



# wwPDB EM Validation Summary Report ⓘ

Nov 28, 2022 – 10:09 PM EST

PDB ID : 7TDZ  
EMDB ID : EMD-25817  
Title : Cryo-EM model of protomer of the cytoplasmic ring of the nuclear pore complex from *Xenopus laevis*  
Authors : Fontana, P.; Wu, H.  
Deposited on : 2022-01-03  
Resolution : 6.90 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:

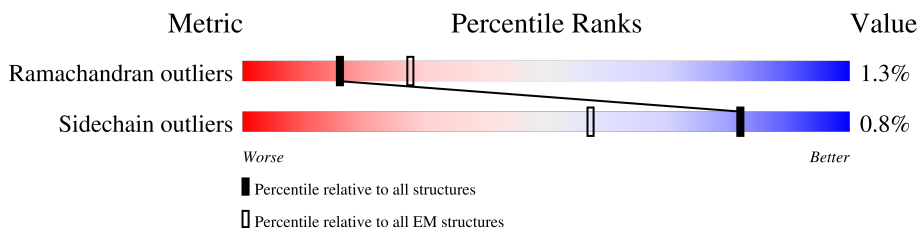
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP)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

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 6.90 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
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	H	916	<div style="display: flex; align-items: center;"> <div style="width: 20%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 82%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 14%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="text-align: center;">20% 82% 14%</p>
1	h	916	<div style="display: flex; align-items: center;"> <div style="width: 69%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 82%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 14%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="text-align: center;">69% 82% 14%</p>
2	T	547	<div style="display: flex; align-items: center;"> <div style="width: 7%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 23%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 76%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="text-align: center;">7% 23% 76%</p>
2	t	547	<div style="display: flex; align-items: center;"> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 95%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="text-align: center;">5% 95%</p>
3	S	2037	<div style="display: flex; align-items: center;"> <div style="width: 7%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 93%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="text-align: center;">7% 93%</p>
3	s	2037	<div style="display: flex; align-items: center;"> <div style="width: 98%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="text-align: center;">98%</p>
4	R	728	<div style="display: flex; align-items: center;"> <div style="width: 14%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 89%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 7%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="text-align: center;">14% 89% 7%</p>
4	r	728	<div style="display: flex; align-items: center;"> <div style="width: 20%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 62%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 35%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="text-align: center;">20% 62% 35%</p>
5	G	306	<div style="display: flex; align-items: center;"> <div style="width: 8%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 98%; height: 10px; background-color: green; margin-right: 5px;"></div> </div> <p style="text-align: center;">8% 98%</p>

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Mol	Chain	Length	Quality of chain
5	g	306	7% 98%
6	L	2011	19% 95% 5%
6	l	2011	16% 95% 5%
7	E	322	7% 97%
7	e	322	12% 97%
8	D	375	9% 95%
8	d	375	18% 95%
9	C	653	18% 97%
9	c	653	17% 90% 5%
10	U	1388	26% 74%
11	M	2905	6% 27% 73%
11	N	2905	6% 27% 73%
11	O	2905	8% 27% 73%
11	P	2905	22% 27% 73%
11	Q	2905	7% 27% 73%
12	B	326	66% 97%
12	b	326	8% 97%
13	A	1435	32% 90% 6%
13	a	1435	21% 90% 6%
14	I	1140	44% 57% 41%
14	i	1140	93% 90% 7%
15	F	673	19% 92% 5%
15	f	673	17% 92% 5%

## 2 Entry composition [i](#)

There are 15 unique types of molecules in this entry. The entry contains 331243 atoms, of which 162589 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 Nuclear pore complex protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	H	789	12767	4080	6346	1085	1224	32	0	0
1	h	789	12767	4080	6346	1085	1224	32	0	0

- Molecule 2 is a protein called Nup62.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			
2	t	29	479	153	235	42	49	0	0	
2	T	130	2140	664	1064	189	220	3	0	0

- Molecule 3 is a protein called Nup214.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			
3	s	32	518	158	261	46	53	0	0	
3	S	142	2333	722	1164	208	236	3	0	0

- Molecule 4 is a protein called Nup88A protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	r	470	7354	2349	3679	598	703	25	0	0
4	R	680	10786	3395	5396	916	1048	31	0	0

- Molecule 5 is a protein called Protein SEC13 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
5	g	306	4657	1506	2270	408	460	13	0	0
5	G	306	4657	1506	2270	408	460	13	0	0

- Molecule 6 is a protein called Nup205.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
6	L	2011	32130	10112	16156	2785	2978	99	0	0
6	l	2011	32130	10112	16156	2785	2978	99	0	0

- Molecule 7 is a protein called Nucleoporin SEH1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
7	E	322	4973	1582	2445	452	476	18	0	0
7	e	322	4973	1582	2445	452	476	18	0	0

- Molecule 8 is a protein called Nup42.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
8	D	375	5727	1813	2800	524	571	19	0	0
8	d	375	5727	1813	2800	524	571	19	0	0

- Molecule 9 is a protein called Nuclear pore complex protein Nup85.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
9	C	653	10494	3341	5226	904	984	39	0	0
9	c	653	5267	3341	904	983	39		0	0

- Molecule 10 is a protein called Nup155-prov protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
10	U	358	5843	1868	2931	490	538	16	0	0

- Molecule 11 is a protein called Nup358.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	P	798	Total	C	H	N	O	S	0	0
			12862	4088	6444	1096	1202	32		
11	O	798	Total	C	H	N	O	S	0	0
			12862	4088	6444	1096	1202	32		
11	Q	798	Total	C	H	N	O	S	0	0
			12862	4088	6444	1096	1202	32		
11	N	798	Total	C	H	N	O	S	0	0
			12862	4088	6444	1096	1202	32		
11	M	798	Total	C	H	N	O	S	0	0
			12862	4088	6444	1096	1202	32		

- Molecule 12 is a protein called Nup37.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	B	326	Total	C	H	N	O	S	0	0
			5076	1640	2503	443	473	17		
12	b	326	Total	C	H	N	O	S	0	0
			5076	1640	2503	443	473	17		

- Molecule 13 is a protein called Nup160.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	A	1352	Total	C	H	N	O	S	0	0
			21491	6819	10745	1855	2005	67		
13	a	1352	Total	C	H	N	O	S	0	0
			21491	6819	10745	1855	2005	67		

- Molecule 14 is a protein called Nup133.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	I	671	Total	C	H	N	O	S	0	0
			10733	3406	5353	899	1048	27		
14	i	1064	Total	C	H	N	O	S	0	0
			16672	5313	8274	1394	1641	50		

- Molecule 15 is a protein called Nuclear pore complex protein Nup96.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	F	639	Total	C	H	N	O	S	0	0
			10336	3298	5128	928	954	28		

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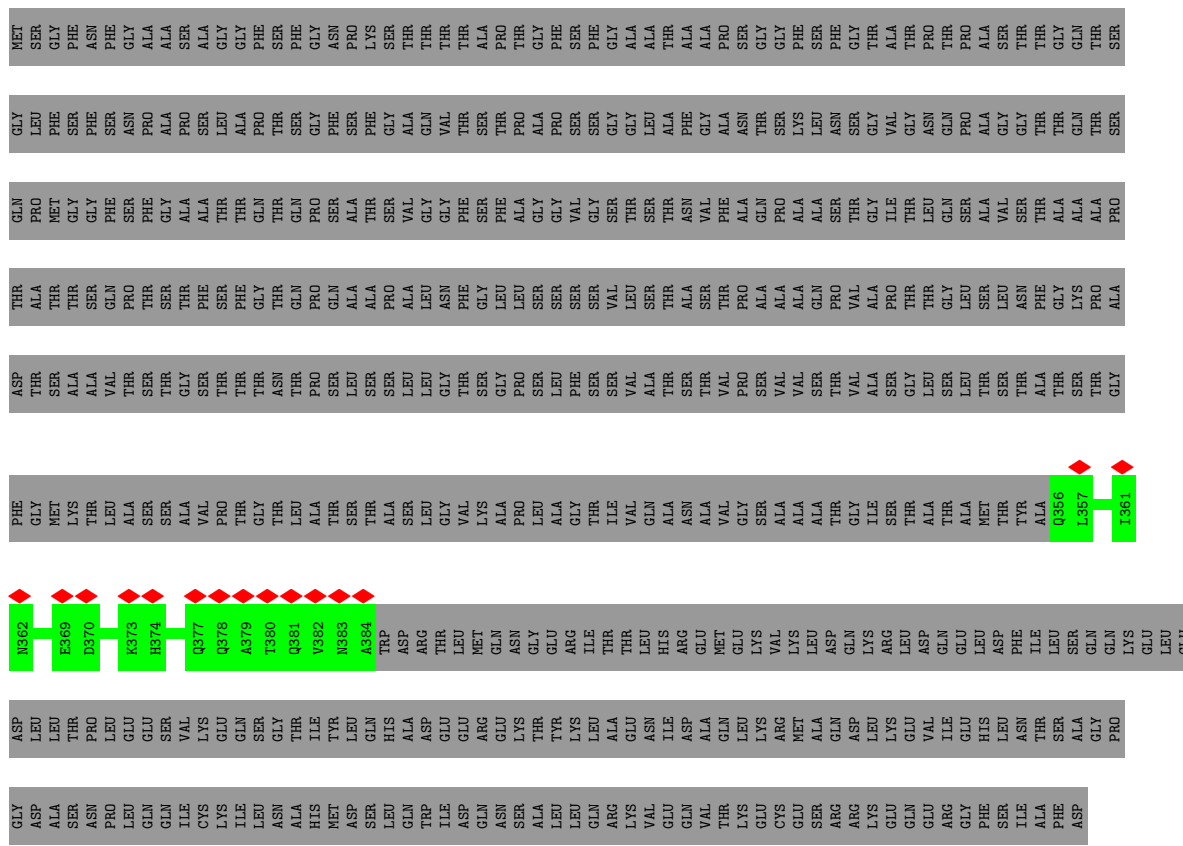
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Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
15	f	639	10336	3298	5128	928	954	28	0	0

