



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 04:37 AM UTC

PDB ID : 7AOR / pdb_00007aor
EMDB ID : EMD-11846
Title : mt-SSU from Trypanosoma cruzi in complex with mt-IF-3.
Authors : Soufari, H.; Waltz, F.; Parrot, C.; Bochler, A.; Hashem, Y.
Deposited on : 2020-10-15
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

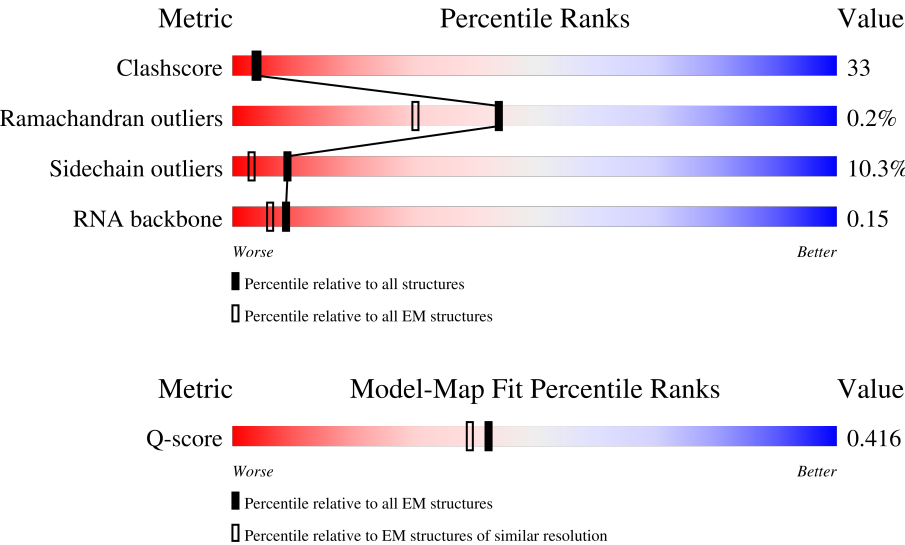
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance ⓘ

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

The reported resolution of this entry is 3.50 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	13950 (3.00 - 4.00)

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	u	874	44% 34% 42% 20%
2	s	180	24% 35% 53% 8%
3	r	500	41% 37% 51% 5% 7%

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Mol	Chain	Length	Quality of chain
4	n	172	
5	h	166	
6	e	818	
7	az	163	
8	ay	218	
9	ax	172	
10	aw	186	
11	au	247	
12	ak	314	
13	aj	396	
14	ag	581	
15	af	677	
16	ae	678	
17	l	714	
18	ac	1152	
19	ab	1175	
20	ad	810	
21	m	319	
22	i	429	
23	f	325	
24	c	285	
25	d	445	
26	ba	217	
27	av	237	
28	at	259	

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Mol	Chain	Length	Quality of chain
29	ar	268	
30	aq	299	
31	ap	277	
32	ao	283	
33	ai	410	
34	an	293	
35	z	1181	
36	y	449	
37	x	345	
38	w	186	
39	v	215	
40	bb	238	
41	t	256	
42	al	308	
43	q	442	
44	p	308	
45	Ca	603	
46	g	193	
47	j	189	
48	b	160	
49	bd	90	
50	a	434	
51	bc	376	
52	aa	1827	
53	k	309	

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Mol	Chain	Length	Quality of chain
54	be	82	
55	as	261	
56	2	8129	
56	A	8129	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	GTP	r	901	-	-	X	-

2 Entry composition [i](#)

There are 60 unique types of molecules in this entry. The entry contains 173743 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 mS35.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	u	697	Total	C	N	O	S	0	0
			5597	3524	1014	1035	24		

- Molecule 2 is a protein called mS33.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	s	165	Total	C	N	O	S	0	0
			1351	851	249	242	9		

- Molecule 3 is a protein called mS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	r	465	Total	C	N	O	S	0	0
			3806	2451	655	681	19		

- Molecule 4 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	n	142	Total	C	N	O	S	0	0
			1169	760	203	201	5		

- Molecule 5 is a protein called uS14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	h	157	Total	C	N	O	S	0	0
			1324	842	252	222	8		

- Molecule 6 is a protein called uS10m.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	e	810	Total	C	N	O	S	0	0
			6577	4157	1153	1237	30		

- Molecule 7 is a protein called mS72.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	az	154	Total	C	N	O	S	0	0
			1292	828	243	217	4		

- Molecule 8 is a protein called mS71.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	ay	141	Total	C	N	O	S	0	0
			1200	765	229	202	4		

- Molecule 9 is a protein called mS70.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	ax	161	Total	C	N	O	S	0	0
			1366	868	263	228	7		

- Molecule 10 is a protein called mS69.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	aw	160	Total	C	N	O	S	0	0
			1338	851	251	232	4		

- Molecule 11 is a protein called Rhodanese domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	au	239	Total	C	N	O	S	0	0
			2069	1331	371	357	10		

- Molecule 12 is a protein called mS58.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	ak	230	Total	C	N	O	S	0	0
			1865	1174	345	338	8		

- Molecule 13 is a protein called mS57.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	aj	315	Total	C	N	O	S	0	0
			2590	1667	450	459	14		

- Molecule 14 is a protein called mS55.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	ag	548	Total	C	N	O	S	0	0
			4472	2804	838	806	24		

- Molecule 15 is a protein called mS54.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	af	558	Total	C	N	O	S	0	0
			4590	2897	829	838	26		

- Molecule 16 is a protein called mS53.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	ae	574	Total	C	N	O	S	0	0
			4634	2918	862	833	21		

- Molecule 17 is a protein called mS52.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	l	588	Total	C	N	O	S	0	0
			4821	3070	855	880	16		

- Molecule 18 is a protein called mS50.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	ac	1125	Total	C	N	O	S	0	0
			8864	5568	1581	1682	33		

- Molecule 19 is a protein called mS49.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	ab	1110	Total	C	N	O	S	0	0
			9094	5669	1697	1697	31		

- Molecule 20 is a protein called mS51.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	ad	801	Total	C	N	O	S	0	0
			6610	4182	1197	1186	45		

- Molecule 21 is a protein called bS18m.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	m	232	Total	C	N	O	S	0	0
			1940	1234	356	344	6		

- Molecule 22 is a protein called uS15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	i	360	Total	C	N	O	S	0	0
			2970	1890	543	522	15		

- Molecule 23 is a protein called uS11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	f	233	Total	C	N	O	S	0	0
			1917	1195	358	354	10		

- Molecule 24 is a protein called uS8m.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	c	263	Total	C	N	O	S	0	0
			2169	1358	417	384	10		

- Molecule 25 is a protein called uS9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	d	445	Total	C	N	O	S	0	0
			3538	2229	635	657	17		

- Molecule 26 is a protein called mS73.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	ba	83	Total	C	N	O	S	0	0
			706	460	115	127	4		

- Molecule 27 is a protein called mS68.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	av	213	Total	C	N	O	S	0	0
			1752	1102	310	333	7		

- Molecule 28 is a protein called mS66.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	at	242	Total	C	N	O	S	0	0
			1946	1216	364	352	14		

- Molecule 29 is a protein called AKAP7_NLS domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	ar	255	Total	C	N	O	S	0	0
			2061	1303	382	368	8		

- Molecule 30 is a protein called mS63.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	aq	198	Total	C	N	O	S	0	0
			1701	1092	304	297	8		

- Molecule 31 is a protein called mS62.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	ap	222	Total	C	N	O	S	0	0
			1796	1109	329	344	14		

- Molecule 32 is a protein called mS61.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	ao	252	Total	C	N	O	S	0	0
			2062	1305	383	362	12		

- Molecule 33 is a protein called mS56.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	ai	390	Total	C	N	O	S	0	0
			3205	2046	554	592	13		

- Molecule 34 is a protein called mS60.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	an	293	Total	C	N	O	S	0	0
			2422	1533	458	419	12		

- Molecule 35 is a protein called mS47.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	z	1071	Total	C	N	O	S	0	0
			8630	5428	1553	1612	37		

- Molecule 36 is a protein called Sod_Fe_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	y	253	Total	C	N	O	S	0	0
			1983	1260	360	350	13		

- Molecule 37 is a protein called Superoxide dismutase, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	x	252	Total	C	N	O	S	0	0
			2016	1294	353	364	5		

- Molecule 38 is a protein called Protein FYV4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	w	175	Total	C	N	O	S	0	0
			1479	945	261	267	6		

- Molecule 39 is a protein called mS37.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	v	196	Total	C	N	O	S	0	0
			1567	964	306	288	9		

- Molecule 40 is a protein called mS38.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	bb	110	Total	C	N	O	S	0	0
			905	580	182	141	2		

- Molecule 41 is a protein called Trafficking protein particle complex subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	t	226	Total	C	N	O	S	0	0
			1797	1138	317	336	6		

- Molecule 42 is a protein called mS59.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	al	292	Total	C	N	O	S	0	0
			2372	1500	444	415	13		

- Molecule 43 is a protein called mS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	q	214	Total	C	N	O	S	0	0
			1840	1169	335	330	6		

- Molecule 44 is a protein called mS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	242	Total	C	N	O	S	0	0
			1998	1264	362	364	8		

- Molecule 45 is a protein called mS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Ca	592	Total	C	N	O	S	0	0
			5070	3247	913	890	20		

- Molecule 46 is a protein called bS21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	g	184	Total	C	N	O	S	0	0
			1544	975	300	258	11		

- Molecule 47 is a protein called bS16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	j	180	Total	C	N	O	S	0	0
			1501	963	280	251	7		

- Molecule 48 is a protein called bS6m.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	b	150	Total	C	N	O	S	0	0
			1271	810	228	227	6		

- Molecule 49 is a protein called MURF5.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	bd	50	Total	C	N	O	S	0	0
			430	296	65	68	1		

- Molecule 50 is a protein called Ribosomal_S5_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	a	425	Total	C	N	O	S	0	0
			3436	2177	633	610	16		

- Molecule 51 is a protein called mt-iF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	bc	151	Total	C	N	O	S	0	0
			1247	792	229	220	6		

- Molecule 52 is a protein called mS48.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	aa	1558	Total	C	N	O	S	0	0
			12549	7926	2247	2337	39		

- Molecule 53 is a protein called 30S Ribosomal protein S17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	k	190	Total	C	N	O	S	0	0
			1577	1009	301	258	9		

- Molecule 54 is a protein called Ribosome protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	be	79	Total	C	N	O	S	0	0
			665	459	101	97	8		

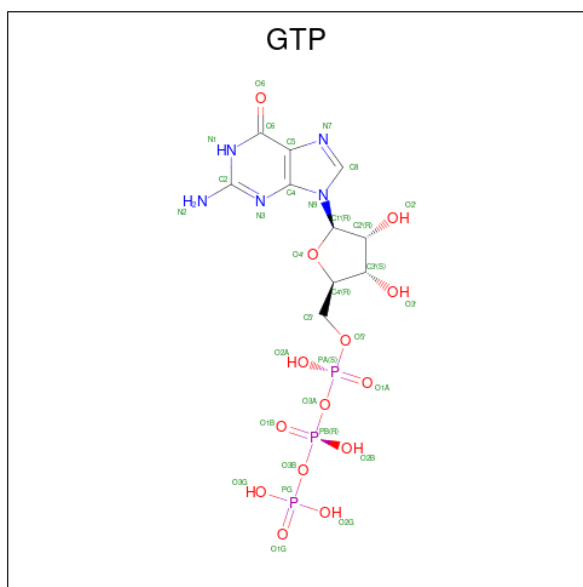
- Molecule 55 is a protein called mS65.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	as	252	Total	C	N	O	S	0	0
			2024	1305	356	353	10		

- Molecule 56 is a RNA chain called RNA (478-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
56	A	143	Total	C	N	O	P	0	0
			3030	1364	522	1001	143		
56	2	470	Total	C	N	O	P	0	0
			9932	4470	1690	3302	470		

- Molecule 57 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

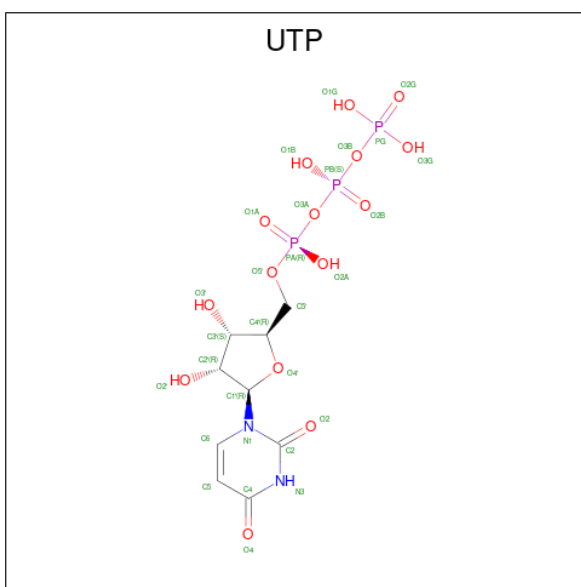


Mol	Chain	Residues	Atoms					AltConf
57	r	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
58	r	1	Total	Mg	0
			1	1	

- Molecule 59 is URIDINE 5'-TRIPHOSPHATE (CCD ID: UTP) (formula: $C_9H_{15}N_2O_{15}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
59	aj	1	Total	C	N	O	P	0
			29	9	2	15	3	

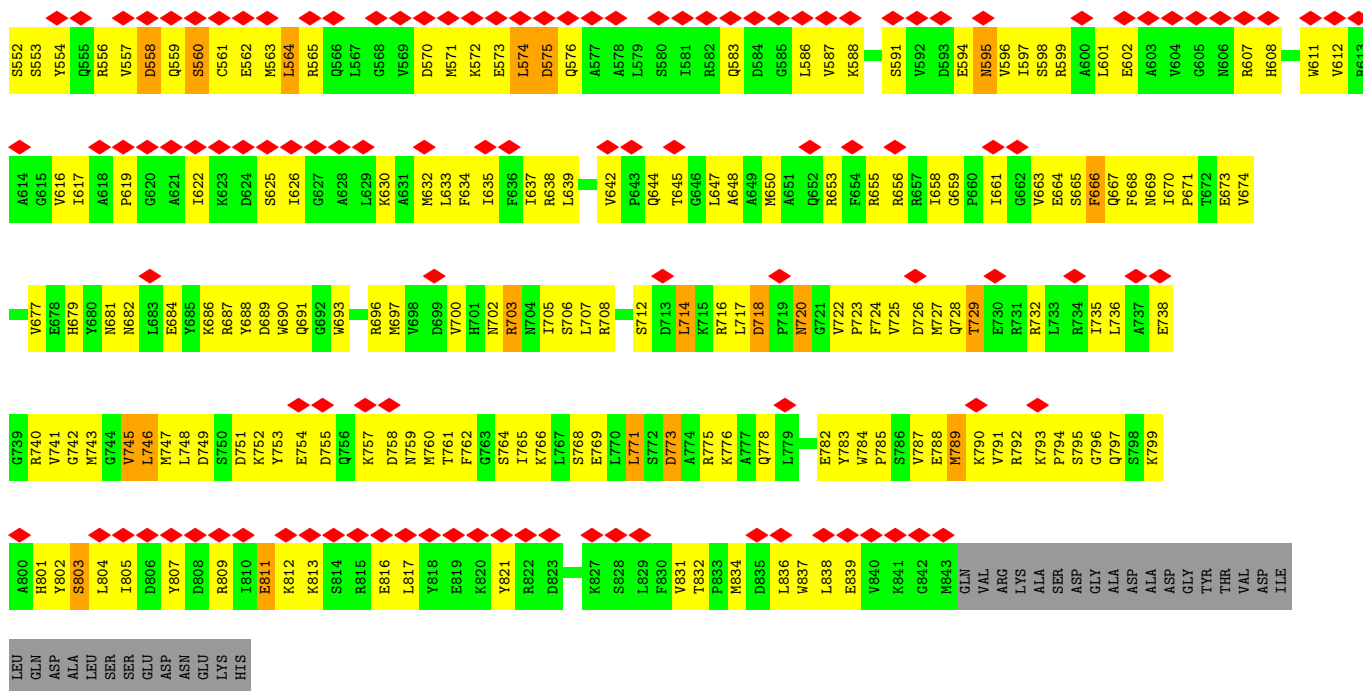
- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
60	at	2	Total Zn 2 2	0
60	y	1	Total Zn 1 1	0
60	aa	1	Total Zn 1 1	0

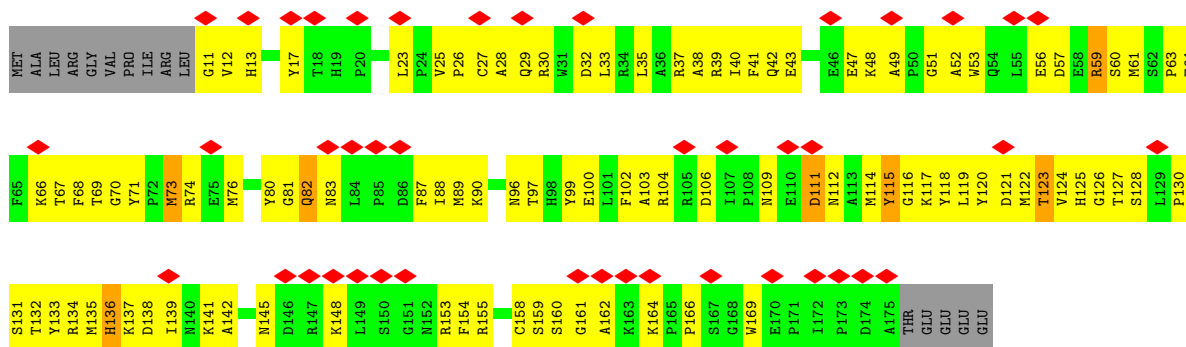
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

Chain u:

