



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:28 AM UTC

PDB ID : 8ETC / pdb_00008etc
EMDB ID : EMD-24398
Title : Fkbp39 associated nascent 60S ribosome State 4
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on : 2022-10-16
Resolution : 3.10 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

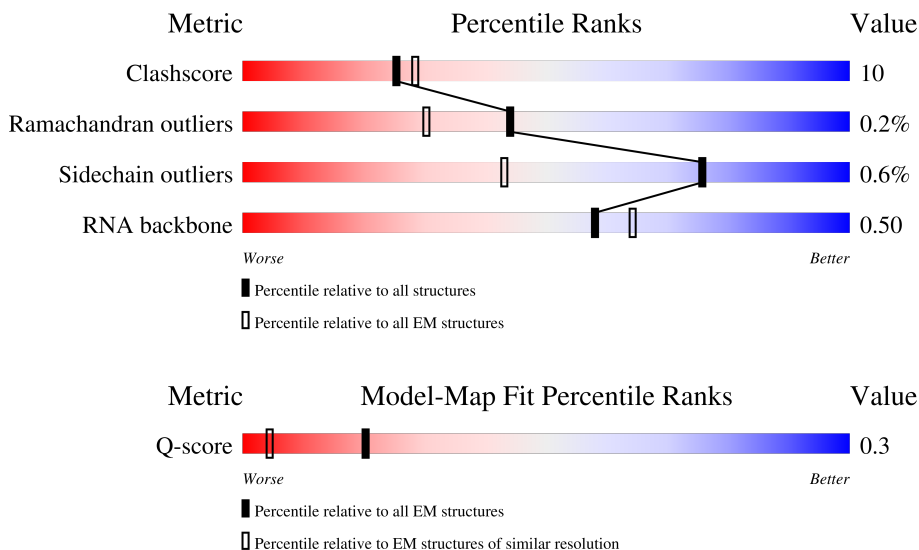
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	1	3497	
2	2	165	
3	3	302	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	8	51	84% 71% 25% .
5	B	388	20% 72% 22% 6%
6	C	363	5% 74% 24% ..
7	E	195	14% 59% 24% . 16%
8	F	250	5% 69% 18% 13%
9	G	259	12% 50% 20% . 30%
10	H	190	40% 72% 24% . .
11	L	208	28% 62% 24% 13%
12	M	134	6% 58% 34% . 7%
13	N	201	. 61% 22% 17%
14	O	197	8% 75% 25% .
15	P	187	28% 70% 20% 10%
16	Q	187	. 60% 12% 28%
17	R	193	42% 41% 23% 36%
18	S	176	23% 70% 25% 5%
19	U	117	68% 82% . 16%
20	V	139	82% 59% 38% ..
21	W	241	86% 87% . 11%
22	X	141	11% 60% 21% 19%
23	Y	126	. 73% 26% .
24	Z	136	88% 97% ..
25	a	148	11% 43% 21% 36%
26	b	642	59% 50% 14% 35%
27	c	117	78% 82% . 17%
28	d	113	39% 56% 35% 10%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	e	127	68% 25% 7%
30	f	108	84% 14%
31	g	112	91% 55% 37% 6%
32	h	122	65% 34%
33	i	99	39% 60% 5%
34	j	91	8% 59% 23% 18%
35	k	74	69% 55% 36% 5%
36	r	260	54% 53% 11% 36%
37	s	470	6% 94%
38	u	192	40% 38% 22% 41%
39	w	802	50% 39% 13% 48%
40	y	244	72% 58% 33% 8%
41	z	117	30% 19% 11% 70%
42	T	160	9% 11% 87%

2 Entry composition [i](#)

There are 43 unique types of molecules in this entry. The entry contains 95651 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called RNA (2151-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	2140	45843	20476	8349	14878	2140	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1746	C	U	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (147-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	147	3131	1401	560	1023	147	0	0

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	114	969	614	181	168	6	0	0

- Molecule 4 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	8	49	428	267	97	63	1	0	0

- Molecule 5 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	B	365	2903	1837	542	514	10	0	0

- Molecule 6 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	359	Total	C	N	O	S	0	0
			2795	1765	536	491	3		

- Molecule 7 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	163	Total	C	N	O	S	0	0
			1260	807	232	218	3		

- Molecule 8 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	218	Total	C	N	O	S	0	0
			1770	1141	324	302	3		

- Molecule 9 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	182	Total	C	N	O	S	2	0
			1453	931	263	257	2		

- Molecule 10 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	183	Total	C	N	O	S	0	0
			1451	914	266	265	6		

- Molecule 11 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	180	Total	C	N	O	S	0	0
			1427	891	284	251	1		

- Molecule 12 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	125	Total	C	N	O	S	0	0
			1007	644	191	168	4		

- Molecule 13 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	166	Total	C	N	O	S	0	0
			1406	883	291	229	3		

- Molecule 14 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	196	Total	C	N	O	S	0	0
			1557	999	297	257	4		

- Molecule 15 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	169	Total	C	N	O	S	0	0
			1339	848	252	236	3		

- Molecule 16 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	135	Total	C	N	O	S	0	0
			1047	658	202	186	1		

- Molecule 17 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	124	Total	C	N	O	S	0	0
			1038	651	217	165	5		

- Molecule 18 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	168	Total	C	N	O	S	0	0
			1408	909	263	231	5		

- Molecule 19 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	U	98	Total	C	N	O	0	0
			484	288	98	98		

- Molecule 20 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	V	138	1032	647	194	183	8	0	0

- Molecule 21 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	W	215	1057	627	215	215		0	0

- Molecule 22 is a protein called 60S ribosomal protein L25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	X	114	914	584	167	162	1	0	0

- Molecule 23 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	Y	125	998	622	201	173	2	0	0

- Molecule 24 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	Z	134	662	393	134	135		0	0

- Molecule 25 is a protein called 60S ribosomal protein L28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	a	94	747	474	142	131		0	0

- Molecule 26 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	b	415	2837	1765	535	534	3	0	0

- Molecule 27 is a protein called 60S ribosomal protein L30-2.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	c	97	Total	C	N	O	0	0
			477	282	97	98		

- Molecule 28 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	102	Total	C	N	O	S	0	0
			849	534	165	147	3		

- Molecule 29 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	e	118	Total	C	N	O	S	0	0
			944	591	191	157	5		

- Molecule 30 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	106	Total	C	N	O	S	0	0
			839	534	162	140	3		

- Molecule 31 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	g	105	Total	C	N	O	S	0	0
			853	534	176	141	2		

- Molecule 32 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	h	121	Total	C	N	O	0	0
			999	629	194	176		

- Molecule 33 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	i	94	Total	C	N	O	S	0	0
			754	469	158	126	1		

- Molecule 34 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	j	75	Total	C	N	O	S	0	0
			600	367	131	95	7		

- Molecule 35 is a protein called 60S ribosomal protein L38-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	k	70	Total	C	N	O	S	0	0
			564	357	104	102	1		

- Molecule 36 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	r	166	Total	C	N	O	S	0	0
			1086	656	224	205	1		

- Molecule 37 is a protein called GTPase grn1.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	s	30	Total	C	N	O	0	0
			253	154	58	41		

- Molecule 38 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	u	114	Total	C	N	O	S	0	0
			944	598	190	147	9		

- Molecule 39 is a protein called AdoMet-dependent rRNA methyltransferase spb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	w	420	Total	C	N	O	S	0	0
			3377	2152	589	621	15		

- Molecule 40 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	y	225	Total	C	N	O	S	0	0
			1697	1058	293	341	5		

- Molecule 41 is a protein called UPF0642 protein C32H8.05.

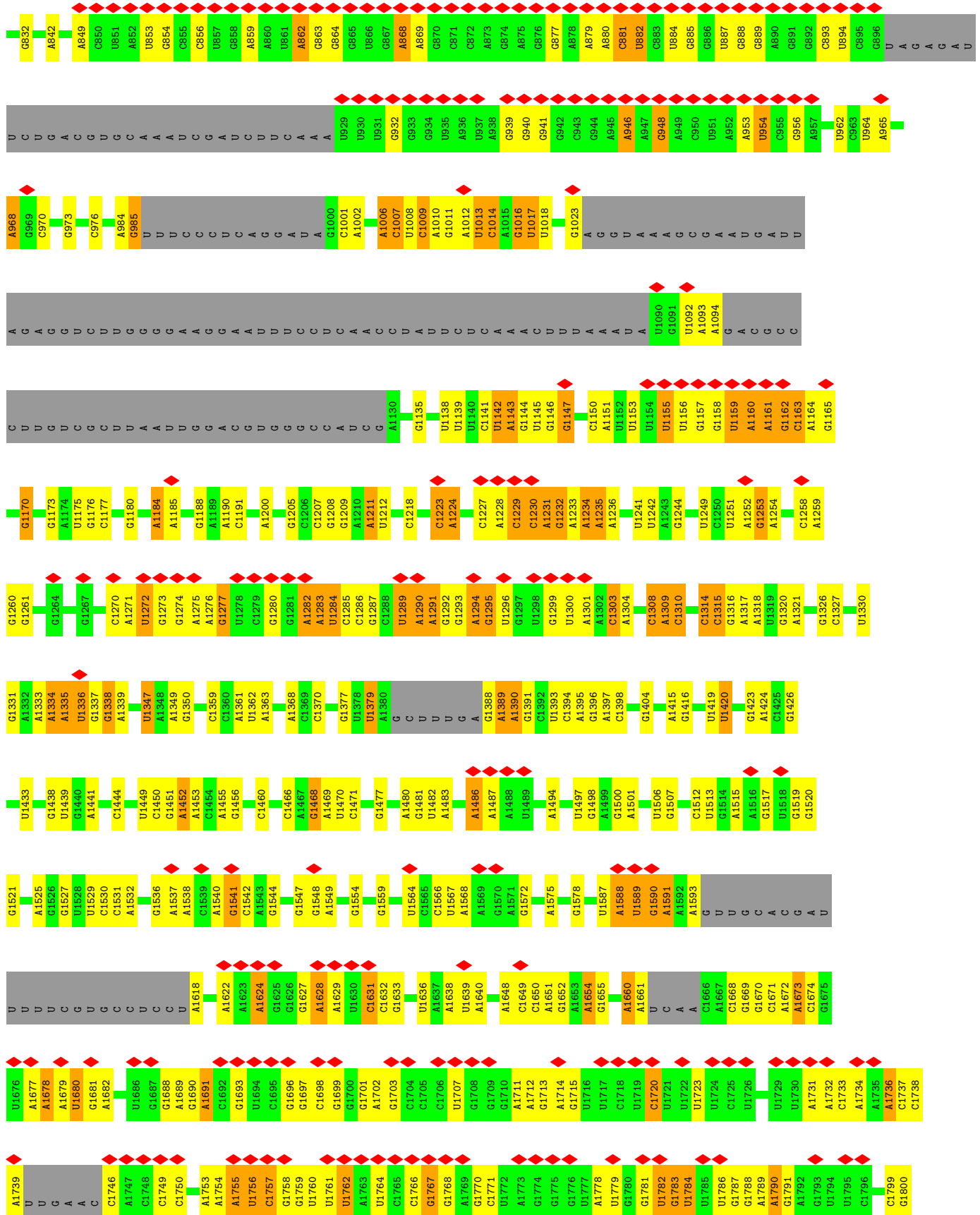
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
41	z	35	292	183	63	46	0	0