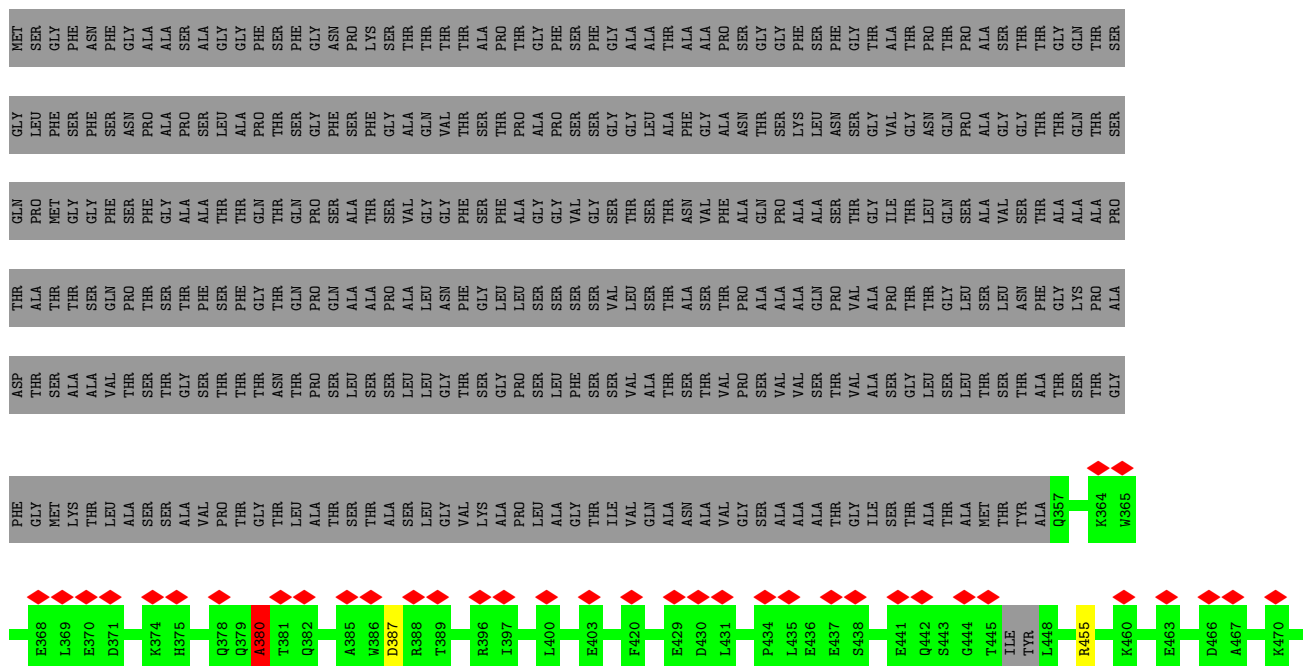








• Molecule 2: Nup62

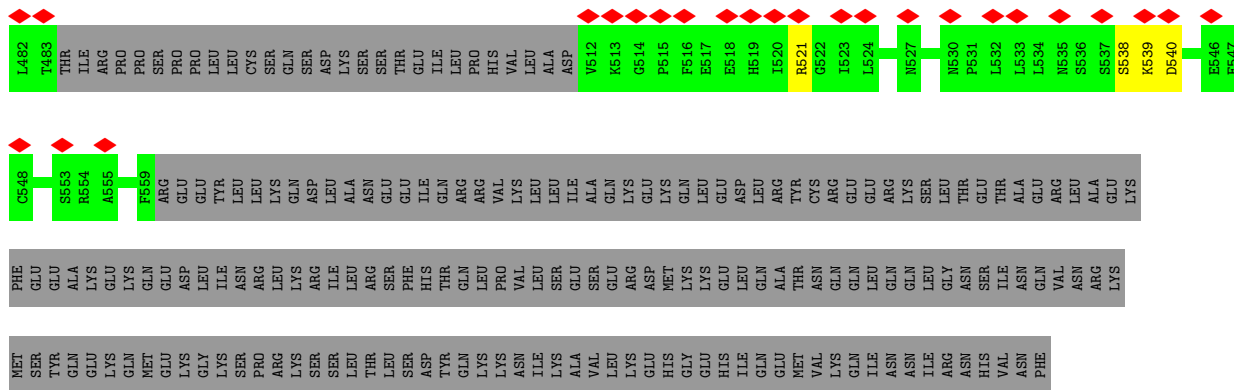




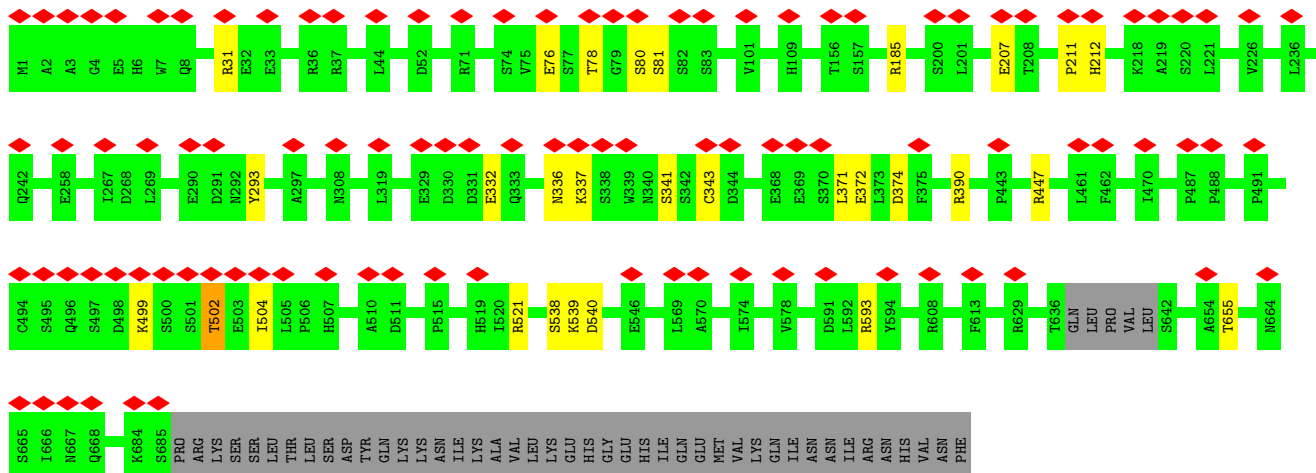
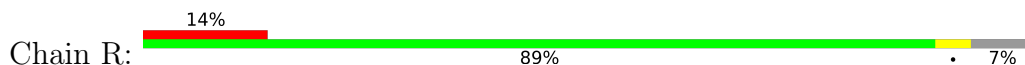








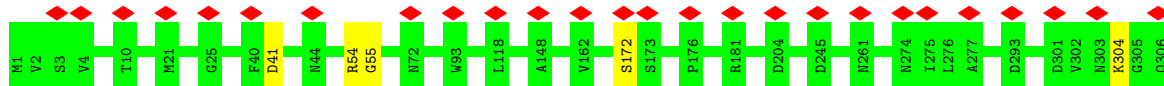
• Molecule 4: Nup88A protein



• Molecule 5: Protein SEC13 homolog

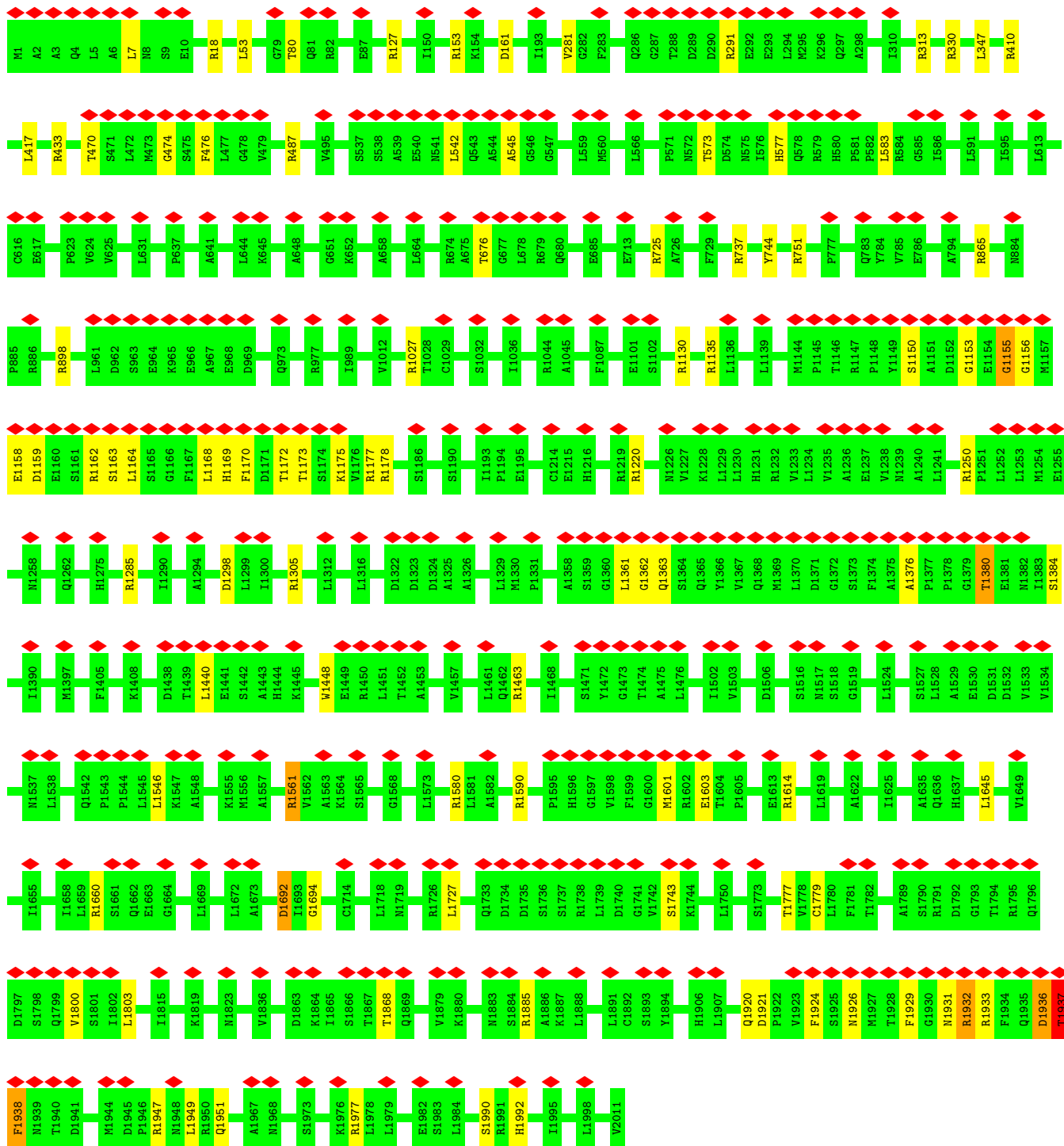


• Molecule 5: Protein SEC13 homolog

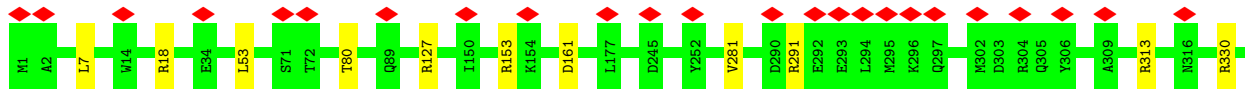
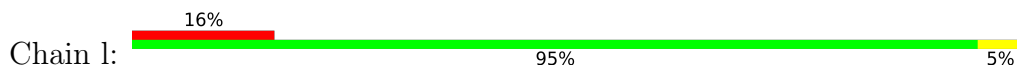


