wwPDB EM Validation Summary Report (i)

Nov 27, 2022 – 07:10 AM EST

PDB ID	:	6ODM
EMDB ID	:	EMD-9860
Title	:	Herpes simplex virus type 1 (HSV-1) portal vertex-adjacent capsid/CATC, asymmetric unit
Authors	:	Liu, Y.T.; Jih, J.; Dai, X.H.; Bi, G.Q.; Zhou, Z.H.
Deposited on	:	2019-03-26
Resolution	:	4.30 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 (i) 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 (i)) were used in the production of this report:

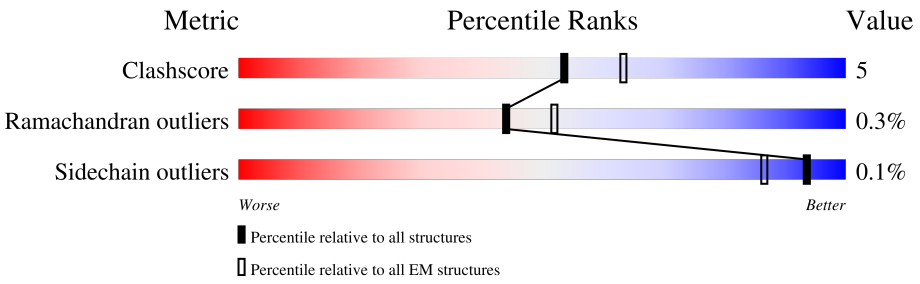
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 4.30 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=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 <=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	S	1374	8% 79% 17% •
1	T	1374	12% 83% 17%
1	W	1374	18% 85% 14% •
1	X	1374	7% 80% 15% 5%
2	E	112	10% 79% 11% 10%
2	F	112	12% 83% 7% 10%
2	L	112	52% 81% 9% 10%
2	P	112	13% 82% 8% 10%

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Mol	Chain	Length	Quality of chain
3	5	465	21% 72% 11% 17%
3	D	465	12% 67% 10% 22%
4	6	318	14% 78% 13% 8%
4	7	318	14% 80% 17%
4	A	318	35% 81% 15%
4	H	318	31% 75% 16% 8%
5	C	703	16% 67% 13% 20%
6	G	580	5% 14% 84%
6	K	580	11% 86%
7	B	3094	98%
7	O	3094	98%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 65560 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 Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	T	1369	10470	6612	1884	1920	54	0	0
1	W	1367	10451	6602	1879	1916	54	0	0
1	S	1328	10151	6418	1823	1858	52	0	0
1	X	1310	10027	6337	1801	1836	53	0	0

- Molecule 2 is a protein called Small capsomere-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	L	101	774	488	146	137	3	0	0
2	P	101	774	488	146	137	3	0	0
2	E	101	774	488	146	137	3	0	0
2	F	101	774	488	146	137	3	0	0

- Molecule 3 is a protein called Triplex capsid protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	5	387	2963	1848	564	532	19	0	0
3	D	363	2786	1741	531	496	18	0	0

- Molecule 4 is a protein called Triplex capsid protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	6	291	2216	1413	393	403	7	0	0
			Total	C	N	O	S		
4	7	310	2355	1497	417	432	9	0	0
			Total	C	N	O	S		
4	H	291	2216	1413	393	403	7	0	0
			Total	C	N	O	S		
4	A	310	2355	1497	417	432	9	0	0

- Molecule 5 is a protein called Capsid vertex component 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	C	565	4305	2734	783	767	21	0	0

- Molecule 6 is a protein called Capsid vertex component 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	G	92	749	475	136	134	4	0	0
			Total	C	N	O	S		
6	K	79	644	407	121	114	2	0	0

- Molecule 7 is a protein called Large tegument protein deneddylase.

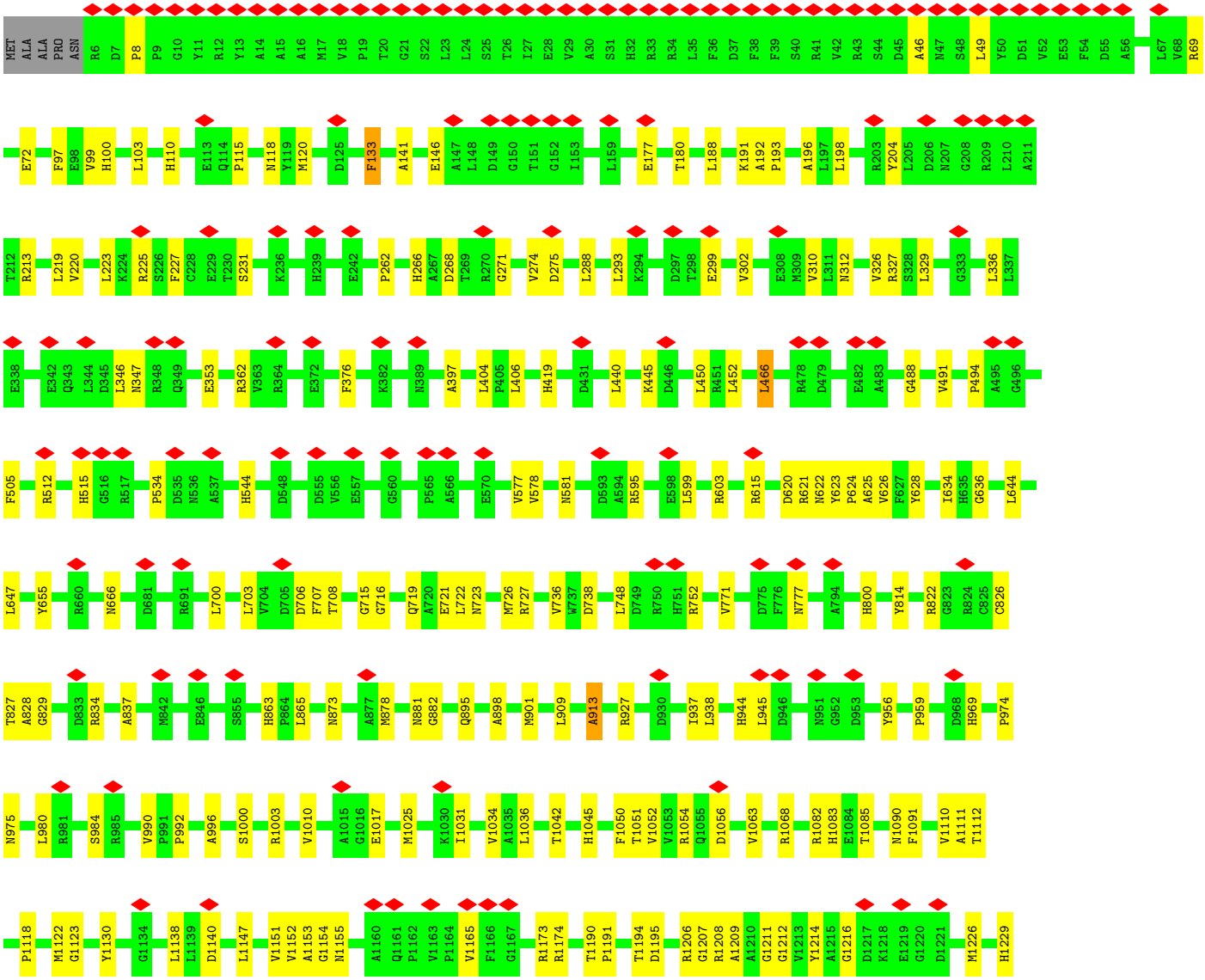
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	O	48	388	239	85	62	2	0	0
			Total	C	N	O	S		
7	B	48	388	239	85	62	2	0	0

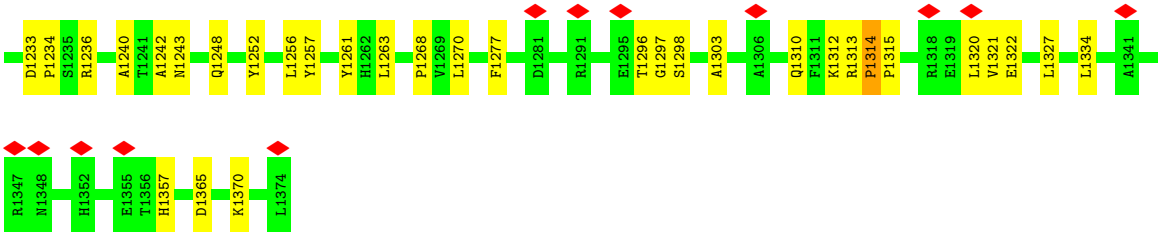
3 Residue-property plots (i)

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: Major capsid protein

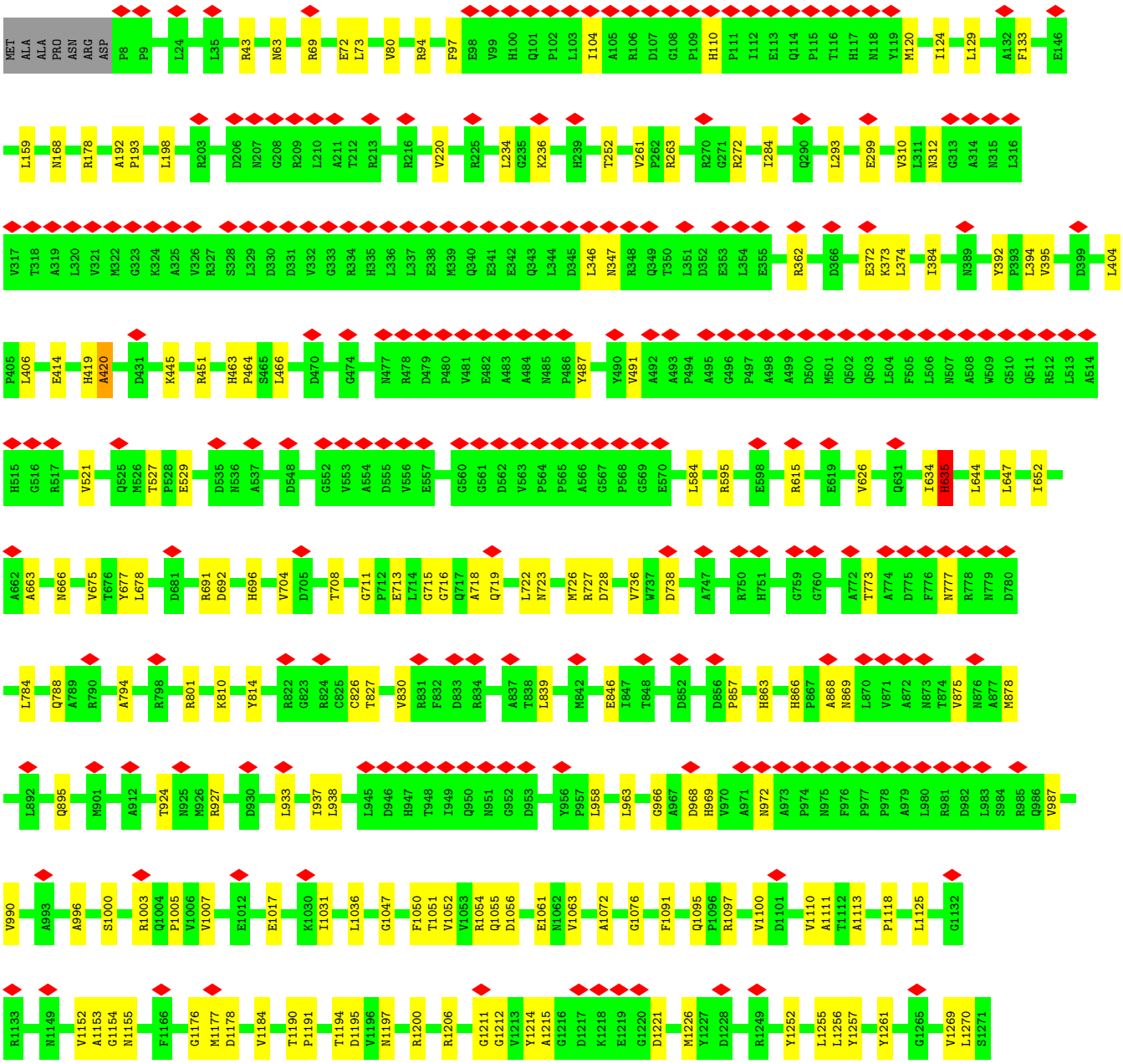
Chain T: 12% 83% 17%

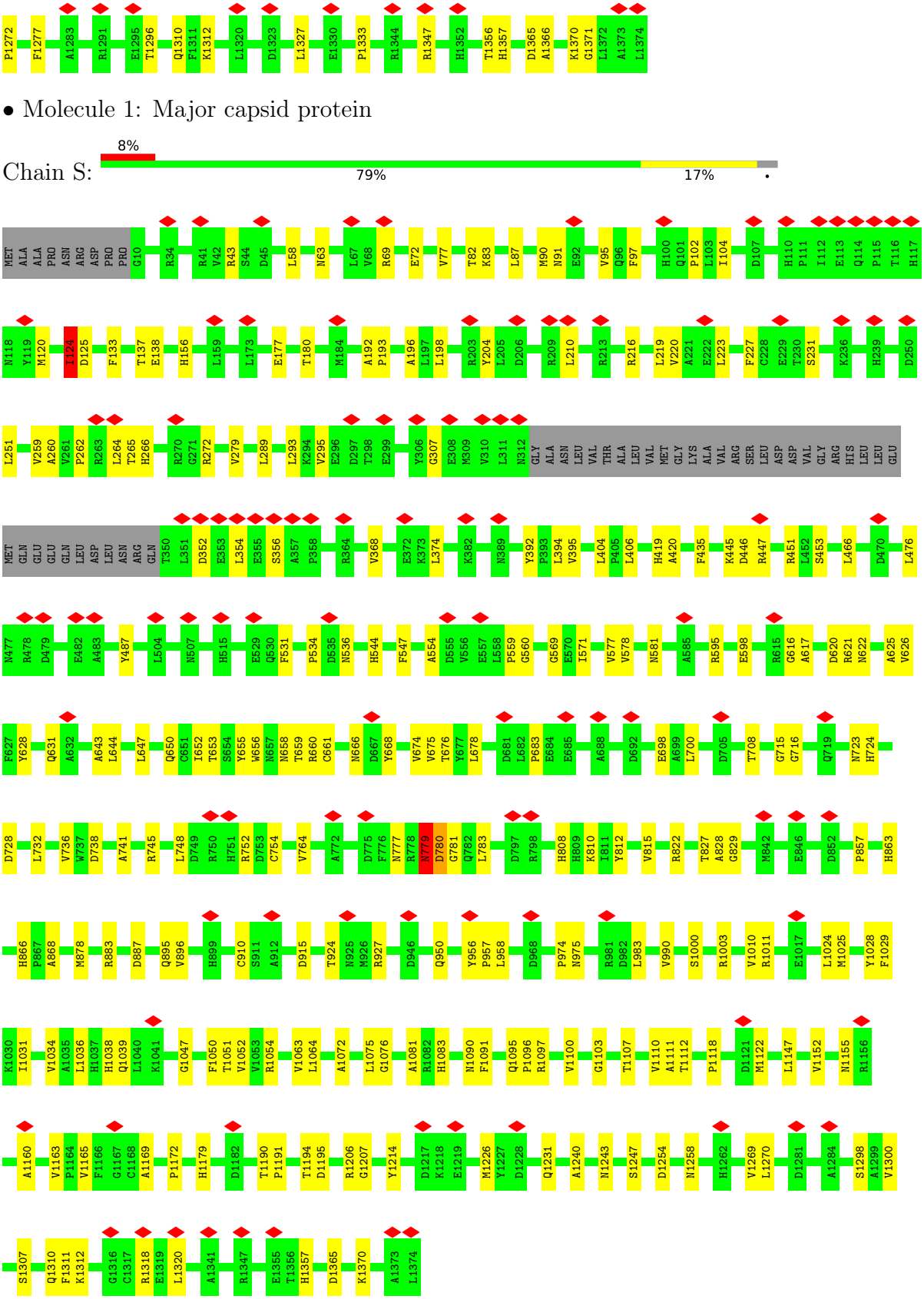




- Molecule 1: Major capsid protein

Chain W:





