



Full wwPDB EM Validation Report ⓘ

Nov 16, 2022 – 03:44 AM JST

PDB ID : 6LK8
EMDB ID : EMD-0909
Title : Structure of *Xenopus laevis* Cytoplasmic Ring subunit.
Authors : Shi, Y.; Huang, G.; Yan, C.; Zhang, Y.
Deposited on : 2019-12-18
Resolution : 5.50 Å (reported)

This is a Full wwPDB EM Validation 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:

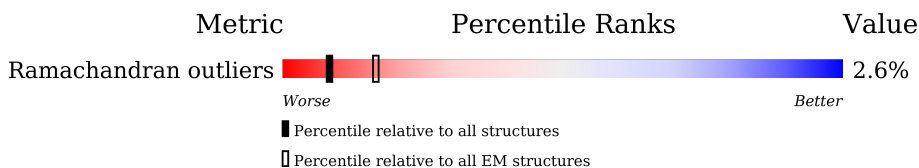
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance i

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

The reported resolution of this entry is 5.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023

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	2011	
1	a	2011	
2	B	653	
2	b	653	
3	C	375	
3	c	375	
4	D	322	
4	d	322	
5	E	1435	
5	e	1435	
6	F	326	

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Mol	Chain	Length	Quality of chain
6	f	326	63% 87% 11%
7	G	923	23% 60% 7% 33%
7	g	923	26% 59% 7% 34%
8	H	320	15% 89% 9%
8	h	320	21% 88% 10%
9	I	916	66% 80% 19%
9	i	916	79% 79% 21%
10	J	1140	90% 88% 10%
10	j	1140	90% 89% 10%
11	S	2905	5% 6% 94%
11	T	2905	6% 6% 94%
11	U	2905	6% 6% 94%
11	V	2905	6% 6% 94%
12	K	69	100%
13	L	80	100%
14	M	73	100%
15	N	31	48% 100%
16	O	35	100%
17	P	26	96% 100%
18	Q	391	58% 99%
18	R	391	87% 90% 10%

2 Entry composition [i](#)

There are 18 unique types of molecules in this entry. The entry contains 72207 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 MGC83295 protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	A	1409	Total 6934	C 4116	N 1409	O 1409	0	0
1	a	1272	Total 6306	C 3762	N 1272	O 1272	0	0

- Molecule 2 is a protein called Nuclear pore complex protein Nup85.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	B	532	Total 2639	C 1575	N 532	O 532	0	0
2	b	519	Total 2574	C 1536	N 519	O 519	0	0

- Molecule 3 is a protein called MGC154553 protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	C	289	Total 1156	C 578	N 289	O 289	0	0
3	c	292	Total 1168	C 584	N 292	O 292	0	0

- Molecule 4 is a protein called Nucleoporin SEH1-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	D	307	Total 1519	C 905	N 307	O 307	0	0
4	d	293	Total 1450	C 864	N 293	O 293	0	0

- Molecule 5 is a protein called outer Nup160.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	E	1030	Total	C	N	O	0	0
			5107	3047	1030	1030		
5	e	1109	Total	C	N	O	0	0
			5497	3279	1109	1109		

- Molecule 6 is a protein called MGC83926 protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	F	289	Total	C	N	O	0	0
			1423	845	289	289		
6	f	291	Total	C	N	O	0	0
			1433	851	291	291		

- Molecule 7 is a protein called Nuclear pore complex protein Nup96.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	G	618	Total	C	N	O	0	0
			3064	1828	618	618		
7	g	607	Total	C	N	O	0	0
			3010	1796	607	607		

- Molecule 8 is a protein called GATOR complex protein SEC13.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	H	291	Total	C	N	O	0	0
			1419	837	291	291		
8	h	287	Total	C	N	O	0	0
			1413	839	287	287		

- Molecule 9 is a protein called Nuclear pore complex protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	738	Total	C	N	O	0	0
			3668	2192	738	738		
9	i	727	Total	C	N	O	0	0
			3613	2159	727	727		

- Molecule 10 is a protein called outer Nup133.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	J	1026	Total	C	N	O	0	0
			5085	3033	1026	1026		

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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	j	1027	5090	3036	1027	1027	0	0

- Molecule 11 is a protein called Nup358 complex, clamps.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	S	169	840	502	169	169	0	0
11	T	169	840	502	169	169	0	0
11	U	173	859	513	173	173	0	0
11	V	169	840	502	169	169	0	0

- Molecule 12 is a protein called Nup214 complex Coiled-coil region 1, helix 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	K	69	345	207	69	69	0	0

- Molecule 13 is a protein called Nup214 complex coiled coil region 1, helix 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	L	80	400	240	80	80	0	0

- Molecule 14 is a protein called Nup214 complex coiled coil region 1, helix 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	M	73	365	219	73	73	0	0

- Molecule 15 is a protein called Nup214 complex Coiled coil region 2, helix 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	N	31	155	93	31	31	0	0

- Molecule 16 is a protein called Nup214 complex Coiled coil region 2, helix 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	O	35	175	105	35	35	0	0

- Molecule 17 is a protein called Nup214 complex Coiled coil region 2, helix 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
17	P	26	130	78	26	26	0	0

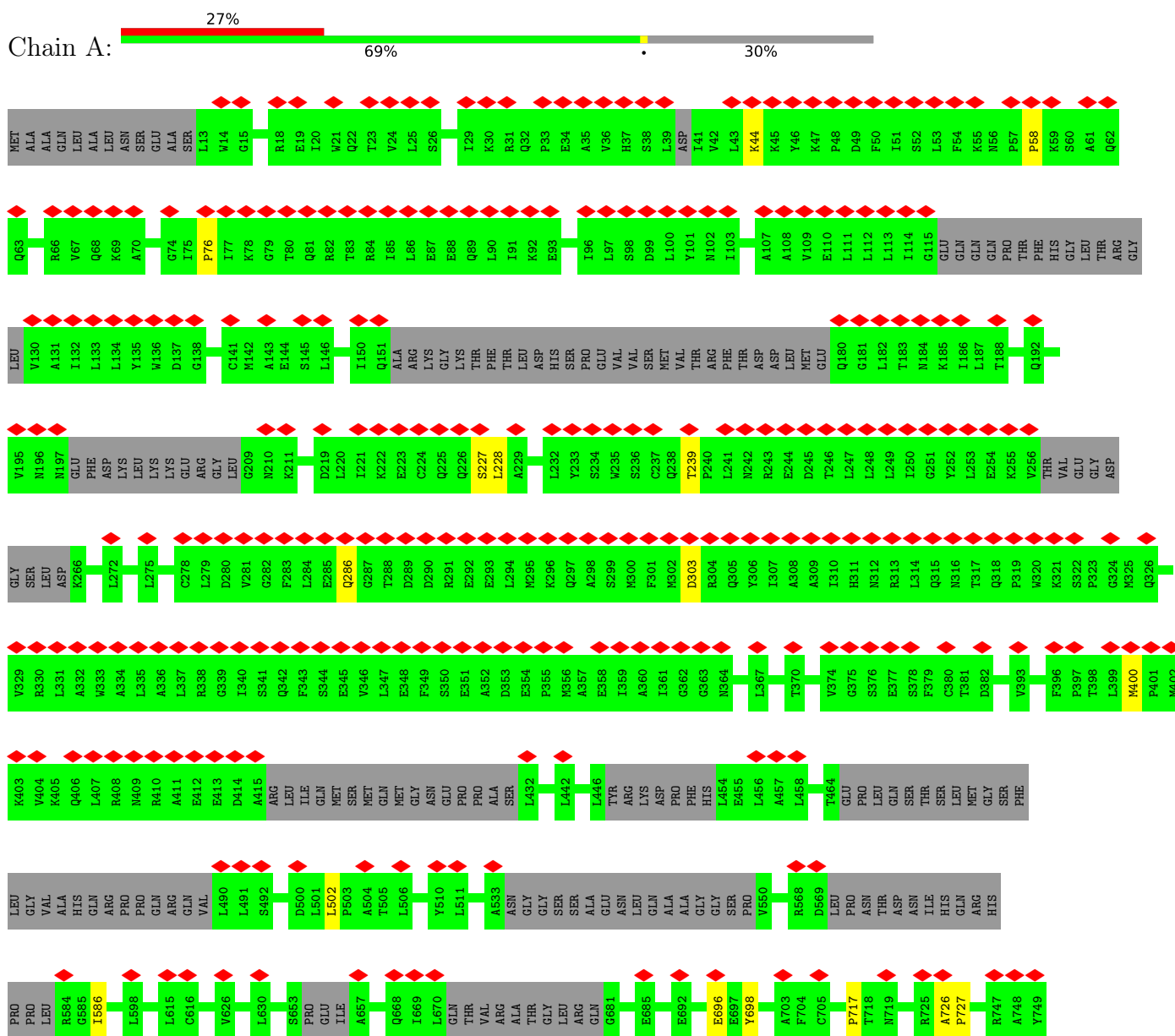
- Molecule 18 is a protein called bridge domain.

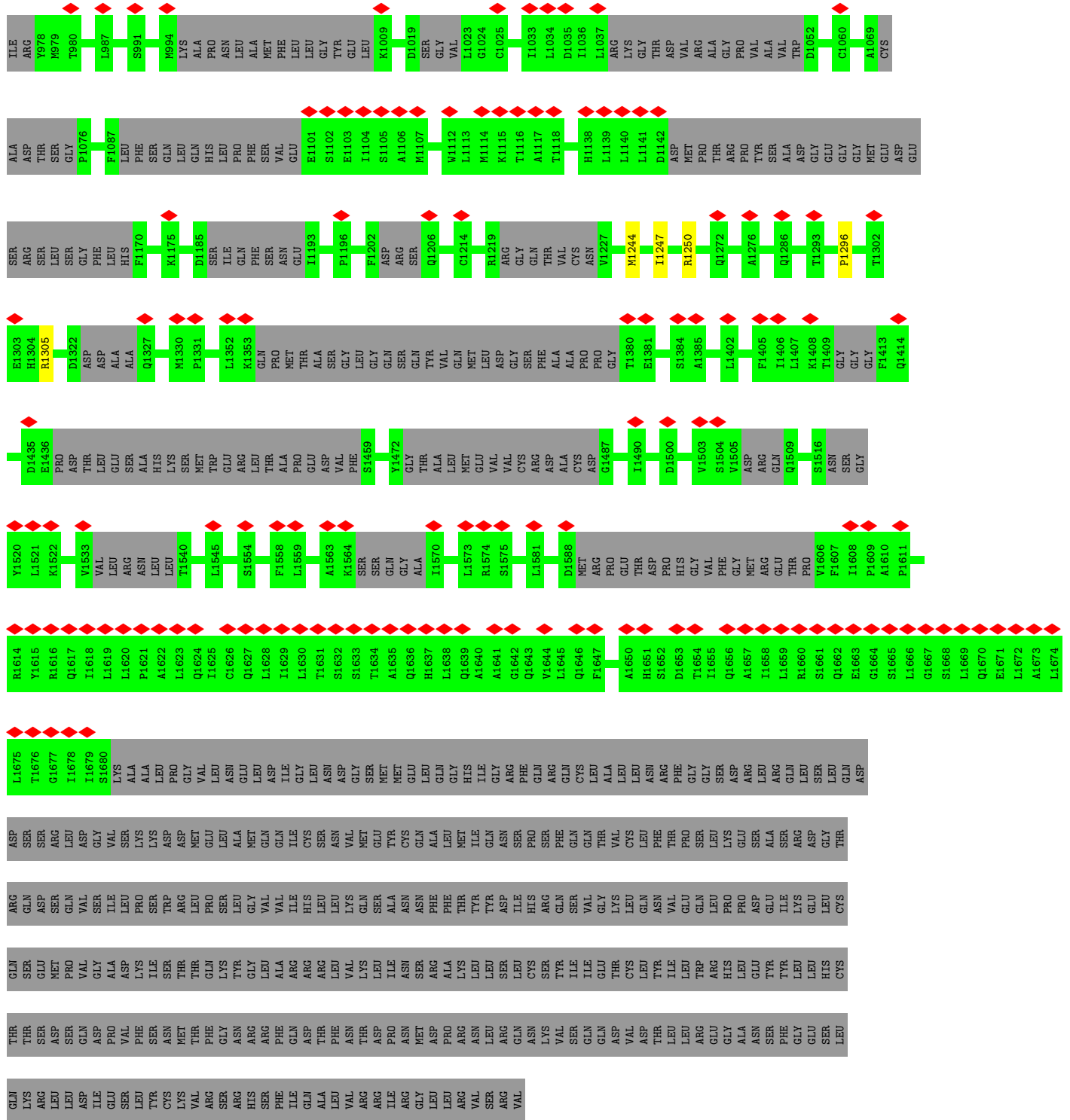
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
18	Q	387	1935	1161	387	387	0	0
18	R	351	1755	1053	351	351	0	0

