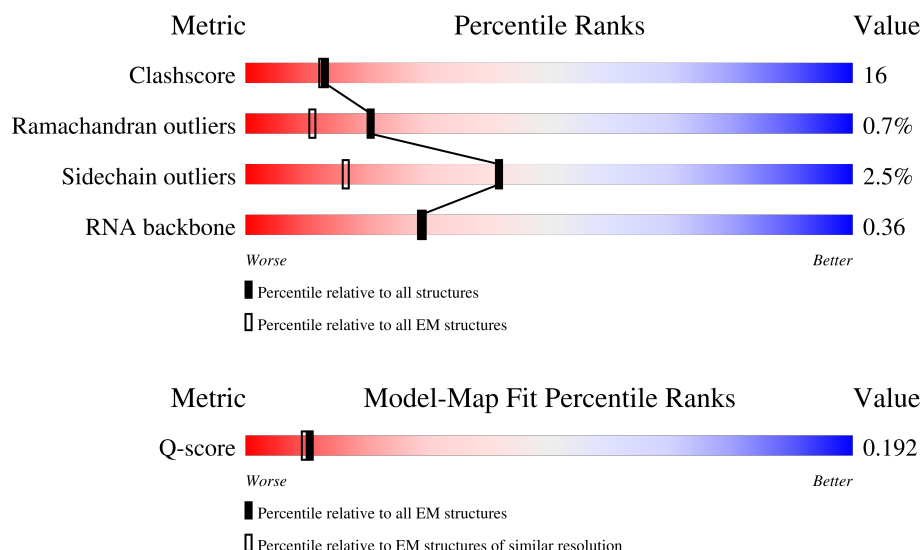
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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

The reported resolution of this entry is 4.30 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	4585 (3.80 - 4.80)

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	A	2335	
2	B	117	
3	C	972	

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Mol	Chain	Length	Quality of chain
4	D	2136	
5	E	357	
6	F	107	
7	4	46	
8	G	174	
9	H	188	
10	I	855	
11	J	848	
12	K	225	
13	L	802	
14	M	243	
15	N	144	
16	O	420	
17	P	229	
18	Q	1485	
19	R	536	
20	S	166	
21	T	514	
22	U	2752	
23	V	908	
24	W	579	
25	Y	1220	
26	Z	758	
27	2	184	
28	z	112	

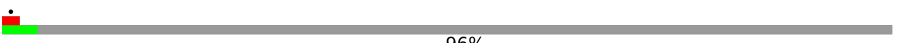
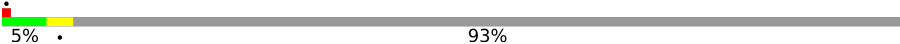
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Mol	Chain	Length	Quality of chain
29	b	240	
29	i	240	
30	y	301	
31	a	126	
31	h	126	
32	c	119	
32	j	119	
33	d	118	
33	k	118	
34	f	86	
34	m	86	
35	e	92	
35	l	92	
36	g	76	
36	n	76	
37	q	504	
37	r	504	
37	s	504	
37	t	504	
38	o	255	
39	p	225	
40	l	586	
41	v	146	
42	w	174	
43	u	411	

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Mol	Chain	Length	Quality of chain
44	x	703	 96%
45	3	415	 5% 93%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
46	IHP	A	3000	-	-	X	-

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 106538 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
			17748	11367	3144	3167	70		

- 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
			6787	4339	1136	1281	31		

- 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	0	0
			8530	5086	1722	1722		

- 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	4	13	Total	C	N	O	P	0	0
			276	123	50	90	13		

- Molecule 8 is a RNA chain called Pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	82	Total	C	N	O	P	0	0
			1510	666	210	552	82		

- Molecule 9 is a RNA chain called U2 snRNA.

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

- Molecule 10 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	618	Total	C	N	O	S	0	0
			3857	2389	722	735	11		

- Molecule 11 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	569	Total	C	N	O	S	0	0
			3819	2379	718	716	6		

- Molecule 12 is a protein called Pre-mRNA-splicing factor SPF27.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	155	Total	C	N	O		0	0
			772	462	155	155			

- Molecule 13 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	437	Total	C	N	O	S	0	0
			3015	1859	584	565	7		

- Molecule 14 is a protein called Pre-mRNA-splicing factor SYF2.

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

- Molecule 15 is a protein called Protein BUD31 homolog.

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

- Molecule 16 is a protein called Pre-mRNA-splicing factor RBM22.

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

- Molecule 17 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	113	Total	C	N	O	S	0	0
			953	583	189	179	2		

- Molecule 18 is a protein called RNA helicase aquarius.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Q	1322	Total	C	N	O	4	0
			6562	3918	1322	1322		

- Molecule 19 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	280	Total	C	N	O	P S	0	0
			2243	1401	411	416	2 13		

- Molecule 20 is a protein called Peptidyl-prolyl cis-trans isomerase-like 1.

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

- Molecule 21 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	312	Total	C	N	O	S	0	0
			2454	1550	446	450	8		

- Molecule 22 is a protein called Serine/arginine repetitive matrix protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	72	Total	C	N	O	S	0	0
			422	257	82	82	1		

- Molecule 23 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	452	Total	C	N	O	S	0	0
			2632	1639	492	495	6		

- Molecule 24 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	509	Total	C	N	O	S	0	0
			4129	2628	715	762	24		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	667	Total	C	N	O	S	4	0
			3431	2057	680	693	1		

- Molecule 26 is a protein called Cactin.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	122	Total	C	N	O	S	0	0
			1084	712	197	173	2		

- Molecule 27 is a protein called PRKR-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	2	123	Total	C	N	O	S	0	0
			1013	635	193	180	5		

- Molecule 28 is a protein called Protein FAM32A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	z	60	Total	C	N	O	S	0	0
			496	306	96	92	2		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	102	Total	C	N	O	S	0	0
			786	492	148	139	7		
29	i	86	Total	C	N	O	S	0	0
			690	434	126	123	7		

- Molecule 30 is a protein called Peptidyl-prolyl cis-trans isomerase E.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	y	79	Total	C	N	O	0	0
			390	232	79	79		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	77	Total	C	N	O	S	0	0
			609	381	108	115	5		
31	h	81	Total	C	N	O	S	0	0
			633	397	112	118	6		

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

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

- Molecule 33 is a protein called Small nuclear ribonucleoprotein Sm D2.

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

- Molecule 34 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	74	Total	C	N	O	S	0	0
			576	373	95	103	5		
34	m	73	Total	C	N	O	S	0	0
			566	367	93	101	5		

- Molecule 35 is a protein called Small nuclear ribonucleoprotein E.

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

- Molecule 36 is a protein called Small nuclear ribonucleoprotein G.

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

- Molecule 37 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	q	132	Total	C	N	O	0	0
			659	395	132	132		
37	r	131	Total	C	N	O	0	0
			654	392	131	131		
37	s	132	Total	C	N	O	0	0
			659	395	132	132		
37	t	131	Total	C	N	O	0	0
			654	392	131	131		

- Molecule 38 is a protein called U2 small nuclear ribonucleoprotein A'.

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

- Molecule 39 is a protein called U2 small nuclear ribonucleoprotein B'.

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

- Molecule 40 is a protein called Pre-mRNA-splicing factor SLU7.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	1	269	Total	C	N	O	S	0	0
			2209	1389	394	418	8		

- Molecule 41 is a protein called Protein mago nashi homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	v	144	Total	C	N	O	0	0
			711	423	144	144		

- Molecule 42 is a protein called RNA-binding protein 8A.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	w	91	Total	C	N	O	0	0
			445	263	91	91		

- Molecule 43 is a protein called Eukaryotic initiation factor 4A-III.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	u	386	Total	C	N	O	0	0
			1907	1135	386	386		

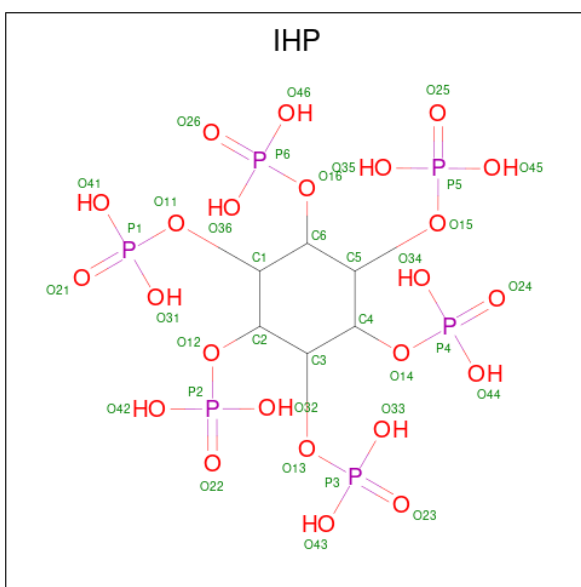
- Molecule 44 is a protein called Protein CASC3.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	x	25	Total	C	N	O	0	0
			124	74	25	25		

- Molecule 45 is a protein called NF-kappa-B-activating protein.

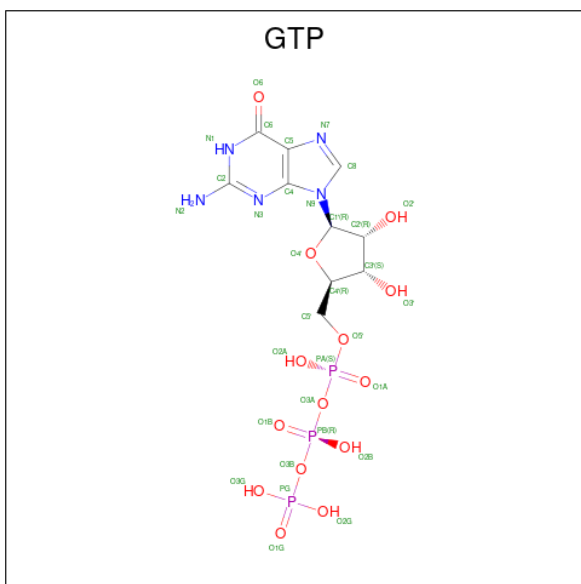
Mol	Chain	Residues	Atoms					AltConf	Trace
45	3	30	Total	C	N	O	S	0	0
			230	140	43	45	2		

- Molecule 46 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: C₆H₁₈O₂₄P₆) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 47 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).



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

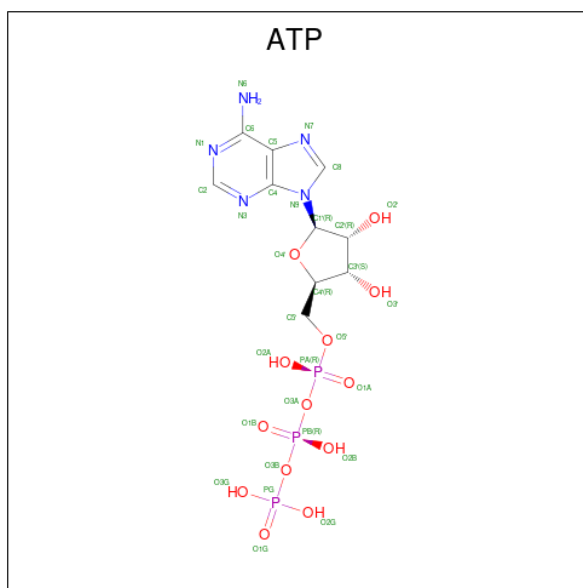
- Molecule 48 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
48	C	1	Total	Mg	0
			1	1	
48	F	6	Total	Mg	0
			6	6	
48	Q	2	Total	Mg	0
			2	2	

- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
49	N	3	Total	Zn	0
			3	3	
49	O	3	Total	Zn	0
			3	3	
49	1	1	Total	Zn	0
			1	1	

- Molecule 50 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).

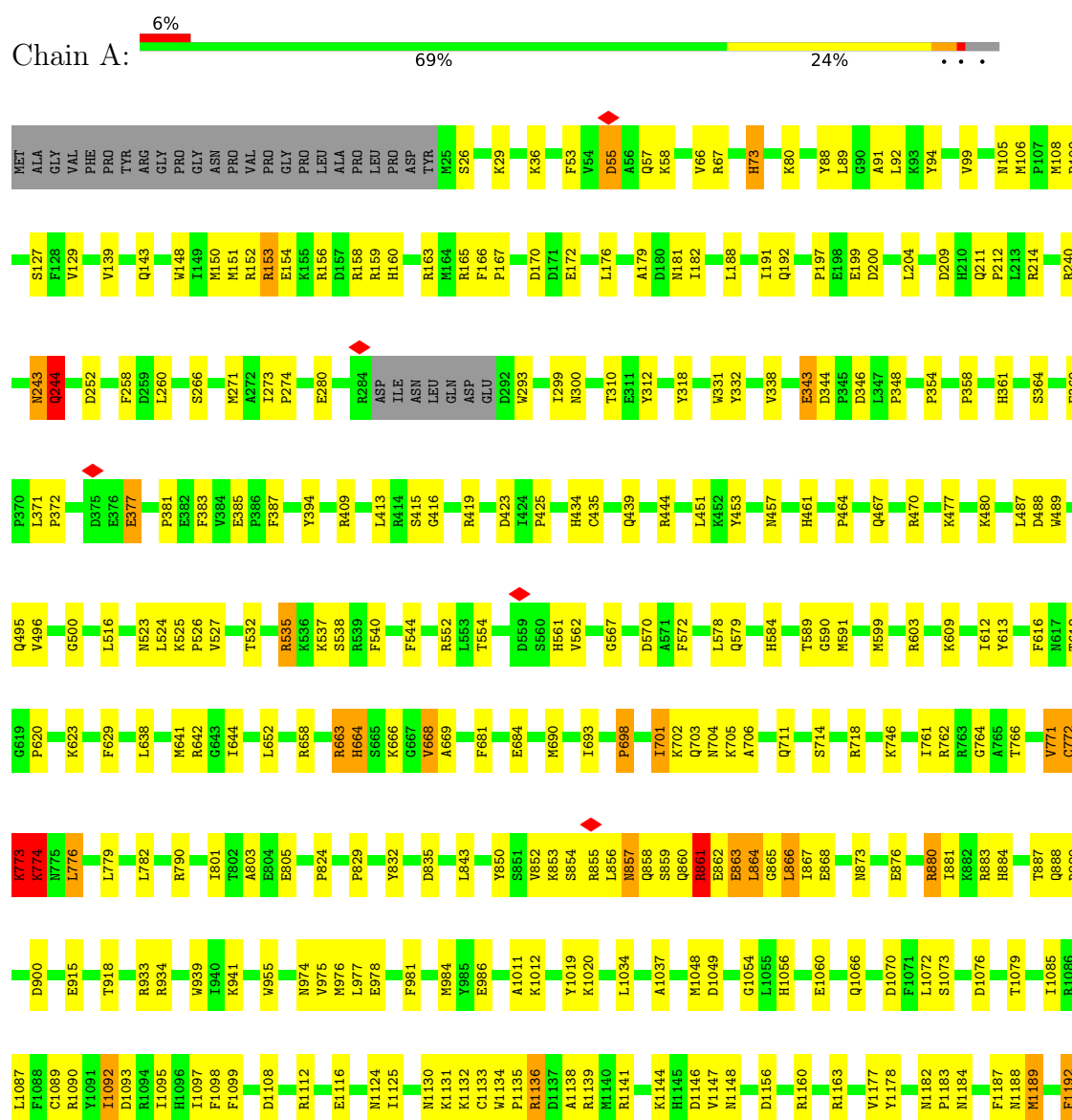


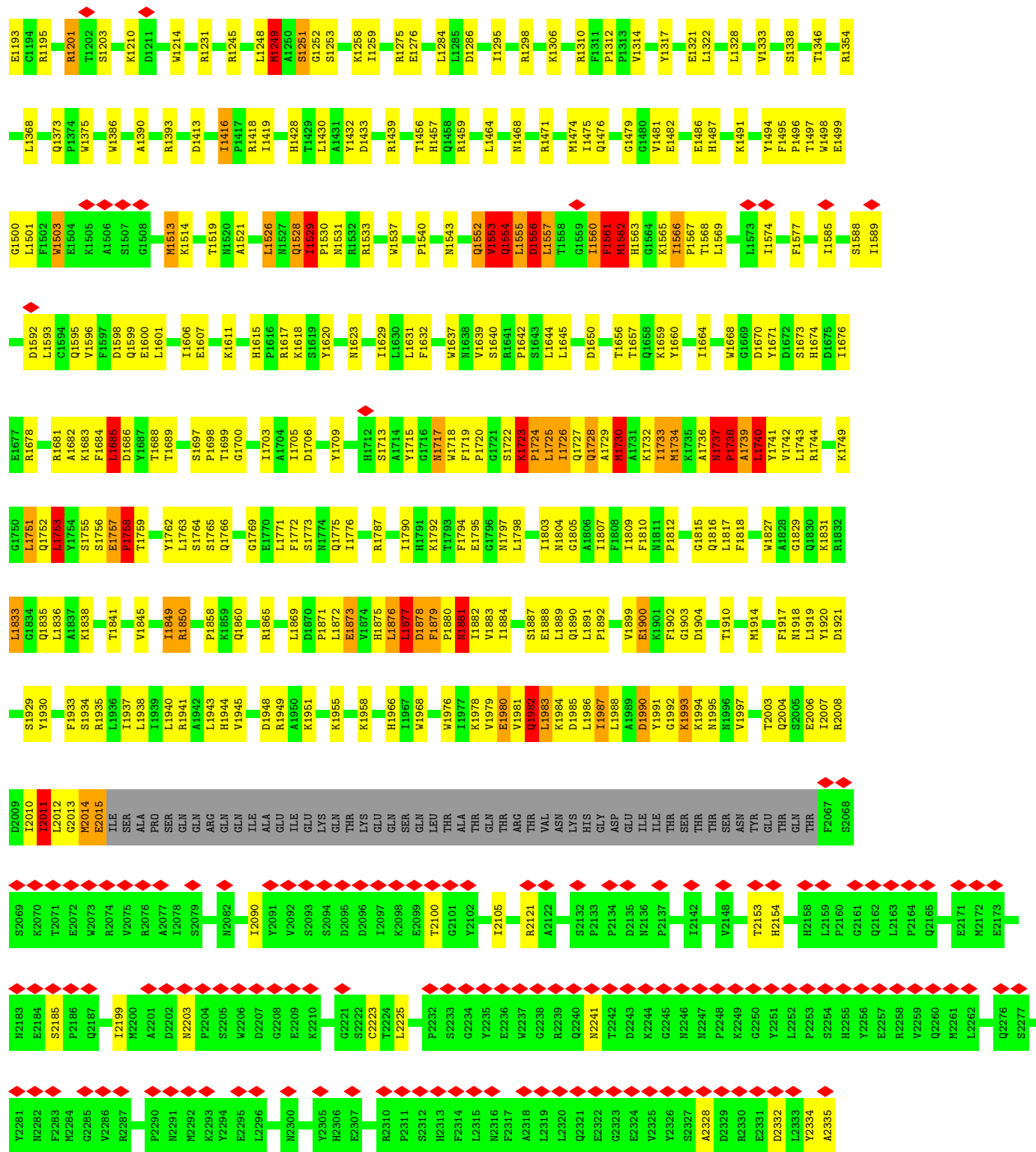
Mol	Chain	Residues	Atoms					AltConf
50	Q	1	Total	C	N	O	P	0
			31	10	5	13	3	

