



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 02:08 PM UTC

PDB ID : 4V92 / pdb_00004v92
EMDB ID : EMD-2604
Title : Kluyveromyces lactis 80S ribosome in complex with CrPV-IRES
Authors : Fernandez, I.S.; Bai, X.; Scheres, S.H.W.; Ramakrishnan, V.
Deposited on : 2014-03-21
Resolution : 3.70 Å(reported)
Based on initial model : 3B31

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

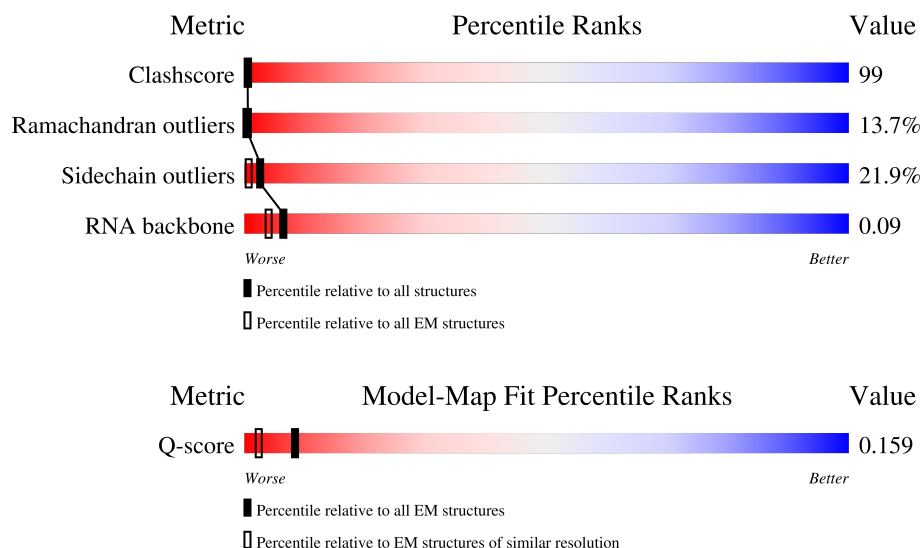
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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	10198 (3.30 - 4.30)

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	A2	1767	
2	AZ	190	
3	BA	206	

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Mol	Chain	Length	Quality of chain
4	BB	213	
5	BC	216	
6	BD	222	
7	BE	260	
8	BF	206	
9	BG	226	
10	BH	184	
11	BI	187	
12	BJ	179	
13	BK	93	
14	BL	142	
15	BM	120	
16	BN	150	
17	BO	127	
18	BP	115	
19	BQ	140	
20	BR	121	
21	BS	140	
22	BT	142	
23	BU	104	
24	BV	87	
25	BW	129	
26	BX	142	
27	BY	134	
28	BZ	64	

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Mol	Chain	Length	Quality of chain
29	Ba	97	
30	Bb	81	
31	Bc	63	
32	Bd	52	
33	Be	55	
34	Bf	64	
35	Bg	315	

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 79002 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 18S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A2	1764	Total	C	N	O	P	0	0
			37579	16801	6644	12370	1764		

- Molecule 2 is a RNA chain called RNA OF CRICKET-PARALYSIS-VIRUS-IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AZ	190	Total	C	N	O	P	0	0
			4018	1801	685	1342	190		

- Molecule 3 is a protein called US2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	BA	206	Total	C	N	O	S	0	0
			1577	1014	278	283	2		

- Molecule 4 is a protein called ES1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	BB	213	Total	C	N	O	S	0	0
			1686	1070	302	310	4		

- Molecule 5 is a protein called US5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	BC	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 6 is a protein called US3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	BD	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

- Molecule 7 is a protein called ES4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	BE	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 8 is a protein called US7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	BF	206	Total	C	N	O	S	0	0
			1603	1004	297	299	3		

- Molecule 9 is a protein called ES6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	BG	226	Total	C	N	O	S	0	0
			1790	1123	343	321	3		

- Molecule 10 is a protein called ES7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	BH	184	Total	C	N	O	S	0	0
			1481	951	265	265			

- Molecule 11 is a protein called ES8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	BI	187	Total	C	N	O	S	0	0
			1480	919	296	263	2		

- Molecule 12 is a protein called US4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	BJ	179	Total	C	N	O	S	0	0
			1452	919	282	250	1		

- Molecule 13 is a protein called ES10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BK	93	Total	C	N	O	S	0	0
			765	496	123	144	2		

- Molecule 14 is a protein called US17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	BL	142	Total	C	N	O	S	0	0
			1146	735	217	191	3		

- Molecule 15 is a protein called ES12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BM	120	Total	C	N	O	S	0	0
			870	548	152	168	2		

- Molecule 16 is a protein called US15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BN	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 17 is a protein called US11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BO	127	Total	C	N	O	S	0	0
			905	555	183	165	2		

- Molecule 18 is a protein called US19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BP	115	Total	C	N	O	S	0	0
			914	585	165	157	7		

- Molecule 19 is a protein called US9.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	BQ	140	Total	C	N	O	0	0
			1082	696	193	193		

- Molecule 20 is a protein called ES17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BR	121	Total	C	N	O	S	0	0
			934	583	179	170	2		

- Molecule 21 is a protein called US13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BS	140	Total	C	N	O	S	0	0
			1150	720	223	205	2		

- Molecule 22 is a protein called ES19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BT	142	Total	C	N	O	S	0	0
			1105	689	207	207	2		

- Molecule 23 is a protein called US10.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	BU	104	Total	C	N	O	S	0	0
			829	525	150	153	1		

- Molecule 24 is a protein called ES21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BV	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 25 is a protein called US8.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 26 is a protein called US12.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BX	142	Total	C	N	O	S	0	0
			1101	698	215	186	2		

- Molecule 27 is a protein called ES24.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	BY	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 28 is a protein called ES25.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	BZ	64	Total	C	N	O	0	0
			518	331	95	92		

- Molecule 29 is a protein called ES26.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ba	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 30 is a protein called ES27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Bb	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 31 is a protein called ES28.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Bc	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 32 is a protein called US14.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Bd	52	Total	C	N	O	S	0	0
			433	269	91	69	4		

- Molecule 33 is a protein called ES30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Be	55	Total	C	N	O	S	0	0
			440	277	90	72	1		

- Molecule 34 is a protein called ES31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Bf	64	Total	C	N	O	S	0	0
			458	289	83	82	4		

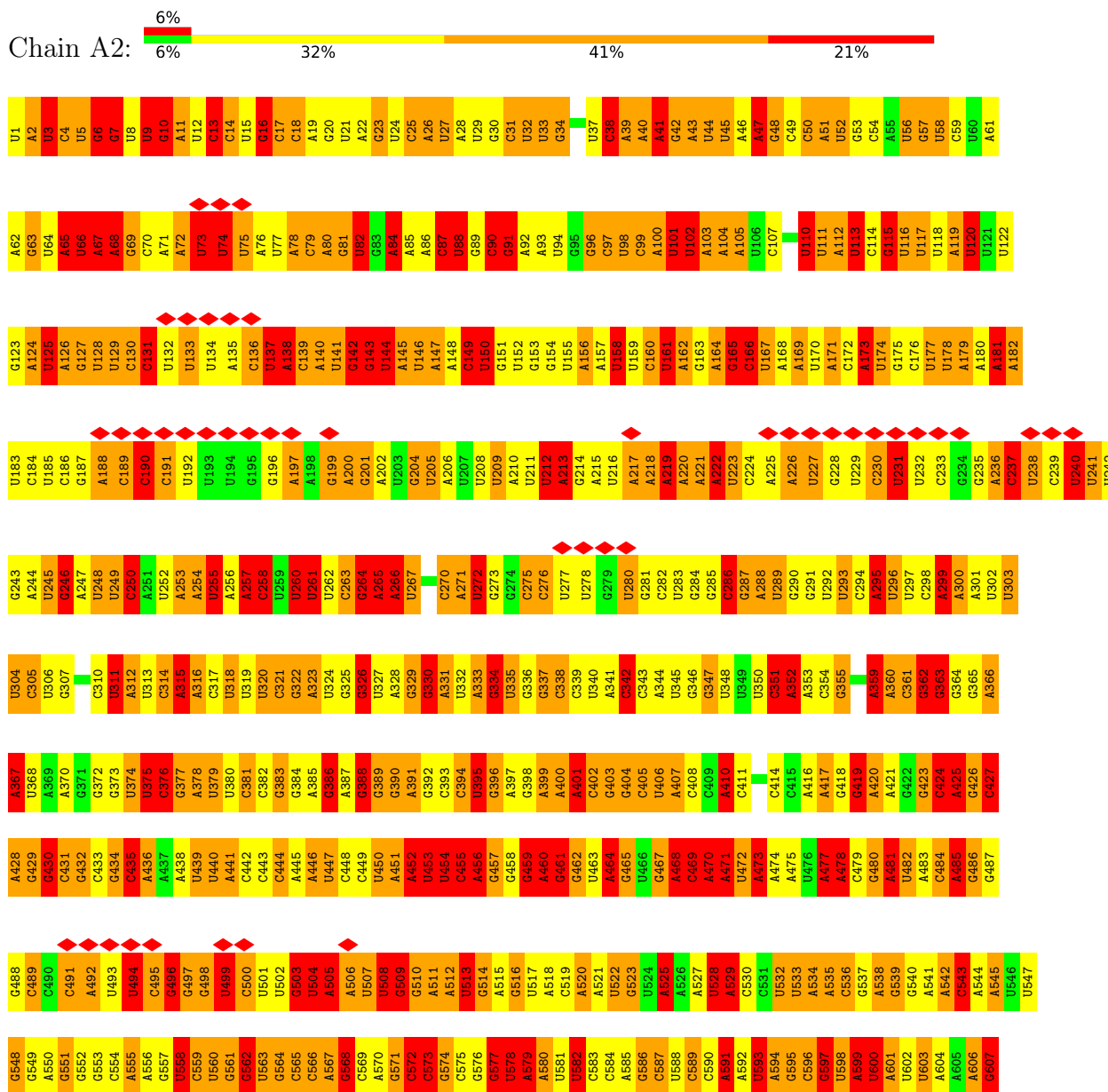
- Molecule 35 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Bg	315	Total	C	N	O	S	0	0
			2417	1531	414	464	8		

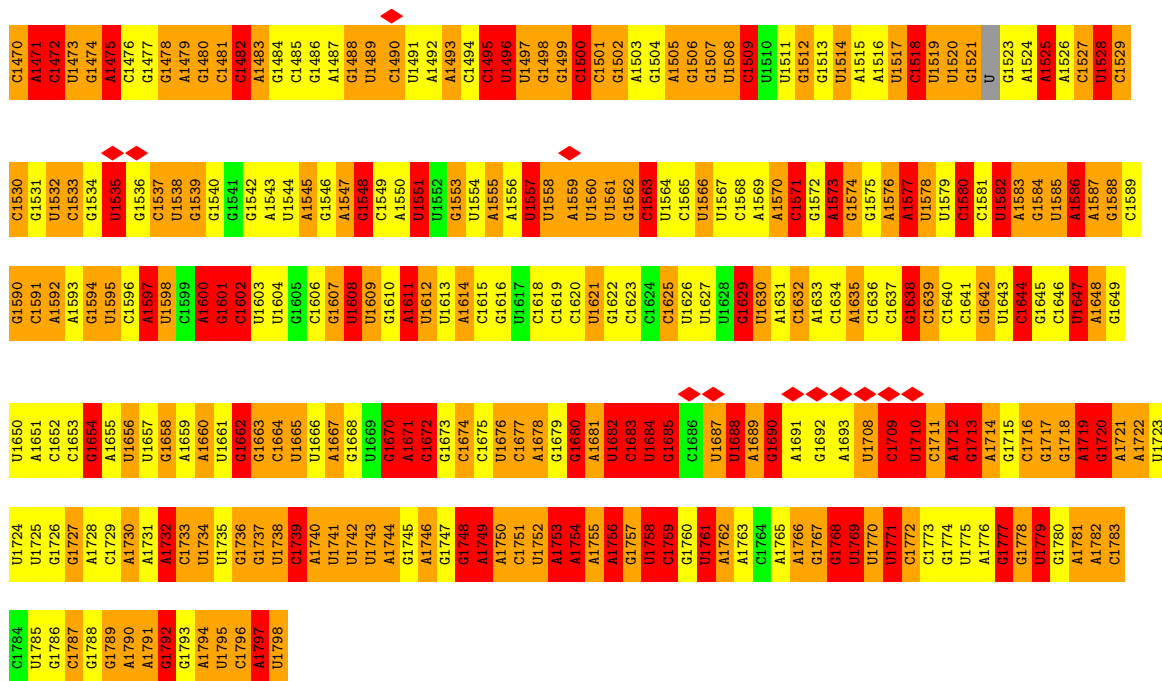
3 Residue-property plots

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.

