



wwPDB EM Validation Summary Report ⓘ

Mar 16, 2026 – 06:38 PM UTC

PDB ID : 7N9F / pdb_00007n9f
EMDB ID : EMD-24258
Title : Structure of the in situ yeast NPC
Authors : Villa, E.; Singh, D.; Ludtke, S.J.; Akey, C.W.; Rout, M.P.; Echeverria, I.;
Suslov, S.
Deposited on : 2021-06-17
Resolution : 37.00 Å(reported)

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

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

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:

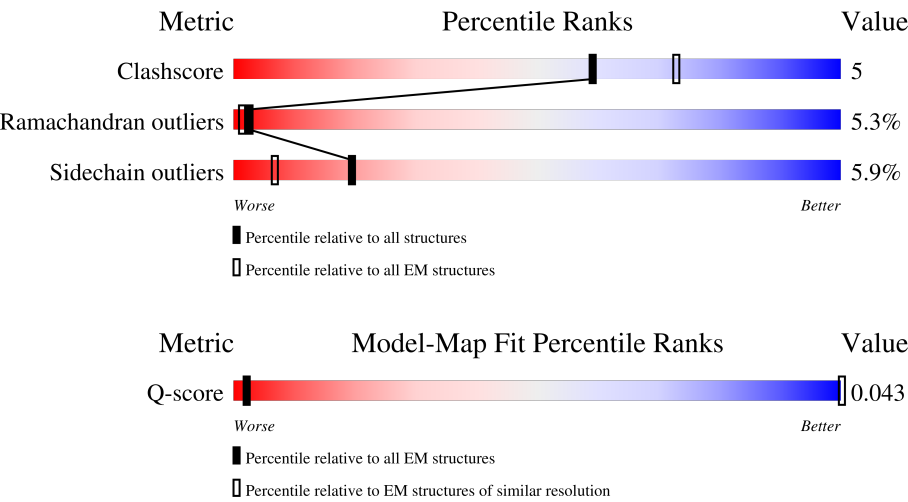
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 37.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	3 (37.00 - 37.00)

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	0	1502	
1	Y	1502	
2	1	1391	
2	Z	1391	





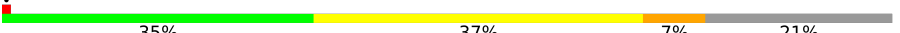






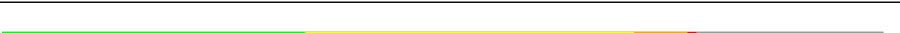













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Mol	Chain	Length	Quality of chain
3	5	36	100%
3	6	36	92% 8%
4	A	823	9% 10% . 80%
4	D	823	8% 10% . 80%
4	G	823	8% 9% . 80%
4	J	823	9% 9% . 80%
4	y	823	13% 10% 77%
4	z	823	14% 9% 77%
5	B	541	16% 21% . . 60%
5	E	541	17% 17% 6% 60%
5	H	541	17% 19% . . 60%
5	K	541	19% 18% . . 60%
6	C	472	13% 20% . 65%
6	F	472	17% 17% . 65%
6	I	472	15% 17% . 65%
6	L	472	16% 17% . . 65%
7	M	1683	34% 47% 9% . 10%
7	O	1683	36% 43% 9% . 10%
8	N	1655	31% 41% 9% . 18%
8	P	1655	30% 41% 10% . 18%
9	Q	839	35% 41% 6% 18%
9	R	839	34% 42% 8% . 16%
9	S	839	35% 40% 7% 18%
9	T	839	34% 42% 7% . 16%
10	U	475	6% 12% . 80%

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Mol	Chain	Length	Quality of chain
10	W	475	 80%
11	V	528	 82%
11	X	528	 82%
12	u	713	 19%
12	v	713	 21%
13	w	1460	 87%
13	x	1460	 86%
14	a	1037	 11%
14	h	1037	 9%
15	b	744	 9%
15	i	744	 11%
16	c	712	 21%
16	j	712	 21%
17	d	297	 8%
17	k	297	 8%
18	e	349	 13%
18	l	349	 12%
19	f	726	 11%
19	m	726	 11%
20	g	1157	 8%
20	n	1157	 8%
21	o	92	 7%
21	p	92	 7%
21	q	92	 7%
21	r	92	 7%

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Mol	Chain	Length	Quality of chain
21	s	92	<div><div></div><div>40%48%<div><div></div><div></div><div></div></div>7%</div></div>
21	t	92	<div><div></div><div>39%47%<div><div></div><div></div><div></div></div>7%7%</div></div>

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 212962 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 Nucleoporin NUP170.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	1085	Total	C	N	O	S	0	0
			8762	5674	1424	1636	28		
1	Y	1086	Total	C	N	O	S	0	0
			8770	5679	1425	1637	29		

- Molecule 2 is a protein called Nucleoporin NUP157.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	1113	Total	C	N	O	S	0	0
			8919	5719	1479	1693	28		
2	Z	1111	Total	C	N	O	S	0	0
			8906	5710	1477	1691	28		

- Molecule 3 is a protein called orphans bound to Nup192 NTD.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	5	36	Total	C	N	O	0	0
			181	108	36	37		
3	6	36	Total	C	N	O	0	0
			181	108	36	37		

- Molecule 4 is a protein called Nucleoporin NSP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	163	Total	C	N	O	S	0	0
			1315	814	220	280	1		
4	D	163	Total	C	N	O	S	0	0
			1315	814	220	280	1		
4	G	164	Total	C	N	O	S	0	0
			1321	817	221	282	1		
4	J	164	Total	C	N	O	S	0	0
			1321	817	221	282	1		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	y	190	Total	C	N	O	0	0
			946	566	190	190		
4	z	193	Total	C	N	O	0	0
			962	575	193	194		

- Molecule 5 is a protein called Nucleoporin NUP57.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	217	Total	C	N	O	S	0	0
			1771	1115	317	336	3		
5	E	217	Total	C	N	O	S	0	0
			1771	1115	317	336	3		
5	H	217	Total	C	N	O	S	0	0
			1771	1115	317	336	3		
5	K	217	Total	C	N	O	S	0	0
			1771	1115	317	336	3		

- Molecule 6 is a protein called Nucleoporin NUP49/NSP49.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	166	Total	C	N	O	S	0	0
			1347	863	217	265	2		
6	F	167	Total	C	N	O	S	0	0
			1351	865	218	266	2		
6	I	166	Total	C	N	O	S	0	0
			1347	863	217	265	2		
6	L	167	Total	C	N	O	S	0	0
			1351	865	218	266	2		

- Molecule 7 is a protein called Nucleoporin NUP192.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	1521	Total	C	N	O	S	0	0
			11909	7694	1943	2241	31		
7	O	1520	Total	C	N	O	S	0	0
			11902	7689	1942	2240	31		

- Molecule 8 is a protein called Nucleoporin NUP188.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	1360	Total	C	N	O	S	0	0
			10971	7162	1746	2038	25		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	P	1360	Total	C	N	O	S	0	0
			10971	7162	1746	2038	25		

- Molecule 9 is a protein called Nucleoporin NIC96.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Q	688	Total	C	N	O	S	0	0
			5184	3294	894	979	17		
9	R	708	Total	C	N	O	S	0	0
			5287	3357	914	999	17		
9	S	690	Total	C	N	O	S	0	0
			5197	3303	896	981	17		
9	T	708	Total	C	N	O	S	0	0
			5287	3357	914	999	17		

- Molecule 10 is a protein called Nucleoporin NUP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	U	94	Total	C	N	O	S	0	0
			745	486	120	137	2		
10	W	94	Total	C	N	O	S	0	0
			745	486	120	137	2		

- Molecule 11 is a protein called Nucleoporin ASM4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	V	94	Total	C	N	O	S	0	0
			739	475	122	139	3		
11	X	94	Total	C	N	O	S	0	0
			739	475	122	139	3		

- Molecule 12 is a protein called Nucleoporin NUP82.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	u	581	Total	C	N	O	S	0	0
			4214	2673	708	821	12		
12	v	564	Total	C	N	O	S	0	0
			4063	2579	681	791	12		

- Molecule 13 is a protein called Nucleoporin NUP159.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	w	195	Total	C	N	O	S	0	0
			1088	664	206	216	2		
13	x	198	Total	C	N	O	S	0	0
			1106	676	209	219	2		

- Molecule 14 is a protein called Nucleoporin NUP120.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	h	1006	Total	C	N	O	S	0	0
			8279	5346	1334	1566	33		
14	a	1006	Total	C	N	O	S	0	0
			8279	5346	1334	1566	33		

- Molecule 15 is a protein called Nucleoporin NUP85.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	i	663	Total	C	N	O	S	0	0
			5327	3431	849	1019	28		
15	b	675	Total	C	N	O	S	0	0
			5424	3493	863	1038	30		

- Molecule 16 is a protein called Nucleoporin 145c.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	j	559	Total	C	N	O	S	0	0
			4520	2884	750	869	17		
16	c	559	Total	C	N	O	S	0	0
			4520	2884	750	869	17		

- Molecule 17 is a protein called Protein transport protein SEC13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	k	274	Total	C	N	O	S	0	0
			2160	1379	369	409	3		
17	d	274	Total	C	N	O	S	0	0
			2160	1379	369	409	3		

- Molecule 18 is a protein called Nucleoporin SEH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	l	307	Total	C	N	O	S	0	0
			2438	1543	422	462	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
18	e	303	Total	C	N	O	S	0	0
			2407	1524	415	457	11		

- Molecule 19 is a protein called Nucleoporin NUP84.

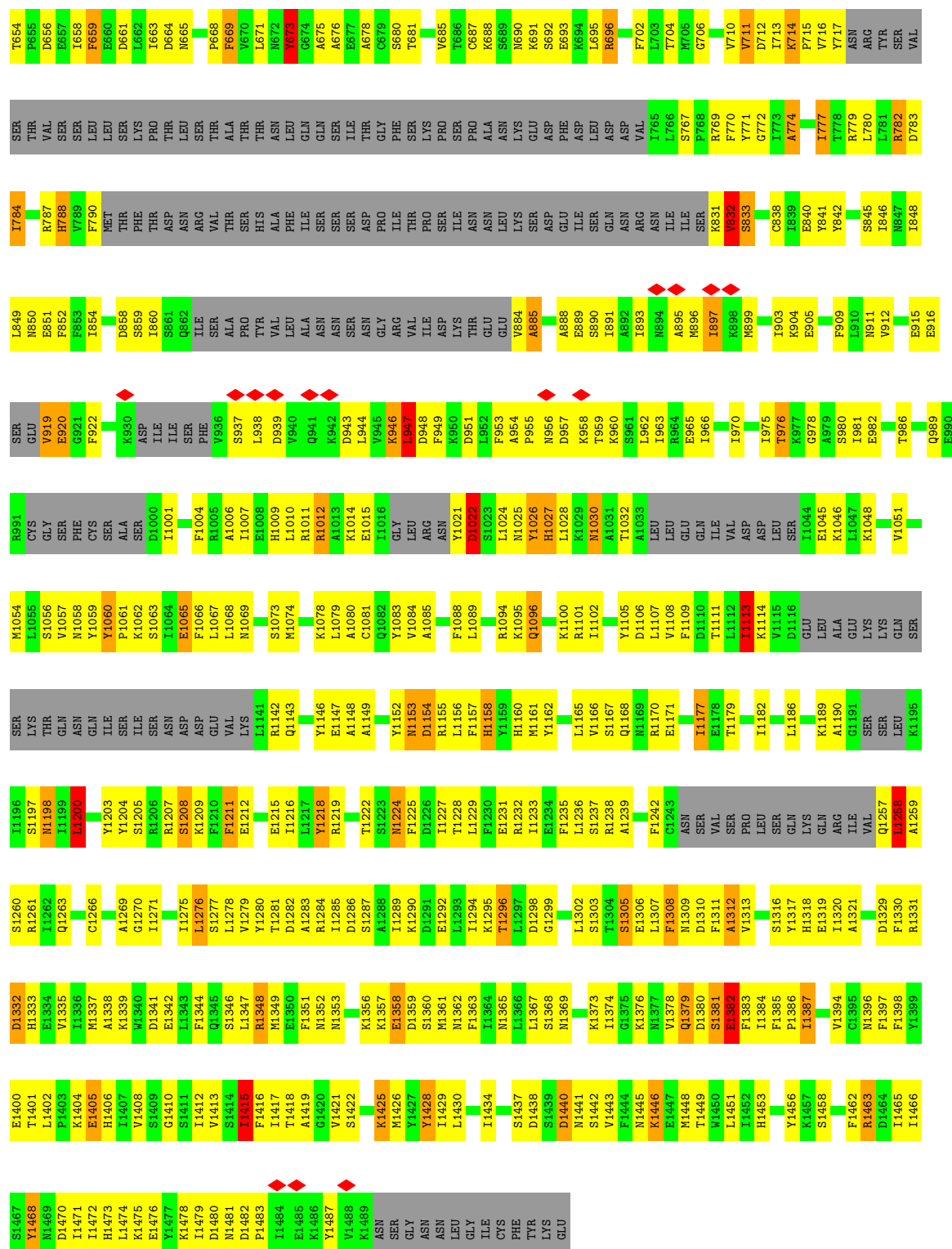
Mol	Chain	Residues	Atoms					AltConf	Trace
19	m	649	Total	C	N	O	S	0	0
			5261	3370	866	1011	14		
19	f	649	Total	C	N	O	S	0	0
			5261	3370	866	1011	14		

- Molecule 20 is a protein called Nucleoporin NUP133.

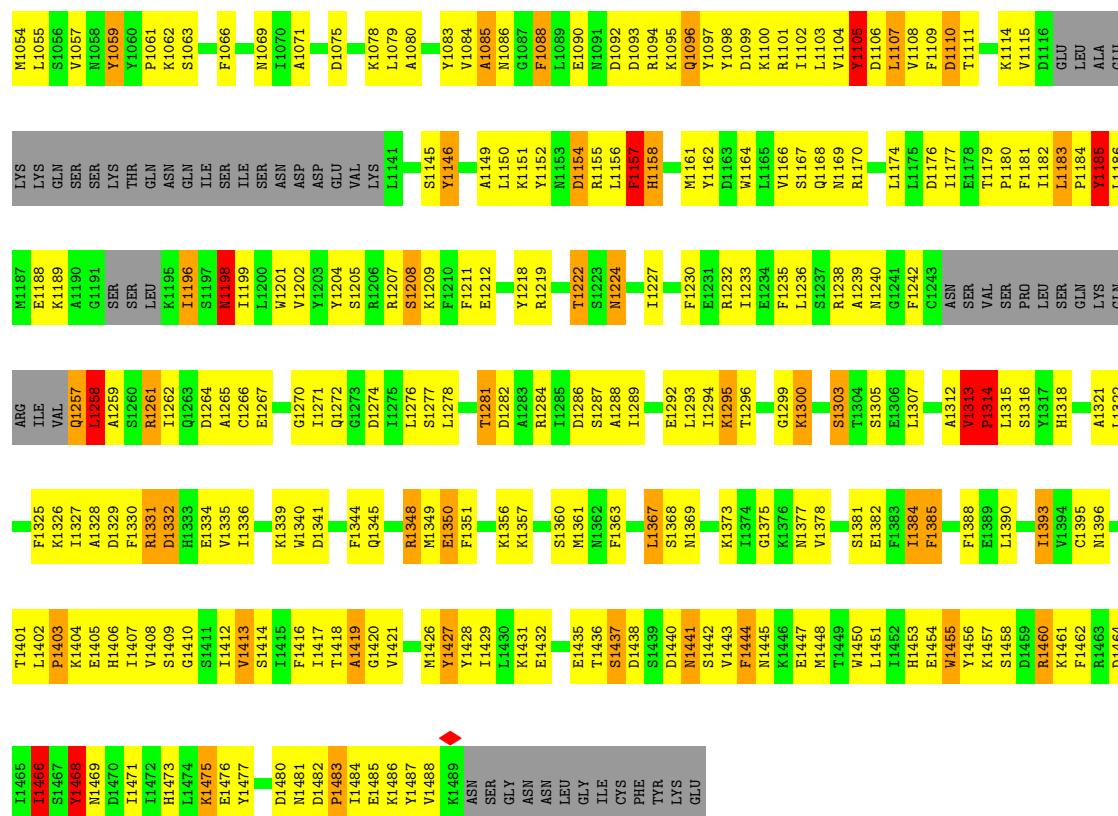
Mol	Chain	Residues	Atoms					AltConf	Trace
20	n	1062	Total	C	N	O	S	0	0
			8627	5541	1393	1664	29		
20	g	1062	Total	C	N	O	S	0	0
			8627	5541	1393	1664	29		

- Molecule 21 is a protein called Dynein light chain 1, cytoplasmic.

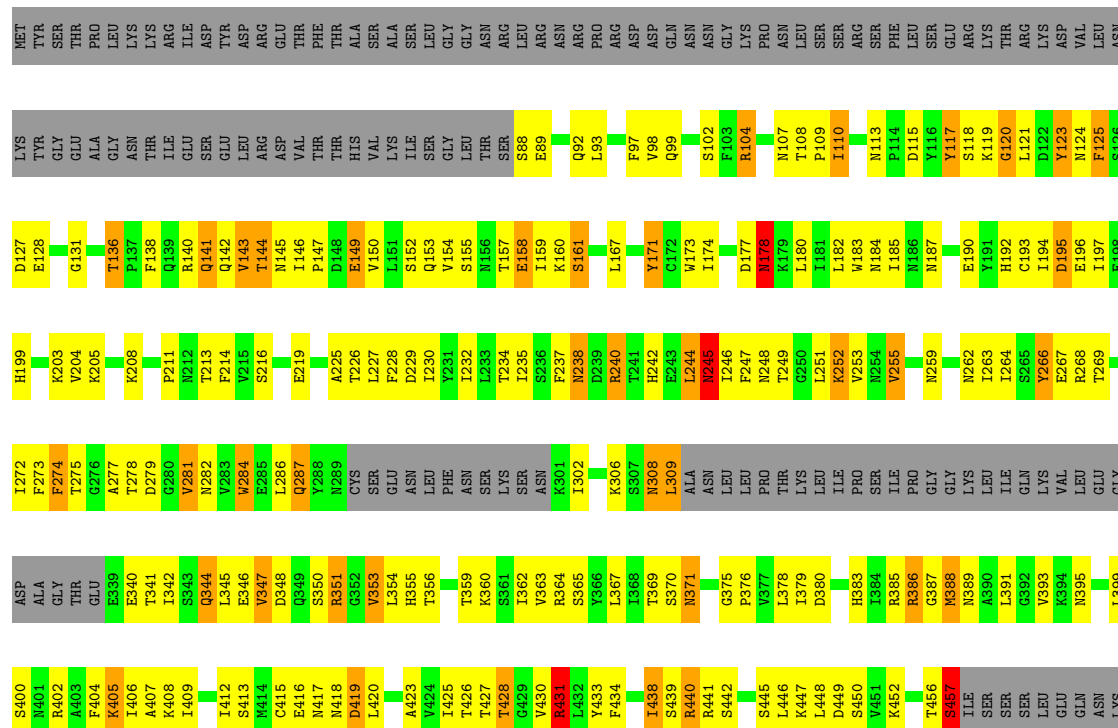
Mol	Chain	Residues	Atoms				AltConf	Trace
21	o	86	Total	C	N	O	0	0
			691	453	111	127		
21	p	86	Total	C	N	O	0	0
			691	453	111	127		
21	q	86	Total	C	N	O	0	0
			691	453	111	127		
21	r	86	Total	C	N	O	0	0
			691	453	111	127		
21	s	86	Total	C	N	O	0	0
			691	453	111	127		
21	t	86	Total	C	N	O	0	0
			691	453	111	127		

