



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 02:09 PM UTC

PDB ID : 7A5P / pdb_00007a5p
EMDB ID : EMD-11570
Title : Human C Complex Spliceosome - Medium-resolution PERIPHERY
Authors : Bertram, K.; Kastner, B.
Deposited on : 2020-08-21
Resolution : 5.00 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:

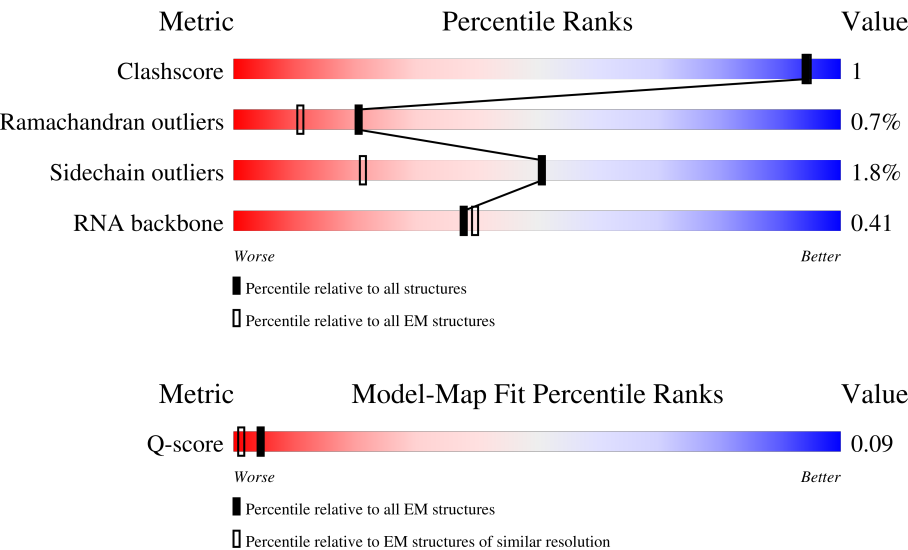
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 5.00 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	10198 (3.30 - 4.30)

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

Mol	Chain	Length	Quality of chain
1	2	975	14% 9% 6% . 84%
2	5	116	16% 12% 6% . 66%
3	6	106	9% 6% 85%

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Mol	Chain	Length	Quality of chain
4	8	204	
5	A	2335	
6	C	536	
7	E	579	
8	G	504	
8	H	504	
8	I	504	
8	J	504	
9	K	225	
10	L	802	
11	M	855	
12	N	243	
13	O	848	
14	P	420	
15	S	2752	
16	T	908	
17	U	1485	
18	W	255	
19	X	225	
20	Y	324	
21	a	126	
21	l	126	
22	b	240	
22	m	240	
23	c	119	

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Mol	Chain	Length	Quality of chain
23	n	119	
24	d	118	
24	h	118	
25	e	92	
25	j	92	
26	f	86	
26	i	86	
27	g	76	
27	k	76	
28	o	301	
29	p	654	
30	q	2136	
31	r	1227	
32	s	285	
33	u	323	
34	v	146	
35	w	174	
36	x	258	
37	y	411	
38	z	646	

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 52703 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	155	Total	C	N	O	P	0	0
			2854	1258	396	1045	155		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5	40	Total	C	N	O	P	0	0
			718	316	93	269	40		

- Molecule 3 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	6	16	Total	C	N	O	P	0	0
			296	130	42	108	16		

- Molecule 4 is a protein called UNKNOWN.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	8	76	Total	C	N	O	0	0
			376	224	76	76		

- Molecule 5 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	A	491	Total	C	N	O	0	0
			2485	1496	497	492		

- Molecule 6 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	C	15	Total	C	N	O	0	0
			75	45	15	15		

- Molecule 7 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	E	305	Total	C	N	O	0	0
			1525	915	305	305		

- Molecule 8 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	G	132	Total	C	N	O	0	0
			679	415	132	132		
8	H	135	Total	C	N	O	0	0
			696	426	135	135		
8	I	133	Total	C	N	O	0	0
			684	418	133	133		
8	J	110	Total	C	N	O	0	0
			561	341	110	110		

- Molecule 9 is a protein called Pre-mRNA-splicing factor SPF27.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	K	138	Total	C	N	O	0	0
			689	413	138	138		

- Molecule 10 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	L	115	Total	C	N	O	0	0
			573	343	115	115		

- Molecule 11 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	M	672	Total	C	N	O	0	0
			3387	2043	672	672		

- Molecule 12 is a protein called Pre-mRNA-splicing factor SYF2.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	N	73	Total	C	N	O	0	0
			369	223	73	73		

- Molecule 13 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	O	261	Total	C	N	O	0	0
			1320	798	261	261		

- Molecule 14 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	P	90	Total	C	N	O	0	0
			452	271	90	91		

- Molecule 15 is a protein called Serine/arginine repetitive matrix protein 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	S	46	Total	C	N	O	0	0
			229	137	46	46		

- Molecule 16 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	T	253	Total	C	N	O	0	0
			1271	765	253	253		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
17	U	1293	Total	C	N	O	0	0
			6546	3960	1293	1293		

- Molecule 18 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	W	174	Total	C	N	O	0	0
			874	526	174	174		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
W	89	ASP	CYS	conflict	UNP P09661
W	119	CYS	SER	conflict	UNP P09661

- Molecule 19 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	X	93	Total	C	N	O	0	0
			466	280	93	93		

- Molecule 20 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	Y	29	Total	C	O	P	0	0
			348	145	174	29		

- Molecule 21 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	a	72	Total	C	N	O	0	0
			358	214	72	72		
21	l	83	Total	C	N	O	0	0
			415	249	83	83		

- Molecule 22 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	b	66	Total	C	N	O	0	0
			327	195	66	66		
22	m	70	Total	C	N	O	0	0
			351	211	70	70		

- Molecule 23 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	c	81	Total	C	N	O	0	0
			407	245	81	81		
23	n	82	Total	C	N	O	0	0
			412	248	82	82		

- Molecule 24 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	d	81	Total	C	N	O	0	0
			406	244	81	81		
24	h	84	Total	C	N	O	0	0
			421	253	84	84		

- Molecule 25 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	e	79	Total	C	N	O	0	0
			393	235	79	79		
25	j	78	Total	C	N	O	0	0
			388	232	78	78		

- Molecule 26 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	f	74	Total	C	N	O	0	0
			369	221	74	74		
26	i	71	Total	C	N	O	0	0
			352	210	71	71		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
27	g	74	Total	C	N	O	0	0
			369	221	74	74		
27	k	73	Total	C	N	O	0	0
			364	218	73	73		

- Molecule 28 is a protein called Peptidyl-prolyl cis-trans isomerase E.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	o	77	Total	C	N	O	0	0
			384	230	77	77		

- Molecule 29 is a protein called WD repeat-containing protein 70.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	p	68	Total	C	N	O	0	0
			333	197	68	68		

- Molecule 30 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	q	1896	Total	C	N	O	0	0
			9558	5766	1896	1896		

- Molecule 31 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	r	593	Total	C	N	O	0	0
			2982	1796	593	593		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
r	855	ASN	GLY	conflict	UNP Q92620

- Molecule 32 is a protein called Pre-mRNA-splicing factor ISY1 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	s	76	Total	C	N	O	0	0
			376	224	76	76		

- Molecule 33 is a protein called Splicing factor YJU2.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	u	43	Total	C	N	O	0	0
			216	129	43	44		

- Molecule 34 is a protein called Protein mago nashi homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	v	144	Total	C	N	O	0	0
			723	435	144	144		

- Molecule 35 is a protein called RNA-binding protein 8A.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	w	91	Total	C	N	O	0	0
			453	271	91	91		

- Molecule 36 is a protein called Protein FRG1.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	x	125	Total	C	N	O	0	0
			621	371	125	125		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
37	y	390	Total 1951	C 1171	N 390	O 390	0	0

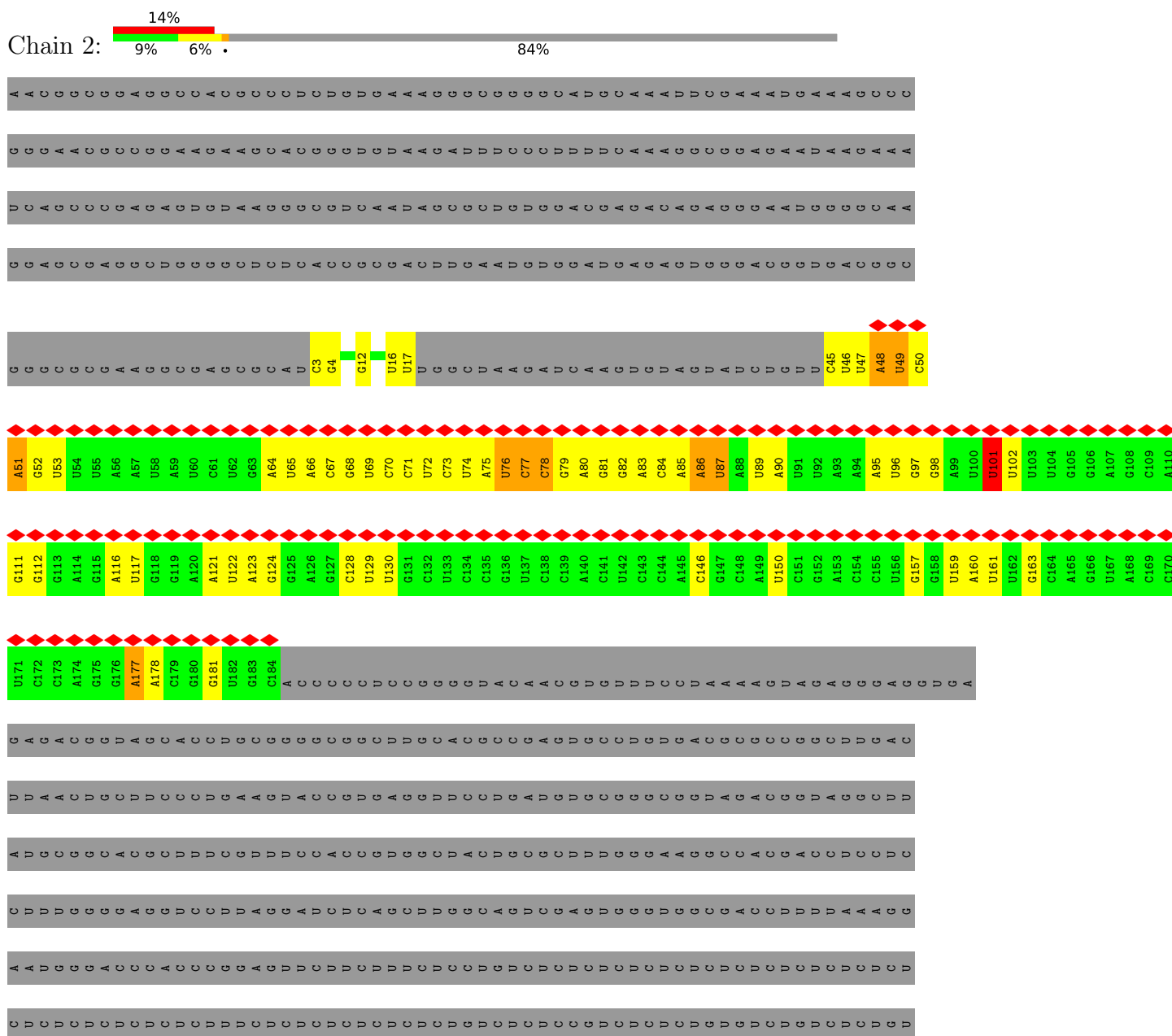
- Molecule 38 is a protein called Peptidylprolyl isomerase domain and WD repeat-containing protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	z	460	Total 2301	C 1381	N 460	O 460	0	0

3 Residue-property plots [i](#)

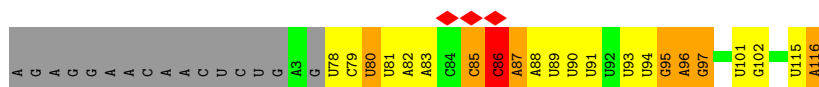
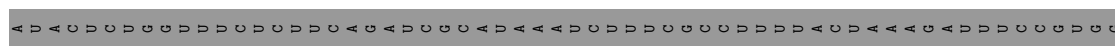
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: U2 snRNA

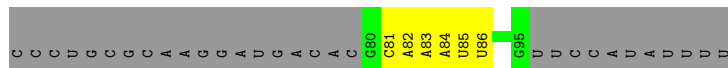
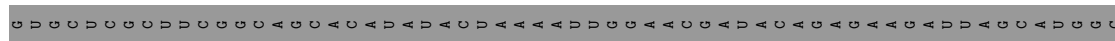




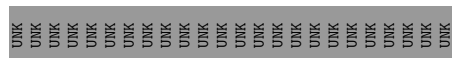
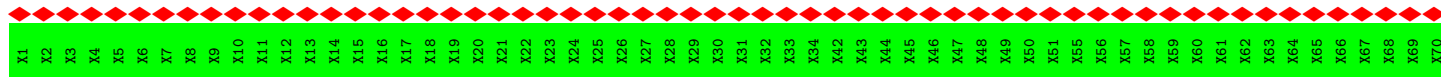
- Molecule 2: U5 snRNA