3 Residue-property plots

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

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





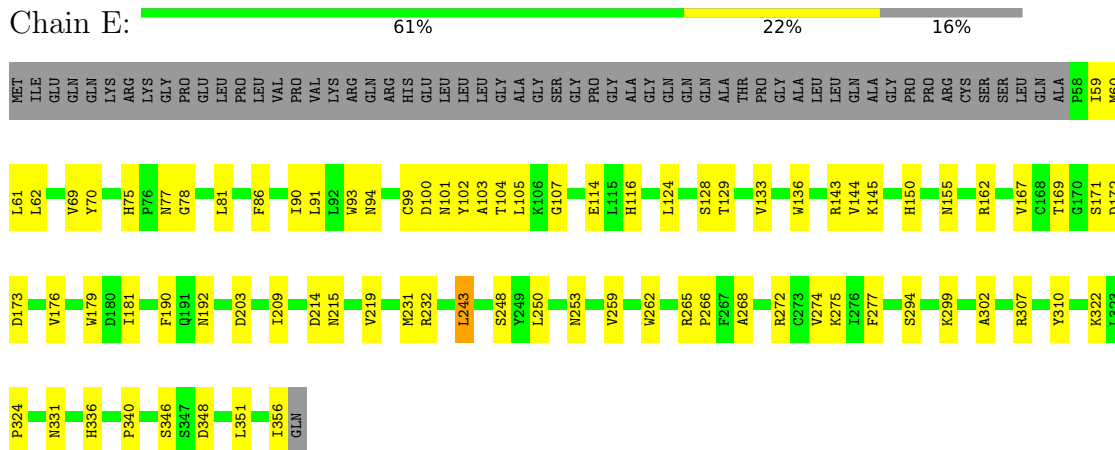
• Molecule 2: U5 snRNA



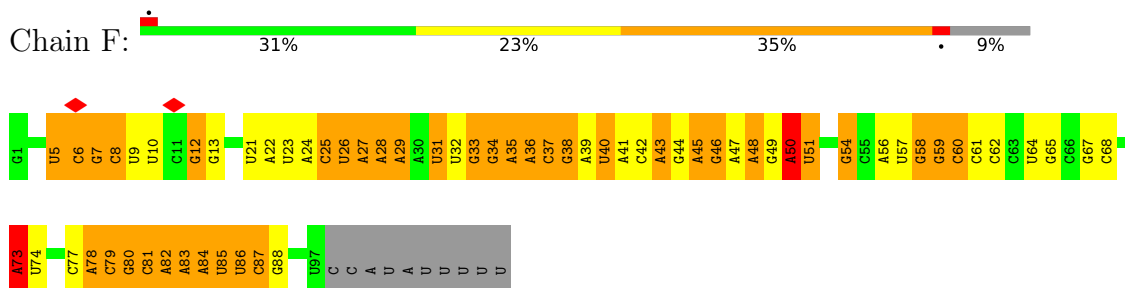


L2019	Y1959	A1897	F1832	V1752	I1641	R1570	R1475	E1395	P1306	E1212	R1133	E1054
S2020	L1960	H1898	S1833	D1753	V1645	L1571	Y1476	K1396	L1307	K1213	R1134	P1055
Y2021	K1961	L1899	M1834			T1572	I1477	F1397	P1308	G1216	K1135	S1056
E2022	Q1962	S1900	L1835	T1756	D1665	T1578	S1478	Q1398	V1309		L1136	A1057
V2023	L1963	R1901	L1836	N1772	T1666	T1579	Q1479	R1400	S1310	W1222	E1137	K1058
V2024	P1964	M1902	A1838		M1670	C1580	S1480	L1401	A1311		E1138	I1059
D2025	H1965	Q1903	K1839	I1776	A1675	A1581	I1481	N1402	L1312	E1226	V1139	N1060
K2026	F1966	S1905	T1840	S1777	A1676	D1583	R1482	K1403	R1313	D1227	V1140	I1061
D2027	P1967	A1906	K1841	H1778	Y1676	A1582	R1483	K1404	K1314	V1228	K1141	L1062
S2028	S1968	E1907	V1842	H1779		I1584	P1484	V1405	S1315			
I2029	E1969	L1908	Q1585	R1586	Y1679	Q1585	S1491	A1316	A1316	D1229	K1142	F1066
R2030	H1970	Q1909	R1587	Q1587	P1680	R1587	K1498	F1317	E1318	S1230	I1143	
S2031	I1971	S1910	I1681	Y1682	T1680	L1590	A1501	G1410	E1319	E1231	E1144	L1070
G2032	K1972	D1911	Y1682			H1591	H1502	E1411	S1319	EL237	K1145	K1071
G2033	R1973	T1912	Q1686			C1592	W1503	T1412	L1320		K1146	L1072
P2034	C1974	E1913	A1691	S1786		E1591	H1502	S1413	Y1321	K1242	N1147	E1073
V2035	D1975	E1914	E1787	E1787		C1592	W1503	T1414	Q1322		F1148	G1074
V2036	D1976	L1915	A1691	L1788		T1593	L1504	D1415	D1323	E1249	P1149	F1075
V2037	K1977	L1916	N1692	V1789		E1594	G1505	L1416	K1324	H1250	F1150	A1076
L2038	G1978	S1917	R1693	E1790		K1595	C1506	L1417	K1325	I1252	E1151	L1077
V2039	V1979	K1918	P1694	Q1791		D1596	S1507	L1418	F1326	T1253	R1152	M1078
Q2040	E1980	A1919	L1695	L1792		L1597	A1508	L1419	F1327		L1153	A1079
L2041	S1981	I1920	Q1696	D1697		I1598	T1509	G1420	F1328	F1259	Y1154	D1080
E2042	V1982	R1921	D1698	D1698		P1599	S1510	G1422	K1421	E1260	L1156	M1081
R2043	F1983	L1922	C1702			L1600	M1517	N1423	N1329	P1261	N1157	V1082
E2044	D1984	I1923	G1708			E1602	V1518	S1427	I1331	L1262	H1158	V1083
E2045	I1985	Q1924	S1709			K1603	P1520	E1430	Q1332	P1263	N1159	L1084
E2046	M1986	A1925	K1710			L1604	V1521		Q1333	R1269	E1160	T1085
V2047	E1987	L1926	K1711			D1606	P1522		Q1334	V1270	I1161	Q1086
T2048	M1988	D1928	K1716			S1607	L1523		F1336		G1162	S1087
G2049	E1989	L1929	E1720			T1608	L1524		R1437	S1277	E1163	M1092
P2050	E1990	L1930	L1728			L1610	L1525		R1438	C1278	L1164	R1093
V2051	E1991	S1931	L1722			E1611	H1526		W1439	E1279	I1165	A1094
T2052	E1992	I1932	L1722			K1612			K1440	T1280	R1166	I1095
A2053	R1993	Q1933	E1720			L1613	G1529		R1441	Q1281	M1167	F1096
P2054	M1994	M1934	L1722			L1614			R1442	L1282	P1168	E1097
L2055	A1995	W1935	H1727			L1615	H1534		K1443	Q1283	K1169	T1098
P2056	Q1973	L1936	L1728			N1615	T1535		N1444	P1283	M1170	V1099
P2057	L1997	S1937	L1729			N1616	Q1536		V1445	V1284	G1171	L1100
Q2058	Q1998	P1938	H1730			G1616	T1537		Q1446	S1285	K1172	
R2059	L1999	P1938	C1731						I1447		T1173	W1104
R2060	T2000	A1939	F1736			G1623	T1551		I1448	L1289	Y1177	A1105
E2061	D2001	L1940	M1737			L1624	K1552		N1449	L1290		
E2062	S2002	A1941	M1737			S1625	H1553		L1450	L1291	K1183	D1109
G2063	Q2003	E1944	T1742			P1626	S1554		V1452	P1292	L1184	K1110
W2064	I2004	L1945	K1743			M1627	P1555		K1368	E1293	T1111	T1112
A2065	A2005	L1946	T1744			K1628	K1556		L1369	K1294	E1185	N1113
D2066	D2006	Q1947	T1745			L1819	K1557		Q1370	V1296	L1186	L1114
V2067	V2007	T1950	I1746			R1630	K1558		S1371	P1297	S1187	C1115
T2068	A2008	Q1951	E1746			L1631	V1559		S1372	P1298	L1190	K1116
G2069	R2009	A1952	M1747			Q1634	I1560		E1373	T1299	R1195	D1119
D2070	F2010	M1953	K1748			L1635	V1561		G1374	E1300	S1196	
A2071	C2011	W1954	Q1749			F1636	P1564		V1377	L1301	T1197	W1123
S2073	R2013	S1955	D1750			S1637	S1565		E1383	L1302		Q1124
N2074	Y2014	K1956	A1751			S1638	R1566			D1303		S1125
S2075	P2015	D1957								L1304		M1126
L2076	N2016	S1958				A1640				Q1305		C1127
T2077	I2017											
S2078												

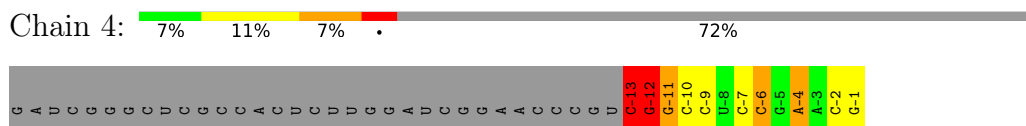
- Molecule 5: U5 small nuclear ribonucleoprotein 40 kDa protein



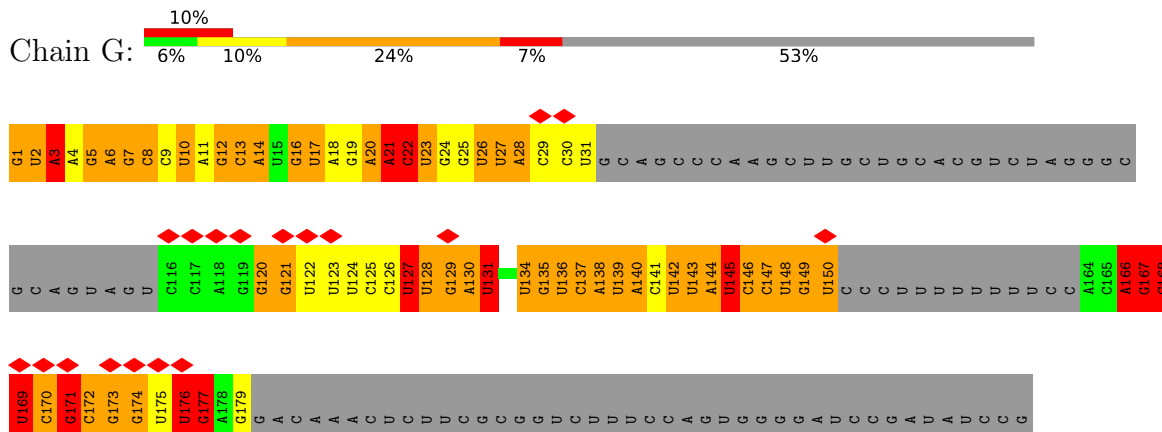
- Molecule 6: U6 snRNA



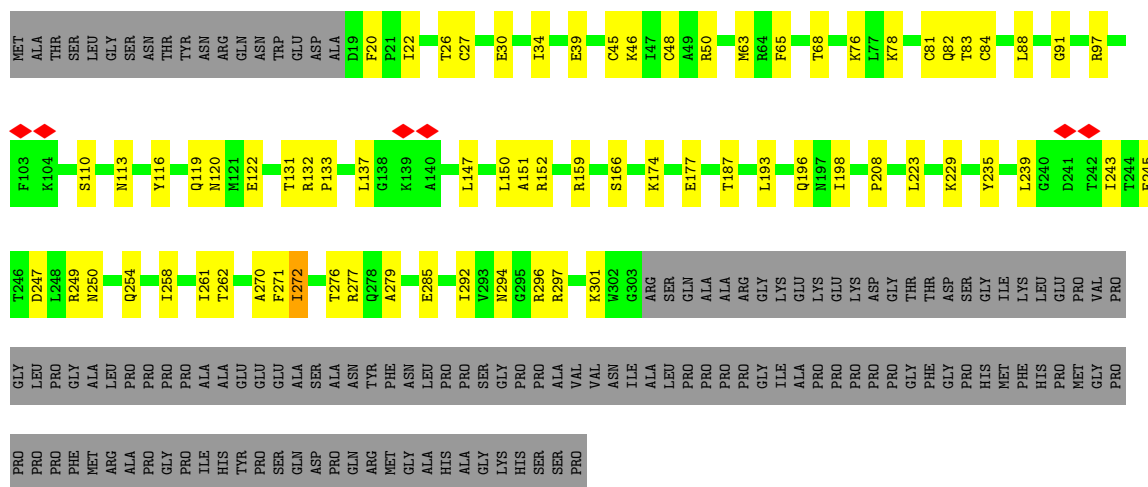
- Molecule 7: Pre-mRNA



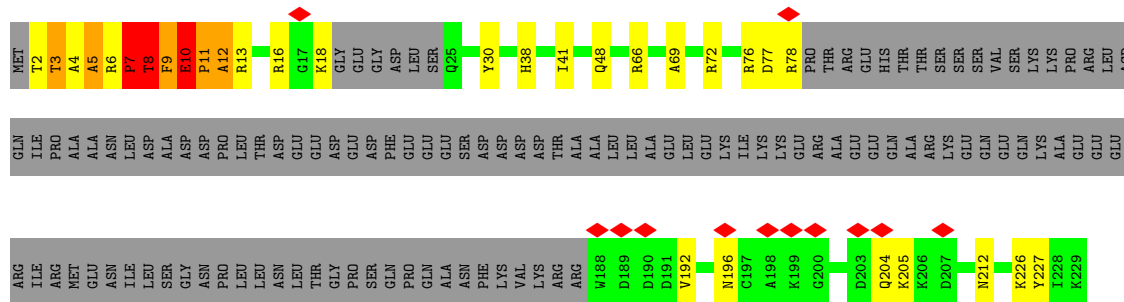
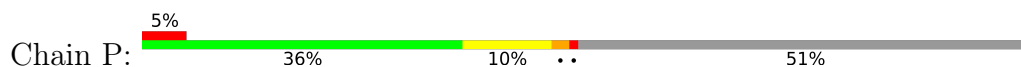
- Molecule 8: Pre-mRNA



