



wwPDB EM Validation Summary Report ⓘ

Oct 6, 2024 – 09:51 am BST

PDB ID : 7ASE
EMDB ID : EMD-11893
Title : 43S preinitiation complex from Trypanosoma cruzi with the kDDX60 helicase
Authors : Bochler, A.; Brito Querido, J.; Prilepskaja, T.; Soufari, H.; Del Cistia, M.L.; Kuhn, L.; Rimoldi Ribeiro, A.; Valasek, L.S.; Hashem, Y.
Deposited on : 2020-10-27
Resolution : 3.33 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:

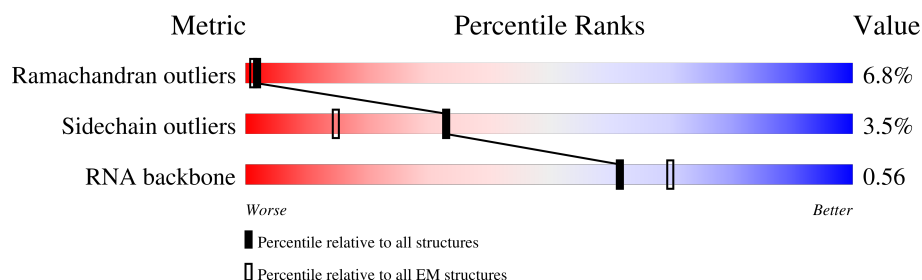
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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 3.33 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	f	2174	<div> <div>54%</div> <div>55% 10% . . 30%</div> </div>
2	1	75	<div> <div>13%</div> <div>85% 15%</div> </div>
3	0	2319	<div> <div>18%</div> <div>74% 17% . 7%</div> </div>
4	y	137	<div> <div>9%</div> <div>88% . 10%</div> </div>
5	s	418	<div> <div>58%</div> <div>58% 9% . 29%</div> </div>
6	j	150	<div> <div>35%</div> <div>46% 7% 47%</div> </div>
7	n	343	<div> <div>43%</div> <div>58% 7% . 34%</div> </div>
8	p	318	<div> <div>38%</div> <div>93% . . .</div> </div>

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Mol	Chain	Length	Quality of chain
9	r	149	
10	u	153	
11	m	143	
12	Z	221	
13	o	190	
14	q	211	
15	R	151	
16	S	86	
17	t	112	
18	U	91	
19	v	144	
20	X	173	
21	B	190	
22	F	245	
23	d	263	
24	g	247	
25	a	110	
26	J	257	
27	h	141	
28	5	477	
29	P	250	
30	i	141	
31	L	117	
32	M	214	
33	N	161	

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Mol	Chain	Length	Quality of chain
34	O	167	
35	b	145	
36	c	66	
37	V	109	
38	w	166	
39	E	407	
40	Y	379	
41	Q	57	
42	D	34	
43	G	345	
44	K	203	
45	T	152	
46	C	716	
47	8	762	
48	W	254	
49	I	489	
50	H	334	
51	A	502	
52	l	273	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 136847 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 kDDX60.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	f	1523	Total	C	N	O	S	0	0
			12257	7734	2165	2292	66		

- Molecule 2 is a RNA chain called initiator tRNA-Met.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	75	Total	C	N	O	P	0	0
			1606	718	300	514	74		

- Molecule 3 is a RNA chain called 18S.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	0	2150	Total	C	N	O	P	0	0
			45795	20471	8144	15037	2143		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	143	C	A	conflict	GB 320364483
0	805	C	U	conflict	GB 320364483
0	2321	U	-	insertion	GB 320364483
0	2322	U	-	insertion	GB 320364483
0	2323	U	-	insertion	GB 320364483

- Molecule 4 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	y	123	Total	C	N	O	S	0	0
			989	628	194	165	2		

- Molecule 5 is a protein called Elongation initiation factor 2 alpha subunit, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	s	295	Total	C	N	O	S	0	0
			2365	1489	436	427	13		

- Molecule 6 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	j	79	Total	C	N	O	S	0	0
			644	409	123	106	6		

- Molecule 7 is a protein called Translation initiation factor, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	n	225	Total	C	N	O	S	0	0
			1796	1111	335	339	11		

- Molecule 8 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	p	310	Total	C	N	O	S	0	0
			2405	1505	424	463	13		

- Molecule 9 is a protein called 40S ribosomal protein S16, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	r	140	Total	C	N	O	S	0	0
			1113	706	212	192	3		

- Molecule 10 is a protein called 40S ribosomal protein S18, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	u	136	Total	C	N	O	S	0	0
			1108	689	224	190	5		

- Molecule 11 is a protein called 40S ribosomal protein S23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	m	142	Total	C	N	O	S	0	0
			1116	706	220	188	2		

- Molecule 12 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Z	175	Total	C	N	O	S	0	0
			1404	885	283	233	3		

- Molecule 13 is a protein called 40S ribosomal protein S5, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	o	190	Total	C	N	O	S	0	0
			1493	932	286	269	6		

- Molecule 14 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	q	200	Total	C	N	O	S	0	0
			1670	1063	324	277	6		

- Molecule 15 is a protein called 40S ribosomal protein S13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	141	Total	C	N	O	S	0	0
			1143	724	221	190	8		

- Molecule 16 is a protein called 40S ribosomal protein S27, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	S	82	Total	C	N	O	S	0	0
			630	384	121	116	9		

- Molecule 17 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	t	104	Total	C	N	O	S	0	0
			829	510	177	132	10		

- Molecule 18 is a protein called 40S ribosomal protein S33.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	U	68	Total	C	N	O	S	0	0
			526	315	107	100	4		

- Molecule 19 is a protein called 40S ribosomal protein S14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	v	135	Total	C	N	O	S	0	0
			1011	620	195	187	9		

- Molecule 20 is a protein called 40S ribosomal protein S11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	X	148	Total	C	N	O	S	0	0
			1212	760	239	207	6		

- Molecule 21 is a protein called Putative 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	B	179	Total	C	N	O	S	0	0
			1483	935	297	243	8		

- Molecule 22 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	F	207	Total	C	N	O	S	0	0
			1658	1060	299	288	11		

- Molecule 23 is a protein called 40S ribosomal protein S2, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	d	223	Total	C	N	O	S	0	0
			1726	1098	304	314	10		

- Molecule 24 is a protein called Putative 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	g	83	Total	C	N	O	S	0	0
			635	395	116	122	2		

- Molecule 25 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	70	Total	C	N	O	S	0	0
			553	356	97	97	3		

- Molecule 26 is a protein called RNA-binding protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	J	173	Total	C	N	O	S	0	0
			1358	862	259	234	3		

- Molecule 27 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	h	121	Total	C	N	O	S	0	0
			958	594	174	185	5		

- Molecule 28 is a protein called Eukaryotic translation initiation factor 2 subunit, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	5	421	Total	C	N	O	S	0	0
			3245	2049	581	596	19		

- Molecule 29 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	P	249	Total	C	N	O	S	0	0
			1983	1244	402	333	4		

- Molecule 30 is a protein called 40S ribosomal protein S17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	i	121	Total	C	N	O	S	0	0
			992	623	190	174	5		

- Molecule 31 is a protein called Ribosomal protein S20, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	L	99	Total	C	N	O	S	0	0
			784	497	144	140	3		

- Molecule 32 is a protein called 40S ribosomal protein S3, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	M	200	Total	C	N	O	S	0	0
			1587	995	302	279	11		

- Molecule 33 is a protein called 40S ribosomal protein S10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	N	93	Total	C	N	O	S	0	0
			780	508	136	132	4		

- Molecule 34 is a protein called Ribosomal protein S19, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	O	140	Total	C	N	O	S	0	0
			1116	702	221	185	8		

- Molecule 35 is a protein called 40S ribosomal protein S15a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	b	129	Total	C	N	O	S	0	0
			1019	647	188	176	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	83	THR	ALA	conflict	UNP Q4CXX2

- Molecule 36 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	c	60	Total	C	N	O	S	0	0
			480	303	98	78	1		

- Molecule 37 is a protein called Protein translation factor SUI1 homolog, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	V	97	Total	C	N	O	S	0	0
			789	490	152	145	2		

- Molecule 38 is a protein called Putative eukaryotic translation initiation factor 1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	w	147	Total	C	N	O	S	0	0
			1162	716	209	236	1		

- Molecule 39 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	E	391	Total	C	N	O	S	0	0
			3119	1977	536	593	13		

- Molecule 40 is a protein called Eukaryotic translation initiation factor 5, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Y	174	Total	C	N	O	S	0	0
			1387	872	243	260	12		

- Molecule 41 is a protein called Ribosomal protein S29, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Q	57	Total	C	N	O	S	0	0
			462	283	96	77	6		

- Molecule 42 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	D	33	Total	C	N	O	S	0	0
			294	178	76	38	2		

- Molecule 43 is a protein called JAB_MPN domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	G	308	Total	C	N	O	S	0	0
			2414	1492	442	466	14		

- Molecule 44 is a protein called CSN8_PSD8_EIF3K domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	K	201	Total	C	N	O	S	0	0
			1566	1001	256	304	5		

- Molecule 45 is a protein called 40S ribosomal protein S15, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	T	132	Total	C	N	O	S	0	0
			1057	670	204	179	4		

- Molecule 46 is a protein called Eukaryotic translation initiation factor 3 subunit 8, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	C	696	Total	C	N	O	S	0	0
			5630	3542	973	1092	23		

- Molecule 47 is a protein called eIF3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	8	576	Total	C	N	O	S	0	0
			4596	2882	845	847	22		

- Molecule 48 is a protein called 40S ribosomal protein S3a-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	W	217	Total	C	N	O	S	0	0
			1781	1124	337	313	7		

- Molecule 49 is a protein called Eukaryotic translation initiation factor 3 (EIF-3) interacting protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	I	344	Total	C	N	O	S	0	0
			2770	1771	479	503	17		

- Molecule 50 is a protein called eIF3H.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	H	297	Total	C	N	O	S	0	0
			2388	1498	421	451	18		

- Molecule 51 is a protein called Eukaryotic translation initiation factor 3 subunit 7-like protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	A	483	Total	C	N	O	S	0	0
			3891	2446	691	729	25		

- Molecule 52 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	1	258	Total	C	N	O	S	0	0
			2038	1290	383	354	11		

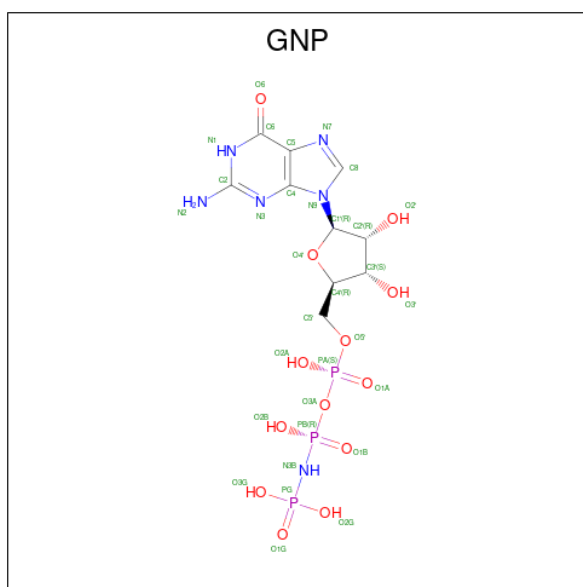
- Molecule 53 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
53	n	1	Total	Zn	0
			1	1	

- Molecule 54 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	5	1	Total	Mg	0
			1	1	


- Molecule 55 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: C₁₀H₁₇N₆O₁₃P₃).

