



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 11:07 PM UTC

PDB ID : 6VZG / pdb_00006vzg
EMDB ID : EMD-21489
Title : Cryo-EM structure of Sth1-Arp7-Arp9-Rtt102
Authors : Leschziner, A.E.; Baker, R.W.
Deposited on : 2020-02-28
Resolution : 4.20 Å (reported)
Based on initial models : 5TGC, 4I6M

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:

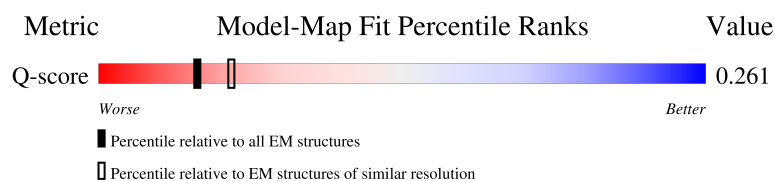
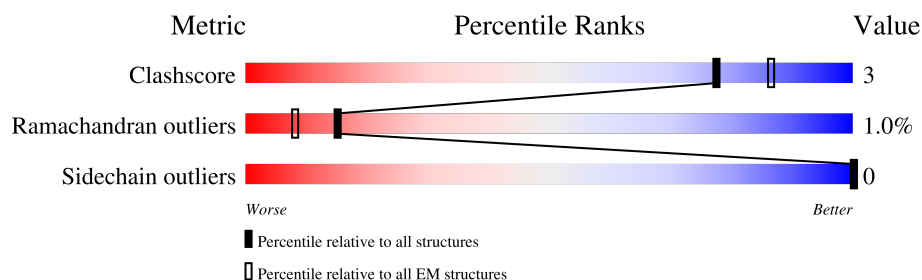
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 4.20 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.



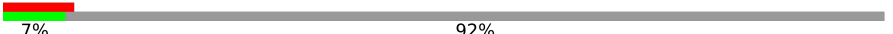
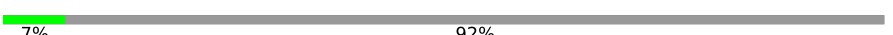
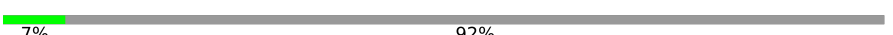
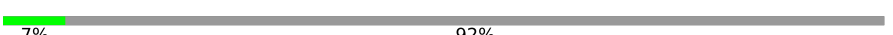
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5410 (3.70 - 4.70)

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	1-L	477	
1	10-L	477	
1	2-L	477	
1	3-L	477	

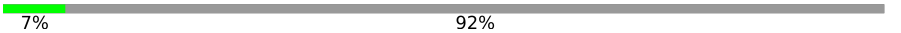
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Mol	Chain	Length	Quality of chain
1	4-L	477	 74%8%18%
1	5-L	477	 75%7%18%
1	6-L	477	 76%6%18%
1	7-L	477	 74%8%18%
1	8-L	477	 74%8%18%
1	9-L	477	 75%7%18%
2	1-M	467	 77%79%6%15%
2	10-M	467	 79%6%15%
2	2-M	467	 78%6%15%
2	3-M	467	 77%7%15%
2	4-M	467	 78%6%15%
2	5-M	467	 78%7%15%
2	6-M	467	 77%7%15%
2	7-M	467	 78%6%15%
2	8-M	467	 79%6%15%
2	9-M	467	 78%6%15%
3	1-K	813	 8%7%92%
3	10-K	813	 7%92%
3	2-K	813	 8%92%
3	3-K	813	 8%92%
3	4-K	813	 7%92%
3	5-K	813	 7%92%
3	6-K	813	 7%92%
3	7-K	813	 7%92%
3	8-K	813	 7%92%

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Mol	Chain	Length	Quality of chain
3	9-K	813	 7% 92%
4	1-N	157	 32% 31% 65%
4	10-N	157	 31% 65%
4	2-N	157	 31% 65%
4	3-N	157	 30% 65%
4	4-N	157	 31% 65%
4	5-N	157	 31% 65%
4	6-N	157	 32% 65%
4	7-N	157	 31% 65%
4	8-N	157	 31% 65%
4	9-N	157	 32% 65%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 74080 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 Actin-related protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		
1	2-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		
1	3-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		
1	4-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		
1	5-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		
1	6-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		
1	7-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		
1	8-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		
1	9-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		
1	10-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		

- Molecule 2 is a protein called Actin-like protein ARP9.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		
2	2-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		
2	3-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		
2	4-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		
2	5-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	6-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		
2	7-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		
2	8-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		
2	9-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		
2	10-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		

- Molecule 3 is a protein called Nuclear protein STH1/NPS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1-K	62	Total	C	N	O	S	0	0
			537	329	110	96	2		
3	2-K	62	Total	C	N	O	S	0	0
			537	329	110	96	2		
3	3-K	62	Total	C	N	O	S	0	0
			537	329	110	96	2		
3	4-K	62	Total	C	N	O	S	0	0
			537	329	110	96	2		
3	5-K	62	Total	C	N	O	S	0	0
			537	329	110	96	2		
3	6-K	62	Total	C	N	O	S	0	0
			537	329	110	96	2		
3	7-K	62	Total	C	N	O	S	0	0
			537	329	110	96	2		
3	8-K	62	Total	C	N	O	S	0	0
			537	329	110	96	2		
3	9-K	62	Total	C	N	O	S	0	0
			537	329	110	96	2		
3	10-K	62	Total	C	N	O	S	0	0
			537	329	110	96	2		

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	285	MET	-	initiating methionine	UNP P32597
K	286	GLY	-	expression tag	UNP P32597
K	287	SER	-	expression tag	UNP P32597
K	288	SER	-	expression tag	UNP P32597

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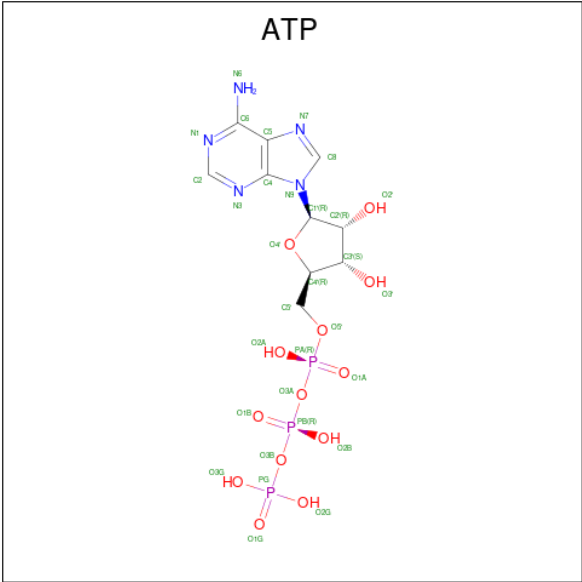
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Chain	Residue	Modelled	Actual	Comment	Reference
K	289	HIS	-	expression tag	UNP P32597
K	290	HIS	-	expression tag	UNP P32597
K	291	HIS	-	expression tag	UNP P32597
K	292	HIS	-	expression tag	UNP P32597
K	293	HIS	-	expression tag	UNP P32597
K	294	HIS	-	expression tag	UNP P32597
K	295	SER	-	expression tag	UNP P32597
K	296	GLN	-	expression tag	UNP P32597
K	297	ASP	-	expression tag	UNP P32597
K	298	PRO	-	expression tag	UNP P32597
K	299	ASN	-	expression tag	UNP P32597
K	300	SER	-	expression tag	UNP P32597
K	372	LYS	ARG	conflict	UNP P32597

- Molecule 4 is a protein called Regulator of Ty1 transposition protein 102.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		
4	2-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		
4	3-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		
4	4-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		
4	5-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		
4	6-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		
4	7-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		
4	8-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		
4	9-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		
4	10-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		

- Molecule 5 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).

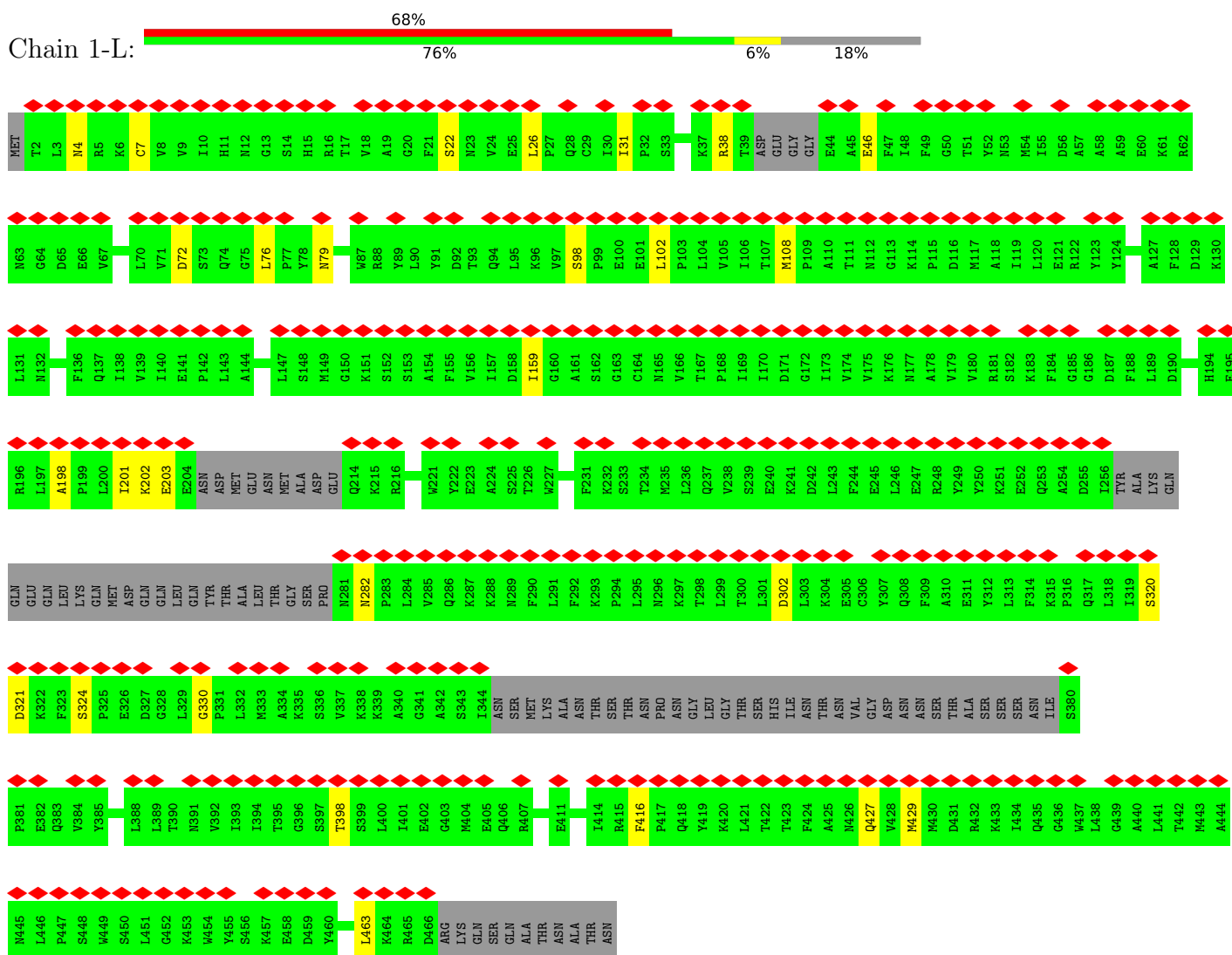


Mol	Chain	Residues	Atoms					AltConf
5	1-L	1	Total	C	N	O	P	0
			31	10	5	13	3	
5	2-L	1	Total	C	N	O	P	0
			31	10	5	13	3	
5	3-L	1	Total	C	N	O	P	0
			31	10	5	13	3	
5	4-L	1	Total	C	N	O	P	0
			31	10	5	13	3	
5	5-L	1	Total	C	N	O	P	0
			31	10	5	13	3	
5	6-L	1	Total	C	N	O	P	0
			31	10	5	13	3	
5	7-L	1	Total	C	N	O	P	0
			31	10	5	13	3	
5	8-L	1	Total	C	N	O	P	0
			31	10	5	13	3	
5	9-L	1	Total	C	N	O	P	0
			31	10	5	13	3	
5	10-L	1	Total	C	N	O	P	0
			31	10	5	13	3	

