



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 02:57 AM UTC

PDB ID : 9ZDW / pdb_00009zdw
EMDB ID : EMD-74075
Title : Pseudomonas phage DEV delta-gp53 mutant neck and tail (portal, head-to-tail and tail tube proteins)
Authors : Bellis, N.F.; Cingolani, G.
Deposited on : 2025-11-26
Resolution : 3.60 Å(reported)

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

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

A user guide is available at
<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

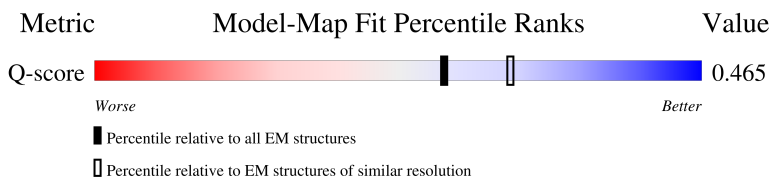
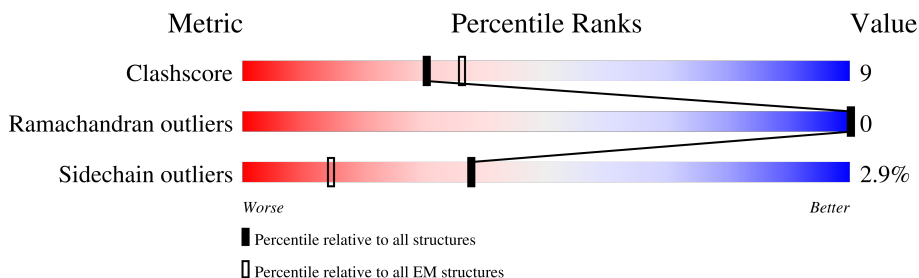
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 Å.

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



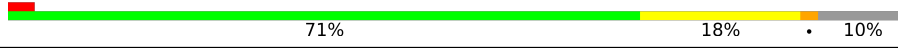
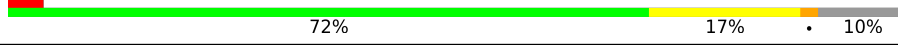
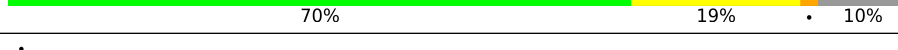
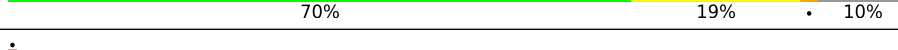
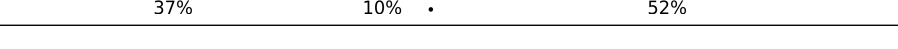
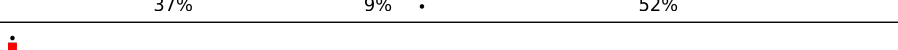
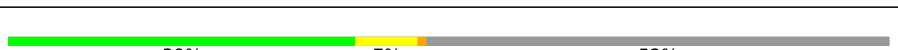
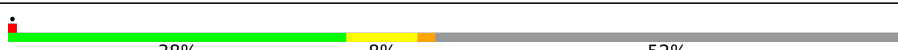
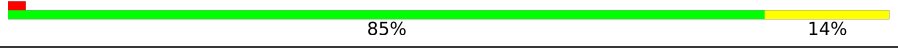
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	12797 (3.10 - 4.10)

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	PA	726	 71% 18% • 10%
1	PB	726	 70% 19% • 10%
1	PC	726	 70% 19% • 10%
1	PD	726	 74% 15% • 10%

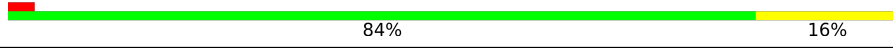
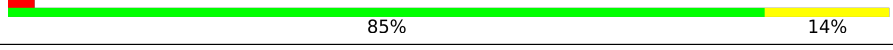
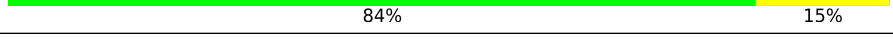
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Mol	Chain	Length	Quality of chain
1	PE	726	
1	PF	726	
1	PG	726	
1	PH	726	
1	PI	726	
1	PJ	726	
1	PK	726	
1	PL	726	
2	TA	321	
2	TB	321	
2	TC	321	
2	TD	321	
2	TE	321	
2	TF	321	
2	TG	321	
2	TH	321	
2	TI	321	
2	TJ	321	
2	TK	321	
2	TL	321	
3	AA	244	
3	AB	244	
3	AC	244	
3	AD	244	
3	AE	244	

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Mol	Chain	Length	Quality of chain
3	AF	244	 87%12%
3	AG	244	 83%17%
3	AH	244	 84%16%
3	AI	244	 85%14%
3	AJ	244	 82%17%
3	AK	244	 88%11%
3	AL	244	 84%15%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 98304 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 gp80 portal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	PA	657	Total	C	N	O	S	0	0
			5187	3235	911	1016	25		
1	PB	657	Total	C	N	O	S	0	0
			5187	3235	911	1016	25		
1	PC	657	Total	C	N	O	S	0	0
			5187	3235	911	1016	25		
1	PD	657	Total	C	N	O	S	0	0
			5187	3235	911	1016	25		
1	PE	657	Total	C	N	O	S	0	0
			5187	3235	911	1016	25		
1	PF	657	Total	C	N	O	S	0	0
			5187	3235	911	1016	25		
1	PG	657	Total	C	N	O	S	0	0
			5187	3235	911	1016	25		
1	PH	657	Total	C	N	O	S	0	0
			5187	3235	911	1016	25		
1	PI	657	Total	C	N	O	S	0	0
			5187	3235	911	1016	25		
1	PJ	657	Total	C	N	O	S	0	0
			5187	3235	911	1016	25		
1	PK	657	Total	C	N	O	S	0	0
			5187	3235	911	1016	25		
1	PL	657	Total	C	N	O	S	0	0
			5187	3235	911	1016	25		

- Molecule 2 is a protein called gp75 tail tube.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	TA	153	Total	C	N	O	S	0	0
			1054	661	186	206	1		
2	TB	153	Total	C	N	O	S	0	0
			1054	661	186	206	1		
2	TC	153	Total	C	N	O	S	0	0
			1054	661	186	206	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	TD	153	Total	C	N	O	S	0	0
			1054	661	186	206	1		
2	TE	153	Total	C	N	O	S	0	0
			1054	661	186	206	1		
2	TF	153	Total	C	N	O	S	0	0
			1054	661	186	206	1		
2	TG	153	Total	C	N	O	S	0	0
			1054	661	186	206	1		
2	TH	153	Total	C	N	O	S	0	0
			1054	661	186	206	1		
2	TI	153	Total	C	N	O	S	0	0
			1054	661	186	206	1		
2	TJ	153	Total	C	N	O	S	0	0
			1054	661	186	206	1		
2	TK	153	Total	C	N	O	S	0	0
			1054	661	186	206	1		
2	TL	153	Total	C	N	O	S	0	0
			1054	661	186	206	1		

- Molecule 3 is a protein called gp83 head-to-tail.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AA	243	Total	C	N	O	S	0	0
			1951	1245	334	364	8		
3	AB	243	Total	C	N	O	S	0	0
			1951	1245	334	364	8		
3	AC	243	Total	C	N	O	S	0	0
			1951	1245	334	364	8		
3	AD	243	Total	C	N	O	S	0	0
			1951	1245	334	364	8		
3	AE	243	Total	C	N	O	S	0	0
			1951	1245	334	364	8		
3	AF	243	Total	C	N	O	S	0	0
			1951	1245	334	364	8		
3	AG	243	Total	C	N	O	S	0	0
			1951	1245	334	364	8		
3	AH	243	Total	C	N	O	S	0	0
			1951	1245	334	364	8		
3	AI	243	Total	C	N	O	S	0	0
			1951	1245	334	364	8		
3	AJ	243	Total	C	N	O	S	0	0
			1951	1245	334	364	8		

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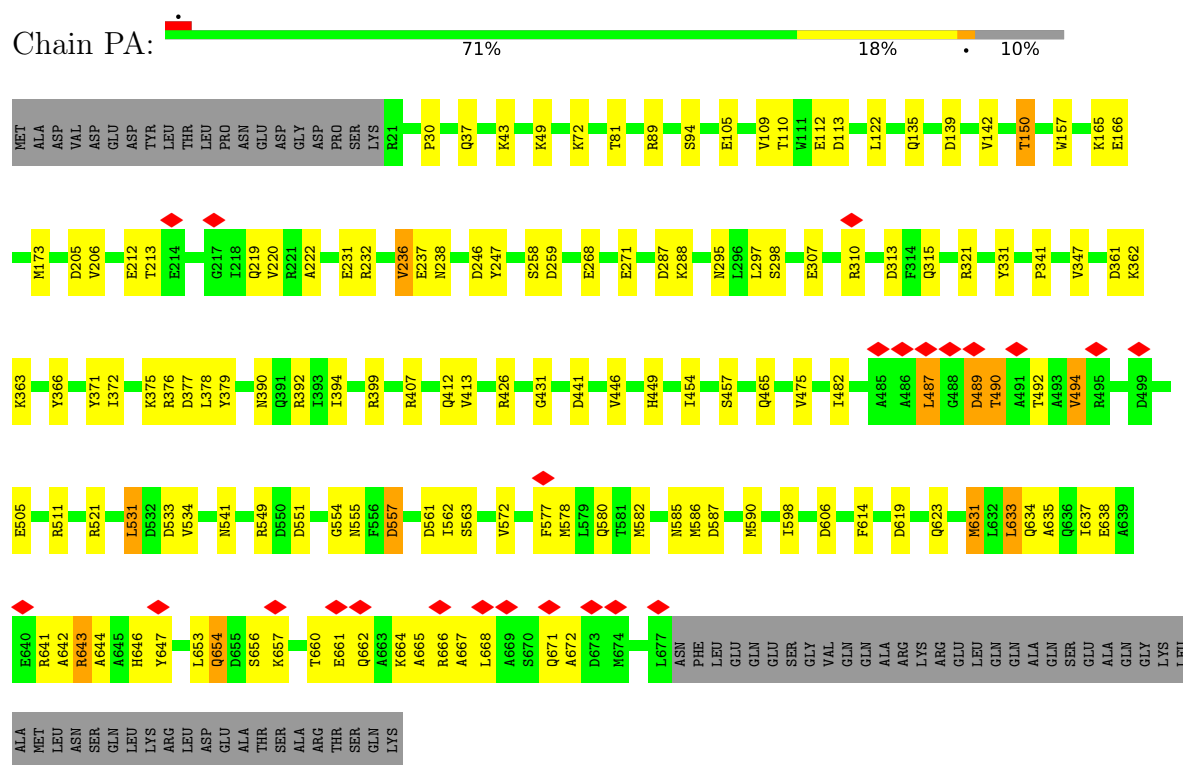
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Mol	Chain	Residues	Atoms					AltConf	Trace
3	AK	243	Total	C	N	O	S	0	0
			1951	1245	334	364	8		
3	AL	243	Total	C	N	O	S	0	0
			1951	1245	334	364	8		