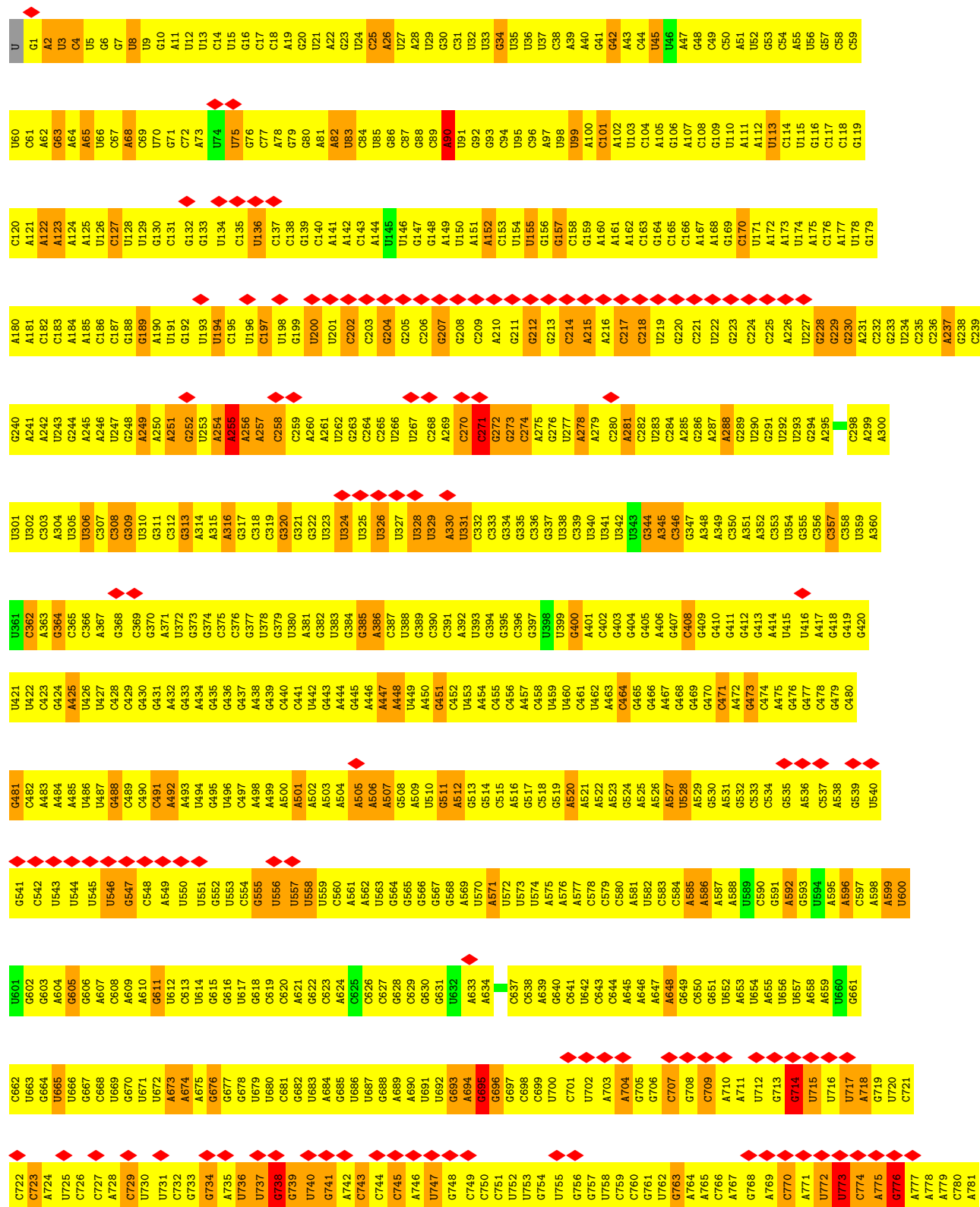


Mol	Chain	Residues	Atoms					AltConf
55	5	1	Total	C	N	O	P	0
			32	10	6	13	3	

ASP	VAL	ILE	ASP	ALA	GLU	GLY	ASP	ALA	ILE	LYS	SER	LYS	ALA	SER	MET	THR	GLU	LYS	GLU	ALA	LYS	ASN	VAL	GLN	GLU	TYR	LYS	LYS	PHE	VAL	ARG	ASN	ALA	LEU	LYS	GLN	ALA	GLN	SER	MET	GLY	ILE	SER	PHE	GLY	ALA	ALA	HIS	GLU	LEU	ALA	MET	VAL	CYS	SER	ASP	ASN	ASP	S668
D669	D670	D671	A672	G673	G674	M675	S676	A677	M678	N679	K680	T681	A682	G683	A684	K685	K686	V687	M688	K689	E690	H691	A692	G693	Q694	G695	M696	K697	T773	L774	G775	S701	K702	E703	D704	E705	I706	R707	E708	R709	S710	N711	V712	I713	A714	A715	T716	A717	T718	V719	A720	E721	W722	H723	K724	Q725	M726	N727	H728
L729	L730	H731	A732	V733	D734	M735	S736	R739	T740	R743	A754	A755	I756	K757	L759	K763	F764	G765	K766	N767	F768	D769	G770	G771	Y772	T773	A774	G775	G776	S777	T778	N779	T780	A781	L784	K785	L786	L787	M788	W789	R790	R791	L792	V793	A794	A795	S796	Q797	L798	R799	E800	V801	E802						
F803	A804	F805	A806	M807	E808	D809	K813	K820	K821	K822	D823	S824	K825	S826	E827	Y828	K829	M830	L831	Y832	G833	F834	H835	V836	I837	F840	R843	E844	A845	V846	K847	G848	N849	H850	R851	G852	K853	L854	D855	P856	L857	R858	K859	A860	K861	P862	D863	M864	T865	I866	V867	E868	A869	R870					
R874	Q886	L887	K890	Q897	L898	E899	N900	W901	A902	A903	E904	R905	E906	A907	A908	R909	L910	A911	Q912	E913	S914	P915	K916	I917	A918	L919	G920	I921	P922	L923	F924	H929	L932	A933	V934	T935	R936	D937	E938	R941	M942	S943	S944	E945	D946	I947	D948	R951	S952	A953	L954	K955							
H956	F957	D958	L959	P960	D961	S962	Y963	Y964	N965	K966	D967	D968	Q969	C970	I971	N976	M977	L979	G980	T981	L982	L983	P984	S985	L986	L987	P988	Q989	D990	K991	Q992	L993	P994	E995	T996	P997	E998	M999	L1000	Q1001	L1002	L1003	H1004	M1005	G1006	H1007	L1008	L1009	E1010	R1011	P1012	F1013	V1014	R1015	E1016	H1017	D1018		
Y1019	R1020	D1021	A1022	F1023	N1024	P1025	D1026	N1027	W1028	Q1029	R1030	E1031	L1032	L1033	D1034	D1037	G1038	R1039	G1040	S1041	A1042	V1043	Y1044	C1045	A1046	P1047	T1048	S1049	A1050	G1051	K1052	T1053	F1054	L1055	S1056	Y1057	Y1058	C1059	M1060	Y1061	K1062	A1063	L1064	R1065	R1066	T1067	N1068	K1069	K1070	V1071	L1075	P1077	A1078	R1079	A1080	L1081			
I1082	D1088	V1089	R1092	Y1093	G1094	S1095	K1099	N1100	P1101	G1102	R1103	Y1104	I1105	Y1106	G1107	A1108	L1109	G1110	G1111	A1112	D1113	Y1114	H1115	Q1116	F1117	H1118	D1119	S1120	C1121	Q1122	V1123	L1124	L1125	T1126	V1127	P1128	E1129	T1130	F1131	M1134	S1137	P1138	K1139	Y1140	T1141	D1142	W1143	V1144	E1145	L1146	D1148	Y1149	V1150						
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K1212	M1213	R1214	D1215	F1216	E1217	V1218	H1219	L1220	L1221	P1222	S1223	E1224	G1225	K1226	S1227	I1228	Q1229	R1230	W1231	N1232	D1233	L1234	K1235	K1236	L1240	P1241	P1242	A1245	A1246	L1247	T1248	Q1249	K1250	K1251	L1252	K1253	A1254	Q1255	Y1256	L1257	N1258	C1259	T1260	I1261	R1262	D1263	L1264	H1265	P1266	L1267	S1268	I1269	F1331	L1270	T1271	A1272	D1273	Q1274	
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● Molecule 3: 18S

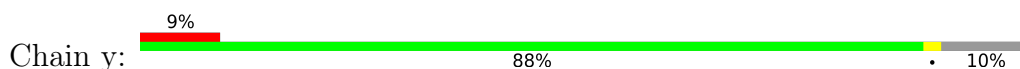
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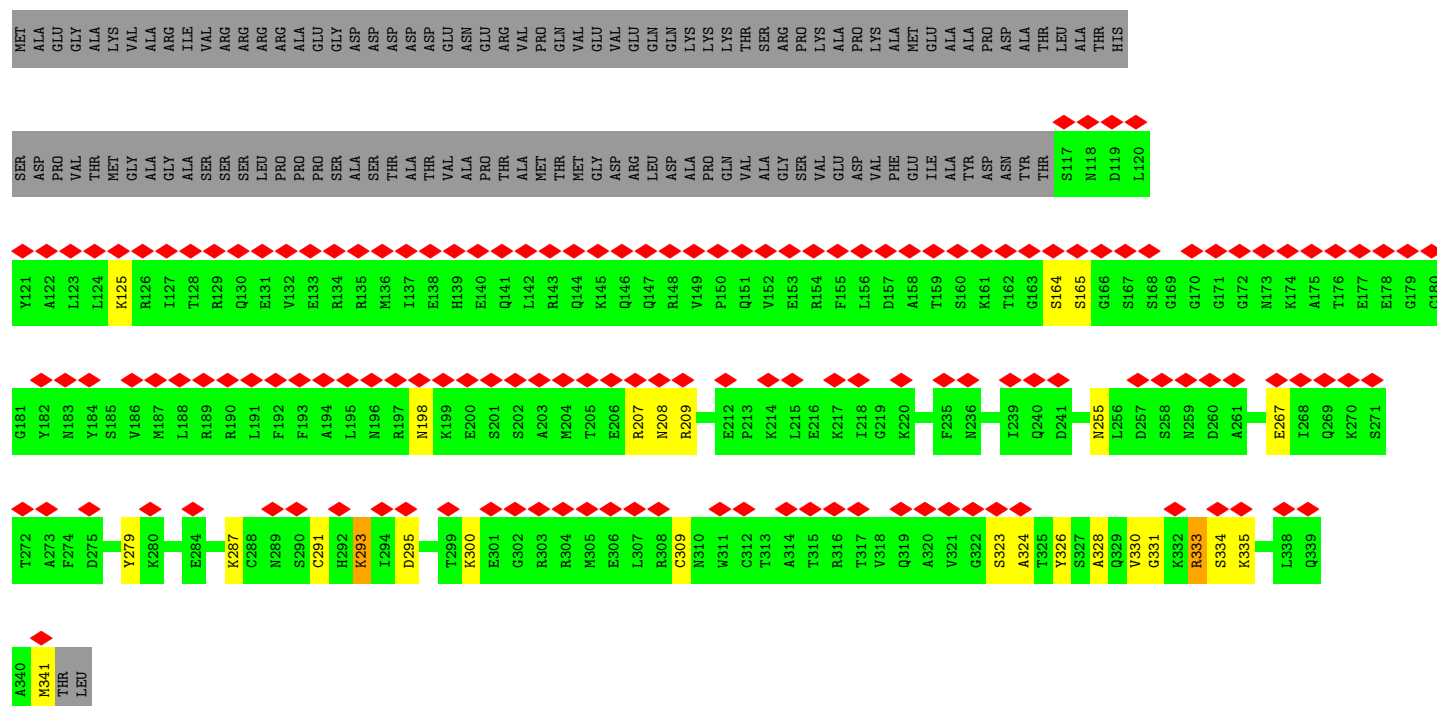


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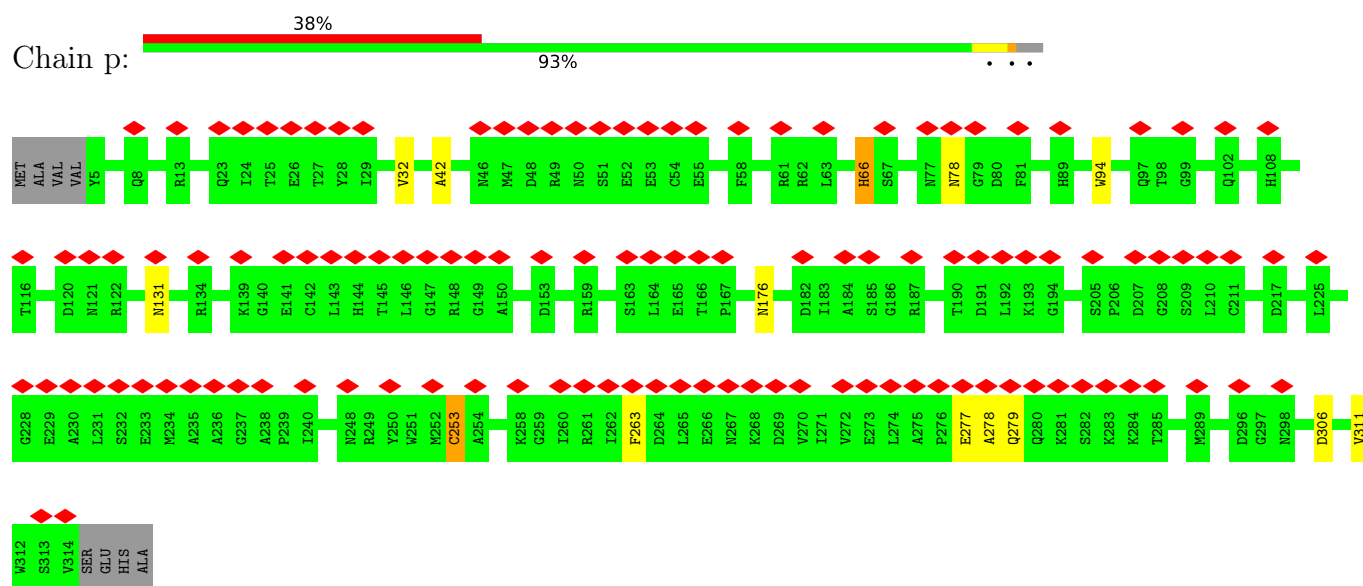
● Molecule 4: 40S ribosomal protein S24



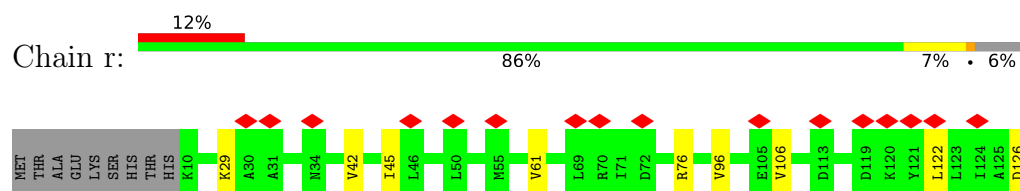




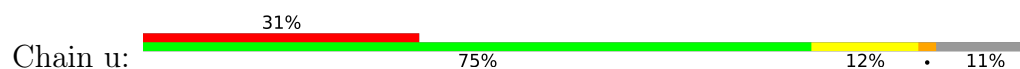
- Molecule 8: Guanine nucleotide-binding protein subunit beta-like protein

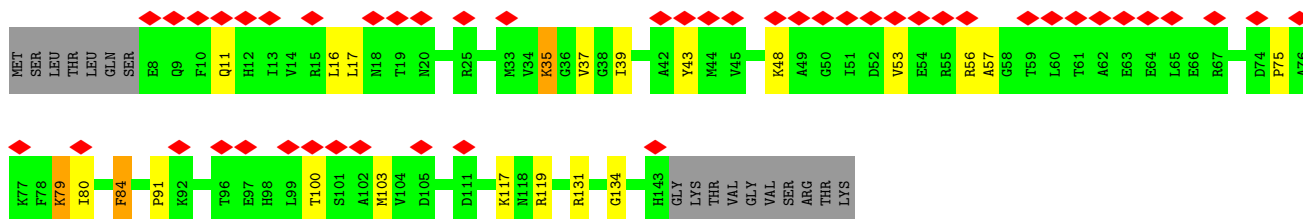


- Molecule 9: 40S ribosomal protein S16, putative

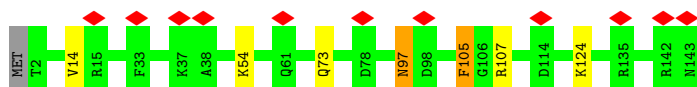


- Molecule 10: 40S ribosomal protein S18, putative

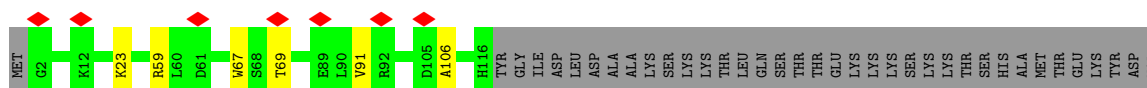
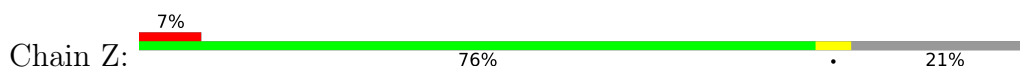




