



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 07:06 AM UTC

PDB ID : 3J8G / pdb_00003j8g
EMDB ID : EMD-6149
Title : Electron cryo-microscopy structure of EngA bound with the 50S ribosomal subunit
Authors : Zhang, X.; Yan, K.; Zhang, Y.; Li, N.; Ma, C.; Li, Z.; Zhang, Y.; Feng, B.; Liu, J.; Sun, Y.; Xu, Y.; Lei, J.; Gao, N.
Deposited on : 2014-10-24
Resolution : 5.00 Å (reported)
Based on initial models : 2WWQ, 2HJG

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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:

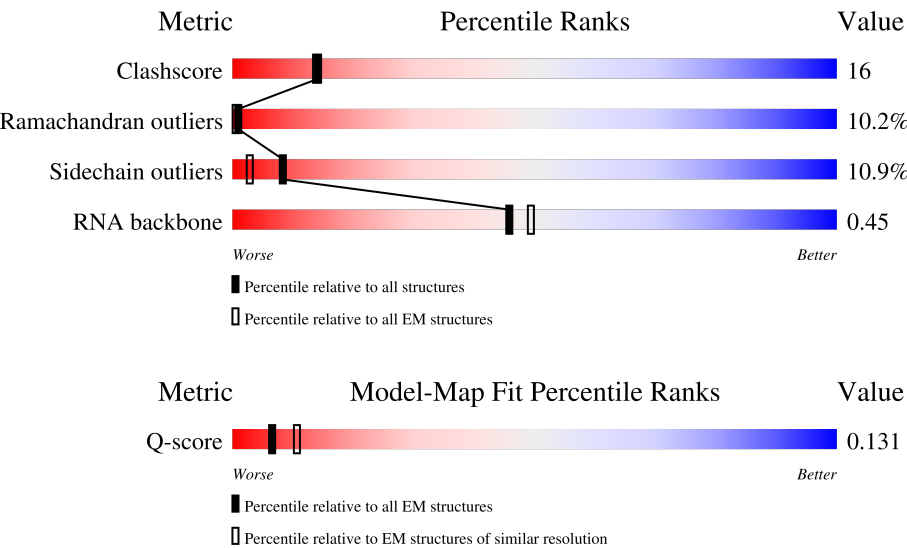
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 5.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1057 (4.50 - 5.50)

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	A	117	
2	B	2903	
3	0	78	

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Mol	Chain	Length	Quality of chain
4	K	123	
5	L	144	
6	1	63	
7	M	136	
8	N	127	
9	O	117	
10	P	115	
11	Q	118	
12	R	103	
13	S	110	
14	D	209	
15	T	100	
16	2	59	
17	U	104	
18	W	94	
19	X	490	
20	E	201	
21	Y	85	
22	3	57	
23	5	234	
24	6	46	
25	7	65	
26	8	38	
27	C	273	
28	F	179	

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Mol	Chain	Length	Quality of chain
29	G	177	20% 28% 46% 21%
30	H	149	85% 30% 52% 17%
31	I	142	94% 38% 49% 12%
32	J	142	38% 20% 49% 23% 8%

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 94855 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 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	115	Total	C	N	O	P	0	0
			2455	1097	451	795	112		

- Molecule 2 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	2874	Total	C	N	O	P	0	0
			61689	27523	11353	19941	2872		

- Molecule 3 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 4 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	K	121	Total	C	N	O	S	0	0
			931	582	179	164	6		

- Molecule 5 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 6 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 7 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 8 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 9 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 10 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 11 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 12 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 13 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 14 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 15 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 16 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	2	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 17 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	U	99	Total	C	N	O		0	0
			755	479	140	136			

- Molecule 18 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	W	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 19 is a protein called GTPase Der.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	X	418	Total	C	N	O	S	0	0
			3280	2074	582	610	14		

- Molecule 20 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 21 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Y	79	Total	C	N	O	S	0	0
			596	367	120	108	1		

- Molecule 22 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	3	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 23 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	5	234	Total	C	N	O	S	0	0
			1733	1081	315	330	7		

- Molecule 24 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 25 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 26 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	8	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 27 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	F	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	G	175	Total	C	N	O	S	0	0
			1316	827	242	245	2		

- Molecule 30 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	H	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 31 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

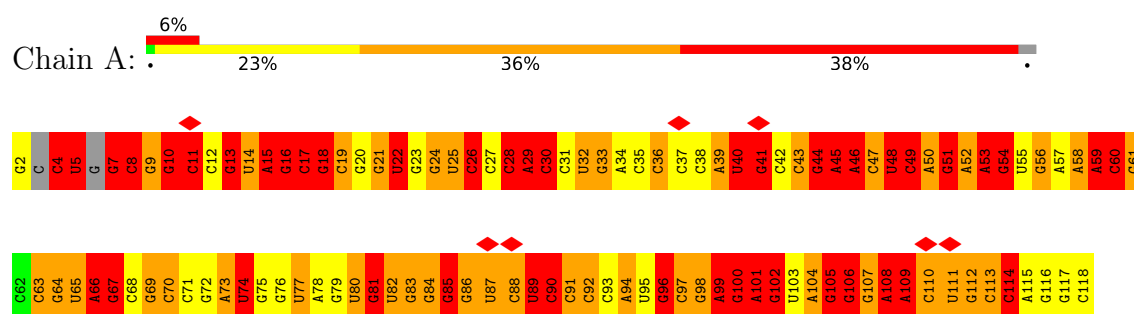
- Molecule 32 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

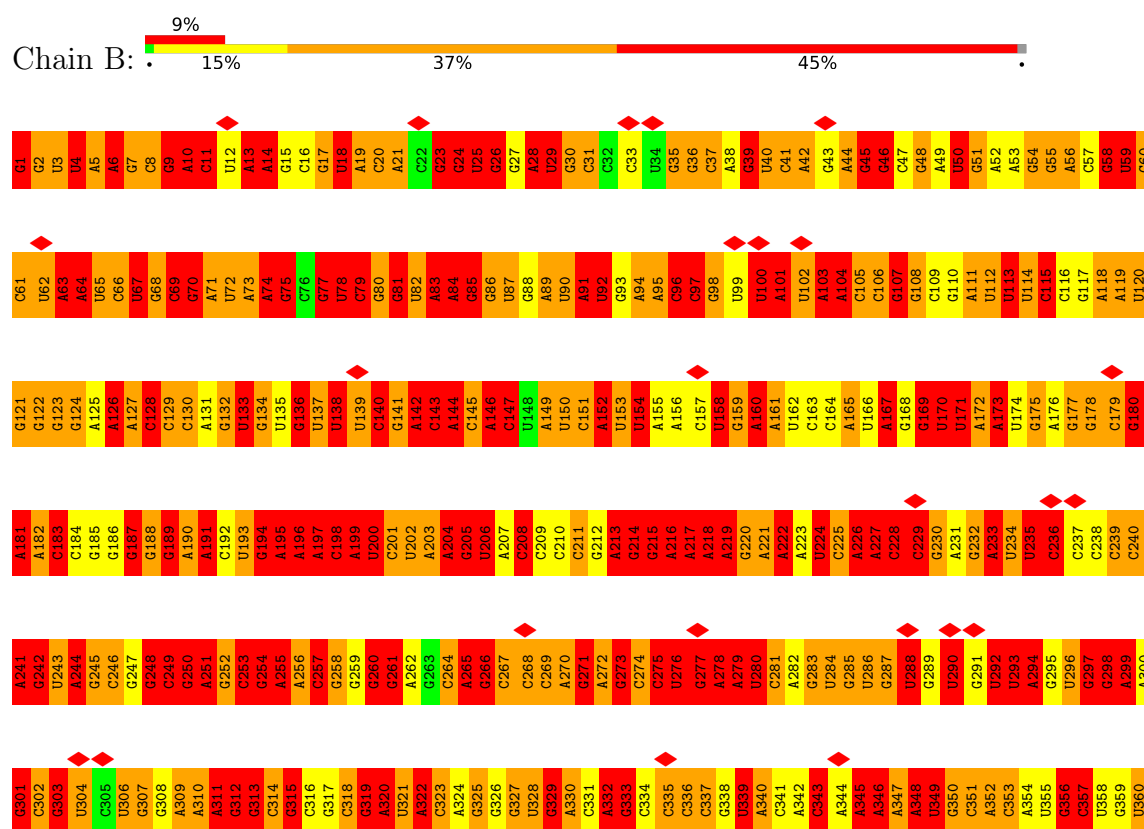
3 Residue-property plots

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

• Molecule 1: 5S rRNA



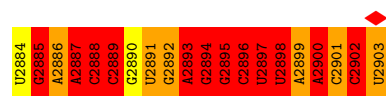
• Molecule 2: 23S rRNA



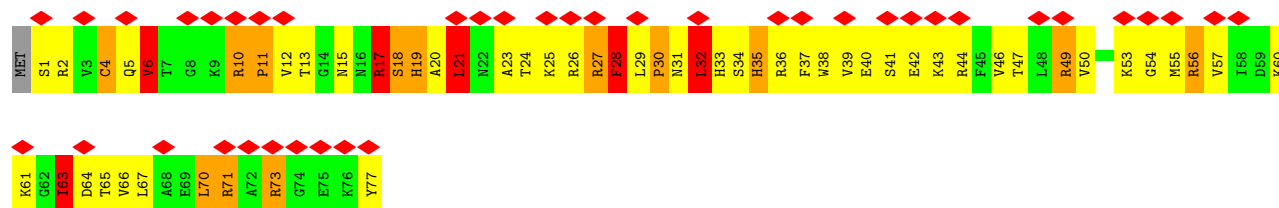
U1141	U1081	A1021	C961	C901	G841	A781	A721	A661	C601	A541	G481	C421	G361
A1142	U1082	G1022	G962	C902	U942	A782	A722	G662	A602	C542	A482	A422	A362
A1143	U1083	U1023	U963	C903	G843	A783	C723	G663	G603	G543	A483	A423	G363
A1144	A1084	G1024	G964	C904	A844	G784	U724	G664	G604	C544	C484	G424	C364
C1145	A1085	G1025	C965	A905	A845	G785	G725	U665	G605	U545	C485	G425	U365
C1146	A1086	G1026	G966	U906	U946	G786	G726	A666	U606	U546	C486	C426	C366
A1147	G1087	A1027	U967	G907	U947	C787	A727	U667	U607	A547	C487	U427	G367
U1148	A1088	A1028	C968	C908	C948	A788	G728	A668	A608	G548	A488	A428	A368
G1149	A1089	A1029	G969	A909	A949	A789	G729	G669	A609	G549	A489	A429	U369
C1150	C1030	C1030	U970	A910	U850	U790	A730	C670	C610	C550	A430	G370	G370
A1151	A1090	G1031	G971	A911	C851	C791	C731	A671	C611	C551	G431	U431	A371
C1152	C1032	A1032	A972	C912	U852	A792	C732	C672	G612	U552	A432	U372	G372
C1153	U1093	U1033	G973	U913	C853	A793	G733	C673	A613	G553	C433	U373	U373
G1154	G1093	G1034	G974	G914	C854	A794	A734	G674	G614	U554	G434	U434	A374
A1155	U1094	U1035	A975	C915	G855	C795	A735	A675	U615	U555	C435	G375	G375
A1156	A1095	G1036	G976	C916	G856	C796	C736	A676	A616	A556	C436	G376	G376
C1157	A1096	G1037	G977	A917	G857	G797	G737	A677	G617	C557	U437	G377	G377
C1158	A1097	G1038	G978	A918	G858	G798	G738	C678	G618	U558	G438	G378	C378
U1159	A1098	A1039	A979	U919	G859	G799	A739	C679	G619	U559	A439	G379	G379
G1160	U1097	A1040	A980	A920	U860	A800	C740	C680	G620	G560	C440	G380	G380
A1161	A1098	G1041	A981	C921	A861	G801	U741	G681	A621	C561	A501	G381	G381
G1162	G1099	G1042	C982	C922	G862	A802	A742	C682	G622	U562	A502	A442	C382
C1163	C1100	C1043	A983	G923	A863	U803	A743	U683	C623	U563	A503	A443	C383
C1164	U1101	G1044	A984	G924	G864	A804	U744	G684	C624	C564	A504	A444	C384
A1165	A1102	A1045	A985	A925	C865	G805	G745	A685	G625	C565	A505	A445	C385
G1166	A1103	A1046	C986	G926	A866	C806	U746	U686	A626	U566	G506	C446	C386
C1167	C1104	A1047	C987	A927	G867	U807	U747	C687	A627	U567	A507	A447	U387
G1168	U1105	A1048	A988	A928	U868	G808	G748	U688	G628	U568	A508	A448	G388
C1169	U1106	C1049	G989	U929	G869	G809	A749	A689	G629	U569	C509	U449	G389
G1170	G1107	A1050	A990	G930	U870	U810	A750	G690	G630	G570	C510	U450	U390
C1171	U1108	G1051	C991	U931	U871	U811	A751	C691	A631	U571	U511	G450	A391
U1172	U1109	C1052	C992	U932	U872	C812	A752	C692	A632	A572	G512	U451	U392
C1173	C1110	A1053	G993	A933	C873	U813	A753	A693	A633	U573	A513	C452	C393
U1174	A1111	U1054	C994	U934	G874	C814	U754	U694	C634	A574	A514	A453	C394
A1175	G1112	G1055	A995	C935	G875	C815	U755	G695	C635	A575	A515	A454	U395
U1176	U1113	G1056	G996	A936	C876	C816	A756	G696	G636	U576	A516	A455	G396
G1177	C1114	A1057	C997	C937	A877	G817	G757	G697	A637	U577	C517	C456	U397
C1178	G1115	U1058	C998	G938	A878	A818	C758	C698	G638	G578	G518	A457	C398
G1179	U1116	G1059	U999	G939	G879	A819	G759	A699	U639	G579	U519	G458	U399
U1180	C1117	U1060	A1000	G940	G880	A820	G760	G700	C640	U580	G520	U459	G400
G1181	U1118	U1061	G1001	A941	G881	A821	A761	U701	U641	C581	A460	A461	A401
U1182	G1119	G1062	G1002	G942	G882	C822	G762	U702	U642	U582	A462	C462	A402
C1183	U1120	A1063	A943	C944	G883	U824	A764	G704	A644	A583	C523	U403	U403
U1184	G1122	G1064	C945	A945	U884	A825	C765	A705	C645	C584	G524	A404	A404
G1185	C1123	U1065	C946	C946	C885	U826	U766	A706	U646	G585	G525	U464	U405
C1186	G1124	A1066	A947	A947	A886	U827	U767	G707	U647	A586	A526	G465	G406
G1187	U1125	U1067	U1008	C948	U887	A829	G768	G708	G648	C587	C527	G467	G407
U1188	A1126	A1068	A1009	G949	U888	G330	G770	U709	G649	U588	A528	G468	G408
A1189	U1127	G1069	G1010	C950	C889	G331	G771	U710	C650	U589	A529	G469	G409
G1190	A1128	A1069	U1011	C951	C889	G332	G772	G712	U652	A590	G530	A470	G410
C1191	U1129	G1070	G1012	G952	C890	A833	U773	G713	U653	U591	C531	A471	A412
G1192	U1130	A1071	C1013	G953	G891	G334	G774	U714	U654	A592	A532	A472	C413
C1193	G1131	G1072	A1014	G954	G892	G335	G775	A715	U655	U594	G533	G473	C414
A1194	U1132	C1073	U1015	U955	A893	G336	G776	A716	A656	C595	G534	G474	A415
G1195	A1133	A1073	G1017	G956	U894	C837	G777	C717	G656	U596	G535	G475	A416
C1196	C1134	U1074	U1018	U958	U895	C838	G778	C718	G657	G597	G536	G476	C417
G1197	U1135	G1075	U1019	U959	A896	U839	G779	C719	U658	U598	A538	A477	C418
U1198	G1136	C1076	U1020	A960	C897	C940	G780	U720	G659	A599	C540	A478	U419
U1199	G1137	A1077	C1076	A960	C898	C941	G781	U721	C660	G600	C541	A479	C420
C1200	G1138	U1078	A960	A960	C899	C942	G782	U722				A480	