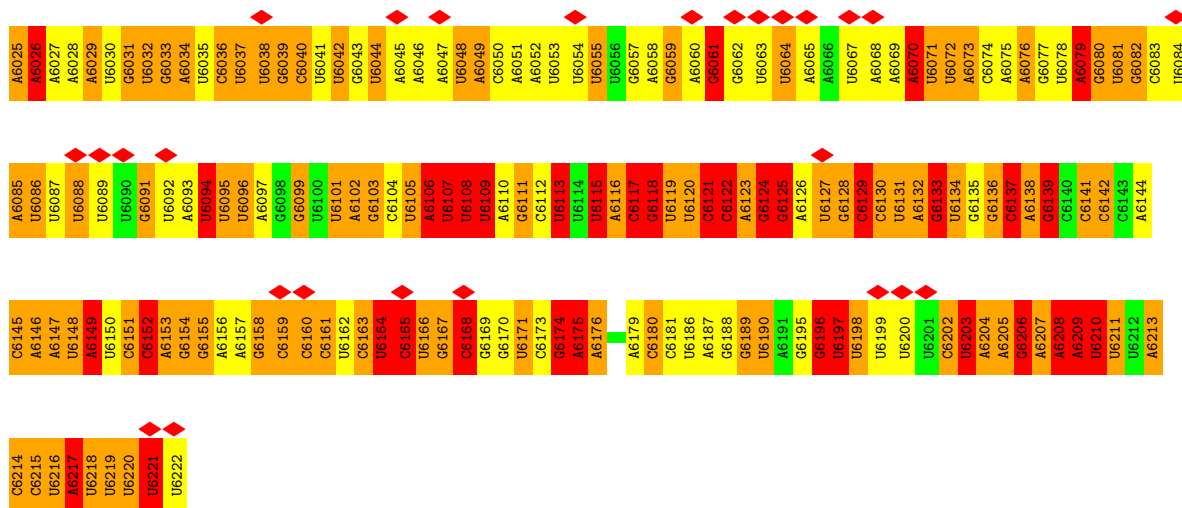
• Molecule 1: 18S RRNA



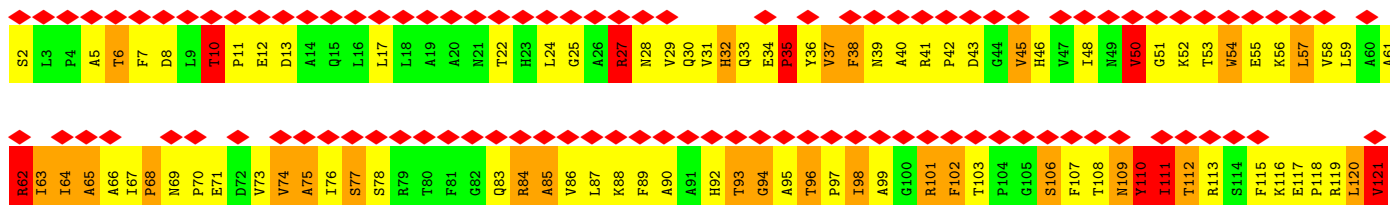
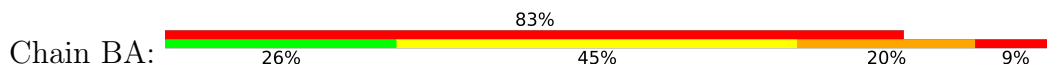
G1409	A1348	G1288	U1168	G1108	G1048	G987	C927	G866	A806	U745	A885	U608
A1410	G1349	G1229	G1169	G1109	U1049	A986	U928	G867	A807	A746	C886	G609
G1411	U1350	A1230	G1170	G1110	G1050	U989	A929	G868	U908		G887	U610
G	G1351	U1231	A1171	G1111	G1051	C990	A930	A969	A809	U749	G888	U611
U1413	G1352	U1232	G1172	G1112	U1052	G991	C931	C970	G810	U750	G889	U612
U1414	U1353	G1233	C1173	G1113	G1053	A992	U932	G871	G811	G751	G890	G613
U1415	G1354	A1234	C1174	G1114	U1054	A993	A933	G872	A812	A752	C691	C614
G1416	C1355	C1235	U1175	U1115	U1055	G994	C934	U873	U813	A753	G692	A615
A1417	U1296	A1236	G1176	A1116	U1056	A995	U935	G874	A814	A754	G693	A616
G1418	A1357	G1237	C1177	U1117	U1057	U996	G936	G875	G	A755	U694	U617
G1419	G1358	A1238	G1178	U1118	U1058	G997	C937	G876	G816	A756	U695	U618
G1420	C1359	U1239	G1179	G1119	U1059	A998	G938	G877	A817	A757	C696	A619
A1421	A1360	U1240	U1180	U1120	U1060		A939	G878	U758		C697	A620
A1422	U1361	G1241	U1181	C1121	U1061	A1001	A940	G879	G819	U759	U698	A621
A1423	U1362	A1242	U1182	G1122	A1062	G1002	A941	C880	U820	A760	A622	A622
A1424	U1363	G1243	A1183	C1123	A1063	A1003	G942	A881	U821	G761	A623	A623
A1425	G1364	A1244	G1184	U1063	U1064	U1004	C943	U882	U822	A762	G701	G624
C1426	C1365	G1245	A1185	G1064	A1005	A1005	A944	C883	G823	G763	G702	C625
A1427	U1366	C1246	U1186	A1065	A1006	C1006	U945	A884	G824	U764	G703	U626
G1428	U1367	U1247	U1187	C1066	C1007	C1007	U946	G885	U825	G765	C704	C627
G1429	G1368	C1248	G1188	C1128	G1008	G1008	U947	U886	U826	U766	C705	G628
U1430	U1369	U1249	A1189	U1129	U1009	U1009	G948	A887	C927	U767	A706	U629
C1431	U1370	G1130	C1190	A1069	C1010	C1010	C949	U888	U828	C768	A707	A630
U1432	A1371	U1251	U1191	C1070	G1011	G1011	C950	U889	A829	A769	G708	G631
G1433	U1372	G1252	C1192	U1071	U1012	U1012	A951	C890	U830	A770	C709	A770
U1434	C1373	U1253	A1193	C1072	A1013	A1013	A952	A891	U831	A771	C709	U633
G1435	C1374	U1254	C1194	G1073	G1014	G1014	G953	A892	U832	G772	C710	U634
A1436	A1375	G1255	U1195	G1074	U1015	U1015	G954	U893	U833	C773	A635	A635
U1437	C1376	A1256	C1196	U1136	C1016	C1016	A955	U894	U834	A774	G711	A636
G1438	U1377	G1257	C1197	A1075	U1017	U1017	C956	G895	U835	G775	G712	C637
C1439	U1378	U1258	G1198	C1076	U1018	U1018	G957	U896	U836	G776	A713	U638
C1440	A1319	U1259	G1199	C1078	A1019	A1019	U958	C997	G837	C777	U639	U639
C1441	U1380	U1260	G1200	U1079	A1020	A1020	U959	A898	U838	G778	U640	U640
U1442	A1321	G1261	G1201	U1080	C1021	C1021	U960	G899	U839	U779	C715	G641
A1443	C1322	U1262	A1202	A1081	C1022	C1022	A900	U900	U840	A780	C716	G642
A1444	G1383	G1263	A1203	G1082	U1023	U1023	C962	G901	U841	G717	C717	G643
A1445	A1384	G1264	A1204	C1083	A1024	A1024	A963	G902	U842	U782	U718	G644
A1446	C1385	G1265	C1205	A1084	A1025	A1025	U964	U903	C943	U783	U719	C645
C1447	A1326	U1266	U1206	A1085	A1026	A1026	U965	G904	U844	C784	C720	C646
G1448	C1327	G1267	C1207	A1086	A1027	A1027	A966	A905	A844	U785	G720	G647
U1449	G1388	G1268	A1208	A1087	C1028	C1028	A967	U906	G845	C786	U721	G648
U1450	U1390	U1269	C1209	A1088	U1029	U1029	U968	A907	G846	G787	G722	U649
U1451	A1391	G1270	C1210	U1089	A1030	A1030	C969	U908	A847	A788	G723	U650
U1452	U1392	G1271	A1211	C1090	U1031	U1031	A970	U909	C848	G789	C724	G651
C1453	C1393	U1272	G1212	A1152	G1032	G1032	A971	C910	C949	U790	C652	G652
G1454	G1394	G1273	G1213	A1092	C1033	C1033	G972	U911	A850	A791	U725	C653
G1455	U1395	C1274	U1214	A1093	C1034	C1034	A974	G912	U851	U792	C726	G655
C1456	U1396	G1154	G1215	G1094	G1035	G1035	C975	G914	G853	A793	C727	G656
C1457	U1397	A1275	C1216	U1095	A1036	A1036	G976	U915	U854	U794	U728	U657
G1458	U1398	G1277	A1217	C1096	C1037	C1037	A977	U916	A855	C795	G729	C658
C1459	C1399	G1278	G1218	U1097	U1038	U1038	A978	U917	A856	G797	G730	G676
A1460	A1400	C1279	A1219	U1098	A1039	A1039	A979	U918	U857	C798	C731	G677
G1461	U1340	G1280	C1220	A1160	U1099	U1099	A980	U919	G858	A799	G732	G678
C1462	A1341	U1281	A1221	G1161	G1041	G1041	G980	U920	A859	U800	A733	A678
C1463	C1342	U1282	C1222	C1162	G1101	G1101	U981	U921	U860	G801	A734	U679
G1464	C1403	A1283	A1223	A1163	G1102	G1102	U982	U922	U861	G802	C735	U680
C1465	U1343	C1284	A1224	U1103	A1043	U1044	A983	G922	A862	A803	C736	U681
G1466	G1405	U1285	U1225	G1164	C1045	C1045	G984	G925	A863	A804	C737	C682
C1467	A1406	U1286	C1226	G1165	C1046	C1046	G985		U864	U805	A738	C683
U1468	U1407	A1287	A1227	A1166	U1106	G1047	G986		A865		G739	A684
A1469	G1408			G1167	G1107						A740	
											C741	
											U742	
											U743	
											U744	

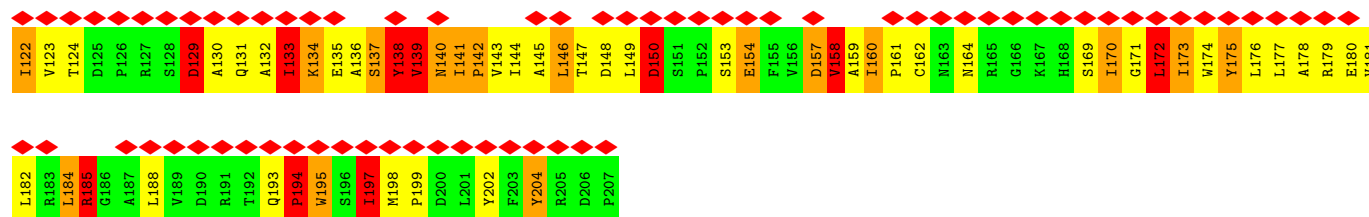


• Molecule 2: RNA OF CRICKET-PARALYSIS-VIRUS-IRES

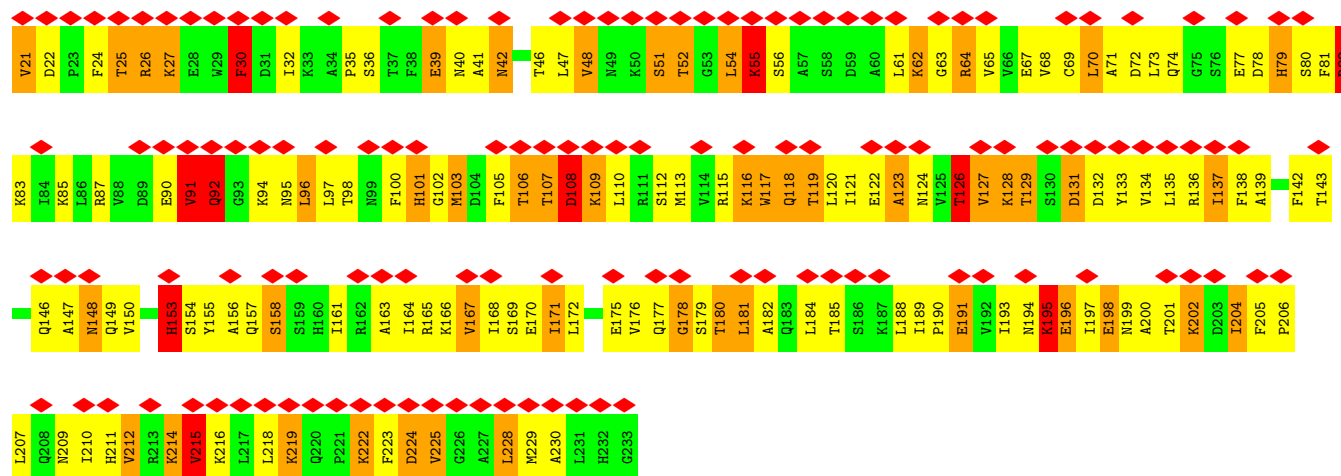


• Molecule 3: US2

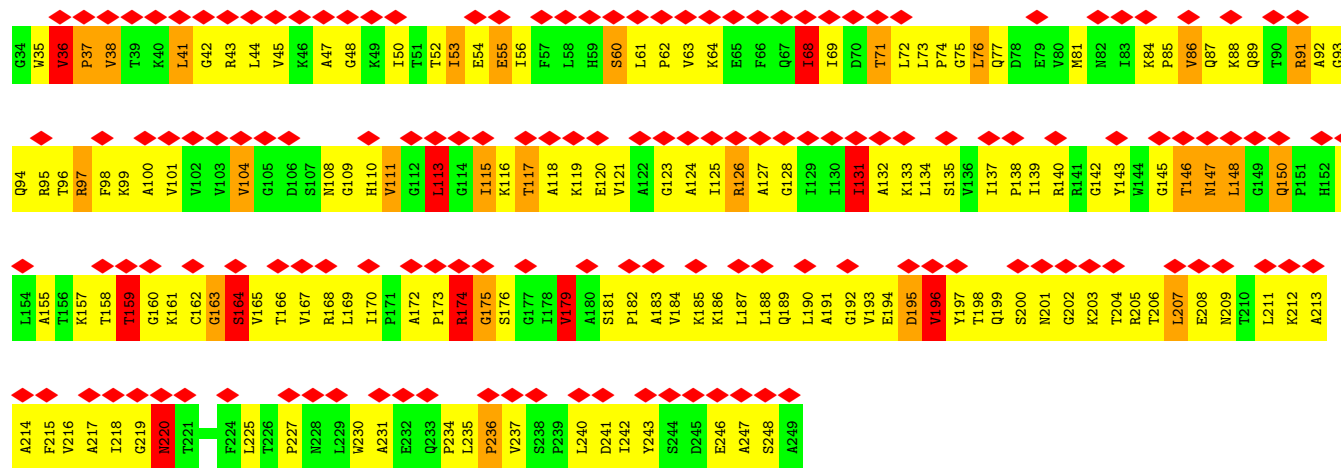




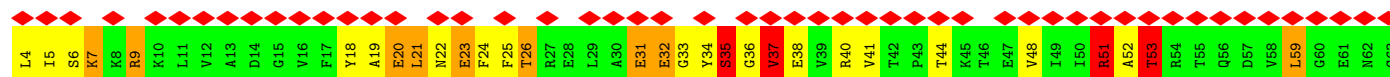
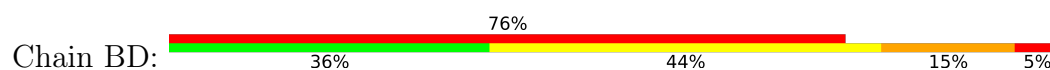
• Molecule 4: ES1

