



wwPDB EM Validation Summary Report ⓘ

Nov 16, 2022 – 03:44 AM JST

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

This is a 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:

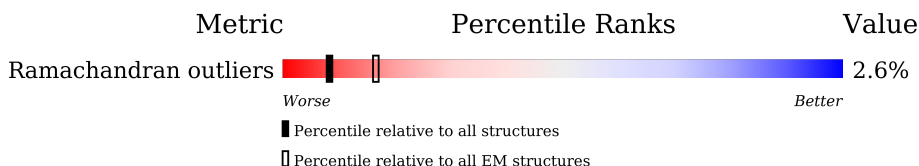
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance i

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

The reported resolution of this entry is 5.50 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2011	
1	a	2011	
2	B	653	
2	b	653	
3	C	375	
3	c	375	
4	D	322	
4	d	322	
5	E	1435	
5	e	1435	
6	F	326	

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

2 Entry composition [i](#)

There are 18 unique types of molecules in this entry. The entry contains 72207 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called MGC83295 protein.

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

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

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

- Molecule 3 is a protein called MGC154553 protein.

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

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

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

- Molecule 5 is a protein called outer Nup160.

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

- Molecule 6 is a protein called MGC83926 protein.

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

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

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

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

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

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

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

- Molecule 10 is a protein called outer Nup133.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

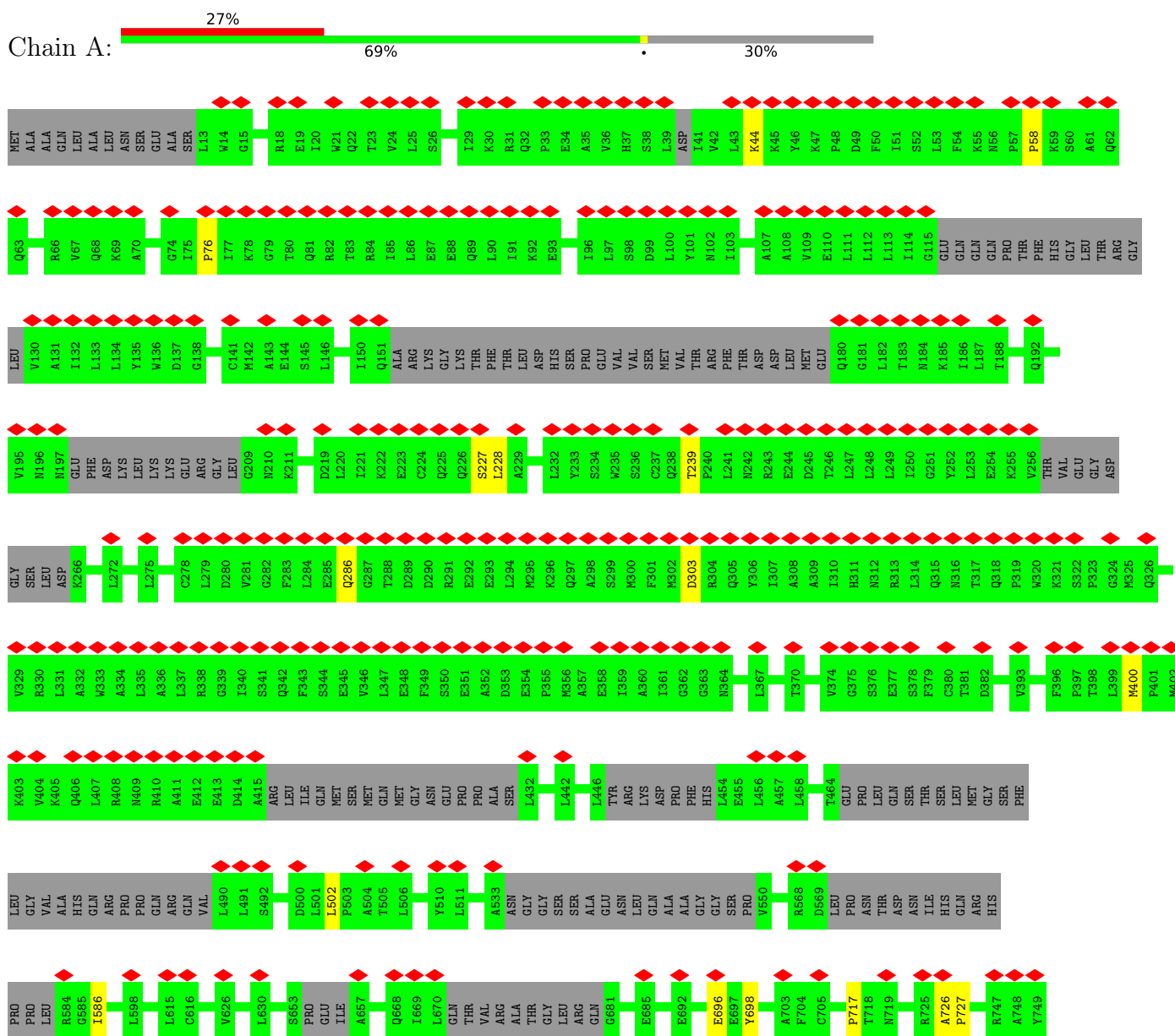
- Molecule 18 is a protein called bridge domain.

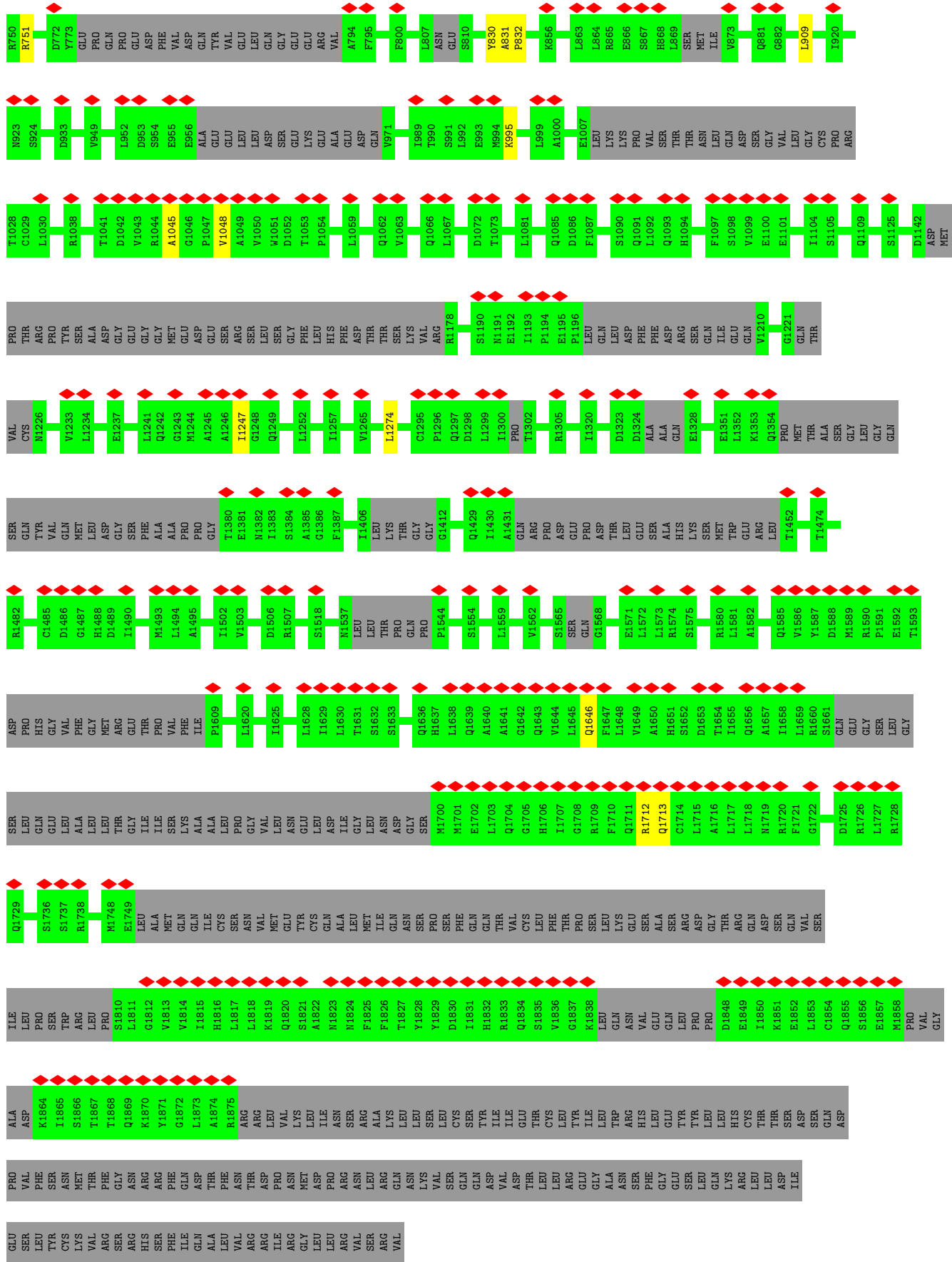
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
18	Q	387	1935	1161	387	387	0	0
18	R	351	1755	1053	351	351	0	0

3 Residue-property plots [i](#)

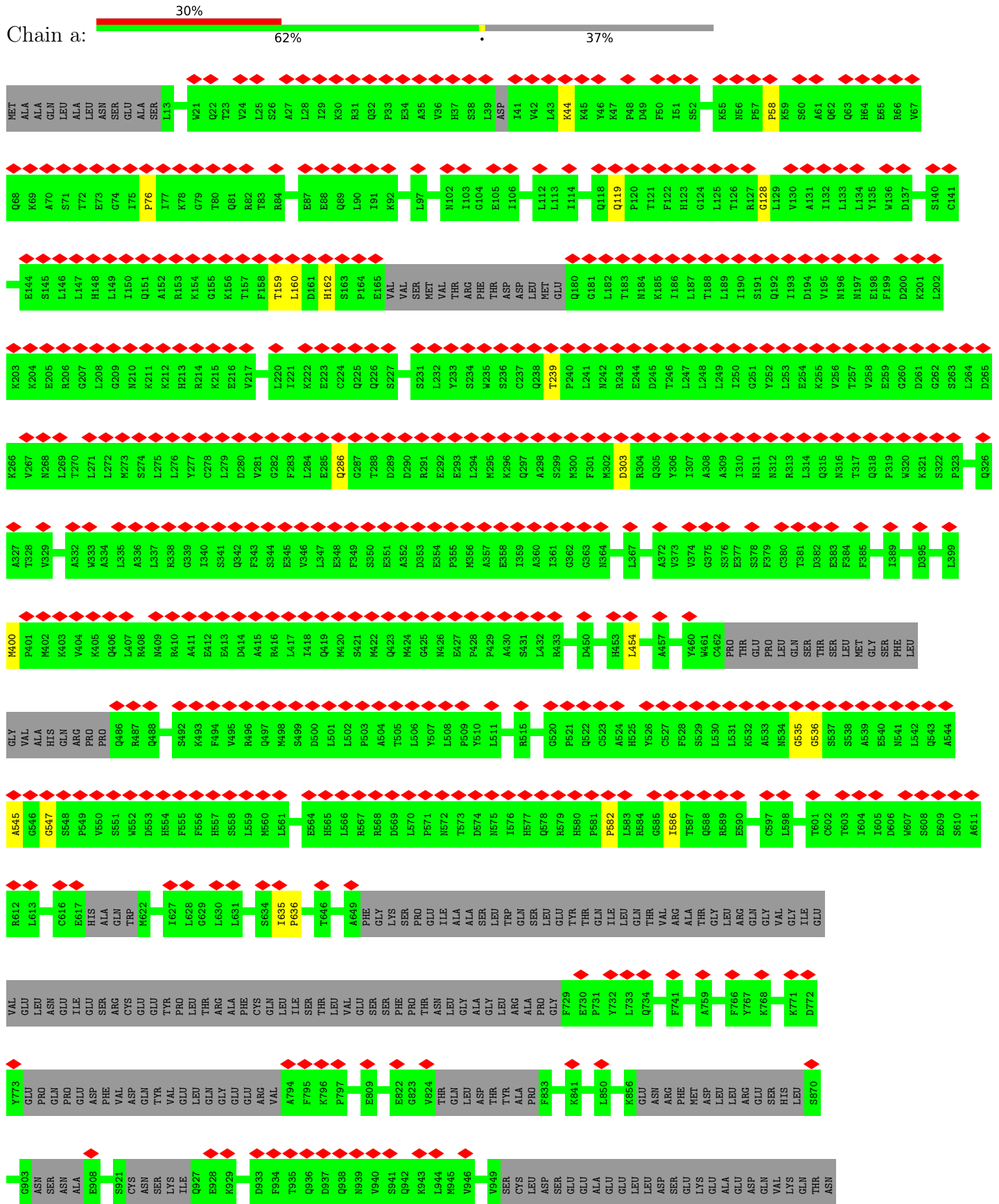
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