G1983	G1984	C1985	C1986	A1987	G1988	C1989	C1990	U1991	G1992	C1993	C1994	U1995	C1996	C1997	A1998	C1999	C2000	C2001	G2002	A2003	G2004	A2005	C2006	U2007	C2008	A2009	G2010	U2011	C2012	A2013	A2014	A2015	U2016	U2017	G2018	A2019	A2020	C2021	U2022	C2023	G2024	C2025	G2026	G2027	U2028	G2029	A2030	A2031	C2032	C2033	U2034	G2035	C2036	A2037	G2038	U2039	G2040	U2041	A2042	
U1923	C1924	C1925	U1926	G1927	A1928	G1929	G1930	U1931	A1932	G1933	C1934	G1935	A1936	A1937	A1938	U1939	U1940	C1941	C1942	U1943	U1944	G1945	U1946	C1947	G1948	G1949	G1950	U1951	A1952	A1953	G1954	U1955	U1956	C1957	C1958	G1959	A1960	C1961	C1962	U1963	G1964	C1965	A1966	G1967	G1968	A1969	U1970	U1971	G1972	C1973	C1974	G1975	U1976	A1977	A1978	U1979	G1980	U1981	U1982	
A1803	C1804	A1805	C1806	G1807	A1808	C1809	A1810	U1811	U1812	G1813	C1814	A1815	C1816	U1817	U1818	A1819	U1820	A1821	C1822	G1823	U1824	U1825	G1826	U1827	G1828	A1829	C1830	G1831	C1832	G1833	U1834	C1835	C1836	U1837	C1838	G1839	U1840	U1841	G1842	C1843	G1844	G1845	G1846	A1847	A1848	G1849	U1850	U1851	U1852	A1853	A1854	U1855	U	A	U	G	G			
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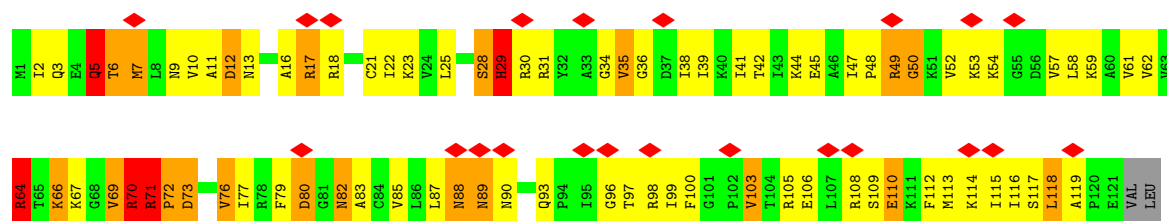
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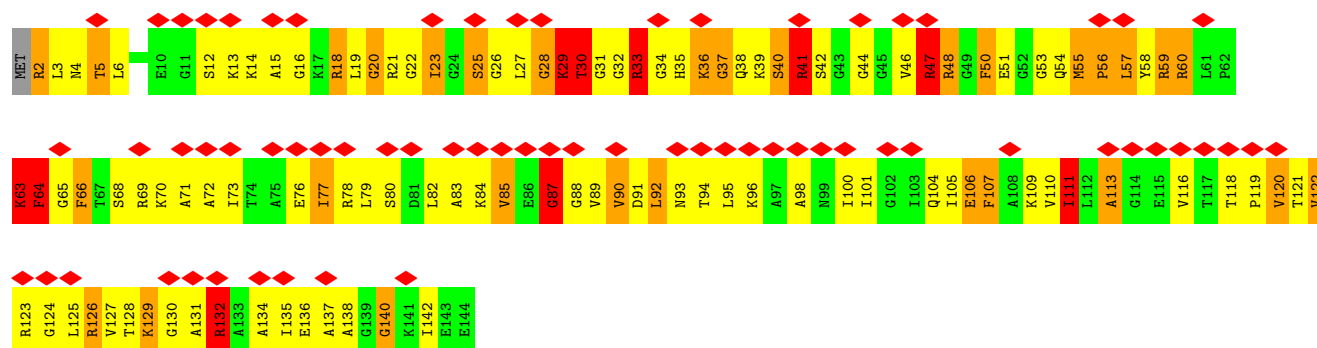
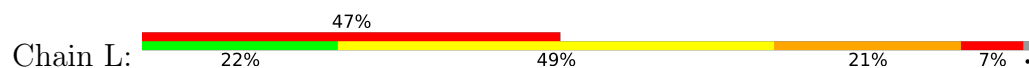
• Molecule 3: 50S ribosomal protein L28



• Molecule 4: 50S ribosomal protein L14



• Molecule 5: 50S ribosomal protein L15

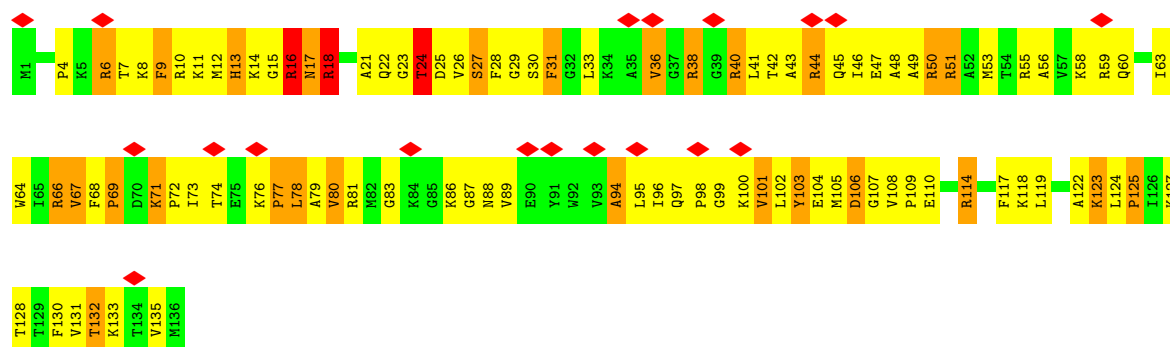


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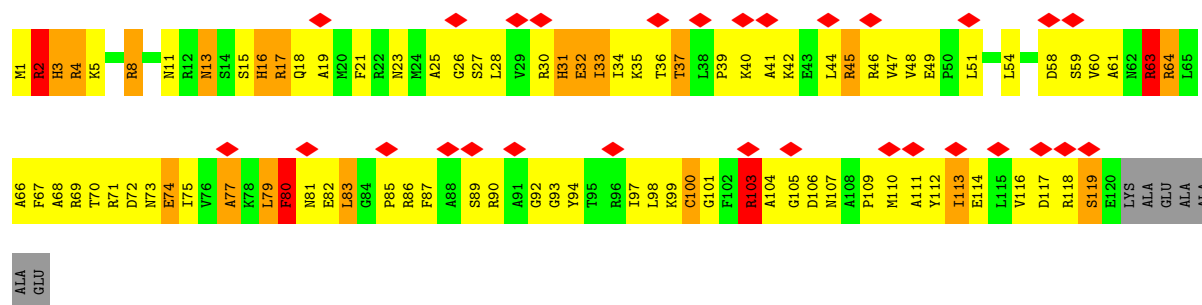




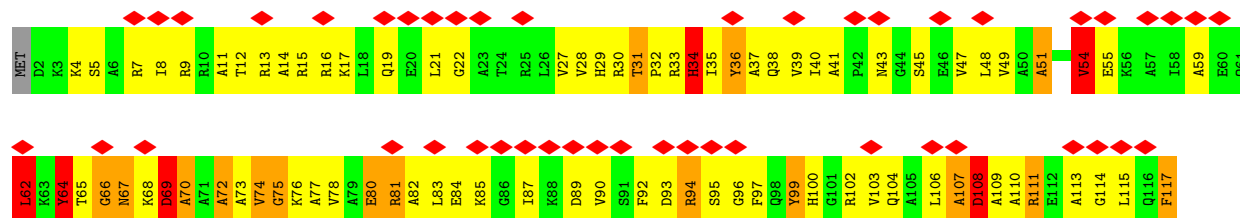
• Molecule 7: 50S ribosomal protein L16



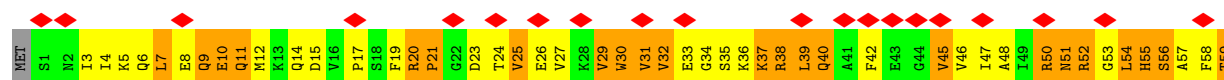
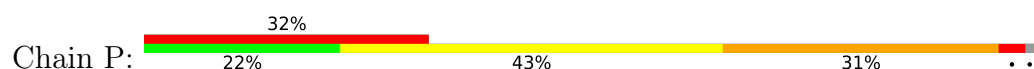
• Molecule 8: 50S ribosomal protein L17

