



wwPDB EM Validation Summary Report ⓘ

Nov 9, 2024 – 11:53 am GMT

PDB ID : 5OPT
EMDB ID : EMD-3844
Title : Structure of KSRP in context of Trypanosoma cruzi 40S
Authors : Brito Querido, J.; Mancera-Martinez, E.; Vicens, Q.; Bochler, A.; Chicher, J.; Simonetti, A.; Hashem, Y.
Deposited on : 2017-08-10
Resolution : 4.00 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:

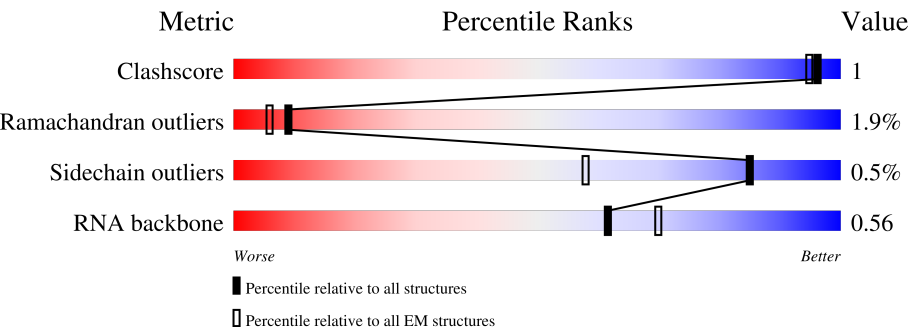
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) :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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.00 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)
Clashscore	210492	15764
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	p	318	<div><div>85%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>95%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>..</div></div>
2	q	57	<div><div>37%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>63%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>33%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>..</div></div>
3	r	149	<div><div>50%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>84%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>9%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>6%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>..</div></div>
4	t	152	<div><div>55%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>74%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>22%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>..</div></div>
5	u	153	<div><div>51%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>74%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>22%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>..</div></div>
6	L	273	<div><div>26%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>94%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>5%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>..</div></div>
7	M	143	<div><div>22%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>99%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>..</div></div>

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Mol	Chain	Length	Quality of chain
8	O	190	
9	Q	211	
10	R	151	
11	S	86	
12	T	112	
13	U	112	
14	V	144	
15	W	261	
16	X	173	
17	Y	137	
18	Z	221	
19	b	190	
20	f	245	
21	d	263	
22	e	130	
23	g	236	
24	a	110	
25	i	141	
26	j	150	
27	P	250	
28	k	196	
29	l	117	
30	m	214	
31	n	161	
32	o	167	

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Mol	Chain	Length	Quality of chain
33	c	66	<div><div></div><div>33%</div><div></div><div>86%</div><div>5%</div><div>9%</div></div>
34	h	257	<div><div></div><div>47%</div><div>53%</div><div>10%</div><div></div><div>33%</div></div>
35	E	2319	<div><div></div><div>12%</div><div></div><div>62%</div><div>20%</div><div></div><div>13%</div></div>

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 82219 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 Activated protein kinase C receptor, putative.

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

- Molecule 2 is a protein called Ribosomal protein S29, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	q	38	Total	C	N	O	S	0	0
			311	191	64	52	4		

- Molecule 3 is a protein called 40S ribosomal protein S16, putative.

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

- Molecule 4 is a protein called 40S ribosomal protein S15, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	t	119	Total	C	N	O	S	0	0
			969	615	185	165	4		

- Molecule 5 is a protein called 40S ribosomal protein S18, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	u	120	Total	C	N	O	S	0	0
			981	614	194	169	4		

- Molecule 6 is a protein called 40S ribosomal protein S4.

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

- Molecule 7 is a protein called 40S ribosomal protein S23, putative.

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

- Molecule 8 is a protein called 40S ribosomal protein S5, putative.

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

- Molecule 9 is a protein called Ribosomal protein S7, putative.

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

- Molecule 10 is a protein called 40S ribosomal protein S13, putative.

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

- Molecule 11 is a protein called 40S ribosomal protein S27, putative.

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

- Molecule 12 is a protein called 40S ribosomal protein S26.

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

- Molecule 13 is a protein called 40S ribosomal protein S33, putative.

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

- Molecule 14 is a protein called 40S ribosomal protein S14, putative.

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

- Molecule 15 is a protein called 40S ribosomal protein S3a-2.

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

- Molecule 16 is a protein called 40S ribosomal protein S11, putative.

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

- Molecule 17 is a protein called 40S ribosomal protein S24.

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

- Molecule 18 is a protein called 40S ribosomal protein S8.

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

- Molecule 19 is a protein called 40S ribosomal protein S9, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	b	164	Total	C	N	O	S	0	0
			1365	864	266	227	8		

- Molecule 20 is a protein called 40S ribosomal protein SA.

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

- Molecule 21 is a protein called 40S ribosomal protein S2, putative.

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

- Molecule 22 is a protein called 40S ribosomal protein S15a, putative.

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

- Molecule 23 is a protein called 40S ribosomal protein S21, putative.

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

- Molecule 24 is a protein called Ribosomal protein S25, putative.

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

- Molecule 25 is a protein called 40S ribosomal protein S12.

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

- Molecule 26 is a protein called Ubiquitin/ribosomal protein S27a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	j	64	Total	C	N	O	S	0	0
			518	324	98	90	6		

- Molecule 27 is a protein called 40S ribosomal protein S6.

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

- Molecule 28 is a protein called 40S ribosomal protein S17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	k	118	Total	C	N	O	S	0	0
			972	610	187	170	5		

- Molecule 29 is a protein called Ribosomal protein S20, putative.

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

- Molecule 30 is a protein called 40S ribosomal protein S3, putative.

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

- Molecule 31 is a protein called 40S ribosomal protein S10, putative.

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

- Molecule 32 is a protein called Ribosomal protein S19, putative.

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

- Molecule 33 is a protein called 40S ribosomal protein S30.

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

- Molecule 34 is a protein called RNA-binding protein, putative.

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

- Molecule 35 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	E	2022	Total	C	N	O	P	0	0
			43106	19268	7710	14111	2017		

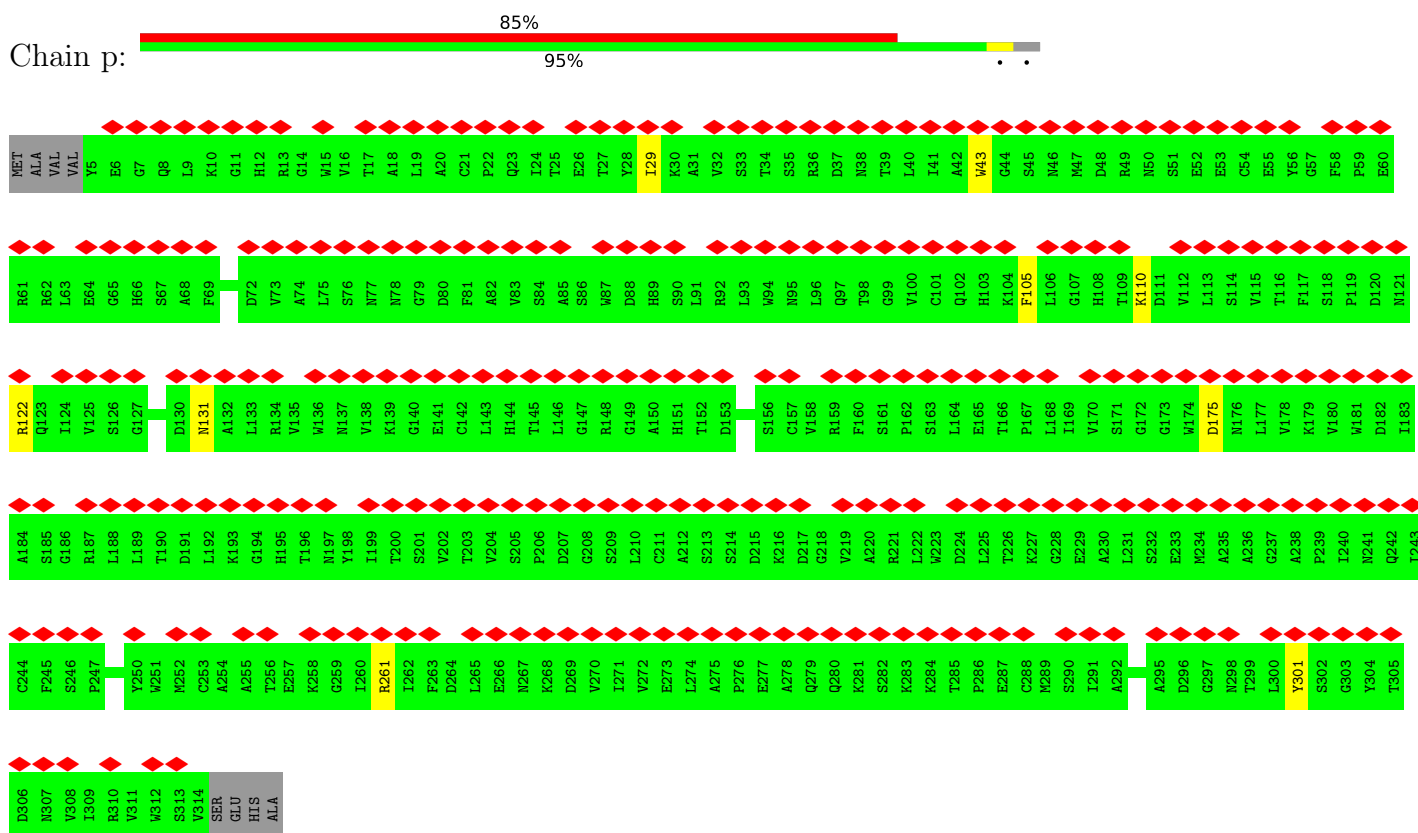
There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	143	C	A	conflict	GB 320364483
E	805	C	U	conflict	GB 320364483
E	2316	U	-	insertion	GB 320364483
E	2317	U	-	insertion	GB 320364483
E	2318	U	-	insertion	GB 320364483

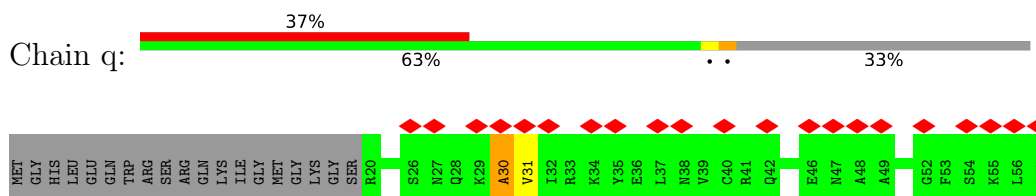
3 Residue-property plots

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

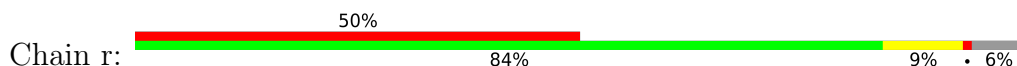
- Molecule 1: Activated protein kinase C receptor, putative