• Molecule 6: Nup205

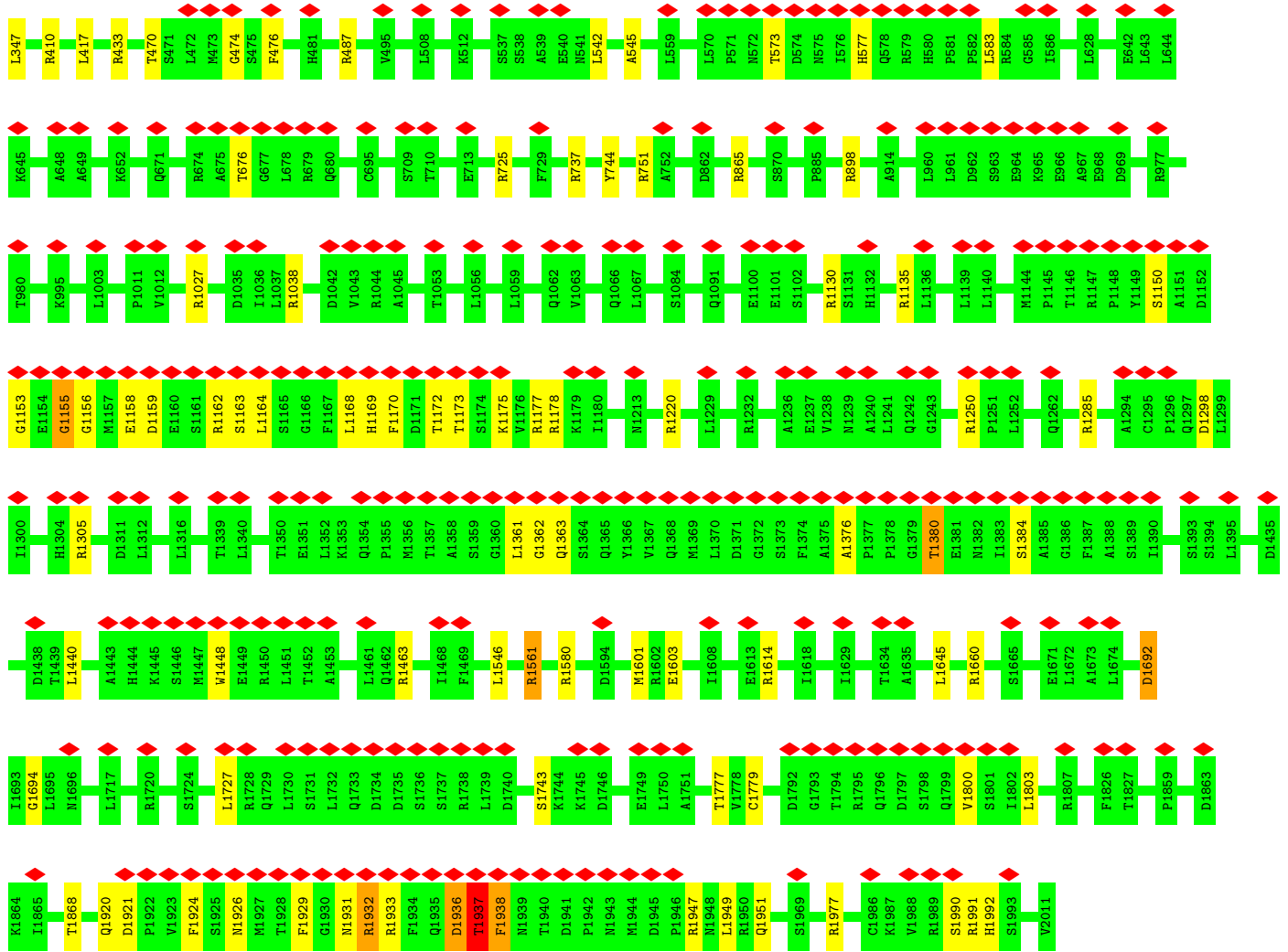




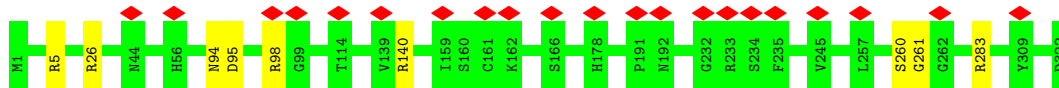
• Molecule 6: Nup205



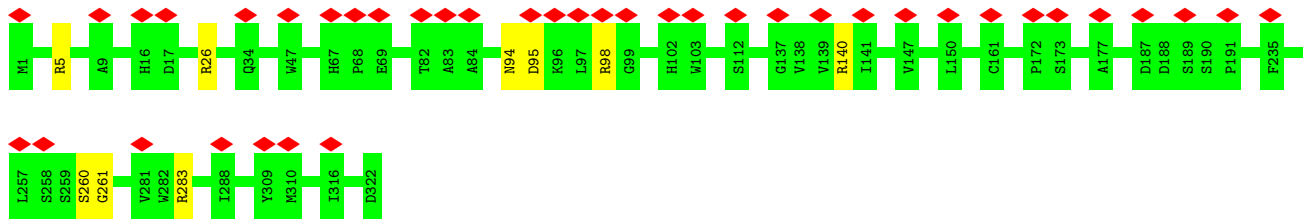




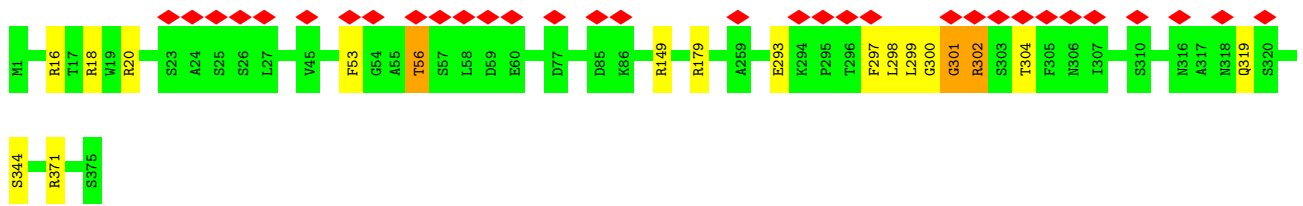
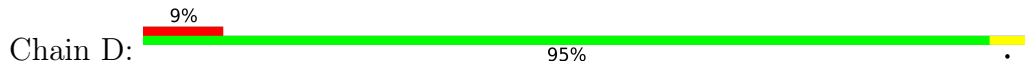
- Molecule 7: Nucleoporin SEH1-A



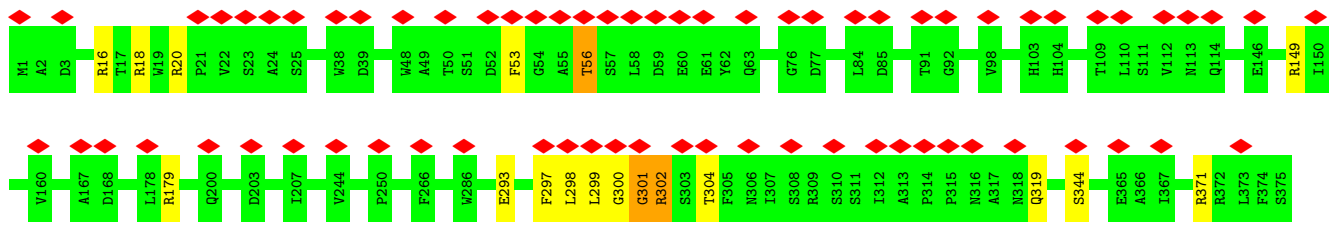
- Molecule 7: Nucleoporin SEH1-A



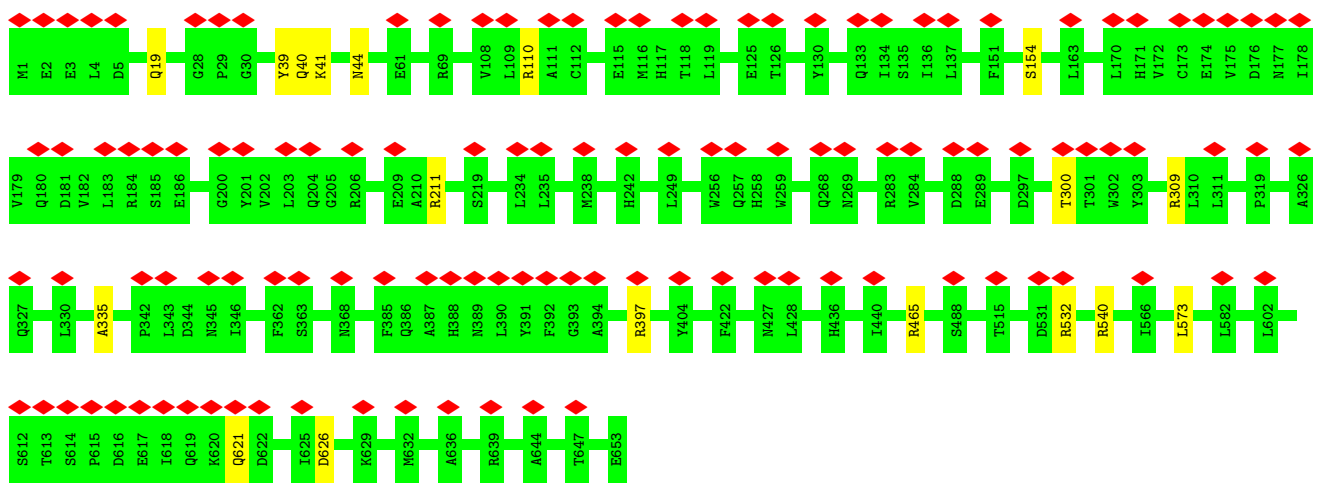
- Molecule 8: Nup42



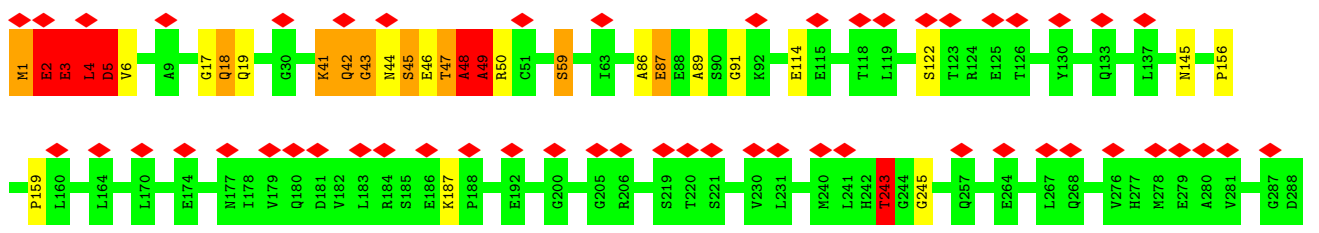
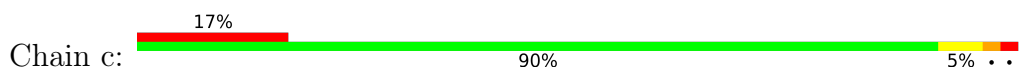
• Molecule 8: Nup42