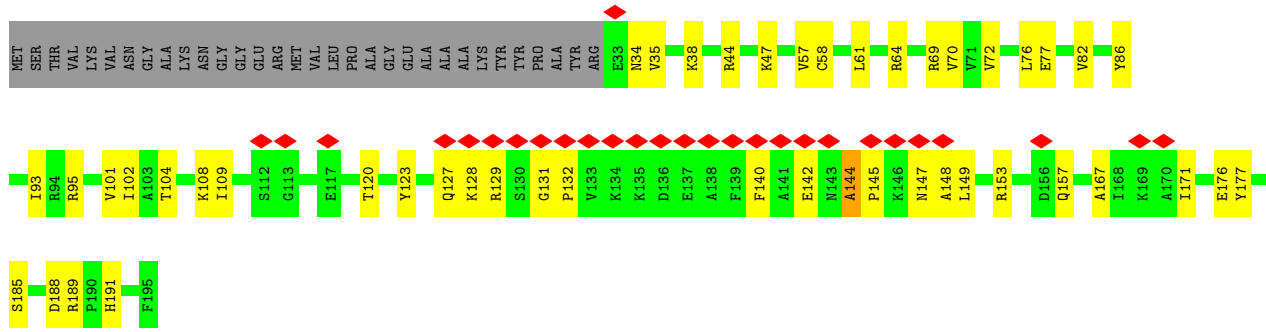
- Molecule 42 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
42	T	21	159	101	28	30	0	0

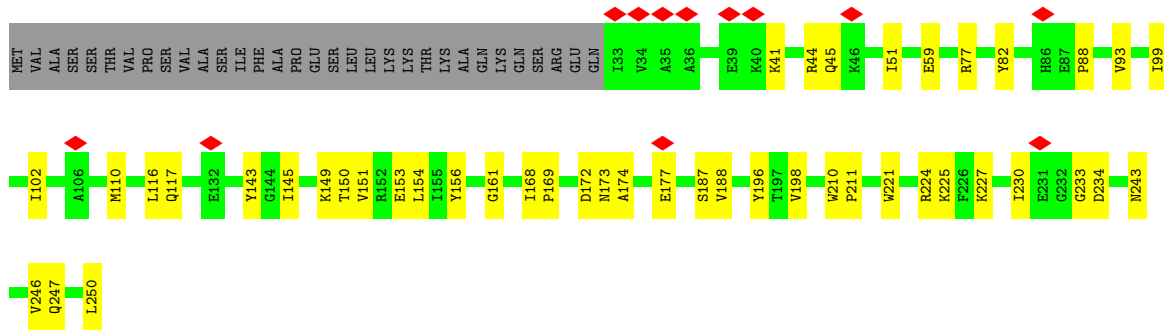
- Molecule 43 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
43	j	1	1	1	0

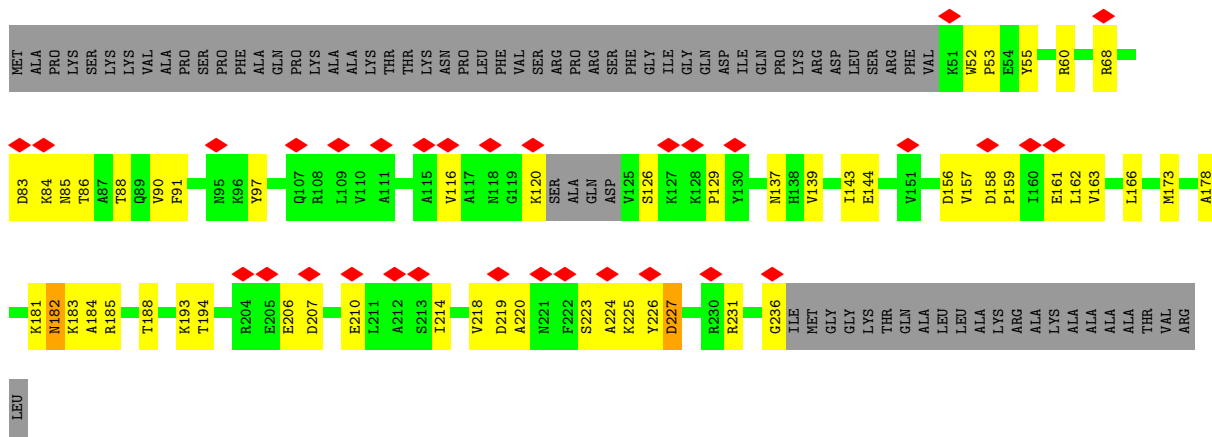




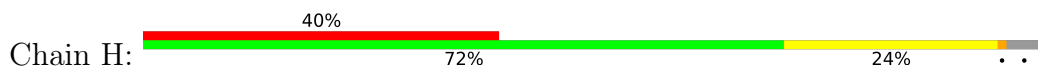
• Molecule 8: 60S ribosomal protein L7-B

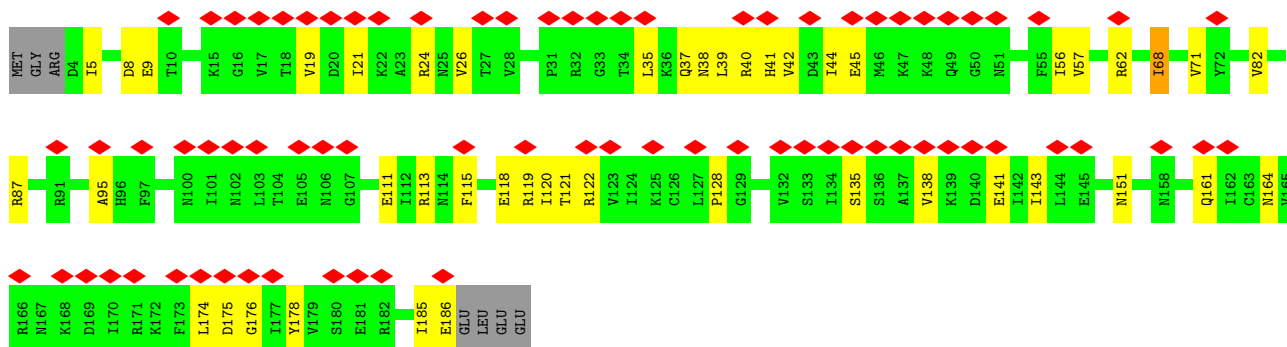


• Molecule 9: 60S ribosomal protein L8

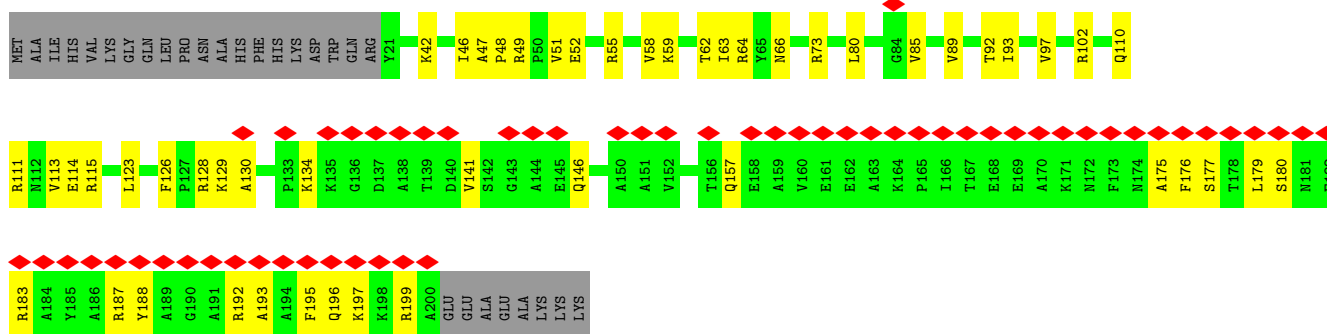


• Molecule 10: 60S ribosomal protein L9-A

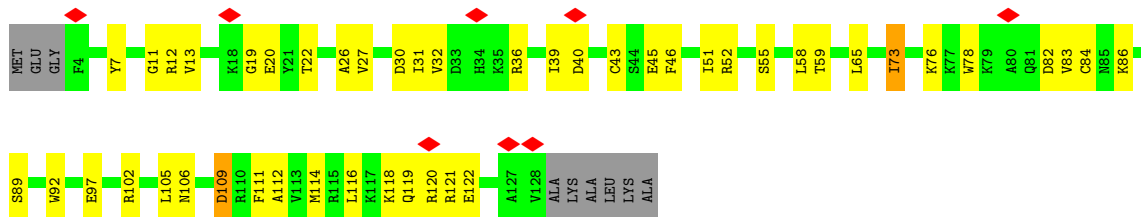




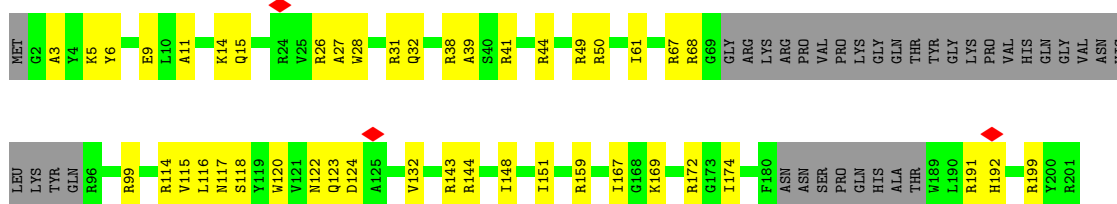
• Molecule 11: 60S ribosomal protein L13