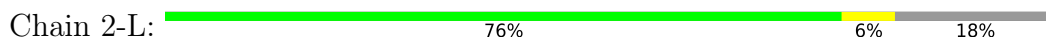
3 Residue-property plots

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: Actin-related protein 7



• Molecule 1: Actin-related protein 7



VAL	LYS	MET
GLY	GLN	T2
ASP	GLU	C7
ASN	GLN	S22
SER	LEU	L26
THR	LYS	I31
ALA	GLN	E44
SER	MET	D72
SER	ASP	L76
SER	THR	N79
ASN	GLN	S98
ILE	LEU	L102
S380	GLN	M108
P381	THR	K114
E382	THR	P115
F416	ALA	F136
W449	LEU	D158
K464	THR	V175
R465	GLY	A198
D466	SER	P199
ARG	PRO	E204
LYS	N281	ASN
GLN	N282	ASP
SER	K293	MET
SER	P294	GLU
GLN	D302	ASN
ALA	S324	ASN
THR	P325	ALA
ALA	E326	ALA
ASN	G330	GLY
	S343	THR
	I344	SER
	ASN	THR
	SER	SER
	MET	THR
	LYS	ASN
	ALA	PRO
	ASN	ASN
	ASN	GLY
	LEU	LEU
	THR	Q214
	SER	K241
	HIS	D242
	ILE	I256
	ASN	TYR
	THR	ALA
	ASN	

Chain 7-L: 74% 8% 18%

THR	THR	K215	MET
SER	SER	T218	T2
ILE	ILE	ASN	N4
ASN	THR	T256	C7
ASN	ASN	ALA	S22
VAL	VAL	GLY	L26
ASP	ASP	GLN	T31
ASN	ASN	GLU	T39
SER	SER	LEU	ASP
THR	THR	GLN	GLU
ALA	ALA	GLY	GLY
SER	SER	MET	E44
SER	SER	GLN	D72
ASN	ASN	LEU	L76
ILE	ILE	GLN	N79
S380	S380	THR	S98
L388	L388	THR	L102
V392	V392	ALA	M108
F416	F416	LEU	N112
T423	T423	THR	R122
Q427	Q427	P80	V133
E458	E458	N281	P134
D466	D466	N282	E141
ARG	ARG	K293	P142
LYS	LYS	P294	F155
GLN	GLN	ALA	D158
SER	SER	G330	A198
SER	SER	I344	P199
THR	THR	ASN	E204
ASN	ASN	ASN	ASP
ASN	ASN	SER	MET
		MET	GLU
		LYS	ASN
		ALA	MET
		THR	ALA
		THR	ASP
		ASN	GLY
		PRO	GLU
		GLY	ASP
		LEU	GLY

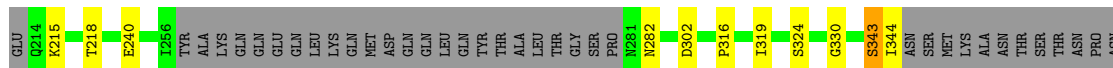
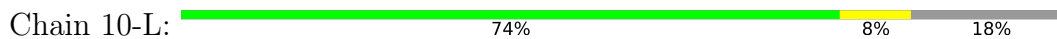
Chain 8-L: 74% 8% 18%

[illegible]

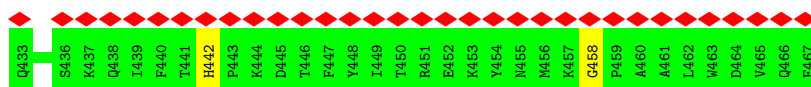
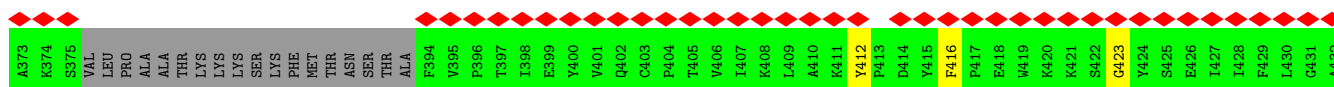
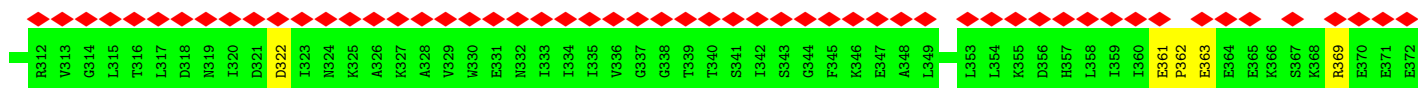
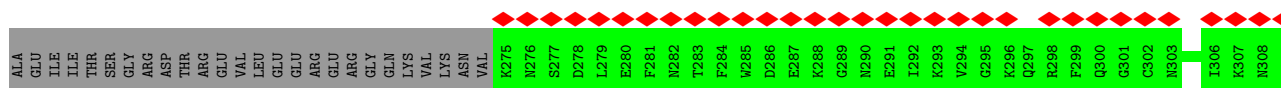
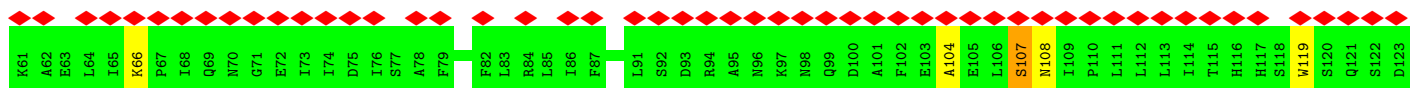
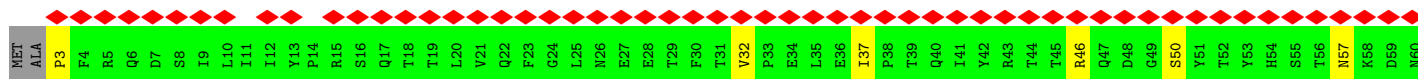
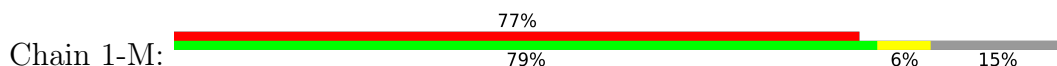
Chain 9-L:

[illegible]

- Molecule 1: Actin-related protein 7

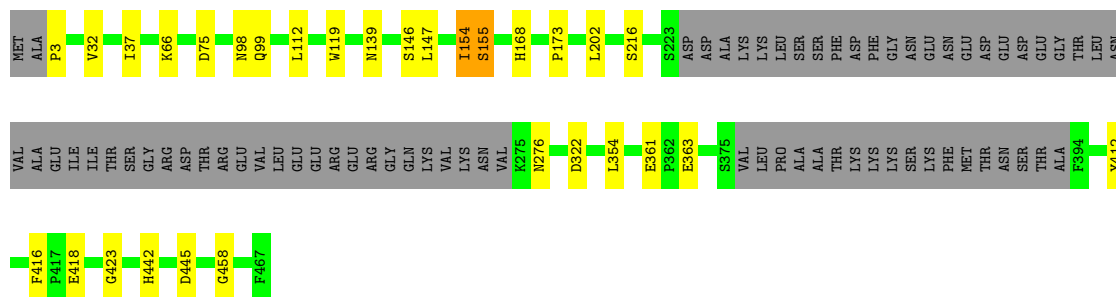


- Molecule 2: Actin-like protein ARP9



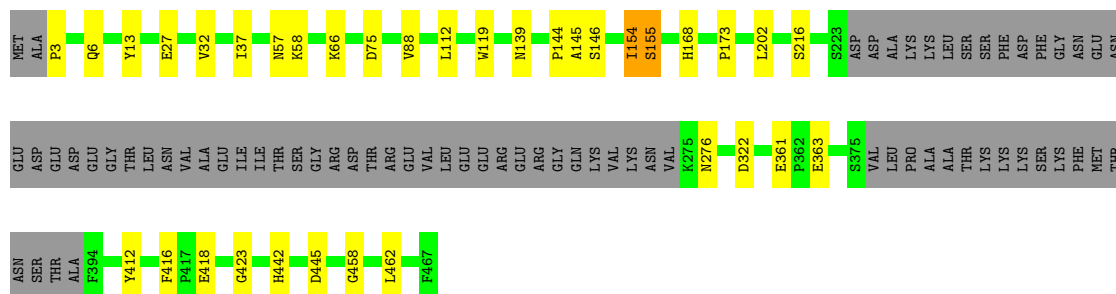
- Molecule 2: Actin-like protein ARP9

Chain 2-M:  78% 6% 15%



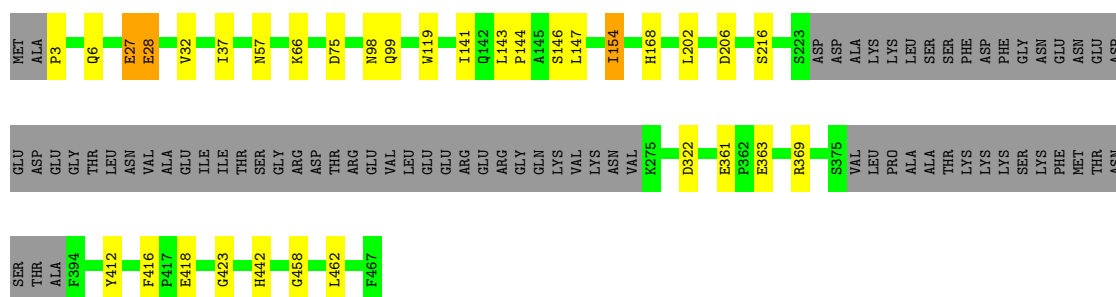
- Molecule 2: Actin-like protein ARP9

Chain 3-M:  77% 7% 15%



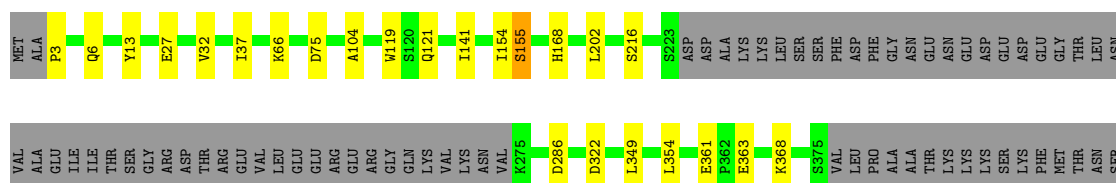
- Molecule 2: Actin-like protein ARP9

Chain 4-M:  78% 6% 15%



- Molecule 2: Actin-like protein ARP9

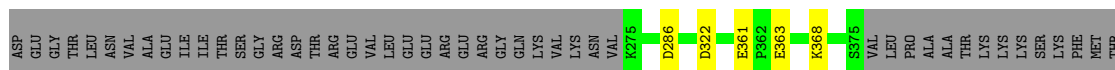
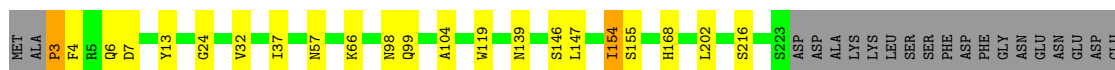
Chain 5-M:  78% 7% 15%