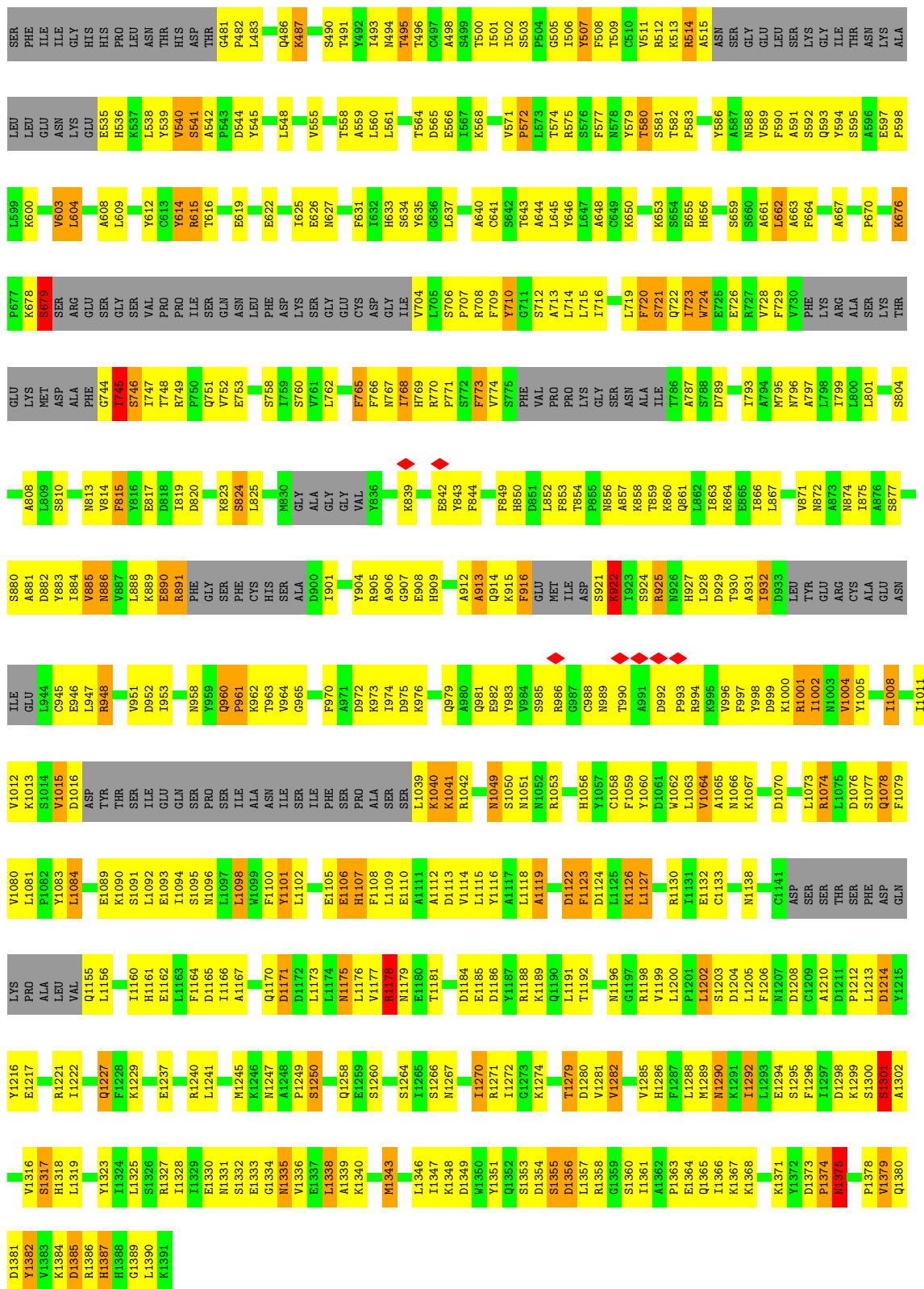


L988	Q889	E916	R853	F790	LEU	Y652	G583	G584	Y583	T519	E458	K391	ASN	V263	M196	S125	THR
E990	R991	GLY	I854	M791	LEU	R653	G585	G586	G587	A522	A459	S392	MET	P264	N197	Y126	GLY
E991	R992	GLY	I855	PHE	SER	T654	I585	I586	I587	A523	L460	I393	LEU	V265	D198	Y127	SER
E992	R993	GLY	I856	THR	PRO	P655	I586	I587	I588	S523	R461	E394	ASN	Q266	N199	N128	ASN
E993	R994	GLY	I857	ASP	THR	D656	I588	I589	I590	T524	L462	I394	PRO	G267	E200	G130	PRO
E994	R995	GLY	I858	ASN	LEU	E657	I590	I591	I592	I525	E463	I395	LEU	G268	Y201	G131	LEU
E995	R996	GLY	I859	ARG	SER	F658	I591	I592	I593	I526	S464	I396	MET	D269	Q202	D132	MET
E996	R997	GLY	I860	VAL	SER	F659	I592	I593	I594	S527	I465	I397	ARG	V270	Q203	D133	ARG
E997	R998	GLY	I861	THR	THR	E660	I593	I594	I595	P528	R466	I402	ALA	I271	V203	S136	ALA
E998	R999	GLY	I862	THR	ALA	D661	I594	I595	I596	G529	P467	G403	SER	D272	V204	S137	SER
E999	R1000	GLY	I863	SER	THR	L662	I595	I596	I597	I530	P468	T404	PHE	I273	D205	R137	ALA
E1000	R1001	GLY	I864	HIS	ASN	L663	I596	I597	I598	F531	P469	T405	ILE	V274	D206	E138	MET
E1001	R1002	GLY	I865	ALA	LEU	D664	I597	I598	I599	V535	SER	T406	ALA	S275	K139	E139	GLY
E1002	R1003	GLY	I866	PHE	LEU	P665	I598	I599	I600	A407	R408	A407	LEU	H276	H209	N140	ALA
E1003	R1004	GLY	I867	THR	GLN	P666	I599	I600	I601	R409	R277	R277	THR	E277	I211	G141	THR
E1004	R1005	GLY	I868	SER	ILE	L667	I600	I601	I602	A410	R278	R278	GLY	G279	I212	A144	GLY
E1005	R1006	GLY	I869	ASP	SER	Y673	I601	I602	I603	GLU	P411	R281	ASP	G280	K213	F145	SER
E1006	R1007	GLY	I870	PRO	THR	G674	I602	I603	I604	VAL	A412	R282	ASN	G281	V214	T146	ILE
E1007	R1008	GLY	I871	ILE	ASN	A675	I603	I604	I605	ILE	L413	R283	SER	I282	A215	P147	ASN
E1008	R1009	GLY	I872	ASN	PRO	G675	I604	I605	I606	GLN	I414	R284	ASN	F284	V217	F148	PRO
E1009	R1010	GLY	I873	ASN	ALA	S680	I605	I606	I607	THR	K416	A285	GLY	A285	P221	Q151	MET
E1010	R1011	GLY	I874	LEU	ASN	T681	I606	I607	I608	GLN	Y417	A286	GLY	G286	N222	D152	SER
E1011	R1012	GLY	I875	PRO	THR	A682	I607	I608	I609	GLN	L418	A287	GLY	G287	M221	V153	ASN
E1012	R1013	GLY	I876	ASN	ASN	I683	I608	I609	I610	VAL	L419	A288	GLY	G288	P222	F154	MET
E1013	R1014	GLY	I877	ASN	ASN	F684	I609	I610	I611	ILE	I420	A289	PHE	ALA	N223	F155	ASN
E1014	R1015	GLY	I878	ASN	ALA	P685	I610	I611	I612	GLN	I421	A290	SER	G289	P226	M155	ASN
E1015	R1016	GLY	I879	LEU	GLN	P686	I611	I612	I613	HIS	V422	A291	GLN	G290	A227	I156	GLU
E1016	R1017	GLY	I880	LEU	GLN	L687	I612	I613	I614	THR	I423	A292	GLN	K222	G229	P157	HIS
E1017	R1018	GLY	I881	LEU	GLN	C687	I613	I614	I615	GLY	I424	A293	GLY	K223	G230	D158	ILE
E1018	R1019	GLY	I882	LEU	GLN	G688	I614	I615	I616	VAL	V425	A294	GLY	K231	H230	E159	ARG
E1019	R1020	GLY	I883	LEU	GLN	P689	I615	I616	I617	SER	I426	A295	GLY	L231	I160	I160	VAL
E1020	R1021	GLY	I884	LEU	GLN	G690	I616	I617	I618	THR	A427	A296	GLY	L232	L161	L161	SER
E1021	R1022	GLY	I885	LEU	GLN	K691	I617	I618	I619	THR	P428	A297	GLY	L233	H162	E163	GLY
E1022	R1023	GLY	I886	LEU	GLN	P692	I618	I619	I620	ALA	E429	A298	GLY	L234	F164	F164	GLY
E1023	R1024	GLY	I887	LEU	GLN	G693	I619	I620	I621	THR	N431	A299	GLY	L235	T236	S167	THR
E1024	R1025	GLY	I888	LEU	GLN	P694	I620	I621	I622	ALA	N432	A300	GLY	L236	T237	Q168	SER
E1025	R1026	GLY	I889	LEU	GLN	G695	I621	I622	I623	THR	N433	A301	GLY	L237	M238	Q169	LYS
E1026	R1027	GLY	I890	LEU	GLN	P696	I622	I623	I624	THR	N434	A302	GLY	L238	T239	T169	LYS
E1027	R1028	GLY	I891	LEU	GLN	G697	I623	I624	I625	ALA	N435	A303	GLY	L239	T240	K170	ASN
E1028	R1029	GLY	I892	LEU	GLN	P698	I624	I625	I626	THR	N436	A304	GLY	L240	T241	T171	ASN
E1029	R1030	GLY	I893	LEU	GLN	G699	I625	I626	I627	ALA	N437	A305	GLY	L241	T242	M172	GLY
E1030	R1031	GLY	I894	LEU	GLN	P699	I626	I627	I628	THR	N438	A306	GLY	L242	T243	D173	GLY
E1031	R1032	GLY	I895	LEU	GLN	G700	I627	I628	I629	THR	N439	A307	GLY	L243	T244	M174	GLY
E1032	R1033	GLY	I896	LEU	GLN	P701	I628	I629	I630	ALA	N440	A308	GLY	L244	T245	G174	GLY
E1033	R1034	GLY	I897	LEU	GLN	G702	I629	I630	I631	THR	N441	A309	GLY	L245	T246	I175	GLY
E1034	R1035	GLY	I898	LEU	GLN	P703	I630	I631	I632	THR	N442	A310	GLY	L246	T247	F176	GLY
E1035	R1036	GLY	I899	LEU	GLN	G704	I631	I632	I633	THR	N443	A311	GLY	L247	T248	L111	GLY
E1036	R1037	GLY	I900	LEU	GLN	P704	I632	I633	I634	THR	N444	A312	GLY	L248	T249	Q112	GLY
E1037	R1038	GLY	I901	LEU	GLN	G705	I633	I634	I635	THR	N445	A313	GLY	L249	T250	Q113	GLY
E1038	R1039	GLY	I902	LEU	GLN	P705	I634	I635	I636	THR	N446	A314	GLY	L250	T251	H113	GLY
E1039	R1040	GLY	I903	LEU	GLN	G706	I635	I636	I637	THR	N447	A315	GLY	L251	T252	K114	GLY
E1040	R1041	GLY	I904	LEU	GLN	P706	I636	I637	I638	THR	N448	A316	GLY	L252	T253	D115	GLY
E1041	R1042	GLY	I905	LEU	GLN	G707	I637	I638	I639	THR	N449	A317	GLY	L253	T254	T118	GLY
E1042	R1043	GLY	I906	LEU	GLN	P708	I638	I639	I640	THR	N450	A318	GLY	L254	T255	P119	GLY
E1043	R1044	GLY	I907	LEU	GLN	G709	I639	I640	I641	THR	N451	A319	GLY	L255	T256	V120	GLY
E1044	R1045	GLY	I908	LEU	GLN	P709	I640	I641	I642	THR	N452	A320	GLY	L256	T257	L121	GLY
E1045	R1046	GLY	I909	LEU	GLN	G710	I641	I642	I643	THR	N453	A321	GLY	L257	T258	E123	GLY
E1046	R1047	GLY	I910	LEU	GLN	P710	I642	I643	I644	THR	N454	A322	GLY	L258	T259	R124	GLY
E1047	R1048	GLY	I911	LEU	GLN	G711	I643	I644	I645	THR	N455	A323	GLY	L259	T260	L192	GLY
E1048	R1049	GLY	I912	LEU	GLN	P711	I644	I645	I646	THR	N456	A324	GLY	L260	T261	W193	GLY
E1049	R1050	GLY	I913	LEU	GLN	G712	I645	I646	I647	THR	N457	A325	GLY	L261	T262	W194	GLY
E1050	R1051	GLY	I914	LEU	GLN	P712	I646	I647	I648	THR	N458	A326	GLY	L262	T263	W195	GLY
E1051	R1052	GLY	I915	LEU	GLN	G713	I647	I648	I649	THR	N459	A327	GLY	L263	T264	W196	GLY
E1052	R1053	GLY	I916	LEU	GLN	P713	I648	I649	I650	THR	N460	A328	GLY	L264	T265	W197	GLY
E1053	R1054	GLY	I917	LEU	GLN	G714	I649	I650	I651	THR	N461	A329	GLY	L265	T266	W198	GLY
E1054	R1055	GLY	I918	LEU	GLN	P714	I650	I651	I652	THR	N462	A330	GLY	L266	T267	W199	GLY
E1055	R1056	GLY	I919	LEU	GLN	G715	I651	I652	I653	THR	N463	A331	GLY	L267	T268	W200	GLY
E1056	R1057	GLY	I920	LEU	GLN	P715	I652	I653	I654	THR	N464	A332	GLY	L268	T269	W201	GLY
E1057	R1058	GLY	I921	LEU	GLN	G716	I653	I654	I655	THR	N465	A333	GLY	L269	T270	W202	GLY
E1058	R1059	GLY	I922	LEU	GLN	P716	I654	I655	I656	THR	N466	A334	GLY	L270	T271	W203	GLY
E1059	R1060	GLY	I923	LEU	GLN	G717	I655	I656	I657	THR	N467	A335	GLY	L271	T272	W204	GLY
E1060	R1061	GLY	I924	LEU	GLN	P717	I656	I657	I658	THR	N468	A336	GLY	L272	T273	W205	GLY
E1061	R1062	GLY	I925	LEU	GLN	G718	I657	I658	I659	THR	N469	A337	GLY	L273	T274	W206	GLY
E1062	R1063	GLY	I926	LEU	GLN	P718	I658	I659	I660	THR	N470	A338	GLY	L274	T275	W207	GLY
E1063	R1064	GLY	I927	LEU	GLN	G719	I659	I660	I661	THR	N471	A339	GLY	L275	T276	W208	GLY
E1064	R1065	GLY	I928	LEU	GLN	P719	I660	I661	I662	THR	N472	A340	GLY	L276	T277	W209	GLY
E1065	R1066	GLY	I929	LEU	GLN	G720	I661	I662	I663	THR	N473	A341	GLY	L277	T278	W210	GLY
E1066	R1067	GLY	I930	LEU	GLN	P720	I662	I663	I664	THR	N474	A342	GLY	L278	T279	W211	GLY
E1067	R1068	GLY	I931	LEU	GLN	G721	I663	I664	I665	THR	N475	A343	GLY	L279	T280	W212	GLY
E1068	R1069	GLY	I932	LEU	GLN	P721	I664	I665	I666	THR	N476	A344	GLY	L280	T281	W213	GLY
E1069	R1070	GLY	I933	LEU	GLN	G722	I665	I666	I667	THR	N477	A345	GLY	L281	T282	W214	GLY
E1070	R1071	GLY	I934	LEU	GLN	P722	I666	I667	I668	THR	N478	A346	GLY	L282	T283	W215	GLY
E1071	R1072	GLY	I935	LEU	GLN	G723	I667	I668	I669	THR	N479	A347	GLY	L283	T284	W216	GLY
E1072	R1073	GLY	I936	LEU	GLN	P723	I668	I669	I670	THR	N480	A348	GLY	L284	T285	W217	GLY
E1073	R1074	GLY	I937	LEU	GLN	G724	I669	I670	I671	THR	N481	A349	GLY	L285	T286	W218	GLY
E1074	R1075	GLY	I938	LEU	GLN	P724	I670	I671	I672	THR	N482	A350	GLY	L286	T287		



• Molecule 2: Nucleoporin NUP157

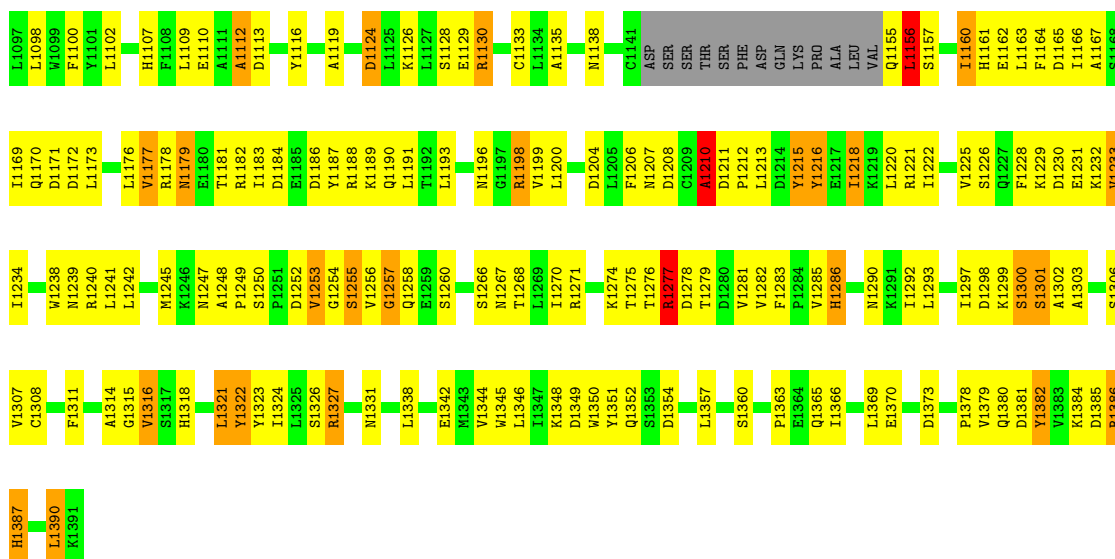




• Molecule 2: Nucleoporin NUP157

Chain Z: 32% 38% 8% 20%

C945	V1012	G131	K208	N282	Q444	E416	Q486	L548	R615	L811	R749	L811	Y883	C945	V1012
E946	K1013	L132	P209	V283	L345	N417	K487	K549	T616	I812	P750	I812	N886	E946	K1013
R948	S1014	G133	GLY	W284	E346	L422	S489	N550	P617	F815	Q751	F815	N887	R948	S1014
R949	V1015	A134	GLY	E285	V347	L422	S489	Y551	D618	F816	Q752	F816	N888	R949	V1015
V950	D1016	T213	ALA	Q287	D348	V423	T491	N557	E619	E817	Y753	E817	K888	V950	D1016
ASP	ASP	F136	GLY	Q287	Q349	V423	Y492	T558	V620	D818	Y755	D818	E890	V951	ASP
THR	THR	F137	ASN	Y288	S350	L425	Y492	T558	F621	D819	Y755	D819	E891	P952	THR
LYS	LYS	F138	THR	N289	R351	T426	Y493	A559	E622	R820	L756	R820	R891	P953	LYS
ILE	ILE	Q139	ILE	CYS	R352	T427	N494	S559	S623	G815	L757	G815	PHE	K956	ILE
ARG	ARG	Q139	GLY	SER	G352	T427	N494	L560	S623	R821	S757	R821	GLY	K957	ARG
ASP	ASP	R140	GLY	GLU	V353	T428	T495	D562	L624	F822	S758	F822	SER	K958	ASP
TYR	TYR	V143	GLY	ASN	R355	V430	T496	T563	I625	K823	S760	K823	PHE	K959	TYR
ASP	ASP	T144	LEU	ASN	R355	R431	S489	T564	N627	S824	V761	S824	HIS	K958	ASP
ARG	ARG	N145	LEU	PHE	S358	F434	T500	T564	H633	T828	A763	T828	ALA	K959	ARG
GLY	GLY	N146	ARG	ASN	T359	F434	T500	T564	H633	T829	A763	T829	ALA	K960	GLY
THR	THR	P147	VAL	SER	K360	K435	S503	S503	S634	L828	D764	L828	ALA	P961	THR
PHE	PHE	D148	THR	LYS	S361	G436	S503	S503	Y635	M930	F765	M930	ALA	P962	PHE
THR	THR	D149	THR	SER	S361	G436	P604	P604	Y635	M931	F766	M931	ALA	P963	THR
ALA	ALA	E149	HIS	ASN	V363	I438	P604	P604	Y635	M932	N767	M932	ALA	F966	ALA
SER	SER	Q153	VAL	K301	R364	S439	S503	S503	Y635	M933	I768	S503	ALA	F967	SER
ALA	ALA	I159	LYS	L302	R364	S439	F508	F508	A640	T840	H769	T840	ALA	F968	ALA
SER	SER	K160	ILE	C303	S365	R441	T509	T509	S642	R841	R770	R841	ALA	F969	SER
LEU	LEU	S161	GLY	S307	L373	G443	C510	C510	S642	R842	P771	R842	ALA	F970	LEU
GLY	GLY	S161	LEU	S307	L373	G443	V511	V511	L645	T843	S772	T843	ALA	F971	GLY
ASN	ASN	I165	THR	N308	F376	K446	R512	R512	Y646	T844	S773	T844	ALA	F972	ASN
ARG	ARG	F166	SER	LEU	V377	K446	R512	R512	L646	T845	S774	T845	ALA	F973	ARG
LEU	LEU	E168	SER	ALA	V377	K446	R512	R512	L646	T846	S775	T846	ALA	F974	LEU
ASN	ASN	E168	ASN	ASN	L378	S581	ASN	ASN	K650	T847	PHE	T847	ALA	F975	ASN
ASN	ASN	P90	LEU	LEU	L378	S581	ASN	ASN	K650	T848	VAL	T848	ALA	F976	ASN
ARG	ARG	N170	LEU	LEU	L378	S581	ASN	ASN	K650	T849	VAL	T849	ALA	F977	ARG
PRO	PRO	N171	LEU	LEU	D380	P454	GLY	GLY	N652	F844	PR0	F844	ALA	F978	PRO
ARG	ARG	G172	PRO	PRO	A381	P455	GLY	GLY	N652	F845	PR0	F845	ALA	F979	ARG
ASP	ASP	N173	ASN	THR	A382	T456	LEU	LEU	S654	D846	LYS	D846	ALA	F980	ASP
GLN	GLN	F97	ASN	LYS	S383	S457	SER	SER	E655	L847	GLY	L847	ALA	F981	GLN
ASN	ASN	D100	ASN	ILE	L384	ILE	LYS	LYS	H656	K848	SER	K848	ALA	F982	ASN
GLY	GLY	N176	GLY	ILE	K388	SER	ILE	ILE	I657	H850	ALA	H850	ALA	F983	GLY
LYS	LYS	N178	LYS	PRO	N389	SER	THR	THR	F590	T854	ILE	T854	ALA	F984	LYS
PRO	PRO	K179	PRO	SER	A390	LEU	ASN	ASN	S592	F855	T786	F855	ALA	F985	PRO
ASN	ASN	I181	R106	PRO	L391	GLY	LYS	LYS	Q593	N856	A787	N856	ALA	F986	ASN
LEU	LEU	L182	N254	GLY	GLY	ASN	ALA	ALA	F664	A857	S788	A857	ALA	F987	LEU
SER	SER	N183	V255	LYS	K394	LYS	LEU	LEU	F665	K858	A790	A790	ALA	F988	SER
SER	SER	N184	F258	LEU	S396	SER	GLY	GLY	S666	E865	E791	E791	ALA	F989	SER
ARG	ARG	I185	N259	ILE	F397	PHE	ASN	ASN	G668	L866	S792	S792	ALA	F990	ARG
ASN	ASN	N186	V260	GLN	L398	ILE	LYS	LYS	L669	L867	M795	M795	ALA	F991	ASN
PHE	PHE	N187	S261	LYS	L399	ILE	GLY	GLY	P670	G671	N796	N796	ALA	F992	PHE
LEU	LEU	Y191	N262	VAL	N401	HIS	H535	H535	V672	V673	A797	A797	ALA	F993	LEU
SER	SER	H192	L263	LEU	R402	HIS	K537	K537	V673	V673	L798	L798	ALA	F994	SER
GLY	GLY	Y116	L263	GLY	A403	PRO	L538	L538	E674	E674	L799	L799	ALA	F995	GLY
ARG	ARG	Y117	L263	ASP	F404	THR	L538	L538	E674	E674	L800	L800	ALA	F996	ARG
THR	THR	G120	LYS	ALA	K408	HIS	L538	L538	E674	E674	L800	L800	ALA	F997	THR
ARG	ARG	F125	THR	GLY	K408	HIS	L538	L538	E674	E674	L800	L800	ALA	F998	ARG
LYS	LYS	K203	ARG	THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F999	LYS
ASP	ASP	V204	LYS	GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1000	ASP
VAL	VAL	K205	VAL	THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1001	VAL
E128	E128	D127	VAL	THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1002	E128
V129	V129	G280	ASN	GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1003	V129
G130	G130	V207		THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1004	G130
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1005	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1006	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1007	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1008	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1009	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1010	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1011	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1012	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1013	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1014	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1015	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1016	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1017	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1018	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1019	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1020	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1021	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1022	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1023	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1024	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1025	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1026	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1027	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1028	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1029	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1030	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1031	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1032	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1033	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1034	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1035	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1036	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1037	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1038	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1039	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1040	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1041	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1042	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1043	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1044	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1045	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1046	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1047	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1048	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1049	
				THR	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1050	
				GLY	L409	ASP	L538	L538	E674	E674	L800	L800	ALA	F1051	
				THR											



- Molecule 3: orphans bound to Nup192 NTD

Chain 5: 100%

There are no outlier residues recorded for this chain.

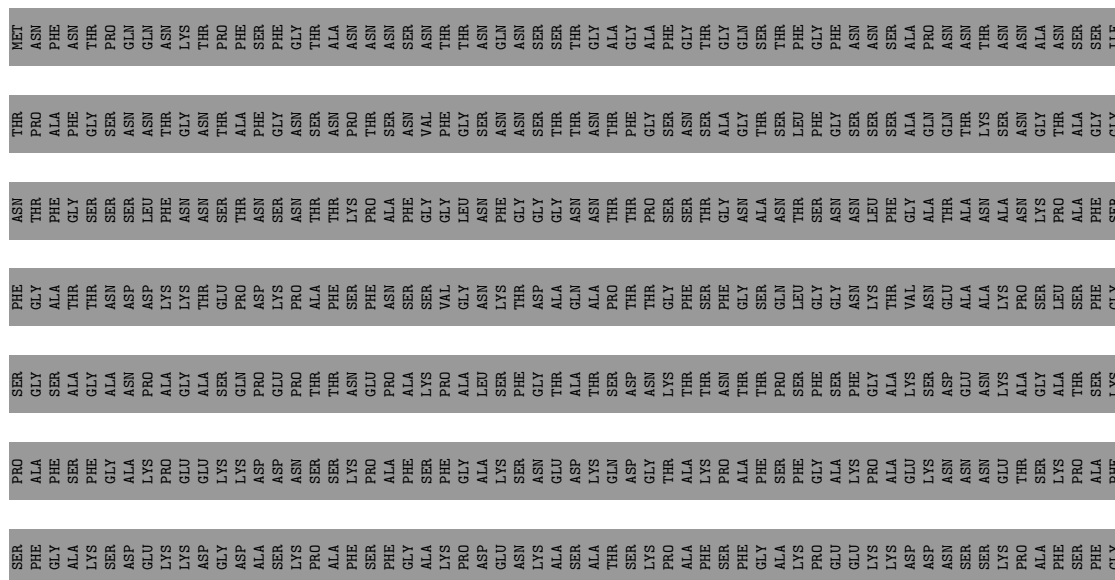
- Molecule 3: orphans bound to Nup192 NTD