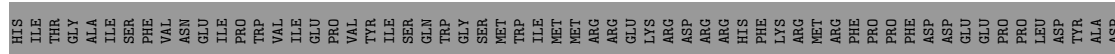
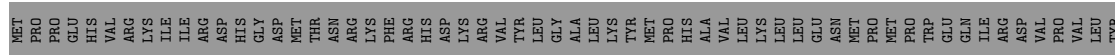
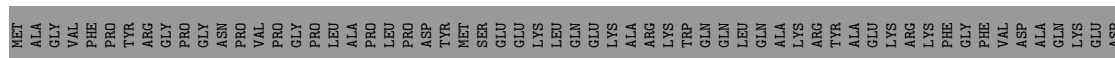
- Molecule 3: U6 snRNA



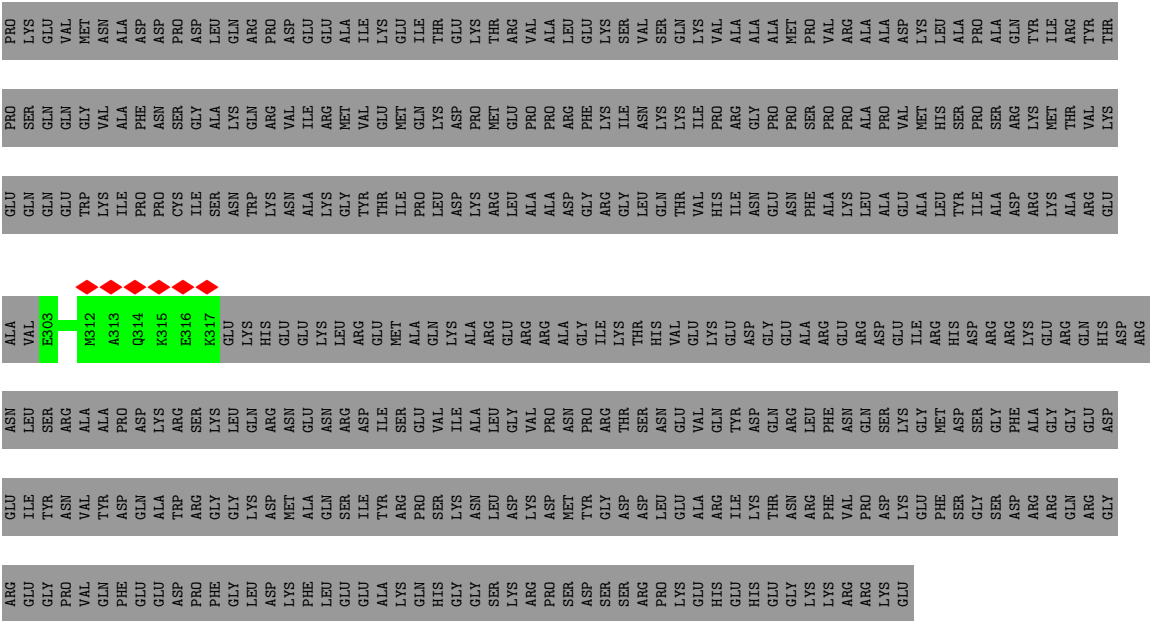
- Molecule 4: UNKNOWN



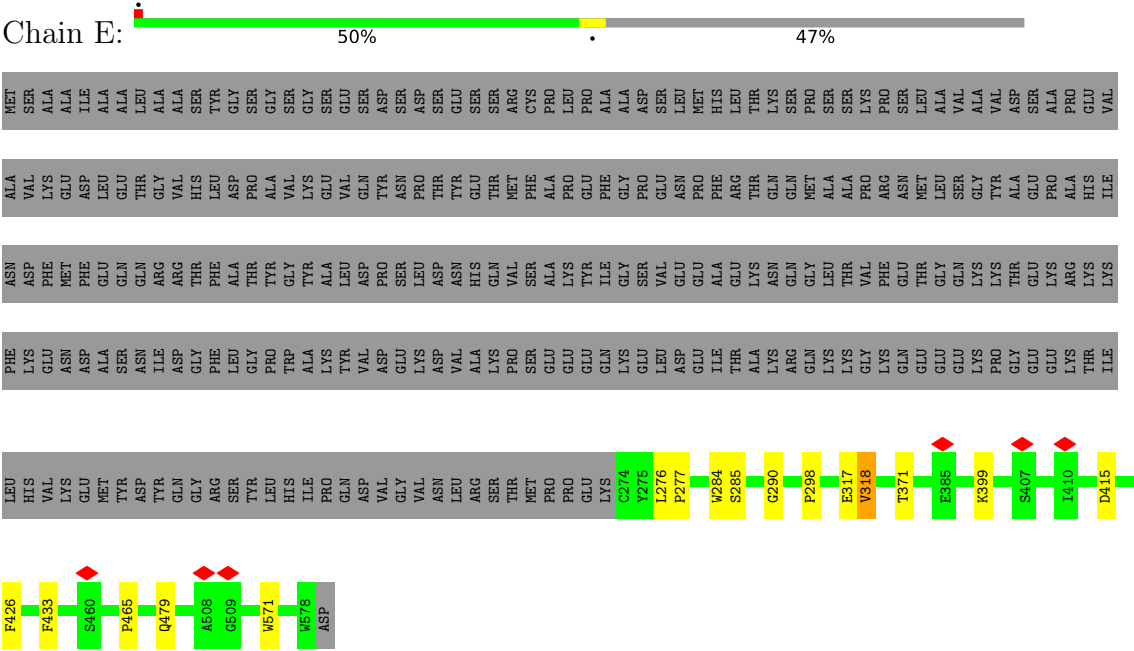
- Molecule 5: Pre-mRNA-processing-splicing factor 8