3 Residue-property plots

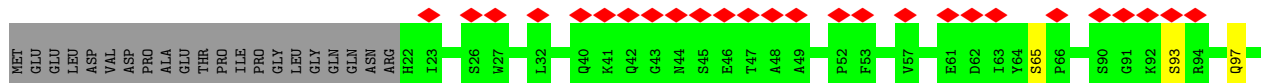
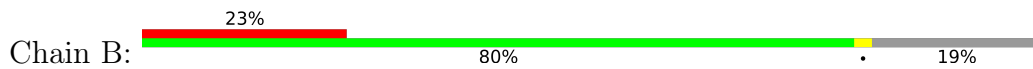
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

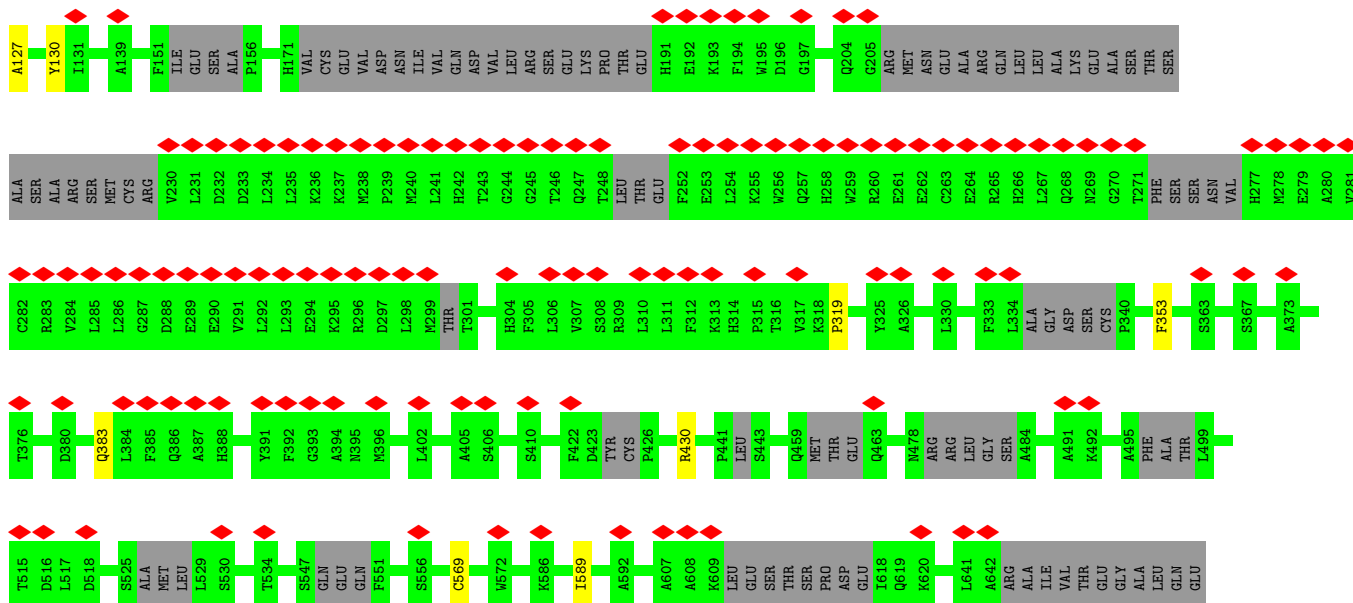
- Molecule 1: MGC83295 protein



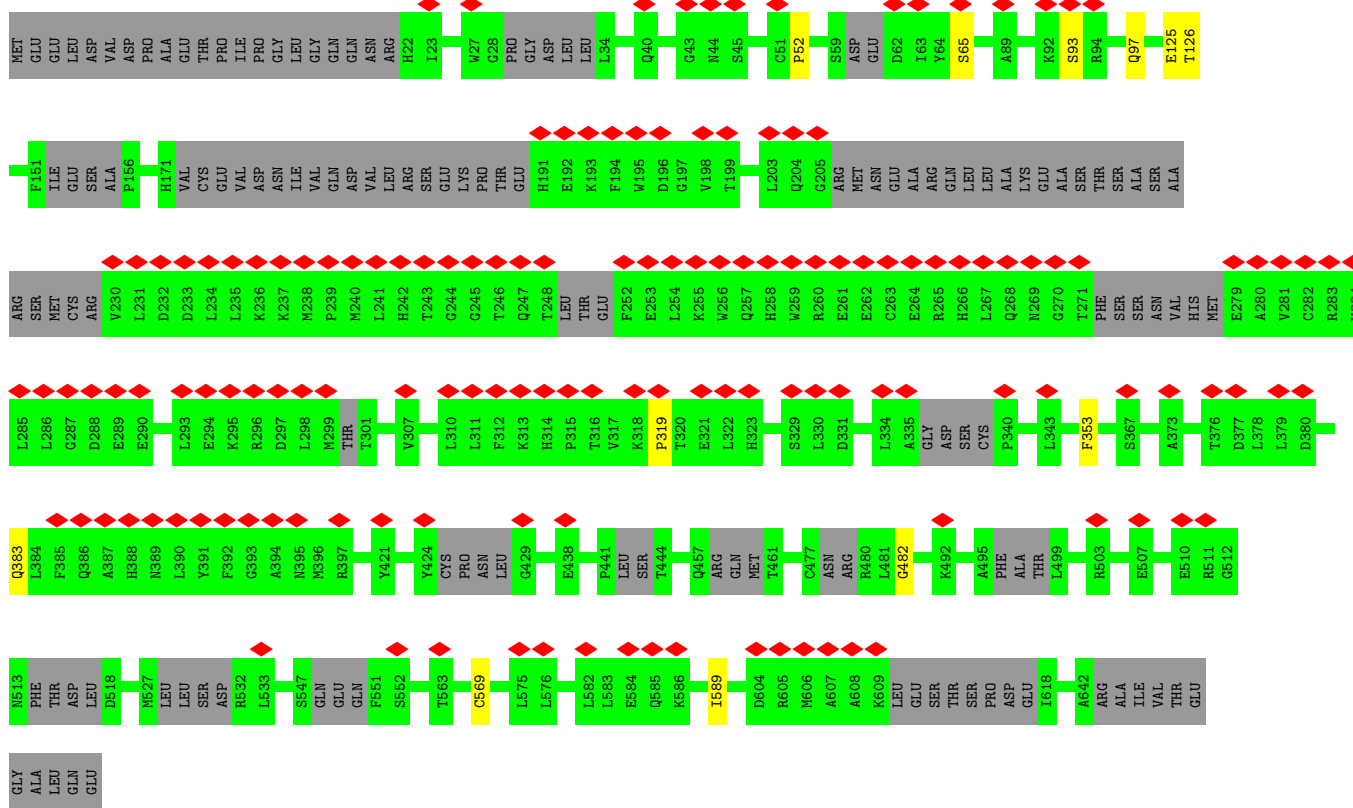
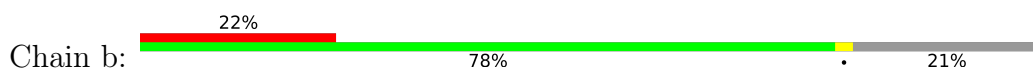


● Molecule 2: Nuclear pore complex protein Nup85

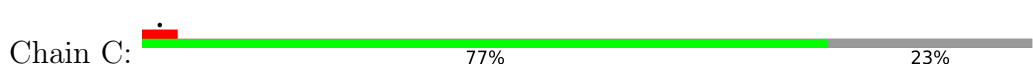


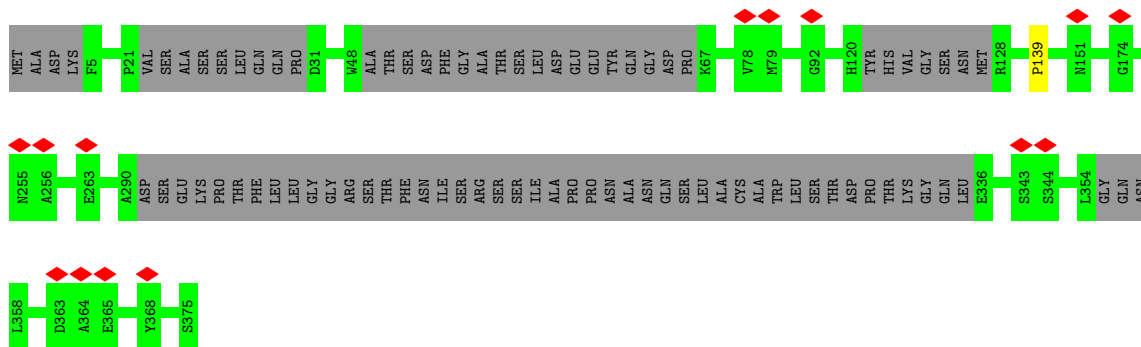


• Molecule 2: Nuclear pore complex protein Nup85

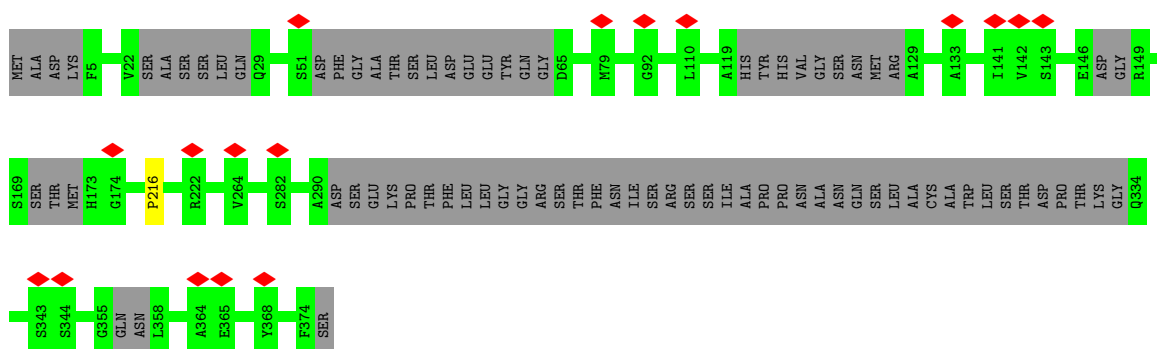
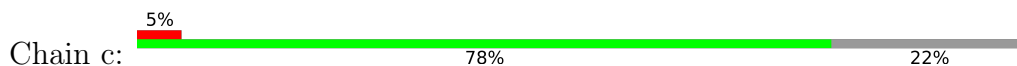


• Molecule 3: MGC154553 protein

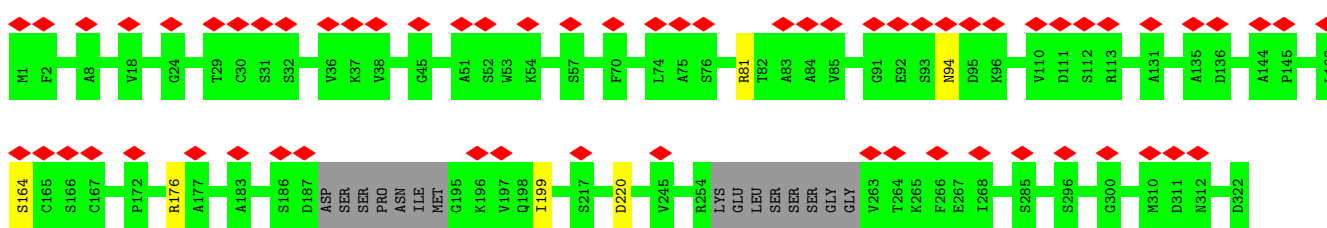




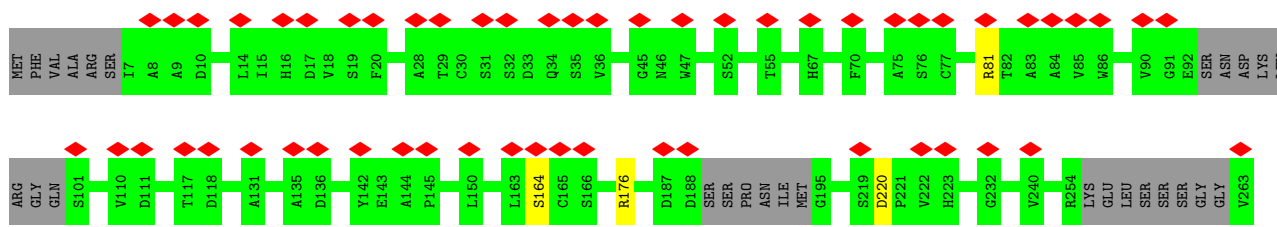
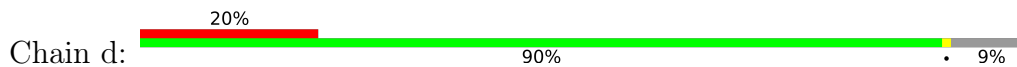
• Molecule 3: MGC154553 protein