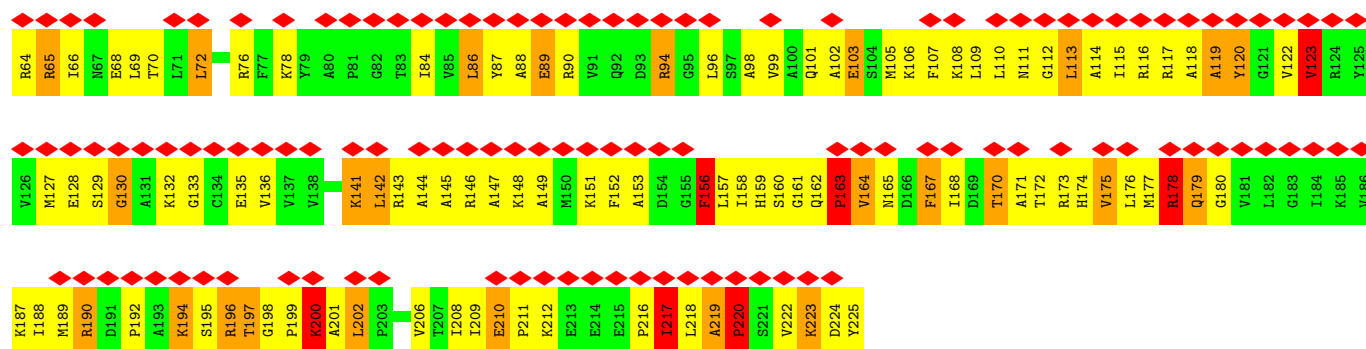


• Molecule 5: US5

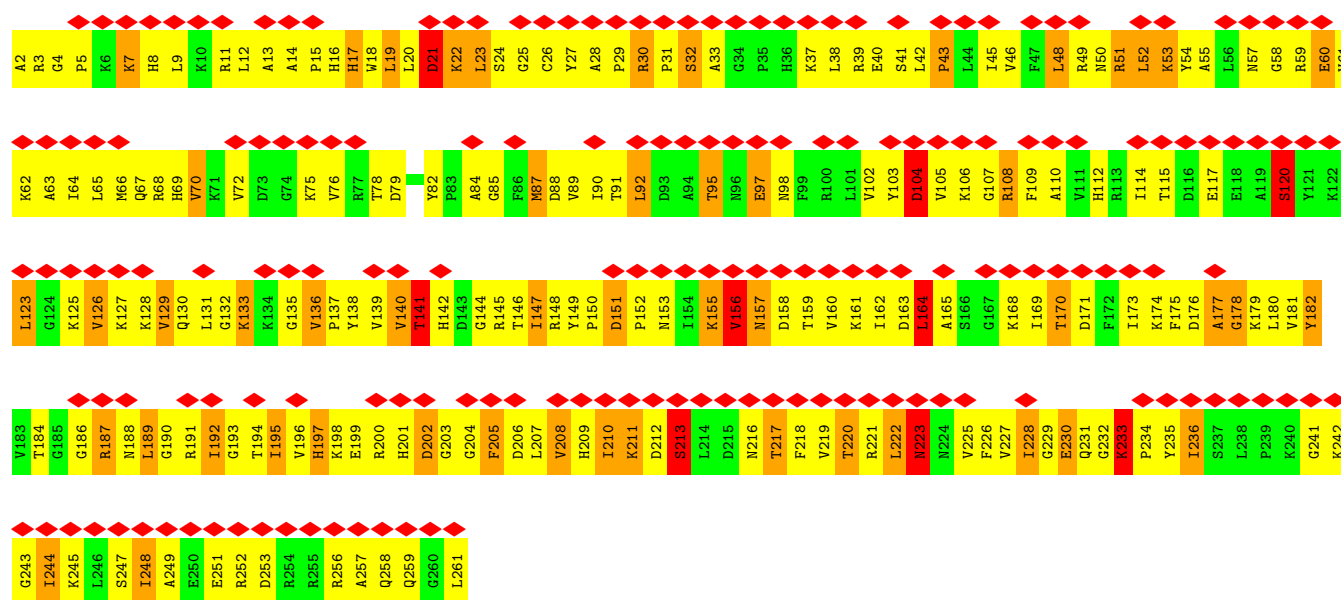


• Molecule 6: US3

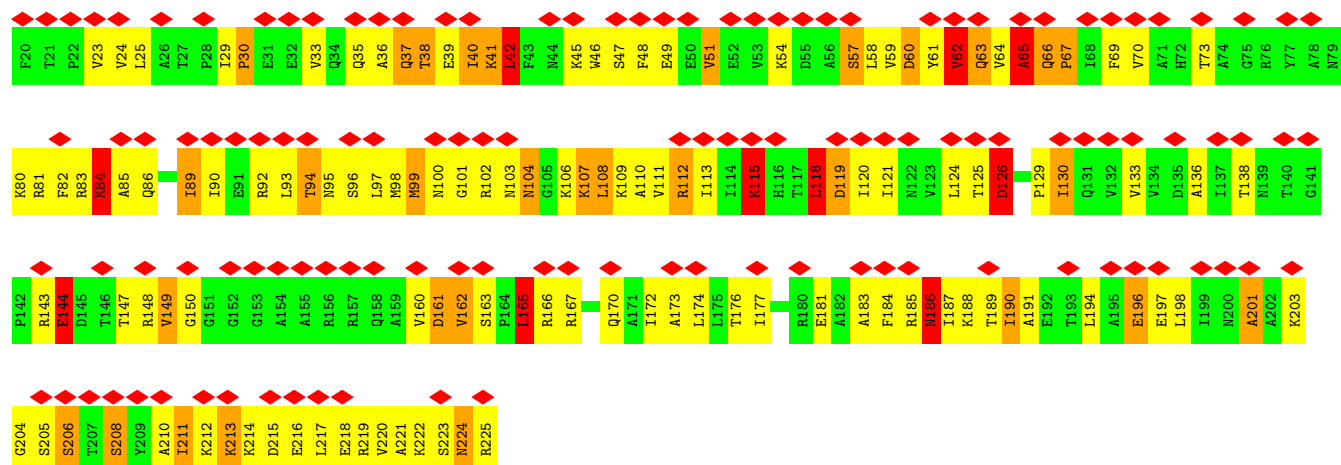




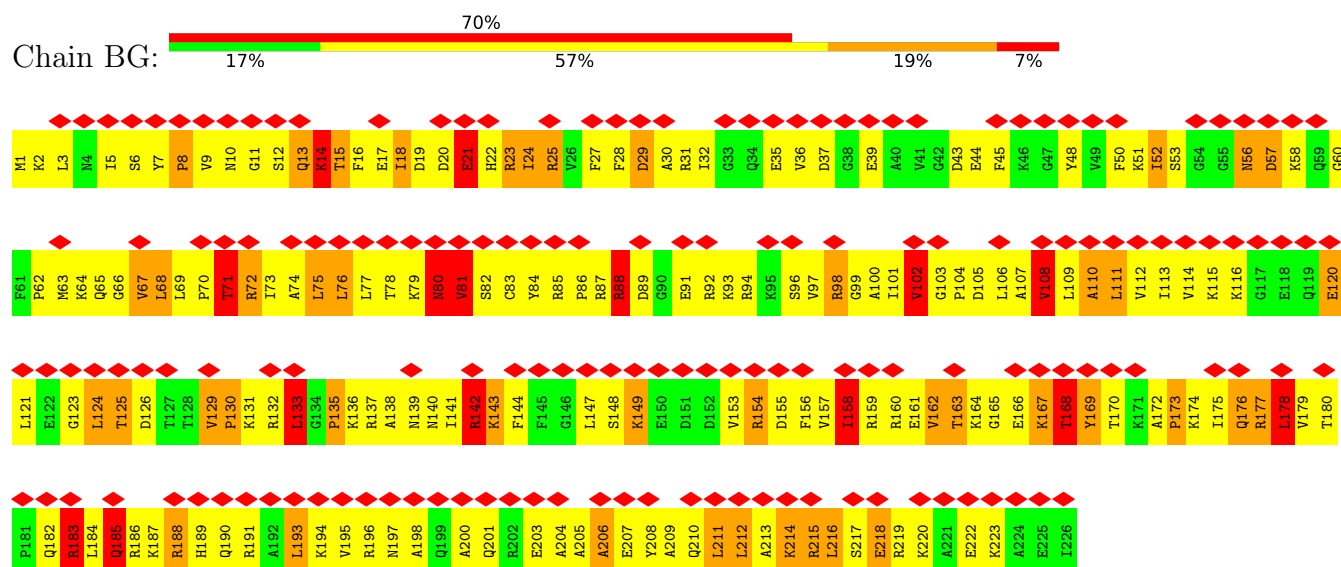
• Molecule 7: ES4



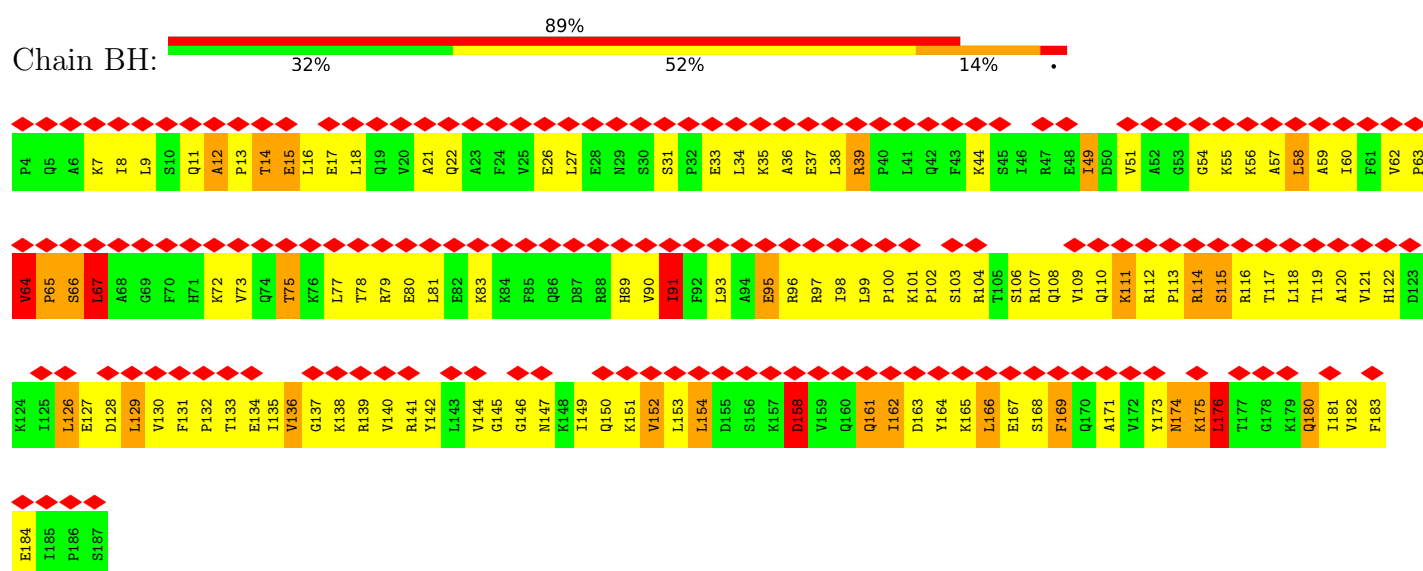
• Molecule 8: US7



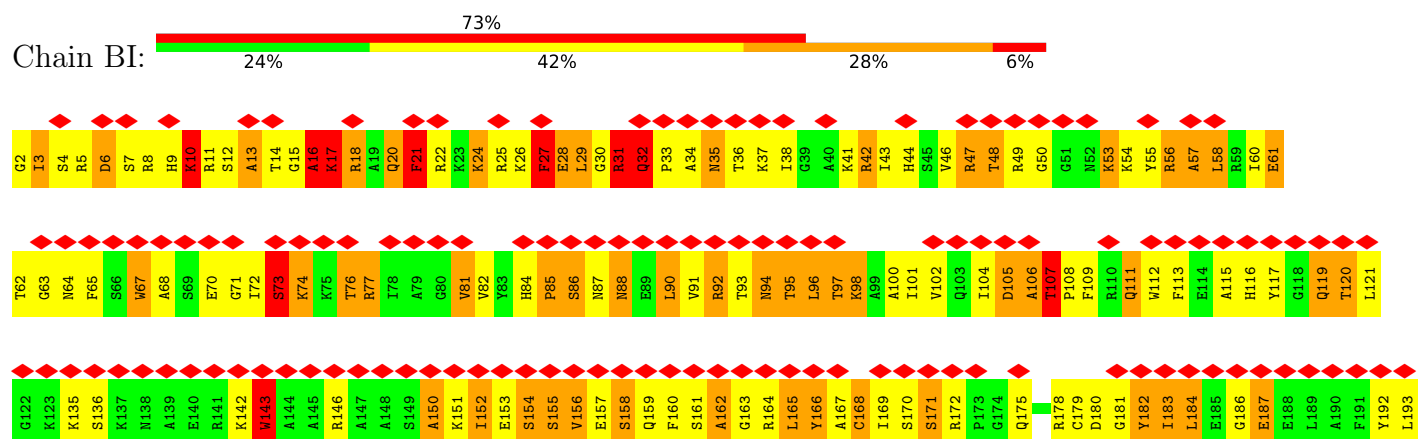
- Molecule 9: ES6

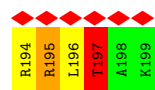


- Molecule 10: ES7

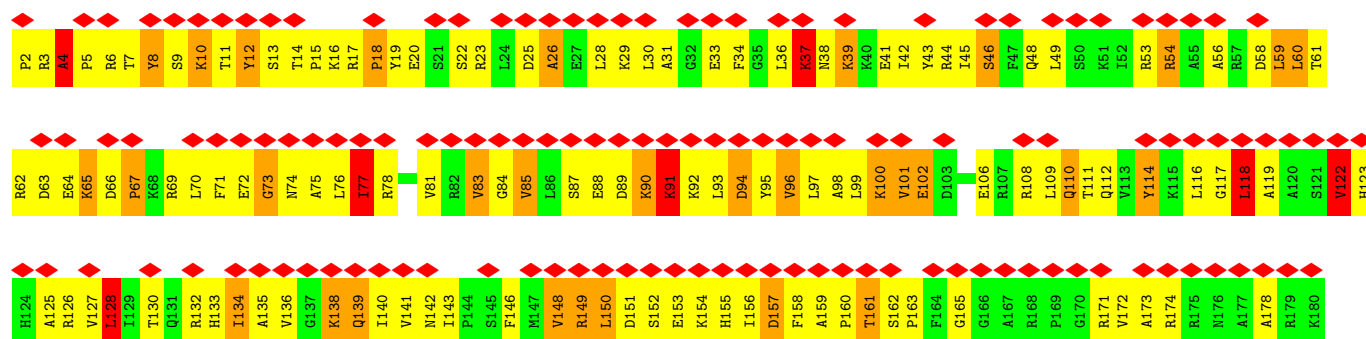
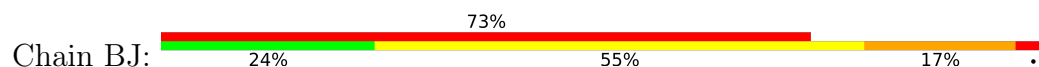


- Molecule 11: ES8





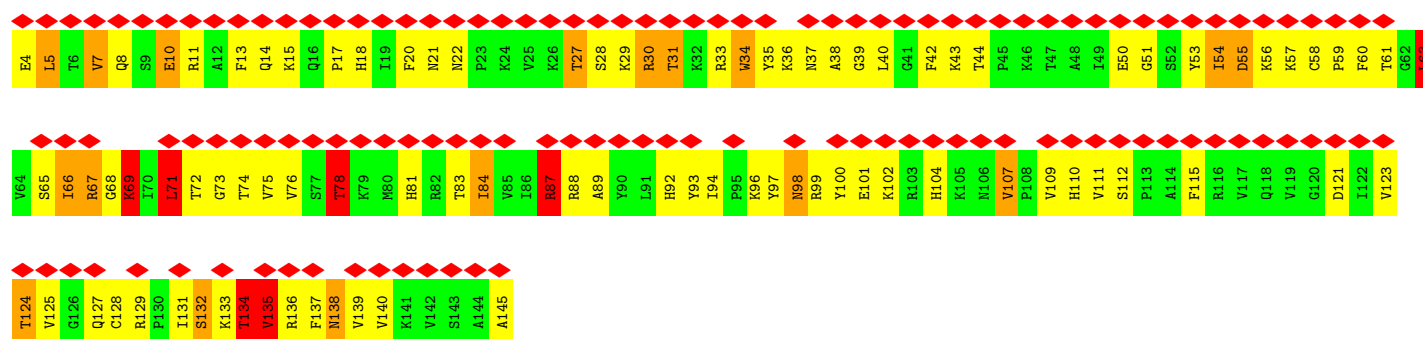
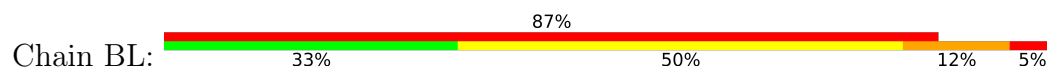