• Molecule 9: Nuclear pore complex protein Nup85



• Molecule 9: Nuclear pore complex protein Nup85





















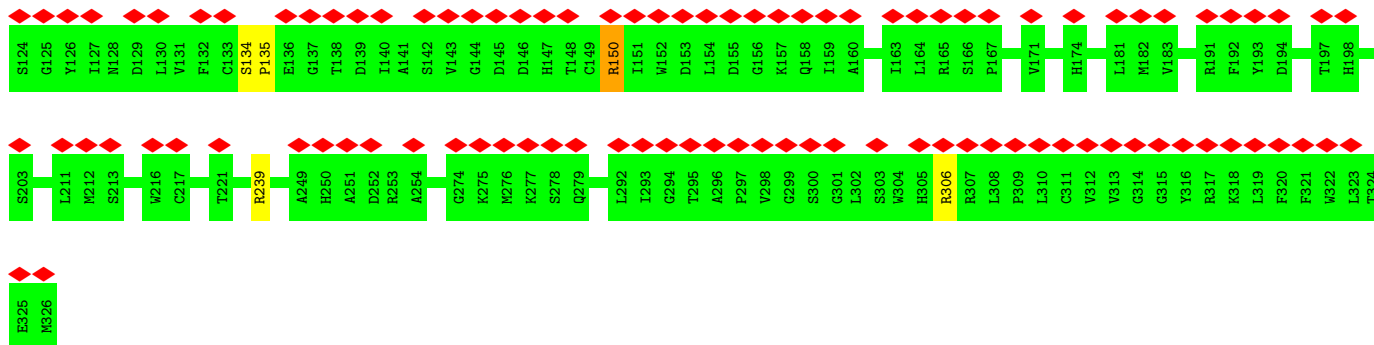




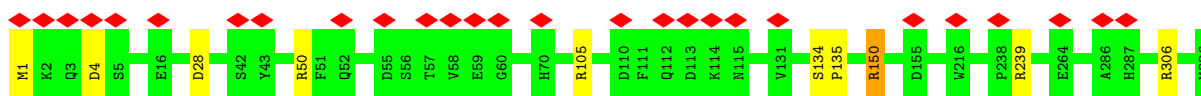




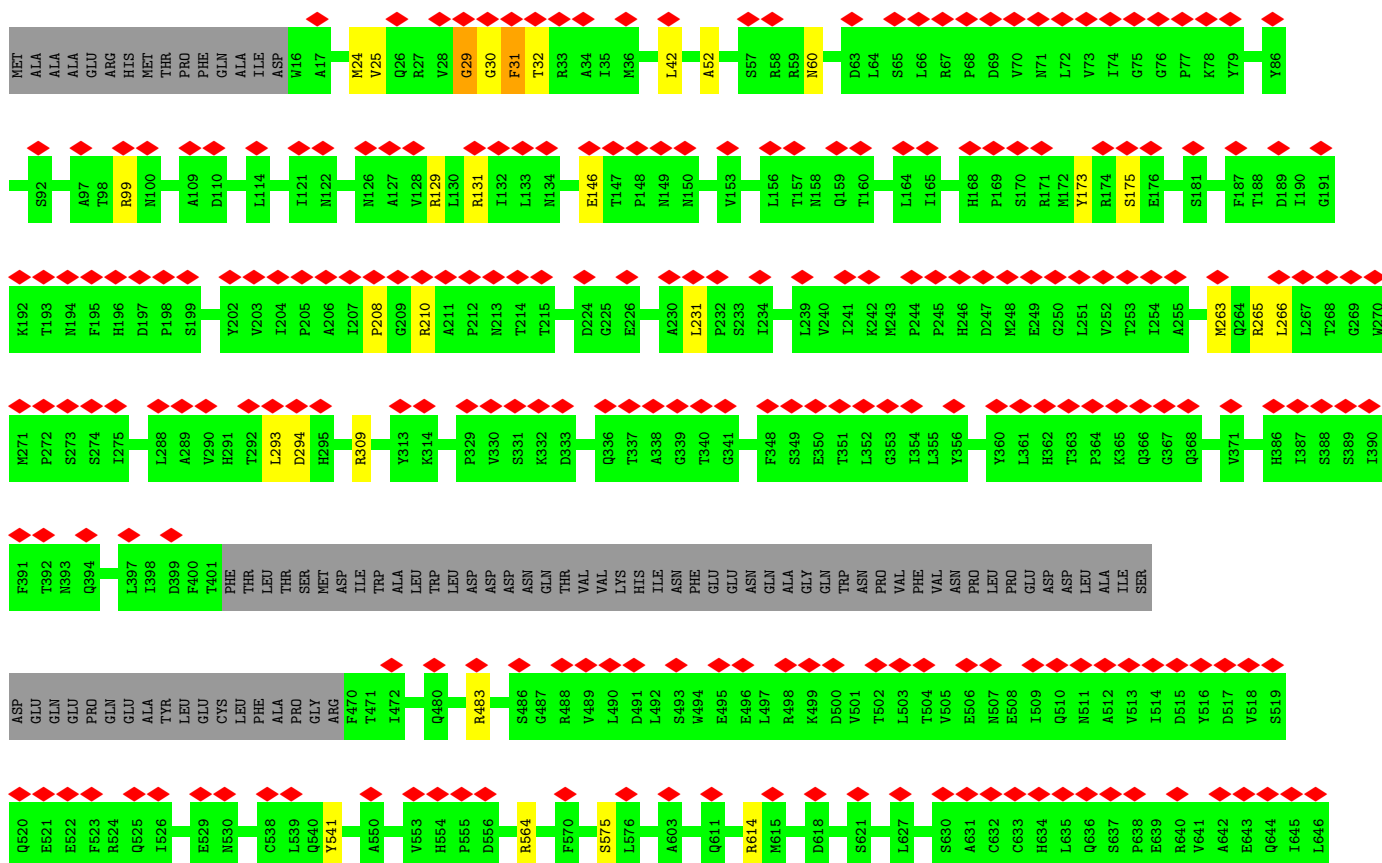
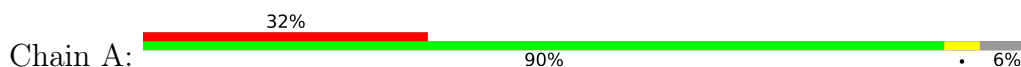




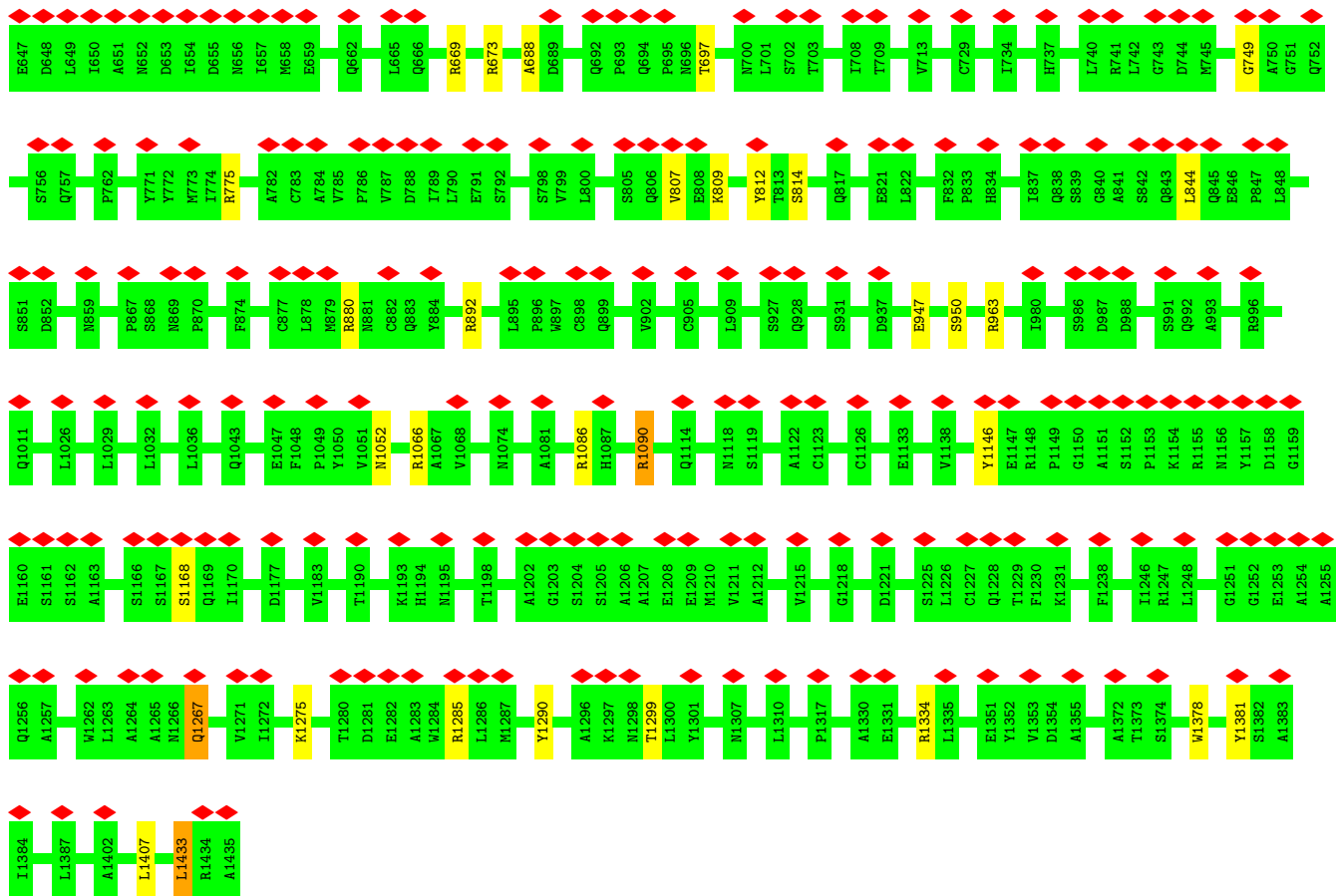
• Molecule 12: Nup37



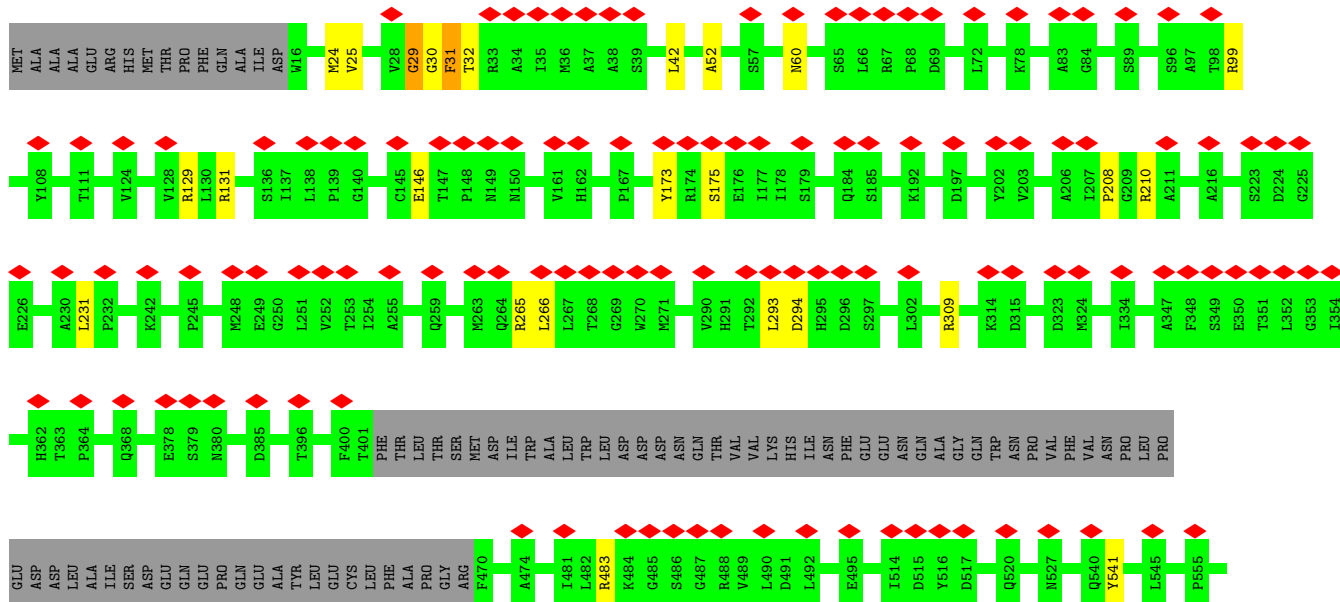
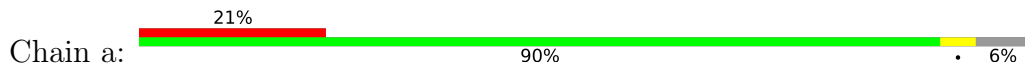
• Molecule 13: Nup160