• Molecule 12: 60S ribosomal protein L14



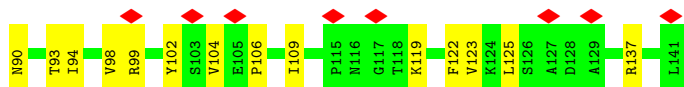
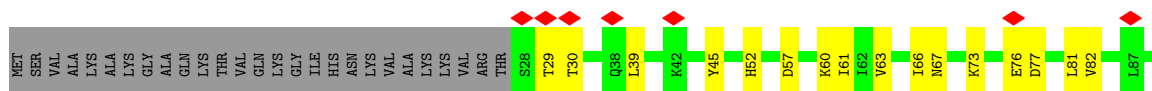
• Molecule 13: 60S ribosomal protein L15-A



• Molecule 14: 60S ribosomal protein L16-B



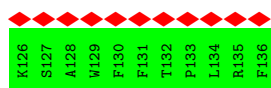
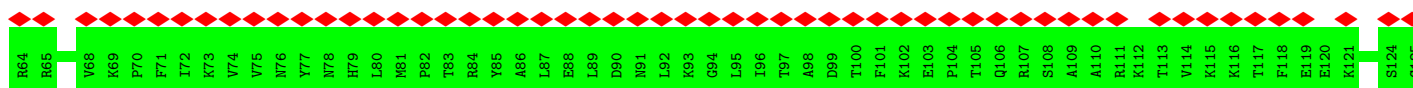
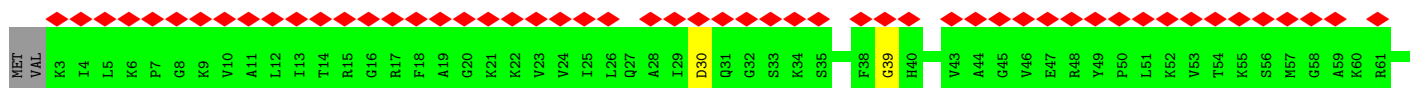
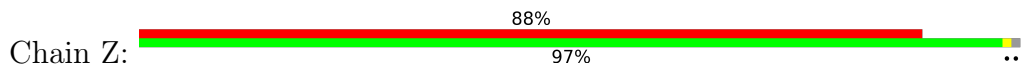
• Molecule 22: 60S ribosomal protein L25-A



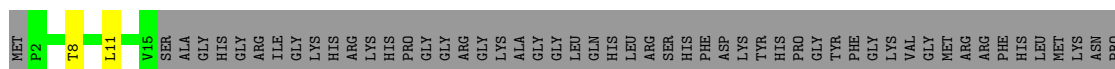
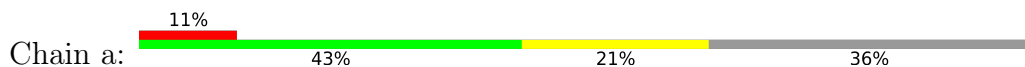
• Molecule 23: 60S ribosomal protein L26



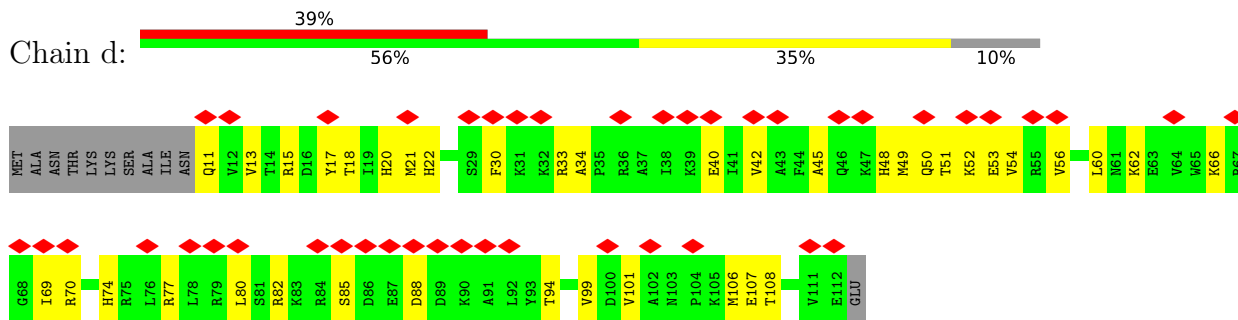
• Molecule 24: 60S ribosomal protein L27-A



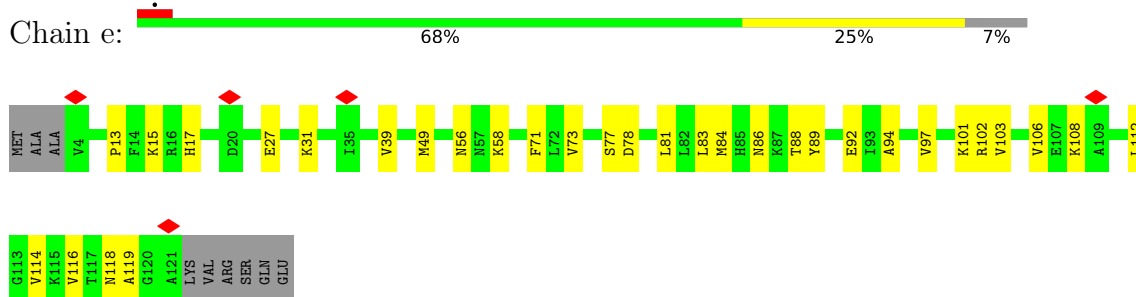
• Molecule 25: 60S ribosomal protein L28-A



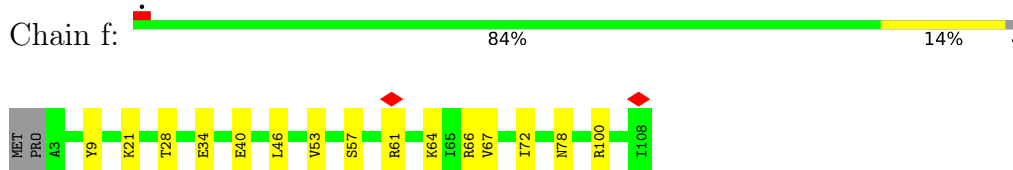
• Molecule 28: 60S ribosomal protein L31



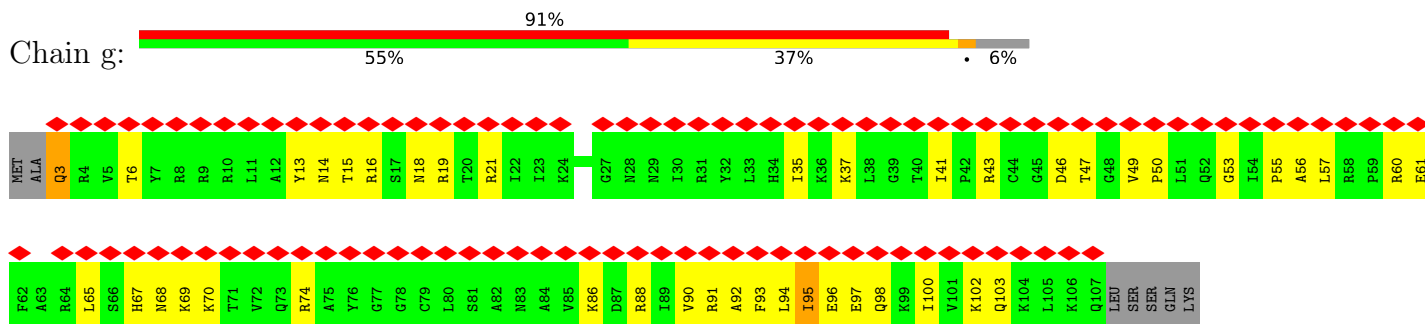
• Molecule 29: 60S ribosomal protein L32-A



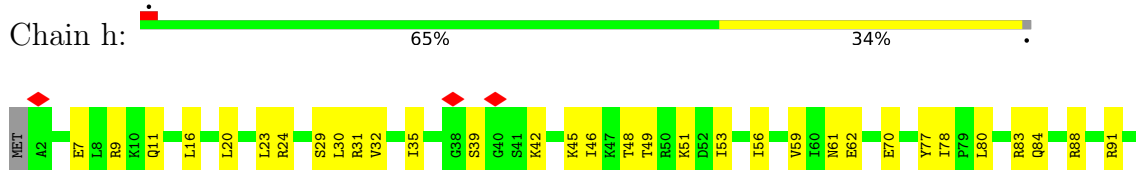
• Molecule 30: 60S ribosomal protein L33-B



• Molecule 31: 60S ribosomal protein L34-A

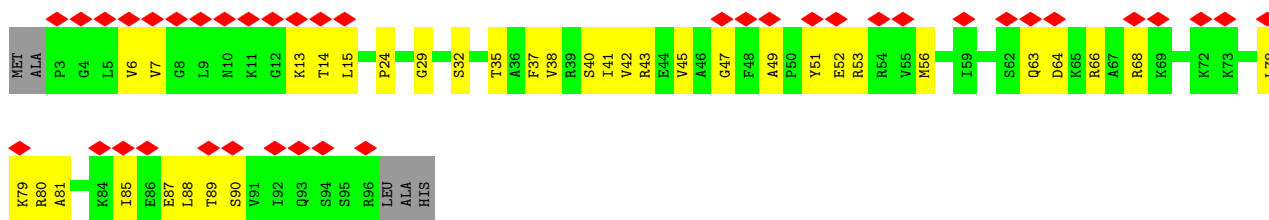


• Molecule 32: 60S ribosomal protein L35





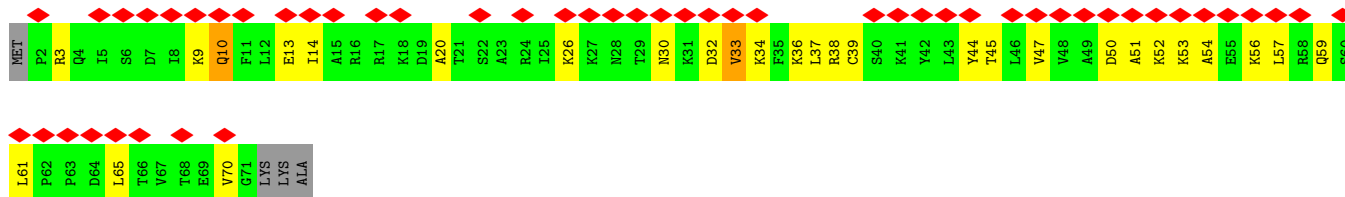
• Molecule 33: 60S ribosomal protein L36-B