• Molecule 12: US4



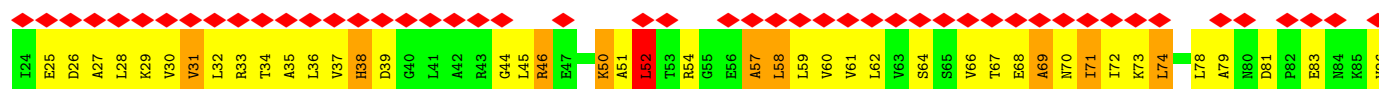
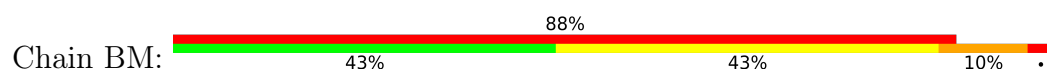
• Molecule 13: ES10



• Molecule 14: US17

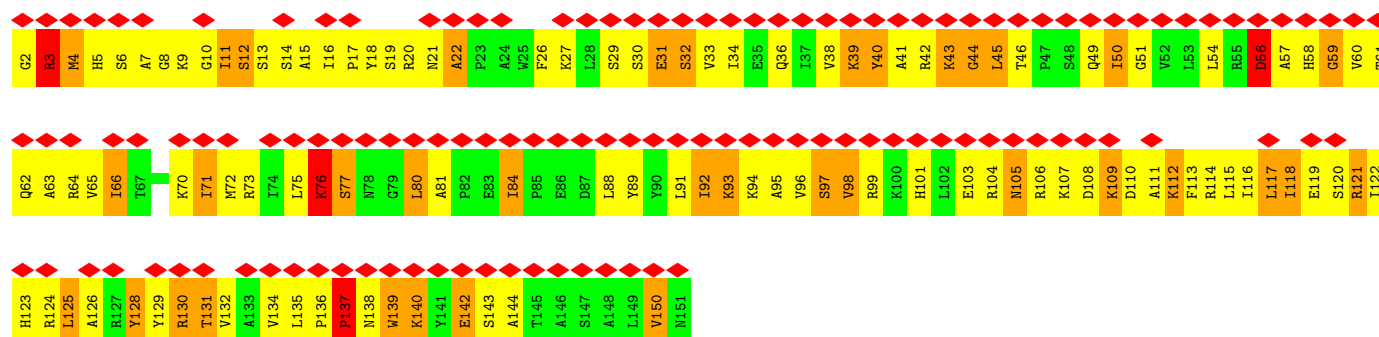
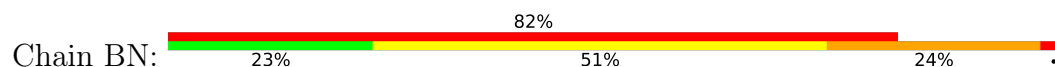


• Molecule 15: ES12

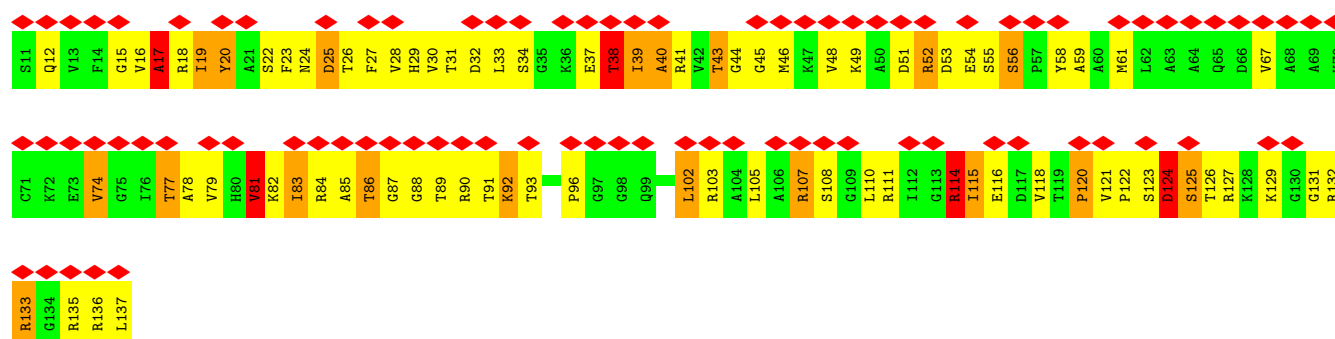




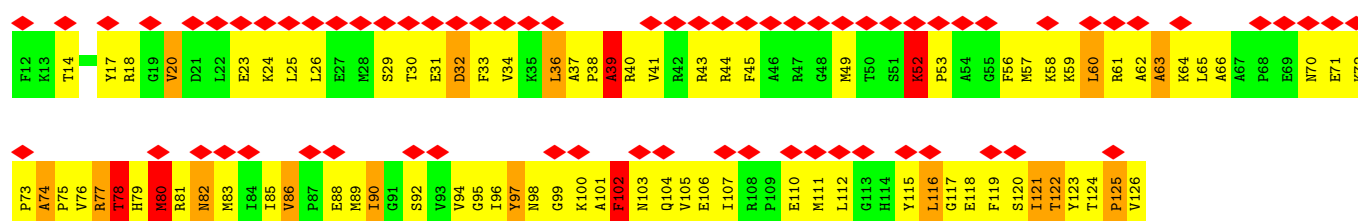
• Molecule 16: US15



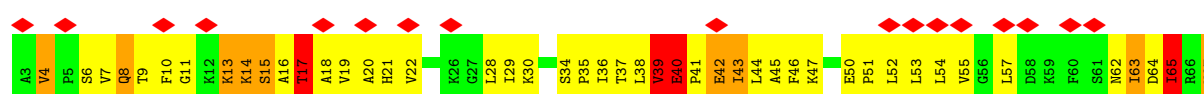
• Molecule 17: US11

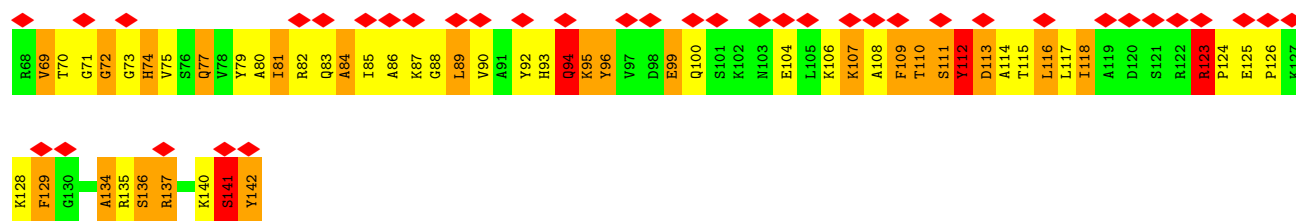


• Molecule 18: US19

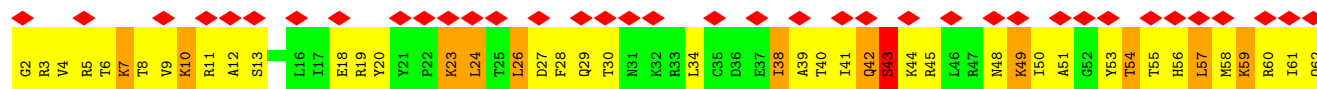
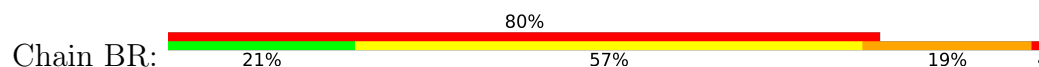