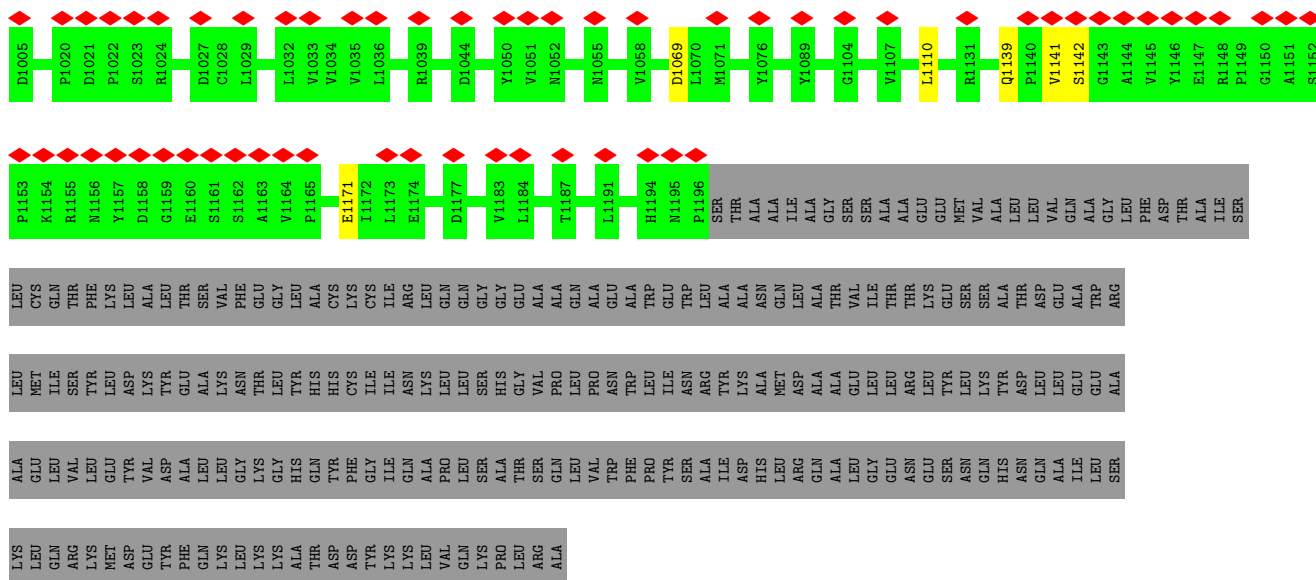
• Molecule 4: Nucleoporin SEH1-A



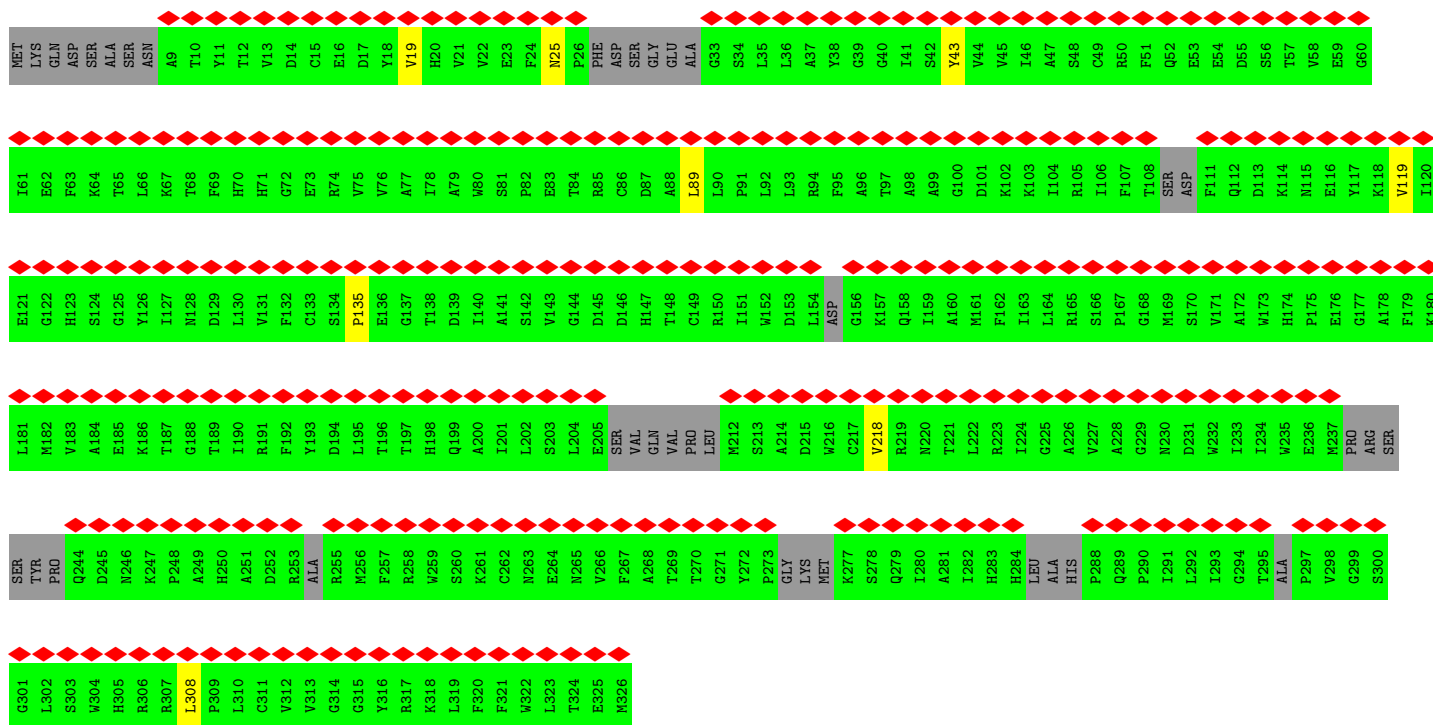
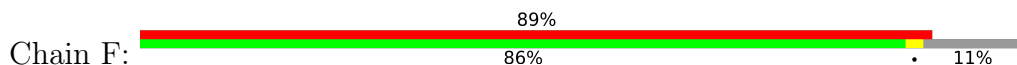
• Molecule 4: Nucleoporin SEH1-A



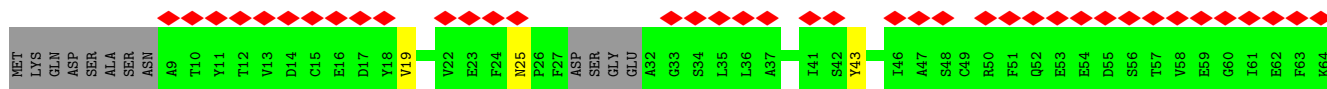
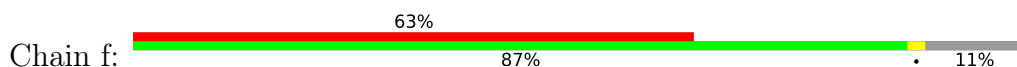
I121	I122	I123	I124	N125	N126	A127	V128	R129	L130	R131	I132	L133	N134	C135	S136	I137	L138	P139	G140	G141	V142	H143	I144	C145	E146	T147	P148	N149	N150	I151	V152	V153	V154	I155	L156	T157	N158	Q159	T160	V161	H162	R163	L164	I165	L166	P167	H168	P169	S170	R171	M172	Y173	R174	S175	E176	I177	I178	S179	D180				
S181	H182	I183	Q184	S185	I186	F187	T188	D189	I190	G191	K192	T193	N194	F195	H196	D197	P198	S199	N200	N201	T202	V203	V204	P205	A206	T207	P208	G209	R210	A211	P212	N213	T214	T215	A216	S217	T218	T219	A219	W220	L221	S222	S223	D224	G225	E226	A227	L228	F229	V230	L231	P232	S233	I234	S235	G236	G237	I238	L239	V240			
I241	K242	M243	P244	P245	H246	K247	M248	E249	G250	L251	V252	T253	I254	A255	E256	K257	K258	Q259	S260	S261	V262	M263	Q264	R265	L266	L267	T268	G269	W270	M271	P272	S273	S274	I275	R276	G277	D278	Q279	G280	P281	A282	H283	L284	P285	E286	S287	L288	A289	V290	H291	T292	L293	D294	H295	D296	S297	I298	L299	F300				
A301	L302	C303	Q304	D305	H306	K307	L308	R309	M310	W311	S312	Y313	K314	D315	Q316	M317	C318	L319	M320	V321	A322	D323	M324	L325	E326	Y327	V328	P329	V330	S331	K332	D333	I334	R335	Q336	T337	A338	G339	T340	G341	H342	K343	L344	R345	L346	A347	F348	S349	A411	T351	L352	G353	I354	L355	Y356	L357	Q358	V359	Y360				
L361	H362	T363	P364	K365	Q366	G367	Q368	F369	C370	V371	F372	Q373	L374	M375	C376	E377	E378	S379	N380	R381	Y382	S383	L384	H385	R386	I387	S388	S389	I390	F391	T392	N393	Q394	E395	T396	L397	I398	D399	F400	T401	F402	THR	LEU	THR	MET	D406	I409	W410	S411	L412	W413	L414	D415	D416	D417	W418	Q419	T420					
V421	V422	K423	H424	I425	N426	F427	E428	GLU	ASN	Q431	A432	G433	Q434	W435	M436	P437	V438	F439	V440	M441	P442	L443	P444	E445	D446	D447	L448	A449	L450	S451	D452	E453	Q454	E455	P456	VAL	E458	A459	V460	L461	E462	C463	L464	F465	A466	P467	G468	R469	F470	T471	L472	A473	A474	V475	Q476	K477	A478	L479	Q480				
I481	L482	R483	K484	G485	S486	G487	R488	V489	L490	D491	L492	S493	Q494	E495	E496	L497	R498	K499	D500	V501	T502	L503	T504	V505	E506	E507	E508	I509	Q510	M511	ALA	VAL	I512	ASP	TYR	ASP	VAL	SER	Q520	E521	E522	F523	E524	Q525	I526	N527	E528	E529	N530	W531	C532	T533	F534	Y535	T536	C537	C538	L539	Q540				
Y541	Q542	E543	T544	L545	S546	R547	P548	L549	A550	L551	L552	V553	H554	P555	D556	T557	N558	M559	V560	C561	L562	L563	R564	K565	G566	F567	L568	S569	F570	L571	A572	P573	C574	S575	L576	V577	E578	H579	L580	E581	F582	V583	P584	A585	E586	H587	L588	L589	T590	V591	D592	E593	S594	V595	L596	S597	D598	D599	I600				
D601	A602	A603	S604	D605	L606	V607	N608	L609	L610	Q611	C612	L613	R614	M615	L616	A617	D618	V619	L620	S621	E622	D623	M624	A625	G566	F567	L568	S569	F570	L571	A572	P573	C574	S575	L576	V577	E578	H579	L580	E581	F582	V583	P584	A585	E586	H587	L588	L589	T590	V591	D592	E593	S594	V595	L596	S597	D598	D599	I600				
T661	Q662	R663	K664	L665	Q666	D667	T668	R669	N670	D671	L672	R673	L734	L735	L736	Q736	H737	L738	L739	Q680	N681	M682	D683	V684	E685	THR	ASN	ALA	ASP	M690	E691	L692	P693	Q694	P695	M696	T697	R698	L699	M700	L701	S702	A642	E643	Q644	L645	L646	E647	T709	A710	L769	S711	S712	V713	W714	C715	Q716	R775	W776	G777	S778	Q779	C780
L781	A782	C783	A784	V785	P786	V787	D788	L789	S790	E791	S792	M793	L794	Q795	H796	L797	S798	V799	L800	E801	L802	S803	D804	S805	P867	S868	N869	F870	N871	F872	O873	F874	A875	E876	C877	L878	M879	R880	N881	C882	Q883	H884	T885	Q886	L887	Q888	E889	Y890	V891	R892	K893	H894	W895	F896	I897	Q898	Q899	V900					
N901	V902	Q911	L914	V915	E918	G919	H920	S931	R935	E936	D937	F938	L939	E940	K941	L942	V951	S952	P953	Y957	Y958	N959	E966	D967	V968	G969	L970	P971	V974	I975	A978	G983	E984	A985	SER	ASP	ASP	W989	A994	L995	R996	T997	F1000	K1001	L1004																		