• Molecule 1: Major capsid protein

• Molecule 1: Major capsid protein

Chain X: 7% 80% 15% 5%

MET ALA ALA PRO ASN ARG ASP PRO PRO GLY TYR ARG TYR ALA ALA ALA MET VAL PRO THR GLY SER LEU LEU LEU SER THR ILE GLU VAL ALA SER HIS ARG ARG LEU PHE ASP PHE PHE SER ARG VAL ARG SER ASP ALA ASN SER LEU Y50 D51 V52 E53 F54 D55 L58 Y61

L67 V68 R69 E72 V77 F97 E98 V99 H100 L103 P109 H110 P111 P115 N118 Y119 M120 D125 S134 L135 A136 L142 L143 T144 GLY GLU ALA LEU ASP GLY THR GLY ILE SER ALA H156 R157 Q158 L159 R160 A161 I162 Q163 R167 V172 E177 R178

G179 T180 A181 D182 L185 A192 P193 A196 L197 L198 D206 N207 GLY ARG LEU ALA T212 F227 C228 E229 T230 S231 H239 D250 L251 H266 R270 E299 A319 L320 V326 L329 D330 Q340 E341 E342 D345 L346 N347 R348 D352 D366

E372 L380 E381 K382 Y385 A386 A387 T388 N389 V390 P391 Y392 P393 L394 V395 L404 P405 L406 H419 A420 G421 F435 L440 F441 F442 K445 L450 R451 L452 E455 D470 G474 G475 L476 Y487 V491 P494 Q503 N507 V518 R519 W520 V521

E529 Q530 F531 D535 N536 A537 N538 D548 A554 D555 V556 E557 L558 P559 G560 G561 D562 G569 R576 V577 V578 N581 E598 R615 E619 D620 R621 N622 A625 V626 F627 Y628 Q631 A632 A633 I634 H635 G636 V648 C651 F664 V665 N666 V674

V675 L678 G679 G680 D681 E684 M687 A688 R691 D692 E698 D705 G715 G716 Q719 L722 D728 V736 W737 D738 R745 R750 V756 S757 A758 A766 V771 A772 T773 N777 L784 D793 A794 R798 F799 H800 K810 R822

G823 R824 C825 C826 T827 A828 G829 F832 D833 R834 M842 V843 E846 I847 E851 D856 D860 H863 P864 L865 N876 A877 M878 N881 G882 R883 E903 R904 L908 L909 C910 S911 F929 D930 H944 L945 D946 N951 Y956 P957 L958 P959 V960 G966

A967 D968 H969 V970 A971 N972 A973 P974 N975 R981 R985 Q986 V987 V990 L994 S1000 R1003 V1010 R1011 E1012 S1013 A1014 E1017 L1020 A1023 I1031 L1036 F1050 T1051 R1054 Q1055 D1056 V1063 A1072 H1083 E1084 T1085 G1086 G1087 G1088 V1089 N1090

L1093 V1100 V1110 A1111 T1112 D1121 R1148 V1152 A1153 G1154 N1155 R1156 Q1161 P1162 V1165 F1166 G1167 R1173 R1174 H1179 E1186 T1190 D1195 R1201 G1207 A1215 G1216 D1217 K1218 E1219 G1220 D1221 D1228 P1234 N1243 F1250 D1254 L1255 L1256 Y1257

N1258 Y1261 H1262 L1263 N1264 G1265 L1270 R1287 R1291 T1296 T1304 A1305 A1306 S1307 Q1310 F1311 K1312 R1313 P1314 P1315 R1318 E1319 L1320 L1327 L1334 N1348 G1349 E1350 A1351 H1352 H1357 F1358 D1365 K1370 A1373 L1374

• Molecule 2: Small capsomere-interacting protein

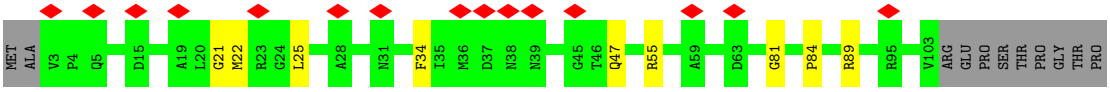
Chain L: 52% 81% 9% 10%

MET ALA V3 P4 Q5 F6 H7 R8 P9 S10 T11 V12 T13 T14 D15 S16 V17 R18 A19 L20 G21 M22 R23 G24 L25 V26 L27 A28 T29 N30 N31 S32 Q33 F34 I35 M36 D37 N38 N39 H40 P41 H42 P43 Q44 G45 T46 Q47 G48 A49 V50 R51 E52 F53 L54 R55 G56 Q57 A58 A59 A60

L61 T62 D63 H68 P84 P90 L94 R95 V103 ARG GLU PRO SER THR PRO GLY THR PRO

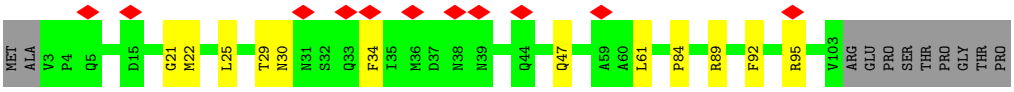
- Molecule 2: Small capsomere-interacting protein

Chain P:



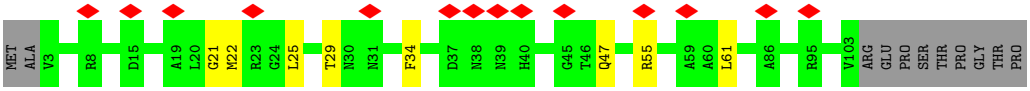
- Molecule 2: Small capsomere-interacting protein

Chain E:



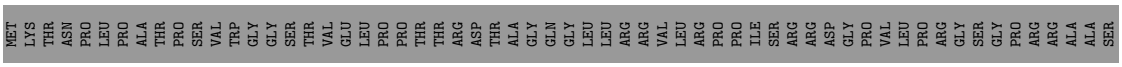
- Molecule 2: Small capsomere-interacting protein

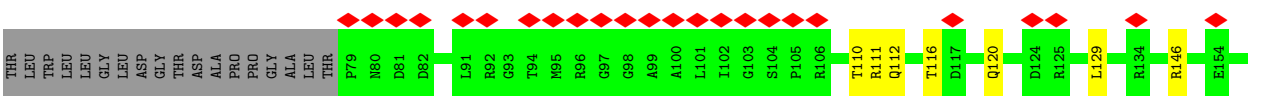
Chain F:

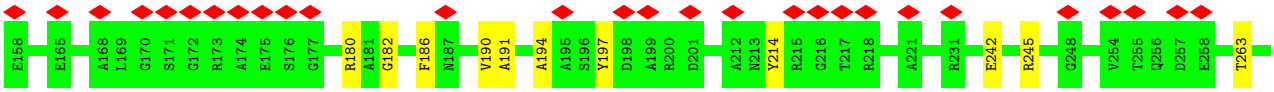


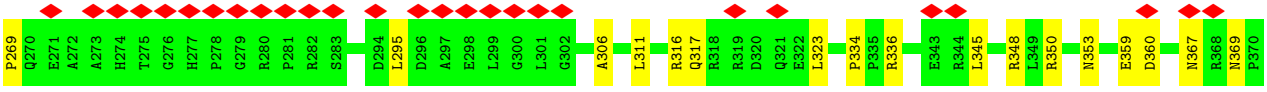
- Molecule 3: Triplex capsid protein 1

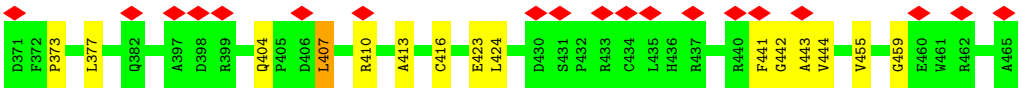
Chain 5:





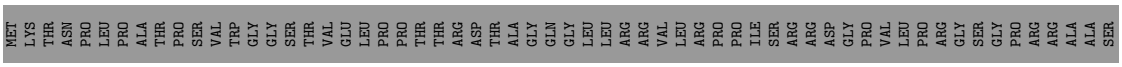


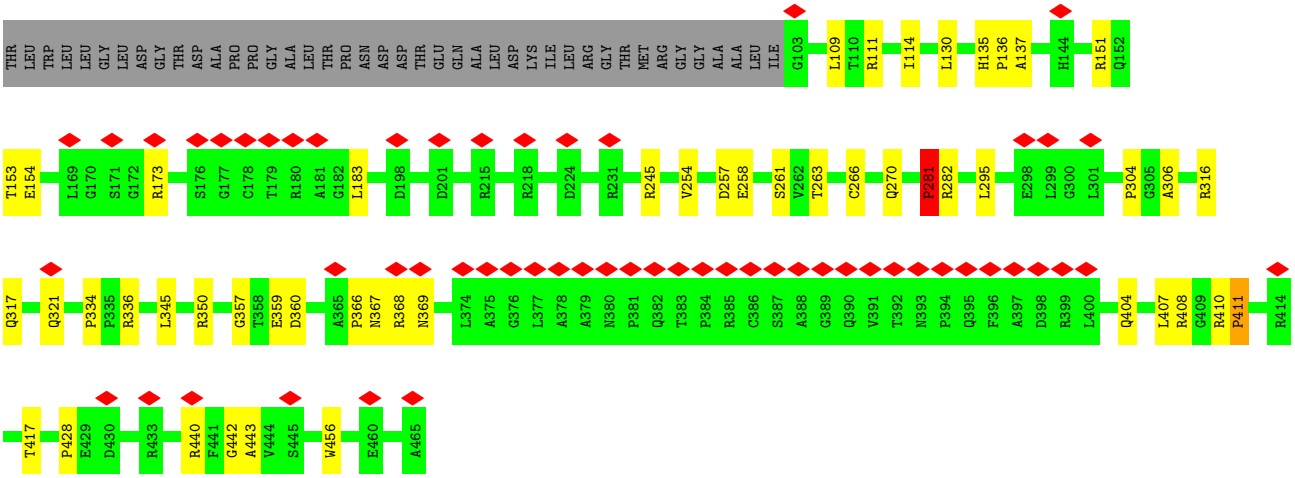




- Molecule 3: Triplex capsid protein 1

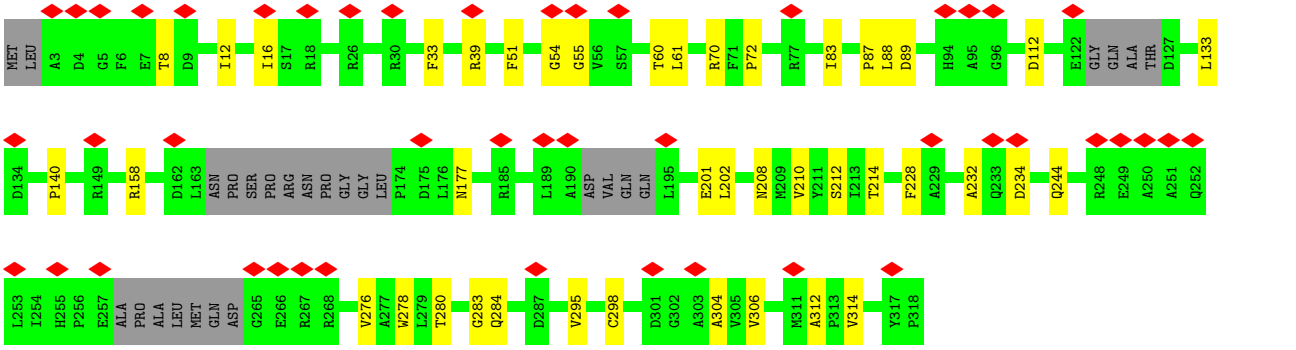
Chain D:





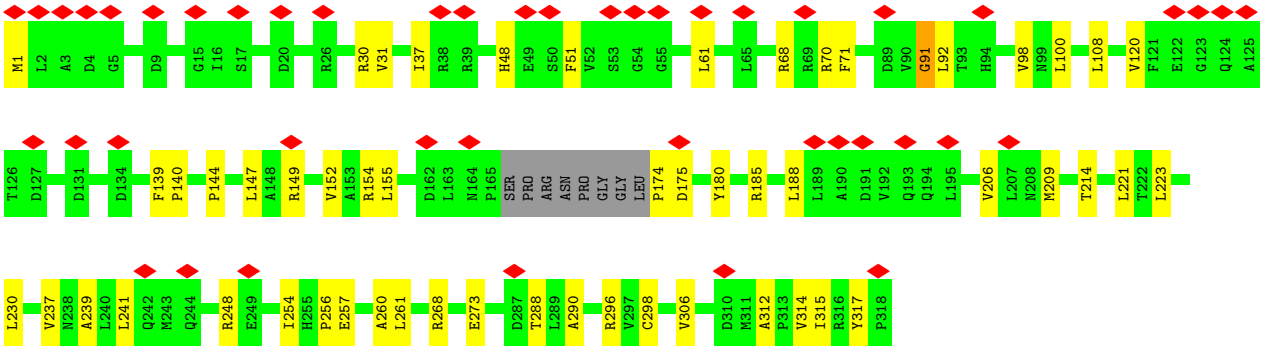
- Molecule 4: Triplex capsid protein 2

Chain 6:



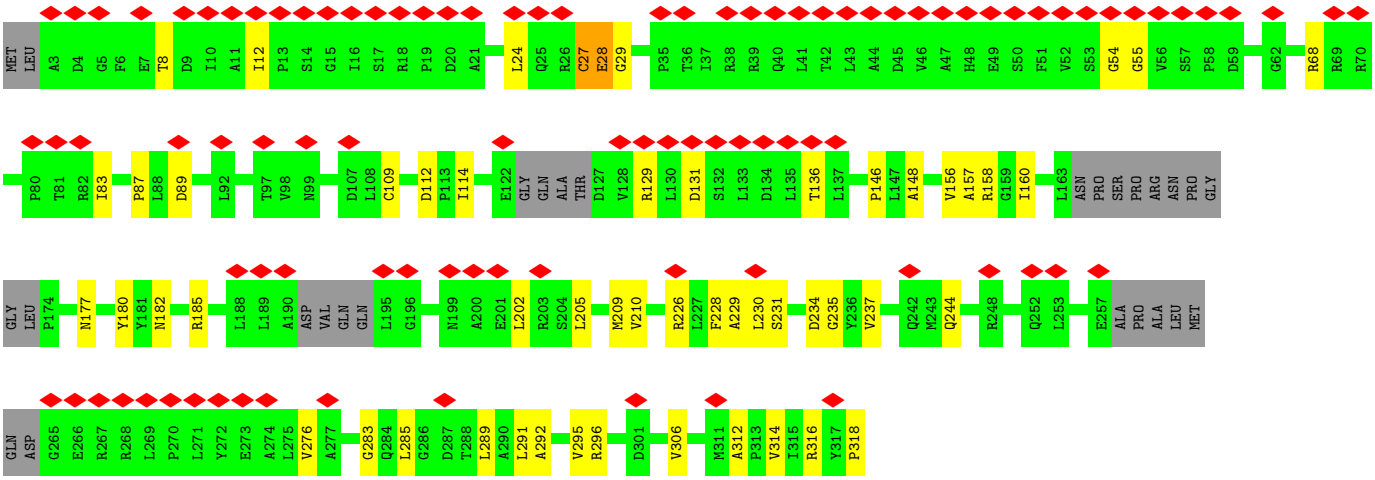
- Molecule 4: Triplex capsid protein 2

Chain 7:



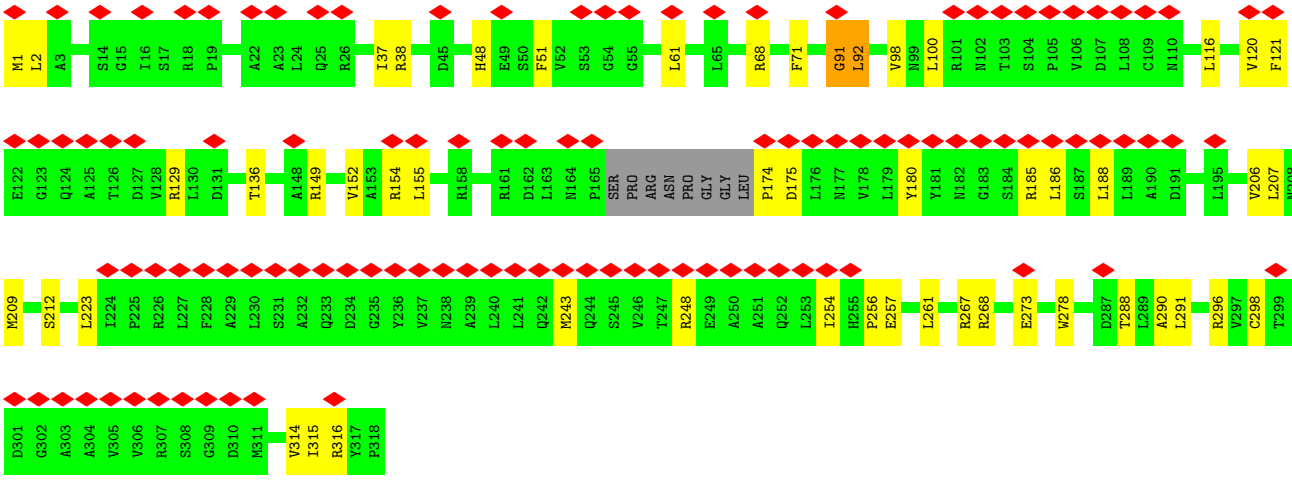
- Molecule 4: Triplex capsid protein 2

Chain H:



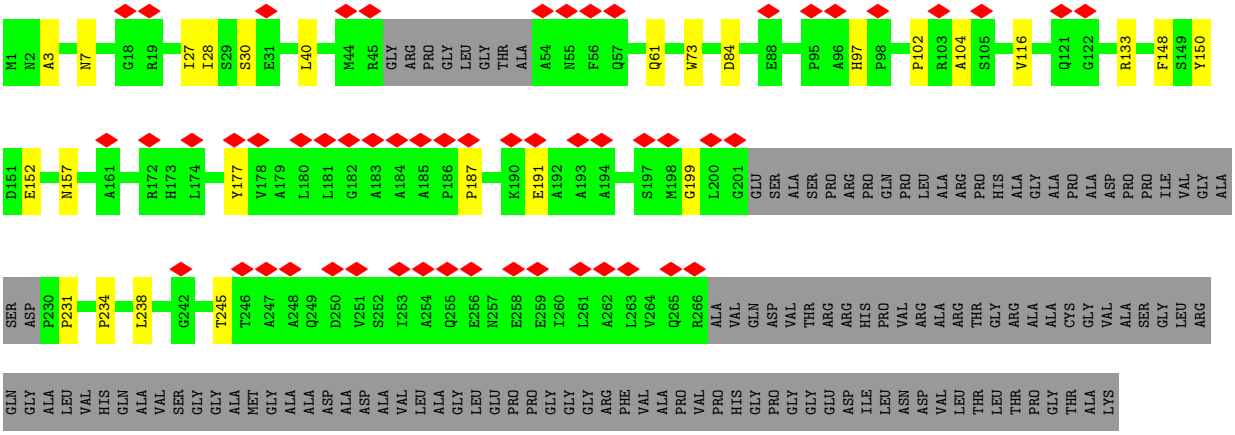
- Molecule 4: Triplex capsid protein 2

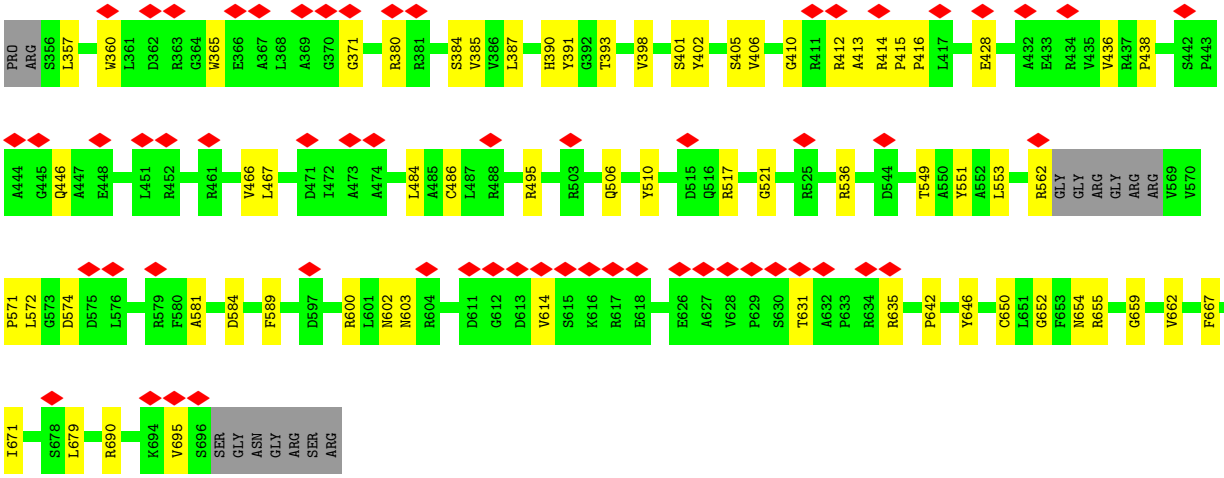
Chain A:



- Molecule 5: Capsid vertex component 1

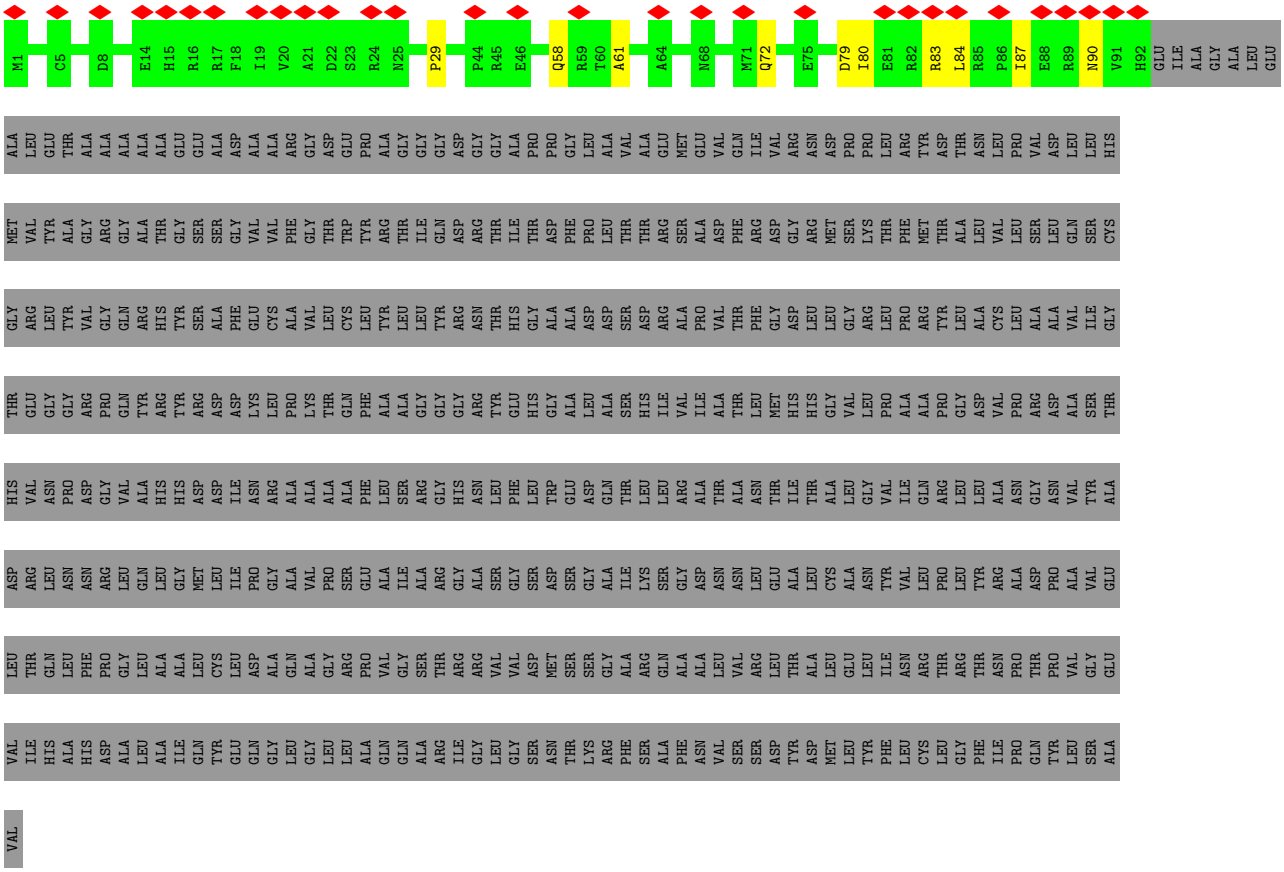
Chain C:





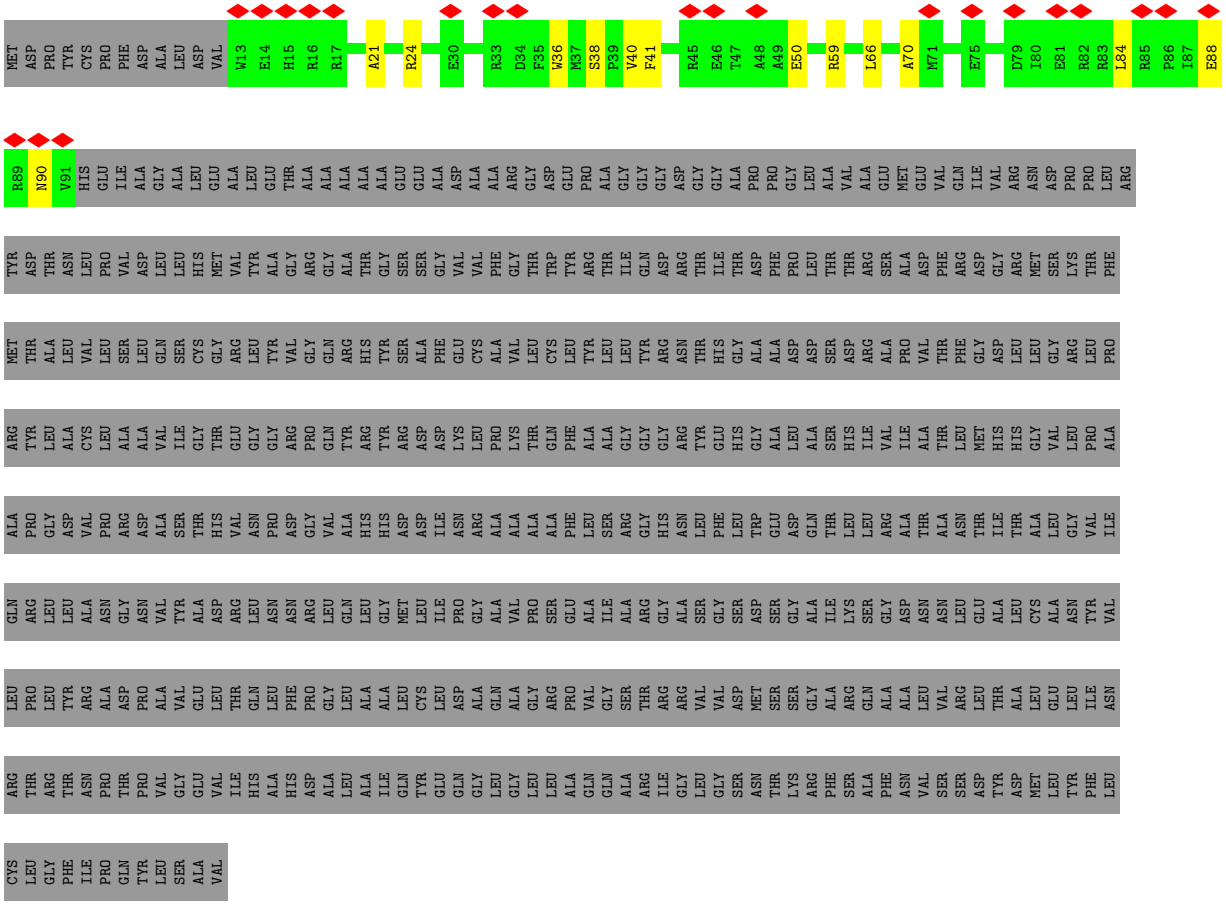
- Molecule 6: Capsid vertex component 2

Chain G: 5% 14% 84%



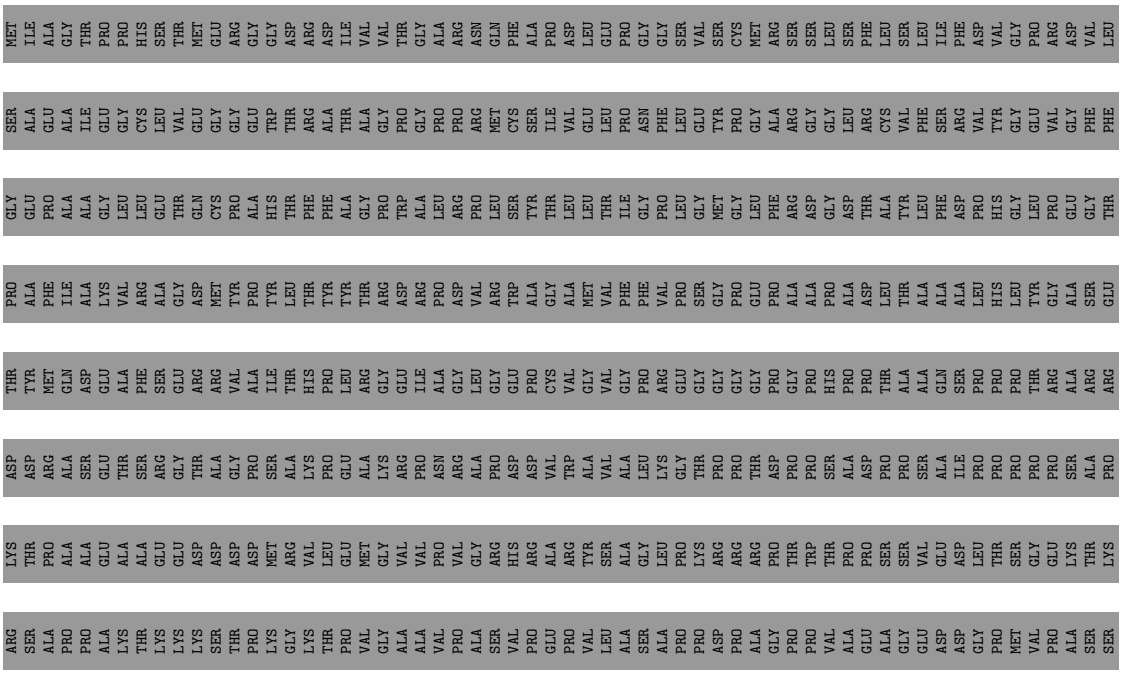
- Molecule 6: Capsid vertex component 2

Chain K: 11% 86%



• Molecule 7: Large tegument protein deneddylase

Chain O: 98%



GLN ALA LEU GLU ALA LEU LYS THR ARG ARG SER PRO GLU PRO PRO GLY ALA ASP LEU ALA GLN LEU PHE GLU ALA HIS PRO ASN VAL ALA ALA THR ALA VAL LYS PHE THR ALA CYS SER ALA THR LEU ALA ARG GLU VAL ALA ALA CYS SER ARG LEU THR ILE SER ALA LEU ARG SER