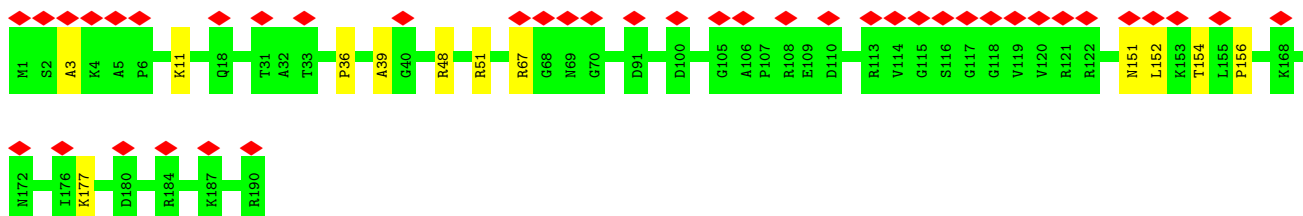
- Molecule 11: 40S ribosomal protein S23, putative



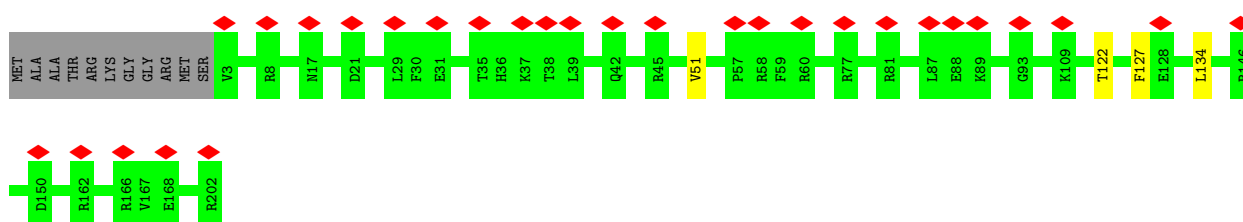
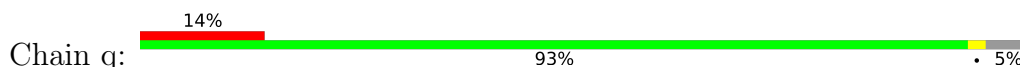
- Molecule 12: 40S ribosomal protein S8



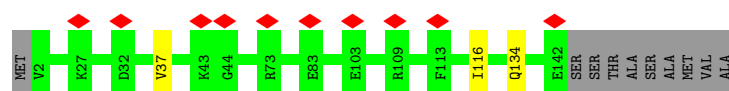
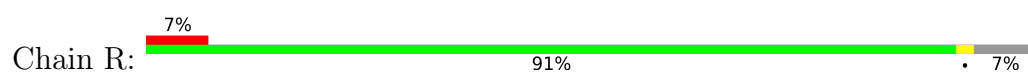
- Molecule 13: 40S ribosomal protein S5, putative



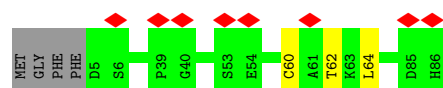
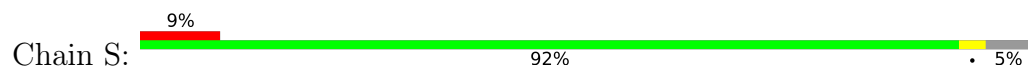
- Molecule 14: 40S ribosomal protein S7



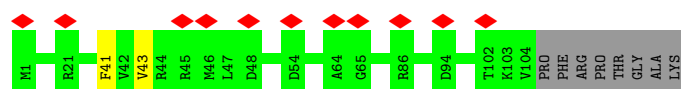
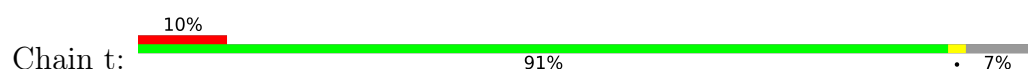
- Molecule 15: 40S ribosomal protein S13, putative



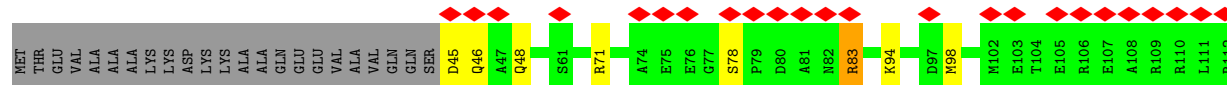
- Molecule 16: 40S ribosomal protein S27, putative



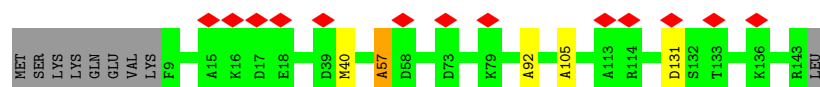
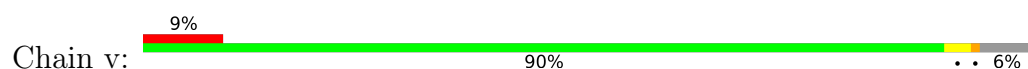
- Molecule 17: 40S ribosomal protein S26



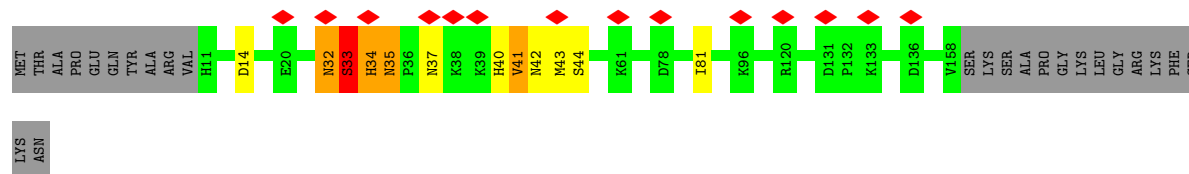
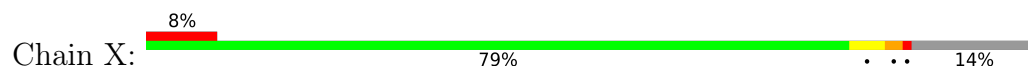
- Molecule 18: 40S ribosomal protein S33



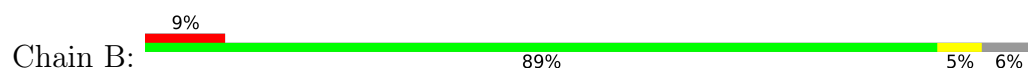
- Molecule 19: 40S ribosomal protein S14, putative

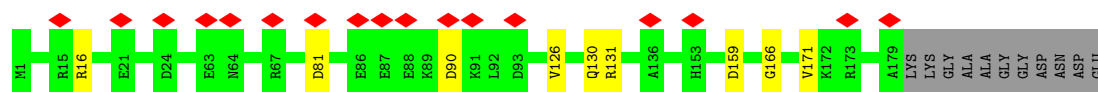


- Molecule 20: 40S ribosomal protein S11, putative

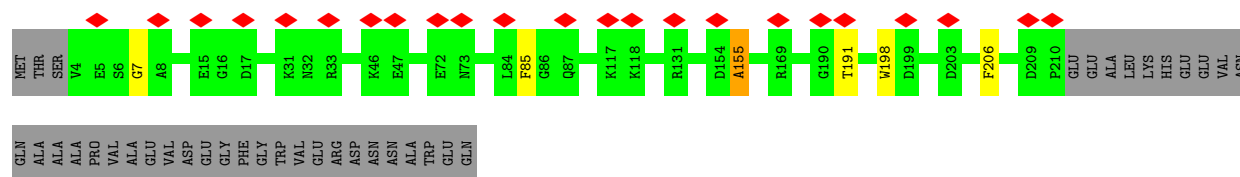
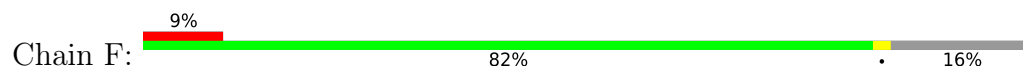


- Molecule 21: Putative 40S ribosomal protein S9

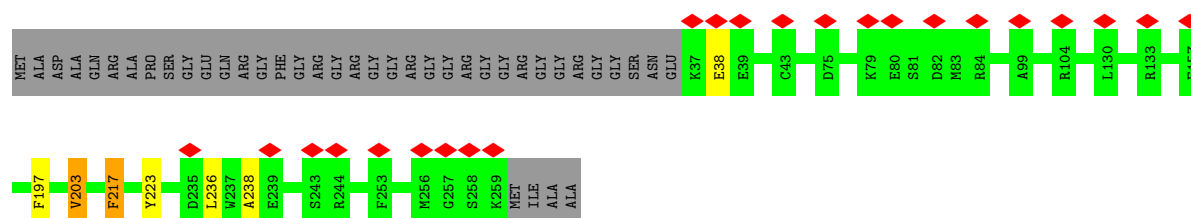
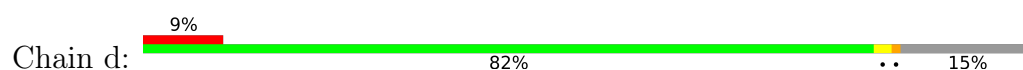




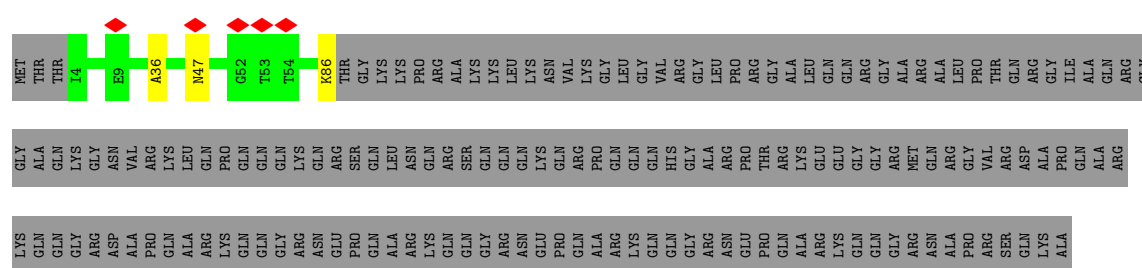
- Molecule 22: 40S ribosomal protein SA



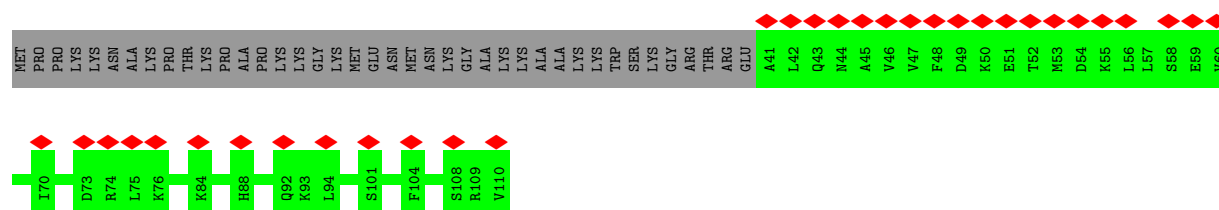
- Molecule 23: 40S ribosomal protein S2, putative



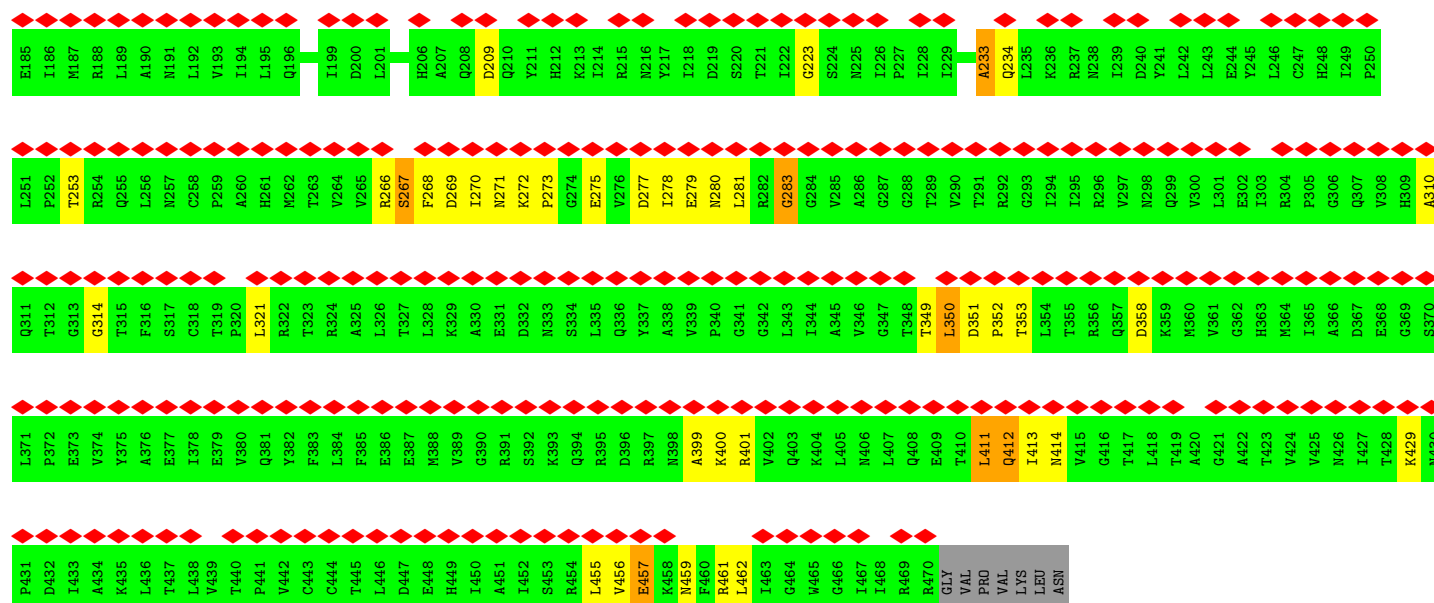
- Molecule 24: Putative 40S ribosomal protein S21



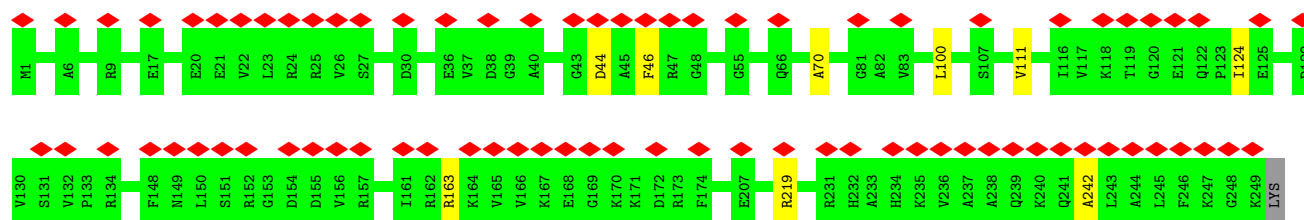
- Molecule 25: 40S ribosomal protein S25