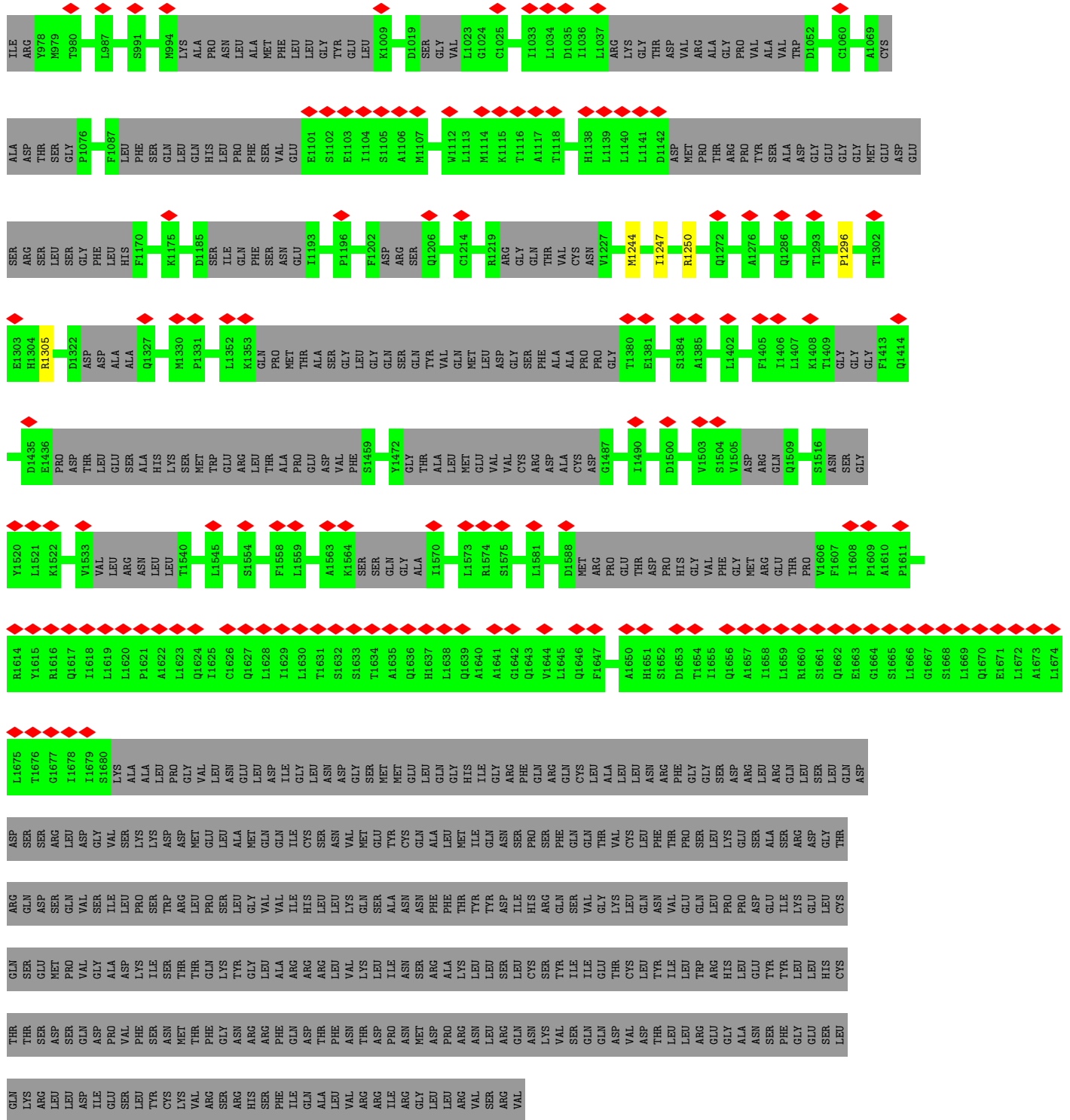
- Molecule 1: MGC83295 protein



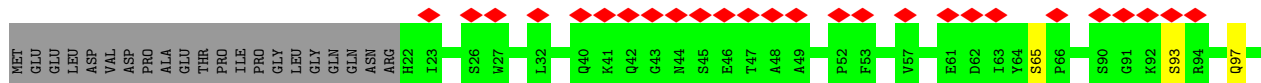
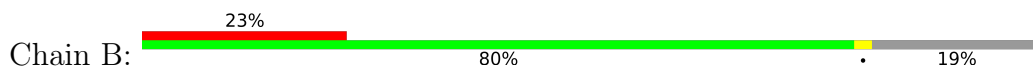


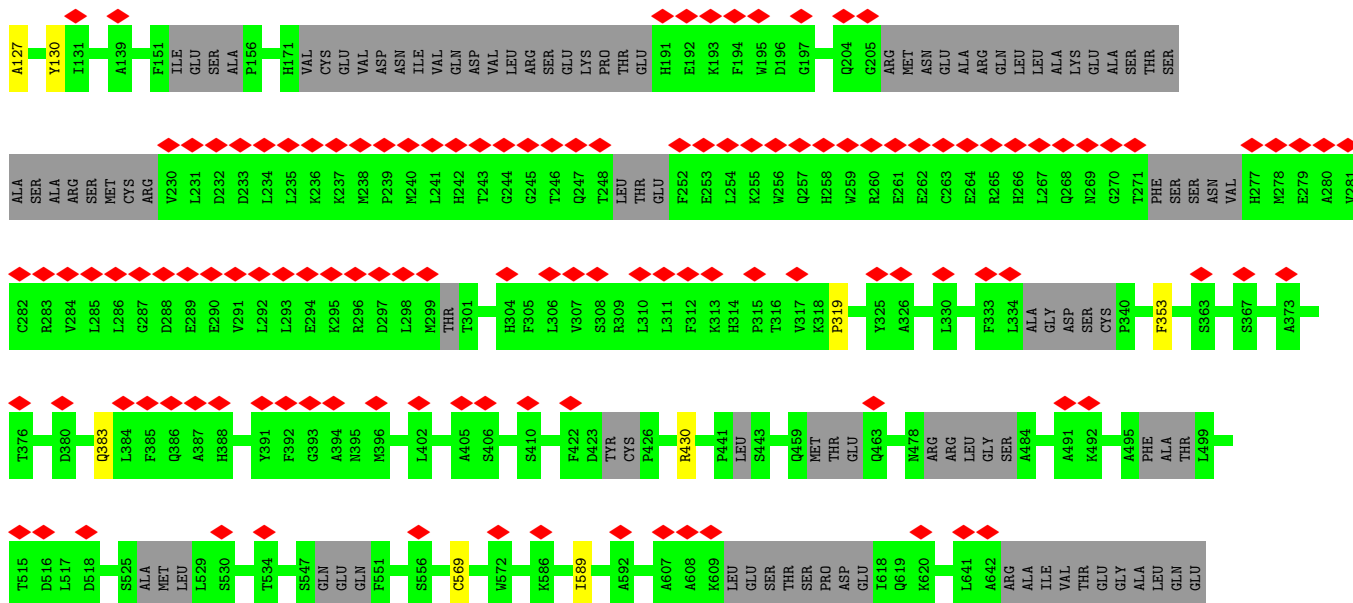
• Molecule 1: MGC83295 protein



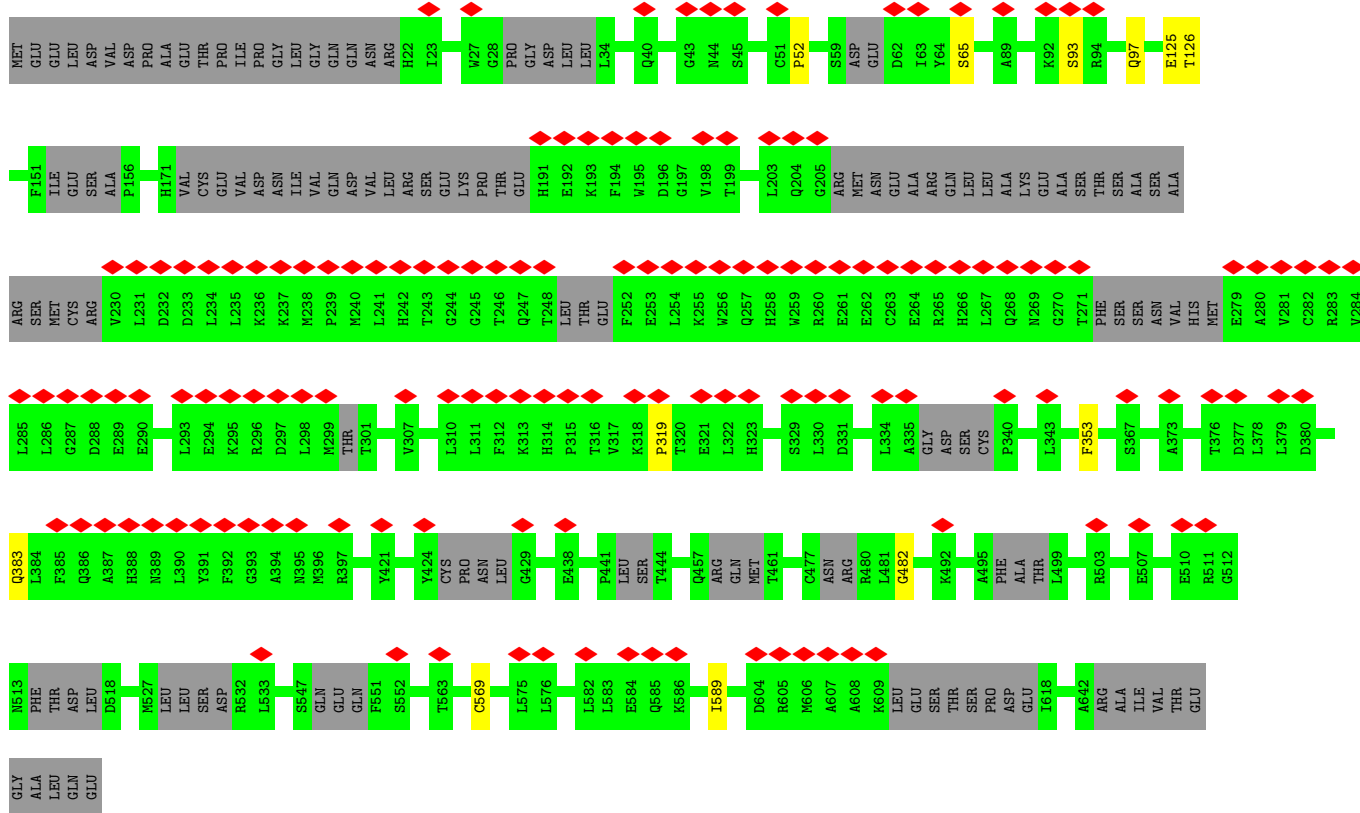
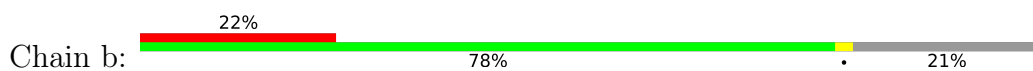


- Molecule 2: Nuclear pore complex protein Nup85

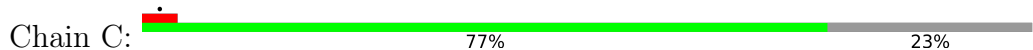


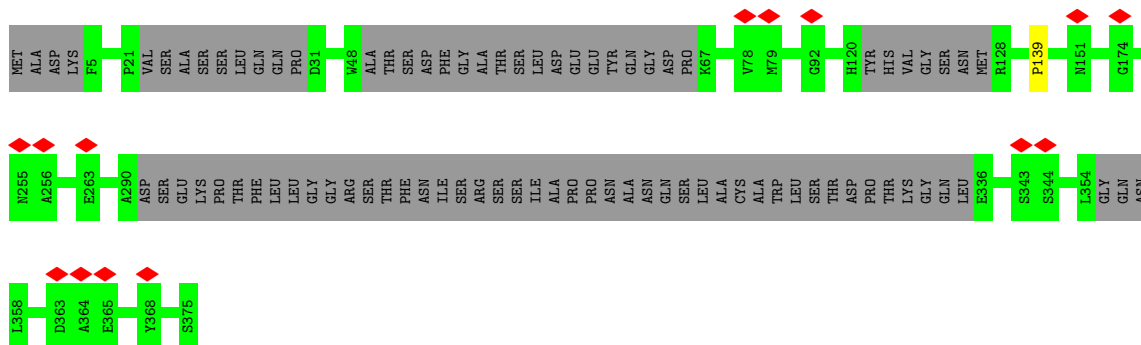


• Molecule 2: Nuclear pore complex protein Nup85

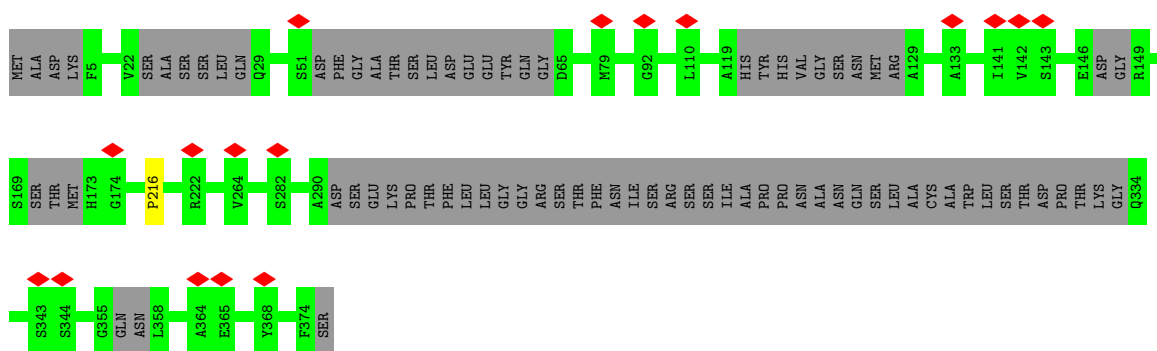
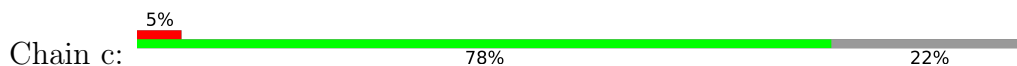


• Molecule 3: MGC154553 protein

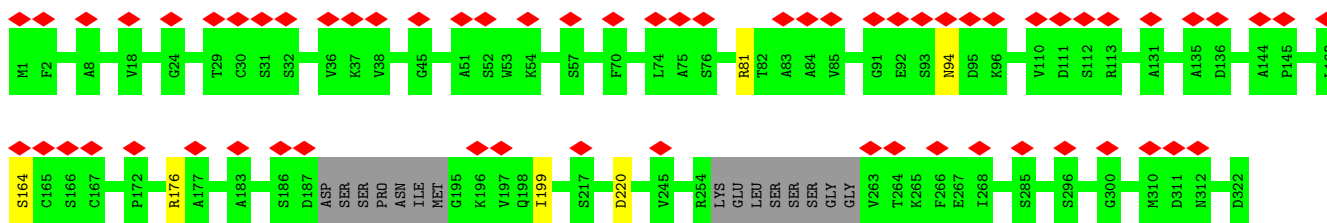




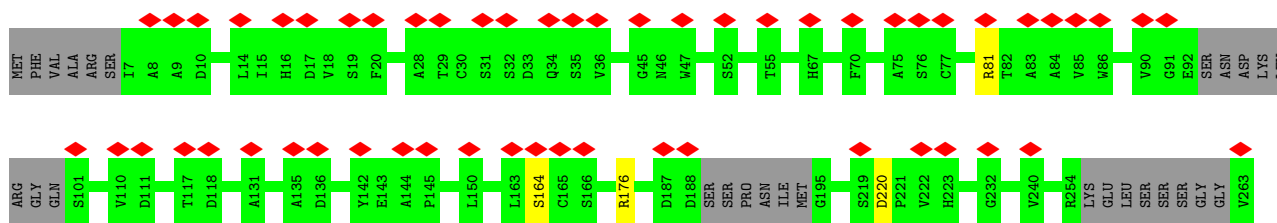
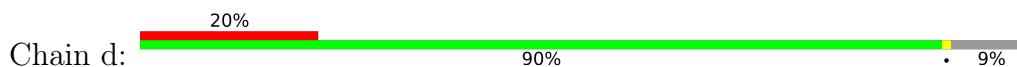
• Molecule 3: MGC154553 protein