PRO TYR PRO ALA SER PRO GLY LEU LEU GLU LEU CYS VAL ILE PHE PHE PHE GLU ARG VAL LEU ALA PHE LEU ILE GLU ASN GLY ALA ARG THR HIS THR GLN ALA GLY VAL ALA GLY PRO ALA ALA ALA LEU LEU GLU PHE THR LEU SER MET LEU PRO ARG LYS THR ALA VAL GLY ASP

PHE LEU ALA SER THR ARG LEU SER LEU ALA ASP VAL ALA ALA HIS LEU PRO LEU VAL GLN HIS VAL LEU ASP GLU ASN SER LEU ILE GLY ARG LEU ALA LEU ALA LYS LEU ILE LEU VAL ALA ARG ASP VAL ILE ARG GLU THR ASP ALA PHE TYR GLY GLU LEU ALA ASP LEU GLU LEU

GLN LEU ARG ALA ALA PRO PRO ALA ASN LEU TYR THR ARG LEU GLY GLU TRP LEU LEU GLU ARG SER GLN ALA HIS PRO ASP THR LEU PHE ALA PRO ALA THR PRO THR HIS PRO GLU PRO LEU LEU TYR ARG VAL GLN ALA LEU ALA LYS PHE ALA ARG GLY GLU GLU ILE ARG VAL GLU

ALA GLU ASP ARG GLN MET ARG GLU ALA LEU ASP ALA LEU ALA ARG GLY VAL ASP ALA VAL SER GLN HIS ALA GLY PRO LEU GLY VAL MET PRO ALA PRO ALA GLY ALA ALA PRO GLN GLY ALA PRO ARG PRO PRO PRO LEU GLY PRO GLU ALA VAL GLN VAL ARG LEU GLU GLU VAL ARG

THR GLN ALA ARG ARG ALA ILE GLU GLY ALA VAL LYS GLU TYR PHE TYR ARG GLY ALA VAL TYR SER ALA LYS ALA LEU GLN ALA SER ASP ASN ASN ASP ARG ARG PHE HIS VAL ALA SER ALA ALA VAL VAL PRO VAL VAL GLN LEU LEU GLU SER LEU PRO VAL PHE ASP GLN HIS THR

ARG ASP ILE ALA GLN ARG ALA ALA ILE PRO ALA PRO PRO PRO ILE ALA THR SER PRO THR ALA ILE LEU LEU ARG ASP LEU ILE GLN ARG GLY GLN THR LEU ASP ALA PRO GLU ASP LEU ALA ALA TRP LEU SER VAL LEU THR ASP ALA ALA ASN GLN GLY LEU ILE GLU ARG LYS PRO

LEU ASP GLU LEU ALA ARG SER ILE ARG ASP ILE ASN ASP GLN GLN ALA ARG ARG SER SER GLY LEU ALA GLU LEU ARG ARG PHE ASP ALA LEU ASP ALA ALA LEU GLY GLN GLN LEU ASP SER ASP ALA ALA PHE VAL PRO ALA PRO GLY ALA SER PRO TYR PRO ASP ASP GLY GLY LEU

SER PRO GLU ALA THR ARG MET ALA GLU GLU ALA LEU ARG GLN ALA ARG ALA MET ASP ALA ALA LYS LEU THR ALA GLU LEU ALA PRO ASP ALA ARG ALA ARG LEU ARG GLU ARG ALA ARG SER LEU GLU ALA MET LEU GLU GLY ALA ARG GLU ARG ALA LYS VAL ALA ARG ASP ALA ARG

GLU LYS PHE LEU HIS LYS LEU GLN GLY VAL LEU ARG PRO LEU PRO ASP PHE VAL GLY LEU LYS ALA CYS PRO ALA VAL LEU ALA THR LEU ARG ALA SER LEU PRO ALA GLY TRP SER ASP LEU PRO GLU ALA VAL ARG GLY ALA PRO PRO GLU VAL THR ALA ALA LEU ARG ALA ASP MET

TRP GLY LEU LEU GLY GLN TYR ARG ASP ALA LEU GLU HIS PRO THR PRO ASP THR ALA THR ALA LEU SER GLY LEU HIS PRO SER PHE VAL VAL VAL LEU LYS ASN LEU PHE ALA ASP ALA PRO GLU THR PRO PHE LEU LEU GLN PHE PHE ALA ASP HIS ALA PRO ILE ILE ALA HIS ALA

VAL SER ASN ALA ILE ASN ALA GLY SER ALA ALA VAL ALA THR ALA ASP PRO ALA SER THR VAL ASP ALA ALA VAL ARG ALA HIS ARG VAL LEU VAL ASP ALA VAL THR ALA LEU GLY ALA ALA ALA SER ASP PRO ALA SER PRO LEU ALA PHE LEU ALA ALA MET ALA ASP SER ALA ALA

GLY TYR VAL LYS ALA THR ARG LEU ALA LEU ASP ALA ARG GLY ALA ILE ALA GLN LEU THR THR LEU GLY SER ALA ALA ALA ASP LEU VAL VAL GLN VAL ARG ARG ALA ALA ASN GLN PRO GLU GLY GLU HIS ALA SER LEU ILE GLN ALA ALA THR ARG ALA THR THR GLY ALA ARG GLU

SER LEU ALA GLY HIS GLU GLY ARG PHE GLY GLY LEU LEU HIS ALA GLU GLY THR ALA GLY ASP HIS SER PRO SER GLY ARG ALA LEU GLN GLU LEU GLY LYS VAL ILE GLY ALA THR ARG ARG ARG ALA ASP GLU LEU GLU ALA ALA ILE ALA ASP LEU ARG GLU LYS MET ALA ALA GLN

ARG ALA ARG SER SER HIS GLU ARG TRP ALA ALA ASP VAL GLU ALA VAL LEU ASP ARG VAL GLU SER GLY ALA GLU PHE ASP VAL VAL GLU LEU ARG ARG LEU GLN ALA LEU ALA GLY THR HIS GLY TYR ASN PRO ARG ASP PHE ARG LYS ARG ALA GLU GLN ALA LEU GLY THR ASN ALA

LYS ALA VAL THR LEU ALA LEU GLU THR ALA LEU ALA PHE ASN PRO TYR THR PRO GLU ASN GLN ARG HIS PRO MET LEU PRO PRO LEU ALA ALA ILE HIS ARG ILE ASP TRP SER ALA ALA PHE GLY ALA ALA ALA ASP THR TYR ALA ASP MET PHE ARG VAL ASP THR GLU PRO LEU ALA

ARG LEU LEU ARG LEU ALA GLY GLY LEU LEU GLU ARG ALA GLN ALA ASN ASP GLY PHE ILE ASP TYR HIS GLU ALA VAL LEU HIS LEU SER GLU ASP LEU GLY GLY VAL PRO ALA LEU ARG GLN TYR VAL PRO PHE PHE GLN LYS GLY TYR ALA GLU TYR VAL ASP ILE ARG ASP ARG LEU

ASP ALA LEU ARG ALA ASP ALA ARG ARG ALA ILE GLY SER VAL ALA LEU ASP LEU ALA ALA ALA ALA GLU GLU ILE SER ALA VAL ARG ASN ASP PRO ALA ALA ALA ALA GLU LEU VAL ARG ALA GLY VAL THR LEU PRO CYS PRO SER GLU ASP ALA LEU VAL ALA CYS VAL ALA ALA LEU

GLU ARG VAL ASP GLN SER PRO VAL LYS ASP THR ALA TYR ALA ASP TYR VAL ALA PHE VAL THR ARG GLN ASP LEU ALA ASP THR LYS ASP ALA VAL VAL ARG ALA LYS GLN GLN ARG ALA GLU ALA THR GLU ARG VAL THR ALA GLY LEU ARG GLU VAL LEU ALA ALA ARG GLU ARG ARG

ALA GLN LEU GLU ALA GLU GLY LEU ALA ASN LEU LYS THR LEU LEU LYS VAL VAL ALA VAL PRO ALA THR VAL ALA LYS THR LEU ASP GLN ALA ARG SER ALA GLU GLU ILE ALA ASP GLN VAL GLU ILE LEU LEU ASP GLN THR GLU LYS ALA ARG GLU LEU ASP VAL GLN ALA VAL ALA

TRP LEU GLU HIS ALA GLN ARG THR PHE GLU THR HIS PRO LEU ASN ALA ALA SER GLY ASP GLY PRO GLY LEU LEU THR ARG GLN GLY ALA ARG LEU GLN ALA LEU PHE ASP THR ARG ARG ARG VAL GLU ALA LEU ARG ARG SER LEU GLU GLU ALA GLU ALA GLU TRP ASP GLU VAL TRP

GLY ARG PHE GLY ARG VAL ARG GLY GLY ALA TRP LYS SER PRO GLU GLY PHE ARG ALA ALA CYS GLU GLN LEU ARG ALA LEU GLN ASP THR THR ASN THR VAL SER GLY LEU ARG ALA GLN ARG ASP TYR GLU ARG LEU PRO ALA LYS TYR GLN GLY VAL LEU GLY ALA LYS SER ALA GLU

ARG ALA GLY ALA VAL GLU GLU LEU GLY GLY ARG VAL ALA GLN HIS ALA ASP LEU SER ALA ARG LEU ARG ASP GLU VAL VAL PRO ARG VAL ALA TRP GLU MET ASN PHE ASP THR LEU GLY GLY LEU LEU ALA GLU PHE ASP ALA VAL ALA GLY ASP LEU ALA PRO TRP ALA VAL GLU GLU

PHE ARG GLY ALA ARG GLU LEU ILE GLN ARG ARG MET GLY LEU TYR SER ALA TYR ALA LYS ALA THR GLY GLN THR GLY ALA GLY ALA ALA ALA PRO ALA PRO LEU LEU VAL ASP LEU ARG ALA LEU ASP ALA ARG ALA ARG ALA SER ALA PRO PRO GLY GLN GLU ALA ASP PRO GLN

MET LEU ARG ARG ARG GLY GLU ALA TYR LEU ARG VAL SER GLY GLY PRO GLY PRO LEU VAL LEU ARG GLU ALA THR SER THR LEU ASP ARG PRO PHE ALA PRO SER PHE LEU VAL PRO ASP GLY THR PRO LEU GLN TYR ALA LEU CYS PHE PRO ALA VAL THR ASP LYS LEU GLY ALA LEU

LEU MET CYS PRO GLU ALA ALA CYS ILE ARG PRO PRO LEU PRO THR ASP THR LEU GLU SER ALA SER THR VAL THR ALA MET TYR VAL ILE THR VAL ILE ASN ARG LEU GLN LEU ALA LEU SER ASP ALA GLN ALA ALA ASN PHE GLN LEU PHE GLY ARG PHE VAL ARG HIS ARG GLN ALA

ARG TRP GLY ALA SER MET ASP ALA ALA ALA GLU LEU TYR VAL ALA LEU VAL ALA THR THR LEU THR ARG GLU PHE GLY CYS ARG TRP ALA GLN LEU GLU TRP GLY GLY ASP ALA ALA ALA PRO GLY PRO PRO LEU GLY PRO HIS SER SER THR ARG HIS ARG VAL SER PHE ASN GLU ASN

ASP VAL LEU VAL ALA LEU VAL ALA SER SER PRO GLU HIS ILE TYR THR PHE TRP ARG LEU ASP LEU VAL ARG GLN HIS GLU TYR MET HIS LEU THR LEU PRO ARG ALA PHE GLN ASN ALA ALA ASP SER MET LEU PHE VAL GLN ARG LEU THR PRO HIS PRO ASP ALA ARG ILE ARG VAL

LEU PRO VAL PHE SER THR GLY GLY PRO PRO THR ARG GLY LEU MET PHE GLY THR ARG LEU ALA ASP TRP ARG ARG GLY LYS LEU SER GLU THR ASP PRO LEU ALA PRO TRP ARG SER VAL PRO GLU LEU GLY THR GLU ARG GLY ALA ALA LEU GLY LYS LEU SER PRO ALA GLN ALA LEU

ALA ALA VAL SER VAL LEU GLY ARG MET CYS LEU PRO SER THR ALA LEU ALA ALA LEU TRP THR CYS MET PHE PRO ASP ASP TYR THR GLU TYR ASP SER PHE ASP ALA LEU LEU THR ALA ARG LEU GLU SER GLY GLN THR LEU SER PRO SER GLY GLY ARG GLU ALA SER PRO PRO ALA

PRO PRO ASN ALA LEU TYR ARG PRO THR GLY GLN HIS VAL ALA VAL PRO ALA ALA ALA THR HIS ARG THR PRO ALA ALA ARG VAL THR ALA MET ASP LEU VAL LEU ALA ALA VAL LEU LEU GLY ALA PRO VAL VAL ALA LEU ARG ASN THR THR ALA PHE SER ARG GLU SER GLU LEU

GLU LEU CYS LEU THR LEU PHE ASP SER ARG ALA ARG GLY PRO ASP ALA ALA LEU ARG ASP ALA VAL SER SER ASP ILE GLU THR TRP ALA VAL ARG LEU LEU HIS ALA ASP LEU ASN PRO ILE GLU ASN ALA CYS LEU ALA ALA GLN LEU PRO ARG LEU SER ALA LEU ILE ALA GLU ARG

PRO LEU ALA ARG GLY PRO PRO CYS LEU VAL LEU VAL ASP ILE SER MET THR PRO VAL ALA ALA VAL LEU TRP GLU ASN PRO ASP PRO PRO GLY PRO PRO ASP VAL ARG PHE VAL GLY SER GLU ALA THR GLU GLU LEU PRO PHE VAL ALA GLY GLY GLU ASP VAL LEU ALA ALA SER ALA THR

ASP GLU ASP PRO PHE LEU ALA ARG ALA ILE LEU GLY ARG PRO PHE ASP ALA SER LEU LEU SER GLY GLU LEU PHE PRO GLY HIS PRO VAL TYR GLN ARG ALA PRO ASP ASP GLN SER PRO SER VAL PRO ASN PRO THR PRO GLY PRO ALA ASP LEU VAL GLY THR GLU GLY SER LEU GLY

PRO GLY SER LEU ALA PRO THR LEU PHE THR ASP ALA THR PRO GLY GLU PRO VAL PRO PRO ARG MET TRP ALA TRP ILE HIS GLY LEU GLU GLU LEU ALA SER ASP ASP SER GLY GLY PRO ALA PRO LEU LEU ALA PRO ASP PRO LEU SER PRO THR ALA ASP GLN SER VAL PRO THR SER

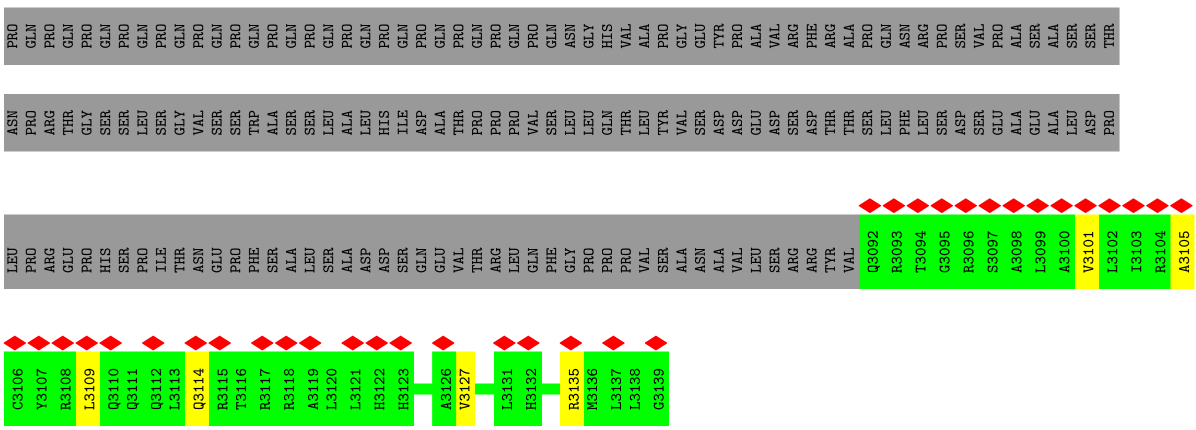
GLN CYS ALA PRO ARG PRO PRO GLY PRO ALA VAL THR ALA ARG GLU ALA ARG PRO GLY VAL PRO ALA GLU SER THR ARG PRO ALA PRO VAL GLY PRO ARG ASP ASP PHE ARG ARG LEU PRO SER PRO GLN SER SER PRO ALA PRO PRO ASP ALA THR ALA PRO ARG PRO PRO ALA SER SER

