



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 07:06 AM UTC

PDB ID : 7FIK / pdb_00007fik
EMDB ID : EMD-31600
Title : The cryo-EM structure of the CR subunit from *X. laevis* NPC
Authors : Shi, Y.; Huang, G.; Zhan, X.
Deposited on : 2021-07-31
Resolution : 3.70 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

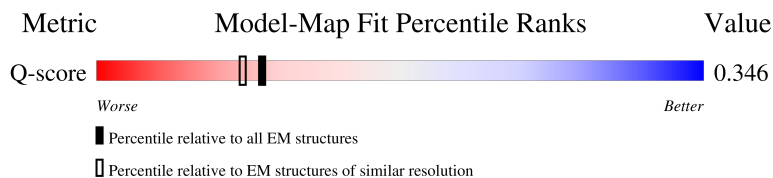
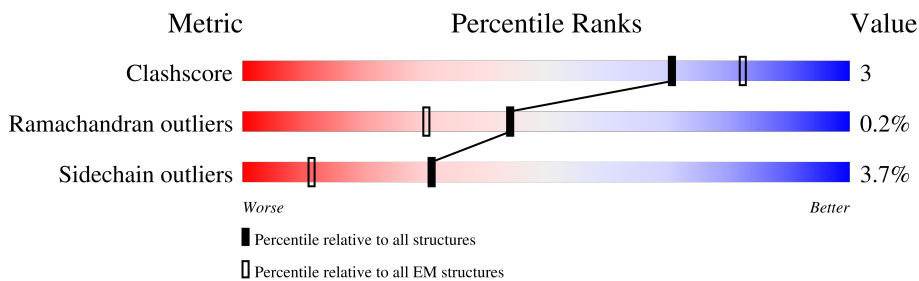
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 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	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	86% (green), 11% (grey), 3% (yellow), 0% (orange), 0% (red)
1	a	2011	82% (green), 14% (grey), 4% (yellow), 0% (orange), 0% (red)
2	B	653	79% (green), 11% (yellow), 8% (grey), 0% (orange), 2% (red)
2	b	653	78% (green), 13% (yellow), 9% (grey), 0% (orange), 0% (red)

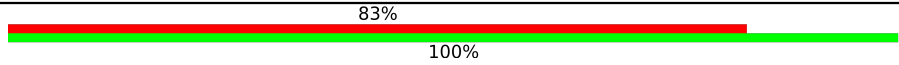

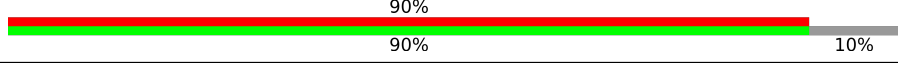
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Mol	Chain	Length	Quality of chain
3	C	375	75% 11% 14%
3	c	375	71% 11% 18%
4	D	360	77% 10% 12%
4	d	360	80% 6% 13%
5	E	1435	24% 83% 7% 9%
5	e	1435	8% 77% 8% 13%
6	F	326	8% 98% 1% 1%
6	f	326	85% 13% 2%
7	G	1742	28% 67%
7	g	1742	28% 6% 65%
8	H	320	83% 6% 10%
8	h	320	81% 8% 10%
9	I	916	9% 76% 20%
9	i	916	46% 73% 27%
10	J	1140	78% 88% 11%
11	K	2905	5% 24% 76%
11	L	2905	10% 23% 77%
11	M	2905	22% 77%
11	N	2905	6% 24% 76%
11	O	2905	23% 76%
12	P	820	70% 28%
12	S	820	5% 94%
12	p	820	52% 52% 44%
12	s	820	6% 94%
13	W	1388	20% 77%

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Mol	Chain	Length	Quality of chain
14	X	161	 83% 100%
15	Y	728	 38% 45% 53%
16	j	1140	 90% 90% 10%

2 Entry composition [i](#)

There are 16 unique types of molecules in this entry. The entry contains 116163 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	S		
1	A	1795	Total	C	N	O	S	0	0
			9238	5541	1851	1841	5		
1	a	1725	Total	C	N	O	S	0	0
			8811	5278	1770	1757	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	598	Total	C	N	O	S	0	0
			4799	3051	833	878	37		
2	b	595	Total	C	N	O	S	0	0
			4549	2894	793	829	33		

- Molecule 3 is a protein called MGC154553 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	324	Total	C	N	O	S	0	0
			2557	1590	461	488	18		
3	c	309	Total	C	N	O	S	0	0
			2445	1518	443	468	16		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	316	Total	C	N	O	S	0	0
			2473	1550	443	463	17		
4	d	312	Total	C	N	O	S	0	0
			2435	1531	435	451	18		

- Molecule 5 is a protein called outer Nup160.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	1310	Total	C	N	O	S	0	0
			7891	4857	1495	1522	17		
5	e	1247	Total	C	N	O	S	0	0
			8134	5074	1497	1533	30		

- Molecule 6 is a protein called MGC83926 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	326	Total	C	N	O		0	0
			1607	954	326	327			
6	f	322	Total	C	N	O	S	0	0
			2524	1612	436	461	15		

- Molecule 7 is a protein called Nuclear pore complex protein Nup98-Nup96.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	567	Total	C	N	O	S	0	0
			4209	2659	769	764	17		
7	g	603	Total	C	N	O	S	0	0
			4770	3022	868	856	24		

- Molecule 8 is a protein called Protein SEC13 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	288	Total	C	N	O	S	0	0
			2235	1417	383	423	12		
8	h	288	Total	C	N	O	S	0	0
			2259	1429	385	433	12		

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

Mol	Chain	Residues	Atoms				AltConf	Trace	
9	I	729	Total	C	N	O		0	0
			3626	2168	729	729			
9	i	673	Total	C	N	O		0	0
			3347	2001	673	673			

- Molecule 10 is a protein called nuclear pore complex protein Nup133.

Mol	Chain	Residues	Atoms				AltConf	Trace	
10	J	1015	Total	C	N	O		0	0
			5029	2999	1015	1015			

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

Mol	Chain	Residues	Atoms				AltConf	Trace
11	K	697	Total	C	N	O	0	0
			3460	2066	697	697		
11	L	679	Total	C	N	O	0	0
			3372	2014	679	679		
11	M	654	Total	C	N	O	0	0
			3246	1938	654	654		
11	N	701	Total	C	N	O	0	0
			3480	2078	701	701		
11	O	683	Total	C	N	O	0	0
			3391	2025	683	683		

- Molecule 12 is a protein called Nuclear pore complex protein Nup93.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	P	593	Total	C	N	O	0	0	
			2945	1759	593	593			
12	S	52	Total	C	N	O	S	0	0
			432	272	77	81	2		
12	s	52	Total	C	N	O	S	0	0
			432	272	77	81	2		
12	p	456	Total	C	N	O	0	0	
			2267	1355	456	456			

- Molecule 13 is a protein called Nup155-prov protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	W	324	Total	C	N	O	S	0	0
			2636	1688	447	485	16		

- Molecule 14 is a protein called Nup98.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	X	161	Total	C	N	O	0	0
			794	472	161	161		

- Molecule 15 is a protein called Nucleoporin Nup88A.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	Y	339	Total	C	N	O	0	0
			1676	998	339	339		

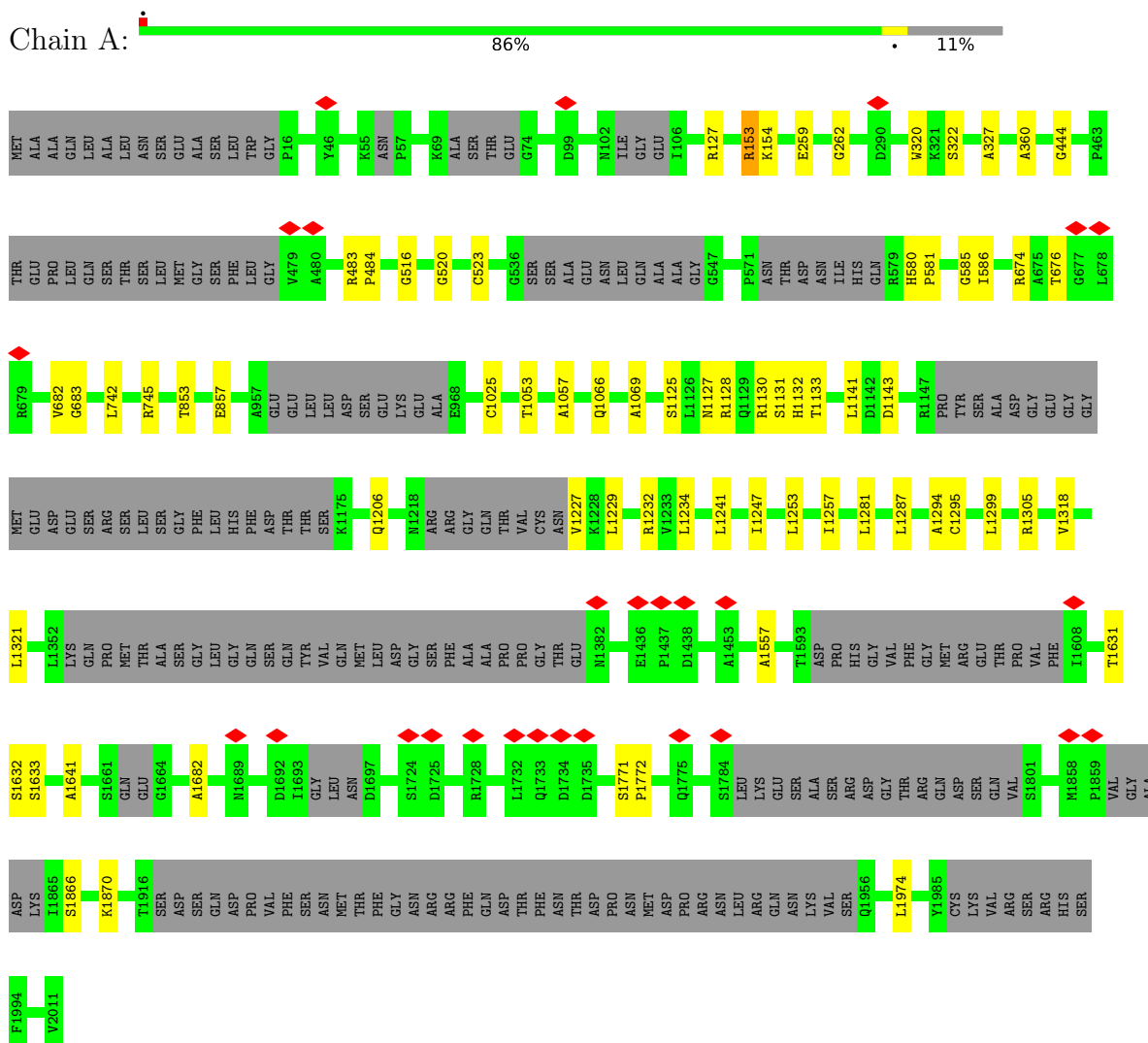
- Molecule 16 is a protein called outer Nup133.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	j	1028	5094	3038	1028	1028	0	0