- Molecule 2: Actin-like protein ARP9

Chain 6-M: 77% 7% 15%



- Molecule 2: Actin-like protein ARP9

Chain 7-M: 78% 6% 15%



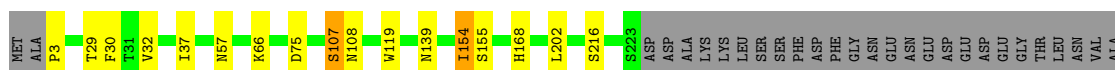
- Molecule 2: Actin-like protein ARP9

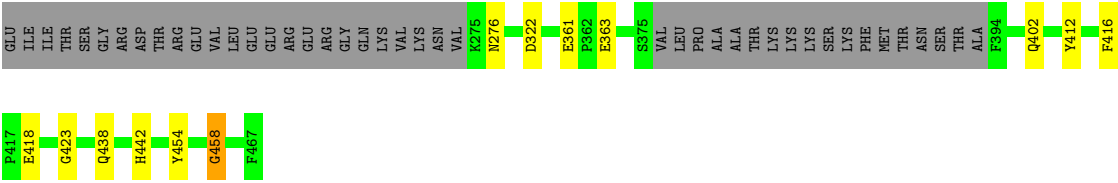
Chain 8-M: 79% 6% 15%



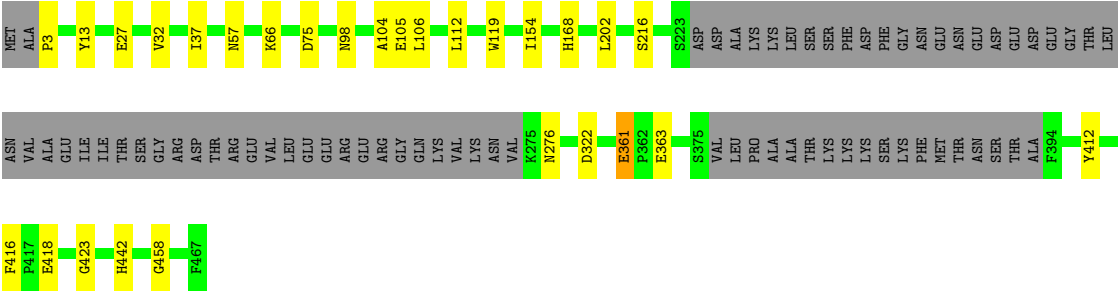
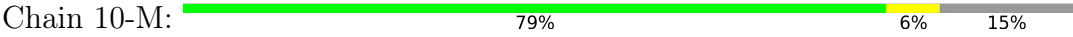
- Molecule 2: Actin-like protein ARP9

Chain 9-M: 78% 6% 15%

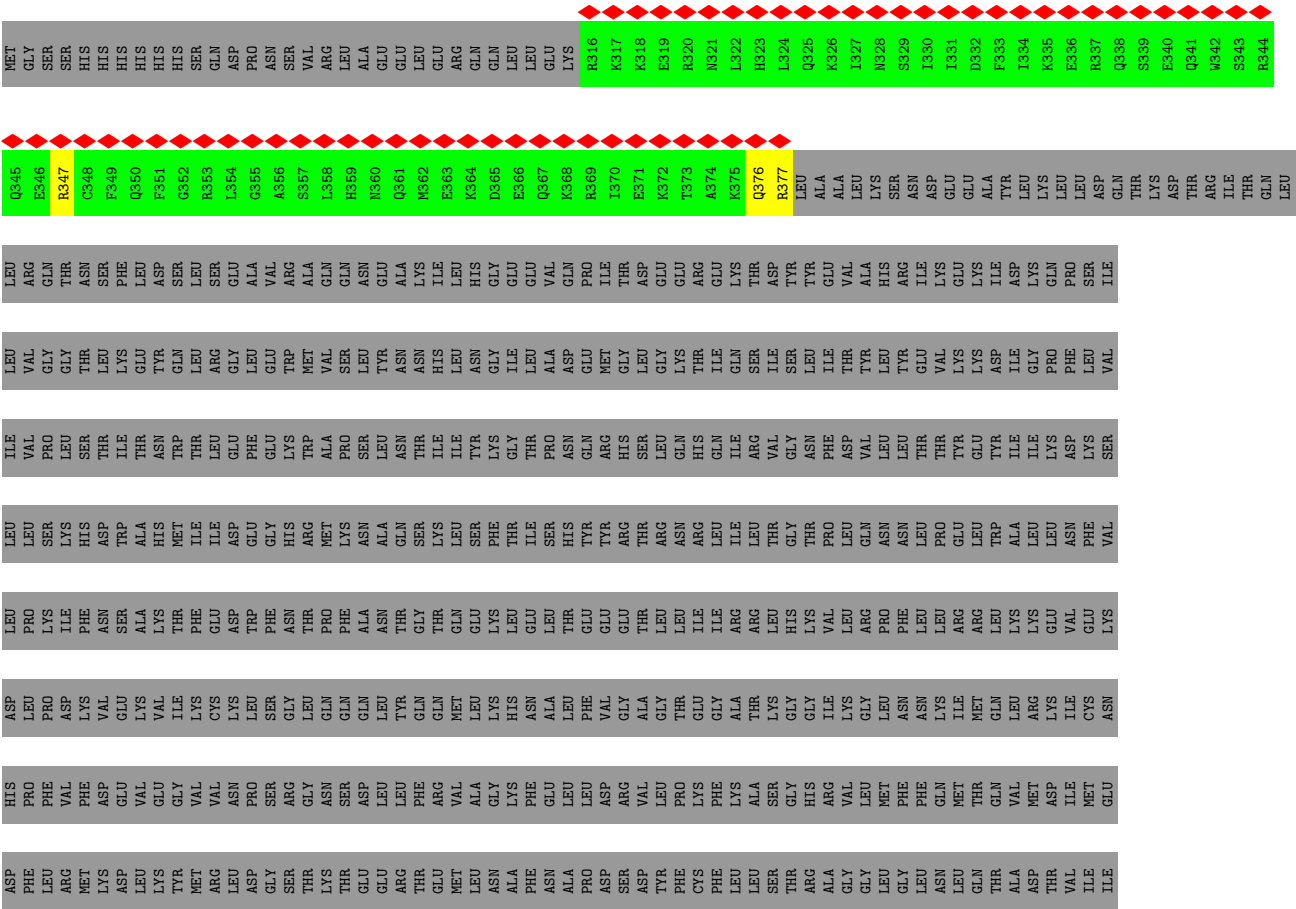




• Molecule 2: Actin-like protein ARP9

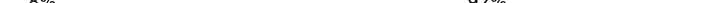


• Molecule 3: Nuclear protein STH1/NPS1



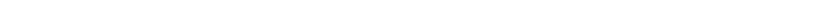
[illegible]

- Molecule 3: Nuclear protein STH1/NPS1

Chain 2-K:  8% 92%

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

- Molecule 3: Nuclear protein STH1/NPS1

Chain 3-K:  8% 92%

[illegible]

- Molecule 3: Nuclear protein STH1/NPS1

Chain 6-K: 7% 92%

[illegible]

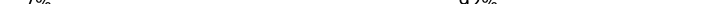
- Molecule 3: Nuclear protein STH1/NPS1

Chain 7-K: 7% 92%

[illegible]

[illegible]

- Molecule 3: Nuclear protein STH1/NPS1

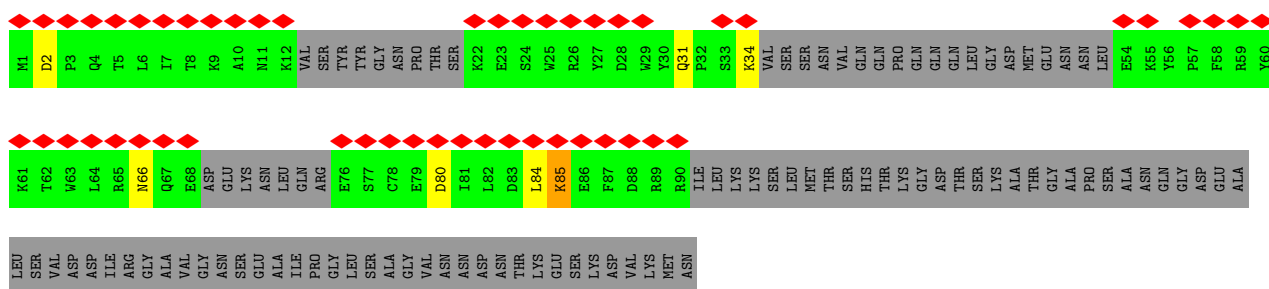
Chain 9-K:  7% 92%

[illegible]

- Molecule 3: Nuclear protein STH1/NPS1

[illegible]

Chain 1-N:

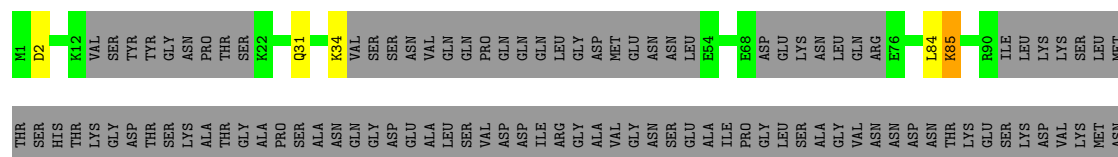


MET ASN	LEU	#1
	THR	D2
	SER	K12
	THR	VAL
	LYS	SER
	GLY	TYR
	ASP	GLY
	THR	ASN
	SER	PRO
	LYS	THR
	ALA	SER
	THR	K22
	GLY	
	ALA	Q31
	PRO	
	SER	K34
	ALA	VAL
	ASN	SER
	GLN	SER
	GLY	ASN
	ASP	VAL
	GLU	GLN
	ALA	GLN
	LEU	PRO
	SER	GLN
	VAL	GLN
	ASP	GLN
	ASP	LEU
	ILE	GLY
	ARG	ASP
	GLY	MET
	ALA	GLU
	VAL	ASN
	GLY	ASN
	ASN	LEU
	SER	E54
	GLU	
	ALA	N66
	ILE	G67
	PRO	E68
	GLY	ASP
	LEU	
	SER	GLU
	LYS	LYS
	ALA	ASN
	GLY	LEU
	VAL	GLN
	ASN	ARG
	ASN	E76
	ASP	
	ASN	L84
	THR	K85
	LYS	
	GLU	R90
	SER	ILE
	LYS	LEU
	ASP	LYS
	VAL	VAL
	LYS	SER

LYS	LEU	#1
ASP	LYS	D2
VAL	LYS	K12
LYS	SER	VAL
MET	MET	SER
ASN	THR	TYR
	SER	GLY
	HIS	ASN
	THR	PRO
	LYS	THR
	GLY	SER
	THR	K22
	SER	
	LYS	Q31
	ALA	K34
	THR	VAL
	GLY	SER
	ALA	SER
	PRO	SER
	SER	ASN
	SER	ASN
	ALA	VAL
	ASN	GLN
	GLN	GLN
	GLY	PRO
	ASP	GLN
	GLU	GLN
	ALA	GLN
	LEU	LEU
	SER	GLY
	VAL	ASP
	ASP	MET
	ASP	GLU
	ILE	ASN
	ARG	ASN
	GLY	LEU
	ALA	F54
	VAL	K55
	GLY	Y56
	ASN	P57
	SER	F58
	GLU	
	ALA	F68
	ILE	ASP
	PRO	GLU
	GLY	LYS
	LEU	ASN
	LEU	LEU
	ALA	GLN
	GLY	ARG
	VAL	E76
	ASN	
	ASP	D80
	ASN	L84
	THR	K85
	LYS	
	GLU	R90
	SER	ILE

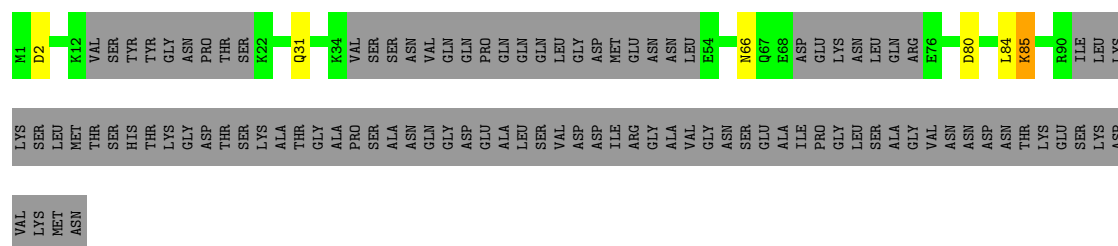
[illegible][illegible]