ARG ALA SER ALA ALA SER SER GLY SER ARG ALA ARG ARG HIS ARG ARG ALA ARG SER LEU ALA ARG ALA THR GLN ALA SER ALA THR THR GLN GLY TRP ARG PRO PRO ALA LEU PRO ASP THR VAL ALA PRO VAL THR ASP PHE ALA ARG PRO PRO ALA PRO PRO LYS PRO PRO GLU

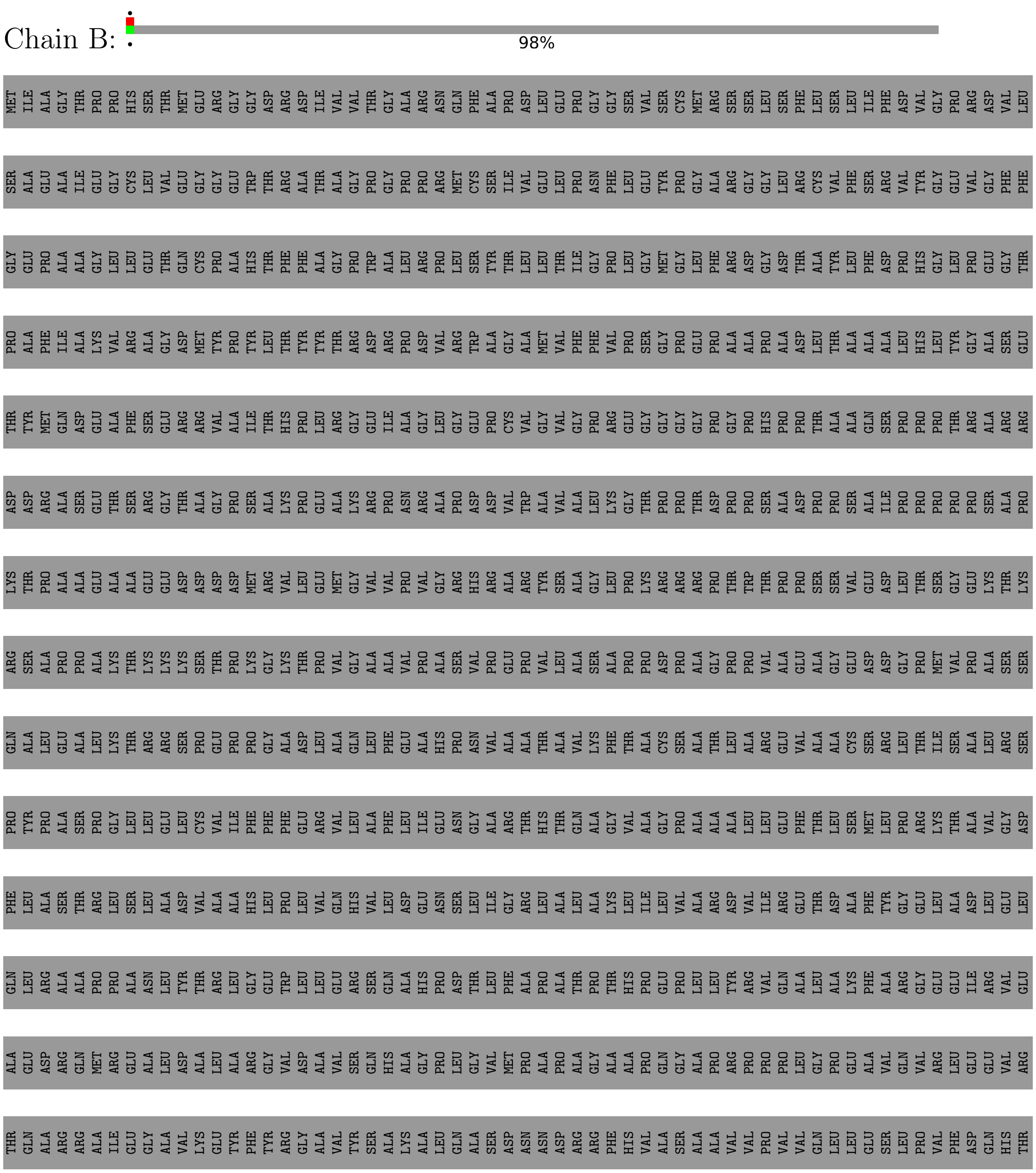
PRO ALA LEU HIS ALA LEU VAL SER GLY VAL PRO LEU PRO LEU GLY PRO GLN PHE ALA GLY GLN ALA SER PRO ALA LEU PRO ILE ASP PRO VAL PRO PRO PRO VAL ALA THR GLY THR VAL LEU PRO GLY GLY GLU ASN ARG ARG PRO PRO LEU THR SER GLY PRO ALA PRO THR PRO PRO

ARG VAL PRO VAL GLY GLY PRO GLN ARG ARG LEU THR ARG PRO ALA VAL ALA SER LEU SER GLU SER ARG GLU SER LEU PRO SER PRO TRP ASP PRO ALA ASP PRO THR ALA PRO VAL LEU GLY ARG ASN PRO ALA GLU PRO THR SER SER SER PRO ALA GLY PRO SER PRO PRO PRO PRO

ALA VAL GLN PRO VAL THR PRO PRO PRO THR SER GLY PRO PRO PRO THR TYR LEU THR LEU GLU GLY GLY VAL THR PRO GLY GLY PRO VAL SER ARG ARG PRO THR THR ARG GLN PRO VAL ALA THR PRO THR THR SER ALA ARG PRO ARG GLY HIS LEU THR VAL ASN ARG LEU SER ALA



• Molecule 7: Large tegument protein deneddylase



ARG ASP ILE ALA GLN ARG ALA ALA ILE PRO ALA PRO PRO PRO ILE ALA THR SER PRO THR ALA ILE LEU LEU ARG ASP LEU ILE GLN ARG GLY GLN THR LEU ASP ALA PRO GLU ASP LEU ALA ALA TRP LEU SER VAL LEU THR ASP ALA ALA ASN GLN GLY LEU ILE GLU ARG LYS PRO

LEU ASP GLU LEU ALA ARG SER ILE ARG ASP ILE ASN ASP GLN GLN ALA ARG ARG SER SER GLY LEU ALA GLU LEU ARG ARG PHE ASP ALA LEU ASP ALA ALA LEU GLY GLN GLN LEU ASP SER ASP ALA ALA PHE VAL PRO ALA PRO GLY ALA SER PRO TYR PRO ASP ASP GLY GLY LEU

SER PRO GLU ALA THR ARG MET ALA GLU GLU ALA LEU ARG GLN ALA ARG ALA MET ASP ALA ALA LYS LEU THR ALA GLU LEU ALA PRO ASP ALA ARG ALA ARG LEU ARG GLU ARG ALA ARG SER LEU GLU ALA MET LEU GLU GLY ALA ARG GLU ARG ALA LYS VAL ALA ARG ASP ALA ARG

GLU LYS PHE LEU HIS LYS LEU GLN GLY VAL LEU ARG PRO LEU PRO ASP PHE VAL GLY LEU LYS ALA CYS PRO ALA VAL LEU ALA THR LEU ARG ALA SER LEU PRO ALA GLY TRP SER ASP LEU PRO GLU ALA VAL ARG GLY ALA PRO PRO GLU VAL THR ALA ALA LEU ARG ALA ASP MET

TRP GLY LEU LEU GLY GLN TYR ARG ASP ALA LEU GLU HIS PRO THR PRO ASP THR ALA THR ALA LEU SER GLY LEU HIS PRO SER PHE VAL VAL VAL LEU LYS ASN LEU PHE ALA ASP ALA PRO GLU THR PRO PHE LEU LEU GLN PHE PHE ALA ASP HIS ALA PRO ILE ILE ALA HIS ALA

VAL SER ASN ALA ILE ASN ALA GLY SER ALA ALA VAL ALA THR ALA ASP PRO ALA SER THR VAL ASP ALA ALA VAL ARG ALA HIS ARG VAL LEU VAL ASP ALA VAL THR ALA LEU GLY ALA ALA ALA SER ASP PRO ALA SER PRO LEU ALA PHE LEU ALA ALA MET ALA ASP SER ALA ALA

GLY TYR VAL LYS ALA THR ARG LEU ALA LEU ASP ALA ARG GLY ALA ILE ALA GLN LEU THR THR LEU GLY SER ALA ALA ALA ASP LEU VAL VAL GLN VAL ARG ARG ALA ALA ASN GLN PRO GLU GLY GLU HIS ALA SER LEU ILE GLN ALA ALA THR ARG ALA THR THR GLY ALA ARG GLU

SER LEU ALA GLY HIS GLU GLY ARG PHE GLY GLY LEU LEU HIS ALA GLU GLY THR ALA GLY ASP HIS SER PRO SER GLY ARG ALA LEU GLN GLU LEU GLY LYS VAL ILE GLY ALA THR ARG ARG ARG ALA ASP GLU LEU GLU ALA ALA ILE ALA ASP LEU ARG GLU LYS MET ALA ALA GLN

ARG ALA ARG SER SER HIS GLU ARG TRP ALA ALA ASP VAL GLU ALA VAL LEU ASP ARG VAL GLU SER GLY ALA GLU PHE ASP VAL VAL GLU LEU ARG ARG LEU GLN ALA LEU ALA GLY THR HIS GLY TYR ASN PRO ARG ASP PHE ARG LYS ARG ALA GLU GLN ALA LEU GLY THR ASN ALA

LYS ALA VAL THR LEU ALA LEU GLU THR ALA LEU ALA PHE ASN PRO TYR THR PRO GLU ASN GLN ARG HIS PRO MET LEU PRO PRO LEU ALA ALA ILE HIS ARG ILE ASP TRP SER ALA ALA PHE GLY ALA ALA ALA ASP THR TYR ALA ASP MET PHE ARG VAL ASP THR GLU PRO LEU ALA

ARG LEU LEU ARG LEU ALA GLY GLY LEU LEU GLU ARG ALA GLN ALA ASN ASP GLY PHE ILE ASP TYR HIS GLU ALA VAL LEU HIS LEU SER GLU ASP LEU GLY GLY VAL PRO ALA LEU ARG GLN TYR VAL PRO PHE PHE GLN LYS GLY TYR ALA GLU TYR VAL ASP ILE ARG ASP ARG LEU

ASP ALA LEU ARG ARG ALA ASP ALA ARG ARG ALA ILE GLY SER VAL ALA LEU ASP LEU ALA ALA ALA ALA GLU GLU ILE SER ALA VAL ARG ASN ASP PRO ALA ALA ALA ALA GLU LEU VAL ARG ALA GLY VAL THR LEU PRO CYS PRO SER GLU ASP ALA LEU VAL ALA CYS VAL ALA ALA LEU

GLU ARG VAL ASP GLN SER PRO VAL LYS ASP THR ALA TYR ALA ASP TYR VAL ALA PHE VAL THR ARG GLN ASP LEU ALA ASP THR LYS ASP ALA VAL VAL ARG ALA LYS GLN GLN ARG ALA GLU ALA THR GLU ARG VAL THR ALA GLY LEU ARG GLU VAL LEU ALA ALA ARG GLU ARG ARG

ALA GLN LEU GLU ALA GLU GLY LEU ALA ASN LEU LYS THR LEU LEU LYS VAL VAL ALA VAL PRO ALA THR VAL ALA LYS THR LEU ASP GLN ALA ARG SER ALA GLU GLU ILE ALA ASP GLN VAL GLU ILE LEU LEU ASP GLN THR GLU LYS ALA ARG GLU LEU ASP VAL GLN ALA VAL ALA

TRP LEU GLU HIS ALA GLN ARG THR PHE GLU THR HIS PRO LEU ASN ALA ALA SER GLY ASP GLY PRO GLY LEU LEU THR ARG GLN GLY ALA ARG LEU GLN ALA LEU PHE ASP THR ARG ARG ARG VAL GLU ALA LEU ARG ARG SER LEU GLU GLU ALA GLU ALA GLU TRP ASP GLU VAL TRP

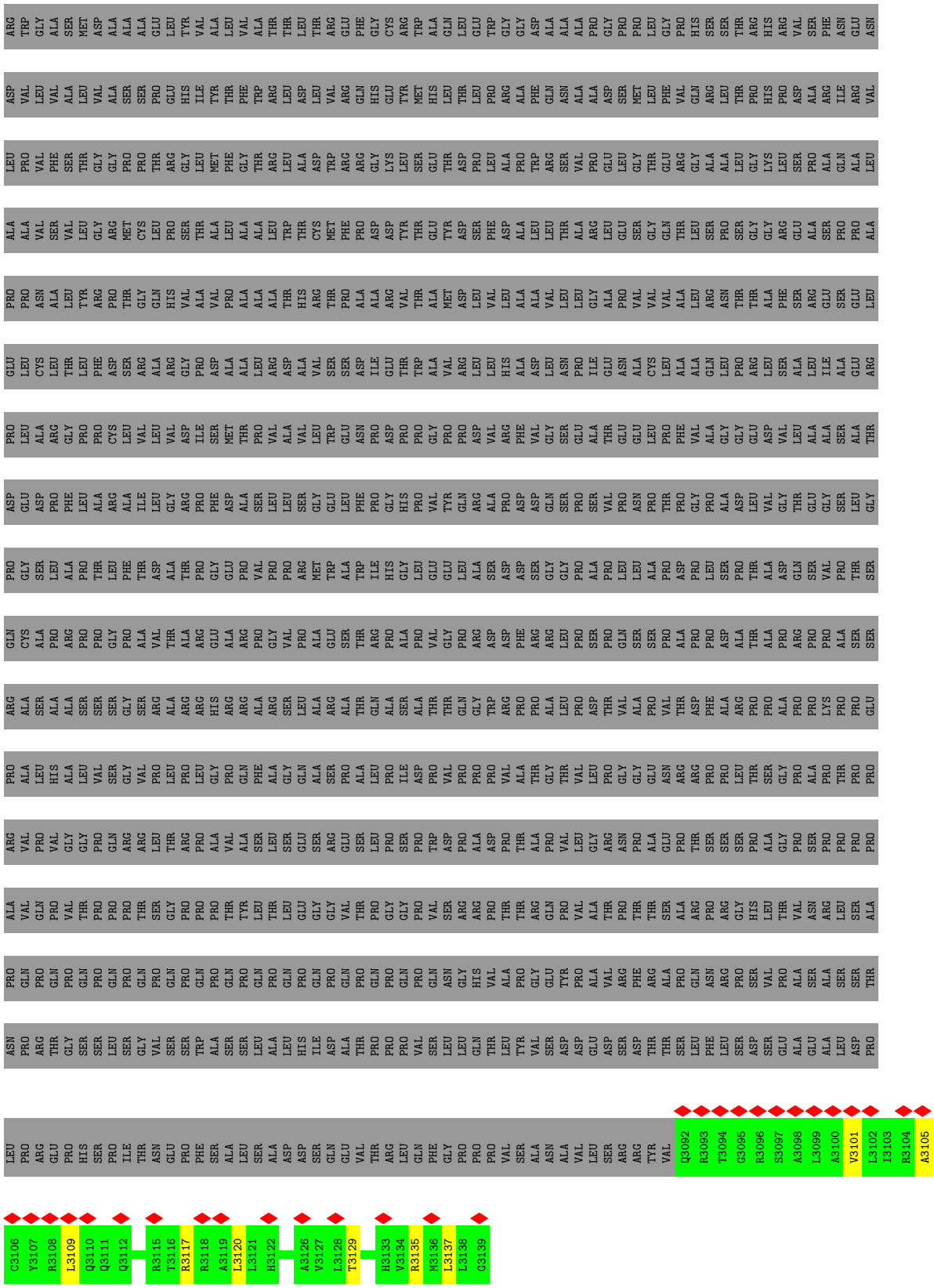
GLY ARG PHE GLY ARG VAL ARG GLY GLY ALA TRP LYS SER PRO GLU GLY PHE ARG ALA ALA CYS GLU GLN LEU ARG ALA LEU GLN ASP THR THR ASN THR VAL SER GLY LEU ARG ALA GLN ARG ASP TYR GLU ARG LEU PRO ALA LYS TYR GLN GLY VAL LEU GLY ALA LYS SER ALA GLU

