



## wwPDB EM Validation Summary Report ⓘ

Nov 13, 2022 – 12:41 AM EST

PDB ID : 6V92  
EMDB ID : EMD-21114  
Title : RSC-NCP  
Authors : Patel, A.B.; Moore, C.M.; Greber, B.J.; Nogales, E.  
Deposited on : 2019-12-13  
Resolution : 20.00 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

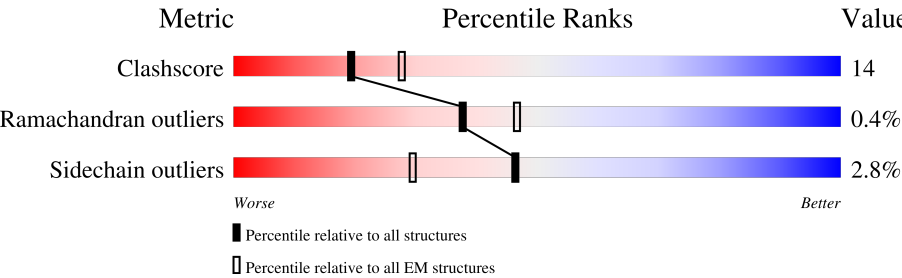
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 20.00 Å.

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



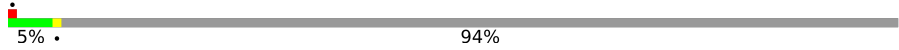

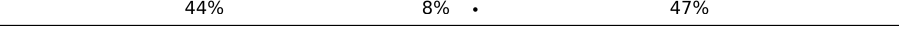
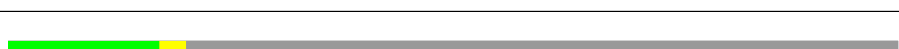
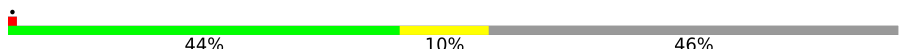


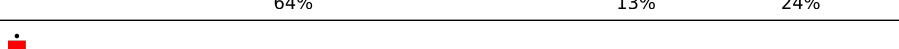
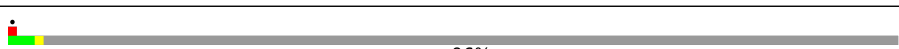
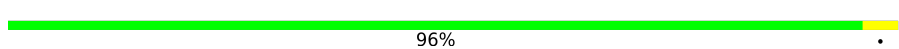
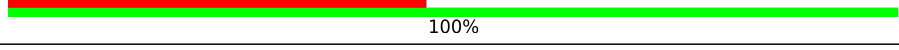
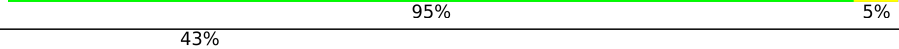
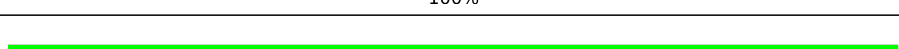
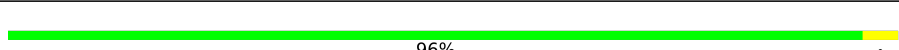
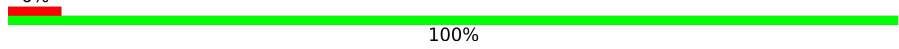
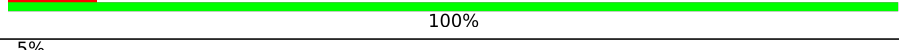
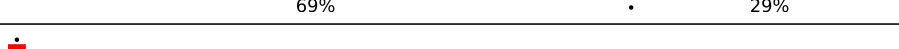







Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	477	<div> <div>23%</div> <div>54%</div> <div>27%</div> <div>16%</div> </div>
2	R	1359	<div> <div>18%</div> <div>6%</div> <div>76%</div> </div>
3	B	467	<div> <div>20%</div> <div>62%</div> <div>22%</div> <div>15%</div> </div>
4	P	157	<div> <div>11%</div> <div>20%</div> <div>13%</div> <div>66%</div> </div>
5	C	78	<div> <div>71%</div> <div>6%</div> <div>23%</div> </div>
6	D	180	<div> <div>6%</div> <div>50%</div> <div>6%</div> <div>44%</div> </div>
7	E	435	<div> <div>21%</div> <div>6%</div> <div>72%</div> </div>
8	F	889	<div> <div>6%</div> <div>92%</div> </div>

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Mol	Chain	Length	Quality of chain
9	G	885	
10	H	625	
11	I	557	
11	J	557	
11	K	557	
11	L	557	
12	M	483	
13	N	581	
14	O	502	
15	Q	426	
16	S	883	
17	2	28	
18	3	19	
18	4	19	
19	5	14	
20	6	15	
21	7	49	
22	i	146	
22	j	146	
23	a	136	
23	e	136	
24	b	103	
24	f	103	
25	c	130	
25	g	130	

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Mol	Chain	Length	Quality of chain
26	d	126	<div><div></div><div>10%</div><div>71%</div><div>5%</div><div>24%</div></div>
26	h	126	<div><div></div><div></div><div>69%</div><div>6%</div><div>25%</div></div>

## 2 Entry composition

There are 27 unique types of molecules in this entry. The entry contains 44583 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 Actin-related protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	399	Total	C	N	O	S	3	0
			3227	2081	528	603	15		

- Molecule 2 is a protein called Nuclear protein STH1/NPS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	R	325	Total	C	N	O	S	0	0
			2663	1668	487	504	4		

- Molecule 3 is a protein called Actin-like protein ARP9.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	396	Total	C	N	O	S	1	0
			3198	2053	523	615	7		

- Molecule 4 is a protein called Regulator of Ty1 transposition protein 102.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	P	54	Total	C	N	O	S	0	0
			490	313	84	92	1		

- Molecule 5 is a protein called High temperature lethal protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	60	Total	C	N	O	S	0	0
			493	301	92	96	4		

- Molecule 6 is a protein called Chromatin structure-remodeling complex protein RSC14.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	100	Total	C	N	O	S	0	0
			772	490	132	148	2		

- Molecule 7 is a protein called Chromatin structure-remodeling complex subunit RSC7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	120	Total	C	N	O	S	0	0
			978	610	166	200	2		

- Molecule 8 is a protein called Chromatin structure-remodeling complex subunit RSC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	67	Total	C	N	O	S	0	0
			536	346	94	95	1		

- Molecule 9 is a protein called Chromatin structure-remodeling complex protein RSC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	53	Total	C	N	O	S	0	0
			422	270	71	79	2		

- Molecule 10 is a protein called Chromatin structure-remodeling complex subunit RSC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	131	Total	C	N	O	S	0	0
			1083	696	175	205	7		

- Molecule 11 is a protein called Chromatin structure-remodeling complex protein RSC8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	293	Total	C	N	O	S	0	0
			2416	1537	423	448	8		
11	J	115	Total	C	N	O	S	0	0
			924	579	149	190	6		
11	K	109	Total	C	N	O	S	0	0
			878	554	139	179	6		
11	L	298	Total	C	N	O	S	0	0
			2445	1557	428	452	8		

- Molecule 12 is a protein called Chromatin structure-remodeling complex protein RSC6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	310	Total	C	N	O	S	0	0
			2474	1558	414	496	6		

- Molecule 13 is a protein called Chromatin structure-remodeling complex subunit RSC9.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	412	Total	C	N	O	S	0	0
			3275	2105	540	612	18		

- Molecule 14 is a protein called Chromatin structure-remodeling complex protein RSC58.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	384	Total	C	N	O	S	0	0
			3145	2025	529	581	10		

- Molecule 15 is a protein called Chromatin structure-remodeling complex subunit SFH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	264	Total	C	N	O	S	0	0
			2137	1349	362	418	8		

- Molecule 16 is a protein called Chromatin structure-remodeling complex protein RSC30.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	S	34	Total	C	N	O	S	0	0
			278	182	41	54	1		

- Molecule 17 is a protein called Unknown Protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	2	28	Total	C	N	O	0	0
			140	84	28	28		

- Molecule 18 is a protein called Unknown Protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	3	19	Total	C	N	O	0	0
			95	57	19	19		
18	4	19	Total	C	N	O	0	0
			95	57	19	19		

- Molecule 19 is a protein called Unknown Protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	5	14	Total	C	N	O	0	0
			70	42	14	14		

- Molecule 20 is a protein called Unknown Protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	6	15	Total	C	N	O	0	0
			75	45	15	15		

- Molecule 21 is a protein called Unknown Protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	7	49	Total	C	N	O	0	0
			245	147	49	49		

- Molecule 22 is a DNA chain called DNA (146-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
22	i	146	Total	C	N	O	P	0	0
			2990	1431	540	874	145		
22	j	146	Total	C	N	O	P	0	0
			2990	1431	540	874	145		

- Molecule 23 is a protein called Histone H3.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	a	97	Total	C	N	O	S	0	0
			801	505	155	137	4		
23	e	99	Total	C	N	O	S	0	0
			816	514	158	140	4		

- Molecule 24 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	b	78	Total	C	N	O	S	0	0
			619	391	120	107	1		
24	f	85	Total	C	N	O	S	0	0
			683	430	136	116	1		

- Molecule 25 is a protein called Histone H2A type 1-B/E.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	c	108	Total	C	N	O	0	0
			835	526	165	144		
25	g	104	Total	C	N	O	0	0
			805	508	157	140		

- Molecule 26 is a protein called Histone H2B type 1-K.