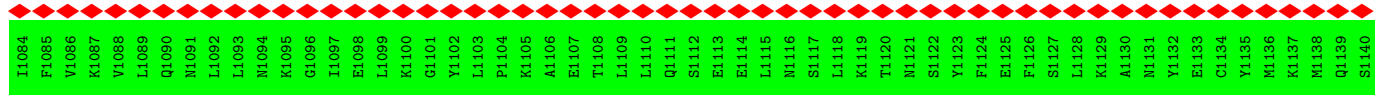
• Molecule 13: Nup160



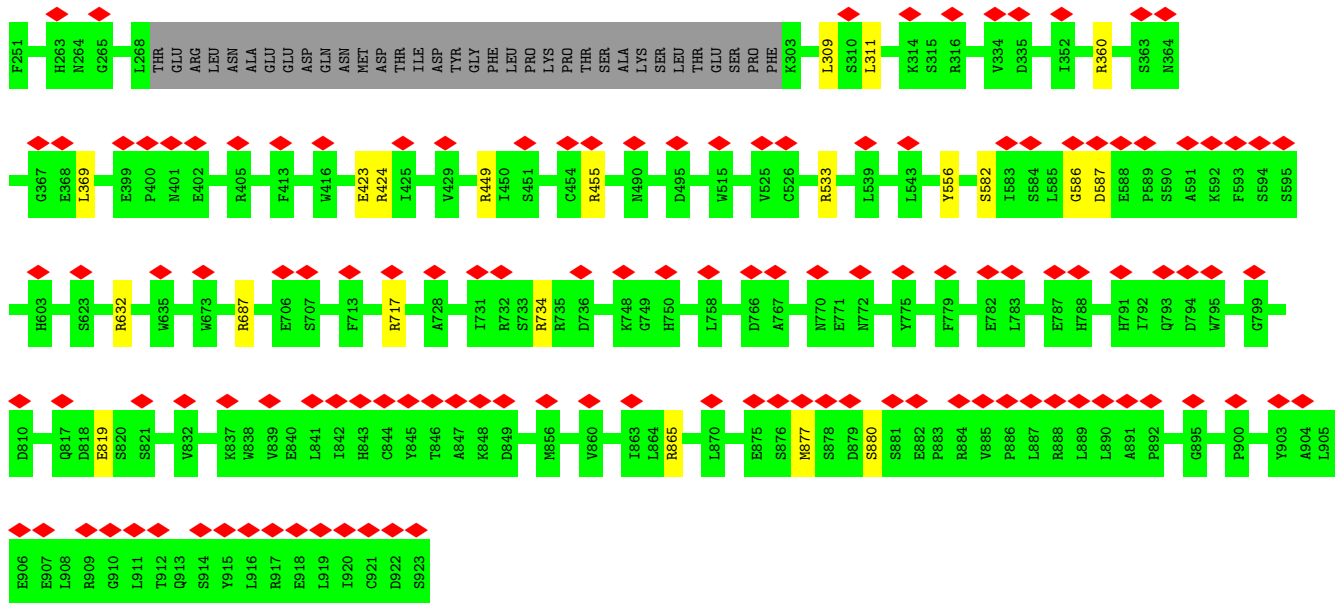
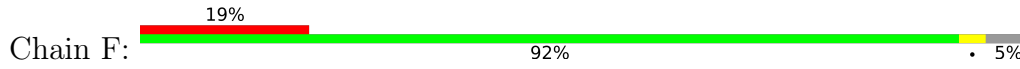




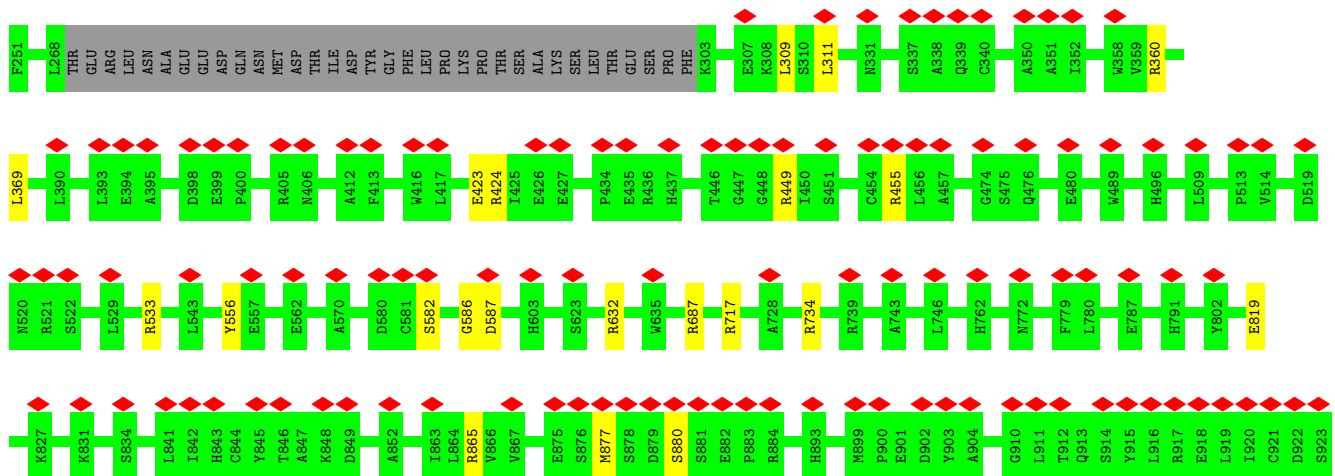
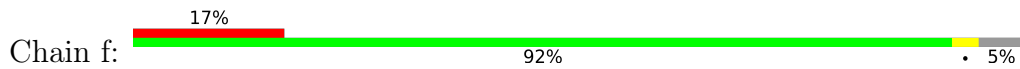
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L601	H602	Q603	V604	G605	L606	F607	S608	R609	L610	S611	T612	C613	Q614	T615	K616	G617	M618	L619	V620	A621	T622	R623	L624	L625	L626	S627	E628	H629	A630	E631	K632	L633	S634	A635	A636	L637	V638	L639	K640	M641	H642	I643	H644	K645	L646	P647	V648	L649	V650	M651	S652	A653	H654	Q655	F656	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	L684	L685	F686	E687	C688	L689	V690	D691	K692	E693	E694	A695	D696	L697	E698	S699	T700	S701	I702	D703	S704	V705	T706	W707	A708	M709	I710	V711	V712	M713	A714	M715	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	P745	E746	H747	V748	P749	M750	T751	A752	S753	S754	G755	T756	A757	G758	I759	R760	V761	E822	V763	T764	R765	Q766	H767	G768	I769	I770	L771	K772	V773	A774	P775	Q776	A777	D778	S779	G780
L781	R782	T783	L784	L785	L786	Q787	Q788	L789	A790	A791	L792	L793	N794	Y795	L796	L797	D798	D799	Y800	M801	T802	Q803	L804	K805	S806	L807	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	T836	L837	Q838	Q839	Y840
A841	W842	A843	S844	N845	L846	A847	E848	R849	Y850	C851	D852	F853	D854	L855	L856	W857	Q858	L859	C860	E861	M862	T863	D864	N865	Q866	S867	R868	L869	Q870	R871	Y872	M873	T874	L875	F876	A877	E878	Q879	N880	F881	S882	D883	F884	L885	F886	R887	W888	Y889	L890	E891	K892	G893	K894	R895	C896	K897	L898	L899	S900
Q901	P902	A903	S904	Q905	H906	G907	Q908	L909	A910	A911	F912	L913	Q914	A915	H916	D917	H918	L919	I920	S921	H922	H923	E924	L925	N926	S927	Q928	E929	F930	E931	K932	A933	H934	R935	T936	L937	Q938	T939	L940	A941	S883	F884	L885	F886	R887	F948	C949	K950	K951	K952	T953	L954	S955	S956	A951	A962	L963		
A964	S965	D966	F967	Q968	E969	D970	V971	L972	Q973	E974	K975	V976	E977	E978	I979	A980	E981	Q982	E983	H984	F985	L986	L987	H988	Q989	E990	T991	L992	P993	K994	K995	L996	L997	E998	E999	K1000	Q1001	L1002	D1003	L1004	N1005	A1006	M1007	P1008	V1009	L1010	A1011	P1012	F1013	Q1014	L1015	I1016	Q1017	L1018	Y1019	V1020	K1021	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	H1048	D1049	V1050	E1051	E1052	L1053	K1054	L1055	E1056	I1057	L1058	C1059	K1060	A1061	I1062	K1063	R1064	D1065	E1066	V1067	S1068	A1069	T1070	D1071	K1072	D1074	D1075	P1076	I1077	E1078	A1079	K1081	D1082	S1083		



• Molecule 15: Nuclear pore complex protein Nup96



• Molecule 15: Nuclear pore complex protein Nup96



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	333214	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	1.25	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	4.753	Depositor
Minimum map value	-0.227	Depositor
Average map value	0.018	Depositor
Map value standard deviation	0.092	Depositor
Recommended contour level	0.366	Depositor
Map size ( $\text{\AA}$ )	840.0, 840.0, 840.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	2.8, 2.8, 2.8	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	H	0.65	0/6553	0.91	21/8867 (0.2%)
1	h	0.65	0/6553	0.91	20/8867 (0.2%)
2	T	0.58	0/1086	0.80	2/1457 (0.1%)
2	t	0.58	0/247	0.75	0/333
3	S	0.78	1/1178 (0.1%)	1.06	3/1567 (0.2%)
3	s	0.58	0/258	0.71	0/343
4	R	0.63	0/5490	0.89	7/7427 (0.1%)
4	r	0.63	0/3755	0.91	5/5107 (0.1%)
5	G	0.60	0/2454	0.91	1/3349 (0.0%)
5	g	0.60	0/2454	0.91	1/3349 (0.0%)
6	L	0.65	0/16272	0.93	34/22021 (0.2%)
6	l	0.65	0/16272	0.94	34/22021 (0.2%)
7	E	0.61	0/2592	0.96	4/3515 (0.1%)
7	e	0.61	0/2592	0.96	5/3515 (0.1%)
8	D	0.61	0/2996	0.98	6/4074 (0.1%)
8	d	0.61	0/2996	0.98	6/4074 (0.1%)
9	C	0.64	0/5377	0.89	8/7265 (0.1%)
9	c	0.79	19/5376 (0.4%)	1.00	35/7265 (0.5%)
10	U	0.64	0/2977	0.85	2/4032 (0.0%)
11	M	0.65	0/6555	0.89	9/8864 (0.1%)
11	N	0.65	0/6555	0.89	9/8864 (0.1%)
11	O	0.65	0/6555	0.89	9/8864 (0.1%)
11	P	0.65	0/6555	0.89	9/8864 (0.1%)
11	Q	0.65	0/6555	0.89	9/8864 (0.1%)
12	B	0.65	0/2643	0.93	6/3587 (0.2%)
12	b	0.65	0/2643	0.93	6/3587 (0.2%)
13	A	0.64	0/10962	0.93	21/14884 (0.1%)
13	a	0.64	0/10962	0.93	21/14884 (0.1%)
14	I	0.63	0/5475	0.88	9/7398 (0.1%)
14	i	0.63	0/8561	0.89	9/11601 (0.1%)
15	F	0.65	0/5338	0.93	13/7245 (0.2%)
15	f	0.65	0/5338	0.93	13/7245 (0.2%)
All	All	0.65	20/172175 (0.0%)	0.92	337/233199 (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	H	0	1
1	h	0	1
2	T	0	1
4	R	0	4
4	r	0	3
6	L	0	18
6	l	0	18
8	D	0	7
8	d	0	7
9	C	0	2
9	c	0	41
10	U	0	1
11	M	0	3
11	N	0	3
11	O	0	3
11	P	0	3
11	Q	0	3
12	B	0	3
12	b	0	3
13	A	0	11
13	a	0	11
14	I	0	5
14	i	0	12
15	F	0	2
15	f	0	2
All	All	0	168

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	S	736	SER	C-N	16.30	1.71	1.34
9	c	615	PRO	N-CD	-11.91	1.31	1.47
9	c	568	PRO	N-CD	-9.19	1.34	1.47
9	c	393	GLY	C-N	9.02	1.54	1.34
9	c	335	ALA	C-N	8.94	1.49	1.33

The worst 5 of 337 bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	S	736	SER	O-C-N	-27.28	79.05	122.70
9	c	387	ALA	O-C-N	-20.77	89.47	122.70
9	c	2	GLU	O-C-N	-19.86	90.92	122.70
9	c	3	GLU	O-C-N	-18.08	93.77	122.70
9	c	48	ALA	O-C-N	-14.74	99.11	122.70

There are no chirality outliers.