ARG ALA GLY ALA VAL GLU GLU LEU GLY GLY ARG VAL ALA GLN HIS ALA ASP LEU SER ALA ARG LEU ARG ASP GLU VAL VAL PRO ARG VAL ALA TRP GLU MET ASN PHE ASP THR LEU GLY GLY LEU LEU ALA GLU PHE ASP ALA VAL ALA GLY ASP LEU ALA PRO TRP ALA VAL GLU GLU

PHE ARG GLY ALA ARG GLU LEU ILE GLN ARG ARG MET GLY LEU TYR SER ALA TYR ALA LYS ALA THR GLY GLN THR GLY ALA GLY ALA ALA ALA ALA PRO ALA PRO LEU LEU VAL ASP LEU ARG ALA LEU ASP ALA ARG ALA ARG ALA SER ALA PRO PRO GLY GLN GLU ALA ASP PRO GLN

MET LEU ARG ARG ARG GLY GLU ALA TYR LEU ARG VAL SER GLY GLY PRO GLY PRO LEU VAL LEU ARG GLU ALA THR SER THR LEU ASP ARG PRO PHE ALA PRO SER PHE LEU VAL PRO ASP GLY THR PRO LEU GLN TYR ALA LEU CYS PHE PRO ALA VAL THR ASP LYS LEU GLY ALA LEU

LEU MET CYS PRO GLU ALA ALA CYS ILE ARG PRO PRO LEU PRO THR ASP THR LEU GLU SER ALA SER THR VAL THR ALA MET TYR VAL ILE THR VAL ILE ASN ARG LEU GLN LEU ALA LEU SER ASP ALA GLN ALA ALA ASN PHE GLN LEU PHE GLY ARG PHE VAL ARG HIS ARG GLN ALA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H3122
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V3127
L3128
T3129
H3133
V3134
R3135
M3136
L3137
L3138
G3139
Q3092
R3093
T3094
G3095
R3096
S3097
A3098
L3099
A3100
V3101
L3102
I3103
R3104
A3105

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C5	Depositor
Number of particles used	42857	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 ($e^-/Å^2$)	25	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	24271	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.034	Depositor
Minimum map value	-0.018	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	395.52, 395.52, 395.52	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.03, 1.03, 1.03	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	S	0.31	0/10405	0.57	5/14207 (0.0%)
1	T	0.31	0/10728	0.56	1/14645 (0.0%)
1	W	0.30	0/10709	0.56	3/14619 (0.0%)
1	X	0.32	0/10274	0.57	2/14027 (0.0%)
2	E	0.28	0/796	0.45	0/1087
2	F	0.28	0/796	0.45	0/1087
2	L	0.28	0/796	0.45	0/1087
2	P	0.28	0/796	0.45	0/1087
3	5	0.30	0/3036	0.54	0/4134
3	D	0.30	0/2858	0.57	1/3895 (0.0%)
4	6	0.29	0/2255	0.57	1/3080 (0.0%)
4	7	0.29	0/2399	0.57	0/3282
4	A	0.28	0/2399	0.56	0/3282
4	H	0.28	0/2255	0.57	0/3080
5	C	0.30	0/4411	0.54	0/6015
6	G	0.28	0/769	0.53	0/1049
6	K	0.29	0/659	0.50	0/897
7	B	0.24	0/392	0.45	0/526
7	O	0.24	0/392	0.45	0/526
All	All	0.30	0/67125	0.56	13/91612 (0.0%)

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	S	0	5
1	T	0	8
1	W	0	8
1	X	0	5
3	D	0	3
4	7	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
4	A	0	1
4	H	0	1
5	C	0	1
All	All	0	33

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	X	745	ARG	NE-CZ-NH2	-7.72	116.44	120.30
1	X	847	ILE	C-N-CA	6.78	138.65	121.70
1	S	466	LEU	CA-CB-CG	6.33	129.85	115.30
1	S	210	LEU	CA-CB-CG	6.09	129.31	115.30
1	T	466	LEU	CA-CB-CG	6.02	129.14	115.30

There are no chirality outliers.

5 of 33 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	T	110	HIS	Peptide
1	T	133	PHE	Peptide
1	T	419	HIS	Peptide
1	T	800	HIS	Peptide
1	T	913	ALA	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	S	10151	0	9955	137	0
1	T	10470	0	10279	131	0
1	W	10451	0	10263	109	0
1	X	10027	0	9841	121	0
2	E	774	0	754	11	0
2	F	774	0	754	7	0
2	L	774	0	754	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	P	774	0	754	9	0
3	5	2963	0	2918	33	0
3	D	2786	0	2737	36	0
4	6	2216	0	2291	31	0
4	7	2355	0	2431	33	0
4	A	2355	0	2431	33	0
4	H	2216	0	2291	37	0
5	C	4305	0	4293	58	0
6	G	749	0	728	9	0
6	K	644	0	635	13	0
7	B	388	0	413	7	0
7	O	388	0	413	5	0
All	All	65560	0	64935	716	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 716 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:X:826:CYS:HG	1:X:969:HIS:HE2	1.31	0.78
1:T:708:THR:HG22	1:T:723:ASN:HD22	1.49	0.76
5:C:603:ASN:HD22	5:C:635:ARG:HH22	1.32	0.75
1:W:1206:ARG:NH1	1:W:1226:MET:SD	2.64	0.70
6:G:72:GLN:HG3	7:O:3127:VAL:HG22	1.73	0.69

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	S	1324/1374 (96%)	1237 (93%)	80 (6%)	7 (0%)	29	68
1	T	1367/1374 (100%)	1292 (94%)	74 (5%)	1 (0%)	51	85
1	W	1365/1374 (99%)	1281 (94%)	80 (6%)	4 (0%)	41	76
1	X	1304/1374 (95%)	1237 (95%)	62 (5%)	5 (0%)	34	72
2	E	99/112 (88%)	96 (97%)	3 (3%)	0	100	100
2	F	99/112 (88%)	96 (97%)	3 (3%)	0	100	100
2	L	99/112 (88%)	96 (97%)	3 (3%)	0	100	100
2	P	99/112 (88%)	96 (97%)	3 (3%)	0	100	100
3	5	385/465 (83%)	365 (95%)	20 (5%)	0	100	100
3	D	361/465 (78%)	341 (94%)	17 (5%)	3 (1%)	19	60
4	6	281/318 (88%)	261 (93%)	20 (7%)	0	100	100
4	7	306/318 (96%)	290 (95%)	16 (5%)	0	100	100
4	A	306/318 (96%)	295 (96%)	11 (4%)	0	100	100
4	H	281/318 (88%)	264 (94%)	16 (6%)	1 (0%)	34	72
5	C	555/703 (79%)	526 (95%)	28 (5%)	1 (0%)	47	81
6	G	90/580 (16%)	82 (91%)	8 (9%)	0	100	100
6	K	77/580 (13%)	74 (96%)	3 (4%)	0	100	100
7	B	46/3094 (2%)	45 (98%)	1 (2%)	0	100	100
7	O	46/3094 (2%)	45 (98%)	1 (2%)	0	100	100
All	All	8490/16197 (52%)	8019 (94%)	449 (5%)	22 (0%)	44	76

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	W	420	ALA
1	W	635	HIS
1	S	420	ALA
1	X	420	ALA
1	X	1358	PHE

5.3.2 Protein sidechains (i)

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	S	1049/1087 (96%)	1048 (100%)	1 (0%)	93	97
1	T	1084/1087 (100%)	1084 (100%)	0	100	100
1	W	1082/1087 (100%)	1081 (100%)	1 (0%)	93	97
1	X	1039/1087 (96%)	1038 (100%)	1 (0%)	93	97
2	E	80/89 (90%)	80 (100%)	0	100	100
2	F	80/89 (90%)	80 (100%)	0	100	100
2	L	80/89 (90%)	80 (100%)	0	100	100
2	P	80/89 (90%)	80 (100%)	0	100	100
3	5	303/365 (83%)	301 (99%)	2 (1%)	84	90
3	D	285/365 (78%)	285 (100%)	0	100	100
4	6	243/264 (92%)	243 (100%)	0	100	100
4	7	258/264 (98%)	257 (100%)	1 (0%)	91	94
4	A	258/264 (98%)	257 (100%)	1 (0%)	91	94
4	H	243/264 (92%)	243 (100%)	0	100	100
5	C	440/531 (83%)	440 (100%)	0	100	100
6	G	78/449 (17%)	78 (100%)	0	100	100
6	K	66/449 (15%)	66 (100%)	0	100	100
7	B	41/2391 (2%)	41 (100%)	0	100	100
7	O	41/2391 (2%)	41 (100%)	0	100	100
All	All	6830/12701 (54%)	6823 (100%)	7 (0%)	93	97

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	5	367	ASN
3	5	407	LEU
4	A	92	LEU
4	7	214	THR
1	X	1054	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 97 such sidechains are listed below:

Mol	Chain	Res	Type
1	X	876	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	E	68	HIS
1	X	972	ASN
2	L	7	HIS
3	5	120	GLN

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)

There are no chain breaks in this entry.

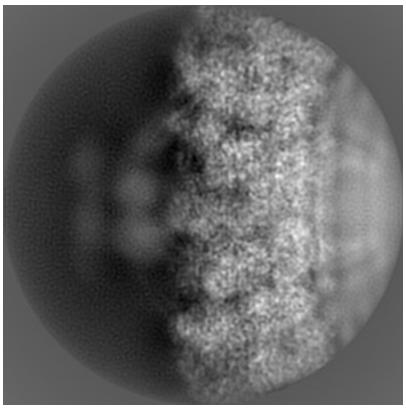
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-9860. These allow visual inspection of the internal detail of the map and identification of artifacts.

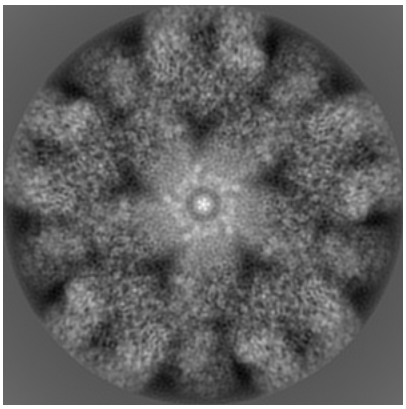
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

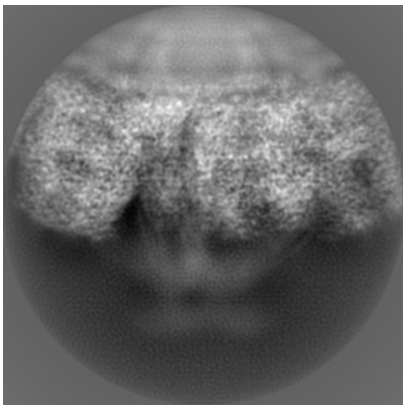
6.1.1 Primary map



X

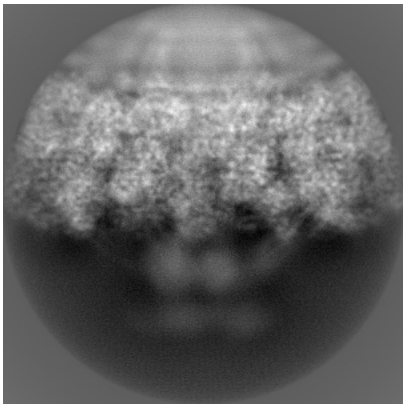


Y

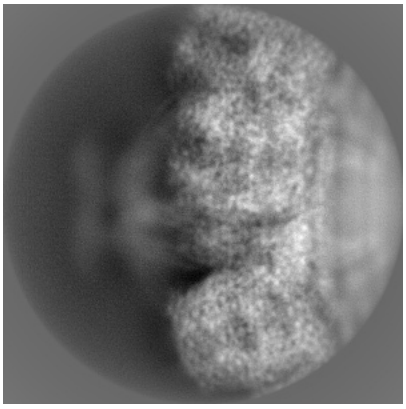


Z

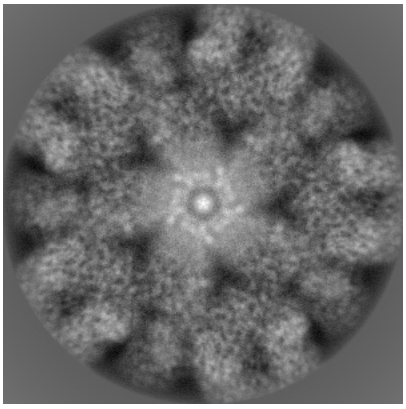
6.1.2 Raw map



X



Y

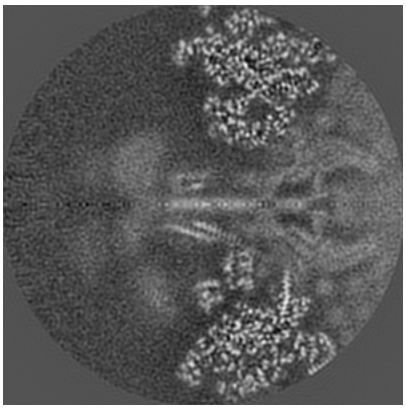


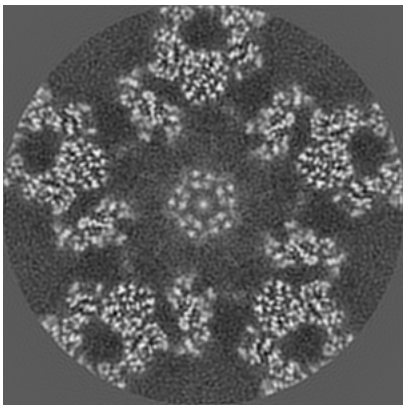
Z

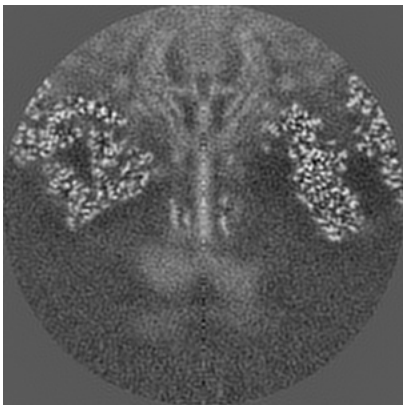
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