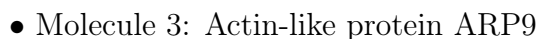


Mol	Chain	Residues	Atoms					AltConf	Trace
26	d	96	Total	C	N	O	S	0	0
			754	473	138	141	2		
26	h	94	Total	C	N	O	S	0	0
			735	461	134	138	2		

- Molecule 27 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
27	I	1	Total	Zn	0
			1	1	











[illegible]

- Molecule 10: Chromatin structure-remodeling complex subunit RSC4

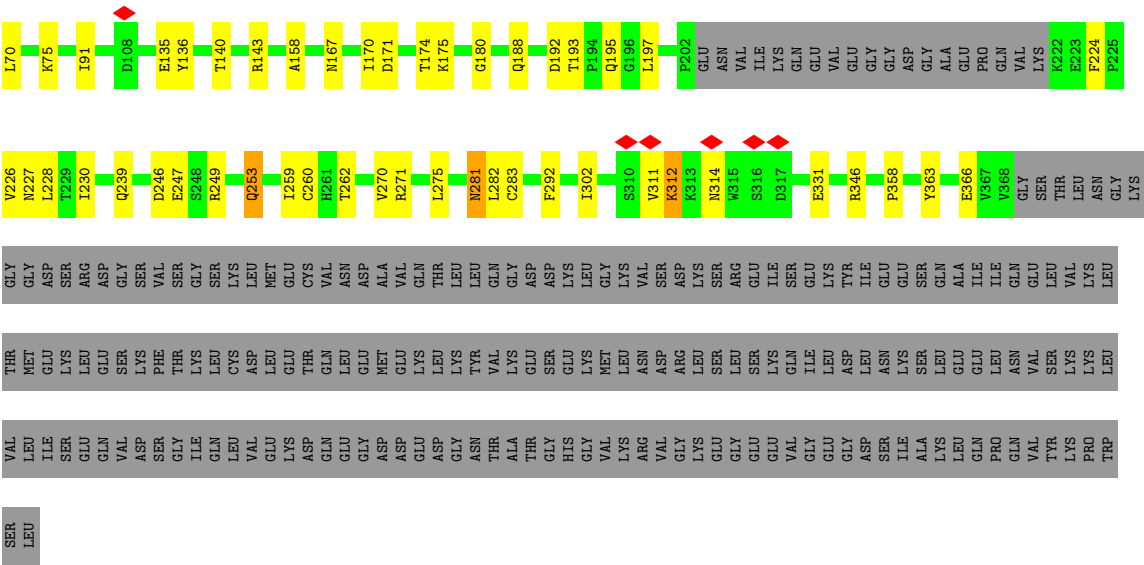
Chain H:  16% 5% 79%

T588	T596	T597	T598	T599	T600	T601	T602	T603	T604	T605	T606	T607	T608	T609	T610	T611	T612	T613	T614	T615	T616	T617	T618	T619	T620	T621	T622	T623	T624	T625	T626	T627	T628	T629	T630	T631	T632	T633	T634	T635	T636	T637	T638	T639	T640	T641	T642	T643	T644	T645	T646	T647	T648	T649	T650	T651	T652	T653	T654	T655	T656	T657	T658	T659	T660	T661	T662	T663	T664	T665	T666	T667	T668	T669	T670	T671	T672	T673	T674	T675	T676	T677	T678	T679	T680	T681	T682	T683	T684	T685	T686	T687	T688	T689	T690	T691	T692	T693	T694	T695	T696	T697	T698	T699	T700	T701	T702	T703	T704	T705	T706	T707	T708	T709	T710	T711	T712	T713	T714	T715	T716	T717	T718	T719	T720	T721	T722	T723	T724	T725	T726	T727	T728	T729	T730	T731	T732	T733	T734	T735	T736	T737	T738	T739	T740	T741	T742	T743	T744	T745	T746	T747	T748	T749	T750	T751	T752	T753	T754	T755	T756	T757	T758	T759	T760	T761	T762	T763	T764	T765	T766	T767	T768	T769	T770	T771	T772	T773	T774	T775	T776	T777	T778	T779	T780	T781	T782	T783	T784	T785	T786	T787	T788	T789	T790	T791	T792	T793	T794	T795	T796	T797	T798	T799	T800	T801	T802	T803	T804	T805	T806	T807	T808	T809	T810	T811	T812	T813	T814	T815	T816	T817	T818	T819	T820	T821	T822	T823	T824	T825	T826	T827	T828	T829	T830	T831	T832	T833	T834	T835	T836	T837	T838	T839	T840	T841	T842	T843	T844	T845	T846	T847	T848	T849	T850	T851	T852	T853	T854	T855	T856	T857	T858	T859	T860	T861	T862	T863	T864	T865	T866	T867	T868	T869	T870	T871	T872	T873	T874	T875	T876	T877	T878	T879	T880	T881	T882	T883	T884	T885	T886	T887	T888	T889	T890	T891	T892	T893	T894	T895	T896	T897	T898	T899	T900	T901	T902	T903	T904	T905	T906	T907	T908	T909	T910	T911	T912	T913	T914	T915	T916	T917	T918	T919	T920	T921	T922	T923	T924	T925	T926	T927	T928	T929	T930	T931	T932	T933	T934	T935	T936	T937	T938	T939	T940	T941	T942	T943	T944	T945	T946	T947	T948	T949	T950	T951	T952	T953	T954	T955	T956	T957	T958	T959	T960	T961	T962	T963	T964	T965	T966	T967	T968	T969	T970	T971	T972	T973	T974	T975	T976	T977	T978	T979	T980	T981	T982	T983	T984	T985	T986	T987	T988	T989	T990	T991	T992	T993	T994	T995	T996	T997	T998	T999	T1000	T1001	T1002	T1003	T1004	T1005	T1006	T1007	T1008	T1009	T1010	T1011	T1012	T1013	T1014	T1015	T1016	T1017	T1018	T1019	T1020	T1021	T1022	T1023	T1024	T1025	T1026	T1027	T1028	T1029	T1030	T1031	T1032	T1033	T1034	T1035	T1036	T1037	T1038	T1039	T1040	T1041	T1042	T1043	T1044	T1045	T1046	T1047	T1048	T1049	T1050	T1051	T1052	T1053	T1054	T1055	T1056	T1057	T1058	T1059	T1060	T1061	T1062	T1063	T1064	T1065	T1066	T1067	T1068	T1069	T1070	T1071	T1072	T1073	T1074	T1075	T1076	T1077	T1078	T1079	T1080	T1081	T1082	T1083	T1084	T1085	T1086	T1087	T1088	T1089	T1090	T1091	T1092	T1093	T1094	T1095	T1096	T1097	T1098	T1099	T1100	T1101	T1102	T1103	T1104	T1105	T1106	T1107	T1108	T1109	T1110	T1111	T1112	T1113	T1114	T1115	T1116	T1117	T1118	T1119	T1120	T1121	T1122	T1123	T1124	T1125	T1126	T1127	T1128	T1129	T1130	T1131	T1132	T1133	T1134	T1135	T1136	T1137	T1138	T1139	T1140	T1141	T1142	T1143	T1144	T1145	T1146	T1147	T1148	T1149	T1150	T1151	T1152	T1153	T1154	T1155	T1156	T1157	T1158	T1159	T1160	T1161	T1162	T1163	T1164	T1165	T1166	T1167	T1168	T1169	T1170	T1171	T1172	T1173	T1174	T1175	T1176	T1177	T1178	T1179	T1180	T1181	T1182	T1183	T1184	T1185	T1186	T1187	T1188	T1189	T1190	T1191	T1192	T1193	T1194	T1195	T1196	T1197	T1198	T1199	T1200	T1201	T1202	T1203	T1204	T1205	T1206	T1207	T1208	T1209	T1210	T1211	T1212	T1213	T1214	T1215	T1216	T1217	T1218	T1219	T1220	T1221	T1222	T1223	T1224	T1225	T1226	T1227	T1228	T1229	T1230	T1231	T1232	T1233	T1234	T1235	T1236	T1237	T1238	T1239	T1240	T1241	T1242	T1243	T1244	T1245	T1246	T1247	T1248	T1249	T1250	T1251	T1252	T1253	T1254	T1255	T1256	T1257	T1258	T1259	T1260	T1261	T1262	T1263	T1264	T1265	T1266	T1267	T1268	T1269	T1270	T1271	T1272	T1273	T1274	T1275	T1276	T1277	T1278	T1279	T1280	T1281	T1282	T1283	T1284	T1285	T1286	T1287	T1288	T1289	T1290	T1291	T1292	T1293	T1294	T1295	T1296	T1297	T1298	T1299	T1300	T1301	T1302	T1303	T1304	T1305	T1306	T1307	T1308	T1309	T1310	T1311	T1312	T1313	T1314	T1315	T1316	T1317	T1318	T1319	T1320	T1321	T1322	T1323	T1324	T1325	T1326	T1327	T1328	T1329	T1330	T1331	T1332	T1333	T1334	T1335	T1336	T1337	T1338	T1339	T1340	T1341	T1342	T1343	T1344	T1345	T1346	T1347	T1348	T1349	T1350	T1351	T1352	T1353	T1354	T1355	T1356	T1357	T1358	T1359	T1360	T1361	T1362	T1363	T1364	T1365	T1366	T1367	T1368	T1369	T1370	T1371	T1372	T1373	T1374	T1375	T1376	T1377	T1378	T1379	T1380	T1381	T1382	T1383	T1384	T1385	T1386	T1387	T1388	T1389	T1390	T1391	T1392	T1393	T1394	T1395	T1396	T1397	T1398	T1399	T1400	T1401	T1402	T1403	T1404	T1405	T1406	T1407	T1408	T1409	T1410	T1411	T1412	T1413	T1414	T1415	T1416	T1417	T1418	T1419	T1420	T1421	T1422	T1423	T1424	T1425	T1426	T1427	T1428	T1429	T1430	T1431	T1432	T1433	T1434	T1435	T1436	T1437	T1438	T1439	T1440	T1441	T1442	T1443	T1444	T1445	T1446	T1447	T1448	T1449	T1450	T1451	T1452	T1453	T1454	T1455	T1456	T1457	T1458	T1459	T1460	T1461	T1462	T1463	T1464	T1465	T1466	T1467	T1468	T1469	T1470	T1471	T1472	T1473	T1474	T1475	T1476	T1477	T1478	T1479	T1480	T1481	T1482	T1483	T1484	T1485	T1486	T1487	T1488	T1489	T1490	T1491	T1492	T1493	T1494	T1495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- Molecule 11: Chromatin structure-remodeling complex protein RSC8