Chain 6-N: 32% .. 65%



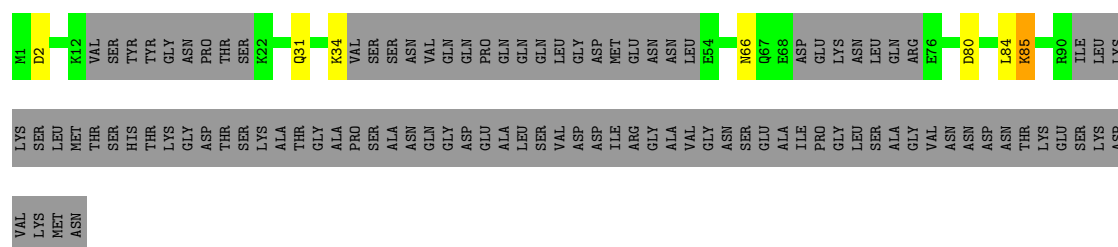
• Molecule 4: Regulator of Ty1 transposition protein 102

Chain 7-N: 31% 65%



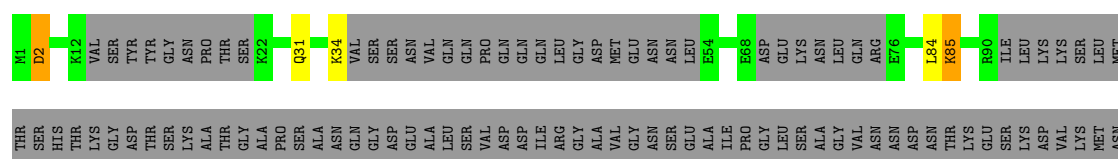
• Molecule 4: Regulator of Ty1 transposition protein 102

Chain 8-N: 31% 65%



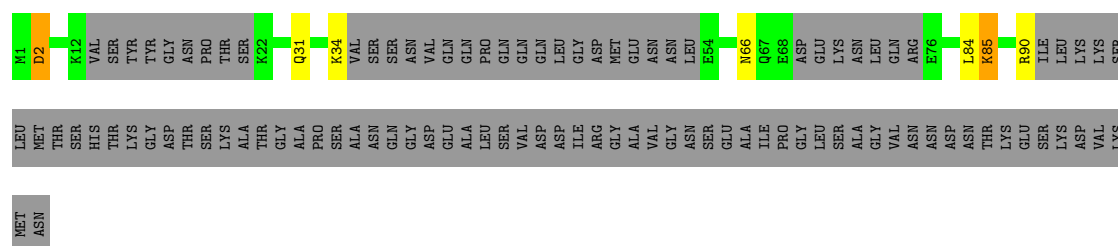
• Molecule 4: Regulator of Ty1 transposition protein 102

Chain 9-N: 32% 65%



• Molecule 4: Regulator of Ty1 transposition protein 102

Chain 10-N: 31% 65%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	415957	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	53	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	36000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.043	Depositor
Minimum map value	-0.014	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.025	Depositor
Map size ($\text{\AA}$)	278.4, 278.4, 278.4	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.16, 1.16, 1.16	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ATP

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	1-L	0.71	0/3220	0.75	22/4355 (0.5%)
1	2-L	0.71	0/3220	0.75	22/4355 (0.5%)
1	3-L	0.71	0/3220	0.75	22/4355 (0.5%)
1	4-L	0.71	0/3220	0.75	22/4355 (0.5%)
1	5-L	0.71	0/3220	0.75	22/4355 (0.5%)
1	6-L	0.71	0/3220	0.75	22/4355 (0.5%)
1	7-L	0.71	0/3220	0.75	22/4355 (0.5%)
1	8-L	0.71	0/3220	0.75	22/4355 (0.5%)
1	9-L	0.71	0/3220	0.75	22/4355 (0.5%)
1	10-L	0.71	0/3220	0.75	22/4355 (0.5%)
2	1-M	0.68	0/3259	0.72	22/4417 (0.5%)
2	2-M	0.68	0/3259	0.72	22/4417 (0.5%)
2	3-M	0.68	0/3259	0.72	22/4417 (0.5%)
2	4-M	0.68	0/3259	0.72	22/4417 (0.5%)
2	5-M	0.68	0/3259	0.72	22/4417 (0.5%)
2	6-M	0.68	0/3259	0.72	22/4417 (0.5%)
2	7-M	0.68	0/3259	0.72	22/4417 (0.5%)
2	8-M	0.68	0/3259	0.72	22/4417 (0.5%)
2	9-M	0.68	0/3259	0.72	22/4417 (0.5%)
2	10-M	0.68	0/3259	0.72	22/4417 (0.5%)
3	1-K	0.64	0/543	0.38	0/716
3	2-K	0.64	0/543	0.38	0/716
3	3-K	0.64	0/543	0.38	0/716
3	4-K	0.64	0/543	0.38	0/716
3	5-K	0.64	0/543	0.38	0/716
3	6-K	0.64	0/543	0.38	0/716
3	7-K	0.64	0/543	0.38	0/716
3	8-K	0.64	0/543	0.38	0/716
3	9-K	0.64	0/543	0.38	0/716
3	10-K	0.64	0/543	0.38	0/716
4	1-N	0.64	0/505	0.77	4/674 (0.6%)
4	2-N	0.64	0/505	0.77	4/674 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	3-N	0.64	0/505	0.77	4/674 (0.6%)
4	4-N	0.64	0/505	0.77	4/674 (0.6%)
4	5-N	0.64	0/505	0.77	4/674 (0.6%)
4	6-N	0.64	0/505	0.77	4/674 (0.6%)
4	7-N	0.64	0/505	0.77	4/674 (0.6%)
4	8-N	0.64	0/505	0.77	4/674 (0.6%)
4	9-N	0.64	0/505	0.77	4/674 (0.6%)
4	10-N	0.64	0/505	0.77	4/674 (0.6%)
All	All	0.69	0/75270	0.72	480/101620 (0.5%)

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	2-L	0	1
1	3-L	0	2
1	6-L	0	2
1	8-L	0	2
1	10-L	0	2
2	1-M	0	2
2	2-M	0	2
2	3-M	0	2
2	4-M	0	2
2	5-M	0	4
2	6-M	0	2
2	7-M	0	4
2	9-M	0	2
2	10-M	0	2
All	All	0	31

There are no bond length outliers.

The worst 5 of 480 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1-L	416	PHE	CA-C-N	8.25	127.89	119.56
1	1-L	416	PHE	C-N-CA	8.25	127.89	119.56
1	2-L	416	PHE	CA-C-N	8.25	127.89	119.56
1	2-L	416	PHE	C-N-CA	8.25	127.89	119.56
1	3-L	416	PHE	CA-C-N	8.25	127.89	119.56

There are no chirality outliers.

5 of 31 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1-M	3	PRO	Mainchain,Peptide
1	2-L	49	PHE	Mainchain
2	2-M	3	PRO	Mainchain,Peptide
1	3-L	343	SER	Mainchain,Peptide
2	3-M	3	PRO	Mainchain

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	1-L	3154	0	3173	12	0
1	2-L	3154	0	3173	12	0
1	3-L	3154	0	3173	25	0
1	4-L	3154	0	3173	18	0
1	5-L	3154	0	3173	22	0
1	6-L	3154	0	3173	17	0
1	7-L	3154	0	3173	22	0
1	8-L	3154	0	3173	25	0
1	9-L	3154	0	3173	20	0
1	10-L	3154	0	3173	20	0
2	1-M	3192	0	3180	10	0
2	2-M	3192	0	3180	14	0
2	3-M	3192	0	3180	17	0
2	4-M	3192	0	3180	18	0
2	5-M	3192	0	3180	17	0
2	6-M	3192	0	3180	17	0
2	7-M	3192	0	3180	18	0
2	8-M	3192	0	3180	13	0
2	9-M	3192	0	3180	16	0
2	10-M	3192	0	3180	18	0
3	1-K	537	0	546	2	0
3	2-K	537	0	546	0	0
3	3-K	537	0	546	1	0
3	4-K	537	0	546	1	0
3	5-K	537	0	546	4	0
3	6-K	537	0	546	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	7-K	537	0	546	2	0
3	8-K	537	0	546	1	0
3	9-K	537	0	546	2	0
3	10-K	537	0	546	5	0
4	1-N	494	0	473	6	0
4	2-N	494	0	473	6	0
4	3-N	494	0	473	4	0
4	4-N	494	0	473	6	0
4	5-N	494	0	473	6	0
4	6-N	494	0	473	4	0
4	7-N	494	0	473	4	0
4	8-N	494	0	473	7	0
4	9-N	494	0	473	5	0
4	10-N	494	0	473	8	0
5	1-L	31	0	12	1	0
5	2-L	31	0	12	2	0
5	3-L	31	0	12	1	0
5	4-L	31	0	12	0	0
5	5-L	31	0	12	2	0
5	6-L	31	0	12	1	0
5	7-L	31	0	12	1	0
5	8-L	31	0	12	1	0
5	9-L	31	0	12	1	0
5	10-L	31	0	12	2	0
All	All	74080	0	73840	432	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 3.

The worst 5 of 432 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)
2:M:154:ILE:HG22	2:M:154:ILE:O	1.74	0.86
2:M:154:ILE:HG22	2:M:154:ILE:O	1.76	0.84
1:L:256:ILE:O	1:L:256:ILE:HG23	1.77	0.83
1:L:465:ARG:O	1:L:465:ARG:NH1	2.15	0.76
3:K:346:GLU:N	3:K:346:GLU:OE1	2.19	0.75

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	1-L	383/477 (80%)	370 (97%)	12 (3%)	1 (0%)	36	71
1	2-L	383/477 (80%)	368 (96%)	10 (3%)	5 (1%)	9	41
1	3-L	383/477 (80%)	366 (96%)	15 (4%)	2 (0%)	24	62
1	4-L	383/477 (80%)	366 (96%)	13 (3%)	4 (1%)	12	47
1	5-L	383/477 (80%)	368 (96%)	12 (3%)	3 (1%)	16	52
1	6-L	383/477 (80%)	362 (94%)	17 (4%)	4 (1%)	12	47
1	7-L	383/477 (80%)	371 (97%)	11 (3%)	1 (0%)	36	71
1	8-L	383/477 (80%)	367 (96%)	12 (3%)	4 (1%)	12	47
1	9-L	383/477 (80%)	369 (96%)	12 (3%)	2 (0%)	24	62
1	10-L	383/477 (80%)	369 (96%)	13 (3%)	1 (0%)	36	71
2	1-M	390/467 (84%)	371 (95%)	13 (3%)	6 (2%)	8	38
2	2-M	390/467 (84%)	373 (96%)	14 (4%)	3 (1%)	16	52
2	3-M	390/467 (84%)	374 (96%)	10 (3%)	6 (2%)	8	38
2	4-M	390/467 (84%)	367 (94%)	20 (5%)	3 (1%)	16	52
2	5-M	390/467 (84%)	373 (96%)	14 (4%)	3 (1%)	16	52
2	6-M	390/467 (84%)	369 (95%)	18 (5%)	3 (1%)	16	52
2	7-M	390/467 (84%)	368 (94%)	20 (5%)	2 (0%)	24	62
2	8-M	390/467 (84%)	369 (95%)	15 (4%)	6 (2%)	8	38
2	9-M	390/467 (84%)	365 (94%)	21 (5%)	4 (1%)	12	47
2	10-M	390/467 (84%)	370 (95%)	18 (5%)	2 (0%)	24	62
3	1-K	60/813 (7%)	59 (98%)	1 (2%)	0	100	100
3	2-K	60/813 (7%)	59 (98%)	0	1 (2%)	7	35
3	3-K	60/813 (7%)	59 (98%)	1 (2%)	0	100	100
3	4-K	60/813 (7%)	57 (95%)	2 (3%)	1 (2%)	7	35
3	5-K	60/813 (7%)	57 (95%)	0	3 (5%)	1	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	6-K	60/813 (7%)	60 (100%)	0	0	100	100
3	7-K	60/813 (7%)	59 (98%)	1 (2%)	0	100	100
3	8-K	60/813 (7%)	59 (98%)	0	1 (2%)	7	35
3	9-K	60/813 (7%)	60 (100%)	0	0	100	100
3	10-K	60/813 (7%)	57 (95%)	1 (2%)	2 (3%)	3	21
4	1-N	47/157 (30%)	44 (94%)	2 (4%)	1 (2%)	5	30
4	2-N	47/157 (30%)	45 (96%)	1 (2%)	1 (2%)	5	30
4	3-N	47/157 (30%)	44 (94%)	1 (2%)	2 (4%)	2	18
4	4-N	47/157 (30%)	43 (92%)	3 (6%)	1 (2%)	5	30
4	5-N	47/157 (30%)	43 (92%)	3 (6%)	1 (2%)	5	30
4	6-N	47/157 (30%)	44 (94%)	2 (4%)	1 (2%)	5	30
4	7-N	47/157 (30%)	44 (94%)	2 (4%)	1 (2%)	5	30
4	8-N	47/157 (30%)	45 (96%)	1 (2%)	1 (2%)	5	30
4	9-N	47/157 (30%)	44 (94%)	2 (4%)	1 (2%)	5	30
4	10-N	47/157 (30%)	45 (96%)	1 (2%)	1 (2%)	5	30
All	All	8800/19140 (46%)	8402 (96%)	314 (4%)	84 (1%)	15	47