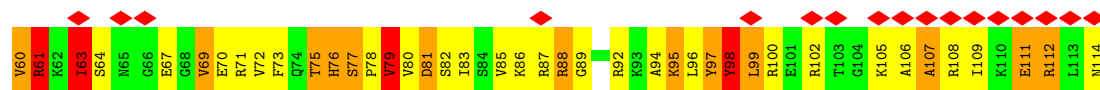


• Molecule 9: 50S ribosomal protein L18

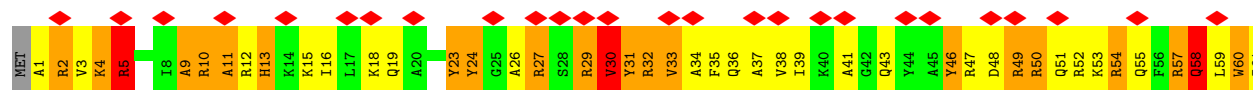
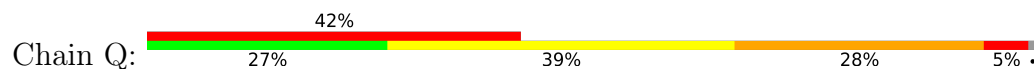


• Molecule 10: 50S ribosomal protein L19

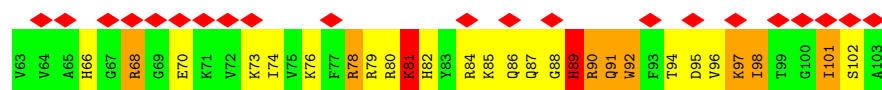
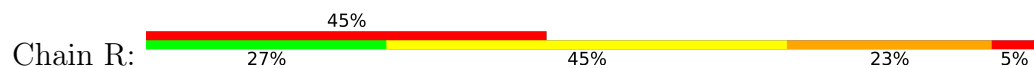




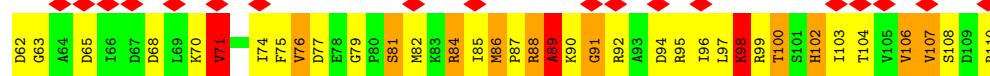
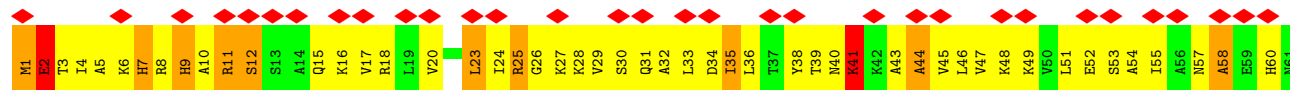
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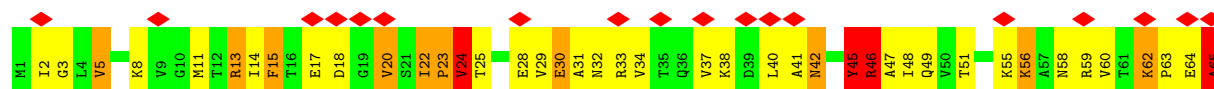
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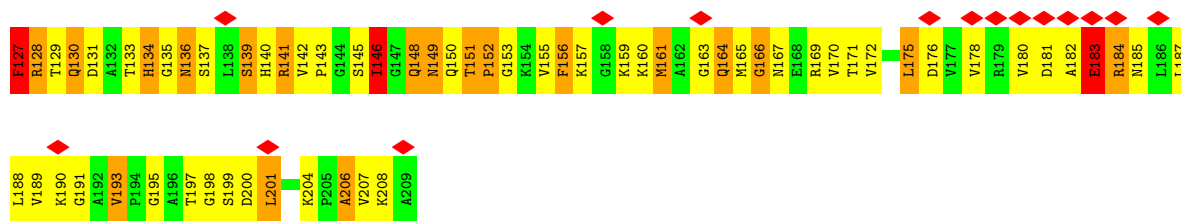


• Molecule 13: 50S ribosomal protein L22

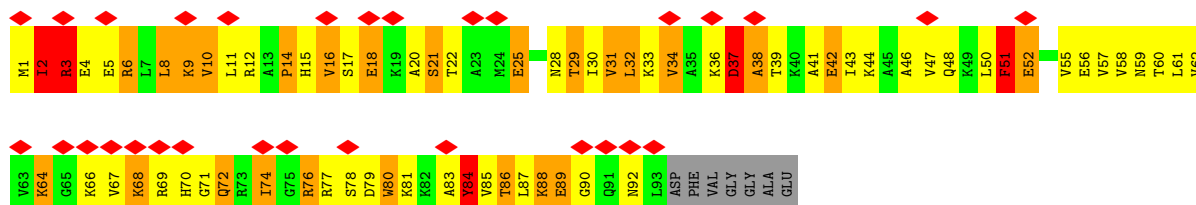
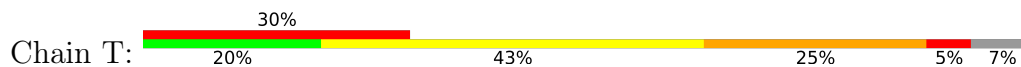


• Molecule 14: 50S ribosomal protein L3

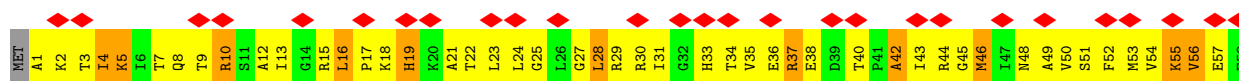




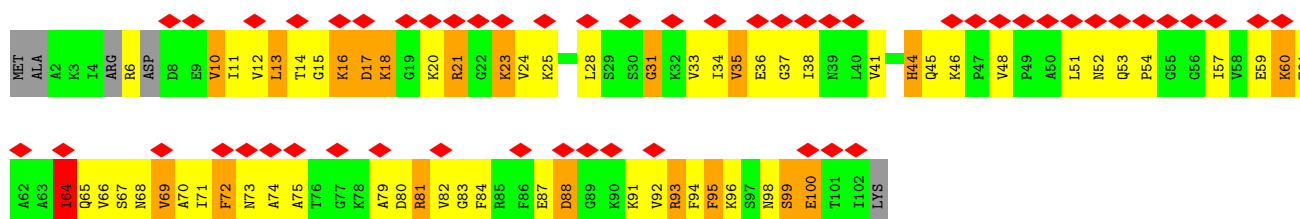
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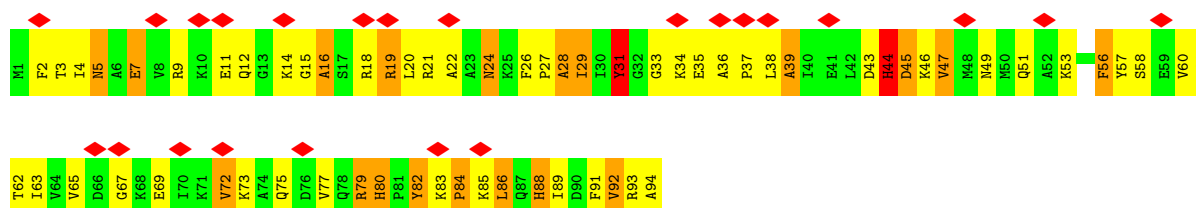
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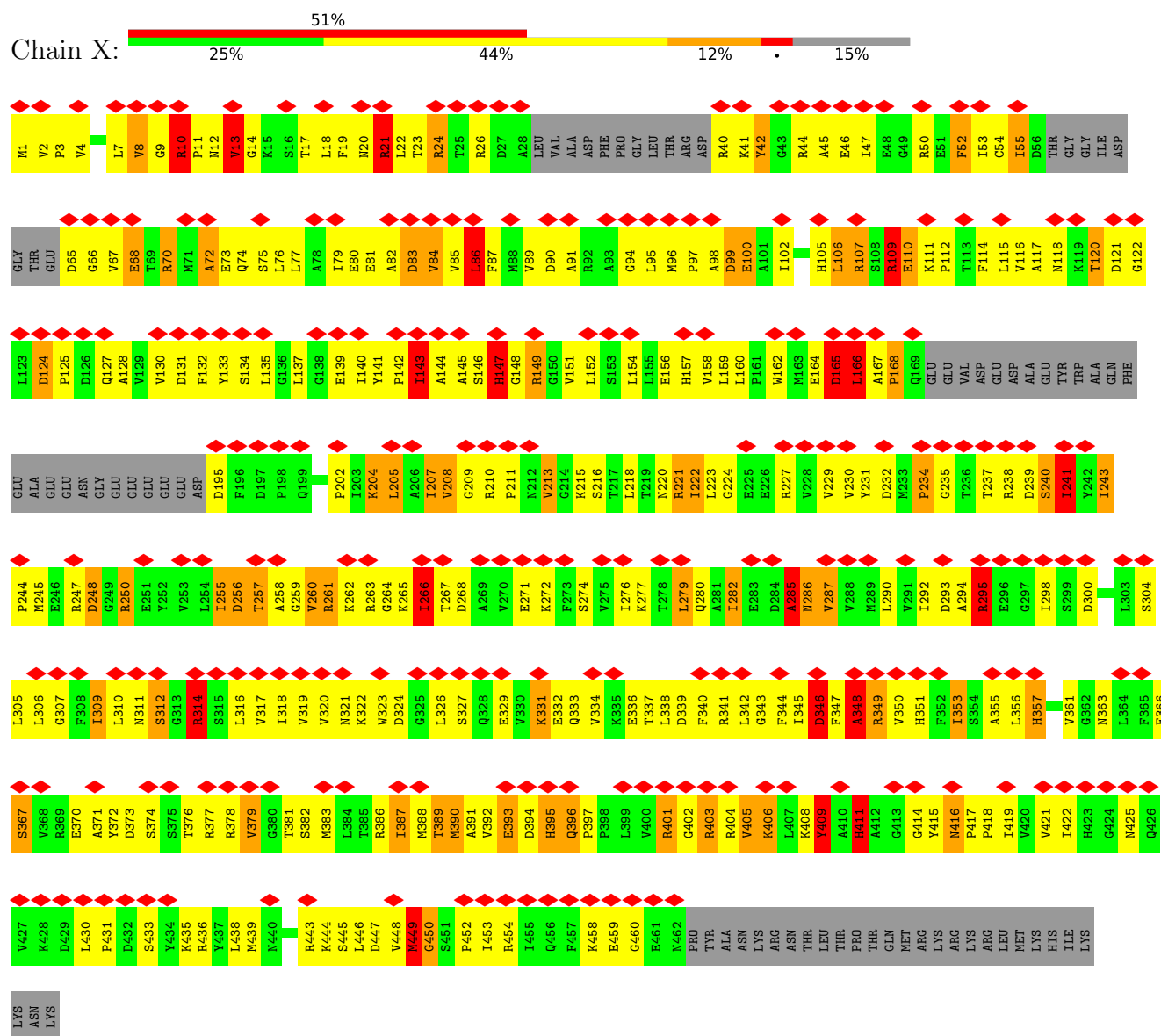
• Molecule 17: 50S ribosomal protein L24



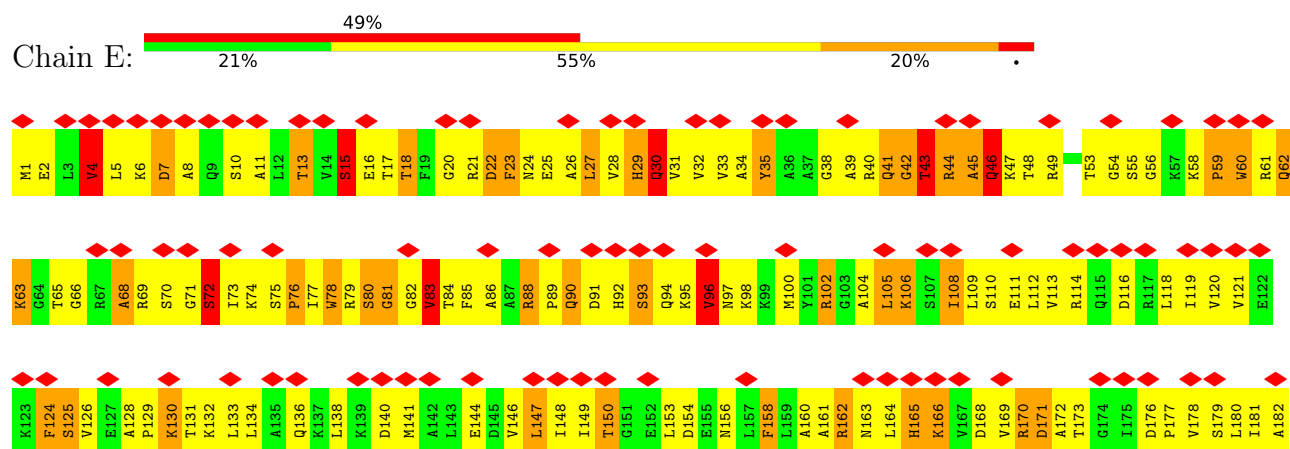
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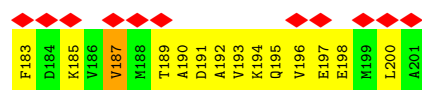