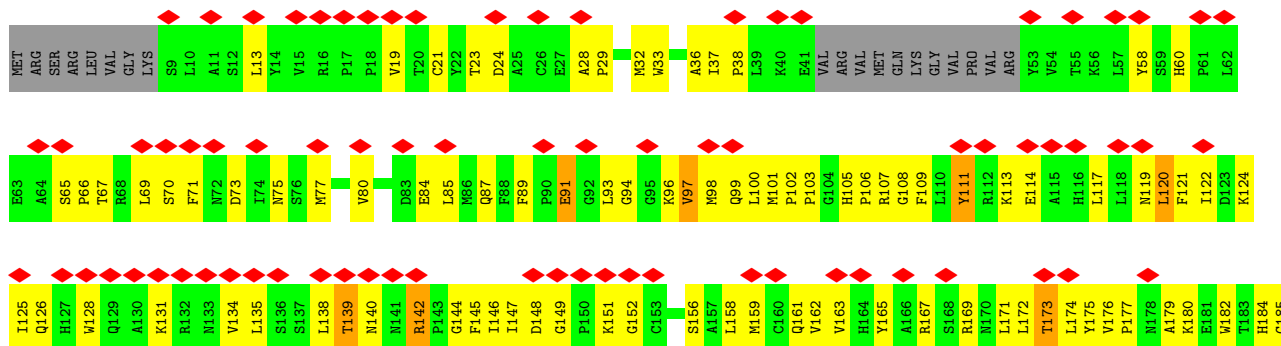


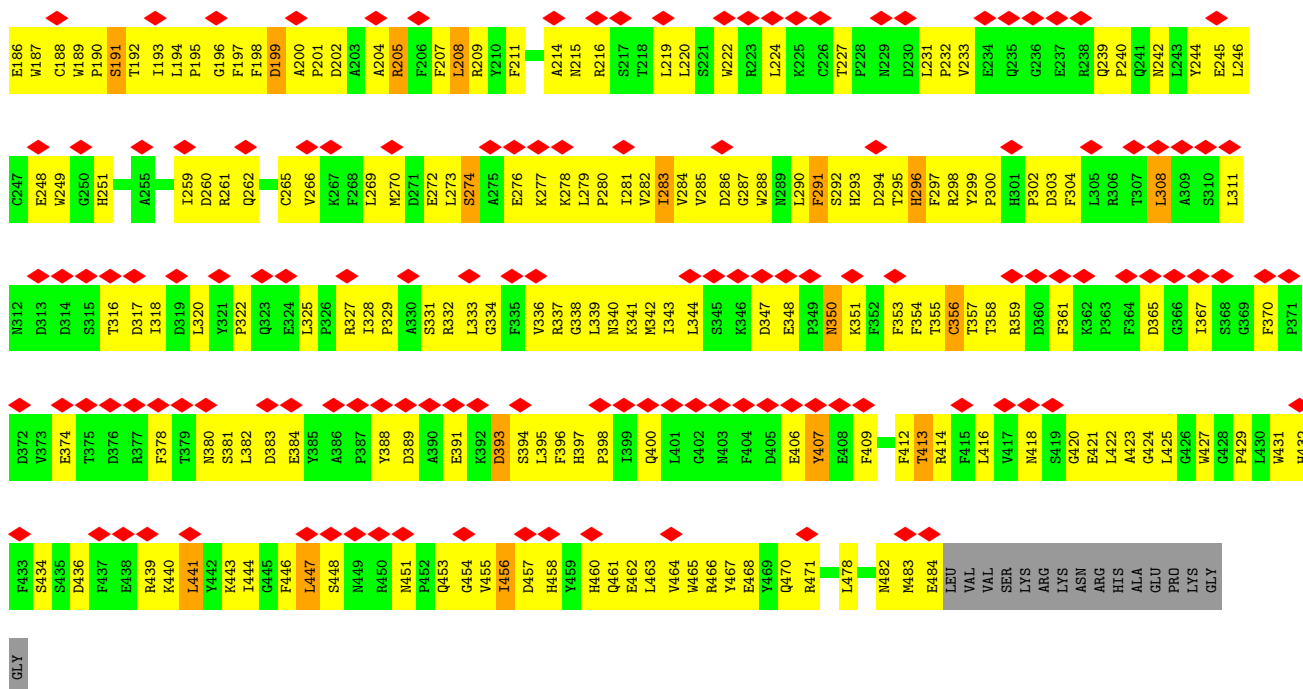


• Molecule 2: mS33

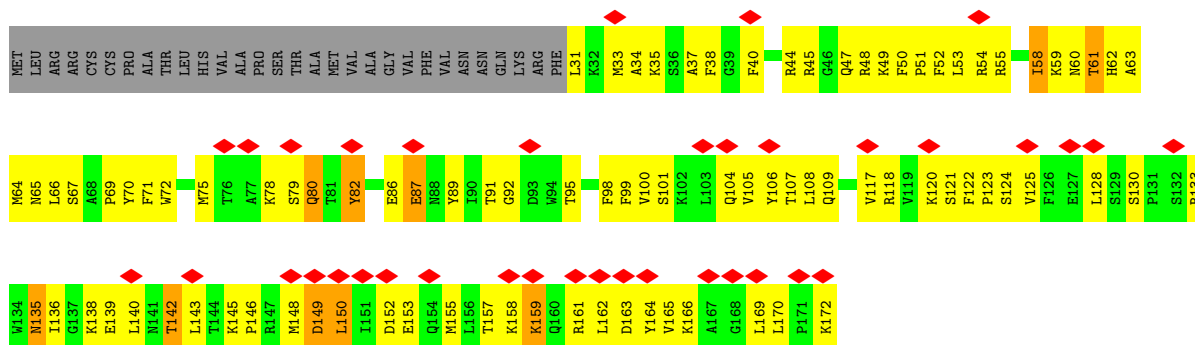


• Molecule 3: mS29

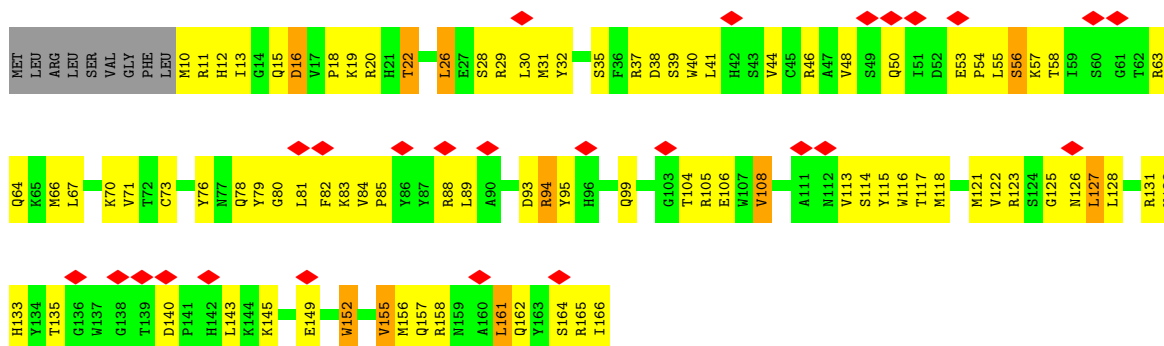




• Molecule 4: uS19

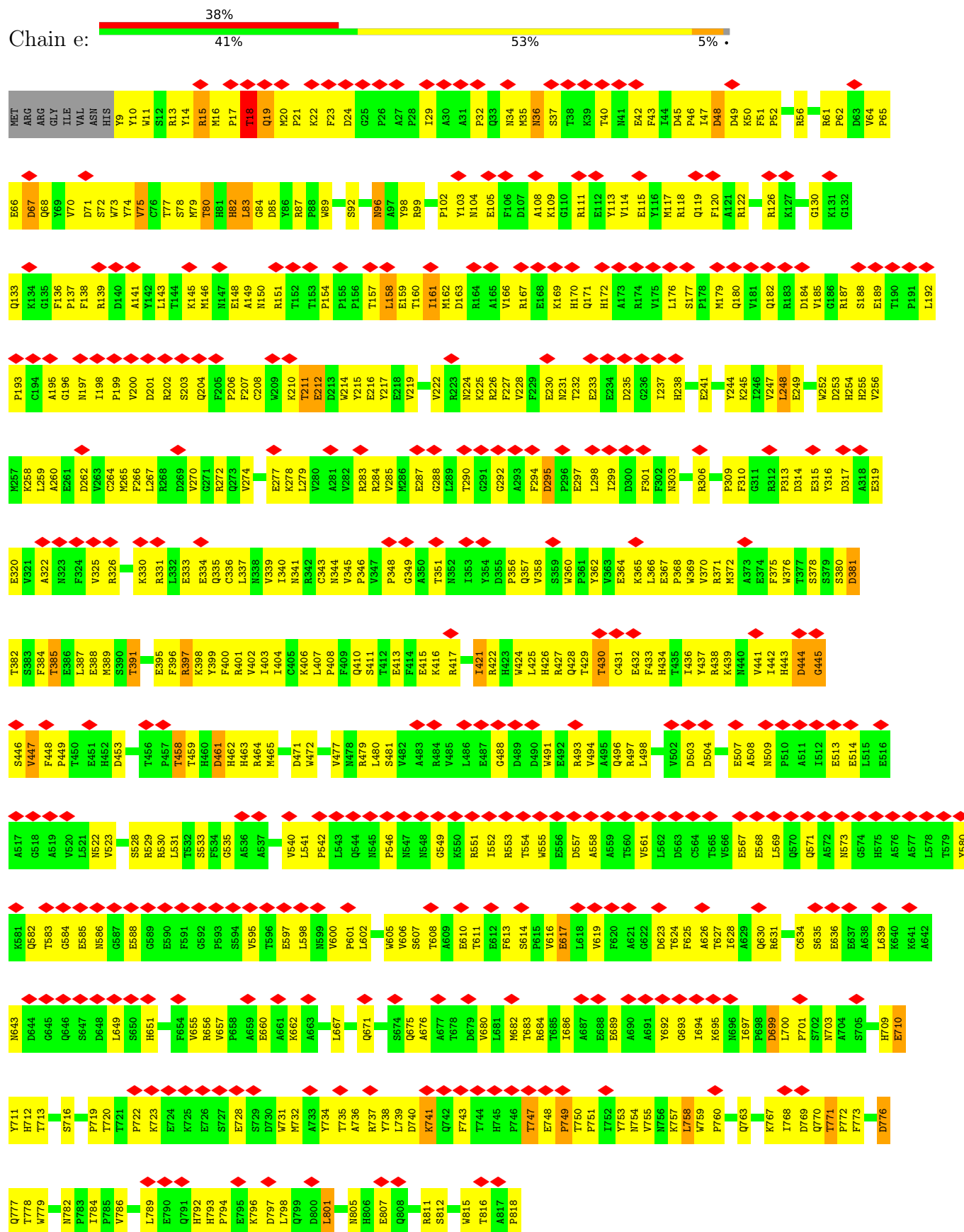


• Molecule 5: uS14m

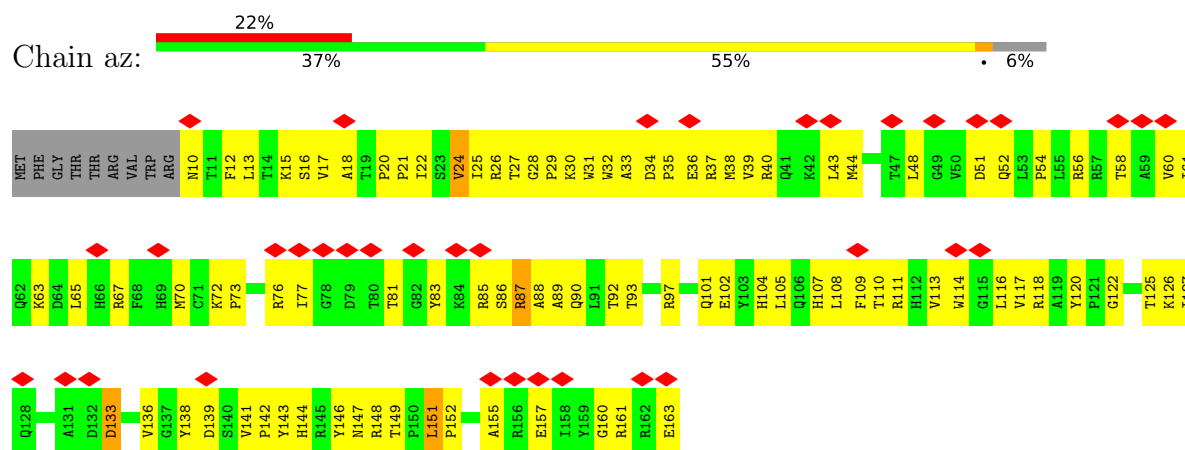


● Molecule 6: uS10m

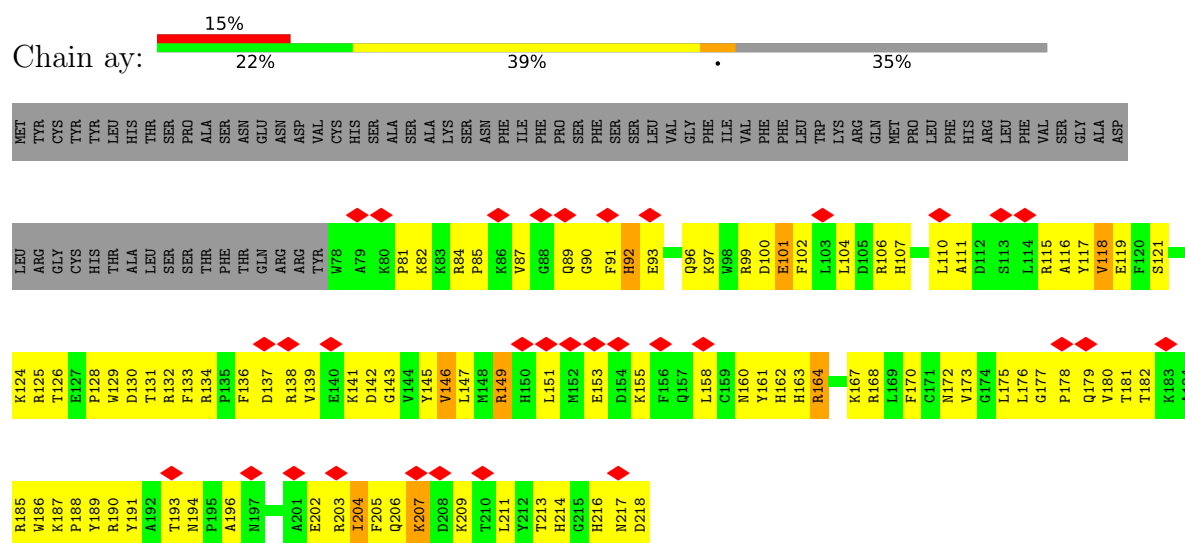
Chain e:



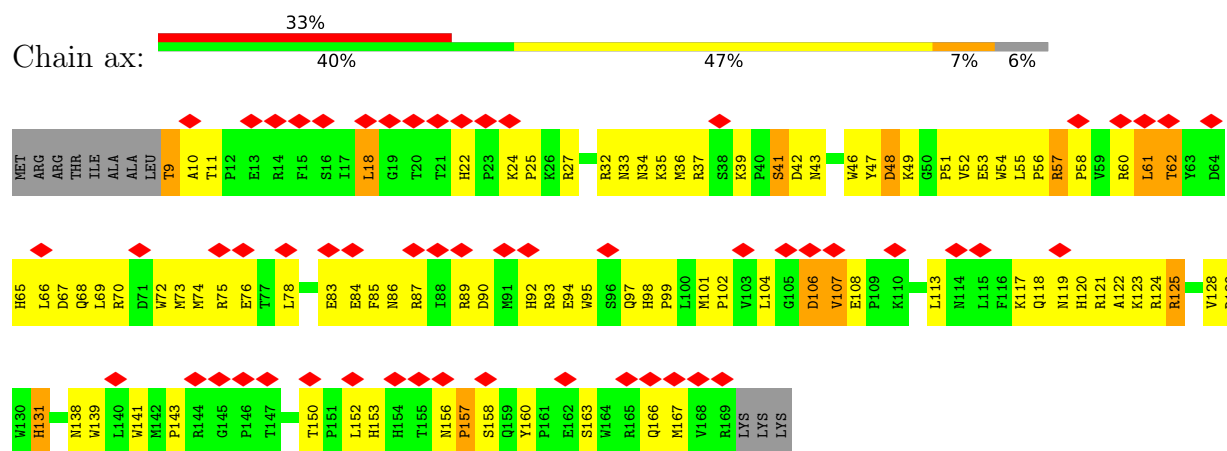
- Molecule 7: mS72



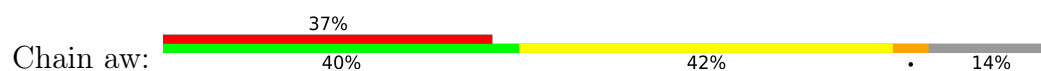
- Molecule 8: mS71

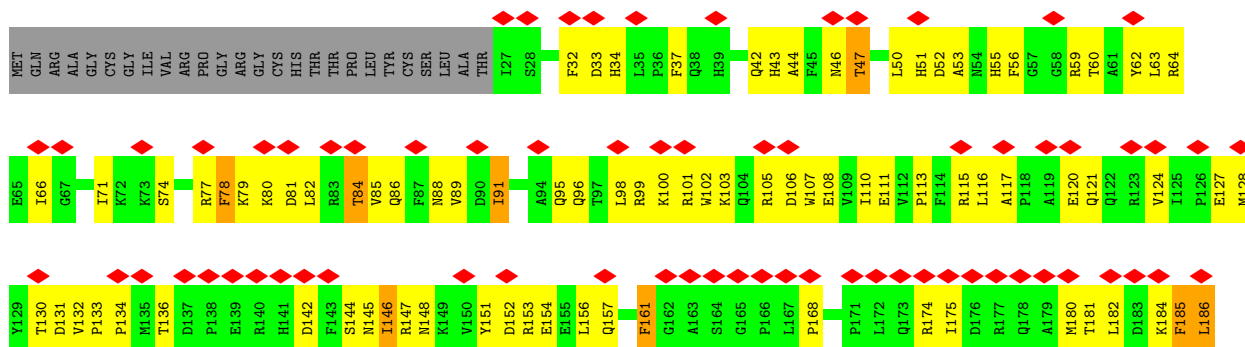


- Molecule 9: mS70

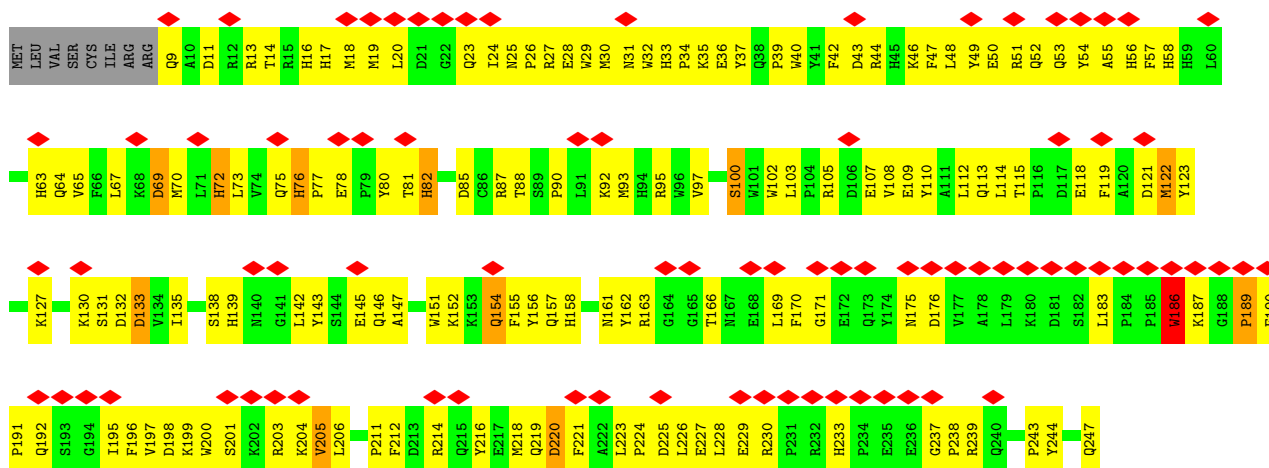


- Molecule 10: mS69

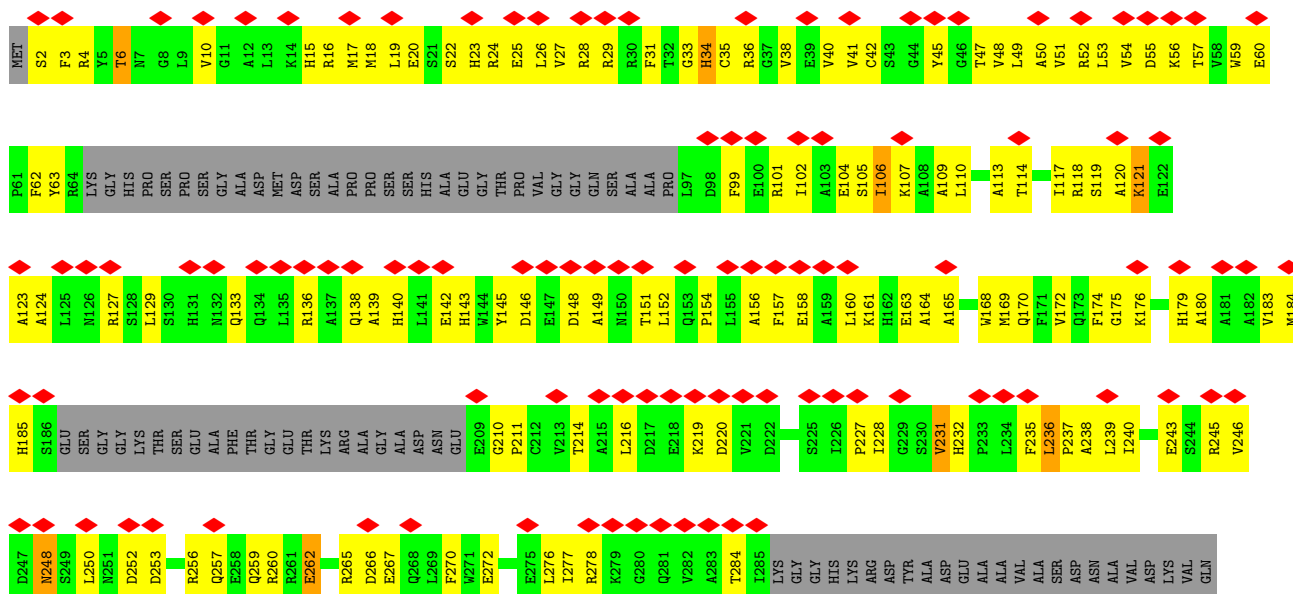


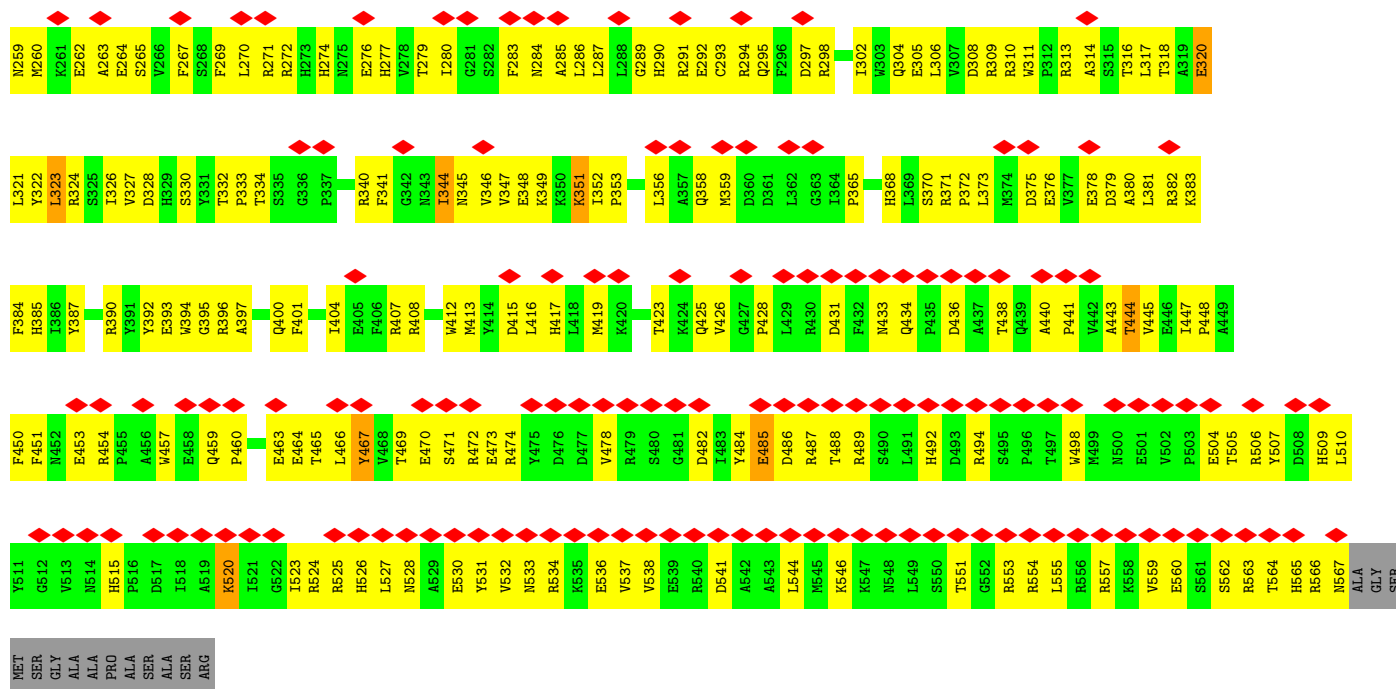


• Molecule 11: Rhodanese domain-containing protein

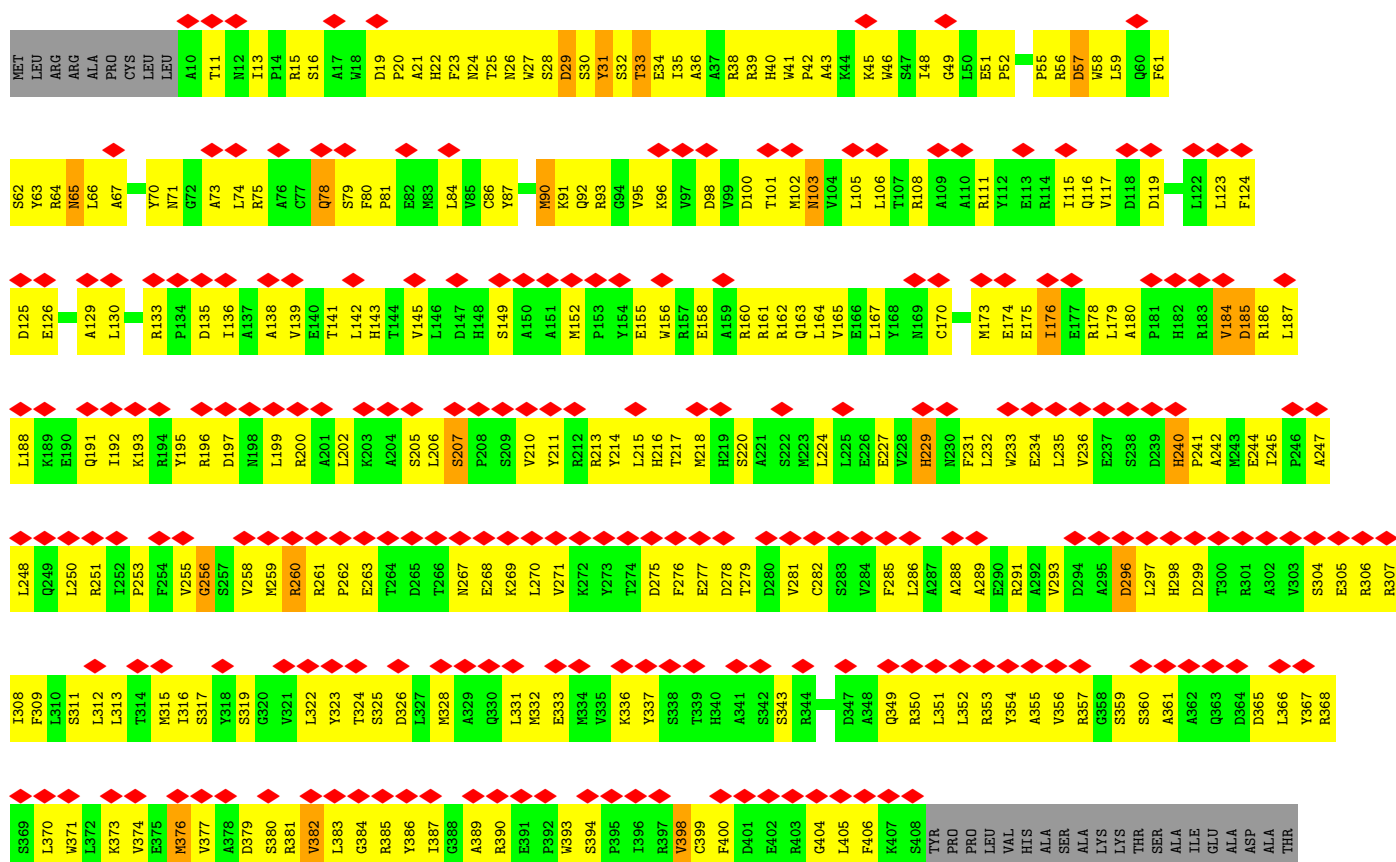


• Molecule 12: mS58

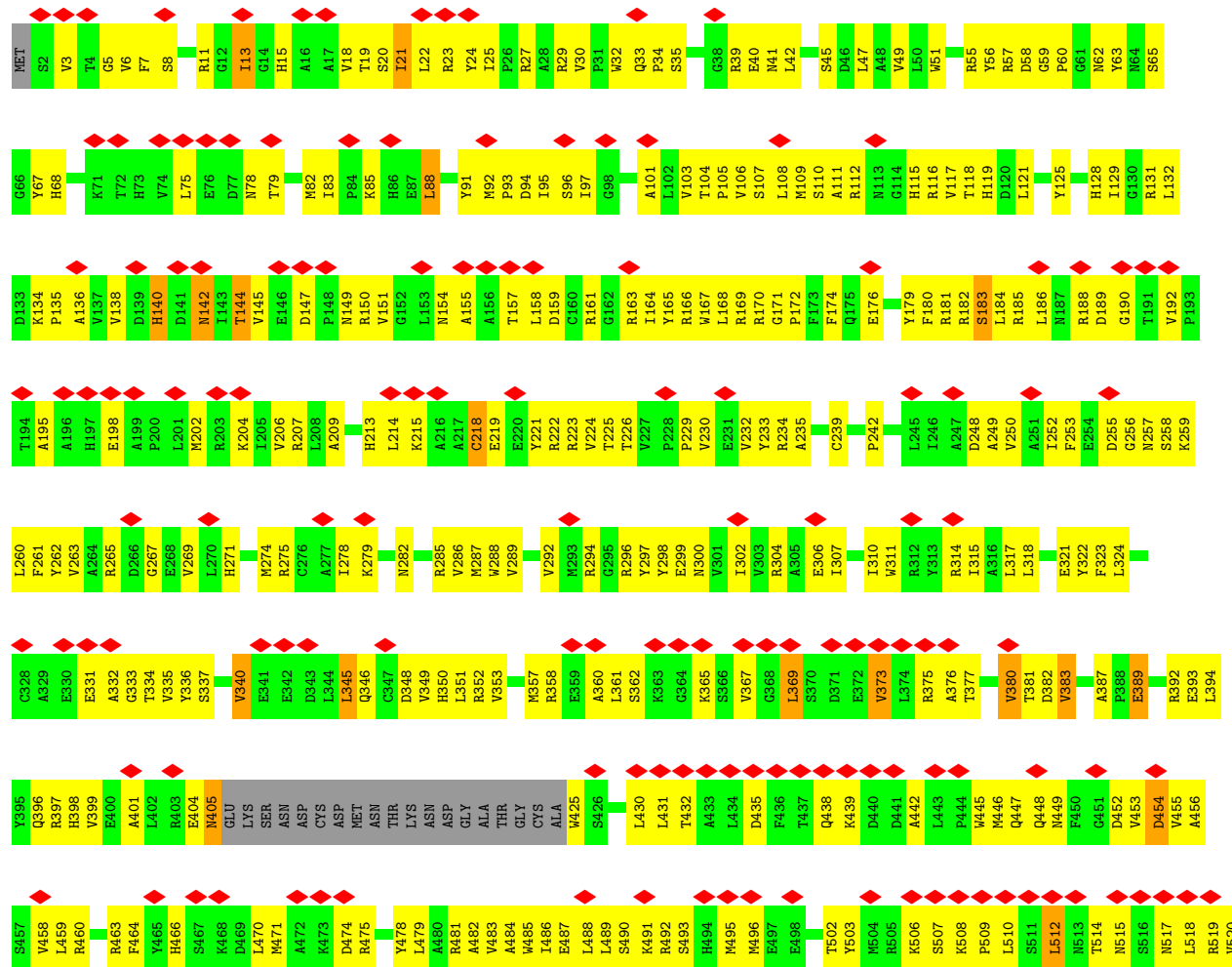


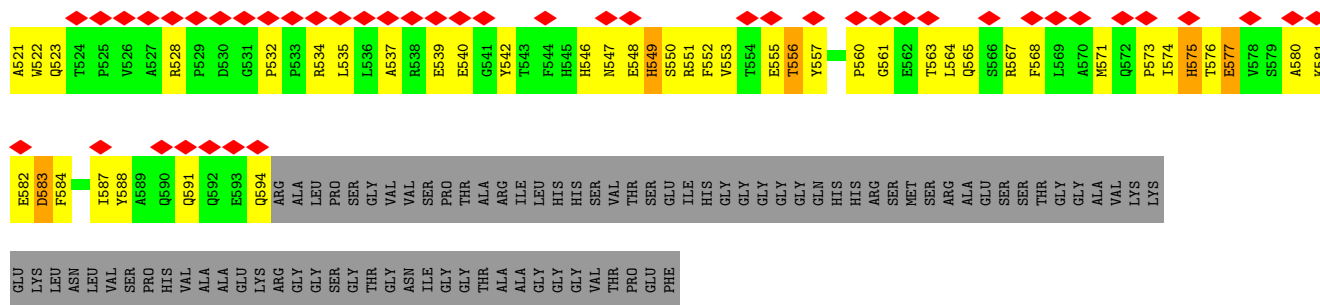


• Molecule 15: mS54



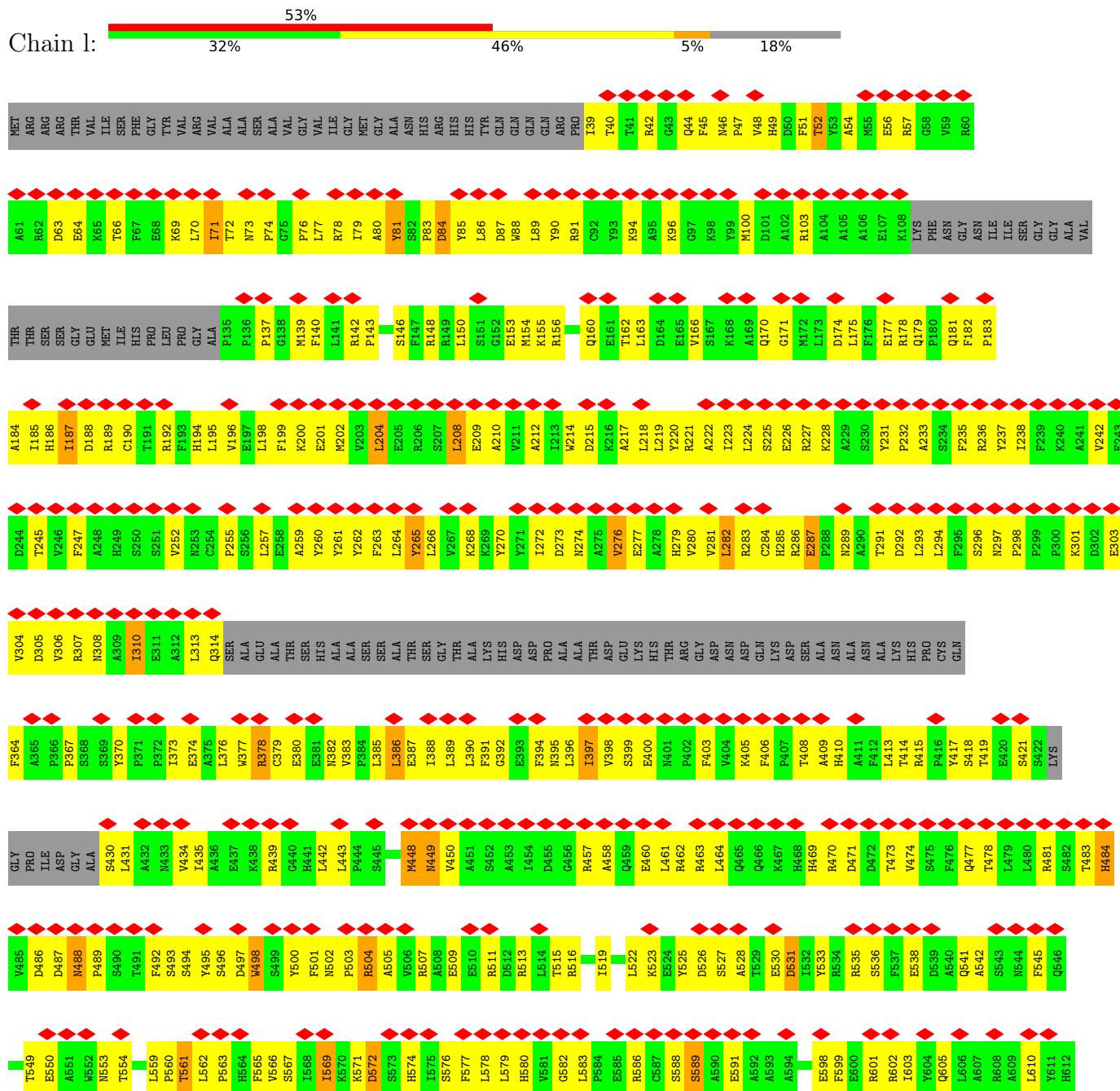
- Molecule 16: mS53

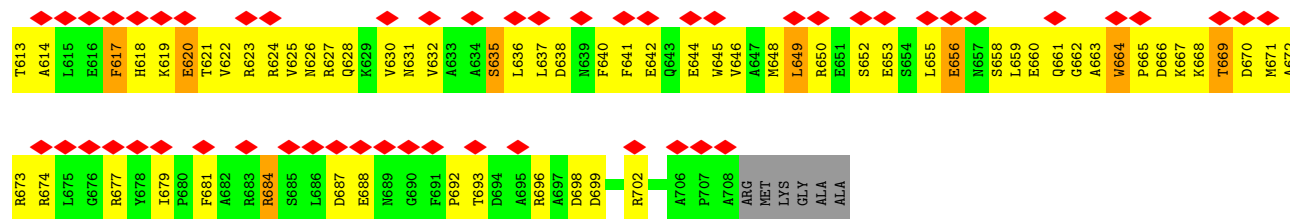




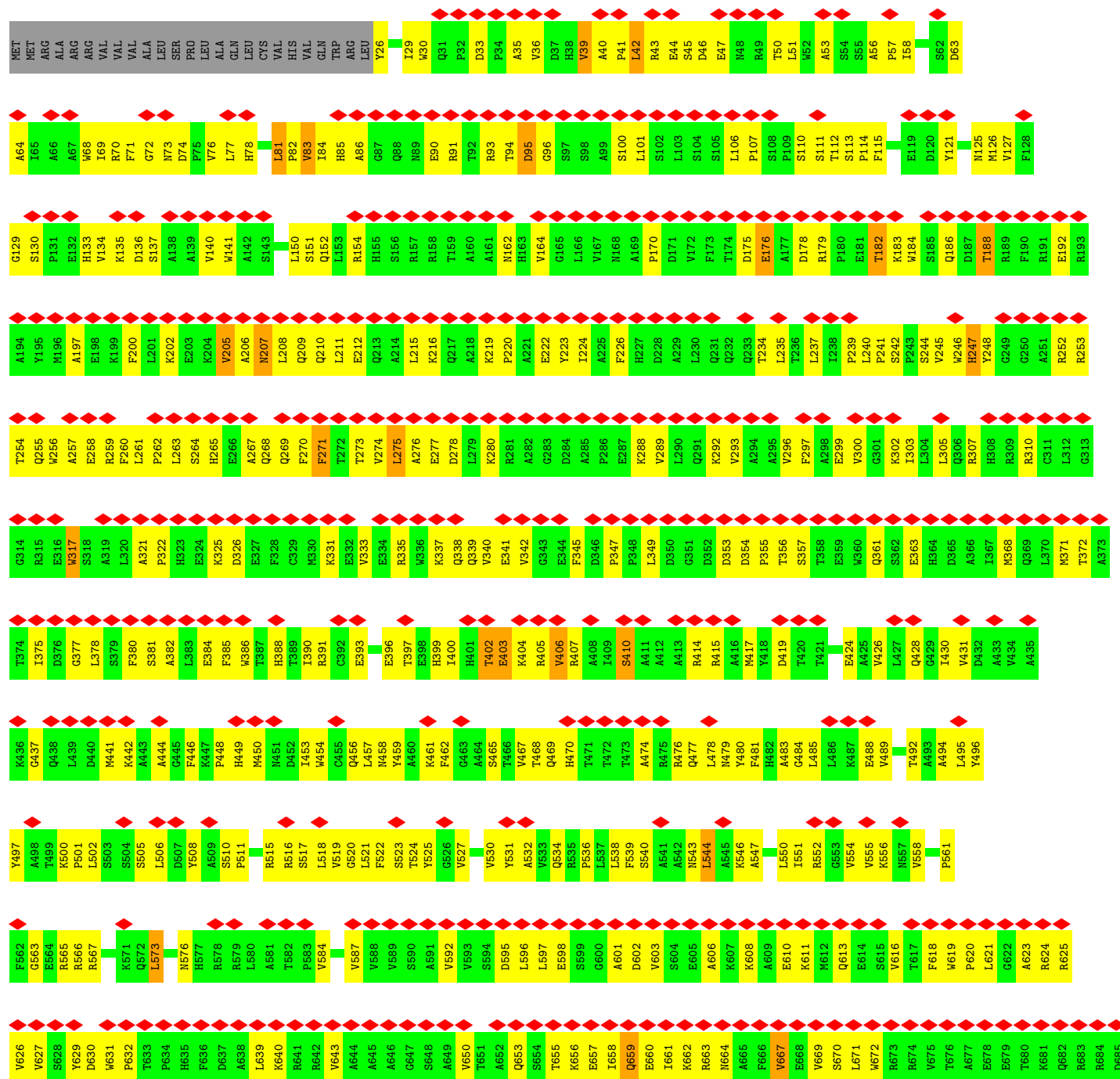
● Molecule 17: mS52

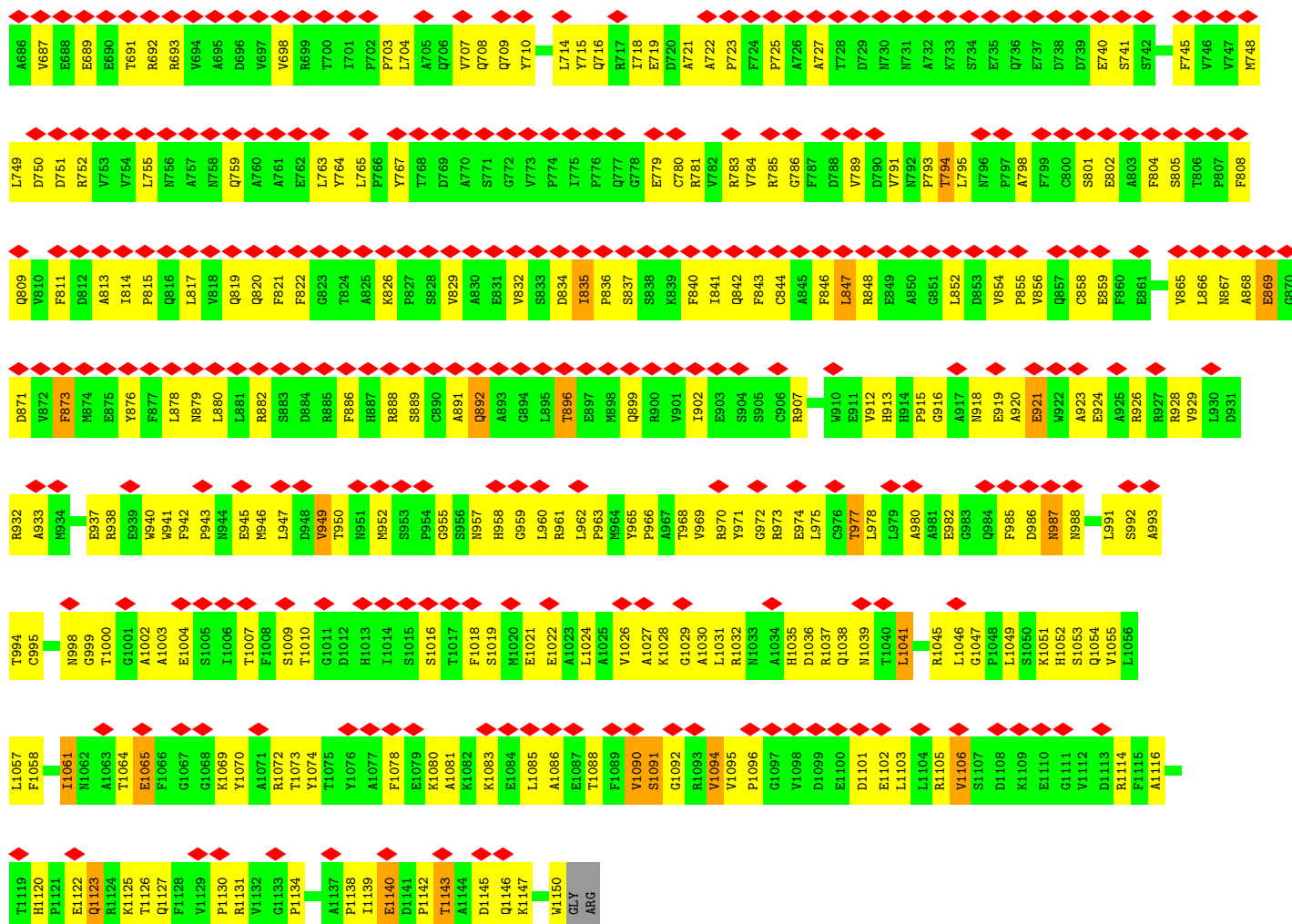
Chain 1:





• Molecule 18: mS50





• Molecule 19: mS49

Chain ab:



MET	ILE	ARG	ASN	ARG	THR	D66	W67	A68	T69	G70	M71	Q72	H73	E74	L75	F76	G77	E78	T79	D80	P81	L82	G83	G84	Q85	K88	D89	Y90	R92	D93	P94	A95	R96	S99	Y102	A103	P104	R105	N106	F107	A108	E109	G110	G111	A112	I113	S114	Y115	H116	H117	A118	Q119	S120	P121	M122	E123
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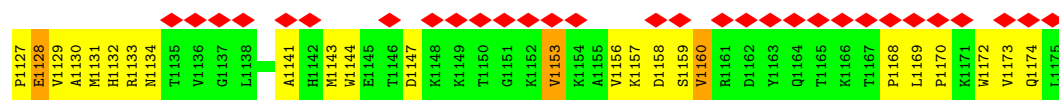
SER	LEU	ASN	SER	THR	D66	W67	A68	T69	G70	M71	Q72	H73	E74	L75	F76	G77	E78	T79	D80	P81	L82	G83	G84	Q85	K88	D89	Y90	R92	D93	P94	A95	R96	S99	Y102	A103	P104	R105	N106	F107	A108	E109	G110	G111	A112	I113	S114	Y115	H116	H117	A118	Q119	S120	P121	M122	E123
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Y124	A125	E126	A127	H128	H129	R130	R131	S132	W133	A139	R140	M141	E142	A143	A144	F145	Q146	E147	F210	R149	A150	M151	L152	R153	G154	M155	E156	S157	A158	T159	E160	R161	D162	E163	L164	A165	R166	R167	Y168	A169	A170	E171	H172	H173	V174	A175	E176	I177	V178	W179	E180	N181	Q182	L184	L185	P186	S187
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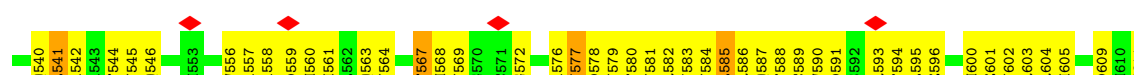
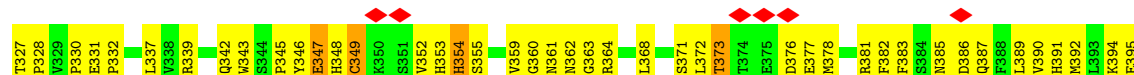
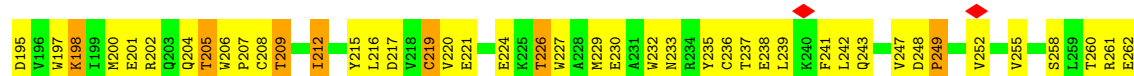
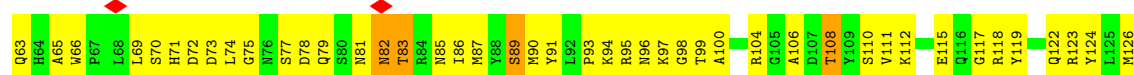
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L256	R257	E258	K259	K261	Y262	D263	F264	T265	V266	L267	Q268	R269	A270	T271	R272	L273	P274	F275	Q276	G277	Y278	D279	M280	D281	R282	F283	L284	A285	Q286	Q287	K288	G289	T290	P291	Y292	G293	A294	Q295	S296	L297	P298	P299	N300	T301	A302	S303	S304	T305	E307	E308	A309	Q310	R311	T312	L313	R314	D315
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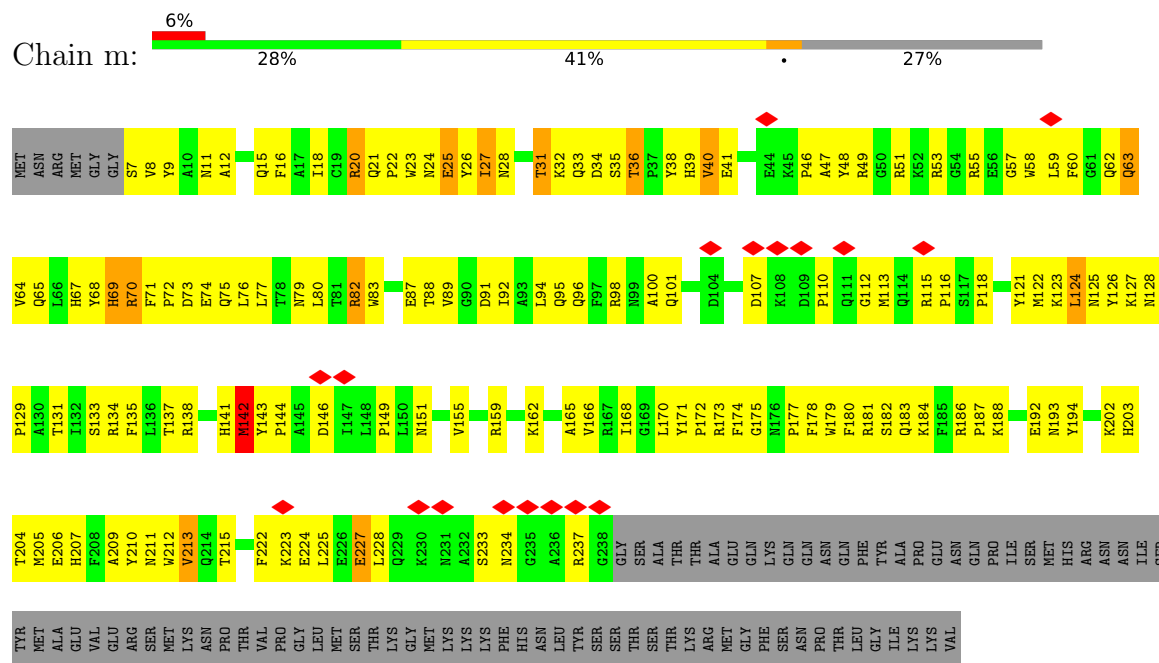
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I1002	D1003	Q1004	W1005	T1006	R1007	F1008	D1009	N1010	S1011	R1012	A1013	D1014	M1015	F1016	R1017	P1018	L1019	S1022	H1023	R1024	R1025	D1026	Y1027	I1028	H1029	G1030	G1031	M1032	W1033	H1034	R1035	Y1036	T1037	P1038	W1039	E1040	W1041	L1042	A1043	V1044	Q1045	E1046	A1047	D1048	Q1049	P1050	L1051	I1052	A1053	E1054	Q1055	T1056	R1057	E1058	E1059	E1060	R1061	A1062	P1063	R1064	L1065	R1066	R1067	A1068
G869	L870	R871	W872	R873	A874	R875	R876	R877	W878	C879	N880	N881	A882	N883	C884	S885	R886	I887	W888	S889	S890	P891	Q892	W895	I896	W897	A898	R899	D900	R901	Q902	P903	F904	F905	N906	P907	F908	P909	R910	L911	V912	R913	V914	S915	D916	D917	E918	D919	V922	E923	E924	L927	A928	N929	I930	M931	T932	V933						
R936	E941	R942	T943	V944	G945	D946	E947	S948	R949	R950	P953	A954	S955	L956	R957	Y958	I960	D961	Y1027	I1028	S963	D964	E968	K969	S970	S971	K972	G973	E974	F976	L977	D978	K979	Y980	T981	R982	A983	R984	T985	S986	E987	V988	A989	A990	G991	R992	Y993	T996	K997	Q998	I999	T1000	E1001											
G809	R810	Y811	E812	L813	E814	L815	L816	P817	R818	R819	W820	N821	H822	N823	C824	S825	Y826	G827	I828	C829	D830	Y831	A832	Y833	N834	R835	C836	N837	Y838	I839	E840	T841	Q842	D843	W844	I845	E846	E847	E848	Q849	A851	S852	C853	E854	E855	G856	W857	P858	T861	H862	A863	D864	G865	R867	A868									
L749	T750	W751	S752	A753	K754	A755	F756	E757	R758	E759	L760	A761	A762	A763	K764	G765	N766	T767	S768	H769	I770	I771	W772	W773	E774	G775	Q776	A777	R778	Q779	L780	R781	R782	D783	S784	E785	R786	F787	V788	W789	F790	L791	S792	V793	R794	L795	E796	S797	Q798	E799	W800	L801	D802	H803	T804	D805	E806	A807	F808					
T687	A688	E689	E690	R691	A692	N693	Y694	Q695	E696	Y697	V698	K699	E700	Q701	T702	S703	K704	Q705	L706	G707	E708	W709	A712	R715	R716	R717	W718	T719	P720	R721	R722	Q723	Q724	W725	N726	G727	H727	V728	V729	A730	Q731	G732	Y733	E734	V735	T736	V737	V738	D739	L740	E741	H742	A743	D744	T745	A746	V747	V748						
D627	E628	M629	G630	T631	A632	D633	T634	R635	E636	N637	V638	L639	S640	S641	R642	Y643	F644	Q645	G646	L647	L648	M650	E651	G652	F653	Q654	N655	R656	L657	G658	R659	A660	F661	M662	Q663	N664	V665	S666	G667	K668	A669	P670	E671	P672	V673	Q674	Q675	V676	M677	Q678	P679	E680	V681	L682	P683	R684	H685	F686						
D566	E567	I568	C569	E570	R571	T572	F573	F574	D575	E576	R577	E578	L579	H580	R581	P582	D583	L584	E585	M586	Q587	V588	S589	G590	E591	T592	L593	R594	F597	G598	V599	Y600	M601	L602	P603	S604	P605	T606	V607	V608	E609	A610	V611	G612	G613	A614	S615	A616	S617	V618	N619	L620	H621	E622	F623	P624	L625	A626						
L437	M438	F441	D442	I443	A444	R445	R446	E447	D448	R449	L450	S451	K452	G453	E454	Q455	D456	L457	T458	E459	R460	S461	V462	M463	H464	F465	G466	V467	Q470	I473	D474	E475	F476	V477	F478	R479	H480	R481	M482	G485	E486	R487	P488	L489	Y491	P496	G497	A498	R499	D500	E501	R502	L503											
N504	R505	M506	Y507	R508	D509	V510	E511	G512	F513	S514	L515	K516	Q517	Q518	R519	P520	E521	F522	L523	E524	W525	E526	L527	F528	Y531	H534	H535	Q536	Q537	R538	R539	R540	L541	A542	L543	L544	H545	G546	L547	E548	P549	V550	A551	N552	E553	T554	A555	Q556	E557	D558	A559	E560	R561	E562	E563	K564	L565							
R377	Q378	G379	A380	L381	V382	Q383	D384	G385	G386	P387	D388	K389	R390	T391	K392	K393	K394	H395	V396	N397	D398	R399	R400	I401	M402	D403	A404	M405	F406	F407	R408	S409	D410	A411	Y412	R413	K414	T415	Q416	T417	D418	E419	H420	W421	M422	F423	Y424	M425	R426	Q427	D428	T429	T430	H431	E432	V433	A434	H435	L436					
P316	T317	A318	T319	V320	P321	S322	F323	E324	A325	I326	S327	K329	A330	F331	R332	N334	T335	V336	R337	D338	H339	P340	T341	E344	E345	L346	T347	Q348	E349	V350	V351	D352	T353	I354	R355	T356	S357	R358	E359	A360	S361	E362	K363	Q364	R365	E366	Q367	E368	R369	A370	Q371	F372	G373	L375	G376									