5 of 84 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-L	202	LYS
2	1-M	155	SER
2	1-M	363	GLU
1	2-L	51	THR
2	3-M	58	LYS

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	1-L	349/420 (83%)	349 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	2-L	349/420 (83%)	349 (100%)	0	100	100
1	3-L	349/420 (83%)	349 (100%)	0	100	100
1	4-L	349/420 (83%)	349 (100%)	0	100	100
1	5-L	349/420 (83%)	349 (100%)	0	100	100
1	6-L	349/420 (83%)	349 (100%)	0	100	100
1	7-L	349/420 (83%)	349 (100%)	0	100	100
1	8-L	349/420 (83%)	349 (100%)	0	100	100
1	9-L	349/420 (83%)	349 (100%)	0	100	100
1	10-L	349/420 (83%)	349 (100%)	0	100	100
2	1-M	362/423 (86%)	362 (100%)	0	100	100
2	2-M	362/423 (86%)	362 (100%)	0	100	100
2	3-M	362/423 (86%)	362 (100%)	0	100	100
2	4-M	362/423 (86%)	362 (100%)	0	100	100
2	5-M	362/423 (86%)	362 (100%)	0	100	100
2	6-M	362/423 (86%)	362 (100%)	0	100	100
2	7-M	362/423 (86%)	362 (100%)	0	100	100
2	8-M	362/423 (86%)	362 (100%)	0	100	100
2	9-M	362/423 (86%)	362 (100%)	0	100	100
2	10-M	362/423 (86%)	362 (100%)	0	100	100
3	1-K	58/735 (8%)	58 (100%)	0	100	100
3	2-K	58/735 (8%)	58 (100%)	0	100	100
3	3-K	58/735 (8%)	58 (100%)	0	100	100
3	4-K	58/735 (8%)	58 (100%)	0	100	100
3	5-K	58/735 (8%)	58 (100%)	0	100	100
3	6-K	58/735 (8%)	58 (100%)	0	100	100
3	7-K	58/735 (8%)	58 (100%)	0	100	100
3	8-K	58/735 (8%)	58 (100%)	0	100	100
3	9-K	58/735 (8%)	58 (100%)	0	100	100
3	10-K	58/735 (8%)	58 (100%)	0	100	100
4	1-N	54/140 (39%)	54 (100%)	0	100	100
4	2-N	54/140 (39%)	54 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	3-N	54/140 (39%)	54 (100%)	0	100	100
4	4-N	54/140 (39%)	54 (100%)	0	100	100
4	5-N	54/140 (39%)	54 (100%)	0	100	100
4	6-N	54/140 (39%)	54 (100%)	0	100	100
4	7-N	54/140 (39%)	54 (100%)	0	100	100
4	8-N	54/140 (39%)	54 (100%)	0	100	100
4	9-N	54/140 (39%)	54 (100%)	0	100	100
4	10-N	54/140 (39%)	54 (100%)	0	100	100
All	All	8230/17180 (48%)	8230 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
1	6-L	391	ASN
1	8-L	391	ASN
2	6-M	17	GLN
1	7-L	214	GLN
3	8-K	323	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

10 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	ATP	5-L	501	-	32,33,33	1.45	6 (18%)	48,52,52	1.83	11 (22%)
5	ATP	7-L	501	-	32,33,33	1.51	8 (25%)	48,52,52	1.85	11 (22%)
5	ATP	3-L	501	-	32,33,33	1.48	6 (18%)	48,52,52	1.86	11 (22%)
5	ATP	9-L	501	-	32,33,33	1.49	7 (21%)	48,52,52	1.86	11 (22%)
5	ATP	2-L	501	-	32,33,33	1.46	7 (21%)	48,52,52	1.80	9 (18%)
5	ATP	4-L	501	-	32,33,33	1.45	6 (18%)	48,52,52	1.83	9 (18%)
5	ATP	8-L	501	-	32,33,33	1.42	6 (18%)	48,52,52	1.84	11 (22%)
5	ATP	1-L	501	-	32,33,33	1.49	8 (25%)	48,52,52	1.85	10 (20%)
5	ATP	6-L	501	-	32,33,33	1.47	7 (21%)	48,52,52	1.87	11 (22%)
5	ATP	10-L	501	-	32,33,33	1.48	7 (21%)	48,52,52	1.82	10 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	ATP	5-L	501	-	-	6/22/38/38	0/3/3/3
5	ATP	7-L	501	-	-	7/22/38/38	0/3/3/3
5	ATP	3-L	501	-	-	6/22/38/38	0/3/3/3
5	ATP	9-L	501	-	-	7/22/38/38	0/3/3/3
5	ATP	2-L	501	-	-	7/22/38/38	0/3/3/3
5	ATP	4-L	501	-	-	6/22/38/38	0/3/3/3
5	ATP	8-L	501	-	-	4/22/38/38	0/3/3/3
5	ATP	1-L	501	-	-	2/22/38/38	0/3/3/3
5	ATP	6-L	501	-	-	4/22/38/38	0/3/3/3
5	ATP	10-L	501	-	-	6/22/38/38	0/3/3/3

The worst 5 of 68 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	7-L	501	ATP	C5-C4	4.01	1.46	1.39
5	5-L	501	ATP	C5-C4	4.00	1.46	1.39
5	3-L	501	ATP	C5-C4	3.98	1.46	1.39
5	1-L	501	ATP	C5-C4	3.98	1.46	1.39
5	6-L	501	ATP	C5-C4	3.97	1.46	1.39

The worst 5 of 104 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	6-L	501	ATP	C5-C4-N3	-6.54	117.72	126.72
5	4-L	501	ATP	C5-C4-N3	-6.40	117.90	126.72
5	3-L	501	ATP	C5-C4-N3	-6.36	117.96	126.72
5	5-L	501	ATP	C5-C4-N3	-6.32	118.02	126.72
5	9-L	501	ATP	C5-C4-N3	-6.31	118.03	126.72

There are no chirality outliers.

5 of 55 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	3-L	501	ATP	PB-O3B-PG-O3G
5	4-L	501	ATP	PB-O3B-PG-O3G
5	6-L	501	ATP	O4'-C4'-C5'-O5'
5	6-L	501	ATP	C3'-C4'-C5'-O5'
5	7-L	501	ATP	C5'-O5'-PA-O1A

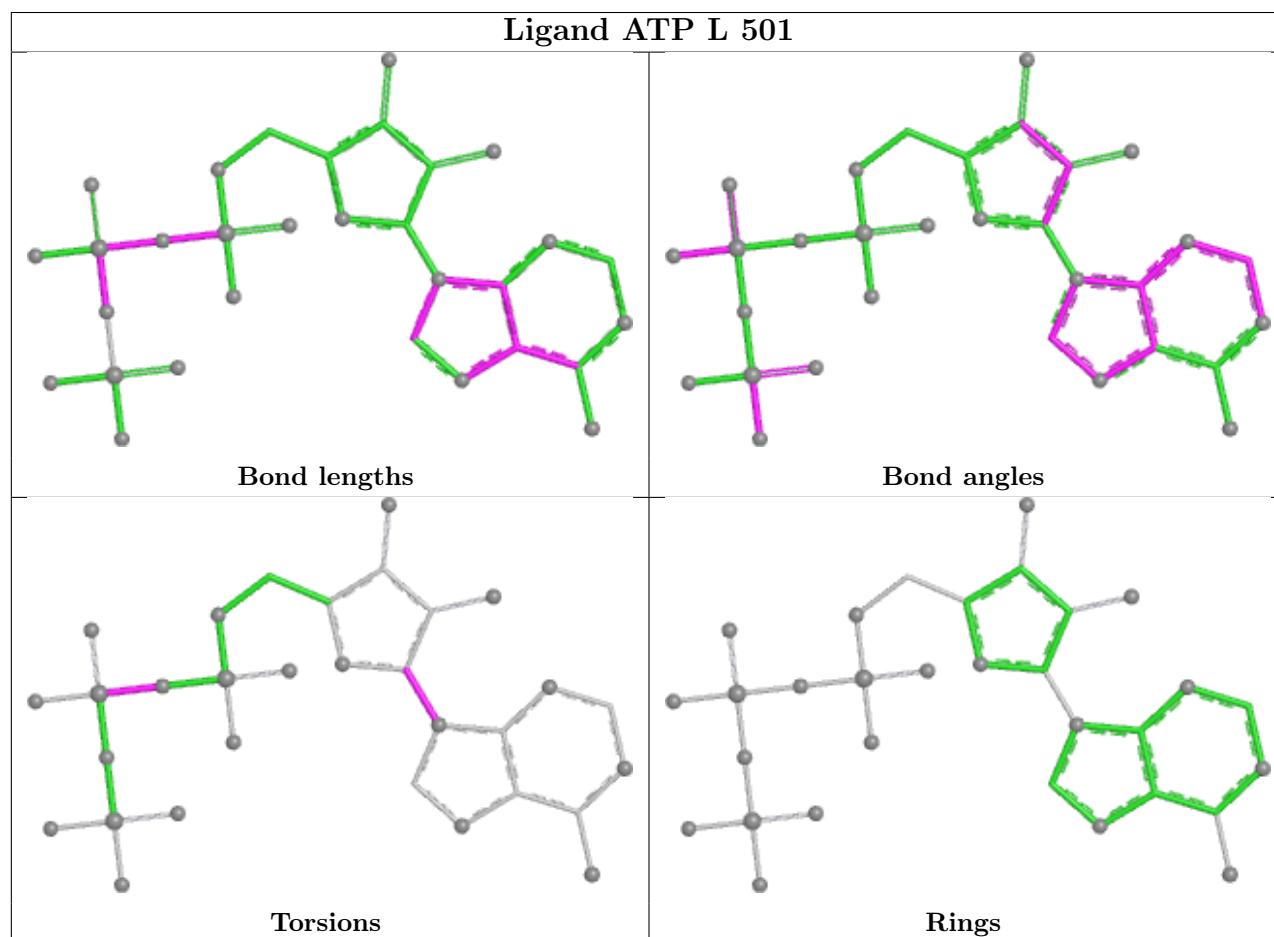
There are no ring outliers.

9 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	5-L	501	ATP	2	0
5	7-L	501	ATP	1	0
5	3-L	501	ATP	1	0
5	9-L	501	ATP	1	0
5	2-L	501	ATP	2	0
5	8-L	501	ATP	1	0
5	1-L	501	ATP	1	0
5	6-L	501	ATP	1	0
5	10-L	501	ATP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

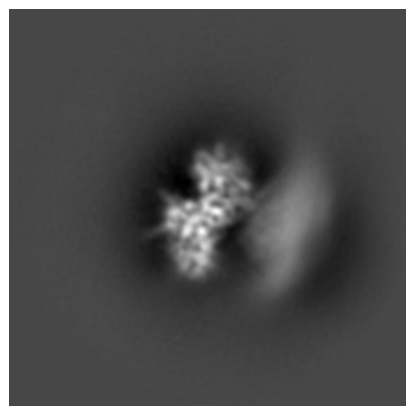
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21489. These allow visual inspection of the internal detail of the map and identification of artifacts.