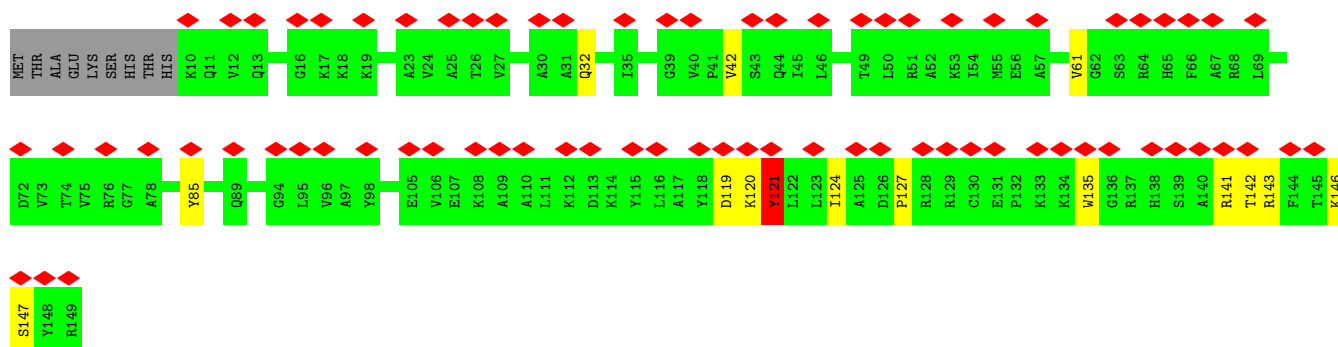


- Molecule 2: Ribosomal protein S29, putative

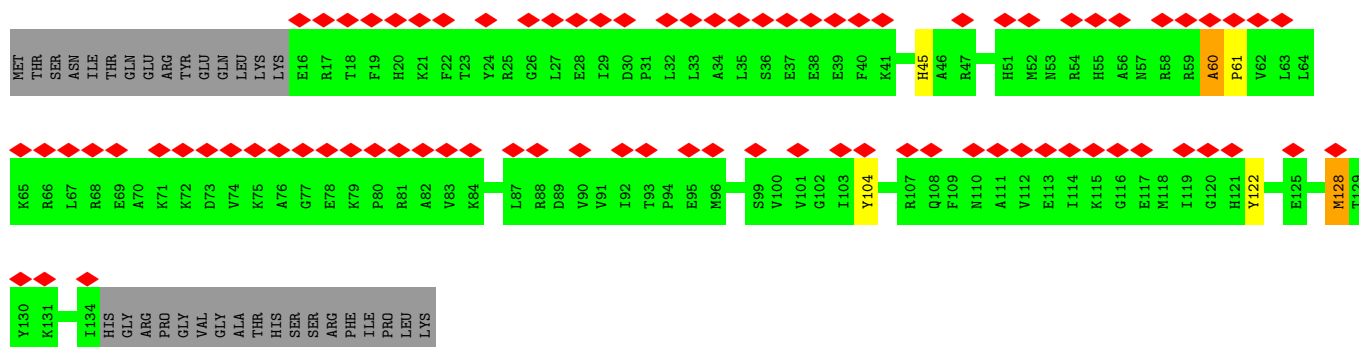


- Molecule 3: 40S ribosomal protein S16, putative

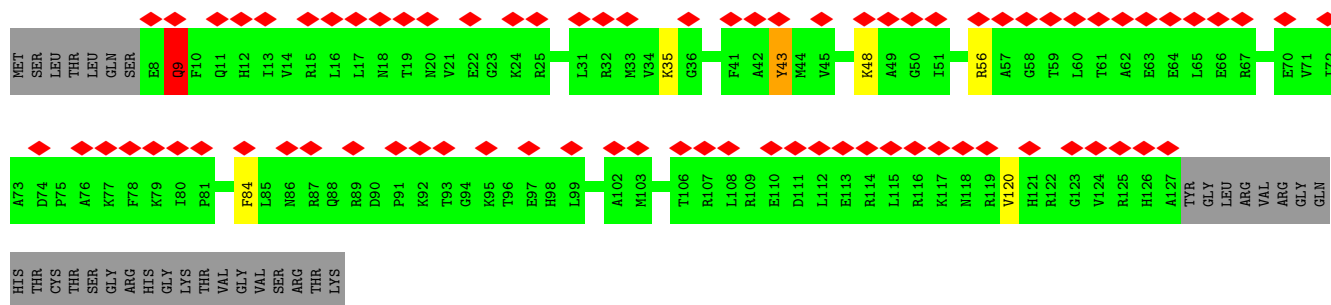
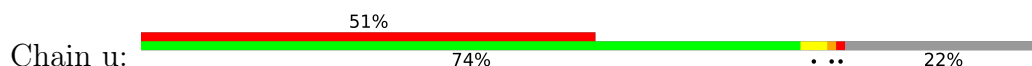




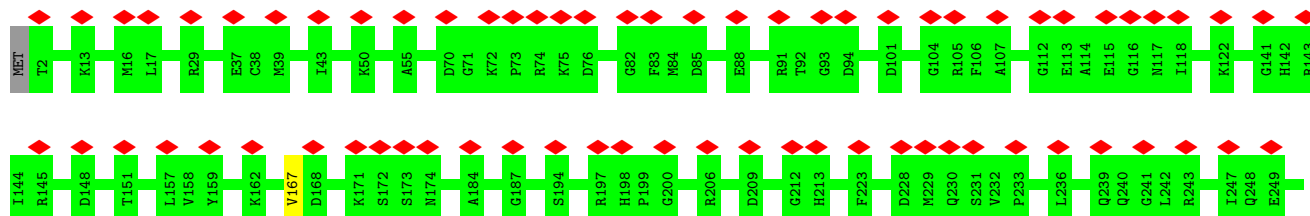
- Molecule 4: 40S ribosomal protein S15, putative

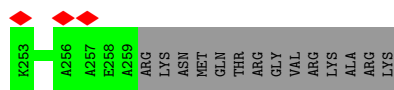


- Molecule 5: 40S ribosomal protein S18, putative

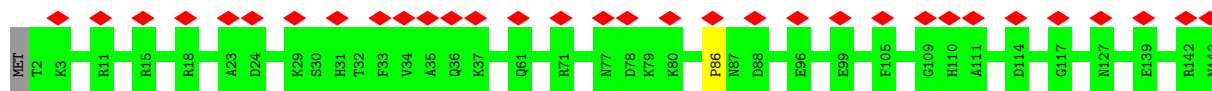


- Molecule 6: 40S ribosomal protein S4

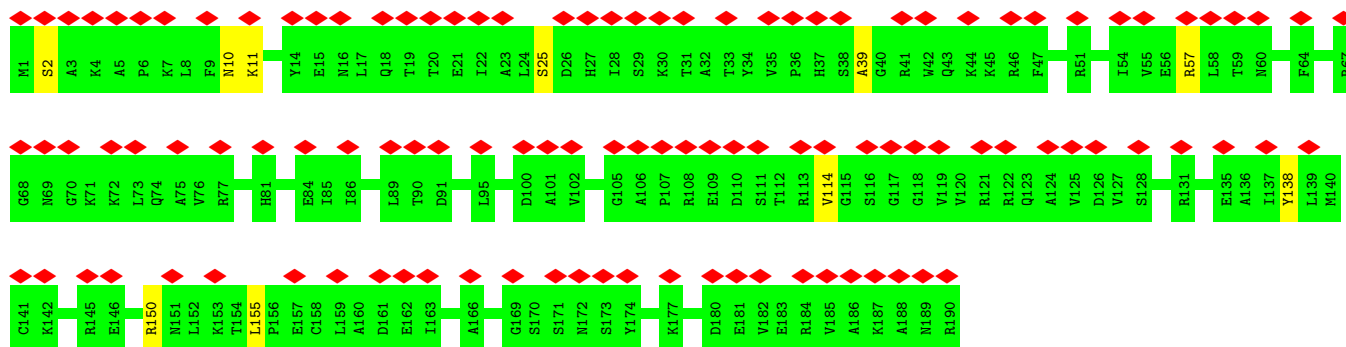




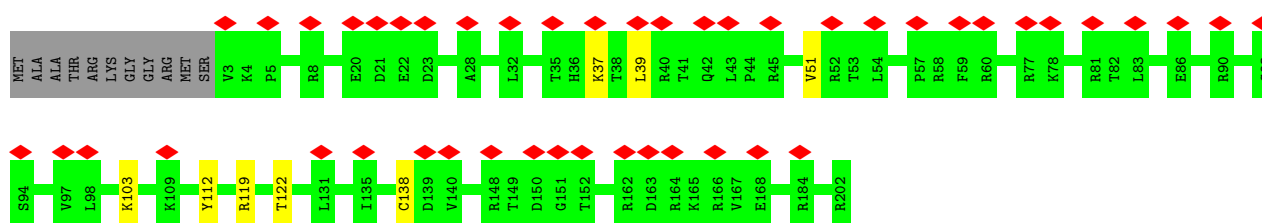
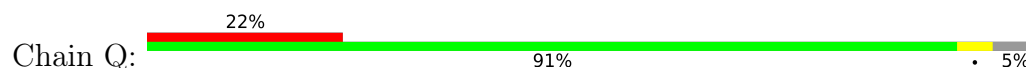
- Molecule 7: 40S ribosomal protein S23, putative



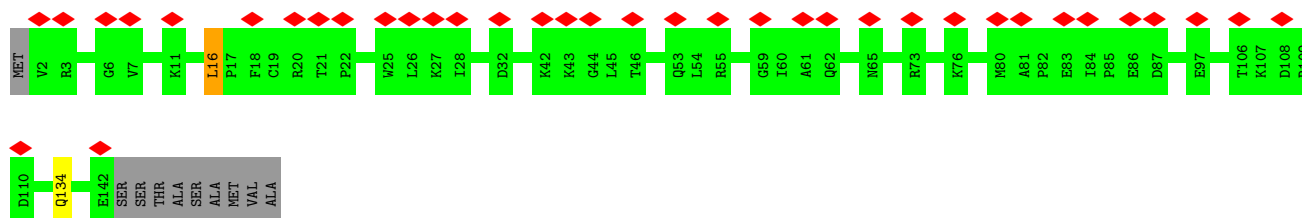
- Molecule 8: 40S ribosomal protein S5, putative



- Molecule 9: Ribosomal protein S7, putative

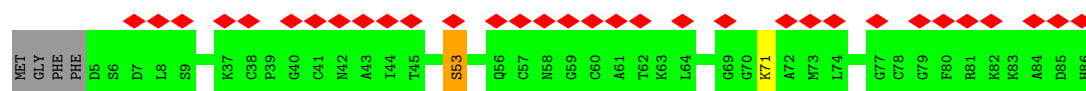


- Molecule 10: 40S ribosomal protein S13, putative



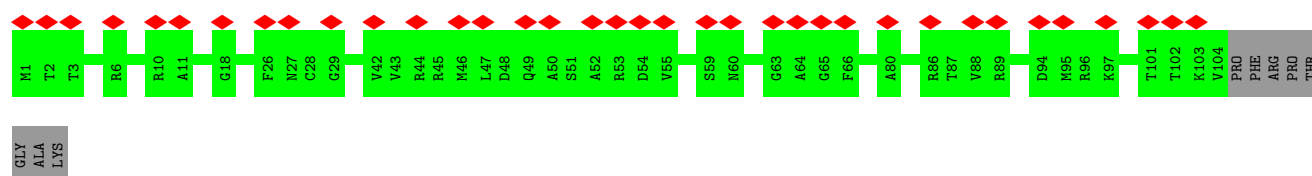
- Molecule 11: 40S ribosomal protein S27, putative

Chain S:



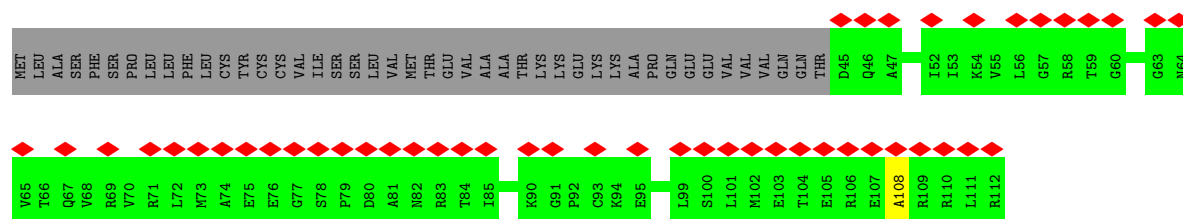
• Molecule 12: 40S ribosomal protein S26

Chain T:



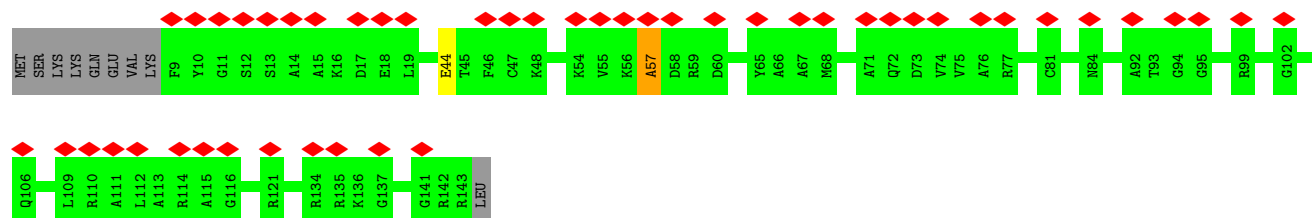
• Molecule 13: 40S ribosomal protein S33, putative

Chain U:



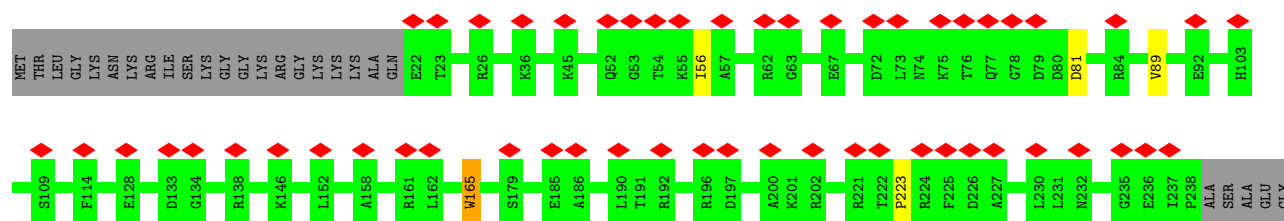
• Molecule 14: 40S ribosomal protein S14, putative

Chain V:



• Molecule 15: 40S ribosomal protein S3a-2

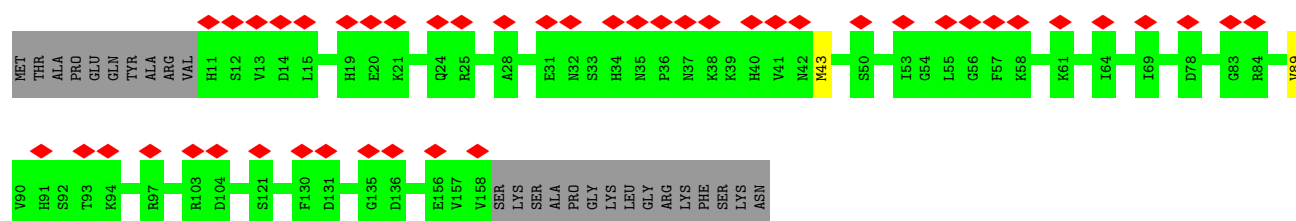
Chain W:



GLU
ALA
ALA
ARG
VAL
PRO
VAL
GLU
GLU
GLU
ALA
GLN
GLU
ALA
PRO
PRO
ALA
ALA
GLU
ALA
ALA
THR
ALA

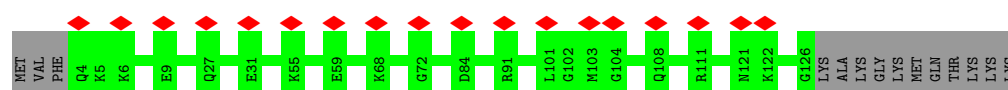
- Molecule 16: 40S ribosomal protein S11, putative

Chain X: 27% 84% 14%



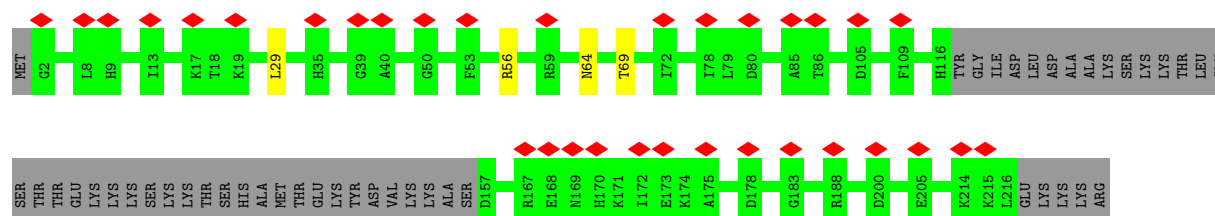
- Molecule 17: 40S ribosomal protein S24

Chain Y: 13% 90% 10%



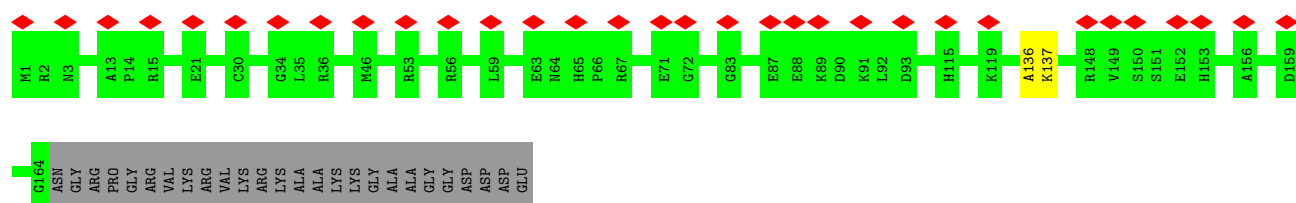
- Molecule 18: 40S ribosomal protein S8

Chain Z: 15% 77% 21%



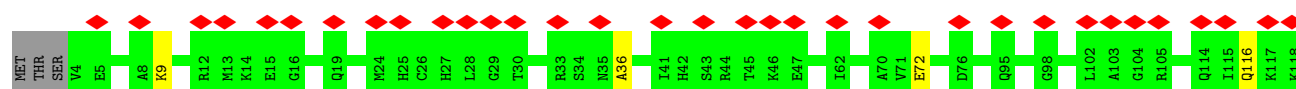
- Molecule 19: 40S ribosomal protein S9, putative

Chain b: 17% 85% 14%

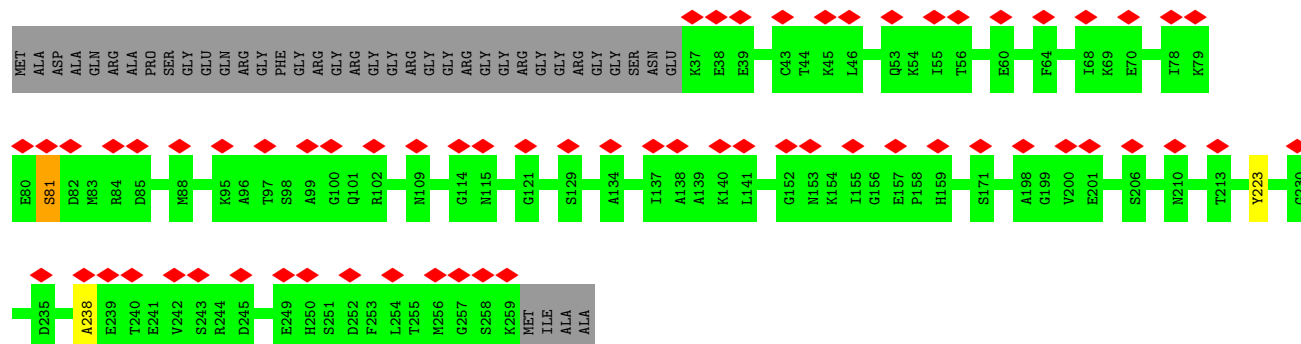
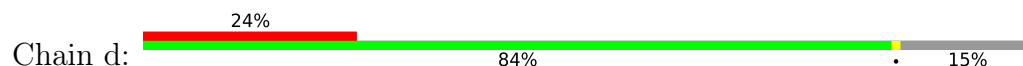


- Molecule 20: 40S ribosomal protein SA

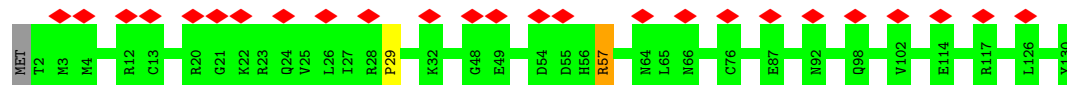
Chain f: 23% 82% 16%



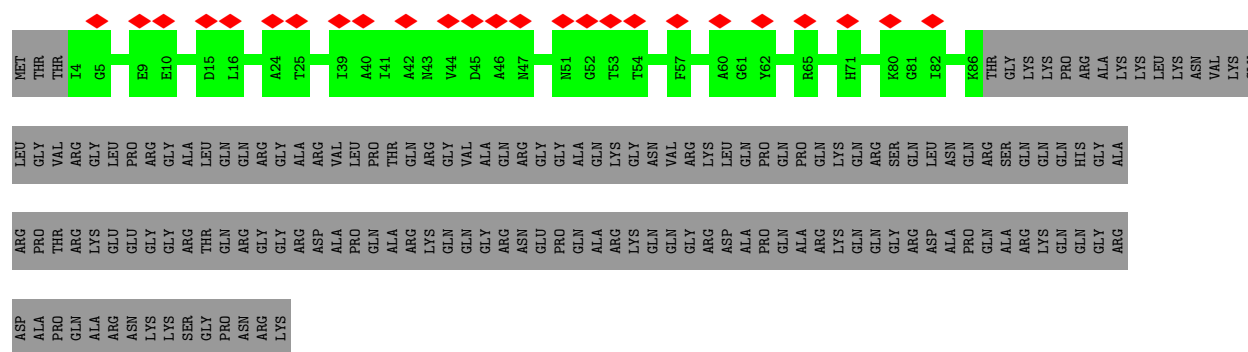
- Molecule 21: 40S ribosomal protein S2, putative



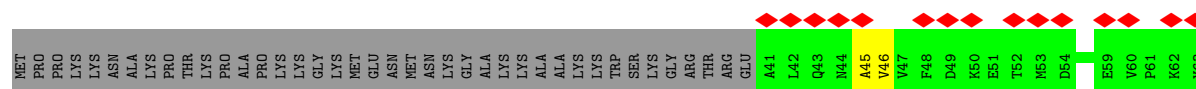
- Molecule 22: 40S ribosomal protein S15a, putative

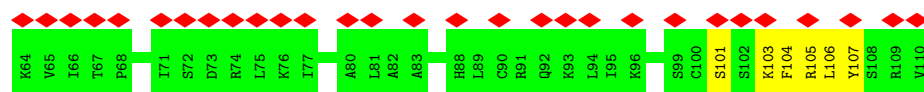


- Molecule 23: 40S ribosomal protein S21, putative



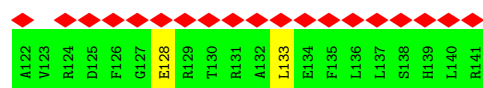
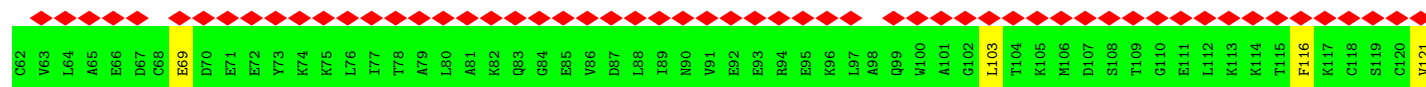
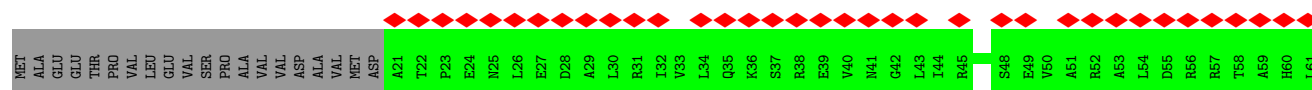
- Molecule 24: Ribosomal protein S25, putative





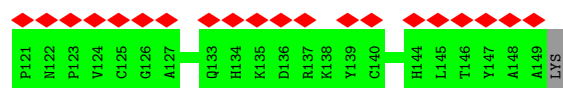
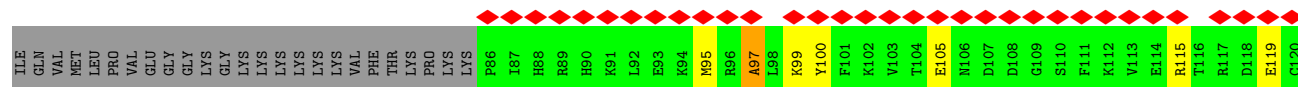
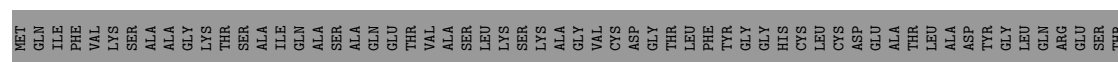
• Molecule 25: 40S ribosomal protein S12

Chain i: 79% 82% 14%



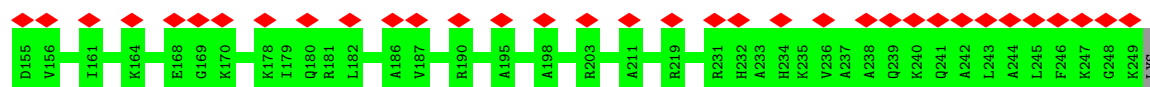
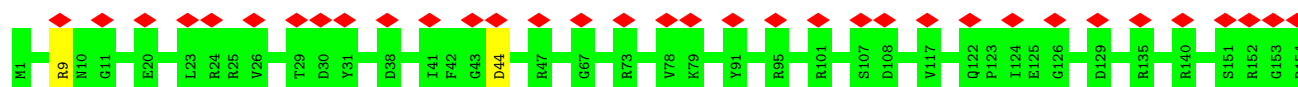
• Molecule 26: Ubiquitin/ribosomal protein S27a, putative

Chain j: 35% 38% 57%



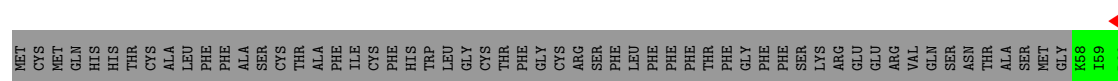
• Molecule 27: 40S ribosomal protein S6

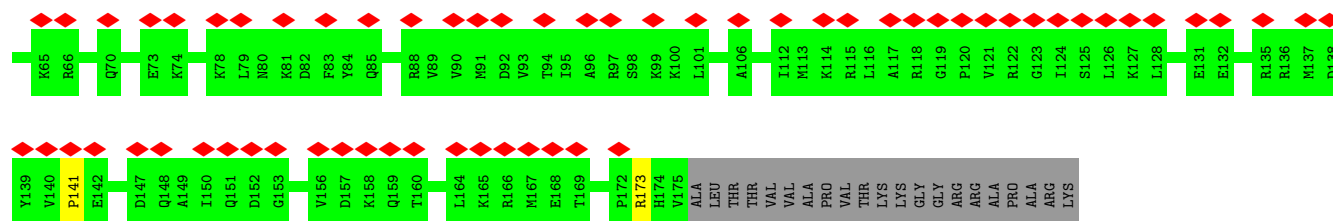
Chain P: 27% 99%



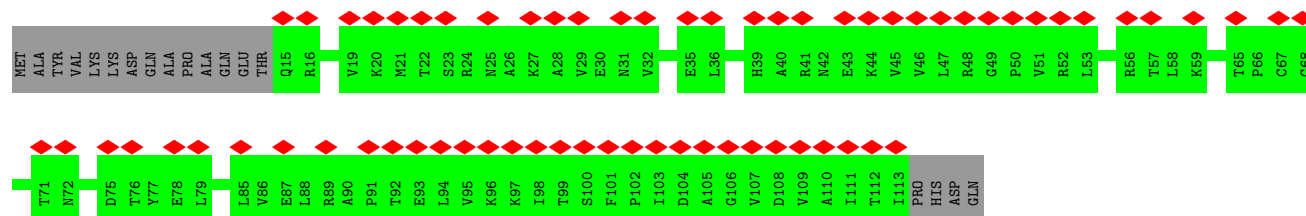
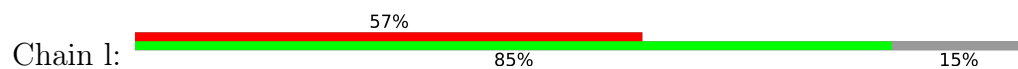
• Molecule 28: 40S ribosomal protein S17, putative