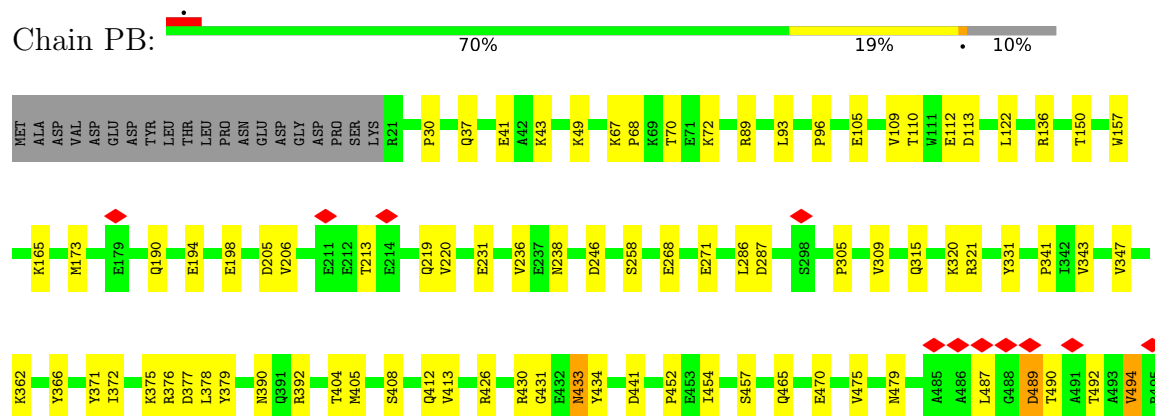
3 Residue-property plots

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

- Molecule 1: gp80 portal protein



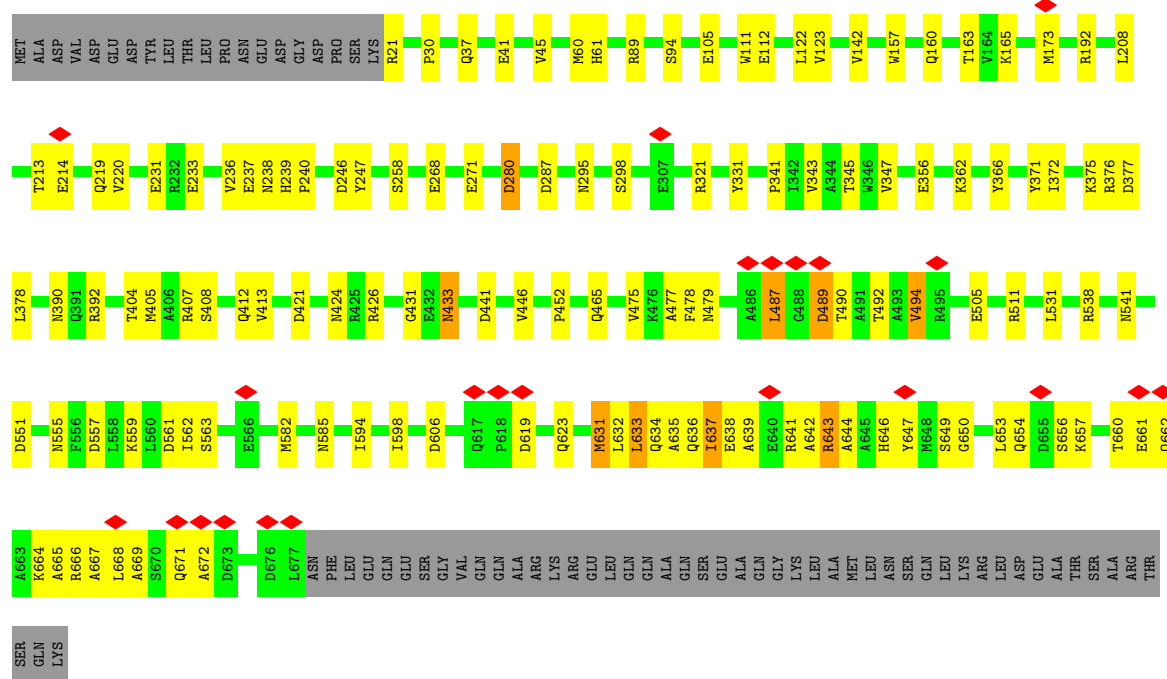
- Molecule 1: gp80 portal protein



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

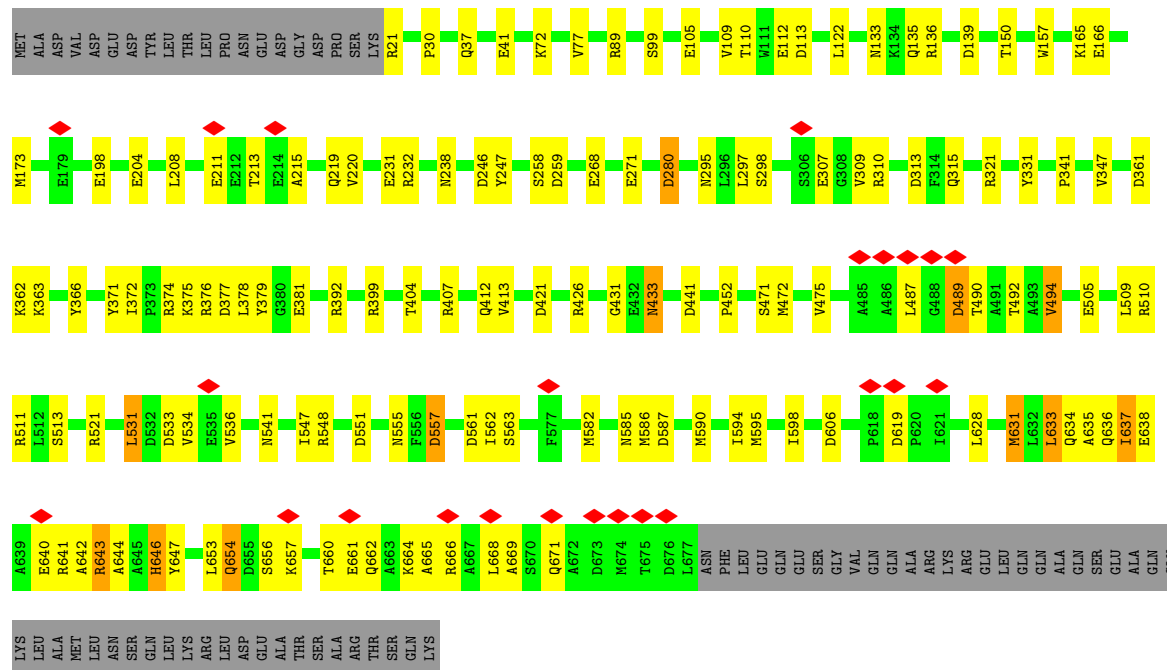
• Molecule 1: gp80 portal protein

Chain PE:



• Molecule 1: gp80 portal protein

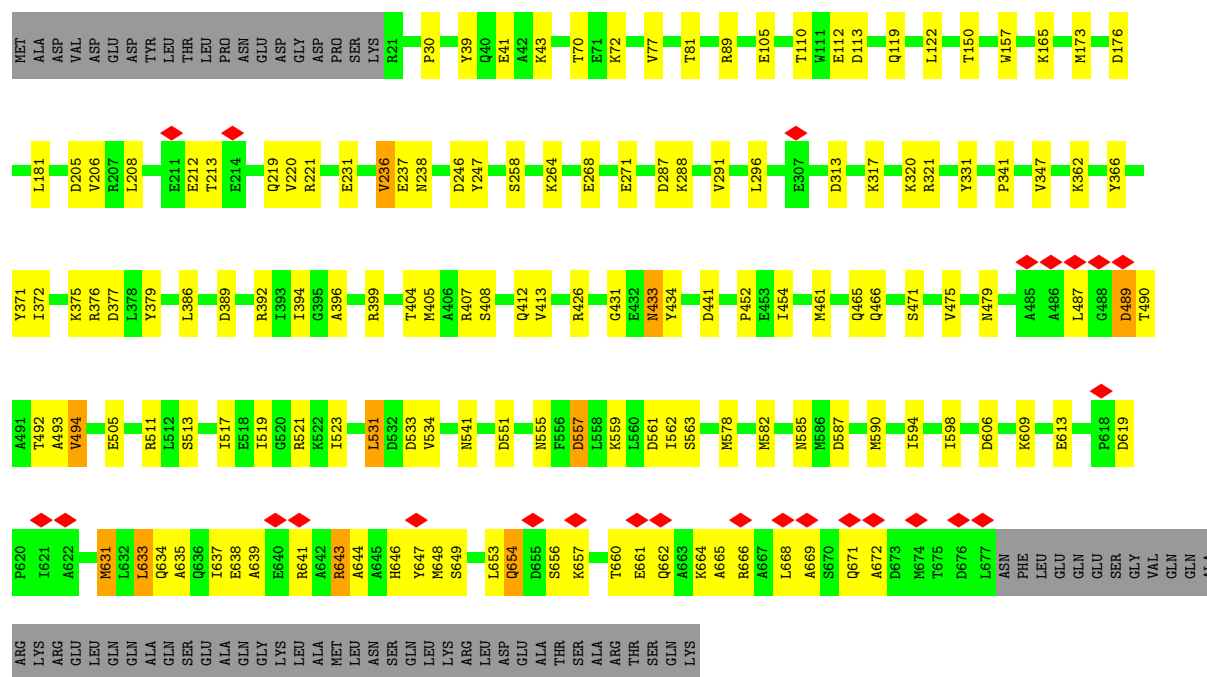
Chain PF:



- Chain PG:  71% 18% 10%

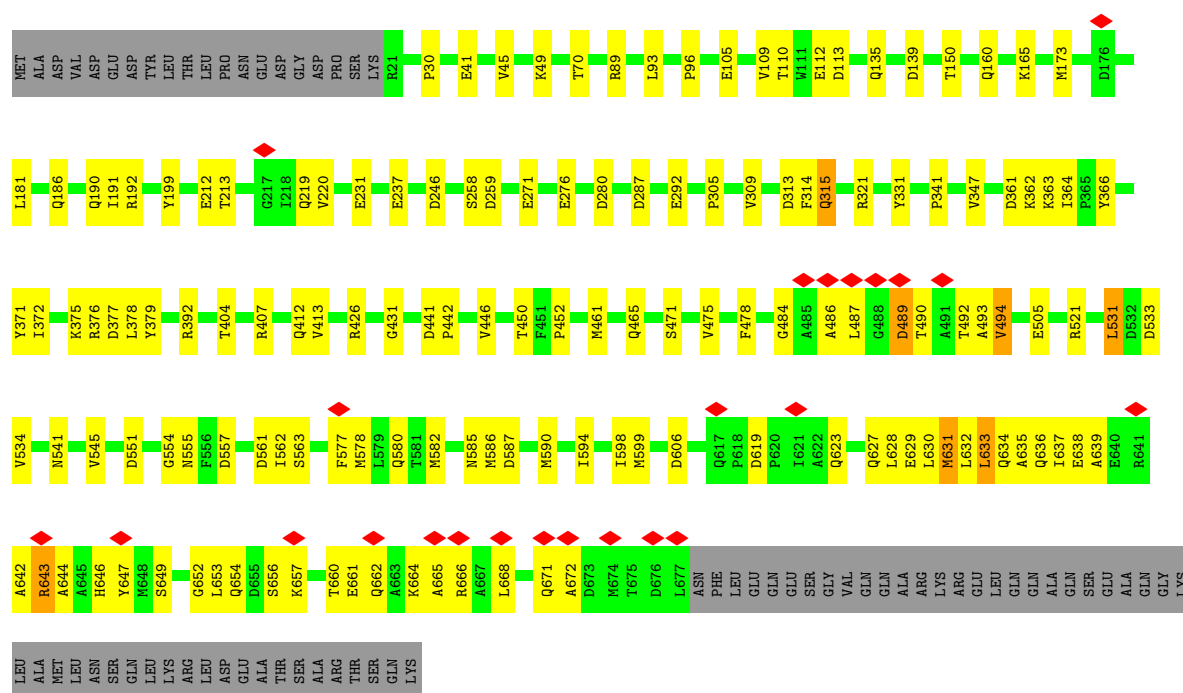


Chain PI: 