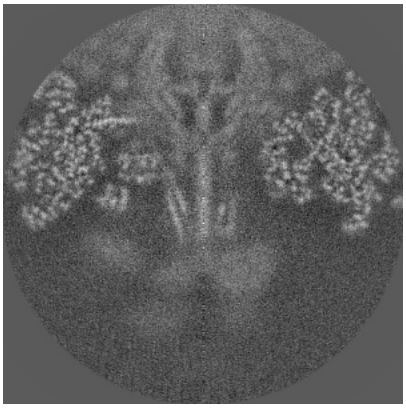
6.2.1 Primary map

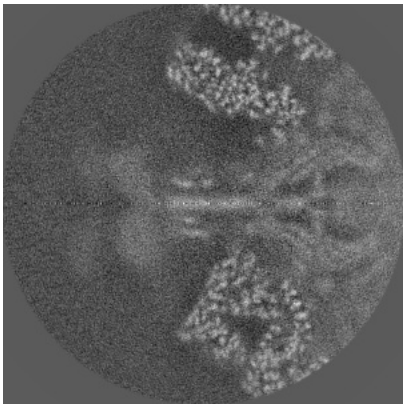

X Index: 192

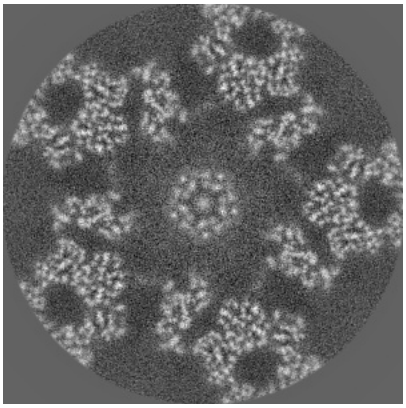

Y Index: 192


Z Index: 192

6.2.2 Raw map


X Index: 192

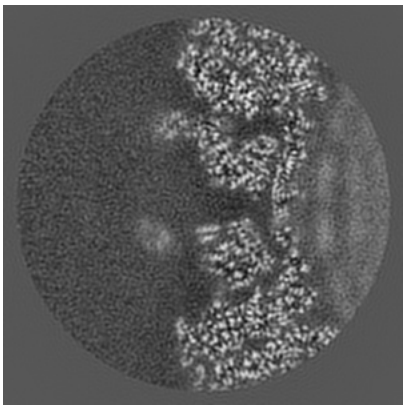

Y Index: 192

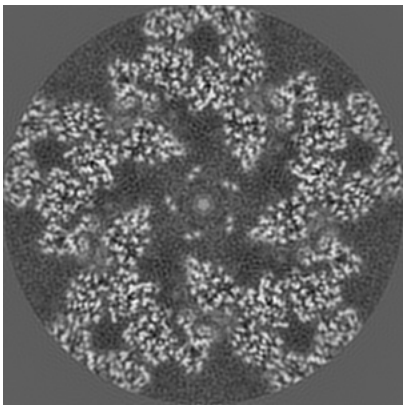

Z Index: 192

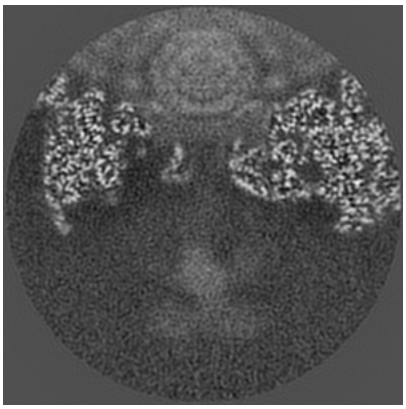
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

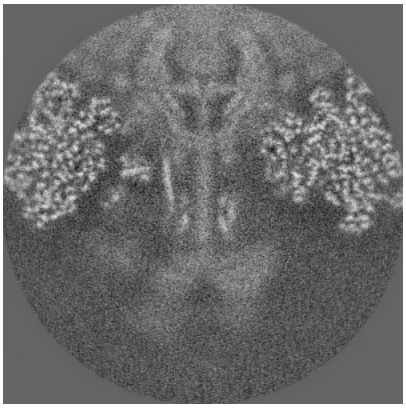
6.3.1 Primary map

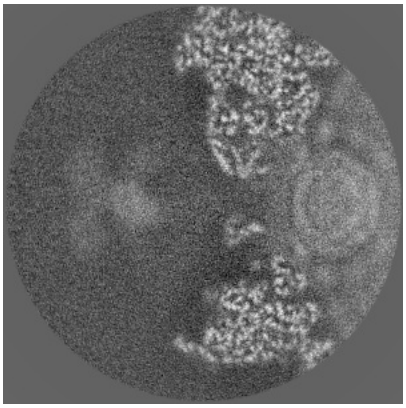

X Index: 265

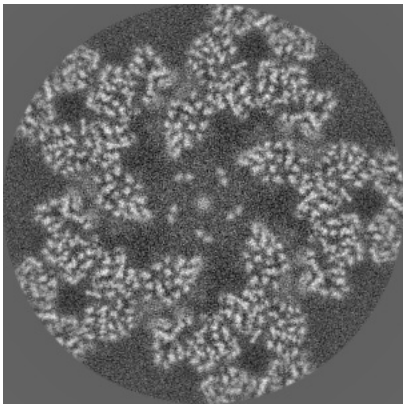

Y Index: 211


Z Index: 231

6.3.2 Raw map


X Index: 197

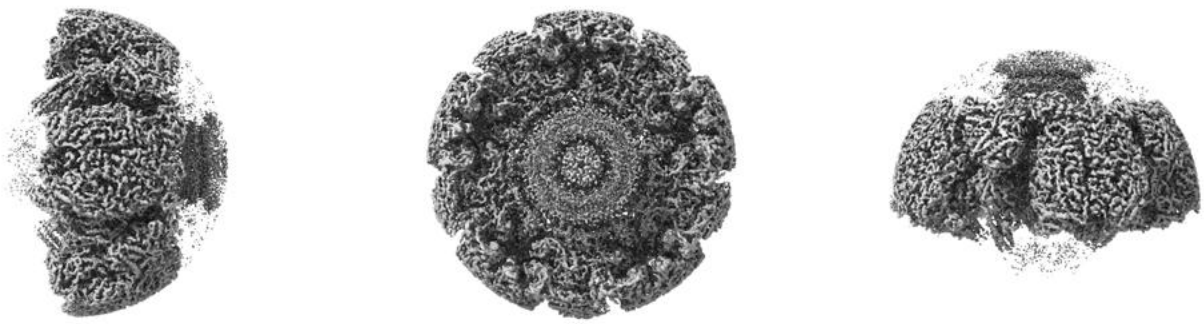

Y Index: 231


Z Index: 211

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

6.4 Orthogonal surface views (i)

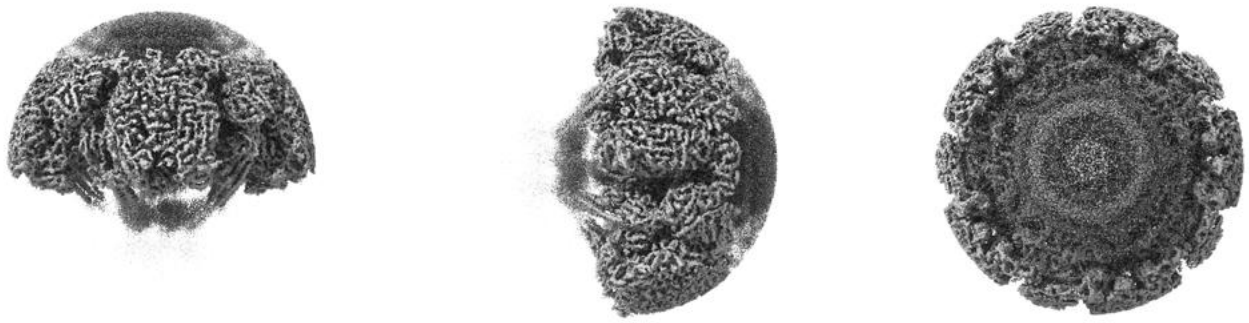
6.4.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



X Y Z

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.

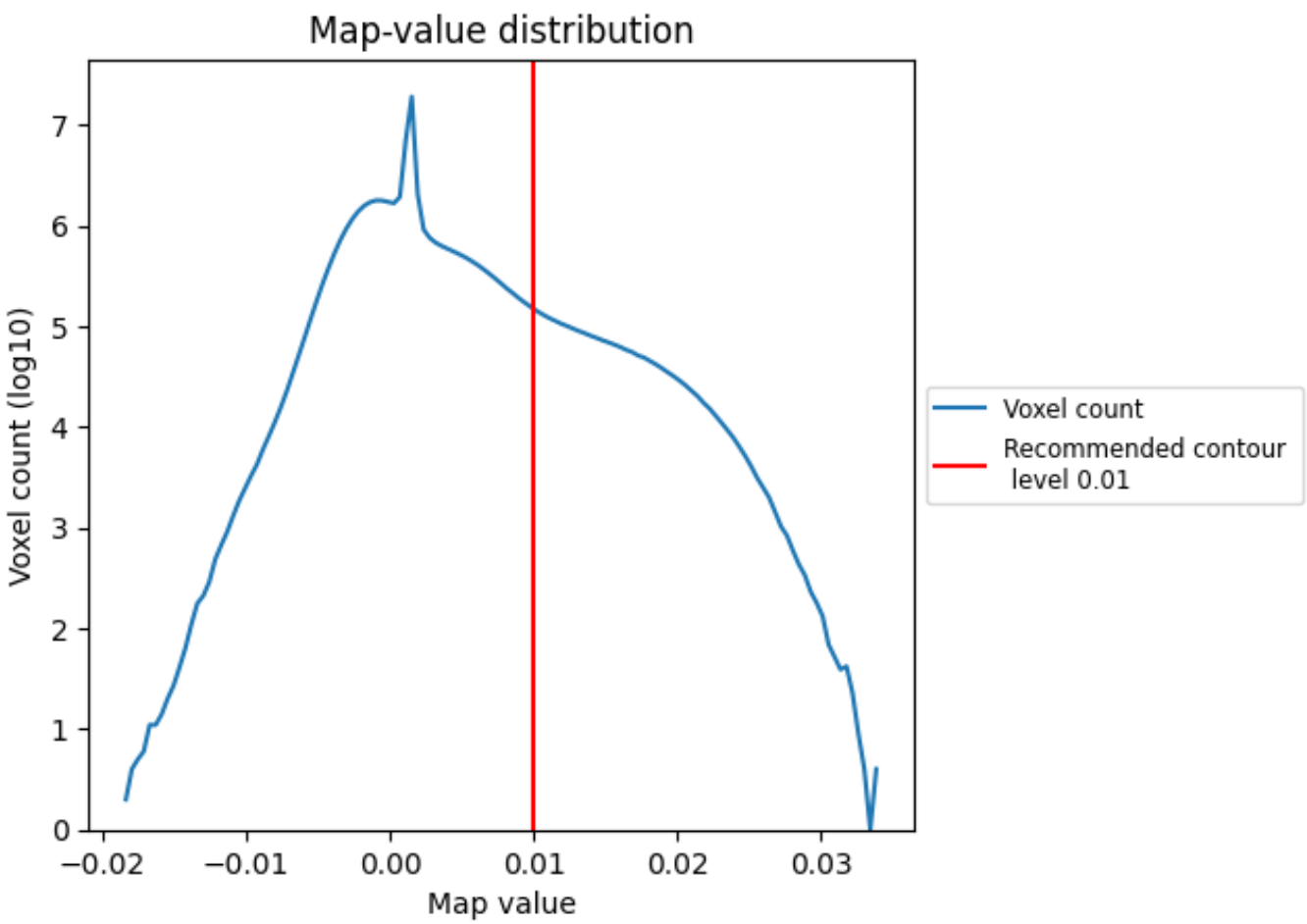
6.5 Mask visualisation (i)

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

7 Map analysis (i)

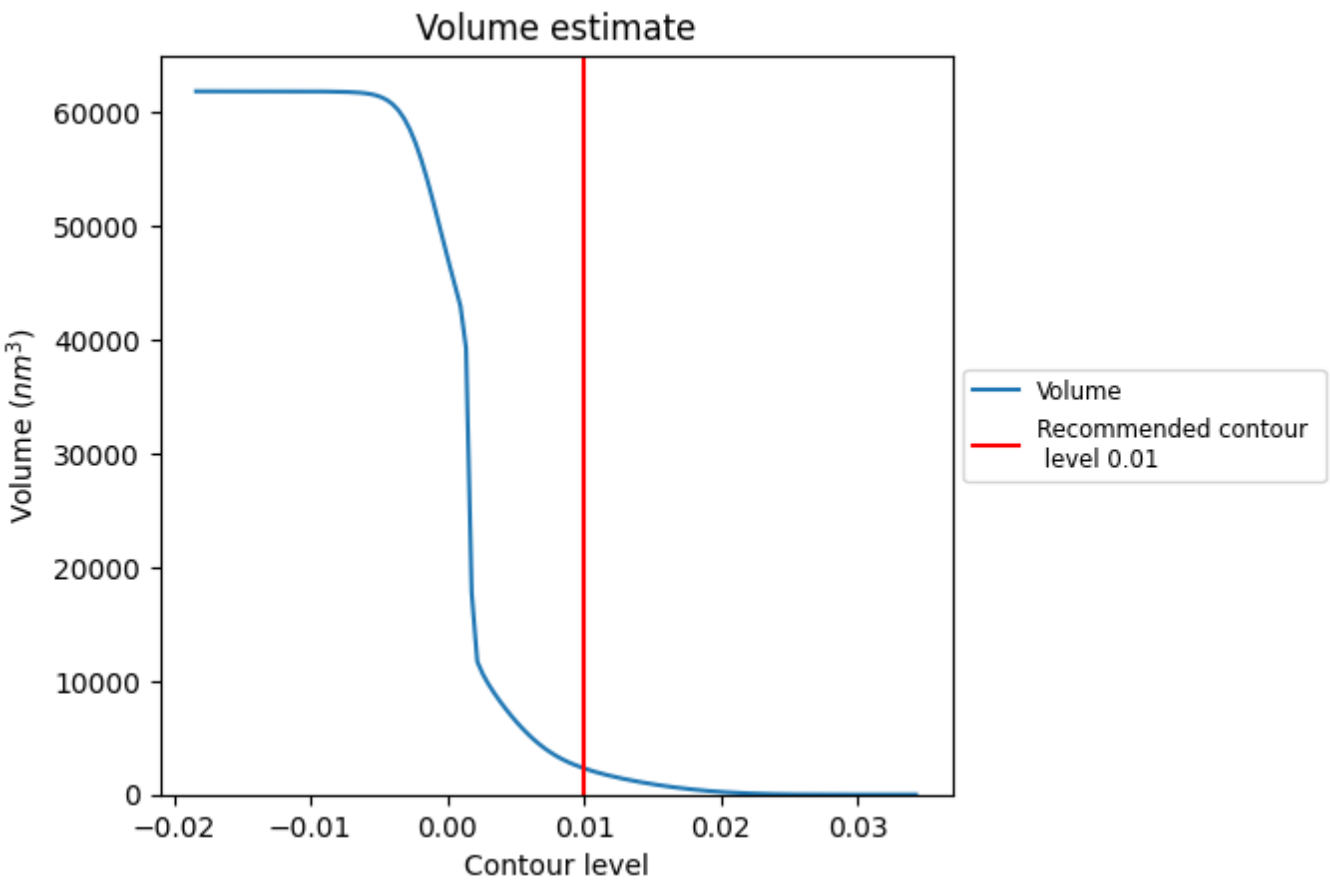
This section contains the results of statistical analysis of the map.

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.