Chain 6: 92%



- Molecule 4: Nucleoporin NSP1

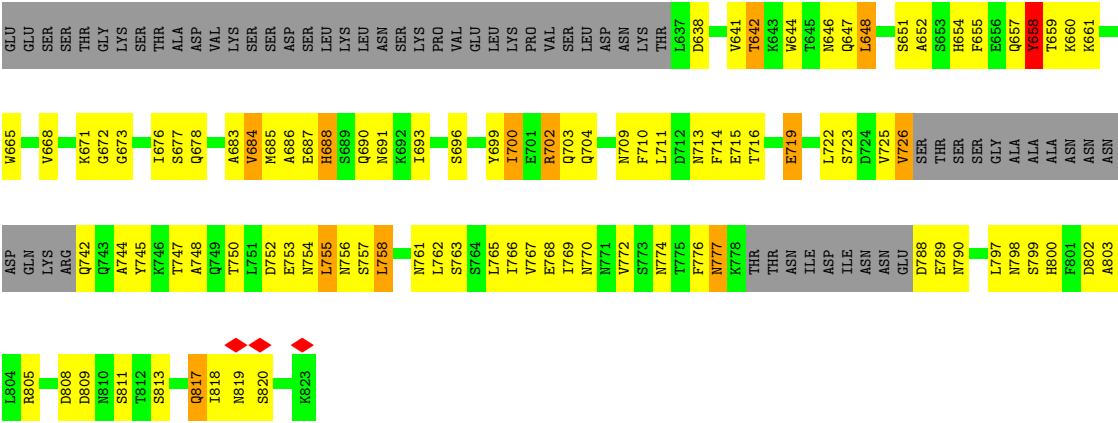
Chain A: 9%



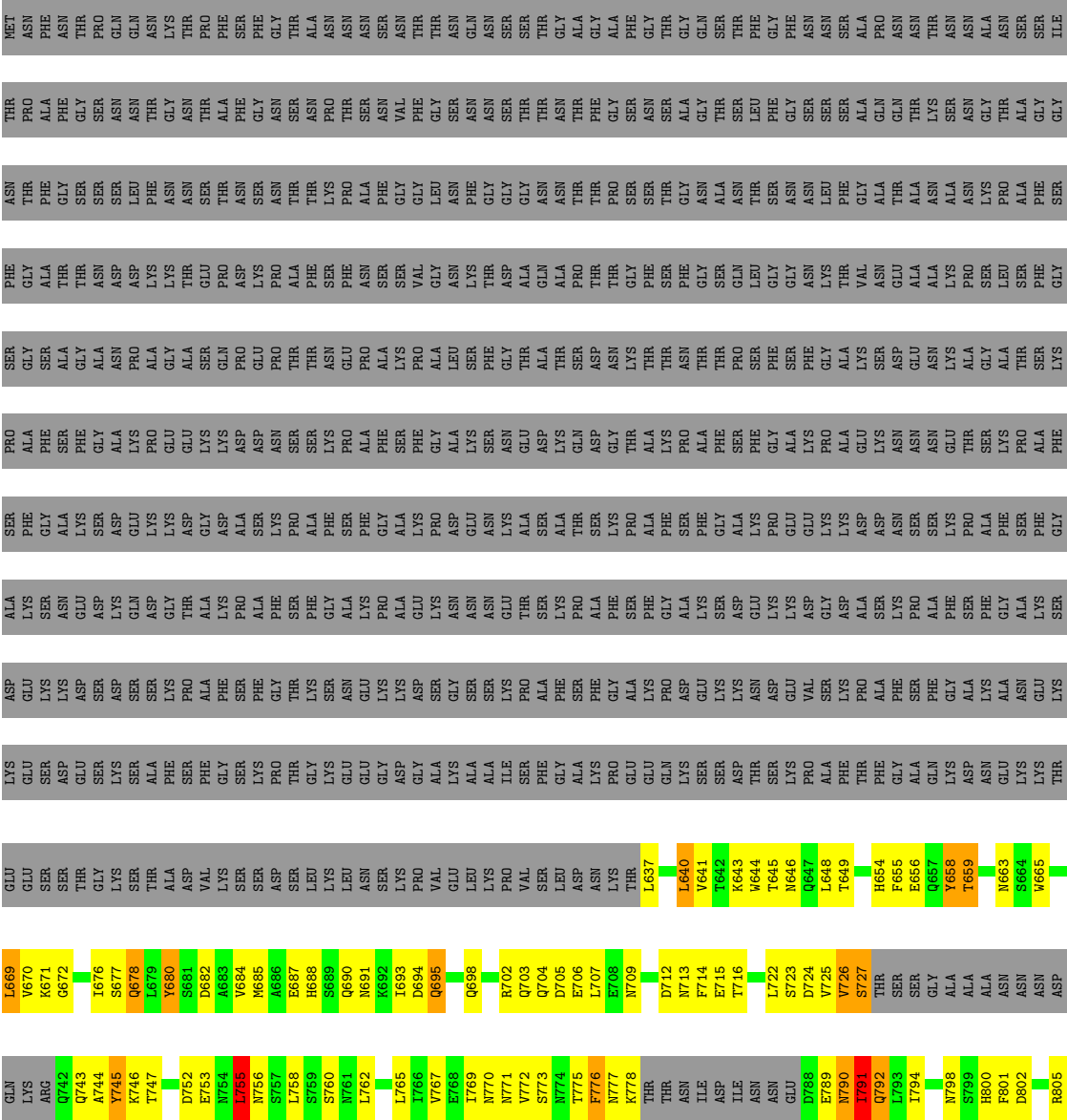
- Molecule 4: Nucleoporin NSP1

Chain D: 8% 10% . 80%

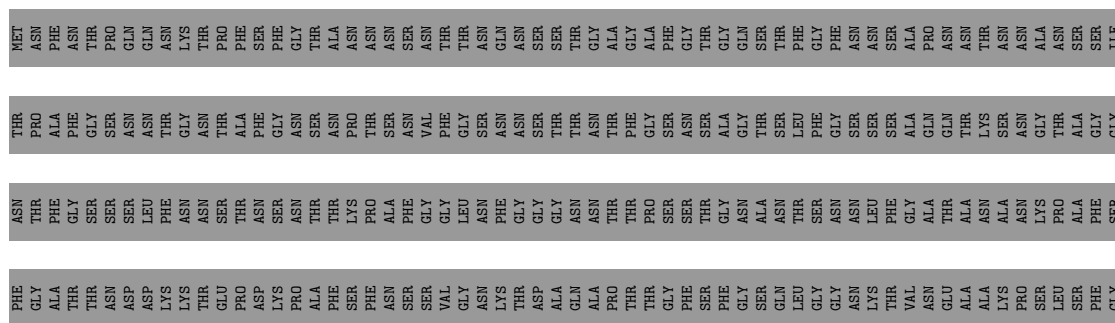
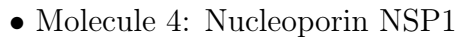
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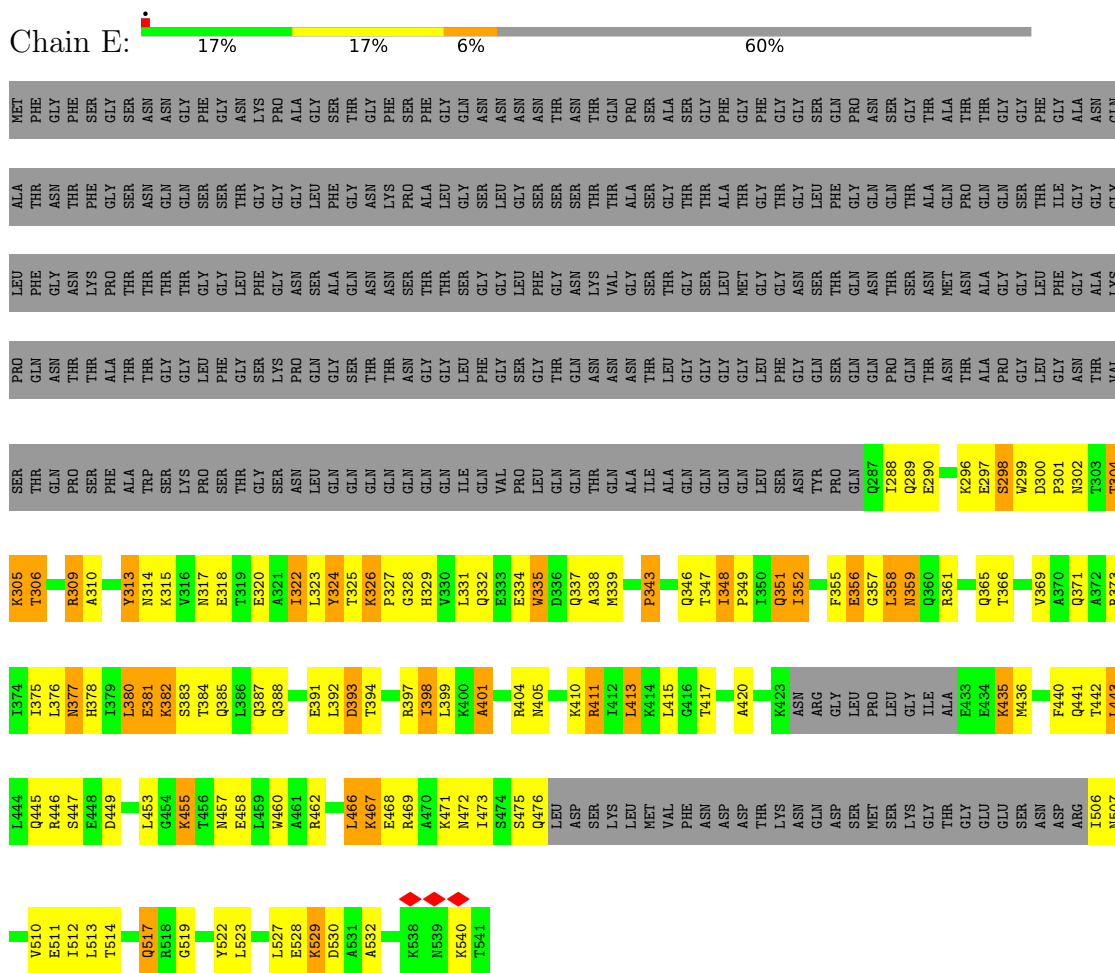
● Molecule 4: Nucleoporin NSP1



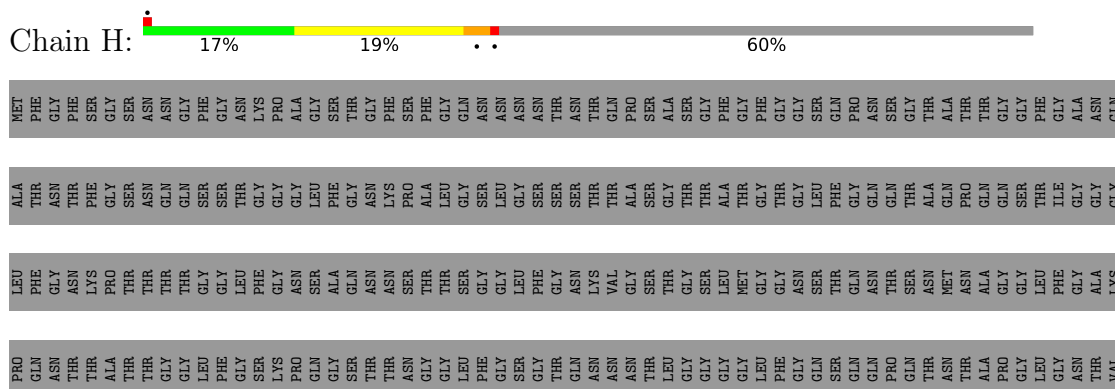


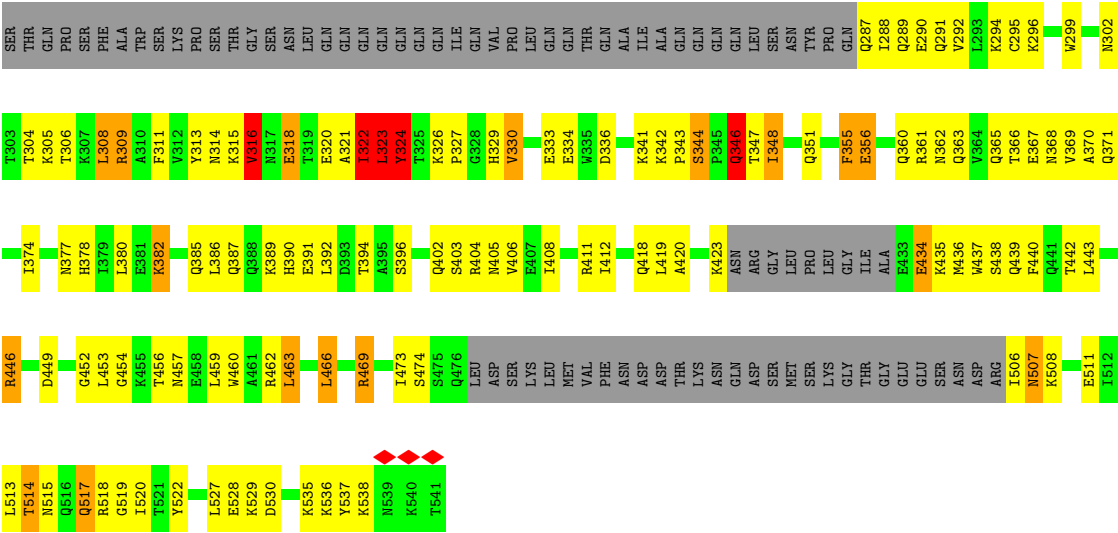


- Molecule 5: Nucleoporin NUP57

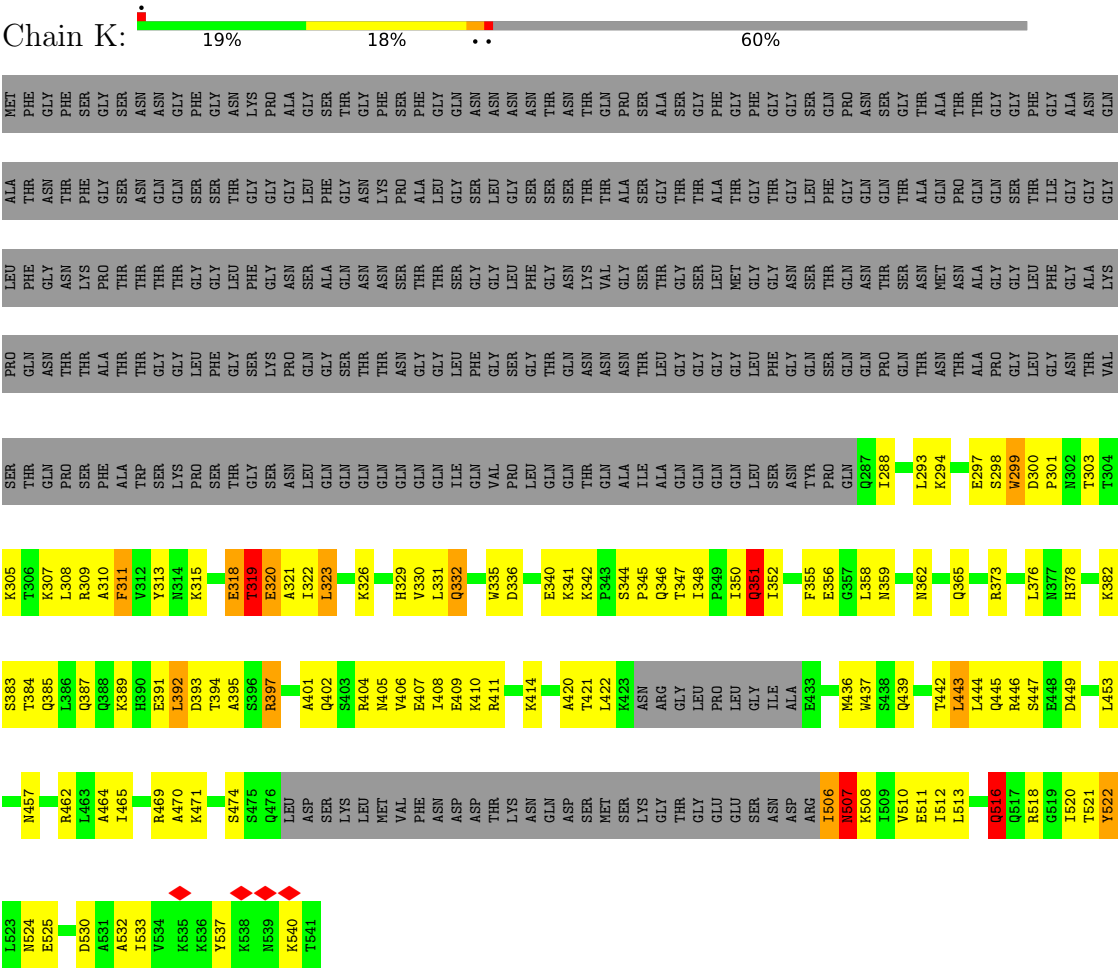


- Molecule 5: Nucleoporin NUP57





• Molecule 5: Nucleoporin NUP57



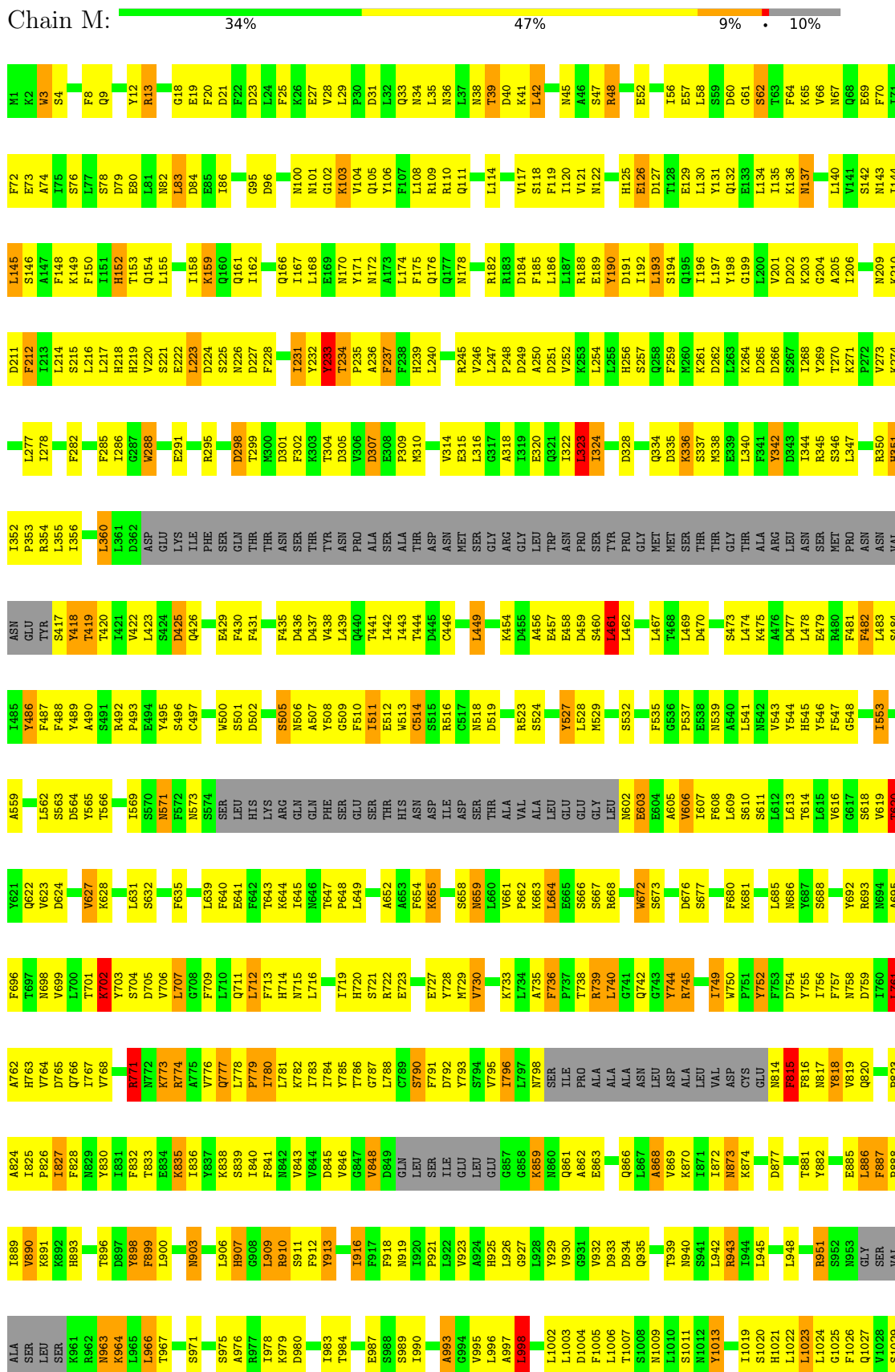
• Molecule 6: Nucleoporin NUP49/NSP49

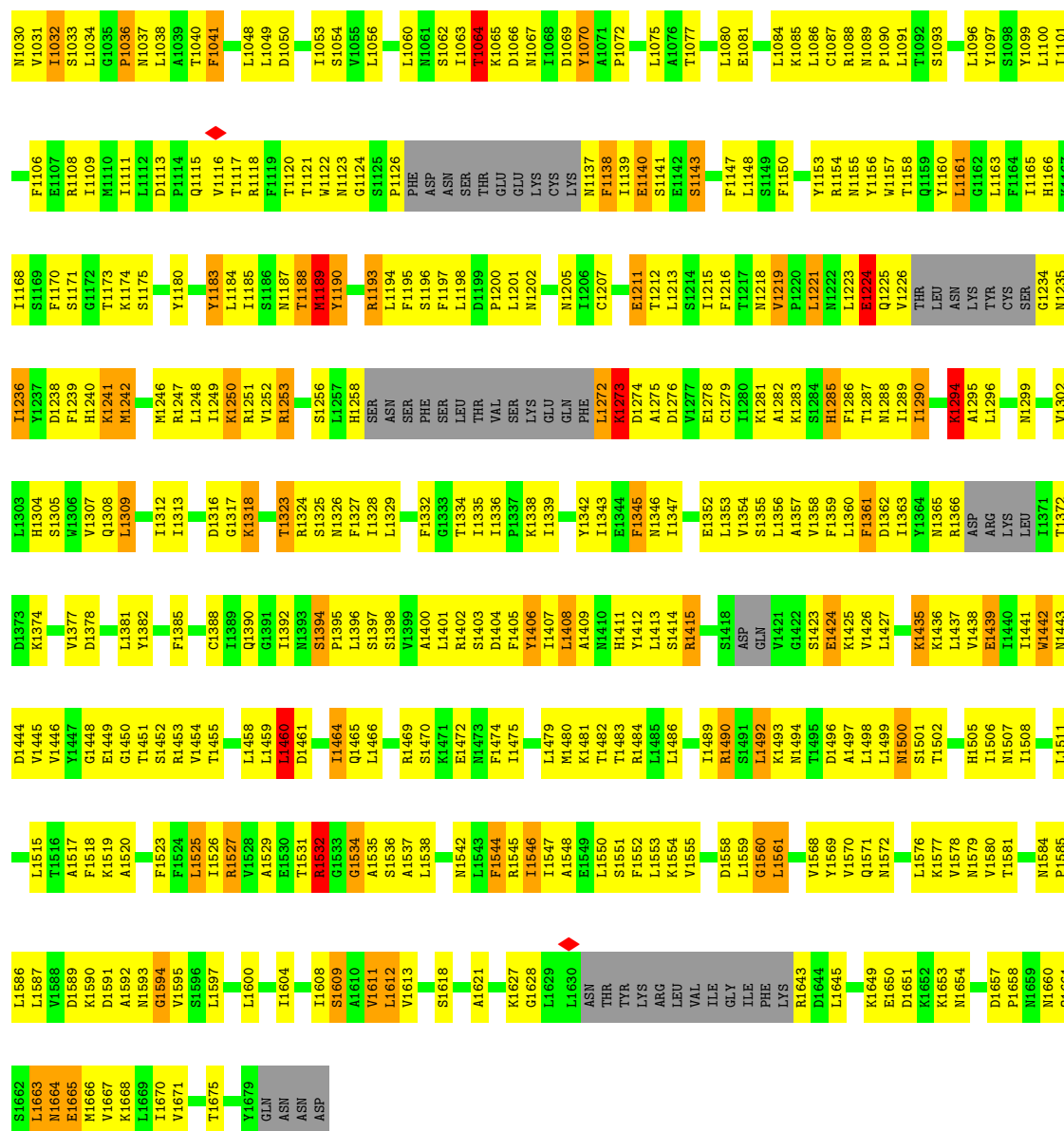


V443	L379	V312	GLN	PRO	GLN	THR	LEU	GLY	THR	GLN	LEU
I444		A313	GLN	GLY	GLY	THR	GLY	ALA	THR	THR	GLY
E445	K382	V314	GLN	THR	GLY	ARG	THR	ALA	THR	THR	ALA
E446	K383	L315	GLN	THR	GLY	GLY	THR	ALA	THR	THR	ALA
F447	L384	L316	GLN	THR	GLY	GLY	THR	ALA	THR	THR	ALA
T448	E385		PRO	PRO	LEU	LEU	LEU	LEU	LEU	LEU	GLY
L449	D386	A321	GLN	GLN	PHE	PHE	GLY	ALA	THR	THR	GLY
F450	Y387	T322	MET	MET	GLN	GLN	GLY	ALA	THR	THR	GLY
M451	C388	S323	GLN	GLN	ASN	ASN	ASN	ASN	ASN	ASN	GLN
D452	R389	Q324	CYS	CYS	ALA	ALA	ALA	ALA	THR	THR	GLN
I453	I390	Y325	ALA	ALA	LEU	LEU	GLY	ALA	THR	THR	GLN
A454	L391	L326	LEU	LEU	GLN	GLN	GLY	ALA	THR	THR	GLN
E455	S392	K327	GLN	GLN	ASN	ASN	ASN	ASN	ASN	ASN	GLN
R456	D393	Q328	ASN	ASN	THR	THR	THR	THR	THR	THR	GLN
I457	I394	D329	LEU	LEU	THR	THR	THR	THR	THR	THR	GLN
		L330	SER	SER	THR	THR	THR	THR	THR	THR	GLN
		K331	GLN	GLN	GLY	GLY	GLY	GLY	GLY	GLY	GLN
H461	A397	K332	LEU	LEU	GLY	GLY	GLY	GLY	GLY	GLY	GLN
Q462	V398	I333	PRO	PRO	GLY	GLY	GLY	GLY	GLY	GLY	GLN
R463		S334	ILE	ILE	LEU	LEU	LEU	LEU	LEU	LEU	GLY
T464			THR	THR	PHE	PHE	PHE	PHE	PHE	PHE	GLY
		K337	PRO	PRO	GLY	GLY	GLY	GLY	GLY	GLY	GLN
A468	D402	S338	MET	MET	SER	SER	SER	SER	SER	SER	GLN
S469	T403	L339	THR	THR	ARG	ARG	ARG	ARG	ARG	ARG	GLY
L470	L405		THR	THR	ILE	ILE	ILE	ILE	ILE	ILE	GLY
S471	F406		GLU	GLU	ALA	ALA	ALA	ALA	ALA	ALA	GLY
I472	G407	D343	LEU	LEU	THR	THR	THR	THR	THR	THR	GLY
	ALA	L344	P270	P270	SER	SER	SER	SER	SER	SER	GLY
	ASN	L345	P271	P271	THR	THR	THR	THR	THR	THR	GLY
	ASN	D346	THR	THR	LEU	LEU	LEU	LEU	LEU	LEU	GLY
	ASN	T347	THR	THR	PHE	PHE	PHE	PHE	PHE	PHE	GLY
	PRO	Q348	PHE	PHE	GLY	GLY	GLY	GLY	GLY	GLY	GLN
	PRO	T349	THR	THR	LEU	LEU	LEU	LEU	LEU	LEU	GLY
	ASN	F350	THR	THR	GLY	GLY	GLY	GLY	GLY	GLY	GLN
	ASN	S351	THR	THR	ASN	ASN	ASN	ASN	ASN	ASN	GLY
	THR	L352	THR	THR	ALA	ALA	ALA	ALA	ALA	ALA	GLY
	ILE	L353	THR	THR	ASN	ASN	ASN	ASN	ASN	ASN	GLY
	THR	L354	THR	THR	THR	THR	THR	THR	THR	THR	GLY
	ALA	Q355	THR	THR	ASN	ASN	ASN	ASN	ASN	ASN	GLY
	ALA	R356	THR	THR	THR	THR	THR	THR	THR	THR	GLY
	ASP	Y283	THR	THR	ASN	ASN	ASN	ASN	ASN	ASN	GLY
	LEU	L357	THR	THR	ASN	ASN	ASN	ASN	ASN	ASN	GLY
	GLY	L358	THR	THR	ASN	ASN	ASN	ASN	ASN	ASN	GLY
	SER	T359	THR	THR	ASN	ASN	ASN	ASN	ASN	ASN	GLY
	SER	PRO	THR	THR	ASN	ASN	ASN	ASN	ASN	ASN	GLY
	GLU	GLY	THR	THR	THR	THR	THR	THR	THR	THR	GLY
	ALA	SER	THR	THR	THR	THR	THR	THR	THR	THR	GLY
	ALA	LYS	THR	THR	THR	THR	THR	THR	THR	THR	GLY
	ASN	ILE	THR	THR	THR	THR	THR	THR	THR	THR	GLY
	LEU	SER	THR	THR	THR	THR	THR	THR	THR	THR	GLY
	LEU	THR	THR</								