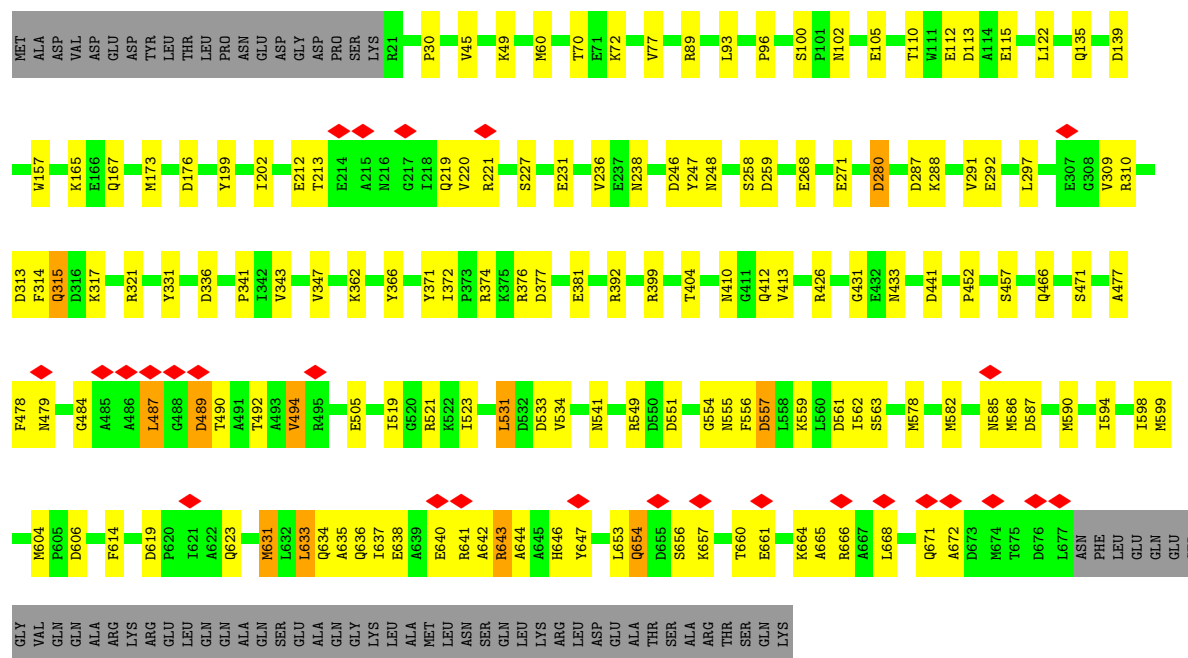
• Molecule 1: gp80 portal protein

Chain PJ: 

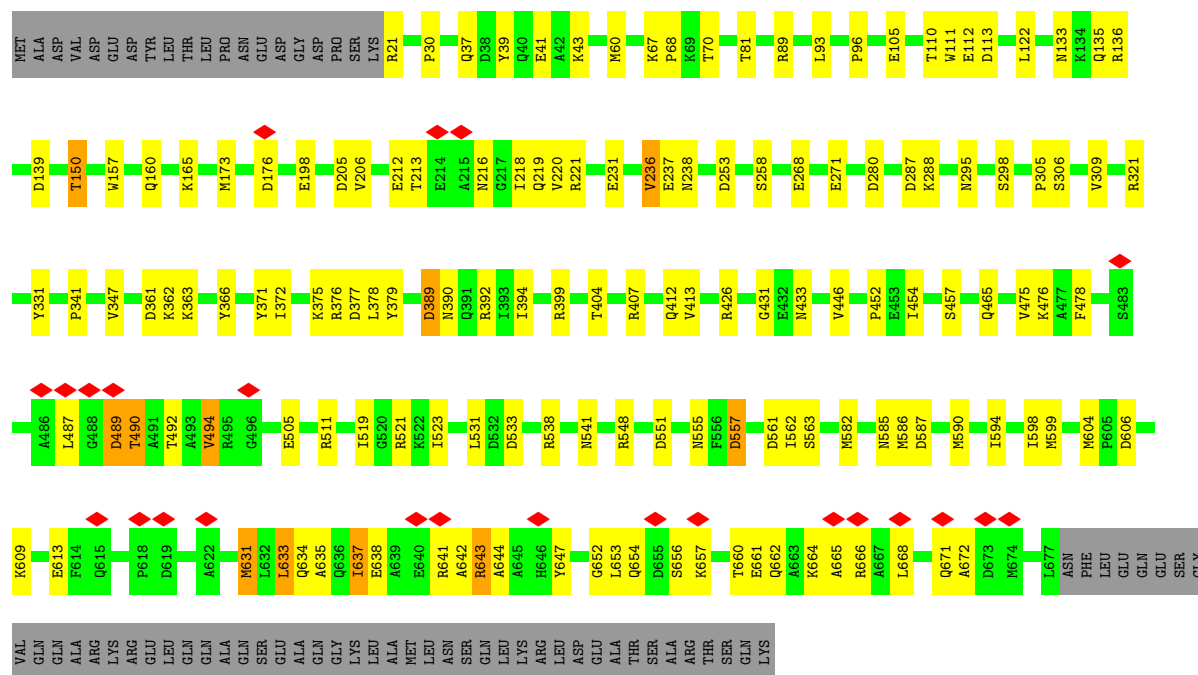


• Molecule 1: gp80 portal protein

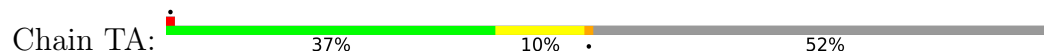
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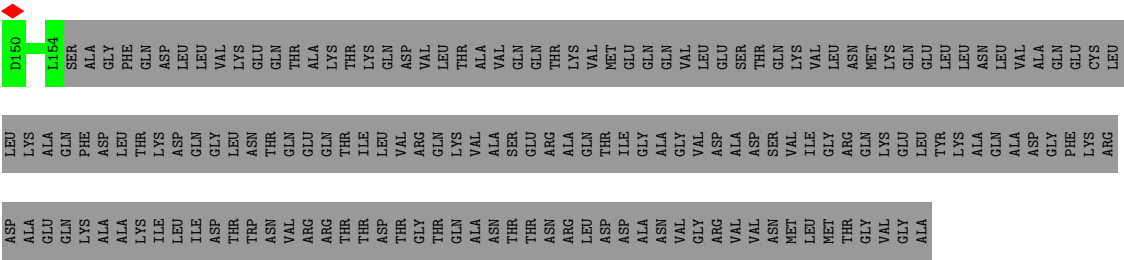


- Molecule 1: gp80 portal protein

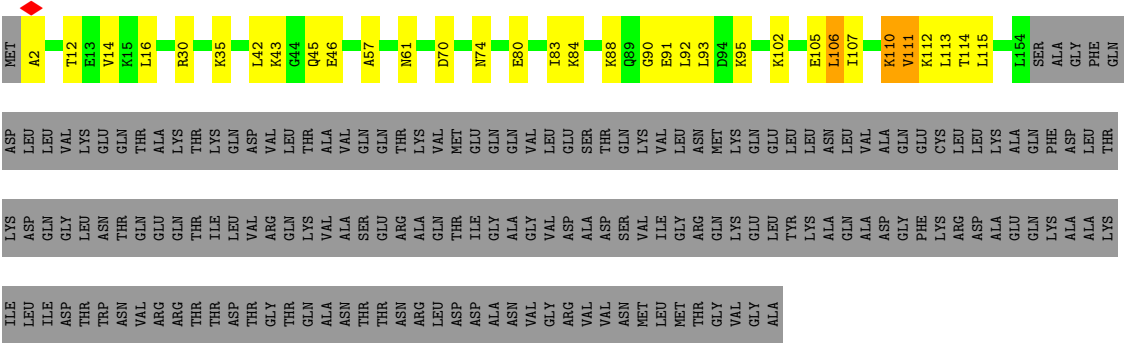
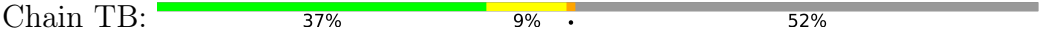


- Molecule 2: gp75 tail tube

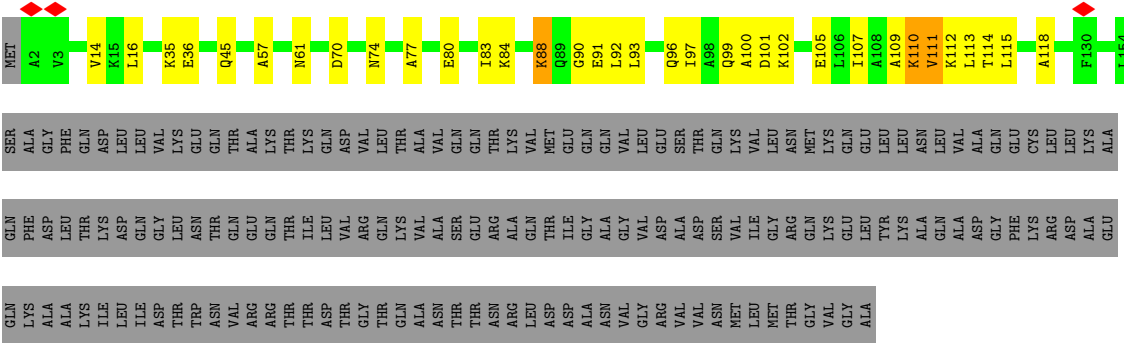
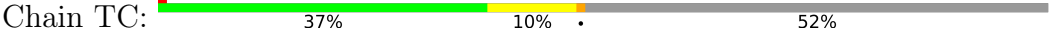




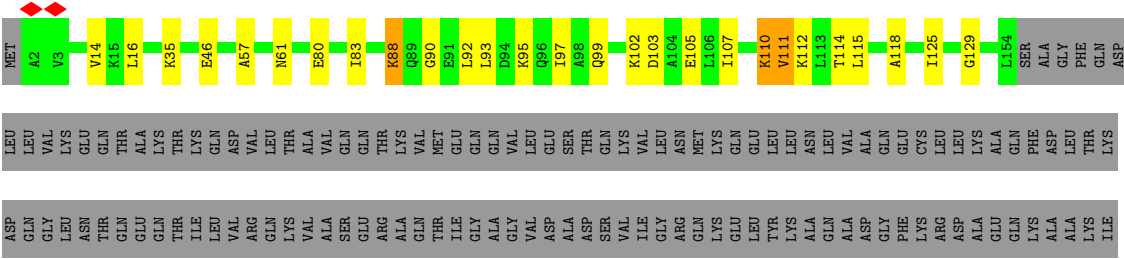
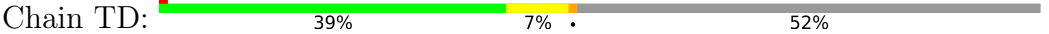
• Molecule 2: gp75 tail tube



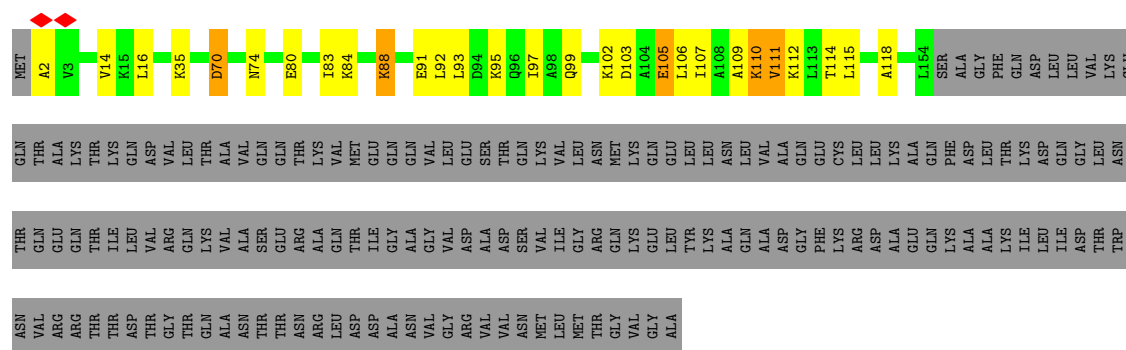
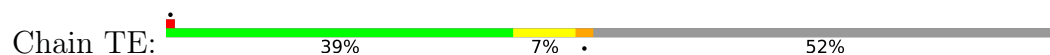
• Molecule 2: gp75 tail tube