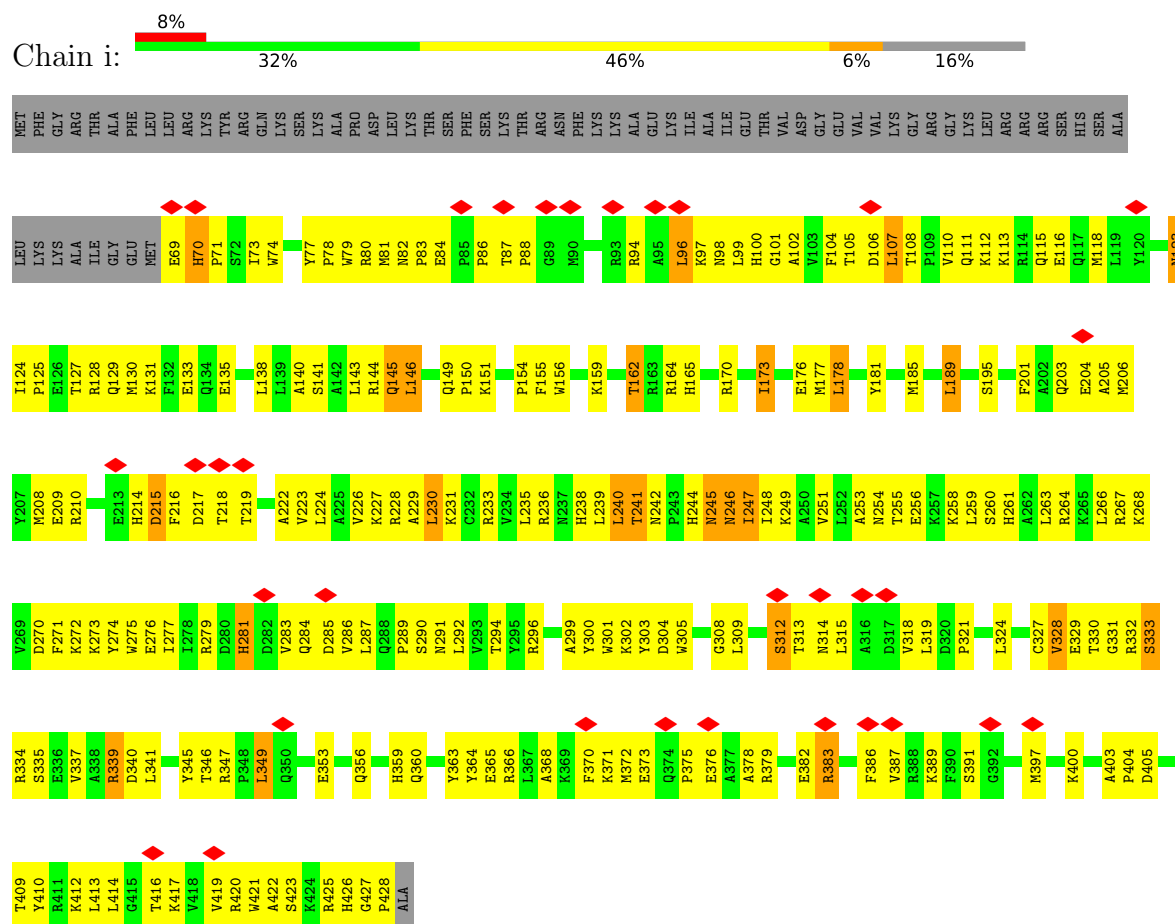
• Molecule 20: mS51



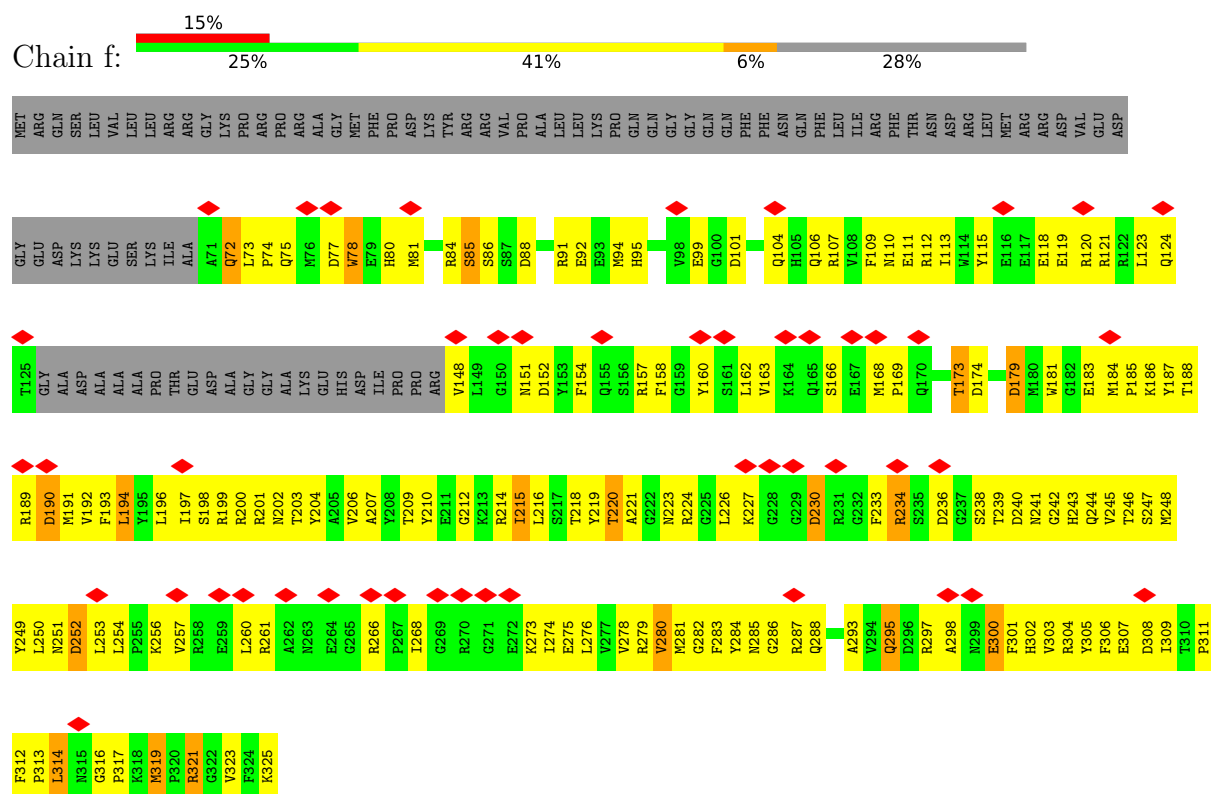
- Molecule 21: bS18m



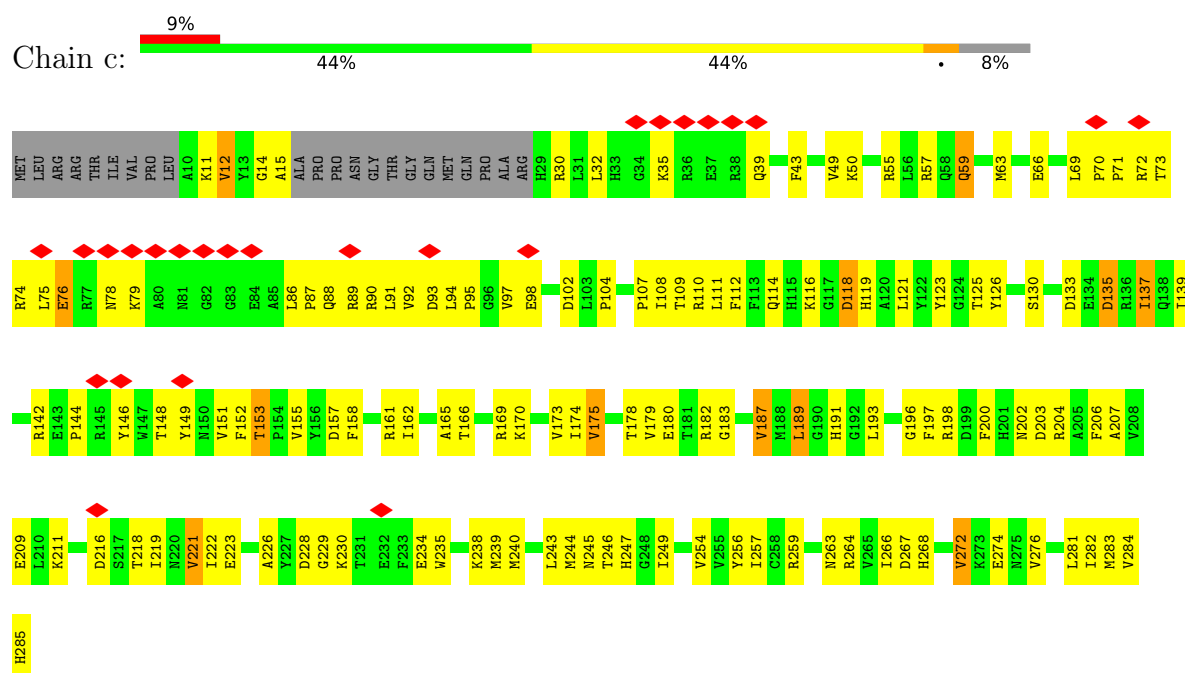
- Molecule 22: uS15m



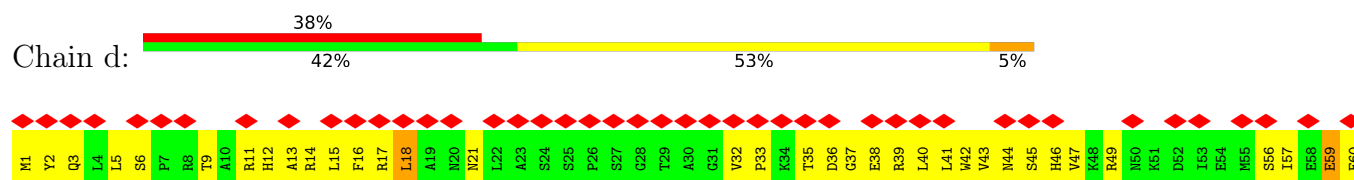
- Molecule 23: uS11m

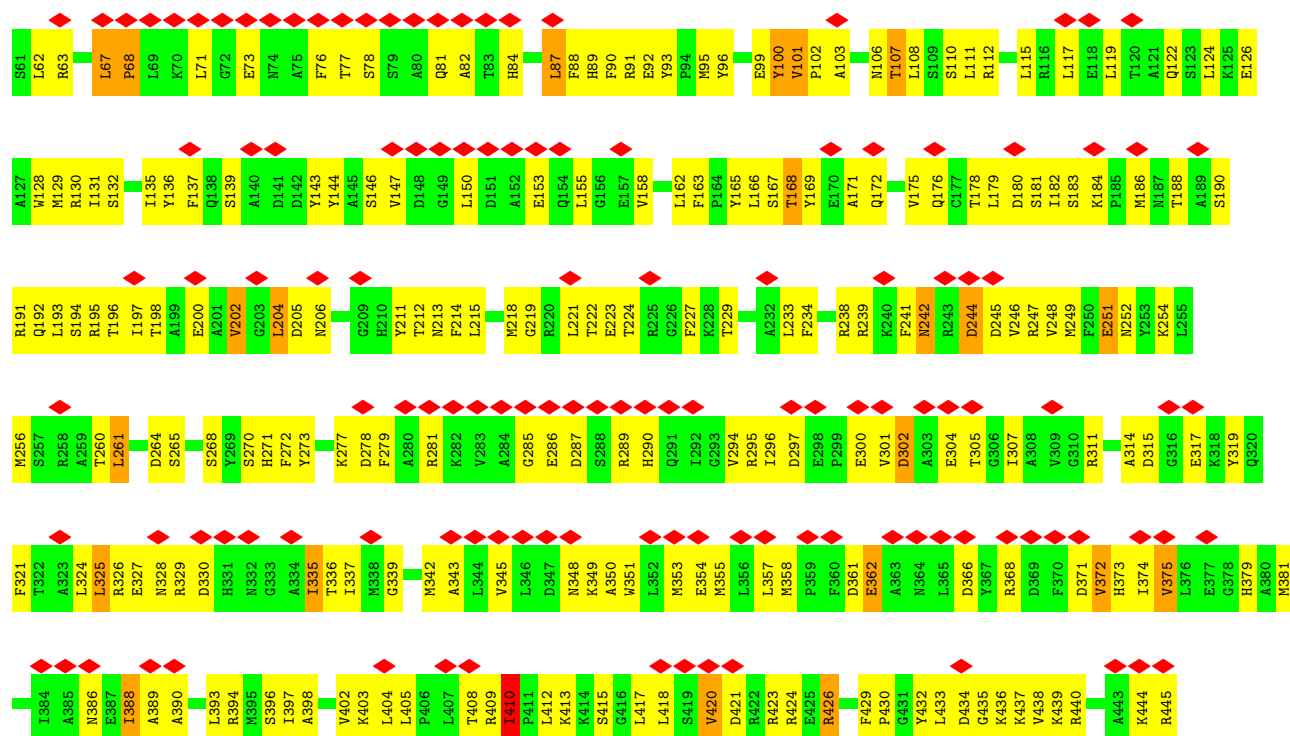


• Molecule 24: uS8m

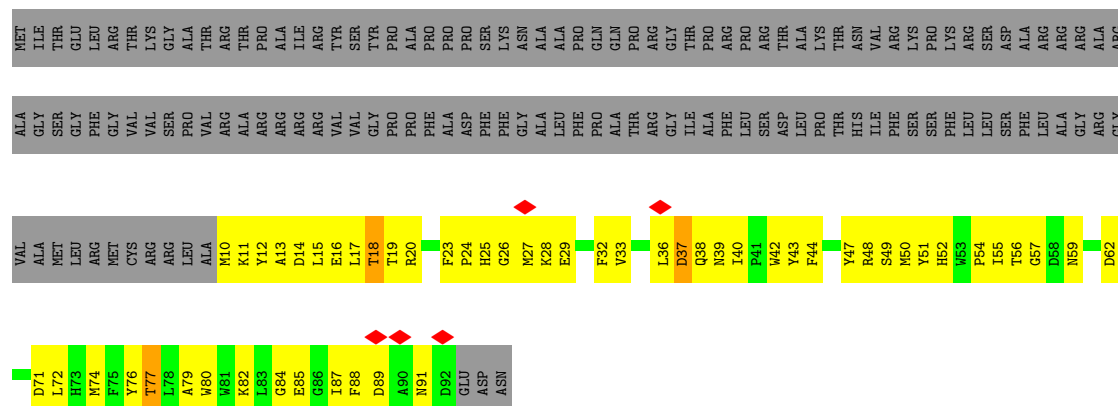


• Molecule 25: uS9m

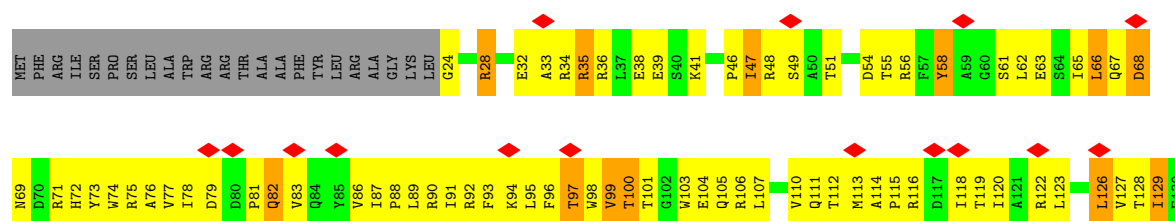


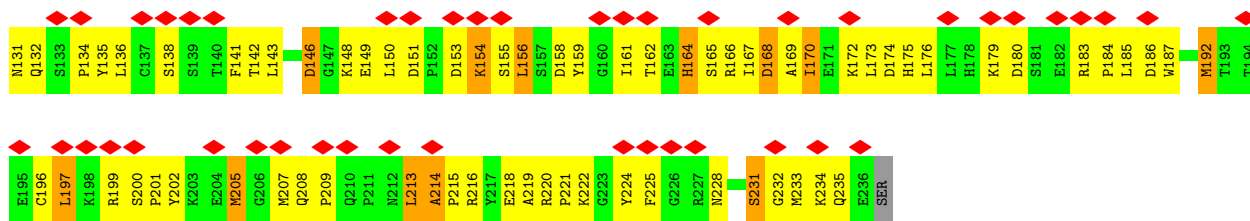


• Molecule 26: mS73

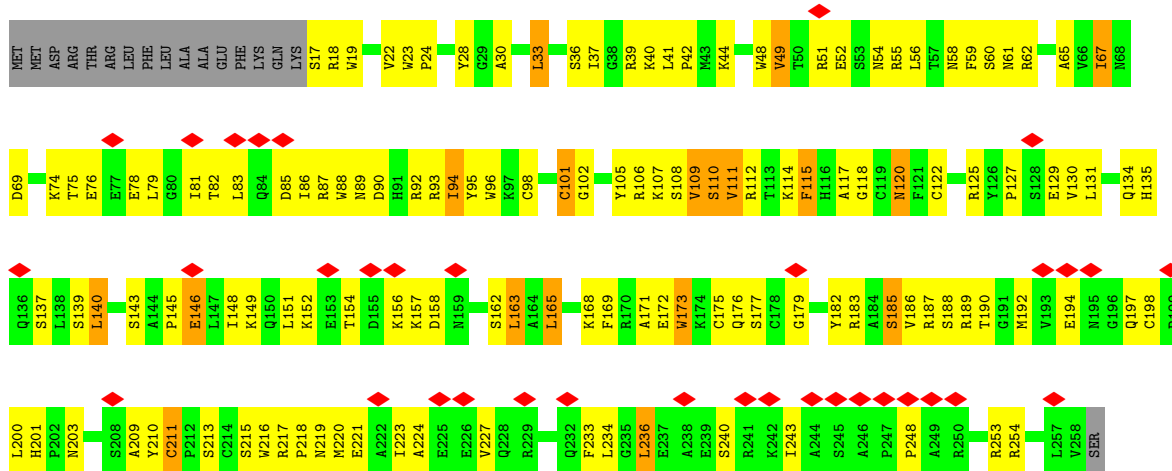
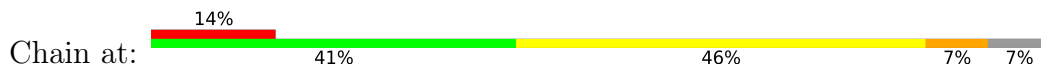