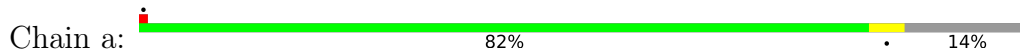
3 Residue-property plots

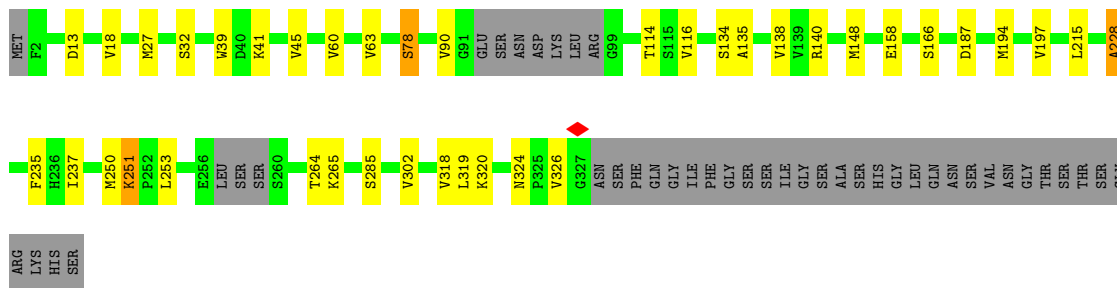
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

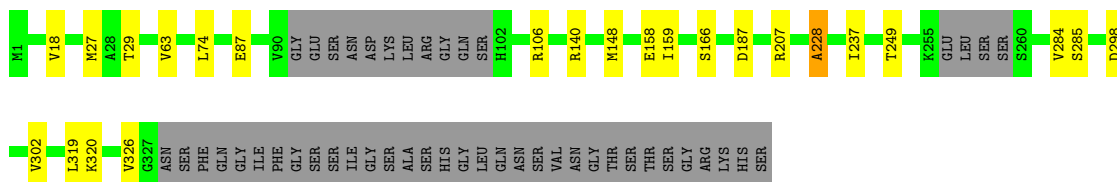
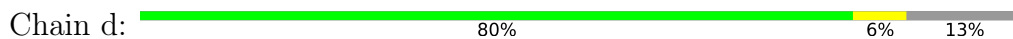


- Molecule 1: MGC83295 protein

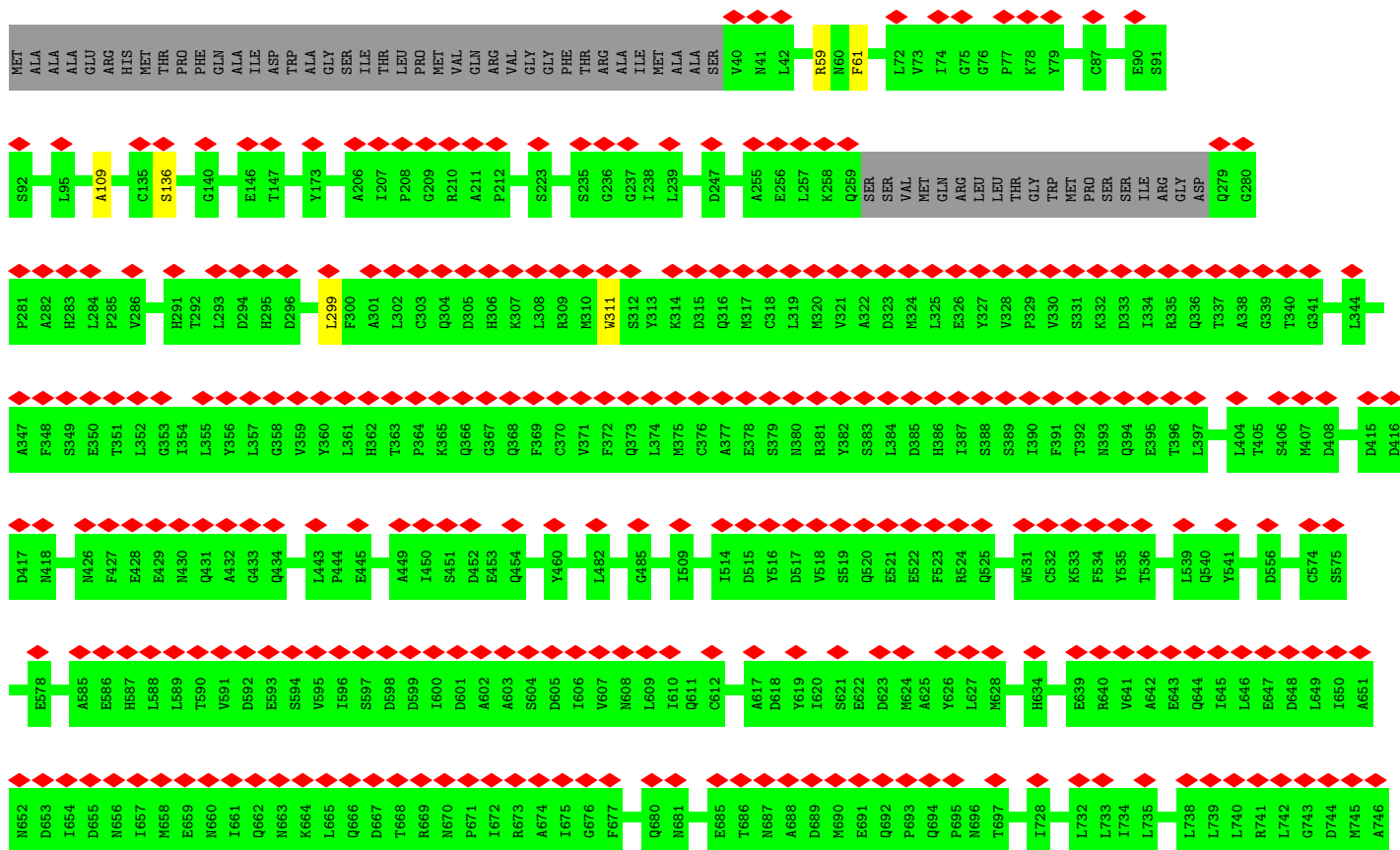
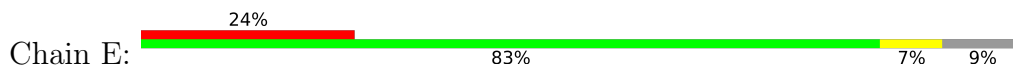