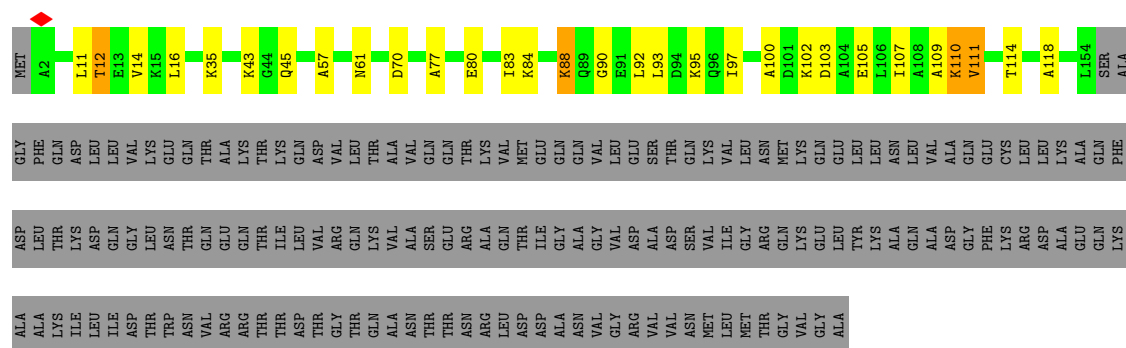
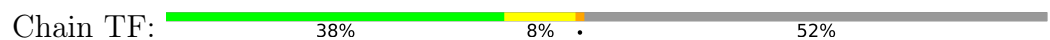
• Molecule 2: gp75 tail tube



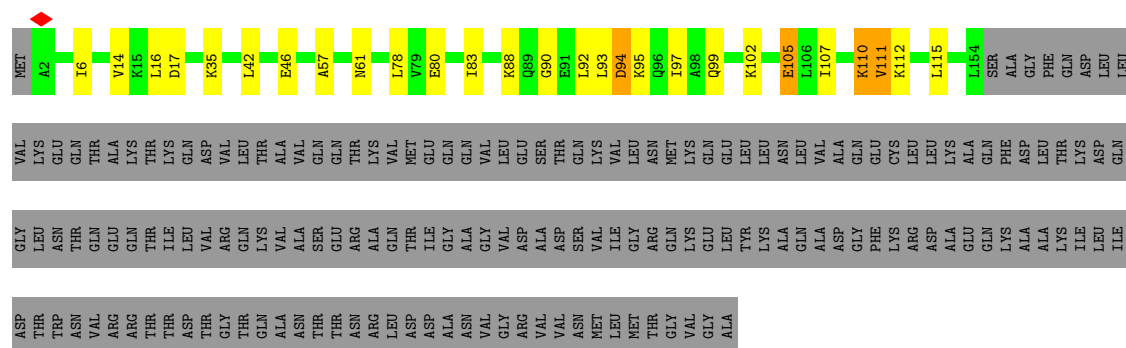
- Molecule 2: gp75 tail tube



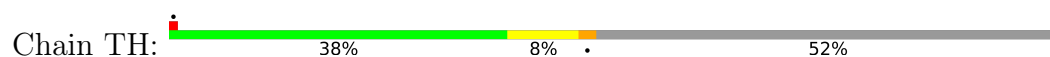
- Molecule 2: gp75 tail tube

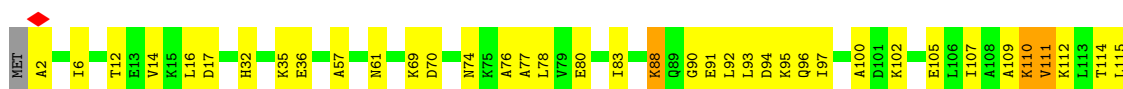
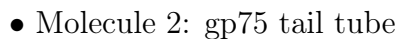
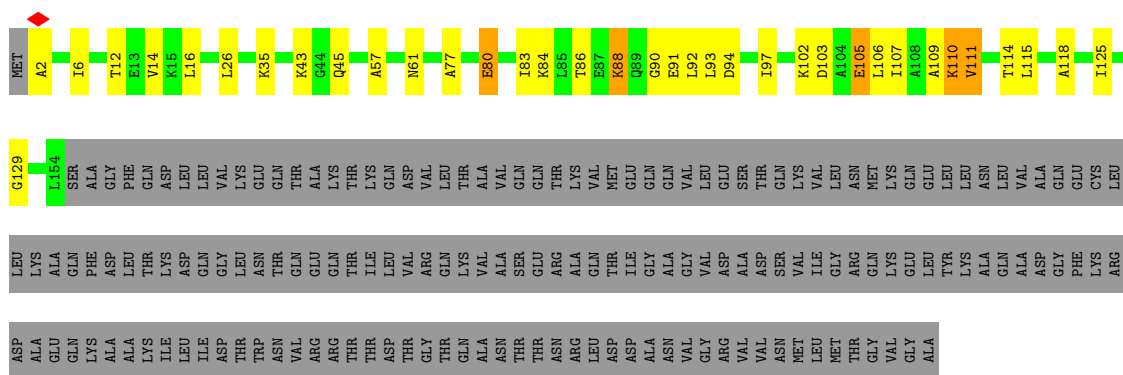
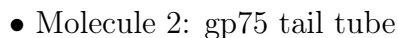
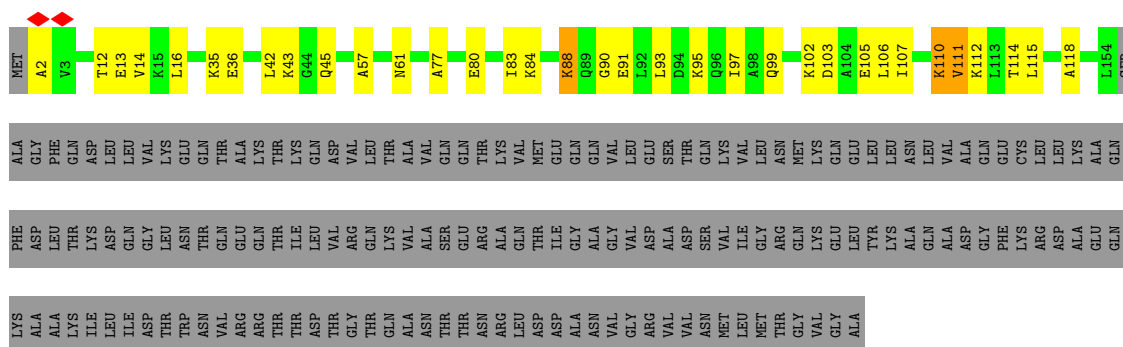
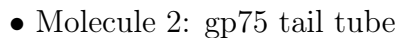


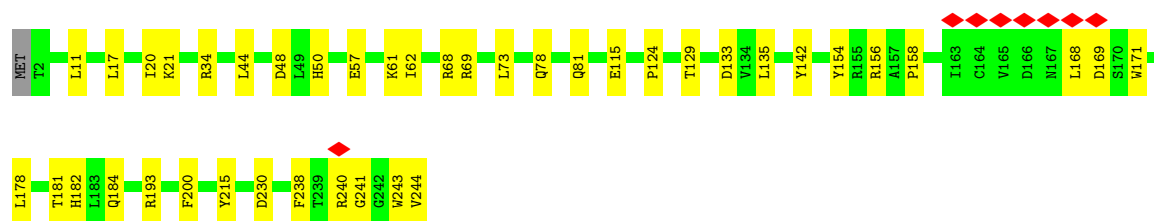
- Molecule 2: gp75 tail tube



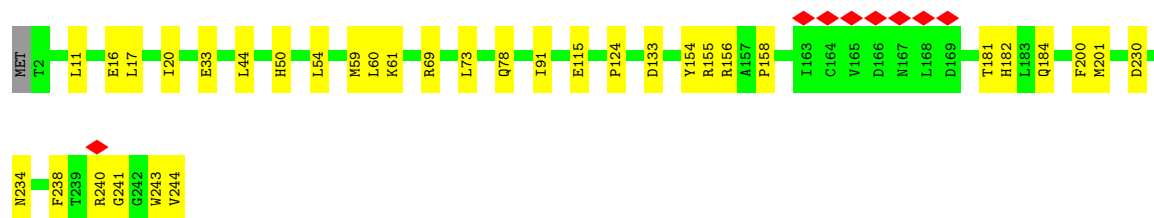
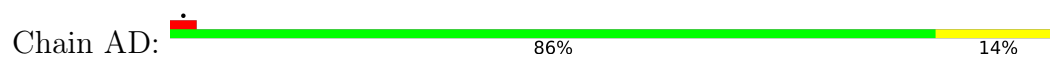
- Molecule 2: gp75 tail tube



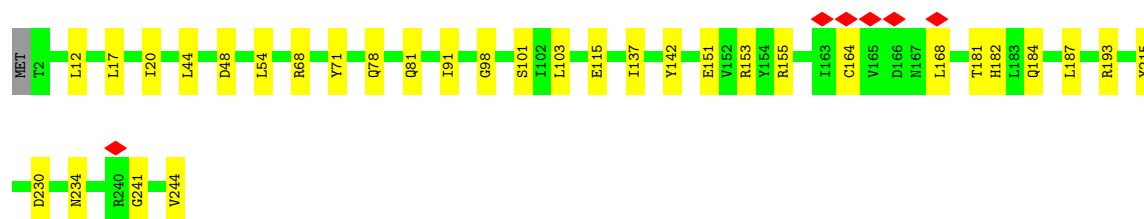




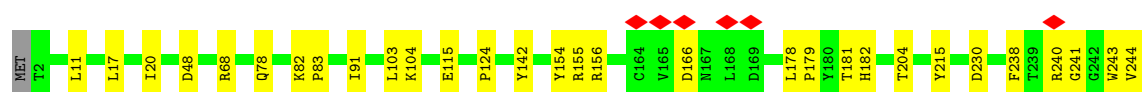
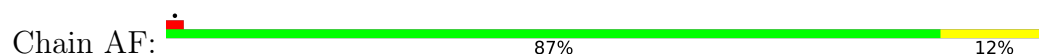
- Molecule 3: gp83 head-to-tail



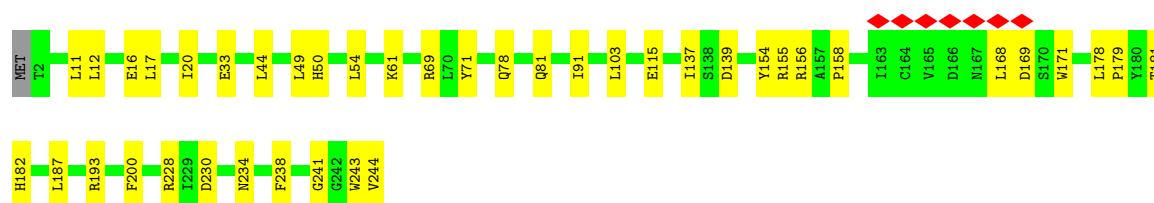
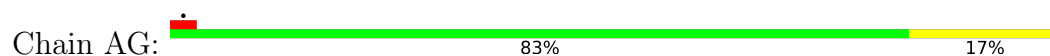
- Molecule 3: gp83 head-to-tail