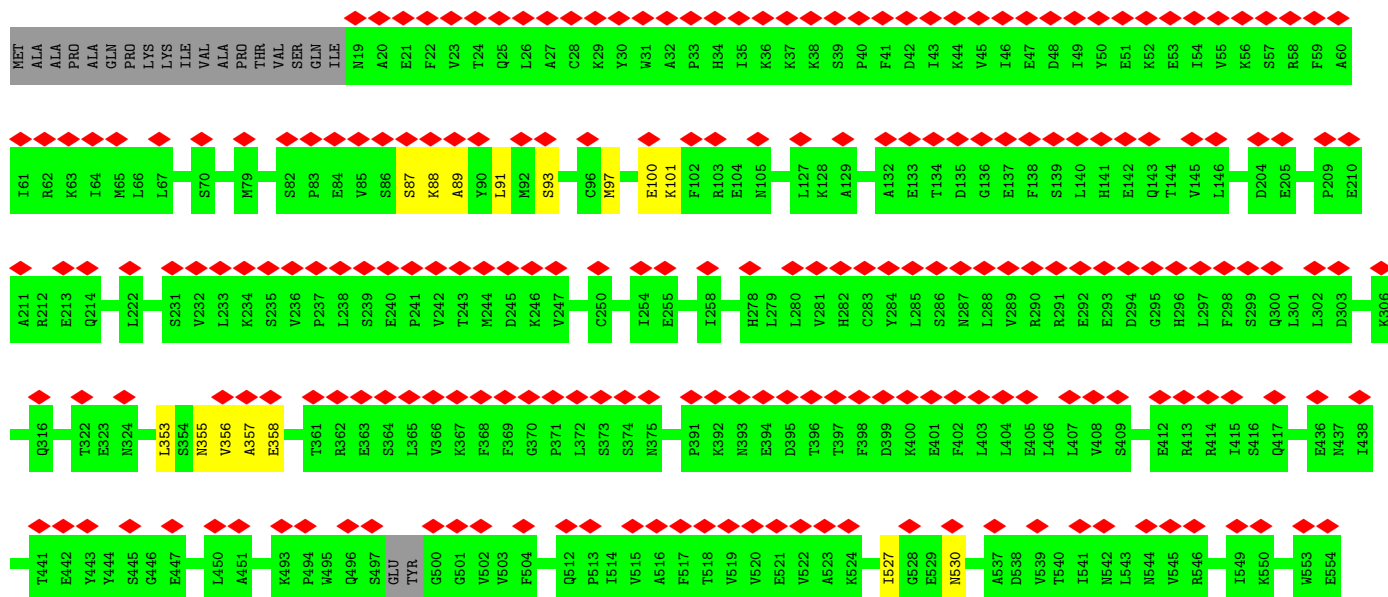
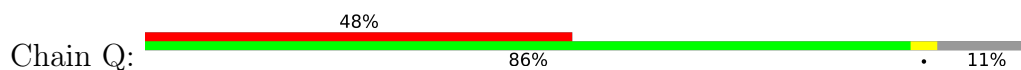


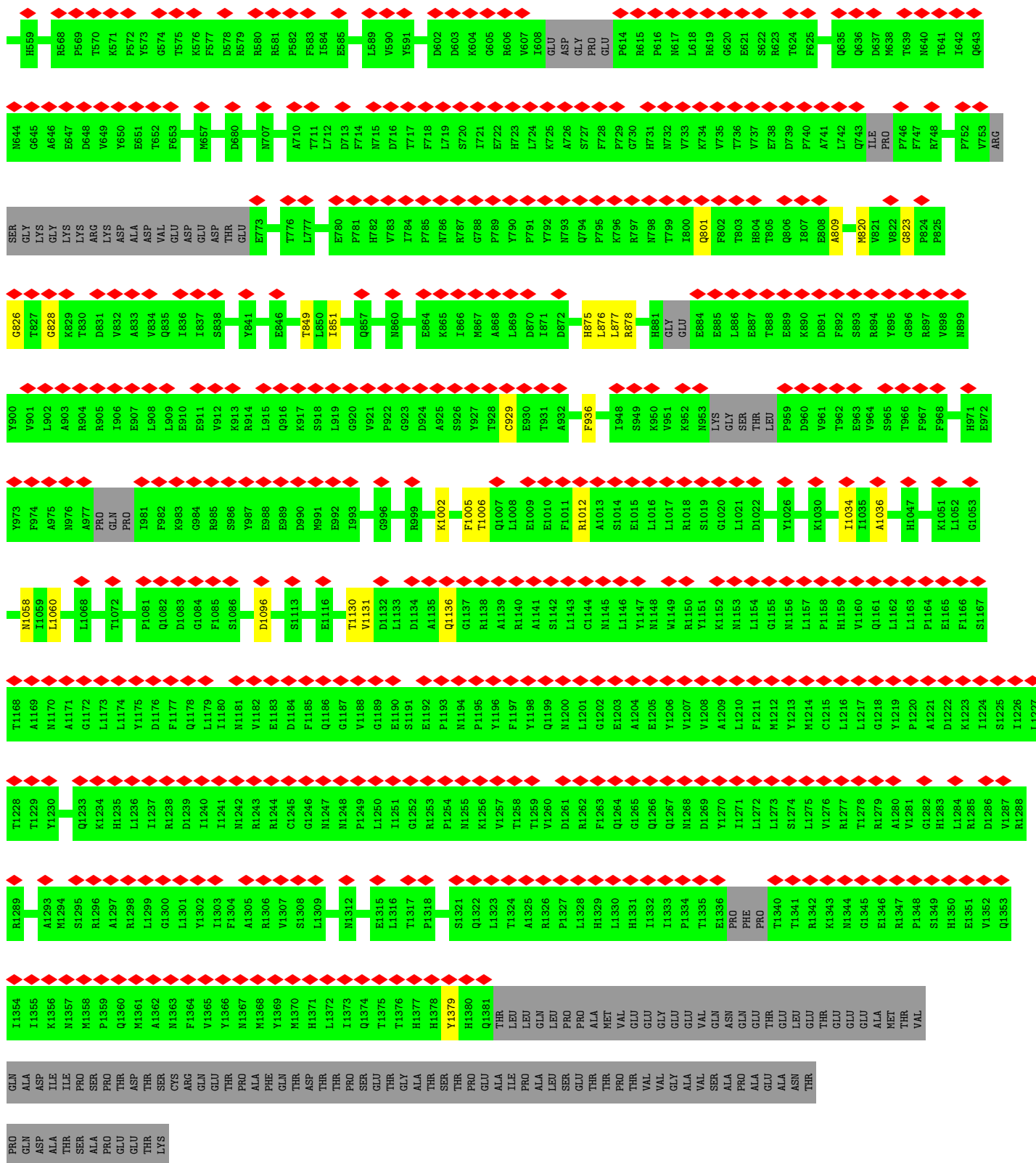


• Molecule 17: Spliceosome-associated protein CWC15 homolog



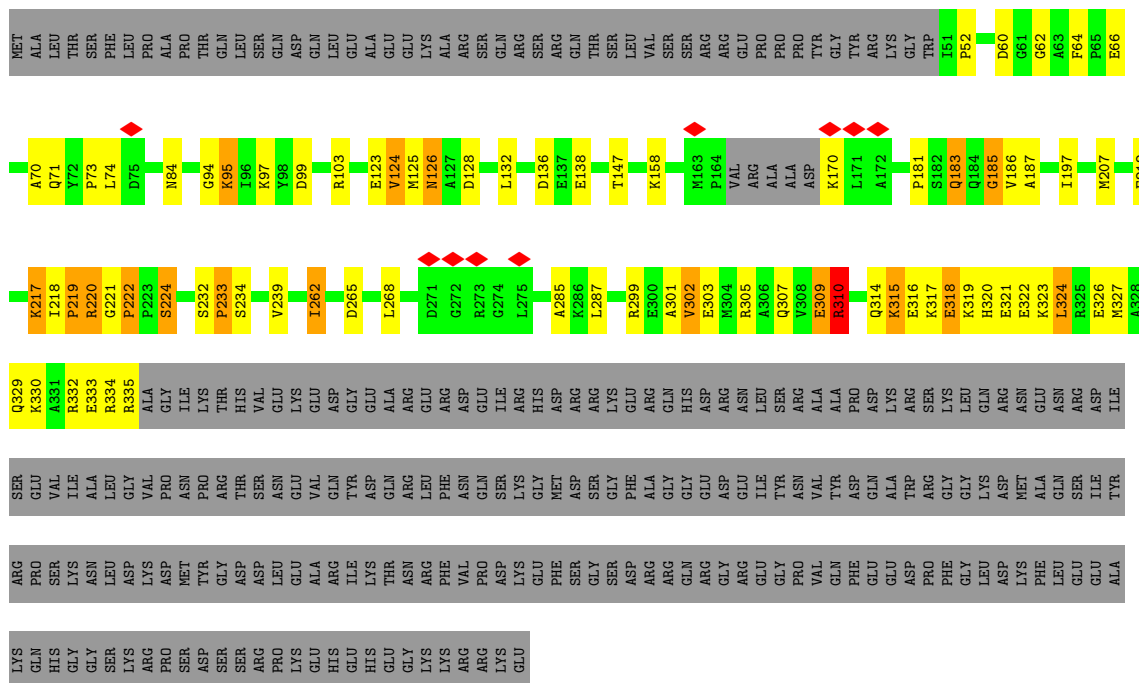
• Molecule 18: RNA helicase aquarius



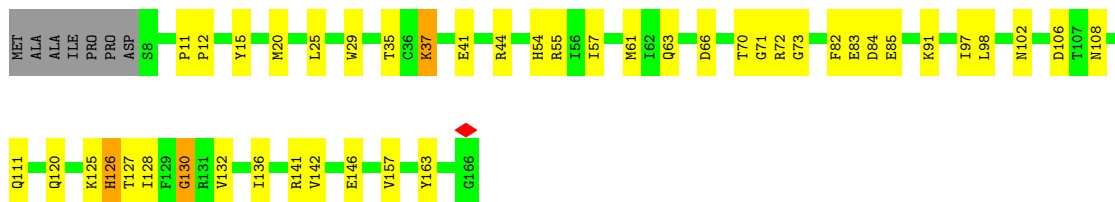


• Molecule 19: SNW domain-containing protein 1

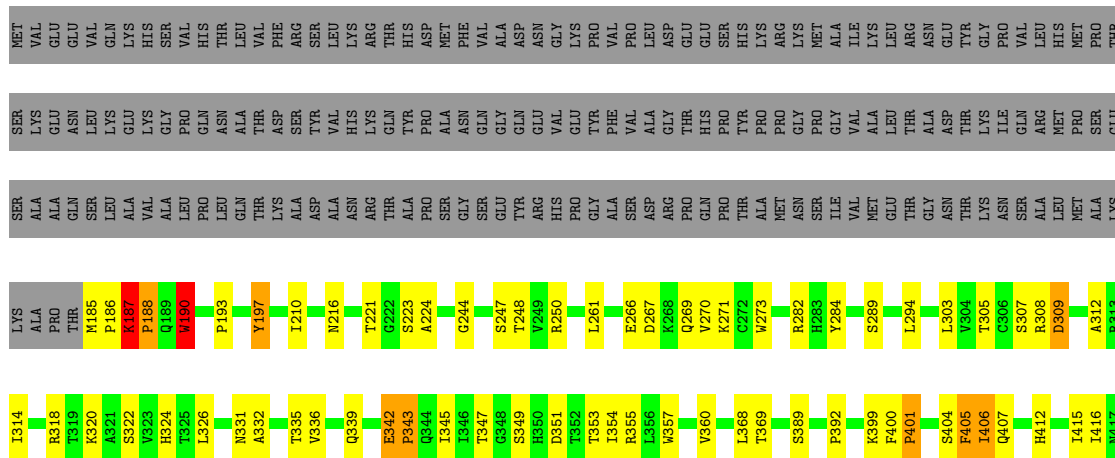
Chain R: 38% 11% 48%



- Molecule 20: Peptidyl-prolyl cis-trans isomerase-like 1



- Molecule 21: Pleiotropic regulator 1







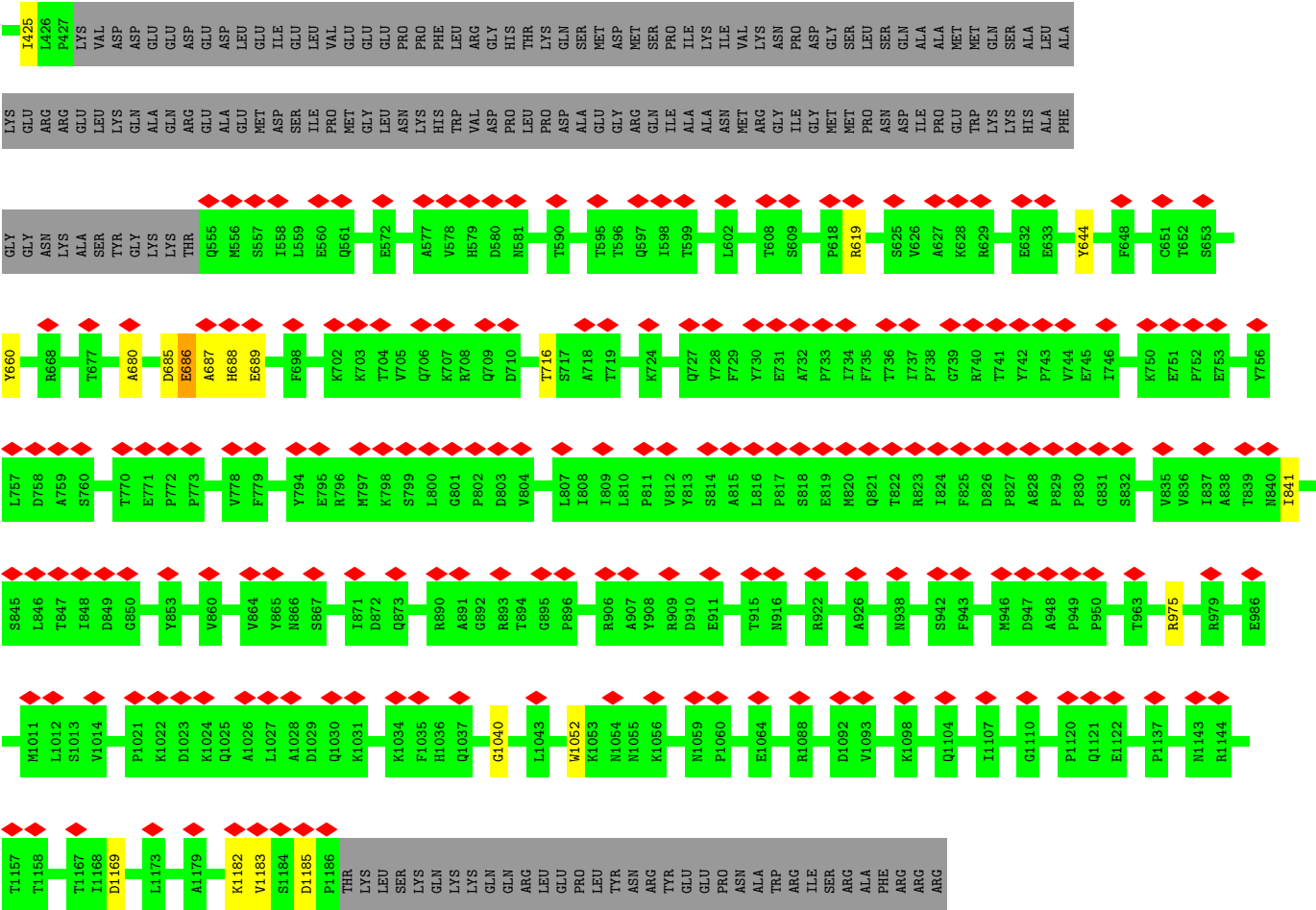
[illegible]

- Molecule 23: Pre-mRNA-splicing factor CWC22 homolog

Chain V: 46% 50%

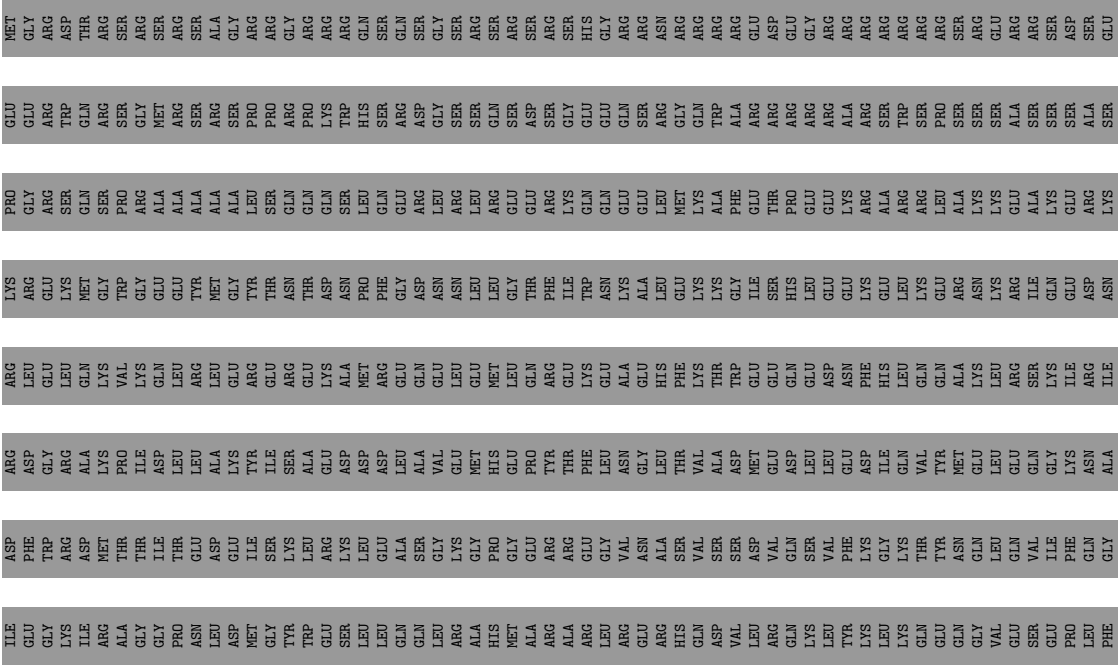
[illegible]