• Molecule 19: GTPase Der

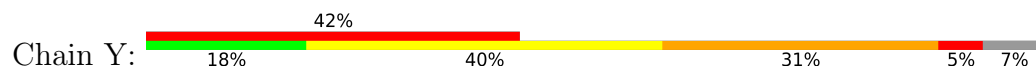


• Molecule 20: 50S ribosomal protein L4

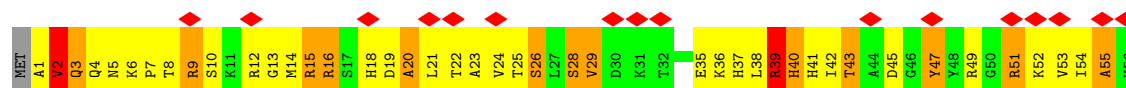
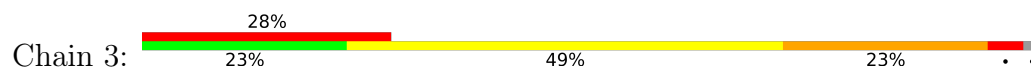




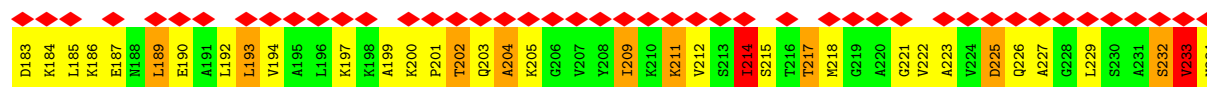
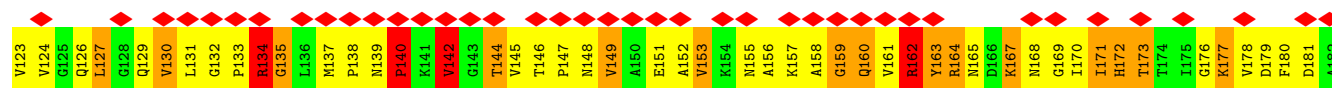
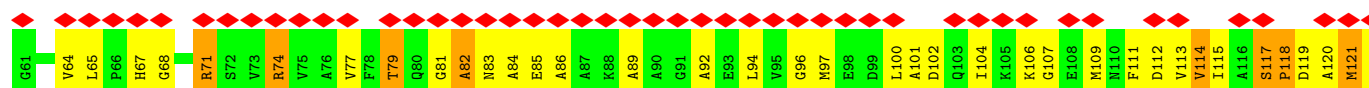
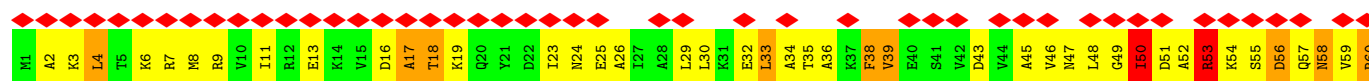
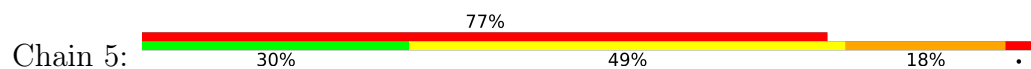
- Molecule 21: 50S ribosomal protein L27



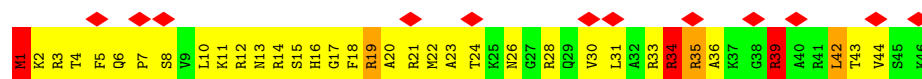
- Molecule 22: 50S ribosomal protein L32



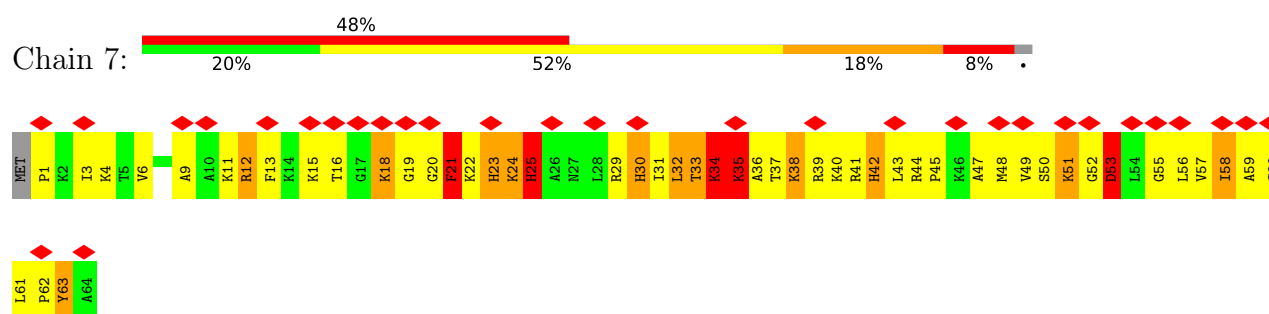
- Molecule 23: 50S ribosomal protein L1



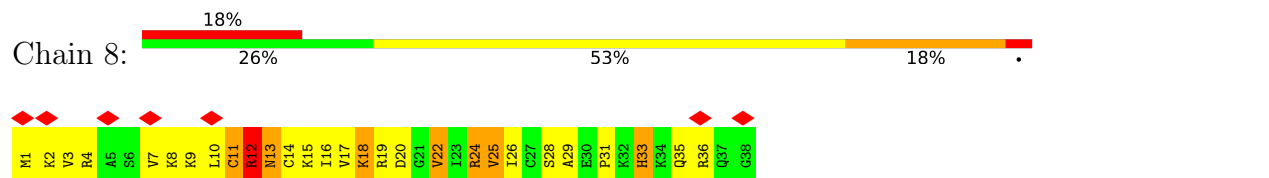
- Molecule 24: 50S ribosomal protein L34



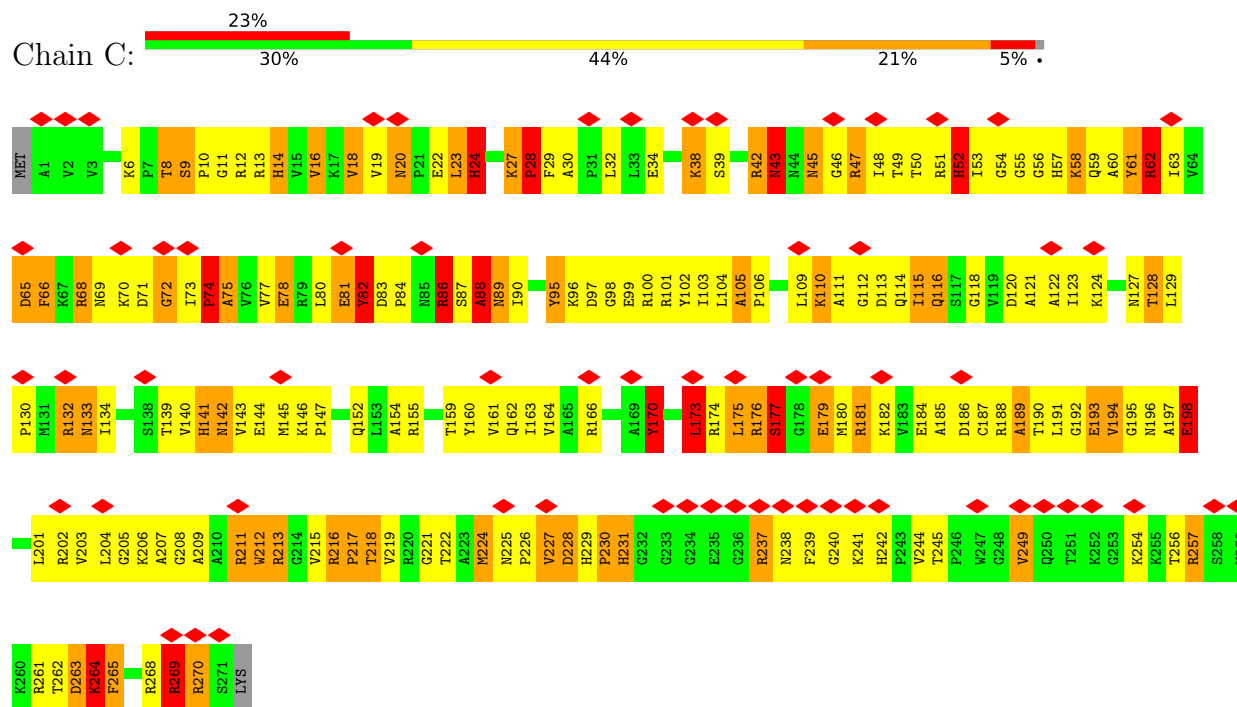
- Molecule 25: 50S ribosomal protein L35



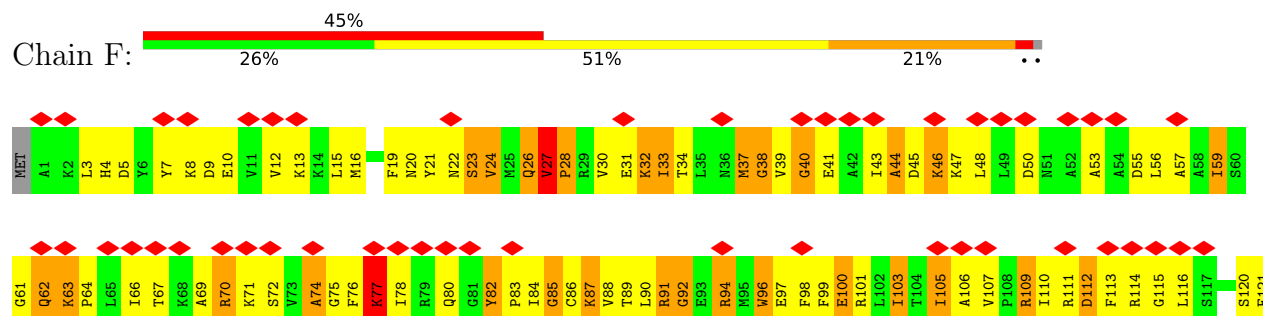
- Molecule 26: 50S ribosomal protein L36