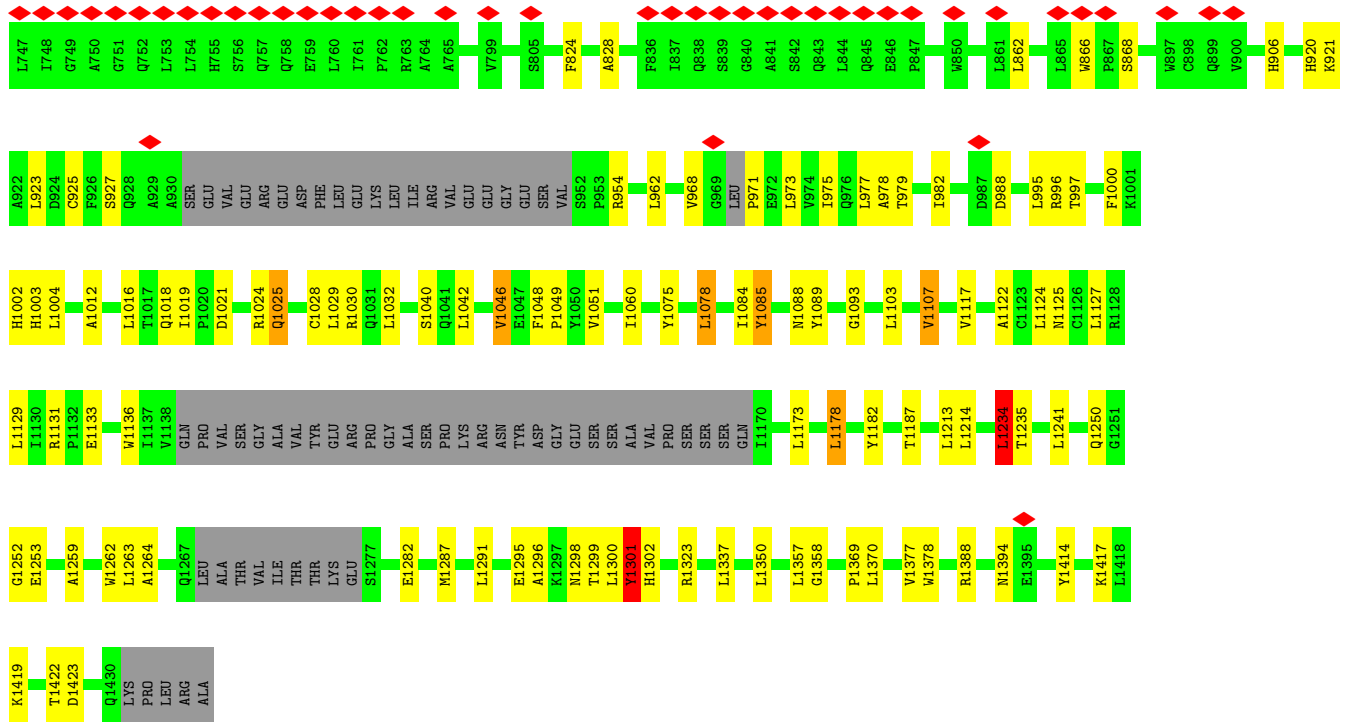


• Molecule 4: Nucleoporin SEH1-B



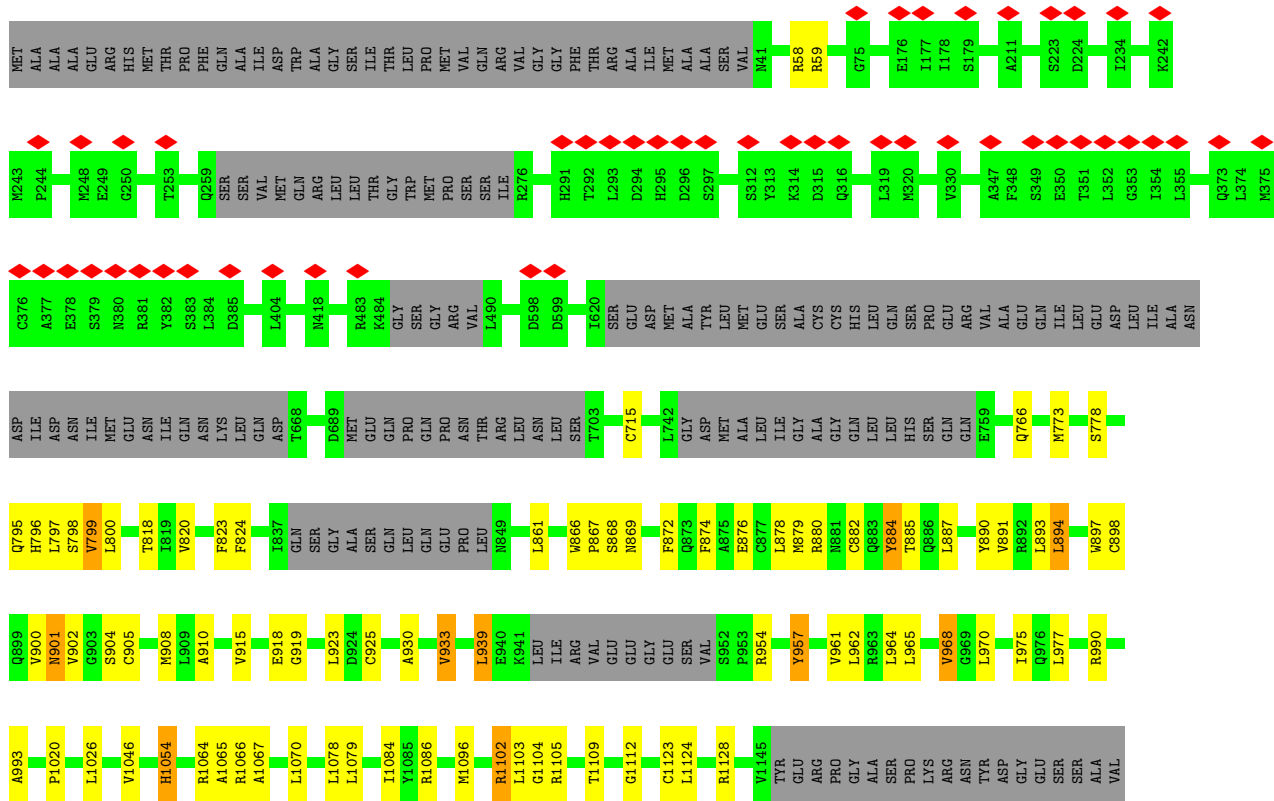
• Molecule 5: outer Nup160





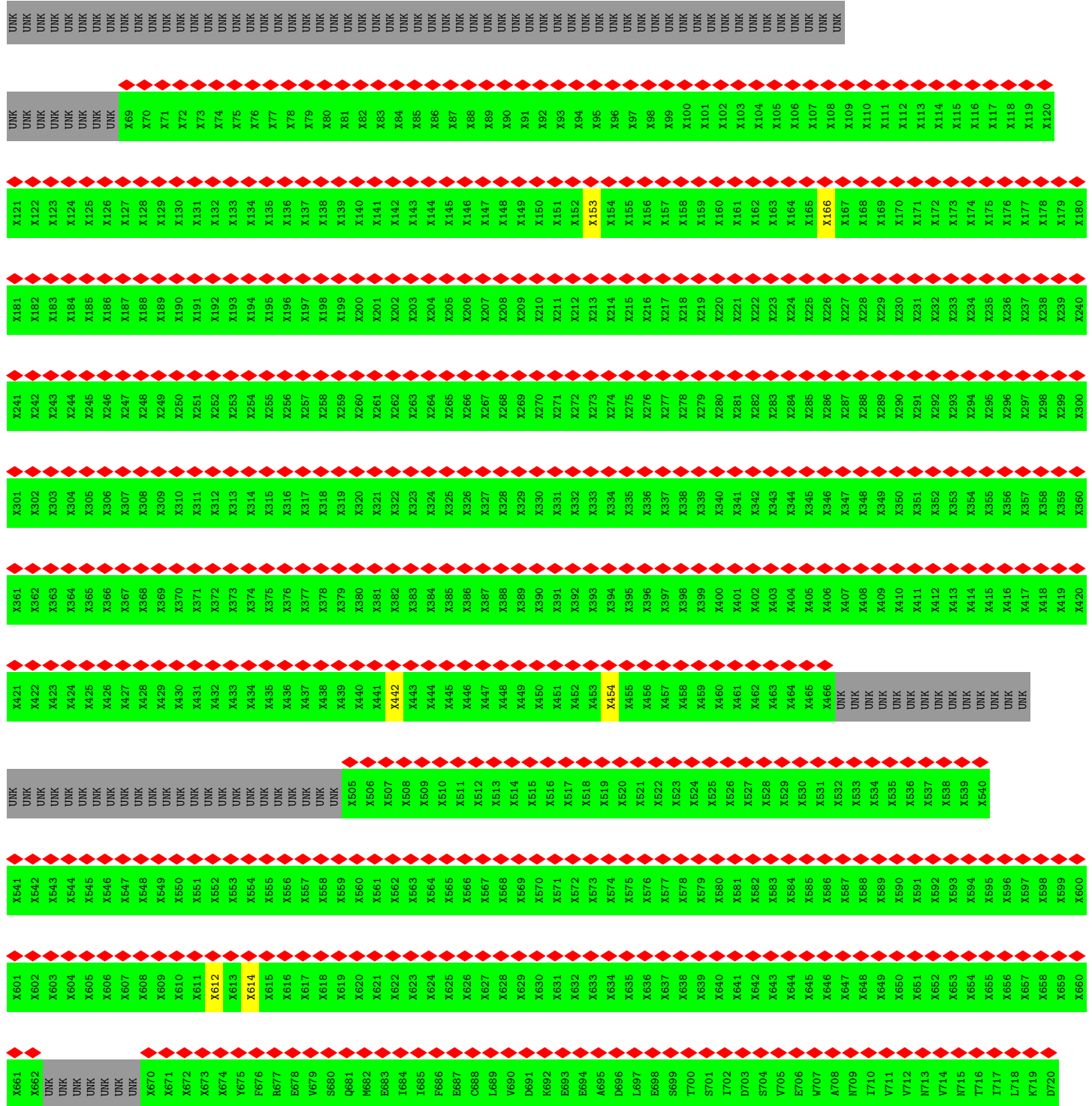
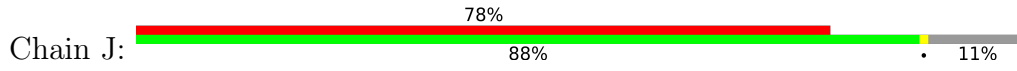
• Molecule 5: outer Nup160