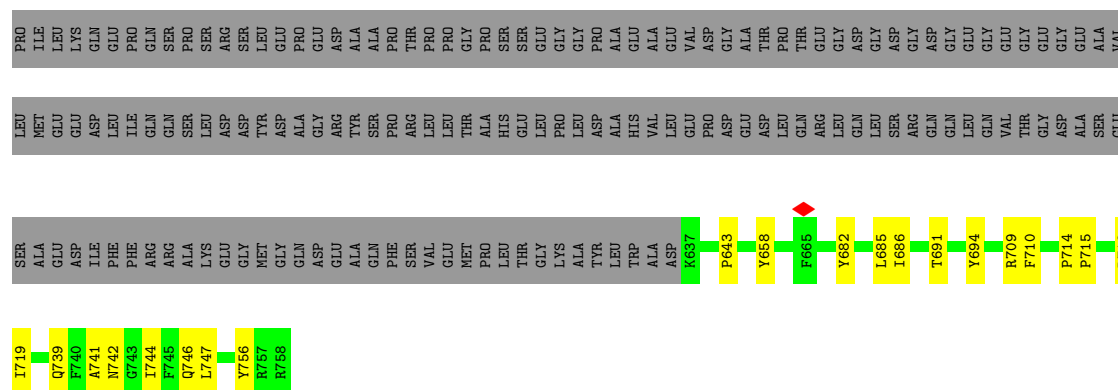




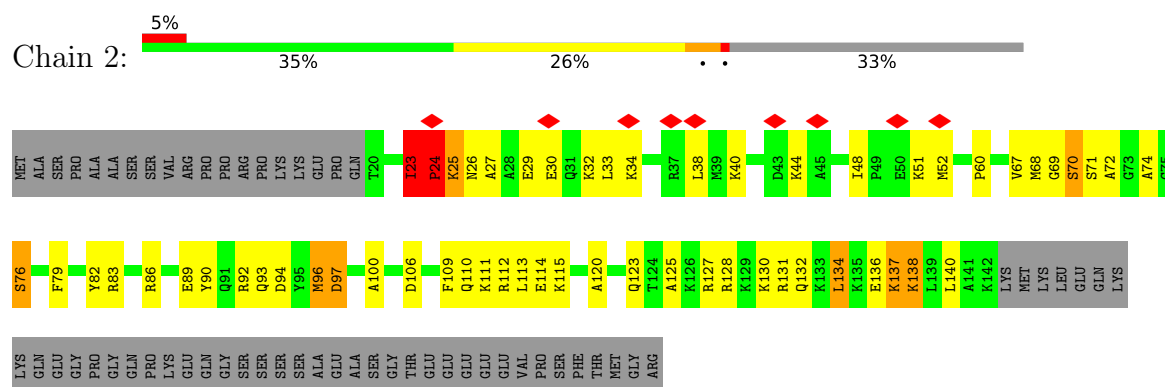
● Molecule 26: Cactin

Chain Z: 13% 84%

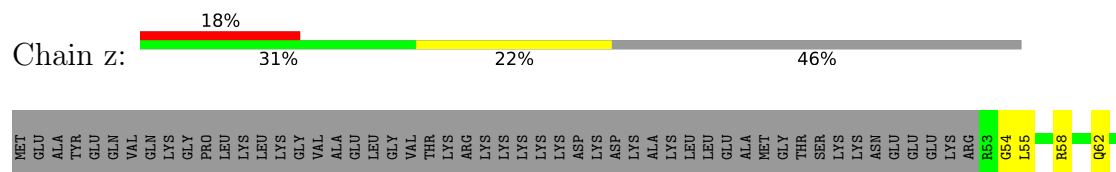




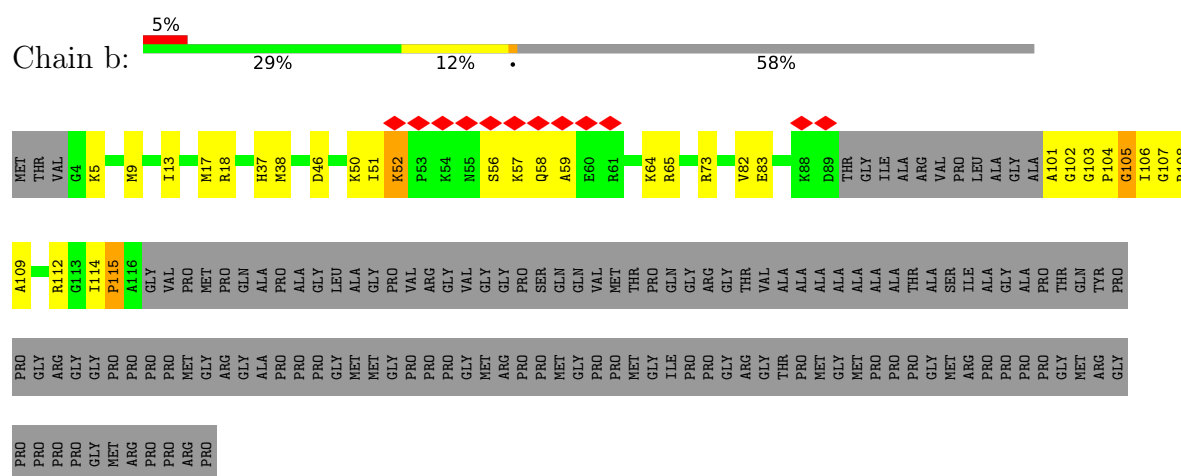
• Molecule 27: PRKR-interacting protein 1

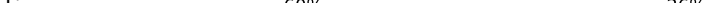


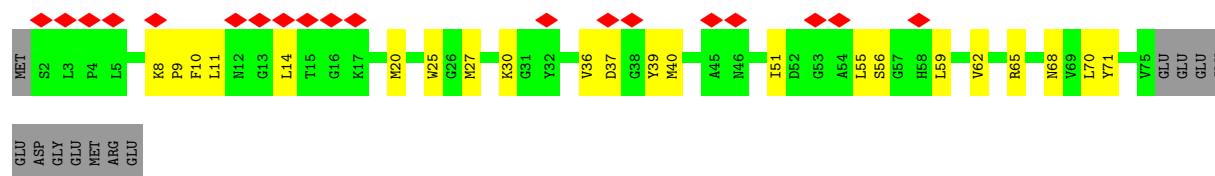
• Molecule 28: Protein FAM32A



• Molecule 29: Small nuclear ribonucleoprotein-associated proteins B and B'

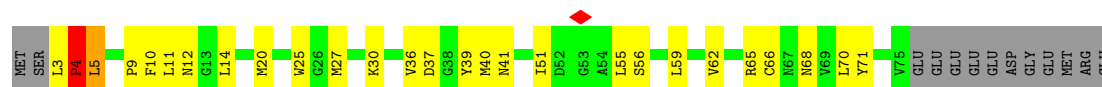


Chain f: 



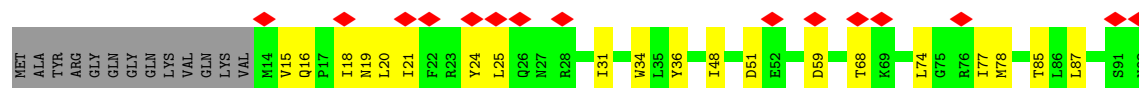
- Molecule 34: Small nuclear ribonucleoprotein F

Chain m: 53% 29% .. 15%



- Molecule 35: Small nuclear ribonucleoprotein E

Chain e: 16% 64% 22% 14%



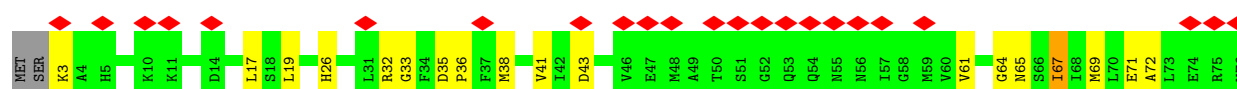
- Molecule 35: Small nuclear ribonucleoprotein E

Chain l: 18% 61% 25% 14%



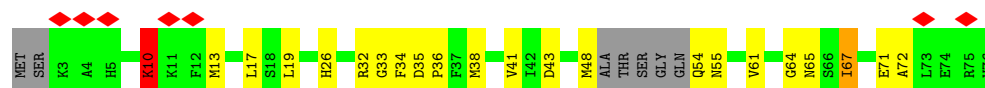
- Molecule 36: Small nuclear ribonucleoprotein G

Chain g: 30% 74% 22% ..