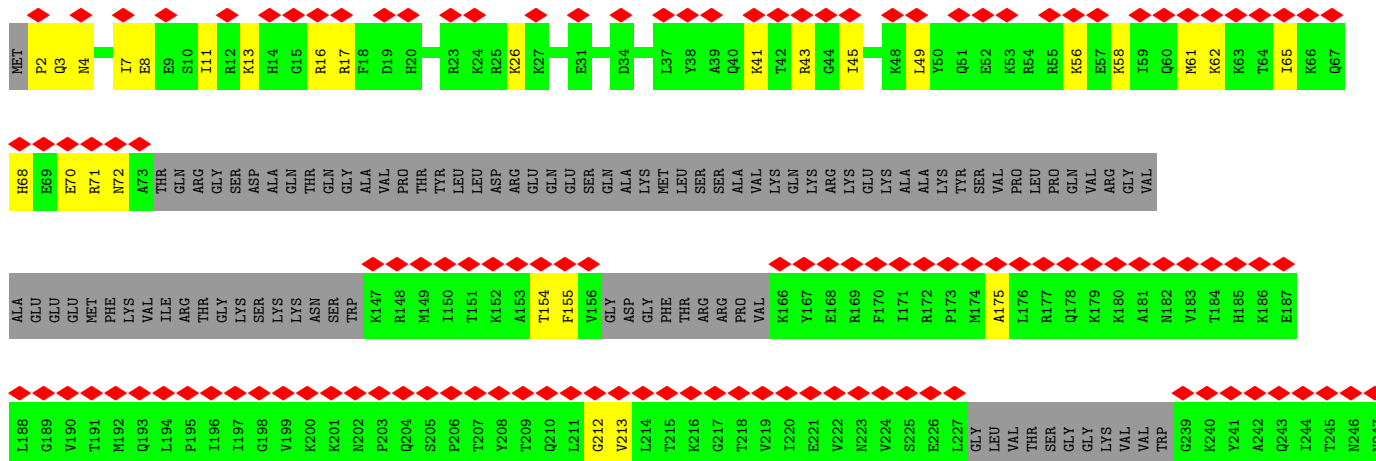
• Molecule 34: 60S ribosomal protein L37-B

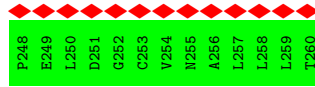


• Molecule 35: 60S ribosomal protein L38-1

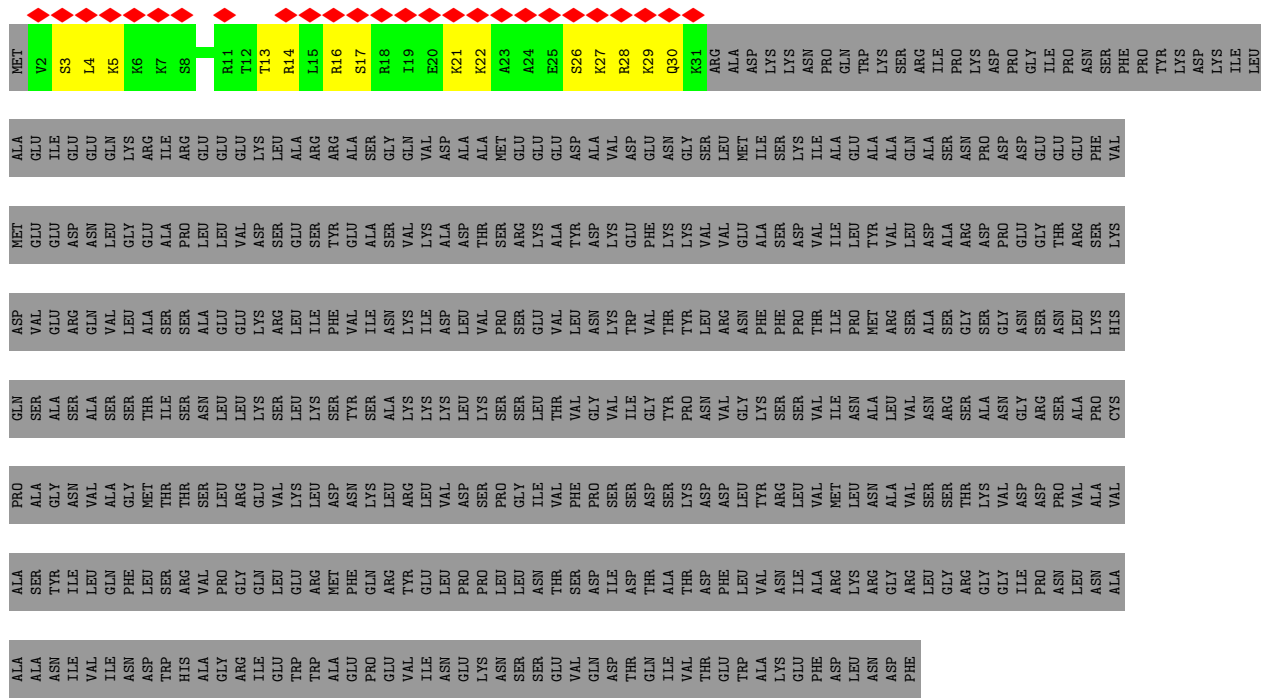


• Molecule 36: Ribosome biogenesis protein nsa2

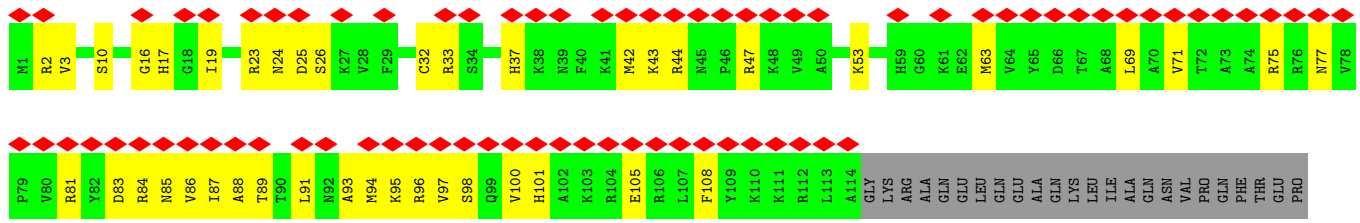




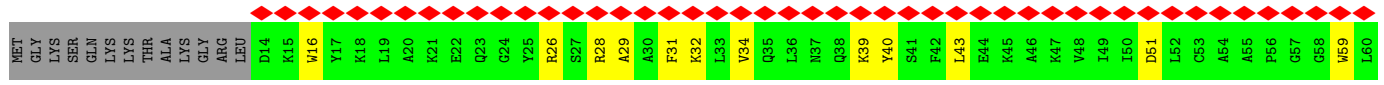
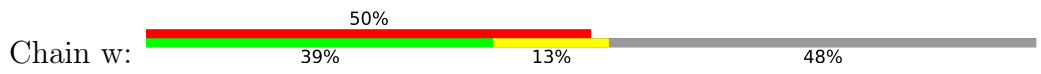
• Molecule 37: GTPase grn1