• Molecule 19: US9

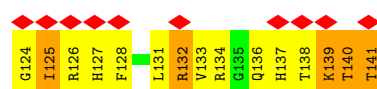




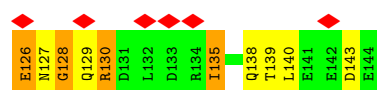
• Molecule 20: ES17



• Molecule 21: US13

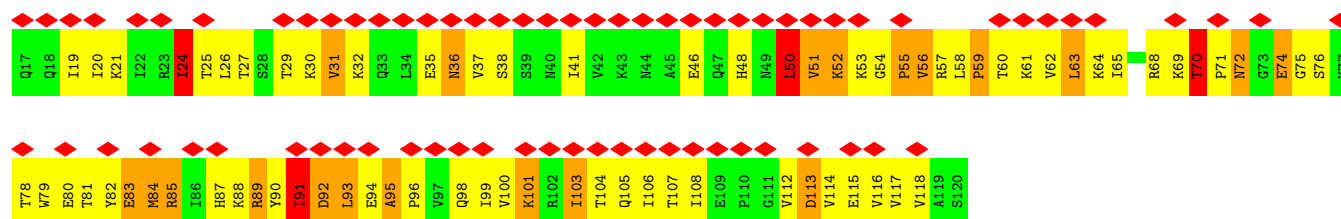


• Molecule 22: ES19

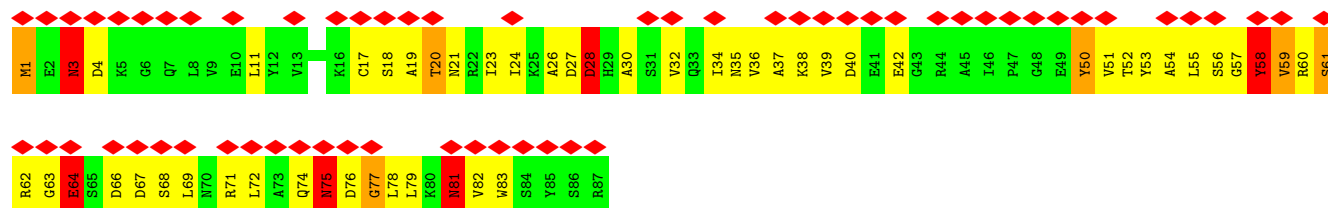


• Molecule 23: US10

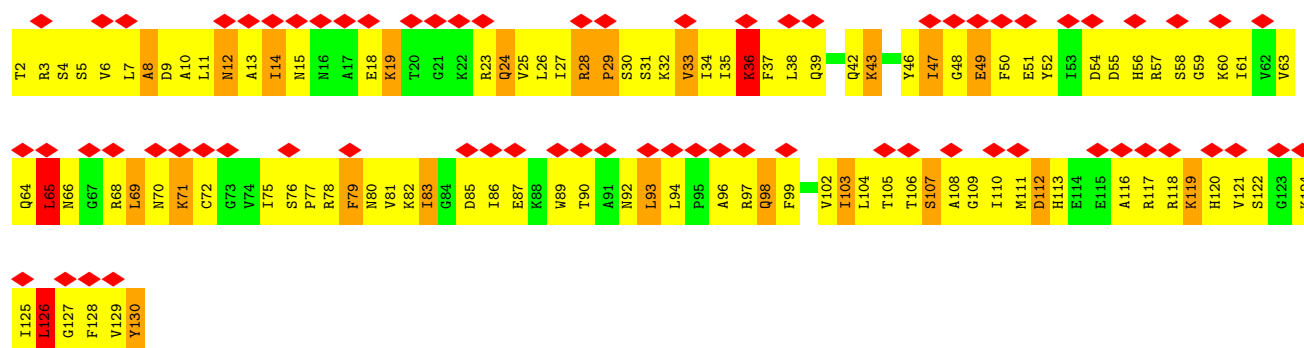




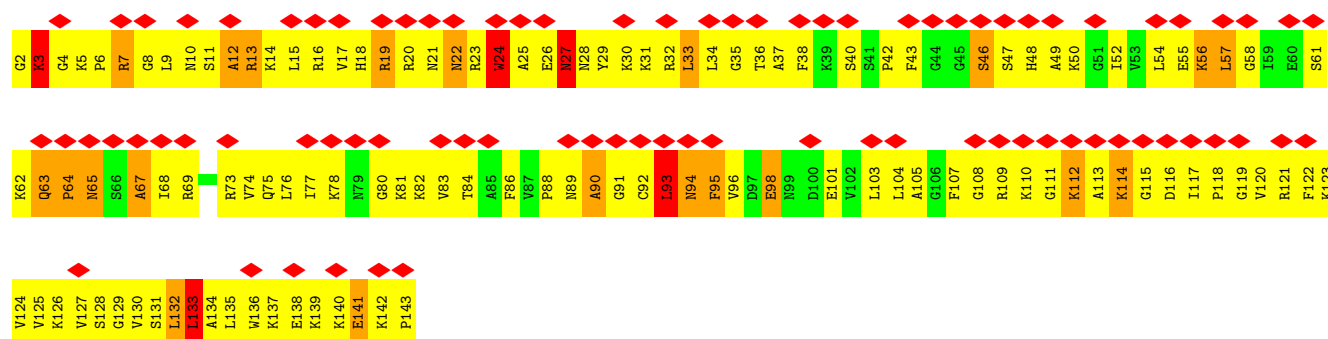
• Molecule 24: ES21



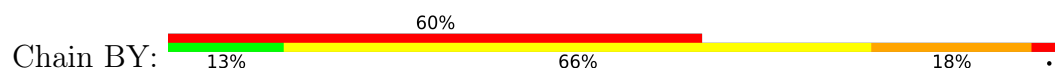
• Molecule 25: US8



• Molecule 26: US12

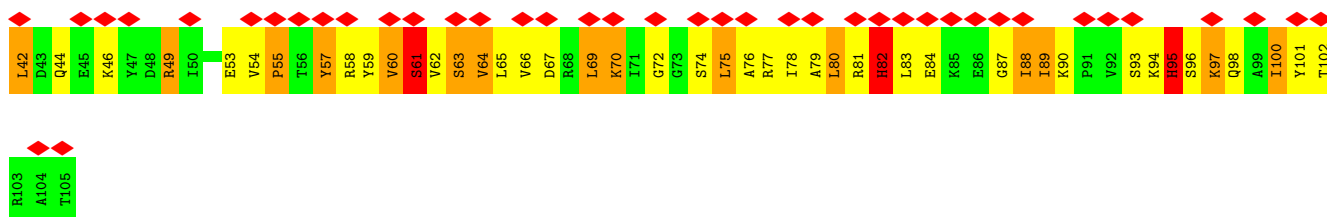


• Molecule 27: ES24

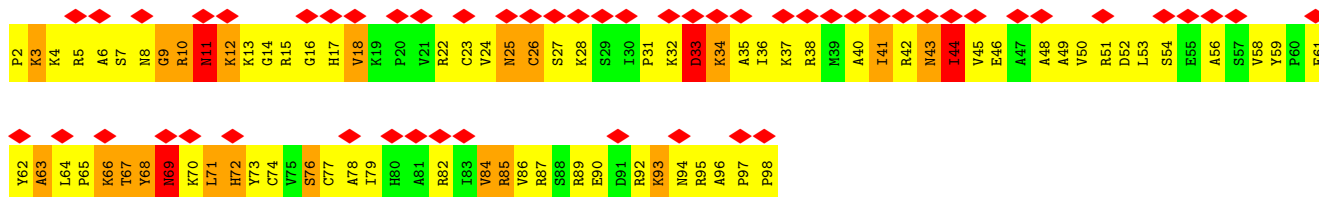
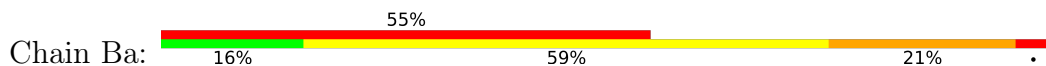




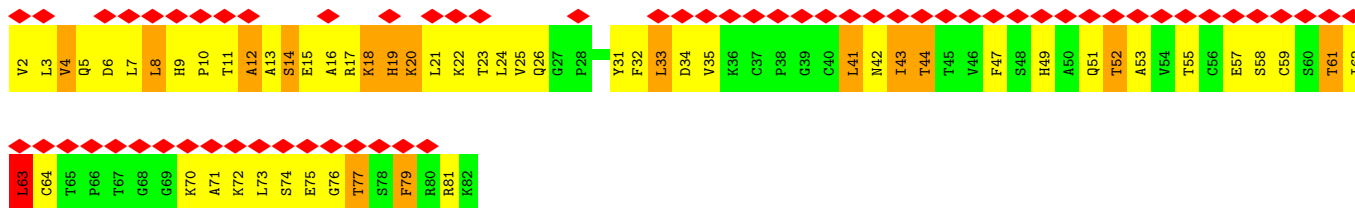
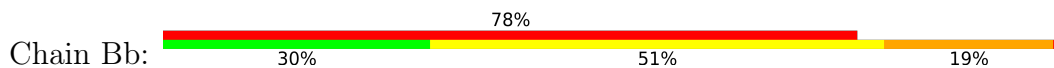
• Molecule 28: ES25



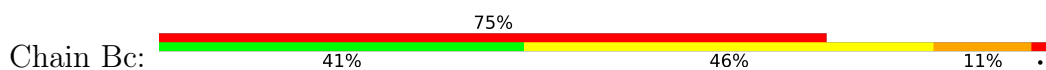
• Molecule 29: ES26



• Molecule 30: ES27

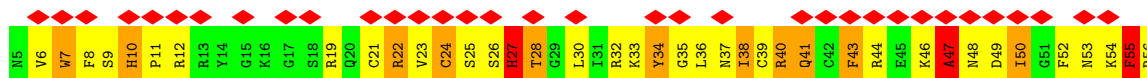


• Molecule 31: ES28

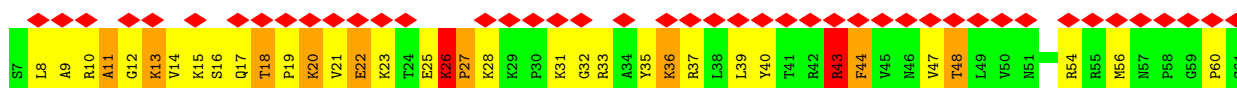
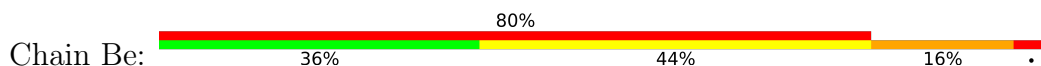




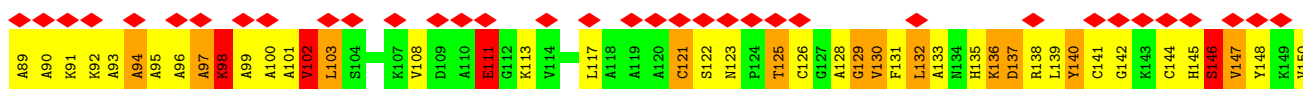
• Molecule 32: US14



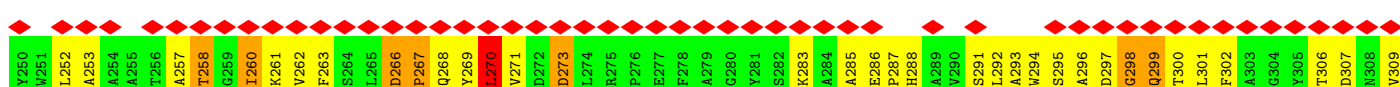
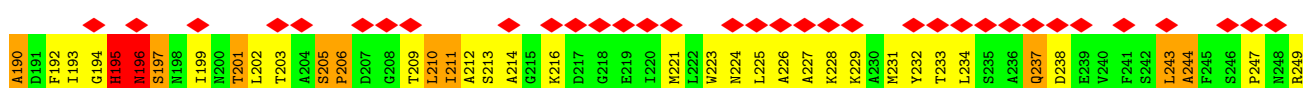
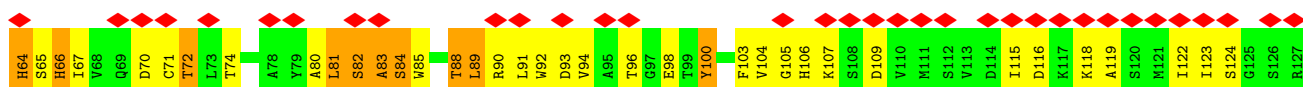
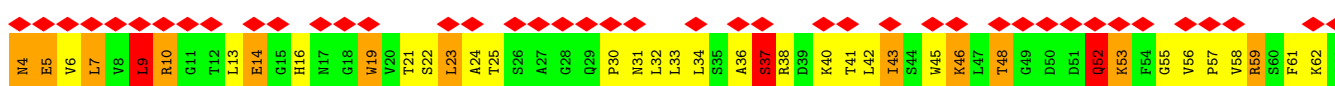
• Molecule 33: ES30