• Molecule 6: MGC83926 protein

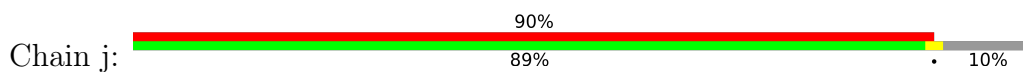


• Molecule 6: MGC83926 protein



L781	A841	Q901	A961	C1021	K1081
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I784	S844	S904	A964	M1024	I1084
L785	N845	H905	S965	K1025	F1085
I786	L846	H906	D966	R1026	V1086
E787	A847	G907	F967	A1027	K1087
Q788	E848	Q908	Q968	M1028	V1088
L789	K849	L909	E969	E1029	L1089
A790	Y850	A910	D970	M1030	Q1090
A791	C851	A911	V971	D1031	M1091
L792	D852	F912	L972	F1032	L1092
L793	F853	L913	Q973	M1033	P1093
N794	D854	Q914	E974	K1034	P1094
Y795	I855	A915	K975	A1035	K1095
L796	L856	HIS	V976	L1036	G1096
L797	V857	ASP	E977	D1037	L1097
D798	Q858	HIS	E978	L1038	E1098
D799	I859	L919	F979	L1039	L1099
Y800	C860	S920	A980	E1040	K1100
V801	E861	W921	E981	Y1041	L1101
T802	S862	L922	Q982	I1042	Y1102
Q803	T863	H923	E983	G1043	L1103
L804	D864	E924	H984	D1044	P1104
K805	N865	L925	F985	D1045	K1105
S806	Q866	N926	L986	S1046	A1106
I807	S867	Q927	L987	E1047	E1107
D808	R868	Q928	H988	V1048	T1108
K809	L869	E929	Q989	D1049	L1109
L810	Q870	F930	E990	V1050	L1110
A811	R871	E931	T991	E1051	Q1111
N812	Y872	K932	L992	E1052	S1112
E813	T873	A933	P993	L1053	E1113
L814	K874	H934	K994	K1054	E1114
R815	L875	R935	K995	L1055	L1115
Y816	F876	T936	L996	E1056	M1116
M817	A877	L937	L997	I1057	S1117
I818	E878	Q938	E998	L1058	L1118
L819	Q879	T939	E999	C1059	K1119
E820	N880	L940	K1000	M1060	T1120
M821	F881	A941	Q1001	A1061	M1121
E822	S882	N942	L1002	I1062	S1122
Y823	D883	M943	D1003	K1063	Y1123
A824	F884	E944	L1004	R1064	F1124
Q825	L885	T945	M1005	D1065	E1125
R826	F886	R946	A1006	E1066	F1126
R827	R887	Y947	M1007	W1067	S1127
S828	V888	F948	P1008	S1068	L1128
E829	Y889	C949	V1009	A1069	K1129
L830	L890	K950	L1010	T1070	A1130
L831	E891	K951	A1011	D1071	M1131
S832	K892	K952	P1012	G1072	Y1132
P833	G893	L953	F1013	K1073	E1133
L834	K894	L954	Q1014	D1074	C1134
L835	R895	L955	L1015	D1075	Y1135
I836	G896	L957	I1016	P1076	M1136
L837	K897	S958	Q1017	I1077	K1137
G838	L898	K959	L1018	E1078	M1138
Q839	L899	L960	Y1019	A1079	GLN
Y840	S900		V1020	I1080	SER

• Molecule 10: outer Nup133

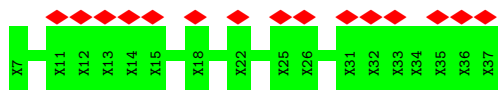


MET	VAL	K121	M181	G241	D301	T361
PHE	TYR	I122	I182	M242	M302	L362
PRO	LEU	S123	L183	L243	S303	V363
SER	HIS	H124	H184	S244	R304	T364
ARG	ALA	S125	E185	G245	V305	V365
ALA	ALA	S126	G186	L246	L306	K366
GLN	SER	S127	T187	G247	R307	D367
GLY	E69	A128	Y188	R248	E308	E368
MET	T70	K129	W189	R249	V309	G369
GLY	W71	L130	E190	V250	I310	Y370
SER	N72	M131	S191	S251	S311	M371
ALA	M73	V132	Y192	T252	D312	I372
ARG	N74	C133	T193	L253	A313	S373
PRO	V75	K134	E194	F254	L314	D374
PHE	Q76	E135	F195	G255	W315	E375
ASN	L77	L136	G196	I256	G316	I376
SER	F78	P137	S197	L257	S317	T377
ARG	G79	L138	SER	S258	E318	V378
LEU	S80	P139	L199	F259	S319	E379
THR	S81	L140	C200	A260	D320	V380
GLY	L82	S141	A201	V261	Y321	T381
ARG	L83	D142	F202	E262	Q322	Q382
GLY	H84	S143	V203	S263	D323	F383
PRO	K85	E144	T204	T264	I324	N384
PRO	V86	M145	A205	L265	K325	P385
VAL	M87	W146	V206	C266	A326	V386
THR	E88	A147	K207	S267	G327	F387
ALA	E89	D148	G208	V268	I328	Q388
ALA	L90	L149	N209	L269	N329	A389
SER	S91	L150	S210	W270	I330	R390
SER	N92	V151	F211	D271	N331	G391
ALA	A93	I152	L212	LYS	K332	M392
TYR	S94	C153	L213	GLY	L333	K393
SER	A95	A154	S214	D274	S334	L394
PRO	D96	Q155	S215	C275	L335	C395
VAL	E97	T156	E216	F276	N336	Q396
GLY	P98	G157	K217	Y277	Q337	L397
ARG	M99	D158	N218	T278	N338	V398
ARG	A100	P159	Q219	L279	C339	V399
VAL	A101	A160	L220	T280	D340	P400
SER	ALA	A161	D281	D281	G341	M401
ALA	C102	A162	R222	S282	F402	F402
GLY	I103	Q163	L223	L284	S403	S403
ALA	H104	S164	T224	N285	S404	S404
ARG	E105	V165	P225	K286	Q405	Q405
SER	G106	A166	D226	W287	S346	A406
PRO	G107	M108	A227	D288	A347	C407
SER	W108	M110	S228	L289	A348	V408
ARG	M110	L111	G229	D290	W349	L409
GLY	L111	A112	K230	D291	Y410	Y410
VAL	C113	M114	M231	T292	F411	T411
THR	D115	E173	Q232	E294	Q412	Q412
THR	L116	G174	R234	S295	E413	E413
PRO	L117	S175	V235	Q296	I415	I415
SER	I118	S176	L236	V297	F416	F416
ARG	I119	R177	Q238	L298	A417	A417
ARG	M120	W178	G239	N299	C418	C418
		P180	Q240	H300	S419	S419

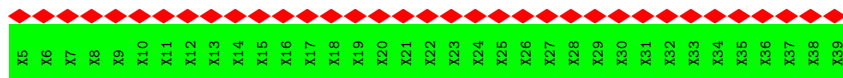
G421	G422	G423	R424	S425	T426	L427	P428	Q429	E430	K431	I432	P433	F434	E435	A436	Q437	G438	D439	N440	I441	G442	G443	A444	G445	A446	C447	E448	G449	W450	P451	V452	F453	F454	I455	R456	K457	S458	G459	M460	L461	T462	V463	V464	A465	R466	E467	THR	ALA	SER	VAL	LEU	PRO	GLU	HIS	MET	GLU	GLU	SER	LEU
SER	SER	VAL	SER	SER	LYS	SER	ARG	GLN	ALA	VAL	VAL	LYS	ASP	SER	SER	ARG	PRO	ASP	GLN	ILE	ALA	ASP	ASP	K505	T506	K507	H508	L509	K510	A511	A512	F513	L514	R515	Y516	C517	R518	K519	D520	I521	L522	G523	A524	Q525	S526	M527	V528	D529	S530	L531	F532	S533	D534	S535	D536	E537	E538	P539	D540
D541	E542	L543	D544	L545	A546	V547	N548	Q549	I550	S551	V552	D553	L554	I555	D556	Y557	Y558	P559	A560	S561	D562	P563	R564	W565	A566	E567	S568	V569	P570	E571	E572	A573	S574	G575	F576	S577	N578	T579	L580	L581	I582	L583	L584	H585	Q586	L587	E588	D589	K590	M591	K592	A593	H594	S595	F596	F597	N598	D599	F600
L601	H602	Q603	V604	G605	L606	F607	S608	R609	SER	T612	C613	Q614	T615	K616	G617	M618	L619	V620	A621	T622	R623	L624	L625	L626	S627	E628	H629	A630	E631	K632	L633	S634	A635	A636	I637	V638	L639	K640	N641	H642	H643	A644	K645	L646	P647	V648	L649	V650	N651	A652	A653	I654	Q655	L656	A657	L658	D659	K660	
R661	M662	C663	T664	V665	P666	Q667	N668	L669	T670	A671	A672	D673	V674	Y675	F676	R677	E678	V679	S680	Q681	M682	E683	I684	I685	F686	E687	C688	L689	V690	D691	K692	E693	E694	A695	D696	L697	E698	S699	T700	S701	I702	D703	S704	V705	E706	W707	A708	N709	I710	V711	V712	N713	I714	N715	T716	I717	L718	K719	D720
M721	L722	H723	V724	A725	C726	Q727	Y728	R729	Q730	S731	K732	M733	S734	L735	Y736	K737	N738	E739	S740	G741	I742	Q743	E744	F745	E746	H747	V748	P749	M750	T751	A752	S753	S754	G755	T756	A757	G758	I759	R760	S761	E762	V763	T764	R765	Q766	H767	G768	I769	I770	L771	K772	V773	V774	F775	Q776	A777	D778	S779	G780
L781	R782	I783	L784	L785	L786	E787	Q788	L789	A790	A791	L792	L793	N794	Y795	L796	L797	D798	D799	Y800	V801	T802	Q803	L804	K805	S806	I807	D808	K809	L810	A811	N812	E813	E814	R815	Y816	M817	L818	L819	E820	M821	E822	Y823	A824	Q825	K826	R827	S828	E829	L830	L831	S832	P833	L834	L835	G836	L837	G838	Q839	E840
A841	W842	A843	S844	N845	L846	A847	E848	K849	Y850	C851	D852	F853	D854	L855	L856	Q858	L859	C860	E861	M862	T863	D864	M865	Q866	S867	R868	L869	F870	R871	Y872	M873	T874	L875	F876	A877	E878	Q879	N880	F881	S882	D883	F884	L885	F886	R887	W888	Y889	K890	K891	K892	G893	L894	L895	G896	K897	L898	L899	S900	
Q901	P902	ALA	SER	GLN	H906	G907	Q908	L909	A910	A911	F912	L913	Q914	A915	H916	D917	H918	L919	S920	N921	L922	H923	E924	L925	N926	S927	Q928	E929	F930	K931	K932	A933	H934	R935	T936	L937	Q938	T939	L940	A941	N942	A943	E944	T945	R946	Y947	F948	C949	K950	L951	K952	T953	L954	L955	G956	L957	S958	K959	L960
A961	A962	L963	A964	S965	D966	F967	Q968	E969	A970	D971	L972	Q973	E974	K975	V976	E977	E978	I979	A980	E981	Q982	E983	H984	F985	S986	L987	H988	Q989	E990	T991	L992	P993	K994	K995	L996	L997	E998	E999	K1000	Q1001	L1002	D1003	L1004	M1005	A1006	M1007	P1008	V1009	L1010	A1011	P1012	F1013	Q1014	L1015	I1016	Q1017	L1018	Y1019	V1020
C1021	E1022	E1023	M1024	K1025	R1026	A1027	M1028	E1029	M1030	D1031	F1032	M1033	K1034	A1035	L1036	D1037	L1038	L1039	E1040	Y1041	I1042	G1043	D1044	D1045	S1046	E1047	V1048	L1049	V1050	E1051	E1052	L1053	K1054	L1055	E1056	L1057	E1058	C1059	K1060	Q1061	I1062	K1063	R1064	M1065	D1066	W1067	S1068	A1069	K1070	D1071	G1072	K1073	D1074	D1075	P1076	I1077	E1078	A1079	T1080
K1081	D1082	S1083	I1084	F1085	V1086	K1087	V1088	Q1089	L1090	N1091	L1092	N1094	K1095	G1096	I1097	E1098	L1099	K1100	G1101	Y1102	L1103	P1104	K1105	A1106	E1107	T1108	L1109	L1110	Q1111	S1112	E1113	I1114	L1115	N1116	S1117	L1118	K1119	T1120	N1121	S1122	Y1123	F1124	E1125	F1126	S1127	L1128	K1129	A1130	N1131	Y1132	E1133	C1134	Y1135	M1136	K1137	L1138	Q1139	SER	

• Molecule 11: Nup358 complex, clamps

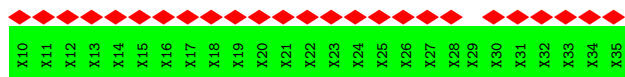
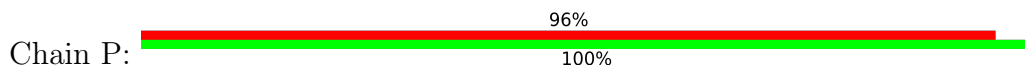