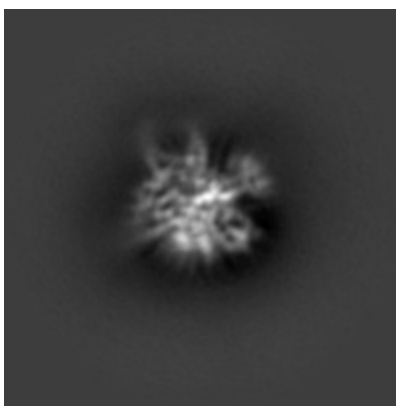
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

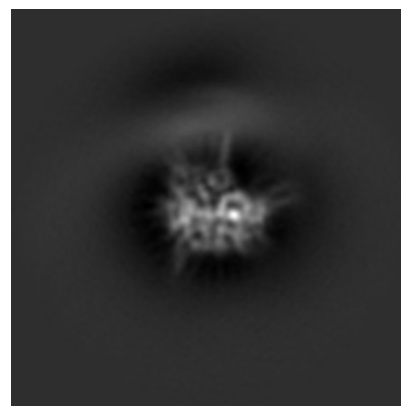
6.1.1 Primary map



X

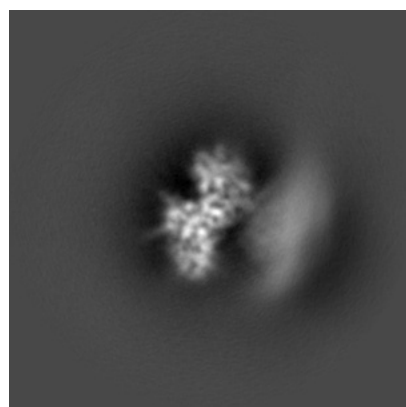


Y

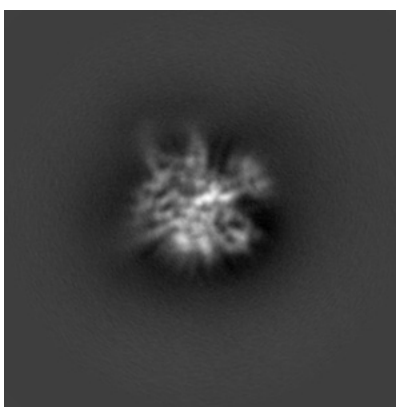


Z

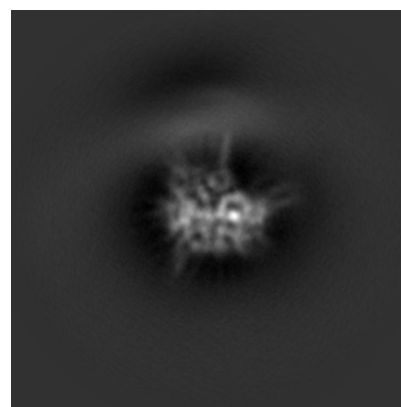
6.1.2 Raw map



X



Y

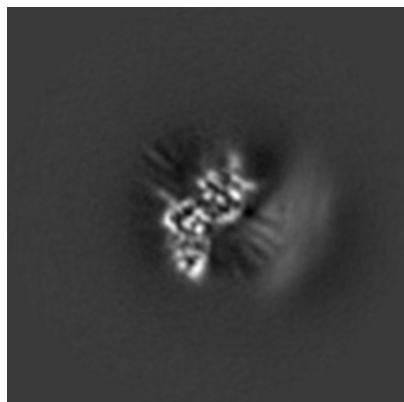


Z

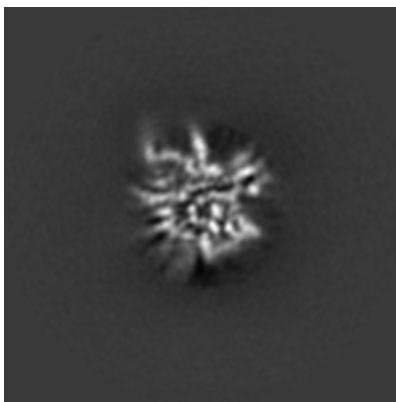
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

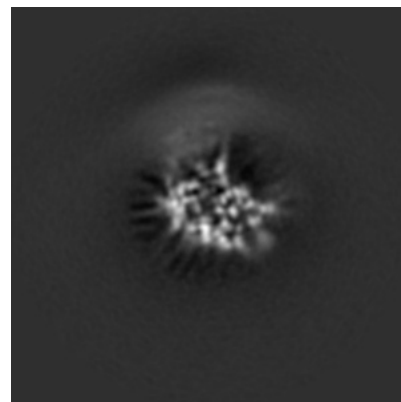
6.2.1 Primary map



X Index: 120

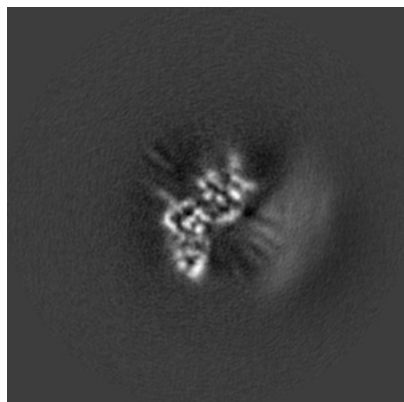


Y Index: 120

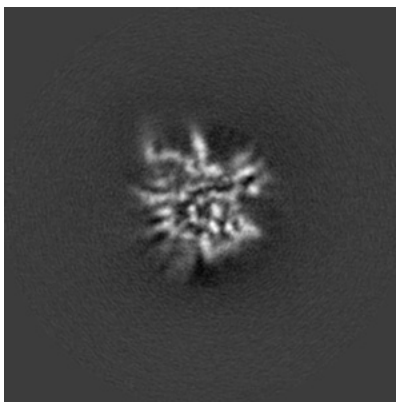


Z Index: 120

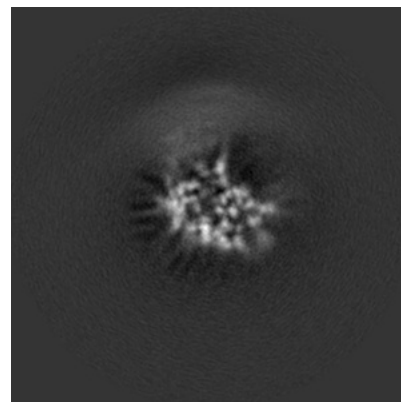
6.2.2 Raw map



X Index: 120



Y Index: 120

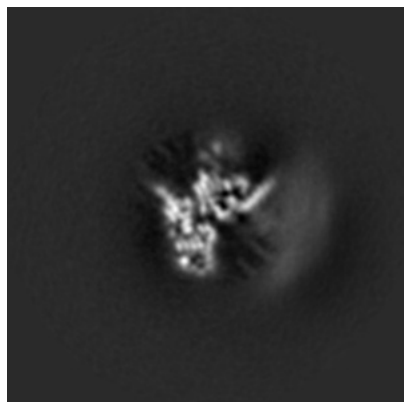


Z Index: 120

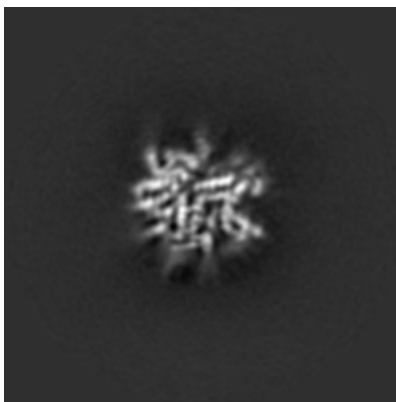
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

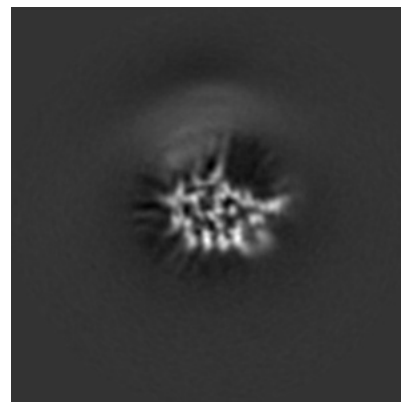
6.3.1 Primary map



X Index: 126

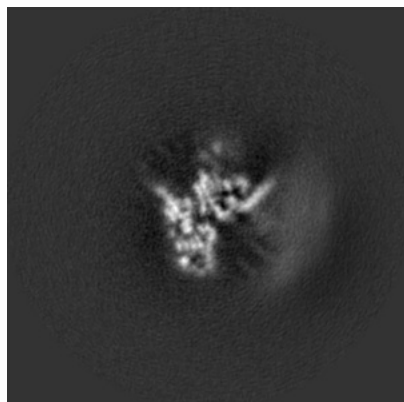


Y Index: 116

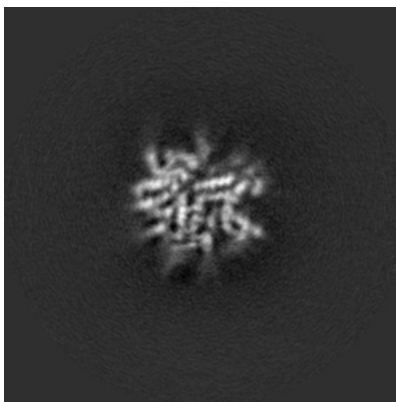


Z Index: 117

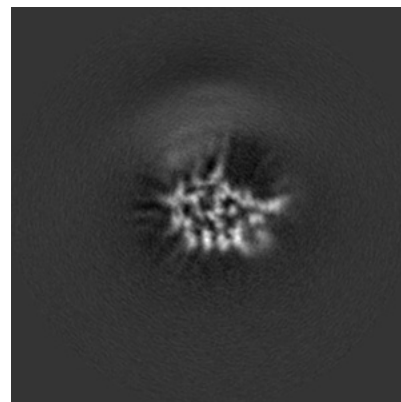
6.3.2 Raw map



X Index: 126



Y Index: 116

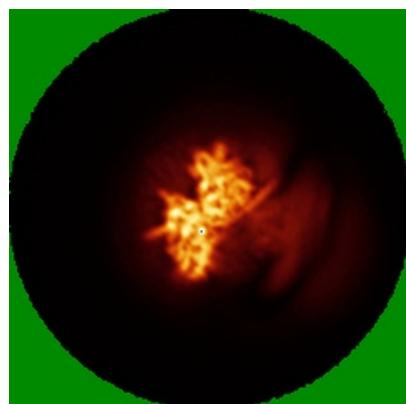


Z Index: 117

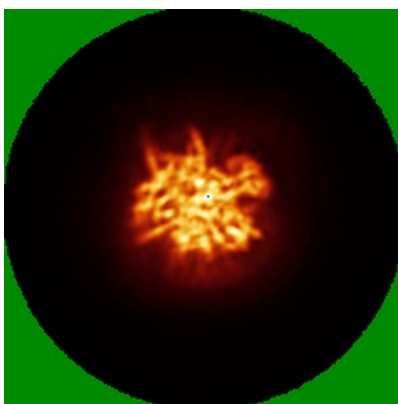
The images above show the largest variance slices of the map in three orthogonal directions.