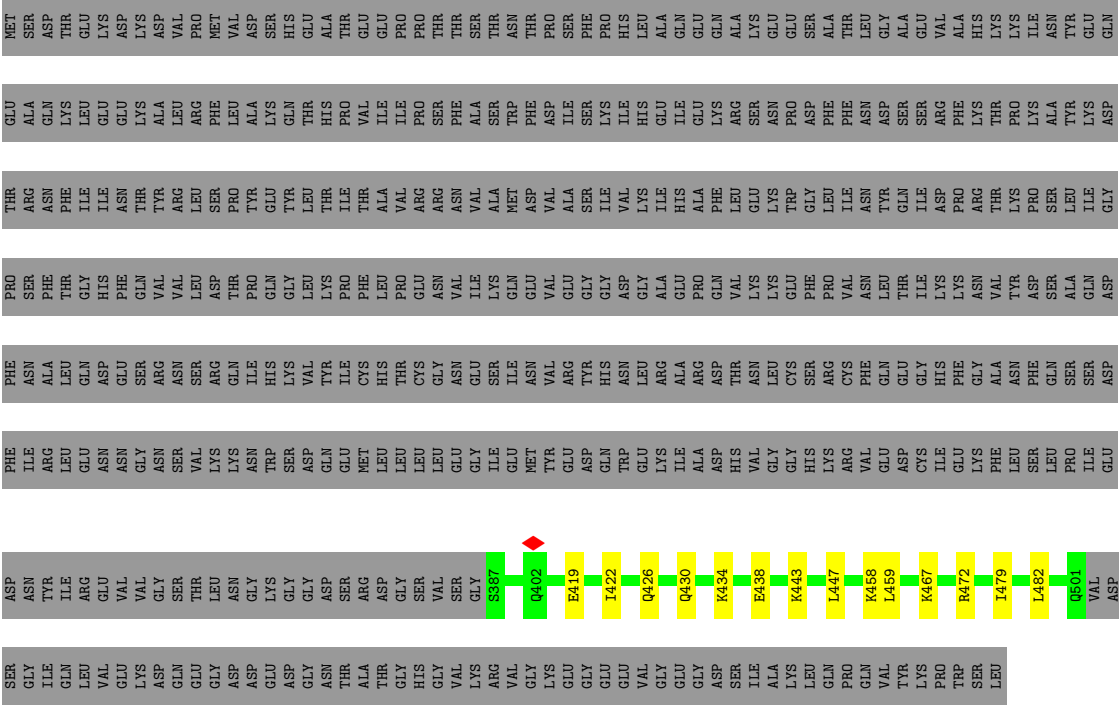
Chain I:  44% 8% 47%

MET	SER	ASP	THR	GLU	LYS	ASP	LYS	ASP	VAL	PRO	MET	VAL	ASP	SER	HIS	GLU	ALA	THR	GLU	GLU	PRO	PRO	THR	THR	SER	THR	ASN	PRO	SER	PHE	PRO	HIS	HIS	LEU	ALA	GLN	GLU	GLN	ALA	LYS	GLU	GLU	SER	ALA	THR	LEU	GLY	ALA	GLU	VAL	ALA	HIS	LYS	LYS	ILE	LYS	MET	Y58	E59
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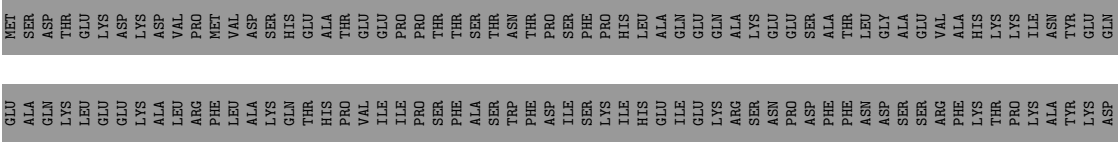
• Molecule 11: Chromatin structure-remodeling complex protein RSC8