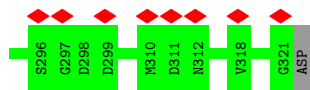


• Molecule 4: Nucleoporin SEH1-A

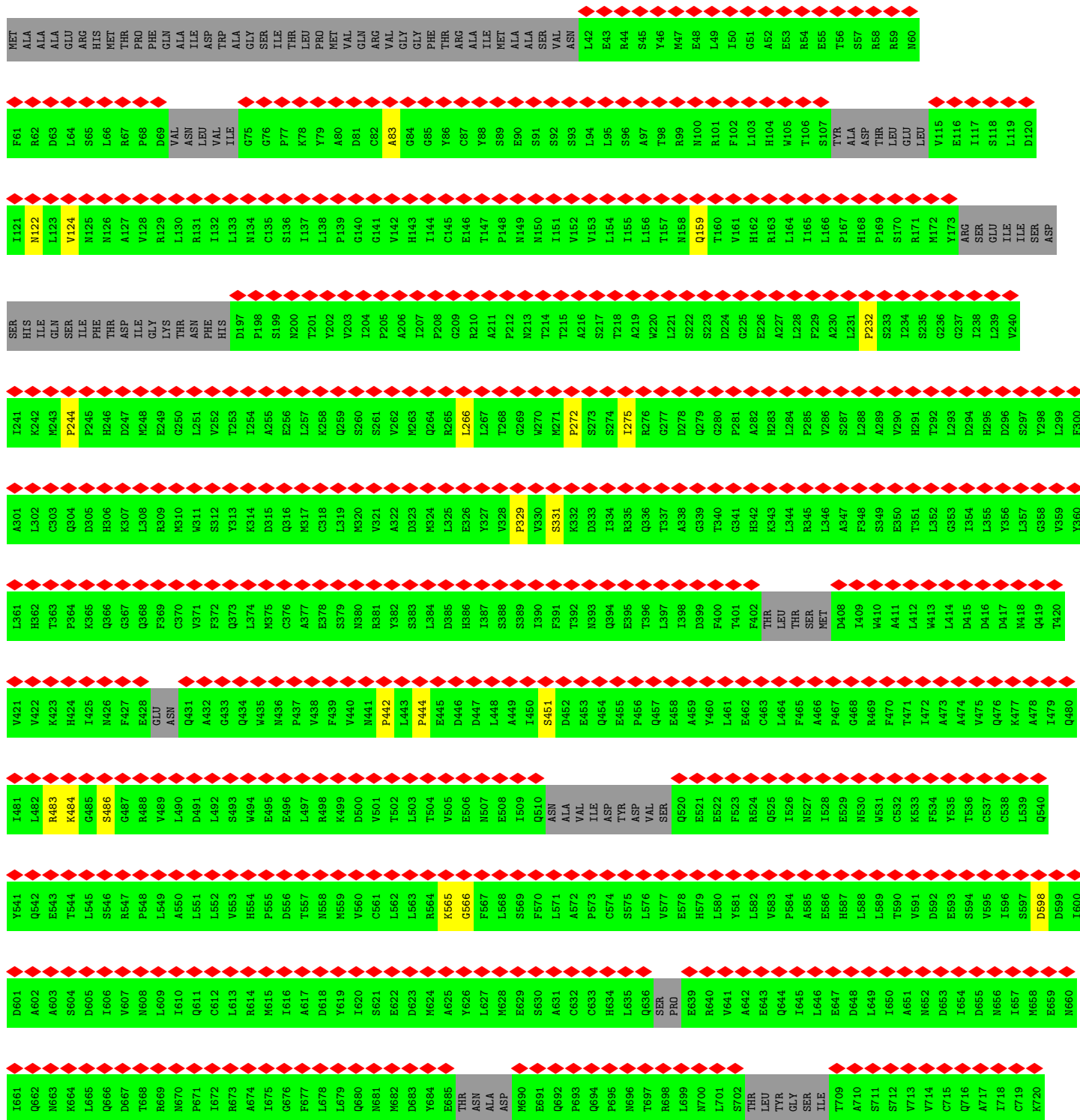


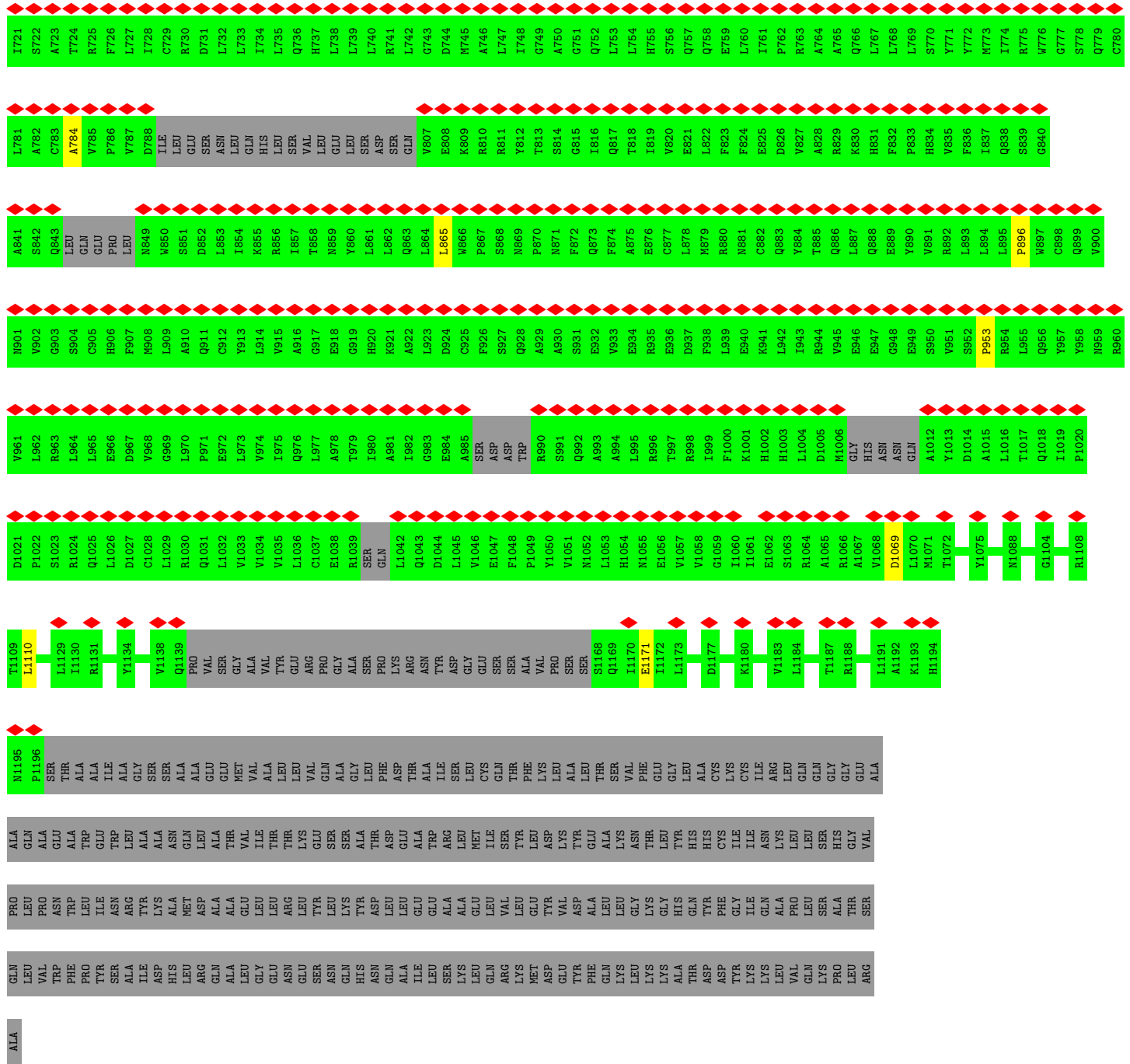
• Molecule 4: Nucleoporin SEH1-A



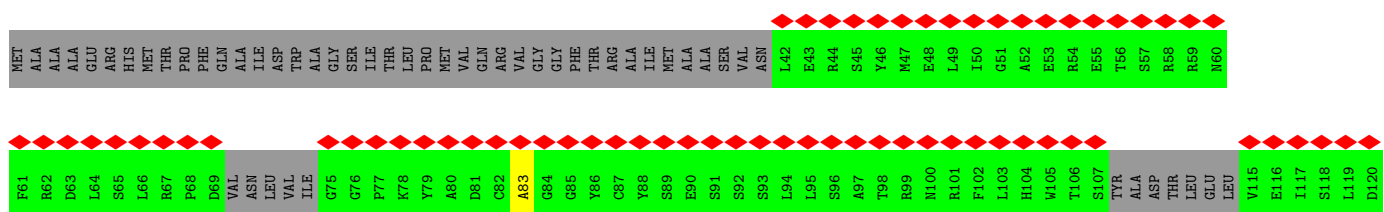
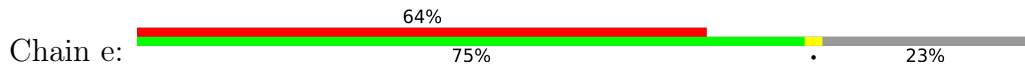


• Molecule 5: outer Nup160

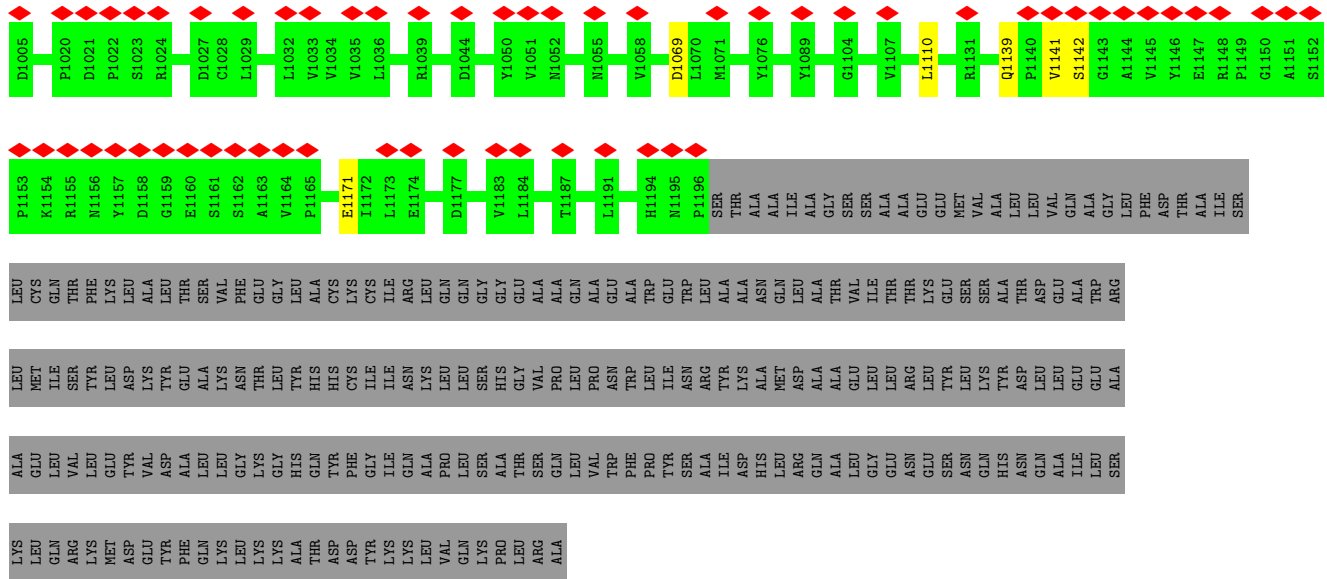




• Molecule 5: outer Nup160

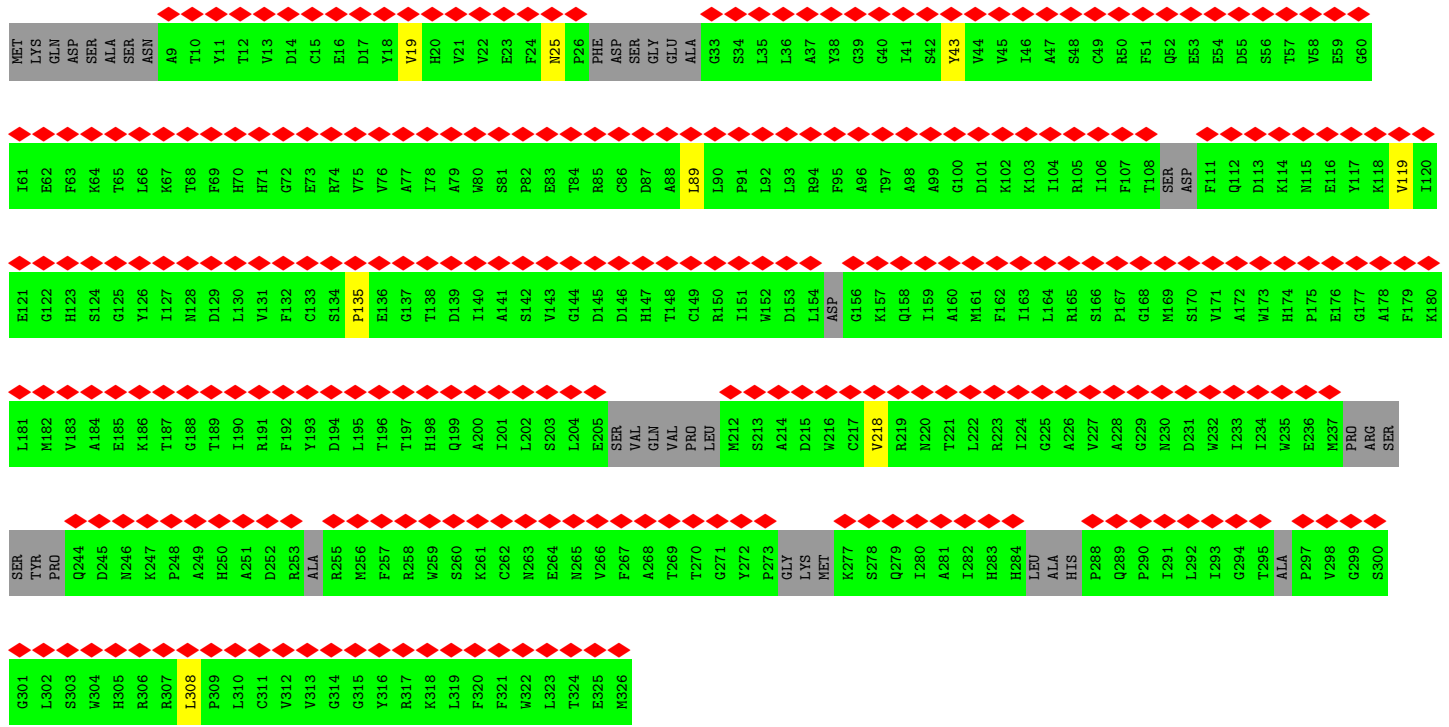


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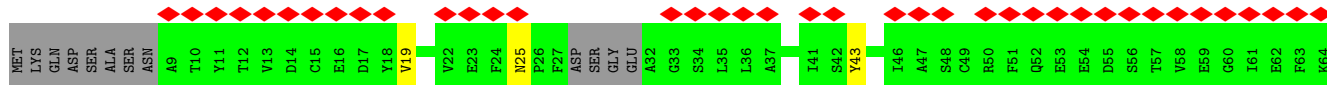
• Molecule 6: MGC83926 protein