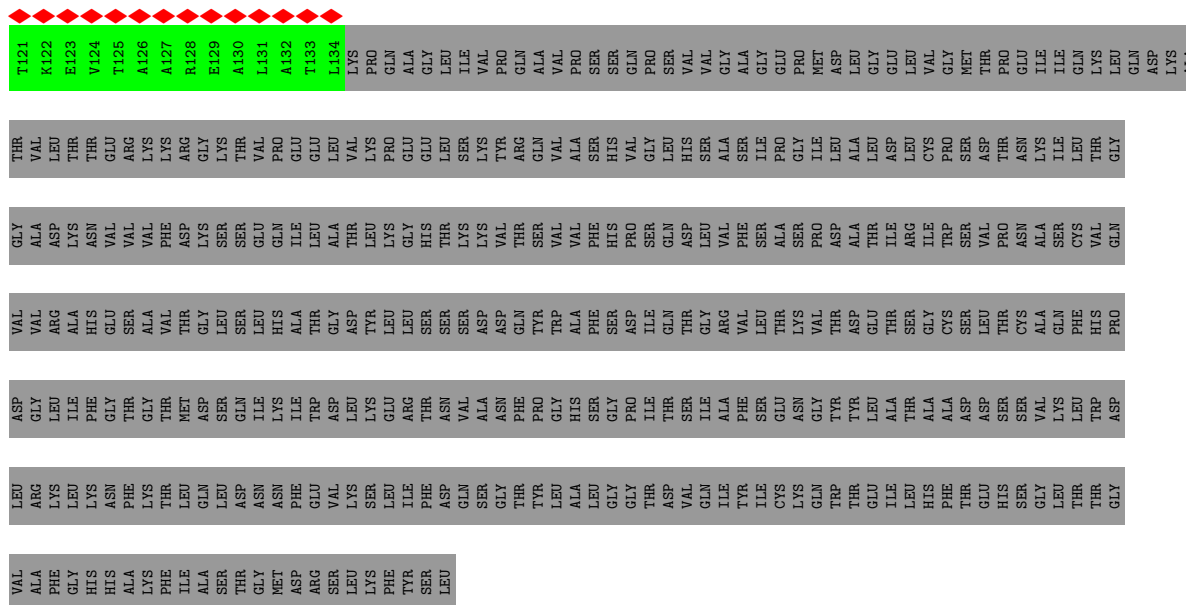


• Molecule 7: Pre-mRNA-processing factor 17

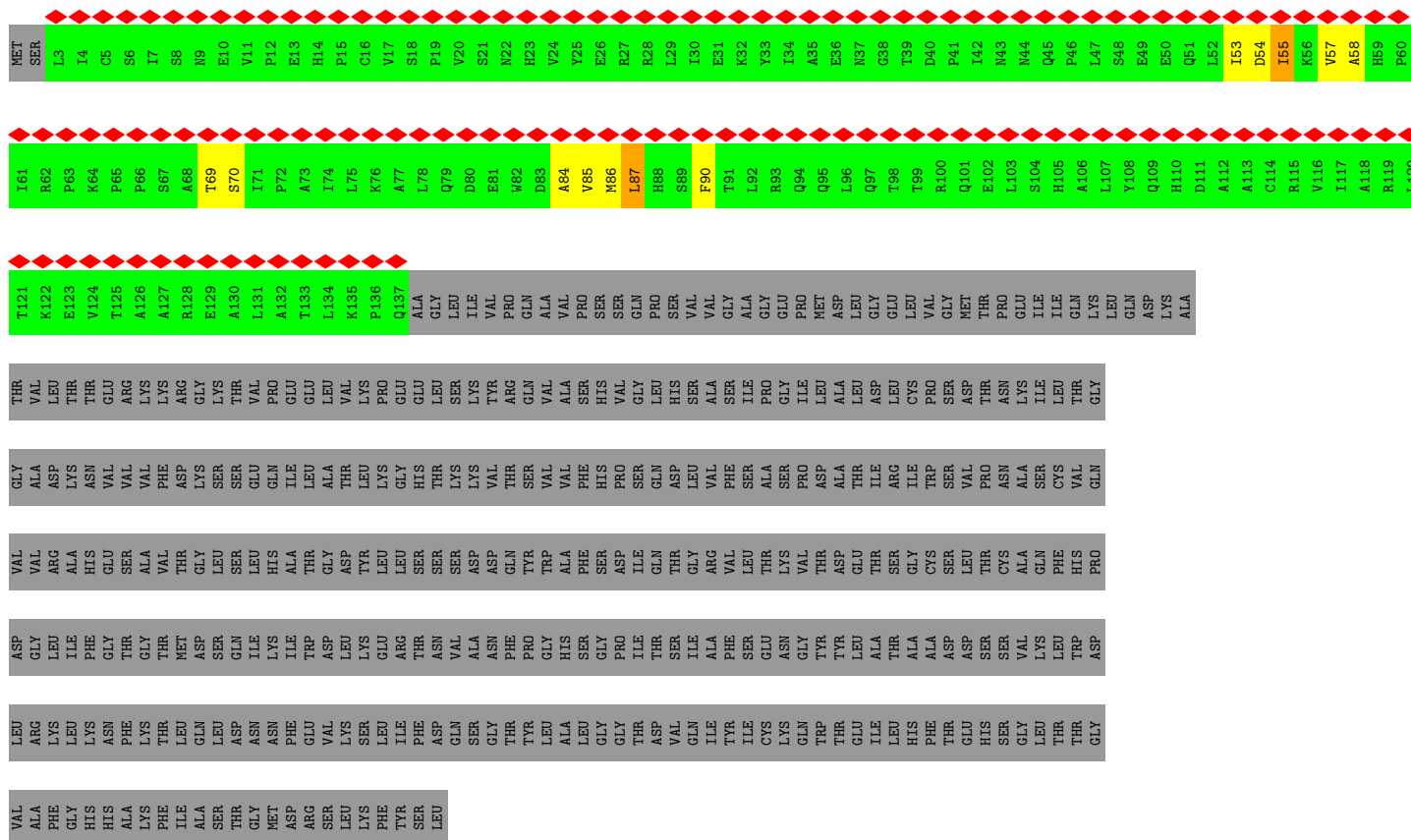


• Molecule 8: Pre-mRNA-processing factor 19

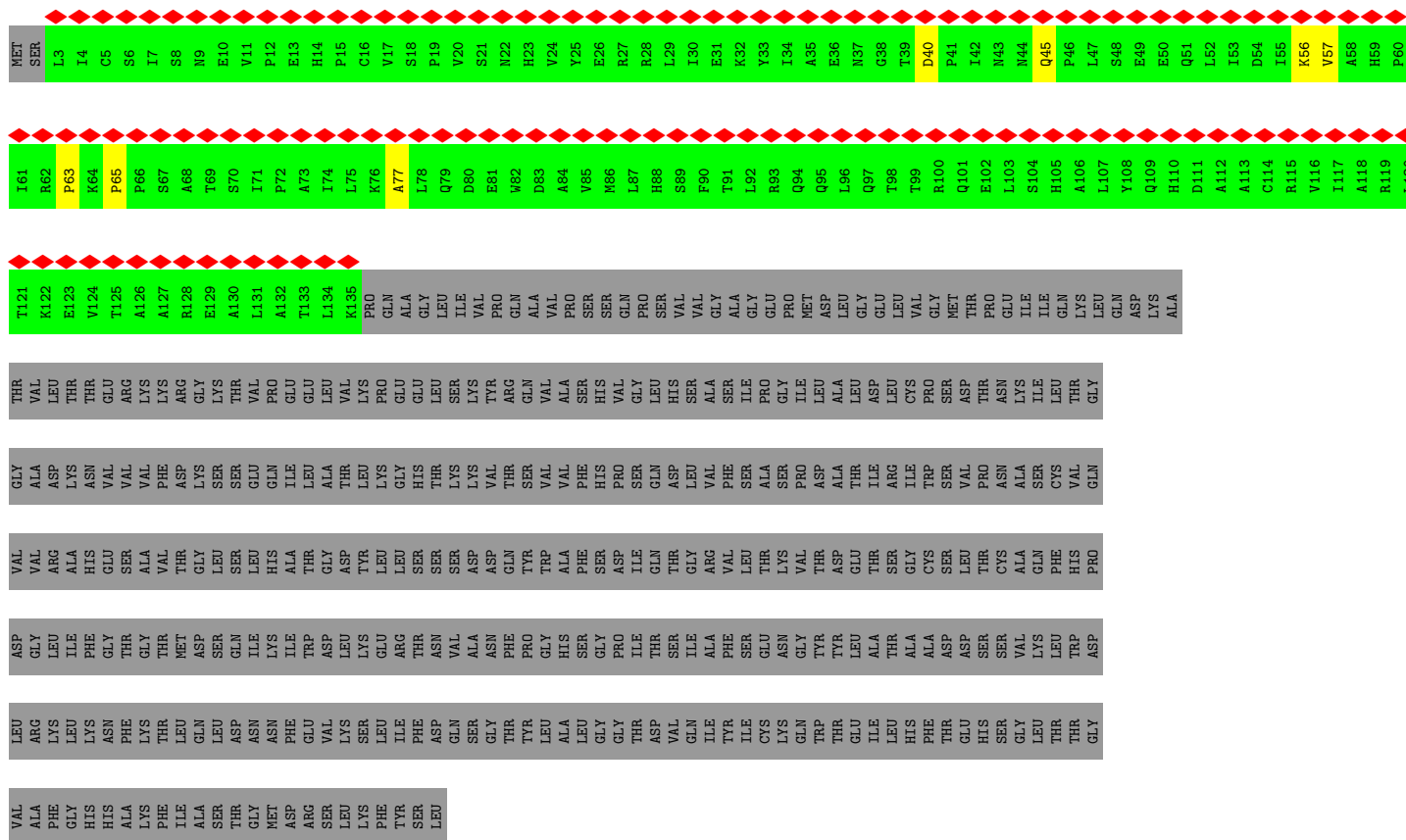




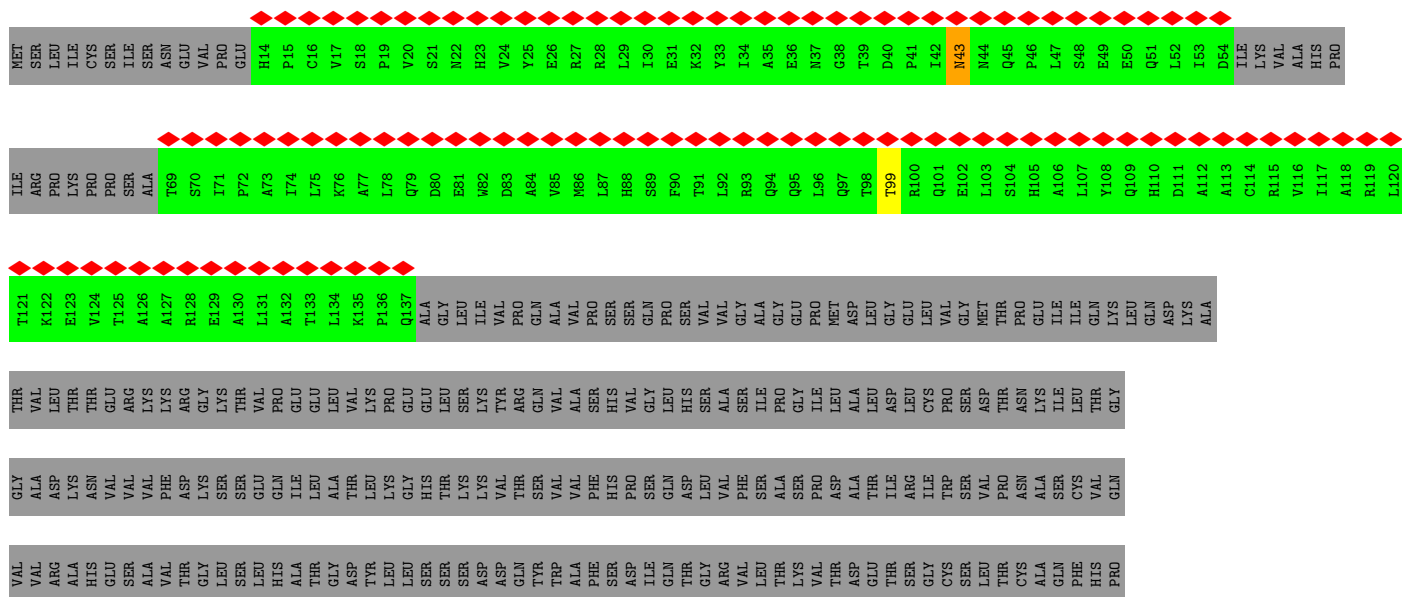
- Molecule 8: Pre-mRNA-processing factor 19



- Molecule 8: Pre-mRNA-processing factor 19



- Molecule 8: Pre-mRNA-processing factor 19





[illegible]

- Molecule 15: Serine/arginine repetitive matrix protein 2

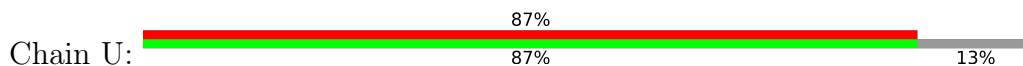
Chain S: 98%

[illegible]



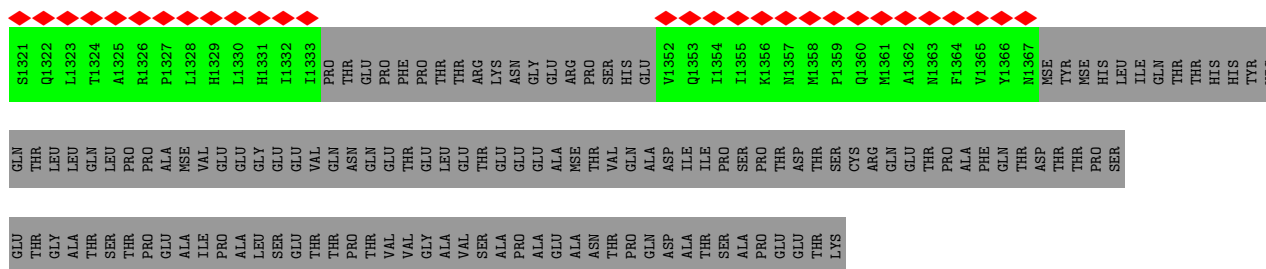
[illegible]

- Molecule 17: Intron-binding protein aquarius

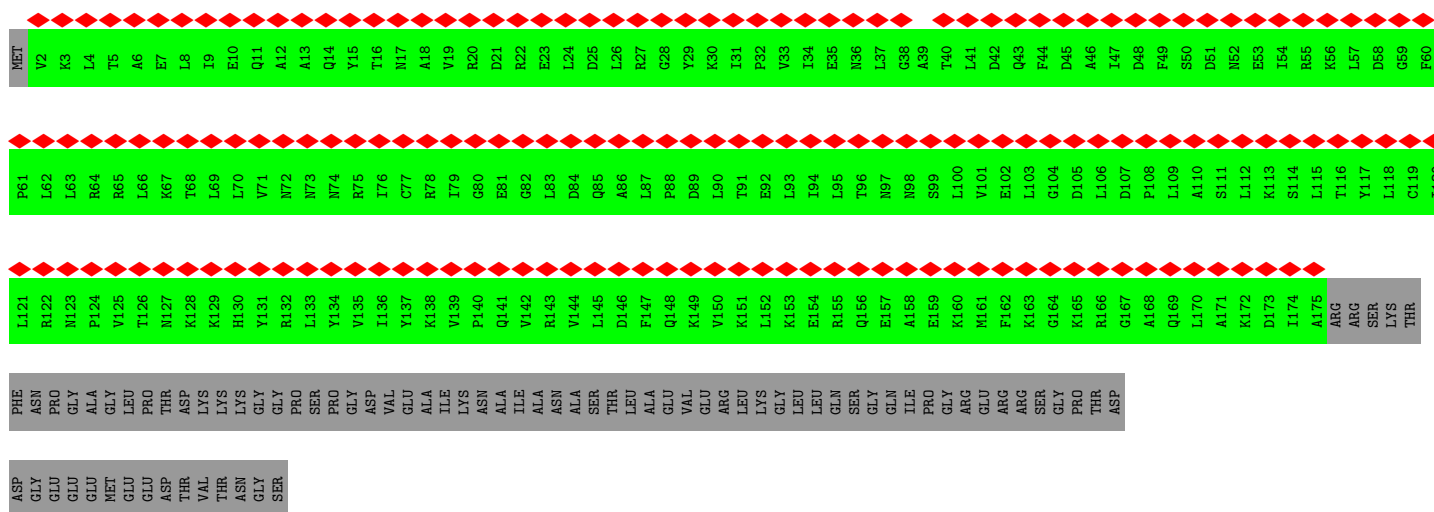


MSE	ALA	ALA	ALA	ALA	GLN	PRO	LYS	ILE	VAL	ALA	PRO	THR	VAL	SER	GLN	ILE	M19	A20	E21	F22	V23	Q25	L26	A27	C28	K29	Y30	X31	A32	P33	H34	I35	K36	K37	K38	S39	P40	F41	D42	I43	K44	V45	I46	E47	D48	I49	Y50	E51	K52	E53	I54	V55	S57	R58	F59	A60								
	R62	R62	F122	F122	K124	H125	I126	L127	K128	A129	A130	L131	A132	E133	L134	E74	M75	Y76	L77	M78	M79	N80	H81	S82	P83	E84	V85	S86	S87	K88	A89	Y90	L91	M92	E93	S93	I94	C95	C96	M97	V98	N99	V100	E101	K101	F102	R103	E104	M105	V106	P107	A108	M109	E110	I111	F112	K113	M114	K115	P116	D117	H118	Y119	P120
	F121	F121	R182	R182	L183	E184	L185	E186	L187	K188	K189	T190	K192	L193	R194	E195	F196	Y197	M198	L199	I200	K201	K202	E203	D204	E205	K206	M207	L208	P209	E210	A211	H212	E213	Q214	A215	Y216	Q217	E218	R219	R220	F221	L222	Q223	Q224	L225	L226	Q227	K228	F229	I230	S231	V232	L233	K234	M235	V236	P237	L238	Y239	E240			
	P241	P242	T243	M244	D245	K246	V247	H248	C250	E251	R252	F253	L254	E255	L256	M257	L258	D259	L260	E261	A262	L263	L264	P265	T266	R267	K268	W269	F270	N271	T272	L273	L274	D275	D276	S277	H278	L279	L280	V281	H282	C283	Y284	L285	S286	N287	L288	V289	R290	R291	E292	E293	D294	G295	H296	L297	F298	S299	Q300					
	L301	L302	E303	M304	L305	K306	F307	Y308	T309	G310	F311	E312	L313	N314	D315	Q316	T317	G318	N319	A320	L321	T322	E323	N324	E325	M326	T327	T328	I329	H330	Y331	D332	R333	I334	T335	S336	L337	Q338	R339	A340	A341	F342	A343	H344	F345	P346	E347	L348	Y349	D350	F351	A352	L353	S354	N355	V356	A357	E358	V359	D360				
	T361	R362	E363	S364	L365	V366	K367	F368	F369	G370	P371	L372	S373	S374	N375	T376	L377	H378	Q379	V380	A381	S382	Y383	L384	C385	L386	L387	P388	T389	L390	P391	K392	N393	E394	D395	T396	T397	F398	D399	K400	E401	F402	L403	L404	E405	L406	L407	V408	S409	R410	H411	E412	R413	R414	I415	S416	Q417	I418	Y419	Q420				
	L421	M422	Q423	M424	P425	L426	Y427	P428	T429	E430	K431	I432	I433	M434	D435	E436	M437	I438	V439	P440	T441	E442	F443	Y444	S445	G446	E447	G448	C449	L450	A451	L452	P453	K454	L455	M456	L457	Q458	F459	L460	T461	L462	H463	D464	Y465	L466	L467	R468	M469	F470	M471	L472	F473	R474	L475	E476	S477	T478	Y479	E480				
	I481	R482	Q483	D484	I485	E486	D487	S488	V489	S490	M491	M492	K493	P494	M495	Q496	S497	E498	Y499	G500	G501	V502	F503	F504	G505	G506	V507	A508	R509	M510	A511	Q512	P513	I514	V515	A516	F517	T518	V519	V520	E521	V522	A523	K524	P525	N526	I527	G528	E529	M530	M531	P532	T533	R534	V535	R536	A537	D538	V539	T540				