• Molecule 27: mS68

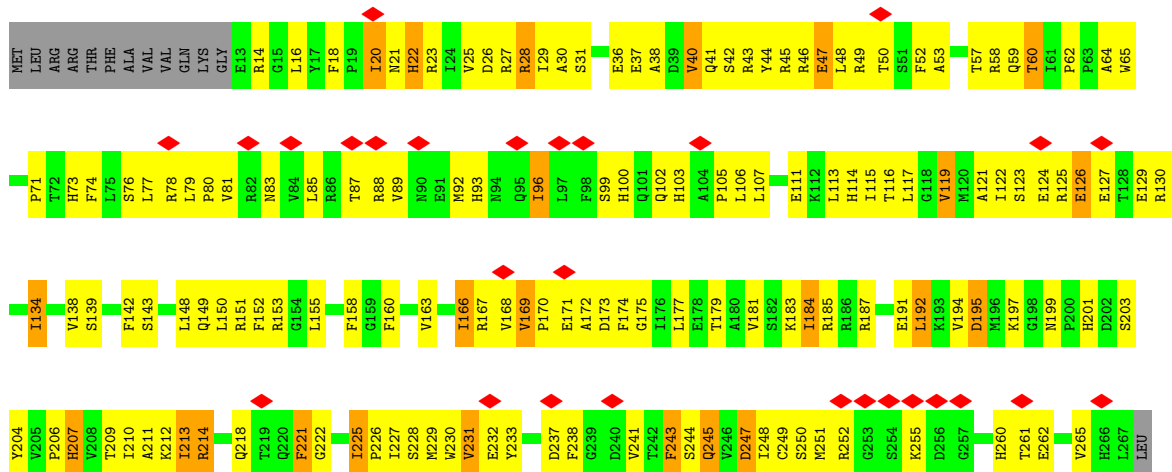




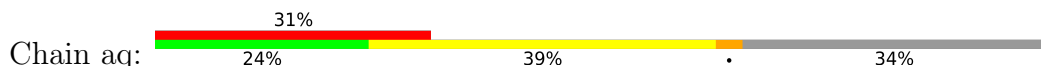
• Molecule 28: mS66

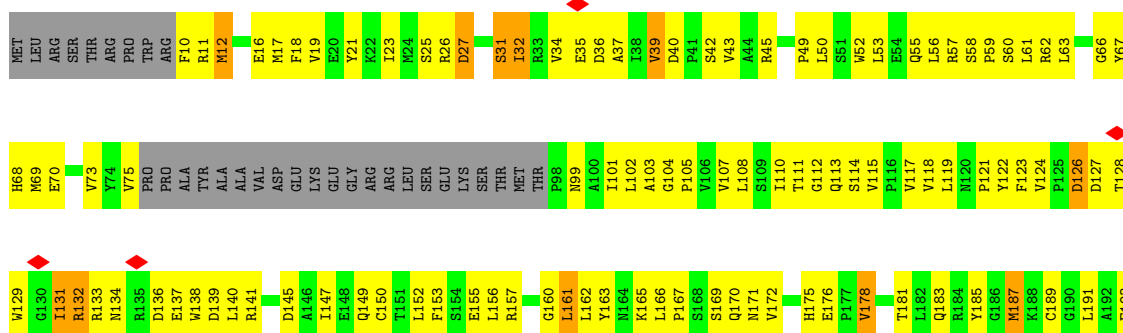


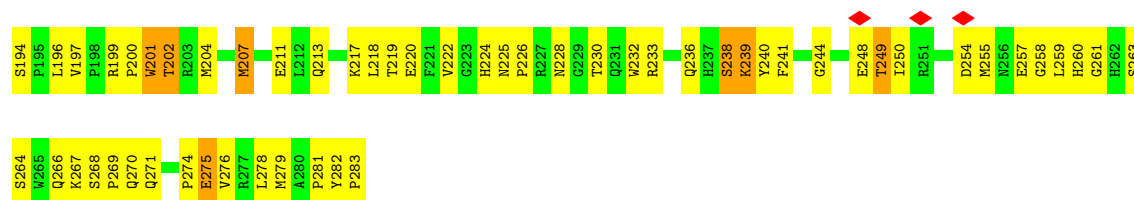
• Molecule 29: AKAP7_NLS domain-containing protein



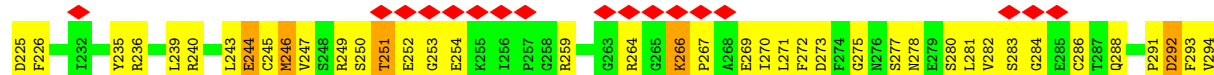
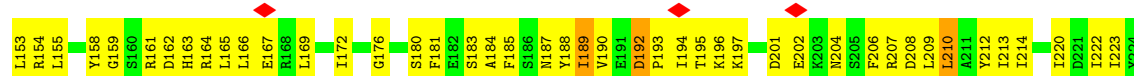
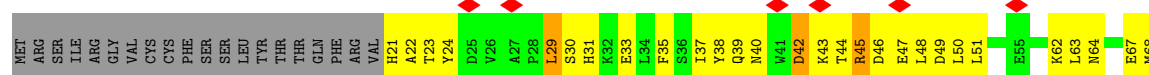
• Molecule 30: mS63



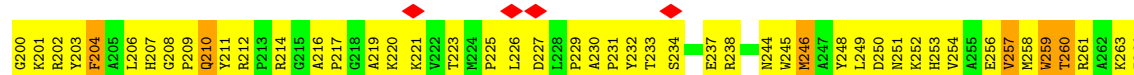
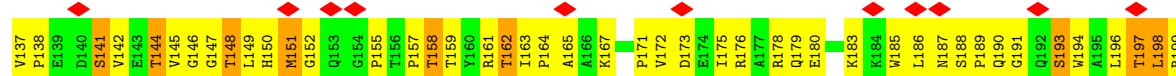




• Molecule 33: mS56

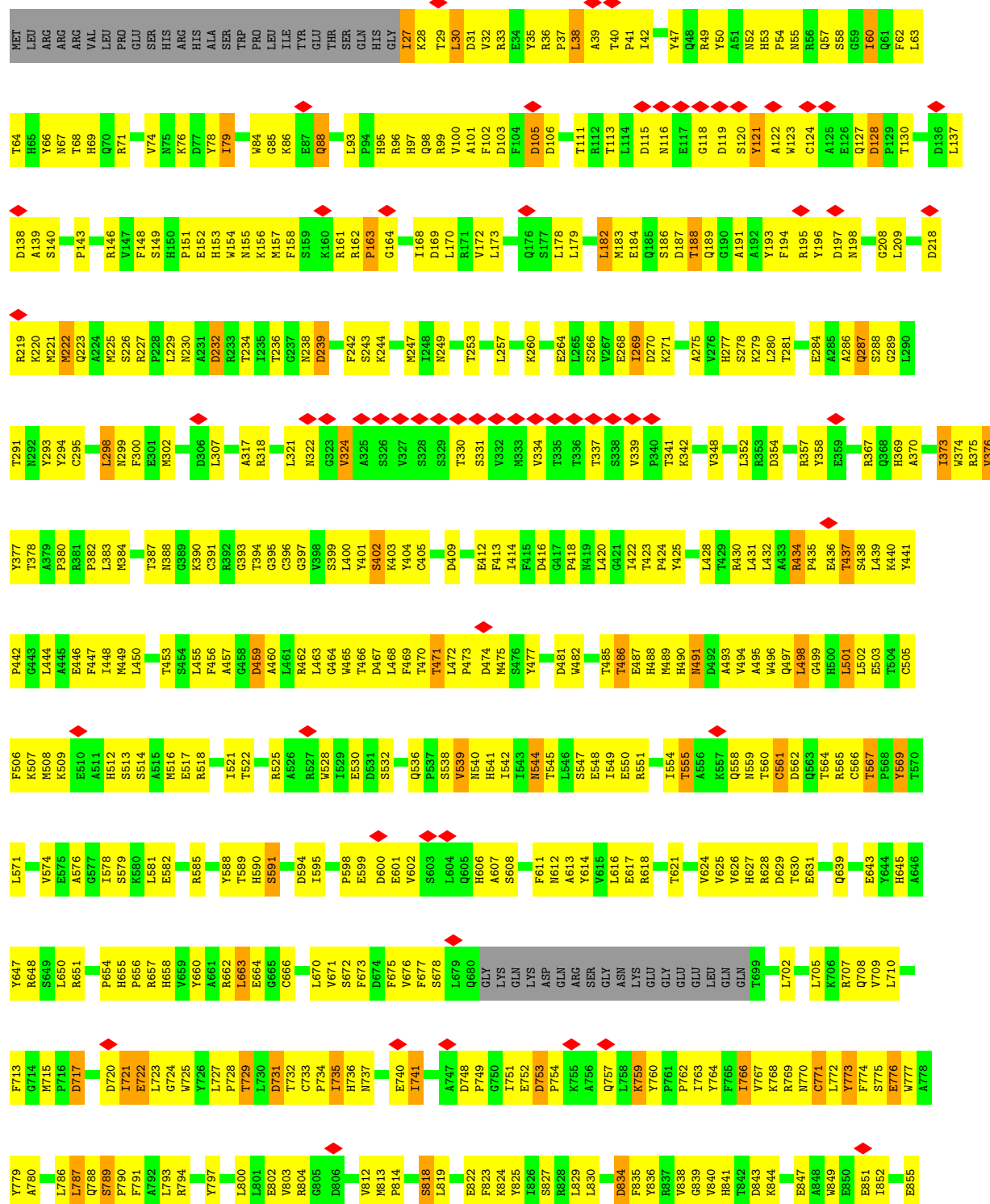


• Molecule 34: mS60

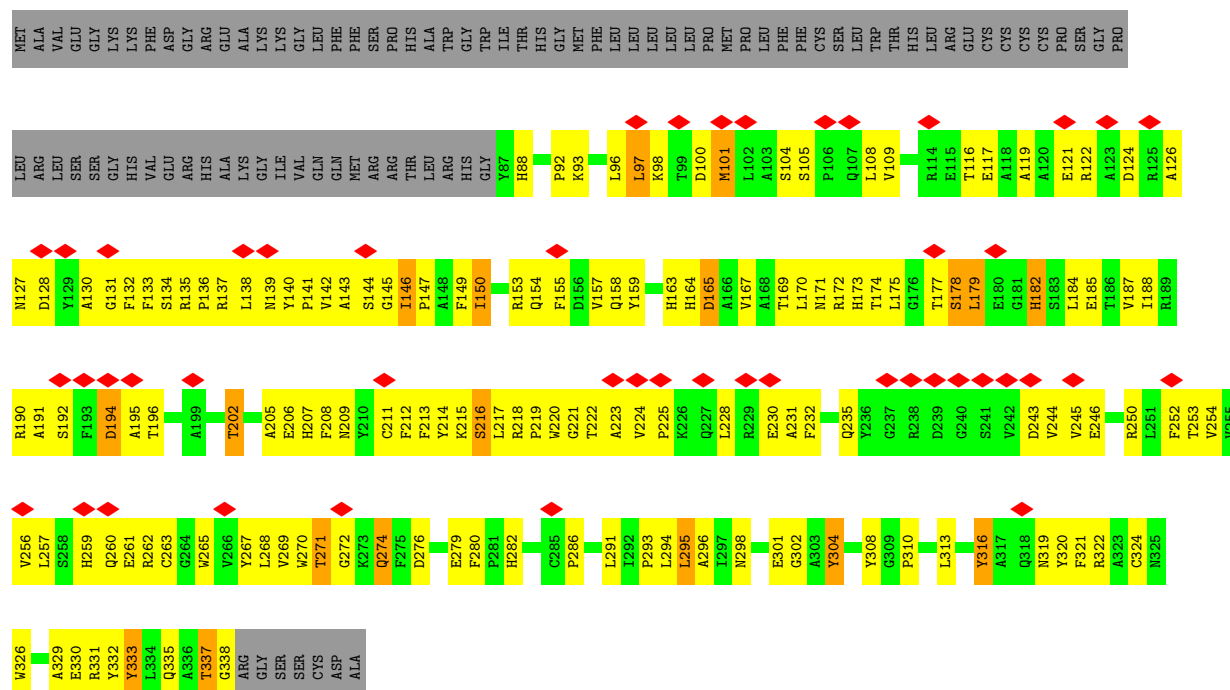




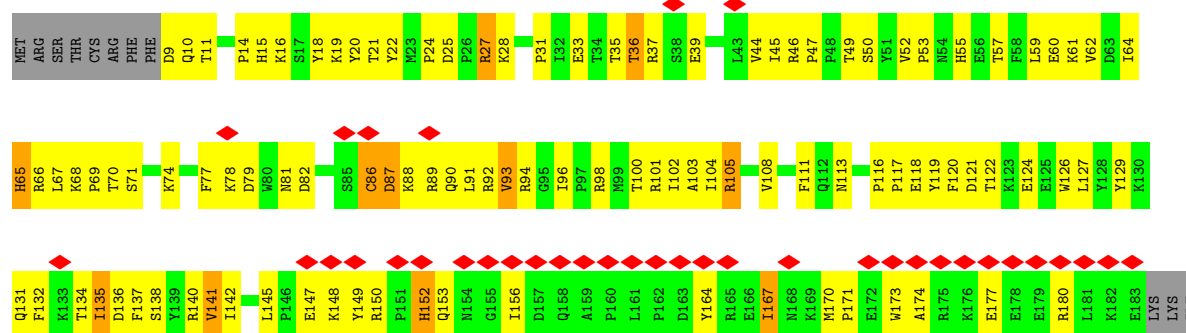
• Molecule 35: mS47



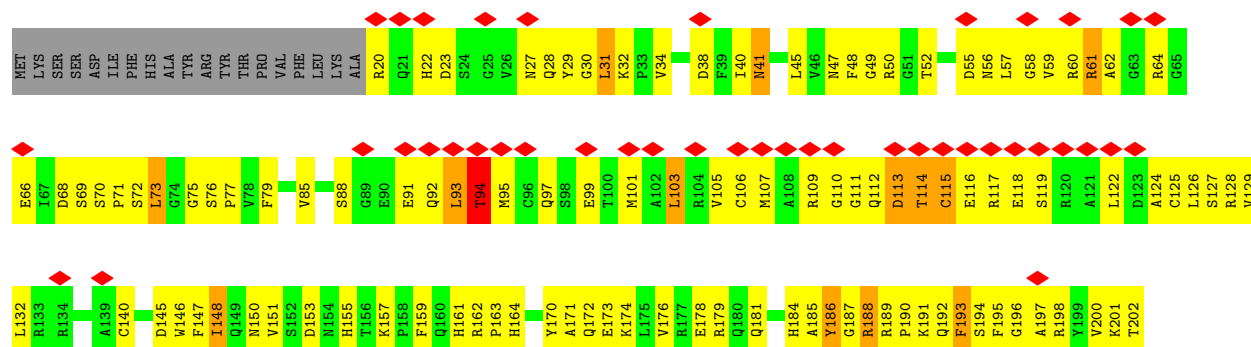




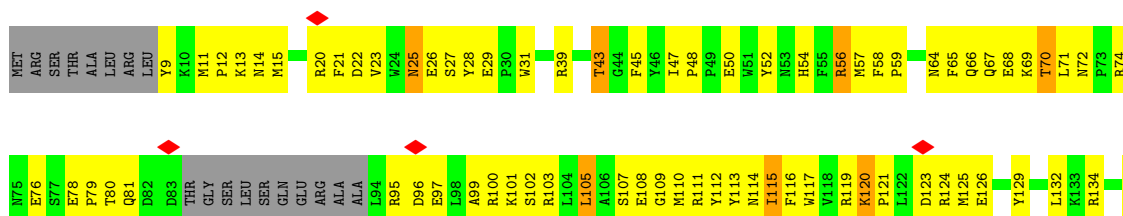
• Molecule 38: Protein FYV4, mitochondrial

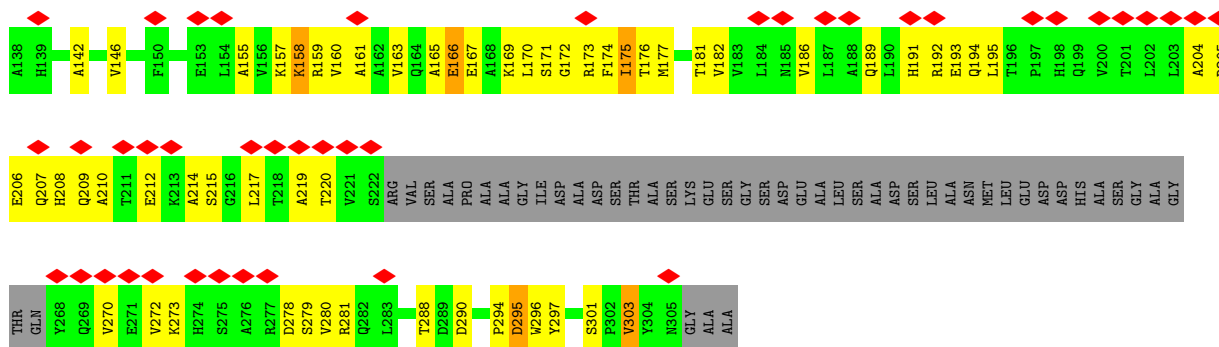


• Molecule 39: mS37

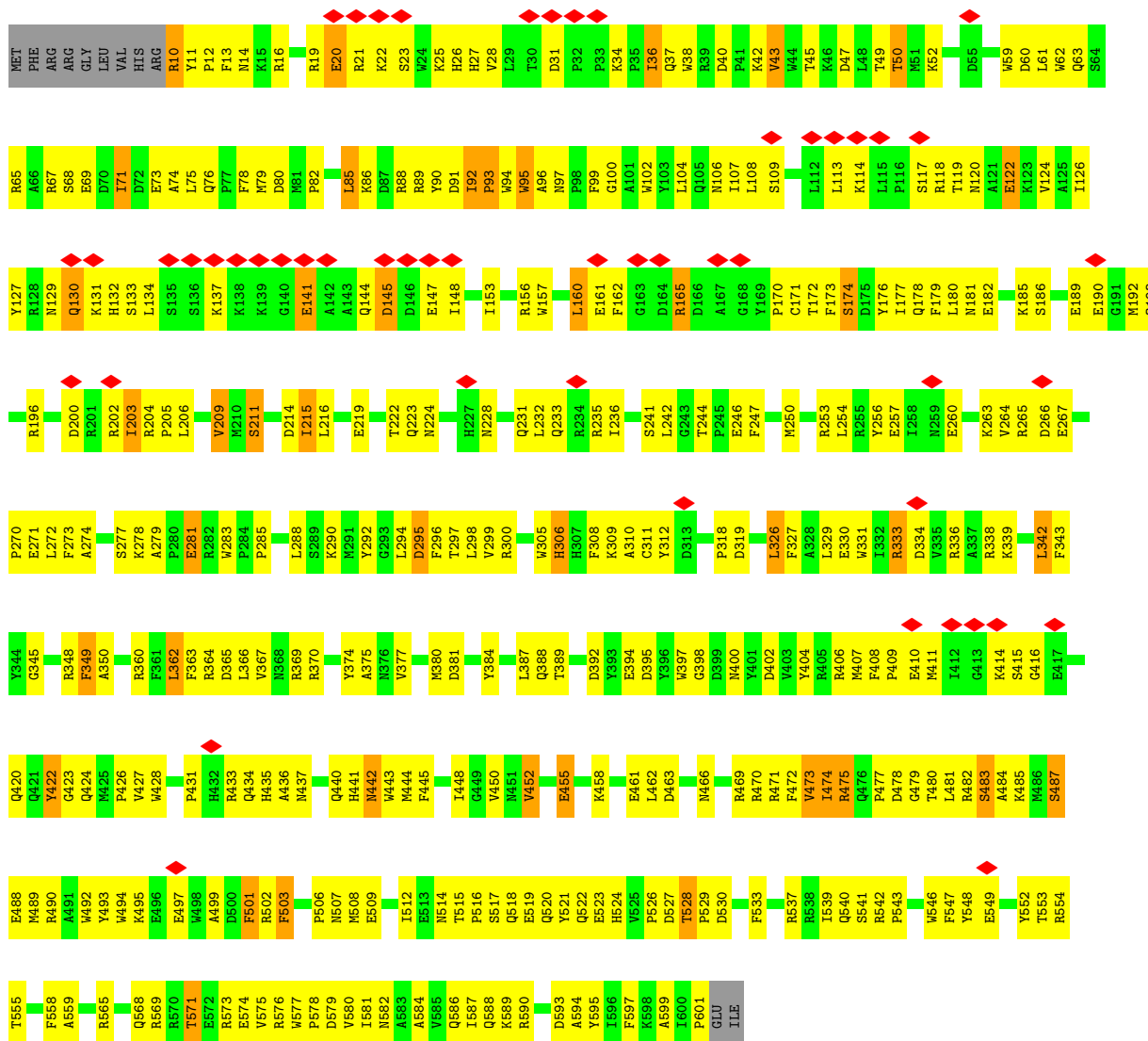


Q63	M64	I65	P66	K67	M68	L69	E70	G71	E72	R73	S74	R75	R76	E77	L78	M79	S80	R81	G82	D83	T84	E85	F86	E87	A88	L89	Y90	E91	F92	I93	A96	S97	Y98	I102	S103	G104	R105	R106	V110	Y111	D112	K113	L114	S115	E116	M117	D118	D119	T120	F121	V122	W123	T127	A128
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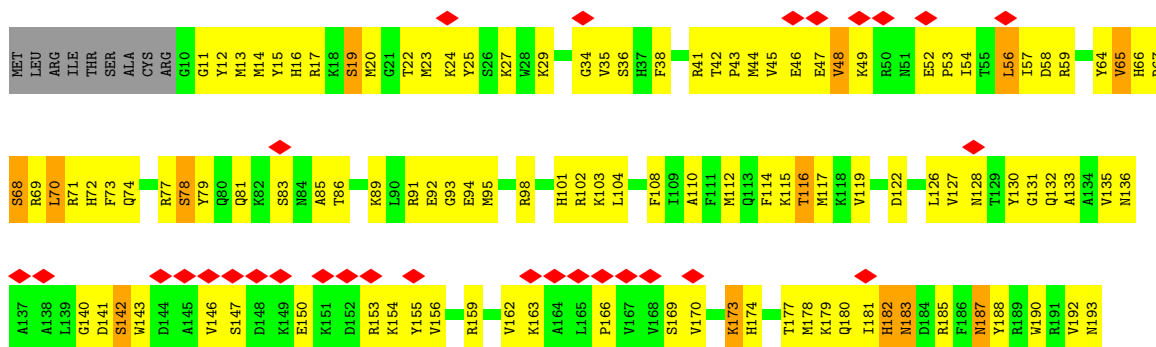