Chain e: 77% 8% 13%





• Molecule 10: nuclear pore complex protein Nup133



K121	M181	G241	D301	T361	G421	SER	D541	L601	R661	M721	L781	A841	Q901
I122	I182	M242	M302	L362	T422	SER	E542	H602	M662	L722	R782	W842	P902
S123	L183	L243	S303	V363	G423	VAL	L643	Q603	C663	H723	T783	A843	A903
H124	H184	S244	R304	T364	R424	LYS	D544	V604	T664	V724	I784	S844	S904
S125	E185	S245	V305	V365	S425	SER	L645	G605	V665	A725	L785	M845	Q905
S126	E186	I246	L306	K366	T426	ARG	A546	L606	A546	C726	T786	L846	H906
S127	G187	G247	R307	D367	L427	GLN	V547	F607	PRO	Q727	E787	A847	G907
A128	Y188	R248	E308	E368	P428	ALA	N548	S608	GLN	Y728	Q788	E848	Q908
K129	I189	R249	Y309	G369	Q429	VAL	Q549	R609	T670	R729	L789	R849	L909
L130	E190	V250	I310	Y370	E430	VAL	L550	L610	A671	Q730	A790	Y850	A910
M131	S191	S251	S311	N371	K431	LYS	S551	S611	A672	S731	A791	C851	A911
V132	Y192	T252	D312	I372	I432	SER	V552	T612	D673	K732	L792	D852	F912
C133	T193	L253	A313	S373	P433	ARG	D553	C613	V674	M733	L793	F853	L913
K134	E194	F254	I314	D374	F434	PRO	L554	Q614	V675	S734	W794	D854	Q914
E135	F195	G255	W315	E375	E435	ASP	L655	T615	F676	L735	Y795	I855	A915
L136	G196	I256	G316	I376	A436	GLN	D556	K616	R677	Y736	L796	L856	H916
P137	S197	L257	S317	T377	Q437	ILE	D557	G617	E678	K737	L797	W857	D917
L138	S198	S258	E318	V378	G438	HIS	Y558	M618	V679	M738	D798	Q858	H918
P139	L199	P259	S319	E379	D439	ASP	P559	L619	S680	E739	D799	I859	L919
L140	C200	A260	D320	V380	N440	ASP	A560	V620	Q681	S740	Y800	C860	S920
S141	A201	V261	Y321	T381	I441	ASP	S561	A621	M682	G741	Y801	E861	W921
D142	F202	E262	D322	Q382	V442	ASP	D562	T622	E683	I742	T802	M862	L922
S143	V203	S263	D323	F383	G443	PRO	P563	R623	L684	Q743	Q803	T863	H923
E144	T204	T264	I324	N384	A444	ASP	R564	L624	L685	E744	L804	D864	E924
W145	A205	L265	K325	P385	G445	GLN	W565	L625	F686	P745	R805	M865	L925
S146	V206	C266	A326	V386	S446	ILE	A566	L626	E687	E746	S806	Q866	N926
A147	K207	S267	G327	F387	C447	ALA	E567	S627	C688	H747	I807	S867	S927
D148	G208	V268	I328	Q388	E448	HIS	S568	E628	L689	W748	D808	R868	Q928
L149	N209	L269	N329	A389	G449	ASP	V569	H629	V690	F749	R809	L869	E929
V150	S210	W270	I330	R390	N450	ASP	P570	A630	D691	W750	K810	Q870	F930
D151	F211	D271	N331	G391	P451	ASP	E571	E631	K692	T751	A811	R871	E931
I152	I212	K272	Y332	M392	V452	ASP	E572	K632	L693	A752	N812	W872	K932
C153	L213	G273	L333	Q393	F453	ASP	A573	L633	E694	S753	E813	M873	A933
A154	S214	D274	S334	L394	F454	ASP	A574	S634	A695	S754	E814	T874	H934
Q155	S215	C275	L335	C395	I455	ASP	G575	A635	D696	G755	R815	L875	A935
T156	E216	F276	N336	Q396	R456	ASP	F576	A636	L697	T756	Y816	F876	N936
G157	K217	Y277	Q337	L397	K457	ASP	S577	L637	E698	A757	M817	R877	L937
D158	N218	T278	N338	V398	S458	ASP	N578	V638	S699	G758	I818	E878	Q938
P159	Q219	L279	C339	V399	G459	ASP	T579	L639	T700	I759	L819	Q879	T939
A160	L220	T280	D340	P400	N460	ASP	S580	K640	S701	R760	E820	N880	L940
A161	V221	D281	G341	M401	L461	ASP	L581	M641	I702	S761	M821	F881	A941
A162	R222	S282	V342	F402	T462	ASP	L582	H642	D703	V762	E822	D882	N942
Q163	L223	S283	V343	S403	V463	ASP	L583	H643	S704	W763	H823	D883	M943
S164	T224	I284	I344	S404	V464	ASP	L584	A644	W705	T764	A824	F884	E944
V165	P225	N285	L345	Q405	A465	ASP	H585	K645	E706	Q765	Q825	L885	T945
A166	D226	K286	S346	A406	R466	ASP	Q586	L646	W707	R766	K826	F886	R946
L167	A227	W287	A347	C407	GLU	THR	L587	P647	A708	H767	R827	R887	Y947
M168	S228	D288	A348	Y408	ALA	ALA	E588	V648	N709	G768	S828	W888	F948
A169	G229	L289	W349	L409	SER	SER	D589	L649	I710	I769	E829	Y889	C949
A170	K230	D290	H350	Y410	VAL	VAL	K590	V650	W711	W770	L830	L890	L950
T171	M231	D291	F351	T411	LEU	LEU	M591	M651	V712	L771	L831	E891	A951
P172	N232	T292	G352	Q412	PRO	PRO	K592	S652	W713	K772	S832	S892	K952
E173	Q233	S293	D353	E413	GLU	GLU	A593	A653	V714	V773	H833	C893	T953
G174	R234	E294	N354	M414	MET	HIS	H594	T654	W715	Y774	L834	K894	K954
S175	V235	S295	F355	I415	GLU	GLU	S595	Q655	T716	F775	L835	R895	L955
S176	L236	Q296	C356	F416	GLU	GLU	F596	L656	I717	Q776	I836	C896	Q956
R177	Q237	L297	Q357	A417	SER	SER	F597	A657	L718	A777	L837	R897	L957
W178	P238	V298	I358	C418	LEU	LEU	W598	L658	K719	D778	L838	L898	S958
W179	G239	N299	Y359	S419			D599	D659	D720	S779	W840	L899	K959
P180	Q240	W300	Y360	T420			F600	K660		G780		S900	L960

A961	C1021	K1081
A962	E1022	D1082
L963	E1023	S1083
A964	N1024	I1084
S965	K1025	F1085
D966	R1026	V1086
F967	A1027	K1087
Q968	N1028	V1088
E969	E1029	L1089
D970	N1030	Q1090
W971	D1031	M1091
L972	F1032	L1092
Q973	M1033	L1093
E974	K1034	M1094
R975	A1035	K1095
W976	L1036	G1096
E977	D1037	I1097
E978	L1038	E1098
I979	L1039	L1099
A980	E1040	K1100
E981	Y1041	G1101
Q982	I1042	Y1102
E983	G1043	L1103
H984	D1044	P1104
F985	D1045	K1105
L986	S1046	A1106
L987	E1047	E1107
H988	V1048	T1108
Q989	D1049	L1109
E990	V1050	L1110
T991	E1051	Q1111
L992	E1052	S1112
P993	L1053	E1113
K994	K1054	E1114
R995	L1055	L1115
L996	E1056	M1116
L997	I1057	S1117
E998	L1058	L1118
E999	C1059	K1119
K1000	K1060	T1120
Q1001	A1061	M1121
L1002	I1062	S1122
D1003	K1063	Y1123
L1004	R1064	F1124
M1005	D1065	E1125
A1006	E1066	F1126
M1007	W1067	S1127
P1008	S1068	L1128
V1009	A1069	K1129
L1010	T1070	A1130
A1011	D1071	M1131
P1012	G1072	Y1132
F1013	K1073	E1133
D1014	D1074	C1134
L1015	D1075	Y1135
I1016	P1076	M1136
Q1017	I1077	K1137
L1018	E1078	M1138
Y1019	A1079	CLN
V1020	T1080	SER