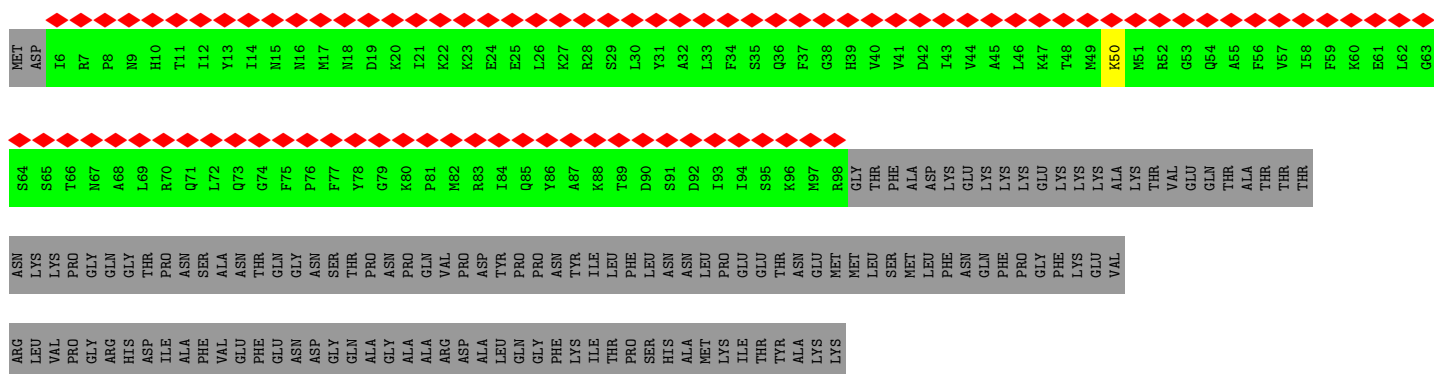
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- Molecule 18: U2 small nuclear ribonucleoprotein A'



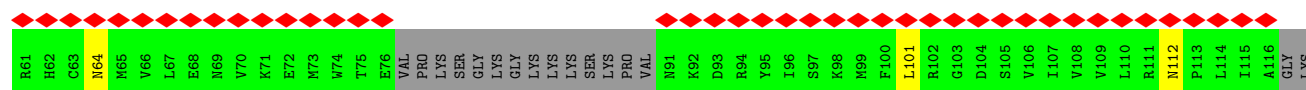
- Molecule 19: U2 small nuclear ribonucleoprotein B''



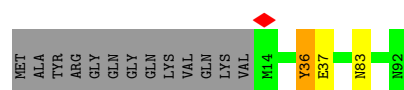
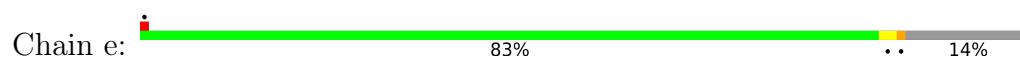
- Molecule 20: pre-mRNA



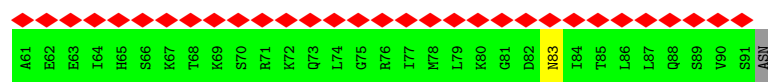
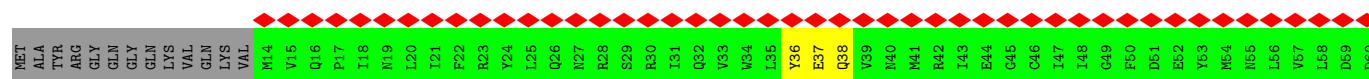
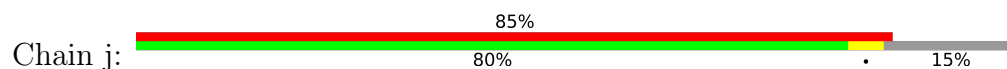
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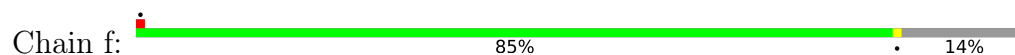
- Molecule 25: Small nuclear ribonucleoprotein E



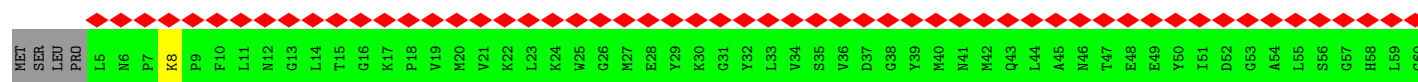
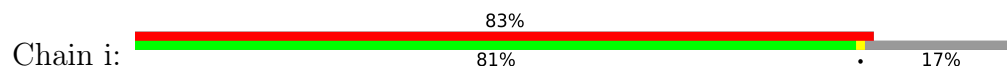
- Molecule 25: Small nuclear ribonucleoprotein E



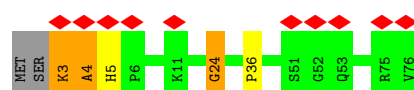
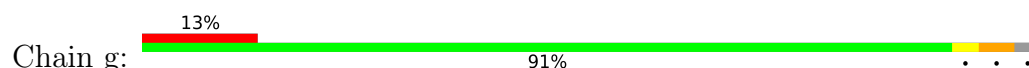
- Molecule 26: Small nuclear ribonucleoprotein F



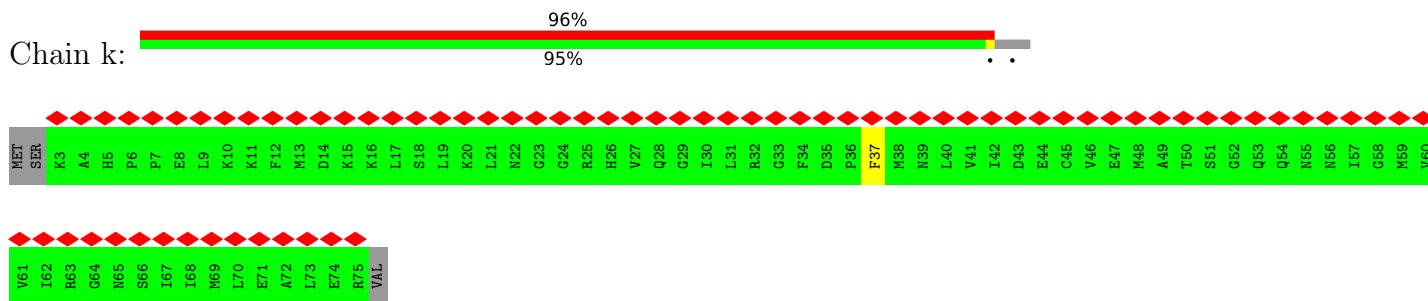
- Molecule 26: Small nuclear ribonucleoprotein F



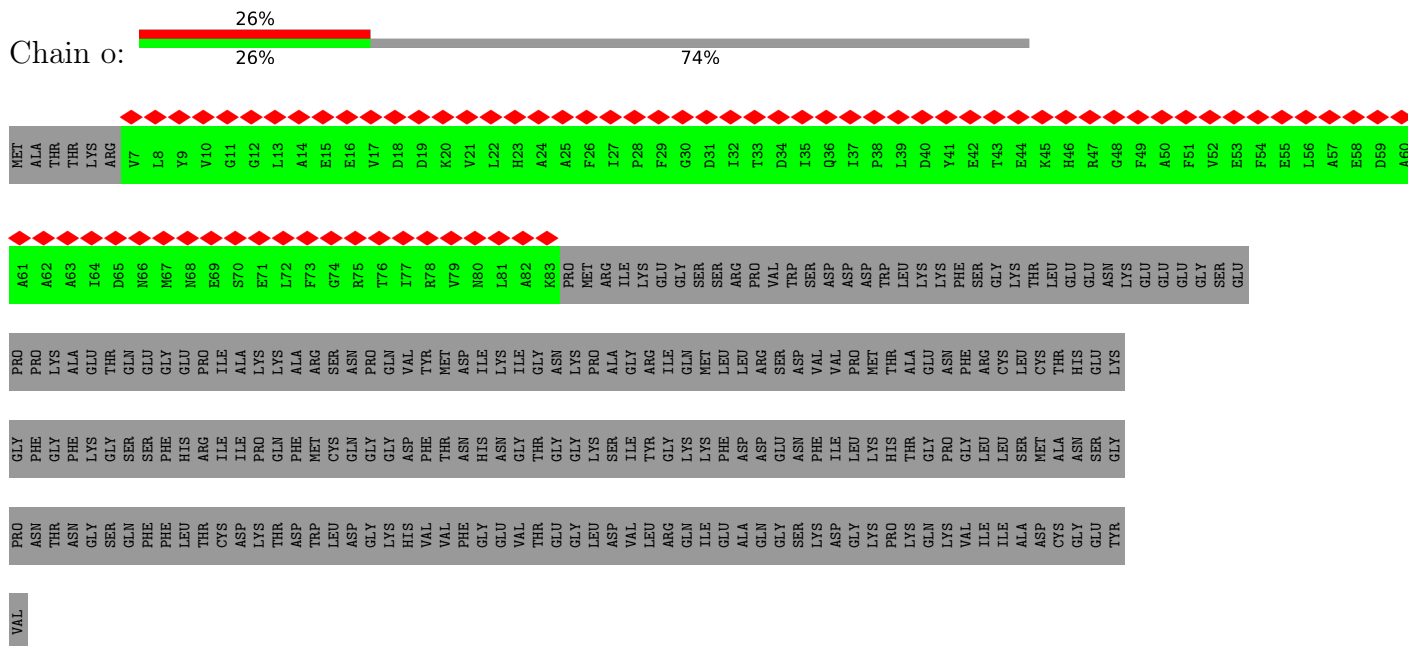
- Molecule 27: Small nuclear ribonucleoprotein G



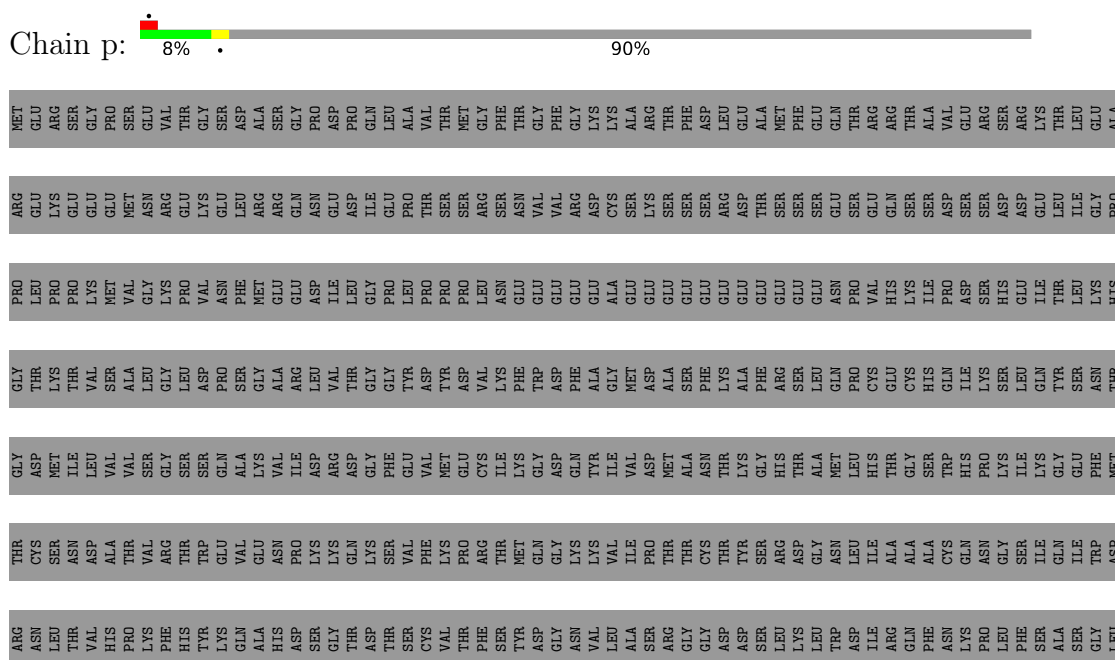
- Molecule 27: Small nuclear ribonucleoprotein G