- Molecule 3: gp83 head-to-tail

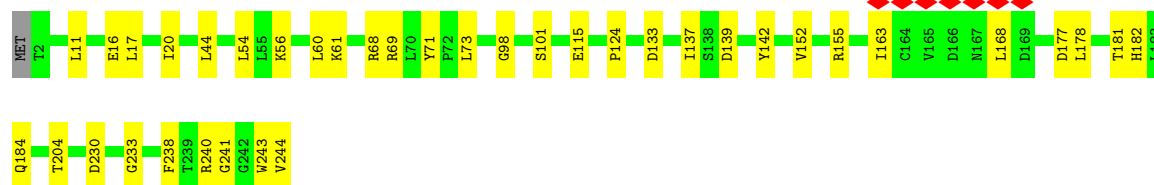


- Molecule 3: gp83 head-to-tail



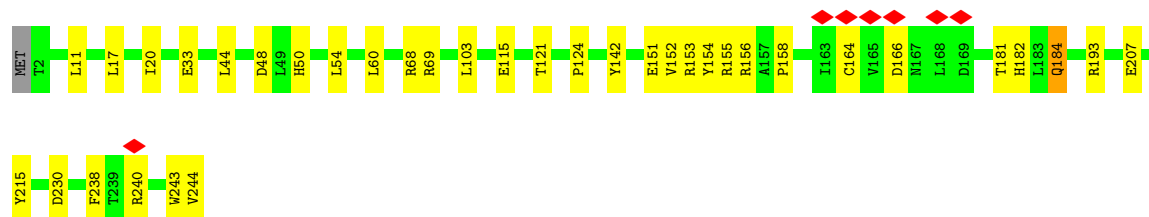
- Molecule 3: gp83 head-to-tail

Chain AH:  84% 16%



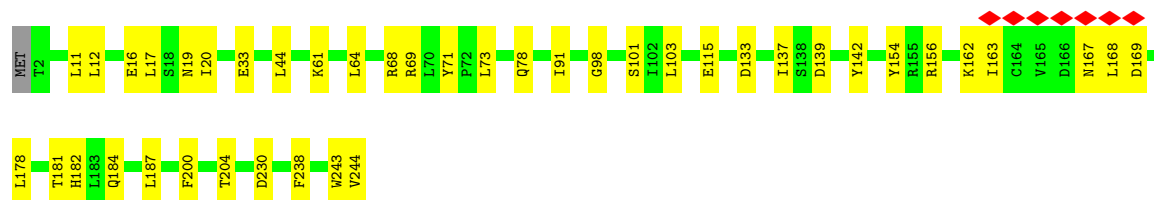
- Molecule 3: gp83 head-to-tail

Chain AI:  85% 14%



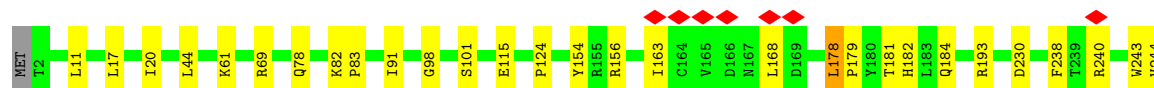
- Molecule 3: gp83 head-to-tail

Chain AJ:  82% 17%



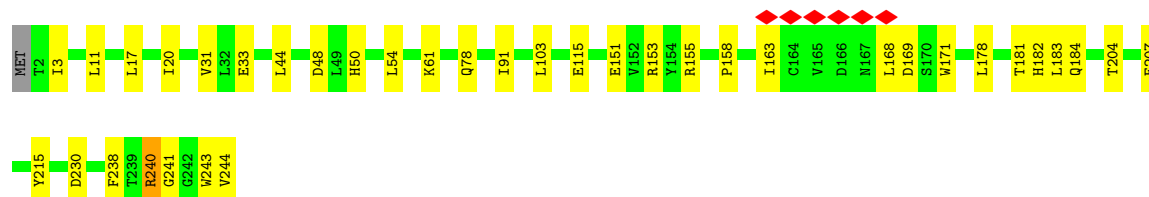
- Molecule 3: gp83 head-to-tail

Chain AK:  88% 11%



- Molecule 3: gp83 head-to-tail

Chain AL:  84% 15%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	64223	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.674	Depositor
Minimum map value	-0.350	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.054	Depositor
Recommended contour level	0.109	Depositor
Map size (Å)	476.00003, 466.48, 447.44003	wwPDB
Map dimensions	376, 392, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.19, 1.19, 1.19	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	PA	0.23	0/5282	0.30	0/7143
1	PB	0.24	0/5282	0.31	0/7143
1	PC	0.23	0/5282	0.30	0/7143
1	PD	0.24	0/5282	0.30	0/7143
1	PE	0.23	0/5282	0.30	0/7143
1	PF	0.24	0/5282	0.30	0/7143
1	PG	0.24	0/5282	0.31	0/7143
1	PH	0.24	0/5282	0.31	0/7143
1	PI	0.24	0/5282	0.30	0/7143
1	PJ	0.24	0/5282	0.31	0/7143
1	PK	0.24	0/5282	0.30	0/7143
1	PL	0.24	0/5282	0.30	0/7143
2	TA	0.19	0/1059	0.28	0/1438
2	TB	0.19	0/1059	0.27	0/1438
2	TC	0.19	0/1059	0.29	0/1438
2	TD	0.20	0/1059	0.29	0/1438
2	TE	0.20	0/1059	0.29	0/1438
2	TF	0.20	0/1059	0.29	0/1438
2	TG	0.19	0/1059	0.28	0/1438
2	TH	0.20	0/1059	0.29	0/1438
2	TI	0.20	0/1059	0.27	0/1438
2	TJ	0.19	0/1059	0.28	0/1438
2	TK	0.19	0/1059	0.28	0/1438
2	TL	0.20	0/1059	0.29	0/1438
3	AA	0.27	0/1991	0.31	0/2699
3	AB	0.26	0/1991	0.31	0/2699
3	AC	0.26	0/1991	0.31	0/2699
3	AD	0.26	0/1991	0.30	0/2699
3	AE	0.26	0/1991	0.31	0/2699
3	AF	0.26	0/1991	0.31	0/2699
3	AG	0.26	0/1991	0.32	0/2699
3	AH	0.26	0/1991	0.33	0/2699
3	AI	0.27	0/1991	0.31	0/2699
3	AJ	0.25	0/1991	0.31	0/2699

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	AK	0.26	0/1991	0.31	0/2699
3	AL	0.26	0/1991	0.31	0/2699
All	All	0.24	0/99984	0.30	0/135360

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	PA	5187	0	5076	158	0
1	PB	5187	0	5076	163	0
1	PC	5187	0	5076	143	0
1	PD	5187	0	5076	133	0
1	PE	5187	0	5076	132	0
1	PF	5187	0	5076	144	0
1	PG	5187	0	5076	144	0
1	PH	5187	0	5076	137	0
1	PI	5187	0	5076	143	0
1	PJ	5187	0	5076	150	0
1	PK	5187	0	5076	151	0
1	PL	5187	0	5076	145	0
2	TA	1054	0	1004	34	0
2	TB	1054	0	1004	28	0
2	TC	1054	0	1004	34	0
2	TD	1054	0	1004	27	0
2	TE	1054	0	1004	33	0
2	TF	1054	0	1004	36	0
2	TG	1054	0	1004	24	0
2	TH	1054	0	1004	31	0
2	TI	1054	0	1004	29	0
2	TJ	1054	0	1004	38	0
2	TK	1054	0	1004	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	TL	1054	0	1004	42	0
3	AA	1951	0	1957	24	0
3	AB	1951	0	1957	30	0
3	AC	1951	0	1957	29	0
3	AD	1951	0	1957	30	0
3	AE	1951	0	1957	23	0
3	AF	1951	0	1957	24	0
3	AG	1951	0	1957	30	0
3	AH	1951	0	1957	28	0
3	AI	1951	0	1957	28	0
3	AJ	1951	0	1957	31	0
3	AK	1951	0	1957	24	0
3	AL	1951	0	1957	27	0
All	All	98304	0	96444	1756	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 9.

The worst 5 of 1756 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:PG:643:ARG:HH21	1:PH:641:ARG:HB2	1.44	0.83
1:PK:487:LEU:HD13	1:PL:494:VAL:HG22	1.61	0.83
1:PJ:665:ALA:HA	1:PJ:668:LEU:HB2	1.60	0.82
1:PG:624:GLN:NE2	1:PG:627:GLN:OE1	2.14	0.80
2:TA:110:LYS:HD3	2:TL:106:LEU:HD22	1.60	0.80

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	PA	655/726 (90%)	639 (98%)	16 (2%)	0	100	100
1	PB	655/726 (90%)	637 (97%)	18 (3%)	0	100	100
1	PC	655/726 (90%)	637 (97%)	18 (3%)	0	100	100
1	PD	655/726 (90%)	637 (97%)	18 (3%)	0	100	100
1	PE	655/726 (90%)	636 (97%)	19 (3%)	0	100	100
1	PF	655/726 (90%)	635 (97%)	20 (3%)	0	100	100
1	PG	655/726 (90%)	638 (97%)	17 (3%)	0	100	100
1	PH	655/726 (90%)	636 (97%)	19 (3%)	0	100	100
1	PI	655/726 (90%)	639 (98%)	16 (2%)	0	100	100
1	PJ	655/726 (90%)	638 (97%)	17 (3%)	0	100	100
1	PK	655/726 (90%)	638 (97%)	17 (3%)	0	100	100
1	PL	655/726 (90%)	637 (97%)	18 (3%)	0	100	100
2	TA	151/321 (47%)	144 (95%)	7 (5%)	0	100	100
2	TB	151/321 (47%)	147 (97%)	4 (3%)	0	100	100
2	TC	151/321 (47%)	146 (97%)	5 (3%)	0	100	100
2	TD	151/321 (47%)	148 (98%)	3 (2%)	0	100	100
2	TE	151/321 (47%)	147 (97%)	4 (3%)	0	100	100
2	TF	151/321 (47%)	148 (98%)	3 (2%)	0	100	100
2	TG	151/321 (47%)	147 (97%)	4 (3%)	0	100	100
2	TH	151/321 (47%)	148 (98%)	3 (2%)	0	100	100
2	TI	151/321 (47%)	148 (98%)	3 (2%)	0	100	100
2	TJ	151/321 (47%)	148 (98%)	3 (2%)	0	100	100
2	TK	151/321 (47%)	146 (97%)	5 (3%)	0	100	100
2	TL	151/321 (47%)	146 (97%)	5 (3%)	0	100	100
3	AA	241/244 (99%)	237 (98%)	4 (2%)	0	100	100
3	AB	241/244 (99%)	237 (98%)	4 (2%)	0	100	100
3	AC	241/244 (99%)	239 (99%)	2 (1%)	0	100	100
3	AD	241/244 (99%)	236 (98%)	5 (2%)	0	100	100
3	AE	241/244 (99%)	237 (98%)	4 (2%)	0	100	100
3	AF	241/244 (99%)	238 (99%)	3 (1%)	0	100	100
3	AG	241/244 (99%)	237 (98%)	4 (2%)	0	100	100
3	AH	241/244 (99%)	236 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	AI	241/244 (99%)	238 (99%)	3 (1%)	0	100	100
3	AJ	241/244 (99%)	237 (98%)	4 (2%)	0	100	100
3	AK	241/244 (99%)	236 (98%)	5 (2%)	0	100	100
3	AL	241/244 (99%)	236 (98%)	5 (2%)	0	100	100
All	All	12564/15492 (81%)	12254 (98%)	310 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	PA	554/615 (90%)	537 (97%)	17 (3%)	35	59
1	PB	554/615 (90%)	539 (97%)	15 (3%)	39	61
1	PC	554/615 (90%)	536 (97%)	18 (3%)	34	58
1	PD	554/615 (90%)	536 (97%)	18 (3%)	34	58
1	PE	554/615 (90%)	531 (96%)	23 (4%)	26	53
1	PF	554/615 (90%)	536 (97%)	18 (3%)	34	58
1	PG	554/615 (90%)	537 (97%)	17 (3%)	35	59
1	PH	554/615 (90%)	535 (97%)	19 (3%)	32	57
1	PI	554/615 (90%)	537 (97%)	17 (3%)	35	59
1	PJ	554/615 (90%)	540 (98%)	14 (2%)	42	63
1	PK	554/615 (90%)	537 (97%)	17 (3%)	35	59
1	PL	554/615 (90%)	532 (96%)	22 (4%)	28	54
2	TA	89/264 (34%)	84 (94%)	5 (6%)	19	47
2	TB	89/264 (34%)	82 (92%)	7 (8%)	11	37
2	TC	89/264 (34%)	84 (94%)	5 (6%)	19	47
2	TD	89/264 (34%)	85 (96%)	4 (4%)	24	51
2	TE	89/264 (34%)	83 (93%)	6 (7%)	15	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	TF	89/264 (34%)	84 (94%)	5 (6%)	19	47
2	TG	89/264 (34%)	83 (93%)	6 (7%)	15	42
2	TH	89/264 (34%)	83 (93%)	6 (7%)	15	42
2	TI	89/264 (34%)	83 (93%)	6 (7%)	15	42
2	TJ	89/264 (34%)	81 (91%)	8 (9%)	9	33
2	TK	89/264 (34%)	84 (94%)	5 (6%)	19	47
2	TL	89/264 (34%)	83 (93%)	6 (7%)	15	42
3	AA	215/216 (100%)	214 (100%)	1 (0%)	81	80
3	AB	215/216 (100%)	213 (99%)	2 (1%)	70	76
3	AC	215/216 (100%)	213 (99%)	2 (1%)	70	76
3	AD	215/216 (100%)	215 (100%)	0	100	100
3	AE	215/216 (100%)	214 (100%)	1 (0%)	81	80
3	AF	215/216 (100%)	215 (100%)	0	100	100
3	AG	215/216 (100%)	214 (100%)	1 (0%)	81	80
3	AH	215/216 (100%)	214 (100%)	1 (0%)	81	80
3	AI	215/216 (100%)	214 (100%)	1 (0%)	81	80
3	AJ	215/216 (100%)	214 (100%)	1 (0%)	81	80
3	AK	215/216 (100%)	213 (99%)	2 (1%)	70	76
3	AL	215/216 (100%)	212 (99%)	3 (1%)	59	71
All	All	10296/13140 (78%)	9997 (97%)	299 (3%)	38	60