Chain k: 32% 59% 40%

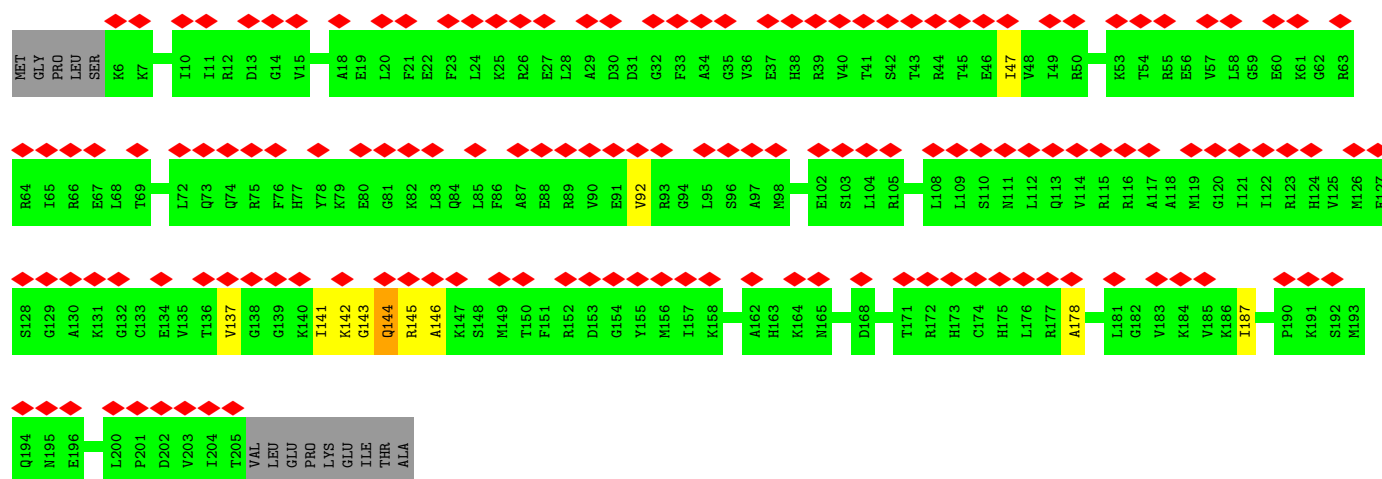
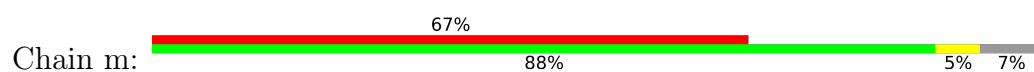




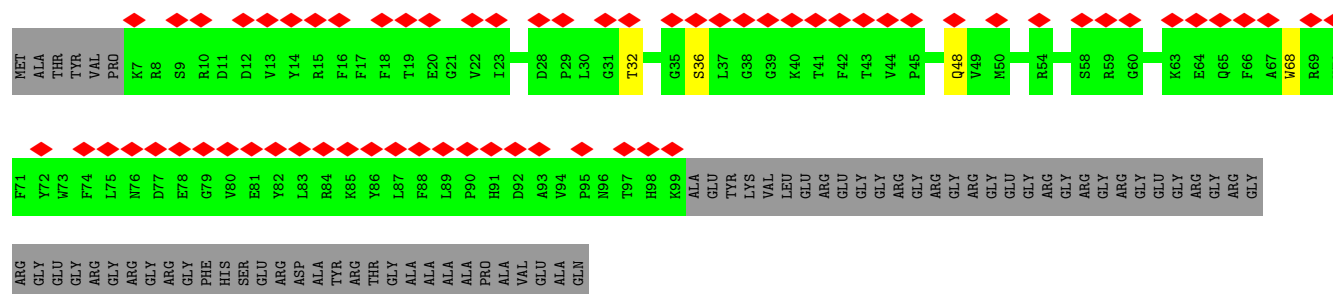
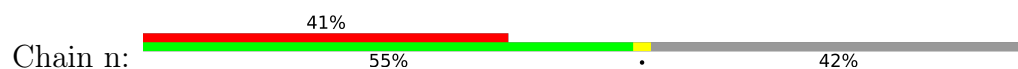
- Molecule 29: Ribosomal protein S20, putative



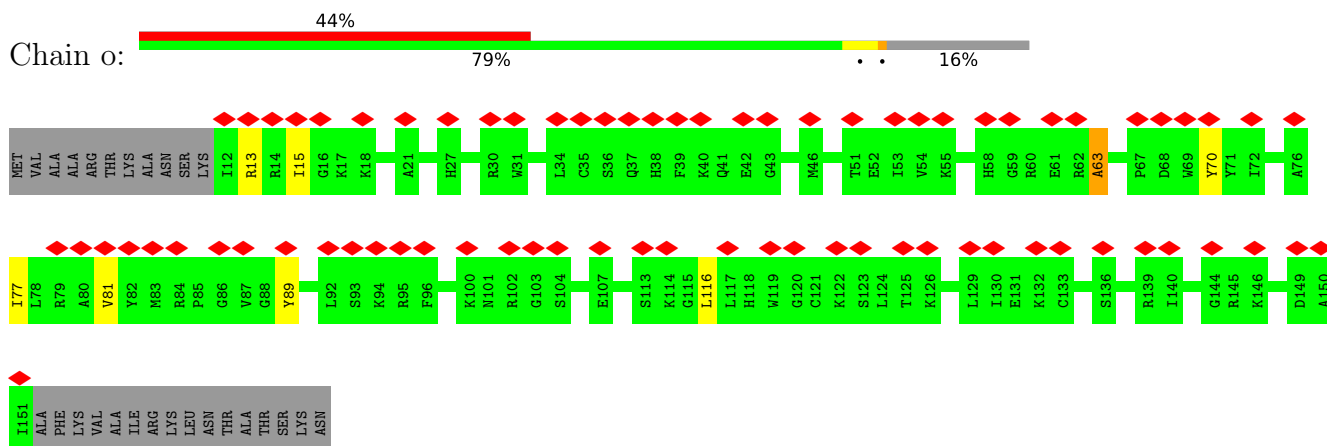
- Molecule 30: 40S ribosomal protein S3, putative



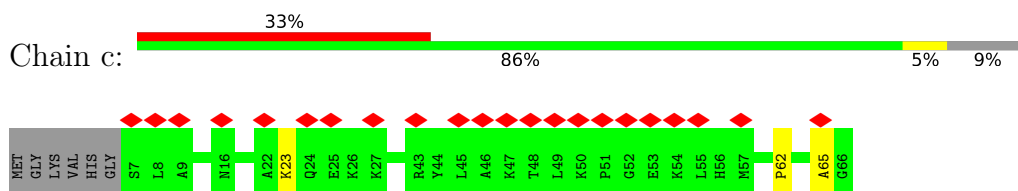
- Molecule 31: 40S ribosomal protein S10, putative



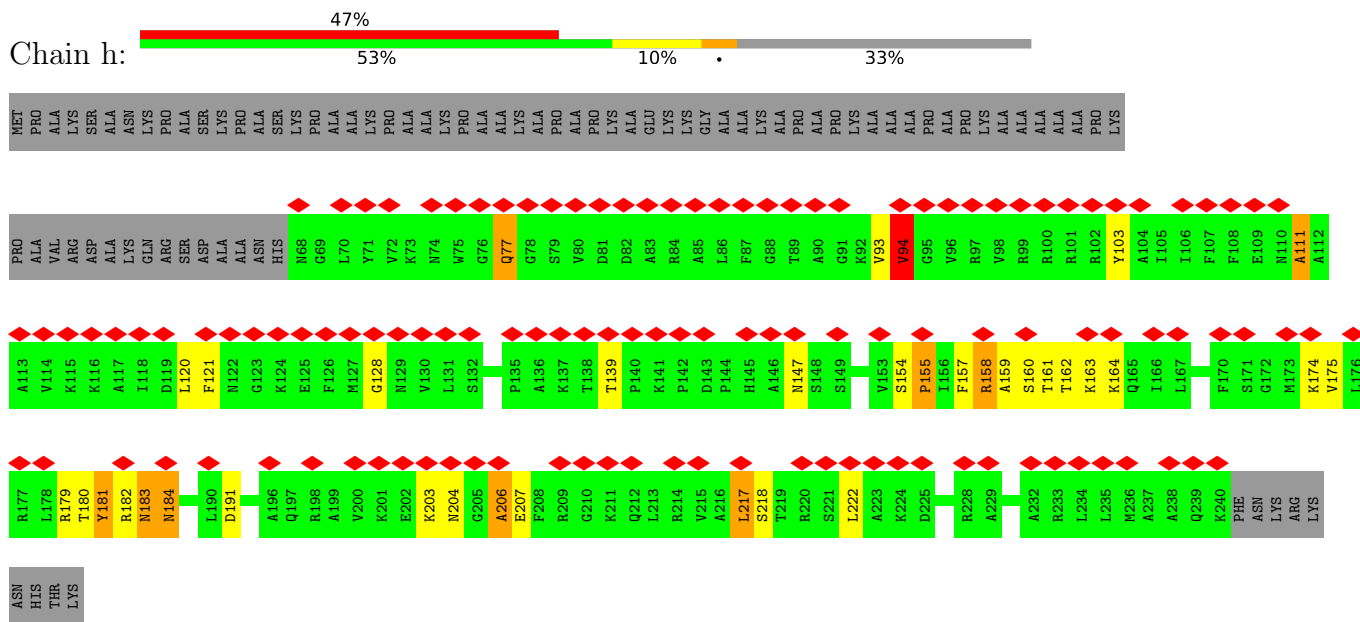
- Molecule 32: Ribosomal protein S19, putative



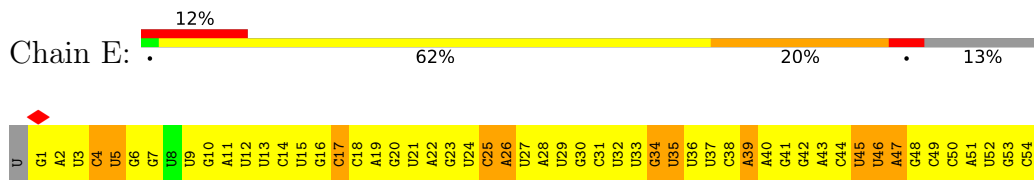
- Molecule 33: 40S ribosomal protein S30