- Molecule 28: Peptidyl-prolyl cis-trans isomerase E



- Molecule 29: WD repeat-containing protein 70



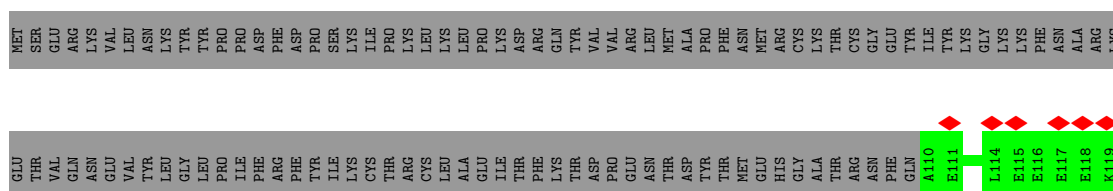


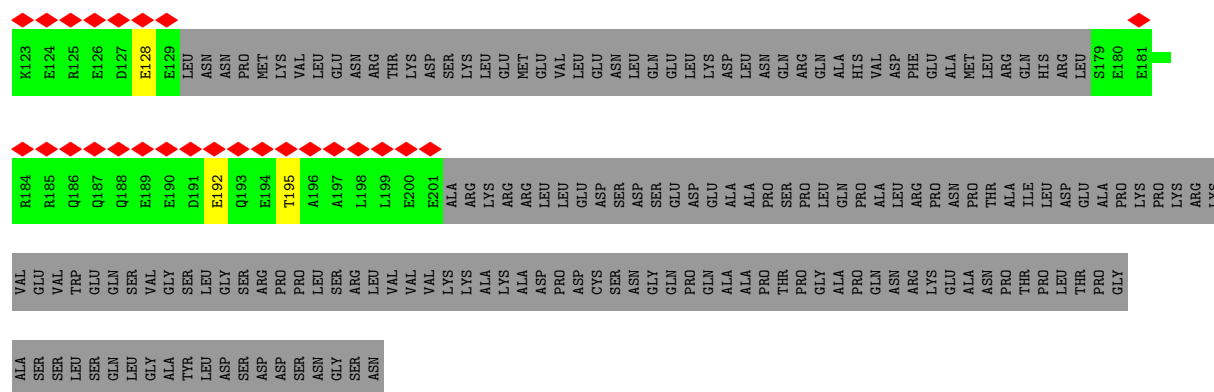
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F1325	Q1265	K1145	T1085	K1025	D965	I905	G845	H785	V725	L665	Y605
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D1343	P1283	E1163	G1103	E1043	E983	A923	T863	D803	L743	D683	D623
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V1358	Y1238	V1178	I1118	K1058	V998	I938	Y878	G818	S758	I698	N638
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R2060	T2000	L1940	N1880	A1820	L1760	G1700	A1640	C1580	P1520	G1460	R1400
E2061	D2001	A1941	N1881	Y1821	Y1761	R1701	I1641	A1581	V1521	G1461	L1401
E2062	S2002	A1942	P1882	Y1822	R1762	C1702	Q1642	A1582	P1522	E1462	M1402
G2063	Q2003	M1943	K1883	Y1823	R1763	V1703	V1643	D1583	L1523	N1463	K1403
V2064	L2004	E1944	F1884	I1824	M1764	I1704	V1644	I1584	E1524	G1464	K1404
V2065	A2005	L1945	N1885	M1825	T1765	M1705	V1645	Q1585	L1525	P1465	V1405
V2066	D2006	A1946	L1886	Y1826	Q1766	C1706	A1646	R1586	H1526	V1466	V1406
V2067	V2007	Q1947	P1887	T1827	M1767	Q1707	S1647	Q1587	I1527	L1467	L1407
I2068	A2008	M1948	H1888	T1828	P1768	G1708	R1648	R1588	Q1528	E1468	L1408
G2069	R2009	V1949	V1889	I1829	M1769	S1709	S1649	F1589	F1529	I1469	T1409
D2070	F2010	L1950	K1890	E1830	Y1770	K1710	L1650	L1590	G1530	G1470	G1410
A2071	C2011	Q1951	T1891	L1831	Y1771	K1711	C1651	H1591	M1531	C1471	E1411
K2072	N2012	A1952	N1892	F1832	M1772	D1712	W1652	C1592	I1532	T1472	T1412
S2073	R2013	M1953	L1893	S1833	L1773	F1713	G1653	T1593	S1533	R1473	S1413
N2074	Y2014	W1954	L1894	M1834	Q1774	F1714	M1654	E1594	H1534	M1474	T1414
S2075	P2015	S1955	L1895	S1835	G1775	K1715	N1655	K1595	T1535	R1475	D1415
L2076	N2016	K1956	Q1896	L1836	I1776	K1716	V1656	D1596	Q1536	Y1476	L1416
I2077	E2017	D1957	A1897	M1837	S1777	F1717	A1657	L1597	T1537	I1477	K1417
S2078	L2018	S1958	H1898	A1838	H1778	L1718	A1658	I1598	R1538	S1478	L1418
I2079	L2019	Y1959	L1899	K1839	R1779	Y1719	H1659	P1599	L1539	S1479	L1419
K2080	S2020	L1960	S1900	T1840	H1780	E1720	L1660	Y1600	L1540	Q1480	G1420
R2081	Y2021	K1961	R1901	K1841	L1781	P1721	V1661	L1601	S1541	I1481	K1421
L2082	E2022	Q1962	M1902	V1842	S1782	L1722	I1662	E1602	M1542	I1482	G1422
T2083	V2023	L1963	Q1903	R1843	D1783	P1723	I1663	K1603	A1543	R1483	N1423
L2084	V2024	P1964	L1904	G1844	H1784	V1724	M1664	L1604	P1544	P1484	I1424
Q2085	D2025	H1965	S1905	L1845	L1785	E1725	D1665	S1605	P1545	I1485	I1425
Q2086	K2026	F1966	A1906	I1846	S1786	S1726	T1666	D1606	V1546	R1486	I1426
K2087	D2027	T1967	E1907	E1847	E1787	H1727	Q1667	S1607	Y1547	I1487	S1427
A2088	S2028	S1968	L1908	I1848	L1788	L1728	Y1668	T1608	H1548	V1488	L1428
K2089	I2029	E1969	Q1909	I1849	V1789	D1729	Y1669	L1609	A1549	A1489	P1429
V2090	R2030	H1970	S1910	S1850	E1790	K1730	M1670	K1610	I1550	L1490	E1430
K2091	S2031	I1971	D1911	M1851	Q1791	C1731	G1671	E1611	T1551	S1491	K1431
L2092	G2032	K1972	T1912	A1852	T1792	M1732	K1672	T1612	K1552	S1492	W1432
D2093	G2033	R1973	E1913	A1853	L1793	D1733	I1673	L1613	H1553	S1493	D1433
F2094	P2034	C1974	E1914	E1854	H1794	H1734	H1674	L1614	S1554	L1494	T1434
V2095	V2035	T1975	I1915	Y1855	D1795	H1735	A1675	N1615	P1555	S1495	L1435
A2096	V2036	D1976	L1916	E1856	L1796	F1736	Y1676	G1616	K1556	N1496	S1436
P2097	V2037	K1977	S1917	M1857	L1797	M1737	V1677	V1617	K1557	A1497	R1437
O2098	L2038	Q1978	K1918	I1858	Q1798	L1738	D1678	G1618	P1558	K1498	R1438
T2099	V2039	V1979	A1919	P1859	S1799	E1739	Y1679	Y1619	V1559	D1499	W1439
G2100	Q2040	E1980	I1920	I1860	K1800	I1740	P1680	L1620	I1560	V1500	L1440
A2101											
H2102											
N2103											
Y2104											
T2105											
L2106											
V2107											
F2108											
T2109											
S2110											
D2111											
A2112											
V2113											
M2114											
G2115											
C2116											
D2117											
Q2118											
E2119											
V2120											
K2121											
F2122											
S2123											
V2124											
V2125											
VAL											
LYS											
GLU											
ALA											
GLU											
THR											
ASP											
SER											
ASP											
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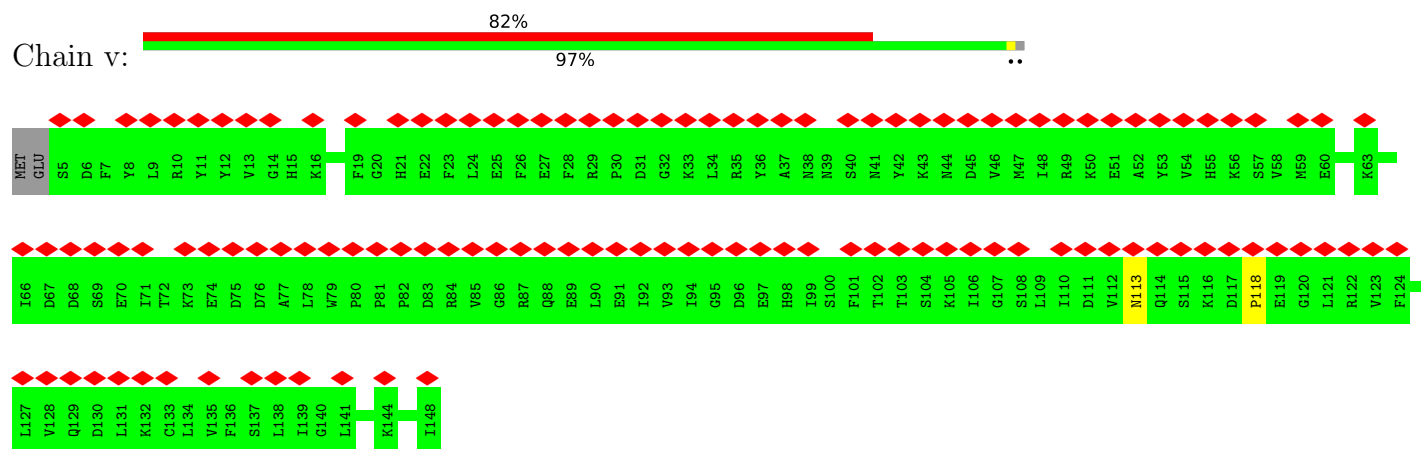
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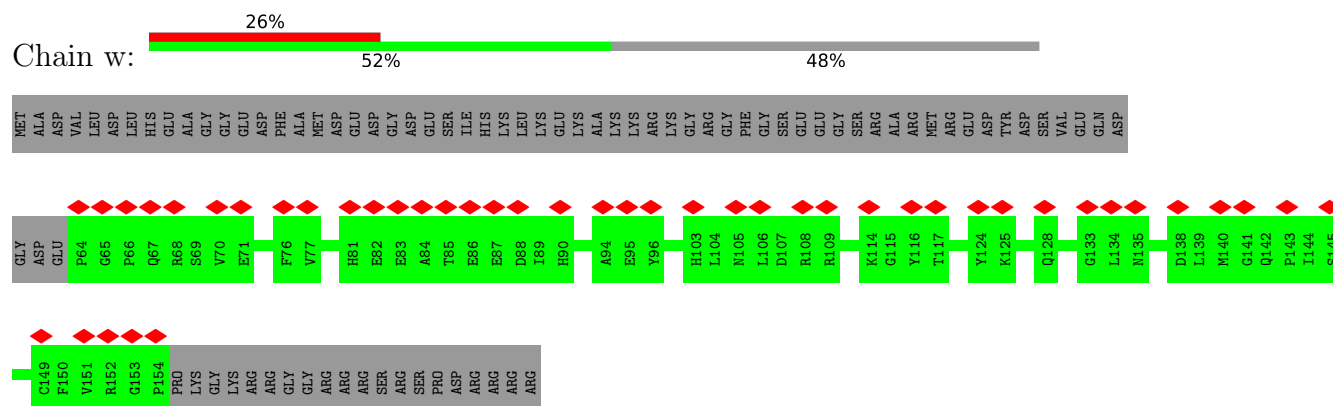




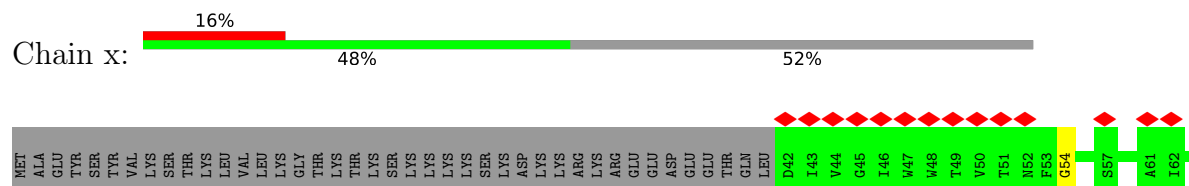
• Molecule 34: Protein mago nashi homolog



• Molecule 35: RNA-binding protein 8A



• Molecule 36: Protein FRG1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	69000	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	6	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.109	Depositor
Minimum map value	-0.033	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.018	Depositor
Map size (Å)	466.39996, 466.39996, 466.39996	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	2	0.30	0/3166	0.66	1/4915 (0.0%)
2	5	1.34	7/794 (0.9%)	1.07	10/1228 (0.8%)
3	6	0.20	0/328	0.58	0/508
5	A	0.29	0/2500	0.72	9/3491 (0.3%)
6	C	0.13	0/74	0.38	0/102
7	E	0.35	0/1534	0.88	3/2142 (0.1%)
8	G	0.53	1/688 (0.1%)	0.96	6/969 (0.6%)
8	H	0.49	0/706	1.02	5/995 (0.5%)
8	I	0.41	0/693	0.89	1/976 (0.1%)
8	J	0.44	0/565	0.93	3/792 (0.4%)
9	K	0.38	0/686	0.80	3/953 (0.3%)
10	L	0.20	0/572	0.50	0/796
11	M	0.30	1/3406 (0.0%)	0.61	4/4767 (0.1%)
12	N	0.64	0/371	1.14	1/519 (0.2%)
13	O	0.38	0/1325	0.95	5/1850 (0.3%)
14	P	0.33	0/454	0.98	5/633 (0.8%)
15	S	0.37	0/228	0.92	2/317 (0.6%)
16	T	0.15	0/1278	0.45	0/1788
17	U	0.26	0/6574	0.58	5/9159 (0.1%)
18	W	0.26	0/879	0.73	0/1229
19	X	0.38	0/468	0.72	0/653
20	Y	0.40	0/375	1.10	0/572
21	a	0.33	0/359	0.62	0/499
21	l	0.64	1/417 (0.2%)	0.79	1/581 (0.2%)
22	b	0.25	0/326	0.67	0/451
22	m	0.23	0/352	0.72	0/489
23	c	0.24	0/409	0.63	0/571
23	n	0.30	0/414	0.64	0/578
24	d	0.24	0/406	0.62	0/565
24	h	0.42	0/421	0.85	0/586
25	e	0.33	0/393	0.70	0/547
25	j	0.28	0/388	0.72	0/540
26	f	0.36	0/372	0.65	0/517
26	i	0.53	1/354 (0.3%)	0.68	0/491