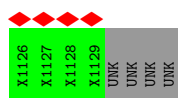
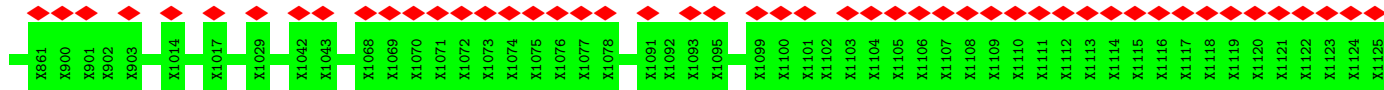
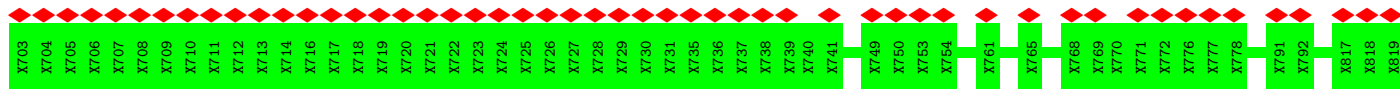
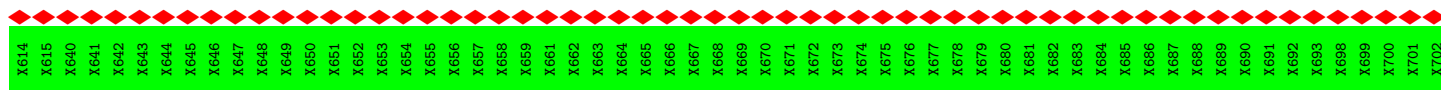
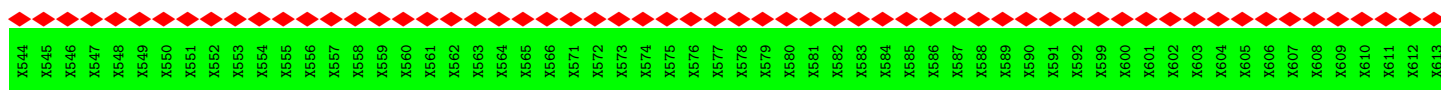
- Molecule 16: Nup214 complex Coiled coil region 2, helix 2



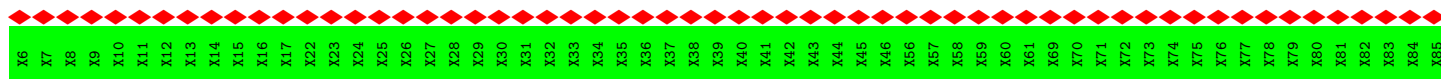
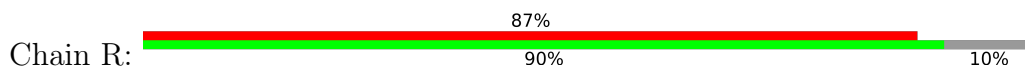
- Molecule 17: Nup214 complex Coiled coil region 2, helix 3



- Molecule 18: bridge domain



- Molecule 18: bridge domain



UNK	X86	X153	X230	X308	X374	UNK
UNK	X87	X154	X231	X309	X375	UNK
UNK	X88	X155	X232	X310	X376	UNK
UNK	X89	X156	X233	X311	X377	UNK
UNK	X90	X157	X234	X312	X378	UNK
UNK	X91	X158	X235	X313	X379	UNK
UNK	X92	X159	X245	X314	X380	UNK
UNK	X93	X160	X246	X315	X385	UNK
UNK	X94	X161	X247	X316	X386	UNK
UNK	X95	X162	X248	X317	X387	UNK
UNK	X96	X163	X249	X319	X416	UNK
UNK	X97	X164	X250	X320	X417	UNK
UNK	X98	X165	X251	X321	X418	UNK
UNK	X99	X166	X252	X322	X419	UNK
UNK	X100	X167	X253	X323	X420	UNK
UNK	X101	X168	X254	X324	X421	UNK
UNK	X102	X169	X255	X325	X422	UNK
UNK	X103	X170	X256	X326	X423	UNK
UNK	X104	X171	X257	X327	X424	UNK
UNK	X105	X172	X258	X328	X425	UNK
UNK	X106	X173	X259	X329	X426	UNK
UNK	X107	X174	X260	X330	X427	UNK
UNK	X108	X175	X261	X331	X428	UNK
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UNK	X116	X188	X269	X339	X437	UNK
UNK	X117	X189	X270	X340	X438	UNK
UNK	X118	X190	X271	X341	X439	UNK
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UNK	X120	X192	X273	X343	X441	UNK
UNK	X121	X193	X274	X345	X442	UNK
UNK	X122	X194	X275	X346	X443	UNK
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UNK	X124	X196	X277	X348	X445	UNK
UNK	X125	X197	X278	X349	X446	UNK
UNK	X126	X198	X279	X350	X447	UNK
UNK	X127	X199	X280	X351	X448	UNK
UNK	X128	X210	X281	X352	X449	UNK
UNK	X129	X211	X282	X353	X451	UNK
UNK	X130	X212	X283	X354	X452	UNK
UNK	X131	X213	X284	X355	UNK	UNK
UNK	X132	X214	X285	X356	UNK	UNK
UNK	X133	X215	X286	X357	UNK	UNK
UNK	X134	X216	X287	X358	UNK	UNK
UNK	X135	X217	X288	X359	UNK	UNK
UNK	X136	X219	X289	X360	UNK	UNK
UNK	X137	X220	X290	X361	UNK	UNK
UNK	X138	X221	X299	X362	UNK	UNK
UNK	X139	X222	X300	X363	UNK	UNK
UNK	X140	X223	X301	X364	UNK	UNK
UNK	X141	X224	X302	X365	UNK	UNK
UNK	X142	X225	X303	X366	UNK	UNK
UNK	X143	X226	X304	X367	UNK	UNK
UNK	X144	X227	X305	X369	UNK	UNK
UNK	X151	X228	X306	X373	UNK	UNK
UNK	X152	X229	X307			UNK

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	616547	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	75	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.151	Depositor
Minimum map value	-0.091	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	568.832, 568.832, 568.832	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.222, 2.222, 2.222	Depositor

5 Model quality i

5.1 Standard geometry i

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	0.46	0/6901	0.77	0/9542
1	a	0.51	0/6275	0.94	0/8703
2	B	0.33	0/2623	0.56	0/3634
2	b	0.31	0/2555	0.55	0/3534
3	C	0.47	0/1150	0.72	0/1427
3	c	0.45	0/1160	0.70	0/1436
4	D	0.69	0/1516	1.11	0/2108
4	d	0.70	0/1446	1.13	0/2009
5	E	0.57	0/5091	1.06	0/7076
5	e	0.57	0/5486	1.07	0/7634
6	F	0.64	0/1413	1.09	0/1949
6	f	0.64	0/1423	1.10	0/1963
7	G	0.42	0/3046	0.73	14/4220 (0.3%)
7	g	0.42	0/2986	0.72	17/4127 (0.4%)
8	H	0.67	0/1417	1.05	0/1959
8	h	0.67	0/1411	1.06	0/1959
9	I	0.53	0/3662	0.96	0/5104
9	i	0.53	0/3607	0.97	0/5027
10	J	0.61	0/5079	1.09	0/7074
10	j	0.61	0/5084	1.08	0/7081
11	S	0.38	0/832	0.90	0/1149
11	T	0.38	0/832	0.90	0/1149
11	U	0.38	0/853	0.90	0/1181
11	V	0.38	0/832	0.90	0/1149
All	All	0.53	0/66680	0.94	31/92194 (0.0%)

There are no bond length outliers.

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	G	198	PRO	N-CA-CB	6.55	111.16	103.30
7	G	146	PRO	N-CA-CB	6.06	110.58	103.30
7	G	134	PRO	N-CA-CB	6.02	110.52	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	g	146	PRO	N-CA-CB	6.01	110.52	103.30
7	G	189	PRO	N-CA-CB	6.01	110.51	103.30
7	G	227	PRO	N-CA-CB	6.01	110.51	103.30
7	g	189	PRO	N-CA-CB	6.00	110.50	103.30
7	G	170	PRO	N-CA-CB	6.00	110.50	103.30
7	G	201	PRO	N-CA-CB	5.99	110.49	103.30
7	g	874	PRO	N-CA-CB	5.99	110.49	103.30
7	g	206	PRO	N-CA-CB	5.99	110.49	103.30
7	g	227	PRO	N-CA-CB	5.98	110.48	103.30
7	g	192	PRO	N-CA-CB	5.97	110.46	103.30
7	G	185	PRO	N-CA-CB	5.96	110.45	103.30
7	g	208	PRO	N-CA-CB	5.96	110.45	103.30
7	g	198	PRO	N-CA-CB	5.96	110.45	103.30
7	g	786	PRO	N-CA-CB	5.94	110.43	103.30
7	g	210	PRO	N-CA-CB	5.94	110.42	103.30
7	g	873	PRO	N-CA-CB	5.94	110.42	103.30
7	g	196	PRO	N-CA-CB	5.93	110.42	103.30
7	g	185	PRO	N-CA-CB	5.92	110.41	103.30
7	G	139	PRO	N-CA-CB	5.92	110.40	103.30
7	G	192	PRO	N-CA-CB	5.91	110.39	103.30
7	g	170	PRO	N-CA-CB	5.91	110.39	103.30
7	g	257	PRO	N-CA-CB	5.90	110.38	103.30
7	g	201	PRO	N-CA-CB	5.90	110.38	103.30
7	G	786	PRO	N-CA-CB	5.89	110.37	103.30
7	G	257	PRO	N-CA-CB	5.86	110.33	103.30
7	G	196	PRO	N-CA-CB	5.84	110.31	103.30
7	G	141	PRO	N-CA-CB	5.81	110.27	103.30
7	g	150	PRO	N-CA-CB	5.79	110.25	103.30

There are no chirality outliers.

There are no planarity outliers.

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

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	1343/2011 (67%)	1264 (94%)	50 (4%)	29 (2%)	6	35
1	a	1210/2011 (60%)	1131 (94%)	53 (4%)	26 (2%)	7	36
2	B	500/653 (77%)	471 (94%)	18 (4%)	11 (2%)	6	35
2	b	481/653 (74%)	454 (94%)	15 (3%)	12 (2%)	5	32
3	C	277/375 (74%)	211 (76%)	65 (24%)	1 (0%)	34	72
3	c	276/375 (74%)	212 (77%)	63 (23%)	1 (0%)	34	72
4	D	301/322 (94%)	275 (91%)	20 (7%)	6 (2%)	7	37
4	d	285/322 (88%)	261 (92%)	20 (7%)	4 (1%)	11	45
5	E	998/1435 (70%)	900 (90%)	71 (7%)	27 (3%)	5	31
5	e	1087/1435 (76%)	967 (89%)	87 (8%)	33 (3%)	4	28
6	F	269/326 (82%)	244 (91%)	17 (6%)	8 (3%)	4	28
6	f	271/326 (83%)	245 (90%)	18 (7%)	8 (3%)	4	28
7	G	582/923 (63%)	473 (81%)	56 (10%)	53 (9%)	1	11
7	g	559/923 (61%)	475 (85%)	39 (7%)	45 (8%)	1	12
8	H	287/320 (90%)	257 (90%)	24 (8%)	6 (2%)	7	36
8	h	283/320 (88%)	255 (90%)	24 (8%)	4 (1%)	11	45
9	I	726/916 (79%)	692 (95%)	28 (4%)	6 (1%)	19	59
9	i	715/916 (78%)	681 (95%)	27 (4%)	7 (1%)	15	53
10	J	1014/1140 (89%)	925 (91%)	69 (7%)	20 (2%)	7	37
10	j	1015/1140 (89%)	930 (92%)	67 (7%)	18 (2%)	8	40
11	S	153/2905 (5%)	146 (95%)	2 (1%)	5 (3%)	4	26
11	T	153/2905 (5%)	146 (95%)	2 (1%)	5 (3%)	4	26
11	U	161/2905 (6%)	148 (92%)	9 (6%)	4 (2%)	5	32
11	V	153/2905 (5%)	146 (95%)	2 (1%)	5 (3%)	4	26
All	All	13099/28462 (46%)	11909 (91%)	846 (6%)	344 (3%)	8	31