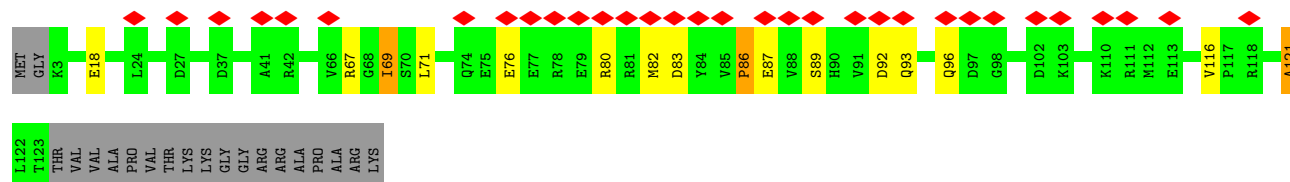
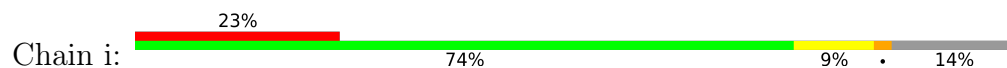
- Molecule 26: RNA-binding protein, putative



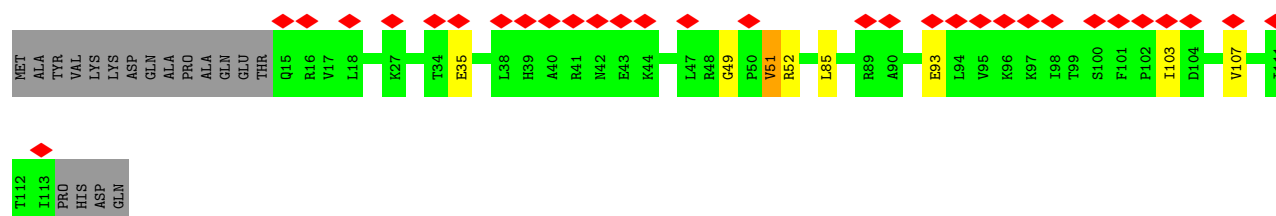
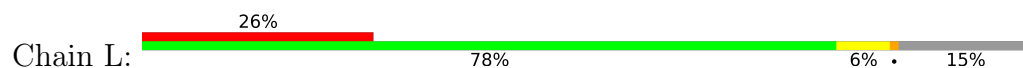
• Molecule 29: 40S ribosomal protein S6

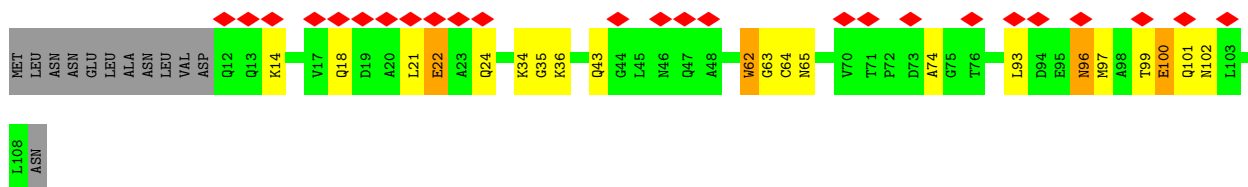


• Molecule 30: 40S ribosomal protein S17, putative

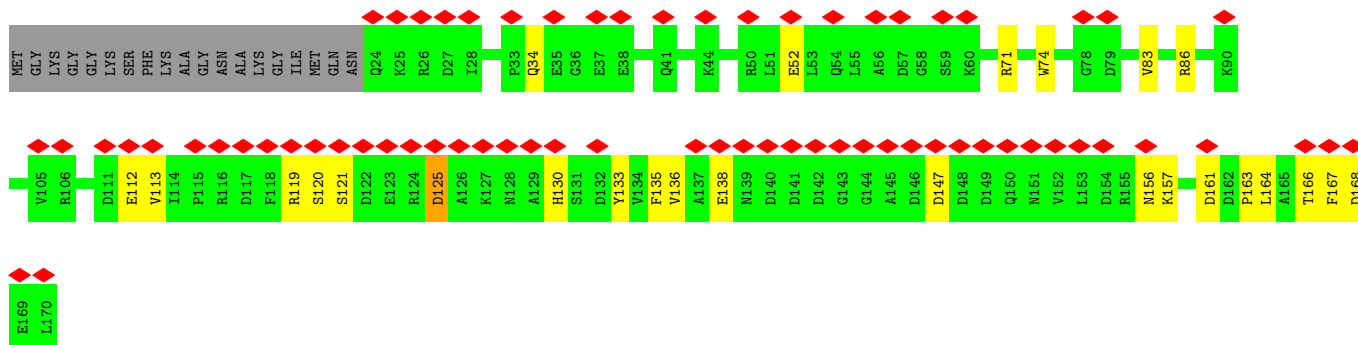
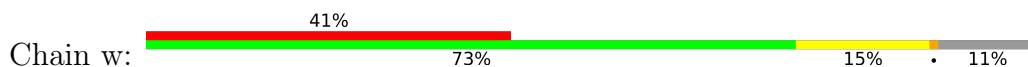


• Molecule 31: Ribosomal protein S20, putative

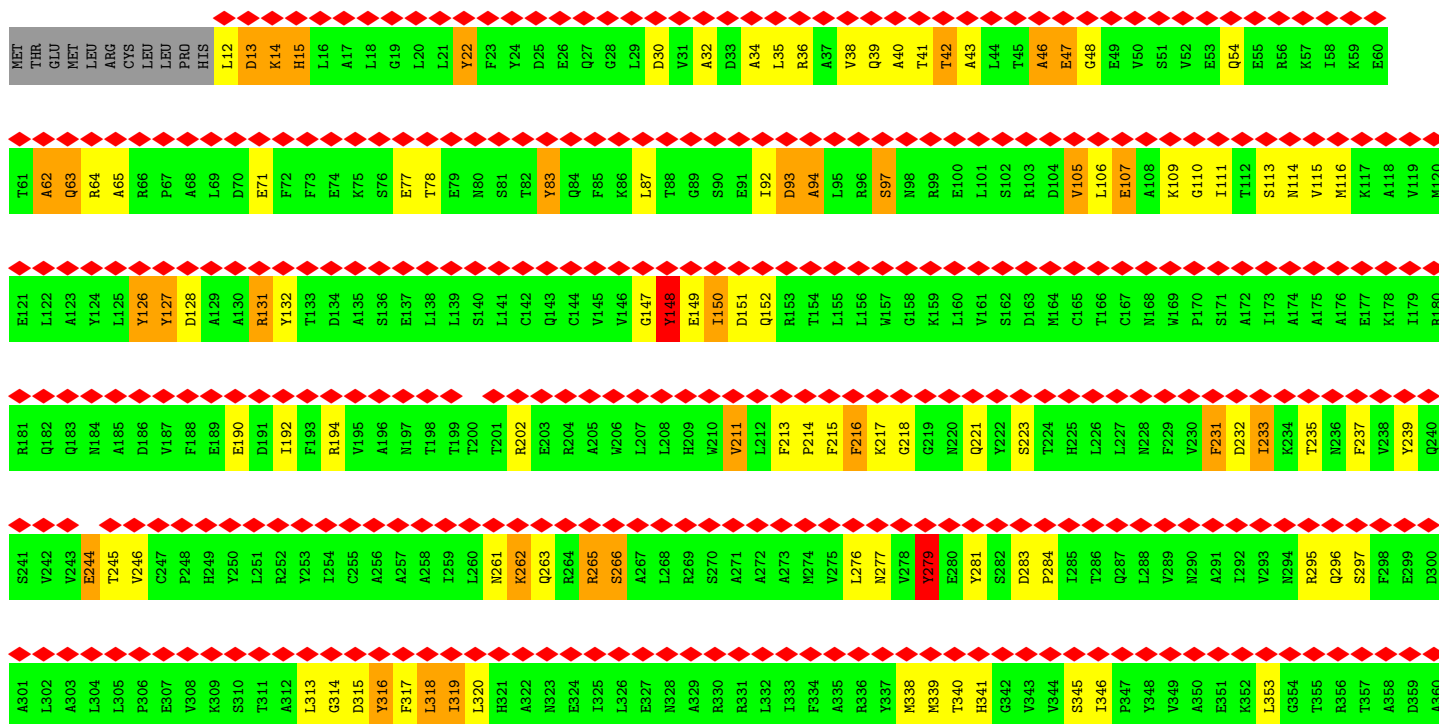


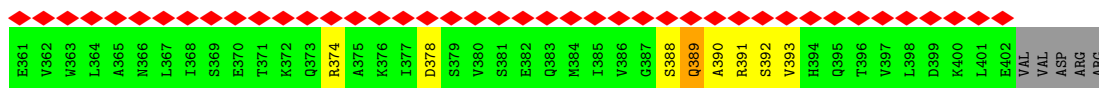


- Molecule 38: Putative eukaryotic translation initiation factor 1A

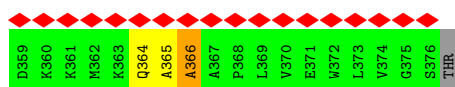
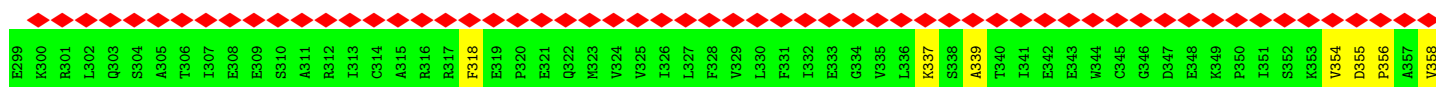
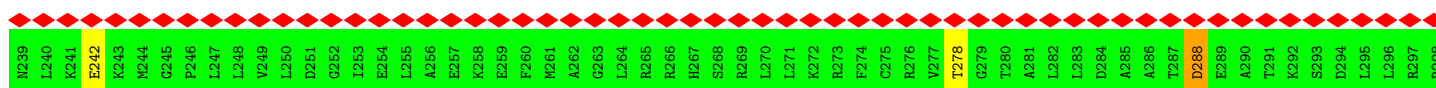
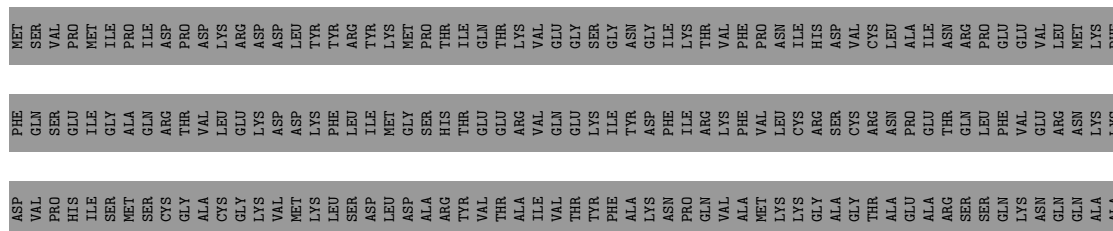
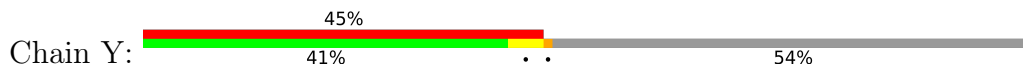


- Molecule 39: Eukaryotic translation initiation factor 3 subunit E

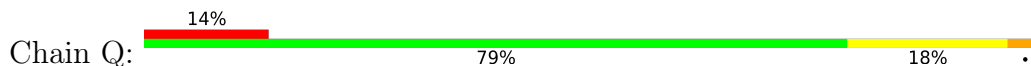




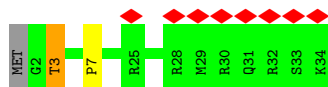
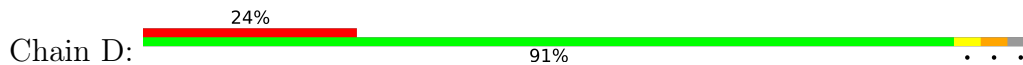
- Molecule 40: Eukaryotic translation initiation factor 5, putative



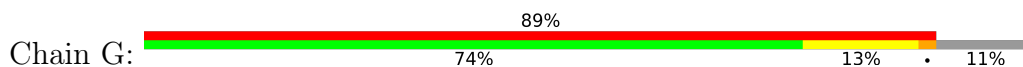
- Molecule 41: Ribosomal protein S29, putative



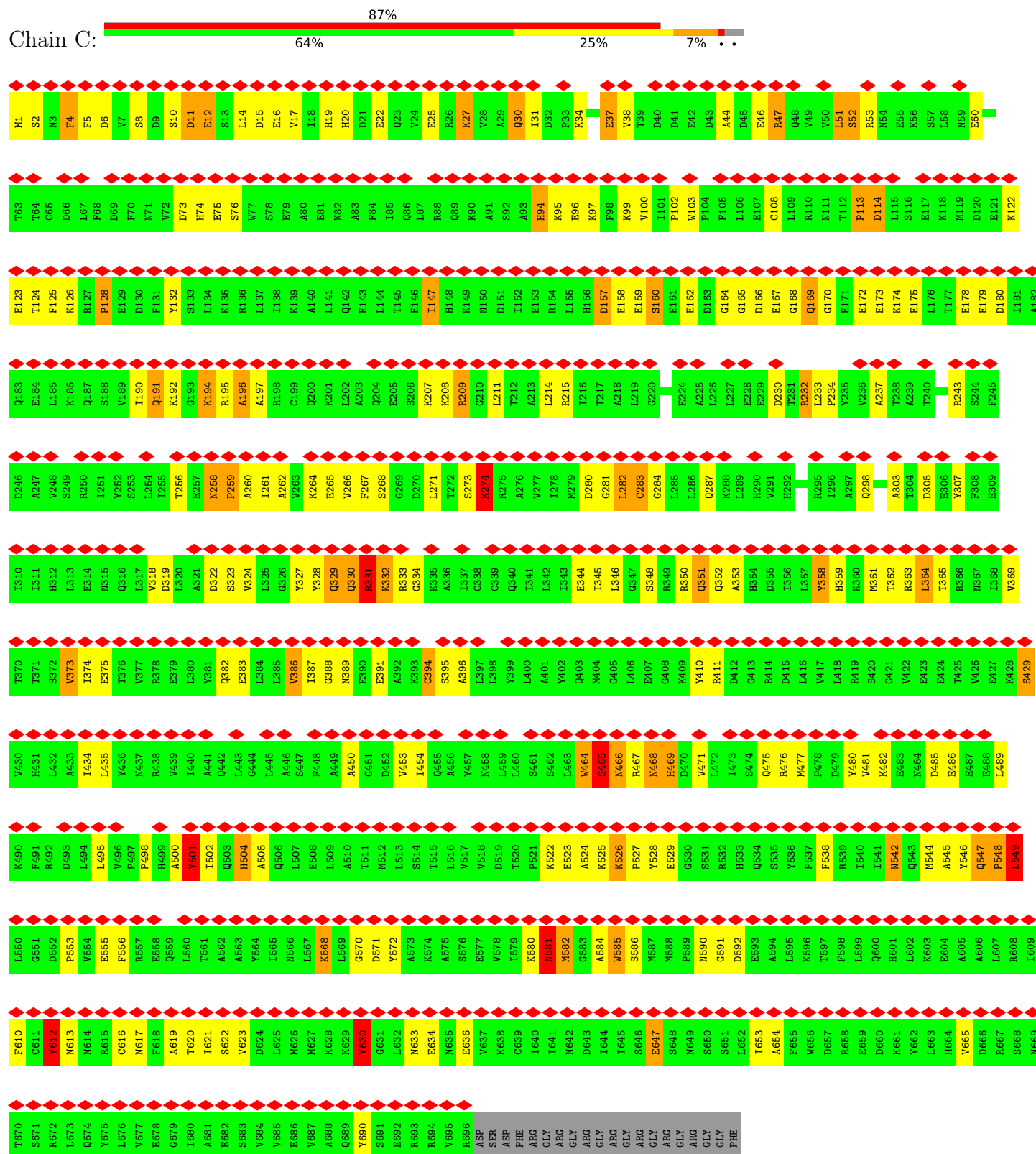
- Molecule 42: eL41



- Molecule 43: JAB_MPN domain-containing protein

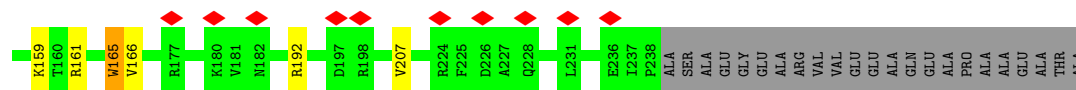


Chain C:

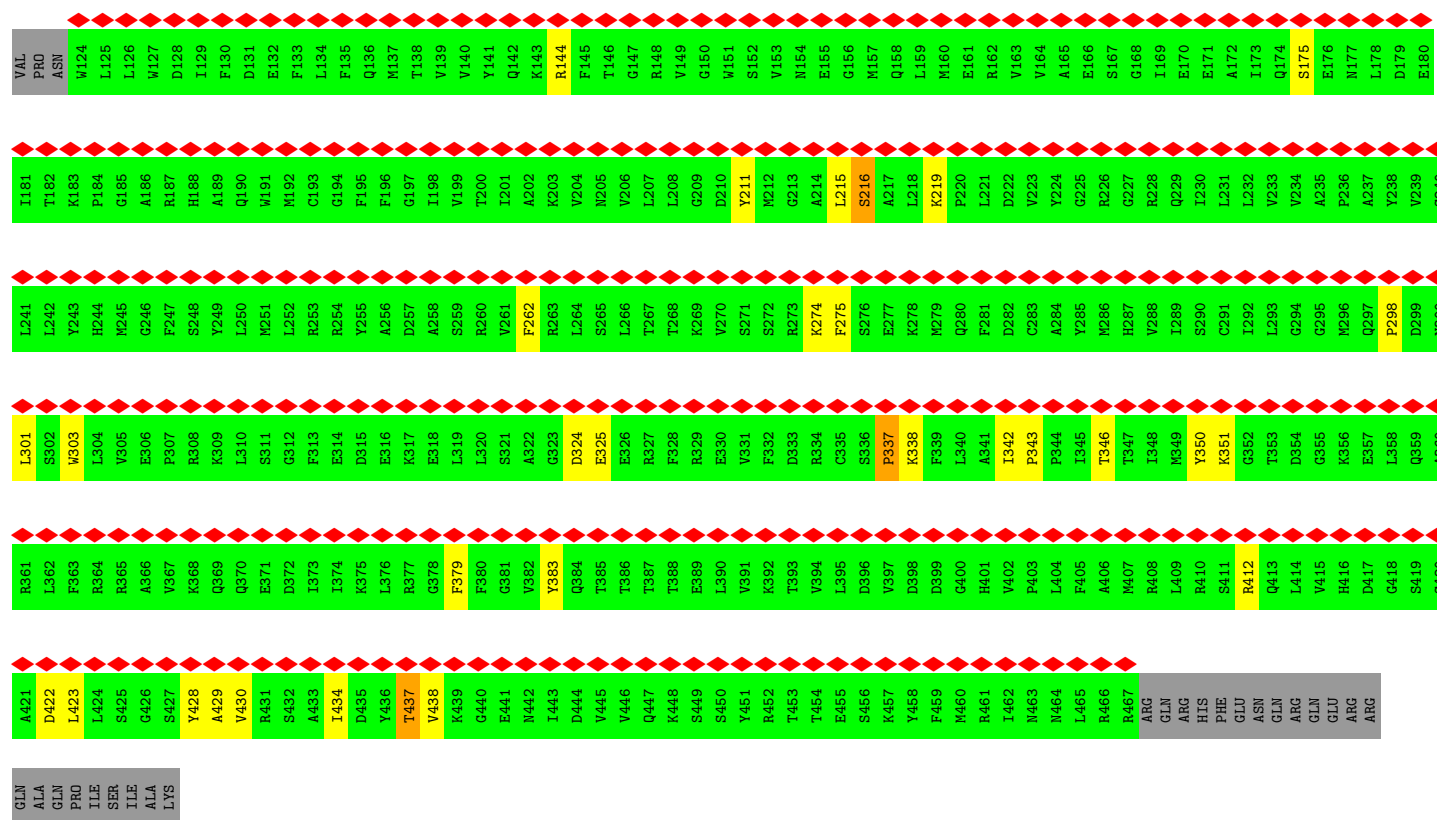
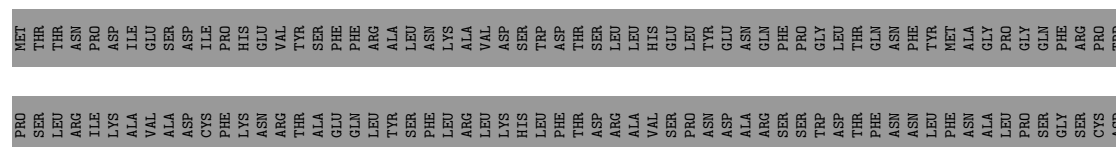


Chain 8:

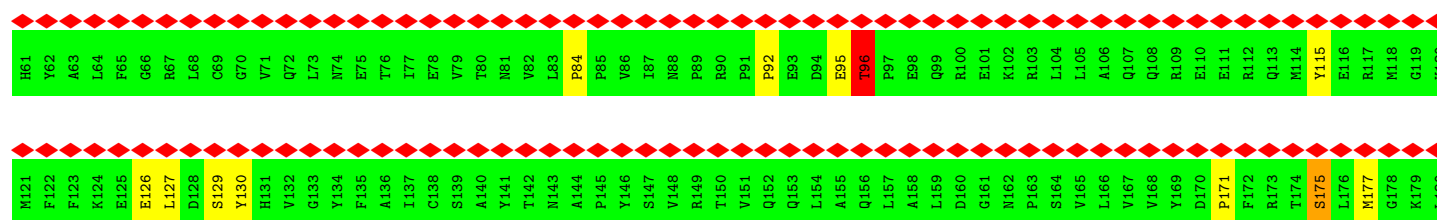
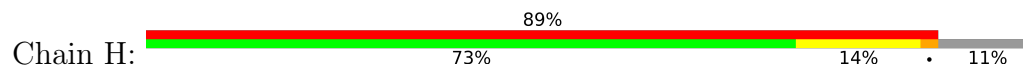




- Molecule 49: Eukaryotic translation initiation factor 3 (EIF-3) interacting protein, putative



- Molecule 50: eIF3H







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	33775	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.118	Depositor
Minimum map value	-0.081	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0193	Depositor
Map size (\AA)	440.0, 440.0, 440.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1, 1.1, 1.1	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GNP, ZN, MG

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	f	1.28	79/12510 (0.6%)	1.48	202/16884 (1.2%)
2	l	1.61	1/1798 (0.1%)	2.50	213/2803 (7.6%)
3	0	1.59	38/51207 (0.1%)	2.44	5849/79792 (7.3%)
4	y	1.02	0/1004	1.01	0/1335
5	s	0.94	0/2405	1.09	8/3247 (0.2%)
6	j	0.94	0/658	1.04	2/871 (0.2%)
7	n	0.92	0/1818	0.93	1/2433 (0.0%)
8	p	0.94	0/2461	1.10	2/3347 (0.1%)
9	r	1.01	0/1131	1.06	1/1520 (0.1%)
10	u	1.06	0/1126	1.20	5/1508 (0.3%)
11	m	0.97	0/1137	1.02	2/1520 (0.1%)
12	Z	1.06	0/1424	1.04	0/1904
13	o	0.96	0/1515	0.97	0/2034
14	q	1.06	0/1703	1.05	2/2290 (0.1%)
15	R	1.01	0/1164	1.00	0/1559
16	S	0.97	0/641	0.95	0/858
17	t	1.14	0/845	1.05	0/1129
18	U	1.05	0/527	1.04	0/702
19	v	1.04	0/1026	1.04	1/1376 (0.1%)
20	X	1.04	1/1238 (0.1%)	1.04	1/1662 (0.1%)
21	B	1.06	0/1513	1.00	0/2030
22	F	0.98	0/1693	1.05	4/2290 (0.2%)
23	d	0.95	0/1760	1.08	5/2376 (0.2%)
24	g	0.93	0/644	1.01	0/875
25	a	0.93	0/559	0.98	0/748
26	J	1.07	0/1381	1.23	7/1857 (0.4%)
27	h	0.97	0/966	0.99	0/1295
28	5	1.02	2/3302 (0.1%)	1.27	12/4483 (0.3%)
29	P	1.09	0/2008	1.04	0/2678
30	i	1.00	0/1005	1.11	3/1341 (0.2%)
31	L	0.99	0/794	1.09	0/1076
32	M	1.04	0/1606	1.05	0/2141

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	N	0.98	0/804	1.07	2/1082 (0.2%)
34	O	1.01	0/1140	1.05	0/1524
35	b	1.00	0/1037	1.04	0/1391
36	c	0.92	0/488	1.02	0/644
37	V	0.75	0/799	0.84	0/1072
38	w	0.92	0/1177	0.94	1/1588 (0.1%)
39	E	1.49	6/3174 (0.2%)	1.15	13/4304 (0.3%)
40	Y	0.91	0/1406	1.00	2/1890 (0.1%)
41	Q	1.07	0/468	1.10	1/618 (0.2%)
42	D	1.30	0/298	1.04	0/385
43	G	1.00	0/2455	1.09	4/3323 (0.1%)
44	K	0.89	0/1597	1.06	12/2170 (0.6%)
45	T	1.00	0/1079	0.98	1/1447 (0.1%)
46	C	1.68	3/5724 (0.1%)	1.11	20/7724 (0.3%)
47	8	0.96	0/4685	1.04	6/6327 (0.1%)
48	W	1.05	4/1809 (0.2%)	1.21	7/2437 (0.3%)
49	I	0.98	0/2826	1.01	8/3809 (0.2%)
50	H	1.01	0/2431	1.11	9/3285 (0.3%)
51	A	0.95	3/3971 (0.1%)	1.04	4/5366 (0.1%)
52	l	1.01	0/2073	1.05	0/2787
All	All	1.31	137/144010 (0.1%)	1.78	6410/205137 (3.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	f	3	200
3	0	2	52
4	y	0	1
5	s	0	17
6	j	0	2
7	n	0	1
8	p	0	2
9	r	0	4
10	u	0	2
11	m	0	2
12	Z	0	2
13	o	0	1
17	t	0	1
19	v	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
20	X	0	10
21	B	0	4
22	F	0	3
23	d	0	3
24	g	0	1
26	J	0	21
28	5	0	12
29	P	0	4
31	L	0	7
32	M	0	2
33	N	0	1
34	O	0	6
35	b	0	1
36	c	0	3
38	w	0	6
39	E	1	73
40	Y	0	4
41	Q	0	3
42	D	0	1
43	G	0	36
44	K	0	2
45	T	0	1
46	C	1	137
47	8	0	69
48	W	0	2
49	I	2	6
50	H	0	26
51	A	0	16
52	l	0	10
All	All	9	759

The worst 5 of 137 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	C	411	ARG	CD-NE	105.86	3.26	1.46
39	E	279	TYR	CE1-CZ	28.41	1.75	1.38
39	E	279	TYR	CE2-CZ	28.18	1.75	1.38
39	E	279	TYR	CG-CD1	28.05	1.75	1.39
39	E	279	TYR	CG-CD2	27.28	1.74	1.39

The worst 5 of 6410 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	5	412	GLN	O-C-N	-35.37	66.11	122.70
1	f	234	GLY	O-C-N	-34.90	66.87	122.70
1	f	307	LEU	O-C-N	-26.57	80.19	122.70
1	f	1147	ILE	O-C-N	23.84	160.84	122.70
1	f	305	TYR	N-CA-CB	19.79	146.23	110.60

5 of 9 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	f	296	TYR	CA
1	f	305	TYR	CA
1	f	772	TYR	CA
3	0	974	A	C1'
3	0	1833	G	C1'