• Molecule 45: mS22

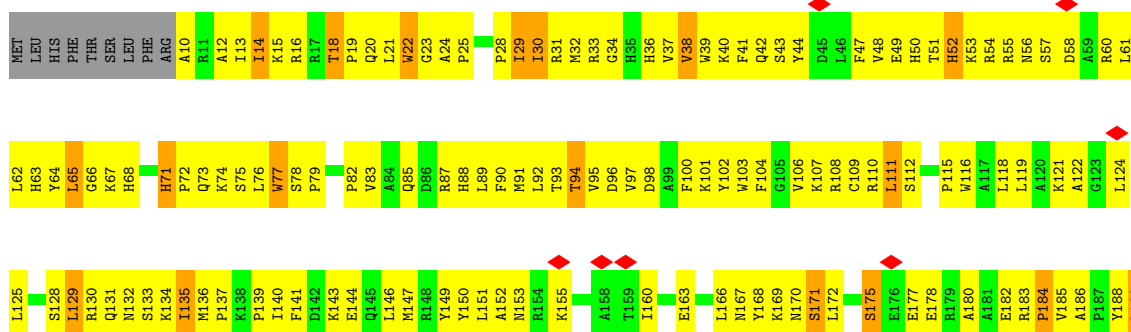


• Molecule 46: bS21m

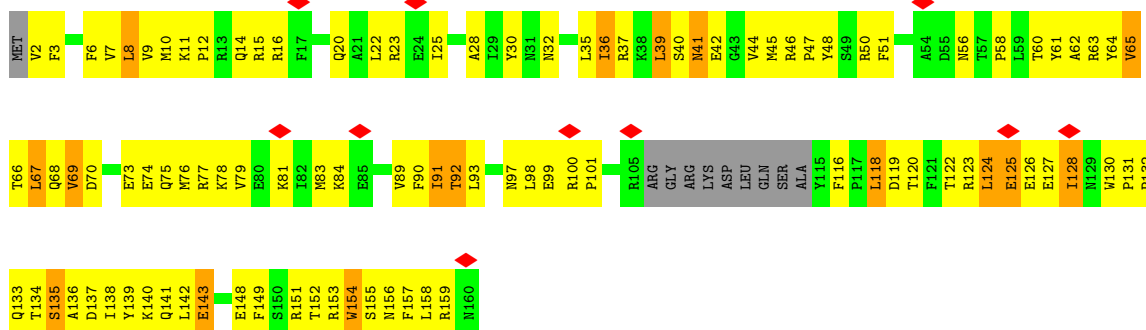




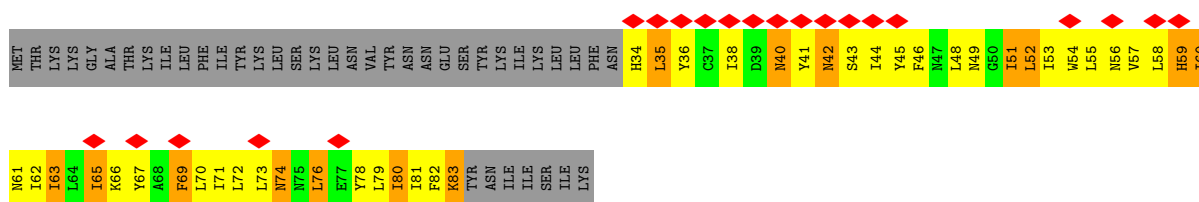
• Molecule 47: bS16m



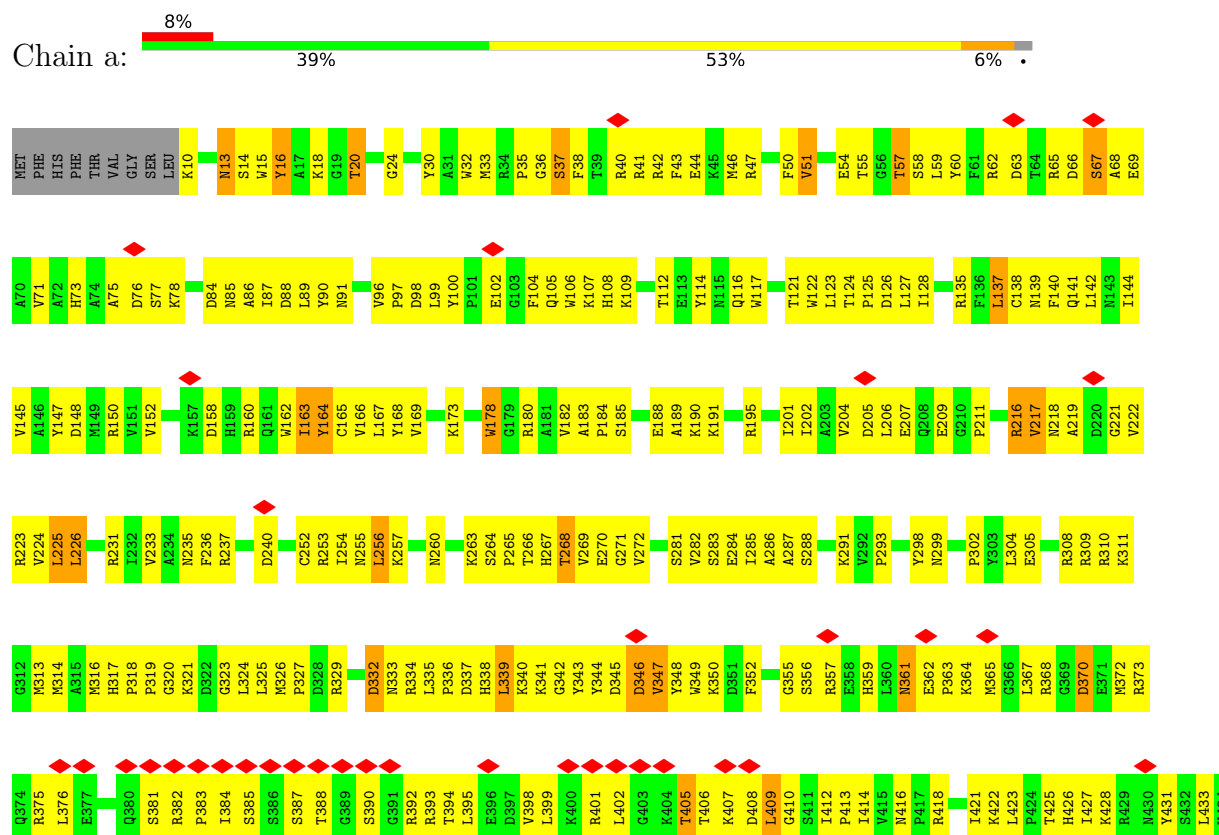
• Molecule 48: bS6m



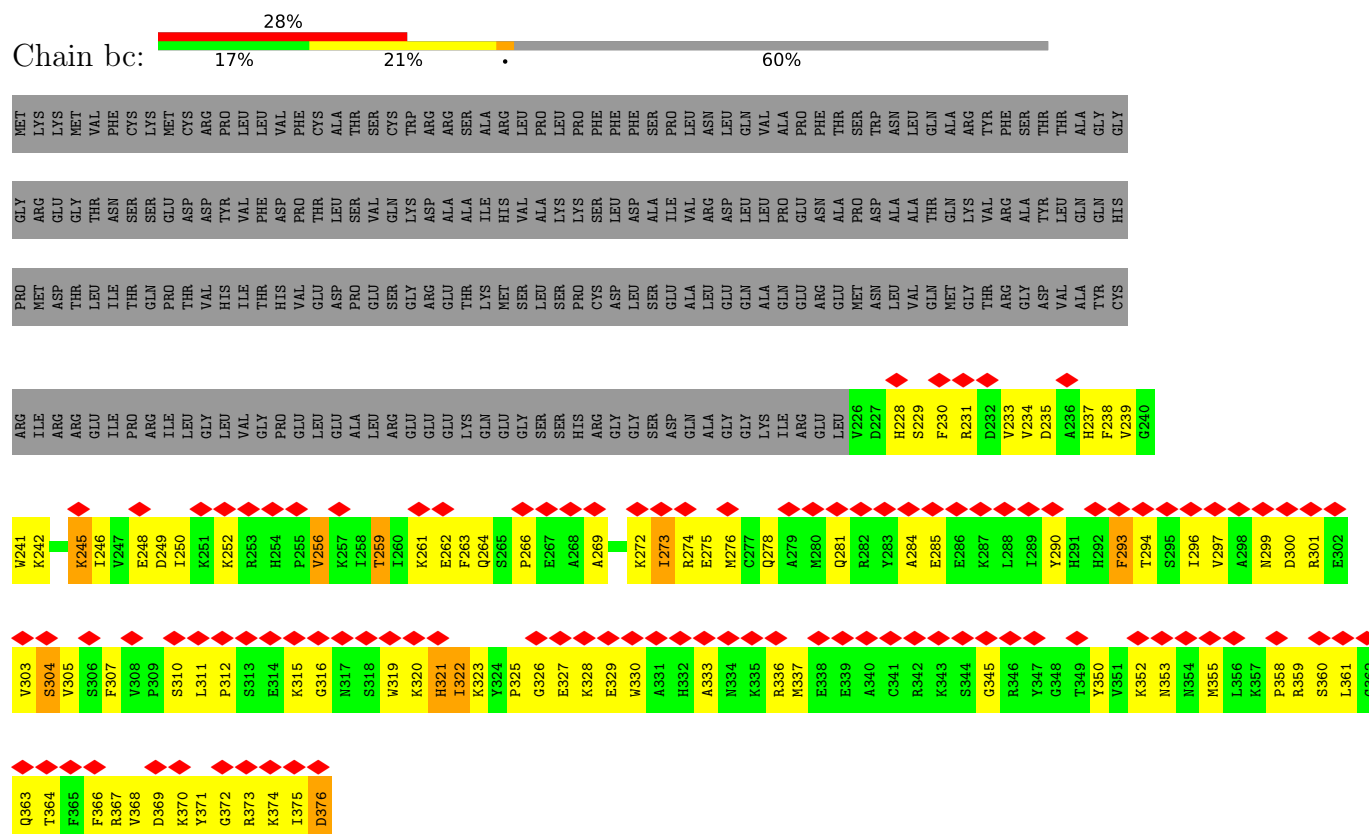
• Molecule 49: MURF5



• Molecule 50: Ribosomal_S5_C domain-containing protein



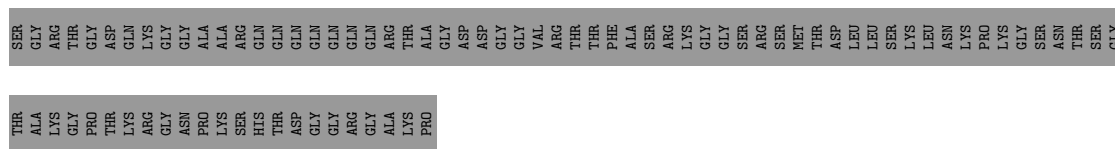
• Molecule 51: mt-iF3



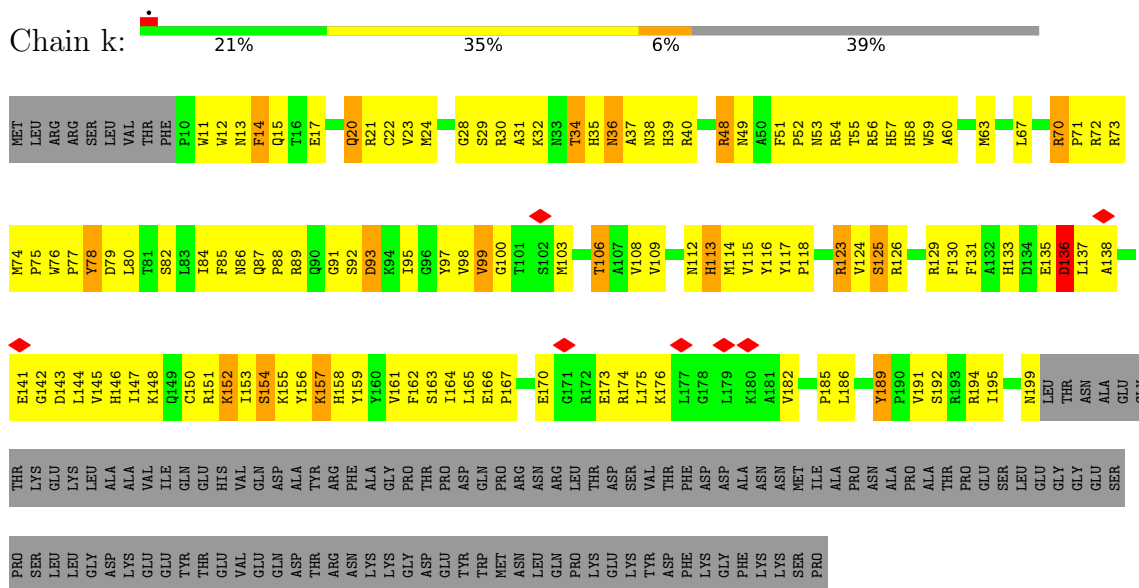
Chain aa: 14% 35% 44% 7% 15%



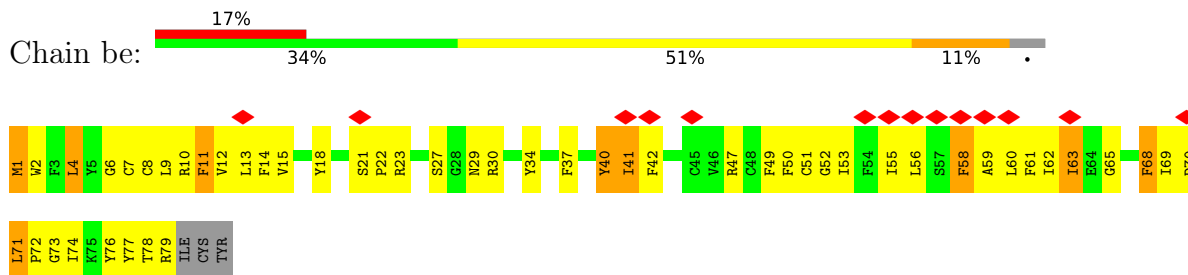




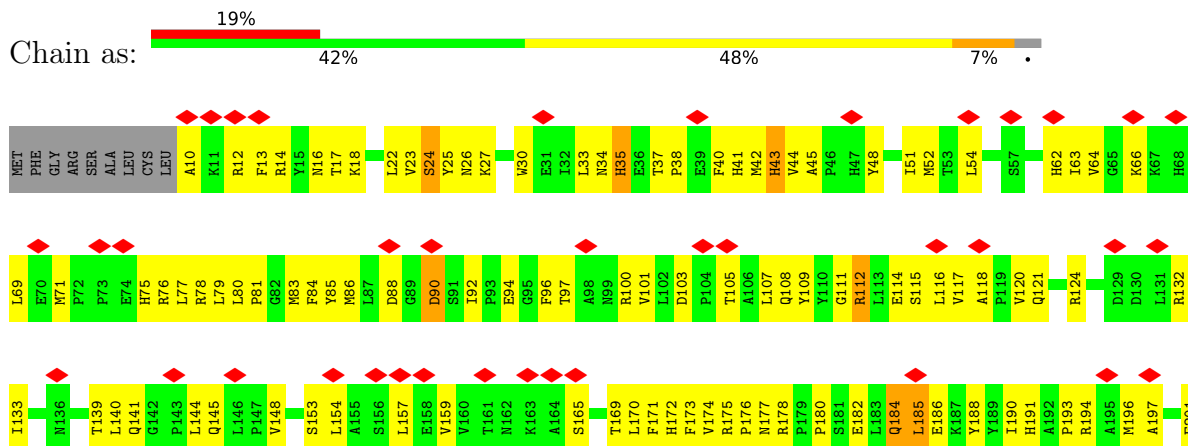
- Molecule 53: 30S Ribosomal protein S17-like protein



- Molecule 54: Ribosome protein S12



- Molecule 55: mS65



G A U U U G U G G G U U U G G A A A U U U U A A U U G U U A A U G U U A A U U U A A G A A A
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A C A U A U A A U G A U A A A A U U U A A A A U U U A A A A U U G A A C U G U A A U U A U
A G U U U A A U A U U A G U U U G U G U A A A A U U A A A G U U A C A G U U G U U C U A U
A U G U A C C A A A A A A U A A A A A G U A A A A A A A A A A A A A A U U A U U U
U C U U U G U A A A A U U A A U G A A A C A A A A A A A A A A A A A A U G U A A A U A U A
A U A A U C C U A A A G U A A A U U U A A A A A A A A A A A C A A A A U U G U A A A A A U
U A A U G G U A U
A U U U G U U A U
U U U A U
G C G U U U G U C U A A G A A U A A U U U A U
U C U U A U
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[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	148180	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.306	Depositor
Minimum map value	-0.176	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	428.40002, 428.40002, 428.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.19, 1.19, 1.19	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	u	0.82	6/5704 (0.1%)	0.60	0/7702
2	s	0.41	0/1391	0.58	0/1880
3	r	0.35	0/3925	0.58	1/5331 (0.0%)
4	n	0.38	0/1202	0.59	0/1618
5	h	0.43	0/1364	0.55	0/1842
6	e	0.57	2/6771 (0.0%)	0.71	6/9218 (0.1%)
7	az	0.39	0/1334	0.66	0/1811
8	ay	0.35	0/1236	0.56	0/1663
9	ax	0.31	0/1415	0.56	0/1923
10	aw	0.38	0/1376	0.58	0/1862
11	au	0.39	0/2151	0.57	0/2920
12	ak	0.34	0/1905	0.61	0/2572
13	aj	0.37	0/2665	0.60	2/3618 (0.1%)
14	ag	0.39	0/4572	0.58	0/6180
15	af	0.33	0/4689	0.60	1/6342 (0.0%)
16	ae	0.35	0/4746	0.58	1/6439 (0.0%)
17	l	0.31	0/4950	0.59	1/6705 (0.0%)
18	ac	0.29	0/9073	0.56	0/12323
19	ab	0.36	0/9319	0.60	0/12610
20	ad	0.57	0/6805	0.68	3/9217 (0.0%)
21	m	0.63	1/1998 (0.1%)	0.71	2/2707 (0.1%)
22	i	0.51	0/3048	0.67	0/4110
23	f	0.42	0/1958	0.61	0/2631
24	c	0.72	0/2216	0.73	1/2984 (0.0%)
25	d	0.45	1/3611 (0.0%)	0.62	0/4871
26	ba	0.64	0/734	0.68	0/996
27	av	0.44	0/1795	0.70	1/2432 (0.0%)
28	at	0.47	1/1992 (0.1%)	0.64	0/2686
29	ar	0.45	0/2109	0.61	0/2852
30	aq	0.36	0/1751	0.59	0/2374
31	ap	0.48	0/1826	0.62	0/2453
32	ao	0.61	0/2119	0.67	0/2871

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	ai	0.56	0/3273	0.65	0/4412
34	an	0.60	0/2484	0.69	0/3357
35	z	0.73	2/8856 (0.0%)	0.69	3/12020 (0.0%)
36	y	0.39	0/2030	0.65	1/2751 (0.0%)
37	x	0.53	0/2075	0.69	0/2825
38	w	0.44	0/1524	0.68	2/2066 (0.1%)
39	v	0.62	0/1603	0.75	0/2154
40	bb	0.47	0/926	0.66	0/1230
41	t	1.14	7/1846 (0.4%)	0.66	0/2511
42	al	0.58	0/2430	0.66	0/3275
43	q	0.60	0/1892	0.68	0/2551
44	p	0.58	0/2047	0.66	0/2762
45	Ca	1.00	7/5233 (0.1%)	0.69	2/7083 (0.0%)
46	g	0.53	0/1580	0.65	0/2113
47	j	0.60	0/1546	0.79	2/2090 (0.1%)
48	b	0.51	0/1299	0.69	1/1751 (0.1%)
49	bd	0.50	0/441	0.74	0/601
50	a	0.68	0/3523	0.70	2/4759 (0.0%)
51	bc	0.29	0/1278	0.54	0/1711
52	aa	0.45	0/12863	0.62	0/17416
53	k	0.65	0/1624	0.80	0/2192
54	be	0.46	0/690	0.71	0/934
55	as	1.11	1/2088 (0.0%)	0.68	1/2844 (0.0%)
56	2	0.50	0/11110	0.60	0/17276
56	A	0.35	0/3392	0.50	0/5275
All	All	0.54	28/179403 (0.0%)	0.64	33/245702 (0.0%)

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	u	0	1
6	e	0	2
11	au	0	3
15	af	0	1
17	l	0	2
20	ad	0	3
25	d	0	2
27	av	0	1
29	ar	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
32	ao	0	2
33	ai	0	1
39	v	0	2
45	Ca	0	2
49	bd	0	2
52	aa	0	1
53	k	0	3
54	be	0	1
All	All	0	30

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	as	236	MET	SD-CE	46.72	2.96	1.79
35	z	1071	ARG	CD-NE	35.62	1.96	1.46
45	Ca	95	TRP	CE3-CZ3	31.82	2.34	1.38
1	u	666	PHE	CE2-CZ	28.17	2.23	1.38
1	u	666	PHE	CD2-CE2	25.44	2.15	1.38

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	e	444	ASP	CA-C-N	22.37	165.26	121.41
6	e	444	ASP	C-N-CA	22.37	165.26	121.41
35	z	1071	ARG	CD-NE-CZ	21.34	154.28	124.40
55	as	236	MET	CG-SD-CE	12.27	127.90	100.90
6	e	749	PRO	CA-C-N	11.55	142.89	120.94

There are no chirality outliers.

5 of 30 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	au	154	GLN	Peptide
11	au	186	TRP	Peptide
6	e	15	ARG	Peptide
6	e	18	THR	Peptide
1	u	229	SER	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	u	5597	0	5628	451	0
2	s	1351	0	1315	135	0
3	r	3806	0	3680	306	0
4	n	1169	0	1188	100	0
5	h	1324	0	1304	107	0
6	e	6577	0	6289	569	0
7	az	1292	0	1287	130	0
8	ay	1200	0	1190	117	0
9	ax	1366	0	1342	115	0
10	aw	1338	0	1322	114	0
11	au	2069	0	1936	158	0
12	ak	1865	0	1836	140	0
13	aj	2590	0	2552	198	0
14	ag	4472	0	4434	338	0
15	af	4590	0	4545	354	0
16	ae	4634	0	4582	342	0
17	l	4821	0	4706	384	0
18	ac	8864	0	8621	548	0
19	ab	9094	0	8739	721	0
20	ad	6610	0	6371	583	0
21	m	1940	0	1882	169	0
22	i	2970	0	2976	273	0
23	f	1917	0	1854	192	0
24	c	2169	0	2146	128	0
25	d	3538	0	3515	309	0
26	ba	706	0	645	66	0
27	av	1752	0	1705	177	0
28	at	1946	0	1927	143	0
29	ar	2061	0	2058	153	0
30	aq	1701	0	1658	119	0
31	ap	1796	0	1747	92	0
32	ao	2062	0	2042	148	0
33	ai	3205	0	3206	180	0
34	an	2422	0	2434	293	0
35	z	8630	0	8339	668	0
36	y	1983	0	1989	139	0
37	x	2016	0	1932	180	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	w	1479	0	1458	129	0
39	v	1567	0	1500	164	0
40	bb	905	0	968	84	0
41	t	1797	0	1752	186	0
42	al	2372	0	2374	195	0
43	q	1840	0	1783	195	0
44	p	1998	0	1965	147	0
45	Ca	5070	0	4897	453	0
46	g	1544	0	1564	141	0
47	j	1501	0	1517	200	0
48	b	1271	0	1263	125	0
49	bd	430	0	448	95	0
50	a	3436	0	3427	283	0
51	bc	1247	0	1249	84	0
52	aa	12549	0	12207	961	0
53	k	1577	0	1587	158	0
54	be	665	0	668	54	0
55	as	2024	0	2025	190	0
56	2	9932	0	4972	685	0
56	A	3030	0	1513	200	0
57	r	32	0	11	10	0
58	r	1	0	0	0	0
59	aj	29	0	10	8	0
60	aa	1	0	0	0	0
60	at	2	0	0	0	0
60	y	1	0	0	0	0
All	All	173743	0	164080	11055	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 33.