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	1279270	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)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	5.334	Depositor
Minimum map value	-0.334	Depositor
Average map value	0.040	Depositor
Map value standard deviation	0.082	Depositor
Recommended contour level	0.35	Depositor
Map size (\AA)	710.144, 710.144, 710.144	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.387, 1.387, 1.387	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	0.40	1/9232 (0.0%)	0.64	7/12806 (0.1%)
1	a	0.33	0/8804	0.60	2/12220 (0.0%)
2	B	0.51	0/4893	0.73	5/6602 (0.1%)
2	b	0.54	1/4636 (0.0%)	0.77	7/6272 (0.1%)
3	C	0.37	0/2615	0.83	4/3550 (0.1%)
3	c	0.40	0/2500	0.84	1/3394 (0.0%)
4	D	0.38	0/2536	0.83	7/3442 (0.2%)
4	d	0.39	0/2498	0.79	2/3392 (0.1%)
5	E	0.43	2/7960 (0.0%)	0.67	6/10948 (0.1%)
5	e	0.45	2/8229 (0.0%)	0.70	12/11264 (0.1%)
6	F	0.23	0/1606	0.44	0/2231
6	f	0.37	0/2594	0.77	2/3526 (0.1%)
7	G	0.48	1/4299 (0.0%)	0.78	8/5856 (0.1%)
7	g	0.58	4/4888 (0.1%)	0.86	9/6644 (0.1%)
8	H	0.40	0/2299	0.83	1/3139 (0.0%)
8	h	0.39	0/2322	0.81	3/3169 (0.1%)
9	I	0.21	0/3621	0.49	0/5050
9	i	0.15	0/3339	0.40	0/4651
10	J	0.15	0/2253	0.40	0/3141
11	K	0.21	0/3452	0.48	0/4805
11	L	0.19	0/3362	0.47	0/4677
11	M	0.26	0/3238	0.57	1/4506 (0.0%)
11	N	0.22	0/3471	0.53	0/4830
11	O	0.21	0/3380	0.53	1/4700 (0.0%)
12	P	0.21	0/2939	0.44	2/4093 (0.0%)
12	S	0.48	0/438	0.71	1/586 (0.2%)
12	p	0.64	0/2251	0.62	0/3118
12	s	0.46	0/438	0.66	0/586
13	W	0.56	0/2692	0.80	3/3638 (0.1%)
15	Y	0.57	0/1668	1.09	3/2311 (0.1%)
16	j	0.13	0/5091	0.39	0/7095
All	All	0.39	11/113544 (0.0%)	0.67	87/156242 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	a	0	2
6	f	0	1
15	Y	0	1
All	All	0	6

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	g	1614	TRP	C-O	-6.41	1.16	1.24
7	g	1594	TYR	C-O	6.16	1.31	1.24
5	E	1234	LEU	N-CA	6.10	1.53	1.46
7	g	1540	PRO	C-O	5.83	1.29	1.23
5	e	1196	PRO	CA-C	5.58	1.60	1.52

The worst 5 of 87 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	683	GLY	N-CA-C	10.10	119.40	110.21
7	g	1321	ARG	N-CA-C	-9.63	100.73	111.14
5	E	988	ASP	N-CA-C	8.56	123.46	108.56
2	b	427	ASN	N-CA-C	7.87	119.64	111.14
12	S	124	MET	N-CA-C	7.08	118.68	110.97

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1053	THR	Peptide
1	A	1771	SER	Peptide
15	Y	286	TYR	Peptide
1	a	1053	THR	Peptide
1	a	1355	PRO	Peptide

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	9238	0	4628	35	0
1	a	8811	0	4324	46	0
2	B	4799	0	4722	51	0
2	b	4549	0	4272	41	0
3	C	2557	0	2454	19	0
3	c	2445	0	2337	17	0
4	D	2473	0	2381	18	0
4	d	2435	0	2340	15	0
5	E	7891	0	5504	81	0
5	e	8134	0	6437	97	0
6	F	1607	0	744	7	0
6	f	2524	0	2439	27	0
7	G	4209	0	3757	47	0
7	g	4770	0	4551	66	0
8	H	2235	0	2100	9	0
8	h	2259	0	2141	17	0
9	I	3626	0	1617	19	0
9	i	3347	0	1497	2	0
10	J	5029	0	1569	5	0
11	K	3460	0	1508	4	0
11	L	3372	0	1473	0	0
11	M	3246	0	1416	9	0
11	N	3480	0	1521	7	0
11	O	3391	0	1485	7	0
12	P	2945	0	1314	12	0
12	S	432	0	433	5	0
12	p	2267	0	1004	25	0
12	s	432	0	433	1	0
13	W	2636	0	2655	33	0
14	X	794	0	155	0	0
15	Y	1676	0	722	2	0
16	j	5094	0	2310	2	0
All	All	116163	0	76243	664	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 3.

The worst 5 of 664 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:a:1627:GLN:O	1:a:1631:THR:CB	1.87	1.22
12:p:614:ALA:HA	12:p:629:LEU:CB	1.70	1.21
5:e:968:VAL:HA	6:f:275:LYS:HA	1.33	1.10
12:p:618:GLU:HA	12:p:626:ALA:HB1	1.33	1.09
12:p:227:MET:CB	12:p:461:TYR:HA	1.83	1.09

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	
1	A	1759/2011 (88%)	1626 (92%)	129 (7%)	4 (0%)	43	72
1	a	1691/2011 (84%)	1552 (92%)	131 (8%)	8 (0%)	24	56
2	B	584/653 (89%)	564 (97%)	19 (3%)	1 (0%)	43	72
2	b	579/653 (89%)	562 (97%)	15 (3%)	2 (0%)	36	65
3	C	315/375 (84%)	303 (96%)	12 (4%)	0	100	100
3	c	299/375 (80%)	284 (95%)	14 (5%)	1 (0%)	36	65
4	D	310/360 (86%)	298 (96%)	12 (4%)	0	100	100
4	d	306/360 (85%)	293 (96%)	13 (4%)	0	100	100
5	E	1298/1435 (90%)	1239 (96%)	56 (4%)	3 (0%)	43	72
5	e	1227/1435 (86%)	1167 (95%)	59 (5%)	1 (0%)	48	78
6	F	324/326 (99%)	312 (96%)	12 (4%)	0	100	100
6	f	320/326 (98%)	308 (96%)	11 (3%)	1 (0%)	36	65
7	G	545/1742 (31%)	508 (93%)	35 (6%)	2 (0%)	30	60
7	g	595/1742 (34%)	543 (91%)	50 (8%)	2 (0%)	36	65
8	H	284/320 (89%)	274 (96%)	9 (3%)	1 (0%)	30	60
8	h	284/320 (89%)	274 (96%)	8 (3%)	2 (1%)	18	50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	719/916 (78%)	675 (94%)	43 (6%)	1 (0%)	48	78
9	i	657/916 (72%)	628 (96%)	29 (4%)	0	100	100
10	J	449/1140 (39%)	422 (94%)	27 (6%)	0	100	100
11	K	681/2905 (23%)	623 (92%)	57 (8%)	1 (0%)	48	78
11	L	659/2905 (23%)	614 (93%)	45 (7%)	0	100	100
11	M	638/2905 (22%)	575 (90%)	62 (10%)	1 (0%)	43	72
11	N	683/2905 (24%)	614 (90%)	68 (10%)	1 (0%)	48	78
11	O	661/2905 (23%)	613 (93%)	47 (7%)	1 (0%)	43	72
12	P	581/820 (71%)	539 (93%)	42 (7%)	0	100	100
12	S	50/820 (6%)	49 (98%)	1 (2%)	0	100	100
12	p	424/820 (52%)	401 (95%)	21 (5%)	2 (0%)	24	56
12	s	50/820 (6%)	46 (92%)	4 (8%)	0	100	100
13	W	318/1388 (23%)	305 (96%)	12 (4%)	1 (0%)	36	65
15	Y	323/728 (44%)	308 (95%)	11 (3%)	4 (1%)	10	40
16	j	1022/1140 (90%)	960 (94%)	62 (6%)	0	100	100
All	All	18635/38477 (48%)	17479 (94%)	1116 (6%)	40 (0%)	44	72

5 of 40 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	I	460	ILE
15	Y	271	LYS
1	a	57	PRO
1	a	58	PRO
1	a	1095	LEU

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	100/1779 (6%)	98 (98%)	2 (2%)	48	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	a	77/1779 (4%)	73 (95%)	4 (5%)	21	47
2	B	517/580 (89%)	500 (97%)	17 (3%)	33	55
2	b	447/580 (77%)	432 (97%)	15 (3%)	32	55
3	C	288/329 (88%)	282 (98%)	6 (2%)	47	64
3	c	276/329 (84%)	267 (97%)	9 (3%)	33	55
4	D	273/310 (88%)	265 (97%)	8 (3%)	37	57
4	d	266/310 (86%)	262 (98%)	4 (2%)	57	68
5	E	382/1256 (30%)	364 (95%)	18 (5%)	23	48
5	e	545/1256 (43%)	520 (95%)	25 (5%)	24	49
6	f	266/275 (97%)	262 (98%)	4 (2%)	57	68
7	G	384/1474 (26%)	356 (93%)	28 (7%)	13	40
7	g	490/1474 (33%)	459 (94%)	31 (6%)	16	43
8	H	236/273 (86%)	230 (98%)	6 (2%)	42	61
8	h	245/273 (90%)	240 (98%)	5 (2%)	48	64
12	S	47/721 (6%)	44 (94%)	3 (6%)	16	43
12	s	47/721 (6%)	44 (94%)	3 (6%)	16	43
13	W	295/1219 (24%)	290 (98%)	5 (2%)	53	67
All	All	5181/14938 (35%)	4988 (96%)	193 (4%)	31	54

5 of 193 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	c	78	VAL
5	e	1079	LEU
3	c	147	ASP
5	e	894	LEU
5	e	1324	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 100 such sidechains are listed below:

Mol	Chain	Res	Type
2	b	436	HIS
5	e	888	GLN
8	h	261	ASN
3	c	68	GLN

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Mol	Chain	Res	Type
4	d	268	ASN

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 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](#)

There are no chain breaks in this entry.