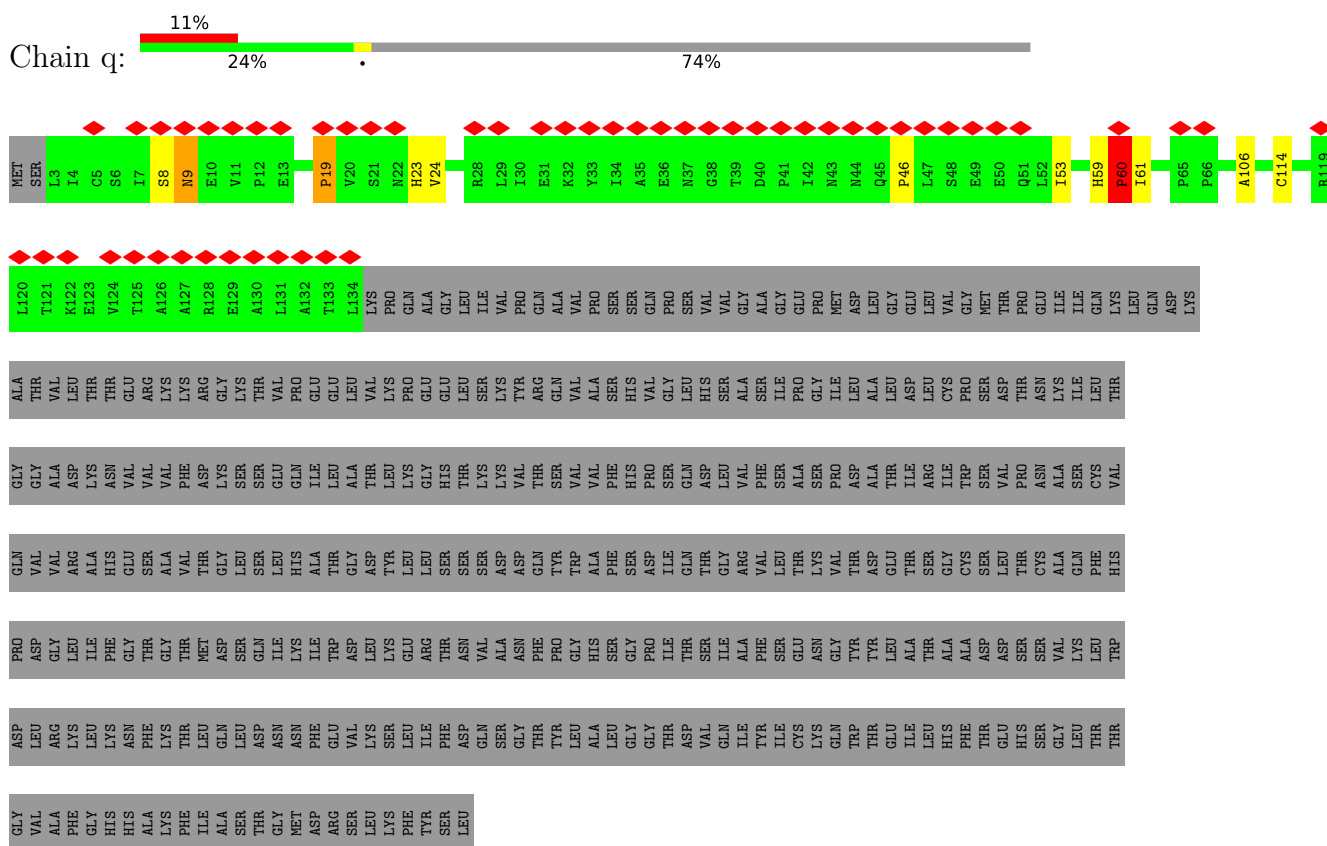


- Molecule 36: Small nuclear ribonucleoprotein G

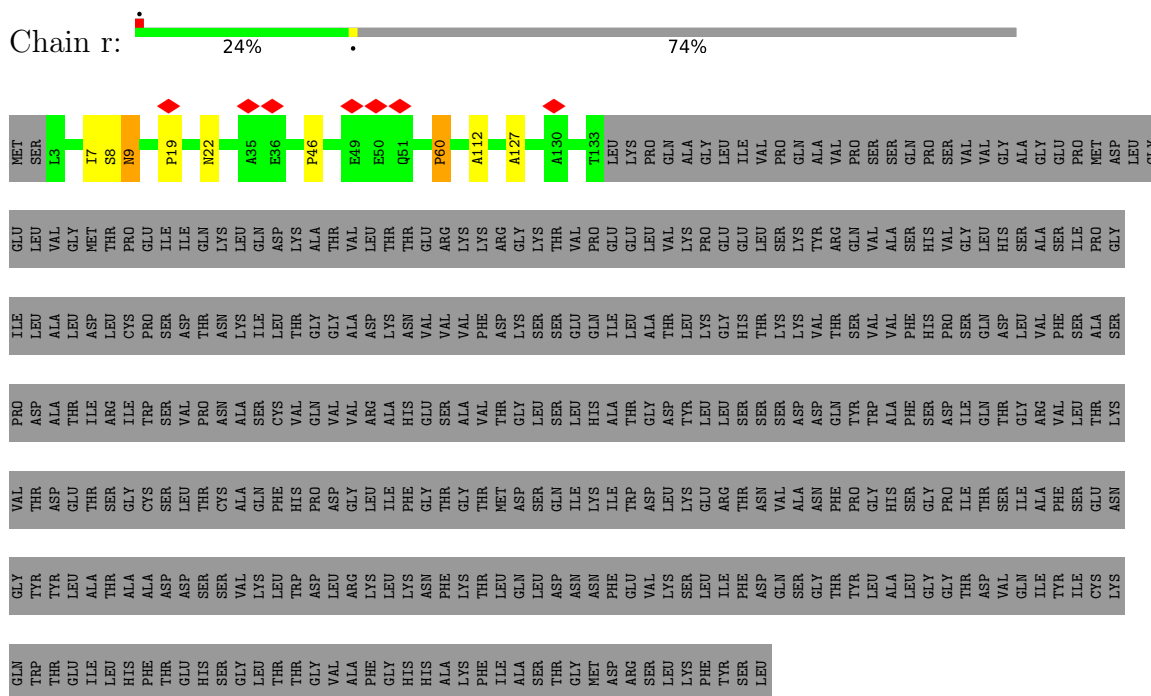
Chain n: 9% 62% 26% .. 9%



- Molecule 37: Pre-mRNA-processing factor 19

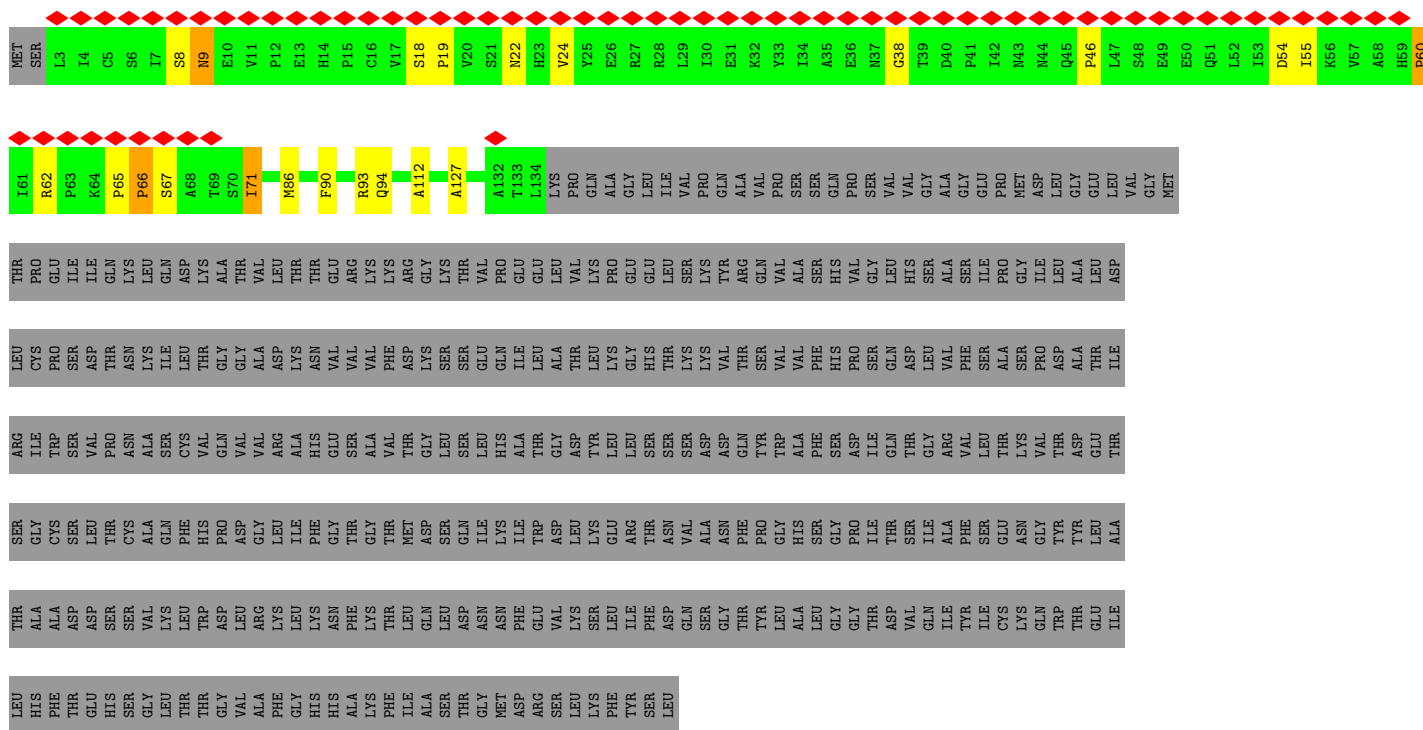


- Molecule 37: Pre-mRNA-processing factor 19

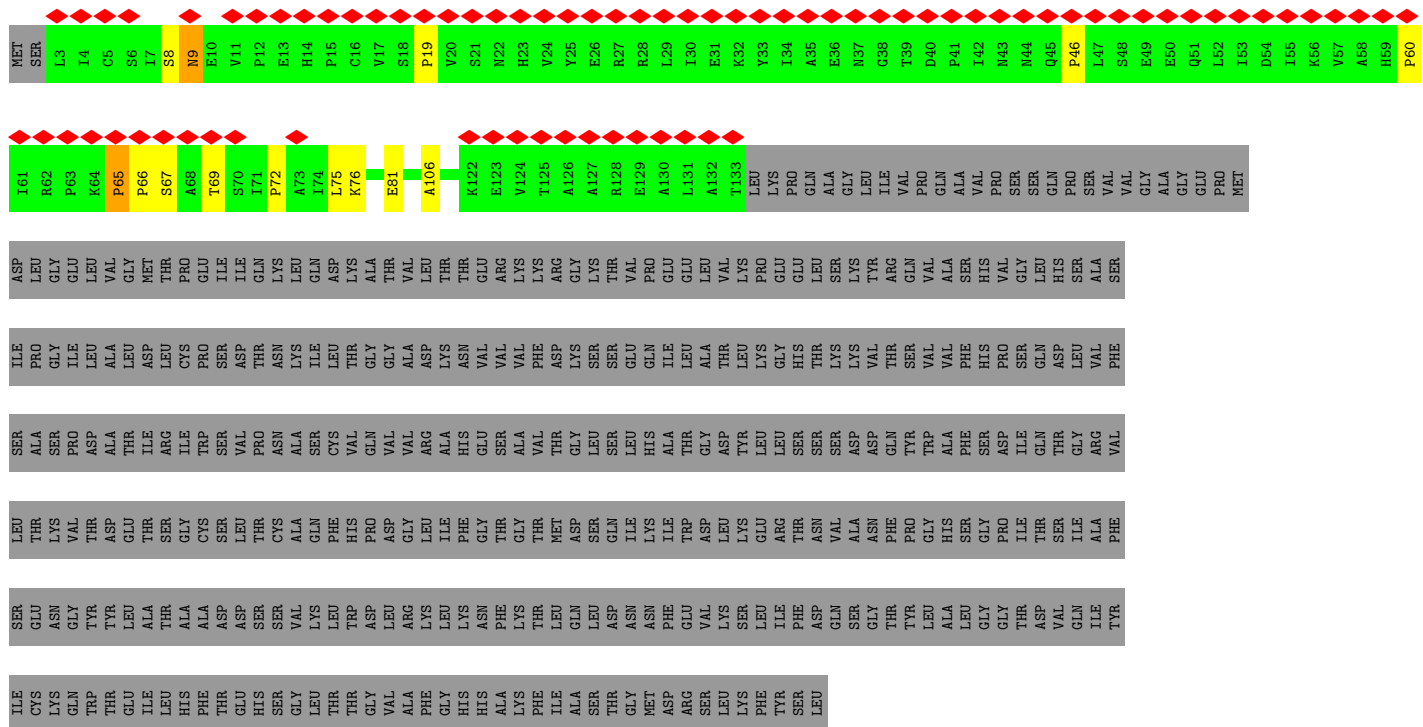


- Molecule 37: Pre-mRNA-processing factor 19





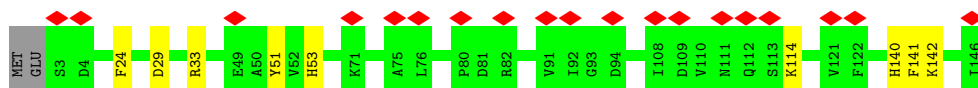
- Molecule 37: Pre-mRNA-processing factor 19



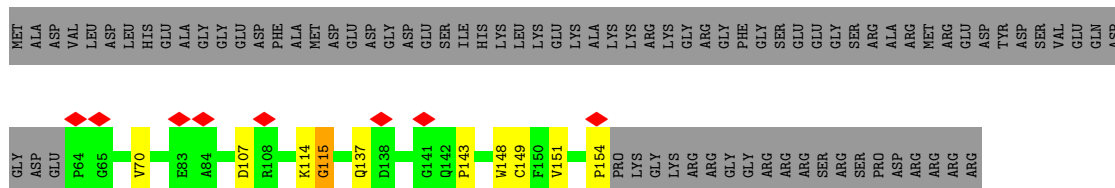
- Molecule 38: U2 small nuclear ribonucleoprotein A'



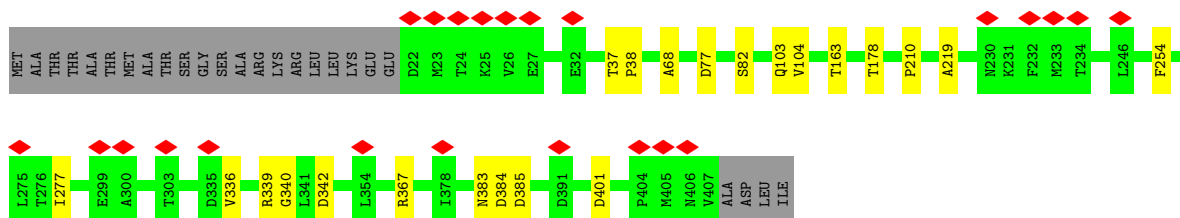
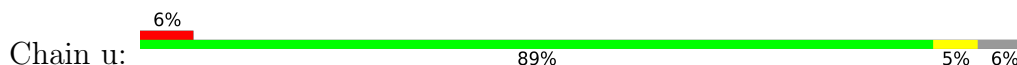
- Molecule 41: Protein mago nashi homolog



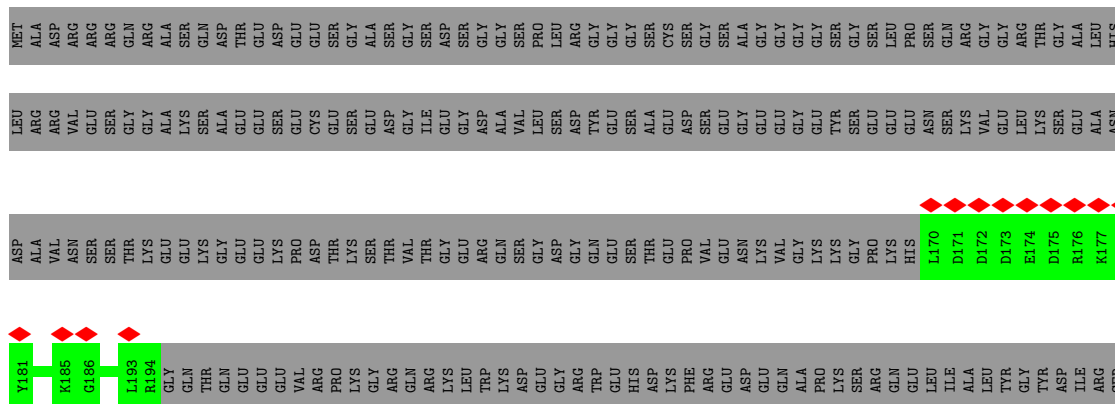
- Molecule 42: RNA-binding protein 8A



- Molecule 43: Eukaryotic initiation factor 4A-III



- Molecule 44: Protein CASC3



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	58374	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.144	Depositor
Minimum map value	-1.098	Depositor
Average map value	0.014	Depositor
Map value standard deviation	0.086	Depositor
Recommended contour level	0.37	Depositor
Map size ($\text{\AA}$)	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	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: GTP, MG, ATP, SEP, IHP, 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	0.78	31/18191 (0.2%)	1.03	94/24720 (0.4%)
2	B	0.60	2/1970 (0.1%)	0.82	6/3060 (0.2%)
3	C	0.53	0/6938	0.83	13/9428 (0.1%)
4	D	0.55	0/8529	1.12	29/11891 (0.2%)
5	E	0.53	0/2392	0.73	0/3242
6	F	0.48	0/2323	0.82	3/3619 (0.1%)
7	4	0.72	0/307	1.00	3/476 (0.6%)
8	G	0.62	2/1674 (0.1%)	1.41	35/2594 (1.3%)
9	H	0.85	26/3305 (0.8%)	1.41	60/5130 (1.2%)
10	I	0.61	0/3884	1.42	24/5301 (0.5%)
11	J	0.54	0/3861	0.85	16/5241 (0.3%)
12	K	0.67	1/768 (0.1%)	1.08	3/1067 (0.3%)
13	L	0.50	0/3046	0.81	10/4115 (0.2%)
14	M	0.54	0/1119	0.90	6/1497 (0.4%)
15	N	0.66	0/1210	0.80	2/1622 (0.1%)
16	O	0.54	0/2344	0.83	4/3163 (0.1%)
17	P	0.74	1/967 (0.1%)	1.18	13/1285 (1.0%)
18	Q	0.41	0/6565	0.91	4/9143 (0.0%)
19	R	0.78	4/2262 (0.2%)	1.21	13/3031 (0.4%)
20	S	0.48	0/1268	0.75	1/1714 (0.1%)
21	T	0.78	0/2519	0.95	9/3433 (0.3%)
22	U	0.50	0/424	0.85	2/582 (0.3%)
23	V	0.43	0/2642	0.82	0/3602
24	W	0.43	0/4237	0.87	5/5723 (0.1%)
25	Y	0.98	0/3436	1.49	20/4774 (0.4%)
26	Z	0.31	1/1129 (0.1%)	0.55	0/1525
27	2	0.59	0/1030	1.02	6/1371 (0.4%)
28	z	0.24	0/505	0.58	0/672
29	b	0.77	0/797	1.05	4/1062 (0.4%)
29	i	0.73	0/700	1.03	4/933 (0.4%)
30	y	0.60	0/389	1.22	3/540 (0.6%)
31	a	0.67	0/616	0.97	2/830 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	h	0.66	0/639	0.86	0/857
32	c	0.74	0/657	0.98	0/888
32	j	0.74	0/657	0.98	0/888
33	d	0.94	1/786 (0.1%)	1.10	2/1053 (0.2%)
33	k	0.95	0/696	1.07	1/935 (0.1%)
34	f	1.04	1/588 (0.2%)	1.08	0/795
34	m	1.05	1/578 (0.2%)	1.15	1/783 (0.1%)
35	e	0.84	0/660	1.06	1/886 (0.1%)
35	l	0.85	0/660	1.06	1/886 (0.1%)
36	g	0.71	0/584	0.95	1/779 (0.1%)
36	n	0.70	0/548	1.00	2/729 (0.3%)
37	q	0.62	0/658	1.04	3/919 (0.3%)
37	r	0.57	0/653	1.00	3/912 (0.3%)
37	s	0.60	0/658	1.08	4/919 (0.4%)
37	t	0.62	0/653	0.94	3/912 (0.3%)
38	o	0.81	0/1299	2.06	54/1761 (3.1%)
39	p	0.78	0/774	1.71	12/1035 (1.2%)
40	l	0.34	0/2262	0.67	1/3045 (0.0%)
41	v	0.47	0/710	1.03	3/987 (0.3%)
42	w	0.47	0/444	1.21	4/614 (0.7%)
43	u	0.51	0/1906	1.20	13/2653 (0.5%)
44	x	0.53	0/123	1.12	0/170
45	3	0.25	0/232	0.60	0/307
All	All	0.65	71/108772 (0.1%)	1.05	503/150099 (0.3%)

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	19
3	C	0	9
4	D	0	1
5	E	0	1
10	I	0	6
11	J	0	5
15	N	0	4
16	O	0	1
17	P	0	3
19	R	0	7
21	T	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
24	W	0	2
33	d	0	1
33	k	0	1
All	All	0	63

The worst 5 of 71 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1724	PRO	N-CA	16.49	1.68	1.47
19	R	219	PRO	C-O	-10.51	1.11	1.23
19	R	222	PRO	N-CA	10.35	1.68	1.46
1	A	771	VAL	C-O	-9.56	1.12	1.24
19	R	221	GLY	C-N	9.29	1.44	1.33

The worst 5 of 503 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	R	221	GLY	CA-C-N	18.39	139.32	120.38
19	R	221	GLY	C-N-CA	18.39	139.32	120.38
1	A	535	ARG	CB-CA-C	18.06	139.35	109.56
8	G	1	G	C1'-C2'-O2'	-16.53	87.00	111.80
38	o	55	ARG	CD-NE-CZ	13.18	142.85	124.40

There are no chirality outliers.

5 of 63 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	166	PHE	Peptide
1	A	346	ASP	Peptide
1	A	377	GLU	Peptide
1	A	55	ASP	Peptide
1	A	73	HIS	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	17748	0	16907	1068	0
2	B	1768	0	897	65	0
3	C	6787	0	6794	123	0
4	D	8530	0	3747	18	0
5	E	2338	0	2275	72	0
6	F	2075	0	1048	174	0
7	4	276	0	142	23	0
8	G	1510	0	760	205	0
9	H	2966	0	1505	289	0
10	I	3857	0	2738	166	0
11	J	3819	0	2904	54	0
12	K	772	0	342	20	0
13	L	3015	0	2570	81	0
14	M	1098	0	1082	39	0
15	N	1184	0	1190	27	0
16	O	2296	0	2284	78	0
17	P	953	0	939	37	0
18	Q	6562	0	2836	49	0
19	R	2243	0	2298	93	0
20	S	1236	0	1210	55	0
21	T	2454	0	2413	81	0
22	U	422	0	291	10	0
23	V	2632	0	1734	56	0
24	W	4129	0	4040	166	0
25	Y	3431	0	1662	35	0
26	Z	1084	0	1019	28	0
27	2	1013	0	1058	168	0
28	z	496	0	484	83	0
29	b	786	0	811	48	0
29	i	690	0	712	15	0
30	y	390	0	190	3	0
31	a	609	0	620	26	0
31	h	633	0	645	14	0
32	c	649	0	693	10	0
32	j	649	0	693	11	0
33	d	776	0	819	32	0
33	k	688	0	709	30	0
34	f	576	0	589	21	0
34	m	566	0	573	53	0
35	e	652	0	668	20	0
35	l	652	0	668	45	0
36	g	577	0	603	15	0
36	n	542	0	568	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	q	659	0	296	19	0
37	r	654	0	294	8	0
37	s	659	0	296	21	0
37	t	654	0	294	18	0
38	o	1282	0	1305	31	0
39	p	760	0	783	12	0
40	l	2209	0	2157	328	0
41	v	711	0	299	6	0
42	w	445	0	203	6	0
43	u	1907	0	845	5	0
44	x	124	0	51	0	0
45	3	230	0	229	48	0
46	A	36	0	6	9	0
47	C	32	0	12	2	0
48	C	1	0	0	0	0
48	F	6	0	0	0	0
48	Q	2	0	0	0	0
49	l	1	0	0	0	0
49	N	3	0	0	0	0
49	O	3	0	0	0	0
50	Q	31	0	12	5	0
All	All	106538	0	83812	3113	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 16.