Chain J: 18% 79%

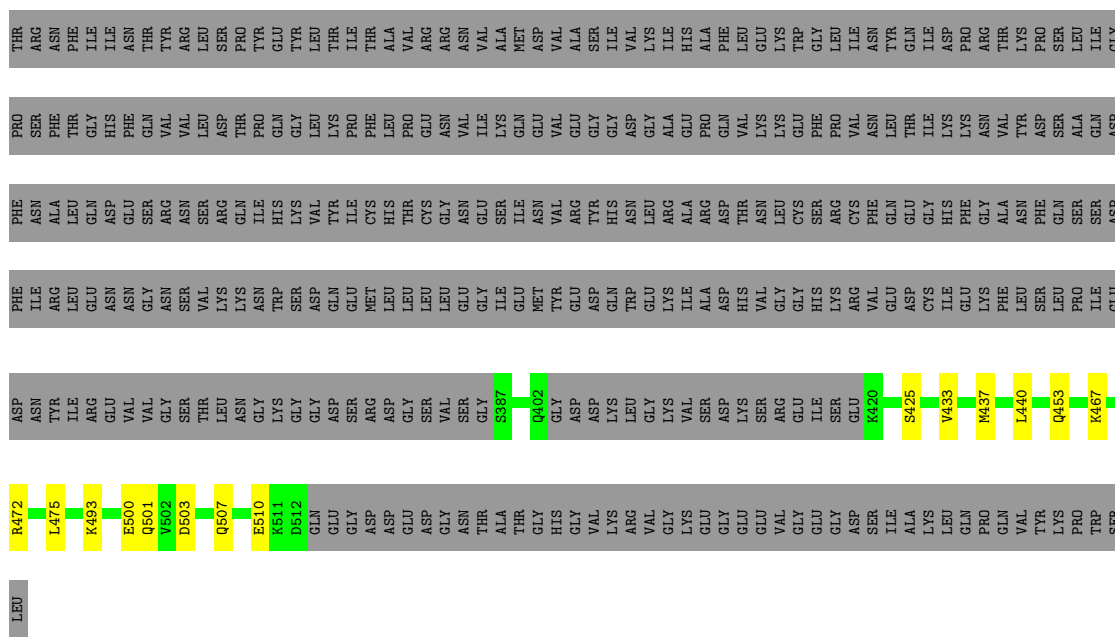


• Molecule 11: Chromatin structure-remodeling complex protein RSC8

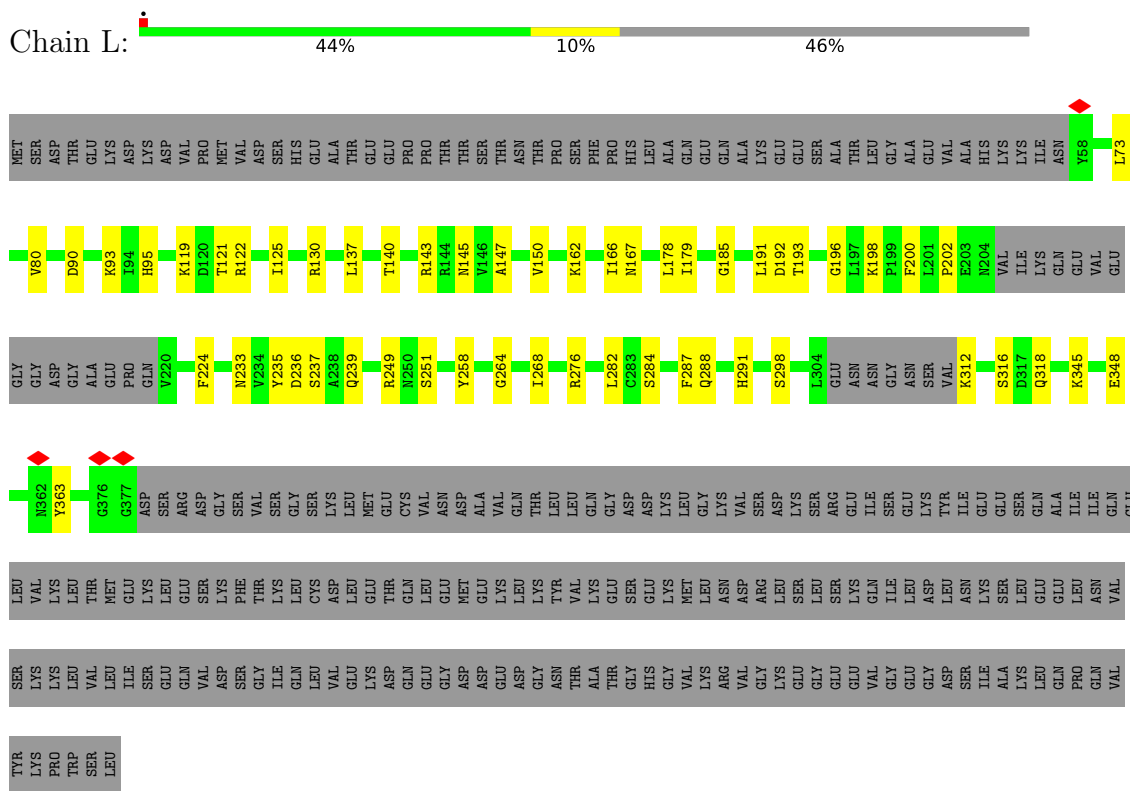
Chain K: 17% 80%



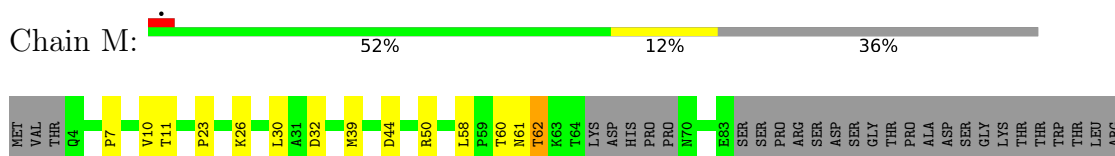


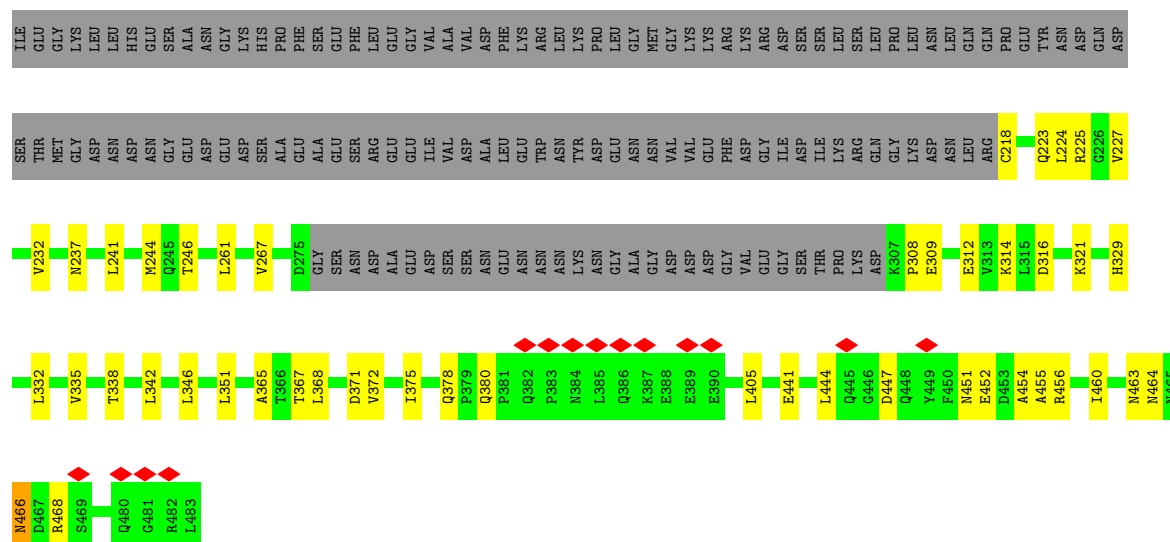


- Molecule 11: Chromatin structure-remodeling complex protein RSC8

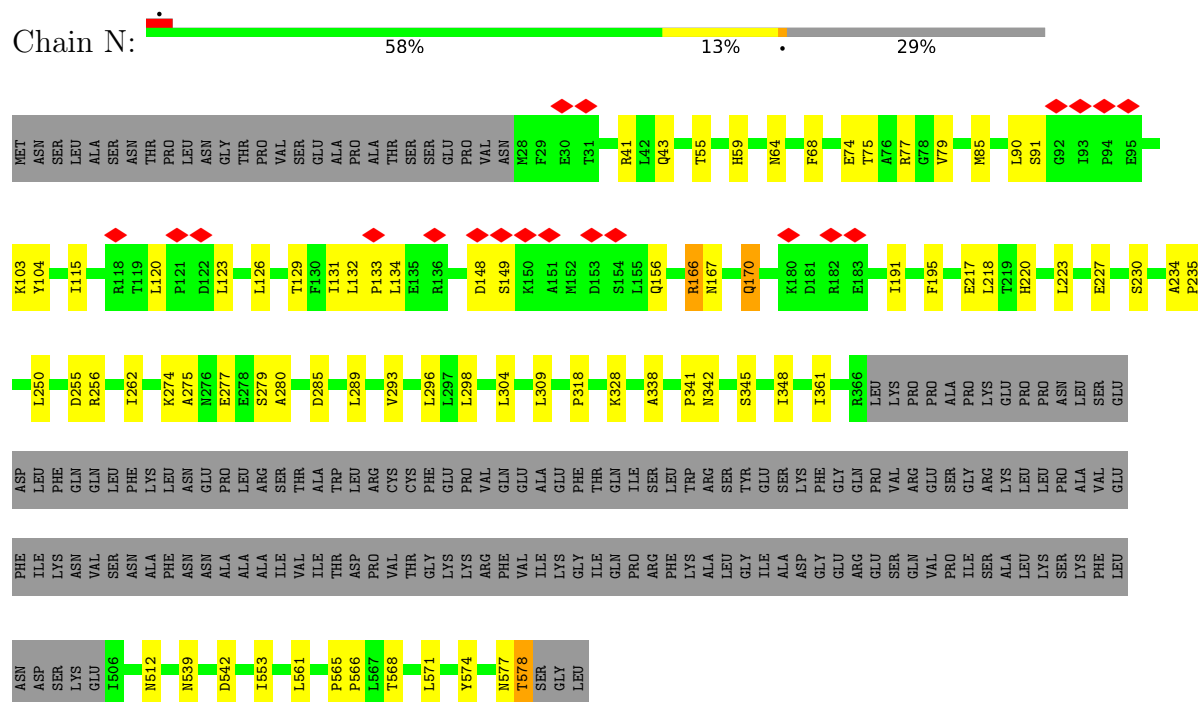


- Molecule 12: Chromatin structure-remodeling complex protein RSC6

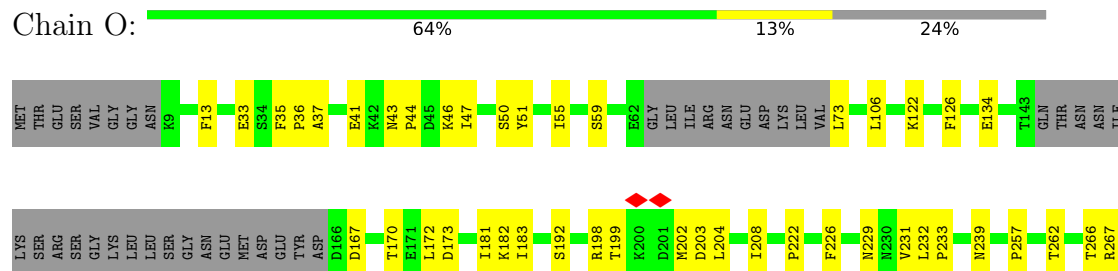


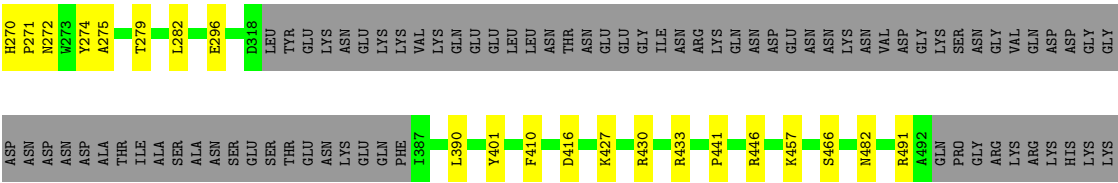


• Molecule 13: Chromatin structure-remodeling complex subunit RSC9

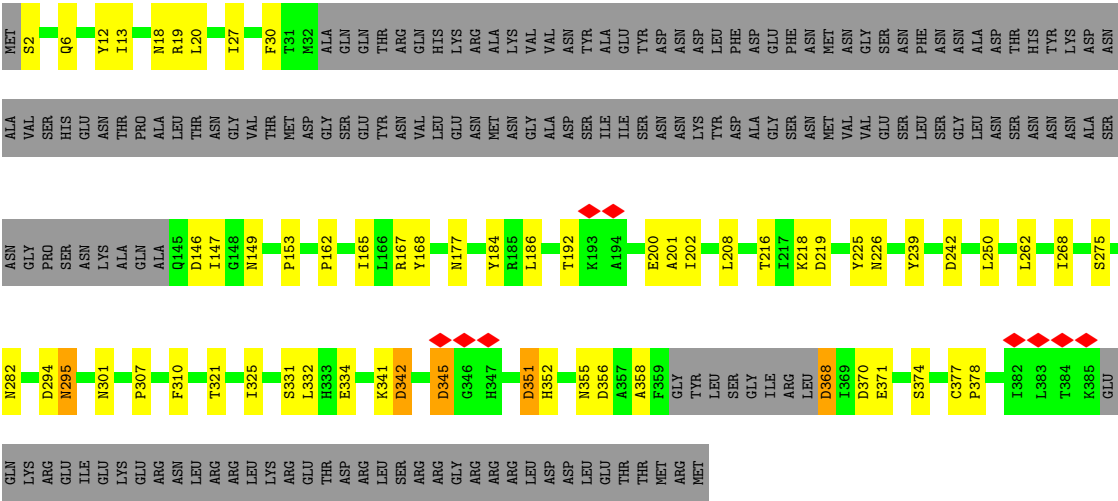


• Molecule 14: Chromatin structure-remodeling complex protein RSC58

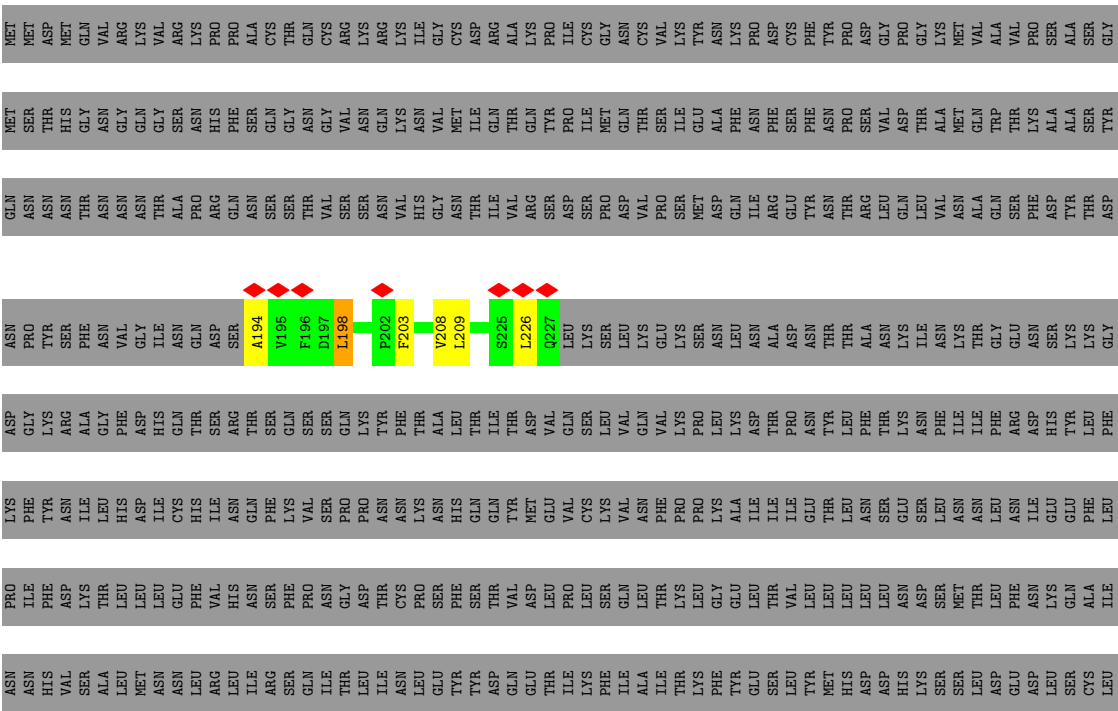




• Molecule 15: Chromatin structure-remodeling complex subunit SFH1



• Molecule 16: Chromatin structure-remodeling complex protein RSC30



[illegible]

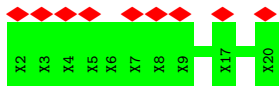
- Molecule 17: Unknown Protein

Chain 2:  96%



- Molecule 18: Unknown Protein

Chain 3:  47% 100%

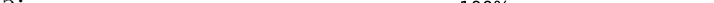


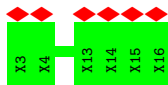
- Molecule 18: Unknown Protein

Chain 4:  95% 5%



- Molecule 19: Unknown Protein

Chain 5:  43% 100%



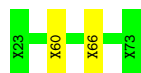
- Molecule 20: Unknown Protein

Chain 6:  100%

There are no outlier residues recorded for this chain.

- Molecule 21: Unknown Protein

Chain 7:  96%



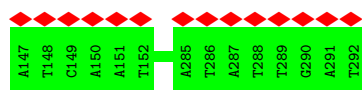
- Molecule 22: DNA (146-MER)

Chain i:  6% 100%



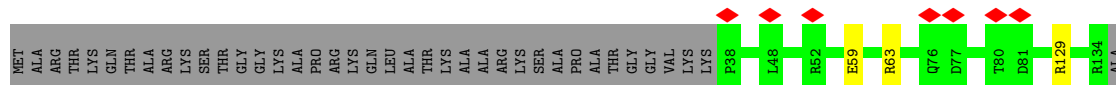
- Molecule 22: DNA (146-MER)

Chain j:  10% 100%



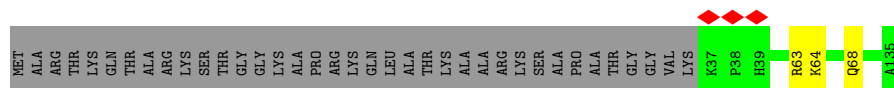
- Molecule 23: Histone H3.1

Chain a:  5% 69% 29%




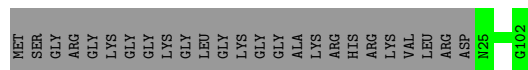
- Molecule 23: Histone H3.1

Chain e:  71% 27%




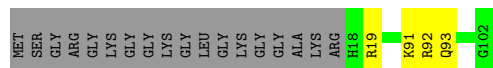
- Molecule 24: Histone H4

Chain b:  76% 24%




- Molecule 24: Histone H4

Chain f:  79% 17%




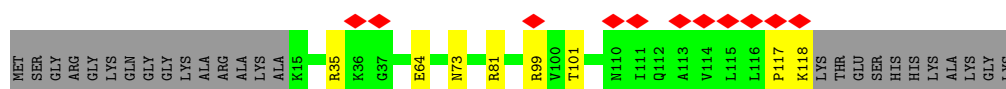
- Molecule 25: Histone H2A type 1-B/E

Chain c:  78% 5% 17%



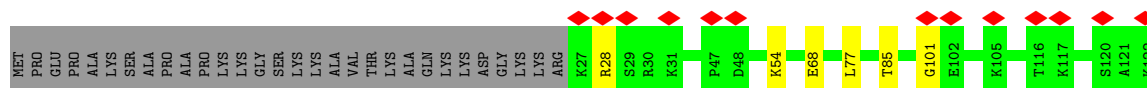
- Molecule 25: Histone H2A type 1-B/E

Chain g:  8% 74% 6% 20%



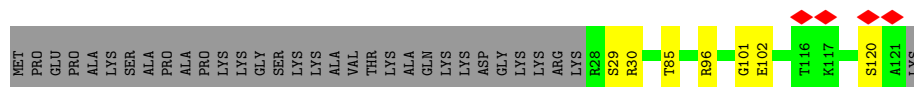
- Molecule 26: Histone H2B type 1-K

Chain d:  10% 71% 5% 24%



- Molecule 26: Histone H2B type 1-K

Chain h:  69% 6% 25%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	13337	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.110	Depositor