5 of 759 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	f	26	SER	Peptide
1	f	38	SER	Peptide
1	f	46	SER	Peptide
1	f	55	VAL	Peptide
1	f	56	THR	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	f	1519/2174 (70%)	1094 (72%)	295 (19%)	130 (9%)	0 4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	y	121/137 (88%)	109 (90%)	10 (8%)	2 (2%)	7	32
5	s	293/418 (70%)	207 (71%)	51 (17%)	35 (12%)	0	2
6	j	77/150 (51%)	68 (88%)	6 (8%)	3 (4%)	2	17
7	n	223/343 (65%)	179 (80%)	33 (15%)	11 (5%)	2	12
8	p	308/318 (97%)	268 (87%)	31 (10%)	9 (3%)	3	22
9	r	138/149 (93%)	101 (73%)	29 (21%)	8 (6%)	1	9
10	u	134/153 (88%)	87 (65%)	33 (25%)	14 (10%)	0	2
11	m	140/143 (98%)	120 (86%)	18 (13%)	2 (1%)	9	35
12	Z	171/221 (77%)	145 (85%)	20 (12%)	6 (4%)	3	19
13	o	188/190 (99%)	147 (78%)	33 (18%)	8 (4%)	2	15
14	q	198/211 (94%)	168 (85%)	28 (14%)	2 (1%)	13	43
15	R	139/151 (92%)	121 (87%)	15 (11%)	3 (2%)	5	27
16	S	80/86 (93%)	69 (86%)	9 (11%)	2 (2%)	4	25
17	t	102/112 (91%)	82 (80%)	19 (19%)	1 (1%)	13	43
18	U	66/91 (72%)	54 (82%)	10 (15%)	2 (3%)	3	22
19	v	133/144 (92%)	121 (91%)	10 (8%)	2 (2%)	8	34
20	X	146/173 (84%)	121 (83%)	20 (14%)	5 (3%)	3	19
21	B	177/190 (93%)	149 (84%)	23 (13%)	5 (3%)	4	23
22	F	205/245 (84%)	180 (88%)	23 (11%)	2 (1%)	13	43
23	d	221/263 (84%)	191 (86%)	28 (13%)	2 (1%)	14	44
24	g	81/247 (33%)	68 (84%)	12 (15%)	1 (1%)	11	39
25	a	68/110 (62%)	56 (82%)	12 (18%)	0	100	100
26	J	171/257 (66%)	132 (77%)	24 (14%)	15 (9%)	0	4
27	h	119/141 (84%)	96 (81%)	19 (16%)	4 (3%)	3	19
28	5	417/477 (87%)	325 (78%)	62 (15%)	30 (7%)	1	7
29	P	247/250 (99%)	219 (89%)	25 (10%)	3 (1%)	11	39
30	i	119/141 (84%)	91 (76%)	16 (13%)	12 (10%)	0	3
31	L	97/117 (83%)	75 (77%)	20 (21%)	2 (2%)	5	28
32	M	198/214 (92%)	160 (81%)	31 (16%)	7 (4%)	3	19
33	N	91/161 (56%)	78 (86%)	10 (11%)	3 (3%)	3	20
34	O	138/167 (83%)	103 (75%)	27 (20%)	8 (6%)	1	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	b	127/145 (88%)	108 (85%)	18 (14%)	1 (1%)	16	47
36	c	58/66 (88%)	47 (81%)	10 (17%)	1 (2%)	7	32
37	V	95/109 (87%)	70 (74%)	15 (16%)	10 (10%)	0	2
38	w	145/166 (87%)	105 (72%)	30 (21%)	10 (7%)	1	7
39	E	389/407 (96%)	288 (74%)	46 (12%)	55 (14%)	0	1
40	Y	172/379 (45%)	139 (81%)	27 (16%)	6 (4%)	3	19
41	Q	55/57 (96%)	40 (73%)	8 (14%)	7 (13%)	0	1
42	D	31/34 (91%)	25 (81%)	5 (16%)	1 (3%)	3	20
43	G	306/345 (89%)	254 (83%)	33 (11%)	19 (6%)	1	9
44	K	199/203 (98%)	185 (93%)	10 (5%)	4 (2%)	6	29
45	T	130/152 (86%)	100 (77%)	21 (16%)	9 (7%)	1	7
46	C	694/716 (97%)	490 (71%)	82 (12%)	122 (18%)	0	0
47	8	574/762 (75%)	462 (80%)	57 (10%)	55 (10%)	0	3
48	W	215/254 (85%)	181 (84%)	27 (13%)	7 (3%)	3	20
49	I	342/489 (70%)	302 (88%)	21 (6%)	19 (6%)	1	10
50	H	295/334 (88%)	231 (78%)	41 (14%)	23 (8%)	1	5
51	A	481/502 (96%)	341 (71%)	89 (18%)	51 (11%)	0	2
52	l	256/273 (94%)	216 (84%)	30 (12%)	10 (4%)	2	17
All	All	11089/13737 (81%)	8768 (79%)	1572 (14%)	749 (7%)	2	7

5 of 749 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	f	56	THR
1	f	91	ASP
1	f	190	ARG
1	f	203	LEU
1	f	235	LEU

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	f	1318/1862 (71%)	1270 (96%)	48 (4%)	30	57
4	y	104/116 (90%)	104 (100%)	0	100	100
5	s	252/362 (70%)	239 (95%)	13 (5%)	19	48
6	j	69/123 (56%)	65 (94%)	4 (6%)	17	45
7	n	196/289 (68%)	181 (92%)	15 (8%)	10	34
8	p	262/268 (98%)	259 (99%)	3 (1%)	70	82
9	r	113/121 (93%)	113 (100%)	0	100	100
10	u	117/132 (89%)	111 (95%)	6 (5%)	20	49
11	m	116/117 (99%)	112 (97%)	4 (3%)	32	59
12	Z	143/184 (78%)	143 (100%)	0	100	100
13	o	160/160 (100%)	157 (98%)	3 (2%)	52	72
14	q	188/195 (96%)	187 (100%)	1 (0%)	86	91
15	R	125/132 (95%)	125 (100%)	0	100	100
16	S	70/73 (96%)	69 (99%)	1 (1%)	62	78
17	t	87/93 (94%)	87 (100%)	0	100	100
18	U	57/74 (77%)	50 (88%)	7 (12%)	4	16
19	v	103/112 (92%)	102 (99%)	1 (1%)	73	84
20	X	137/157 (87%)	135 (98%)	2 (2%)	60	77
21	B	159/165 (96%)	159 (100%)	0	100	100
22	F	182/212 (86%)	182 (100%)	0	100	100
23	d	187/208 (90%)	186 (100%)	1 (0%)	86	91
24	g	68/197 (34%)	67 (98%)	1 (2%)	60	77
25	a	64/96 (67%)	64 (100%)	0	100	100
26	J	138/191 (72%)	125 (91%)	13 (9%)	7	27
27	h	103/120 (86%)	102 (99%)	1 (1%)	73	84
28	5	358/408 (88%)	337 (94%)	21 (6%)	16	44
29	P	204/205 (100%)	202 (99%)	2 (1%)	73	84
30	i	110/124 (89%)	106 (96%)	4 (4%)	30	57
31	L	89/104 (86%)	89 (100%)	0	100	100
32	M	167/179 (93%)	161 (96%)	6 (4%)	30	57
33	N	84/125 (67%)	82 (98%)	2 (2%)	44	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	O	118/139 (85%)	117 (99%)	1 (1%)	79	87
35	b	110/123 (89%)	110 (100%)	0	100	100
36	c	49/53 (92%)	47 (96%)	2 (4%)	26	54
37	V	86/97 (89%)	71 (83%)	15 (17%)	1	7
38	w	125/137 (91%)	115 (92%)	10 (8%)	10	33
39	E	334/350 (95%)	322 (96%)	12 (4%)	30	57
40	Y	152/327 (46%)	145 (95%)	7 (5%)	23	52
41	Q	49/49 (100%)	46 (94%)	3 (6%)	15	43
42	D	30/31 (97%)	29 (97%)	1 (3%)	33	60
43	G	260/289 (90%)	256 (98%)	4 (2%)	60	77
44	K	176/178 (99%)	174 (99%)	2 (1%)	70	82
45	T	111/131 (85%)	108 (97%)	3 (3%)	40	65
46	C	616/628 (98%)	585 (95%)	31 (5%)	20	49
47	8	485/648 (75%)	465 (96%)	20 (4%)	26	54
48	W	194/217 (89%)	186 (96%)	8 (4%)	26	54
49	I	300/430 (70%)	295 (98%)	5 (2%)	56	75
50	H	266/299 (89%)	261 (98%)	5 (2%)	52	72
51	A	425/441 (96%)	380 (89%)	45 (11%)	5	22
52	l	217/230 (94%)	214 (99%)	3 (1%)	62	78
All	All	9633/11701 (82%)	9297 (96%)	336 (4%)	33	58

5 of 336 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	C	190	ILE
50	H	304	LEU
46	C	274	LYS
47	8	82	GLN
51	A	48	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 91 such sidechains are listed below:

Mol	Chain	Res	Type
38	w	34	GLN

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Mol	Chain	Res	Type
46	C	359	HIS
38	w	130	HIS
43	G	231	ASN
46	C	635	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	1	74/75 (98%)	11 (14%)	1 (1%)
3	0	2144/2319 (92%)	389 (18%)	28 (1%)
All	All	2218/2394 (92%)	400 (18%)	29 (1%)

5 of 400 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	1	16	U
2	1	17	G
2	1	20	A
2	1	25	G
2	1	32	U

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	0	1196	G
3	0	2073	C
3	0	1450	G
3	0	1979	C
3	0	1393	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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
55	GNP	5	502	54	29,34,34	2.06	8 (27%)	33,54,54	2.39	9 (27%)

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
55	GNP	5	502	54	-	6/14/38/38	0/3/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	5	502	GNP	PB-O3A	-7.46	1.49	1.59
55	5	502	GNP	C6-N1	3.87	1.39	1.33
55	5	502	GNP	PB-O2B	-3.60	1.47	1.56
55	5	502	GNP	PG-O3G	-2.43	1.50	1.56
55	5	502	GNP	C8-N7	-2.33	1.30	1.34

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	5	502	GNP	C5-C6-N1	-8.57	111.71	123.43
55	5	502	GNP	C2-N1-C6	5.52	124.69	115.93
55	5	502	GNP	O3G-PG-O1G	-3.59	104.44	113.45
55	5	502	GNP	PB-O3A-PA	-3.42	120.56	132.62
55	5	502	GNP	C3'-C2'-C1'	3.38	106.07	100.98

There are no chirality outliers.

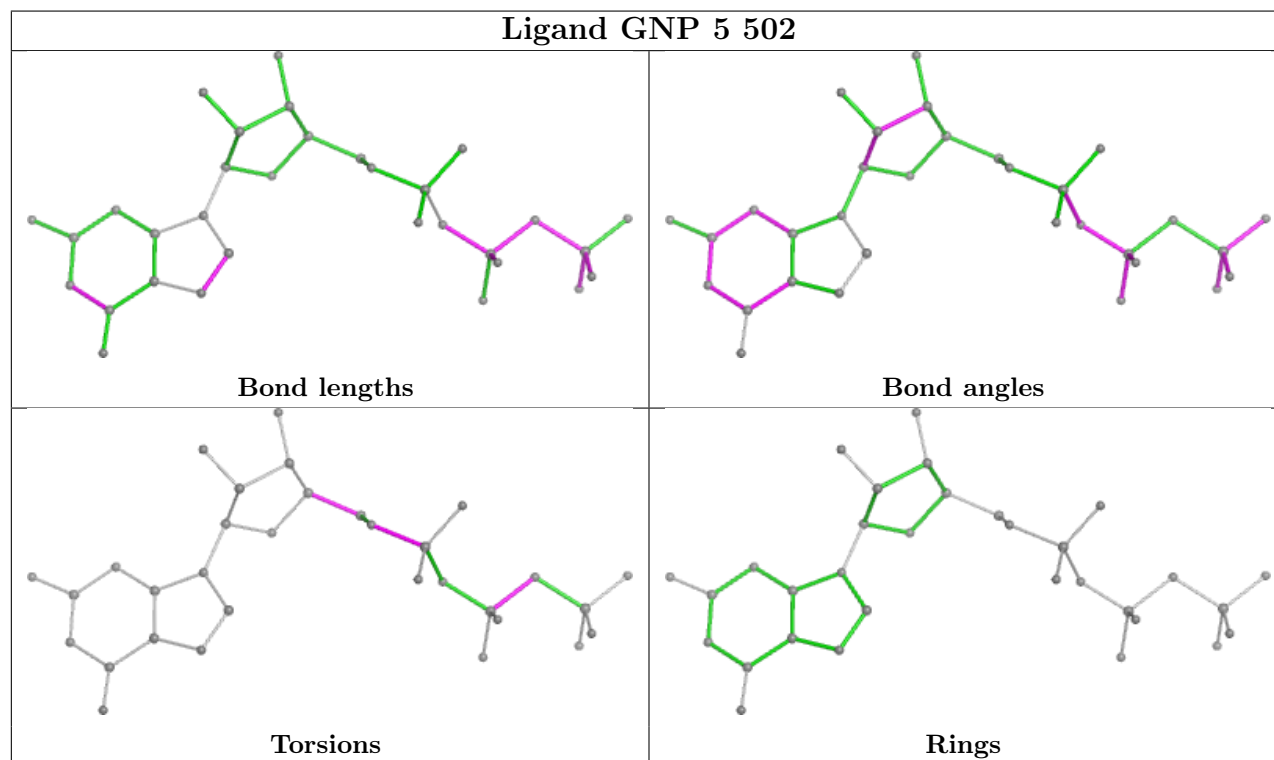
5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	5	502	GNP	PG-N3B-PB-O1B
55	5	502	GNP	PG-N3B-PB-O3A
55	5	502	GNP	C5'-O5'-PA-O3A
55	5	502	GNP	O4'-C4'-C5'-O5'
55	5	502	GNP	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	f	20
28	5	2
46	C	1
48	W	1

The worst 5 of 24 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	282:ARG	C	283:GLY	N	2.09
1	f	1149:TYR	C	1150:VAL	N	1.72
1	f	1221:LEU	C	1222:PRO	N	1.71
1	f	1254:ALA	C	1255:GLN	N	1.68
1	C	53:ARG	C	54:ASN	N	1.67

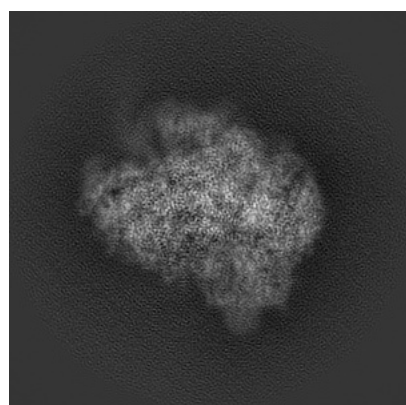
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11893. These allow visual inspection of the internal detail of the map and identification of artifacts.