5 of 168 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	117	LEU	Peptide
1	h	117	LEU	Peptide
4	r	336	ASN	Peptide
4	r	337	LYS	Peptide
4	r	539	LYS	Peptide

## 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 [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	H	787/916 (86%)	762 (97%)	17 (2%)	8 (1%)	15	54
1	h	787/916 (86%)	762 (97%)	17 (2%)	8 (1%)	15	54
2	T	126/547 (23%)	124 (98%)	1 (1%)	1 (1%)	19	60
2	t	27/547 (5%)	27 (100%)	0	0	100	100
3	S	136/2037 (7%)	134 (98%)	1 (1%)	1 (1%)	22	63
3	s	30/2037 (2%)	30 (100%)	0	0	100	100
4	R	674/728 (93%)	627 (93%)	30 (4%)	17 (2%)	5	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	r	464/728 (64%)	433 (93%)	19 (4%)	12 (3%)	5	31
5	G	304/306 (99%)	293 (96%)	8 (3%)	3 (1%)	15	54
5	g	304/306 (99%)	294 (97%)	7 (2%)	3 (1%)	15	54
6	L	2009/2011 (100%)	1889 (94%)	93 (5%)	27 (1%)	12	48
6	l	2009/2011 (100%)	1889 (94%)	93 (5%)	27 (1%)	12	48
7	E	320/322 (99%)	305 (95%)	10 (3%)	5 (2%)	9	44
7	e	320/322 (99%)	305 (95%)	10 (3%)	5 (2%)	9	44
8	D	373/375 (100%)	345 (92%)	20 (5%)	8 (2%)	7	36
8	d	373/375 (100%)	345 (92%)	20 (5%)	8 (2%)	7	36
9	C	651/653 (100%)	630 (97%)	15 (2%)	6 (1%)	17	57
9	c	651/653 (100%)	614 (94%)	20 (3%)	17 (3%)	5	31
10	U	356/1388 (26%)	352 (99%)	4 (1%)	0	100	100
11	M	796/2905 (27%)	768 (96%)	21 (3%)	7 (1%)	17	57
11	N	796/2905 (27%)	768 (96%)	21 (3%)	7 (1%)	17	57
11	O	796/2905 (27%)	768 (96%)	21 (3%)	7 (1%)	17	57
11	P	796/2905 (27%)	768 (96%)	21 (3%)	7 (1%)	17	57
11	Q	796/2905 (27%)	768 (96%)	21 (3%)	7 (1%)	17	57
12	B	324/326 (99%)	307 (95%)	15 (5%)	2 (1%)	25	66
12	b	324/326 (99%)	307 (95%)	15 (5%)	2 (1%)	25	66
13	A	1350/1435 (94%)	1268 (94%)	61 (4%)	21 (2%)	9	44
13	a	1350/1435 (94%)	1268 (94%)	61 (4%)	21 (2%)	9	44
14	I	669/1140 (59%)	639 (96%)	19 (3%)	11 (2%)	9	44
14	i	1060/1140 (93%)	997 (94%)	41 (4%)	22 (2%)	7	36
15	F	635/673 (94%)	615 (97%)	16 (2%)	4 (1%)	25	66
15	f	635/673 (94%)	615 (97%)	16 (2%)	4 (1%)	25	66
All	All	21028/38851 (54%)	20016 (95%)	734 (4%)	278 (1%)	16	48

5 of 278 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	770	GLN
1	h	770	GLN
4	r	332	GLU

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Mol	Chain	Res	Type
4	r	540	ASP
5	g	172	SER

### 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	H	704/816 (86%)	695 (99%)	9 (1%)	69	82
1	h	704/816 (86%)	695 (99%)	9 (1%)	69	82
2	T	120/429 (28%)	119 (99%)	1 (1%)	81	89
2	t	27/429 (6%)	27 (100%)	0	100	100
3	S	130/1634 (8%)	130 (100%)	0	100	100
3	s	29/1634 (2%)	29 (100%)	0	100	100
4	R	614/660 (93%)	612 (100%)	2 (0%)	92	95
4	r	424/660 (64%)	424 (100%)	0	100	100
5	G	261/261 (100%)	260 (100%)	1 (0%)	91	94
5	g	261/261 (100%)	260 (100%)	1 (0%)	91	94
6	L	1779/1779 (100%)	1745 (98%)	34 (2%)	57	75
6	l	1779/1779 (100%)	1745 (98%)	34 (2%)	57	75
7	E	280/280 (100%)	280 (100%)	0	100	100
7	e	280/280 (100%)	280 (100%)	0	100	100
8	D	329/329 (100%)	328 (100%)	1 (0%)	92	95
8	d	329/329 (100%)	328 (100%)	1 (0%)	92	95
9	C	580/580 (100%)	578 (100%)	2 (0%)	92	95
9	c	580/580 (100%)	576 (99%)	4 (1%)	84	90
10	U	327/1219 (27%)	327 (100%)	0	100	100
11	M	716/2521 (28%)	714 (100%)	2 (0%)	92	95
11	N	716/2521 (28%)	714 (100%)	2 (0%)	92	95
11	O	716/2521 (28%)	714 (100%)	2 (0%)	92	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	P	716/2521 (28%)	714 (100%)	2 (0%)	92	95
11	Q	716/2521 (28%)	714 (100%)	2 (0%)	92	95
12	B	275/275 (100%)	274 (100%)	1 (0%)	91	94
12	b	275/275 (100%)	274 (100%)	1 (0%)	91	94
13	A	1184/1256 (94%)	1168 (99%)	16 (1%)	67	80
13	a	1184/1256 (94%)	1169 (99%)	15 (1%)	69	82
14	I	600/993 (60%)	598 (100%)	2 (0%)	92	95
14	i	935/993 (94%)	929 (99%)	6 (1%)	86	92
15	F	571/602 (95%)	568 (100%)	3 (0%)	88	93
15	f	571/602 (95%)	568 (100%)	3 (0%)	88	93
All	All	18712/33612 (56%)	18556 (99%)	156 (1%)	82	89

5 of 156 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	A	266	LEU
15	F	369	LEU
13	A	814	SER
13	a	266	LEU
14	i	158	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 149 such sidechains are listed below:

Mol	Chain	Res	Type
13	a	1267	GLN
2	T	392	GLN
14	I	767	HIS
15	f	791	HIS
9	c	171	HIS

### 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
3	S	2
4	R	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R	544:PRO	C	545:PRO	N	4.80
1	S	728:SER	C	729:ARG	N	3.21
1	S	736:SER	C	737:GLU	N	1.71

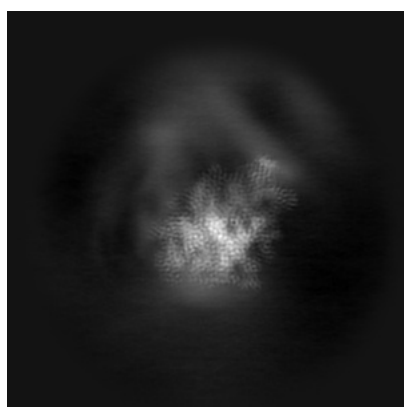
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25817. These allow visual inspection of the internal detail of the map and identification of artifacts.

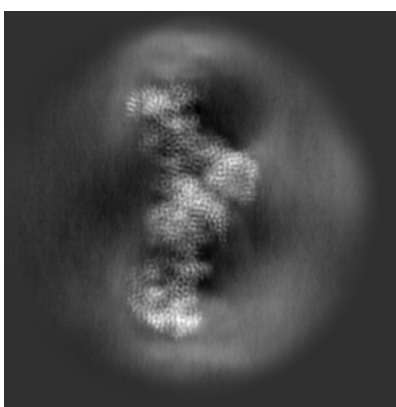
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

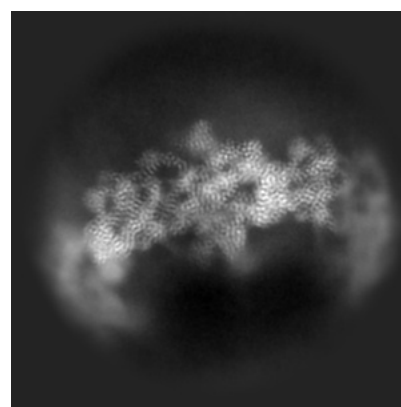
#### 6.1.1 Primary map



X



Y

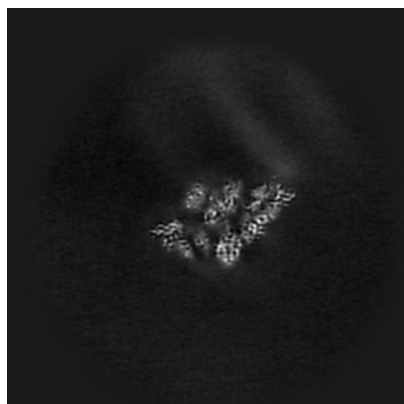


Z

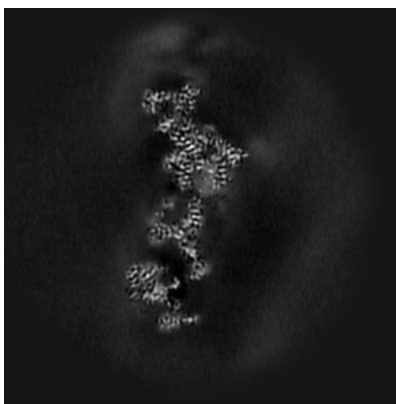
The images above show the map projected in three orthogonal directions.