Minimum map value	-0.064	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.03	Depositor
Map size ( $\text{\AA}$ )	437.76, 437.76, 437.76	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	3.42, 3.42, 3.42	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.43	0/3303	0.60	1/4465 (0.0%)
2	R	0.36	2/2697 (0.1%)	0.49	3/3616 (0.1%)
3	B	0.45	0/3269	0.59	0/4432
4	P	0.41	0/501	0.57	0/669
5	C	0.24	0/495	0.36	0/662
6	D	0.27	0/786	0.38	0/1062
7	E	0.28	0/997	0.44	0/1356
8	F	0.27	0/551	0.41	0/748
9	G	0.26	0/431	0.43	0/584
10	H	0.29	0/1108	0.48	0/1497
11	I	0.32	0/2474	0.41	0/3343
11	J	0.30	0/926	0.40	0/1233
11	K	0.27	0/879	0.39	0/1172
11	L	0.29	0/2502	0.40	0/3376
12	M	0.28	0/2515	0.42	0/3423
13	N	0.30	0/3334	0.42	0/4515
14	O	0.30	0/3216	0.42	1/4358 (0.0%)
15	Q	0.28	0/2181	0.45	0/2964
16	S	0.26	0/281	0.35	0/378
22	i	0.38	0/3354	0.79	0/5175
22	j	0.36	0/3354	0.78	0/5175
23	a	0.40	0/813	0.59	0/1090
23	e	0.46	0/828	0.61	0/1109
24	b	0.38	0/626	0.62	0/837
24	f	0.44	0/691	0.63	0/923
25	c	0.39	0/845	0.60	0/1139
25	g	0.39	0/815	0.65	0/1100
26	d	0.41	0/765	0.63	0/1025
26	h	0.40	0/746	0.58	0/1003
All	All	0.35	2/45283 (0.0%)	0.55	5/62429 (0.0%)



All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	R	328	LYS	C-O	5.96	1.34	1.23
2	R	333	ILE	C-O	5.93	1.34	1.23

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	380	SER	C-N-CD	5.93	140.86	128.40
14	O	231	VAL	C-N-CA	5.36	135.09	121.70
2	R	333	ILE	CA-C-O	5.28	131.19	120.10
2	R	367	ASP	CB-CG-OD2	5.17	122.95	118.30
2	R	328	LYS	CA-C-O	5.10	130.81	120.10

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3227	0	3251	150	0
2	R	2663	0	2746	159	0
3	B	3198	0	3187	136	0
4	P	490	0	467	19	0
5	C	493	0	507	4	0
6	D	772	0	754	11	0
7	E	978	0	935	25	0
8	F	536	0	533	13	0
9	G	422	0	423	9	0
10	H	1083	0	1062	21	0
11	I	2416	0	2358	36	0
11	J	924	0	976	12	0
11	K	878	0	930	13	0
11	L	2445	0	2402	48	0
12	M	2474	0	2465	48	0
13	N	3275	0	3373	47	0
14	O	3145	0	3168	50	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	Q	2137	0	2069	42	0
16	S	278	0	287	6	0
17	2	140	0	34	1	0
18	3	95	0	21	0	0
18	4	95	0	21	1	0
19	5	70	0	16	0	0
20	6	75	0	17	0	0
21	7	245	0	63	2	0
22	i	2990	0	1652	0	0
22	j	2990	0	1652	0	0
23	a	801	0	839	0	0
23	e	816	0	856	0	0
24	b	619	0	659	0	0
24	f	683	0	729	0	0
25	c	835	0	897	0	0
25	g	805	0	861	0	0
26	d	754	0	782	0	0
26	h	735	0	756	0	0
27	I	1	0	0	0	0
All	All	44583	0	41748	652	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 14.