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
27	g	0.70	2/371 (0.5%)	0.99	4/516 (0.8%)
27	k	0.43	0/366	0.74	1/509 (0.2%)
28	o	0.22	0/385	0.56	0/536
29	p	0.72	0/332	1.55	4/459 (0.9%)
30	q	0.27	0/9636	0.73	23/13498 (0.2%)
31	r	0.39	3/3001 (0.1%)	0.81	13/4192 (0.3%)
32	s	0.20	0/374	0.62	0/518
33	u	0.52	0/214	1.10	2/296 (0.7%)
34	v	0.27	0/728	0.63	0/1017
35	w	0.19	0/456	0.50	0/633
36	x	0.29	0/622	0.63	0/860
37	y	0.23	0/1962	0.64	0/2741
38	z	0.39	1/2313 (0.0%)	0.82	6/3222 (0.2%)
All	All	0.37	17/53035 (0.0%)	0.74	117/74766 (0.2%)

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
2	5	1	0
5	A	0	5
7	E	0	3
8	G	0	3
8	H	0	4
8	I	0	1
8	J	0	1
9	K	0	1
11	M	0	2
12	N	0	1
13	O	0	3
17	U	0	2
24	d	0	1
24	h	0	1
25	e	0	1
26	f	0	1
27	g	0	1
29	p	0	3
30	q	0	12
31	r	0	5
33	u	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
37	y	0	1
38	z	0	5
All	All	1	58

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5	86	C	P-O5'	25.29	1.97	1.59
2	5	86	C	P-OP1	16.32	1.81	1.49
2	5	86	C	C5'-C4'	10.20	1.66	1.51
2	5	86	C	C4'-C3'	-9.08	1.39	1.52
2	5	86	C	C3'-C2'	8.21	1.65	1.52

The worst 5 of 117 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	86	C	C5'-C4'-C3'	13.56	136.34	116.00
8	J	43	ASN	CB-CA-C	-10.97	92.58	110.79
2	5	86	C	O4'-C4'-C3'	10.21	114.21	104.00
2	5	86	C	OP2-P-O3'	-9.81	78.56	108.00
2	5	85	C	OP1-P-O3'	-9.79	78.64	108.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	5	86	C	C4'

5 of 58 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	A	1757	GLU	Mainchain,Peptide
5	A	1759	THR	Peptide
5	A	1760	GLU	Mainchain
5	A	1773	SER	Peptide
7	E	284	TRP	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	2854	0	1442	18	0
2	5	718	0	363	12	0
3	6	296	0	149	1	0
4	8	376	0	82	0	0
5	A	2485	0	1164	10	0
6	C	75	0	35	0	0
7	E	1525	0	724	5	0
8	G	679	0	356	2	0
8	H	696	0	367	3	0
8	I	684	0	358	3	0
8	J	561	0	285	0	0
9	K	689	0	315	5	0
10	L	573	0	264	0	0
11	M	3387	0	1651	4	0
12	N	369	0	171	0	0
13	O	1320	0	635	4	0
14	P	452	0	229	1	0
15	S	229	0	95	1	0
16	T	1271	0	594	0	0
17	U	6546	0	3178	0	0
18	W	874	0	421	0	0
19	X	466	0	220	1	0
20	Y	348	0	176	0	0
21	a	358	0	168	1	0
21	l	415	0	198	1	0
22	b	327	0	143	1	0
22	m	351	0	161	2	0
23	c	407	0	186	1	0
23	n	412	0	188	0	0
24	d	406	0	179	0	0
24	h	421	0	185	1	0
25	e	393	0	169	2	0
25	j	388	0	167	2	0
26	f	369	0	182	0	0
26	i	352	0	171	0	0
27	g	369	0	178	4	0
27	k	364	0	176	0	0
28	o	384	0	198	0	0
29	p	333	0	153	2	0
30	q	9558	0	4623	12	0
31	r	2982	0	1461	3	0
32	s	376	0	172	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	u	216	0	96	1	0
34	v	723	0	335	1	0
35	w	453	0	227	0	0
36	x	621	0	315	1	0
37	y	1951	0	928	0	0
38	z	2301	0	1090	6	0
All	All	52703	0	25323	94	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 1.

The worst 5 of 94 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)
2:5:86:C:P	2:5:86:C:O5'	1.97	1.22
5:A:1853:PRO:CB	36:x:54:GLY:O	1.98	1.10
38:z:201:GLY:HA3	38:z:222:HIS:HA	1.59	0.84
38:z:377:GLY:HA2	38:z:393:GLY:HA2	1.69	0.74
2:5:86:C:P	2:5:86:C:C5'	2.82	0.66

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	
5	A	483/2335 (21%)	418 (86%)	58 (12%)	7 (1%)	9	38
6	C	13/536 (2%)	13 (100%)	0	0	100	100
7	E	303/579 (52%)	275 (91%)	26 (9%)	2 (1%)	18	55
8	G	130/504 (26%)	115 (88%)	10 (8%)	5 (4%)	2	18
8	H	133/504 (26%)	115 (86%)	15 (11%)	3 (2%)	5	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	I	131/504 (26%)	122 (93%)	8 (6%)	1 (1%)	16	53
8	J	106/504 (21%)	102 (96%)	4 (4%)	0	100	100
9	K	130/225 (58%)	119 (92%)	7 (5%)	4 (3%)	3	21
10	L	111/802 (14%)	110 (99%)	1 (1%)	0	100	100
11	M	662/855 (77%)	590 (89%)	71 (11%)	1 (0%)	43	77
12	N	71/243 (29%)	58 (82%)	10 (14%)	3 (4%)	2	17
13	O	249/848 (29%)	214 (86%)	27 (11%)	8 (3%)	3	20
14	P	88/420 (21%)	70 (80%)	18 (20%)	0	100	100
15	S	44/2752 (2%)	41 (93%)	3 (7%)	0	100	100
16	T	251/908 (28%)	245 (98%)	6 (2%)	0	100	100
17	U	1281/1485 (86%)	1258 (98%)	21 (2%)	2 (0%)	43	77
18	W	172/255 (68%)	162 (94%)	10 (6%)	0	100	100
19	X	91/225 (40%)	87 (96%)	4 (4%)	0	100	100
21	a	70/126 (56%)	68 (97%)	2 (3%)	0	100	100
21	l	81/126 (64%)	80 (99%)	1 (1%)	0	100	100
22	b	62/240 (26%)	61 (98%)	1 (2%)	0	100	100
22	m	66/240 (28%)	65 (98%)	1 (2%)	0	100	100
23	c	79/119 (66%)	78 (99%)	1 (1%)	0	100	100
23	n	80/119 (67%)	79 (99%)	1 (1%)	0	100	100
24	d	77/118 (65%)	75 (97%)	2 (3%)	0	100	100
24	h	80/118 (68%)	77 (96%)	3 (4%)	0	100	100
25	e	77/92 (84%)	75 (97%)	2 (3%)	0	100	100
25	j	76/92 (83%)	75 (99%)	0	1 (1%)	9	40
26	f	72/86 (84%)	70 (97%)	2 (3%)	0	100	100
26	i	69/86 (80%)	68 (99%)	1 (1%)	0	100	100
27	g	72/76 (95%)	72 (100%)	0	0	100	100
27	k	71/76 (93%)	71 (100%)	0	0	100	100
28	o	75/301 (25%)	74 (99%)	1 (1%)	0	100	100
29	p	66/654 (10%)	38 (58%)	20 (30%)	8 (12%)	0	4
30	q	1888/2136 (88%)	1796 (95%)	80 (4%)	12 (1%)	21	58
31	r	581/1227 (47%)	544 (94%)	33 (6%)	4 (1%)	18	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	s	72/285 (25%)	68 (94%)	4 (6%)	0	100	100
33	u	39/323 (12%)	36 (92%)	3 (8%)	0	100	100
34	v	142/146 (97%)	141 (99%)	1 (1%)	0	100	100
35	w	89/174 (51%)	88 (99%)	1 (1%)	0	100	100
36	x	117/258 (45%)	109 (93%)	8 (7%)	0	100	100
37	y	388/411 (94%)	382 (98%)	6 (2%)	0	100	100
38	z	448/646 (69%)	411 (92%)	34 (8%)	3 (1%)	18	55
All	All	9386/22759 (41%)	8815 (94%)	507 (5%)	64 (1%)	20	55

5 of 64 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	A	1758	PRO
5	A	1760	GLU
5	A	1762	TYR
7	E	318	VAL
8	G	57	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	
5	A	20/2108 (1%)	19 (95%)	1 (5%)	22	43
7	E	10/502 (2%)	10 (100%)	0	100	100
8	G	10/435 (2%)	8 (80%)	2 (20%)	1	7
8	H	11/435 (2%)	11 (100%)	0	100	100
8	I	10/435 (2%)	10 (100%)	0	100	100
8	J	6/435 (1%)	6 (100%)	0	100	100
9	K	1/196 (0%)	1 (100%)	0	100	100
10	L	1/709 (0%)	1 (100%)	0	100	100
11	M	24/749 (3%)	24 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	N	3/209 (1%)	2 (67%)	1 (33%)	0	2
13	O	11/751 (2%)	10 (91%)	1 (9%)	9	28
14	P	4/361 (1%)	4 (100%)	0	100	100
16	T	8/838 (1%)	8 (100%)	0	100	100
17	U	68/1297 (5%)	68 (100%)	0	100	100
18	W	6/218 (3%)	6 (100%)	0	100	100
19	X	3/195 (2%)	3 (100%)	0	100	100
21	a	2/101 (2%)	2 (100%)	0	100	100
21	l	3/101 (3%)	3 (100%)	0	100	100
22	b	1/177 (1%)	1 (100%)	0	100	100
22	m	3/177 (2%)	3 (100%)	0	100	100
23	c	3/101 (3%)	3 (100%)	0	100	100
23	n	3/101 (3%)	3 (100%)	0	100	100
24	d	2/110 (2%)	2 (100%)	0	100	100
24	h	2/110 (2%)	2 (100%)	0	100	100
25	e	1/84 (1%)	1 (100%)	0	100	100
25	j	1/84 (1%)	1 (100%)	0	100	100
26	f	4/74 (5%)	4 (100%)	0	100	100
26	i	3/74 (4%)	3 (100%)	0	100	100
27	g	3/66 (4%)	3 (100%)	0	100	100
27	k	3/66 (4%)	3 (100%)	0	100	100
28	o	2/252 (1%)	2 (100%)	0	100	100
30	q	82/1908 (4%)	81 (99%)	1 (1%)	63	74
31	r	25/1075 (2%)	25 (100%)	0	100	100
33	u	1/289 (0%)	1 (100%)	0	100	100
34	v	6/134 (4%)	6 (100%)	0	100	100
35	w	4/143 (3%)	4 (100%)	0	100	100
36	x	5/223 (2%)	5 (100%)	0	100	100
37	y	12/361 (3%)	12 (100%)	0	100	100
38	z	18/572 (3%)	17 (94%)	1 (6%)	19	41
All	All	385/16256 (2%)	378 (98%)	7 (2%)	51	67

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	N	162	PRO
13	O	208	PRO
38	z	283	PRO
30	q	128	PRO
8	G	65	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	153/975 (15%)	53 (34%)	0
2	5	38/116 (32%)	18 (47%)	0
20	Y	27/324 (8%)	18 (66%)	0
3	6	15/106 (14%)	5 (33%)	0
All	All	233/1521 (15%)	94 (40%)	0

5 of 94 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	16	U
1	2	17	U
1	2	46	U
1	2	47	U
1	2	48	A

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	8	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	8	70:UNK	C	92:UNK	N	23.10
1	8	34:UNK	C	42:UNK	N	21.26
1	8	51:UNK	C	55:UNK	N	10.71

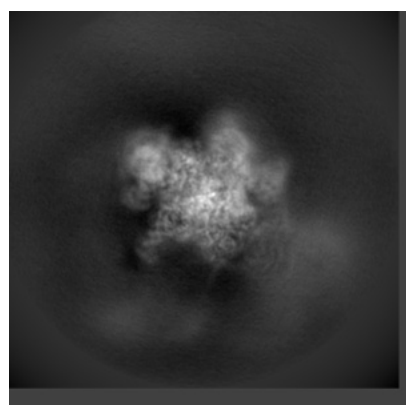
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11570. These allow visual inspection of the internal detail of the map and identification of artifacts.