All (344) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	227	SER
1	A	228	LEU
1	A	239	THR
1	A	586	ILE
1	A	696	GLU
1	A	698	TYR
1	A	726	ALA
1	A	727	PRO
1	A	831	ALA
1	A	832	PRO
1	A	909	LEU
1	A	1048	VAL
1	A	1247	ILE
1	A	1646	GLN
1	A	1713	GLN
2	B	383	GLN
2	B	569	CYS
2	B	589	ILE
3	C	139	PRO
4	D	94	ASN
4	D	164	SER
5	E	451	SER
5	E	896	PRO
5	E	953	PRO
6	F	43	TYR
6	F	119	VAL
6	F	308	LEU
7	G	198	PRO
7	G	288	LEU
7	G	293	SER
7	G	294	ALA
7	G	295	LYS
7	G	309	LEU
7	G	322	LEU
7	G	347	ALA
7	G	422	GLU
7	G	423	GLU
7	G	426	GLU
7	G	438	VAL
7	G	473	VAL
7	G	616	CYS
7	G	667	ASN

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Mol	Chain	Res	Type
7	G	682	PRO
7	G	686	ILE
7	G	708	LEU
8	H	14	ASP
9	I	188	THR
9	I	224	SER
9	I	323	LYS
10	J	252	THR
10	J	538	GLU
10	J	561	SER
10	J	567	GLU
10	J	574	ALA
10	J	609	ARG
10	J	666	PRO
10	J	851	CYS
10	J	1066	GLU
11	S	59	ASP
11	S	90	ASN
11	S	92	THR
11	S	179	GLN
11	T	59	ASP
11	T	90	ASN
11	T	92	THR
11	T	179	GLN
11	U	23	ARG
11	U	92	THR
11	V	59	ASP
11	V	90	ASN
11	V	92	THR
11	V	179	GLN
1	a	239	THR
1	a	454	LEU
1	a	582	PRO
1	a	586	ILE
1	a	636	PRO
1	a	1244	MET
1	a	1247	ILE
1	a	1250	ARG
1	a	1296	PRO
1	a	1305	ARG
2	b	52	PRO
2	b	383	GLN

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Mol	Chain	Res	Type
2	b	569	CYS
2	b	589	ILE
4	d	164	SER
5	e	451	SER
5	e	896	PRO
5	e	953	PRO
5	e	1141	VAL
6	f	43	TYR
6	f	119	VAL
6	f	308	LEU
7	g	282	THR
7	g	294	ALA
7	g	302	PHE
7	g	315	SER
7	g	321	TYR
7	g	323	MET
7	g	422	GLU
7	g	423	GLU
7	g	426	GLU
7	g	438	VAL
7	g	473	VAL
7	g	486	LEU
7	g	487	VAL
7	g	627	ASP
7	g	667	ASN
7	g	682	PRO
7	g	684	PRO
7	g	708	LEU
9	i	188	THR
9	i	224	SER
9	i	323	LYS
10	j	252	THR
10	j	538	GLU
10	j	561	SER
10	j	567	GLU
10	j	574	ALA
10	j	609	ARG
10	j	666	PRO
10	j	1066	GLU
1	A	1274	LEU
2	B	93	SER
2	B	319	PRO

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Mol	Chain	Res	Type
4	D	176	ARG
5	E	83	ALA
5	E	266	LEU
5	E	331	SER
6	F	19	VAL
6	F	89	LEU
6	F	218	VAL
7	G	433	GLY
7	G	434	PRO
7	G	439	GLU
7	G	479	ARG
7	G	481	LEU
7	G	483	SER
7	G	560	PHE
7	G	615	LEU
8	H	11	SER
8	H	105	SER
8	H	223	ILE
10	J	575	GLY
1	a	159	THR
1	a	535	GLY
1	a	635	ILE
2	b	93	SER
2	b	319	PRO
4	d	176	ARG
4	d	220	ASP
5	e	83	ALA
5	e	186	ILE
5	e	266	LEU
5	e	331	SER
5	e	1142	SER
6	f	19	VAL
6	f	89	LEU
6	f	218	VAL
7	g	328	GLU
7	g	371	ALA
7	g	433	GLY
7	g	434	PRO
7	g	439	GLU
7	g	479	ARG
7	g	481	LEU
7	g	483	SER

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Mol	Chain	Res	Type
7	g	560	PHE
8	h	105	SER
8	h	223	ILE
10	j	575	GLY
1	A	58	PRO
1	A	303	ASP
1	A	751	ARG
1	A	995	LYS
1	A	1712	ARG
2	B	97	GLN
5	E	122	ASN
5	E	232	PRO
5	E	329	PRO
5	E	442	PRO
5	E	483	ARG
5	E	486	SER
5	E	566	GLY
5	E	1171	GLU
7	G	289	PRO
7	G	291	PRO
7	G	311	LEU
7	G	346	ASN
7	G	364	ASN
7	G	371	ALA
7	G	435	GLU
7	G	436	ARG
7	G	542	MET
7	G	651	GLU
8	H	199	GLY
9	I	460	ILE
10	J	560	ALA
10	J	571	GLU
10	J	742	ILE
10	J	751	THR
10	J	852	ASP
11	U	91	PRO
1	a	58	PRO
1	a	162	HIS
1	a	303	ASP
1	a	545	ALA
2	b	97	GLN
2	b	126	THR

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Mol	Chain	Res	Type
5	e	122	ASN
5	e	232	PRO
5	e	329	PRO
5	e	442	PRO
5	e	483	ARG
5	e	486	SER
5	e	566	GLY
5	e	1069	ASP
5	e	1171	GLU
7	g	317	GLU
7	g	319	GLN
7	g	364	ASN
7	g	435	GLU
7	g	436	ARG
7	g	651	GLU
8	h	199	GLY
9	i	460	ILE
10	j	560	ALA
10	j	571	GLU
10	j	742	ILE
10	j	751	THR
1	A	44	LYS
1	A	286	GLN
1	A	717	PRO
1	A	830	TYR
1	A	1045	ALA
2	B	130	TYR
2	B	353	PHE
2	B	430	ARG
4	D	220	ASP
5	E	159	GLN
5	E	244	PRO
5	E	444	PRO
5	E	484	LYS
5	E	565	LYS
5	E	598	ASP
5	E	1069	ASP
5	E	1110	LEU
6	F	135	PRO
7	G	146	PRO
7	G	290	LYS
7	G	314	LYS

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Mol	Chain	Res	Type
7	G	370	GLU
7	G	477	GLU
7	G	555	LEU
7	G	705	PRO
8	H	55	GLY
9	I	513	ALA
1	a	44	LYS
1	a	160	LEU
1	a	286	GLN
2	b	125	GLU
2	b	353	PHE
5	e	159	GLN
5	e	244	PRO
5	e	444	PRO
5	e	484	LYS
5	e	565	LYS
5	e	598	ASP
5	e	1110	LEU
5	e	1139	GLN
6	f	135	PRO
7	g	293	SER
7	g	301	PRO
7	g	346	ASN
7	g	370	GLU
7	g	477	GLU
7	g	485	GLN
7	g	555	LEU
7	g	705	PRO
8	h	55	GLY
9	i	513	ALA
1	A	76	PRO
1	A	502	LEU
2	B	65	SER
2	B	127	ALA
4	D	199	ILE
5	E	124	VAL
5	E	272	PRO
5	E	784	ALA
5	E	865	LEU
7	G	341	PRO
7	G	612	GLN
7	G	613	TYR

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Mol	Chain	Res	Type
7	G	617	GLN
10	J	570	PRO
1	a	76	PRO
1	a	547	GLY
2	b	65	SER
5	e	124	VAL
5	e	272	PRO
5	e	784	ALA
5	e	866	TRP
7	g	324	PRO
7	g	325	LEU
7	g	414	SER
10	j	301	ASP
10	j	570	PRO
4	D	81	ARG
6	F	25	ASN
7	G	279	ASN
7	G	280	MET
7	G	414	SER
7	G	557	GLU
10	J	301	ASP
10	J	536	ASP
10	J	1103	LEU
4	d	81	ARG
5	e	197	ASP
6	f	25	ASN
7	g	557	GLU
10	j	536	ASP
10	j	1103	LEU
5	E	275	ILE
10	J	605	GLY
1	a	119	GLN
1	a	128	GLY
1	a	536	GLY
5	e	177	ILE
5	e	275	ILE
9	i	183	ILE
10	j	605	GLY
1	A	400	MET
1	a	400	MET
7	G	195	VAL
7	G	545	PRO

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Mol	Chain	Res	Type
11	S	129	PRO
11	T	129	PRO
11	U	129	PRO
11	V	129	PRO
2	b	482	GLY
3	c	216	PRO
9	I	274	GLY
9	i	274	GLY

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

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](#)

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
18	Q	21
18	R	18
13	L	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R	235:UNK	C	245:UNK	N	21.64
1	Q	861:UNK	C	900:UNK	N	21.11
1	R	387:UNK	C	416:UNK	N	18.78
1	Q	1112:UNK	C	1113:UNK	N	18.48
1	R	198:UNK	C	210:UNK	N	17.94
1	Q	1076:UNK	C	1077:UNK	N	17.45
1	Q	693:UNK	C	698:UNK	N	17.08
1	R	290:UNK	C	299:UNK	N	16.87
1	R	177:UNK	C	183:UNK	N	16.41
1	Q	1056:UNK	C	1057:UNK	N	15.19
1	Q	1016:UNK	C	1017:UNK	N	14.44
1	Q	731:UNK	C	735:UNK	N	13.78
1	Q	592:UNK	C	599:UNK	N	13.32
1	L	307:UNK	C	312:UNK	N	13.26
1	Q	1029:UNK	C	1030:UNK	N	12.80
1	Q	916:UNK	C	1011:UNK	N	12.52
1	Q	1040:UNK	C	1041:UNK	N	12.26
1	Q	1093:UNK	C	1095:UNK	N	12.08
1	R	17:UNK	C	22:UNK	N	11.85
1	Q	714:UNK	C	716:UNK	N	9.51
1	Q	750:UNK	C	753:UNK	N	9.51
1	Q	566:UNK	C	571:UNK	N	9.34
1	Q	819:UNK	C	828:UNK	N	8.54
1	Q	772:UNK	C	776:UNK	N	7.99
1	R	46:UNK	C	56:UNK	N	7.67
1	Q	837:UNK	C	846:UNK	N	7.48
1	Q	615:UNK	C	640:UNK	N	6.57
1	R	61:UNK	C	69:UNK	N	5.86
1	R	143:UNK	C	151:UNK	N	4.88
1	R	217:UNK	C	219:UNK	N	4.68
1	R	282:UNK	C	284:UNK	N	4.67
1	R	449:UNK	C	451:UNK	N	4.52
1	R	428:UNK	C	430:UNK	N	4.18
1	R	354:UNK	C	356:UNK	N	4.11
1	R	343:UNK	C	345:UNK	N	3.88
1	R	367:UNK	C	369:UNK	N	3.59
1	Q	794:UNK	C	797:UNK	N	3.52

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Q	659:UNK	C	661:UNK	N	3.49
1	R	317:UNK	C	319:UNK	N	3.37
1	R	451:UNK	C	452:UNK	N	3.13

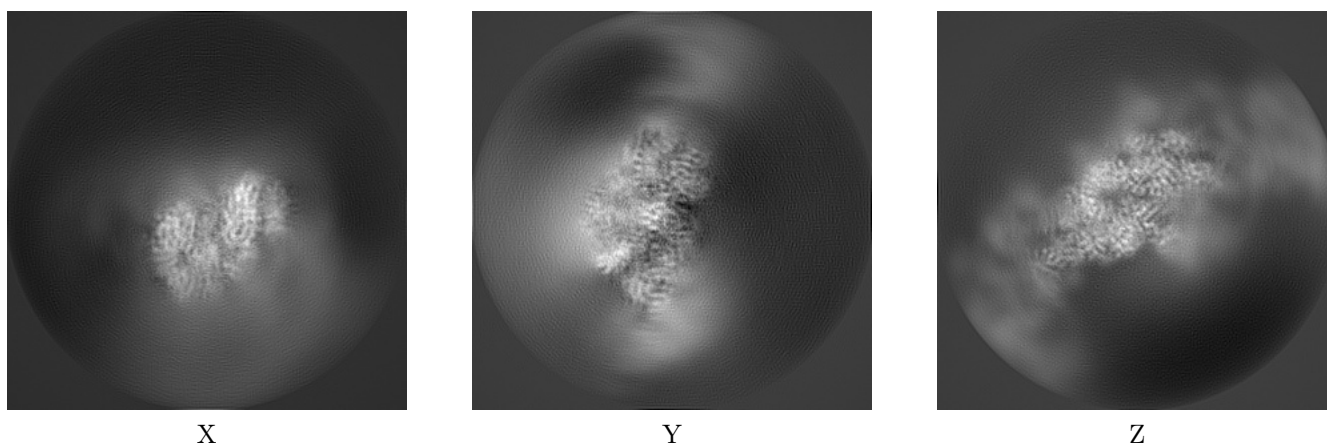
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0909. 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](#)