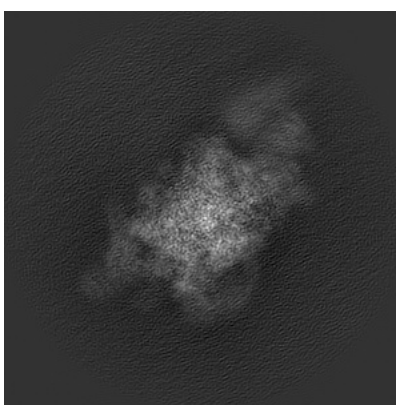
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

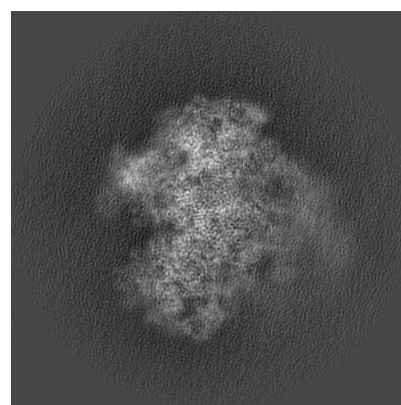
6.1.1 Primary map



X



Y

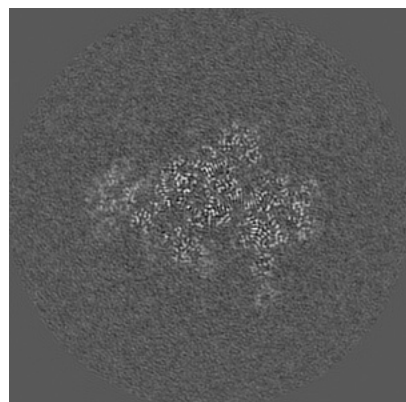


Z

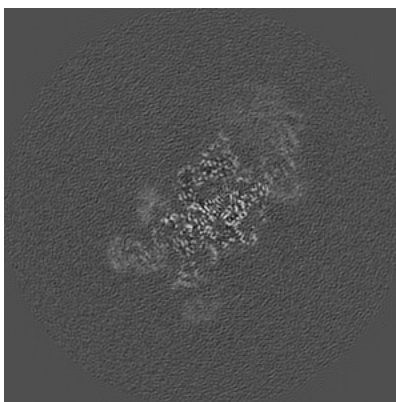
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

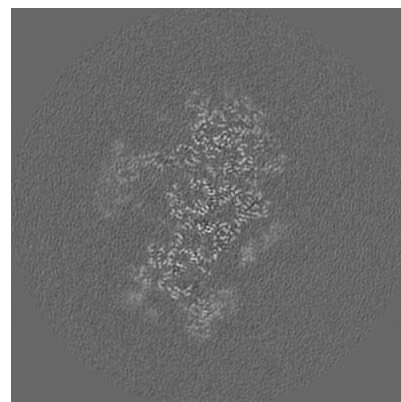
6.2.1 Primary map



X Index: 200



Y Index: 200

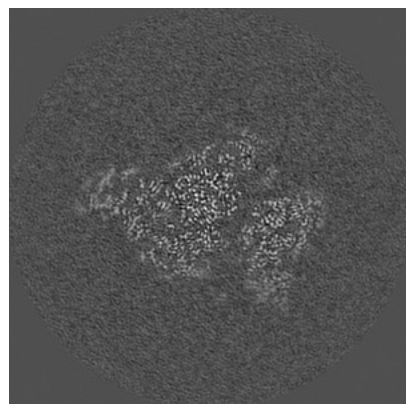


Z Index: 200

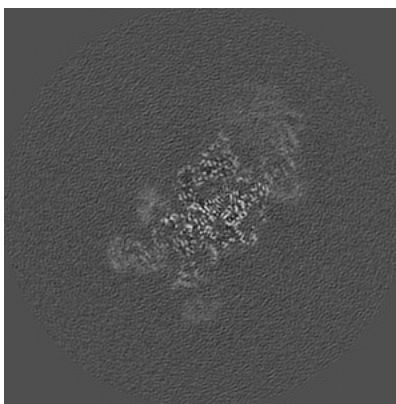
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

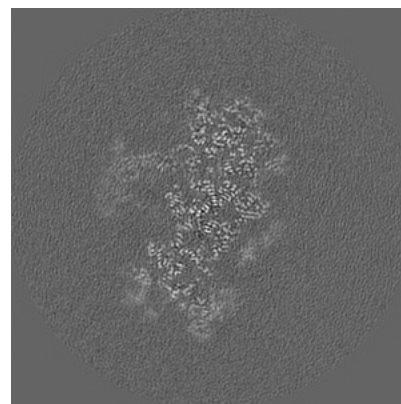
6.3.1 Primary map



X Index: 188



Y Index: 200

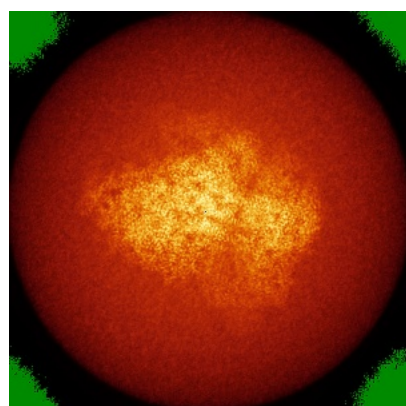


Z Index: 199

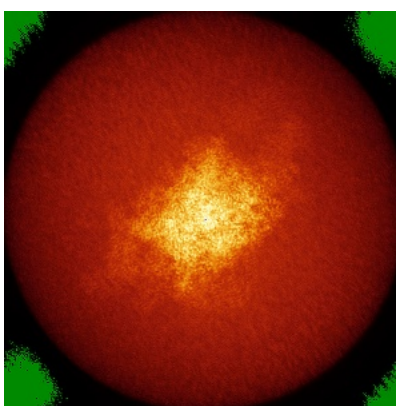
The images above show the largest variance slices of the map in three orthogonal directions.

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

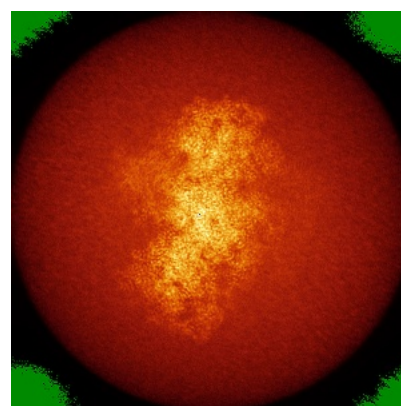
6.4.1 Primary map



X



Y

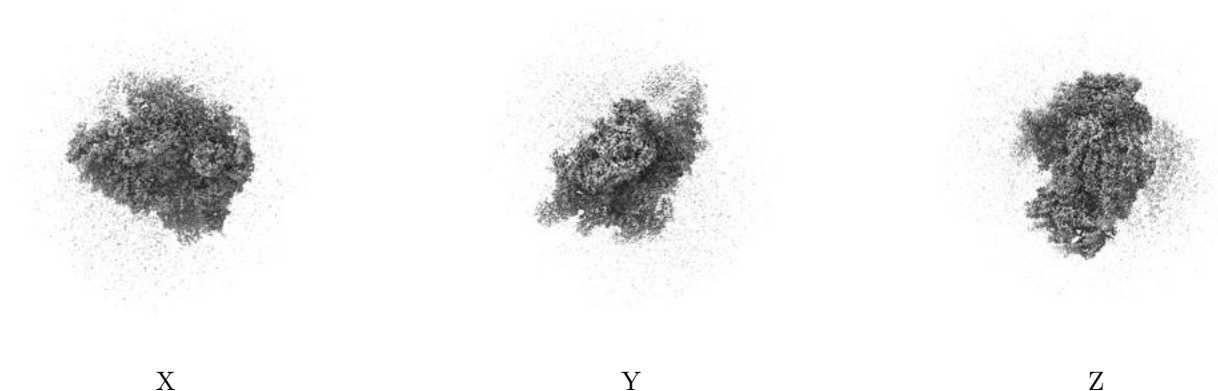


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0193. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

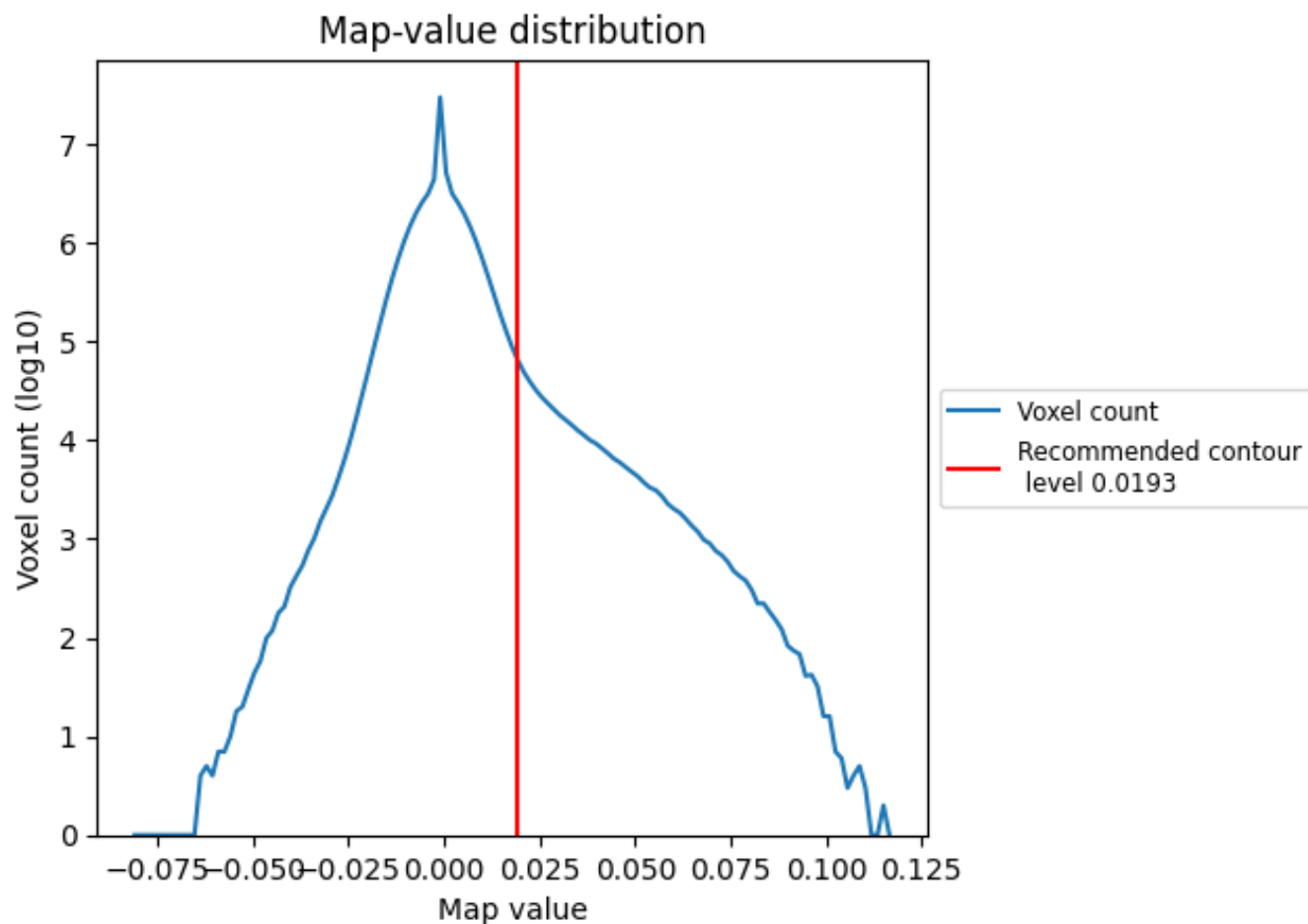
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

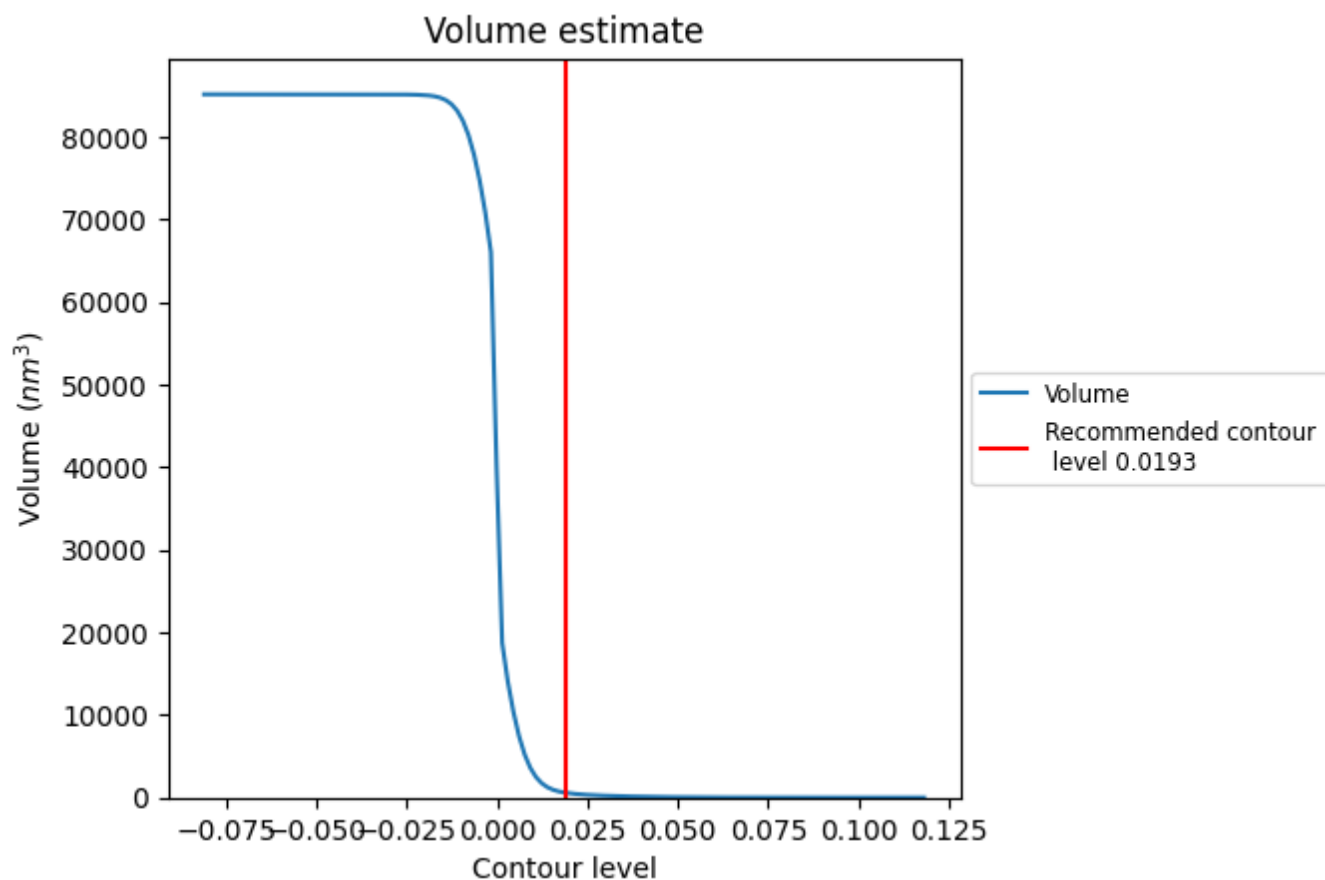
This section contains the results of statistical analysis of the map.

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.