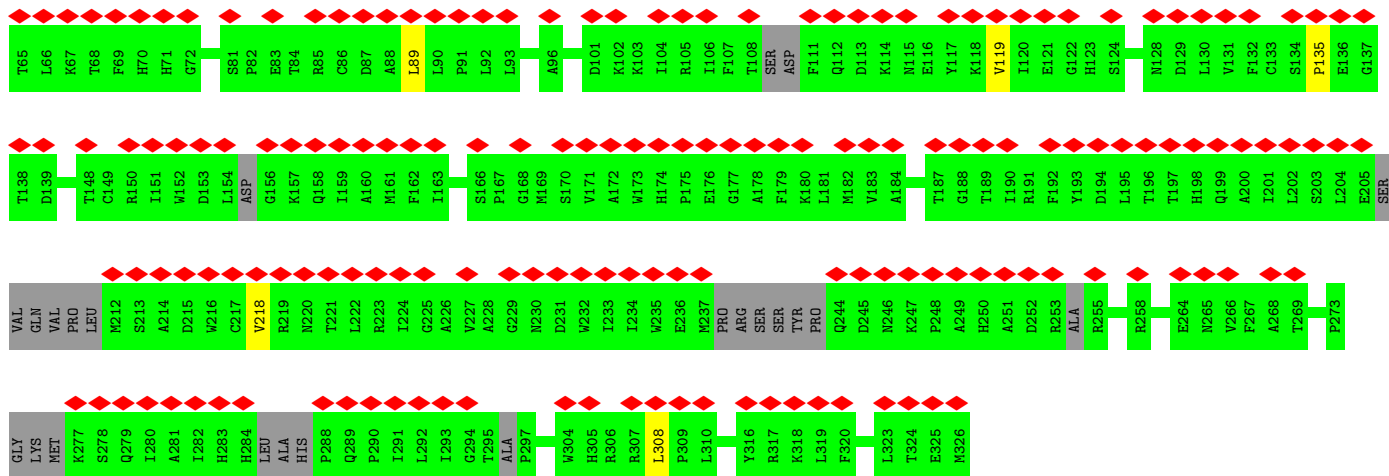
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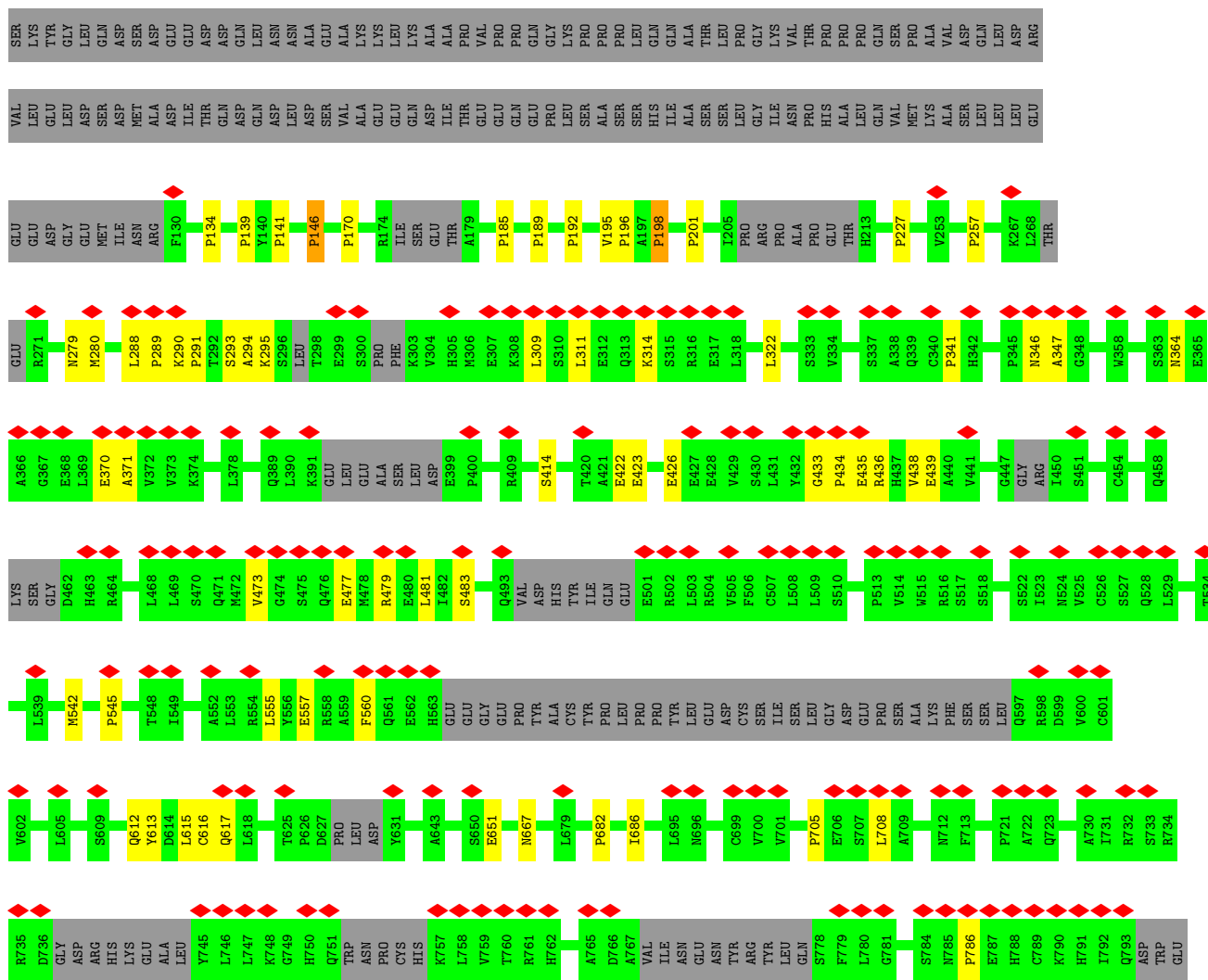
• Molecule 6: MGC83926 protein

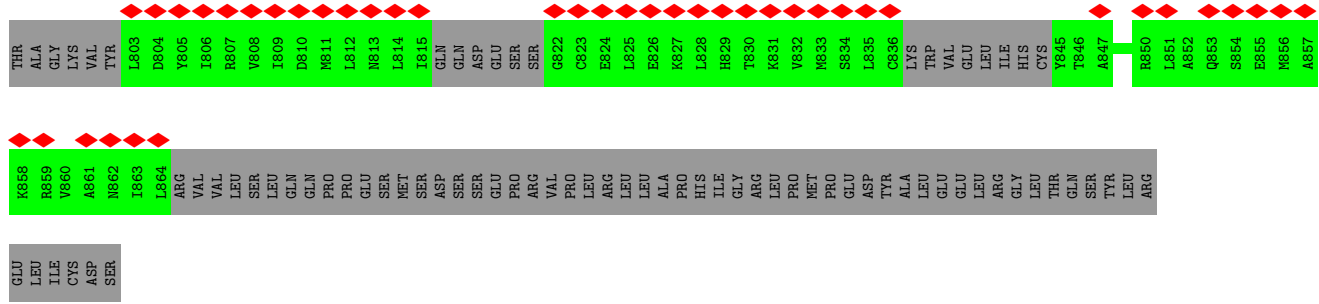
Chain f:



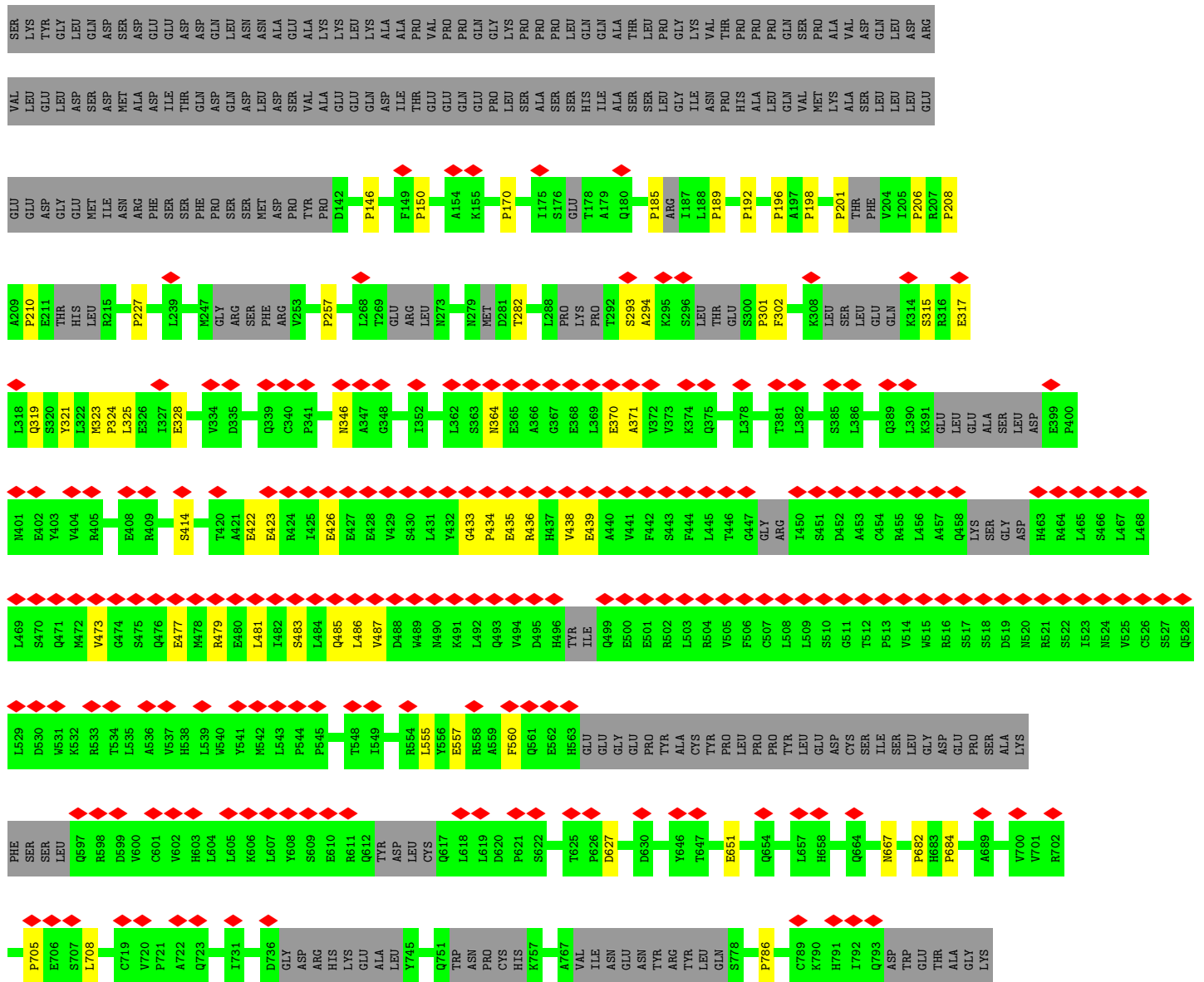


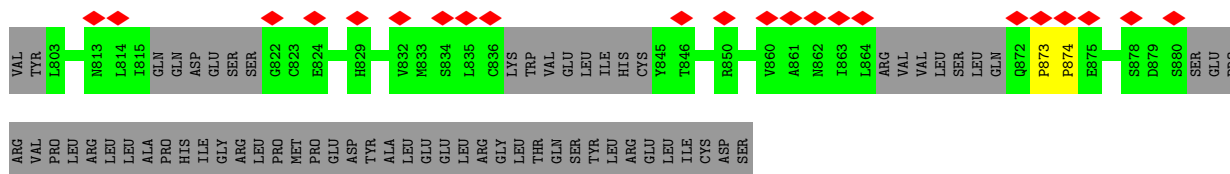
● Molecule 7: Nuclear pore complex protein Nup96