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

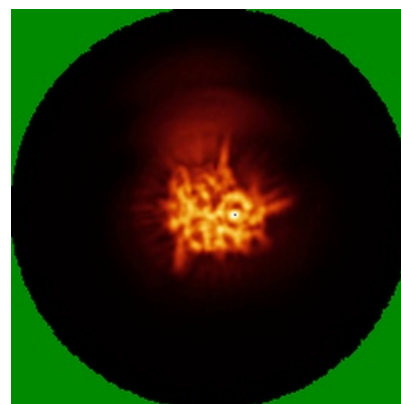
6.4.1 Primary map



X

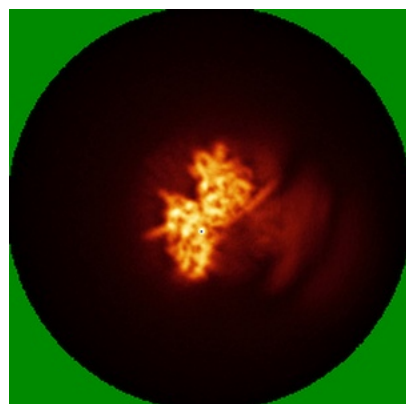


Y

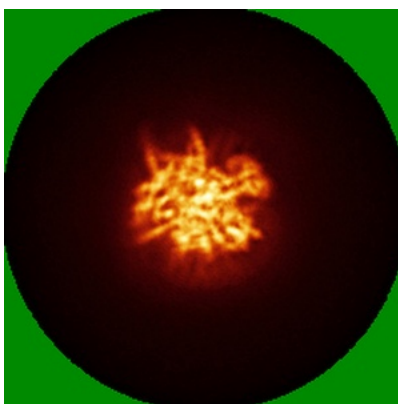


Z

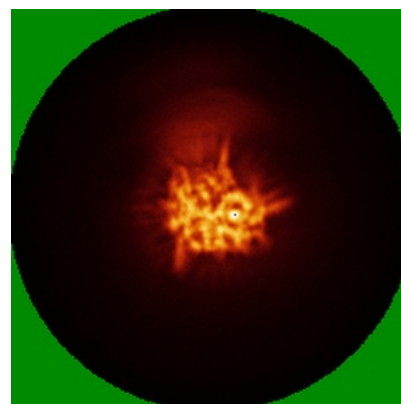
6.4.2 Raw map



X



Y



Z

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

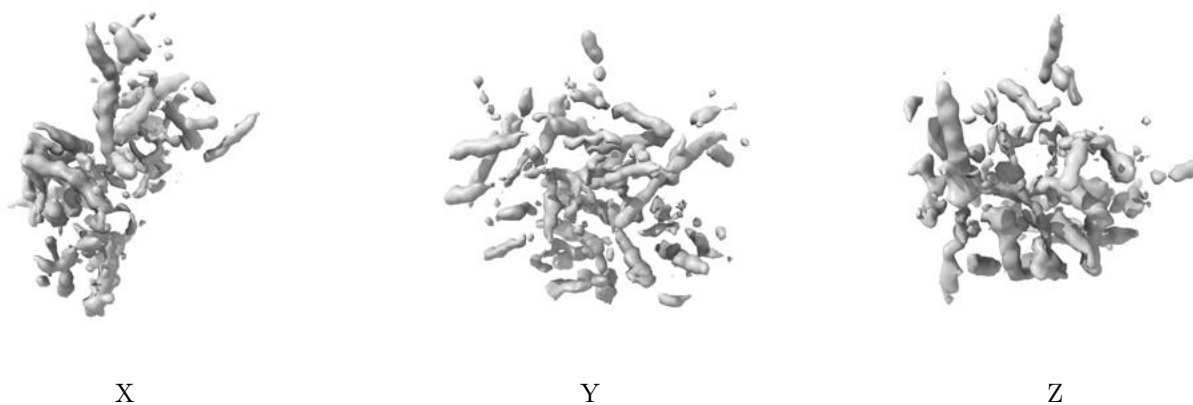
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

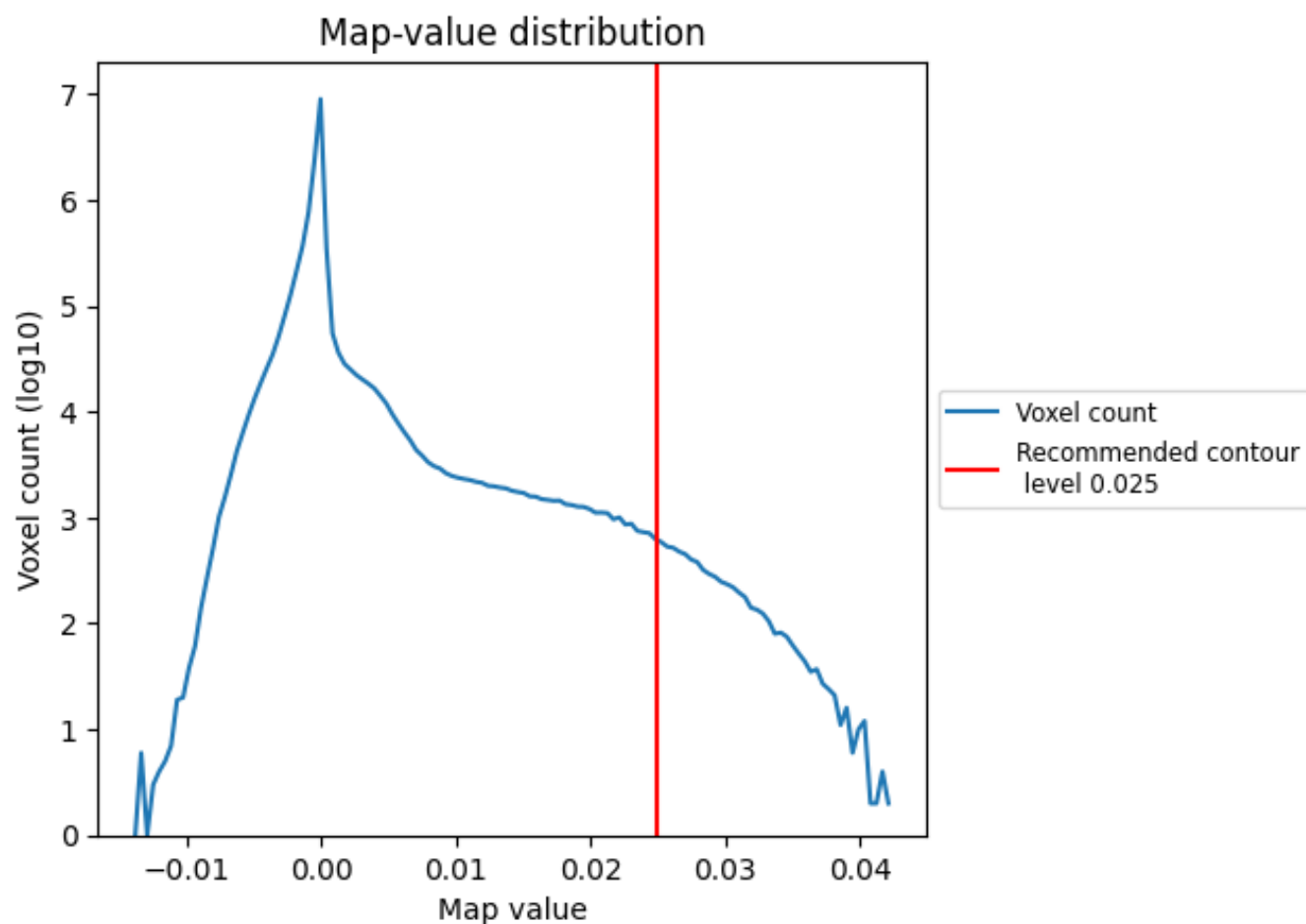
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

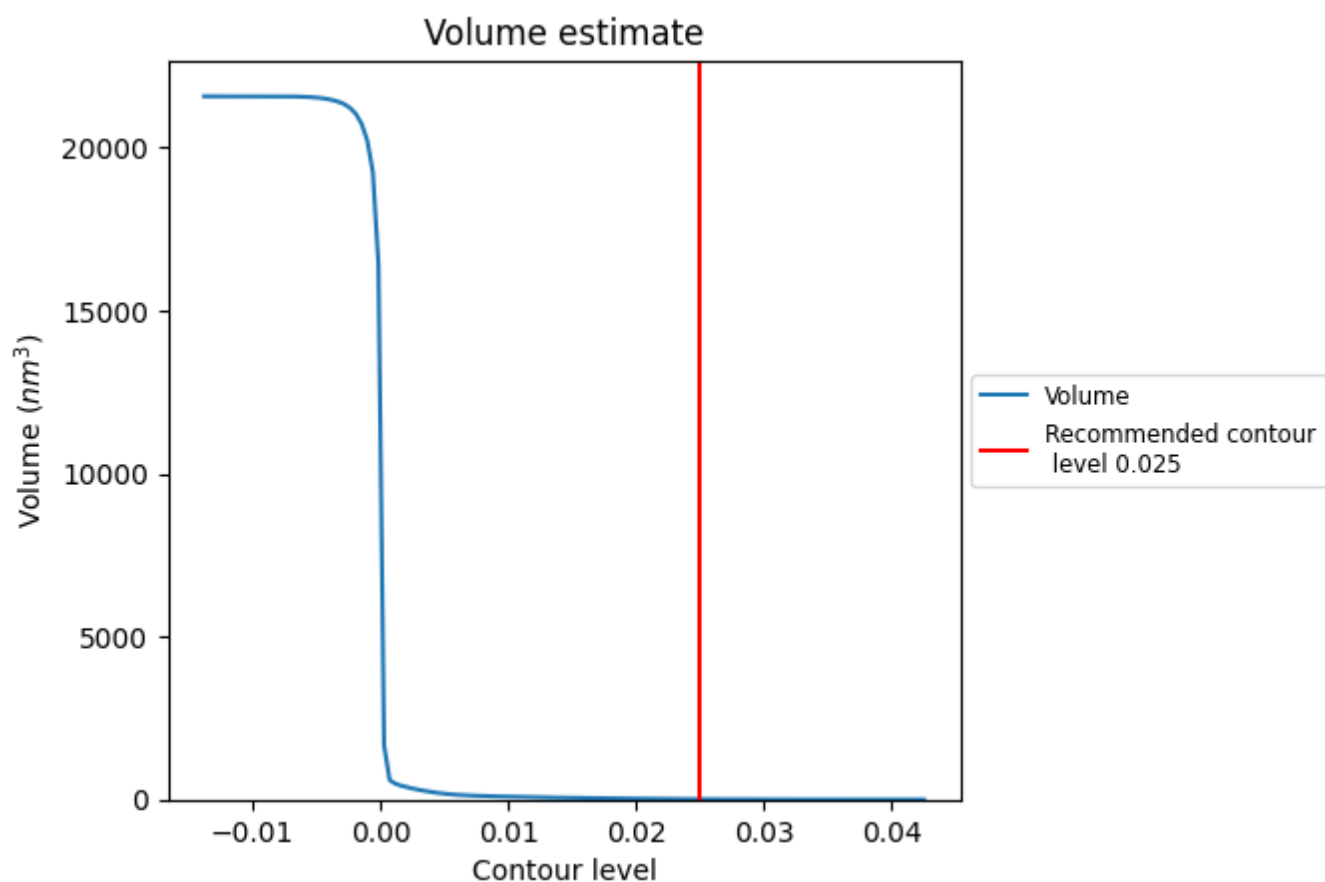
This section contains the results of statistical analysis of the map.

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.