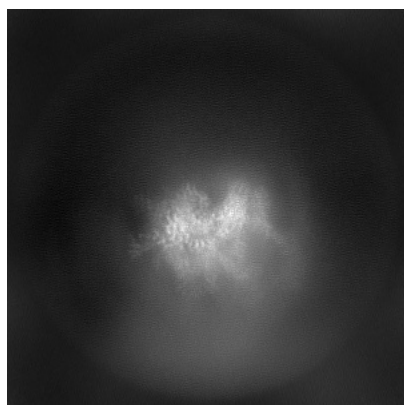
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31600. 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](#)

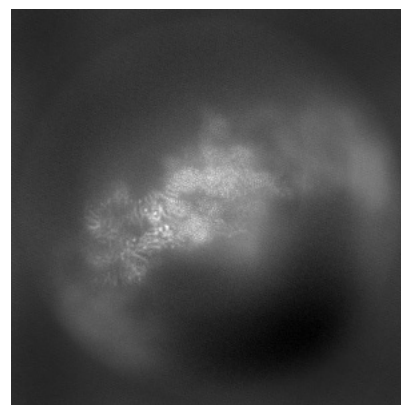
6.1.1 Primary map



X



Y

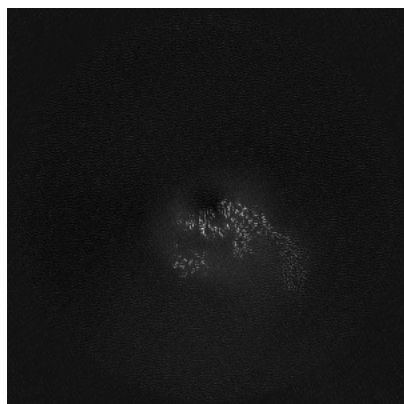


Z

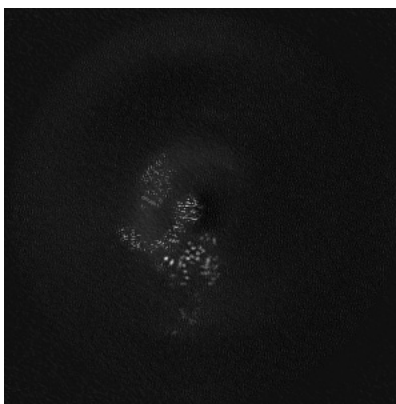
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

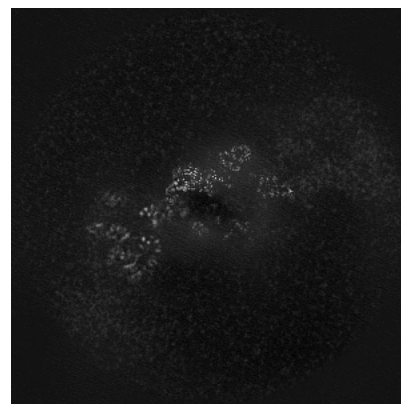
6.2.1 Primary map



X Index: 256



Y Index: 256

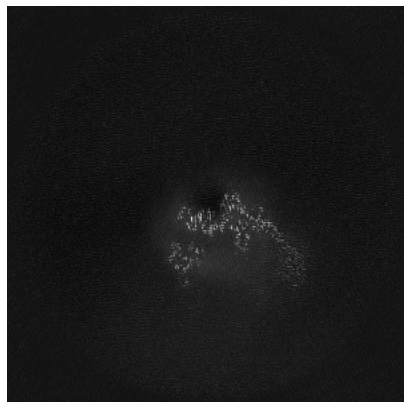


Z Index: 256

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

6.3 Largest variance slices [i](#)

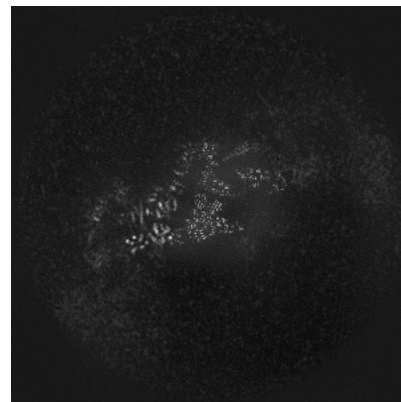
6.3.1 Primary map



X Index: 252



Y Index: 223

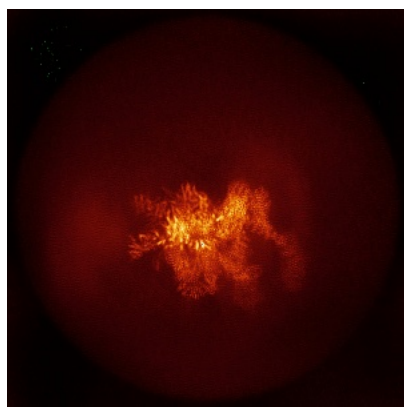


Z Index: 236

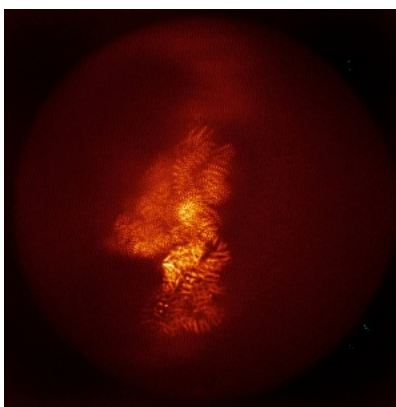
The images above show the largest variance slices of the map in three orthogonal directions.

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

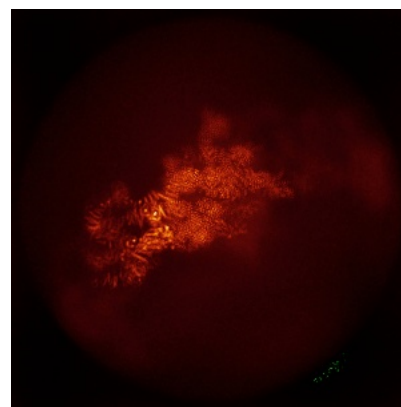
6.4.1 Primary map



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.