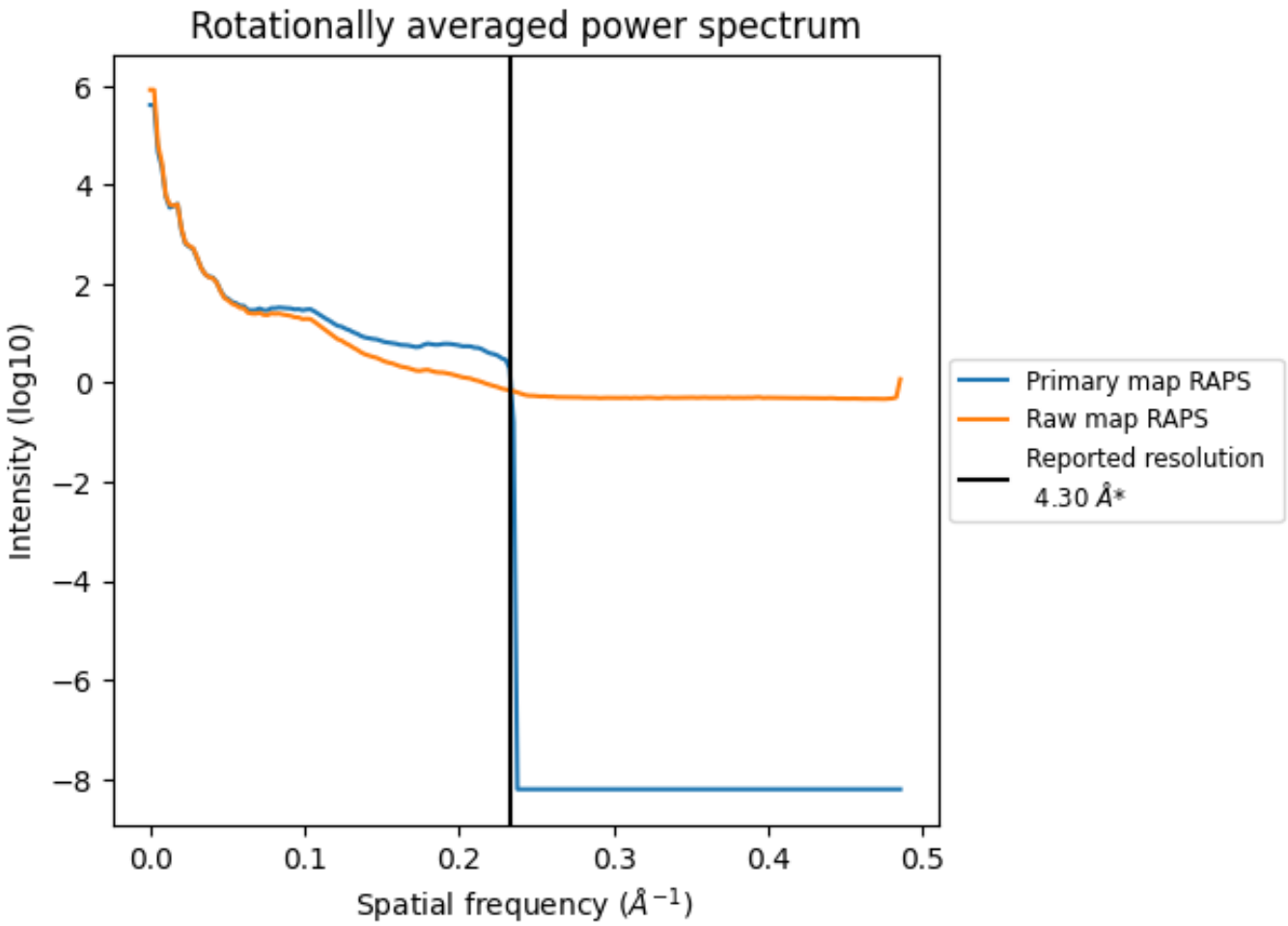
7.2 Volume estimate (i)



The volume at the recommended contour level is 2305 nm^3; this corresponds to an approximate mass of 2082 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)

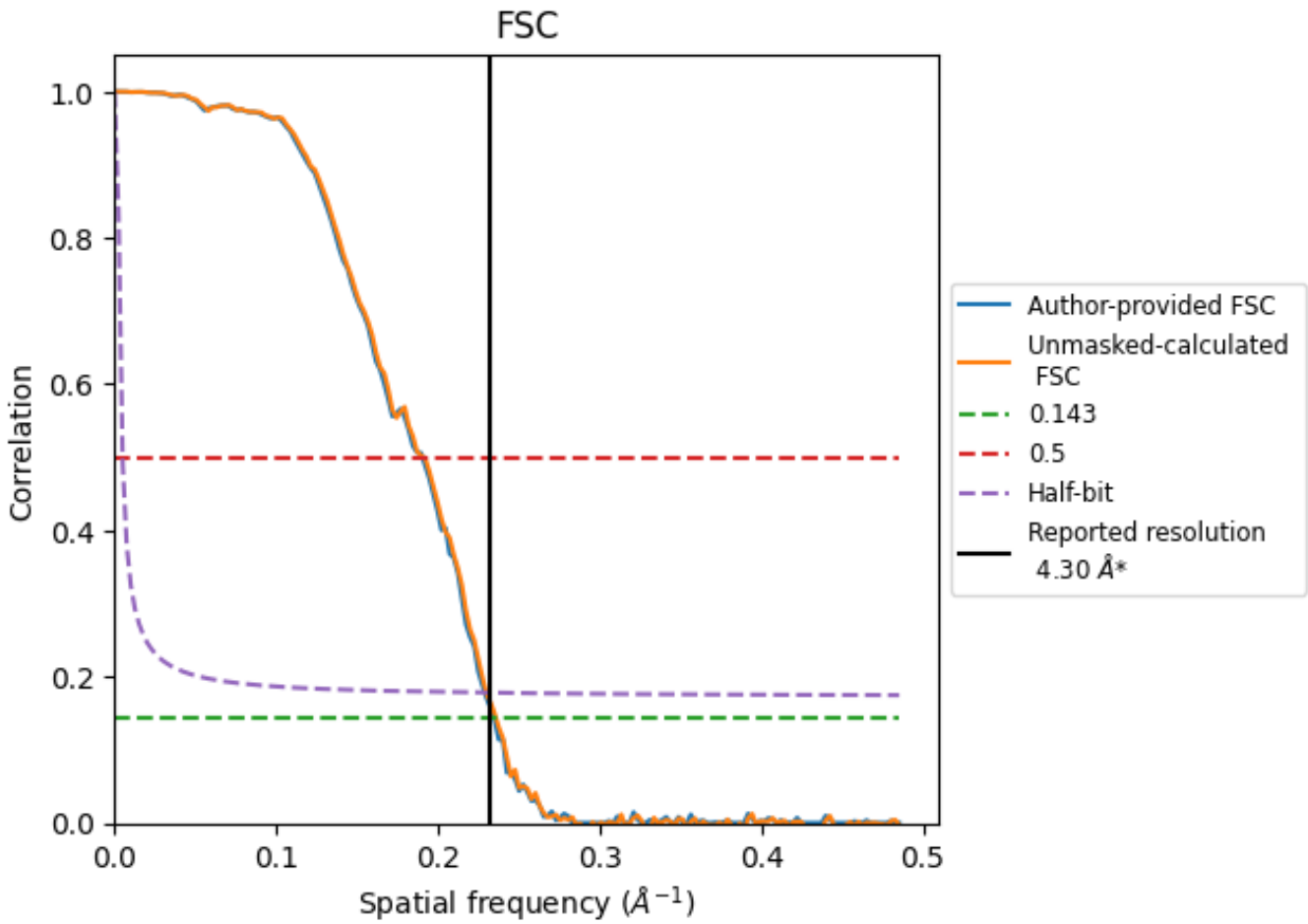


*Reported resolution corresponds to spatial frequency of 0.233 Å^{-1}

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 0.233 Å^{-1}

8.2 Resolution estimates (i)

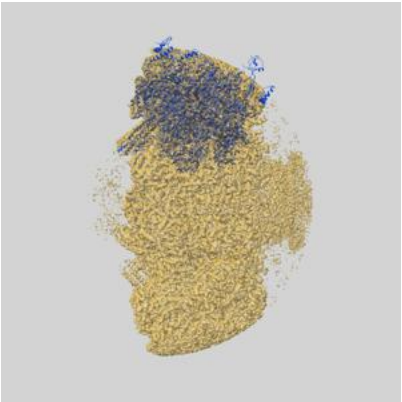
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	4.26	5.25	4.37
Unmasked-calculated*	4.24	5.23	4.35

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

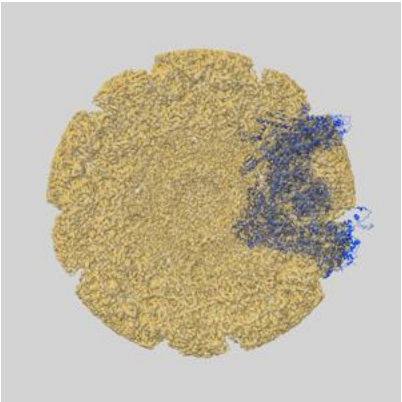
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-9860 and PDB model 6ODM. Per-residue inclusion information can be found in section 3 on page 6.

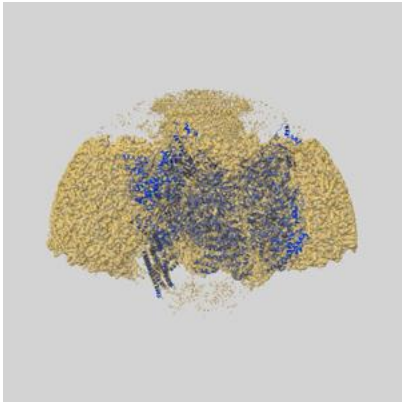
9.1 Map-model overlay (i)



X



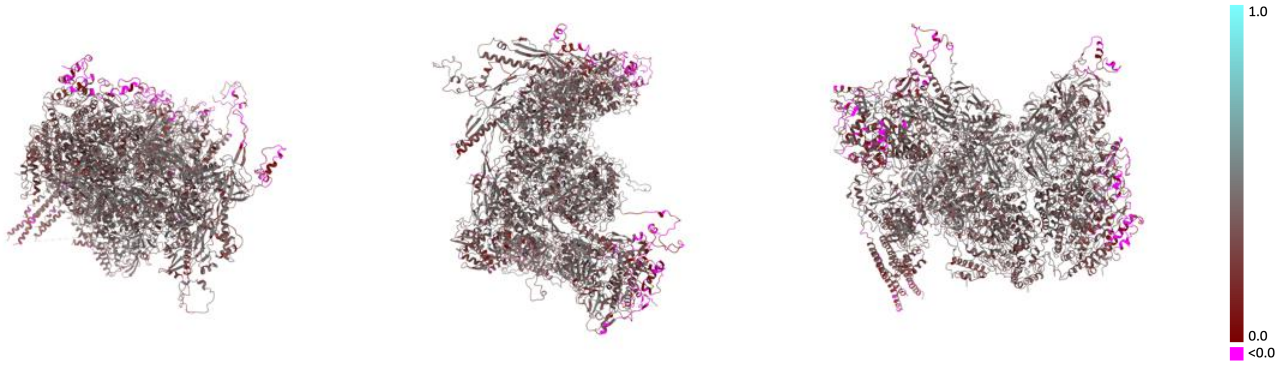
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.01 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.

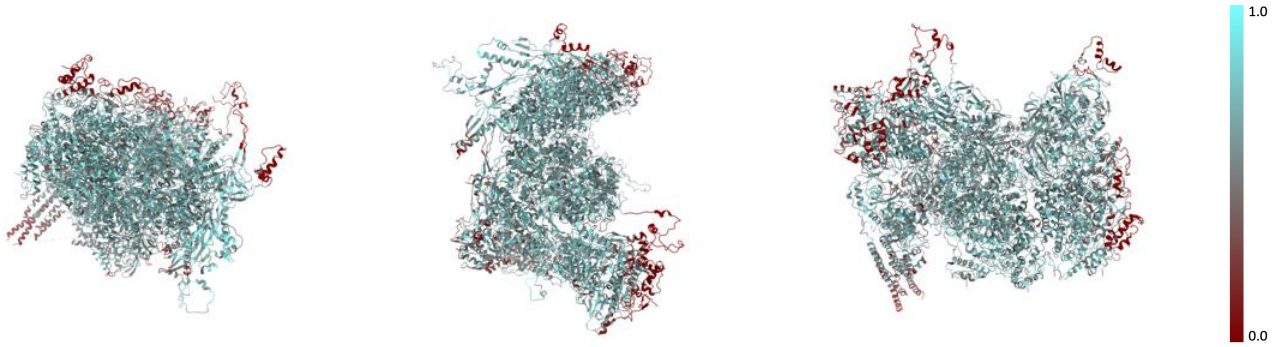
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

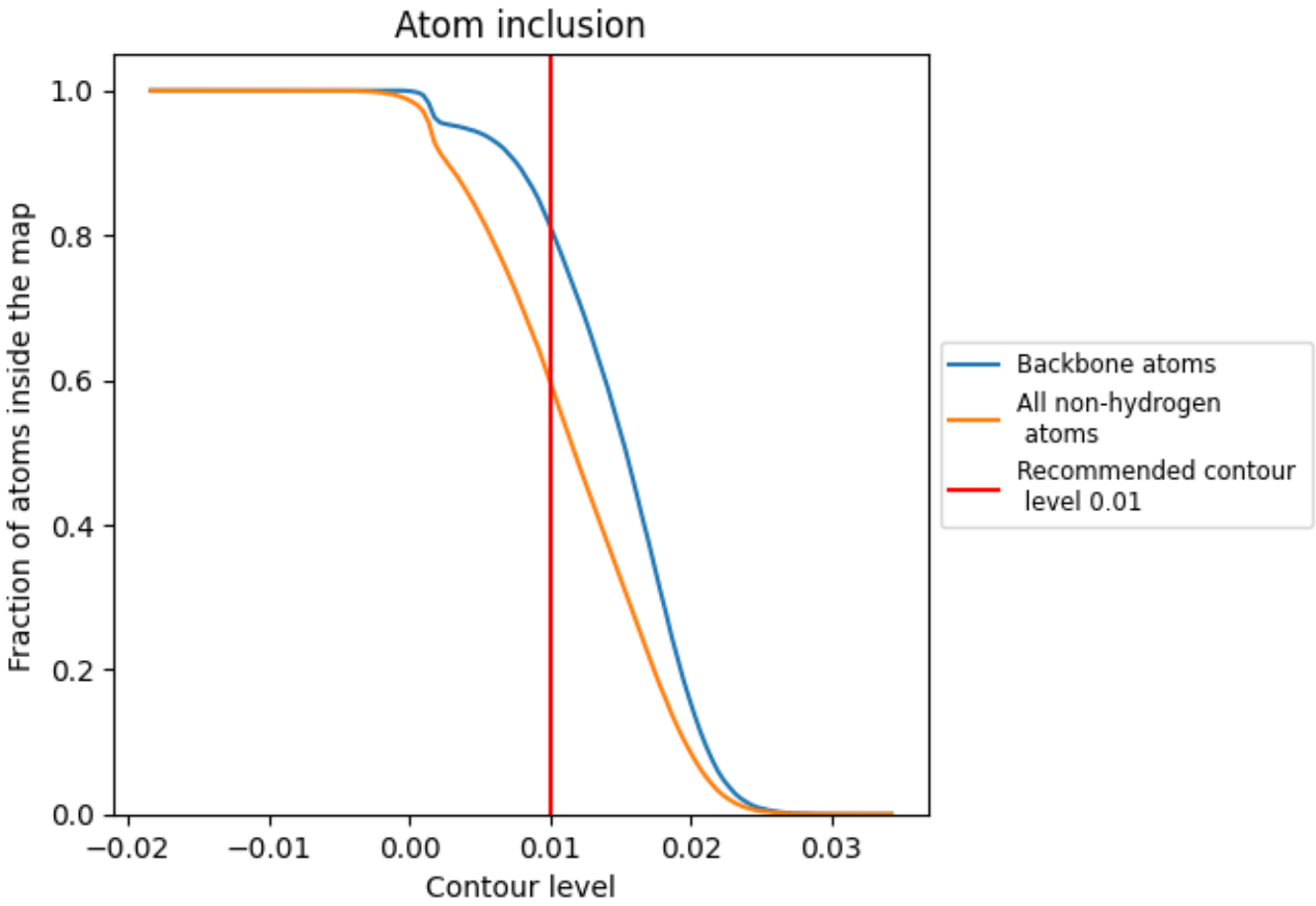
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.01).

9.4 Atom inclusion (i)



At the recommended contour level, 81% of all backbone atoms, 60% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5970	0.3510
5	0.5604	0.3520
6	0.5904	0.3650
7	0.5956	0.3770
A	0.4497	0.2730
B	0.3639	0.2060
C	0.5896	0.3430
D	0.6049	0.3550
E	0.6495	0.3560
F	0.6243	0.3550
G	0.4904	0.2630
H	0.4773	0.2990
K	0.5482	0.2930
L	0.3003	0.1480
O	0.2965	0.1260
P	0.6389	0.3590
S	0.6482	0.3840
T	0.6282	0.3670
W	0.5769	0.3320
X	0.6524	0.3810