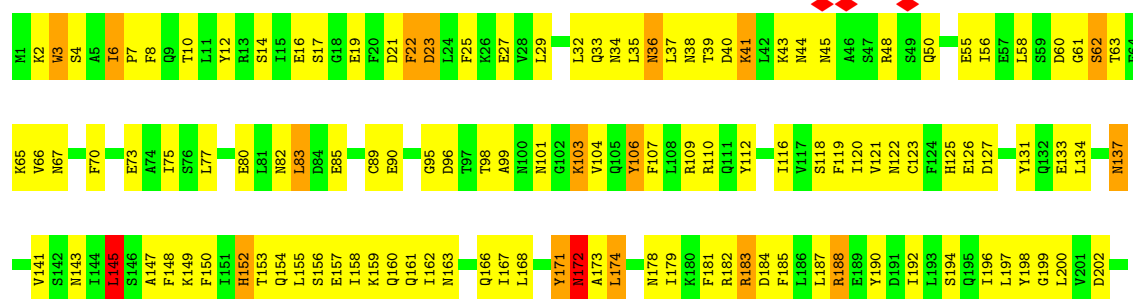
A454	E381	V312	GLN	PRO
A455	K382	A313	LEU	ALA
R456	E385	Y314	GLN	GLY
A458	D386	S318	GLN	THR
V459	E389	E319	PRO	SER
L460	I390	S320	GLN	LEU
	I391		MET	PHE
K463	L392	Y325	GLN	GLY
T464	D393	L326	CYS	ASN
K465	D393	K327	ALA	ASN
T466	I394	Q328	LEU	GLY
	E395	D329	GLN	ASN
S469	T396	L330	ASN	THR
	A397	K331	LEU	THR
		K332	SER	THR
	D402	I333	GLN	GLY
		S334	LEU	GLY
	L405	S335	PRO	GLY
	R406	F336	ILE	LEU
	G407		PHE	PHE
	ALA	I340	THR	GLY
	PRO	D341	MET	SER
	ASN	E342	THR	LYS
	ASN	D343	ARG	PRO
	PRO	L344	ILE	THR
	ASN	L345	SER	GLY
	SER	D346	LEU	GLY
	THR	T347	ALA	THR
	ALA	Q348	THR	SER
	ILE	T349	P270	LEU
	THR	F350	P271	LEU
	ALA		Q275	PHE
	ASP	L353	LYS	GLY
	LEU	L354	SER	PRO
	GLY		ALA	ALA
	SER	L357	ASN	GLY
	SER	L358	ASN	GLN
	GLU	T359	ASN	THR
	ALA	PRO	LEU	GLY
	GLU	GLY	ASN	GLY
	ASN	SER	ASN	GLN
	LEU	LYS	ASN	GLY
	LEU	ILE	S291	GLY
	GLN	SER	H292	THR
	LEU	SER	H293	THR
	LYS	ASN	ILE	ASN
	THR	ASP	MET	SER
	G495	L369	ALA	ASN
	L436	B370	D300	SER
	A437	K371	H301	ALA
		F372	D302	GLY
		F373	E303	GLN
	V443	Q374	L304	ASN
	I444	K375	I305	LEU
		K376	D306	PHE
	L449	I377	S307	GLY
	F450	H378	GLN	PHE
	M451		ASN	GLY
	D452	L379	GLN	ASN
	F453	R340	CTR	ASN
		S341	LYS	GLY