The worst 5 of 3113 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:1685:LEU:HD21	40:1:173:TYR:CZ	1.30	1.66
1:A:1496:PRO:HG2	45:3:338:GLY:CA	1.29	1.61
1:A:1498:TRP:CZ3	40:1:63:ILE:HG23	1.08	1.58
1:A:1698:PRO:CB	40:1:182:VAL:HG22	1.17	1.57
1:A:1496:PRO:CG	45:3:338:GLY:HA3	1.30	1.56

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	2247/2335 (96%)	2044 (91%)	191 (8%)	12 (0%)	24	62
3	C	856/972 (88%)	781 (91%)	71 (8%)	4 (0%)	24	62
4	D	1720/2136 (80%)	1632 (95%)	85 (5%)	3 (0%)	43	77
5	E	297/357 (83%)	275 (93%)	22 (7%)	0	100	100
10	I	576/855 (67%)	558 (97%)	14 (2%)	4 (1%)	18	55
11	J	530/848 (62%)	489 (92%)	33 (6%)	8 (2%)	8	38
12	K	147/225 (65%)	136 (92%)	8 (5%)	3 (2%)	6	31
13	L	425/802 (53%)	408 (96%)	15 (4%)	2 (0%)	24	62
14	M	128/243 (53%)	117 (91%)	11 (9%)	0	100	100
15	N	141/144 (98%)	124 (88%)	16 (11%)	1 (1%)	18	55
16	O	283/420 (67%)	259 (92%)	23 (8%)	1 (0%)	30	66
17	P	107/229 (47%)	89 (83%)	15 (14%)	3 (3%)	4	24
18	Q	1308/1485 (88%)	1280 (98%)	26 (2%)	2 (0%)	43	77
19	R	274/536 (51%)	247 (90%)	23 (8%)	4 (2%)	8	38
20	S	157/166 (95%)	148 (94%)	9 (6%)	0	100	100
21	T	310/514 (60%)	275 (89%)	29 (9%)	6 (2%)	6	32
22	U	68/2752 (2%)	60 (88%)	8 (12%)	0	100	100
23	V	444/908 (49%)	431 (97%)	12 (3%)	1 (0%)	43	77
24	W	507/579 (88%)	432 (85%)	69 (14%)	6 (1%)	10	42
25	Y	667/1220 (55%)	642 (96%)	23 (3%)	2 (0%)	36	71
26	Z	120/758 (16%)	107 (89%)	13 (11%)	0	100	100
27	2	121/184 (66%)	110 (91%)	7 (6%)	4 (3%)	3	21
28	z	58/112 (52%)	56 (97%)	2 (3%)	0	100	100
29	b	98/240 (41%)	93 (95%)	2 (2%)	3 (3%)	3	22
29	i	84/240 (35%)	82 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	y	77/301 (26%)	75 (97%)	2 (3%)	0	100	100
31	a	75/126 (60%)	74 (99%)	1 (1%)	0	100	100
31	h	77/126 (61%)	76 (99%)	1 (1%)	0	100	100
32	c	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
32	j	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
33	d	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
33	k	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
34	f	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
34	m	71/86 (83%)	67 (94%)	3 (4%)	1 (1%)	9	39
35	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
35	l	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
36	g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
36	n	65/76 (86%)	63 (97%)	2 (3%)	0	100	100
37	q	130/504 (26%)	117 (90%)	7 (5%)	6 (5%)	2	17
37	r	129/504 (26%)	118 (92%)	9 (7%)	2 (2%)	7	37
37	s	130/504 (26%)	116 (89%)	6 (5%)	8 (6%)	1	13
37	t	129/504 (26%)	116 (90%)	9 (7%)	4 (3%)	3	22
38	o	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	9	41
39	p	92/225 (41%)	90 (98%)	2 (2%)	0	100	100
40	l	265/586 (45%)	246 (93%)	19 (7%)	0	100	100
41	v	142/146 (97%)	138 (97%)	4 (3%)	0	100	100
42	w	89/174 (51%)	87 (98%)	1 (1%)	1 (1%)	11	45
43	u	384/411 (93%)	372 (97%)	9 (2%)	3 (1%)	16	52
44	x	23/703 (3%)	22 (96%)	1 (4%)	0	100	100
45	3	28/415 (7%)	27 (96%)	1 (4%)	0	100	100
All	All	14373/25726 (56%)	13438 (94%)	839 (6%)	96 (1%)	20	55

5 of 96 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1092	ILE
1	A	1831	LYS
1	A	1881	ASN

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Mol	Chain	Res	Type
3	C	801	LEU
4	D	957	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	1775/2108 (84%)	1707 (96%)	68 (4%)	29	51
3	C	758/866 (88%)	755 (100%)	3 (0%)	84	82
5	E	256/300 (85%)	255 (100%)	1 (0%)	84	82
10	I	199/749 (27%)	185 (93%)	14 (7%)	14	36
11	J	241/751 (32%)	239 (99%)	2 (1%)	73	77
13	L	218/709 (31%)	211 (97%)	7 (3%)	34	56
14	M	117/209 (56%)	115 (98%)	2 (2%)	53	67
15	N	130/130 (100%)	129 (99%)	1 (1%)	73	77
16	O	255/361 (71%)	253 (99%)	2 (1%)	73	77
17	P	101/203 (50%)	97 (96%)	4 (4%)	28	49
19	R	236/457 (52%)	224 (95%)	12 (5%)	21	44
20	S	129/134 (96%)	127 (98%)	2 (2%)	55	69
21	T	268/441 (61%)	264 (98%)	4 (2%)	57	70
22	U	21/2432 (1%)	19 (90%)	2 (10%)	8	26
23	V	98/838 (12%)	95 (97%)	3 (3%)	35	56
24	W	448/502 (89%)	441 (98%)	7 (2%)	55	69
25	Y	32/1085 (3%)	29 (91%)	3 (9%)	8	27
26	Z	110/655 (17%)	110 (100%)	0	100	100
27	2	106/157 (68%)	101 (95%)	5 (5%)	23	46
28	z	51/99 (52%)	51 (100%)	0	100	100
29	b	83/177 (47%)	80 (96%)	3 (4%)	31	52
29	i	77/177 (44%)	74 (96%)	3 (4%)	28	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	a	68/101 (67%)	66 (97%)	2 (3%)	37	58
31	h	70/101 (69%)	70 (100%)	0	100	100
32	c	77/101 (76%)	75 (97%)	2 (3%)	40	60
32	j	77/101 (76%)	75 (97%)	2 (3%)	40	60
33	d	90/110 (82%)	89 (99%)	1 (1%)	65	74
33	k	80/110 (73%)	79 (99%)	1 (1%)	61	72
34	f	63/74 (85%)	61 (97%)	2 (3%)	34	56
34	m	61/74 (82%)	58 (95%)	3 (5%)	22	45
35	e	74/84 (88%)	74 (100%)	0	100	100
35	l	74/84 (88%)	74 (100%)	0	100	100
36	g	64/66 (97%)	63 (98%)	1 (2%)	55	69
36	n	60/66 (91%)	58 (97%)	2 (3%)	33	55
38	o	139/218 (64%)	133 (96%)	6 (4%)	26	48
39	p	82/195 (42%)	79 (96%)	3 (4%)	30	51
40	1	235/520 (45%)	230 (98%)	5 (2%)	47	65
45	3	25/366 (7%)	25 (100%)	0	100	100
All	All	7048/15911 (44%)	6870 (98%)	178 (2%)	42	62

5 of 178 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	R	334	ARG
29	b	57	LYS
21	T	412	HIS
24	W	243	VAL
34	f	27	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 135 such sidechains are listed below:

Mol	Chain	Res	Type
34	f	58	HIS
29	i	22	GLN
40	1	92	GLN
3	C	208	HIS
3	C	154	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	82/117 (70%)	17 (20%)	4 (4%)
6	F	96/107 (89%)	46 (47%)	16 (16%)
7	4	13/46 (28%)	8 (61%)	3 (23%)
8	G	80/174 (45%)	63 (78%)	20 (25%)
9	H	133/188 (70%)	34 (25%)	10 (7%)
All	All	404/632 (63%)	168 (41%)	53 (13%)

5 of 168 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 53 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	G	23	U
8	G	166	A
9	H	40	C
8	G	137	C
8	G	144	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
19	SEP	R	224	19	8,9,10	1.03	0	7,12,14	1.51	1 (14%)
19	SEP	R	232	19	8,9,10	1.62	1 (12%)	7,12,14	1.00	1 (14%)

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
19	SEP	R	224	19	-	0/6/8/10	-
19	SEP	R	232	19	-	2/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	R	232	SEP	P-O1P	3.55	1.61	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	R	224	SEP	OG-CB-CA	-2.66	105.55	108.14
19	R	232	SEP	OG-CB-CA	2.37	110.45	108.14

There are no chirality outliers.

All (2) torsion outliers are listed below:

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

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	R	224	SEP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 16 are monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
47	GTP	C	1500	48	33,34,34	1.07	2 (6%)	50,54,54	1.77	11 (22%)
50	ATP	Q	1501	48	32,33,33	2.05	8 (25%)	48,52,52	1.87	16 (33%)
46	IHP	A	3000	-	36,36,36	0.72	0	60,60,60	1.09	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
47	GTP	C	1500	48	-	2/22/38/38	0/3/3/3
50	ATP	Q	1501	48	-	4/22/38/38	0/3/3/3
46	IHP	A	3000	-	-	3/30/54/54	0/1/1/1

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	Q	1501	ATP	PB-O3B	7.32	1.67	1.59
50	Q	1501	ATP	C6-N6	4.71	1.46	1.34
50	Q	1501	ATP	C4-N3	3.17	1.40	1.34
50	Q	1501	ATP	C2'-C3'	-2.78	1.45	1.53
47	C	1500	GTP	C5-N7	-2.32	1.34	1.39

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	C	1500	GTP	C5-C4-N3	-5.13	120.22	128.39
50	Q	1501	ATP	C5-C4-N3	-4.88	120.00	126.72
47	C	1500	GTP	C2-N3-C4	4.45	119.97	112.30
50	Q	1501	ATP	N3-C2-N1	-4.26	122.14	128.58
50	Q	1501	ATP	N3-C4-N9	3.72	133.50	127.17

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

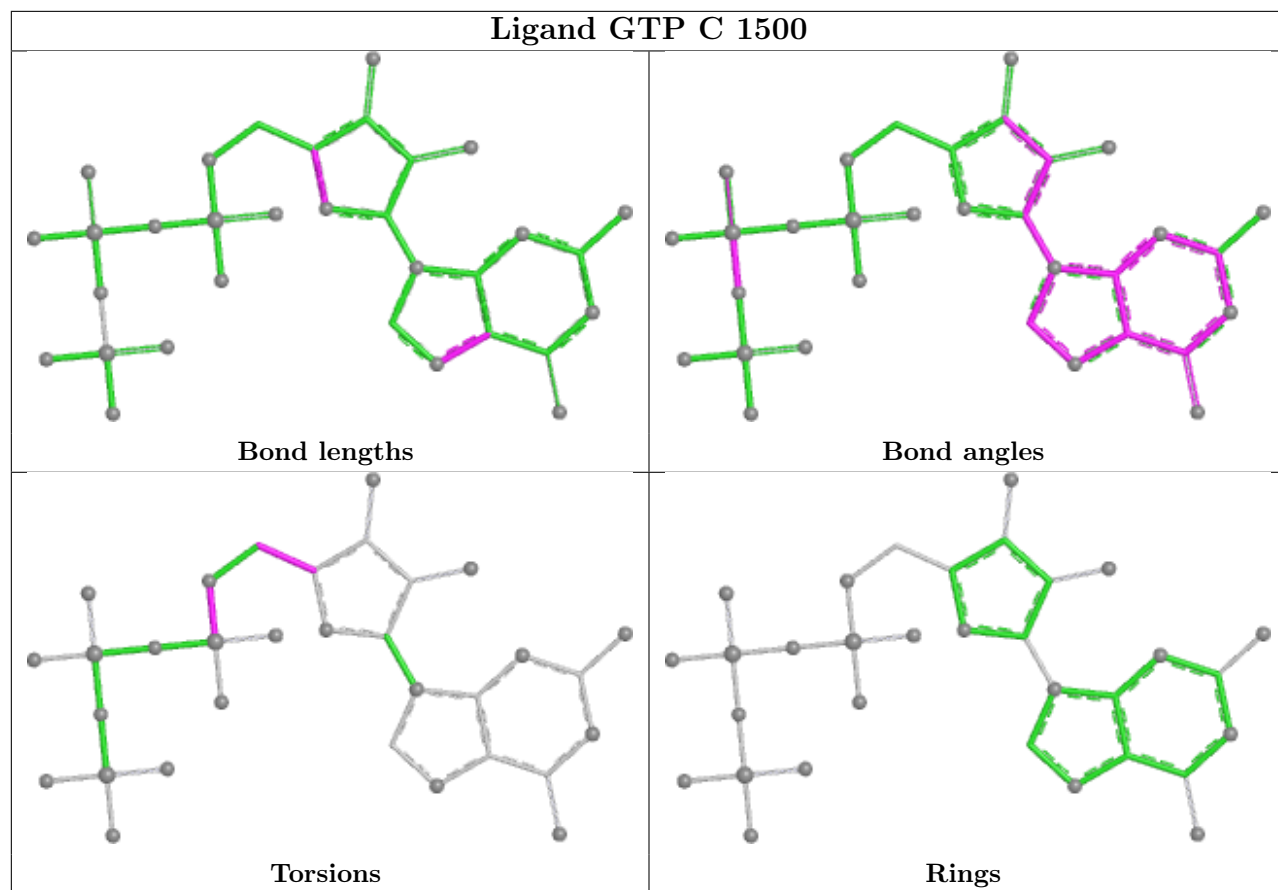
Mol	Chain	Res	Type	Atoms
50	Q	1501	ATP	C5'-O5'-PA-O1A
50	Q	1501	ATP	C5'-O5'-PA-O2A
50	Q	1501	ATP	C5'-O5'-PA-O3A
47	C	1500	GTP	O4'-C4'-C5'-O5'
47	C	1500	GTP	C5'-O5'-PA-O1A

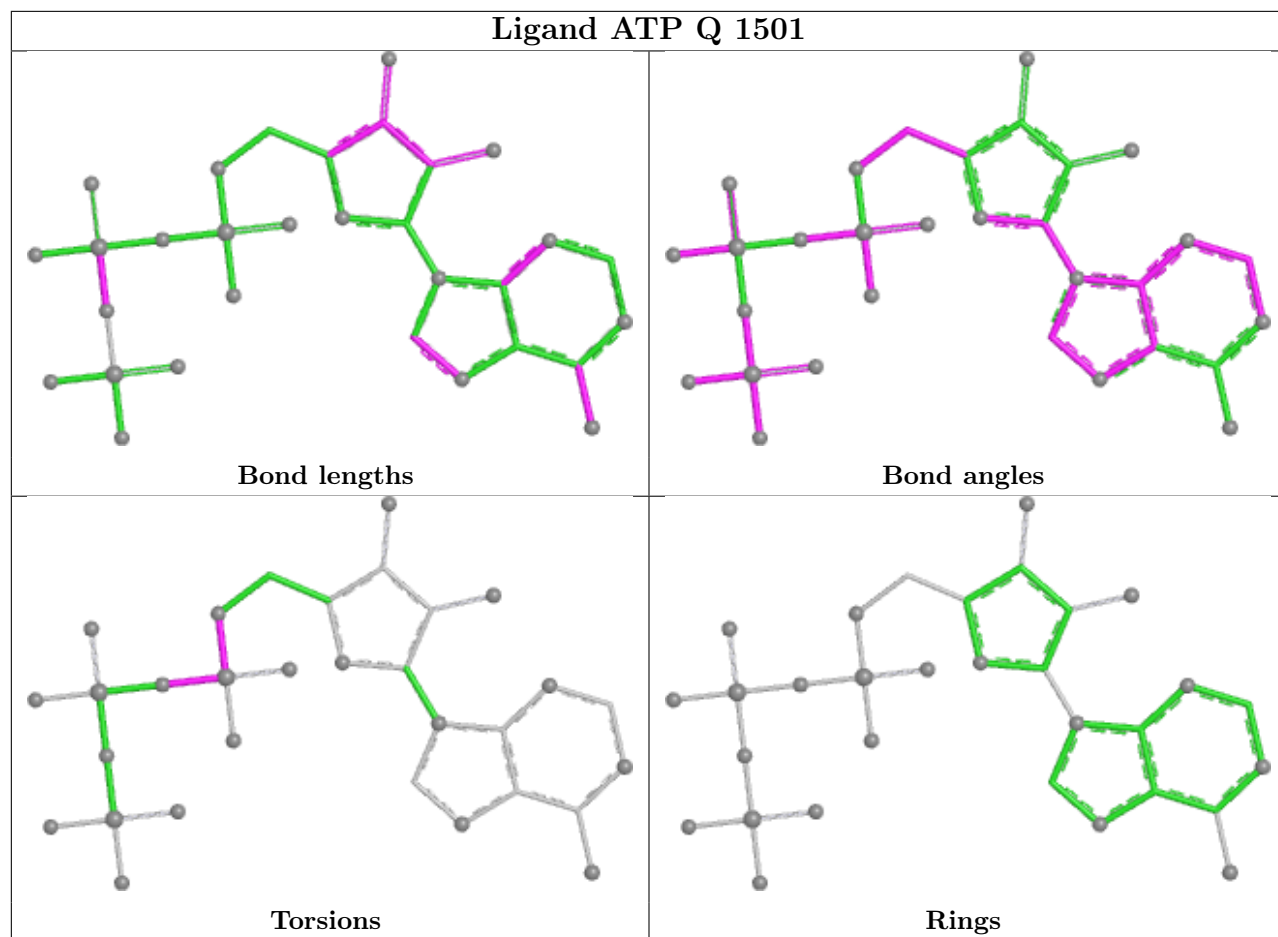
There are no ring outliers.