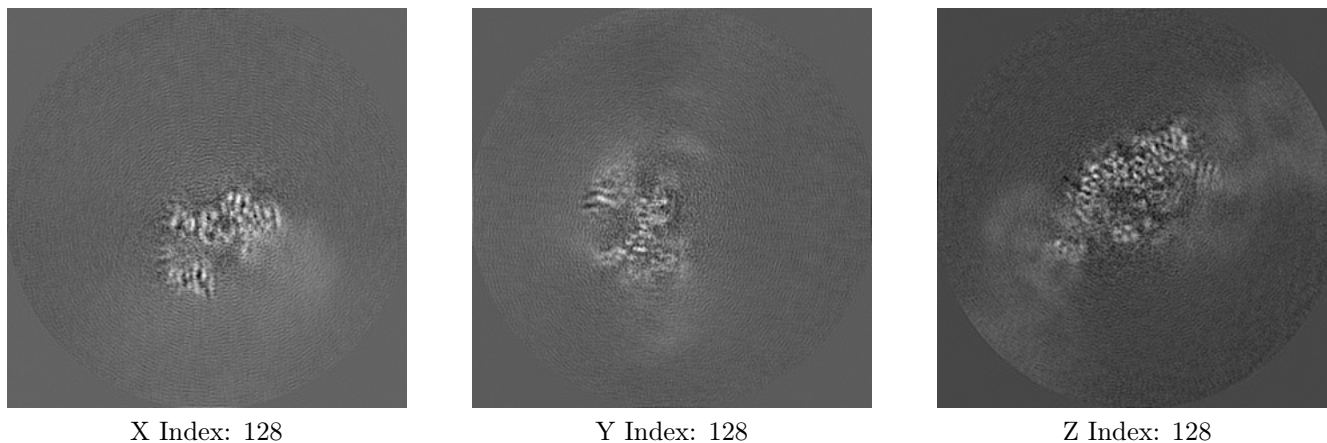
6.1.1 Primary map



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

6.2 Central slices [i](#)

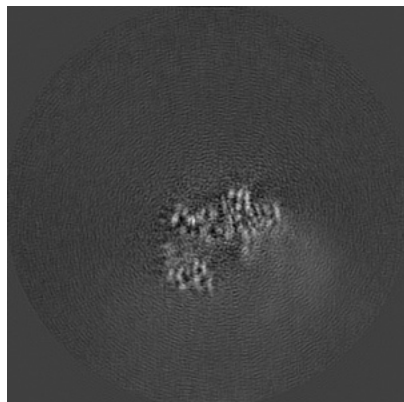
6.2.1 Primary map



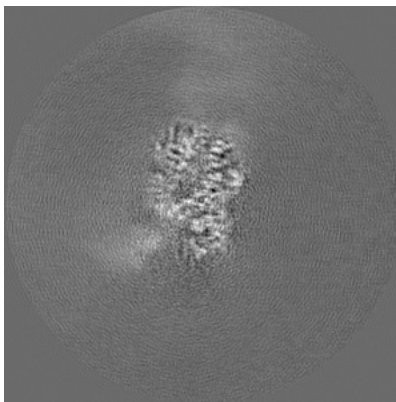
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

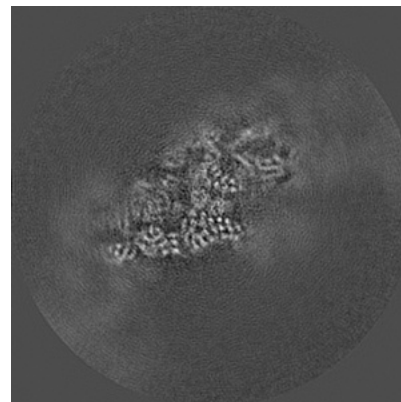
6.3.1 Primary map



X Index: 127



Y Index: 152



Z Index: 117

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.

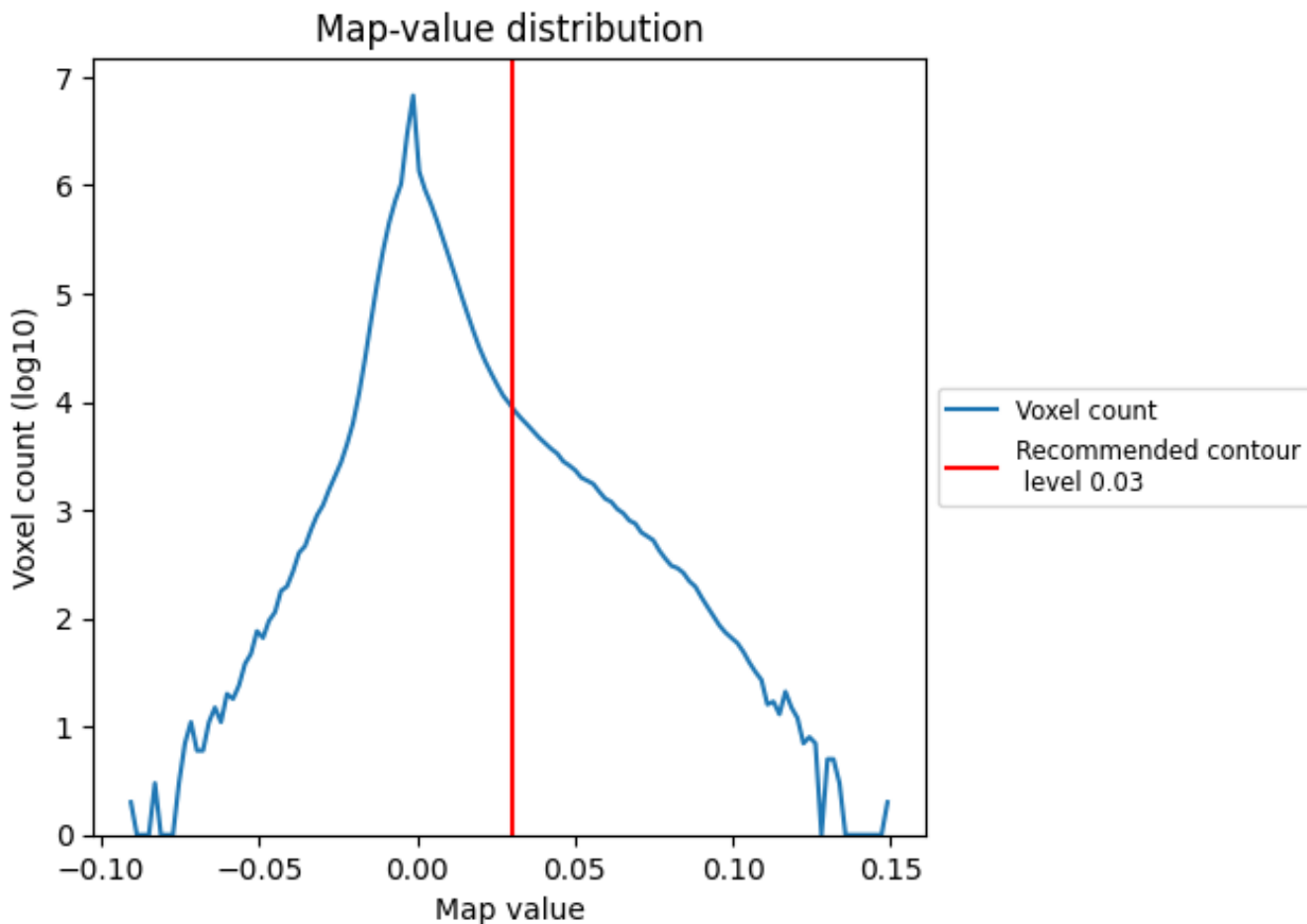
6.5 Mask visualisation

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

7 Map analysis [i](#)

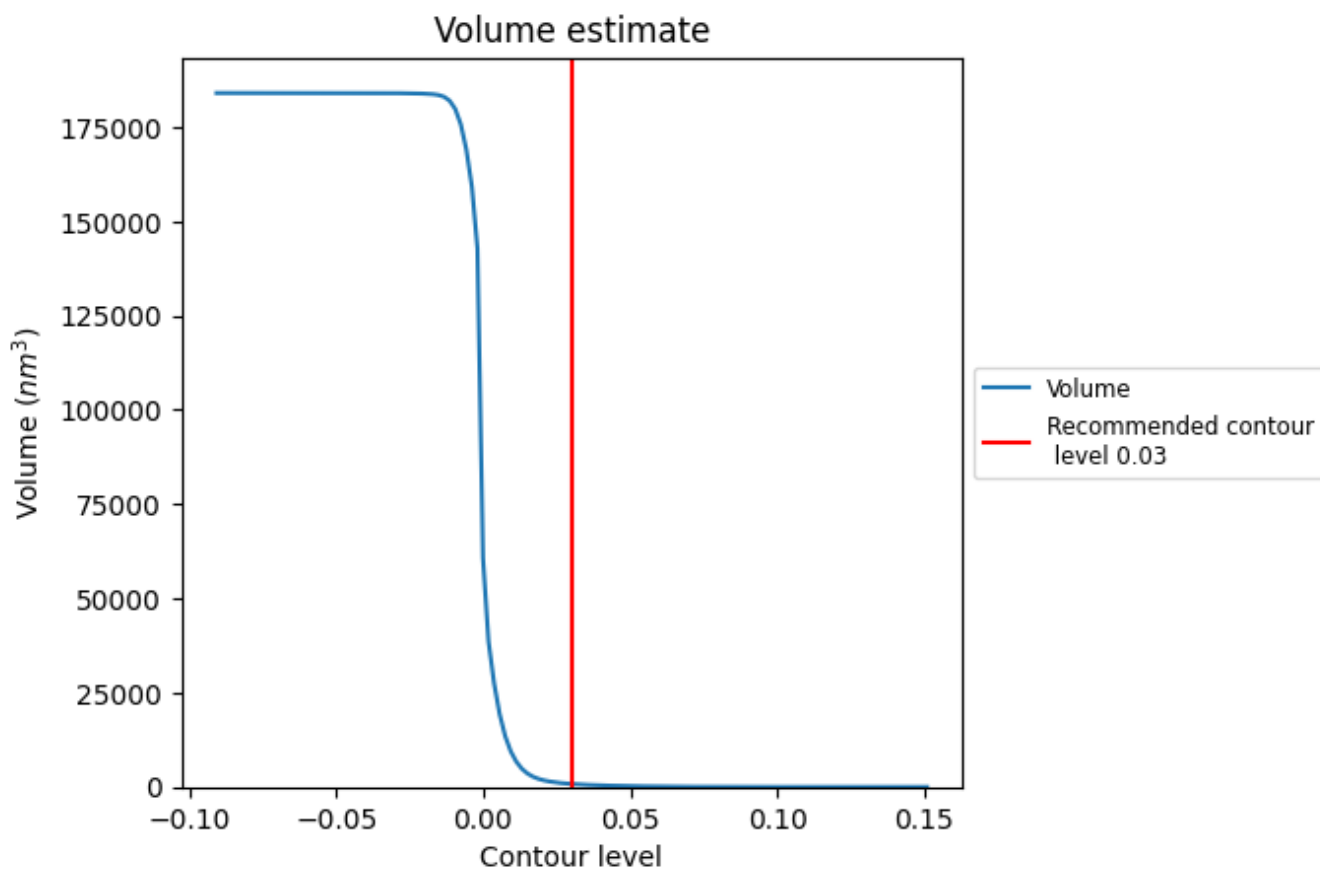
This section contains the results of statistical analysis of the map.

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.