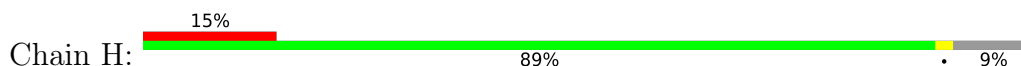


● Molecule 7: Nuclear pore complex protein Nup96

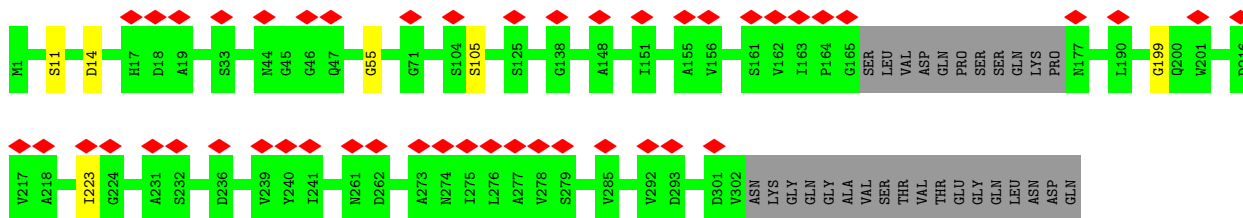




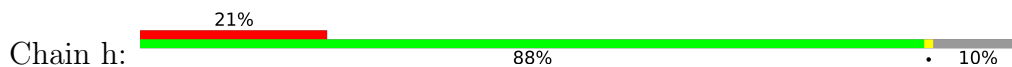
• Molecule 8: GATOR complex protein SEC13



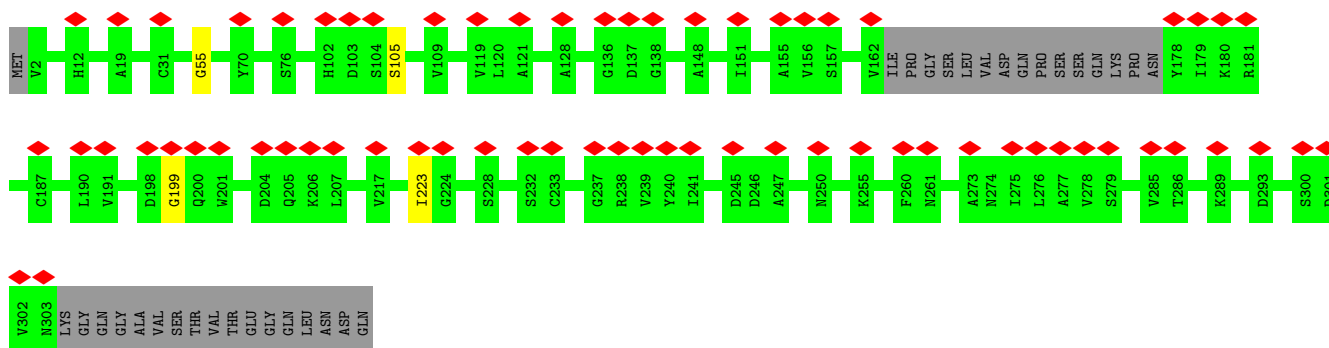
Chain H:



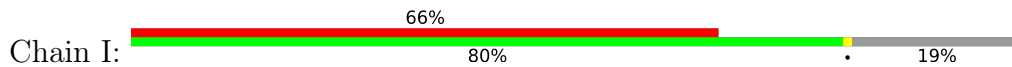
• Molecule 8: GATOR complex protein SEC13



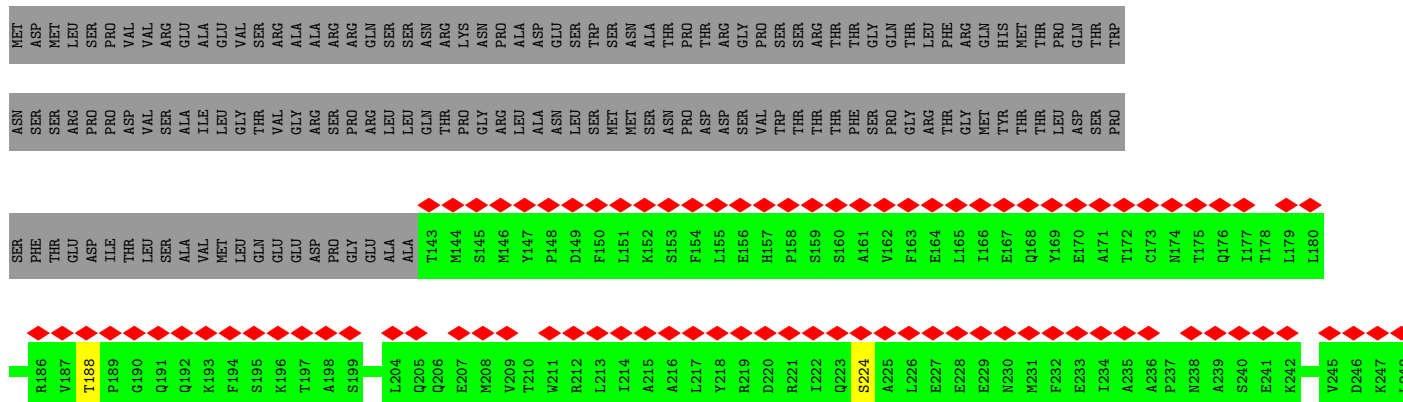
Chain h:



• Molecule 9: Nuclear pore complex protein

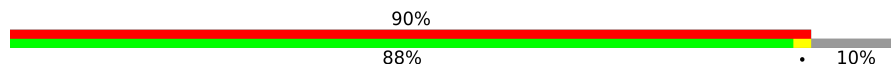


Chain I:



• Molecule 10: outer Nup133

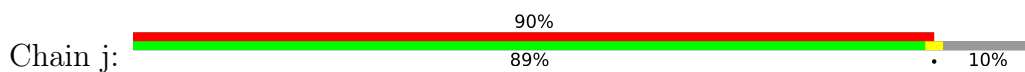
Chain J:



MEI PHE PRD PRO PRO PRO ARG ALA GLN GLY GLY GLY SER ALA ARG ARG PRO PHE ASN SER ARG LEU THR GLY GLY ARG LYS ALA LEU GLY PRO GLY GLY VAL THR ALA SER SER SER PRO SER ALA TYR SER PRO VAL GLY ARG VAL SER ALA SER ALA GLY ALA ARG SER THR PRO SER ARG	VAL TYR LEU HIS PRO ALA ALA SER	E69 T70 V71 N72 Y73 N74 V75 Q76 L77 F78 G79 S80 S81 L82 P83 V84 K85 V86 M87 E88 A89 L90 S91 N92 S93 A93 S94 A95 D96 E97 P98 M99 A100 A101 C102 S103 I103 H104 E105 G106 G107 M108 A109 M110 L111 A112 C113 M114 D115 R116 L117 I118 I119 M120	K121 I122 S123 H124 S125 S126 S127 A128 K129 L130 M131 V132 C133 K134 E135 L136 P137 L138 P139 L140 S141 D142 S143 E144 W145 M146 A147 D148 L149 V150 D151 I152 C153 A154 Q155 T156 G157 D158 P159 A160 A161 A162 Q163 S164 V165 A166 L167 M168 A169 G229 K230 M231 P172 E173 G174 S175 S176 Y177 I178 W179 P180	N181 I182 L183 H184 E185 G186 T187 Y188 I189 E190 S191 Y192 V193 T193 F194 F195 G196 S197 SER	L199 C200 A201 F202 V203 T204 A205 V206 K207 G208 N209 S210 F211 I212 L213 S214 S215 E216 K217 N218 Q219 L220 V221 R222 L223 T224 P225 D226 A227 S228 L289 D290 D291 S292 Q293 E294 S295 Q296 V297 L298 N299 W300	G241 M242 L243 S244 E245 I246 G247 R248 I249 V250 S251 T252 L253 P254 G255 I256 L257 S258 P259 A260 V261 S262 S263 T264 L265 C266 S267 V268 L269 W270 D271 GLY	D774 C275 F276 Y277 T278 L279 D280 D281 S282 S283 L284 N285 K286 W287 D288 L289 D290 D291 S292 Q293 E294 S295 Q296 V297 L298 N299 W300	D801 M302 S303 R304 V305 L306 R307 E308 Y309 I310 S311 D312 A313 I314 W315 G316 S317 E318 S319 D320 Y321 D322 D323 I324 K325 A326 G327 I328 N329 I330 N331 Y332 L333 S334 L335 N336 Q337 N338 C339 D340 G341 S342 V343 I344 L345 S346 A347 A348 W349 H350 P351 G352 D353 N354 P355 C356 I357 Y359 Y360	T361 L362 V363 T364 V365 K366 D367 E368 G369 Y370 N371 I372 S373 D374 E375 I376 T377 V378 E379 V380 T381 Q382 F383 N384 P385 V386 F387 Q388 A389 R390 G391 M392 Q393 L394 C395 Q396 L397 V398 V399 M400 M401 F402 S403 S404 Q405 A406 C407 Y408 L409 Y410 Q412 E413 M414 I415 F416 A417 C418 S419 T420	G421 T422 G423 R424 S425 T426 L427 P428 Q429 E430 K431 I432 F433 P434 E435 A436 G438 D439 M440 I441 V442 G443 A444 G445 S446 C447 E448 G449 W450 P451 V452 F453 F454 I455 R456 K457 S458 G459 M460 L461 T462 V463 V464 A465 R466 E467 THR	ALA SER VAL LEU PRO GLU HIS MET GLU LEU	SER VAL SER LYS SER SER GLN ALA VAL VAL LYS ASP SER ARG PRO ASP GLN ILE HIS ASP ASP	K505 T506 K507 H508 L509 K510 A511 A512 F513 L514 R515 Y516 C517 R518 K519 D520 I521 L522 G523 A524 Q525 S526 M527 V528 D529 S530 L531 F532 S533 D534 S535 D536 M537 E538 P539 D540	D541 E542 L543 D544 L545 A546 V547 N548 Q549 I550 S551 V552 D553 L554 I555 D556 D557 Y558 P559 A560 S561 D562 P563 R564 W565 A566 E567 S568 V569 P570 E571 E572 A573 A574 G575 F576 S577 N578 T579 S580 L581 I582 L583 L584 H585 Q586 L587 E588 D589 K590 M591 K592 A593 H594 S595 F596 F597 V598 D599 F600	L601 H602 Q603 V604 G605 L606 F607 S608 R609 L610 SER T612 C613 Q614 T615 K616 G617 M618 L619 V620 A621 T622 R623 L624 L625 L626 S627 E628 H629 A630 E631 K632 L633 S634 A635 A636 I637 V638 L639 K640 N641 H642 H643 A644 K645 H646 P647 V648 L649 V650 N651 S652 A653 L654 Q655 L656 A657 D658 D659 K660	R661 W662 C663 T664 V665 P666 Q667 N668 L669 T670 A671 A672 D673 W674 V675 F676 R677 E678 V679 S680 Q681 W682 E683 L684 L685 F686 E687 C688 L689 V690 D691 K692 E693 E694 A695 D696 L697 G698 S699 T700 S701 I702 D703 S704 W705 R706 W707 A708 W709 I710 N711 W712 M713 W714 N715 T716 I717 L718 K719 D720	W721 L722 H723 W724 A725 C726 Q727 Y728 R729 Q730 S731 K732 M733 S734 L735 Y736 K737 N738 E739 S740 I742 Q743 E744 P745 E746 H747 W748 P749 W750 T751 A752 S753 S754 G755 T756 A757 G758 I759 R760 S761 I762 W763 T764 R765 Q766 H767 G768 I769 I770 L771 K772 W773 Y774 P775 Q776 A777 D778 S779 G780
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L781	A841	Q901	A961	C1021	K1081
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I784	S844	S904	A964	M1024	I1084
L785	N845	H905	S965	K1025	F1085
I786	L846	H906	D966	M1026	V1086
E787	A847	G907	F967	A1027	K1087
Q788	E848	Q908	Q968	M1028	V1088
L789	K849	L909	E969	G1029	L1089
A790	Y850	A910	D970	M1030	Q1090
A791	C851	A911	V971	D1031	M1091
L792	D852	F912	L972	F1032	L1092
L793	F853	L913	Q973	M1033	L1093
N794	D854	Q914	E974	A1034	M1094
Y795	I855	A915	K975	A1035	K1095
L796	L856	HIS	V976	L1036	G1096
L797	V857	ASP	E977	D1037	L1097
D798	Q858	HIS	E978	L1038	E1098
D799	I859	L919	F979	G1039	G1099
Y800	C860	S920	A980	E1040	K1100
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L804	D864	E924	H984	D1044	P1104
K805	N865	L925	F985	D1045	K1105
S806	Q866	N926	L986	S1046	A1106
I807	S867	Q927	L987	E1047	E1107
D808	R868	Q928	H988	V1048	T1108
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L810	Q870	F930	E990	V1050	L1110
A811	R871	E931	T991	E1051	Q1111
N812	Y872	K932	L992	E1052	S1112
E813	M873	A933	P993	L1053	E1113
L814	T874	H934	K994	K1054	E1114
R815	L875	R935	K995	L1055	L1115
Y816	F876	T936	L996	E1056	M1116
M817	A877	L937	L997	I1057	S1117
L818	E878	Q938	E998	L1058	L1118
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E820	N880	A941	K1000	M1060	T1120
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A824	F884	T945	L1004	R1064	F1124
Q825	L885	R946	M1005	D1065	E1125
R826	F886	Y947	A1006	E1066	F1126
R827	R887	F948	M1007	W1067	S1127
S828	V888	C949	P1008	S1068	L1128
E829	Y889	K950	V1009	A1069	K1129
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I836	G896	L957	I1016	P1076	M1136
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• Molecule 10: outer Nup133