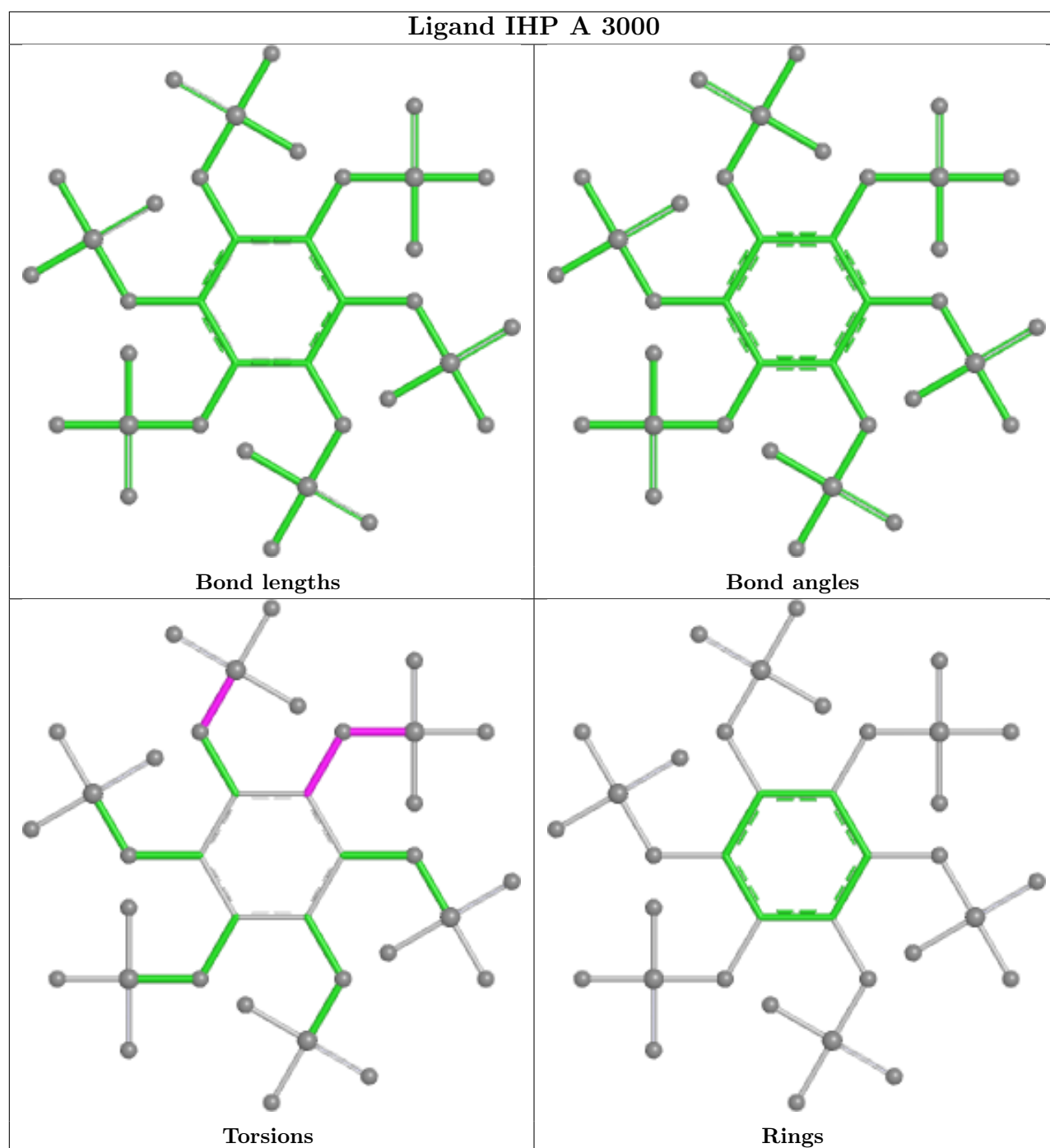
3 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
47	C	1500	GTP	2	0
50	Q	1501	ATP	5	0
46	A	3000	IHP	9	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.

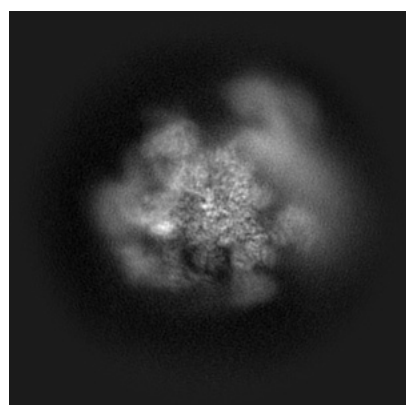
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32321. These allow visual inspection of the internal detail of the map and identification of artifacts.

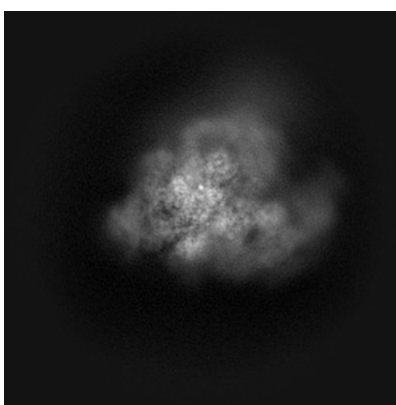
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

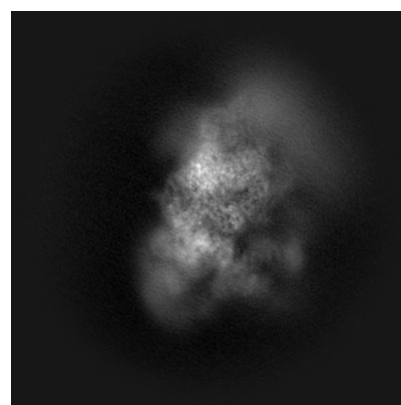
6.1.1 Primary map



X



Y

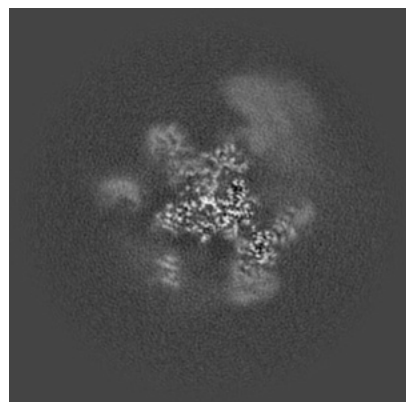


Z

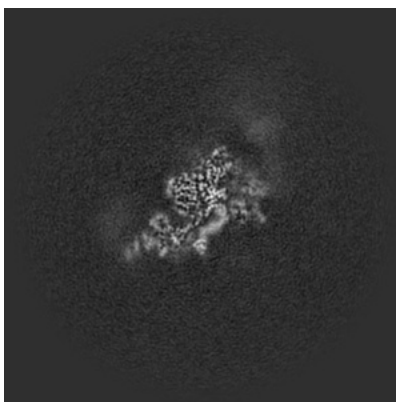
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

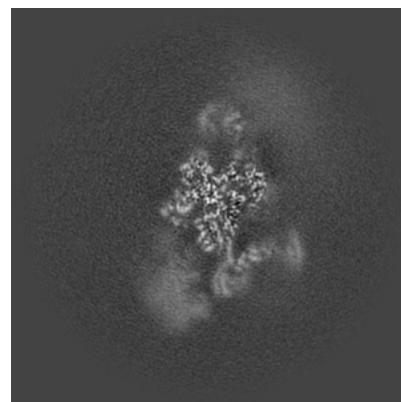
6.2.1 Primary map



X Index: 200



Y Index: 200

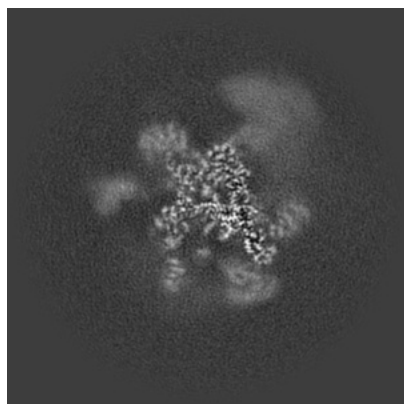


Z Index: 200

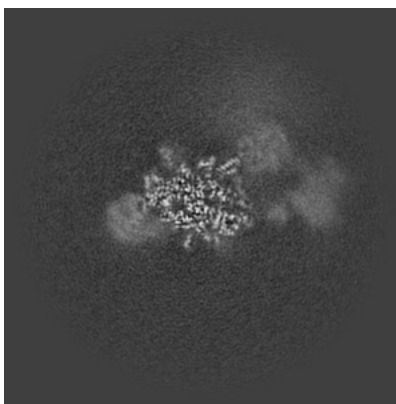
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

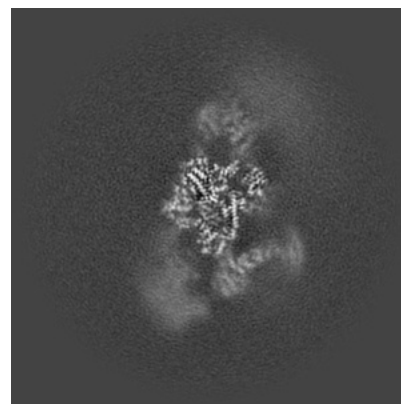
6.3.1 Primary map



X Index: 194



Y Index: 238

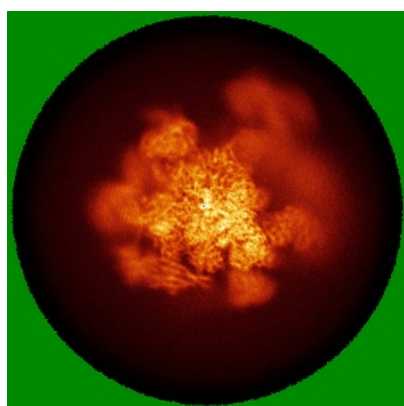


Z Index: 197

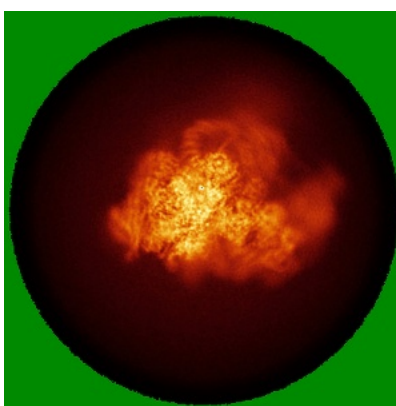
The images above show the largest variance slices of the map in three orthogonal directions.

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

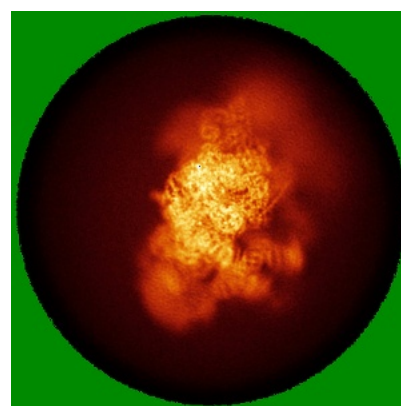
6.4.1 Primary map



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

This section was not generated.

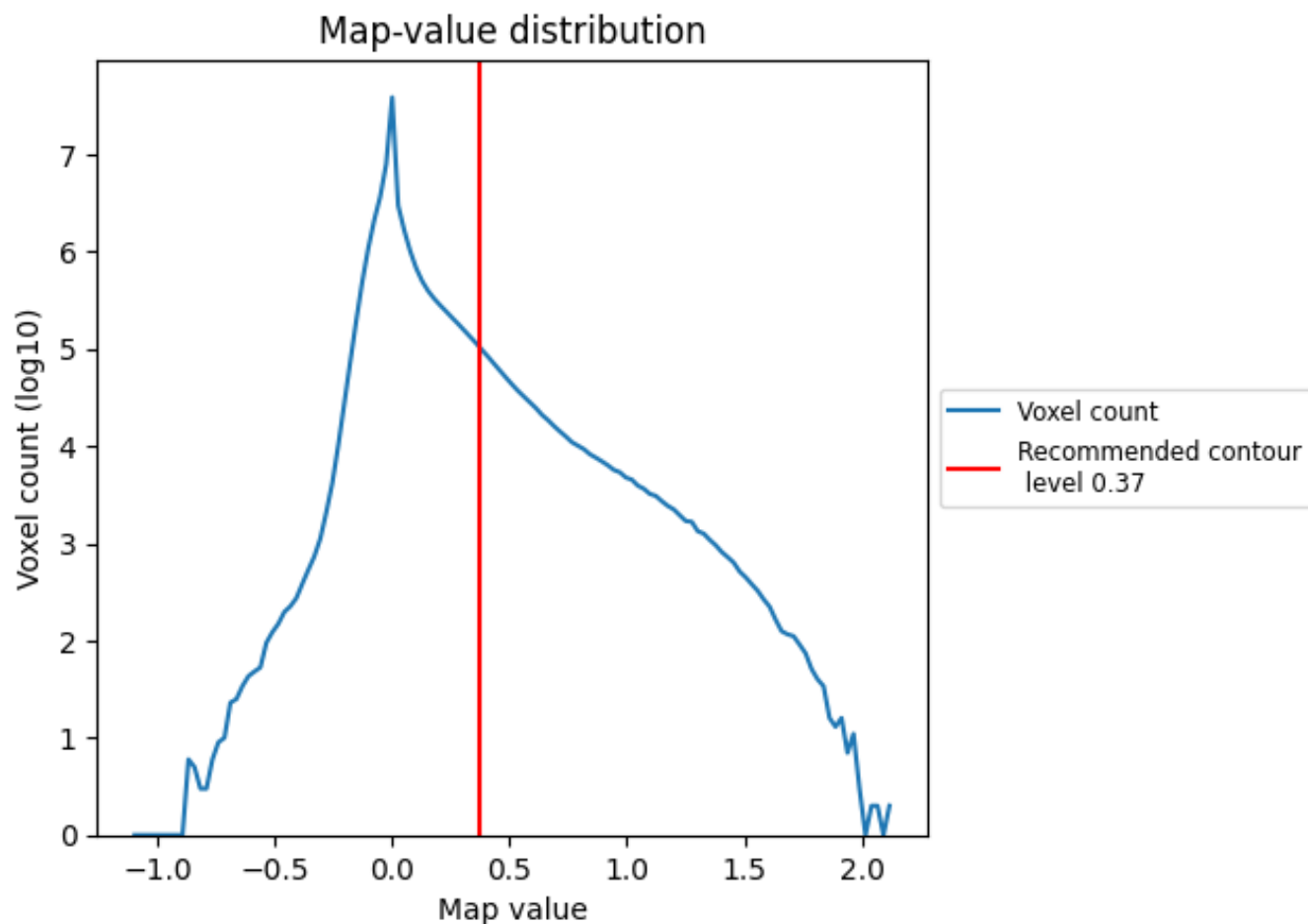
6.6 Mask visualisation

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

7 Map analysis [i](#)

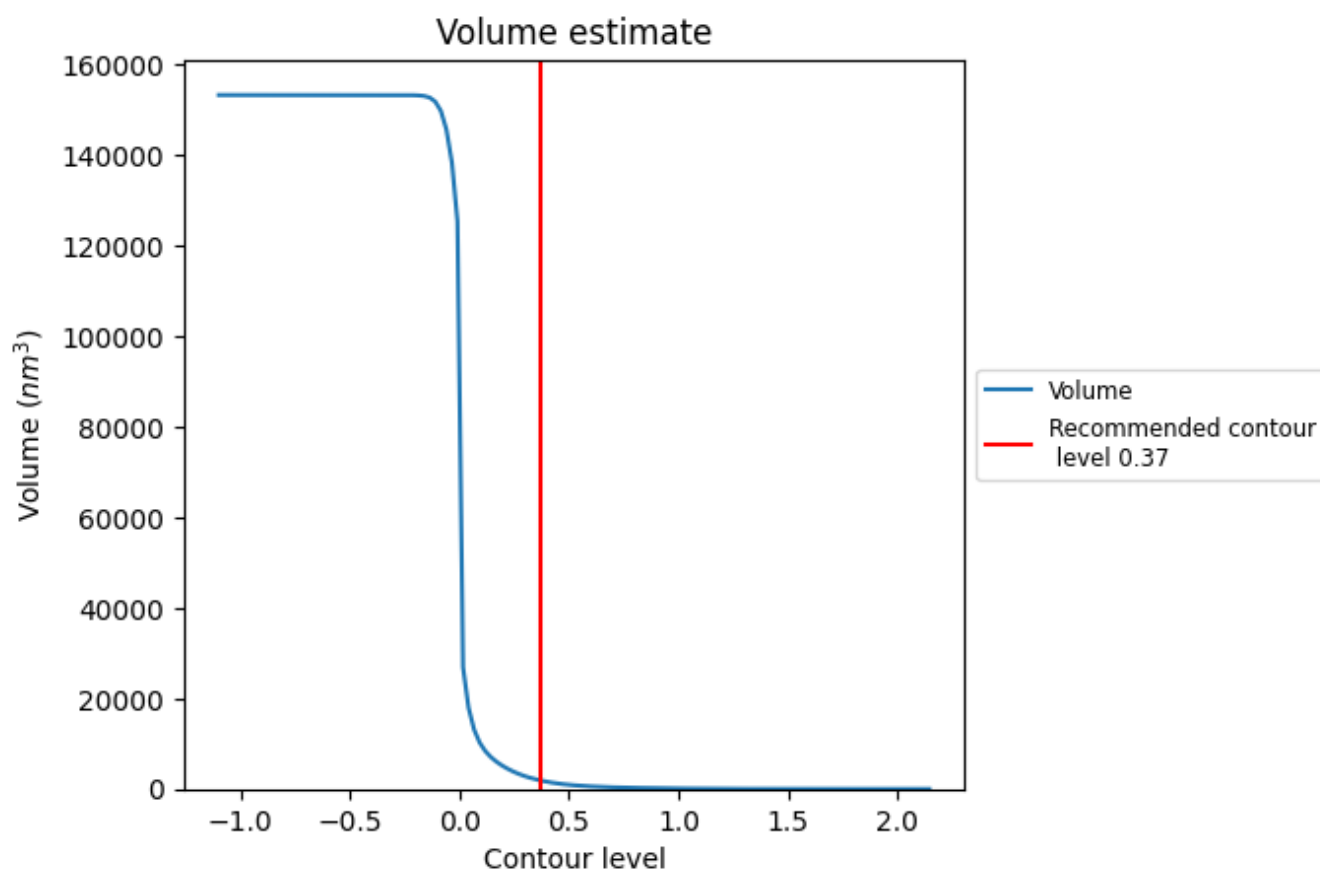
This section contains the results of statistical analysis of the map.