- Molecule 34: RNA-binding protein, putative



- Molecule 35: 18S rRNA



C842	A843	G844	A784	A845	A785	A846	U847	A788	U848	C789	U849	U850	U851	A852	C853	U854	U855	U856	C857	A858	C859	U860	A861	A862	C863	A864	A865	A866	C867	U868	C869	U870	U871	U872	U873	A774	U875	U876	U877	U878	U879	U880	U881	A882	A883	U884	U885	U886	U887	U888	U889	U890	A901							
A782	A783	A784	A785	A786	C787	A788	C789	U790	C791	C792	A793	C794	U795	C796	U797	U798	U799	A799	C800	C801	U802	U803	C804	A805	C806	U807	G808	U809	C810	U811	A812	U813	C814	C815	C816	A817	U818	C819	U820	C821	A822	U823	C824	C825	A826	U827	C828	C829	C830	C831	C832	C833	A834	U835	A836	U837	C838	C839	C840	C841
C722	C723	A724	U725	C726	C727	U728	C729	U730	U731	C732	C733	C734	U735	U736	U737	U738	U739	C739	U740	C741	A742	C743	C744	C745	A746	U747	U748	U749	U750	U751	U752	U753	U754	U755	C756	U757	U758	C759	U760	C761	U762	C763	A764	A765	C766	A767	A768	A769	U770	C771	U772	U773	C774	A775	C776	A777	U778	U779	C780	A781
U601	G602	G603	G604	G605	G606	G607	C608	G609	G610	G611	U612	C613	U614	G615	G616	U617	G618	G619	C620	A621	G622	C623	A624	C625	C626	C627	G628	C629	G630	G631	U632	A633	U634	U635	U636	U637	U638	C639	U640	U641	U642	C643	C644	A645	A646	A647	A648	G649	C650	U651	U652	A653	U654	A655	U656	U657	A658	A659	U660	G661
C541	C542	U543	U544	U545	U546	C547	C548	C549	C550	C551	C552	U553	C554	C555	U556	U557	U558	U559	C560	A561	A562	U563	A564	C565	C566	C567	C568	C569	C570	C571	C572	C573	C574	C575	C576	C577	C578	C579	C580	C581	C582	C583	C584	C585	C586	C587	C588	C589	C590	C591	C592	C593	C594	C595	C596	C597	C598	C599	U600	
G481	C482	A483	A484	A485	U486	U487	G488	C489	C490	C491	A492	A493	U494	G495	U496	C497	A498	A499	A500	A501	A502	A503	A504	A505	A506	A507	G508	U509	C510	U511	G512	C513	C514	C515	A516	G517	C518	C519	A520	A521	A522	A523	G524	A525	A526	U527	U528	C529	A530	A531	C532	C533	C534	G535	A536	C537	A538	C539	U540	
U421	U422	C423	C424	A425	U426	U427	C428	C429	G430	C431	A432	G433	A434	G435	C436	C437	A438	G439	C440	C441	U442	G443	A444	G445	A446	A447	A448	U449	U450	A451	C452	U453	A454	C455	C456	A457	C458	U459	U460	C461	A462	A463	C464	G465	G466	A467	C468	G469	G470	C471	G472	C473	C474	A475	U476	G477	C478	G479	C480	
A360	U361	C362	C363	A364	A365	C366	C367	C368	C369	U370	C371	U372	G373	C374	C375	C376	C377	U378	C379	U380	C381	C382	U383	G384	G385	A386	C387	U388	C389	U390	C391	A392	U393	C394	C395	C396	C397	G400	A401	C402	G403	C404	G405	A406	C407	C408	G409	C410	C411	C412	C413	U414	U415	U416	U417	C418	G419	G420		
A300	U301	U302	C303	C304	U305	U306	C307	C308	C309	U310	C311	C312	G313	A314	A315	A316	G317	C318	C319	C320	C321	C322	U323	U324	U325	U326	U327	U328	U329	A330	C331	C332	C333	C334	C335	C336	C337	U338	C339	U340	U341	U342	U343	G344	A345	C346	C347	A348	A349	C350	A351	A352	C353	U354	G355	C356	C357	U358	U359	
G240	A241	A242	U243	C244	A245	A246	U247	A248	A249	A250	A251	C252	U253	U254	A255	A256	C257	C258	C259	A260	A261	U262	G263	C264	C265	U266	U267	C268	A269	C270	C271	G272	G273	C274	A275	G276	U277	A278	C279	A280	C281	C282	U283	C284	A285	G286	A287	A288	G289	U290	G291	U292	U293	C294	A295	U296	U297	C298	A299	
U180	A181	C182	C183	A184	A185	C186	C187	C188	C189	U190	U191	G192	U193	U194	C195	U196	C197	U198	C199	U200	U201	C202	C203	G204	G205	C206	C207	C208	C209	A210	G211	C212	A213	G214	C215	C216	C217	C218	U219	G220	C221	U222	C223	C224	C225	A226	U227	A228	G229	A230	C231	C232	C233	U234	C235	C236	A237	G238	C239	
C120	A121	A122	C123	A124	A125	U126	C127	U128	U129	U130	C131	G132	C133	U134	C135	U136	C137	C138	C139	C140	A141	A142	C143	A144	U145	U146	G147	C148	C149	U150	A151	A152	C153	U154	U155	U156	G157	C158	G159	A160	A161	A162	C163	G164	C165	C166	A167	A168	G169	C170	U171	A172	U173	U174	A175	C176	C177	U178	G179	
U60	C61	A62	G63	A64	A65	U66	C67	A68	C69	U70	G71	C72	A73	U74	C75	G76	C77	A78	C79	G80	A81	A82	U83	C84	U85	G86	C87	G88	C89	A90	U91	G92	G93	C94	U95	C96	A97	U98	U99	A100	C101	A102	U103	C104	A105	G106	A107	C108	G109	U110	A111	A112	U113	C114	U115	G116	C117	C118	G119	



A2284	G2284	A2104	G2043	U1983	U1923	C1863	A1803	C1742
G2285	A2165	C2105	G2044	A1984	G1924	C1864	A1804	A1743
U2286	C2166	A2106	A2045	C1985	G1925	A1865	G1805	U1744
U2287	A2167	A2107	A2046	C1986	G1926	A1866	C1806	G1745
A2288	C2168	G2108	A2047	U1988	A1927	G1867	G1807	G1746
C2289	A2169	A2109	A2048	G1989	U1928	G1868	G1808	C1747
A2290	C2170	A2110	C2049	U1990	U1929	G1869	C1809	G1748
U2291	G2171	A2111	C2050	C1991	U1930	G1870	C1810	C1749
G2292	C2172	G2112	C2051	A1992	U1931	G1871	A1812	U1751
A2293	C2173	G2113	C2052	U1993	G1932	G1872	G1813	U1754
G2294	C2174	U2114	G2053	U1994	G1933	G1873	U1814	G1755
G2295	C2175	C2115	G2054	G1995	G1934	C1874	A1815	G1756
U2296	G2176	U2116	A2055	A1996	C1935	G1875	G1816	U1757
C2297	U2177	C2117	A2056	G1997	A1936	G1876	G1817	C1758
G2298	C2178	U2118	U2057	A1998	A1937	U1877	A1818	G1759
A2299	G2179	A2119	C2058	A1999	C1938	U1878	U1819	G1760
C2300	U2180	G2120	A2059	C2000	A1939	U1879	U1820	U1761
A2301	U2181	G2121	C2060	A2001	C1940	U1880	C1821	G1762
G2302	U2182	C2122	G2061	G2002	C1941	C1881	A1822	G1763
U2303	U2183	G2123	U2062	G2003	A1942	G1882	G1823	A1764
G2304	C2184	U2124	A2063	A2004	G1943	G1883	A1824	G1765
C2305	U2185	C2125	G2064	A2005	G1944	C1884	U1826	U1766
A2306	C2186	A2126	A2065	A2006	U1945	U1885	U1827	G1767
G2307	C2187	G2127	C2066	A2007	U1946	U1886	G1828	A1768
C2308	U2188	C2128	C2067	A2008	G1947	U1887	C1829	U1769
U2309	G2189	U2129	C2068	C2009	G1948	G1888	C1830	U1770
G2310	U2190	C2130	A2069	G2010	U1949	U1889	G1831	U1771
C2311	U2191	U2131	C2070	A2011	G1950	C1890	A1832	G1772
A2312	A2192	C2132	C2071	C2012	U1951	U1891	U1833	U1773
U2313	U2193	C2133	U2072	U2013	U1952	U1892	A	U1774
G2314	G2194	A2134	G2073	C2014	G1953	C1893	G	U1775
A2315	U2195	A2135	C2074	C2015	C1954	C1894	G	G1776
C2316	U2196	G2136	G2075	U2016	U1955	U1895	U	U1777
U2317	C2197	C2137	C2076	G2017	C1956	U1896	A	U1778
U2318	G2198	U2138	C2077	U2018	U1957	C1897	U	U1779
	U2199	G2139	C2078	G2019	C1958	U1898	A	G1780
	A2200	U2140	G2079	G2020	U1959	C1899	C	A1781
	U2201	G2141	C2080	G2021	A1960	U1900	C	U1782
	A2202	C2142	G2081	A2022	U1961	G1898	A	U1783
	C2203	C2143	U2082	C2023	U1962	G1900	A	C1784
	A2204	G2144	A2083	C2024	G1963	G1901	U	G1785
	G2205	A2145	U2084	U2025	U1964	G1902	C1845	C1786
	C2206	U2146	U2085	A2026	U1965	C1903	C1846	U1787
	U2207	U2147	G2086	U2027	C1966	U1904	C1847	A1789
	G2208	A2148	C2087	U2028	U1967	U1905	U1848	C1790
	A2209	G2149	A2088	G2029	G1968	C1906	U1849	G1791
	U2210	U2151	U2089	U2030	G1969	C1907	C1850	G1792
	C2211	C2152	A2090	A2031	C1970	U1908	C1851	G1793
	G2212	C2153	U2091	U2032	C1971	U1909	G1852	A1794
	A2213	U2154	A2092	C2033	G1972	G1910	C1853	C1795
	C2214	G2155	G2093	A2034	A1973	U1911	G1854	G1796
	U2215	C2156	G2094	A2035	A1974	U1912	G1855	A1797
	A2216	G2157	C2095	A2036	C1975	U1913	U1800	G1798
	C2217	U2158	U2096	A2037	G1976	U1914	G1856	A1799
	U2218	C2159	C2097	G2038	C1977	G1915	U1857	C1801
	G2219	A2160	C2098	A2039	G1978	C1916	U1858	U1802
	C2220	U2161	G2099	G2040	C1979	G1917	U1859	
	A2221	U2162	G2100	U2041	G1980	C1918	U1860	
	G2222	G2163	C2101	G2042	A1981	A1919	A1861	
	U2223		C2102		C1982	G1921	C1862	
			A2103			G1922		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	86000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.257	Depositor
Minimum map value	-0.132	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.0549	Depositor
Map size (Å)	499.19998, 499.19998, 499.19998	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.56, 1.56, 1.56	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	p	0.94	0/2461	1.01	3/3347 (0.1%)
2	q	1.09	0/314	1.04	1/416 (0.2%)
3	r	1.02	0/1131	1.11	5/1520 (0.3%)
4	t	1.02	0/988	1.05	3/1325 (0.2%)
5	u	1.05	0/996	1.10	5/1334 (0.4%)
6	L	0.99	0/2073	0.98	0/2787
7	M	0.97	0/1137	0.94	0/1520
8	O	0.99	0/1515	0.96	0/2034
9	Q	1.06	0/1703	1.01	0/2290
10	R	1.00	0/1164	0.96	0/1559
11	S	0.99	0/641	1.01	1/858 (0.1%)
12	T	1.13	0/845	1.00	0/1129
13	U	1.13	0/527	1.04	0/702
14	V	1.04	0/1026	1.02	1/1376 (0.1%)
15	W	1.03	0/1809	1.01	1/2437 (0.0%)
16	X	1.02	0/1238	0.96	0/1662
17	Y	1.01	0/1004	0.98	0/1335
18	Z	1.06	0/1424	1.01	0/1904
19	b	1.03	0/1394	0.95	0/1874
20	f	0.97	0/1693	1.01	5/2290 (0.2%)
21	d	0.94	0/1760	1.03	2/2376 (0.1%)
22	e	1.00	0/1037	1.03	0/1391
23	g	0.92	0/644	0.89	0/875
24	a	0.92	0/559	1.03	1/748 (0.1%)
25	i	0.98	0/966	0.97	2/1295 (0.2%)
26	j	0.98	0/530	1.10	3/707 (0.4%)
27	P	1.09	0/2008	0.98	0/2678
28	k	1.00	0/985	0.98	0/1313
29	l	0.99	0/794	1.06	0/1076
30	m	1.03	0/1606	1.02	4/2141 (0.2%)
31	n	0.98	0/804	0.99	0/1082
32	o	1.00	0/1140	1.09	2/1524 (0.1%)
33	c	0.98	0/488	0.97	0/644
34	h	1.06	0/1381	1.22	4/1857 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	E	1.63	86/48215 (0.2%)	2.51	5573/75140 (7.4%)
All	All	1.38	86/88000 (0.1%)	2.03	5616/128546 (4.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	p	0	3
3	r	0	7
4	t	0	2
5	u	0	4
8	O	0	3
9	Q	0	3
15	W	0	1
18	Z	0	1
22	e	0	1
24	a	0	2
26	j	0	1
27	P	0	2
28	k	0	1
30	m	0	2
32	o	0	2
33	c	0	2
34	h	0	22
35	E	4	121
All	All	4	180

The worst 5 of 86 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	E	724	A	N9-C4	-14.62	1.29	1.37
35	E	734	G	N9-C4	-13.56	1.27	1.38
35	E	711	A	N9-C4	-10.05	1.31	1.37
35	E	718	A	N9-C4	-9.61	1.32	1.37
35	E	738	G	N9-C4	-8.96	1.30	1.38

The worst 5 of 5616 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	E	774	C	P-O3'-C3'	37.91	165.19	119.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	E	1187	C	P-O3'-C3'	33.90	160.37	119.70
35	E	976	U	O5'-P-OP2	-24.56	81.23	110.70
35	E	976	U	O5'-P-OP1	-24.39	81.44	110.70
35	E	703	A	P-O3'-C3'	23.77	148.22	119.70