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

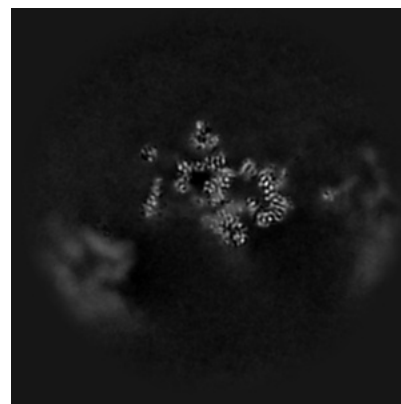
#### 6.2.1 Primary map



X Index: 150



Y Index: 150

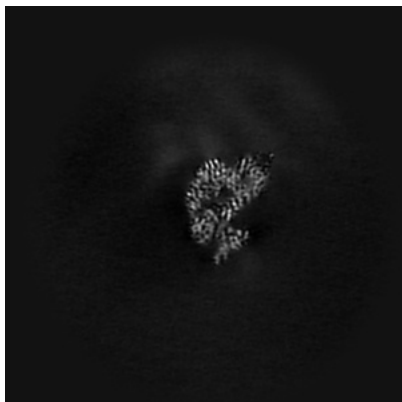


Z Index: 150

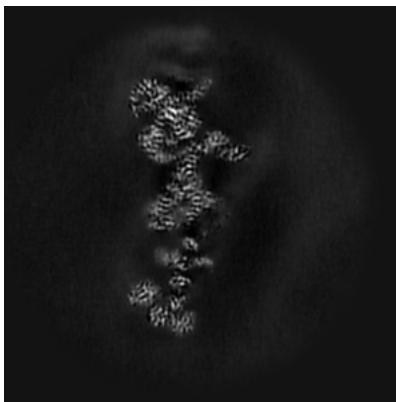
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

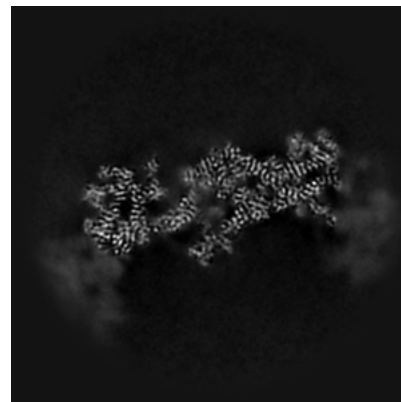
### 6.3.1 Primary map



X Index: 189



Y Index: 161

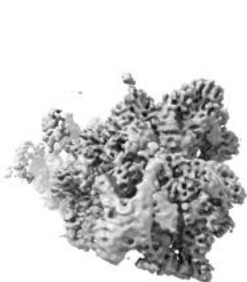


Z Index: 130

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

## 6.5 Mask visualisation

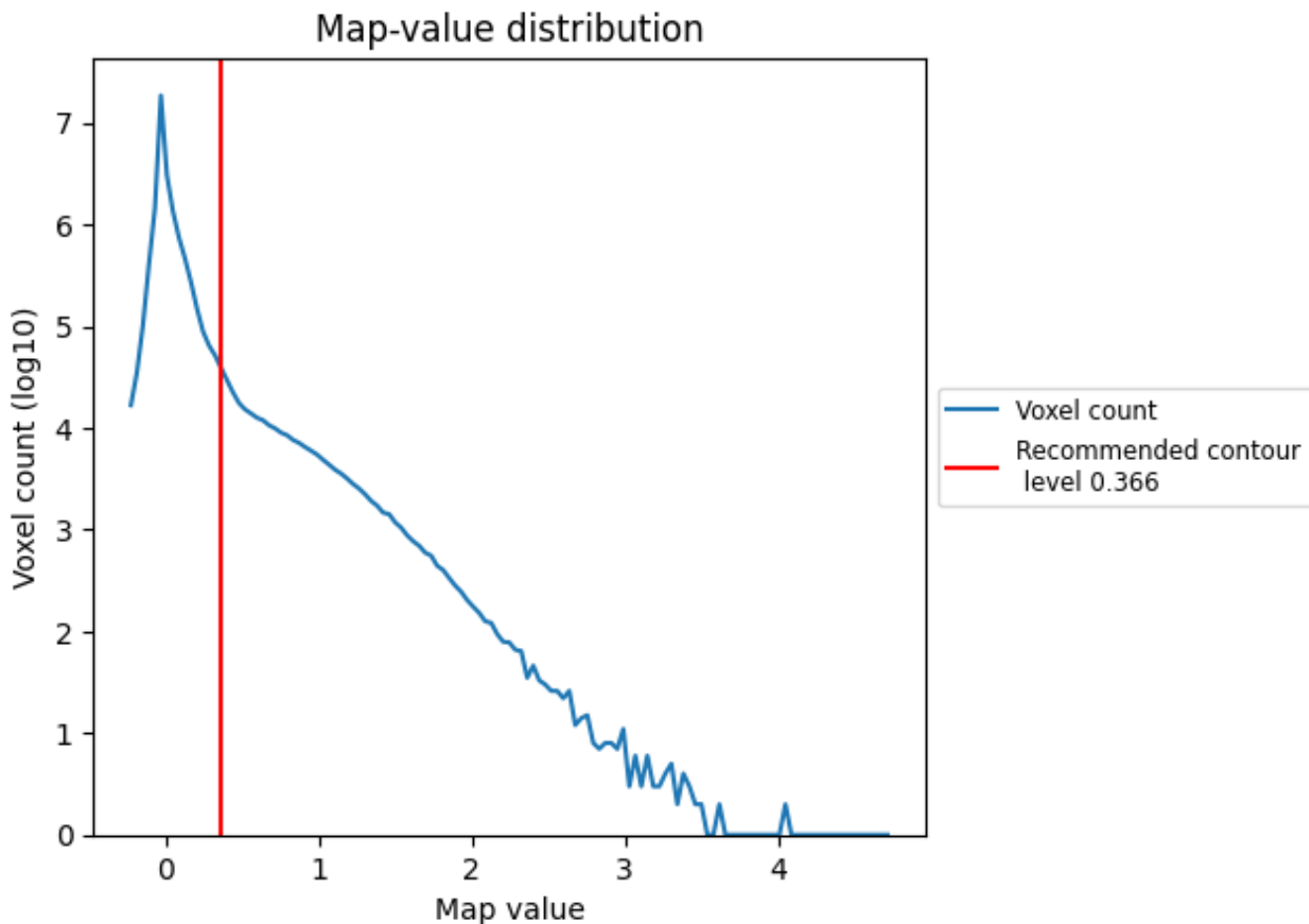
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

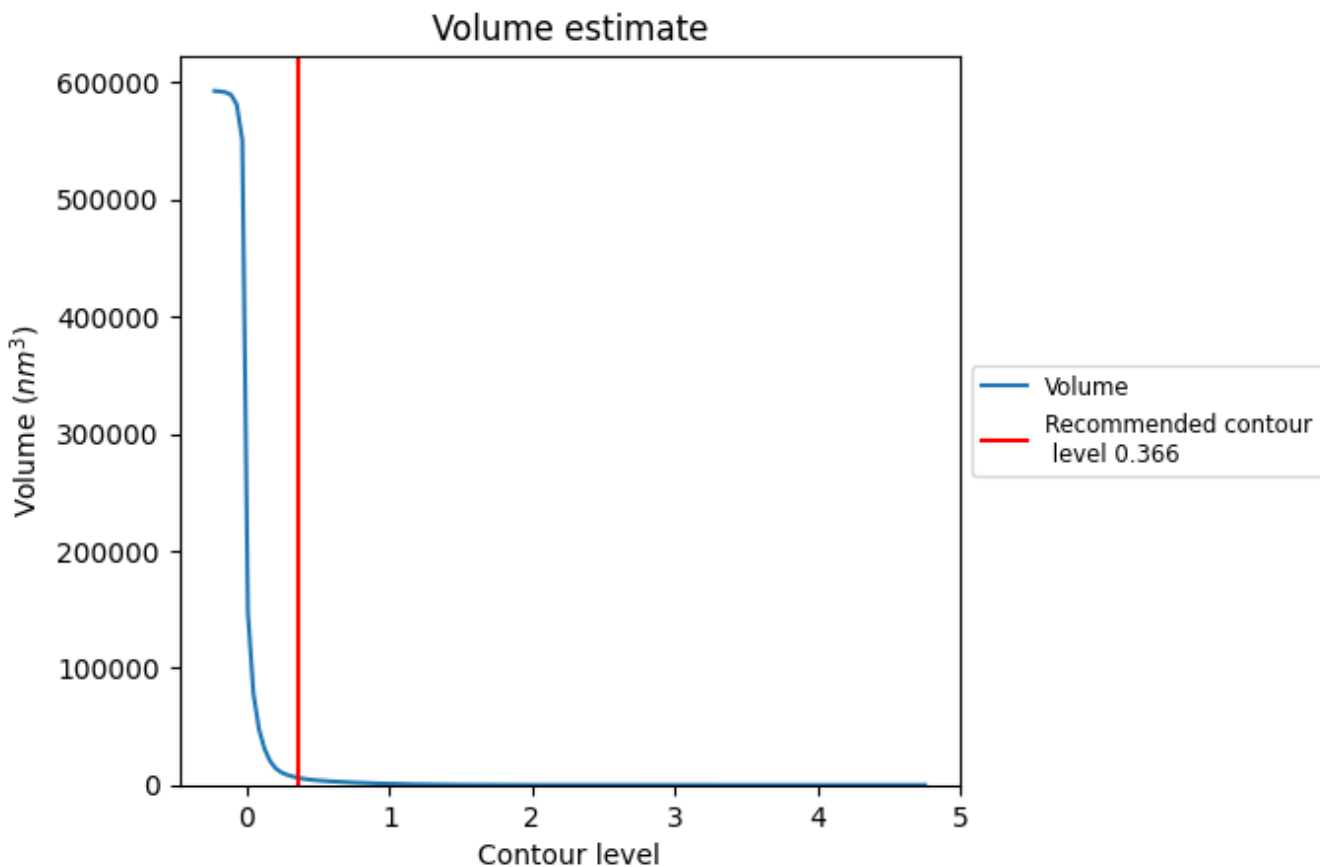
This section contains the results of statistical analysis of the map.

### 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.

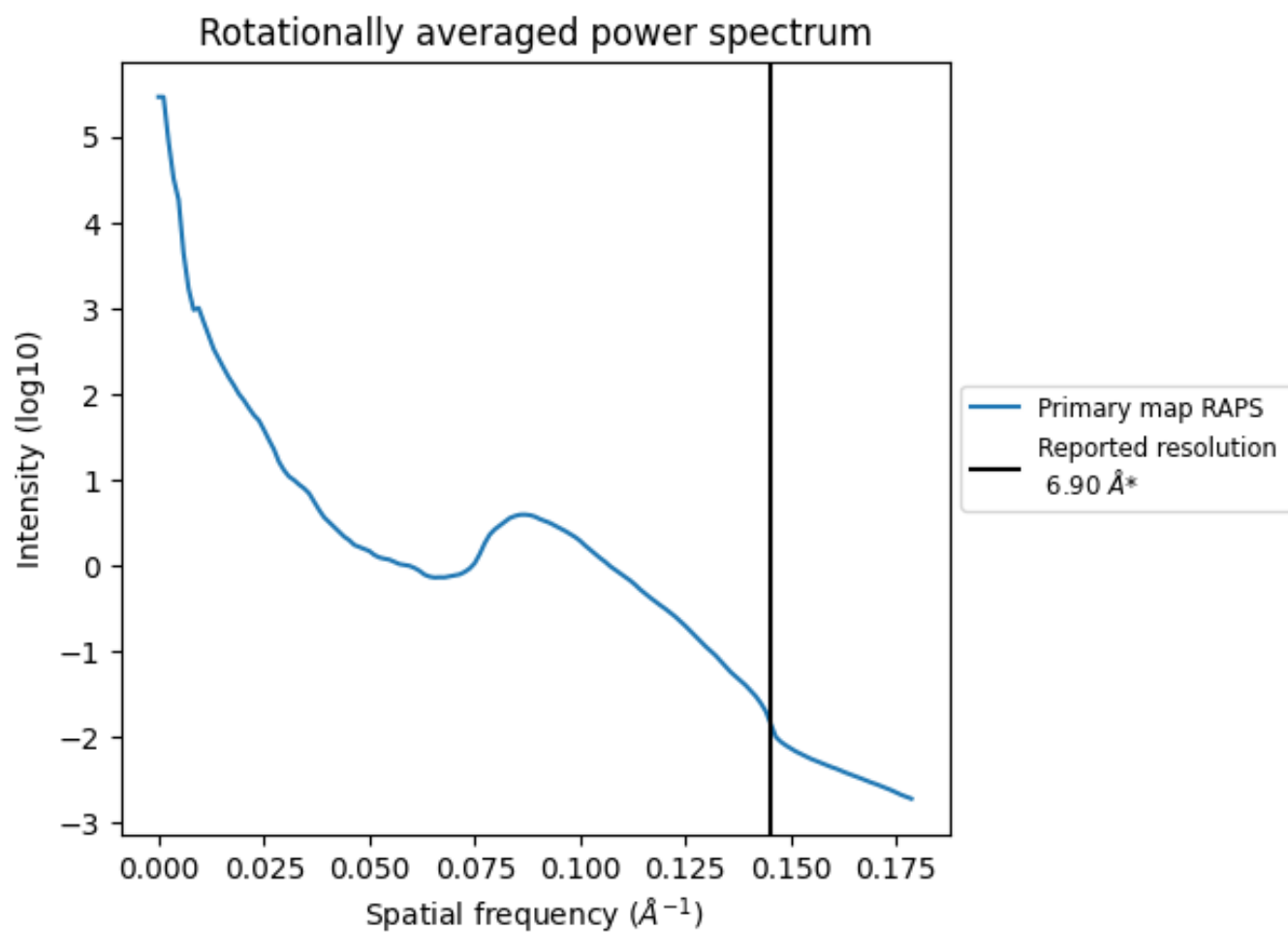
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5957  $\text{nm}^3$ ; this corresponds to an approximate mass of 5381 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 0.145 Å<sup>-1</sup>