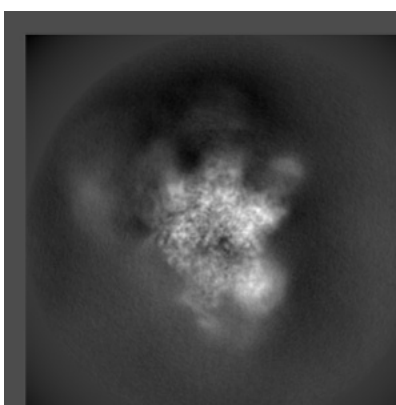
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

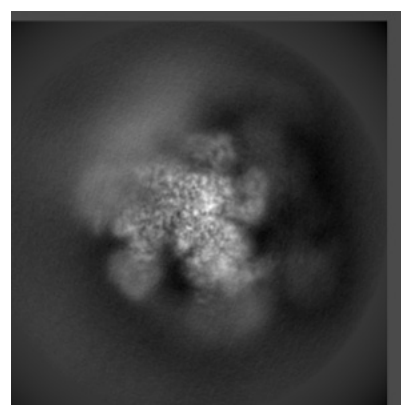
6.1.1 Primary map



X



Y

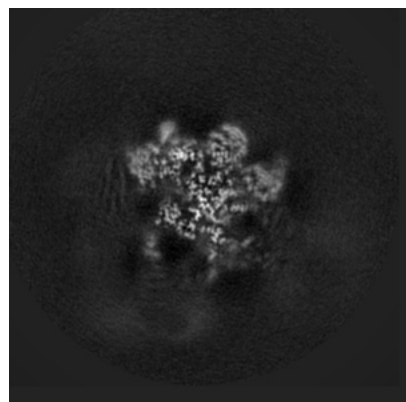


Z

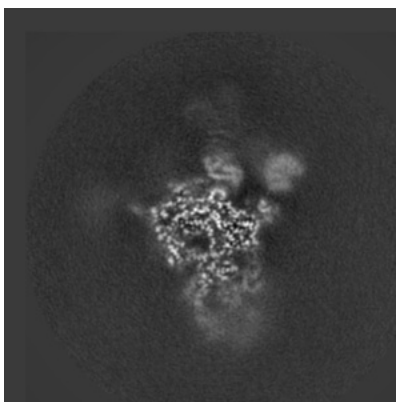
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

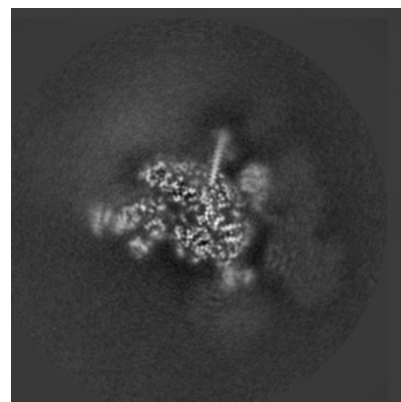
6.2.1 Primary map



X Index: 220



Y Index: 220

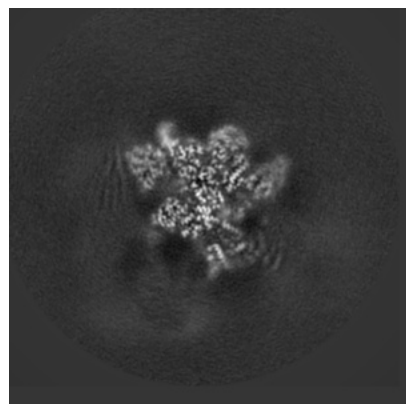


Z Index: 220

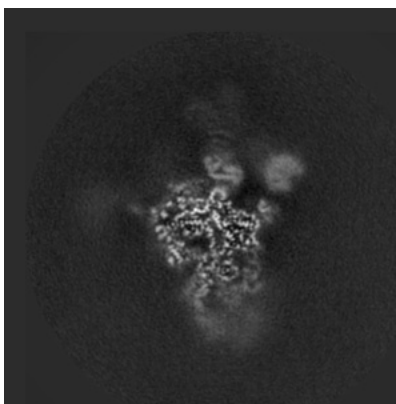
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

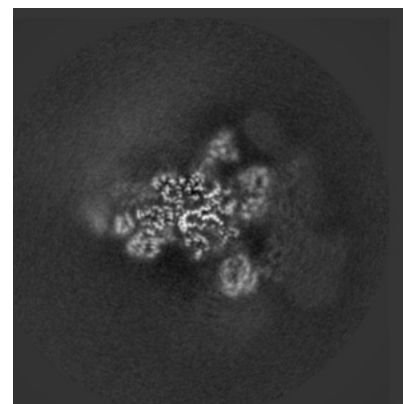
6.3.1 Primary map



X Index: 215



Y Index: 219

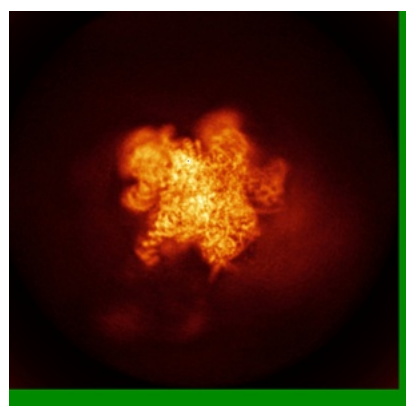


Z Index: 231

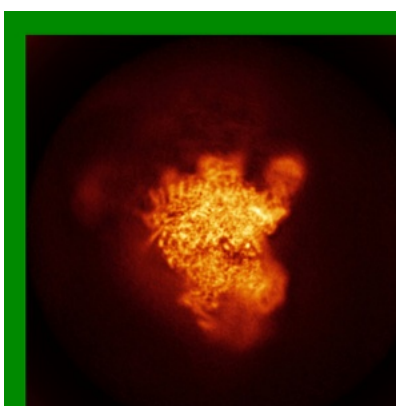
The images above show the largest variance slices of the map in three orthogonal directions.

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

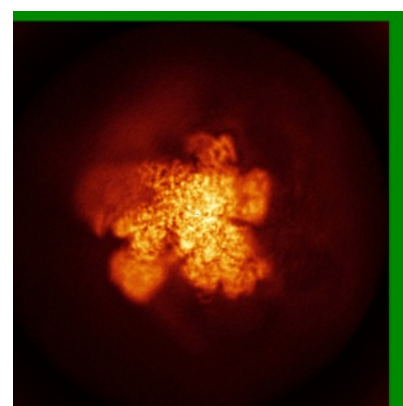
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.018. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

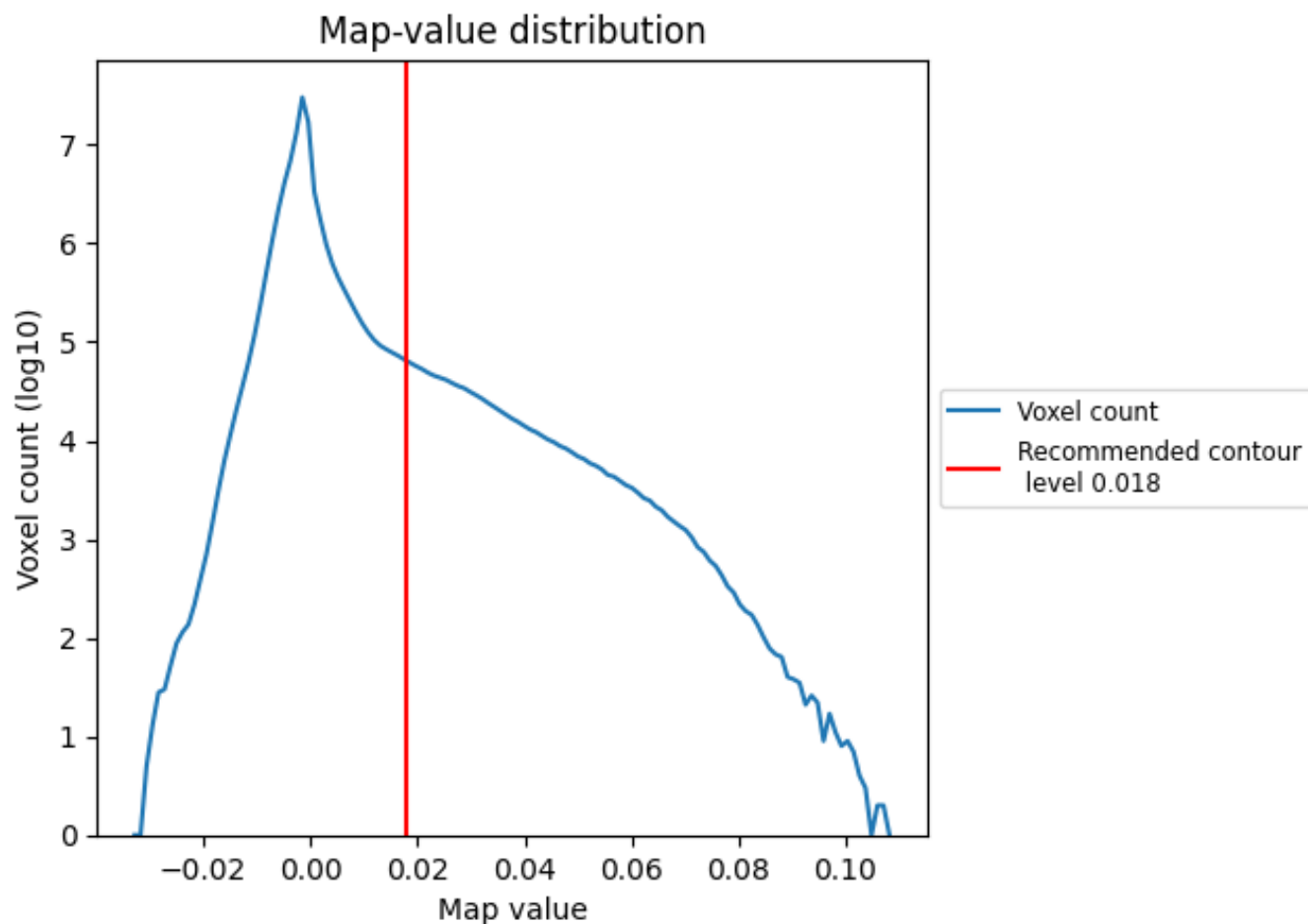
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

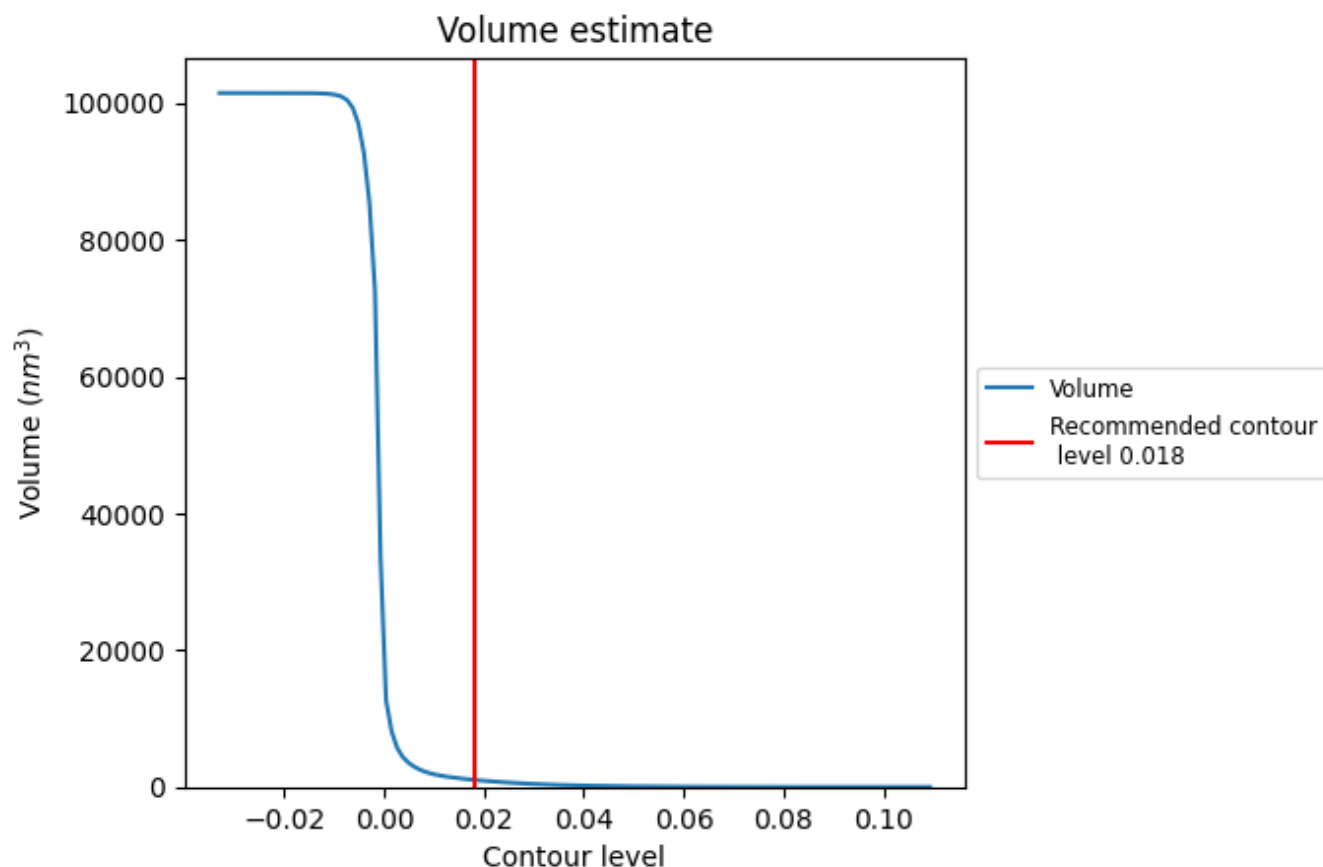
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