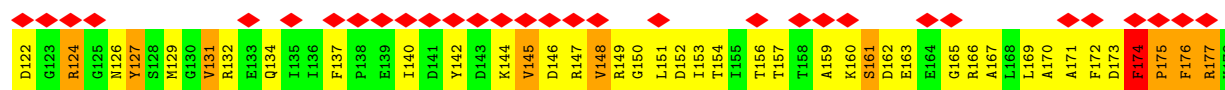


- Molecule 27: 50S ribosomal protein L2

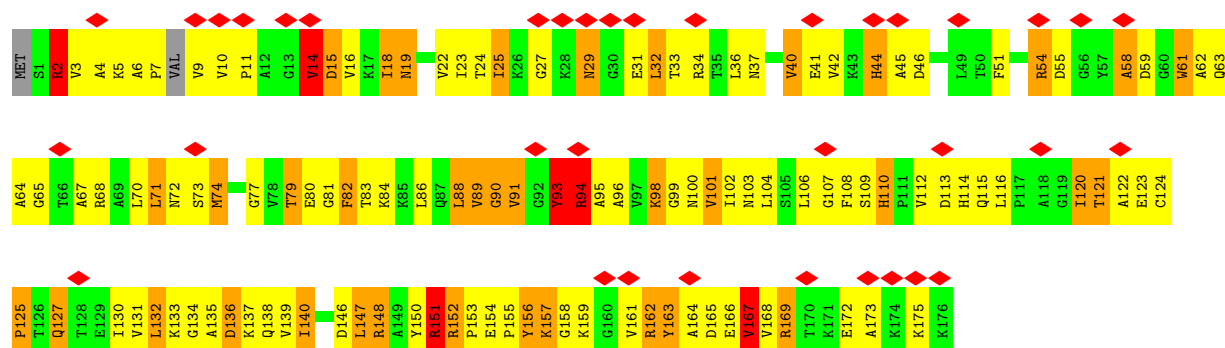


- Molecule 28: 50S ribosomal protein L5

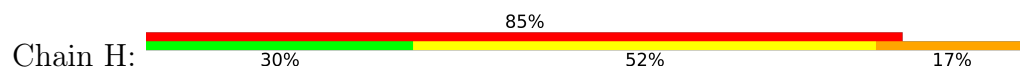




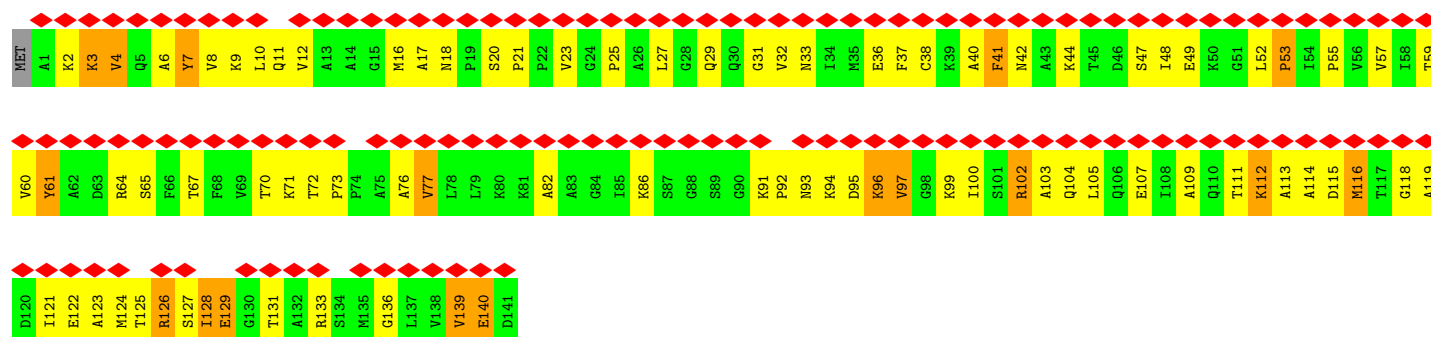
• Molecule 29: 50S ribosomal protein L6



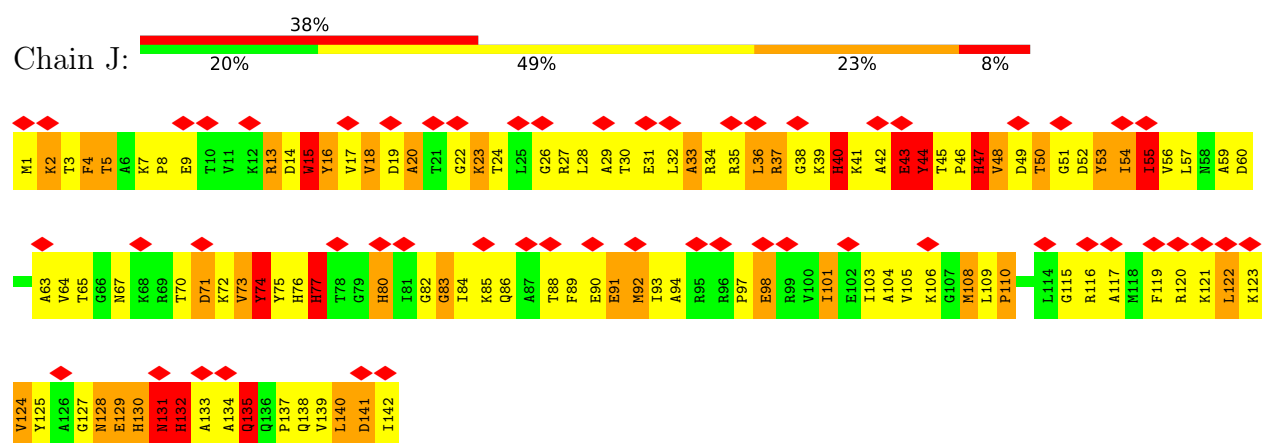
• Molecule 30: 50S ribosomal protein L9



• Molecule 31: 50S ribosomal protein L11



• Molecule 32: 50S ribosomal protein L13



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	189614	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI EAGLE (4k x 4k)	Depositor
Maximum map value	0.232	Depositor
Minimum map value	-0.093	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.045	Depositor
Map size ($\text{\AA}$)	373.088, 373.088, 373.088	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1659, 1.1659, 1.1659	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	2.17	83/2744 (3.0%)	1.96	140/4276 (3.3%)
2	B	2.22	2425/69092 (3.5%)	2.05	3683/107787 (3.4%)
3	0	2.62	44/635 (6.9%)	2.58	50/848 (5.9%)
4	K	2.36	36/940 (3.8%)	2.50	64/1258 (5.1%)
5	L	2.56	73/1054 (6.9%)	2.67	98/1403 (7.0%)
6	1	2.39	25/510 (4.9%)	2.52	34/677 (5.0%)
7	M	2.41	59/1093 (5.4%)	2.46	67/1460 (4.6%)
8	N	2.45	55/973 (5.7%)	2.58	82/1301 (6.3%)
9	O	2.56	63/902 (7.0%)	2.59	74/1209 (6.1%)
10	P	2.49	52/929 (5.6%)	2.55	74/1242 (6.0%)
11	Q	2.47	50/960 (5.2%)	2.77	80/1278 (6.3%)
12	R	2.48	46/829 (5.5%)	2.46	58/1107 (5.2%)
13	S	2.64	60/864 (6.9%)	2.55	59/1156 (5.1%)
14	D	2.51	94/1586 (5.9%)	2.61	131/2134 (6.1%)
15	T	2.65	53/744 (7.1%)	2.73	64/994 (6.4%)
16	2	2.59	25/453 (5.5%)	2.69	41/605 (6.8%)
17	U	2.33	32/761 (4.2%)	2.46	50/1013 (4.9%)
18	W	2.42	34/766 (4.4%)	2.53	57/1025 (5.6%)
19	X	2.34	145/3334 (4.3%)	2.54	266/4502 (5.9%)
20	E	2.52	92/1571 (5.9%)	2.58	127/2113 (6.0%)
21	Y	2.45	28/603 (4.6%)	2.67	54/797 (6.8%)
22	3	2.63	29/450 (6.4%)	2.64	34/599 (5.7%)
23	5	2.37	76/1748 (4.3%)	2.63	153/2355 (6.5%)
24	6	2.64	26/380 (6.8%)	2.54	28/498 (5.6%)
25	7	2.50	32/513 (6.2%)	2.66	45/676 (6.7%)
26	8	2.38	13/303 (4.3%)	2.45	15/397 (3.8%)
27	C	2.52	116/2121 (5.5%)	2.60	180/2852 (6.3%)
28	F	2.26	53/1444 (3.7%)	2.57	111/1937 (5.7%)
29	G	2.44	71/1335 (5.3%)	2.53	96/1803 (5.3%)
30	H	2.30	40/1122 (3.6%)	2.46	94/1515 (6.2%)
31	I	2.26	40/1046 (3.8%)	2.55	83/1410 (5.9%)
32	J	2.56	64/1152 (5.6%)	2.52	90/1551 (5.8%)
All	All	2.29	4134/102957 (4.0%)	2.20	6282/153778 (4.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	69
2	B	0	1764
3	O	0	5
4	K	0	4
5	L	0	10
6	1	0	6
7	M	0	9
8	N	0	4
9	O	0	5
10	P	0	7
11	Q	0	11
12	R	0	8
13	S	0	3
14	D	0	11
15	T	0	3
16	2	0	4
17	U	0	4
18	W	0	2
19	X	0	25
20	E	0	7
21	Y	0	6
22	3	0	4
23	5	0	7
24	6	0	3
25	7	0	3
26	8	0	1
27	C	0	11
28	F	0	6
29	G	0	9
30	H	0	9
31	I	0	3
32	J	0	9
All	All	0	2032

The worst 5 of 4134 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	J	57	LEU	CA-C	-18.93	1.40	1.52
20	E	165	HIS	N-CA	-17.39	1.31	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	L	106	GLU	CA-C	-12.69	1.37	1.52
20	E	197	GLU	N-CA	-12.58	1.31	1.46
16	2	31	ILE	CA-CB	-12.27	1.38	1.54

The worst 5 of 6282 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	T	25	GLU	N-CA-C	-18.98	92.99	114.62
11	Q	35	PHE	N-CA-C	-17.07	90.87	112.72
2	B	680	C	C5'-C4'-C3'	16.81	141.22	116.00
2	B	471	A	P-O3'-C3'	16.42	144.82	120.20
19	X	272	LYS	N-CA-C	15.92	128.10	111.07

There are no chirality outliers.

5 of 2032 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2	G	Sidechain
1	A	4	C	Sidechain
1	A	5	U	Sidechain
1	A	7	G	Sidechain
1	A	8	C	Sidechain

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	A	2455	0	1253	65	0
2	B	61689	0	30889	2040	0
3	O	625	0	655	9	0
4	K	931	0	1003	13	0
5	L	1045	0	1117	18	0
6	1	509	0	543	8	0
7	M	1074	0	1157	17	0
8	N	960	0	1000	15	0
9	O	892	0	923	10	0
10	P	917	0	965	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	Q	947	0	1022	17	0
12	R	816	0	839	13	0
13	S	857	0	922	18	0
14	D	1565	0	1616	27	0
15	T	738	0	807	8	0
16	2	449	0	491	7	0
17	U	755	0	807	6	0
18	W	753	0	780	11	0
19	X	3280	0	3334	51	0
20	E	1552	0	1619	27	0
21	Y	596	0	610	14	0
22	3	444	0	461	7	0
23	5	1733	0	1824	20	0
24	6	377	0	418	6	0
25	7	504	0	574	9	0
26	8	302	0	343	8	0
27	C	2082	0	2157	32	0
28	F	1420	0	1460	18	0
29	G	1316	0	1364	15	0
30	H	1111	0	1148	13	0
31	I	1032	0	1088	4	0
32	J	1129	0	1162	34	0
All	All	94855	0	64351	2486	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 16.

The worst 5 of 2486 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)
19:X:347:PHE:CD2	19:X:449:MET:CG	2.00	1.45
19:X:347:PHE:CD2	19:X:449:MET:HG2	1.49	1.26
19:X:449:MET:HA	19:X:449:MET:HE2	1.20	1.10
19:X:347:PHE:CD2	19:X:449:MET:HG3	1.84	0.97
19:X:449:MET:HA	19:X:449:MET:CE	1.97	0.94

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	
3	0	75/78 (96%)	54 (72%)	11 (15%)	10 (13%)	0	3
4	K	119/123 (97%)	84 (71%)	21 (18%)	14 (12%)	0	5
5	L	141/144 (98%)	108 (77%)	23 (16%)	10 (7%)	1	10
6	1	61/63 (97%)	49 (80%)	12 (20%)	0	100	100
7	M	134/136 (98%)	97 (72%)	18 (13%)	19 (14%)	0	3
8	N	118/127 (93%)	91 (77%)	20 (17%)	7 (6%)	1	13
9	O	114/117 (97%)	96 (84%)	12 (10%)	6 (5%)	1	14
10	P	112/115 (97%)	81 (72%)	18 (16%)	13 (12%)	0	5
11	Q	115/118 (98%)	87 (76%)	17 (15%)	11 (10%)	0	7
12	R	101/103 (98%)	71 (70%)	23 (23%)	7 (7%)	1	11
13	S	108/110 (98%)	83 (77%)	16 (15%)	9 (8%)	0	9
14	D	207/209 (99%)	143 (69%)	42 (20%)	22 (11%)	0	6
15	T	91/100 (91%)	58 (64%)	17 (19%)	16 (18%)	0	2
16	2	56/59 (95%)	46 (82%)	7 (12%)	3 (5%)	1	14
17	U	94/104 (90%)	66 (70%)	16 (17%)	12 (13%)	0	4
18	W	92/94 (98%)	77 (84%)	10 (11%)	5 (5%)	1	14
19	X	410/490 (84%)	329 (80%)	46 (11%)	35 (8%)	0	8
20	E	199/201 (99%)	145 (73%)	28 (14%)	26 (13%)	0	3
21	Y	77/85 (91%)	43 (56%)	15 (20%)	19 (25%)	0	1
22	3	54/57 (95%)	36 (67%)	10 (18%)	8 (15%)	0	3
23	5	232/234 (99%)	185 (80%)	23 (10%)	24 (10%)	0	6
24	6	44/46 (96%)	33 (75%)	7 (16%)	4 (9%)	0	8
25	7	62/65 (95%)	44 (71%)	11 (18%)	7 (11%)	0	5
26	8	36/38 (95%)	26 (72%)	6 (17%)	4 (11%)	0	6
27	C	269/273 (98%)	201 (75%)	35 (13%)	33 (12%)	0	4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	F	176/179 (98%)	119 (68%)	41 (23%)	16 (9%)	0	8
29	G	171/177 (97%)	128 (75%)	26 (15%)	17 (10%)	0	7
30	H	147/149 (99%)	109 (74%)	25 (17%)	13 (9%)	0	8
31	I	139/142 (98%)	114 (82%)	16 (12%)	9 (6%)	1	12
32	J	140/142 (99%)	102 (73%)	21 (15%)	17 (12%)	0	4
All	All	3894/4078 (96%)	2905 (75%)	593 (15%)	396 (10%)	1	6