The worst 5 of 652 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)
2:R:353:PHE:CZ	3:B:447:PHE:CE2	2.05	1.45
2:R:353:PHE:CZ	3:B:447:PHE:HE2	1.34	1.41
2:R:353:PHE:CE1	3:B:447:PHE:HE2	1.47	1.33
2:R:365:GLU:HG2	3:B:415:TYR:CD2	1.65	1.32
2:R:353:PHE:CE2	3:B:447:PHE:CE2	2.21	1.29

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	A	392/477 (82%)	369 (94%)	18 (5%)	5 (1%)	12	48
2	R	319/1359 (24%)	296 (93%)	23 (7%)	0	100	100
3	B	391/467 (84%)	368 (94%)	21 (5%)	2 (0%)	29	69
4	P	46/157 (29%)	43 (94%)	2 (4%)	1 (2%)	6	35
5	C	58/78 (74%)	56 (97%)	2 (3%)	0	100	100
6	D	96/180 (53%)	90 (94%)	6 (6%)	0	100	100
7	E	118/435 (27%)	108 (92%)	10 (8%)	0	100	100
8	F	63/889 (7%)	56 (89%)	7 (11%)	0	100	100
9	G	51/885 (6%)	49 (96%)	2 (4%)	0	100	100
10	H	127/625 (20%)	114 (90%)	10 (8%)	3 (2%)	6	33
11	I	289/557 (52%)	274 (95%)	15 (5%)	0	100	100
11	J	113/557 (20%)	109 (96%)	4 (4%)	0	100	100
11	K	105/557 (19%)	101 (96%)	4 (4%)	0	100	100
11	L	292/557 (52%)	277 (95%)	15 (5%)	0	100	100
12	M	302/483 (62%)	281 (93%)	21 (7%)	0	100	100
13	N	408/581 (70%)	380 (93%)	28 (7%)	0	100	100
14	O	376/502 (75%)	352 (94%)	24 (6%)	0	100	100
15	Q	258/426 (61%)	224 (87%)	34 (13%)	0	100	100
16	S	32/883 (4%)	32 (100%)	0	0	100	100
23	a	95/136 (70%)	92 (97%)	3 (3%)	0	100	100
23	e	97/136 (71%)	95 (98%)	2 (2%)	0	100	100
24	b	76/103 (74%)	75 (99%)	1 (1%)	0	100	100
24	f	83/103 (81%)	80 (96%)	3 (4%)	0	100	100
25	c	106/130 (82%)	101 (95%)	5 (5%)	0	100	100
25	g	102/130 (78%)	98 (96%)	3 (3%)	1 (1%)	15	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	d	94/126 (75%)	89 (95%)	4 (4%)	1 (1%)	14	52
26	h	92/126 (73%)	88 (96%)	0	4 (4%)	2	22
All	All	4581/11645 (39%)	4297 (94%)	267 (6%)	17 (0%)	38	72

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	48	ASP
10	H	528	ILE
26	h	120	SER
1	A	343	SER
26	d	101	GLY

### 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	
1	A	357/420 (85%)	338 (95%)	19 (5%)	22	47
2	R	297/1228 (24%)	294 (99%)	3 (1%)	76	86
3	B	363/423 (86%)	343 (94%)	20 (6%)	21	47
4	P	53/140 (38%)	52 (98%)	1 (2%)	57	75
5	C	58/75 (77%)	58 (100%)	0	100	100
6	D	82/151 (54%)	82 (100%)	0	100	100
7	E	113/388 (29%)	105 (93%)	8 (7%)	14	39
8	F	60/810 (7%)	60 (100%)	0	100	100
9	G	48/832 (6%)	47 (98%)	1 (2%)	53	72
10	H	126/578 (22%)	124 (98%)	2 (2%)	62	79
11	I	268/500 (54%)	261 (97%)	7 (3%)	46	66
11	J	111/500 (22%)	110 (99%)	1 (1%)	78	87
11	K	106/500 (21%)	106 (100%)	0	100	100
11	L	270/500 (54%)	270 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	M	286/435 (66%)	281 (98%)	5 (2%)	60	78
13	N	374/521 (72%)	366 (98%)	8 (2%)	53	72
14	O	358/462 (78%)	355 (99%)	3 (1%)	81	89
15	Q	243/384 (63%)	233 (96%)	10 (4%)	30	55
16	S	33/824 (4%)	32 (97%)	1 (3%)	41	63
23	a	85/111 (77%)	82 (96%)	3 (4%)	36	59
23	e	86/111 (78%)	83 (96%)	3 (4%)	36	59
24	b	63/79 (80%)	63 (100%)	0	100	100
24	f	70/79 (89%)	66 (94%)	4 (6%)	20	45
25	c	85/100 (85%)	79 (93%)	6 (7%)	14	39
25	g	83/100 (83%)	76 (92%)	7 (8%)	11	33
26	d	82/105 (78%)	77 (94%)	5 (6%)	18	44
26	h	80/105 (76%)	77 (96%)	3 (4%)	33	57
All	All	4240/10461 (40%)	4120 (97%)	120 (3%)	46	65

5 of 120 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	I	270	VAL
25	g	35	ARG
13	N	166	ARG
24	f	93	GLN
26	h	96	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
12	M	61	ASN
26	d	92	GLN
13	N	559	HIS
26	d	60	ASN
25	g	73	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
21	7	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	7	57:UNK	C	60:UNK	N	4.98

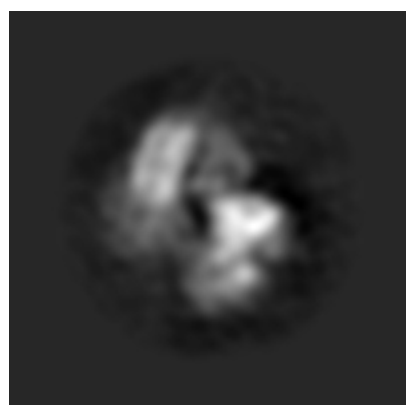
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21114. These allow visual inspection of the internal detail of the map and identification of artifacts.

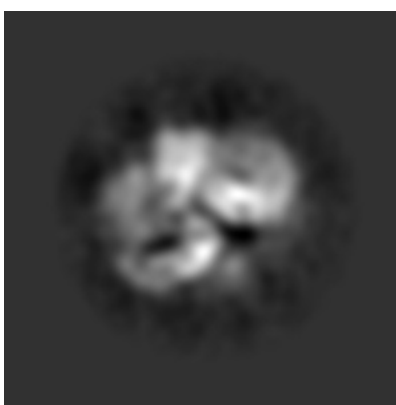
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

#### 6.1.1 Primary map



X



Y

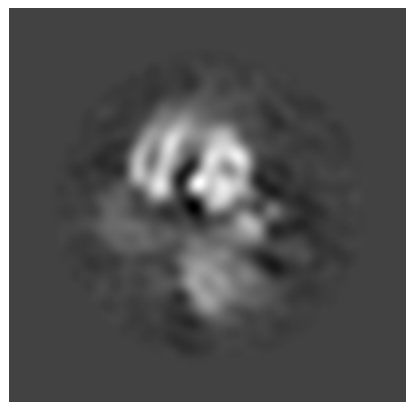


Z

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

### 6.2 Central slices [i](#)

#### 6.2.1 Primary map



X Index: 64



Y Index: 64



Z Index: 64

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: 68



Y Index: 71



Z Index: 59

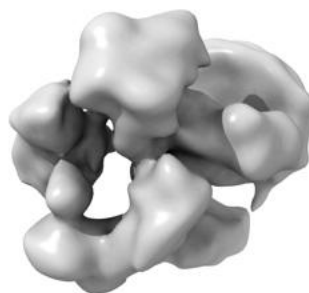
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.



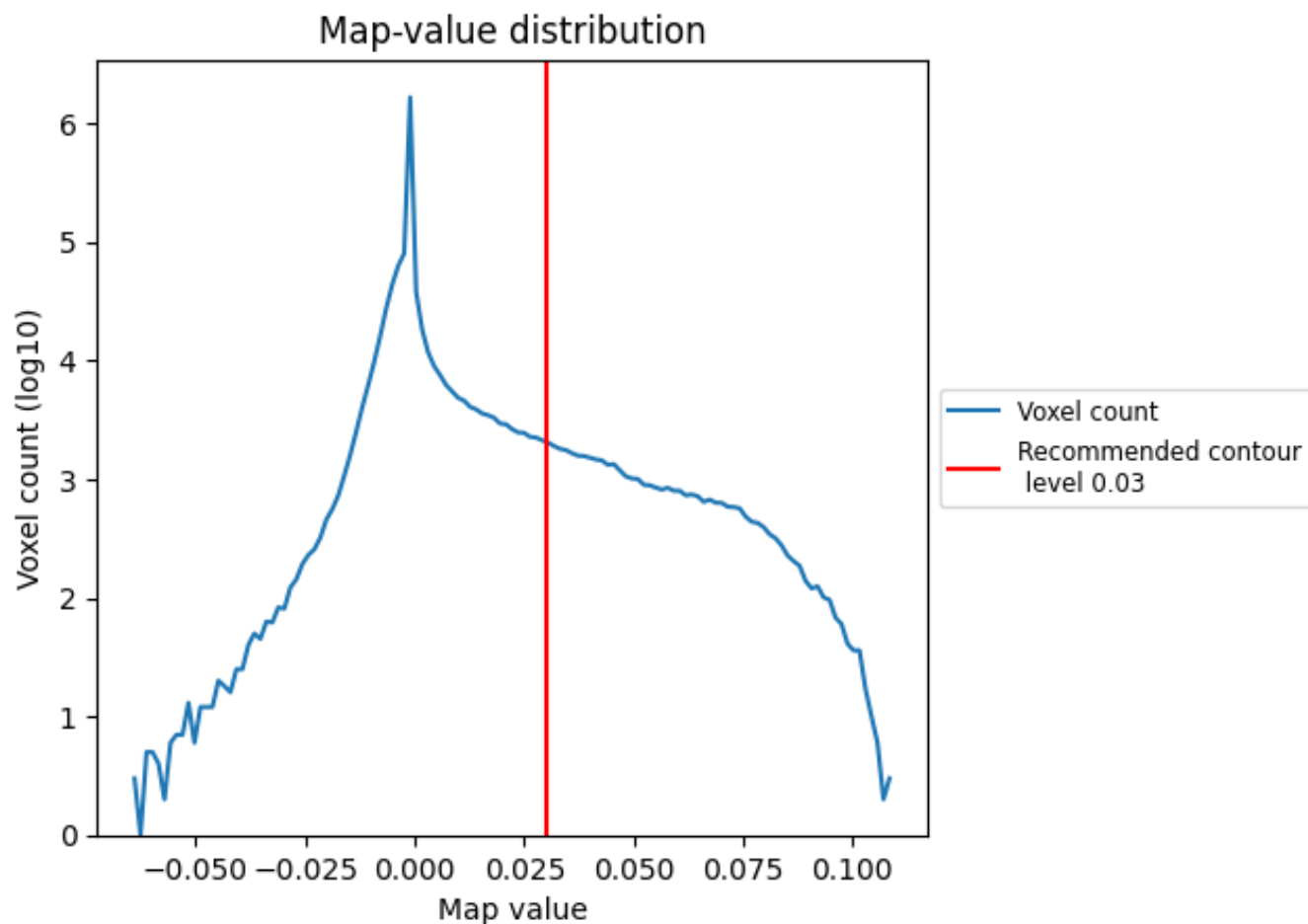
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