• Molecule 38: Ribosome biogenesis protein rlp24

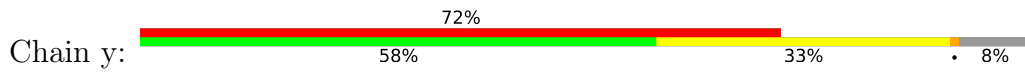


• Molecule 39: AdoMet-dependent rRNA methyltransferase spb1



Q61	V62	A63	S64	K65	T66	C67	K68	P69	G70	S71	L72	I73	V74	G75	V76	D77	L78	A79	P80	K81	P83	I84	P85	N86	C87	H88	T89	F90	V91	E92	D93	I94	T95	S96	D97	K98	C99	R100	S101	Q102	L103	R104	G105	Y106	L107	K108	T109	W110	R161	S162	R163	D164	Y165	N166	N167	L168	L169	W170	V171	F172	K173	Q174	L175	F176	N177	K178	G119	A120																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
P121	N122	V123	G124	S125	A126	W127	L128	Q129	D130	A131	Y132	G133	Q134	A135	Q136	L137	V138	L139	M140	S141	M142	K143	L144	A145	C146	E147	F148	L149	V150	A151	G152	G153	T154	F155	V156	T157	K158	V159	F160	R161	S162	R163	D164	Y165	N166	N167	L168	L169	W170	V171	F172	K173	Q174	L175	F176	N177	K178	V179	E180																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
A181	T182	K183	P184	P185	S186	S187	R188	N189	V190	S191	A192	E193	I194	F195	V196	V197	C198	R199	G200	I81	K202	A203	P204	K205	K206	L207	D208	P209	R210	F211	T212	D213	P214	R215	T216	V217	F218	E219	E220	V221	Q222	E223	P224	V225	T226	N227	V228	D229	A230	K231	V232	F233	H234	P235	E236	K237	R238	K239	R240																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
S241	R242	E243	G244	Y245	A246	D247	D248	D249	Y250	T251	L252	K253	H254	T255	V256	L257	A258	S259	E260	F261	V262	T263	A264	M265	D266	P267	I268	Q269	I270	L271	G272	T273	S274	A275	E276	I277	V278	F279	P280	K281	Q282	D283	E284	E285	C286	Q287	R288	L289	Y290	M291	L292	D293	V294	T295	T296	E297	E298	I299	L300																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
L301	C302	S303	S304	D305	L306	Q307	V308	L309	G310	K311	K312	E313	F314	R315	D316	I317	L318	R319	W320	R321	L322	K323	I324	R325	D326	E327	M328	G329	I330	L331	L332	L333	L334	L335	L336	L337	L338	L339	L340	L341	L342	L343	L344	L345	L346	L347	L348	L349	L350	L351	L352	L353	L354	L355	L356	L357	L358	L359	L360	L361	L362	L363	L364	L365	L366	L367	L368	L369	L370	L371	L372	L373	L374	L375	L376	L377	L378	L379	L380	L381	L382	L383	L384	L385	L386	L387	L388	L389	L390	L391	L392	L393	L394	L395	L396	L397	L398	L399	L400	L401	L402	L403	L404	L405	L406	L407	L408	L409	L410	L411	L412	L413	L414	L415	L416	L417	L418	L419	L420	L421	L422	L423	L424	L425	L426	L427	L428	L429	L430	L431	L432	L433	L434	L435	L436	L437	L438	L439	L440	L441	L442	L443	L444	L445	L446	L447	L448	L449	L450	L451	L452	L453	L454	L455	L456	L457	L458	L459	L460	L461	L462	L463	L464	L465	L466	L467	L468	L469	L470	L471	L472	L473	L474	L475	L476	L477	L478	L479	L480	L481	L482	L483	L484	L485	L486	L487	L488	L489	L490	L491	L492	L493	L494	L495	L496	L497	L498	L499	L500	L501	L502	L503	L504	L505	L506	L507	L508	L509	L510	L511	L512	L513	L514	L515	L516	L517	L518	L519	L520	L521	L522	L523	L524	L525	L526	L527	L528	L529	L530	L531	L532	L533	L534	L535	L536	L537	L538	L539	L540	L541	L542	L543	L544	L545	L546	L547	L548	L549	L550	L551	L552	L553	L554	L555	L556	L557	L558	L559	L560	L561	L562	L563	L564	L565	L566	L567	L568	L569	L570	L571	L572	L573	L574	L575	L576	L577	L578	L579	L580	L581	L582	L583	L584	L585	L586	L587	L588	L589	L590	L591	L592	L593	L594	L595	L596	L597	L598	L599	L600	L601	L602	L603	L604	L605	L606	L607	L608	L609	L610	L611	L612	L613	L614	L615	L616	L617	L618	L619	L620	L621	L622	L623	L624	L625	L626	L627	L628	L629	L630	L631	L632	L633	L634	L635	L636	L637	L638	L639	L640	L641	L642	L643	L644	L645	L646	L647	L648	L649	L650	L651	L652	L653	L654	L655	L656	L657	L658	L659	L660	L661	L662	L663	L664	L665	L666	L667	L668	L669	L670	L671	L672	L673	L674	L675	L676	L677	L678	L679	L680	L681	L682	L683	L684	L685	L686	L687	L688	L689	L690	L691	L692	L693	L694	L695	L696	L697	L698	L699	L700	L701	L702	L703	L704	L705	L706	L707	L708	L709	L710	L711	L712	L713	L714	L715	L716	L717	L718	L719	L720	L721	L722	L723	L724	L725	L726	L727	L728	L729	L730	L731	L732	L733	L734	L735	L736	L737	L738	L739	L740	L741	L742	L743	L744	L745	L746	L747	L748	L749	L750	L751	L752	L753	L754	L755	L756	L757	L758	L759	L760	L761	L762	L763	L764	L765	L766	L767	L768	L769	L770	L771	L772	L773	L774	L775	L776	L777	L778	L779	L780	L781	L782	L783	L784	L785	L786	L787	L788	L789	L790	L791	L792	L793	L794	L795	L796	L797	L798	L799	L800	L801	L802	L803	L804	L805	L806	L807	L808	L809	L810	L811	L812	L813	L814	L815	L816	L817	L818	L819	L820	L821	L822	L823	L824	L825	L826	L827	L828	L829	L830	L831	L832	L833	L834	L835	L836	L837	L838	L839	L840	L841	L842	L843	L844	L845	L846	L847	L848	L849	L850	L851	L852	L853	L854	L855	L856	L857	L858	L859	L860	L861	L862	L863	L864	L865	L866	L867	L868	L869	L870	L871	L872	L873	L874	L875	L876	L877	L878	L879	L880	L881	L882	L883	L884	L885	L886	L887	L888	L889	L890	L891	L892	L893	L894	L895	L896	L897	L898	L899	L900	L901	L902	L903	L904	L905	L906	L907	L908	L909	L910	L911	L912	L913	L914	L915	L916	L917	L918	L919	L920	L921	L922	L923	L924	L925	L926	L927	L928	L929	L930	L931	L932	L933	L934	L935	L936	L937	L938	L939	L940	L941	L942	L943	L944	L945	L946	L947	L948	L949	L950	L951	L952	L953	L954	L955	L956	L957	L958	L959	L960	L961	L962	L963	L964	L965	L966	L967	L968	L969	L970	L971	L972	L973	L974	L975	L976	L977	L978	L979	L980	L981	L982	L983	L984	L985	L986	L987	L988	L989	L990	L991	L992	L993	L994	L995	L996	L997	L998	L999	L1000

• Molecule 40: Eukaryotic translation initiation factor 6



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.558	Depositor
Minimum map value	-0.297	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1	0.09	0/51306	0.22	0/79930
2	2	0.10	0/3500	0.20	0/5446
3	3	0.16	0/990	0.44	0/1333
4	8	0.11	0/439	0.33	0/586
5	B	0.12	0/2965	0.33	0/3988
6	C	0.16	0/2848	0.37	1/3842 (0.0%)
7	E	0.15	0/1284	0.37	0/1731
8	F	0.11	0/1806	0.30	0/2424
9	G	0.14	0/1475	0.35	0/1988
10	H	0.13	0/1470	0.38	0/1982
11	L	0.15	0/1452	0.39	0/1955
12	M	0.15	0/1024	0.40	0/1375
13	N	0.10	0/1436	0.27	0/1920
14	O	0.13	0/1588	0.32	0/2128
15	P	0.12	0/1361	0.34	0/1823
16	Q	0.11	0/1057	0.32	0/1419
17	R	0.12	0/1054	0.36	0/1404
18	S	0.13	0/1444	0.35	0/1939
19	U	0.05	0/483	0.19	0/671
20	V	0.14	0/1048	0.40	0/1410
21	W	0.06	0/1053	0.28	0/1457
22	X	0.14	0/930	0.40	0/1251
23	Y	0.11	0/1008	0.31	0/1341
24	Z	0.06	0/661	0.17	0/917
25	a	0.15	0/760	0.42	0/1026
26	b	0.23	0/2868	0.48	1/3902 (0.0%)
27	c	0.06	0/476	0.16	0/658
28	d	0.11	0/864	0.31	0/1161
29	e	0.13	0/958	0.32	0/1278
30	f	0.10	0/859	0.26	0/1152
31	g	0.16	0/865	0.50	2/1159 (0.2%)
32	h	0.12	0/1008	0.35	0/1340

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i	0.18	0/761	0.48	0/1009
34	j	0.10	0/613	0.31	0/811
35	k	0.22	0/570	0.57	0/762
36	r	0.13	0/1091	0.36	0/1464
37	s	0.15	0/252	0.40	0/325
38	u	0.20	0/966	0.49	0/1292
39	w	0.12	0/3444	0.37	0/4638
40	y	0.12	0/1720	0.34	0/2345
41	z	0.14	0/297	0.42	0/388
42	T	0.22	0/165	0.45	0/228
All	All	0.12	0/102219	0.29	4/149198 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	345	SER	N-CA-C	-6.50	104.40	112.72
26	b	162	PRO	CA-N-CD	-5.19	104.74	112.00
31	g	95	ILE	CA-C-N	-5.00	112.18	120.68
31	g	95	ILE	C-N-CA	-5.00	112.18	120.68

There are no chirality outliers.

There are no planarity outliers.

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	1	45843	0	23070	659	0
2	2	3131	0	1583	39	0
3	3	969	0	964	60	0
4	8	428	0	452	16	0
5	B	2903	0	2974	74	0
6	C	2795	0	2918	73	0
7	E	1260	0	1343	40	0
8	F	1770	0	1848	35	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	G	1453	0	1545	37	0
10	H	1451	0	1511	34	0
11	L	1427	0	1482	45	0
12	M	1007	0	1072	37	0
13	N	1406	0	1441	43	0
14	O	1557	0	1652	40	0
15	P	1339	0	1380	35	0
16	Q	1047	0	1143	18	0
17	R	1038	0	1113	39	0
18	S	1408	0	1462	33	0
19	U	484	0	222	1	0
20	V	1032	0	1081	53	0
21	W	1057	0	487	4	0
22	X	914	0	970	25	0
23	Y	998	0	1090	31	0
24	Z	662	0	305	1	0
25	a	747	0	790	37	0
26	b	2837	0	2413	90	0
27	c	477	0	233	1	0
28	d	849	0	885	29	0
29	e	944	0	1005	24	0
30	f	839	0	866	10	0
31	g	853	0	919	34	0
32	h	999	0	1092	36	0
33	i	754	0	836	28	0
34	j	600	0	613	17	0
35	k	564	0	611	31	0
36	r	1086	0	842	29	0
37	s	253	0	300	16	0
38	u	944	0	983	49	0
39	w	3377	0	3430	93	0
40	y	1697	0	1679	53	0
41	z	292	0	317	16	0
42	T	159	0	150	8	0
43	j	1	0	0	0	0
All	All	95651	0	71072	1692	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 10.