The worst 5 of 11055 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:u:666:PHE:CD2	1:u:666:PHE:CG	1.76	1.70
41:t:46:TYR:CZ	41:t:46:TYR:CE2	1.78	1.68
1:u:666:PHE:CG	1:u:666:PHE:CD1	1.76	1.60
41:t:46:TYR:CZ	41:t:46:TYR:CE1	1.81	1.60
45:Ca:95:TRP:CE2	45:Ca:95:TRP:CZ2	1.89	1.56

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	u	693/874 (79%)	638 (92%)	55 (8%)	0	100	100
2	s	163/180 (91%)	138 (85%)	23 (14%)	2 (1%)	10	41
3	r	461/500 (92%)	408 (88%)	53 (12%)	0	100	100
4	n	140/172 (81%)	122 (87%)	18 (13%)	0	100	100
5	h	155/166 (93%)	143 (92%)	12 (8%)	0	100	100
6	e	808/818 (99%)	712 (88%)	94 (12%)	2 (0%)	43	74
7	az	152/163 (93%)	138 (91%)	14 (9%)	0	100	100
8	ay	139/218 (64%)	127 (91%)	11 (8%)	1 (1%)	18	51
9	ax	159/172 (92%)	148 (93%)	10 (6%)	1 (1%)	21	54
10	aw	158/186 (85%)	135 (85%)	23 (15%)	0	100	100
11	au	237/247 (96%)	205 (86%)	31 (13%)	1 (0%)	30	62
12	ak	224/314 (71%)	205 (92%)	19 (8%)	0	100	100
13	aj	313/396 (79%)	274 (88%)	38 (12%)	1 (0%)	36	67
14	ag	544/581 (94%)	500 (92%)	43 (8%)	1 (0%)	43	74
15	af	552/677 (82%)	505 (92%)	46 (8%)	1 (0%)	43	74
16	ae	570/678 (84%)	518 (91%)	52 (9%)	0	100	100
17	l	580/714 (81%)	520 (90%)	60 (10%)	0	100	100
18	ac	1123/1152 (98%)	1022 (91%)	101 (9%)	0	100	100
19	ab	1108/1175 (94%)	994 (90%)	113 (10%)	1 (0%)	48	79
20	ad	799/810 (99%)	692 (87%)	102 (13%)	5 (1%)	21	54
21	m	230/319 (72%)	201 (87%)	29 (13%)	0	100	100
22	i	358/429 (83%)	306 (86%)	51 (14%)	1 (0%)	36	67
23	f	229/325 (70%)	196 (86%)	33 (14%)	0	100	100
24	c	259/285 (91%)	228 (88%)	31 (12%)	0	100	100
25	d	443/445 (100%)	398 (90%)	44 (10%)	1 (0%)	43	74

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	ba	81/217 (37%)	68 (84%)	13 (16%)	0	100	100
27	av	211/237 (89%)	174 (82%)	35 (17%)	2 (1%)	14	47
28	at	240/259 (93%)	201 (84%)	38 (16%)	1 (0%)	30	62
29	ar	253/268 (94%)	220 (87%)	33 (13%)	0	100	100
30	aq	196/299 (66%)	177 (90%)	19 (10%)	0	100	100
31	ap	220/277 (79%)	196 (89%)	24 (11%)	0	100	100
32	ao	248/283 (88%)	209 (84%)	39 (16%)	0	100	100
33	ai	388/410 (95%)	333 (86%)	55 (14%)	0	100	100
34	an	291/293 (99%)	248 (85%)	41 (14%)	2 (1%)	18	51
35	z	1067/1181 (90%)	901 (84%)	163 (15%)	3 (0%)	36	67
36	y	249/449 (56%)	196 (79%)	51 (20%)	2 (1%)	16	49
37	x	250/345 (72%)	213 (85%)	36 (14%)	1 (0%)	30	62
38	w	173/186 (93%)	150 (87%)	22 (13%)	1 (1%)	21	54
39	v	194/215 (90%)	153 (79%)	37 (19%)	4 (2%)	5	31
40	bb	108/238 (45%)	95 (88%)	12 (11%)	1 (1%)	14	47
41	t	224/256 (88%)	193 (86%)	30 (13%)	1 (0%)	30	62
42	al	290/308 (94%)	257 (89%)	32 (11%)	1 (0%)	36	67
43	q	212/442 (48%)	185 (87%)	26 (12%)	1 (0%)	24	57
44	p	236/308 (77%)	206 (87%)	30 (13%)	0	100	100
45	Ca	590/603 (98%)	509 (86%)	80 (14%)	1 (0%)	43	74
46	g	182/193 (94%)	163 (90%)	19 (10%)	0	100	100
47	j	178/189 (94%)	140 (79%)	38 (21%)	0	100	100
48	b	146/160 (91%)	123 (84%)	23 (16%)	0	100	100
49	bd	48/90 (53%)	41 (85%)	7 (15%)	0	100	100
50	a	423/434 (98%)	363 (86%)	59 (14%)	1 (0%)	43	74
51	bc	149/376 (40%)	138 (93%)	11 (7%)	0	100	100
52	aa	1554/1827 (85%)	1363 (88%)	186 (12%)	5 (0%)	36	67
53	k	188/309 (61%)	156 (83%)	32 (17%)	0	100	100
54	be	77/82 (94%)	67 (87%)	9 (12%)	1 (1%)	9	39
55	as	250/261 (96%)	211 (84%)	39 (16%)	0	100	100
All	All	19513/22991 (85%)	17122 (88%)	2345 (12%)	46 (0%)	44	74

5 of 46 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
54	be	41	ILE
13	aj	36	GLN
37	x	178	SER
39	v	94	THR
2	s	42	GLN

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	u	613/762 (80%)	544 (89%)	69 (11%)	5	25
2	s	144/157 (92%)	132 (92%)	12 (8%)	10	34
3	r	413/443 (93%)	380 (92%)	33 (8%)	11	35
4	n	127/152 (84%)	114 (90%)	13 (10%)	7	28
5	h	142/150 (95%)	128 (90%)	14 (10%)	7	29
6	e	712/719 (99%)	648 (91%)	64 (9%)	9	32
7	az	136/144 (94%)	126 (93%)	10 (7%)	13	37
8	ay	126/195 (65%)	114 (90%)	12 (10%)	8	31
9	ax	149/158 (94%)	136 (91%)	13 (9%)	9	33
10	aw	144/164 (88%)	132 (92%)	12 (8%)	10	34
11	au	220/228 (96%)	199 (90%)	21 (10%)	8	31
12	ak	197/257 (77%)	178 (90%)	19 (10%)	8	30
13	aj	280/351 (80%)	258 (92%)	22 (8%)	11	36
14	ag	477/502 (95%)	443 (93%)	34 (7%)	13	38
15	af	490/583 (84%)	452 (92%)	38 (8%)	11	36
16	ae	492/567 (87%)	460 (94%)	32 (6%)	15	42
17	l	514/606 (85%)	467 (91%)	47 (9%)	9	32
18	ac	934/957 (98%)	860 (92%)	74 (8%)	11	36
19	ab	954/1011 (94%)	870 (91%)	84 (9%)	9	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	ad	703/712 (99%)	626 (89%)	77 (11%)	6	26
21	m	202/278 (73%)	182 (90%)	20 (10%)	7	29
22	i	314/371 (85%)	279 (89%)	35 (11%)	6	25
23	f	201/276 (73%)	179 (89%)	22 (11%)	6	26
24	c	228/246 (93%)	203 (89%)	25 (11%)	6	26
25	d	373/373 (100%)	339 (91%)	34 (9%)	9	32
26	ba	73/180 (41%)	67 (92%)	6 (8%)	10	34
27	av	191/210 (91%)	163 (85%)	28 (15%)	3	17
28	at	212/227 (93%)	190 (90%)	22 (10%)	7	27
29	ar	227/238 (95%)	199 (88%)	28 (12%)	4	22
30	aq	181/253 (72%)	162 (90%)	19 (10%)	6	27
31	ap	189/233 (81%)	167 (88%)	22 (12%)	5	24
32	ao	225/252 (89%)	194 (86%)	31 (14%)	3	19
33	ai	351/370 (95%)	320 (91%)	31 (9%)	9	32
34	an	250/250 (100%)	214 (86%)	36 (14%)	3	18
35	z	920/1011 (91%)	813 (88%)	107 (12%)	5	24
36	y	209/366 (57%)	182 (87%)	27 (13%)	4	21
37	x	206/284 (72%)	177 (86%)	29 (14%)	3	18
38	w	163/174 (94%)	148 (91%)	15 (9%)	8	32
39	v	164/181 (91%)	146 (89%)	18 (11%)	6	26
40	bb	92/197 (47%)	83 (90%)	9 (10%)	7	30
41	t	193/220 (88%)	167 (86%)	26 (14%)	4	20
42	al	247/262 (94%)	225 (91%)	22 (9%)	9	32
43	q	196/390 (50%)	186 (95%)	10 (5%)	21	48
44	p	213/258 (83%)	195 (92%)	18 (8%)	10	34
45	Ca	534/544 (98%)	477 (89%)	57 (11%)	6	27
46	g	163/171 (95%)	139 (85%)	24 (15%)	3	17
47	j	159/168 (95%)	136 (86%)	23 (14%)	3	17
48	b	138/146 (94%)	119 (86%)	19 (14%)	3	19
49	bd	48/86 (56%)	36 (75%)	12 (25%)	0	4
50	a	364/372 (98%)	328 (90%)	36 (10%)	7	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	bc	134/327 (41%)	123 (92%)	11 (8%)	10	34
52	aa	1340/1552 (86%)	1166 (87%)	174 (13%)	4	21
53	k	169/272 (62%)	139 (82%)	30 (18%)	2	10
54	be	70/73 (96%)	60 (86%)	10 (14%)	3	18
55	as	221/228 (97%)	195 (88%)	26 (12%)	5	23
All	All	17127/19857 (86%)	15365 (90%)	1762 (10%)	9	28

5 of 1762 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	aq	100	ARG
35	z	852	ILE
55	as	223	THR
52	aa	805	ILE
31	ap	144	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 470 such sidechains are listed below:

Mol	Chain	Res	Type
20	ad	561	HIS
52	aa	1164	GLN
30	aq	116	HIS
52	aa	957	HIS
45	Ca	518	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
56	2	468/8129 (5%)	249 (53%)	8 (1%)
56	A	142/8129 (1%)	90 (63%)	2 (1%)
All	All	610/16258 (3%)	339 (55%)	10 (1%)

5 of 339 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
56	A	397	U
56	A	398	U
56	A	399	A

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Mol	Chain	Res	Type
56	A	400	U
56	A	401	A

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
56	2	262	A
56	2	324	A
56	2	366	U
56	2	87	U
56	2	97	U

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 7 ligands modelled in this entry, 5 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
57	GTP	r	901	58	33,34,34	3.59	17 (51%)	50,54,54	2.15	16 (32%)
59	UTP	aj	401	-	29,30,30	3.08	11 (37%)	43,47,47	1.68	7 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	GTP	r	901	58	-	5/22/38/38	0/3/3/3
59	UTP	aj	401	-	-	3/22/38/38	0/2/2/2

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	r	901	GTP	C3'-C4'	-9.70	1.28	1.53
59	aj	401	UTP	O4'-C1'	8.26	1.61	1.42
57	r	901	GTP	O4'-C4'	7.41	1.61	1.45
57	r	901	GTP	C4-N3	6.50	1.49	1.34
59	aj	401	UTP	C2'-C1'	-5.91	1.34	1.53

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	aj	401	UTP	C4-N3-C2	-5.64	119.61	126.61
57	r	901	GTP	C1'-N9-C4	-5.03	111.64	126.49
57	r	901	GTP	C2'-C1'-N9	-4.81	99.85	113.25
59	aj	401	UTP	N3-C2-N1	4.55	120.81	114.89
57	r	901	GTP	C5-C4-N3	-4.53	121.18	128.39

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	r	901	GTP	C5'-O5'-PA-O1A
57	r	901	GTP	C5'-O5'-PA-O2A
59	aj	401	UTP	O4'-C4'-C5'-O5'
59	aj	401	UTP	C3'-C4'-C5'-O5'
57	r	901	GTP	C3'-C4'-C5'-O5'

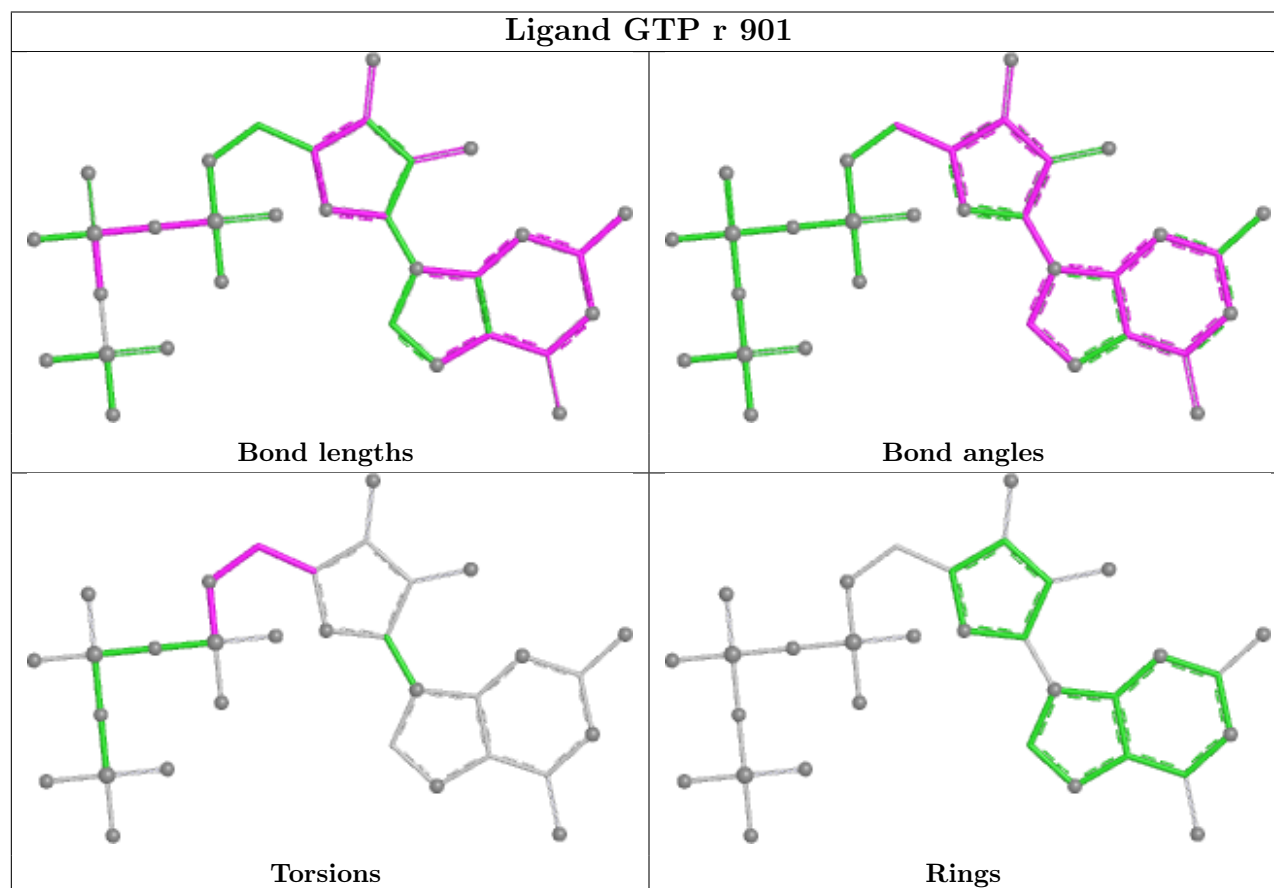
There are no ring outliers.

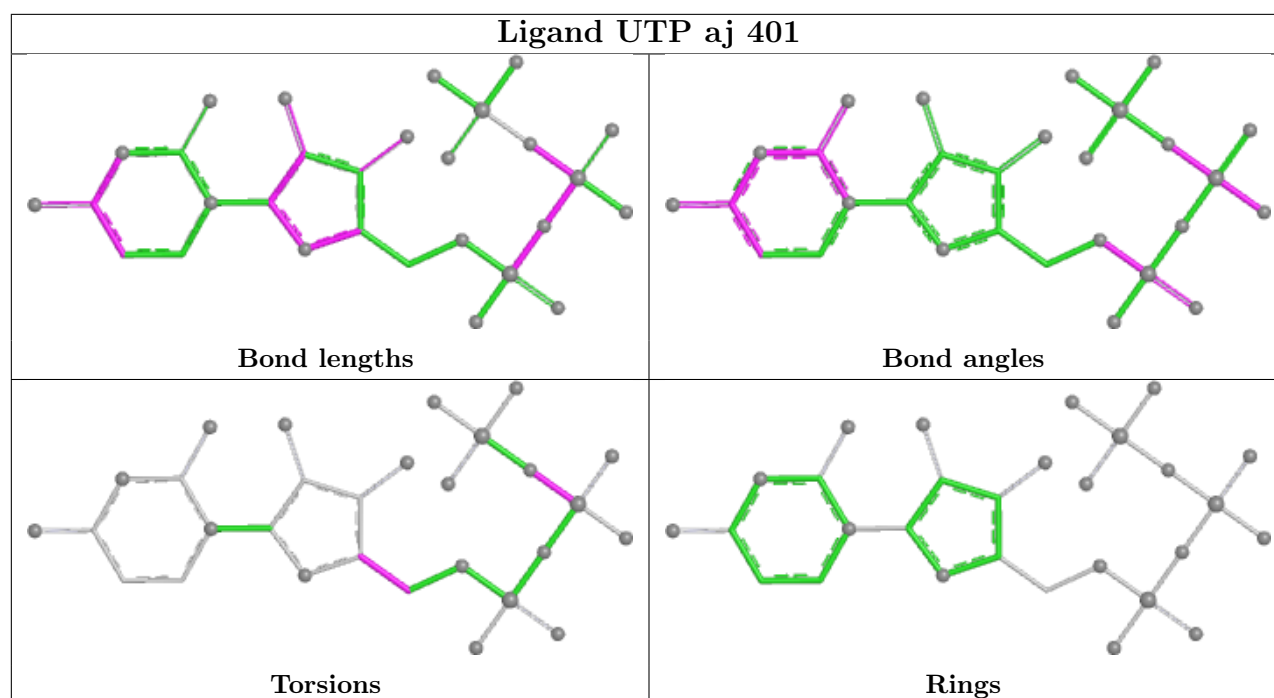
2 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	r	901	GTP	10	0
59	aj	401	UTP	8	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
6	e	1
21	m	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	e	444:ASP	C	445:GLY	N	1.67
1	m	70:ARG	C	71:PHE	N	1.17

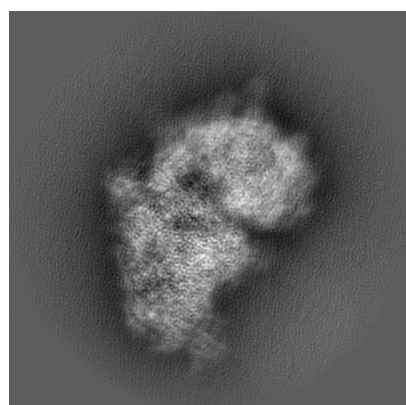
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11846. These allow visual inspection of the internal detail of the map and identification of artifacts.

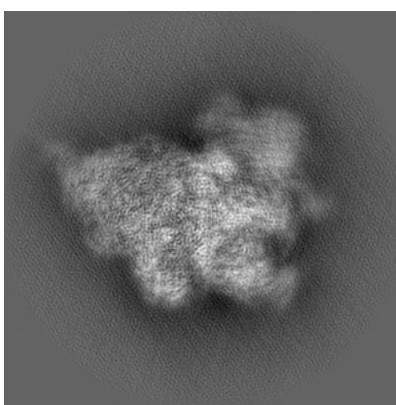
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

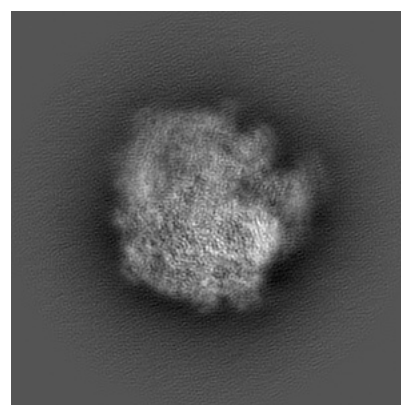
6.1.1 Primary map



X



Y

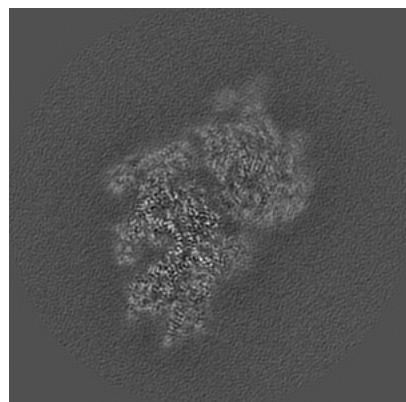


Z

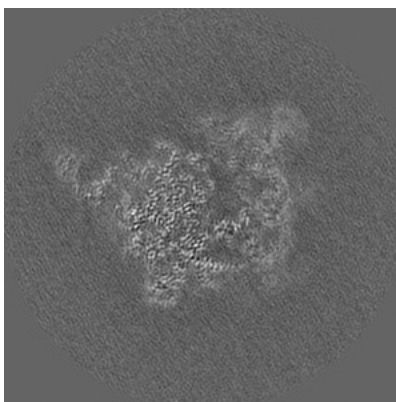
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

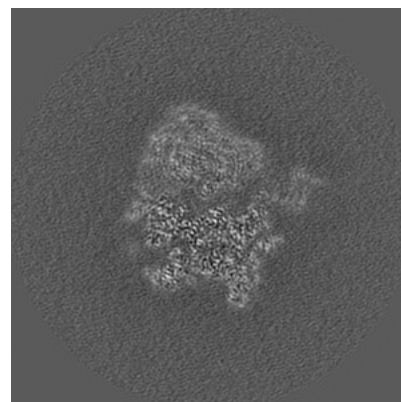
6.2.1 Primary map



X Index: 180



Y Index: 180

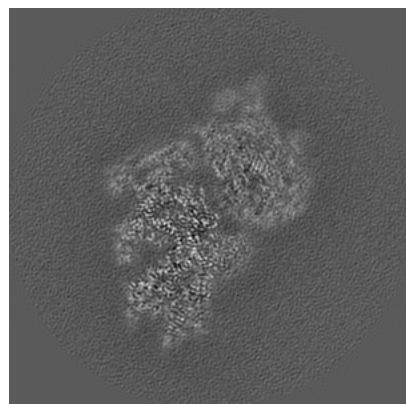


Z Index: 180

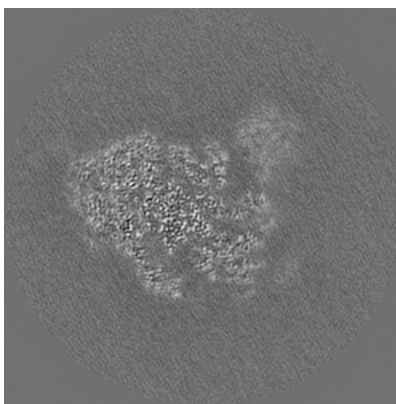
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

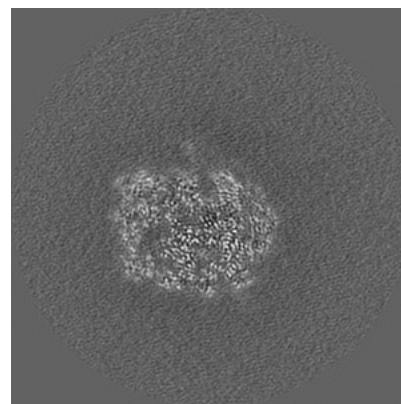
6.3.1 Primary map



X Index: 181



Y Index: 155

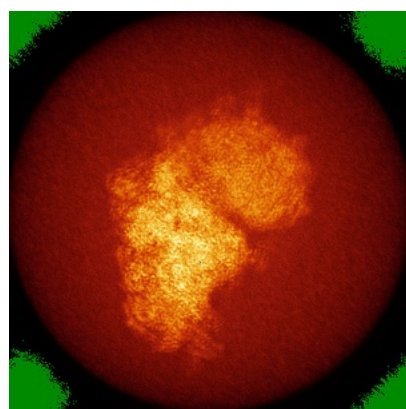


Z Index: 155

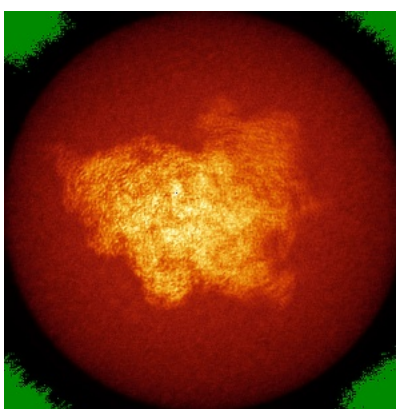
The images above show the largest variance slices of the map in three orthogonal directions.