5 of 396 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	0	15	ASN
3	0	28	PHE
3	0	70	LEU
5	L	29	LYS
5	L	41	ARG

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	0	67/68 (98%)	62 (92%)	5 (8%)	12	33
4	K	102/104 (98%)	91 (89%)	11 (11%)	6	21
5	L	102/103 (99%)	89 (87%)	13 (13%)	4	17
6	1	55/55 (100%)	50 (91%)	5 (9%)	9	28
7	M	109/109 (100%)	103 (94%)	6 (6%)	19	42
8	N	100/103 (97%)	89 (89%)	11 (11%)	6	21
9	O	86/87 (99%)	73 (85%)	13 (15%)	3	13
10	P	99/100 (99%)	86 (87%)	13 (13%)	4	16
11	Q	89/90 (99%)	78 (88%)	11 (12%)	4	18
12	R	84/84 (100%)	68 (81%)	16 (19%)	1	8
13	S	93/93 (100%)	85 (91%)	8 (9%)	10	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	D	164/164 (100%)	143 (87%)	21 (13%)	4	17
15	T	80/84 (95%)	67 (84%)	13 (16%)	2	11
16	2	48/49 (98%)	44 (92%)	4 (8%)	10	30
17	U	81/85 (95%)	73 (90%)	8 (10%)	7	24
18	W	78/78 (100%)	72 (92%)	6 (8%)	12	32
19	X	357/419 (85%)	324 (91%)	33 (9%)	8	27
20	E	165/165 (100%)	151 (92%)	14 (8%)	10	29
21	Y	59/63 (94%)	54 (92%)	5 (8%)	10	29
22	3	47/48 (98%)	39 (83%)	8 (17%)	2	11
23	5	181/181 (100%)	158 (87%)	23 (13%)	4	17
24	6	38/38 (100%)	35 (92%)	3 (8%)	11	32
25	7	51/52 (98%)	44 (86%)	7 (14%)	3	15
26	8	34/34 (100%)	31 (91%)	3 (9%)	9	29
27	C	216/218 (99%)	192 (89%)	24 (11%)	6	20
28	F	149/150 (99%)	134 (90%)	15 (10%)	7	23
29	G	136/138 (99%)	115 (85%)	21 (15%)	2	12
30	H	114/114 (100%)	105 (92%)	9 (8%)	11	32
31	I	109/110 (99%)	100 (92%)	9 (8%)	10	30
32	J	116/116 (100%)	103 (89%)	13 (11%)	6	20
All	All	3209/3302 (97%)	2858 (89%)	351 (11%)	8	21

5 of 351 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	5	109	MET
28	F	10	GLU
23	5	184	LYS
27	C	18	VAL
29	G	14	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 93 such sidechains are listed below:

Mol	Chain	Res	Type
21	Y	75	ASN

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Mol	Chain	Res	Type
27	C	199	HIS
22	3	5	ASN
25	7	23	HIS
28	F	22	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	112/117 (95%)	20 (17%)	4 (3%)
2	B	2873/2903 (98%)	586 (20%)	122 (4%)
All	All	2985/3020 (98%)	606 (20%)	126 (4%)

5 of 606 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	G
1	A	13	G
1	A	14	U
1	A	15	A
1	A	16	G

5 of 126 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	1284	A
2	B	2402	U
2	B	1730	C
2	B	2336	A
2	B	2601	C

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

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

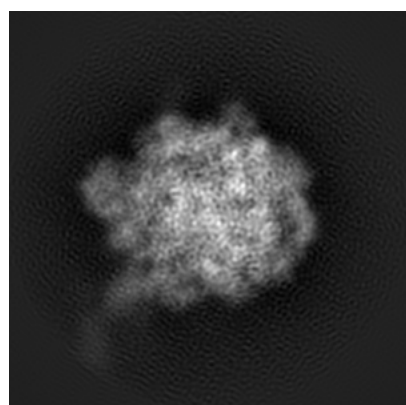
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6149. These allow visual inspection of the internal detail of the map and identification of artifacts.

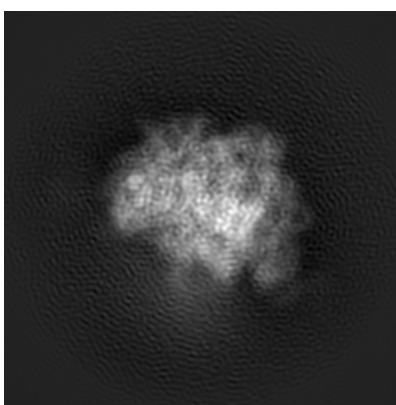
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

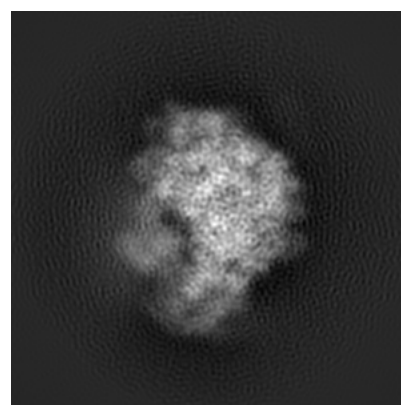
6.1.1 Primary map



X



Y

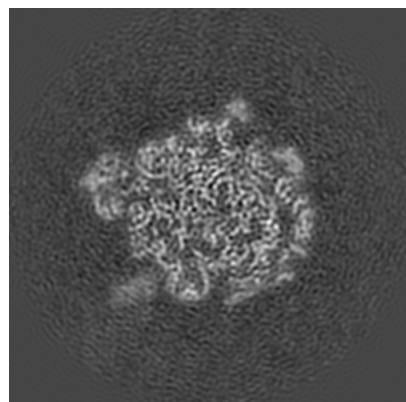


Z

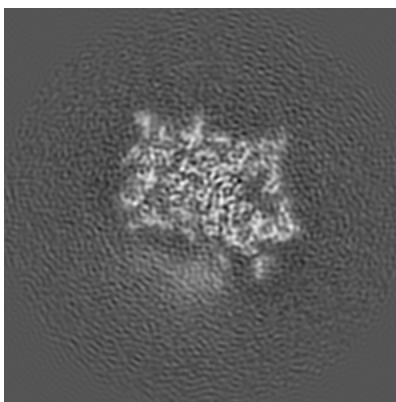
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

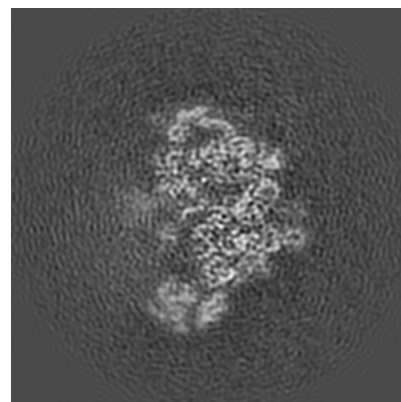
6.2.1 Primary map



X Index: 160



Y Index: 160

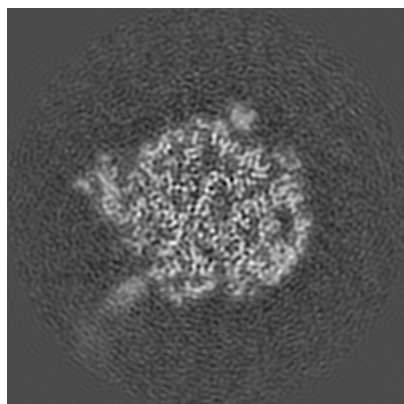


Z Index: 160

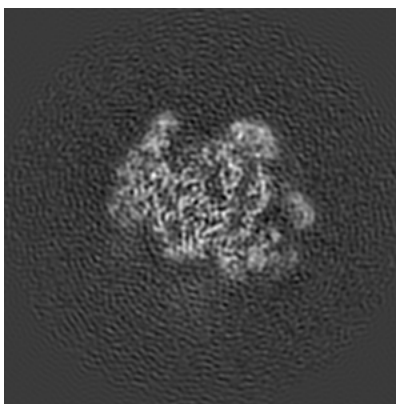
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

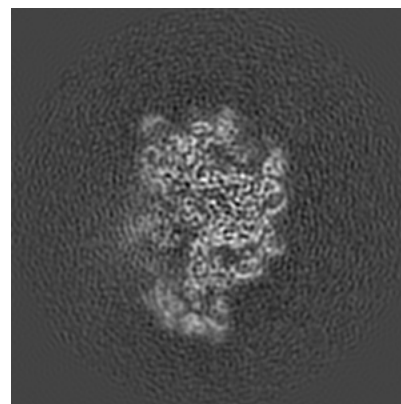
6.3.1 Primary map



X Index: 166



Y Index: 181

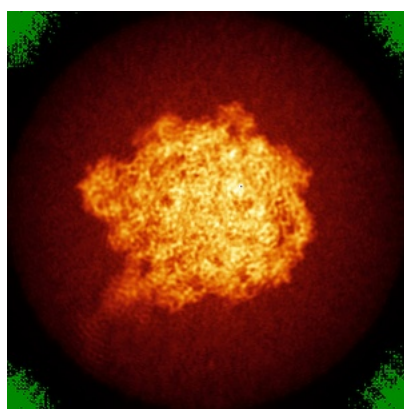


Z Index: 176

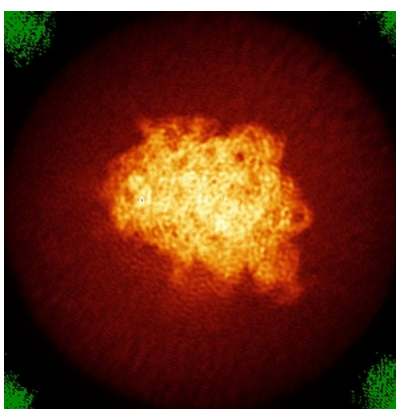
The images above show the largest variance slices of the map in three orthogonal directions.