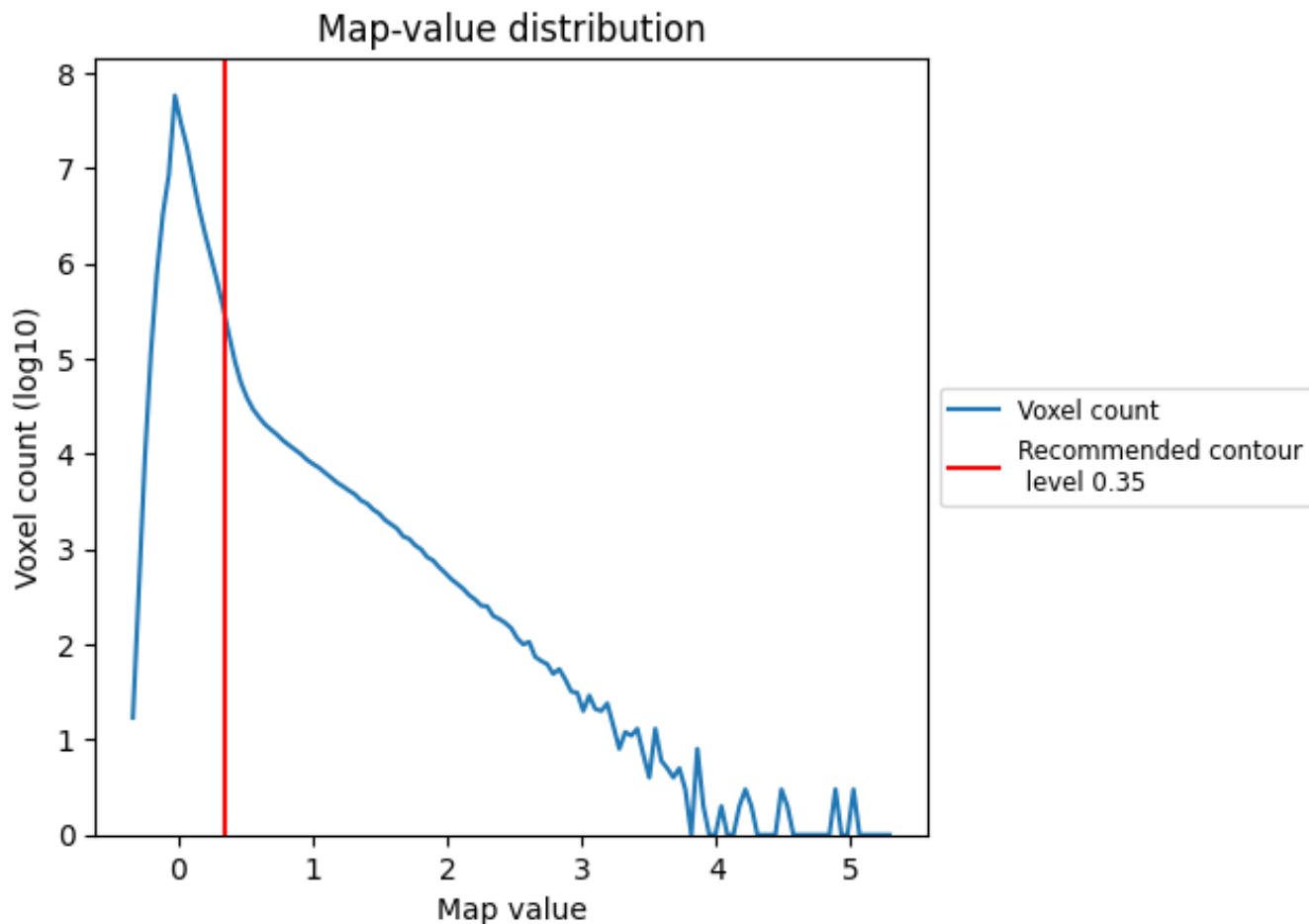
6.6 Mask visualisation

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

7 Map analysis [i](#)

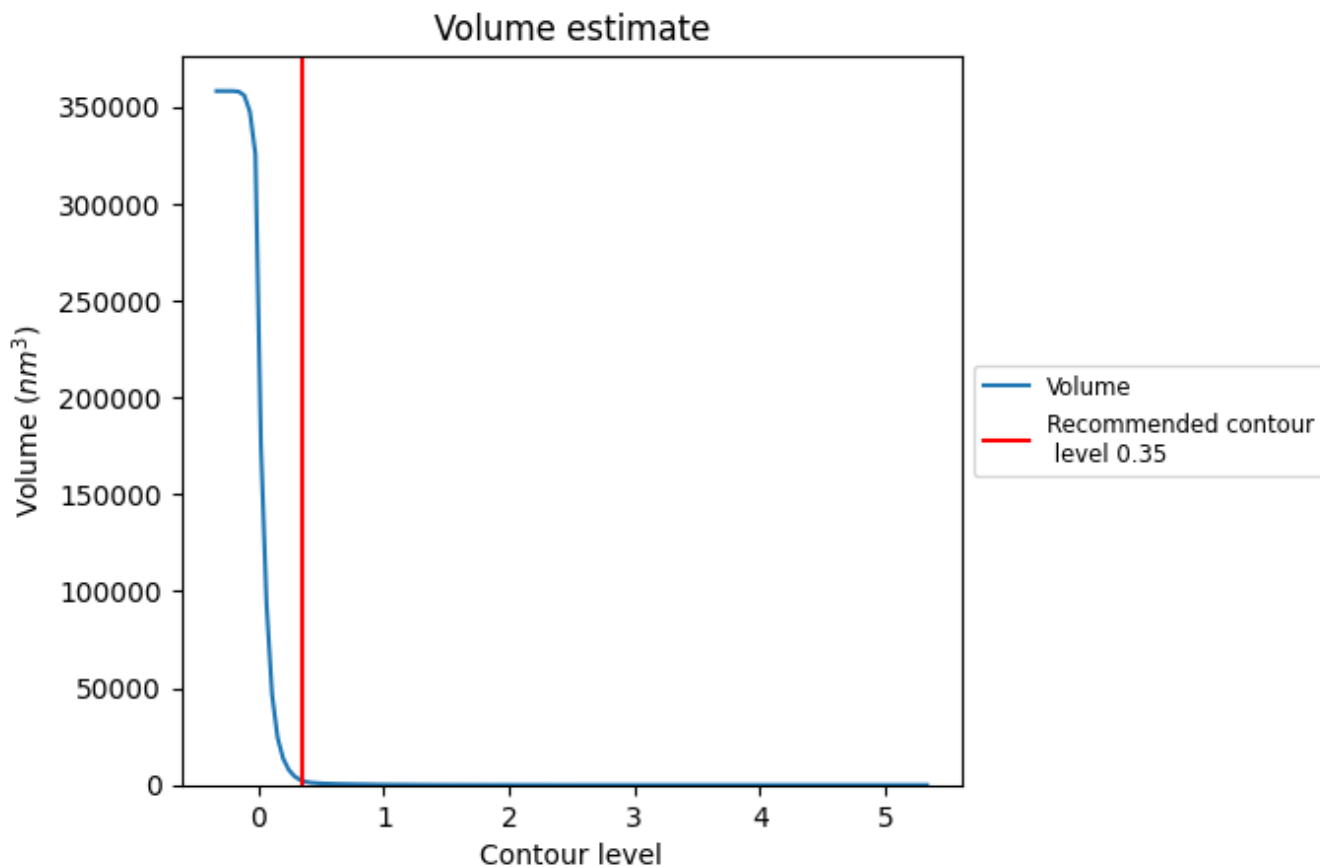
This section contains the results of statistical analysis of the map.

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.

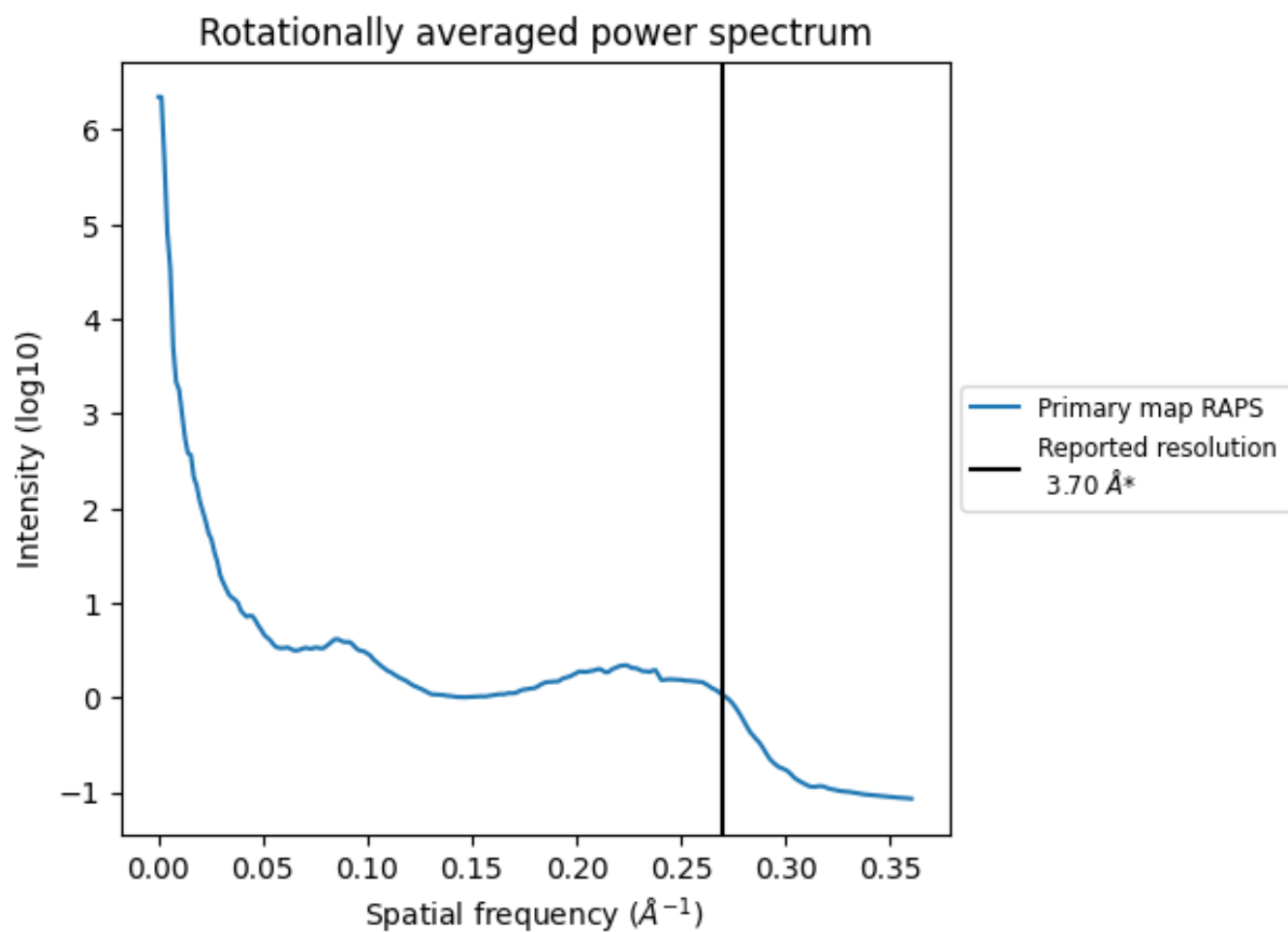
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2248 nm^3 ; this corresponds to an approximate mass of 2031 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 0.270 Å⁻¹

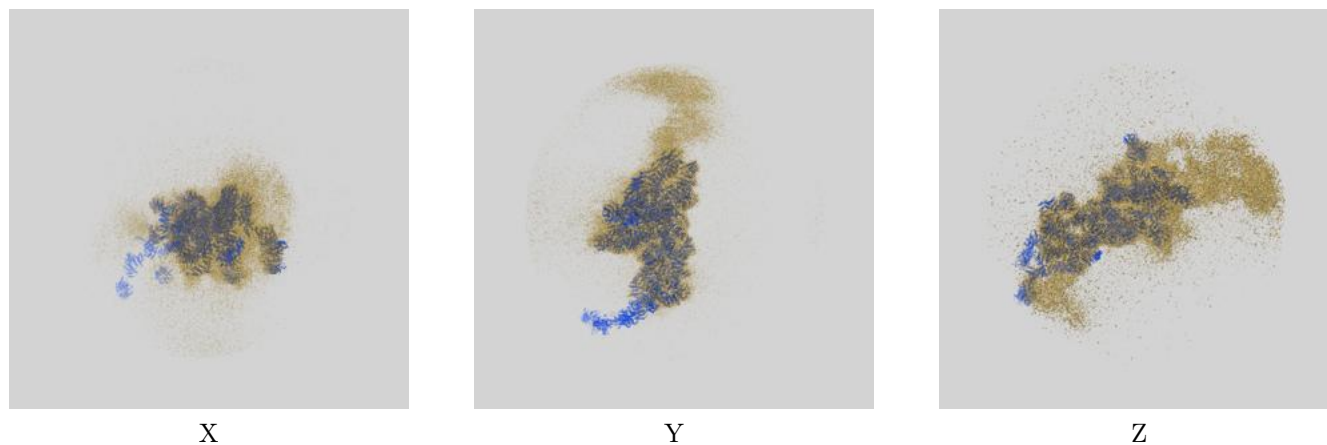
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