The worst 5 of 1692 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)
26:b:117:LEU:HD13	26:b:129:LEU:HD22	1.50	0.94
36:r:71:ARG:NH1	36:r:71:ARG:O	2.07	0.88
25:a:75:LEU:HA	25:a:78:LEU:HD23	1.57	0.86
1:1:591:G:H1'	1:1:592:U:H3'	1.58	0.85
12:M:51:ILE:HD11	12:M:55:SER:HB3	1.58	0.84

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	3	110/302 (36%)	105 (96%)	5 (4%)	0	100	100
4	8	47/51 (92%)	44 (94%)	3 (6%)	0	100	100
5	B	361/388 (93%)	343 (95%)	18 (5%)	0	100	100
6	C	357/363 (98%)	338 (95%)	17 (5%)	2 (1%)	21	52
7	E	161/195 (83%)	148 (92%)	11 (7%)	2 (1%)	10	37
8	F	216/250 (86%)	210 (97%)	5 (2%)	1 (0%)	24	57
9	G	180/259 (70%)	169 (94%)	8 (4%)	3 (2%)	7	30
10	H	181/190 (95%)	173 (96%)	8 (4%)	0	100	100
11	L	178/208 (86%)	168 (94%)	9 (5%)	1 (1%)	21	52
12	M	123/134 (92%)	118 (96%)	5 (4%)	0	100	100
13	N	160/201 (80%)	156 (98%)	4 (2%)	0	100	100
14	O	194/197 (98%)	189 (97%)	4 (2%)	1 (0%)	24	57
15	P	163/187 (87%)	157 (96%)	6 (4%)	0	100	100
16	Q	133/187 (71%)	128 (96%)	5 (4%)	0	100	100
17	R	120/193 (62%)	116 (97%)	4 (3%)	0	100	100
18	S	164/176 (93%)	156 (95%)	8 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	U	96/117 (82%)	92 (96%)	4 (4%)	0	100	100
20	V	136/139 (98%)	132 (97%)	3 (2%)	1 (1%)	18	49
21	W	207/241 (86%)	195 (94%)	12 (6%)	0	100	100
22	X	112/141 (79%)	107 (96%)	5 (4%)	0	100	100
23	Y	123/126 (98%)	119 (97%)	4 (3%)	0	100	100
24	Z	132/136 (97%)	129 (98%)	3 (2%)	0	100	100
25	a	90/148 (61%)	88 (98%)	2 (2%)	0	100	100
26	b	407/642 (63%)	399 (98%)	7 (2%)	1 (0%)	43	73
27	c	95/117 (81%)	95 (100%)	0	0	100	100
28	d	100/113 (88%)	99 (99%)	1 (1%)	0	100	100
29	e	116/127 (91%)	113 (97%)	3 (3%)	0	100	100
30	f	104/108 (96%)	98 (94%)	6 (6%)	0	100	100
31	g	103/112 (92%)	98 (95%)	5 (5%)	0	100	100
32	h	119/122 (98%)	116 (98%)	3 (2%)	0	100	100
33	i	92/99 (93%)	90 (98%)	2 (2%)	0	100	100
34	j	73/91 (80%)	71 (97%)	2 (3%)	0	100	100
35	k	68/74 (92%)	66 (97%)	2 (3%)	0	100	100
36	r	158/260 (61%)	156 (99%)	2 (1%)	0	100	100
37	s	28/470 (6%)	28 (100%)	0	0	100	100
38	u	112/192 (58%)	107 (96%)	5 (4%)	0	100	100
39	w	412/802 (51%)	378 (92%)	33 (8%)	1 (0%)	43	73
40	y	223/244 (91%)	214 (96%)	9 (4%)	0	100	100
41	z	33/117 (28%)	32 (97%)	1 (3%)	0	100	100
42	T	19/160 (12%)	17 (90%)	2 (10%)	0	100	100
All	All	6006/8379 (72%)	5757 (96%)	236 (4%)	13 (0%)	44	73

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	L	175	ALA
20	V	3	ARG
6	C	346	GLU
39	w	476	LYS
7	E	144	ALA

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	
3	3	104/271 (38%)	104 (100%)	0	100	100
4	8	45/47 (96%)	45 (100%)	0	100	100
5	B	308/326 (94%)	307 (100%)	1 (0%)	86	87
6	C	296/297 (100%)	296 (100%)	0	100	100
7	E	133/155 (86%)	132 (99%)	1 (1%)	73	81
8	F	182/210 (87%)	182 (100%)	0	100	100
9	G	154/212 (73%)	149 (97%)	5 (3%)	34	64
10	H	164/170 (96%)	163 (99%)	1 (1%)	78	83
11	L	144/167 (86%)	144 (100%)	0	100	100
12	M	108/113 (96%)	105 (97%)	3 (3%)	38	66
13	N	146/176 (83%)	146 (100%)	0	100	100
14	O	161/162 (99%)	160 (99%)	1 (1%)	78	83
15	P	138/149 (93%)	138 (100%)	0	100	100
16	Q	115/159 (72%)	115 (100%)	0	100	100
17	R	111/162 (68%)	111 (100%)	0	100	100
18	S	150/154 (97%)	150 (100%)	0	100	100
20	V	106/107 (99%)	103 (97%)	3 (3%)	38	66
22	X	101/122 (83%)	100 (99%)	1 (1%)	68	79
23	Y	110/111 (99%)	110 (100%)	0	100	100
25	a	81/122 (66%)	81 (100%)	0	100	100
26	b	214/556 (38%)	212 (99%)	2 (1%)	70	80
28	d	93/102 (91%)	93 (100%)	0	100	100
29	e	100/107 (94%)	100 (100%)	0	100	100
30	f	89/91 (98%)	88 (99%)	1 (1%)	65	78
31	g	91/97 (94%)	90 (99%)	1 (1%)	65	78
32	h	106/107 (99%)	105 (99%)	1 (1%)	70	80

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	i	81/84 (96%)	81 (100%)	0	100	100
34	j	62/71 (87%)	62 (100%)	0	100	100
35	k	63/66 (96%)	61 (97%)	2 (3%)	34	64
36	r	63/224 (28%)	63 (100%)	0	100	100
37	s	28/409 (7%)	28 (100%)	0	100	100
38	u	99/168 (59%)	98 (99%)	1 (1%)	68	79
39	w	369/697 (53%)	366 (99%)	3 (1%)	73	81
40	y	189/206 (92%)	186 (98%)	3 (2%)	55	75
41	z	31/107 (29%)	31 (100%)	0	100	100
42	T	18/139 (13%)	18 (100%)	0	100	100
All	All	4553/6623 (69%)	4523 (99%)	30 (1%)	76	82

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	V	76	MET
40	y	28	LEU
26	b	458	GLU
40	y	178	GLN
39	w	82	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
29	e	17	HIS
34	j	48	ASN
31	g	3	GLN
32	h	15	ASN
36	r	40	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2109/3497 (60%)	502 (23%)	28 (1%)
2	2	144/165 (87%)	22 (15%)	1 (0%)
All	All	2253/3662 (61%)	524 (23%)	29 (1%)

5 of 524 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	12	A
1	1	14	U
1	1	26	A
1	1	49	A

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1272	U
1	1	3328	U
1	1	1338	G
1	1	3081	U
1	1	1333	A

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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

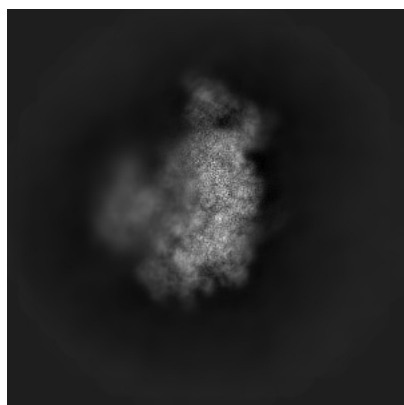
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24398. These allow visual inspection of the internal detail of the map and identification of artifacts.

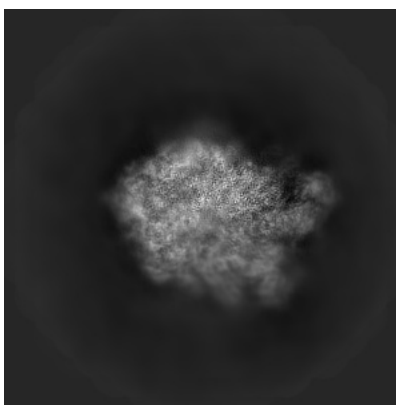
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

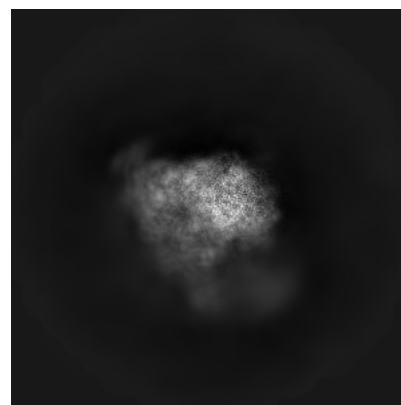
6.1.1 Primary map



X



Y

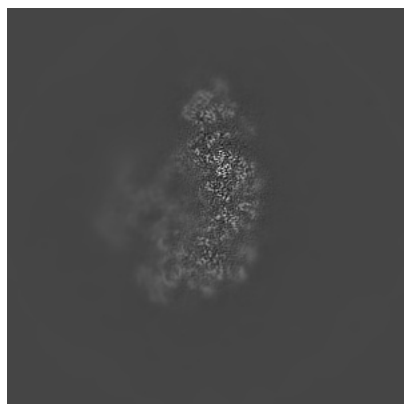


Z

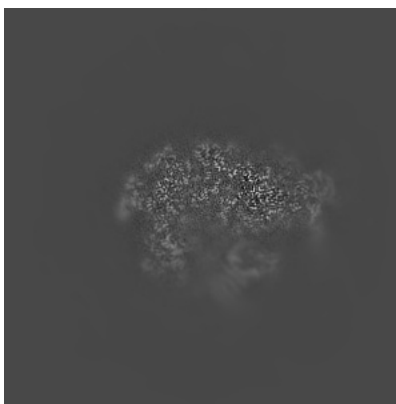
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