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
35	E	325	U	C3'
35	E	702	U	C1'
35	E	810	U	C3'
35	E	1903	A	C3'

5 of 180 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	p	110	LYS	Peptide
1	p	261	ARG	Sidechain
1	p	43	TRP	Peptide
3	r	32	GLN	Peptide
3	r	42	VAL	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	p	2405	0	2323	0	0
2	q	311	0	319	0	0
3	r	1113	0	1175	0	0
4	t	969	0	1003	0	0
5	u	981	0	1021	0	0
6	L	2038	0	2142	0	0
7	M	1116	0	1169	0	0
8	O	1493	0	1562	0	0
9	Q	1670	0	1778	1	0
10	R	1143	0	1226	1	0
11	S	630	0	630	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	T	829	0	866	0	0
13	U	526	0	550	0	0
14	V	1011	0	1019	0	0
15	W	1781	0	1853	0	0
16	X	1212	0	1250	0	0
17	Y	989	0	1065	0	0
18	Z	1404	0	1503	1	0
19	b	1365	0	1410	0	0
20	f	1658	0	1704	0	0
21	d	1726	0	1774	0	0
22	e	1019	0	1050	0	0
23	g	635	0	631	0	0
24	a	553	0	608	0	0
25	i	958	0	981	0	0
26	j	518	0	513	0	0
27	P	1983	0	2131	0	0
28	k	972	0	1031	0	0
29	l	784	0	848	0	0
30	m	1587	0	1662	0	0
31	n	780	0	771	0	0
32	o	1116	0	1166	0	0
33	c	480	0	532	0	0
34	h	1358	0	1419	0	0
35	E	43106	0	21756	87	0
All	All	82219	0	62441	87	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 87 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:E:725:U:H3	35:E:733:G:H1	1.12	0.96
35:E:1849:U:H3	35:E:1869:G:H1	1.26	0.83
35:E:207:G:H1	35:E:222:U:H3	1.30	0.78
35:E:2220:G:H1	35:E:2232:U:H3	1.32	0.77
35:E:711:A:N1	35:E:746:A:N1	2.33	0.77

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	p	308/318 (97%)	288 (94%)	18 (6%)	2 (1%)	22	58
2	q	36/57 (63%)	28 (78%)	6 (17%)	2 (6%)	1	18
3	r	138/149 (93%)	113 (82%)	18 (13%)	7 (5%)	1	19
4	t	117/152 (77%)	105 (90%)	8 (7%)	4 (3%)	3	25
5	u	118/153 (77%)	102 (86%)	13 (11%)	3 (2%)	4	30
6	L	256/273 (94%)	239 (93%)	16 (6%)	1 (0%)	30	66
7	M	140/143 (98%)	131 (94%)	8 (6%)	1 (1%)	19	55
8	O	188/190 (99%)	165 (88%)	16 (8%)	7 (4%)	2	23
9	Q	198/211 (94%)	178 (90%)	16 (8%)	4 (2%)	6	34
10	R	139/151 (92%)	127 (91%)	11 (8%)	1 (1%)	19	55
11	S	80/86 (93%)	73 (91%)	5 (6%)	2 (2%)	4	30
12	T	102/112 (91%)	90 (88%)	12 (12%)	0	100	100
13	U	66/112 (59%)	62 (94%)	3 (4%)	1 (2%)	8	40
14	V	133/144 (92%)	116 (87%)	16 (12%)	1 (1%)	16	53
15	W	215/261 (82%)	200 (93%)	13 (6%)	2 (1%)	14	49
16	X	146/173 (84%)	133 (91%)	11 (8%)	2 (1%)	9	40
17	Y	121/137 (88%)	113 (93%)	8 (7%)	0	100	100
18	Z	171/221 (77%)	157 (92%)	12 (7%)	2 (1%)	11	43
19	b	162/190 (85%)	143 (88%)	17 (10%)	2 (1%)	11	43
20	f	205/245 (84%)	190 (93%)	12 (6%)	3 (2%)	8	40
21	d	221/263 (84%)	205 (93%)	14 (6%)	2 (1%)	14	49
22	e	127/130 (98%)	118 (93%)	8 (6%)	1 (1%)	16	53
23	g	81/236 (34%)	78 (96%)	3 (4%)	0	100	100
24	a	68/110 (62%)	58 (85%)	6 (9%)	4 (6%)	1	17
25	i	119/141 (84%)	111 (93%)	7 (6%)	1 (1%)	16	53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	j	62/150 (41%)	47 (76%)	11 (18%)	4 (6%)	1	16
27	P	247/250 (99%)	226 (92%)	21 (8%)	0	100	100
28	k	116/196 (59%)	102 (88%)	13 (11%)	1 (1%)	14	49
29	l	97/117 (83%)	82 (84%)	15 (16%)	0	100	100
30	m	198/214 (92%)	179 (90%)	14 (7%)	5 (2%)	4	30
31	n	91/161 (56%)	83 (91%)	5 (6%)	3 (3%)	3	25
32	o	138/167 (83%)	112 (81%)	21 (15%)	5 (4%)	3	24
33	c	58/66 (88%)	53 (91%)	4 (7%)	1 (2%)	7	37
34	h	171/257 (66%)	123 (72%)	31 (18%)	17 (10%)	0	8
All	All	4833/5936 (81%)	4330 (90%)	412 (8%)	91 (2%)	9	35

5 of 91 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	r	121	TYR
3	r	124	ILE
5	u	120	VAL
9	Q	138	CYS
21	d	81	SER

5.3.2 Protein sidechains [i](#)

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	p	262/268 (98%)	260 (99%)	2 (1%)	79	84
2	q	34/49 (69%)	34 (100%)	0	100	100
3	r	113/121 (93%)	113 (100%)	0	100	100
4	t	102/131 (78%)	102 (100%)	0	100	100
5	u	104/132 (79%)	104 (100%)	0	100	100
6	L	217/230 (94%)	217 (100%)	0	100	100
7	M	116/117 (99%)	116 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	O	160/160 (100%)	160 (100%)	0	100	100
9	Q	188/195 (96%)	188 (100%)	0	100	100
10	R	125/132 (95%)	124 (99%)	1 (1%)	79	84
11	S	70/73 (96%)	70 (100%)	0	100	100
12	T	87/93 (94%)	87 (100%)	0	100	100
13	U	57/97 (59%)	57 (100%)	0	100	100
14	V	103/112 (92%)	102 (99%)	1 (1%)	73	81
15	W	194/223 (87%)	192 (99%)	2 (1%)	73	81
16	X	137/157 (87%)	137 (100%)	0	100	100
17	Y	104/116 (90%)	104 (100%)	0	100	100
18	Z	143/184 (78%)	143 (100%)	0	100	100
19	b	148/165 (90%)	148 (100%)	0	100	100
20	f	182/211 (86%)	181 (100%)	1 (0%)	86	89
21	d	187/208 (90%)	187 (100%)	0	100	100
22	e	110/111 (99%)	109 (99%)	1 (1%)	75	83
23	g	68/186 (37%)	68 (100%)	0	100	100
24	a	64/96 (67%)	63 (98%)	1 (2%)	58	74
25	i	103/120 (86%)	99 (96%)	4 (4%)	27	50
26	j	55/123 (45%)	54 (98%)	1 (2%)	54	71
27	P	204/205 (100%)	204 (100%)	0	100	100
28	k	108/172 (63%)	108 (100%)	0	100	100
29	l	89/104 (86%)	89 (100%)	0	100	100
30	m	167/179 (93%)	166 (99%)	1 (1%)	84	88
31	n	84/125 (67%)	83 (99%)	1 (1%)	67	78
32	o	118/139 (85%)	117 (99%)	1 (1%)	79	84
33	c	49/53 (92%)	49 (100%)	0	100	100
34	h	138/191 (72%)	133 (96%)	5 (4%)	30	52
All	All	4190/4978 (84%)	4168 (100%)	22 (0%)	85	89

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	m	137	VAL

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Mol	Chain	Res	Type
34	h	94	VAL
32	o	116	LEU
34	h	103	TYR
20	f	72	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
15	W	193	ASN
16	X	11	HIS
30	m	163	HIS
18	Z	64	ASN
20	f	121	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
35	E	2017/2319 (86%)	437 (21%)	86 (4%)

5 of 437 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
35	E	4	C
35	E	5	U
35	E	17	C
35	E	25	C
35	E	26	A

5 of 86 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	E	1187	C
35	E	1903	A
35	E	1191	G
35	E	1712	U
35	E	2017	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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](#)

There are no chain breaks in this entry.

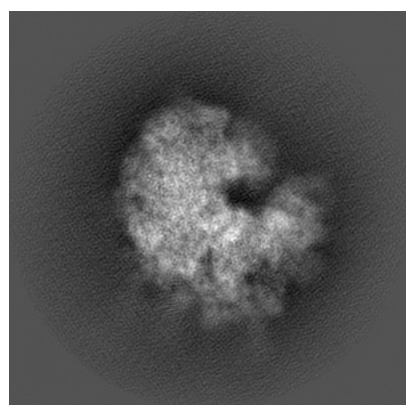
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3844. These allow visual inspection of the internal detail of the map and identification of artifacts.

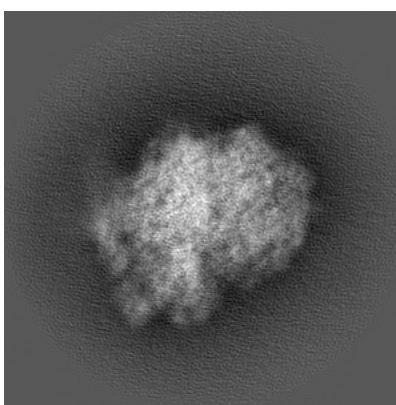
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

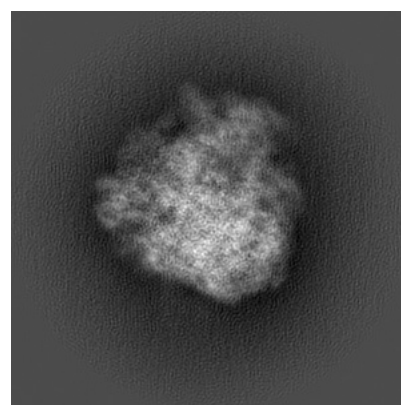
6.1.1 Primary map



X



Y

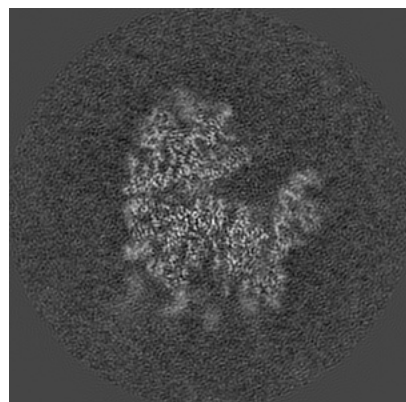


Z

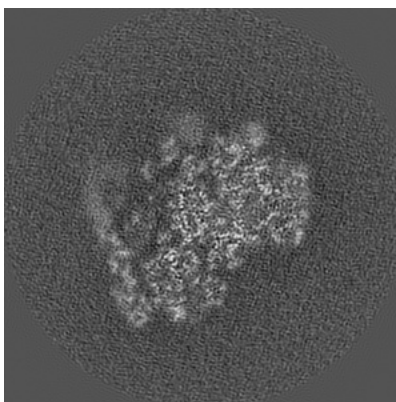
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

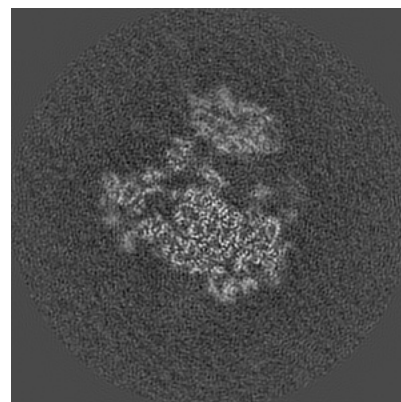
6.2.1 Primary map



X Index: 160



Y Index: 160

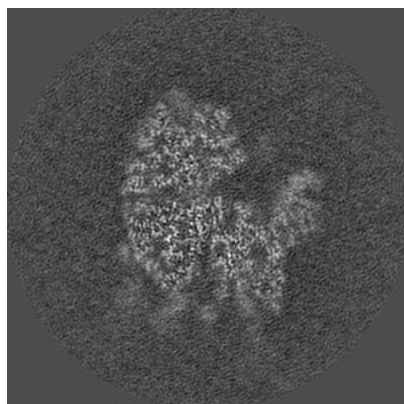


Z Index: 160

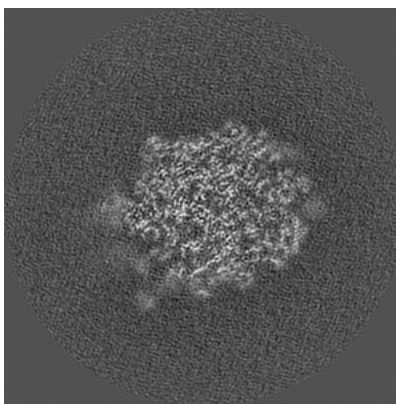
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

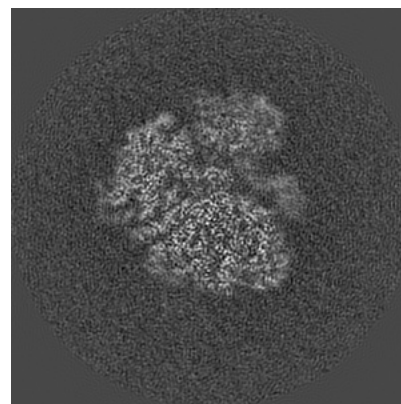
6.3.1 Primary map



X Index: 157



Y Index: 134

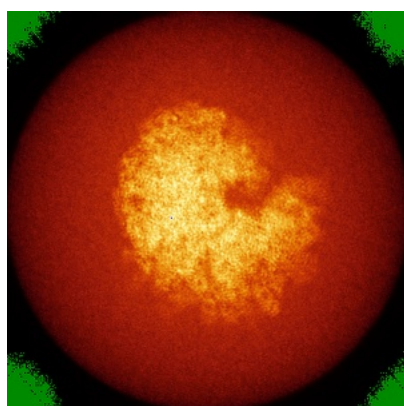


Z Index: 147

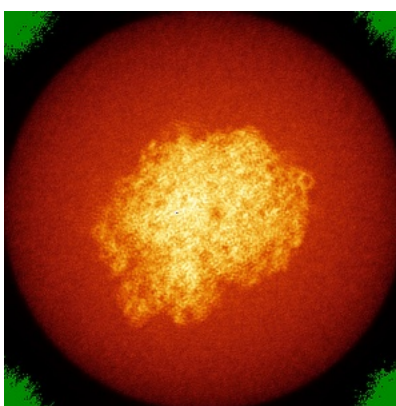
The images above show the largest variance slices of the map in three orthogonal directions.