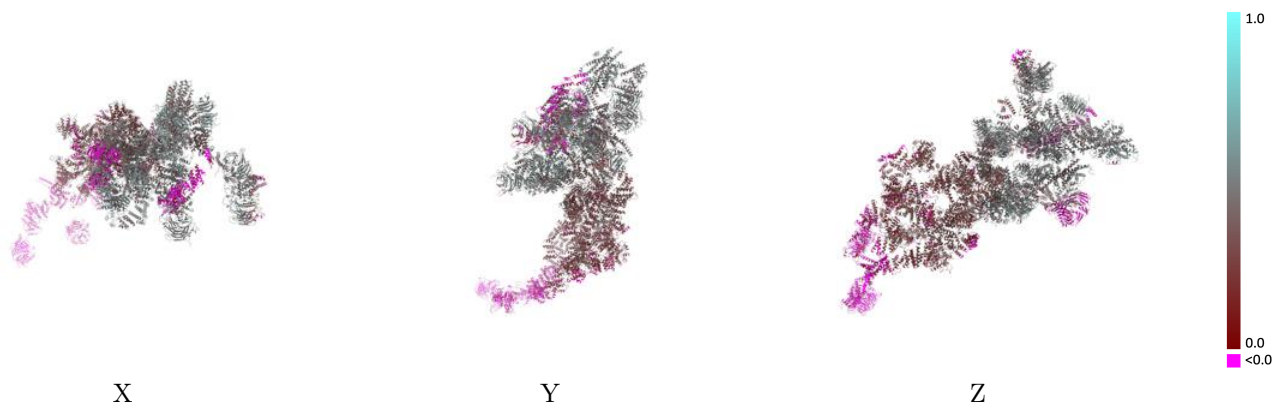
This section contains information regarding the fit between EMDB map EMD-31600 and PDB model 7FIK. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



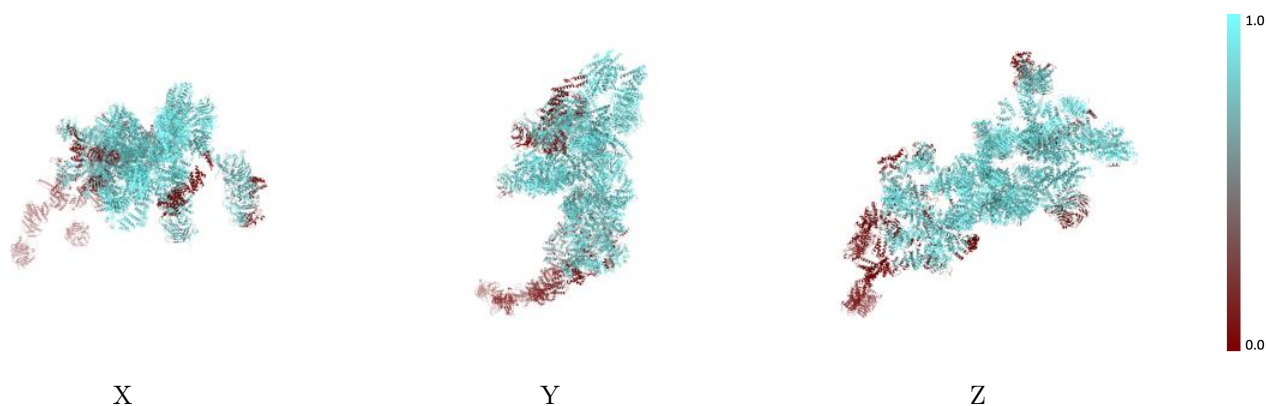
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



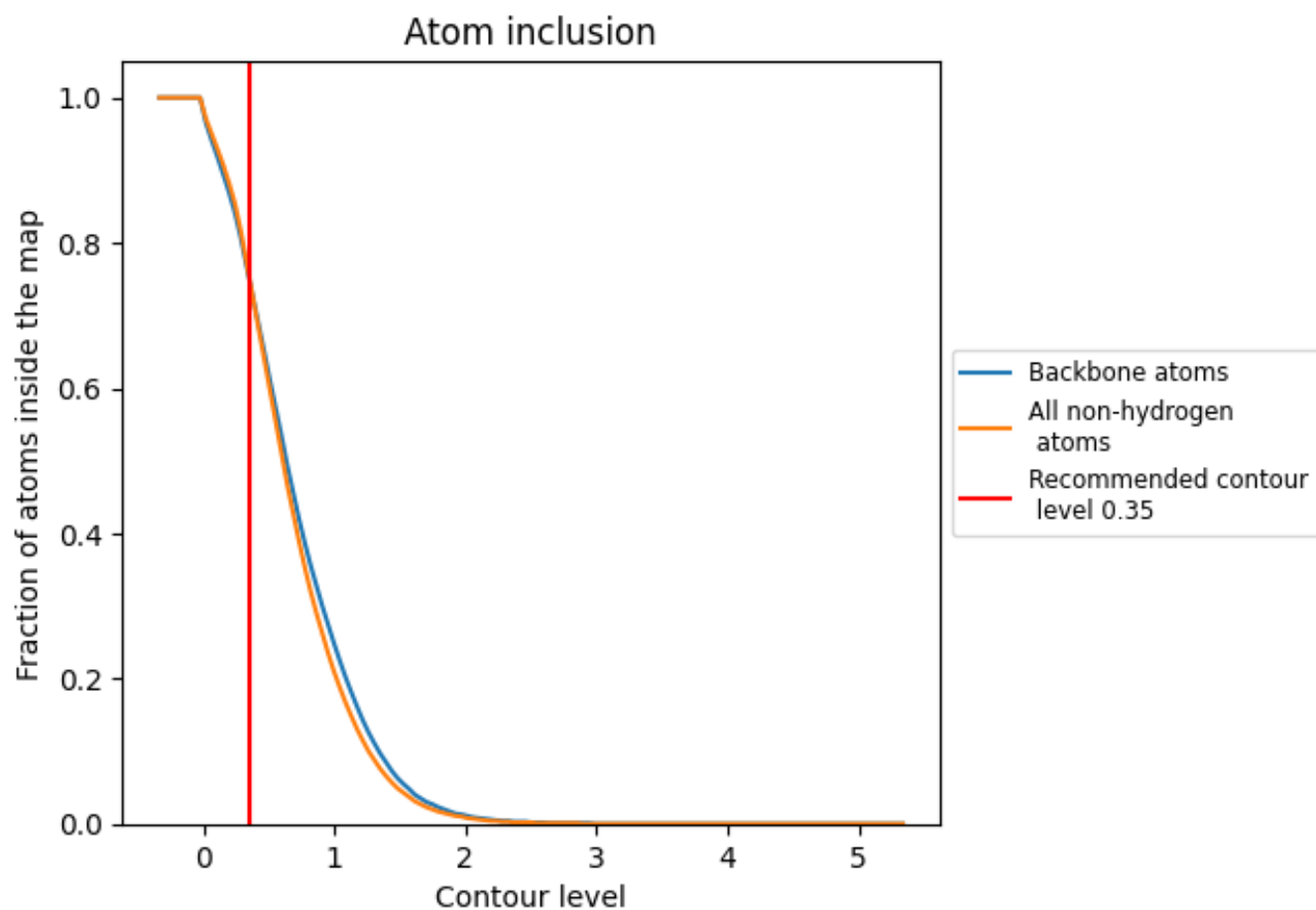
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.35).



































































9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 75% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7540	 0.3460
A	 0.9580	 0.4790
B	 0.8710	 0.4340
C	 0.9490	 0.5030
D	 0.9220	 0.4710
E	 0.7110	 0.4090
F	 0.7750	 0.4700
G	 0.8890	 0.3440
H	 0.9590	 0.4710
I	 0.8330	 0.2830
J	 0.1110	 0.0820
K	 0.7490	 0.2950
L	 0.5250	 0.2780
M	 0.9400	 0.3220
N	 0.6850	 0.2870
O	 0.7840	 0.2290
P	 0.8780	 0.2830
S	 0.9190	 0.4340
W	 0.9640	 0.4950
X	 0.2370	 0.0090
Y	 0.2550	 -0.0240
a	 0.9670	 0.4830
b	 0.8760	 0.4240
c	 0.9290	 0.4670
d	 0.9660	 0.4690
e	 0.8850	 0.4500
f	 0.9850	 0.5100
g	 0.8900	 0.3330
h	 0.9510	 0.3740
i	 0.3530	 0.1570
j	 0.0000	 -0.0560
p	 0.1080	 -0.0130
s	 0.9530	 0.3980