• Molecule 34: ES31



• Molecule 35: RACK1



T310	R311	V312	W313	Q314	V315	M316	T317	A318
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	18132	Depositor
Resolution determination method	Not provided	
CTF correction method	EACH PARTICLE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1.8	Depositor
Maximum defocus (nm)	3	Depositor
Magnification	47000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.990	Depositor
Minimum map value	-0.618	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.07	Depositor
Map size ($\text{\AA}$)	428.80002, 428.80002, 428.80002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.34, 1.34, 1.34	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	A2	0.88	25/41655 (0.1%)	1.57	1236/63991 (1.9%)
2	AZ	0.85	4/4449 (0.1%)	1.55	130/6827 (1.9%)
3	BA	1.29	8/1574 (0.5%)	1.54	38/2086 (1.8%)
4	BB	0.63	1/1661 (0.1%)	1.30	32/2154 (1.5%)
5	BC	0.53	0/1610	1.25	25/2113 (1.2%)
6	BD	0.60	0/1692	1.27	32/2175 (1.5%)
7	BE	0.52	0/2045	1.15	25/2647 (0.9%)
8	BF	0.72	0/1571	1.21	21/2039 (1.0%)
9	BG	0.63	0/1767	1.32	33/2288 (1.4%)
10	BH	0.53	0/1455	1.16	21/1875 (1.1%)
11	BI	0.63	0/1448	1.38	35/1839 (1.9%)
12	BJ	0.52	1/1435 (0.1%)	1.23	24/1854 (1.3%)
13	BK	0.73	0/759	1.25	13/988 (1.3%)
14	BL	0.65	1/1140 (0.1%)	1.31	18/1484 (1.2%)
15	BM	0.98	0/845	1.22	10/1093 (0.9%)
16	BN	0.59	1/1186 (0.1%)	1.23	18/1551 (1.2%)
17	BO	0.56	0/893	1.14	10/1167 (0.9%)
18	BP	0.85	1/903 (0.1%)	1.32	15/1162 (1.3%)
19	BQ	0.76	1/1072 (0.1%)	1.38	27/1392 (1.9%)
20	BR	0.59	0/908	1.19	11/1159 (0.9%)
21	BS	0.98	0/1140	1.51	29/1487 (2.0%)
22	BT	1.05	3/1083 (0.3%)	1.29	20/1389 (1.4%)
23	BU	0.83	0/812	1.34	16/1053 (1.5%)
24	BV	0.62	0/675	1.11	7/881 (0.8%)
25	BW	0.50	0/999	1.12	10/1278 (0.8%)
26	BX	0.48	0/1079	1.19	11/1372 (0.8%)
27	BY	0.64	0/1056	1.44	22/1356 (1.6%)
28	BZ	1.02	0/511	1.27	9/663 (1.4%)
29	Ba	0.59	0/758	1.40	16/975 (1.6%)
30	Bb	0.48	0/596	1.26	10/766 (1.3%)
31	Bc	0.63	0/485	1.24	4/628 (0.6%)
32	Bd	0.54	0/427	1.28	8/540 (1.5%)
33	Be	0.60	0/436	1.59	9/562 (1.6%)
34	Bf	1.06	0/456	1.29	7/599 (1.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Bg	0.74	0/2390	1.26	37/3123 (1.2%)
All	All	0.81	46/82971 (0.1%)	1.46	1989/118556 (1.7%)

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	A2	98	0
2	AZ	8	0
3	BA	8	3
4	BB	11	2
5	BC	8	1
6	BD	6	1
7	BE	8	0
8	BF	6	1
9	BG	10	3
10	BH	7	2
11	BI	12	2
12	BJ	5	1
13	BK	2	0
14	BL	8	0
15	BM	2	0
16	BN	6	0
17	BO	4	1
18	BP	4	0
19	BQ	8	2
20	BR	5	0
21	BS	6	4
22	BT	6	0
23	BU	1	1
24	BV	2	1
25	BW	3	0
26	BX	5	2
27	BY	6	0
28	BZ	1	0
29	Ba	4	1
30	Bb	5	0
31	Bc	2	0
32	Bd	3	1
33	Be	3	0

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Mol	Chain	#Chirality outliers	#Planarity outliers
34	Bf	2	1
35	Bg	9	1
All	All	284	31

The worst 5 of 46 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A2	897	C	O3'-P	39.17	2.19	1.61
1	A2	633	U	O3'-P	38.96	2.19	1.61
1	A2	1797	A	O3'-P	38.17	2.18	1.61
1	A2	1388	A	O3'-P	36.95	2.16	1.61
1	A2	388	G	O3'-P	36.79	2.16	1.61

The worst 5 of 1989 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	1797	A	O3'-P-O5'	37.83	160.74	104.00
1	A2	104	A	P-O3'-C3'	33.24	170.06	120.20
1	A2	56	U	P-O3'-C3'	28.75	163.33	120.20
1	A2	104	A	O3'-P-O5'	-23.14	69.29	104.00
1	A2	862	A	P-O3'-C3'	21.13	151.90	120.20

5 of 284 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A2	7	G	C3'
1	A2	41	A	C3'
1	A2	67	A	C3'
1	A2	102	U	C3'
1	A2	124	A	C2'

5 of 31 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	BA	138	TYR	Peptide
3	BA	35	PRO	Peptide
3	BA	62	ARG	Peptide
4	BB	177	GLN	Peptide
4	BB	178	GLY	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	A2	37579	0	18988	10931	0
2	AZ	4018	0	2058	293	0
3	BA	1577	0	1518	360	0
4	BB	1686	0	1693	204	0
5	BC	1626	0	1633	614	0
6	BD	1729	0	1743	299	0
7	BE	2068	0	2055	1041	0
8	BF	1603	0	1601	331	0
9	BG	1790	0	1764	1216	0
10	BH	1481	0	1515	213	0
11	BI	1480	0	1432	509	0
12	BJ	1452	0	1479	322	0
13	BK	765	0	711	65	0
14	BL	1146	0	1175	171	0
15	BM	870	0	843	43	0
16	BN	1192	0	1210	289	0
17	BO	905	0	852	374	0
18	BP	914	0	886	537	0
19	BQ	1082	0	1104	215	0
20	BR	934	0	889	352	0
21	BS	1150	0	1130	456	0
22	BT	1105	0	1056	498	0
23	BU	829	0	853	243	0
24	BV	684	0	652	76	0
25	BW	1021	0	996	598	0
26	BX	1101	0	1103	799	0
27	BY	1073	0	1061	949	0
28	BZ	518	0	534	170	0
29	Ba	769	0	770	198	0
30	Bb	610	0	599	190	0
31	Bc	497	0	521	28	0
32	Bd	433	0	404	99	0
33	Be	440	0	473	152	0
34	Bf	458	0	452	239	0
35	Bg	2417	0	2290	140	0
All	All	79002	0	58043	13570	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 99.

The worst 5 of 13570 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:A2:782:U:P	27:BY:39:GLU:HG3	1.23	1.72
1:A2:811:A:C2	10:BH:107:ARG:HA	1.19	1.72
1:A2:1722:A:P	9:BG:73:ILE:HG13	1.23	1.72
1:A2:59:C:P	27:BY:111:LYS:HD3	1.28	1.69
1:A2:803:A:H4'	25:BW:120:HIS:CE1	1.25	1.69

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	BA	129/206 (63%)	60 (46%)	39 (30%)	30 (23%)	0	0
4	BB	118/213 (55%)	88 (75%)	17 (14%)	13 (11%)	0	5
5	BC	136/216 (63%)	84 (62%)	31 (23%)	21 (15%)	0	2
6	BD	116/222 (52%)	83 (72%)	17 (15%)	16 (14%)	0	3
7	BE	143/260 (55%)	100 (70%)	26 (18%)	17 (12%)	0	4
8	BF	116/206 (56%)	81 (70%)	20 (17%)	15 (13%)	0	3
9	BG	141/226 (62%)	88 (62%)	32 (23%)	21 (15%)	0	2
10	BH	100/184 (54%)	61 (61%)	22 (22%)	17 (17%)	0	2
11	BI	87/187 (46%)	51 (59%)	22 (25%)	14 (16%)	0	2
12	BJ	101/179 (56%)	58 (57%)	27 (27%)	16 (16%)	0	2
13	BK	48/93 (52%)	29 (60%)	9 (19%)	10 (21%)	0	1
14	BL	85/142 (60%)	53 (62%)	25 (29%)	7 (8%)	0	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	BM	63/120 (52%)	36 (57%)	20 (32%)	7 (11%)	0	5
16	BN	97/150 (65%)	62 (64%)	22 (23%)	13 (13%)	0	3
17	BO	84/127 (66%)	58 (69%)	16 (19%)	10 (12%)	0	4
18	BP	60/115 (52%)	40 (67%)	14 (23%)	6 (10%)	0	6
19	BQ	85/140 (61%)	56 (66%)	19 (22%)	10 (12%)	0	4
20	BR	59/121 (49%)	45 (76%)	9 (15%)	5 (8%)	0	8
21	BS	89/140 (64%)	61 (68%)	13 (15%)	15 (17%)	0	2
22	BT	72/142 (51%)	47 (65%)	14 (19%)	11 (15%)	0	2
23	BU	57/104 (55%)	38 (67%)	12 (21%)	7 (12%)	0	4
24	BV	53/87 (61%)	38 (72%)	10 (19%)	5 (9%)	0	7
25	BW	58/129 (45%)	41 (71%)	11 (19%)	6 (10%)	0	6
26	BX	70/142 (49%)	49 (70%)	12 (17%)	9 (13%)	0	3
27	BY	77/134 (58%)	55 (71%)	15 (20%)	7 (9%)	0	8
28	BZ	37/64 (58%)	22 (60%)	9 (24%)	6 (16%)	0	2
29	Ba	51/97 (53%)	29 (57%)	12 (24%)	10 (20%)	0	1
30	Bb	38/81 (47%)	24 (63%)	11 (29%)	3 (8%)	1	10
31	Bc	38/63 (60%)	29 (76%)	7 (18%)	2 (5%)	1	16
32	Bd	25/52 (48%)	15 (60%)	8 (32%)	2 (8%)	1	9
33	Be	33/55 (60%)	16 (48%)	12 (36%)	5 (15%)	0	2
34	Bf	45/64 (70%)	18 (40%)	14 (31%)	13 (29%)	0	0
35	Bg	170/315 (54%)	115 (68%)	38 (22%)	17 (10%)	0	6
All	All	2681/4776 (56%)	1730 (64%)	585 (22%)	366 (14%)	0	3

5 of 366 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	BA	27	ARG
3	BA	43	ASP
3	BA	50	VAL
3	BA	121	VAL
3	BA	122	ILE

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	BA	164/173 (95%)	123 (75%)	41 (25%)	0	4
4	BB	187/187 (100%)	135 (72%)	52 (28%)	0	3
5	BC	175/175 (100%)	146 (83%)	29 (17%)	2	14
6	BD	182/182 (100%)	146 (80%)	36 (20%)	1	9
7	BE	221/221 (100%)	174 (79%)	47 (21%)	1	7
8	BF	172/172 (100%)	130 (76%)	42 (24%)	1	5
9	BG	185/191 (97%)	135 (73%)	50 (27%)	0	3
10	BH	165/165 (100%)	138 (84%)	27 (16%)	2	14
11	BI	149/149 (100%)	100 (67%)	49 (33%)	0	1
12	BJ	154/154 (100%)	127 (82%)	27 (18%)	2	12
13	BK	80/84 (95%)	61 (76%)	19 (24%)	1	6
14	BL	127/127 (100%)	99 (78%)	28 (22%)	1	7
15	BM	88/97 (91%)	67 (76%)	21 (24%)	1	5
16	BN	127/127 (100%)	102 (80%)	25 (20%)	1	9
17	BO	84/96 (88%)	63 (75%)	21 (25%)	0	4
18	BP	97/97 (100%)	80 (82%)	17 (18%)	2	12
19	BQ	114/114 (100%)	83 (73%)	31 (27%)	0	3
20	BR	94/109 (86%)	69 (73%)	25 (27%)	0	4
21	BS	125/125 (100%)	94 (75%)	31 (25%)	1	5
22	BT	114/114 (100%)	89 (78%)	25 (22%)	1	7
23	BU	97/97 (100%)	73 (75%)	24 (25%)	1	5
24	BV	74/74 (100%)	63 (85%)	11 (15%)	3	16
25	BW	110/110 (100%)	93 (84%)	17 (16%)	2	15
26	BX	116/116 (100%)	102 (88%)	14 (12%)	5	22
27	BY	112/112 (100%)	93 (83%)	19 (17%)	2	13
28	BZ	57/57 (100%)	39 (68%)	18 (32%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	Ba	83/83 (100%)	68 (82%)	15 (18%)	2	12
30	Bb	70/70 (100%)	57 (81%)	13 (19%)	1	10
31	Bc	56/56 (100%)	43 (77%)	13 (23%)	1	6
32	Bd	46/46 (100%)	33 (72%)	13 (28%)	0	3
33	Be	48/48 (100%)	41 (85%)	7 (15%)	3	17
34	Bf	43/43 (100%)	31 (72%)	12 (28%)	0	3
35	Bg	257/259 (99%)	205 (80%)	52 (20%)	1	8
All	All	3973/4030 (99%)	3102 (78%)	871 (22%)	2	7

5 of 871 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	BM	99	GLU
20	BR	71	PHE
32	Bd	55	PHE
16	BN	50	ILE
15	BM	97	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 119 such sidechains are listed below:

Mol	Chain	Res	Type
14	BL	92	HIS
35	Bg	29	GLN
21	BS	12	GLN
35	Bg	17	ASN
35	Bg	314	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A2	1659/1767 (93%)	1115 (67%)	14 (0%)
2	AZ	169/190 (88%)	145 (85%)	0
All	All	1828/1957 (93%)	1260 (68%)	14 (0%)

5 of 1260 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A2	2	A
1	A2	3	U
1	A2	4	C
1	A2	5	U
1	A2	6	G

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A2	835	U
1	A2	836	U
1	A2	1716	C
1	A2	1710	U
1	A2	1712	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A2	393
35	Bg	80
7	BE	64

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Mol	Chain	Number of breaks
6	BD	62
11	BI	58
8	BF	52
10	BH	51
4	BB	51
9	BG	47
5	BC	46
3	BA	43
12	BJ	42
2	AZ	40
26	BX	40
22	BT	39
25	BW	39
20	BR	36
15	BM	33
14	BL	32
18	BP	31
27	BY	31
19	BQ	30
21	BS	29
16	BN	29
23	BU	27
13	BK	25
30	Bb	24
29	Ba	24
17	BO	23
24	BV	18
32	Bd	16
28	BZ	14
31	Bc	14
33	Be	11
34	Bf	9

The worst 5 of 1603 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	1693:A	O3'	1708:U	P	22.38
1	A2	658:C	O3'	676:G	P	18.27
1	BI	123:LYS	C	135:LYS	N	16.74
1	BA	190:ASP	C	191:ARG	N	10.15
1	BR	124:VAL	C	125:SER	N	8.71

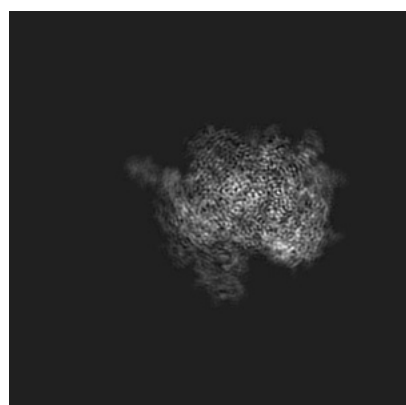
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2604. These allow visual inspection of the internal detail of the map and identification of artifacts.