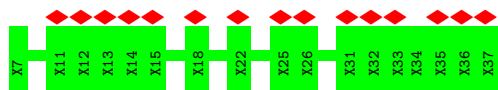


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SER	HIS	H124	H184	S244	R304	T364
ARG	ALA	S125	E185	G245	V305	V365
ALA	ALA	S126	G186	I246	L306	K366
GLN	GLY	S127	T187	G247	R307	D367
MET	GLY	A128	Y188	R248	E308	E368
GLY	TYR	K129	I189	R249	V309	G369
SER	W71	L130	E190	V250	I310	V370
ALA	N72	M131	S191	S251	S311	M371
ARG	Y73	V132	Y192	T252	D312	I372
ARG	N74	C133	T193	L253	A313	S373
PRO	V75	K134	E194	F254	L314	D374
PHE	Q76	E135	F195	G255	W315	E375
ASN	L77	L136	G196	I256	G316	I376
SER	F78	P137	S197	L257	S317	T377
ARG	G79	L138	L199	S258	E318	V378
LEU	S80	P139	C200	F259	S319	E379
THR	ARG	L140	A201	A260	D320	V380
GLY	L82	S141	F202	V261	Y321	T381
ARG	P83	D142	E262	E263	Q322	Q382
GLY	H84	S143	V203	T264	D323	F383
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ALA	S94	C153	L213	GLY	L333	K393
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ARG	M100	P159	Q219	L279	C339	V399
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ARG	THR	V165	G106	N285	Q405	Q405
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ARG	ARG	M168	W110	D288	A408	C407
		A169	L111	S228	A348	A408
		L112	L111	L289	W349	L409
		A113	A112	D290	V410	L409
		C113	C113	D291	D291	Y410
		M114	M114	M231	F351	T411
		D115	D115	N232	G352	Q412
		L116	L116	R234	D353	E413
		I117	I117	V235	E294	M414
		I118	I118	W236	S295	I415
		I119	I119	L236	Q296	F416
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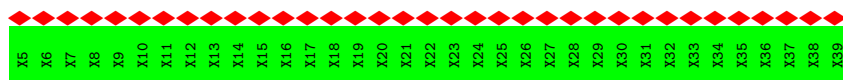
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L601	H602	Q603	V604	G605	L606	F607	S608	R609	L610	SER	T612	C613	Q614	T615	K616	G617	M618	L619	V620	A621	T622	R623	L624	L625	L626	S627	E628	H629	A630	E631	K632	L633	S634	A635	A636	I637	V638	L639	K640	N641	H642	H643	A644	K645	L646	P647	V648	L649	V650	N651	A652	A653	I654	Q655	L656	A657	L658	D659	K660
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M721	L722	H723	V724	A725	C726	Q727	Y728	R729	Q730	S731	K732	M733	S734	L735	Y736	K737	N738	E739	S740	G741	I742	Q743	E744	F745	E746	H747	V748	P749	M750	T751	A752	S753	S754	G755	T756	A757	G758	I759	R760	S761	V762	V763	T764	R765	Q766	H767	G768	I769	I770	L771	K772	V773	V774	F775	Q776	A777	D778	S779	G780
L781	R782	I783	L784	L785	L786	E787	Q788	L789	A790	A791	L792	L793	N794	Y795	L796	L797	D798	D799	Y800	V801	T802	Q803	L804	K805	S806	I807	D808	K809	L810	A811	N812	E813	E814	R815	Y816	M817	L818	L819	E820	M821	E822	Y823	A824	Q825	K826	R827	S828	E829	L830	L831	S832	P833	L834	L835	G836	L837	G838	Q839	E840
A841	W842	A843	S844	N845	L846	A847	E848	K849	Y850	C851	D852	F853	D854	L855	L856	Q857	Q858	L859	C860	E861	M862	T863	D864	M865	Q866	S867	R868	L869	Q870	R871	Y872	M873	T874	L875	F876	A877	E878	Q879	N880	F881	S882	D883	F884	L885	F886	R887	W888	Y889	K890	K891	K892	G893	L894	L895	G896	K897	L898	L899	S900
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A961	A962	L963	A964	S965	D966	F967	Q968	E969	A970	A971	L972	Q973	E974	K975	V976	E977	E978	I979	A980	E981	Q982	E983	H984	F985	A986	L987	H988	Q989	E990	T991	L992	P993	K994	K995	L996	L997	E998	E999	K1000	Q1001	L1002	D1003	L1004	M1005	A1006	M1007	P1008	V1009	L1010	A1011	P1012	F1013	Q1014	L1015	I1016	Q1017	L1018	Y1019	V1020
C1021	E1022	E1023	M1024	K1025	R1026	A1027	M1028	E1029	M1030	D1031	F1032	M1033	K1034	A1035	L1036	D1037	L1038	L1039	E1040	Y1041	I1042	G1043	D1044	D1045	S1046	E1047	V1048	L1049	V1050	E1051	E1052	L1053	K1054	L1055	E1056	L1057	C1058	K1059	K1060	Q1061	I1062	K1063	R1064	M1065	D1066	W1067	S1068	A1069	T1070	D1071	G1072	K1073	D1074	D1075	P1076	I1077	E1078	A1079	T1080
K1081	D1082	S1083	I1084	F1085	V1086	K1087	V1088	L1089	Q1090	N1091	L1092	L1093	N1094	K1095	G1096	I1097	E1098	L1099	K1100	G1101	Y1102	L1103	P1104	K1105	A1106	E1107	T1108	L1109	L1110	Q1111	S1112	E1113	I1114	L1115	N1116	S1117	L1118	K1119	T1120	N1121	S1122	Y1123	F1124	E1125	F1126	S1127	L1128	K1129	A1130	N1131	Y1132	E1133	C1134	Y1135	M1136	K1137	L1138	Q1139	SER

● Molecule 11: Nup358 complex, clamps

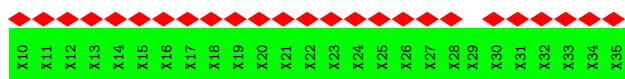




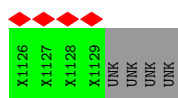
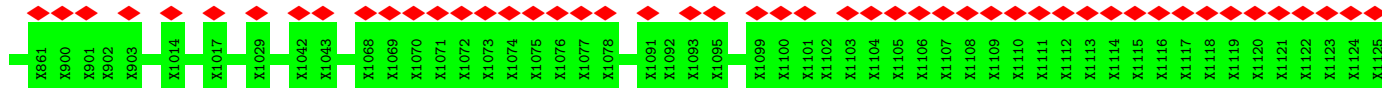
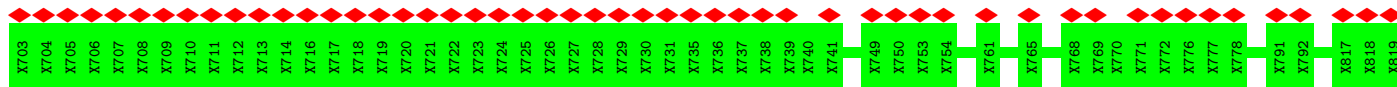
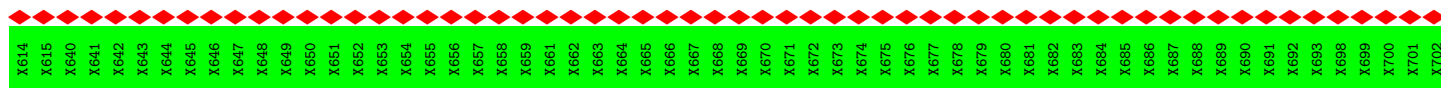
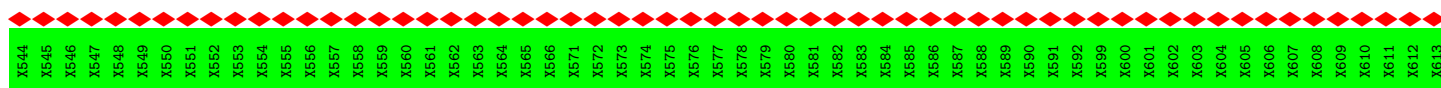
- Molecule 16: Nup214 complex Coiled coil region 2, helix 2



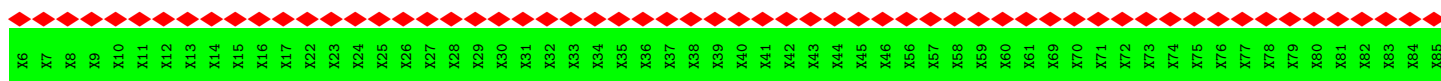
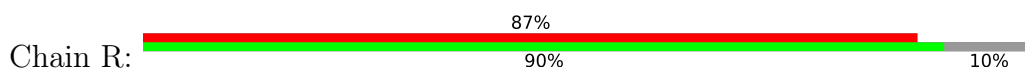
- Molecule 17: Nup214 complex Coiled coil region 2, helix 3



- Molecule 18: bridge domain



- Molecule 18: bridge domain



UNK	X86	X153	X230	X308	X374	UNK	X152
UNK	X87	X154	X231	X309	X375	UNK	X151
UNK	X88	X155	X232	X310	X376	UNK	X143
UNK	X89	X156	X233	X311	X377	UNK	X142
UNK	X90	X157	X234	X312	X378	UNK	X141
UNK	X91	X158	X235	X313	X379	UNK	X139
UNK	X92	X159	X245	X314	X380	UNK	X138
UNK	X93	X160	X246	X315	X385	UNK	X137
UNK	X94	X161	X247	X316	X386	UNK	X136
UNK	X95	X162	X248	X317	X387	UNK	X135
UNK	X96	X163	X249	X319	X416	UNK	X134
UNK	X97	X164	X250	X320	X417	UNK	X133
UNK	X98	X165	X251	X321	X418	UNK	X132
UNK	X99	X166	X252	X322	X419	UNK	X131
UNK	X100	X167	X253	X323	X420	UNK	X129
UNK	X101	X168	X254	X324	X421	UNK	X128
UNK	X102	X169	X255	X325	X422	UNK	X127
UNK	X103	X170	X256	X326	X423	UNK	X126
UNK	X104	X171	X257	X327	X424	UNK	X125
UNK	X105	X172	X258	X328	X425	UNK	X124
UNK	X106	X173	X259	X329	X426	UNK	X123
UNK	X107	X174	X260	X330	X427	UNK	X122
UNK	X108	X175	X261	X331	X428	UNK	X121
UNK	X109	X176	X262	X332	X430	UNK	X120
UNK	X110	X177	X263	X333	X431	UNK	X119
UNK	X111	X183	X264	X334	X432	UNK	X118
UNK	X112	X184	X265	X335	X433	UNK	X117
UNK	X113	X185	X266	X336	X434	UNK	X116
UNK	X114	X186	X267	X337	X435	UNK	X115
UNK	X115	X187	X268	X338	X436	UNK	X114
UNK	X116	X188	X269	X339	X437	UNK	X113
UNK	X117	X189	X270	X340	X438	UNK	X112
UNK	X118	X190	X271	X341	X439	UNK	X111
UNK	X119	X191	X272	X342	X440	UNK	X110
UNK	X120	X192	X273	X343	X441	UNK	X109
UNK	X121	X193	X274	X345	X442	UNK	X108
UNK	X122	X194	X275	X346	X443	UNK	X107
UNK	X123	X195	X276	X347	X444	UNK	X106
UNK	X124	X196	X277	X348	X445	UNK	X105
UNK	X125	X197	X278	X349	X446	UNK	X104
UNK	X126	X198	X279	X350	X447	UNK	X103
UNK	X127	X199	X280	X351	X448	UNK	X102
UNK	X128	X210	X281	X352	X449	UNK	X101
UNK	X129	X211	X282	X353	X451	UNK	X100
UNK	X130	X212	X283	X354	X452	UNK	X99
UNK	X131	X213	X284	X355	UNK	UNK	X98
UNK	X132	X214	X285	X356	UNK	UNK	X97
UNK	X133	X215	X286	X357	UNK	UNK	X96
UNK	X134	X216	X287	X358	UNK	UNK	X95
UNK	X135	X217	X288	X359	UNK	UNK	X94
UNK	X136	X219	X289	X360	UNK	UNK	X93
UNK	X137	X220	X290	X361	UNK	UNK	X92
UNK	X138	X221	X299	X362	UNK	UNK	X91
UNK	X139	X222	X300	X363	UNK	UNK	X90
UNK	X140	X223	X301	X364	UNK	UNK	X89
UNK	X141	X224	X302	X365	UNK	UNK	X88
UNK	X142	X225	X303	X366	UNK	UNK	X87
UNK	X143	X226	X304	X367	UNK	UNK	X86
UNK	X144	X227	X305	X369	UNK	UNK	X85
UNK	X151	X228	X306	X373	UNK	UNK	X84
UNK	X152	X229	X307		UNK	UNK	X83

4 Experimental information

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

There are no bond length outliers.

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
7	G	198	PRO	N-CA-CB	6.55	111.16	103.30
7	G	146	PRO	N-CA-CB	6.06	110.58	103.30
7	G	134	PRO	N-CA-CB	6.02	110.52	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	g	146	PRO	N-CA-CB	6.01	110.52	103.30
7	G	189	PRO	N-CA-CB	6.01	110.51	103.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1343/2011 (67%)	1264 (94%)	50 (4%)	29 (2%)	6	35
1	a	1210/2011 (60%)	1131 (94%)	53 (4%)	26 (2%)	7	36
2	B	500/653 (77%)	471 (94%)	18 (4%)	11 (2%)	6	35
2	b	481/653 (74%)	454 (94%)	15 (3%)	12 (2%)	5	32
3	C	277/375 (74%)	211 (76%)	65 (24%)	1 (0%)	34	72
3	c	276/375 (74%)	212 (77%)	63 (23%)	1 (0%)	34	72
4	D	301/322 (94%)	275 (91%)	20 (7%)	6 (2%)	7	37
4	d	285/322 (88%)	261 (92%)	20 (7%)	4 (1%)	11	45
5	E	998/1435 (70%)	900 (90%)	71 (7%)	27 (3%)	5	31
5	e	1087/1435 (76%)	967 (89%)	87 (8%)	33 (3%)	4	28
6	F	269/326 (82%)	244 (91%)	17 (6%)	8 (3%)	4	28
6	f	271/326 (83%)	245 (90%)	18 (7%)	8 (3%)	4	28
7	G	582/923 (63%)	473 (81%)	56 (10%)	53 (9%)	1	11
7	g	559/923 (61%)	475 (85%)	39 (7%)	45 (8%)	1	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H	287/320 (90%)	257 (90%)	24 (8%)	6 (2%)	7	36
8	h	283/320 (88%)	255 (90%)	24 (8%)	4 (1%)	11	45
9	I	726/916 (79%)	692 (95%)	28 (4%)	6 (1%)	19	59
9	i	715/916 (78%)	681 (95%)	27 (4%)	7 (1%)	15	53
10	J	1014/1140 (89%)	925 (91%)	69 (7%)	20 (2%)	7	37
10	j	1015/1140 (89%)	930 (92%)	67 (7%)	18 (2%)	8	40
11	S	153/2905 (5%)	146 (95%)	2 (1%)	5 (3%)	4	26
11	T	153/2905 (5%)	146 (95%)	2 (1%)	5 (3%)	4	26
11	U	161/2905 (6%)	148 (92%)	9 (6%)	4 (2%)	5	32
11	V	153/2905 (5%)	146 (95%)	2 (1%)	5 (3%)	4	26
All	All	13099/28462 (46%)	11909 (91%)	846 (6%)	344 (3%)	8	31