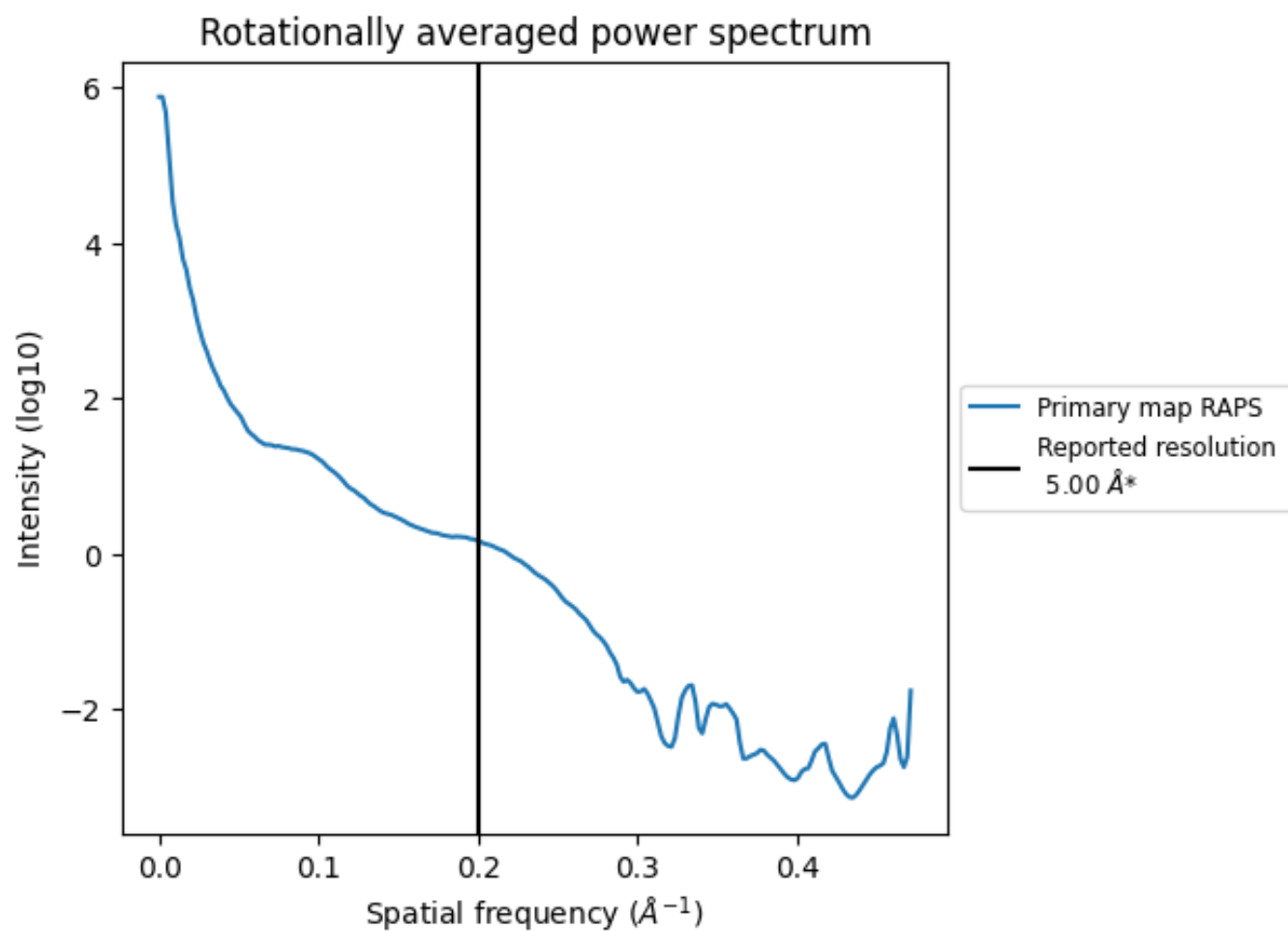
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1034 nm^3 ; this corresponds to an approximate mass of 934 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 0.200 Å⁻¹

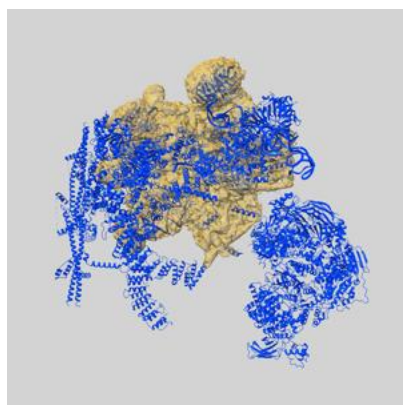
8 Fourier-Shell correlation

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

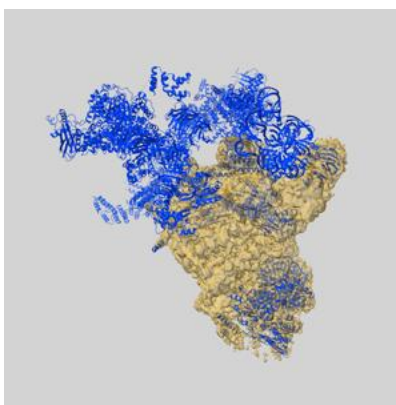
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11570 and PDB model 7A5P. Per-residue inclusion information can be found in section [3](#) on page [12](#).

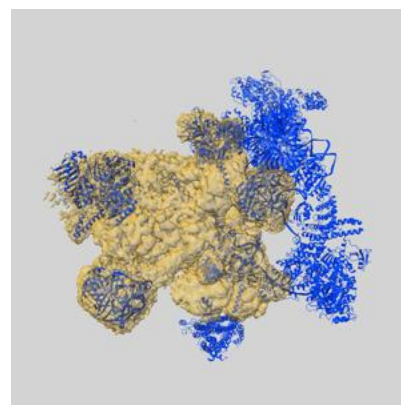
9.1 Map-model overlay [i](#)



X



Y



Z

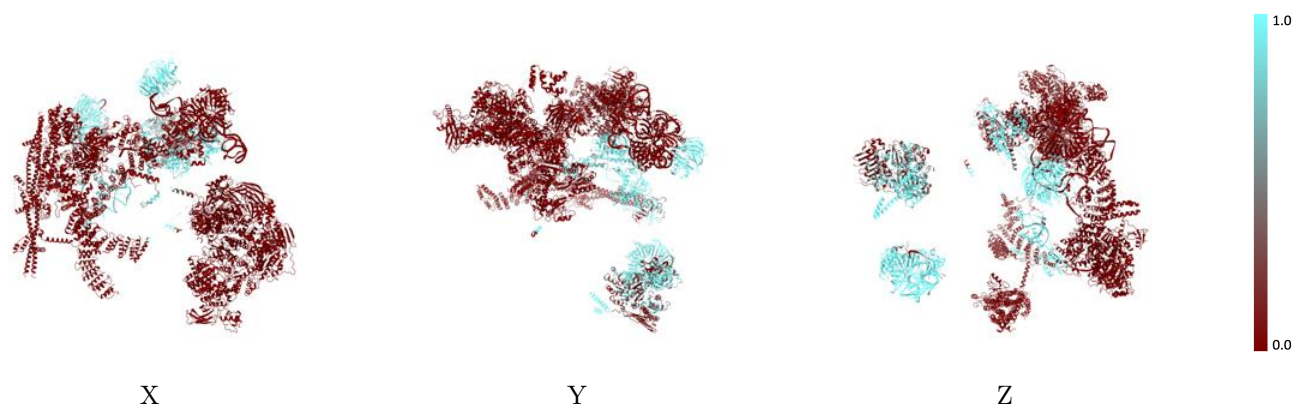
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



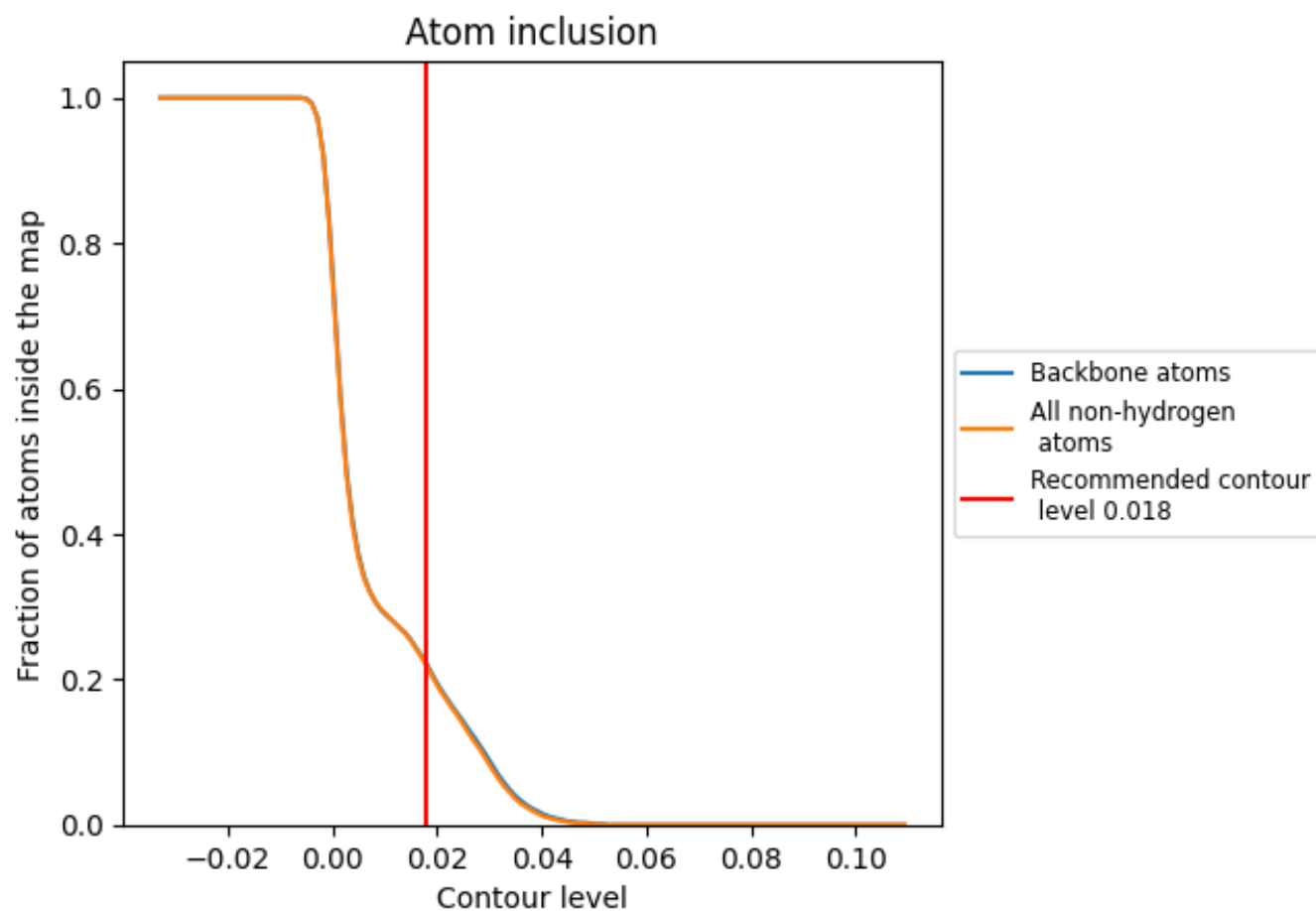
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.018).

9.4 Atom inclusion ⓘ



At the recommended contour level, 22% of all backbone atoms, 22% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.2180	 0.0900
2	 0.1120	 0.0670
5	 0.9250	 0.1000
6	 0.8450	 0.1020
8	 0.0000	 0.0250
A	 0.4880	 0.1660
C	 0.6000	 0.1890
E	 0.9660	 0.1410
G	 0.0000	 0.0170
H	 0.0000	 -0.0120
I	 0.0000	 0.0270
J	 0.0000	 0.0530
K	 0.0020	 0.0950
L	 0.0870	 0.1010
M	 0.0010	 0.0910
N	 0.8100	 0.2420
O	 0.0530	 0.0600
P	 0.9230	 0.2320
S	 1.0000	 0.2050
T	 0.6450	 0.1840
U	 0.0000	 0.0620
W	 0.0070	 0.0270
X	 0.0000	 0.1030
Y	 0.4450	 0.1130
a	 0.9410	 0.1320
b	 0.9450	 0.1530
c	 0.9560	 0.2580
d	 0.9460	 0.1890
e	 0.9870	 0.1260
f	 0.9810	 0.0910
g	 0.8810	 0.0980
h	 0.0070	 0.1890
i	 0.0000	 0.1530
j	 0.0000	 0.1070
k	 0.0000	 0.0930



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Chain	Atom inclusion	Q-score
l	 0.0000	 0.1030
m	 0.0000	 0.1420
n	 0.0610	 0.1550
o	 0.0000	 0.1650
p	 0.6880	 0.2740
q	 0.0000	 0.0070
r	 0.0010	 0.1540
s	 0.6570	 0.2240
u	 0.2640	 0.1360
v	 0.1770	 0.0500
w	 0.4550	 0.0820
x	 0.6230	 0.1030
y	 0.4940	 0.1930
z	 0.3290	 0.0870