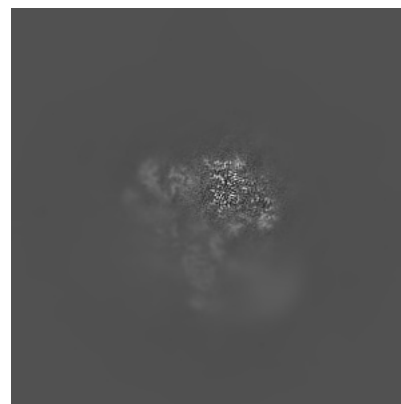
6.2.1 Primary map



X Index: 256



Y Index: 256

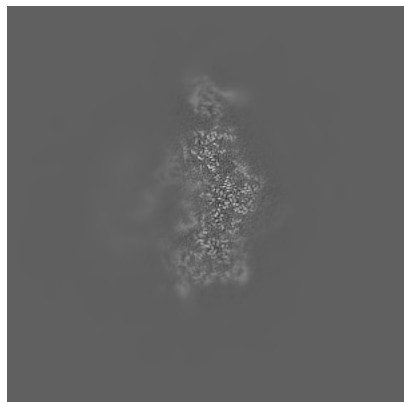


Z Index: 256

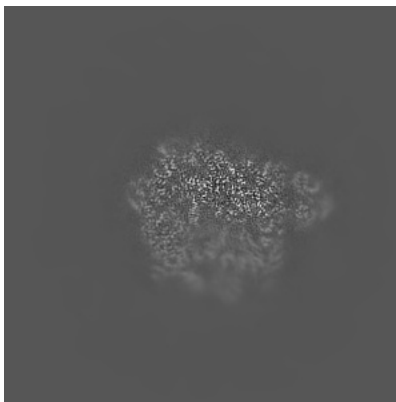
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

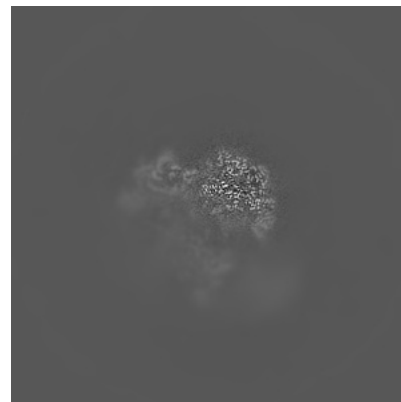
6.3.1 Primary map



X Index: 282



Y Index: 272

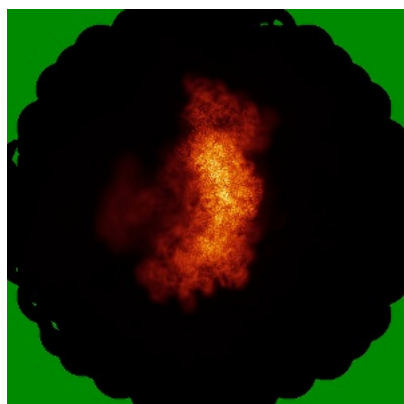


Z Index: 273

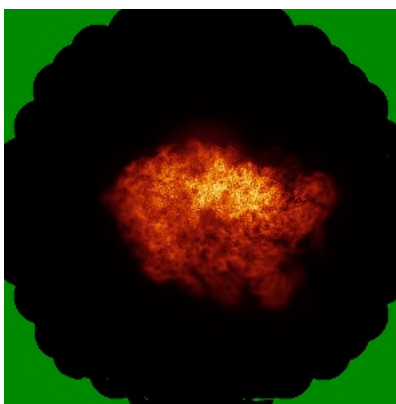
The images above show the largest variance slices of the map in three orthogonal directions.

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

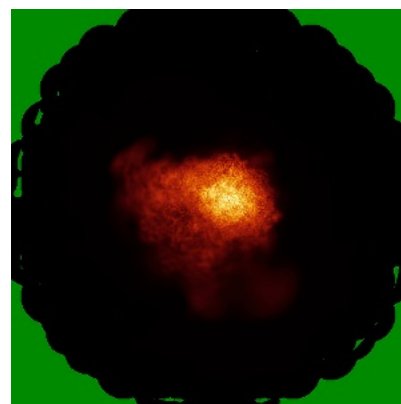
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

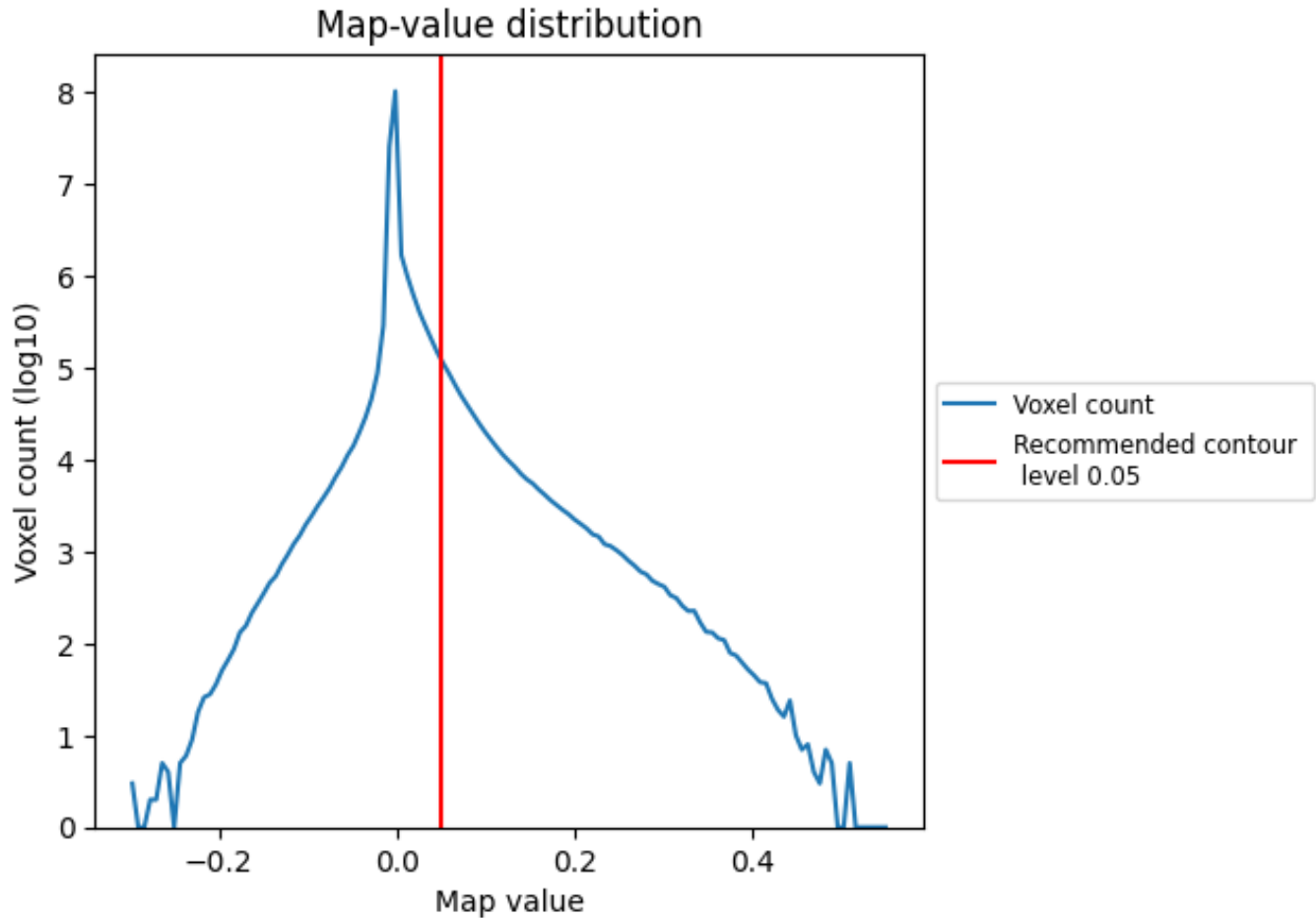
6.6 Mask visualisation

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

7 Map analysis [i](#)

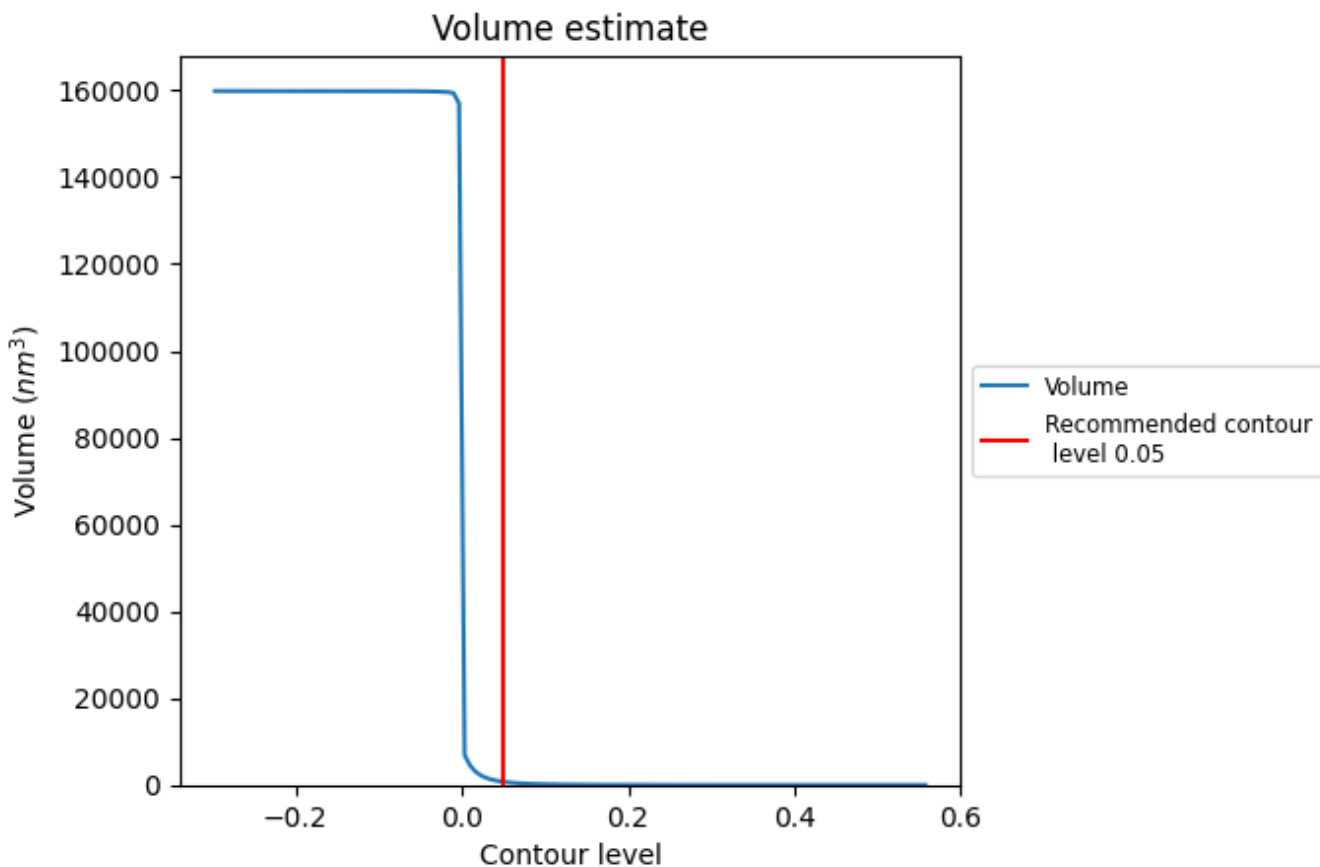
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 720 nm^3 ; this corresponds to an approximate mass of 650 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.323\AA^{-1}