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.

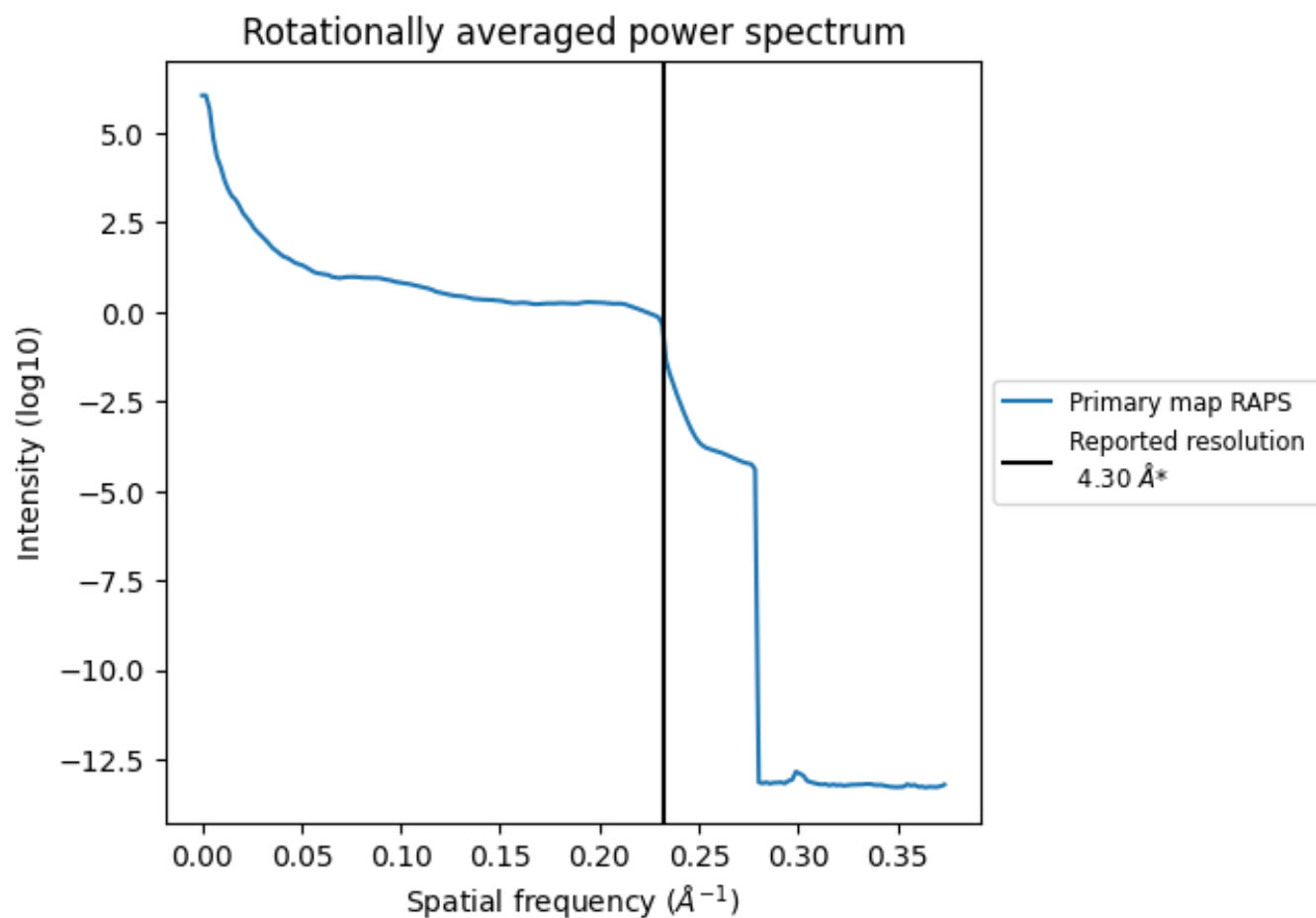
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1869 nm³; this corresponds to an approximate mass of 1688 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 0.233 Å⁻¹

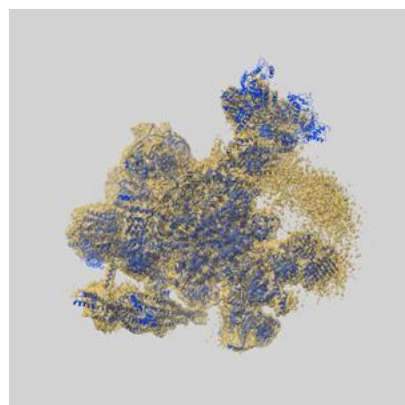
8 Fourier-Shell correlation ⓘ

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

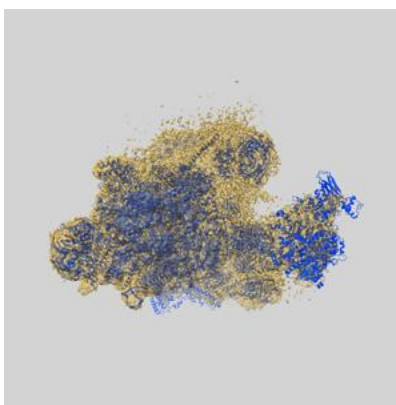
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32321 and PDB model 7W5B. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

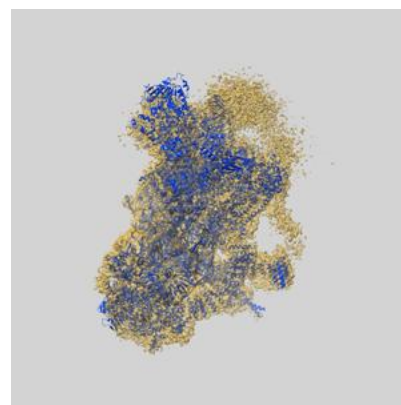
9.1 Map-model overlay [i](#)



X



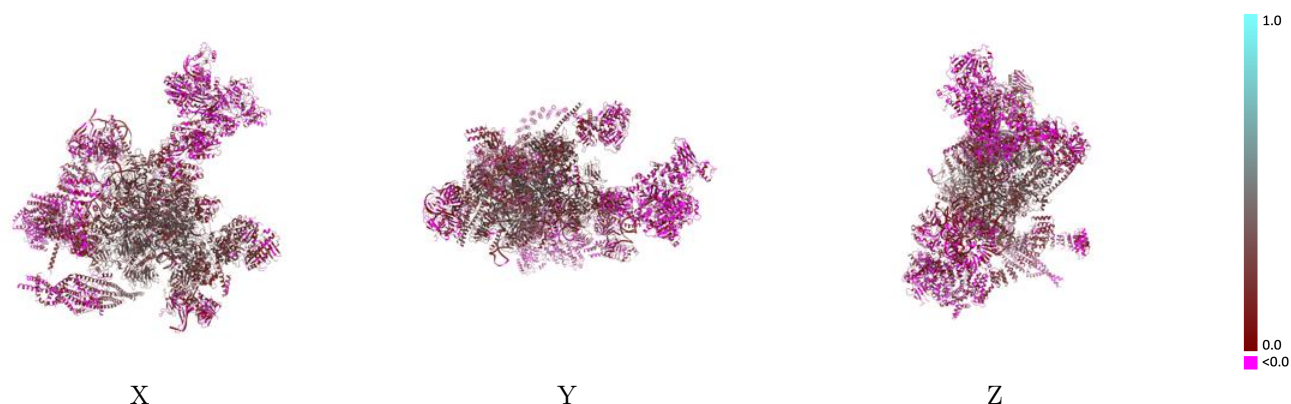
Y



Z

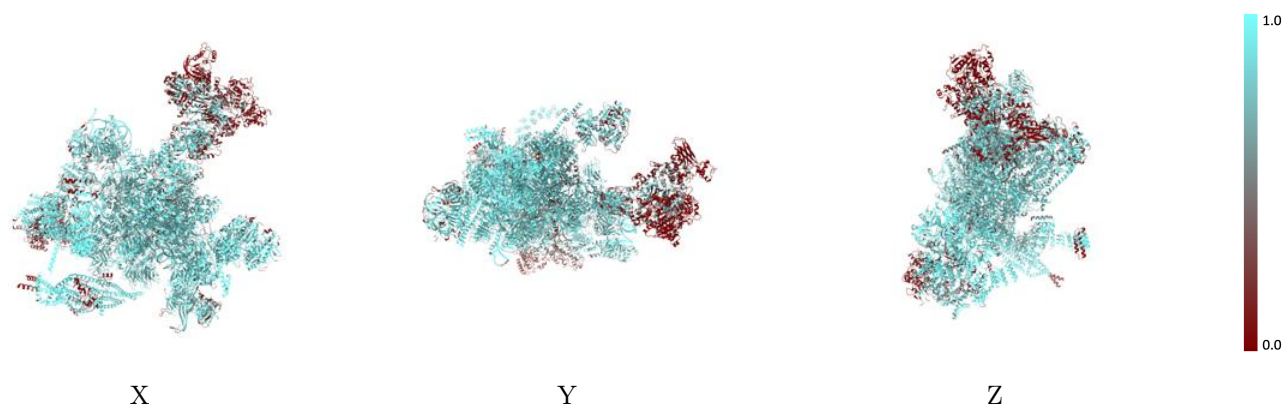
The images above show the 3D surface view of the map at the recommended contour level 0.37 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



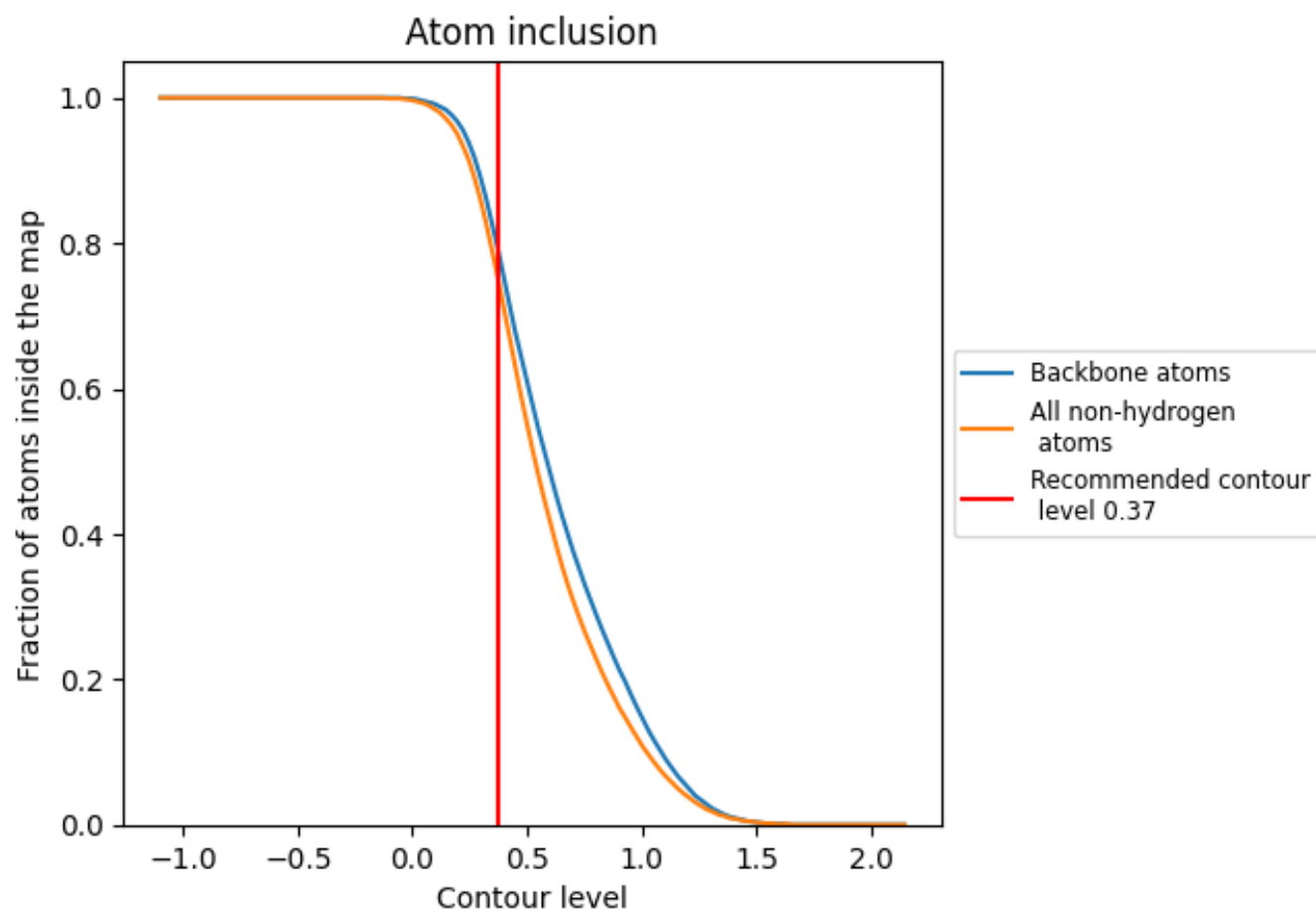
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.37).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 76% 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 (0.37) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7550	 0.1920
1	 0.6780	 0.2120
2	 0.7950	 0.1810
3	 0.6740	 0.2640
4	 0.9860	 0.3870
A	 0.8190	 0.2900
B	 0.9440	 0.2580
C	 0.8620	 0.2950
D	 0.2740	 0.0240
E	 0.9100	 0.2900
F	 0.9610	 0.3000
G	 0.7620	 0.1640
H	 0.9120	 0.1490
I	 0.8920	 0.1500
J	 0.8430	 0.1950
K	 0.9520	 0.2010
L	 0.8500	 0.2470
M	 0.8040	 0.2660
N	 0.8740	 0.3000
O	 0.8590	 0.2530
P	 0.7430	 0.2680
Q	 0.4580	 0.0290
R	 0.8280	 0.3040
S	 0.8900	 0.2590
T	 0.9120	 0.3710
U	 0.9180	 0.2580
V	 0.8400	 0.2200
W	 0.8180	 0.2180
Y	 0.6650	 0.0970
Z	 0.8400	 0.2360
a	 0.7800	 0.1570
b	 0.7990	 0.1220
c	 0.8970	 0.0790
d	 0.7990	 0.0610
e	 0.7010	 0.0590



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Chain	Atom inclusion	Q-score
f	 0.7170	 0.0680
g	 0.5610	 0.0740
h	 0.7390	 0.0730
i	 0.6150	 0.0230
j	 0.8330	 0.0500
k	 0.7490	 0.0550
l	 0.6900	 0.0660
m	 0.9190	 0.1090
n	 0.7640	 0.0740
o	 0.8050	 0.0720
p	 0.8980	 0.0790
q	 0.6060	 0.0700
r	 0.9400	 0.1470
s	 0.4960	 0.1050
t	 0.4110	 0.0150
u	 0.9030	 0.2540
v	 0.7860	 0.1330
w	 0.8720	 0.1370
x	 0.4110	 0.0800
y	 0.8210	 0.0850
z	 0.5410	 0.1300