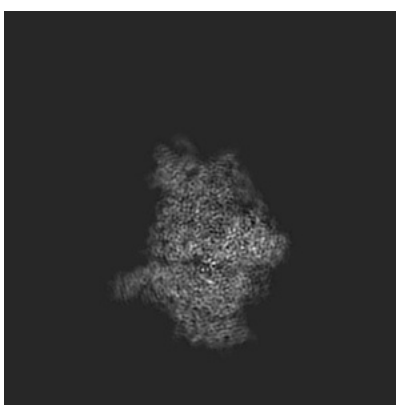
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

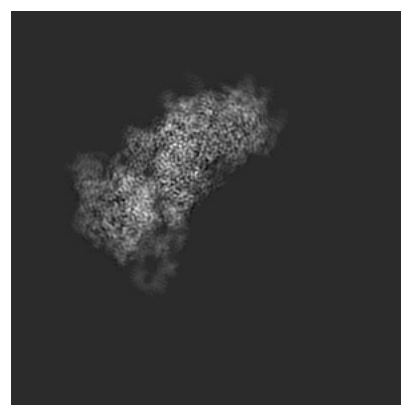
6.1.1 Primary map



X



Y

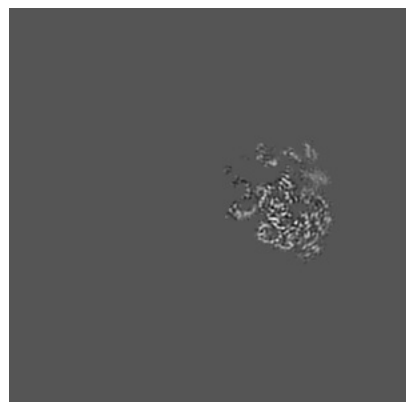


Z

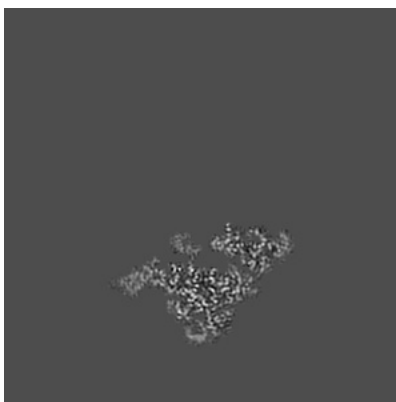
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

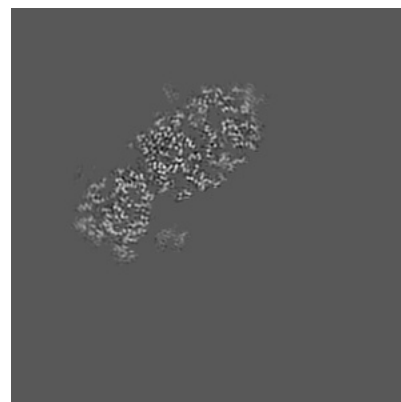
6.2.1 Primary map



X Index: 160



Y Index: 160

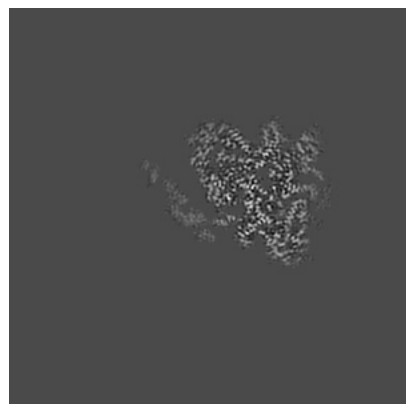


Z Index: 160

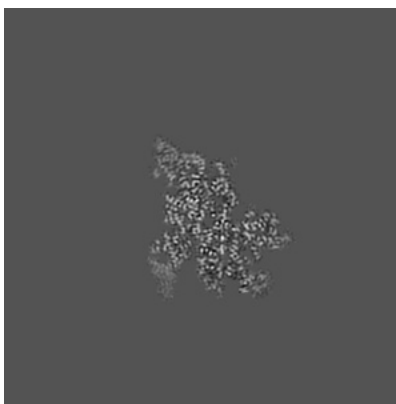
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

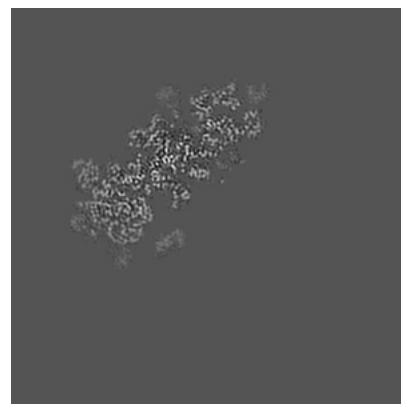
6.3.1 Primary map



X Index: 132



Y Index: 215

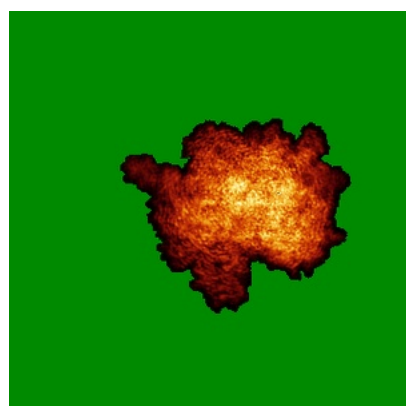


Z Index: 166

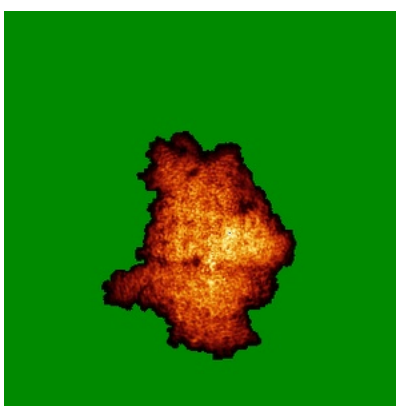
The images above show the largest variance slices of the map in three orthogonal directions.

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

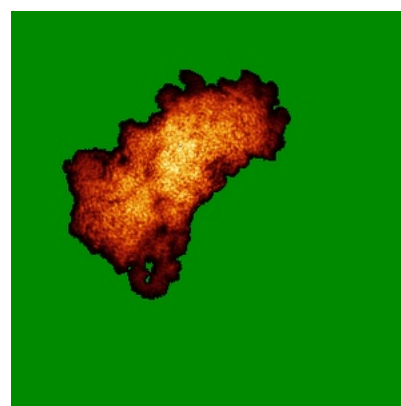
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

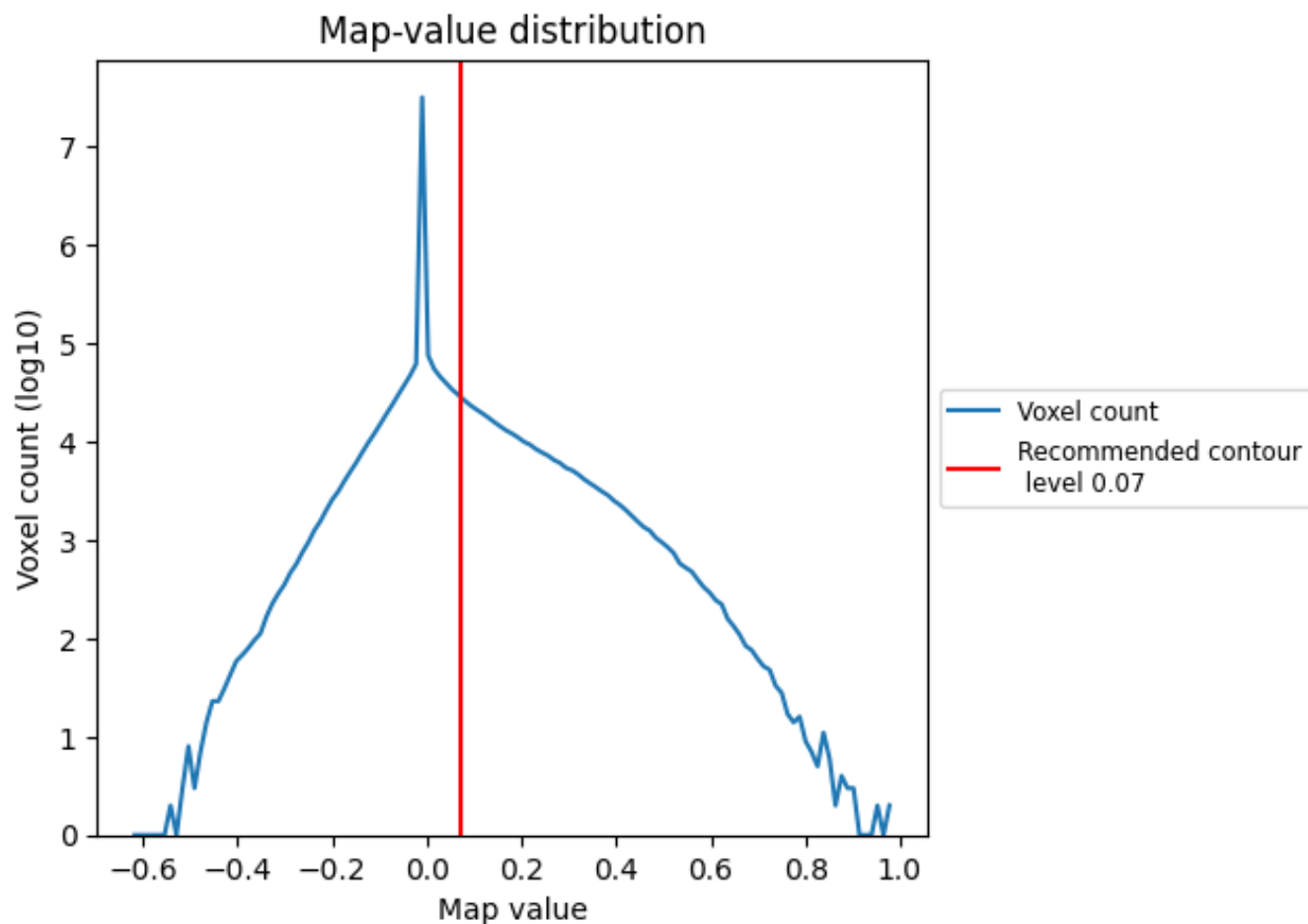
6.6 Mask visualisation

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

7 Map analysis [i](#)

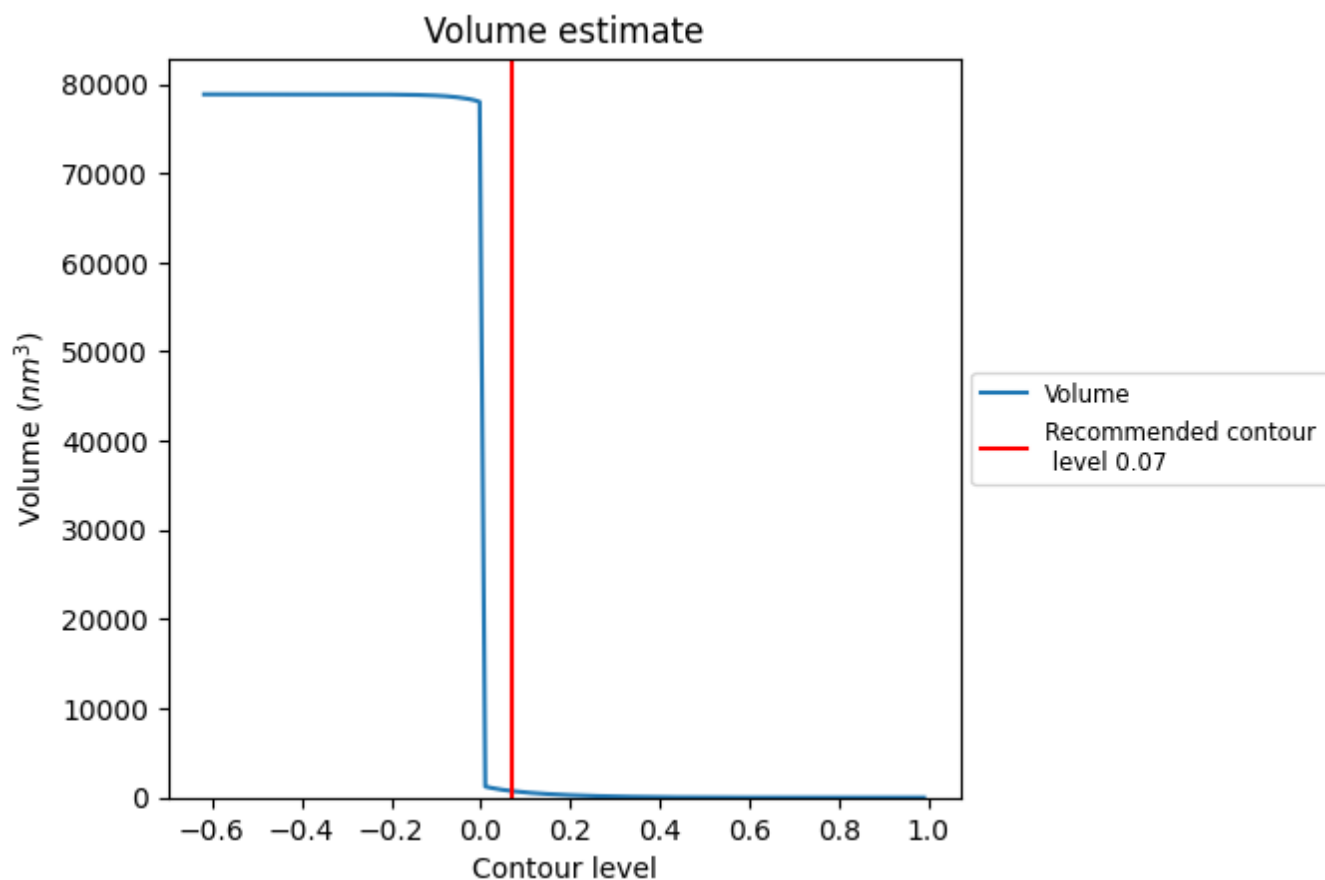
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