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

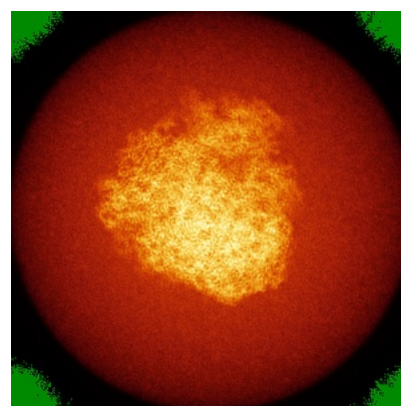
6.4.1 Primary map



X



Y

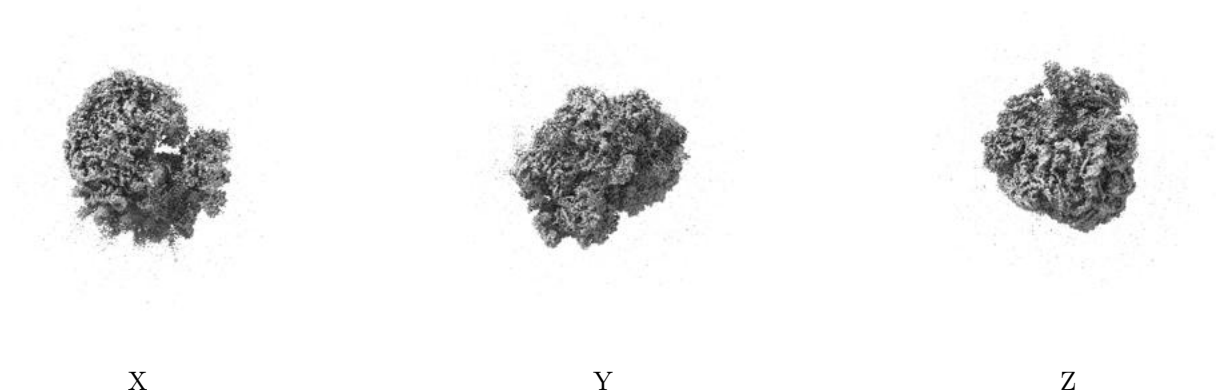


Z

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 0.0549. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

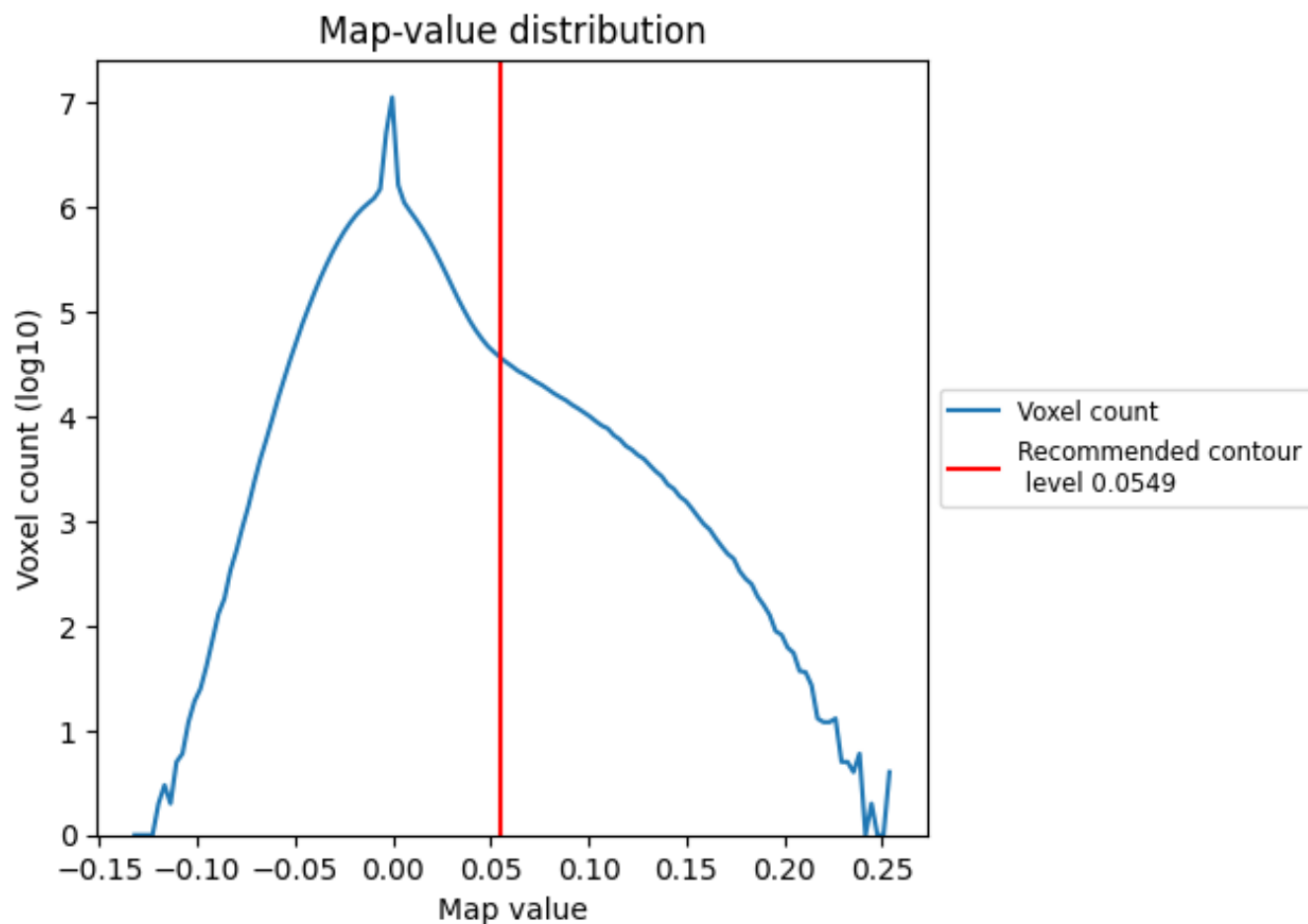
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

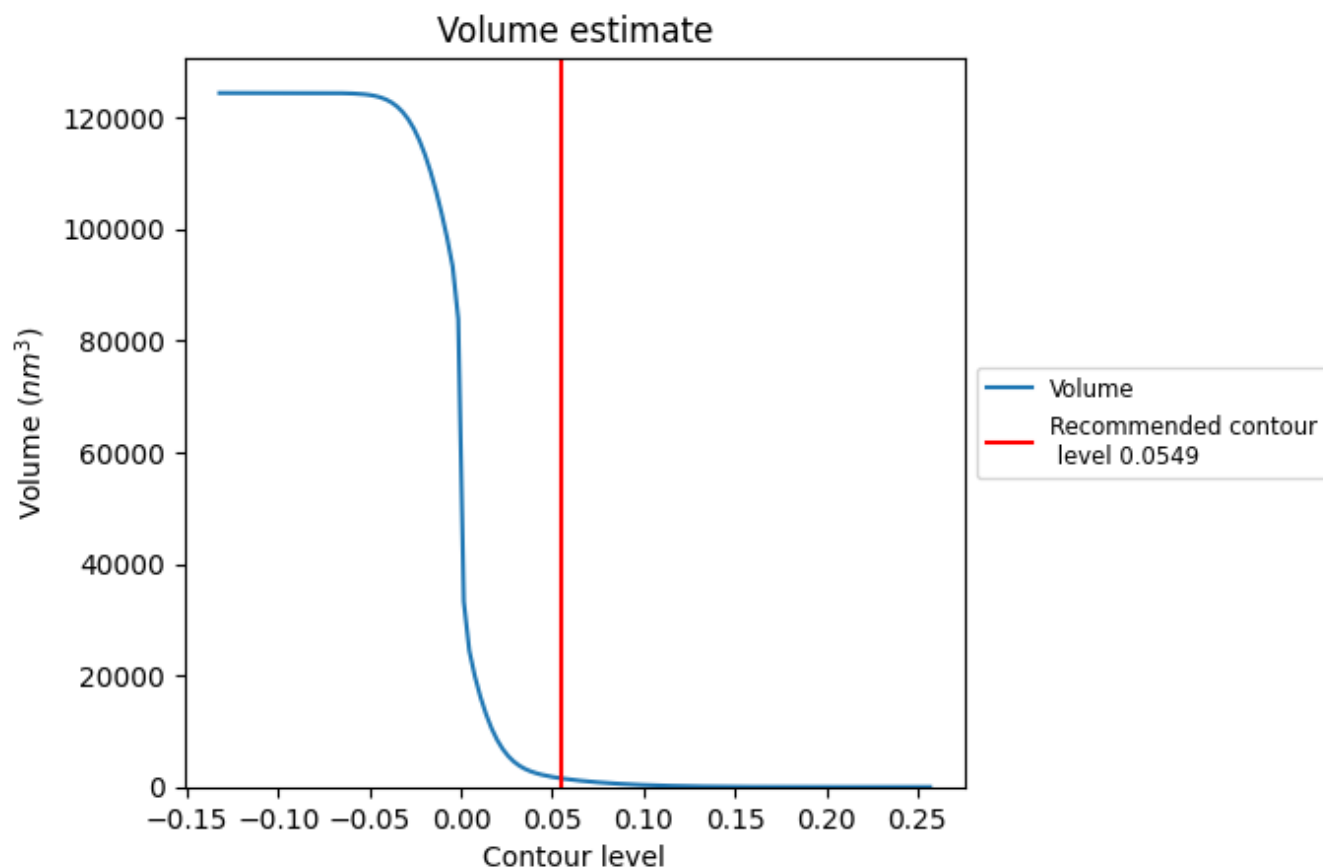
This section contains the results of statistical analysis of the map.

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.