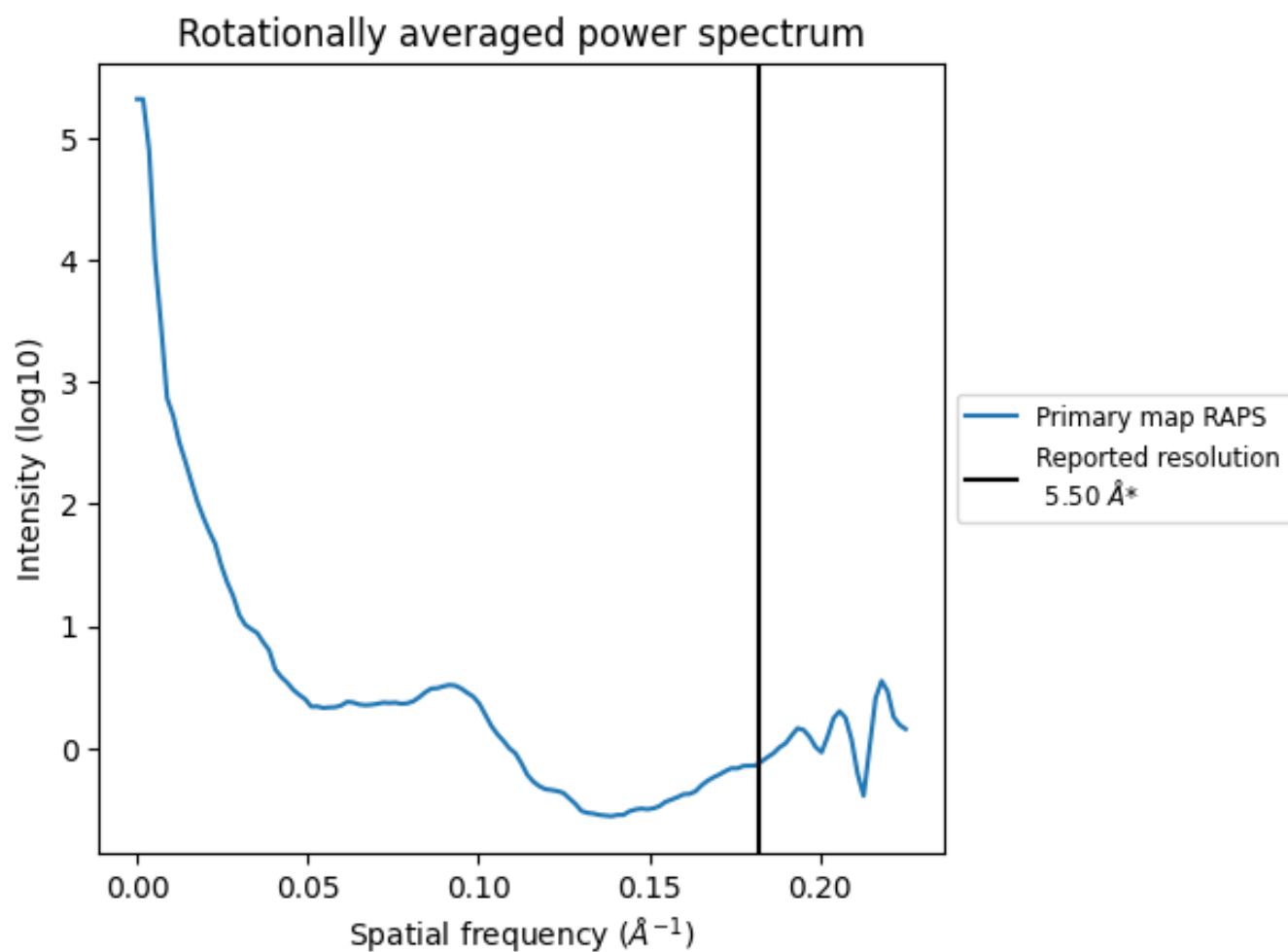
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 803 nm^3 ; this corresponds to an approximate mass of 725 kDa.

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

7.3 Rotationally averaged power spectrum i



*Reported resolution corresponds to spatial frequency of 0.182\AA^{-1}

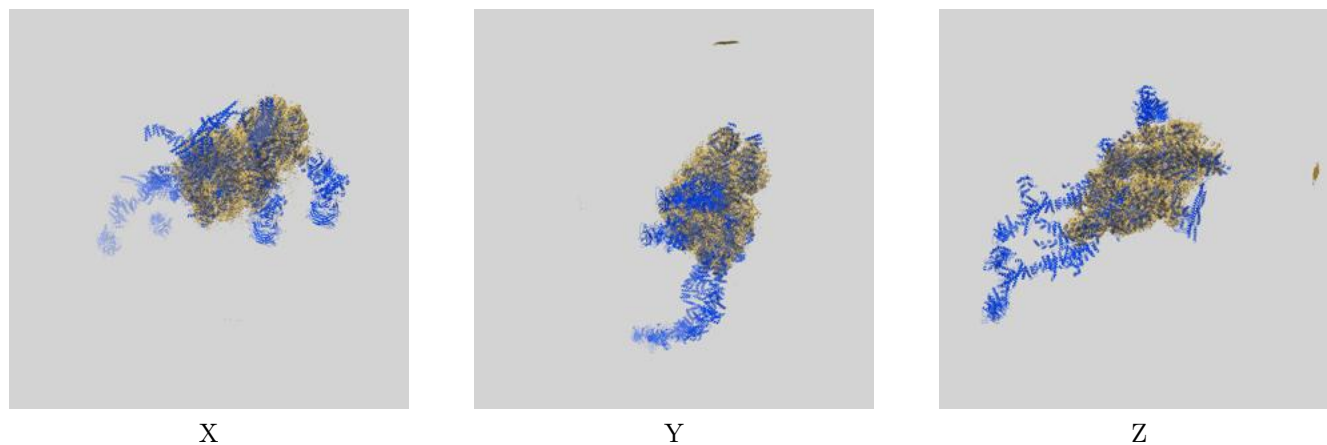
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

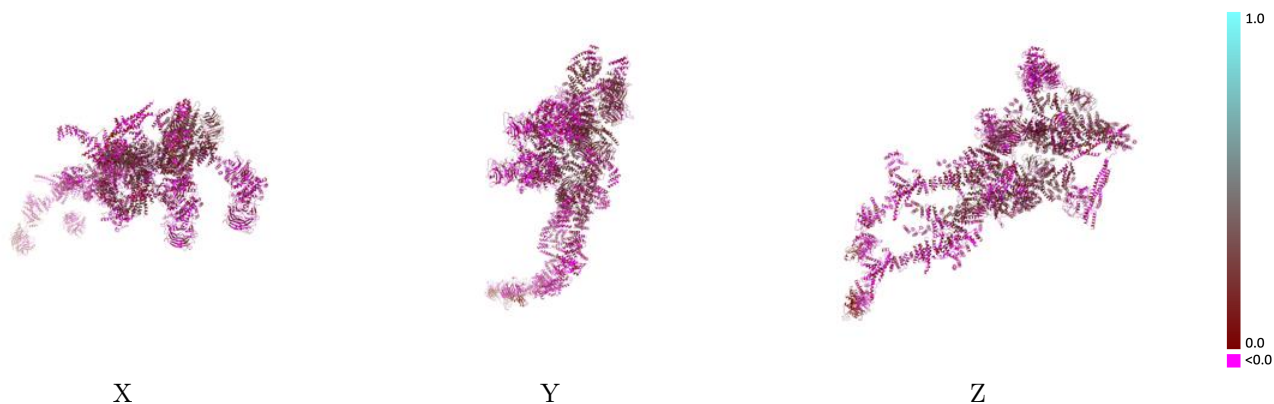
This section contains information regarding the fit between EMDB map EMD-0909 and PDB model 6LK8. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)



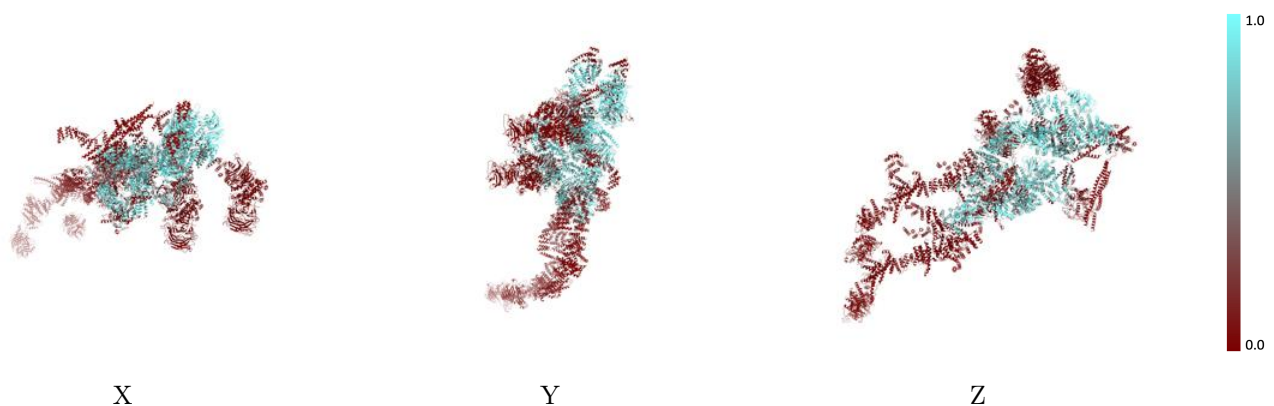
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



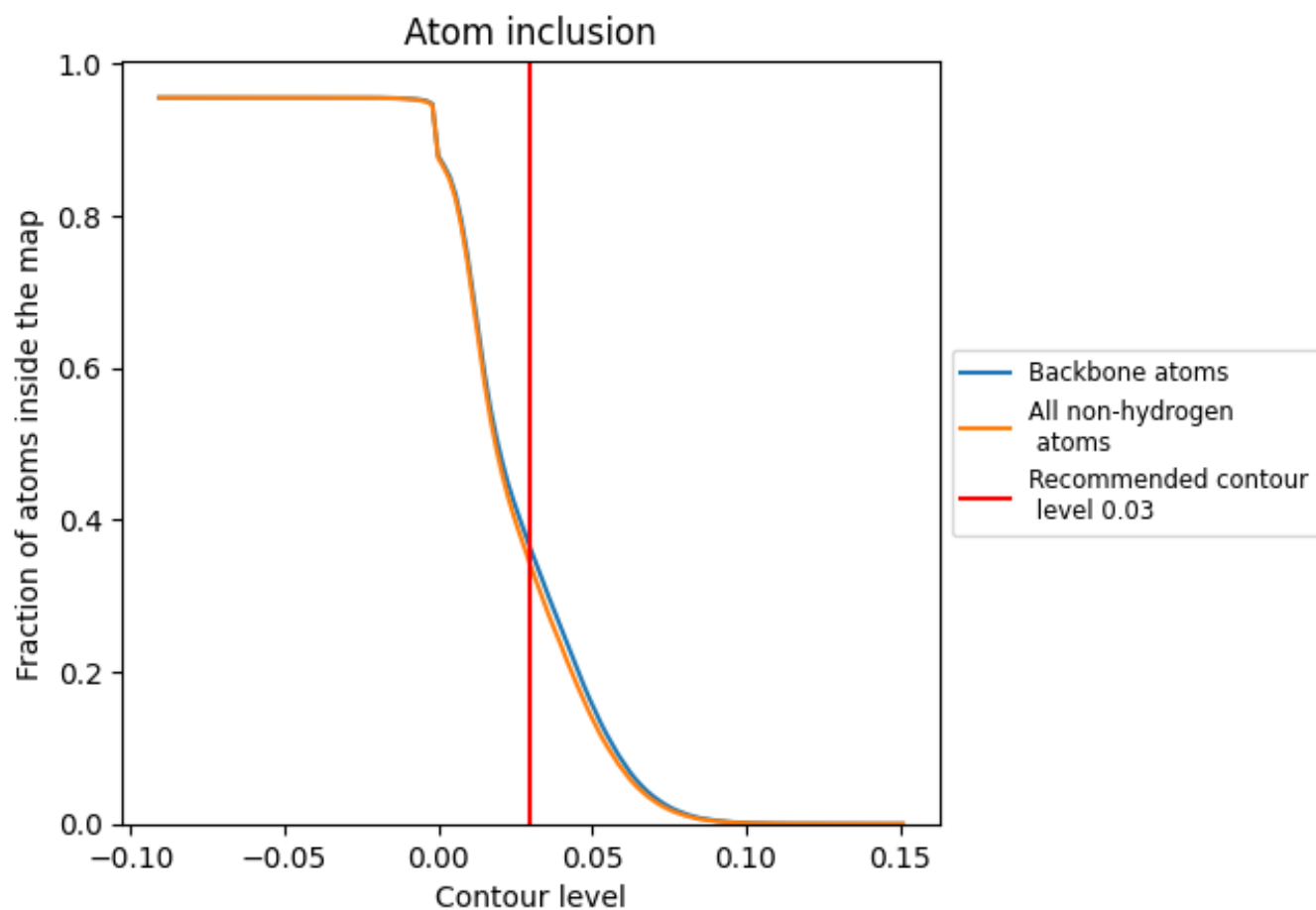
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 36% of all backbone atoms, 34% 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	 0.3389	 0.0890
A	 0.6004	 0.1430
B	 0.6840	 0.1880
C	 0.8953	 0.2270
D	 0.7459	 0.1650
E	 0.0748	 0.0220
F	 0.0000	 0.0160
G	 0.6472	 0.1730
H	 0.7815	 0.1790
I	 0.1832	 0.0930
J	 0.0000	 0.0030
K	 0.0000	 0.0110
L	 0.0000	 0.0100
M	 0.0000	 0.0220
N	 0.4516	 0.1270
O	 0.0800	 0.0580
P	 0.0846	 0.0380
Q	 0.4124	 0.1510
R	 0.0547	 0.0080
S	 0.0667	 0.0560
T	 0.0500	 0.0150
U	 0.0000	 0.0300
V	 0.0000	 0.0190
a	 0.5030	 0.1030
b	 0.6740	 0.1800
c	 0.8776	 0.2470
d	 0.7290	 0.1740
e	 0.1730	 0.0260
f	 0.2994	 0.0300
g	 0.5757	 0.1550
h	 0.7091	 0.1850
i	 0.0000	 0.0190
j	 0.0000	 0.0120