5 of 344 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	227	SER
1	A	228	LEU
1	A	239	THR
1	A	586	ILE
1	A	696	GLU

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
18	Q	21
18	R	18
13	L	1

The worst 5 of 40 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R	235:UNK	C	245:UNK	N	21.64
1	Q	861:UNK	C	900:UNK	N	21.11
1	R	387:UNK	C	416:UNK	N	18.78
1	Q	1112:UNK	C	1113:UNK	N	18.48
1	R	198:UNK	C	210:UNK	N	17.94

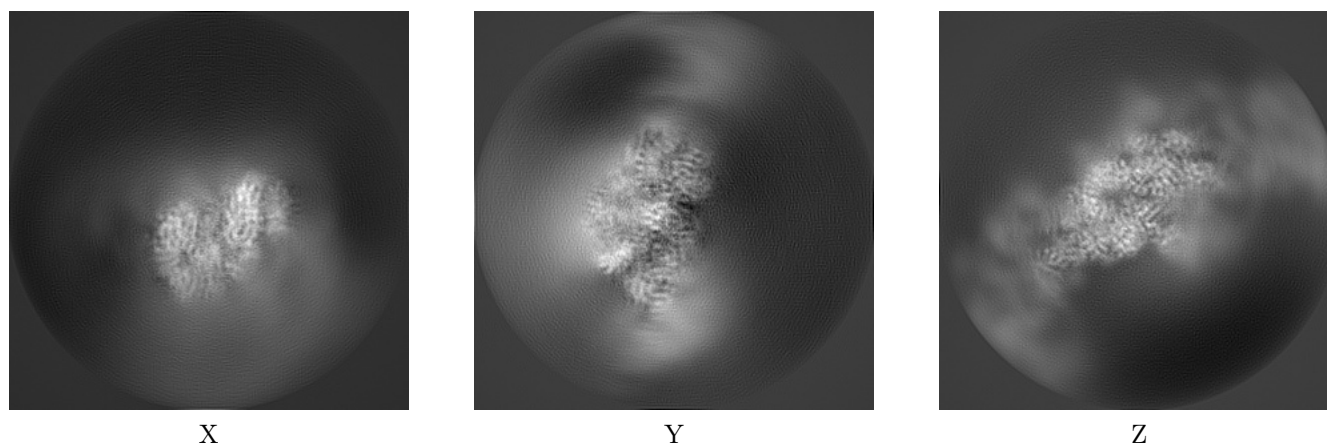
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0909. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

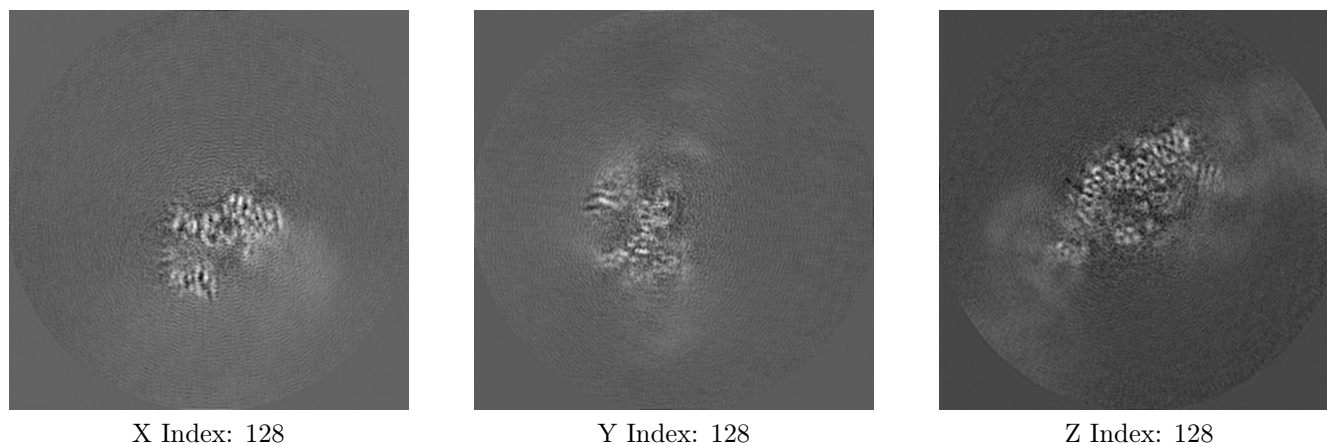
6.1.1 Primary map



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

6.2 Central slices [i](#)

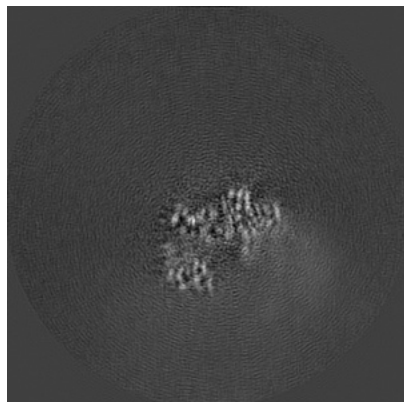
6.2.1 Primary map



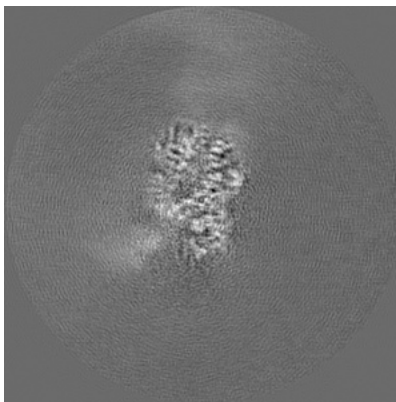
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

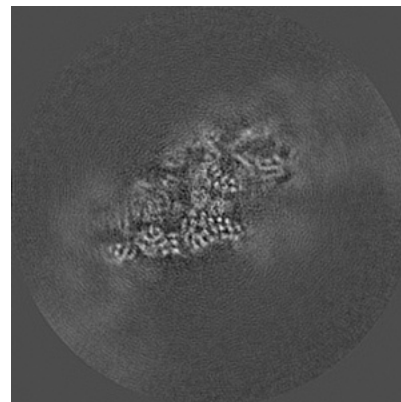
6.3.1 Primary map



X Index: 127



Y Index: 152



Z Index: 117

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

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

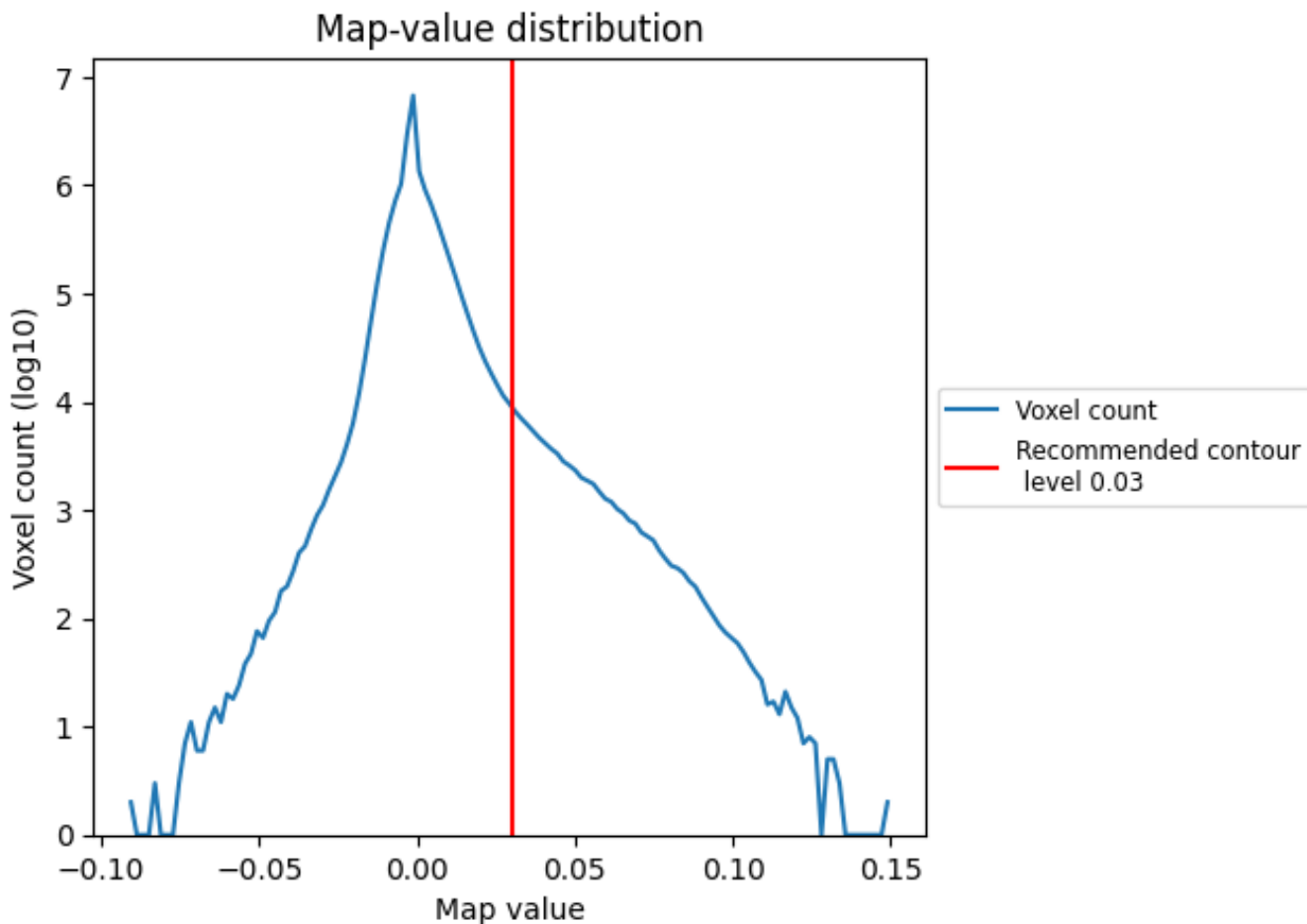
6.5 Mask visualisation

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

7 Map analysis [i](#)

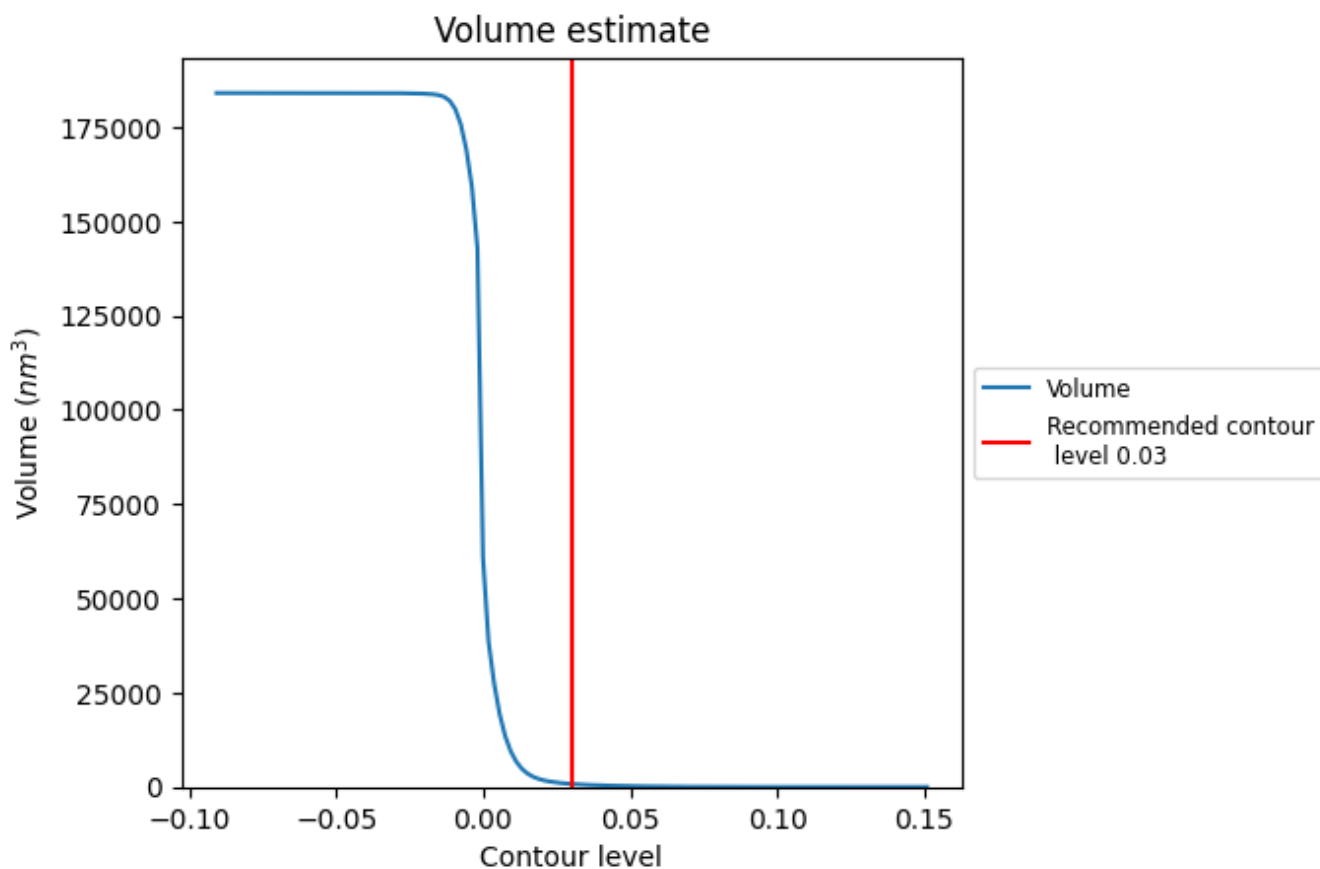
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