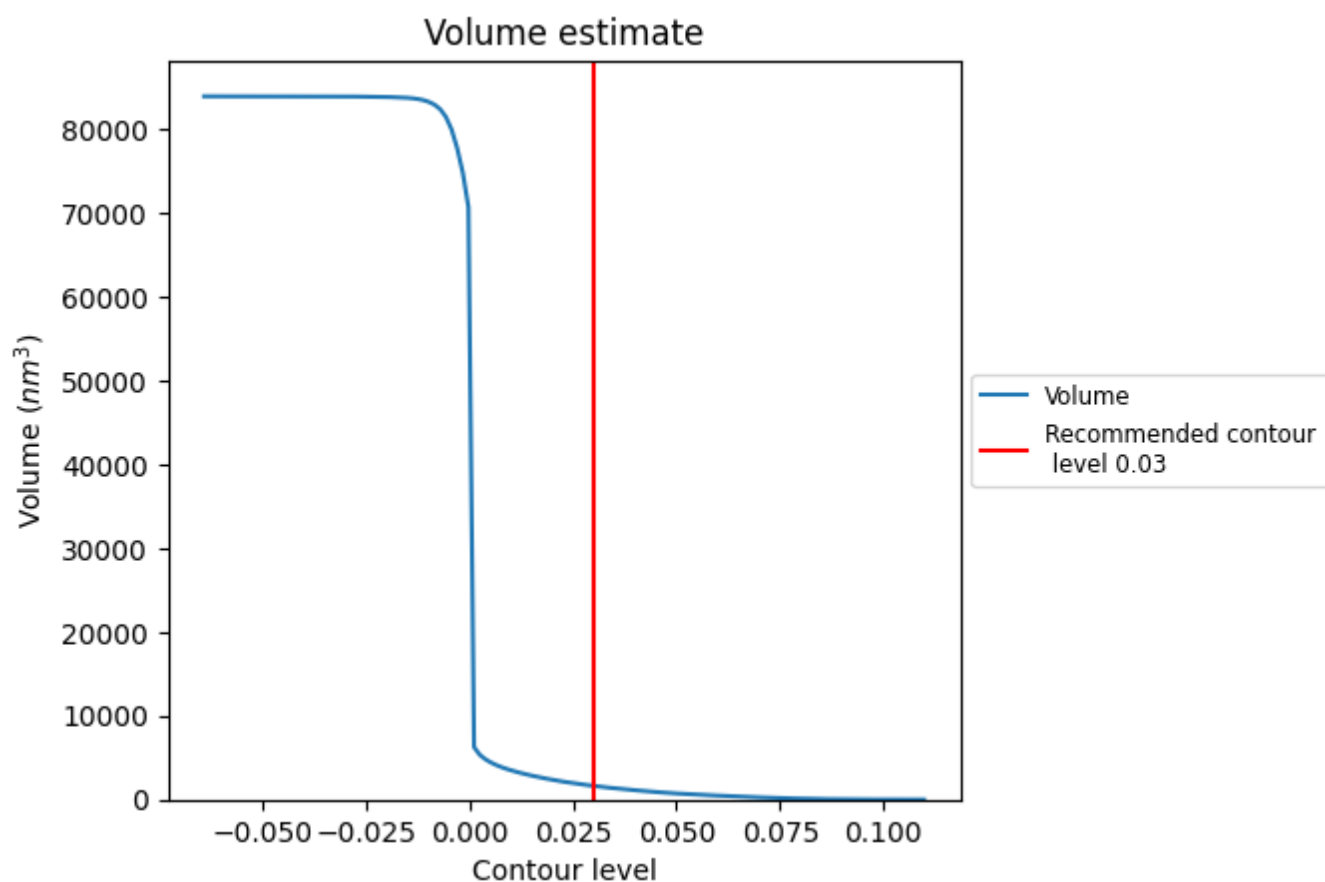
This section contains the results of statistical analysis of the map.

### 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.

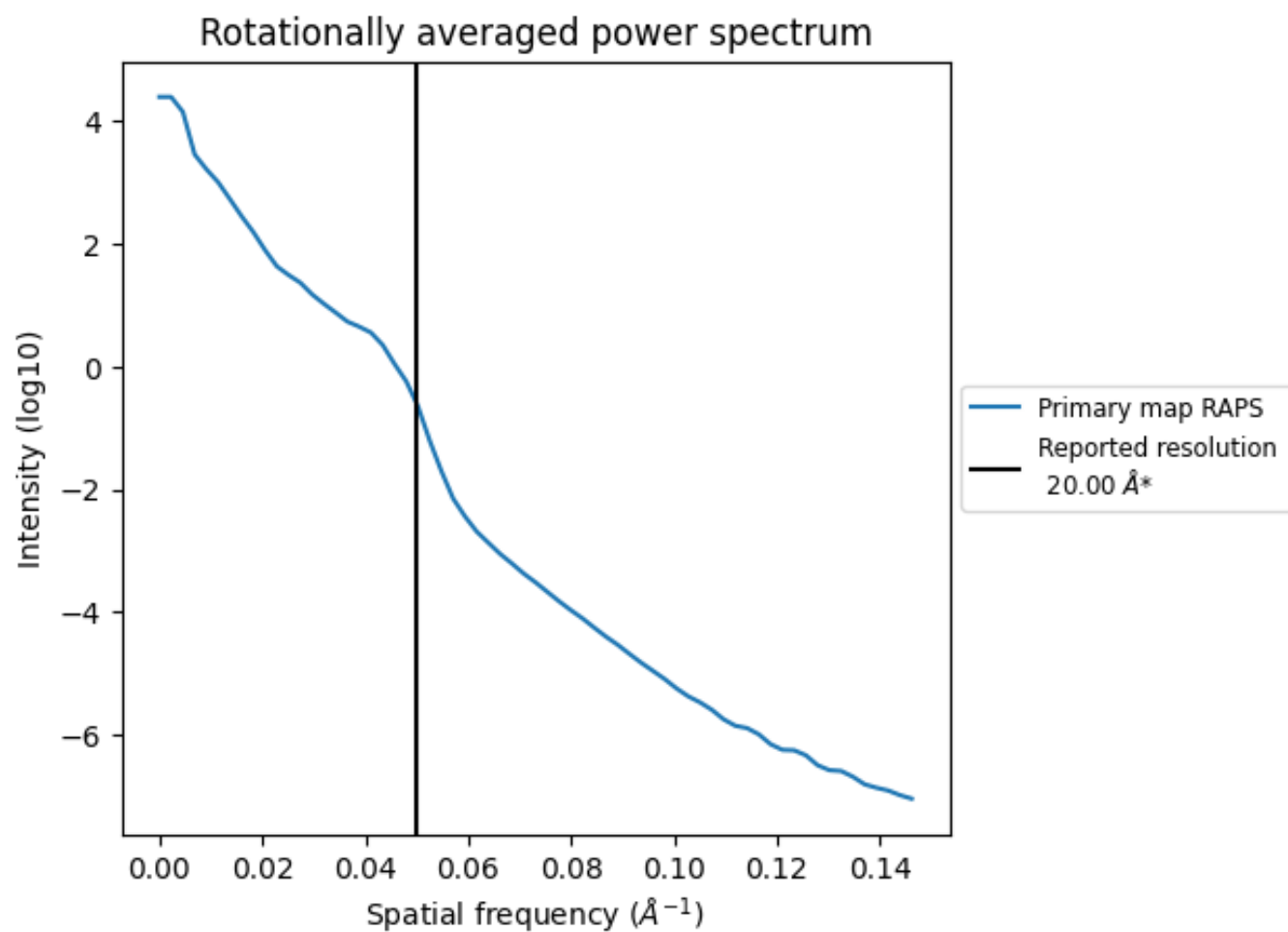
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1633 nm<sup>3</sup>; this corresponds to an approximate mass of 1475 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 0.050 Å<sup>-1</sup>

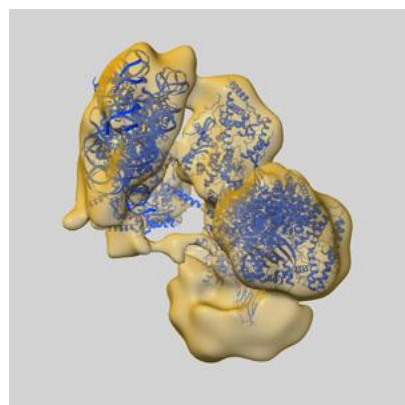
## 8 Fourier-Shell correlation

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

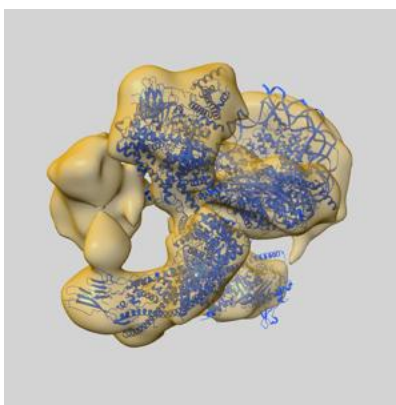
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21114 and PDB model 6V92. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