5 of 299 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	PJ	631	MET
1	PL	633	LEU
2	TJ	86	THR
1	PK	654	GLN
1	PE	236	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 142 such sidechains are listed below:

Mol	Chain	Res	Type
1	PJ	160	GLN

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Mol	Chain	Res	Type
1	PJ	527	ASN
1	PK	555	ASN
1	PE	294	GLN
1	PE	160	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

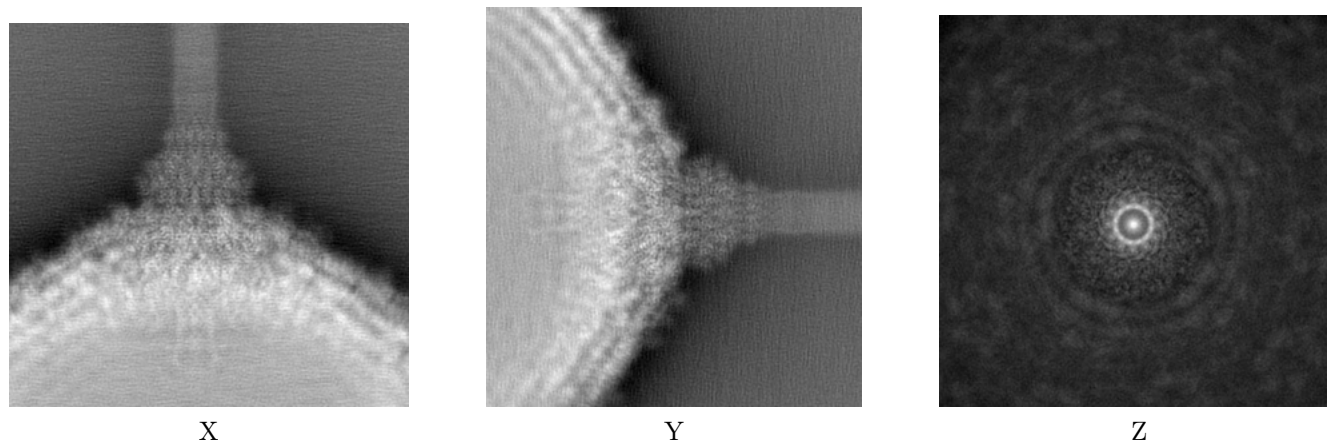
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-74075. These allow visual inspection of the internal detail of the map and identification of artifacts.

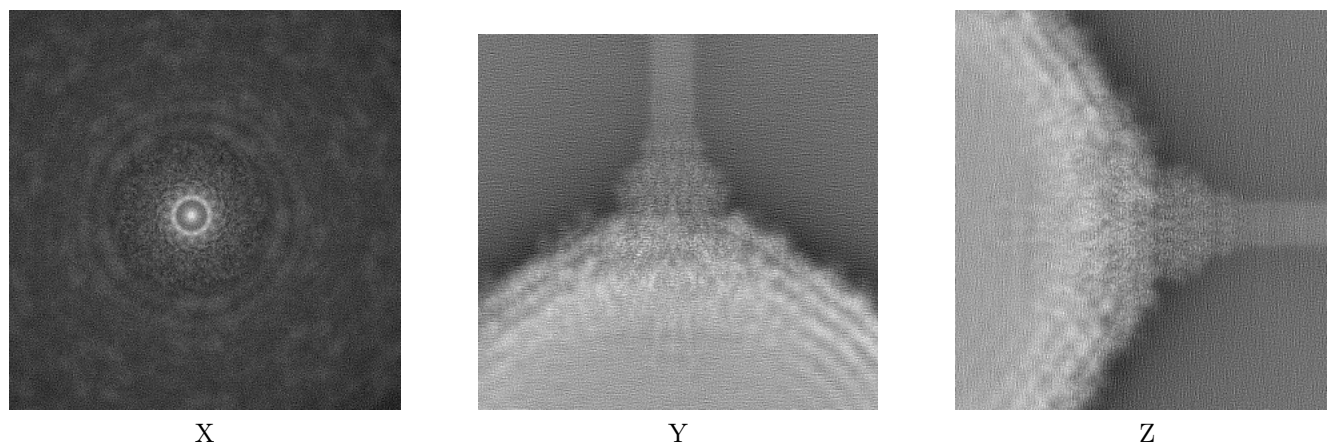
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



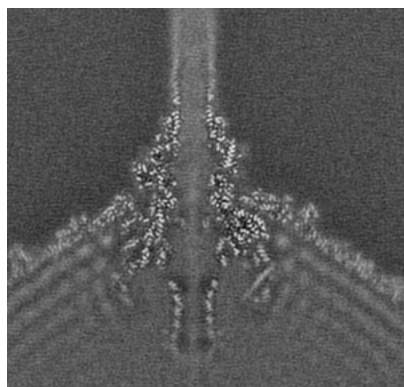
6.1.2 Raw map



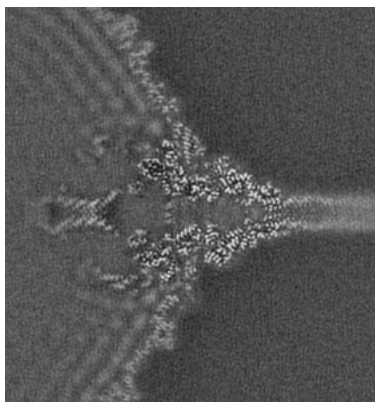
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

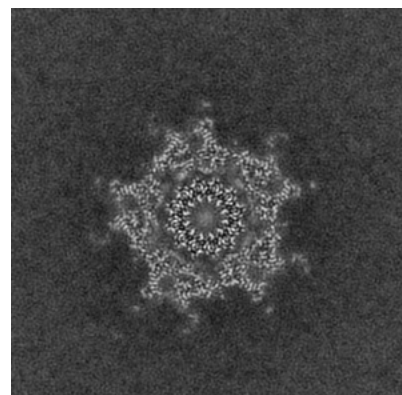
6.2.1 Primary map



X Index: 200

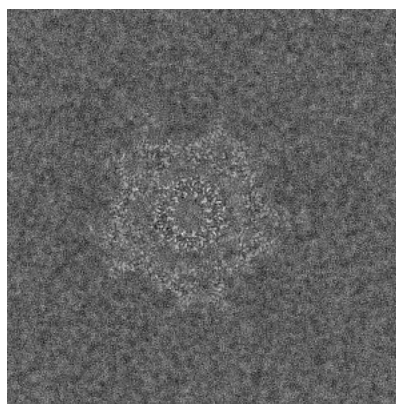


Y Index: 196

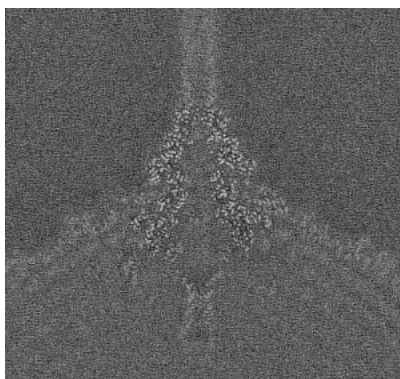


Z Index: 188

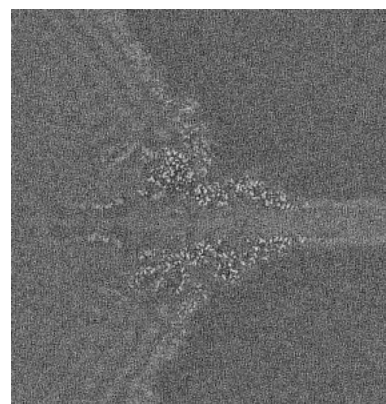
6.2.2 Raw map



X Index: 188



Y Index: 196

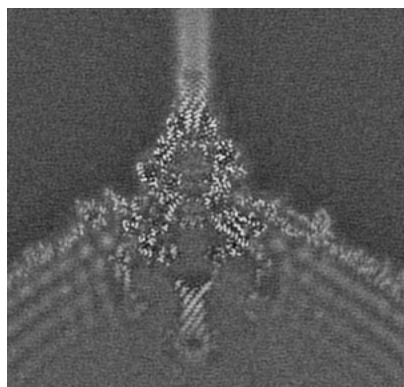


Z Index: 200

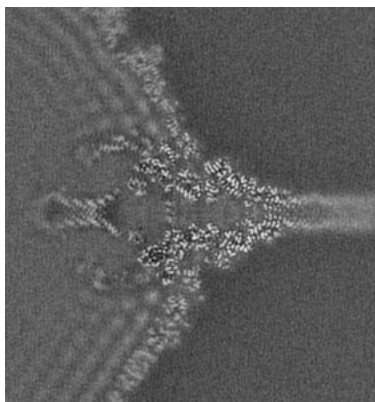
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