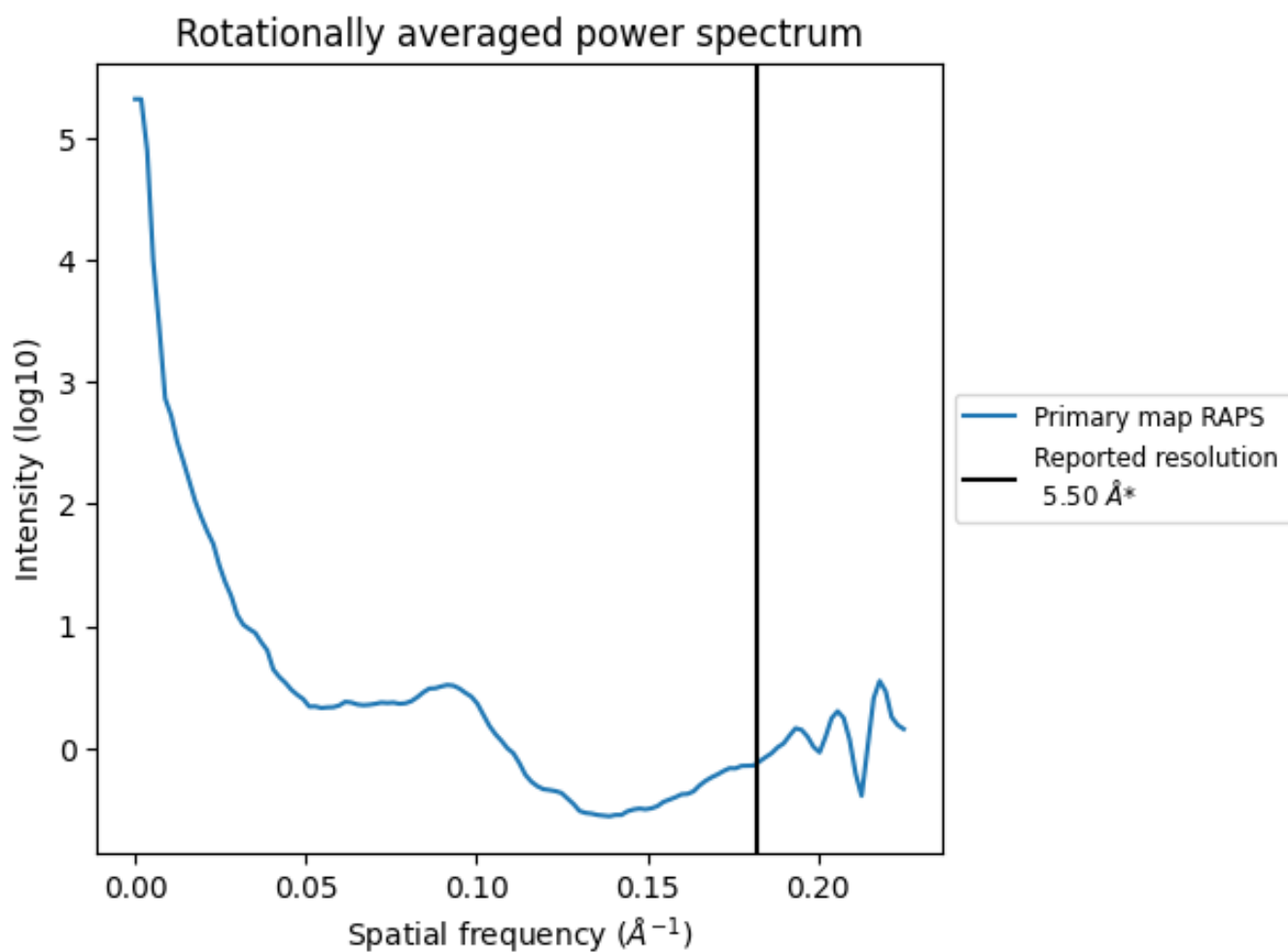
7.2 Volume estimate [i](#)



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

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

7.3 Rotationally averaged power spectrum [\(i\)](#)



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

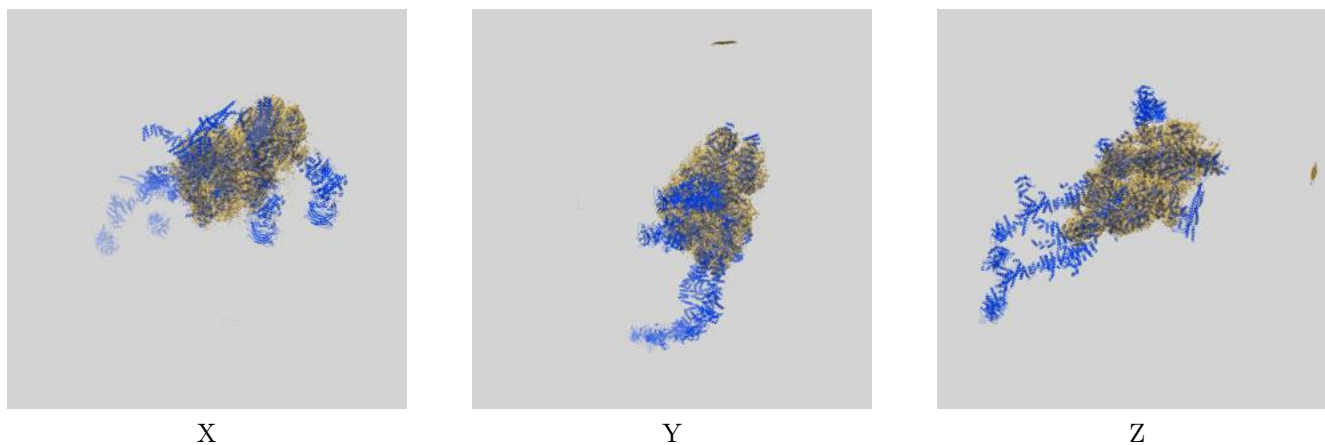
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

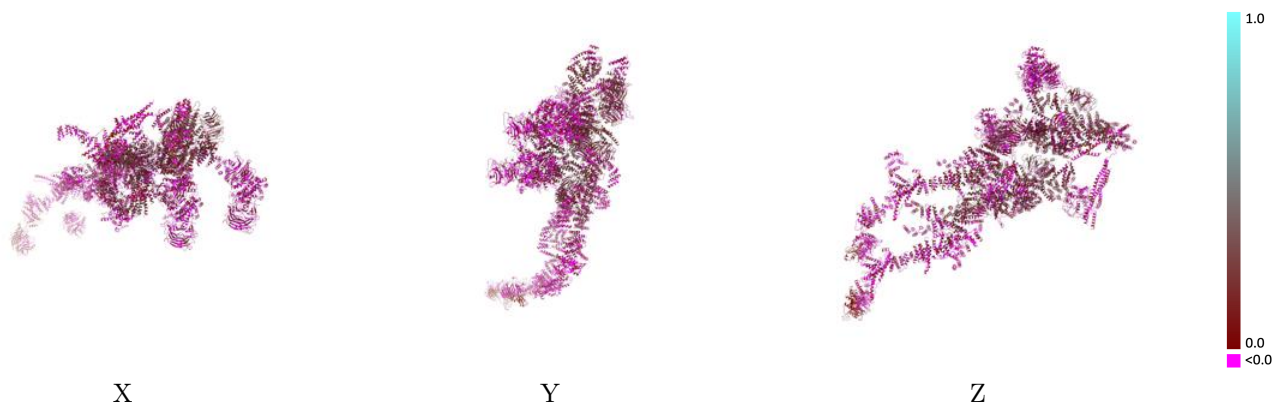
This section contains information regarding the fit between EMDB map EMD-0909 and PDB model 6LK8. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



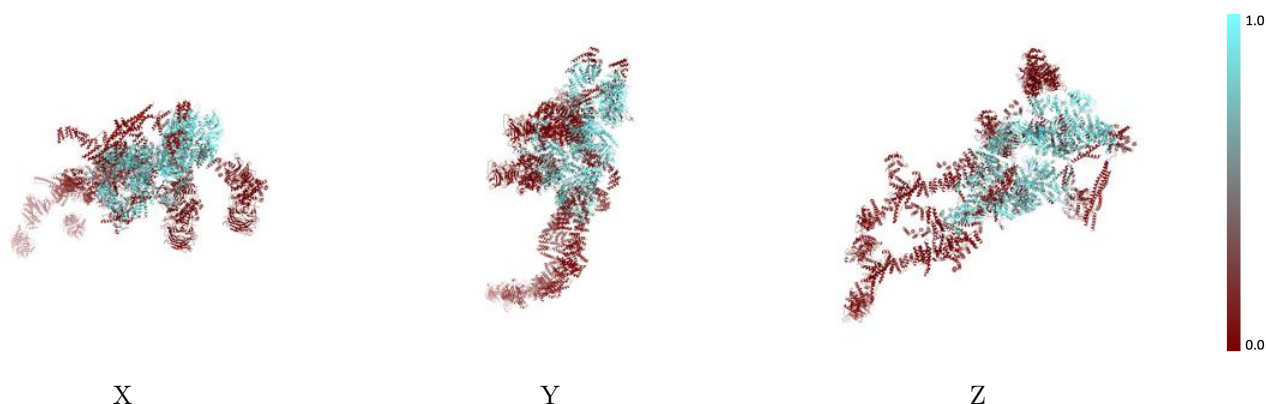
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



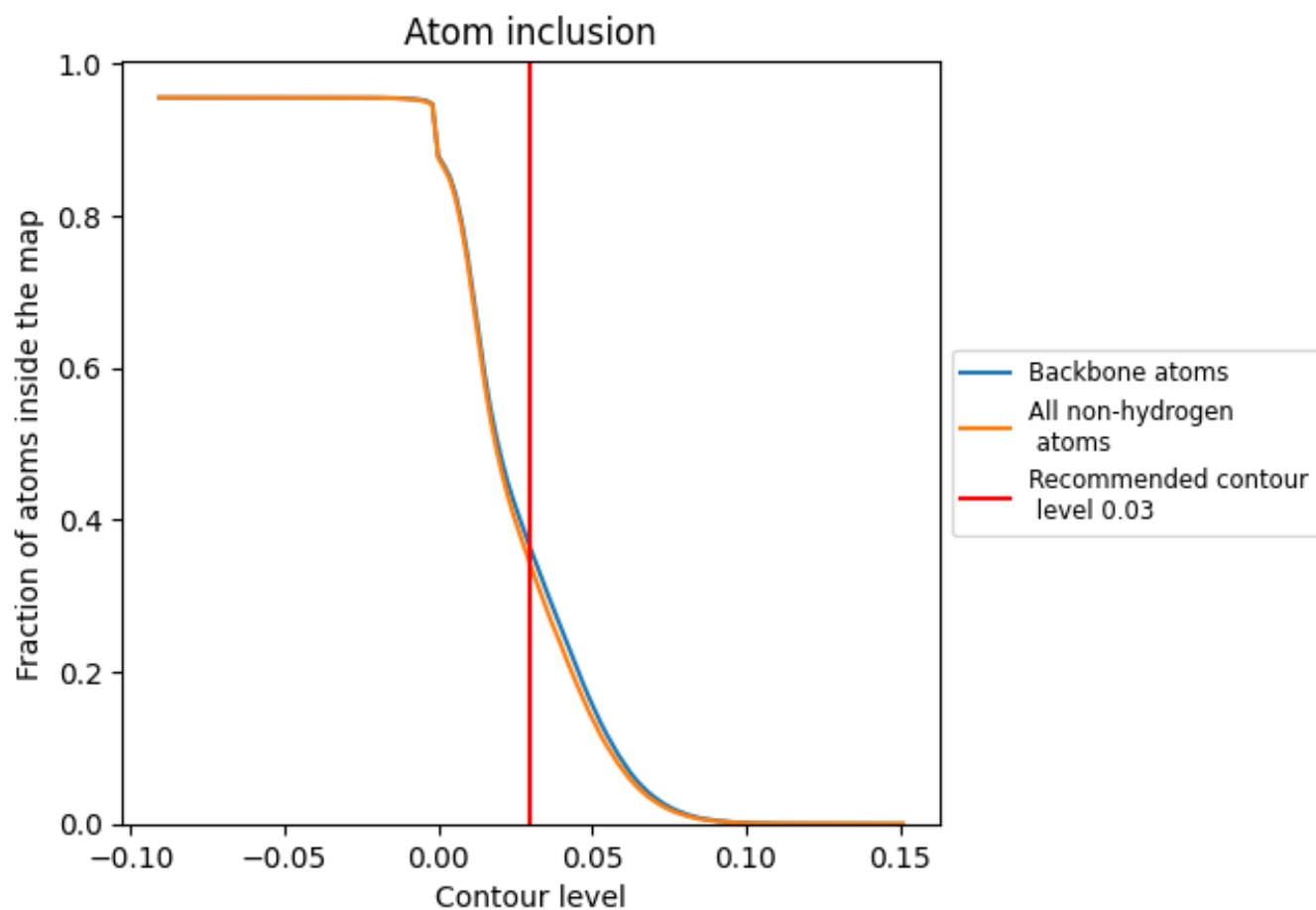
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).



































































9.4 Atom inclusion [i](#)



At the recommended contour level, 36% of all backbone atoms, 34% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3389	 0.0890
A	 0.6004	 0.1430
B	 0.6840	 0.1880
C	 0.8953	 0.2270
D	 0.7459	 0.1650
E	 0.0748	 0.0220
F	 0.0000	 0.0160
G	 0.6472	 0.1730
H	 0.7815	 0.1790
I	 0.1832	 0.0930
J	 0.0000	 0.0030
K	 0.0000	 0.0110
L	 0.0000	 0.0100
M	 0.0000	 0.0220
N	 0.4516	 0.1270
O	 0.0800	 0.0580
P	 0.0846	 0.0380
Q	 0.4124	 0.1510
R	 0.0547	 0.0080
S	 0.0667	 0.0560
T	 0.0500	 0.0150
U	 0.0000	 0.0300
V	 0.0000	 0.0190
a	 0.5030	 0.1030
b	 0.6740	 0.1800
c	 0.8776	 0.2470
d	 0.7290	 0.1740
e	 0.1730	 0.0260
f	 0.2994	 0.0300
g	 0.5757	 0.1550
h	 0.7091	 0.1850
i	 0.0000	 0.0190
j	 0.0000	 0.0120