● Molecule 7: Nucleoporin NUP192

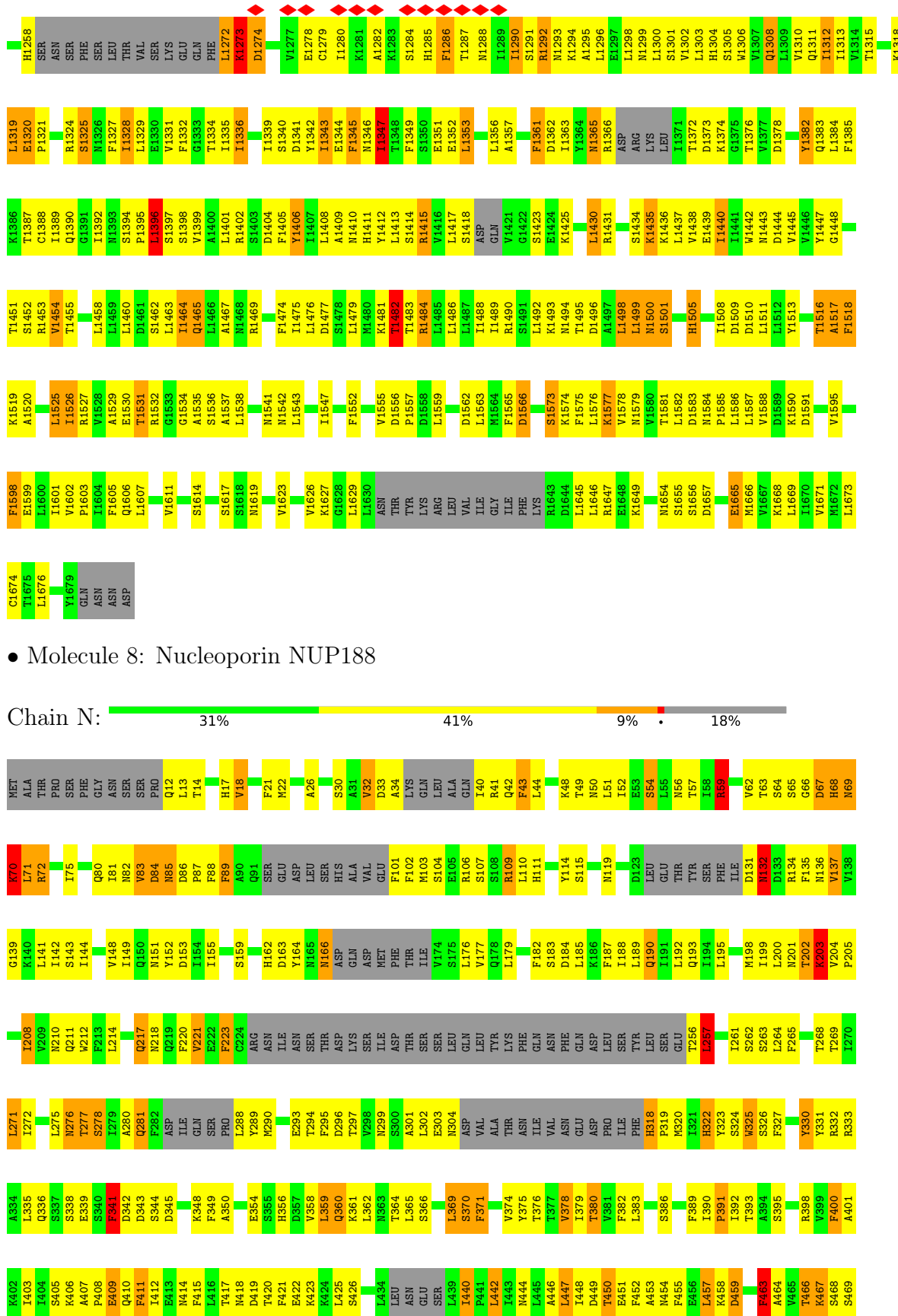




• Molecule 7: Nucleoporin NUP192



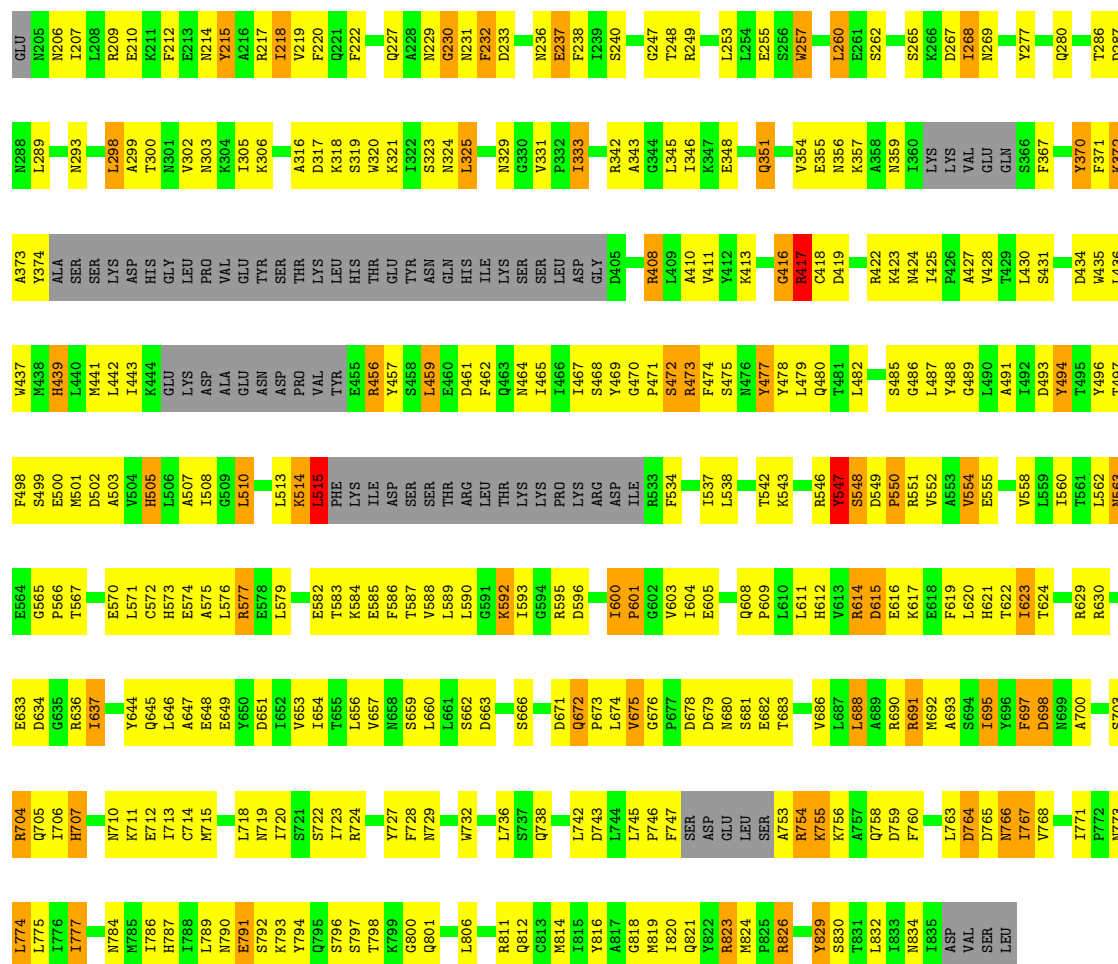






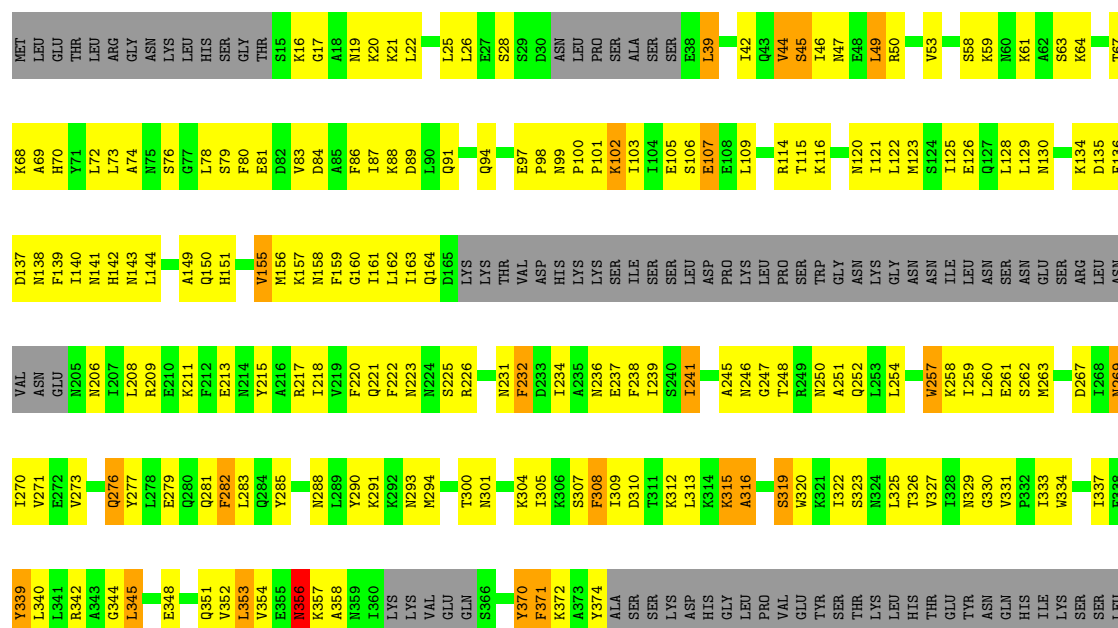






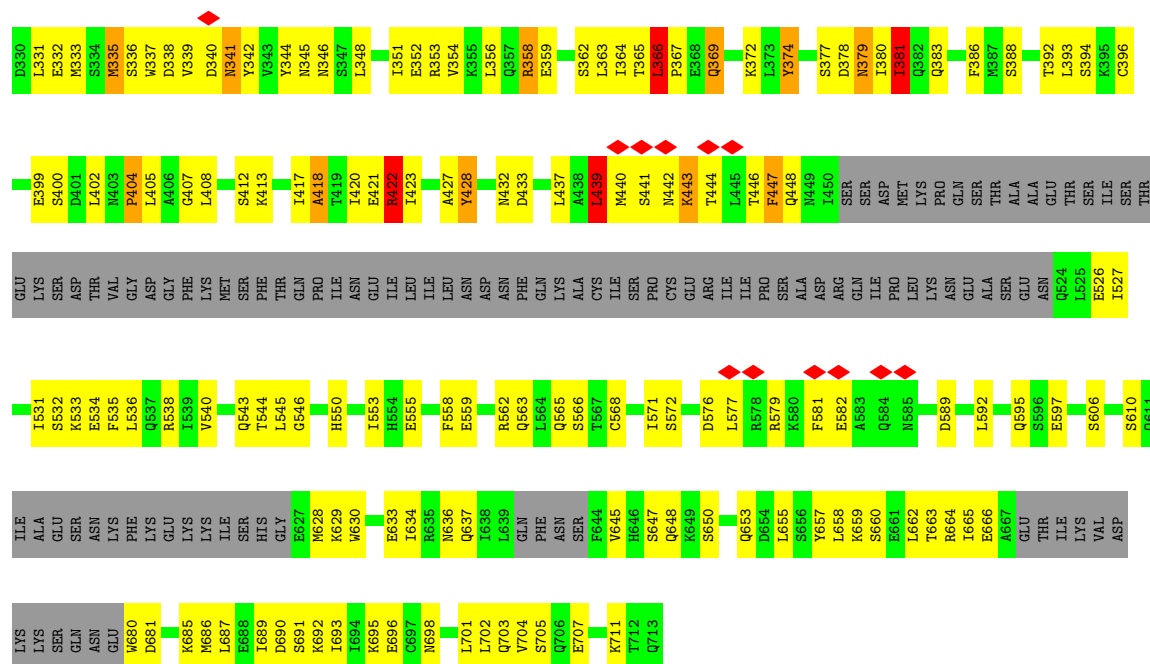
• Molecule 9: Nucleoporin NIC96

Chain T: 34% 42% 7% 16%

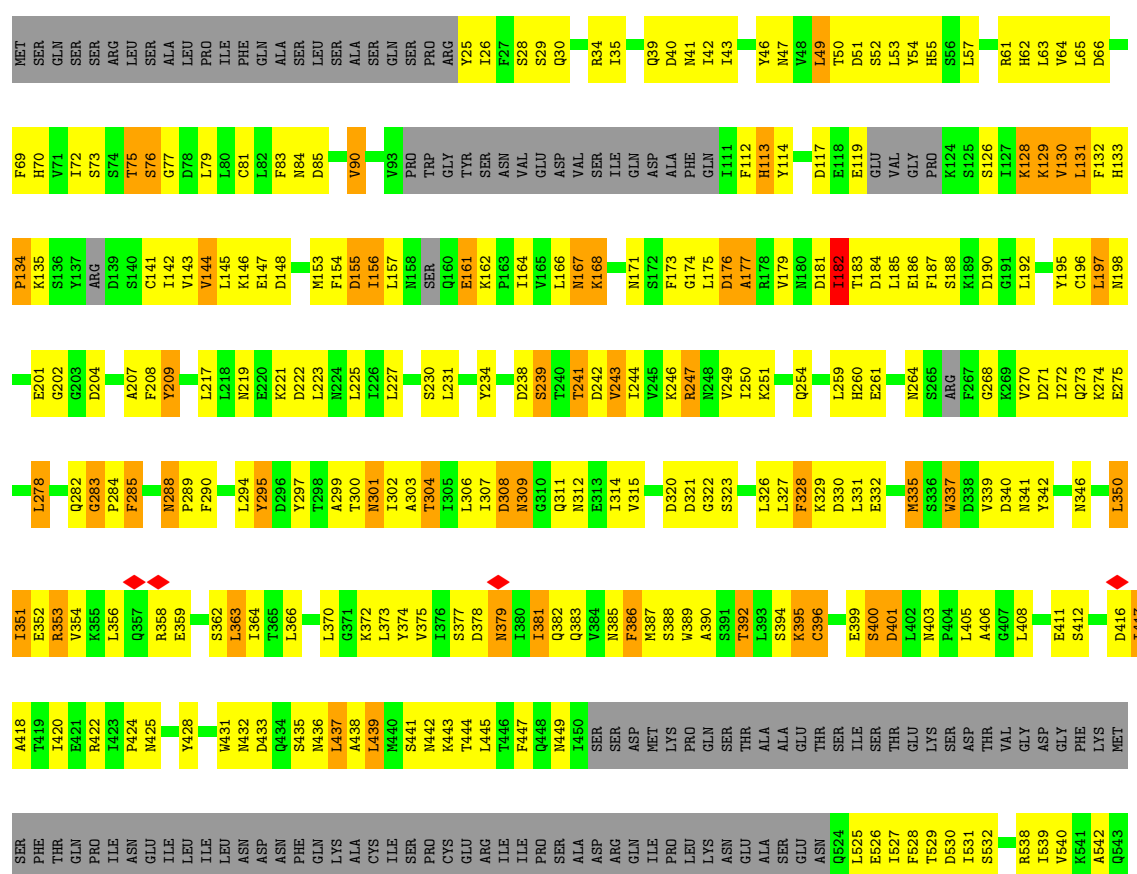


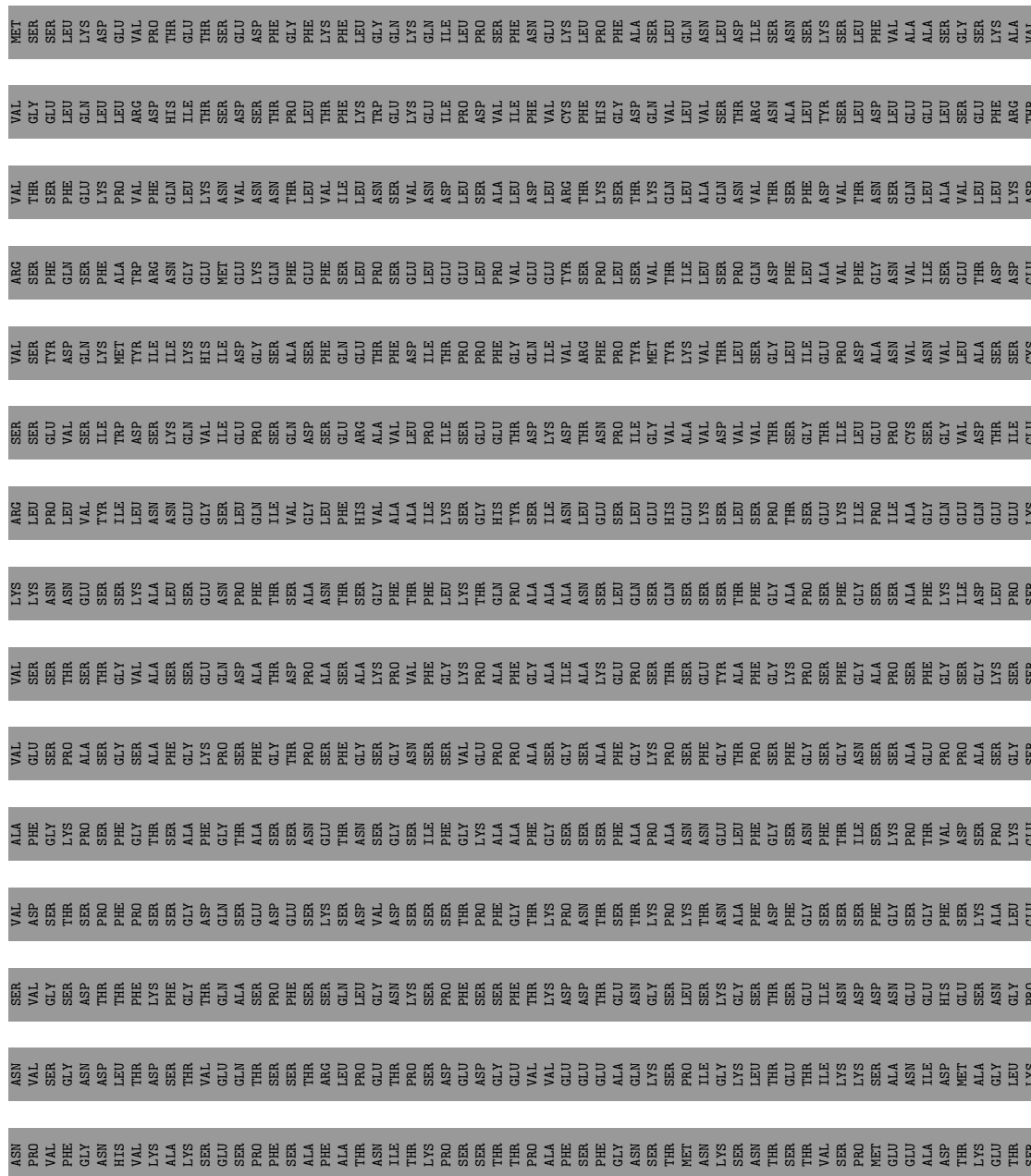


- Molecule 11: Nucleoporin ASM4

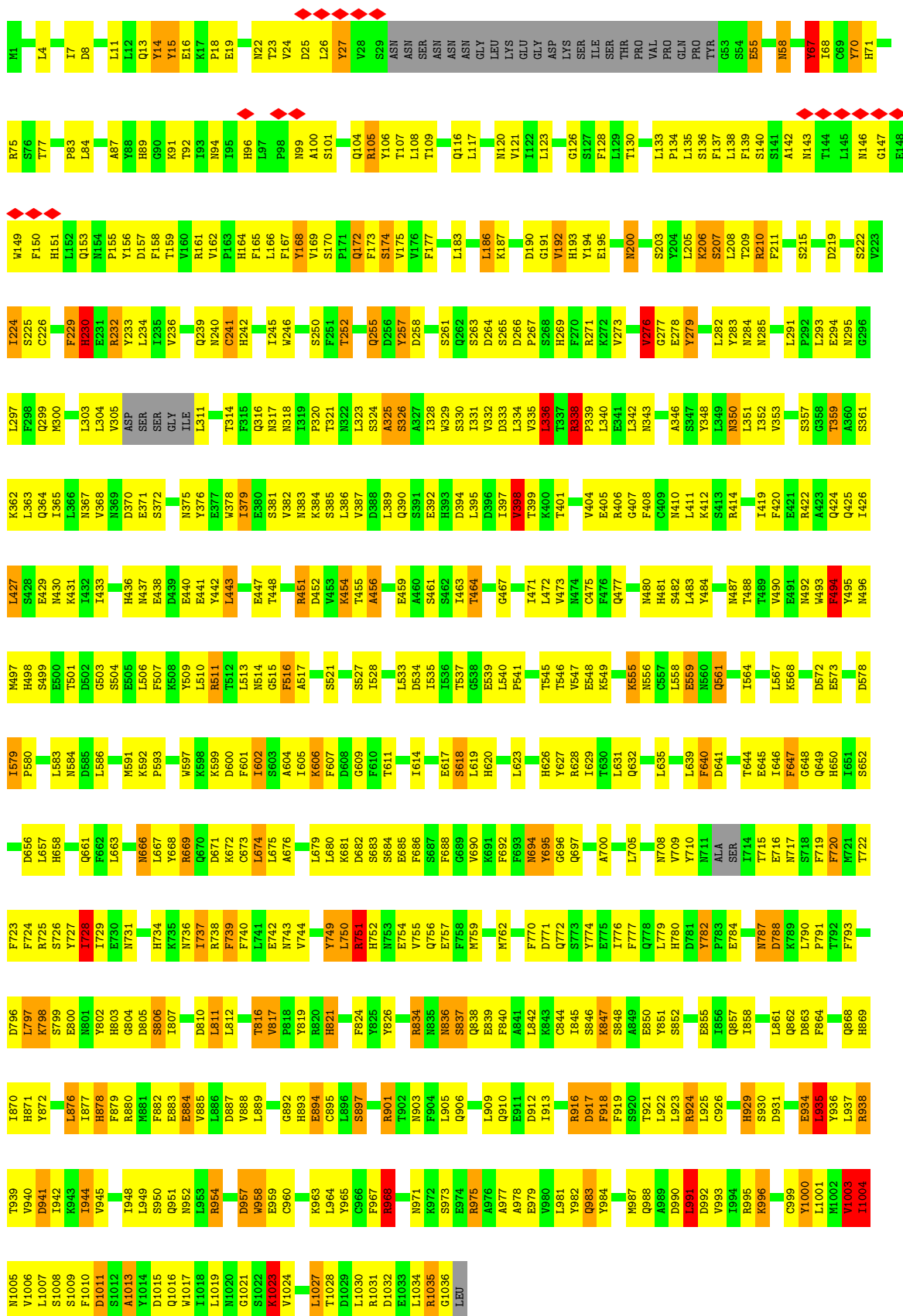


• Molecule 12: Nucleoporin NUP82





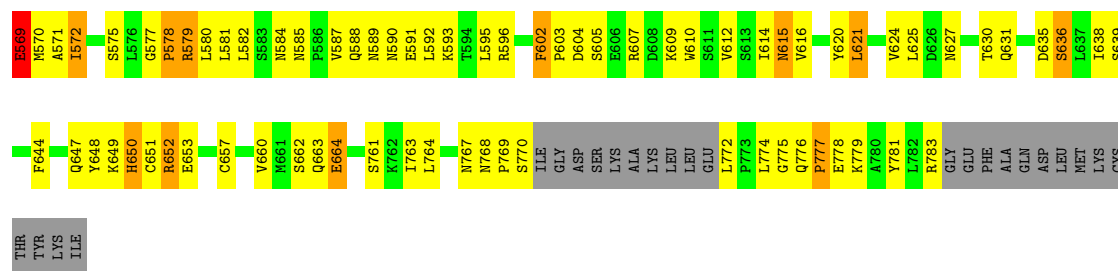




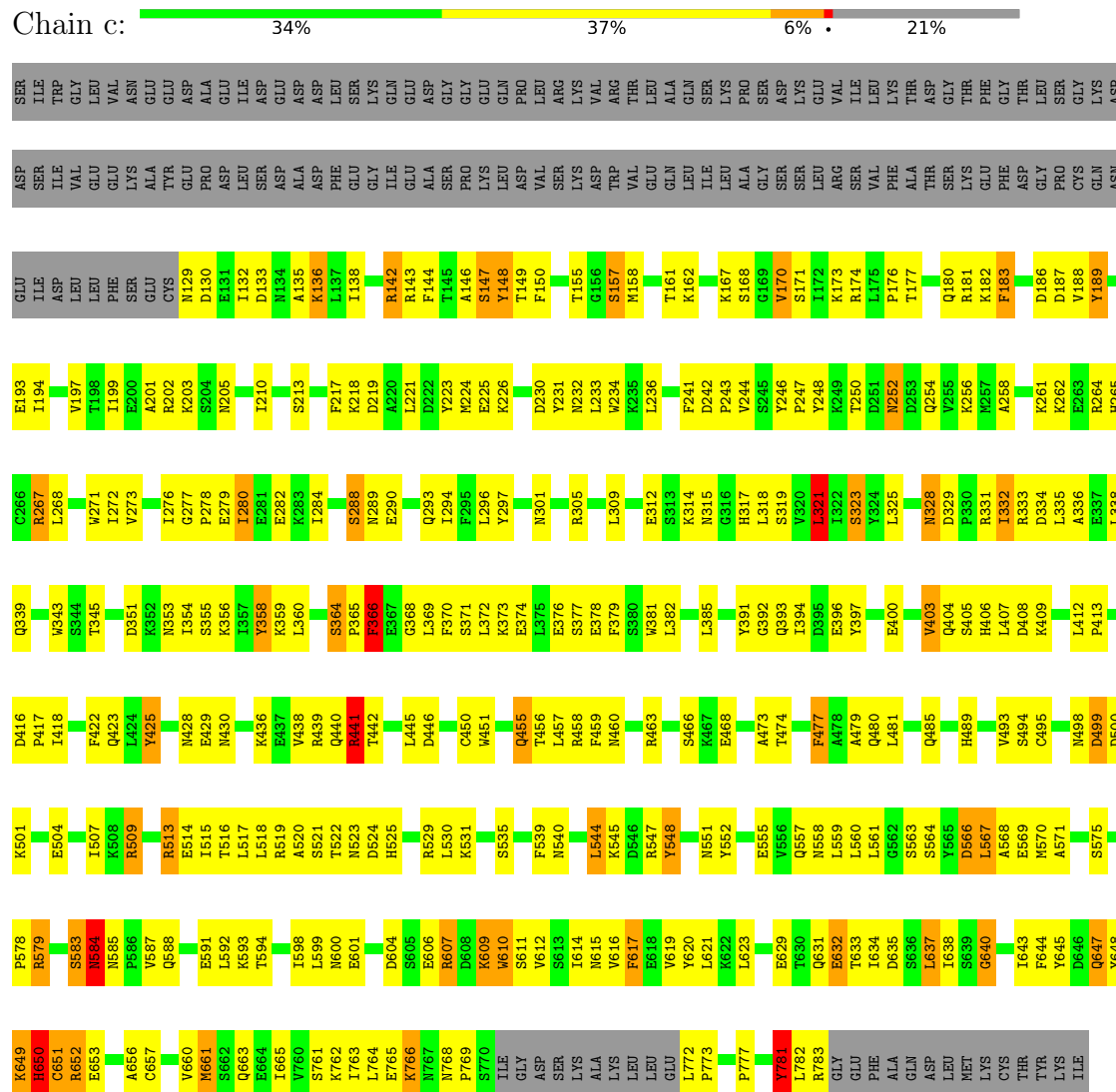
● Molecule 14: Nucleoprotein NUP120

38% 47% 11% . .

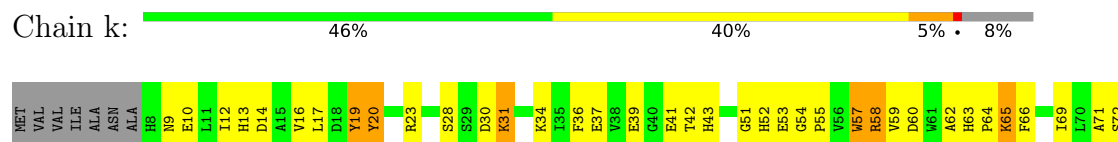


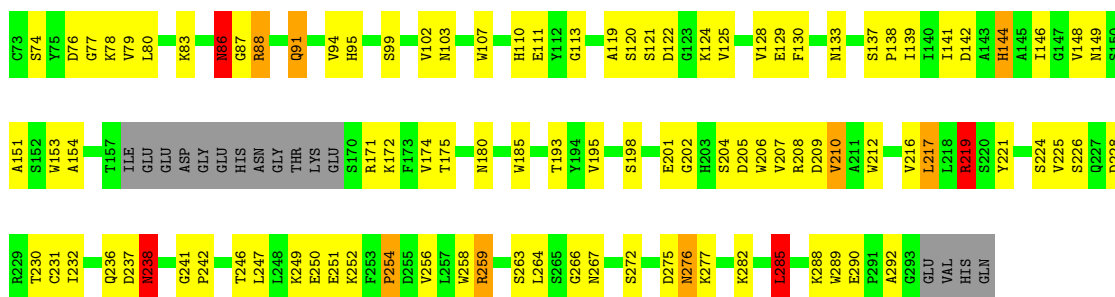


• Molecule 16: Nucleoporin 145c



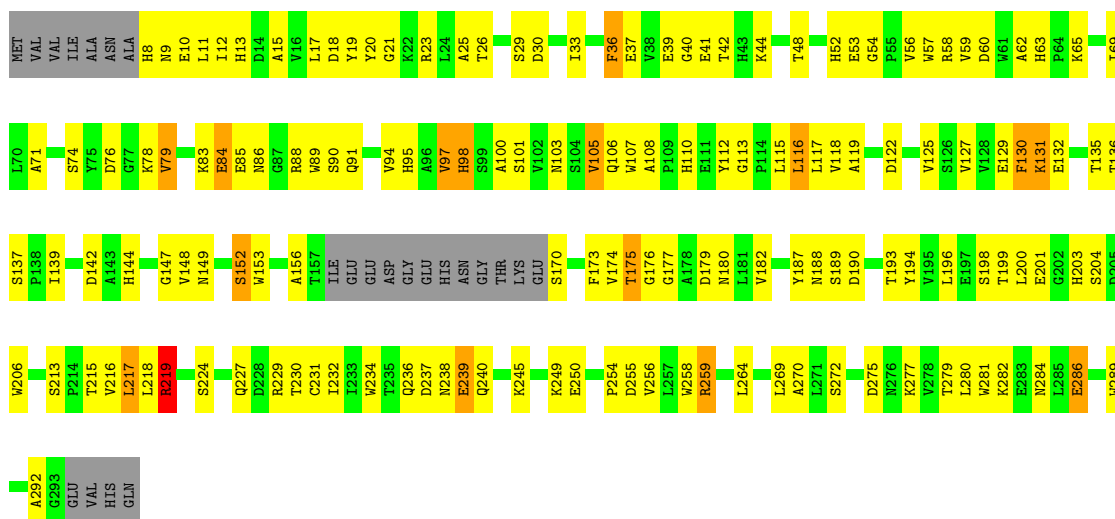
• Molecule 17: Protein transport protein SEC13





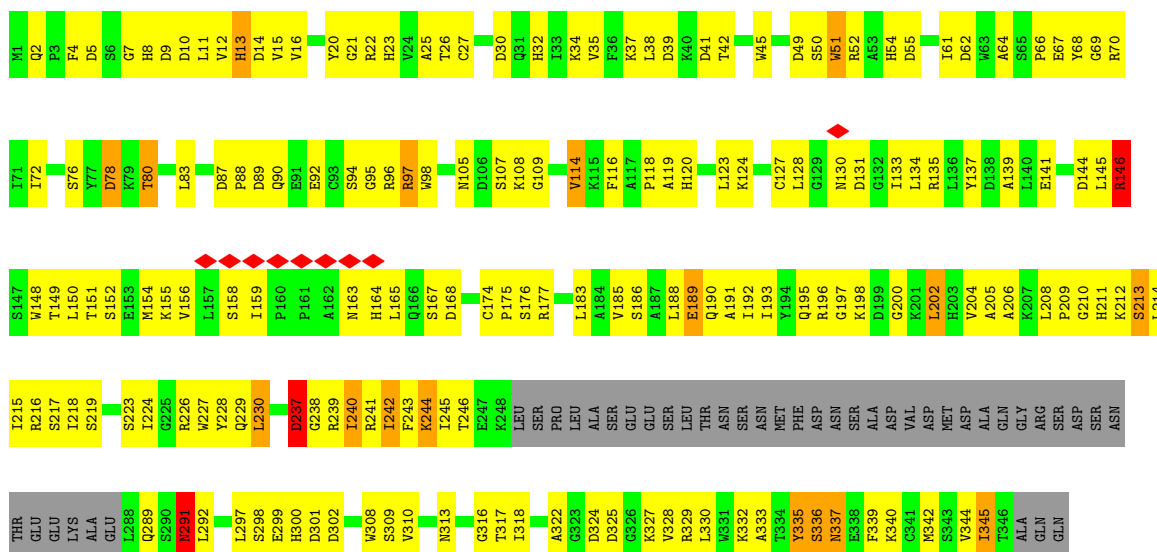
• Molecule 17: Protein transport protein SEC13

Chain d: 41% 46% 5% 8%



• Molecule 18: Nucleoporin SEH1

Chain l: 36% 46% 5% 12%

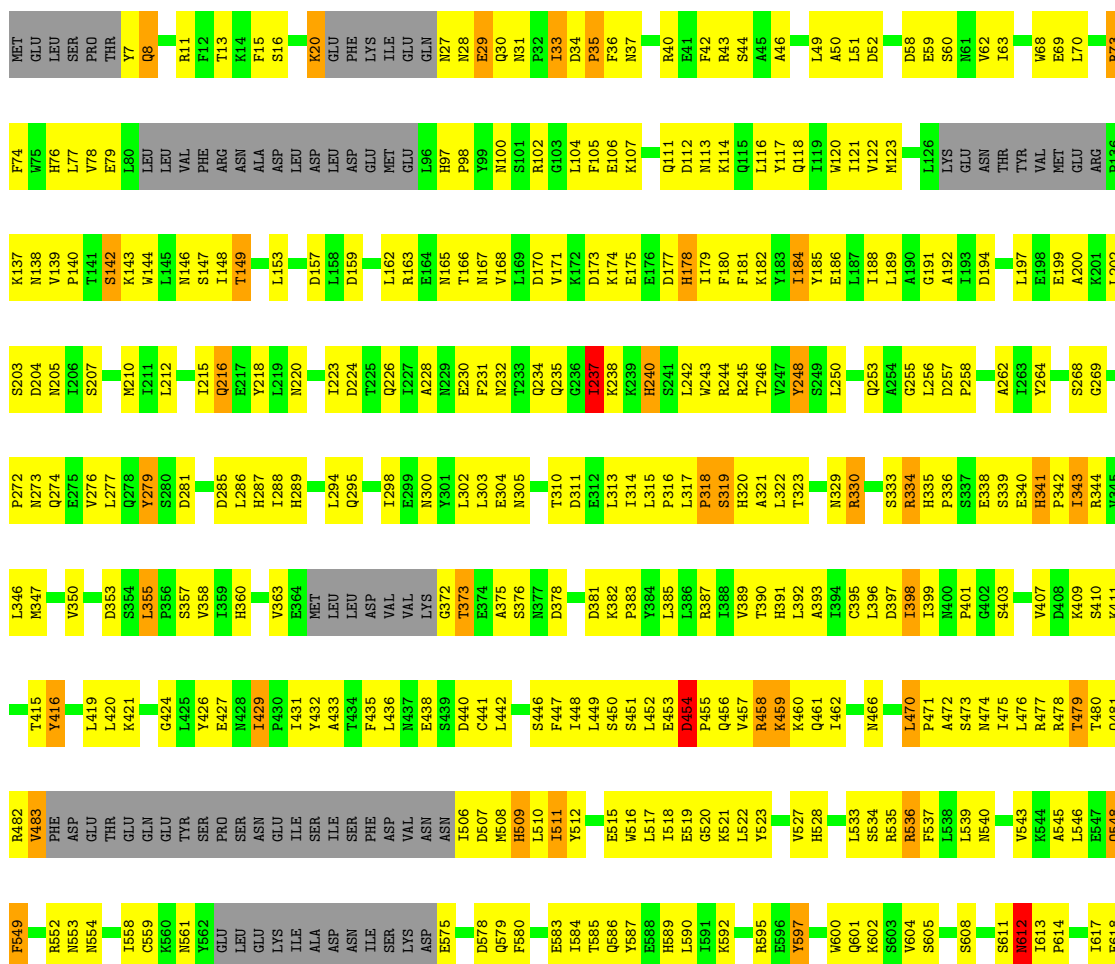


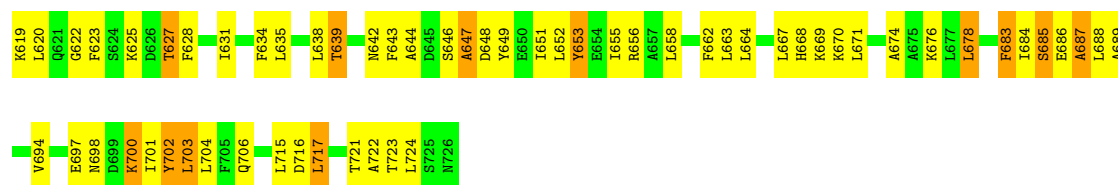
• Molecule 18: Nucleoporin SEH1

Response	Percentage
Yes, we should take action to address climate change	37%
No, we should focus on other issues	41%
Don't know	8%
Other	13%



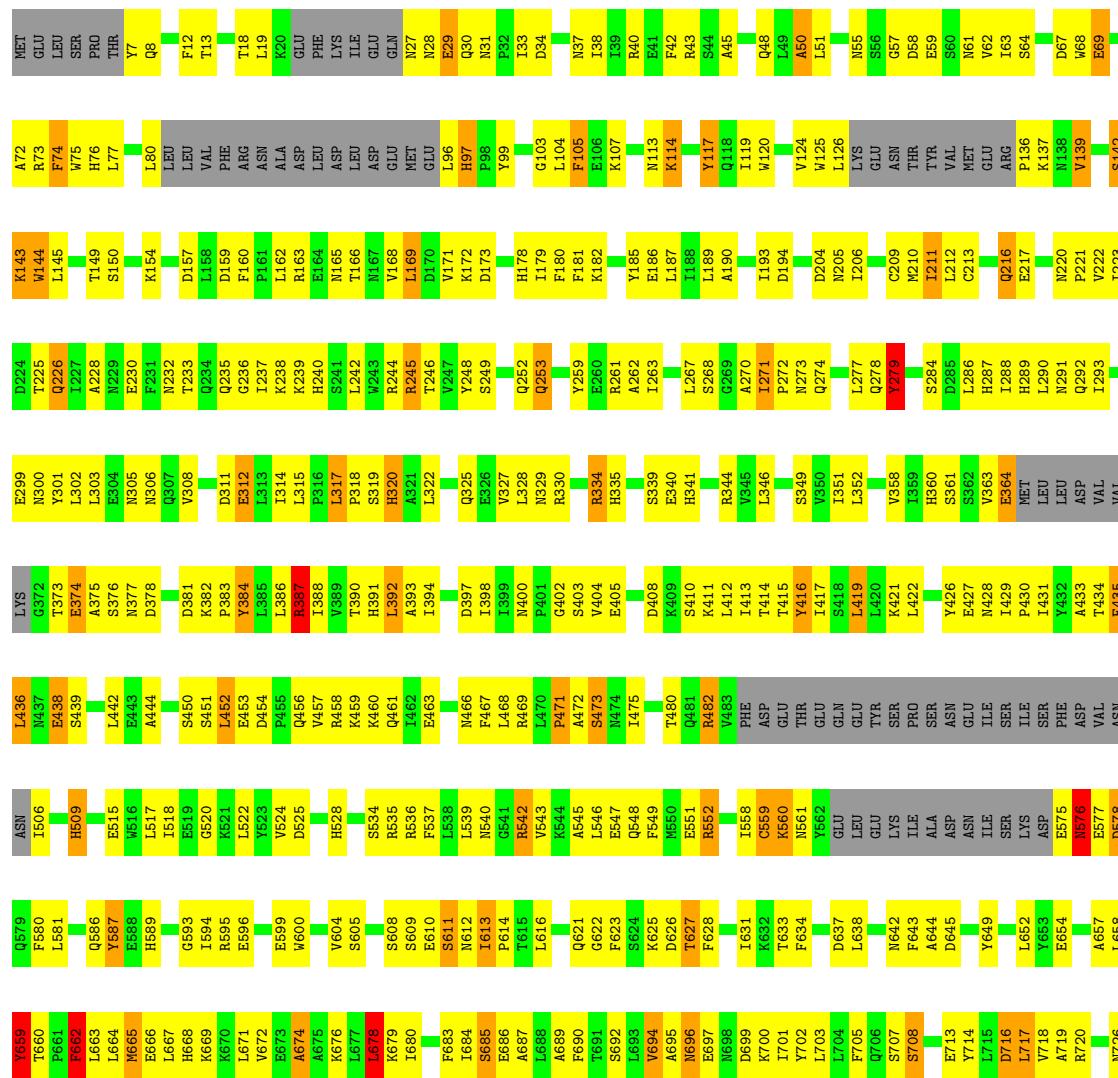
Response	Percentage
Yes, the U.S. should take action to protect the environment	35%
No, the U.S. should focus on the economy	47%
Don't know	7%
Other	11%





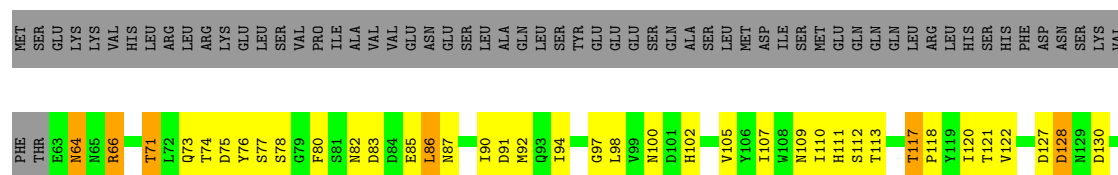
• Molecule 19: Nucleoporin NUP84

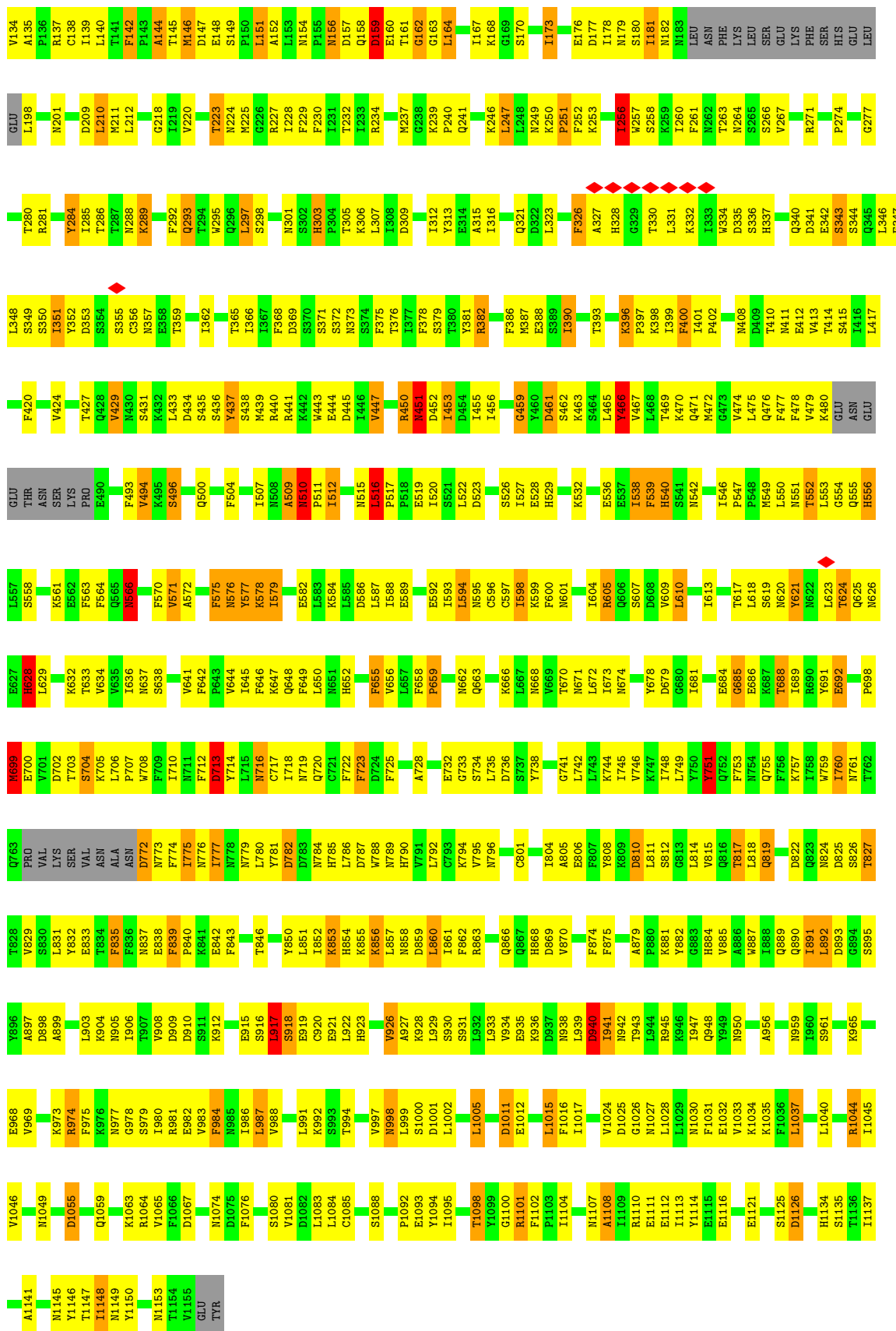
Chain f: 38% 44% 7% 11%



• Molecule 20: Nucleoporin NUP133

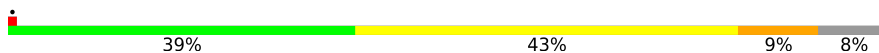
Chain n: 38% 44% 9% 8%





- Molecule 20: Nucleoporin NUP133

Chain g:



MET	THR	GLU	LYS	VAL	HIS	LEU	ARG	LEU	ARG	LYS	GLU	LEU	SER	PRO	ILE	ALA	VAL	VAL	GLU	ASN	GLU	SER	LEU	ALA	GLN	LEU	SER	LEU	GLU	GLU	GLU	GLN	GLN	LEU	ARG	LEU	HIS	HIS	PHE	ASP	ASN	SER	LYS	VAL																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
PHE	THR	GLU	LYS	VAL	HIS	LEU	ARG	LEU	ARG	LYS	GLU	LEU	SER	PRO	ILE	ALA	VAL	VAL	GLU	ASN	GLU	SER	LEU	ALA	GLN	LEU	SER	LEU	GLU	GLU	GLU	GLN	GLN	LEU	ARG	LEU	HIS	HIS	PHE	ASP	ASN	SER	LYS	VAL																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
N219	D130	V134	A135	P136	R137	C138	L139	L140	L141	L142	P143	A144	D145	E146	F147	S148	P149	F150	L151	A152	Q153	L154	D155	E156	L157	L158	D159	E160	L161	L162	L163	L164	L165	L166	L167	L168	L169	L170	L171	L172	L173	L174	L175	L176	L177	L178	L179	L180	L181	L182	L183	L184	L185	L186	L187	L188	L189	L190	L191	L192	L193	L194	L195	L196	L197	L198	L199	L200	L201	L202	L203	L204	L205	L206	L207	L208	L209	L210	L211	L212	L213	L214	L215	L216	L217	L218	L219	L220	L221	L222	L223	L224	L225	L226	L227	L228	L229	L230	L231	L232	L233	L234	L235	L236	L237	L238	L239	L240	L241	L242	L243	L244	L245	L246	L247	L248	L249	L250	L251	L252	L253	L254	L255	L256	L257	L258	L259	L260	L261	L262	L263	L264	L265	L266	L267	L268	L269	L270	L271	L272	L273	L274	L275	L276	L277	L278	L279	L280	L281	L282	L283	L284	L285	L286	L287	L288	L289	L290	L291	L292	L293	L294	L295	L296	L297	L298	L299	L300	L301	L302	L303	L304	L305	L306	L307	L308	L309	L310	L311	L312	L313	L314	L315	L316	L317	L318	L319	L320	L321	L322	L323	L324	L325	L326	L327	L328	L329	L330	L331	L332	L333	L334	L335	L336	L337	L338	L339	L340	L341	L342	L343	L344	L345	L346	L347	L348	L349	L350	L351	L352	L353	L354	L355	L356	L357	L358	L359	L360	L361	L362	L363	L364	L365	L366	L367	L368	L369	L370	L371	L372	L373	L374	L375	L376	L377	L378	L379	L380	L381	L382	L383	L384	L385	L386	L387	L388	L389	L390	L391	L392	L393	L394	L395	L396	L397	L398	L399	L400	L401	L402	L403	L404	L405	L406	L407	L408	L409	L410	L411	L412	L413	L414	L415	L416	L417	L418	L419	L420	L421	L422	L423	L424	L425	L426	L427	L428	L429	L430	L431	L432	L433	L434	L435	L436	L437	L438	L439	L440	L441	L442	L443	L444	L445	L446	L447	L448	L449	L450	L451	L452	L453	L454	L455	L456	L457	L458	L459	L460	L461	L462	L463	L464	L465	L466	L467	L468	L469	L470	L471	L472	L473	L474	L475	L476	L477	L478	L479	L480	L481	L482	L483	L484	L485	L486	L487	L488	L489	L490	L491	L492	L493	L494	L495	L496	L497	L498	L499	L500	L501	L502	L503	L504	L505	L506	L507	L508	L509	L510	L511	L512	L513	L514	L515	L516	L517	L518	L519	L520	L521	L522	L523	L524	L525	L526	L527	L528	L529	L530	L531	L532	L533	L534	L535	L536	L537	L538	L539	L540	L541	L542	L543	L544	L545	L546	L547	L548	L549	L550	L551	L552	L553	L554	L555	L556	L557	L558	L559	L560	L561	L562	L563	L564	L565	L566	L567	L568	L569	L570	L571	L572	L573	L574	L575	L576	L577	L578	L579	L580	L581	L582	L583	L584	L585	L586	L587	L588	L589	L590	L591	L592	L593	L594	L595	L596	L597	L598	L599	L600	L601	L602	L603	L604	L605	L606	L607	L608	L609	L610	L611	L612	L613	L614	L615	L616	L617	L618	L619	L620	L621	L622	L623	L624	L625	L626	L627	L628	L629	L630	L631	L632	L633	L634	L635	L636	L637	L638	L639	L640	L641	L642	L643	L644	L645	L646	L647	L648	L649	L650	L651	L652	L653	L654	L655	L656	L657	L658	L659	L660	L661	L662	L663	L664	L665	L666	L667	L668	L669	L670	L671	L672	L673	L674	L675	L676	L677	L678	L679	L680	L681	L682	L683	L684	L685	L686	L687	L688	L689	L690	L691	L692	L693	L694	L695	L696	L697	L698	L699	L700	L701	L702	L703	L704	L705	L706	L707	L708	L709	L710	L711	L712	L713	L714	L715	L716	L717	L718	L719	L720	L721	L722	L723	L724	L725	L726	L727	L728	L729	L730	L731	L732	L733	L734	L735	L736	L737	L738	L739	L740	L741	L742	L743	L744	L745	L746	L747	L748	L749	L750	L751	L752	L753	L754	L755	L756	L757	L758	L759	L760	L761	L762	L763	L764	L765	L766	L767	L768	L769	L770	L771	L772	L773	L774	L775	L776	L777	L778	L779	L780	L781	L782	L783	L784	L785	L786	L787	L788	L789	L790	L791	L792	L793	L794	L795	L796	L797	L798	L799	L800	L801	L802	L803	L804	L805	L806	L807	L808	L809	L810	L811	L812	L813	L814	L815	L816	L817	L818	L819	L820	L821	L822	L823	L824	L825	L826	L827	L828	L829	L830	L831	L832	L833	L834	L835	L836	L837	L838	L839	L840	L841	L842	L843	L844	L845	L846	L847	L848	L849	L850	L851	L852	L853	L854	L855	L856	L857	L858	L859	L860	L861	L862	L863	L864	L865	L866	L867	L868	L869	L870	L871	L872	L873	L874	L875	L876	L877	L878	L879	L880	L881	L882	L883	L884	L885	L886	L887	L888	L889	L890	L891	L892	L893	L894	L895	L896	L897	L898	L899	L900	L901	L902	L903	L904	L905	L906	L907	L908	L909	L910	L911	L912	L913	L914	L915	L916	L917	L918	L919	L920	L921	L922	L923	L924	L925	L926	L927	L928	L929	L930	L931	L932	L933	L934	L935	L936	L937	L938	L939	L940	L941	L942	L943	L944	L945	L946	L947	L948	L949	L950	L951	L952	L953	L954	L955	L956	L957	L958	L959	L960	L961	L962	L963	L964	L965	L966	L967	L968	L969	L970	L971	L972	L973	L974	L975	L976	L977	L978	L979	L980	L981	L982	L983	L984	L985	L986	L987	L988	L989	L990	L991	L992	L993	L994	L995	L996	L997	L998	L999	L1000	L1001	L1002	L1003	L1004	L1005	L1006	L1007	L1008	L1009	L1010	L1011	L1012	L1013	L1014	L1015	L1016	L1017	L1018	L1019	L1020	L1021	L1022	L1023	L1024	L1025	L1026	L1027	L1028	L1029	L1030	L1031	L1032	L1033	L1034	L1035	L1036	L1037	L1038	L1039	L1040	L1041	L1042	L1043	L1044	L1045	L1046	L1047	L1048	L1049	L1050	L1051	L1052	L1053	L1054	L1055	L1056	L1057	L1058	L1059	L1060	L1061	L1062	L1063	L1064	L1065	L1066	L1067	L1068	L1069	L1070	L1071	L1072	L1073	L1074	L1075	L1076	L1077	L1078	L1079	L1080	L1081	L1082	L1083	L1084	L1085	L1086	L1087	L1088	L1089	L1090	L1091	L1092	L1093	L1094	L1095	L1096	L1097	L1098	L1099	L1100	L1101	L1102	L1103	L1104	L1105	L1106	L1107	L1108	L1109	L1110	L1111	L1112	L1113	L1114	L1115	L1116	L1117	L1118	L1119	L1120	L1121	L1122	L1123	L1124	L1125	L1126	L1127	L1128	L1129	L1130	L1131	L1132	L1133	L1134	L1135	L1136	L1137	L1138	L1139	L1140	L1141	L1142	L1143	L1144	L1145	L1146	L1147	L1148	L1149	L1150	L1151	L1152	L1153	L1154	L1155	L1156	L1157	L1158	L1159	L1160	L1161	L1162	L1163	L1164	L1165	L1166	L1167	L1168	L1169	L1170	L1171	L1172	L1173	L1174	L1175	L1176	L1177	L1178	L1179	L1180	L1181	L1182	L1183	L1184	L1185	L1186	L1187	L1188	L1189	L1190	L1191	L1192	L1193	L1194	L1195	L1196	L1197	L1198	L1199	L1200	L1201	L1202	L1203	L1204	L1205	L1206	L1207	L1208	L1209	L1210	L1211	L1212	L1213	L1214	L1215	L1216	L1217	L1218	L1219	L1220	L1221	L1222	L1223	L1224	L1225	L1226	L1227	L1228	L1229	L1230	L1231	L1232	L1233	L1234	L1235	L1236	L1237	L1238	L1239	L1240	L1241	L1242	L1243	L1244	L1245	L1246	L1247	L1248	L1249	L1250	L1251	L1252	L1253	L1254	L1255	L1256	L1257	L1258	L1259	L1260	L1261	L1262	L1263	L1264	L1265	L1266	L1267	L1268	L1269	L1270	L1271	L1272	L1273	L1274	L1275	L1276	L1277	L1278	L1279	L1280	L1281	L1282	L1283	L1284	L1285	L1286	L1287	L1288	L1289	L1290	L1291	L1292	L1293	L1294	L1295	L1296	L1297	L1298	L1299	L1300	L1301	L1302	L1303	L1304	L1305	L1306	L1307	L1308	L1309	L1310	L1311	L1312	L1313	L1314	L1315	L1316	L1317	L1318	L1319	L1320	L1321	L1322	L1323	L1324	L1325	L1326	L1327	L1328	L1329	L1330	L1331	L1332	L1333	L1334	L1335	L1336	L1337	L1338	L1339	L1340	L1341	L1342	L1343	L1344	L1345	L1346	L1347	L1348	L1349	L1350	L1351	L1352	L1353	L1354	L1355	L1356	L1357	L1358	L1359	L1360	L1361	L1362	L1363	L1364	L1365	L1366	L1367	L1368	L1369	L1370	L1371	L1372	L1373	L1374	L1375	L1376	L1377	L1378	L1379	L1380	L1381	L1382	L1383	L1384	L1385	L1386	L1387	L1388	L1389	L1390	L1391	L1392	L1393	L1394	L1395	L1396	L1397	L1398	L1399	L1400	L1401	L1402	L1403	L1404	L1405	L1406	L1407	L1408	L1409	L1410	L1411	L1412	L1413	L1414	L1415	L1416	L1417	L1418	L1419	L1420	L1421	L1422	L1423	L1424	L1425	L1426	L1427	L1428	L1429	L1430	L1431	L1432	L1433	L1434	L1435	L1436	L1437	L1438	L1439	L1440	L1441	L1442	L1443	L1444	L1445	L1446	L1447	L1448	L1449	L1450	L1451	L1452	L1453	L1454	L1455	L1456	L1457	L1458	L1459	L1460	L1461	L1462	L1463	L1464	L1465	L1466	L1467	L1468	L1469	L1470	L1471	L1472	L1473	L1474	L1475	L1476	L1477	L1478	L1479	L1480	L1481	L1482	L1483	L1484	L1485	L1486	L1487	L1488	L1489	L1490	L1491	L1492	L1493	L1494	L1495	L1496	L1497	L1498	L1499	L1500	L1501	L1502	L1503	L1504	L1505	L1506	L1507	L1508	L15



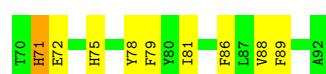
- Molecule 21: Dynein light chain 1, cytoplasmic



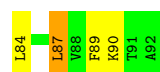
- Molecule 21: Dynein light chain 1, cytoplasmic



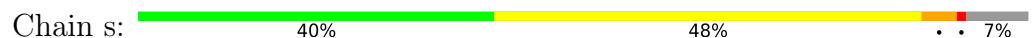
- Molecule 21: Dynein light chain 1, cytoplasmic



- Molecule 21: Dynein light chain 1, cytoplasmic

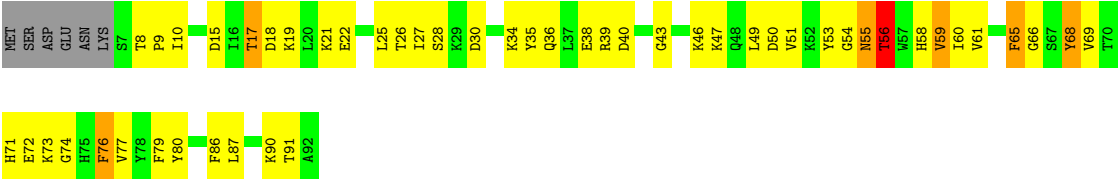
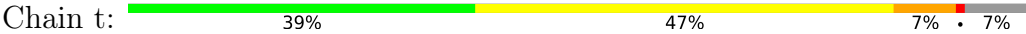


- Molecule 21: Dynein light chain 1, cytoplasmic





• Molecule 21: Dynein light chain 1, cytoplasmic



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C8	Depositor
Number of subtomograms used	518	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY; e2spt_ctf.py was used to identify the precise z height of the particle in the tomogram. This precise height was then used for computing the CTF and performing the CTF correction.	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	4.5	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	6000	Depositor
Magnification	42000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	4082.771	Depositor
Minimum map value	-3.928	Depositor
Average map value	1772.170	Depositor
Map value standard deviation	428.825	Depositor
Recommended contour level	1950	Depositor
Map size (\AA)	2156.7998, 2156.7998, 2156.7998	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	6.7399993, 6.7399993, 6.7399993	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	2.25	302/8936 (3.4%)	2.48	599/12074 (5.0%)
1	Y	2.34	313/8944 (3.5%)	2.51	641/12084 (5.3%)
2	1	2.31	288/9089 (3.2%)	2.54	632/12299 (5.1%)
2	Z	2.24	289/9076 (3.2%)	2.49	609/12281 (5.0%)
4	A	2.17	42/1327 (3.2%)	2.49	86/1788 (4.8%)
4	D	2.20	38/1328 (2.9%)	2.39	75/1791 (4.2%)
4	G	2.22	41/1334 (3.1%)	2.63	105/1799 (5.8%)
4	J	2.21	43/1334 (3.2%)	2.44	88/1799 (4.9%)
4	y	2.35	40/941 (4.3%)	2.65	88/1307 (6.7%)
4	z	2.21	28/957 (2.9%)	2.55	82/1328 (6.2%)
5	B	2.44	63/1793 (3.5%)	2.66	149/2411 (6.2%)
5	E	2.11	47/1793 (2.6%)	2.39	99/2411 (4.1%)
5	H	2.37	60/1793 (3.3%)	2.45	122/2411 (5.1%)
5	K	2.29	70/1793 (3.9%)	2.41	102/2411 (4.2%)
6	C	2.21	45/1364 (3.3%)	2.44	97/1837 (5.3%)
6	F	2.27	47/1368 (3.4%)	2.49	85/1842 (4.6%)
6	I	2.36	58/1364 (4.3%)	2.53	106/1837 (5.8%)
6	L	2.25	39/1368 (2.9%)	2.64	110/1842 (6.0%)
7	M	2.24	400/12132 (3.3%)	2.59	1018/16441 (6.2%)
7	O	2.27	416/12125 (3.4%)	2.58	964/16431 (5.9%)
8	N	2.27	355/11158 (3.2%)	2.57	857/15090 (5.7%)
8	P	2.21	361/11158 (3.2%)	2.49	804/15090 (5.3%)
9	Q	2.27	192/5257 (3.7%)	2.55	416/7126 (5.8%)
9	R	2.29	207/5361 (3.9%)	2.60	448/7273 (6.2%)
9	S	2.24	183/5270 (3.5%)	2.52	388/7144 (5.4%)
9	T	2.32	195/5361 (3.6%)	2.58	447/7273 (6.1%)
10	U	2.42	33/761 (4.3%)	2.82	67/1027 (6.5%)
10	W	2.89	38/761 (5.0%)	3.04	74/1027 (7.2%)
11	V	2.48	32/756 (4.2%)	2.98	82/1021 (8.0%)
11	X	2.37	31/756 (4.1%)	2.57	56/1021 (5.5%)
12	u	2.32	175/4278 (4.1%)	2.55	312/5833 (5.3%)
12	v	2.32	156/4119 (3.8%)	2.52	307/5612 (5.5%)
13	w	2.39	43/1084 (4.0%)	2.78	117/1485 (7.9%)
13	x	2.42	40/1102 (3.6%)	2.75	108/1510 (7.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
14	a	2.23	290/8464 (3.4%)	2.41	503/11469 (4.4%)
14	h	2.25	297/8464 (3.5%)	2.42	537/11469 (4.7%)
15	b	2.17	169/5533 (3.1%)	2.37	322/7493 (4.3%)
15	i	2.21	177/5434 (3.3%)	2.37	316/7362 (4.3%)
16	c	2.18	148/4600 (3.2%)	2.42	269/6211 (4.3%)
16	j	2.21	153/4600 (3.3%)	2.38	243/6211 (3.9%)
17	d	2.29	83/2220 (3.7%)	2.32	114/3028 (3.8%)
17	k	2.27	81/2220 (3.6%)	2.31	109/3028 (3.6%)
18	e	2.30	94/2466 (3.8%)	2.36	130/3341 (3.9%)
18	l	2.34	111/2499 (4.4%)	2.35	146/3388 (4.3%)
19	f	2.23	183/5359 (3.4%)	2.37	300/7258 (4.1%)
19	m	2.25	192/5359 (3.6%)	2.44	361/7258 (5.0%)
20	g	2.20	276/8806 (3.1%)	2.40	554/11936 (4.6%)
20	n	2.20	289/8806 (3.3%)	2.39	532/11936 (4.5%)
21	o	2.66	34/707 (4.8%)	2.59	54/954 (5.7%)
21	p	2.60	28/707 (4.0%)	2.72	58/954 (6.1%)
21	q	2.64	35/707 (5.0%)	2.59	46/954 (4.8%)
21	r	2.48	20/707 (2.8%)	2.43	40/954 (4.2%)
21	s	2.59	27/707 (3.8%)	2.70	55/954 (5.8%)
21	t	2.67	35/707 (5.0%)	2.74	60/954 (6.3%)
All	All	2.27	7432/216413 (3.4%)	2.50	15089/293068 (5.1%)

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	0	4	34
1	Y	6	30
2	1	12	30
2	Z	9	25
4	A	0	1
4	D	0	3
4	G	2	3
4	J	0	2
5	B	4	4
5	E	0	3
5	H	2	3
5	K	2	2
6	C	0	2
6	F	1	3

Continued on next page...

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Mol	Chain	#Chirality outliers	#Planarity outliers
6	I	1	5
6	L	2	5
7	M	5	44
7	O	6	49
8	N	14	44
8	P	6	41
9	Q	2	16
9	R	2	11
9	S	0	14
9	T	4	19
10	U	4	4
10	W	6	2
11	V	3	2
11	X	2	1
12	u	0	8
12	v	0	14
13	x	0	2
14	a	1	57
14	h	1	49
15	b	0	23
15	i	0	31
16	c	0	21
16	j	0	22
17	d	0	9
17	k	0	3
18	e	0	10
18	l	0	10
19	f	0	21
19	m	1	12
20	g	0	37
20	n	0	34
21	o	2	3
21	p	2	6
21	q	2	5
21	r	2	4
21	s	2	5
21	t	2	6
All	All	114	794

The worst 5 of 7432 bond length outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Y	791	MET	C-O	60.97	2.45	1.23
8	N	794	ILE	CA-CB	-33.88	1.08	1.54
21	p	55	ASN	N-CA	-30.14	1.07	1.46
2	Z	678	LYS	N-CA	-28.38	1.13	1.46
21	s	55	ASN	N-CA	-27.09	1.10	1.46

The worst 5 of 15089 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	1	309	LEU	N-CA-CB	36.30	172.21	110.50
8	N	794	ILE	N-CA-CB	32.75	165.27	111.23
11	V	402	ASN	N-CA-CB	26.18	155.00	110.50
5	B	324	TYR	N-CA-CB	25.82	154.12	110.49
2	1	678	LYS	N-CA-C	-25.14	80.28	110.44

5 of 114 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	0	832	VAL	CA
1	0	1021	TYR	CA
1	0	1022	ASP	CA
1	0	1258	LEU	CA
2	1	308	ASN	CA

5 of 794 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	107	TYR	Sidechain
1	0	127	TYR	Sidechain
1	0	133	TYR	Sidechain
1	0	201	TYR	Sidechain
1	0	257	PHE	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	8762	0	8808	270	0
1	Y	8770	0	8821	123	0
2	1	8919	0	8932	108	0
2	Z	8906	0	8917	109	0
3	5	181	0	38	0	0
3	6	181	0	38	7	0
4	A	1315	0	1274	9	0
4	D	1315	0	1275	16	0
4	G	1321	0	1280	6	0
4	J	1321	0	1280	22	0
4	y	946	0	404	19	0
4	z	962	0	410	24	0
5	B	1771	0	1832	11	0
5	E	1771	0	1832	70	0
5	H	1771	0	1832	39	0
5	K	1771	0	1832	11	0
6	C	1347	0	1376	10	0
6	F	1351	0	1379	12	0
6	I	1347	0	1376	8	0
6	L	1351	0	1379	8	0
7	M	11909	0	11617	105	0
7	O	11902	0	11608	120	0
8	N	10971	0	11316	148	0
8	P	10971	0	11315	215	0
9	Q	5184	0	4900	24	0
9	R	5287	0	4948	61	0
9	S	5197	0	4913	90	0
9	T	5287	0	4948	21	0
10	U	745	0	752	23	0
10	W	745	0	752	16	0
11	V	739	0	722	23	0
11	X	739	0	722	30	0
12	u	4214	0	3713	9	0
12	v	4063	0	3567	18	0
13	w	1088	0	656	1	0
13	x	1106	0	671	9	0
14	a	8279	0	8125	49	0
14	h	8279	0	8125	29	0
15	b	5424	0	5397	14	0
15	i	5327	0	5309	19	0
16	c	4520	0	4539	21	0
16	j	4520	0	4539	12	0
17	d	2160	0	2096	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	k	2160	0	2096	6	0
18	e	2407	0	2348	17	0
18	l	2438	0	2378	6	0
19	f	5261	0	5261	41	0
19	m	5261	0	5261	56	0
20	g	8627	0	8539	36	0
20	n	8627	0	8539	61	0
21	o	691	0	702	1	0
21	p	691	0	702	11	0
21	q	691	0	702	0	0
21	r	691	0	702	3	0
21	s	691	0	702	0	0
21	t	691	0	702	1	0
All	All	212962	0	208199	1948	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 5.

The worst 5 of 1948 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)
1:0:413:LEU:HD11	1:0:467:PHE:CD1	1.34	1.62
1:Y:412:ILE:CG2	1:Y:444:VAL:CG2	1.77	1.62
13:x:1300:ARG:CB	21:p:51:VAL:HG21	1.28	1.59
8:N:322:HIS:CE1	8:N:359:LEU:HB3	1.34	1.58
1:Y:412:ILE:CG2	1:Y:444:VAL:HG21	1.20	1.58

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	1053/1502 (70%)	857 (81%)	118 (11%)	78 (7%)	1	10
1	Y	1054/1502 (70%)	864 (82%)	114 (11%)	76 (7%)	1	11
2	1	1087/1391 (78%)	919 (84%)	115 (11%)	53 (5%)	1	16
2	Z	1085/1391 (78%)	918 (85%)	113 (10%)	54 (5%)	1	16
4	A	156/823 (19%)	150 (96%)	2 (1%)	4 (3%)	4	25
4	D	157/823 (19%)	150 (96%)	6 (4%)	1 (1%)	21	59
4	G	158/823 (19%)	151 (96%)	1 (1%)	6 (4%)	2	19
4	J	158/823 (19%)	150 (95%)	6 (4%)	2 (1%)	9	42
4	y	180/823 (22%)	180 (100%)	0	0	100	100
4	z	183/823 (22%)	181 (99%)	2 (1%)	0	100	100
5	B	211/541 (39%)	189 (90%)	9 (4%)	13 (6%)	1	13
5	E	211/541 (39%)	189 (90%)	17 (8%)	5 (2%)	4	27
5	H	211/541 (39%)	179 (85%)	21 (10%)	11 (5%)	1	15
5	K	211/541 (39%)	193 (92%)	11 (5%)	7 (3%)	3	21
6	C	160/472 (34%)	149 (93%)	8 (5%)	3 (2%)	6	32
6	F	161/472 (34%)	153 (95%)	6 (4%)	2 (1%)	10	44
6	I	160/472 (34%)	151 (94%)	6 (4%)	3 (2%)	6	32
6	L	161/472 (34%)	152 (94%)	5 (3%)	4 (2%)	4	26
7	M	1497/1683 (89%)	1249 (83%)	170 (11%)	78 (5%)	1	15
7	O	1496/1683 (89%)	1245 (83%)	173 (12%)	78 (5%)	1	15
8	N	1310/1655 (79%)	994 (76%)	208 (16%)	108 (8%)	0	9
8	P	1310/1655 (79%)	1015 (78%)	191 (15%)	104 (8%)	1	10
9	Q	670/839 (80%)	576 (86%)	63 (9%)	31 (5%)	2	17
9	R	692/839 (82%)	590 (85%)	60 (9%)	42 (6%)	1	13
9	S	672/839 (80%)	584 (87%)	66 (10%)	22 (3%)	3	21
9	T	692/839 (82%)	588 (85%)	68 (10%)	36 (5%)	1	15
10	U	90/475 (19%)	78 (87%)	6 (7%)	6 (7%)	1	12
10	W	90/475 (19%)	74 (82%)	9 (10%)	7 (8%)	1	10
11	V	90/528 (17%)	70 (78%)	15 (17%)	5 (6%)	1	14
11	X	90/528 (17%)	74 (82%)	9 (10%)	7 (8%)	1	10
12	u	569/713 (80%)	500 (88%)	38 (7%)	31 (5%)	1	15
12	v	546/713 (77%)	481 (88%)	40 (7%)	25 (5%)	2	17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	w	179/1460 (12%)	172 (96%)	5 (3%)	2 (1%)	11	46
13	x	182/1460 (12%)	177 (97%)	4 (2%)	1 (0%)	24	63
14	a	996/1037 (96%)	815 (82%)	119 (12%)	62 (6%)	1	13
14	h	996/1037 (96%)	825 (83%)	107 (11%)	64 (6%)	1	12
15	b	667/744 (90%)	532 (80%)	92 (14%)	43 (6%)	1	12
15	i	655/744 (88%)	522 (80%)	91 (14%)	42 (6%)	1	12
16	c	551/712 (77%)	472 (86%)	51 (9%)	28 (5%)	1	15
16	j	551/712 (77%)	475 (86%)	52 (9%)	24 (4%)	2	17
17	d	270/297 (91%)	233 (86%)	29 (11%)	8 (3%)	3	23
17	k	270/297 (91%)	230 (85%)	28 (10%)	12 (4%)	2	17
18	e	297/349 (85%)	262 (88%)	25 (8%)	10 (3%)	3	21
18	l	303/349 (87%)	261 (86%)	28 (9%)	14 (5%)	2	17
19	f	635/726 (88%)	539 (85%)	68 (11%)	28 (4%)	2	17
19	m	635/726 (88%)	548 (86%)	61 (10%)	26 (4%)	2	18
20	g	1052/1157 (91%)	864 (82%)	126 (12%)	62 (6%)	1	13
20	n	1052/1157 (91%)	844 (80%)	142 (14%)	66 (6%)	1	13
21	o	84/92 (91%)	78 (93%)	4 (5%)	2 (2%)	4	27
21	p	84/92 (91%)	80 (95%)	3 (4%)	1 (1%)	10	44
21	q	84/92 (91%)	78 (93%)	4 (5%)	2 (2%)	4	27
21	r	84/92 (91%)	76 (90%)	5 (6%)	3 (4%)	2	20
21	s	84/92 (91%)	79 (94%)	4 (5%)	1 (1%)	10	44
21	t	84/92 (91%)	77 (92%)	5 (6%)	2 (2%)	4	27
All	All	26366/41756 (63%)	22232 (84%)	2729 (10%)	1405 (5%)	2	15