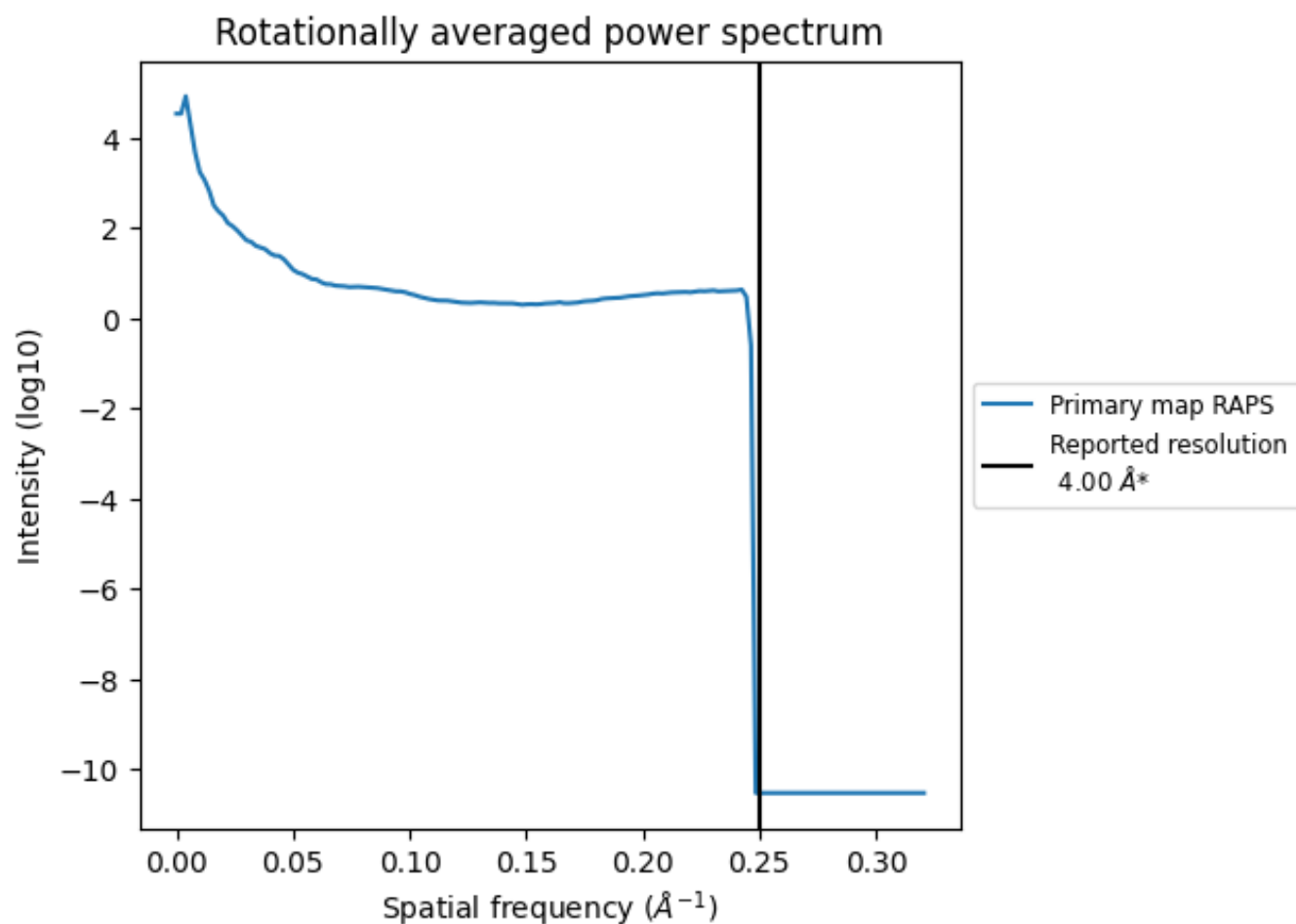
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1549 nm³; this corresponds to an approximate mass of 1400 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 0.250 Å⁻¹

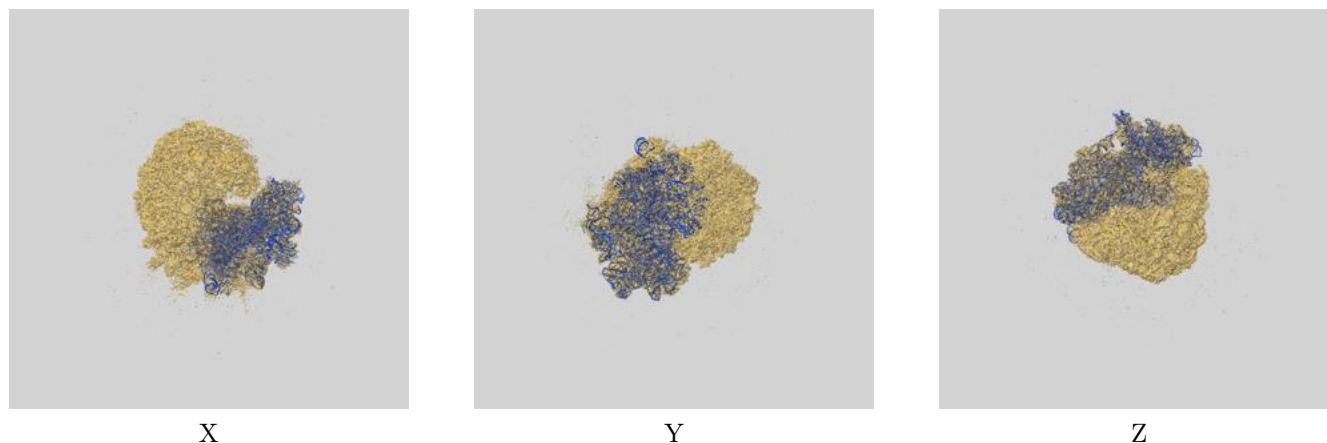
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

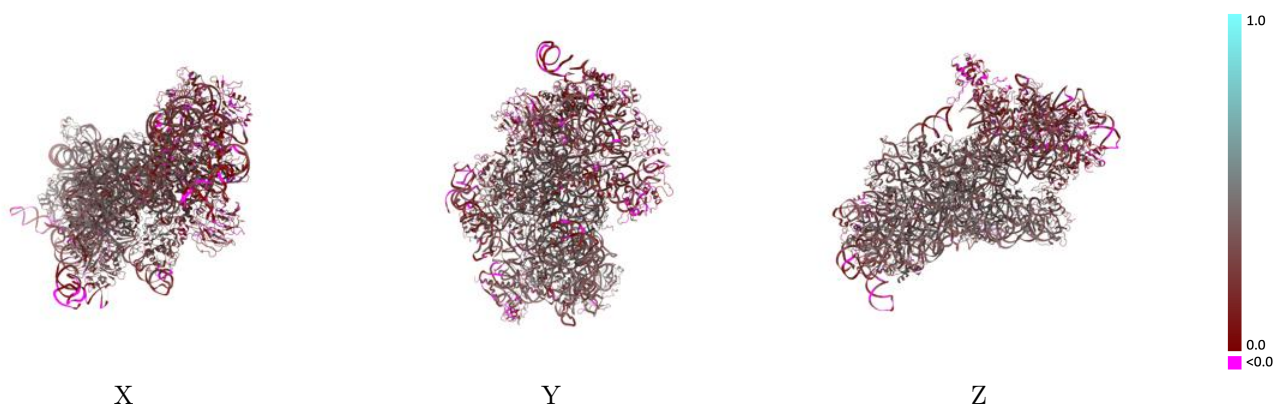
This section contains information regarding the fit between EMDB map EMD-3844 and PDB model 5OPT. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



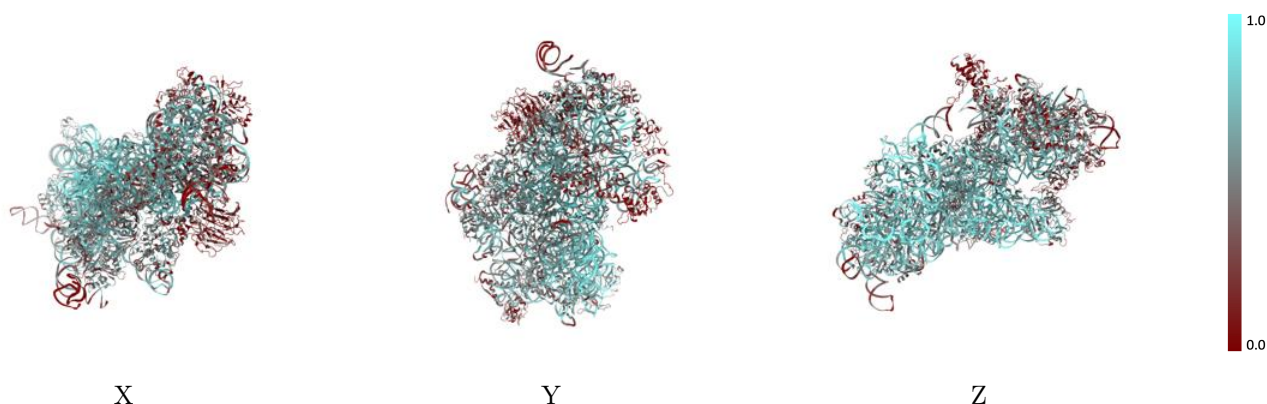
The images above show the 3D surface view of the map at the recommended contour level 0.0549 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



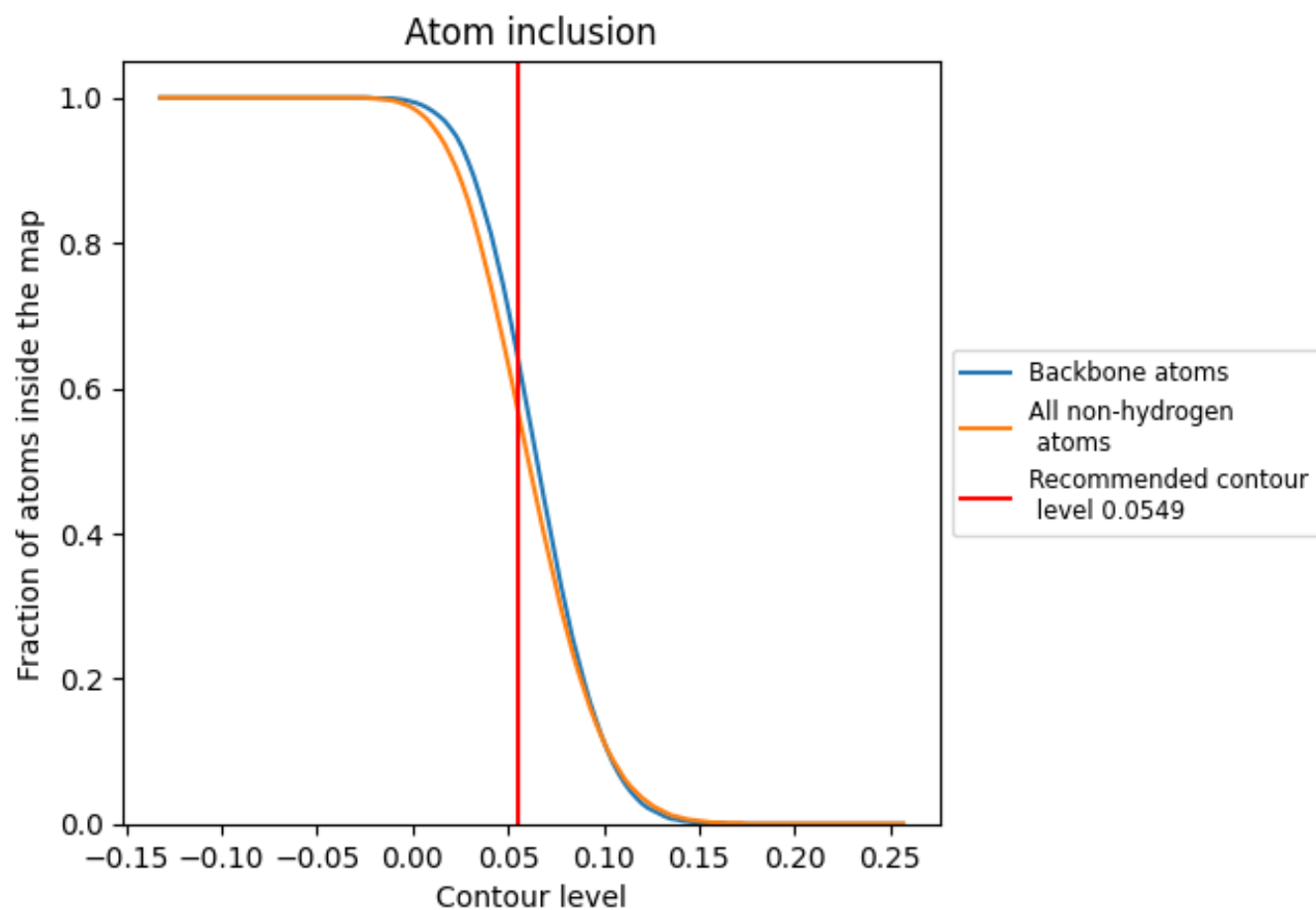
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0549).









































































9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 57% 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 (0.0549) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5720	 0.2840
E	 0.6990	 0.2970
L	 0.5230	 0.3590
M	 0.5610	 0.3500
O	 0.3580	 0.2240
P	 0.5280	 0.2910
Q	 0.5310	 0.3060
R	 0.5200	 0.3280
S	 0.4420	 0.3200
T	 0.5040	 0.3360
U	 0.2610	 0.2090
V	 0.4920	 0.3140
W	 0.5510	 0.3340
X	 0.5150	 0.3370
Y	 0.5850	 0.3250
Z	 0.5970	 0.3600
a	 0.2980	 0.1260
b	 0.5500	 0.3240
c	 0.4760	 0.2910
d	 0.5230	 0.3260
e	 0.5470	 0.3480
f	 0.5210	 0.3120
g	 0.5170	 0.3330
h	 0.2970	 0.1270
i	 0.1110	 0.0940
j	 0.1860	 0.1000
k	 0.3770	 0.2550
l	 0.2940	 0.2240
m	 0.2930	 0.2600
n	 0.2960	 0.2120
o	 0.3840	 0.1690
p	 0.1710	 0.1680
q	 0.3770	 0.2290
r	 0.3920	 0.2380
t	 0.2790	 0.1820
u	 0.3230	 0.1910