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

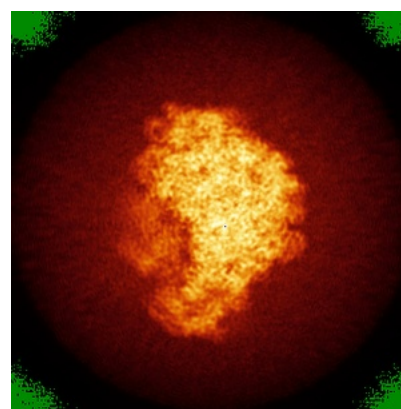
6.4.1 Primary map



X



Y

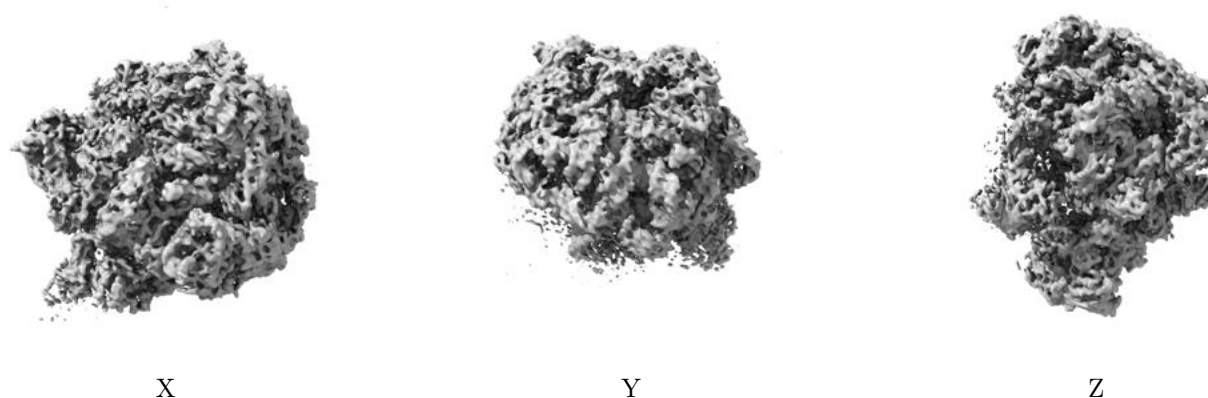


Z

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

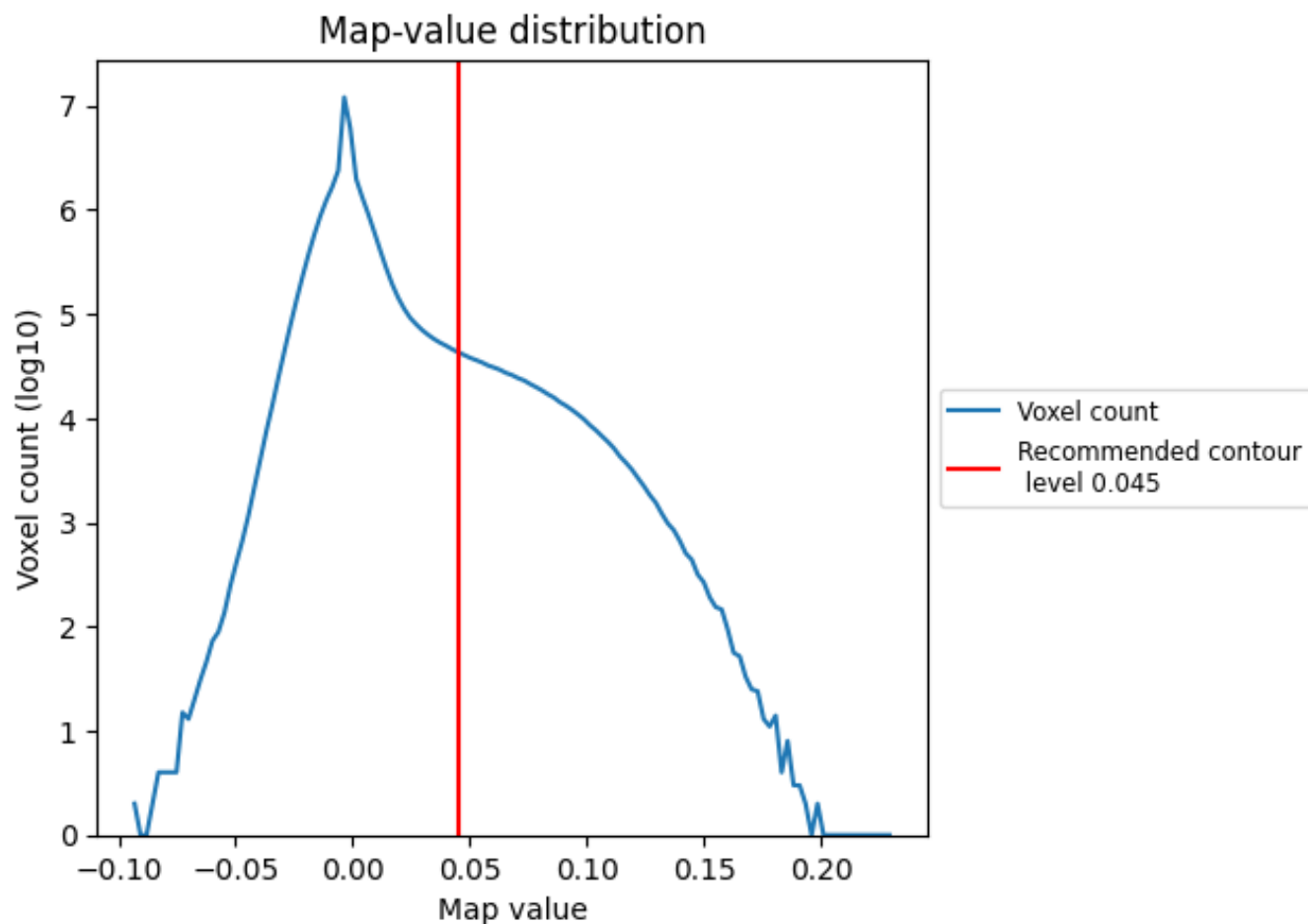
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

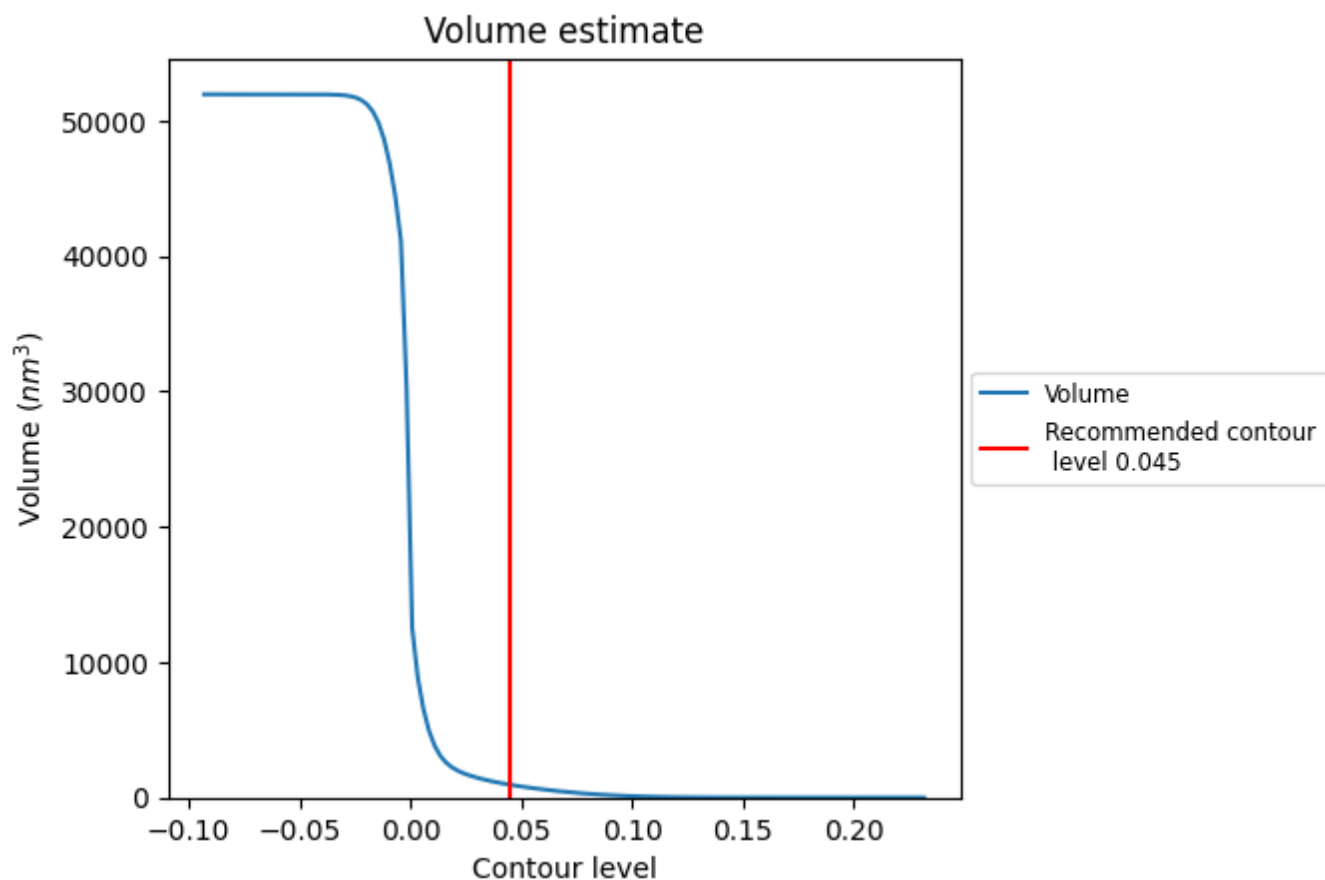
This section contains the results of statistical analysis of the map.

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.

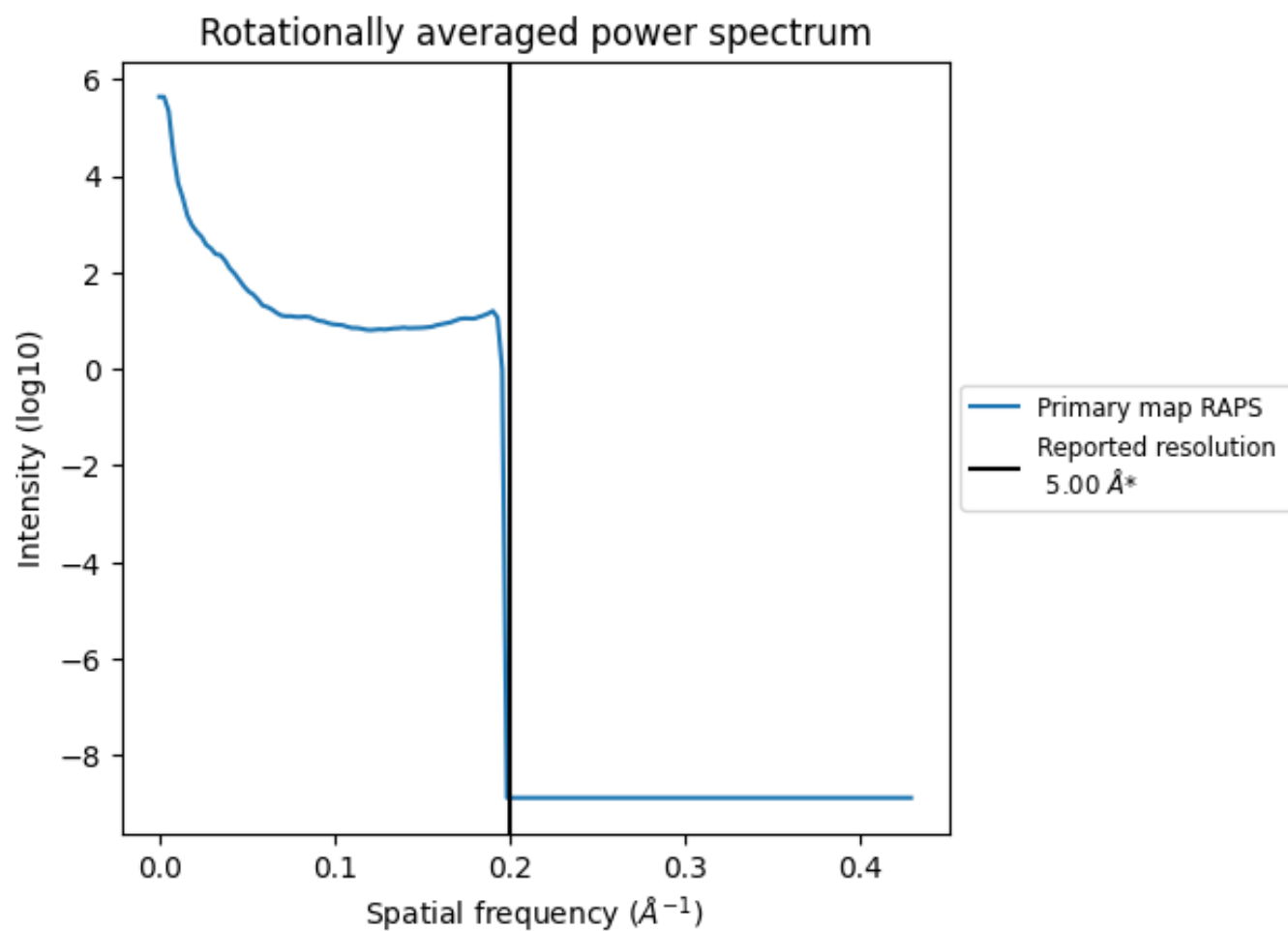
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 946 nm³; this corresponds to an approximate mass of 854 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