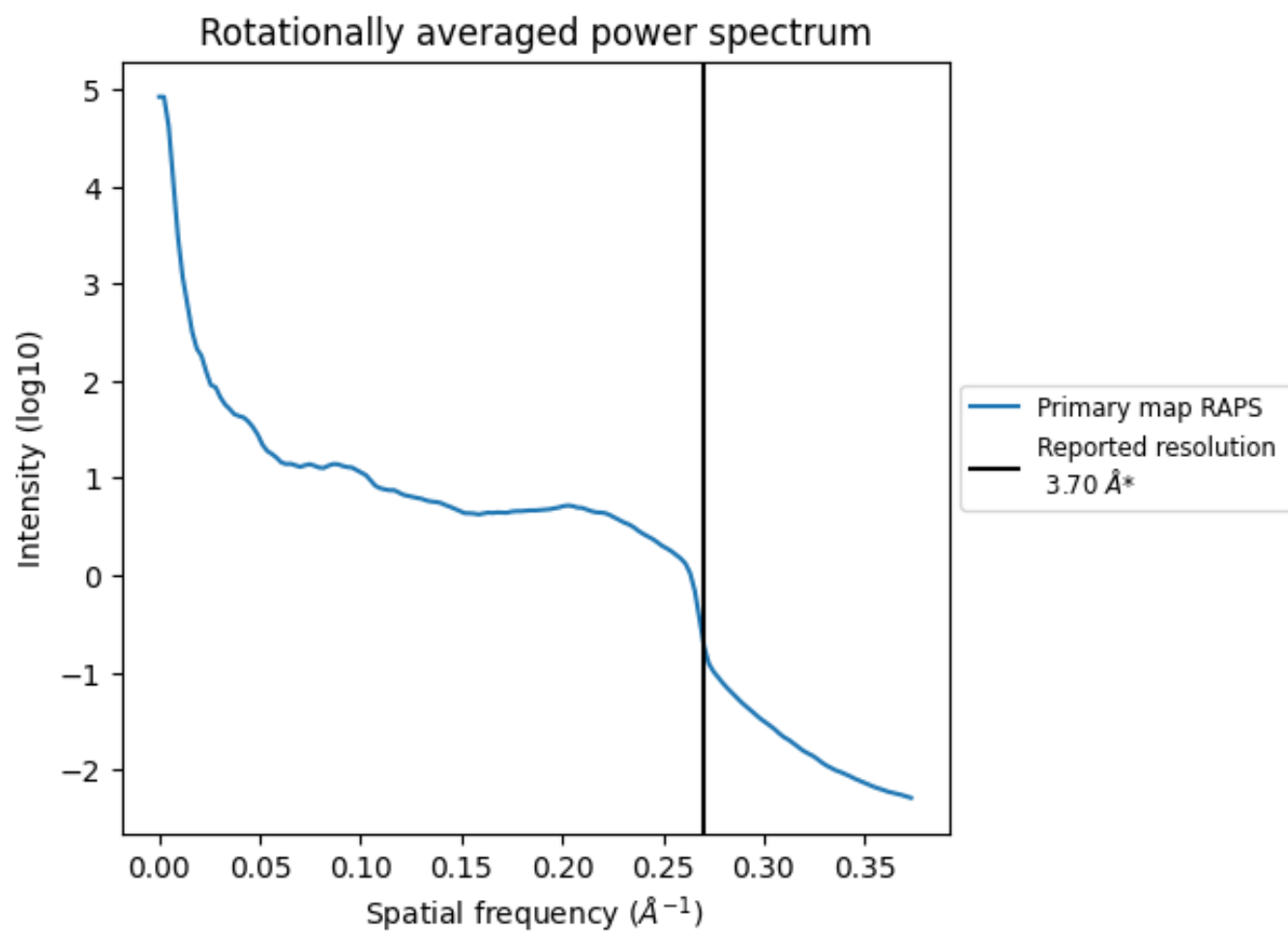
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 732 nm³; this corresponds to an approximate mass of 661 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 0.270 Å⁻¹

8 Fourier-Shell correlation

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

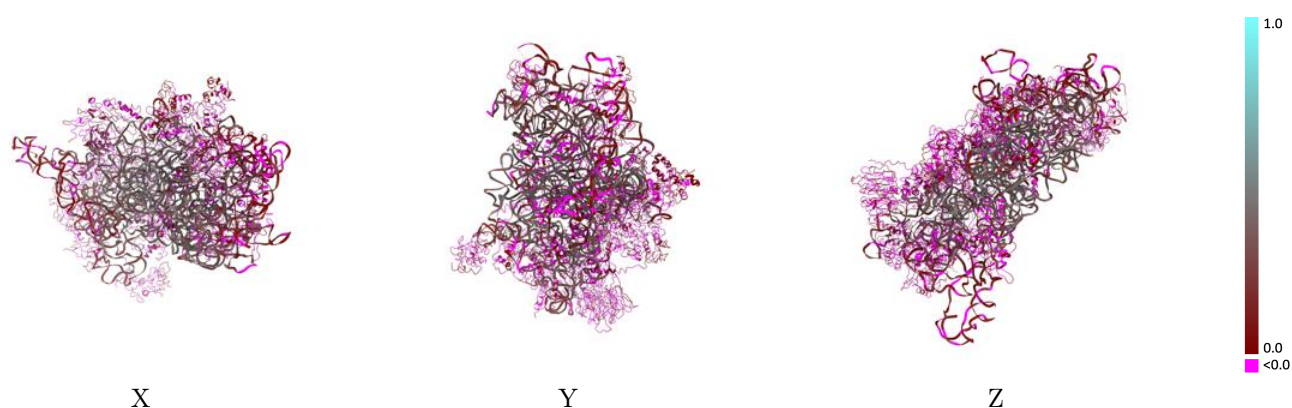
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2604 and PDB model 4V92. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

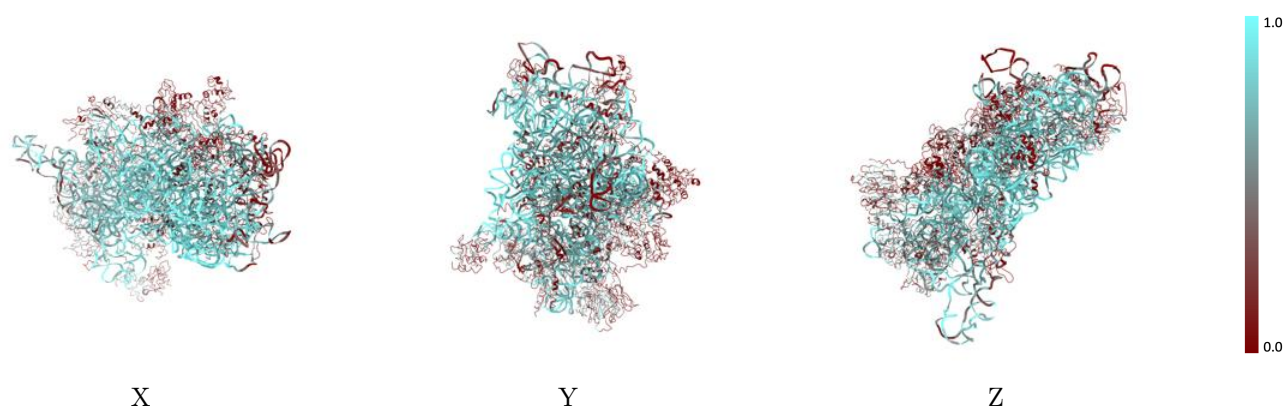
This section was not generated.

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



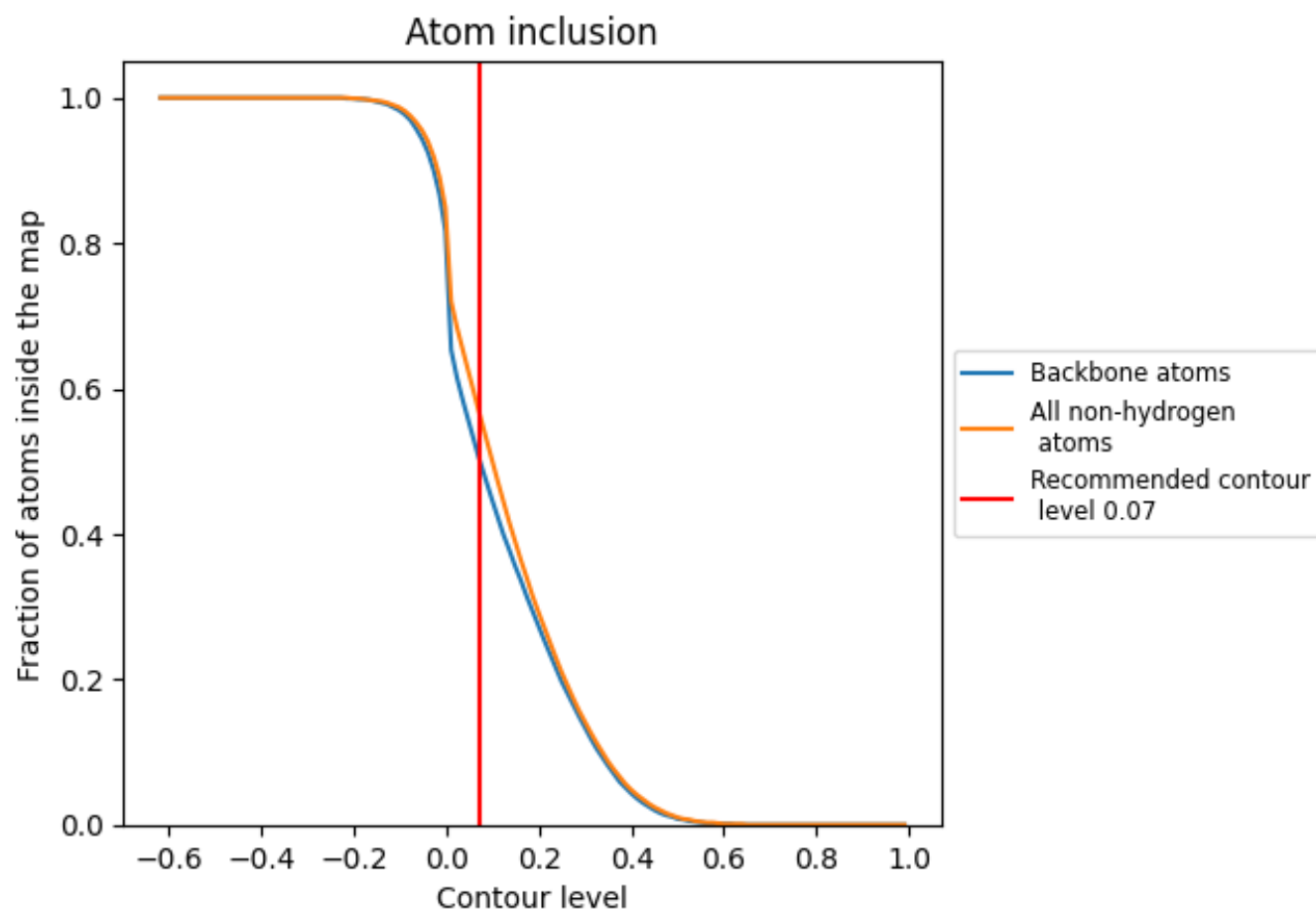
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 57% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5690	 0.1590
A2	 0.8410	 0.3170
AZ	 0.6810	 0.1240
BA	 0.1470	 -0.0090
BB	 0.3000	 0.0170
BC	 0.2880	 0.0070
BD	 0.2120	 -0.0100
BE	 0.2780	 0.0090
BF	 0.3500	 -0.0310
BG	 0.2790	 0.0230
BH	 0.1180	 0.0010
BI	 0.2240	 -0.0070
BJ	 0.2530	 0.0090
BK	 0.3050	 -0.0060
BL	 0.1120	 0.0110
BM	 0.1190	 -0.0310
BN	 0.1840	 0.0090
BO	 0.3120	 0.0220
BP	 0.3540	 0.0130
BQ	 0.4810	 0.0470
BR	 0.1720	 -0.0170
BS	 0.3780	 0.0120
BT	 0.4070	 -0.0030
BU	 0.2490	 -0.0000
BV	 0.2350	 0.0060
BW	 0.3910	 0.0410
BX	 0.3360	 0.0340
BY	 0.3310	 0.0280
BZ	 0.3330	 -0.0250
Ba	 0.3710	 0.0150
Bb	 0.1850	 0.0230
Bc	 0.2330	 -0.0630
Bd	 0.2990	 -0.0060
Be	 0.1890	 0.0040
Bf	 0.3940	 -0.0040
Bg	 0.3250	 -0.0060