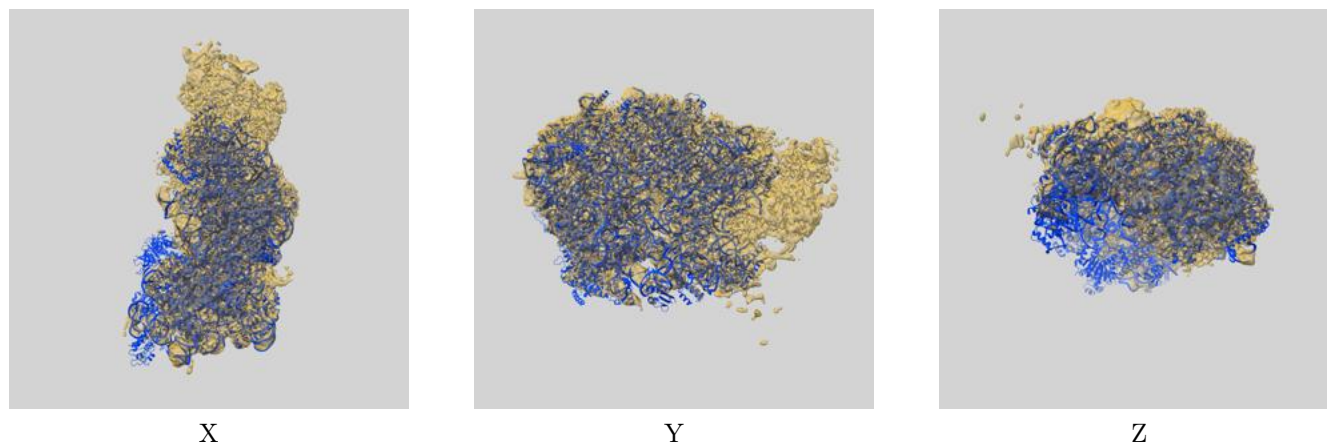
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

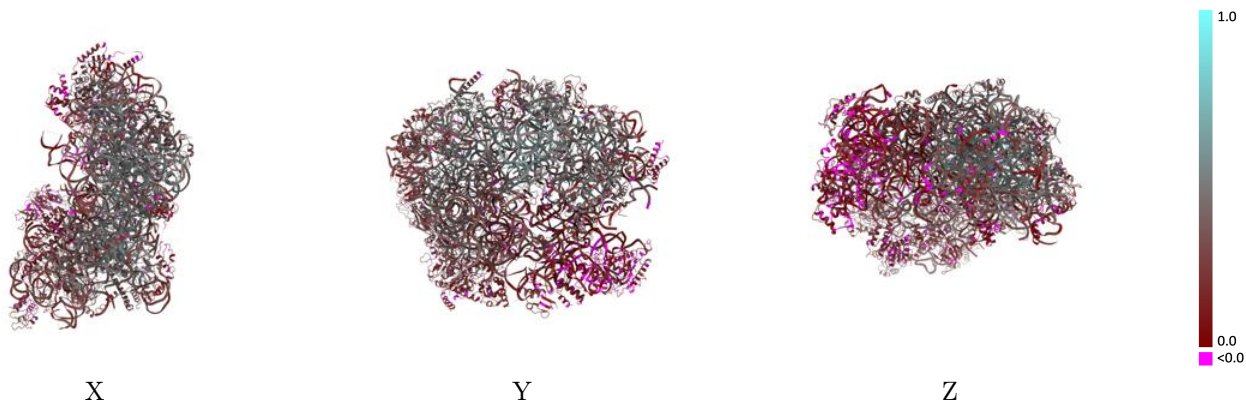
This section contains information regarding the fit between EMDB map EMD-24398 and PDB model 8ETC. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



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

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

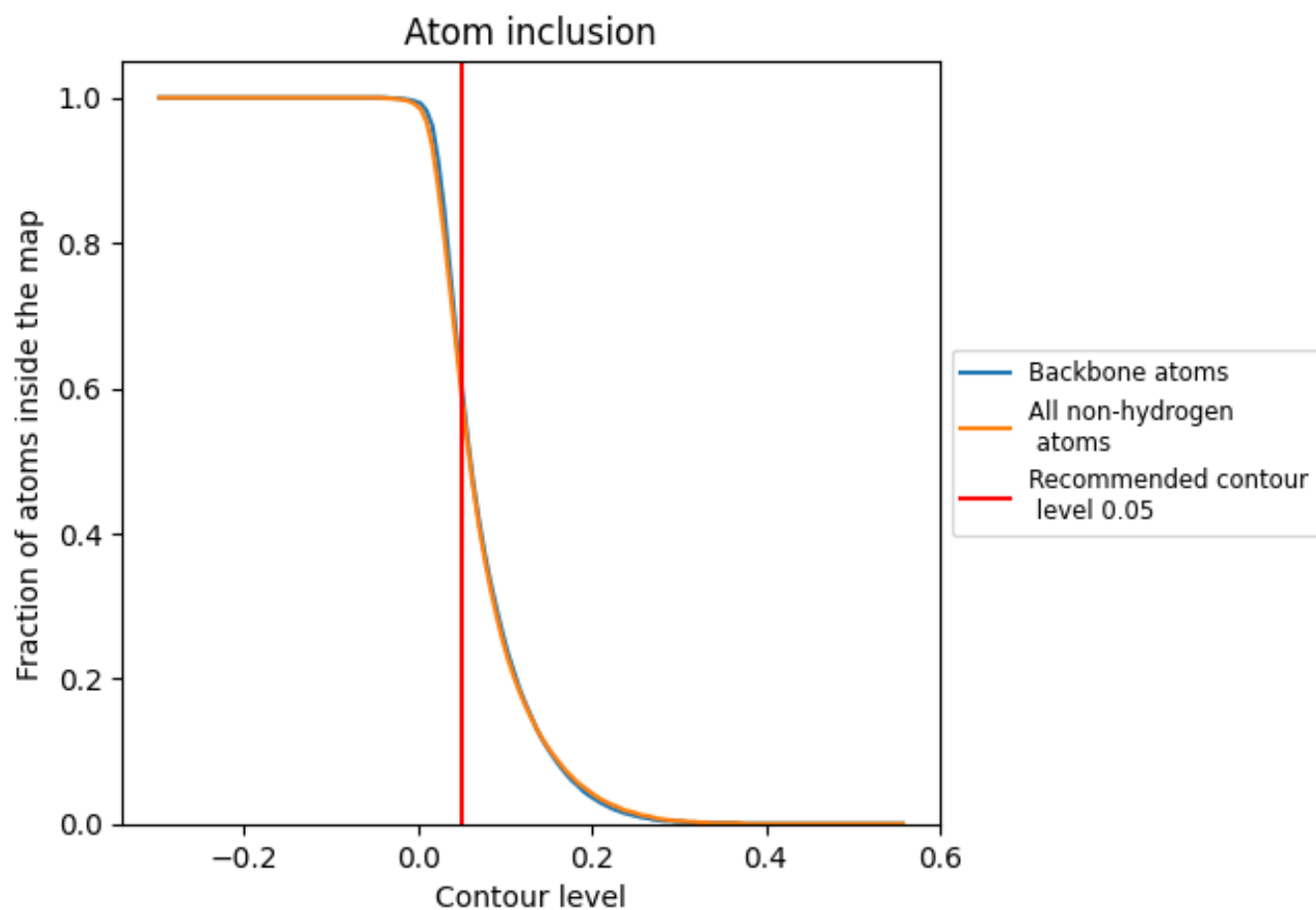


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 59% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

















The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5920	 0.3000
1	 0.7050	 0.3110
2	 0.8570	 0.4040
3	 0.2830	 0.2110
8	 0.1820	 0.1040
B	 0.5870	 0.3250
C	 0.7940	 0.4560
E	 0.5960	 0.3320
F	 0.7400	 0.3960
G	 0.6100	 0.2220
H	 0.4430	 0.2780
L	 0.5720	 0.3200
M	 0.7040	 0.3570
N	 0.8210	 0.4210
O	 0.6970	 0.4020
P	 0.5230	 0.2620
Q	 0.7530	 0.4250
R	 0.2560	 0.1580
S	 0.5840	 0.3140
T	 0.3520	 0.3050
U	 0.1690	 0.2040
V	 0.1950	 0.2250
W	 0.0440	 0.2350
X	 0.6450	 0.3210
Y	 0.7920	 0.4310
Z	 0.1220	 0.0450
a	 0.6120	 0.3680
b	 0.0950	 0.1760
c	 0.0690	 0.0840
d	 0.4690	 0.2520
e	 0.8050	 0.4590
f	 0.7930	 0.4660
g	 0.0560	 0.0230
h	 0.7480	 0.3690
i	 0.5090	 0.1890



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
j	 0.7880	 0.4290
k	 0.2560	 0.0370
r	 0.2040	 0.2060
s	 0.1620	 0.1830
u	 0.2910	 0.1950
w	 0.0500	 0.1440
y	 0.2130	 0.1980
z	 0.0810	 0.2270