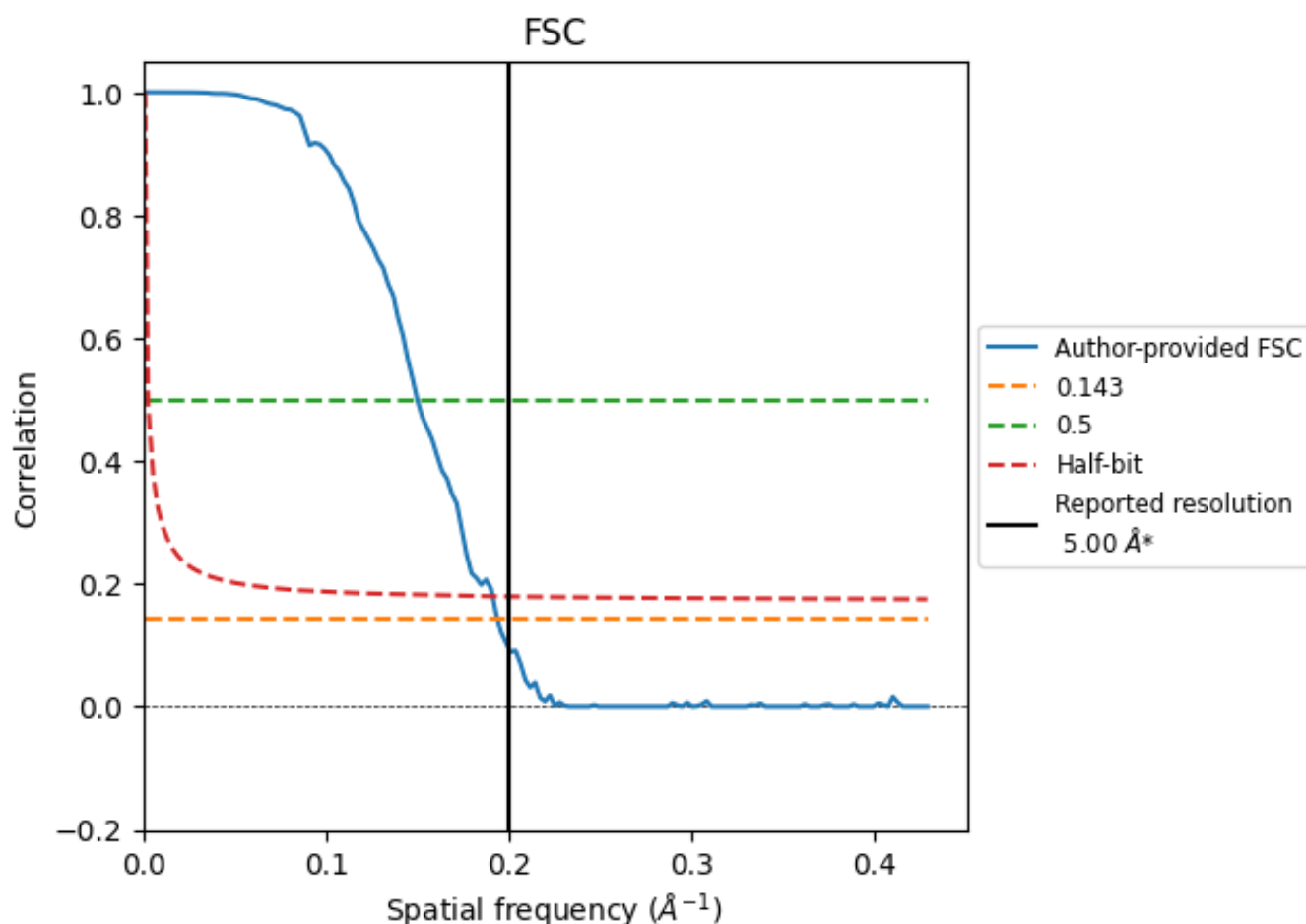


*Reported resolution corresponds to spatial frequency of 0.200 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.200 Å⁻¹

8.2 Resolution estimates [i](#)

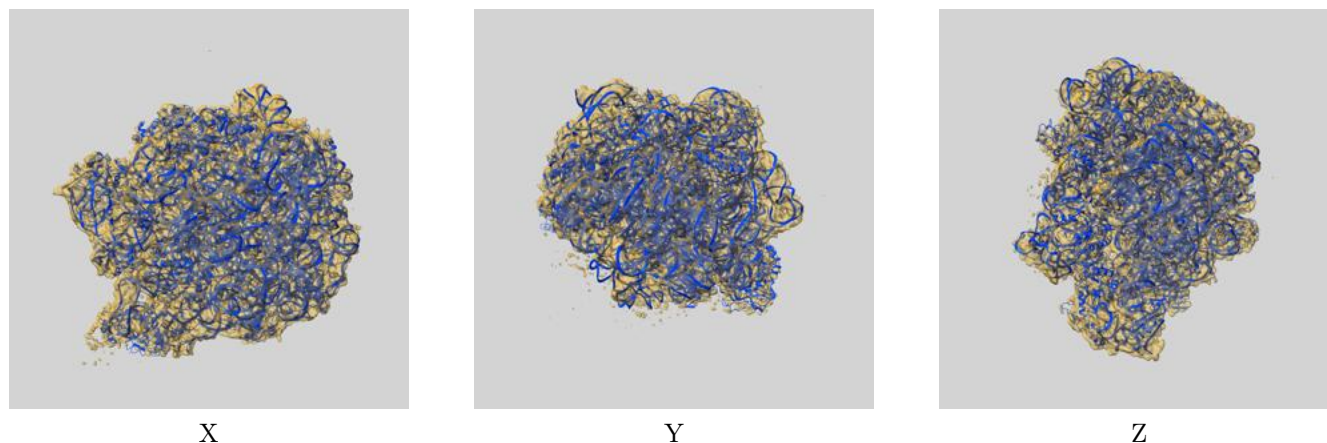
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.00	-	-
Author-provided FSC curve	5.16	6.67	5.23
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

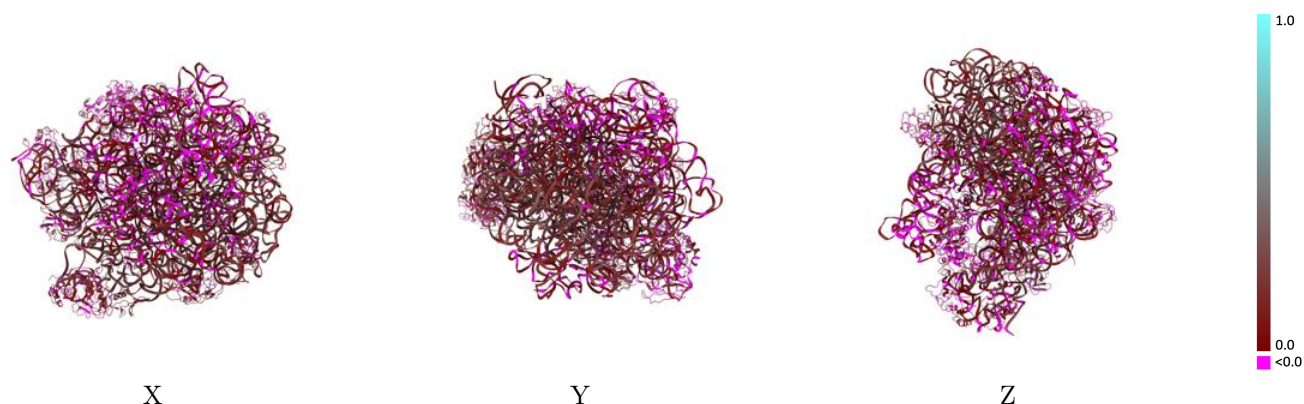
This section contains information regarding the fit between EMDB map EMD-6149 and PDB model 3J8G. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



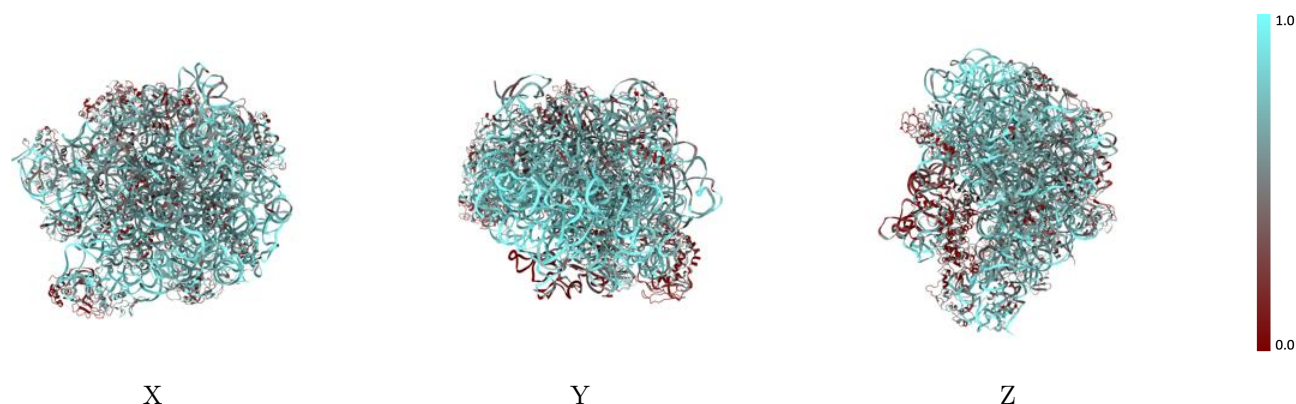
The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



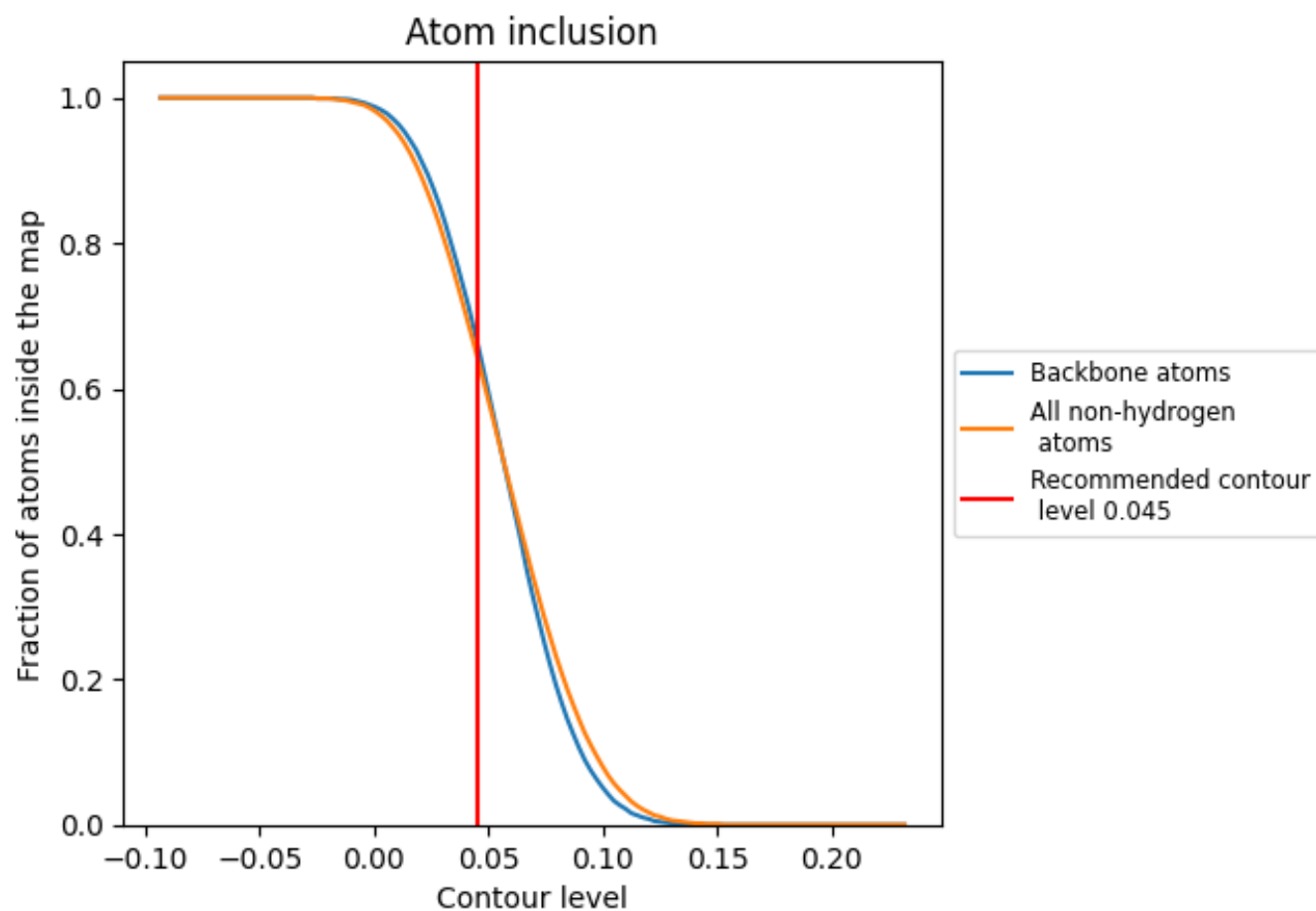
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.045).

9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 65% 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 (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6460	 0.1310
0	 0.4330	 0.0960
1	 0.4370	 0.0650
2	 0.4600	 0.0490
3	 0.5190	 0.1010
5	 0.2170	 0.0350
6	 0.5320	 0.1150
7	 0.4440	 0.0550
8	 0.6370	 0.1510
A	 0.7770	 0.1370
B	 0.7330	 0.1480
C	 0.5890	 0.1510
D	 0.6000	 0.1610
E	 0.4220	 0.0490
F	 0.4560	 0.0680
G	 0.6020	 0.1610
H	 0.1650	 0.0600
I	 0.0460	 0.0270
J	 0.5010	 0.1070
K	 0.6060	 0.1510
L	 0.4460	 0.0560
M	 0.6140	 0.1780
N	 0.6190	 0.1280
O	 0.5280	 0.0920
P	 0.5610	 0.1610
Q	 0.5000	 0.0650
R	 0.4560	 0.0500
S	 0.4400	 0.0580
T	 0.5250	 0.1040
U	 0.4280	 0.0400
W	 0.5580	 0.1540
X	 0.3430	 0.0850
Y	 0.4840	 0.0580