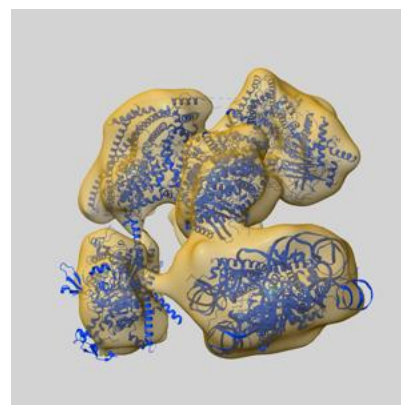
### 9.1 Map-model overlay [i](#)



X



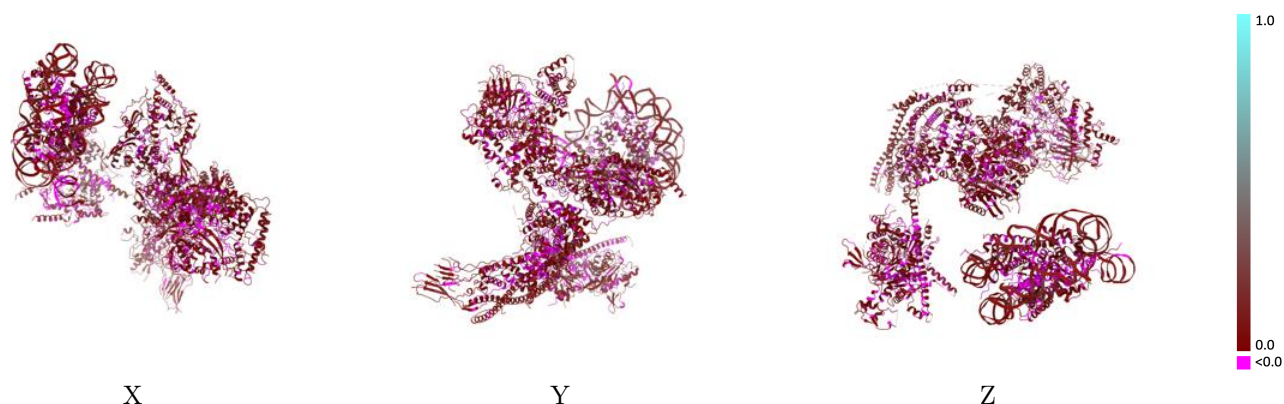
Y



Z

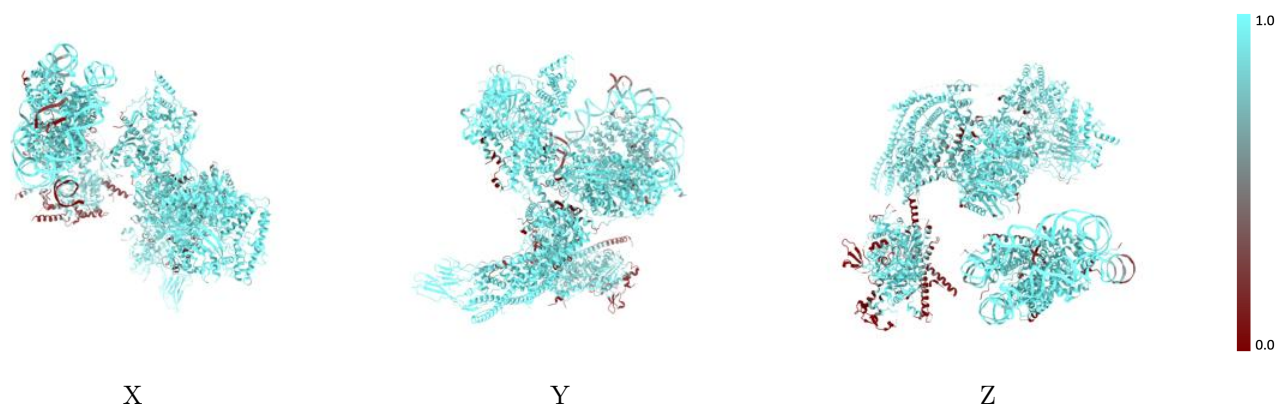
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



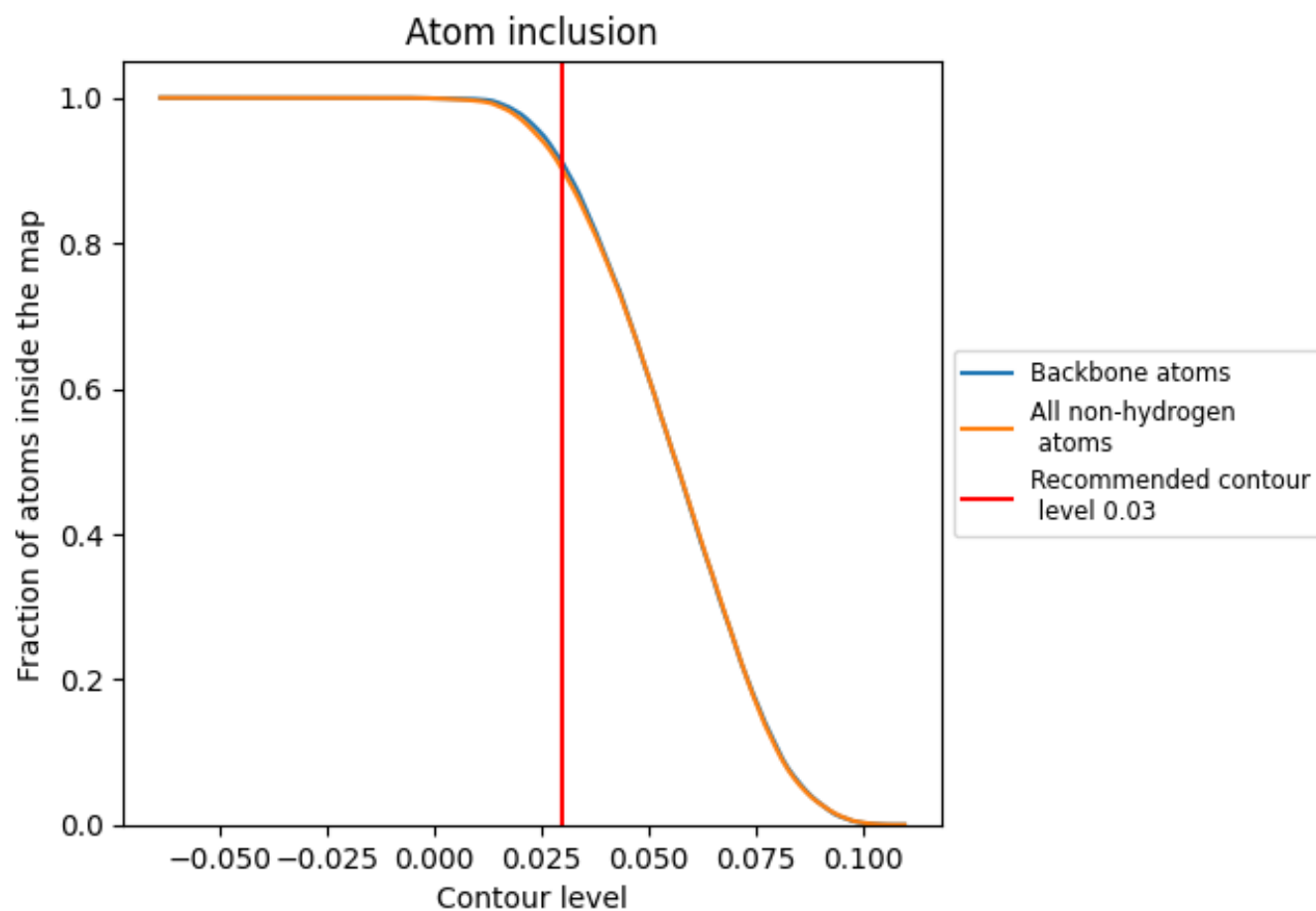
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

## 9.4 Atom inclusion [i](#)











































































At the recommended contour level, 91% of all backbone atoms, 90% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8997	 0.0530
2	 1.0000	 0.0480
3	 0.5789	 0.0250
4	 0.9895	 0.0570
5	 0.5714	 0.0050
6	 1.0000	 0.0500
7	 0.9878	 0.0500
A	 0.6959	 0.0330
B	 0.7389	 0.0370
C	 0.9917	 0.0650
D	 0.8765	 0.0380
E	 0.9687	 0.0740
F	 1.0000	 0.0290
G	 0.8230	 0.0470
H	 0.9570	 0.0530
I	 0.9709	 0.0510
J	 0.9717	 0.0800
K	 0.9691	 0.0810
L	 0.9720	 0.0510
M	 0.9429	 0.0480
N	 0.9367	 0.0490
O	 0.9942	 0.0650
P	 0.6977	 0.0590
Q	 0.9560	 0.0660
R	 0.8229	 0.0410
S	 0.7626	 0.0680
a	 0.9364	 0.0280
b	 0.9899	 0.0440
c	 0.9579	 0.0380
d	 0.8558	 0.0200
e	 0.9554	 0.0430
f	 0.9954	 0.0050
g	 0.8833	 0.0110
h	 0.9372	 0.0120
i	 0.8987	 0.0860
j	 0.8970	 0.0930