5 of 1405 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	180	ASN
1	0	250	ALA
1	0	293	ILE
1	0	420	ILE
1	0	517	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	978/1353 (72%)	924 (94%)	54 (6%)	19	41
1	Y	979/1353 (72%)	918 (94%)	61 (6%)	16	38
2	1	1008/1250 (81%)	929 (92%)	79 (8%)	11	32
2	Z	1007/1250 (81%)	942 (94%)	65 (6%)	15	37
4	A	154/674 (23%)	148 (96%)	6 (4%)	28	49
4	D	154/674 (23%)	147 (96%)	7 (4%)	24	46
4	G	155/674 (23%)	143 (92%)	12 (8%)	12	32
4	J	155/674 (23%)	148 (96%)	7 (4%)	24	46
5	B	196/439 (45%)	182 (93%)	14 (7%)	13	35
5	E	196/439 (45%)	181 (92%)	15 (8%)	12	32
5	H	196/439 (45%)	181 (92%)	15 (8%)	12	32
5	K	196/439 (45%)	184 (94%)	12 (6%)	17	38
6	C	155/377 (41%)	146 (94%)	9 (6%)	18	40
6	F	155/377 (41%)	146 (94%)	9 (6%)	18	40
6	I	155/377 (41%)	148 (96%)	7 (4%)	24	46
6	L	155/377 (41%)	146 (94%)	9 (6%)	18	40
7	M	1279/1538 (83%)	1191 (93%)	88 (7%)	14	36
7	O	1278/1538 (83%)	1197 (94%)	81 (6%)	16	37
8	N	1278/1557 (82%)	1186 (93%)	92 (7%)	13	35
8	P	1278/1557 (82%)	1178 (92%)	100 (8%)	11	32
9	Q	507/762 (66%)	479 (94%)	28 (6%)	19	41
9	R	508/762 (67%)	481 (95%)	27 (5%)	20	41
9	S	508/762 (67%)	476 (94%)	32 (6%)	16	37
9	T	508/762 (67%)	484 (95%)	24 (5%)	23	45
10	U	80/421 (19%)	74 (92%)	6 (8%)	12	33
10	W	80/421 (19%)	75 (94%)	5 (6%)	16	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	V	82/477 (17%)	71 (87%)	11 (13%)	4	14
11	X	82/477 (17%)	71 (87%)	11 (13%)	4	14
12	u	397/670 (59%)	370 (93%)	27 (7%)	14	36
12	v	379/670 (57%)	362 (96%)	17 (4%)	24	46
13	w	35/1290 (3%)	33 (94%)	2 (6%)	18	40
13	x	36/1290 (3%)	34 (94%)	2 (6%)	19	40
14	a	945/972 (97%)	896 (95%)	49 (5%)	21	42
14	h	945/972 (97%)	903 (96%)	42 (4%)	25	47
15	b	606/670 (90%)	581 (96%)	25 (4%)	27	49
15	i	596/670 (89%)	569 (96%)	27 (4%)	24	46
16	c	513/646 (79%)	481 (94%)	32 (6%)	16	38
16	j	513/646 (79%)	489 (95%)	24 (5%)	23	45
17	d	233/252 (92%)	226 (97%)	7 (3%)	36	57
17	k	233/252 (92%)	221 (95%)	12 (5%)	21	42
18	e	266/305 (87%)	257 (97%)	9 (3%)	32	54
18	l	269/305 (88%)	257 (96%)	12 (4%)	24	46
19	f	594/669 (89%)	561 (94%)	33 (6%)	19	40
19	m	594/669 (89%)	560 (94%)	34 (6%)	18	40
20	g	997/1088 (92%)	956 (96%)	41 (4%)	27	49
20	n	997/1088 (92%)	945 (95%)	52 (5%)	21	42
21	o	75/81 (93%)	73 (97%)	2 (3%)	39	61
21	p	75/81 (93%)	71 (95%)	4 (5%)	20	41
21	q	75/81 (93%)	73 (97%)	2 (3%)	39	61
21	r	75/81 (93%)	70 (93%)	5 (7%)	15	36
21	s	75/81 (93%)	69 (92%)	6 (8%)	11	31
21	t	75/81 (93%)	71 (95%)	4 (5%)	20	41
All	All	23060/35810 (64%)	21704 (94%)	1356 (6%)	19	39

5 of 1356 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	v	379	ASN
21	r	12	LYS

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Mol	Chain	Res	Type
14	h	464	THR
12	v	363	LEU
18	l	80	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 744 such sidechains are listed below:

Mol	Chain	Res	Type
12	v	301	ASN
20	n	663	GLN
14	h	418	GLN
12	v	288	ASN
16	j	615	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
16	j	2
16	c	2
20	n	1
20	g	1
4	A	1
14	a	1
14	h	1
1	0	1

The worst 5 of 10 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	n	807:PHE	C	808:TYR	N	28.87
1	g	807:PHE	C	808:TYR	N	9.13
1	j	665:ILE	C	760:VAL	N	8.70
1	A	637:LEU	C	638:ASP	N	7.22
1	a	486:LEU	C	487:ASN	N	6.29

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24258. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

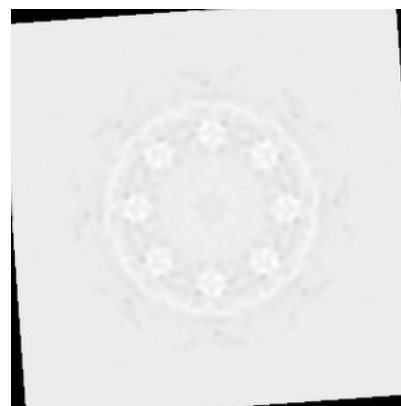
6.1.1 Primary map



X

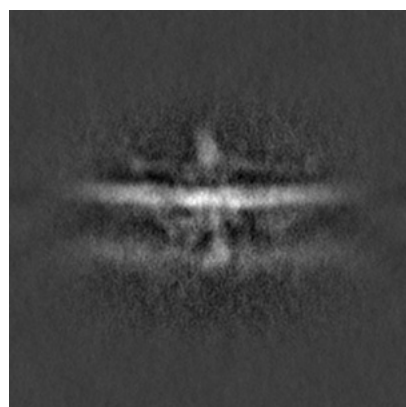


Y

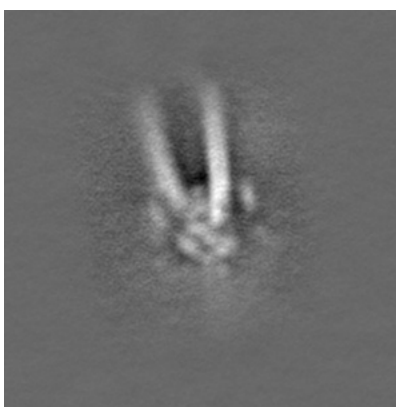


Z

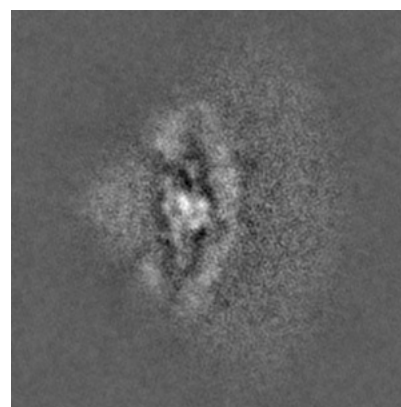
6.1.2 Raw map



X



Y

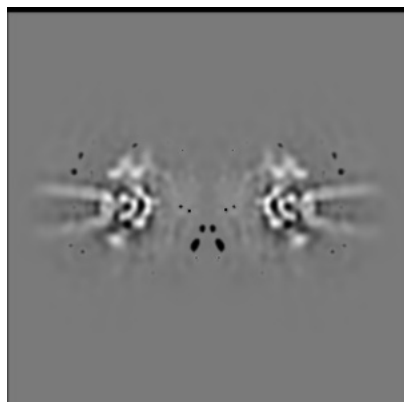


Z

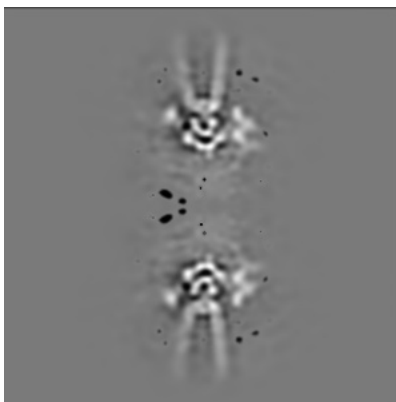
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

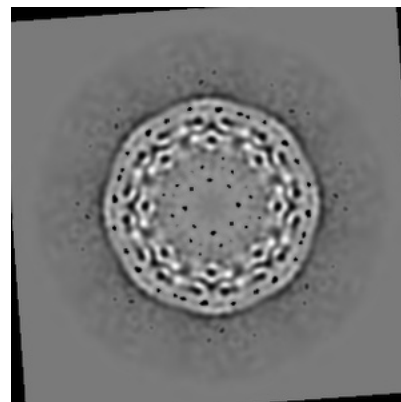
6.2.1 Primary map



X Index: 160

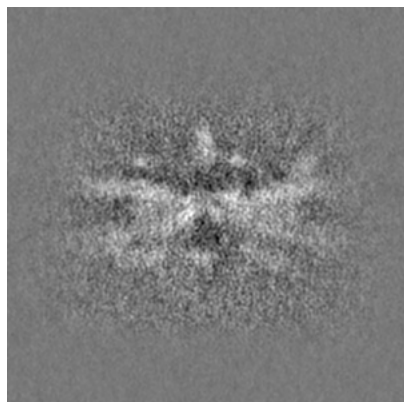


Y Index: 160

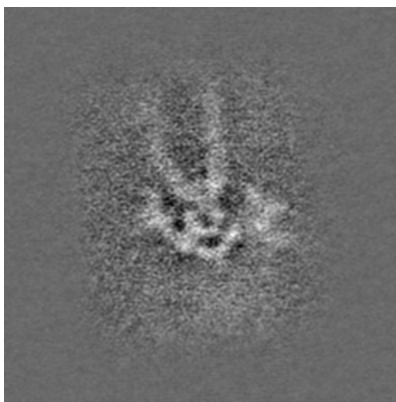


Z Index: 160

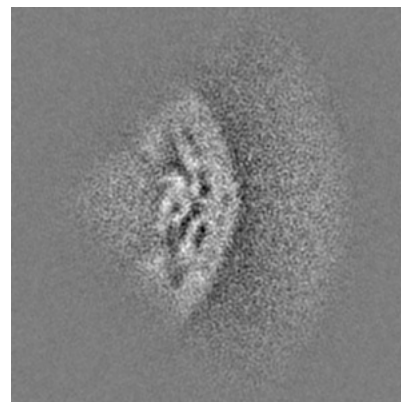
6.2.2 Raw map



X Index: 104



Y Index: 104

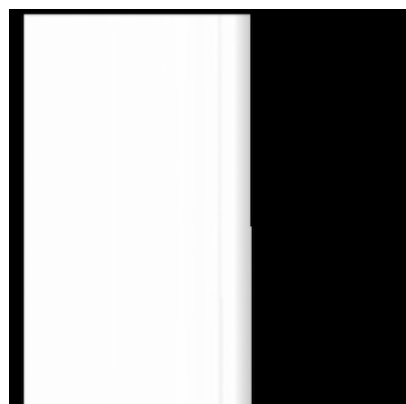


Z Index: 104

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

6.3 Largest variance slices [i](#)

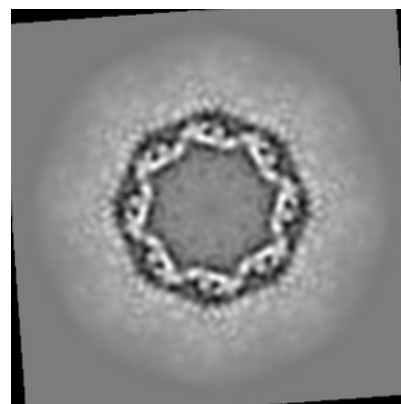
6.3.1 Primary map



X Index: 317

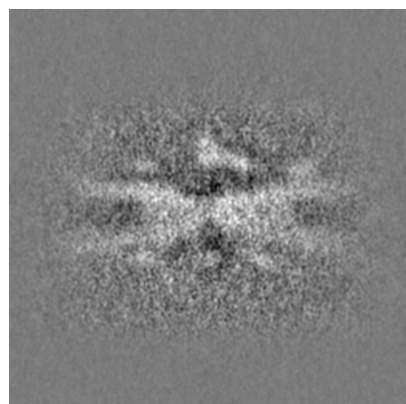


Y Index: 317

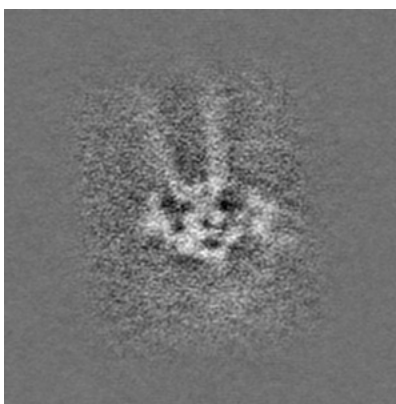


Z Index: 171

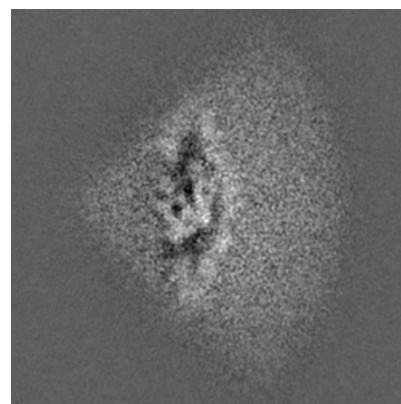
6.3.2 Raw map



X Index: 106



Y Index: 105

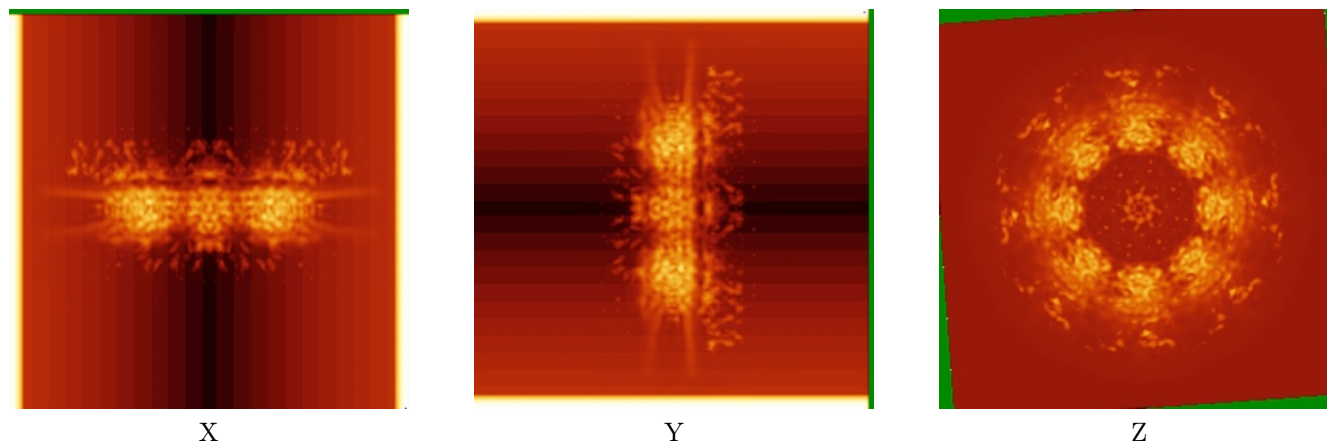


Z Index: 110

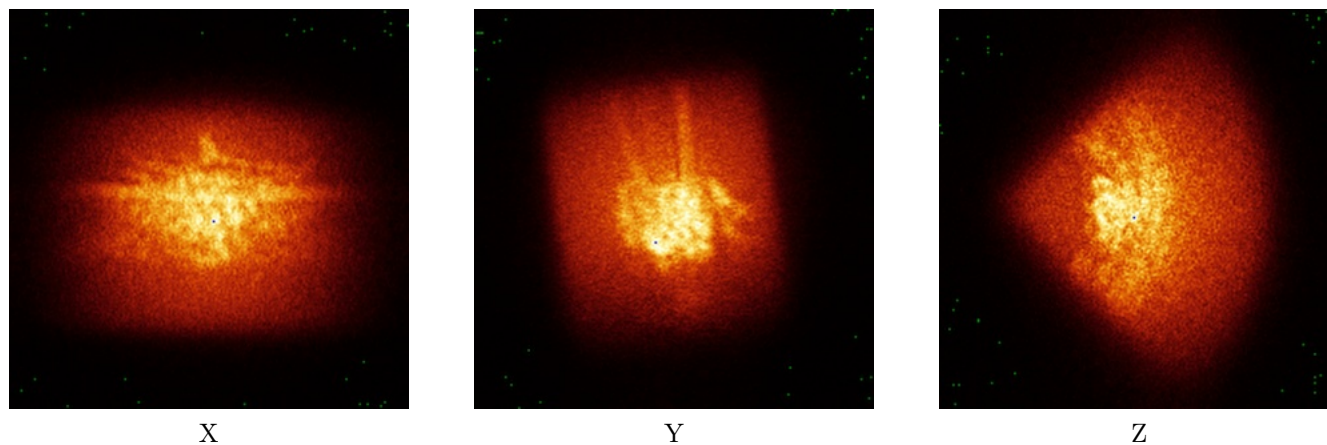
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



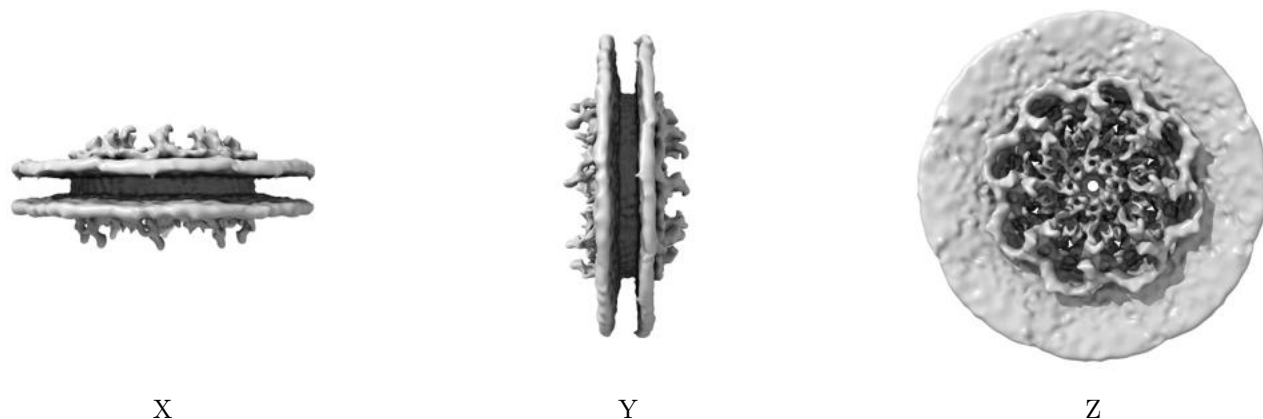
6.4.2 Raw map



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.

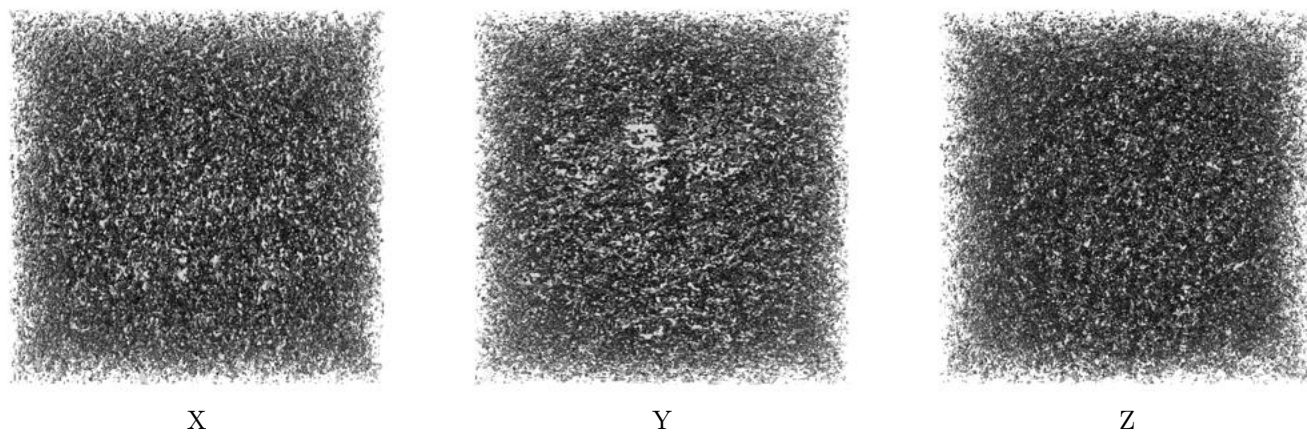
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1950.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

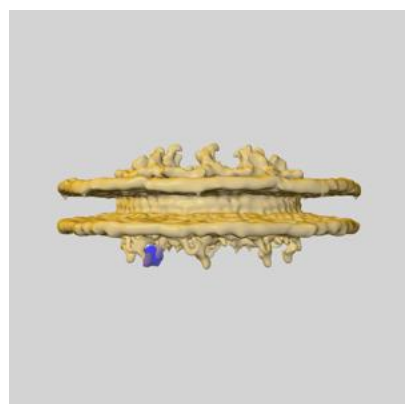
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

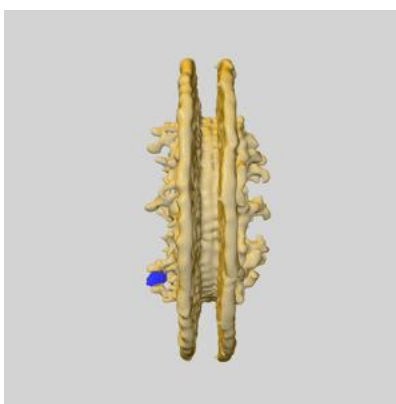
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

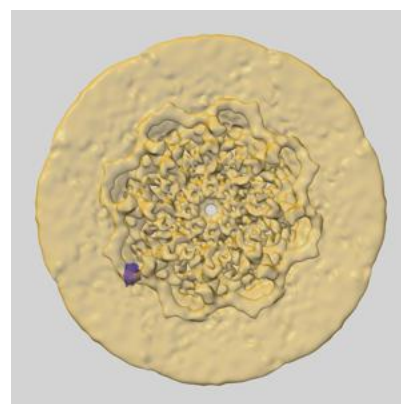
6.6.1 emd_24258_msk_1.map [i](#)



X

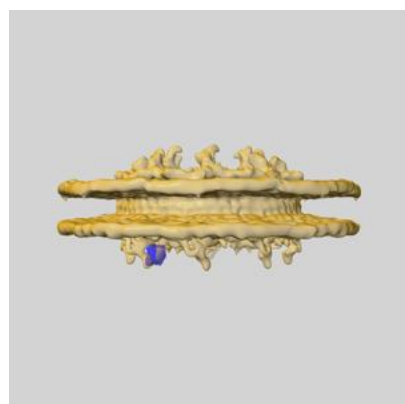


Y

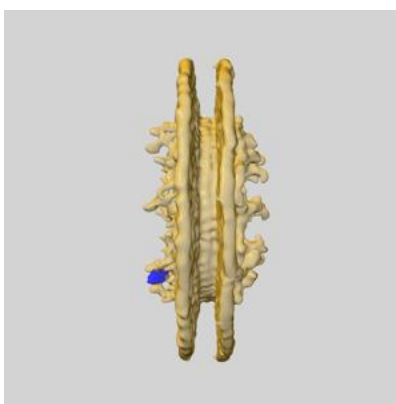


Z

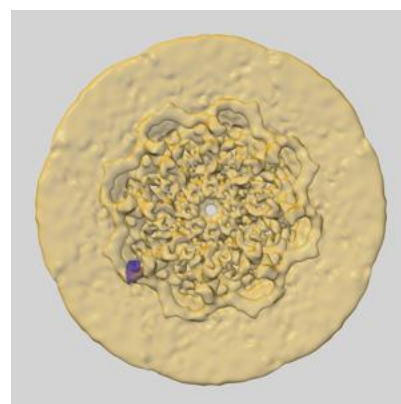
6.6.2 emd_24258_msk_2.map [i](#)



X



Y

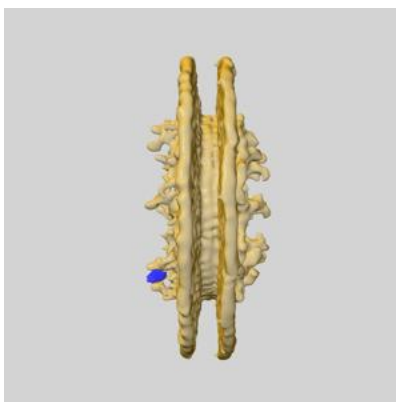


Z

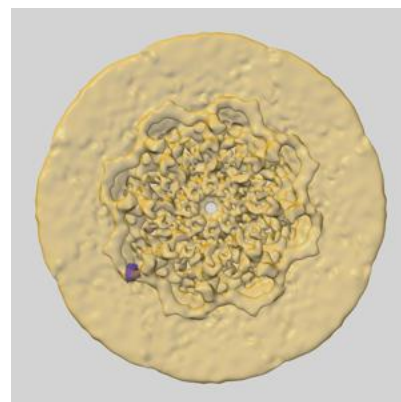
6.6.3 emd_24258_msk_3.map [i](#)