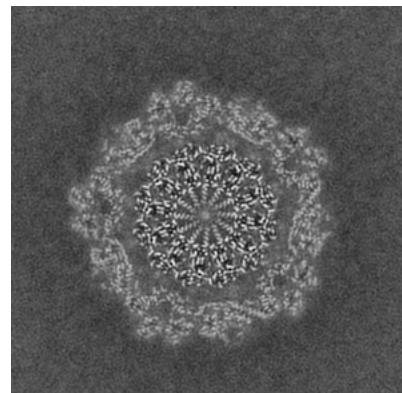
6.3.1 Primary map



X Index: 178

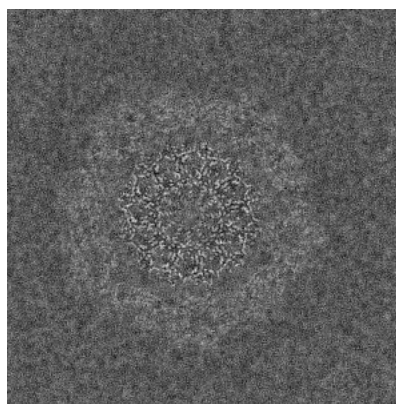


Y Index: 168

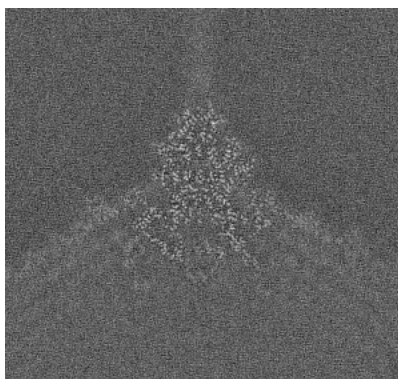


Z Index: 162

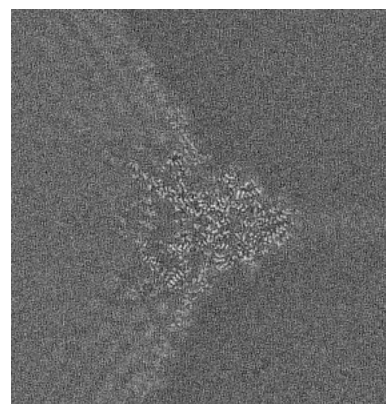
6.3.2 Raw map



X Index: 162



Y Index: 160

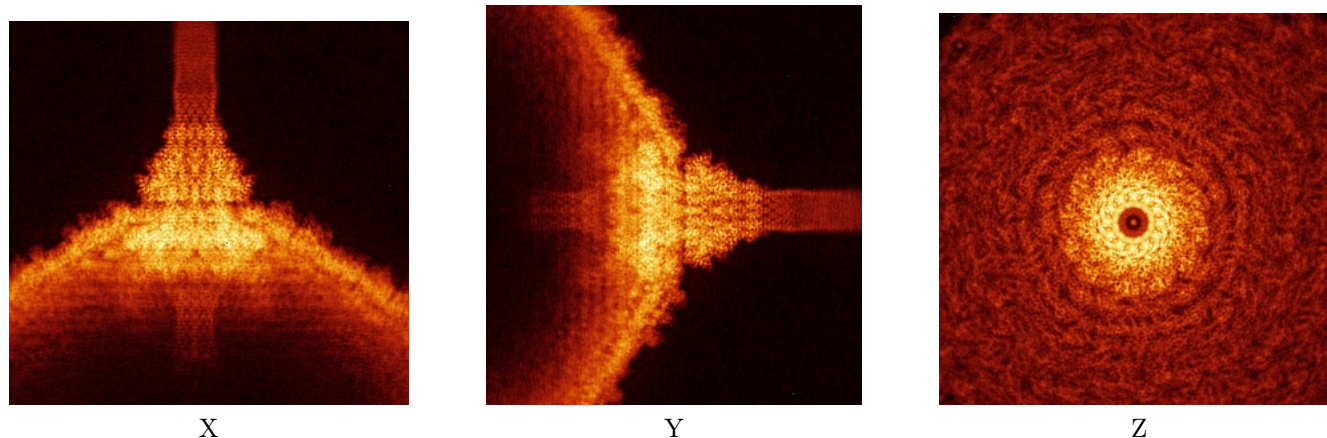


Z Index: 217

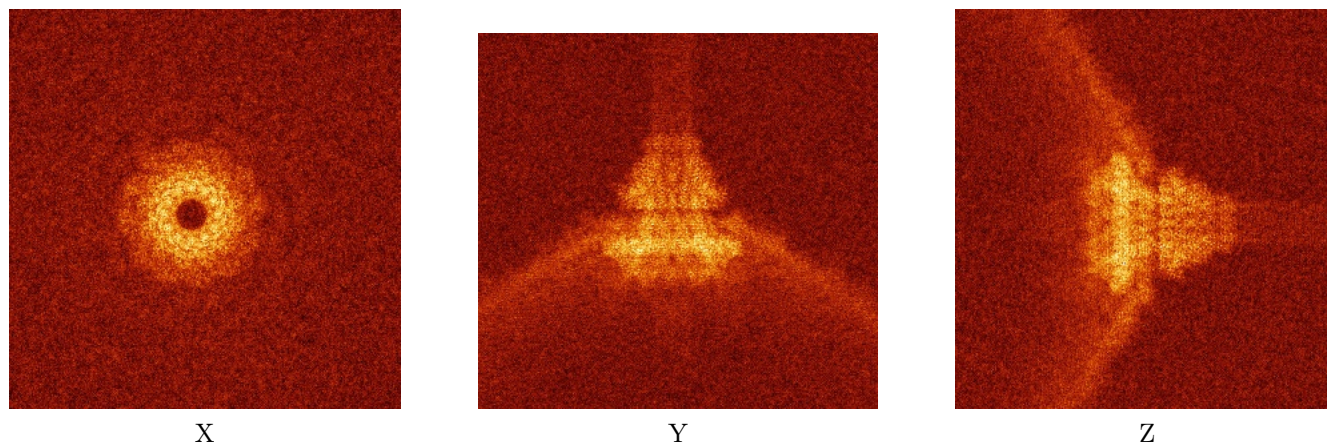
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

This section was not generated.

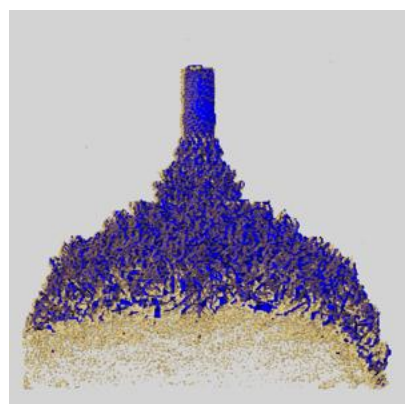
6.6 Mask visualisation [i](#)

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

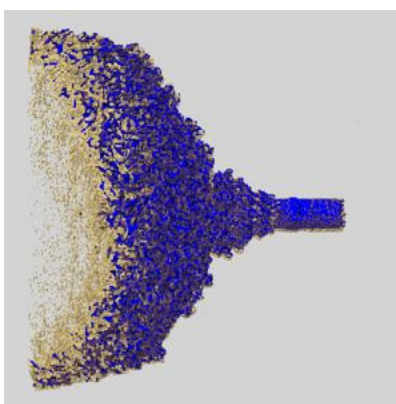
A mask typically either:

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

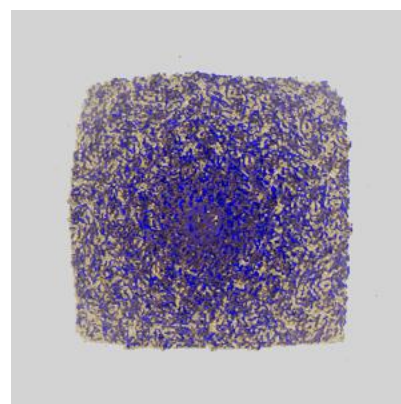
6.6.1 emd_74075_msk_1.map [i](#)



X



Y

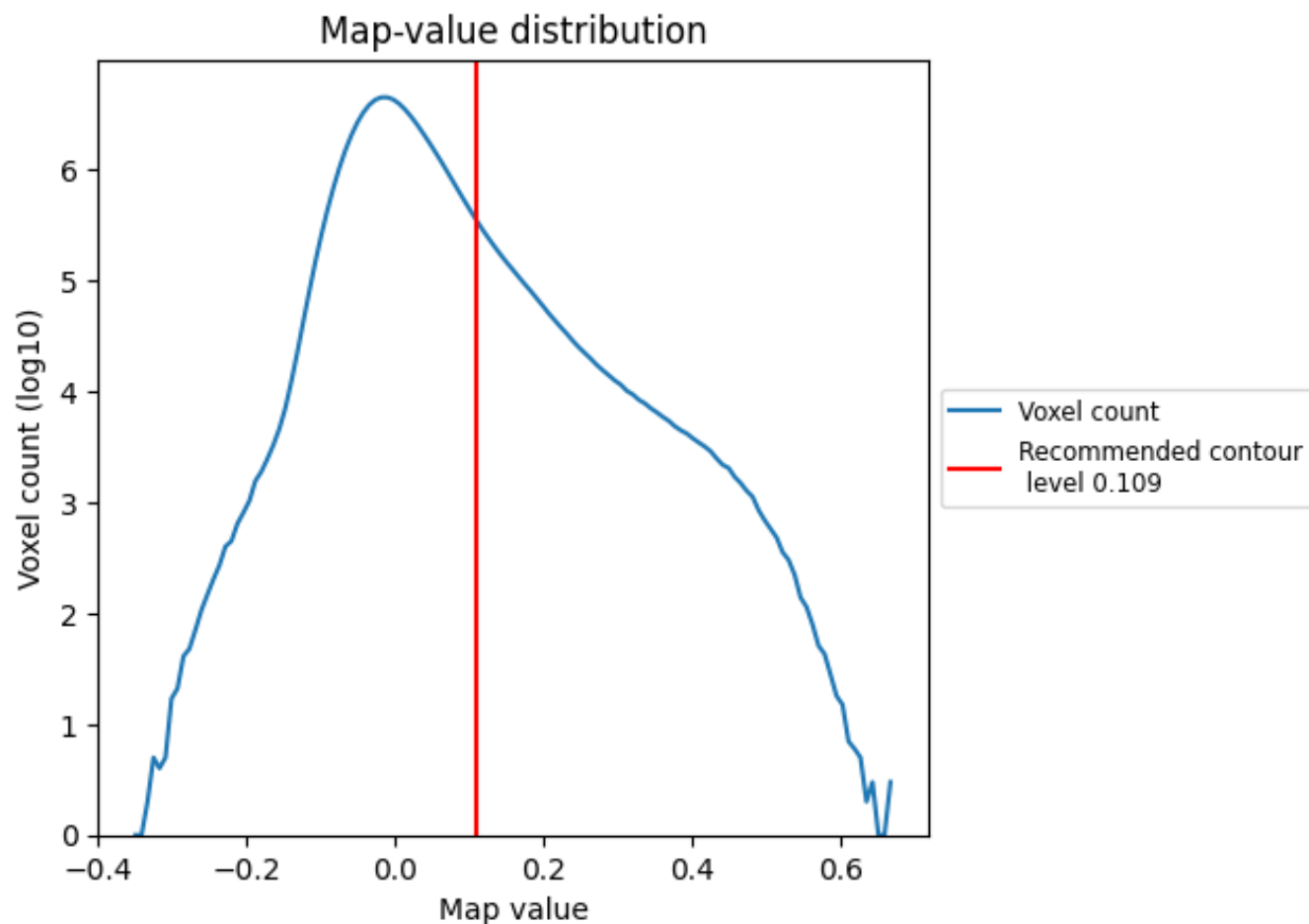


Z

7 Map analysis [i](#)

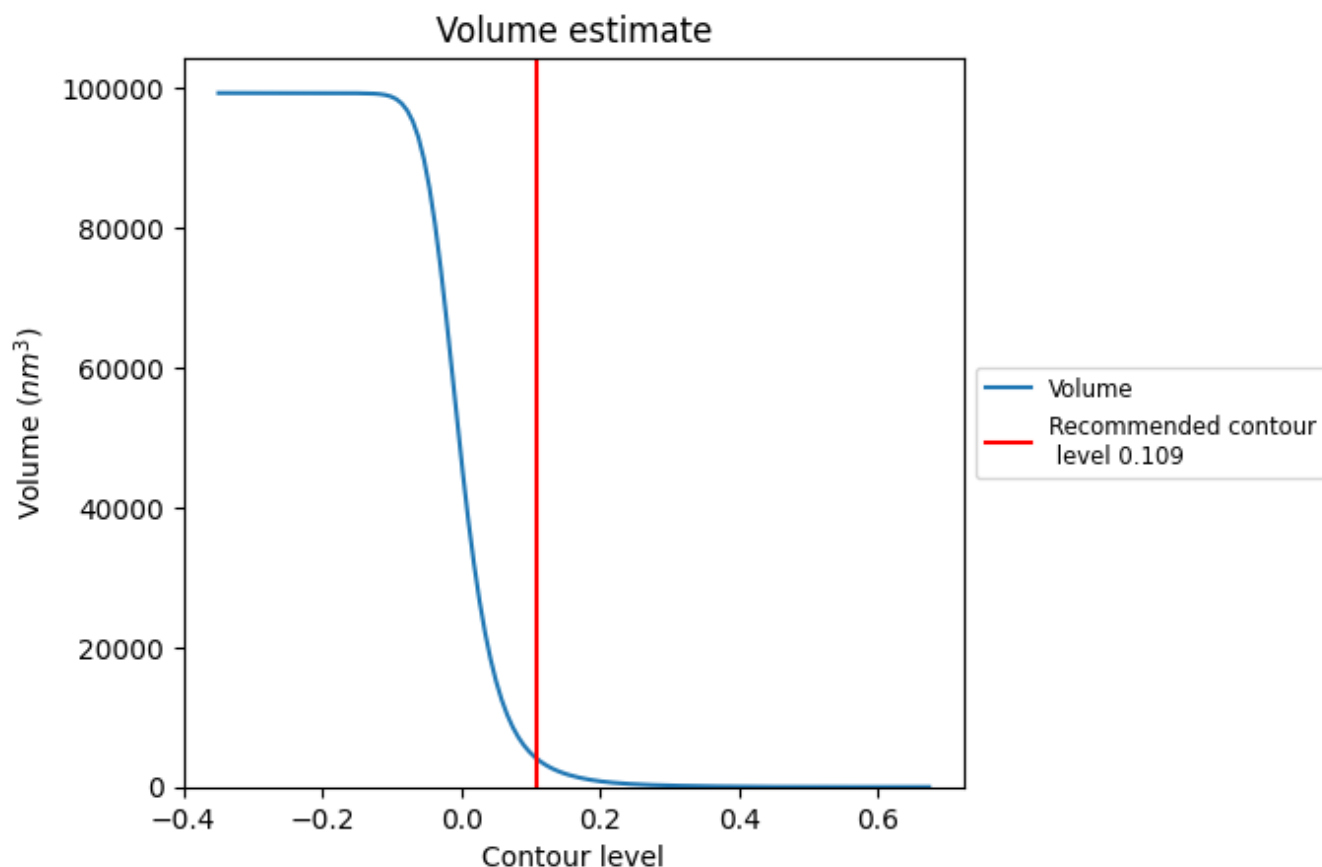
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4065 nm³; this corresponds to an approximate mass of 3672 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](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