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

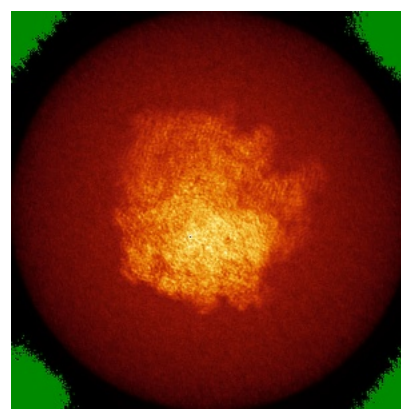
6.4.1 Primary map



X



Y

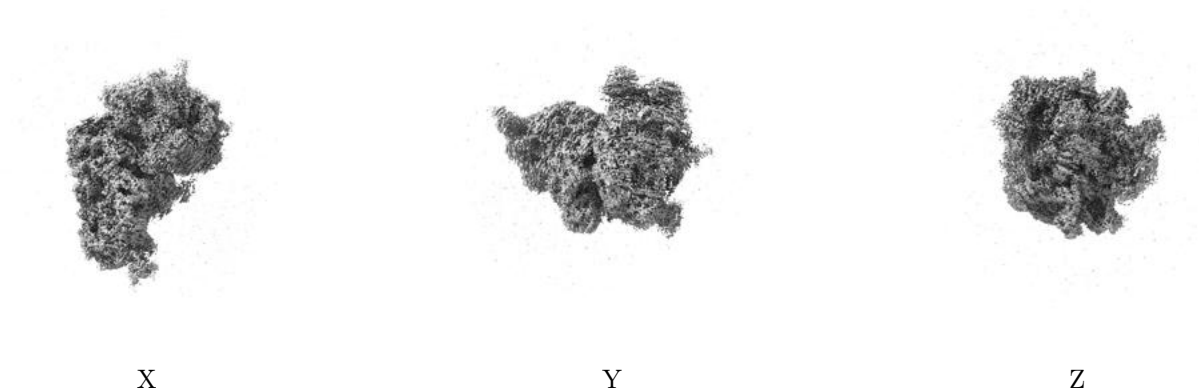


Z

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

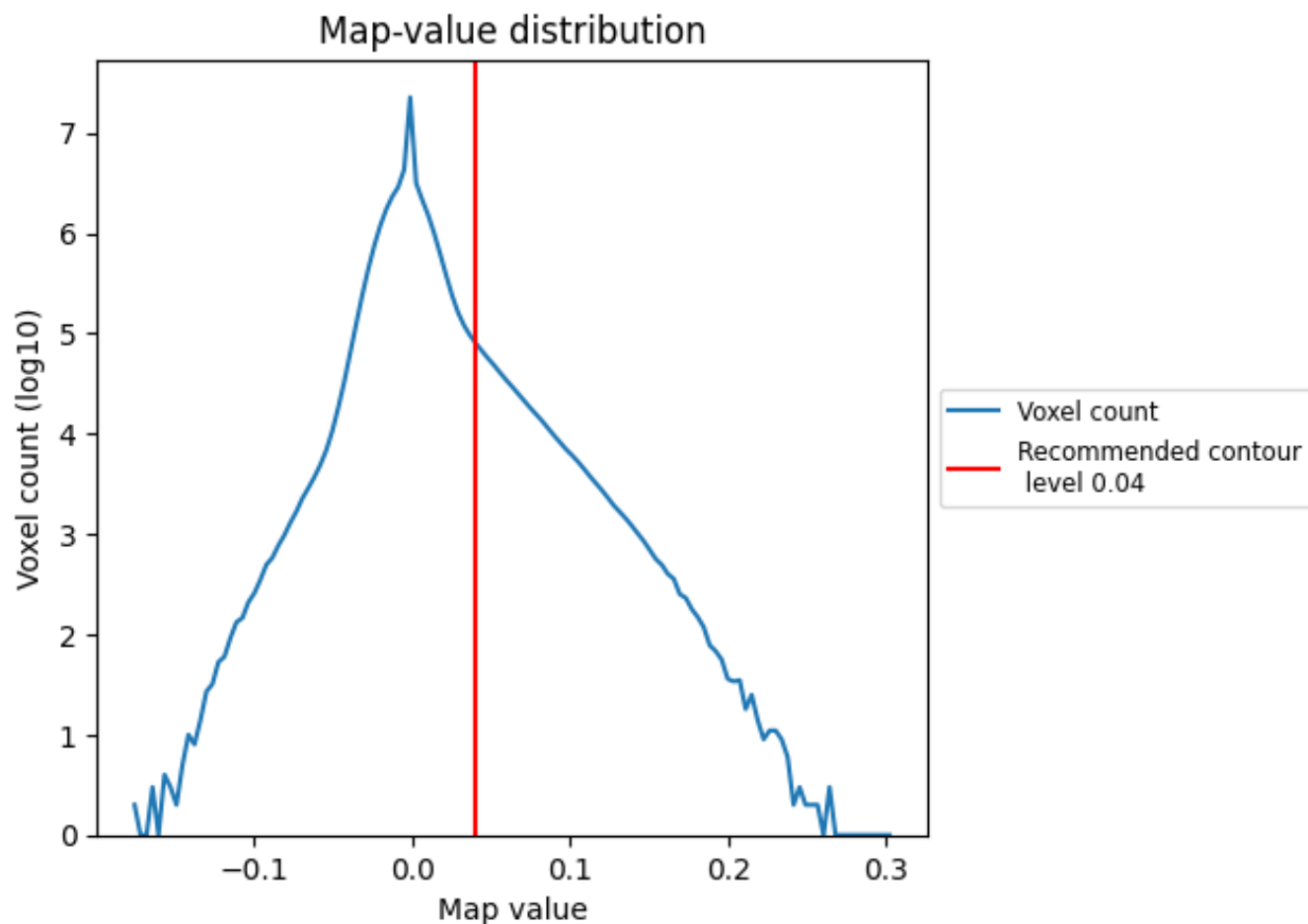
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

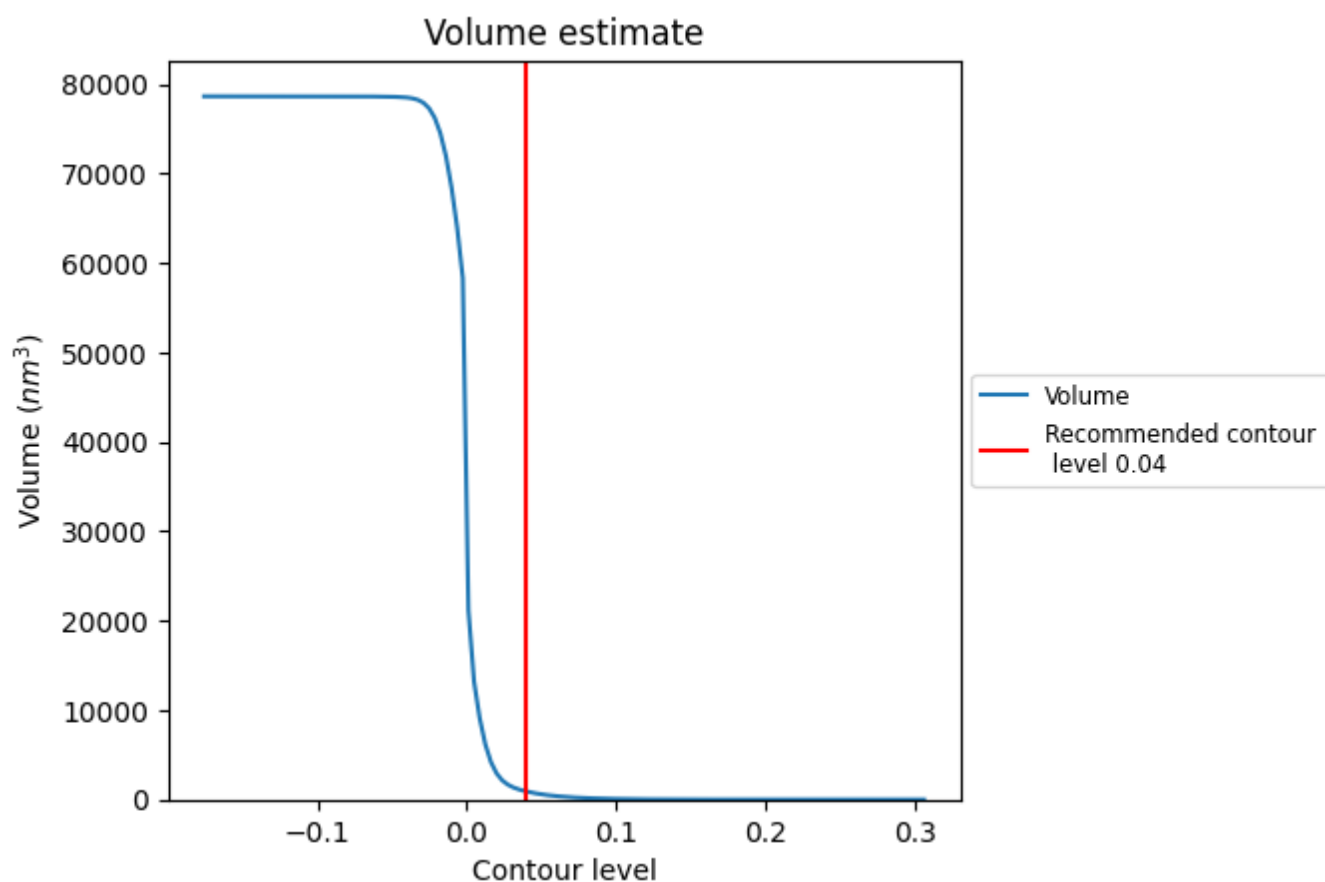
This section contains the results of statistical analysis of the map.

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.

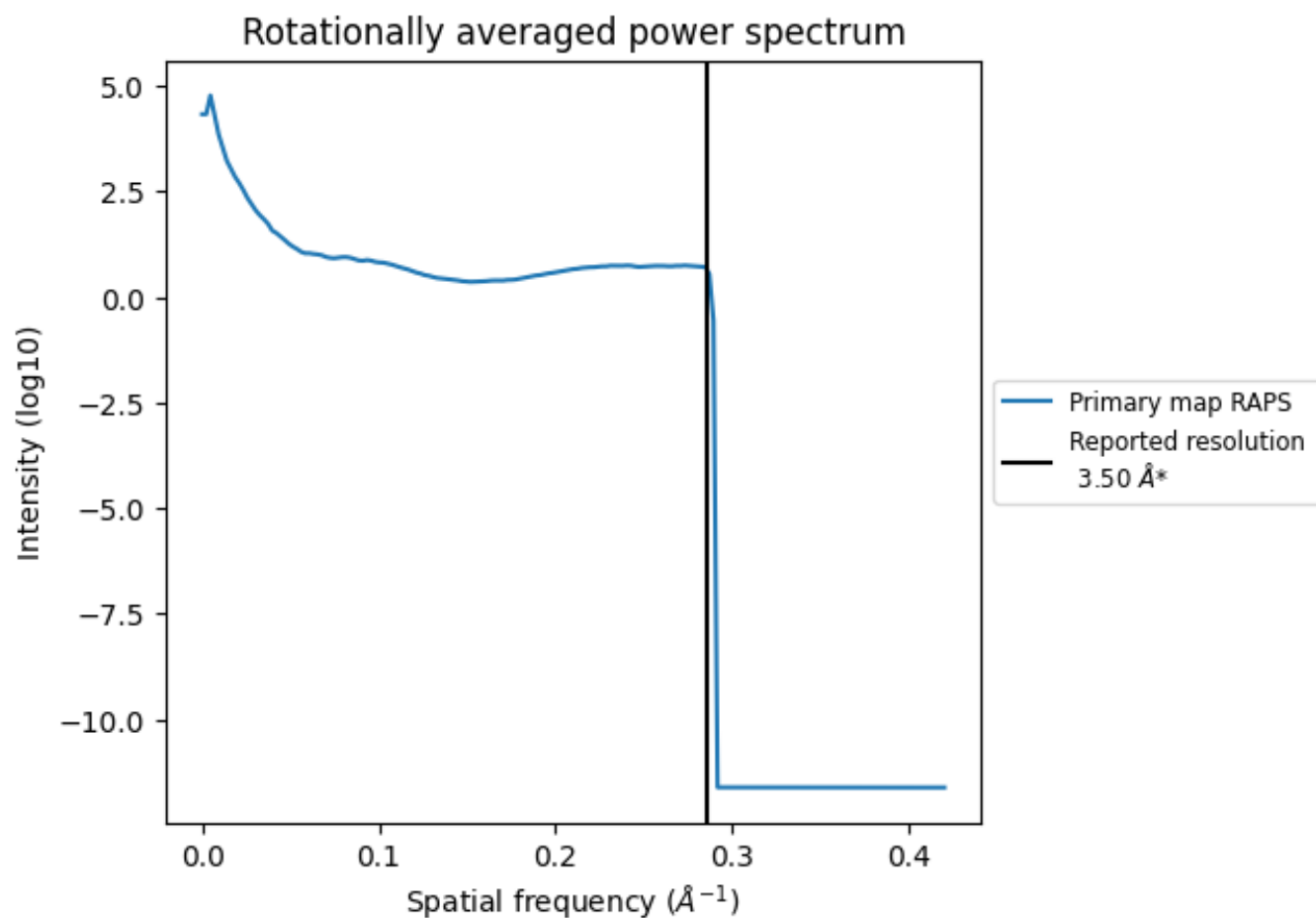
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 906 nm³; this corresponds to an approximate mass of 819 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 0.286 $\text{\AA}^{-1}$

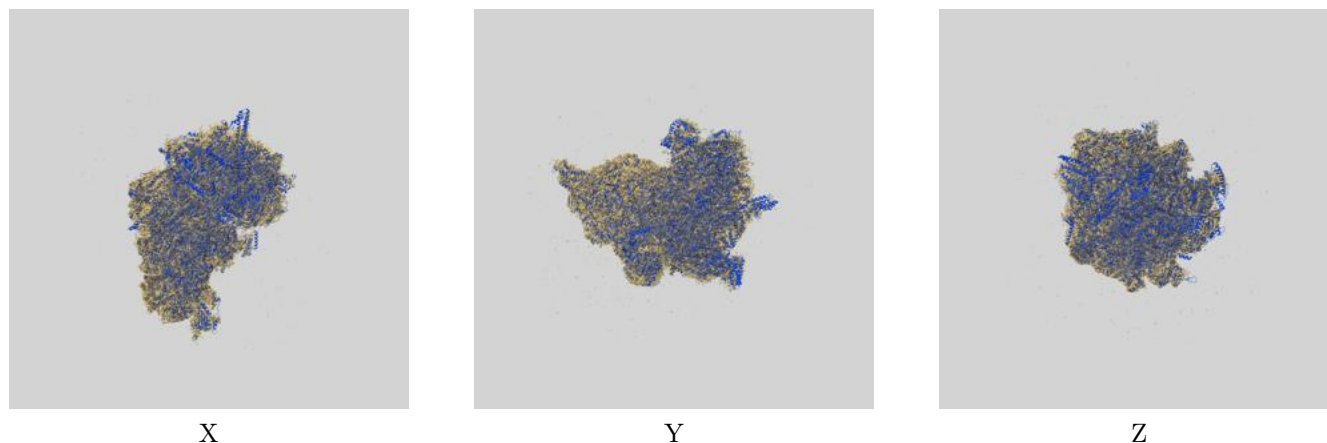
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

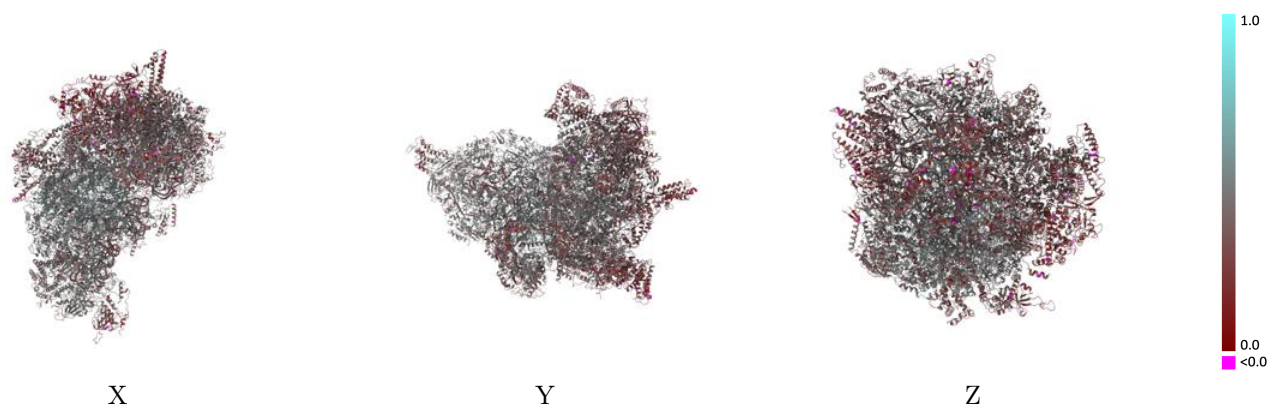
This section contains information regarding the fit between EMDB map EMD-11846 and PDB model 7AOR. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



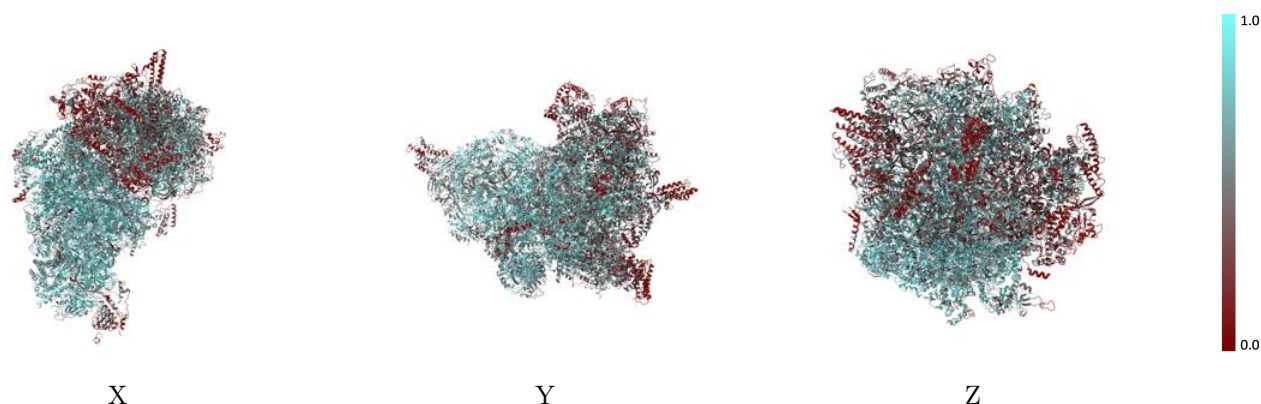
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



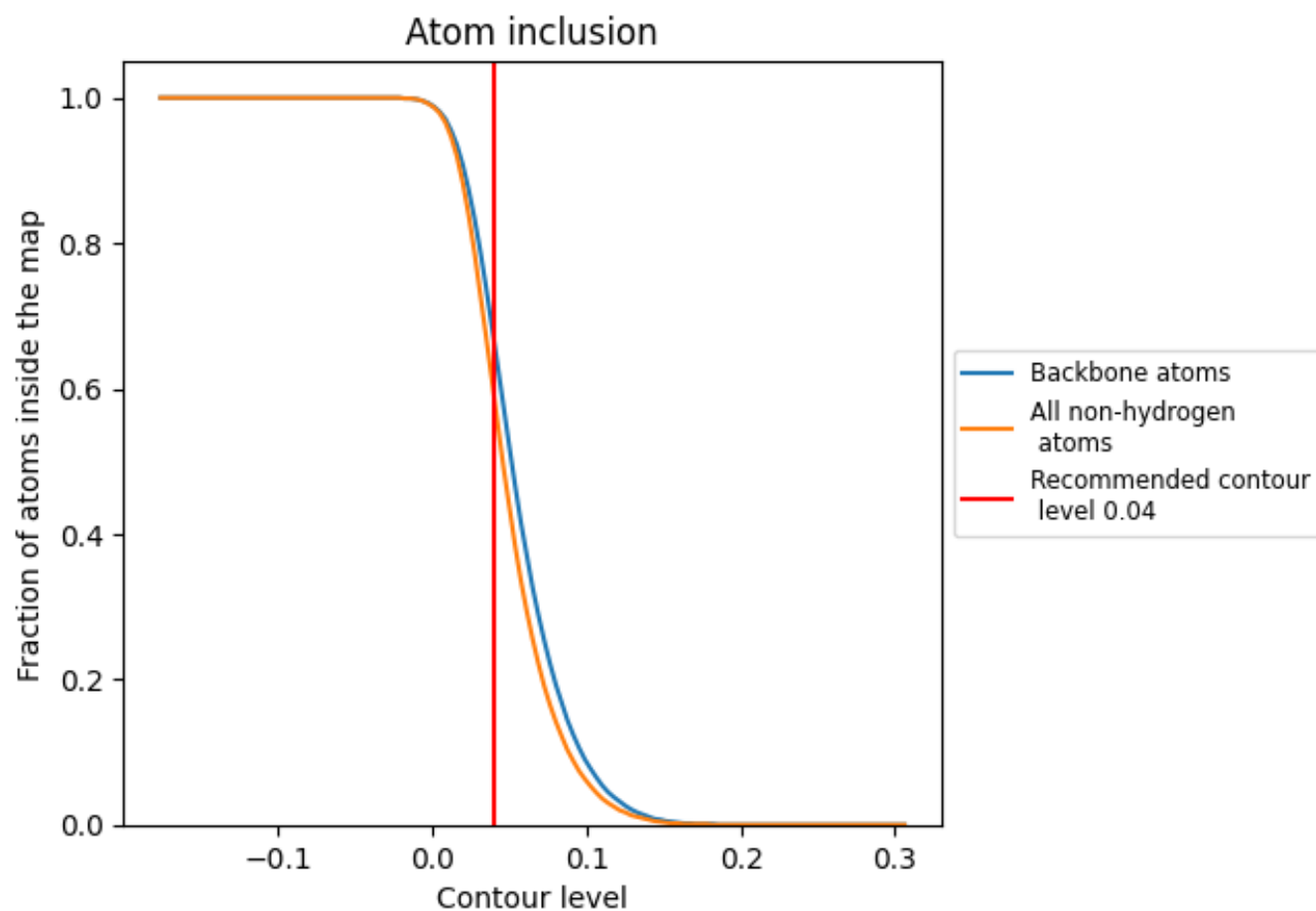
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 67% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5920	 0.4160
2	 0.7410	 0.4140
A	 0.6600	 0.3980
Ca	 0.7420	 0.4910
a	 0.7320	 0.4960
aa	 0.6640	 0.4110
ab	 0.4430	 0.3700
ac	 0.3200	 0.3360
ad	 0.7430	 0.4560
ae	 0.5340	 0.3860
af	 0.3260	 0.3100
ag	 0.4690	 0.4070
ai	 0.7240	 0.4790
aj	 0.5950	 0.4130
ak	 0.4270	 0.3980
al	 0.6320	 0.4760
an	 0.7690	 0.4550
ao	 0.7900	 0.5040
ap	 0.7140	 0.4600
aq	 0.4730	 0.3900
ar	 0.7100	 0.4430
as	 0.6550	 0.4210
at	 0.6870	 0.4310
au	 0.5240	 0.4330
av	 0.5850	 0.4390
aw	 0.4640	 0.4270
ax	 0.5110	 0.3730
ay	 0.5850	 0.3680
az	 0.5990	 0.3830
b	 0.7190	 0.4210
ba	 0.7380	 0.5020
bb	 0.5980	 0.4280
bc	 0.2980	 0.3440
bd	 0.3990	 0.3240
be	 0.6450	 0.4130



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Chain	Atom inclusion	Q-score
c	 0.7270	 0.5110
d	 0.4970	 0.4040
e	 0.5110	 0.4220
f	 0.6000	 0.4110
g	 0.6660	 0.4350
h	 0.6420	 0.4530
i	 0.7040	 0.4490
j	 0.7670	 0.4550
k	 0.7950	 0.4860
l	 0.3250	 0.3050
m	 0.7270	 0.4820
n	 0.5820	 0.4020
p	 0.6470	 0.4570
q	 0.7380	 0.4480
r	 0.4620	 0.3730
s	 0.5790	 0.4350
t	 0.6100	 0.4240
u	 0.3920	 0.3530
v	 0.6630	 0.4600
w	 0.6220	 0.4190
x	 0.6450	 0.4280
y	 0.5930	 0.3770
z	 0.7460	 0.4810