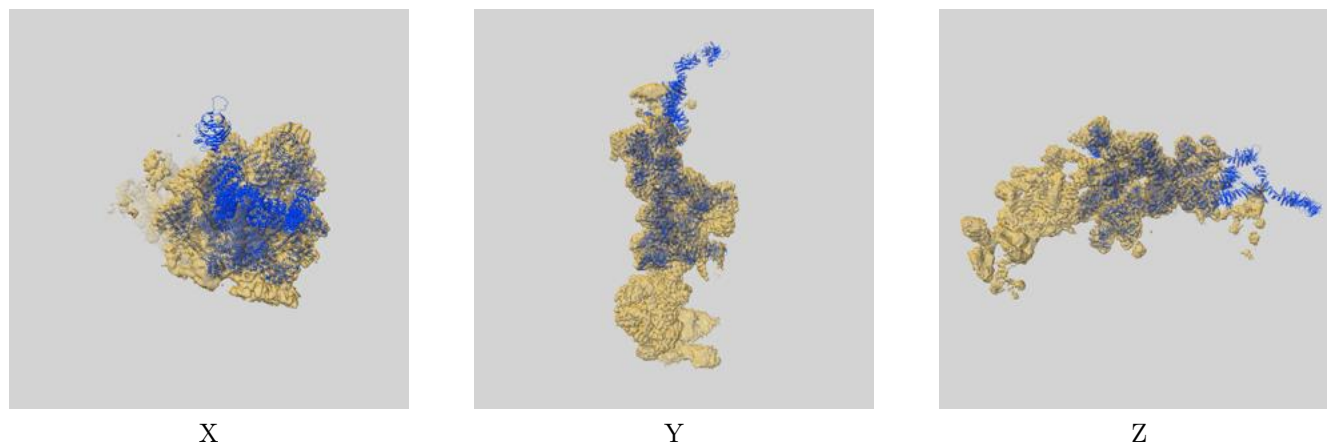
## 8 Fourier-Shell correlation

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

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

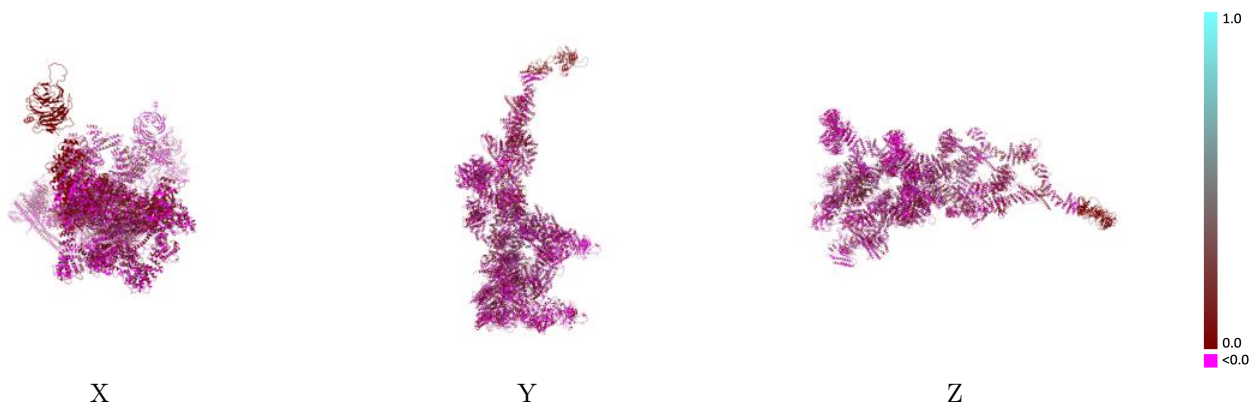
This section contains information regarding the fit between EMDB map EMD-25817 and PDB model 7TDZ. Per-residue inclusion information can be found in section 3 on page 8.

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



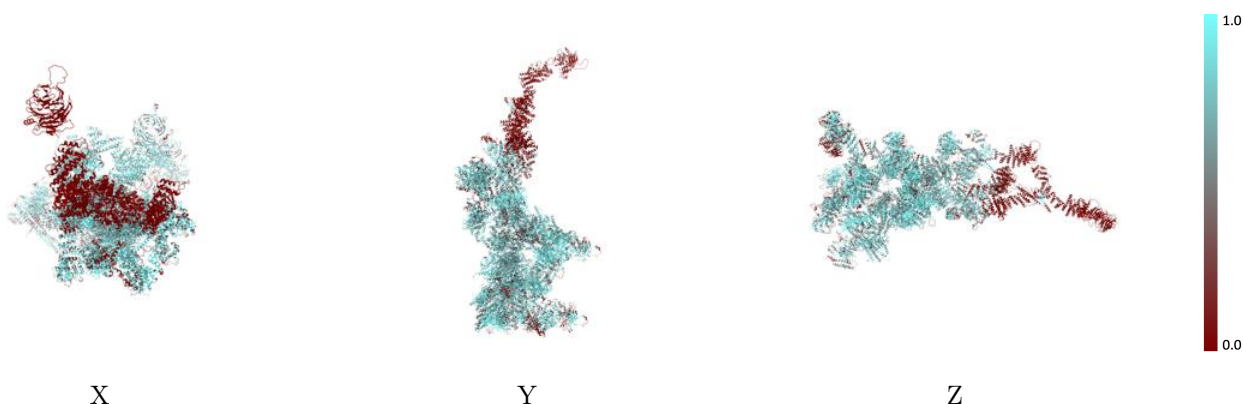
The images above show the 3D surface view of the map at the recommended contour level 0.366 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



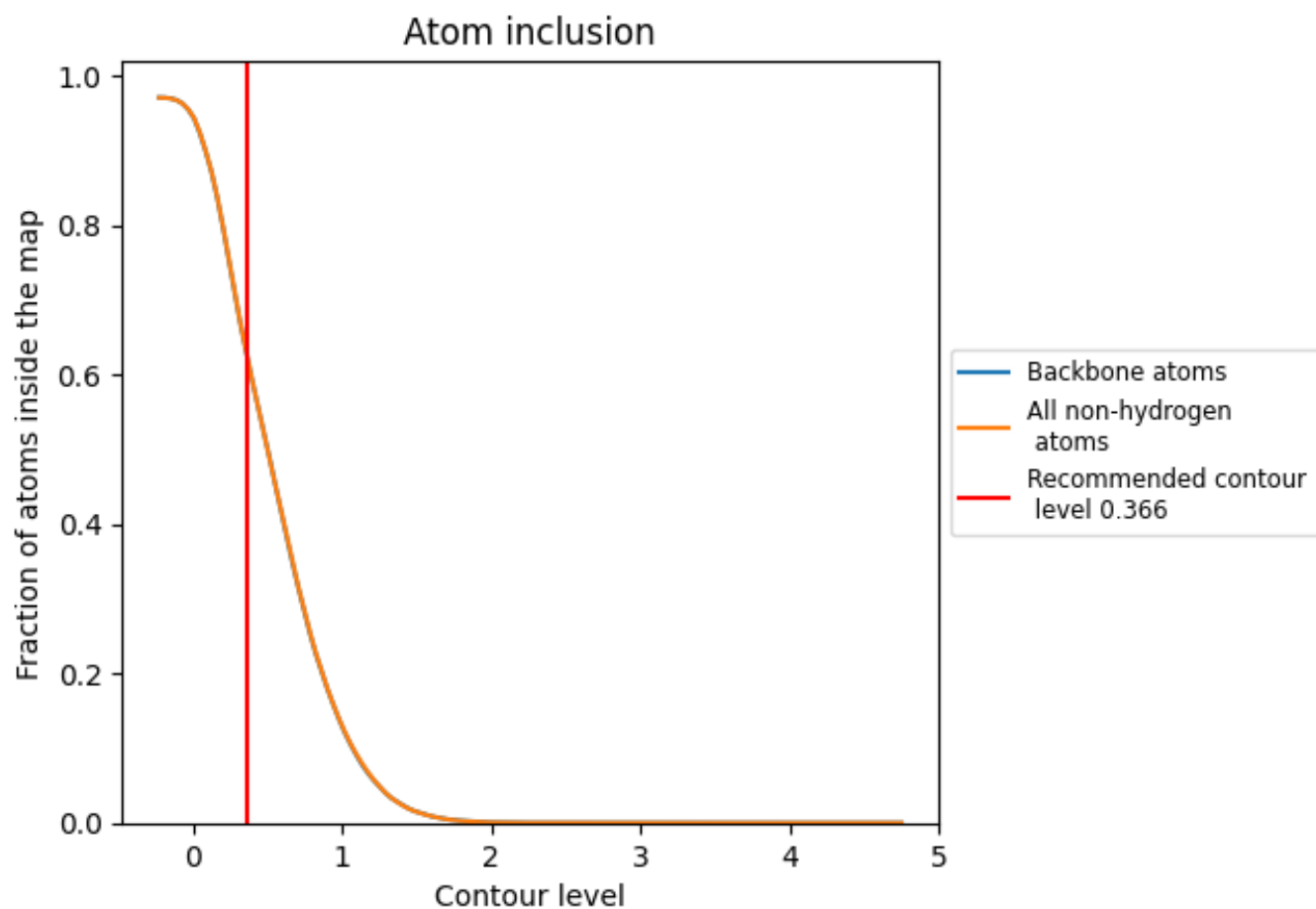
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.366).



































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 62% 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 (0.366) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6220	 0.0290
A	 0.6037	 -0.0080
B	 0.3254	 -0.0010
C	 0.7385	 0.0430
D	 0.8671	 0.0250
E	 0.8309	 0.0590
F	 0.7001	 0.0550
G	 0.8474	 0.0510
H	 0.6747	 0.0520
I	 0.2369	 0.0510
L	 0.7364	 0.0390
M	 0.7048	 0.0300
N	 0.7149	 0.0430
O	 0.6407	 0.0060
P	 0.2043	 0.0450
Q	 0.6769	 0.0090
R	 0.7803	 0.0310
S	 0.6603	 0.0230
T	 0.6098	 0.0250
U	 0.8410	 0.0100
a	 0.7142	 -0.0090
b	 0.8655	 0.0210
c	 0.7182	 0.0410
d	 0.7220	 0.0360
e	 0.7793	 0.0410
f	 0.7048	 0.0480
g	 0.8342	 0.0730
h	 0.1750	 0.0450
i	 0.0047	 0.0110
l	 0.7798	 0.0320
r	 0.6062	 0.0290
s	 0.5099	 -0.0110
t	 0.4403	 -0.0510