X



Y

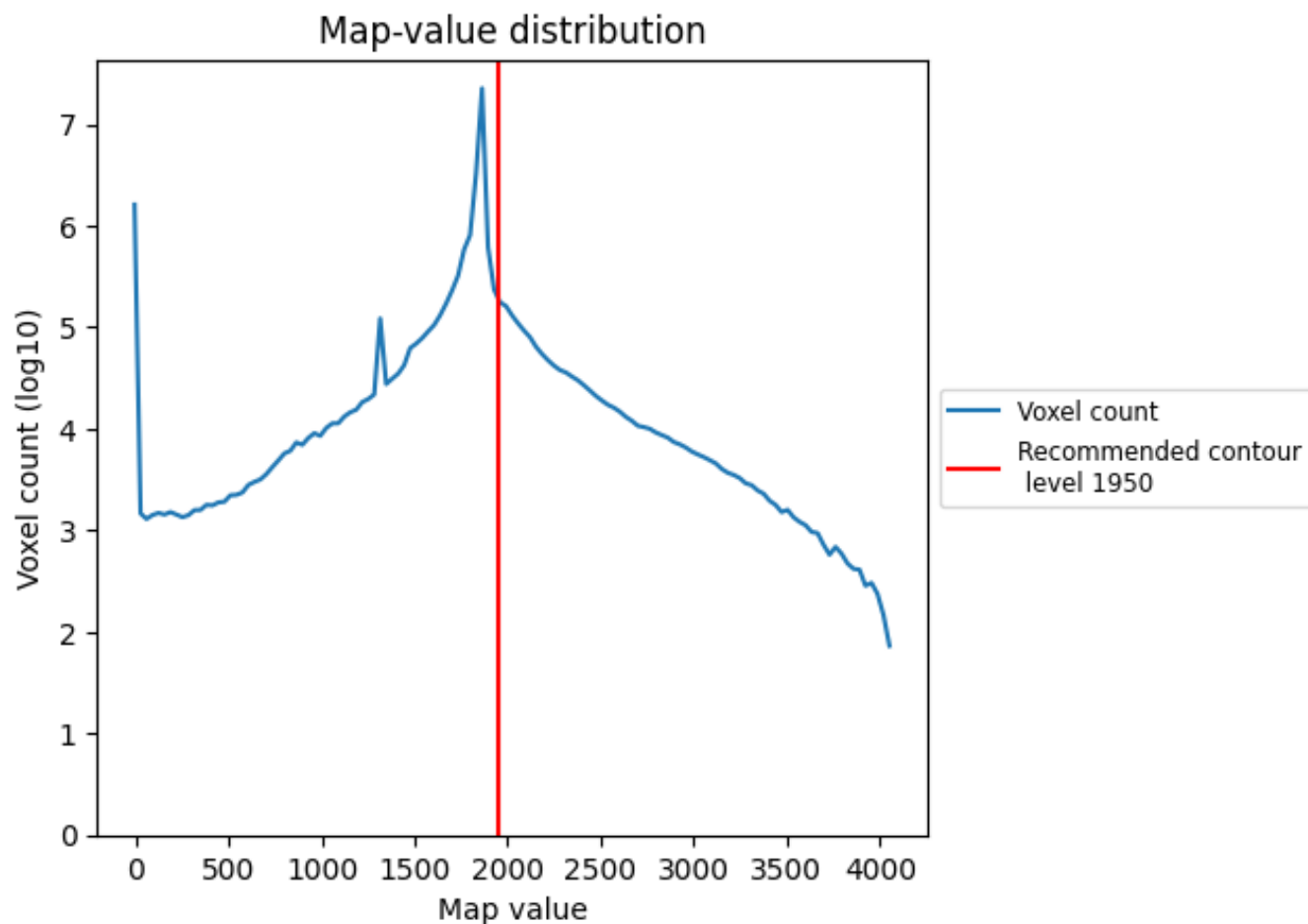


Z

7 Map analysis [i](#)

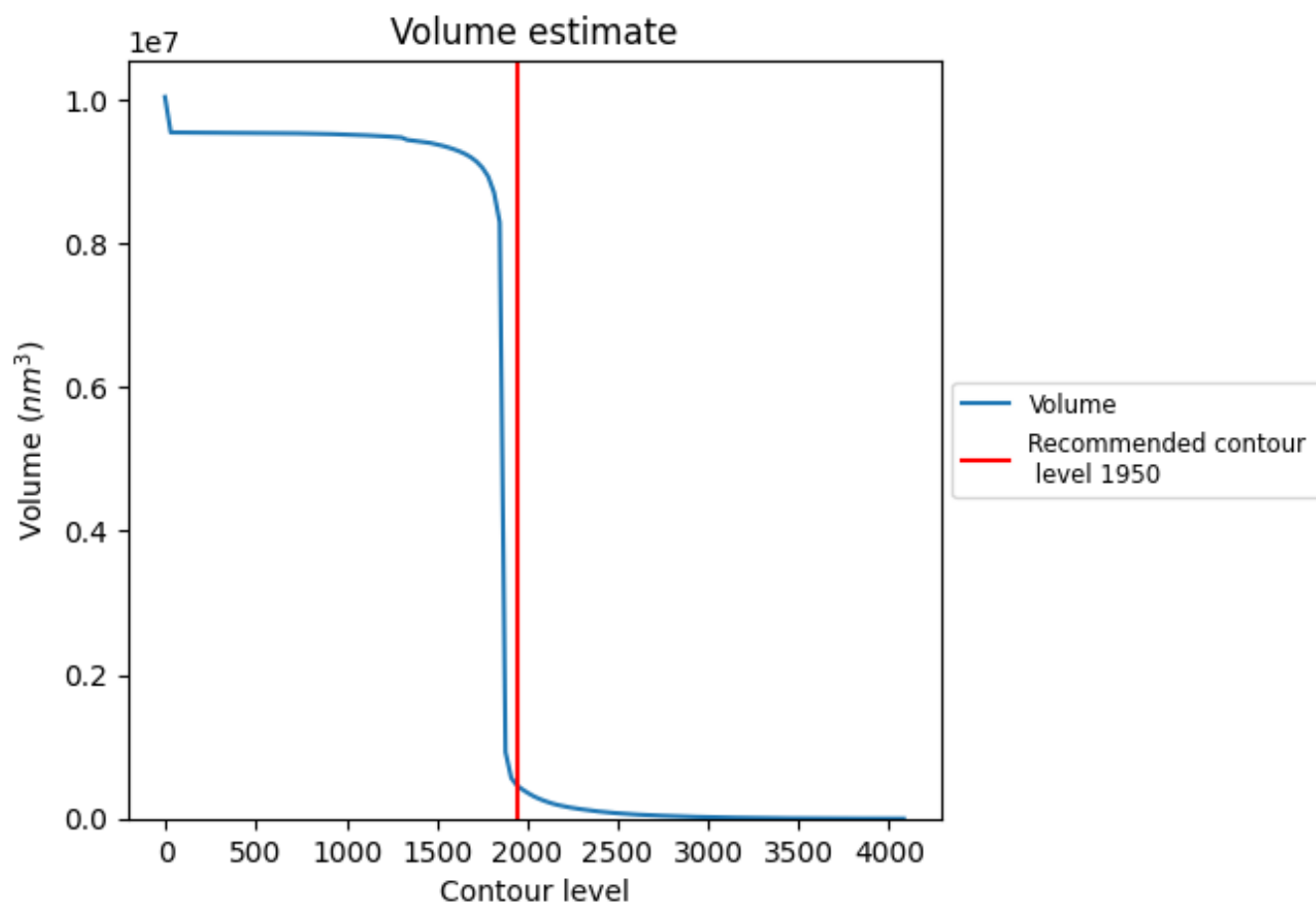
This section contains the results of statistical analysis of the map.

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.

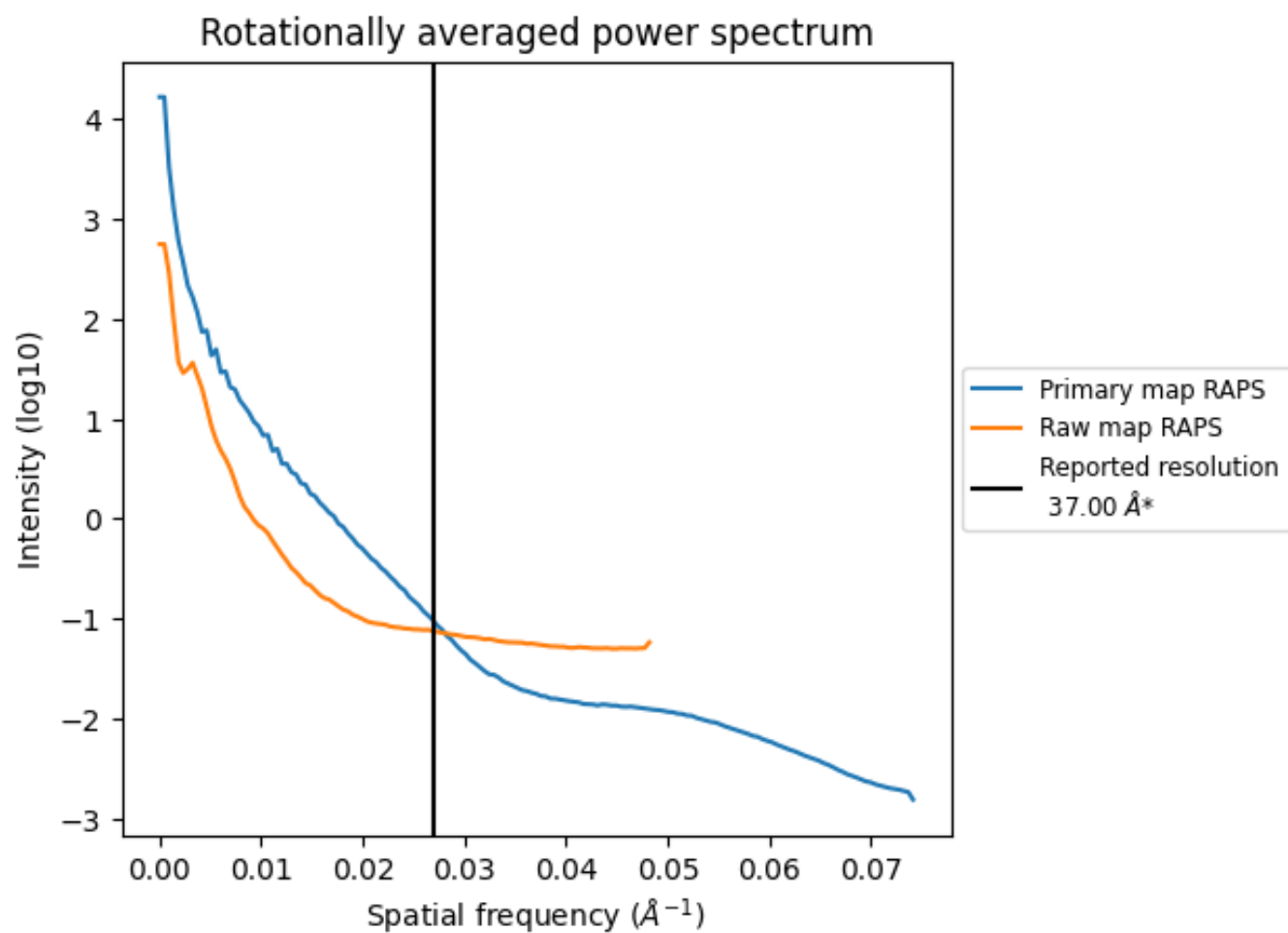
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 447442 nm³; this corresponds to an approximate mass of 404186 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

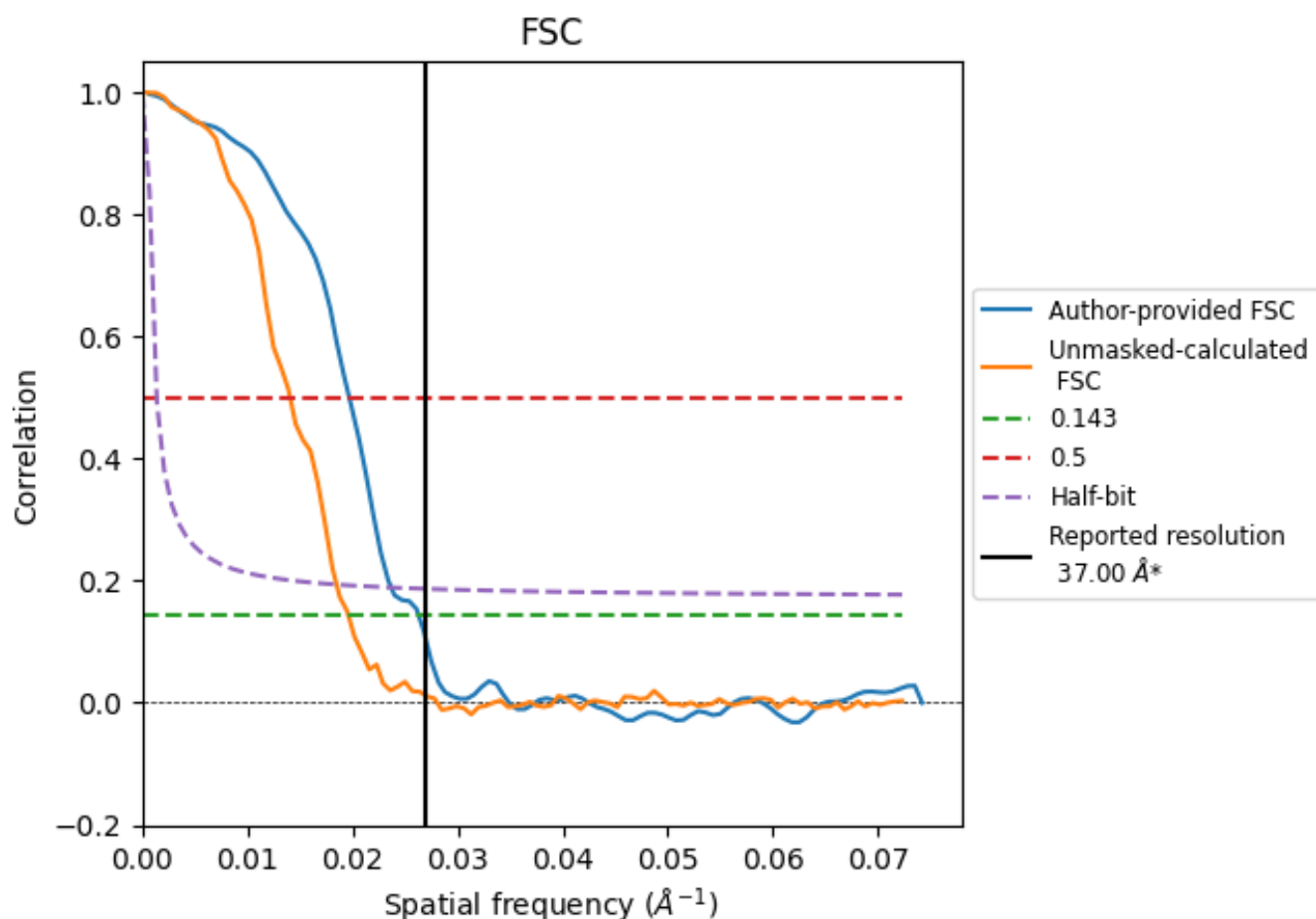


*Reported resolution corresponds to spatial frequency of 0.027 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.027 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	37.00	-	-
Author-provided FSC curve	38.02	50.76	42.19
Unmasked-calculated*	51.02	70.92	54.05

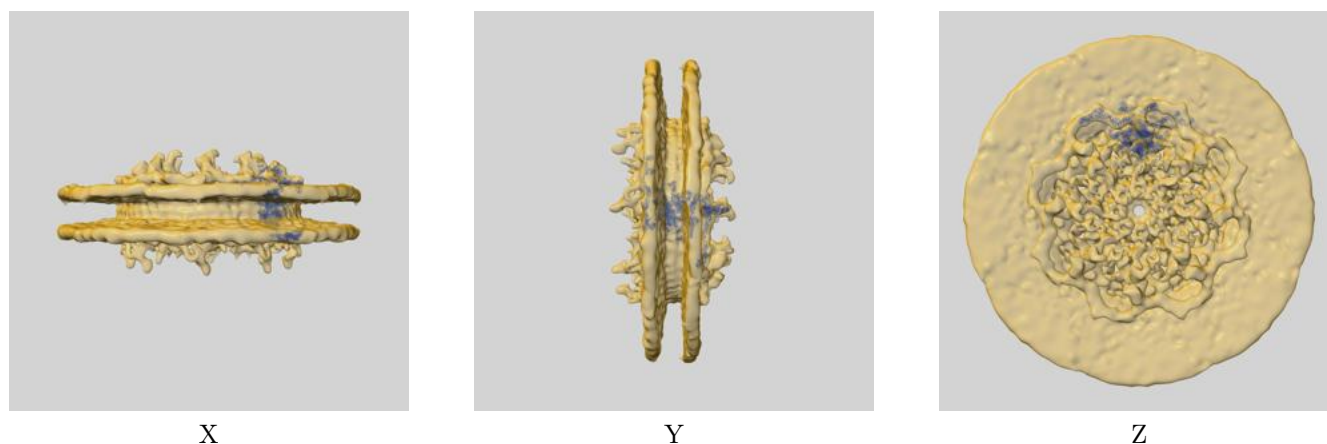
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 51.02 differs from the reported value 37.0 by more than 10 %

9 Map-model fit [i](#)

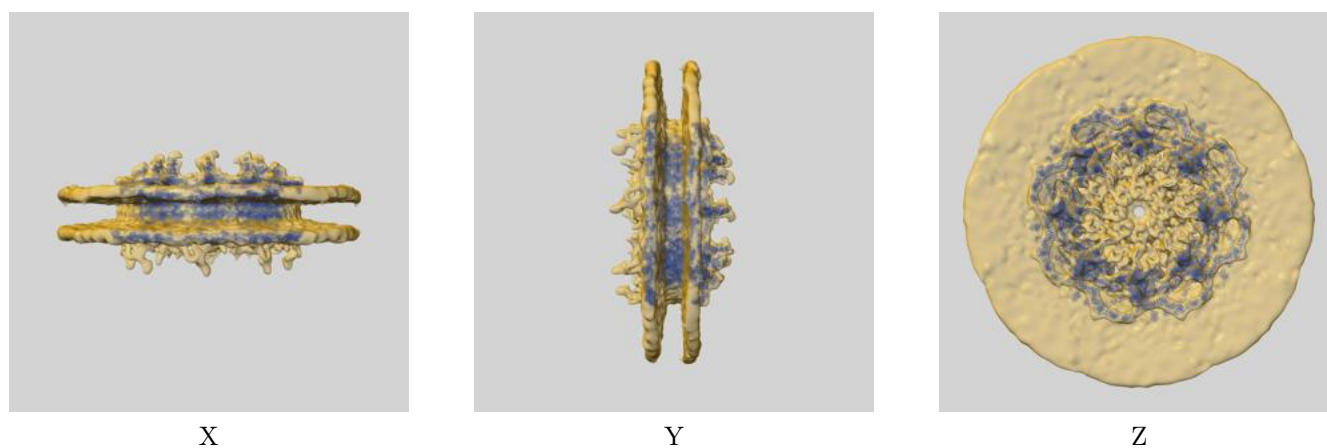
This section contains information regarding the fit between EMDB map EMD-24258 and PDB model 7N9F. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)



9.1.2 Map-model assembly overlay [i](#)



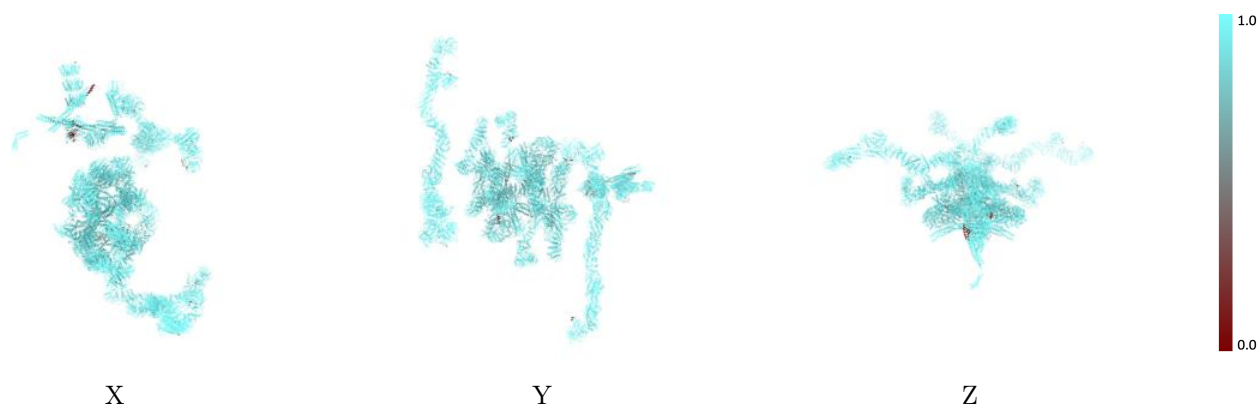
The images above show the 3D surface view of the map at the recommended contour level 1950.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



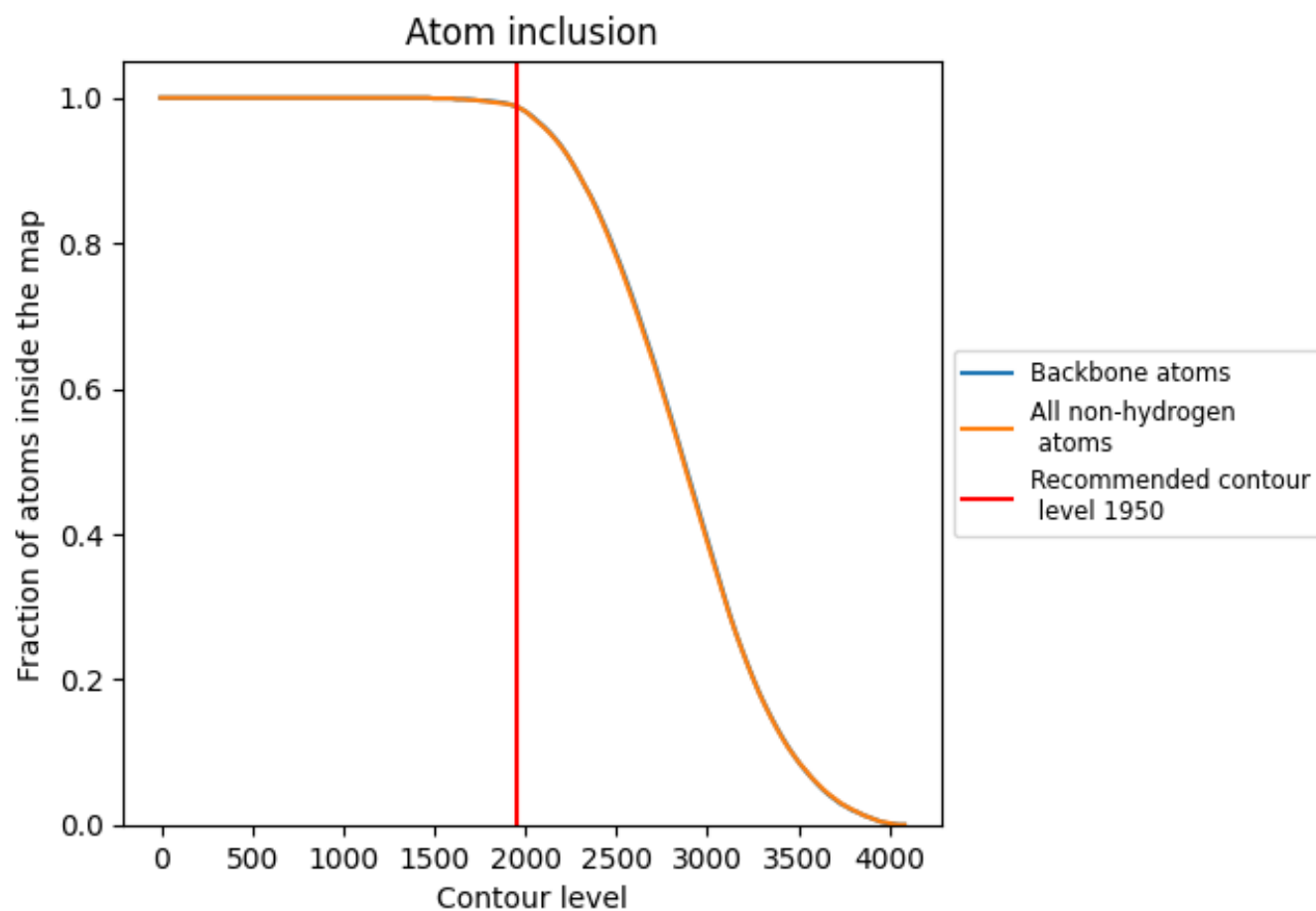
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1950).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% 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 (1950) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9880	 0.0430
0	 0.9750	 0.0430
1	 0.9920	 0.0510
5	 1.0000	 0.0080
6	 1.0000	 -0.0200
A	 0.9980	 0.0610
B	 0.9770	 0.0690
C	 1.0000	 0.0580
D	 0.9750	 0.0500
E	 0.9860	 0.0410
F	 1.0000	 0.0580
G	 0.9830	 0.0490
H	 0.9860	 0.0540
I	 0.9990	 0.0550
J	 0.9460	 0.0560
K	 0.9770	 0.0560
L	 0.9990	 0.0590
M	 0.9960	 0.0350
N	 1.0000	 0.0480
O	 0.9840	 0.0400
P	 1.0000	 0.0440
Q	 1.0000	 0.0580
R	 0.9900	 0.0440
S	 1.0000	 0.0440
T	 0.9940	 0.0520
U	 1.0000	 0.0560
V	 1.0000	 0.0100
W	 1.0000	 0.0550
X	 1.0000	 0.0650
Y	 0.9930	 0.0490
Z	 0.9970	 0.0450
a	 0.9930	 0.0390
b	 1.0000	 0.0480
c	 0.9990	 0.0400
d	 1.0000	 0.0400



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Chain	Atom inclusion	Q-score
e	 1.0000	 0.0260
f	 1.0000	 0.0450
g	 0.9880	 0.0290
h	 0.9820	 0.0340
i	 1.0000	 0.0470
j	 1.0000	 0.0400
k	 1.0000	 0.0580
l	 0.9660	 0.0330
m	 0.9990	 0.0480
n	 0.9910	 0.0430
o	 1.0000	 0.0600
p	 1.0000	 0.0310
q	 1.0000	 0.0530
r	 1.0000	 0.0680
s	 1.0000	 0.0450
t	 0.9930	 0.0280
u	 0.7990	 0.0020
v	 0.9870	 0.0240
w	 0.8960	 0.0270
x	 0.9820	 0.0260
y	 0.9150	 0.0470
z	 0.9230	 0.0420