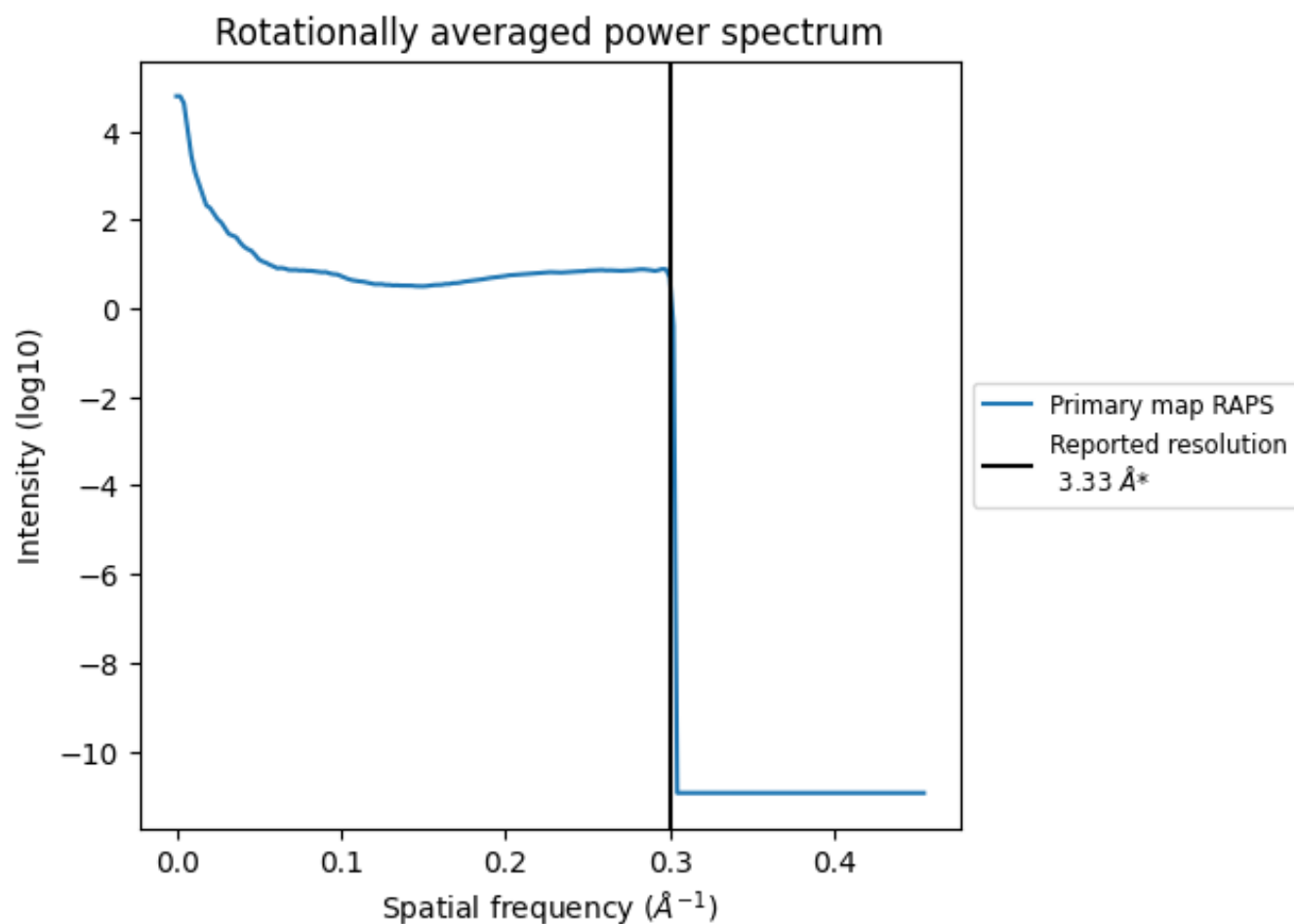
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 566 nm³; this corresponds to an approximate mass of 511 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 0.300 Å⁻¹

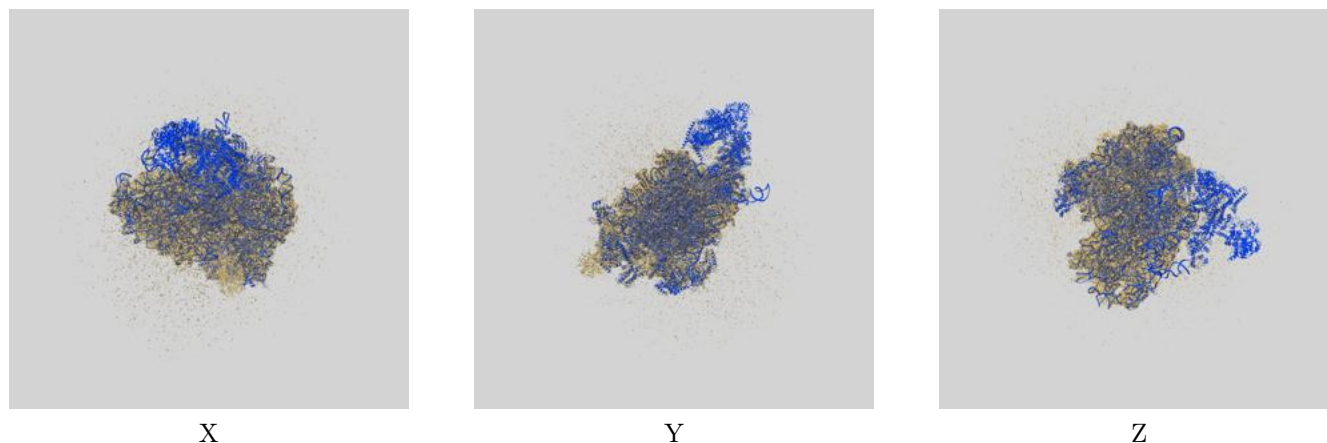
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

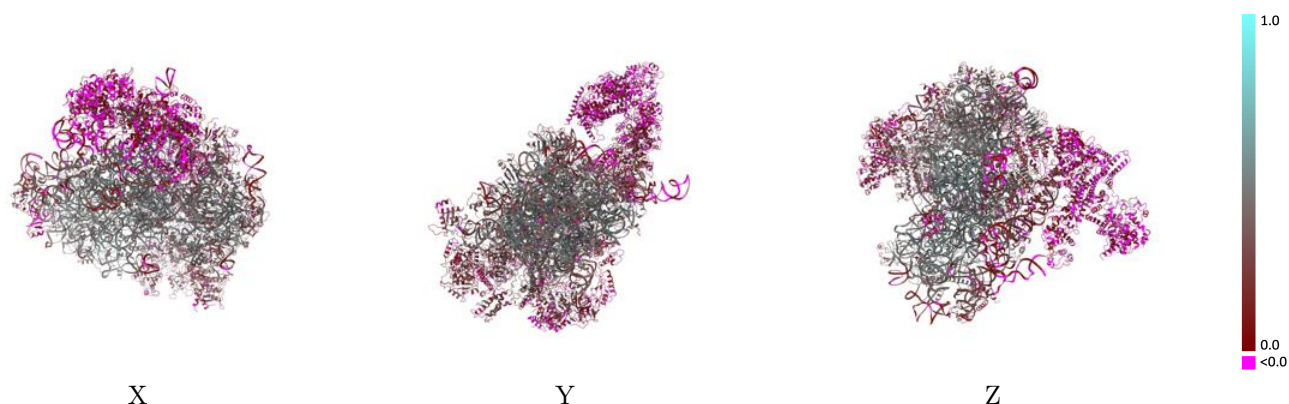
This section contains information regarding the fit between EMDB map EMD-11893 and PDB model 7ASE. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



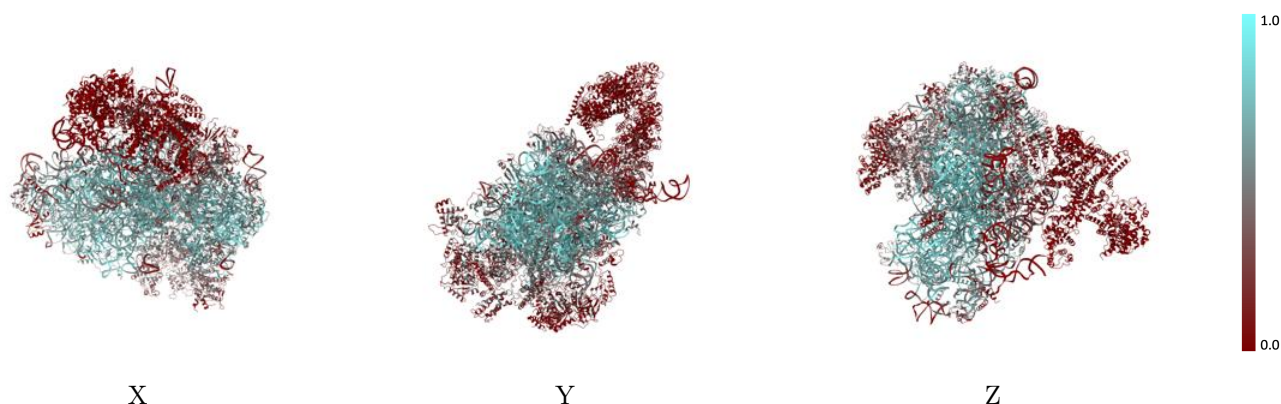
The images above show the 3D surface view of the map at the recommended contour level 0.0193 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



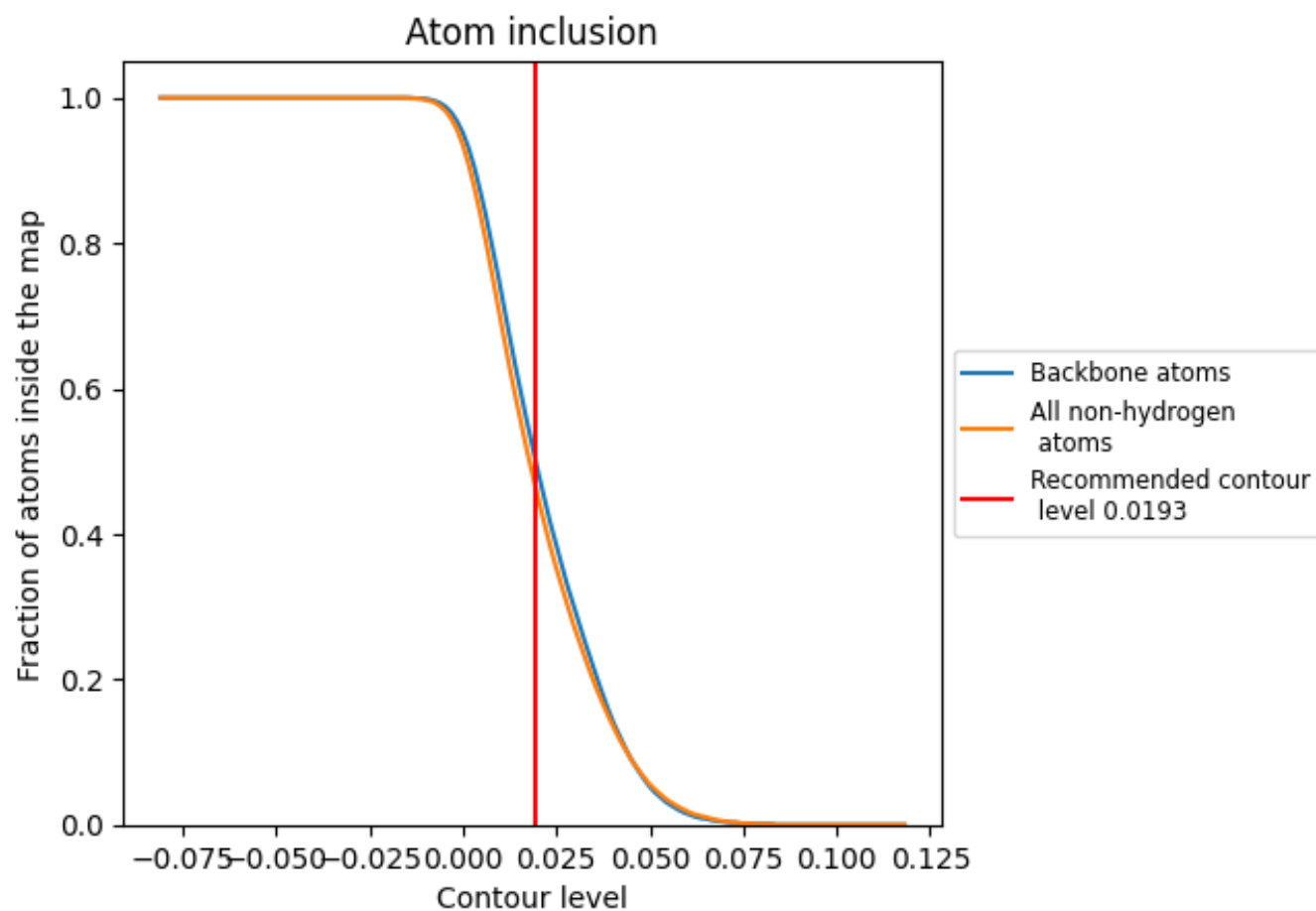
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0193).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 46% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





































The table lists the average atom inclusion at the recommended contour level (0.0193) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4650	 0.3140
0	 0.6860	 0.4100
1	 0.6240	 0.3900
5	 0.1770	 0.1970
8	 0.1050	 0.1110
A	 0.1800	 0.2290
B	 0.6630	 0.4450
C	 0.1370	 0.1530
D	 0.6490	 0.4030
E	 0.0180	 0.0580
F	 0.6590	 0.4440
G	 0.0090	 0.0310
H	 0.0060	 0.0140
I	 0.0000	 0.0270
J	 0.2140	 0.1620
K	 0.0000	 0.0090
L	 0.5220	 0.3740
M	 0.5820	 0.4010
N	 0.5150	 0.3200
O	 0.5160	 0.2710
P	 0.5250	 0.3680
Q	 0.6170	 0.3660
R	 0.6710	 0.4560
S	 0.6560	 0.4530
T	 0.5680	 0.3920
U	 0.4510	 0.3740
V	 0.5590	 0.4390
W	 0.6410	 0.4440
X	 0.7030	 0.4570
Y	 0.0510	 0.1140
Z	 0.6630	 0.4390
a	 0.4440	 0.3150
b	 0.7230	 0.4770
c	 0.5110	 0.3610
d	 0.6770	 0.4640



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Chain	Atom inclusion	Q-score
f	 0.2540	 0.2210
g	 0.6680	 0.4600
h	 0.2370	 0.1980
i	 0.5450	 0.3570
j	 0.3190	 0.2750
l	 0.6780	 0.4450
m	 0.7000	 0.4630
n	 0.2780	 0.2490
o	 0.5770	 0.3930
p	 0.4880	 0.3530
q	 0.6080	 0.4110
r	 0.6470	 0.4160
s	 0.2070	 0.1950
t	 0.6920	 0.4720
u	 0.5260	 0.3220
v	 0.6550	 0.4420
w	 0.3930	 0.3050
y	 0.6420	 0.4190