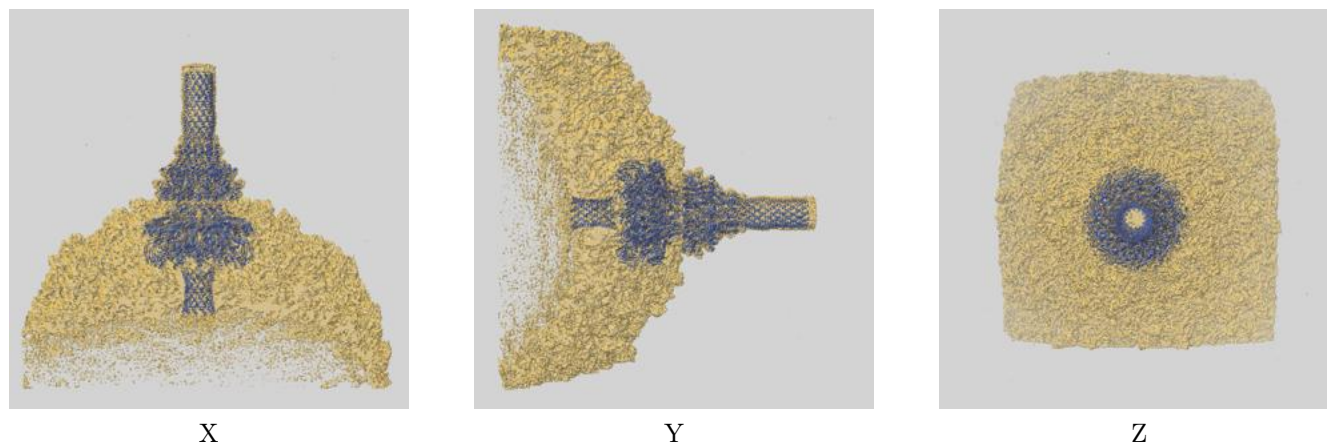
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

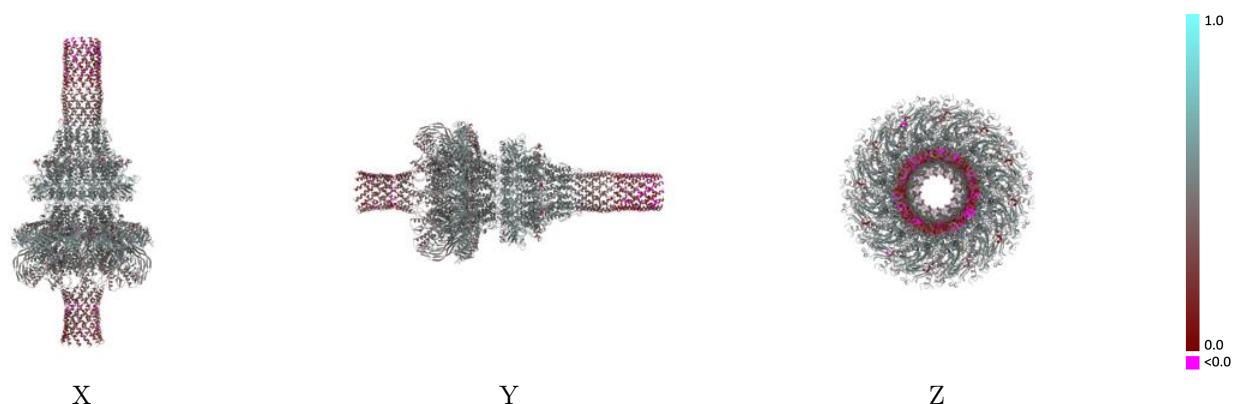
This section contains information regarding the fit between EMDB map EMD-74075 and PDB model 9ZDW. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



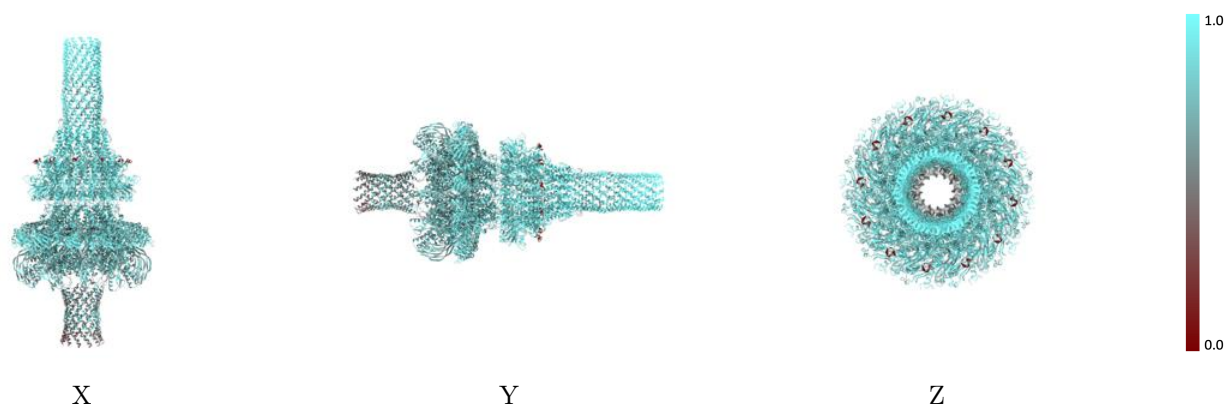
The images above show the 3D surface view of the map at the recommended contour level 0.109 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



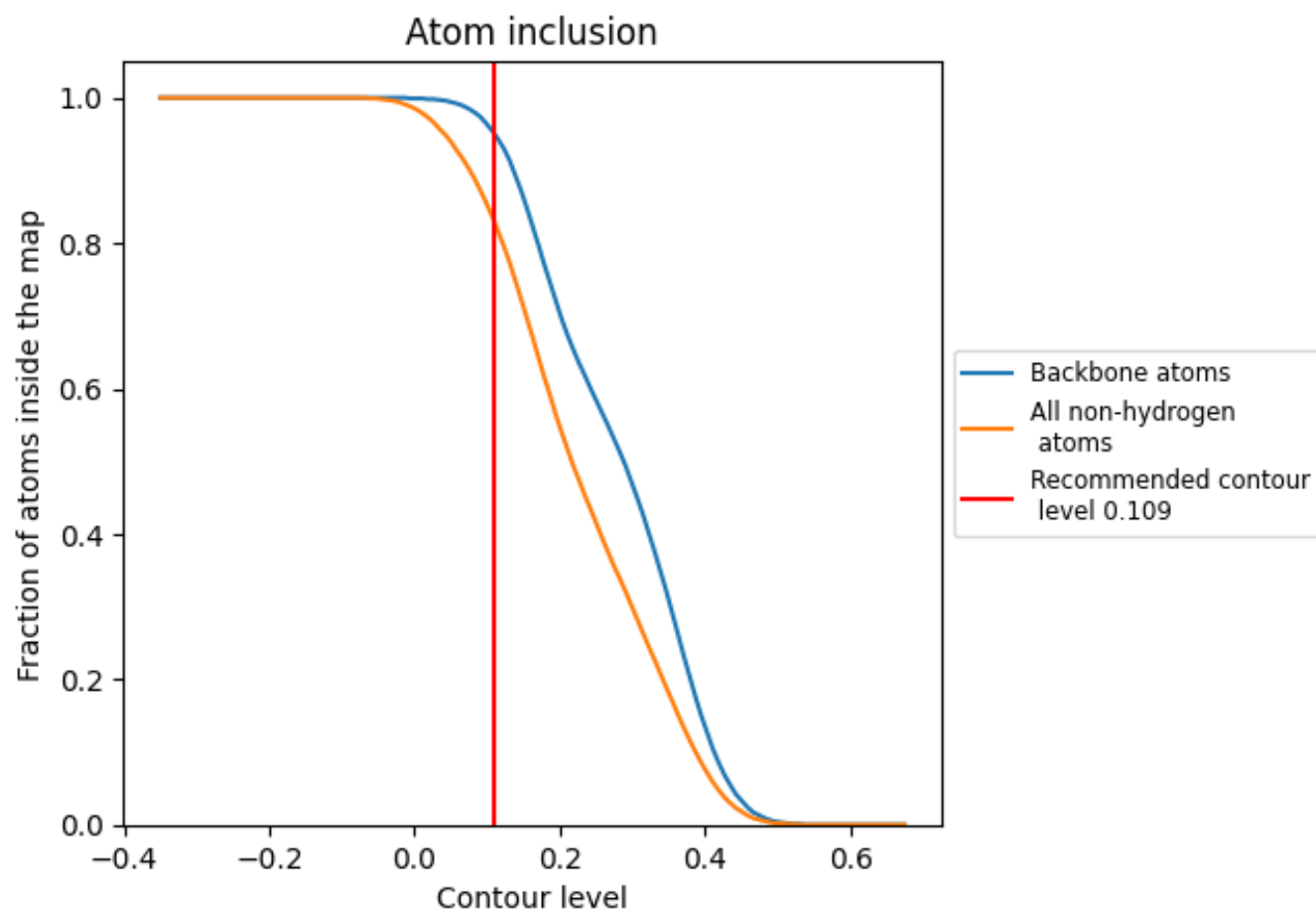
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.109).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 83% 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 (0.109) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8320	 0.4650
AA	 0.8940	 0.5010
AB	 0.9030	 0.5050
AC	 0.9000	 0.5050
AD	 0.9020	 0.5030
AE	 0.8970	 0.5030
AF	 0.8940	 0.5050
AG	 0.9050	 0.5060
AH	 0.8900	 0.5040
AI	 0.8990	 0.5050
AJ	 0.8960	 0.5030
AK	 0.8980	 0.5060
AL	 0.9020	 0.5010
PA	 0.7930	 0.4710
PB	 0.7900	 0.4640
PC	 0.7870	 0.4650
PD	 0.7860	 0.4670
PE	 0.7880	 0.4700
PF	 0.7920	 0.4660
PG	 0.7880	 0.4690
PH	 0.7870	 0.4640
PI	 0.7890	 0.4720
PJ	 0.7900	 0.4690
PK	 0.7860	 0.4670
PL	 0.7890	 0.4670
TA	 0.9070	 0.3650
TB	 0.9320	 0.3850
TC	 0.9160	 0.3810
TD	 0.9180	 0.3880
TE	 0.9200	 0.3830
TF	 0.9230	 0.3830
TG	 0.9250	 0.3840
TH	 0.9190	 0.3890
TI	 0.9120	 0.3710
TJ	 0.9210	 0.3920



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Chain	Atom inclusion	Q-score
TK	 0.9260	 0.3790
TL	 0.9170	 0.3800