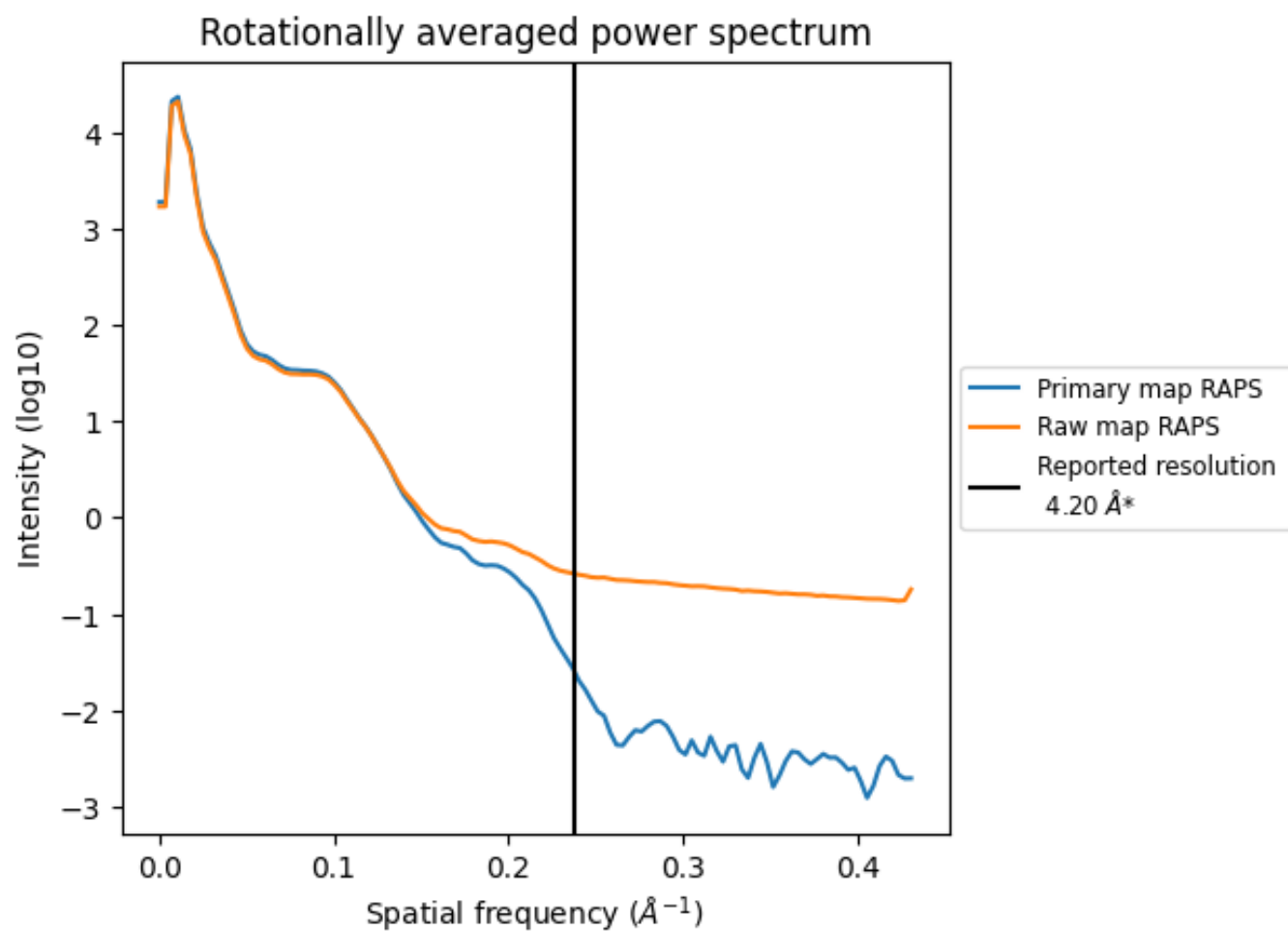
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 11 nm³; this corresponds to an approximate mass of 10 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](#)

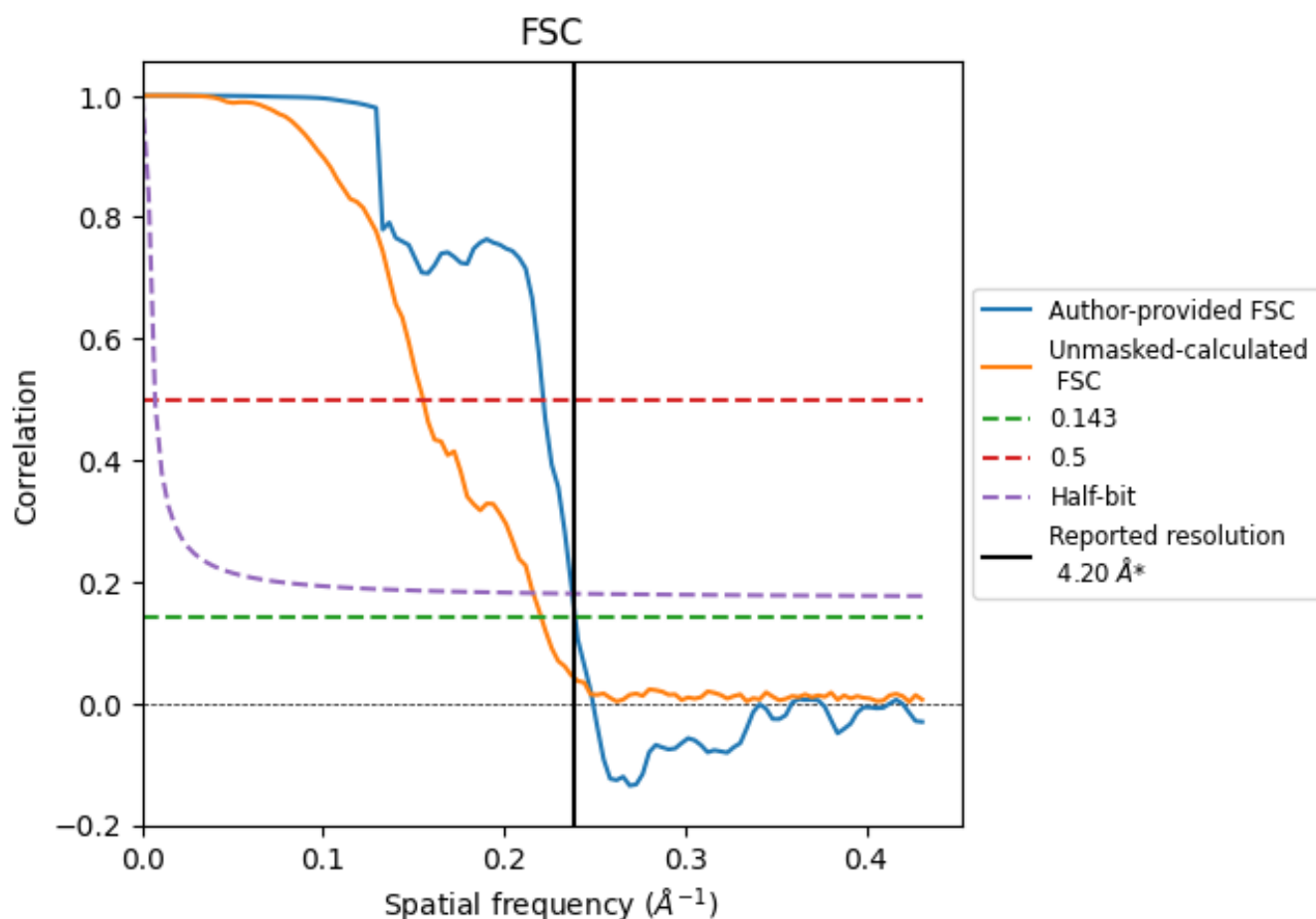


*Reported resolution corresponds to spatial frequency of 0.238 Å⁻¹

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 $0.238 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

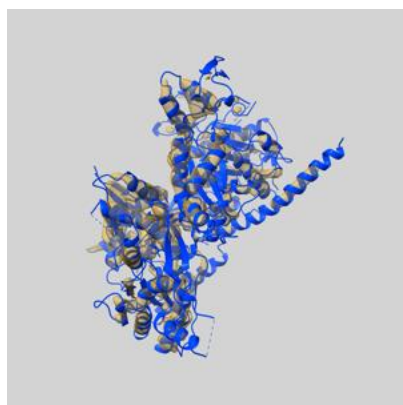
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	4.18	4.51	4.21
Unmasked-calculated*	4.54	6.45	4.63

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

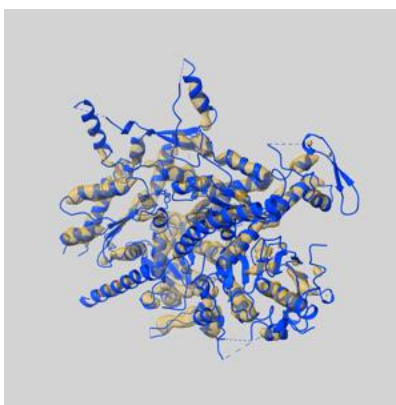
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21489 and PDB model 6VZG. Per-residue inclusion information can be found in section [3](#) on page [9](#).

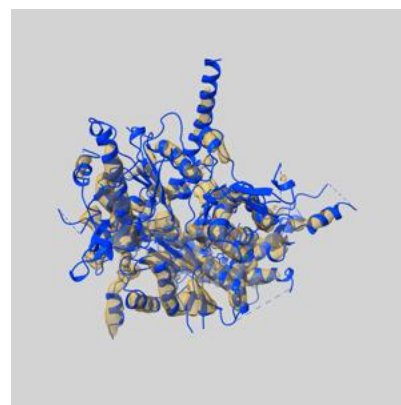
9.1 Map-model overlay [i](#)



X



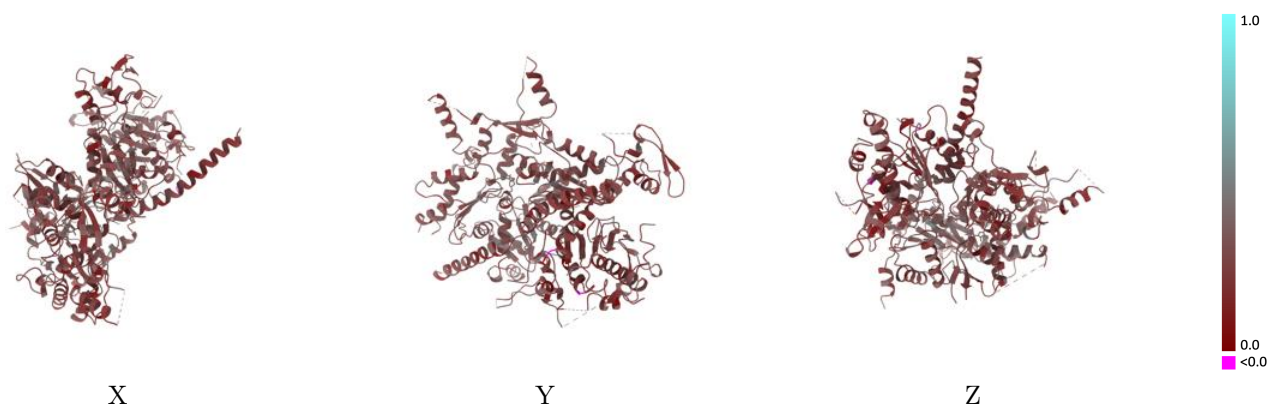
Y



Z

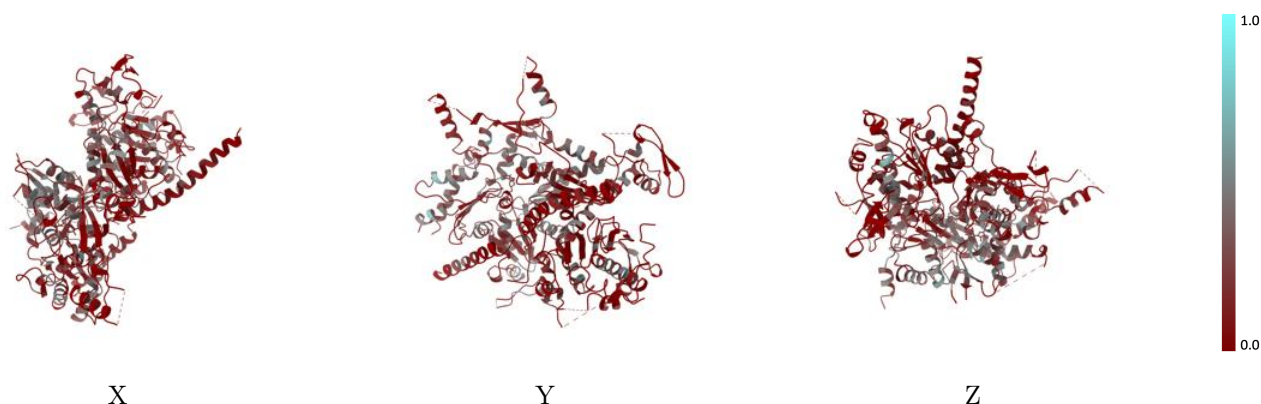
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



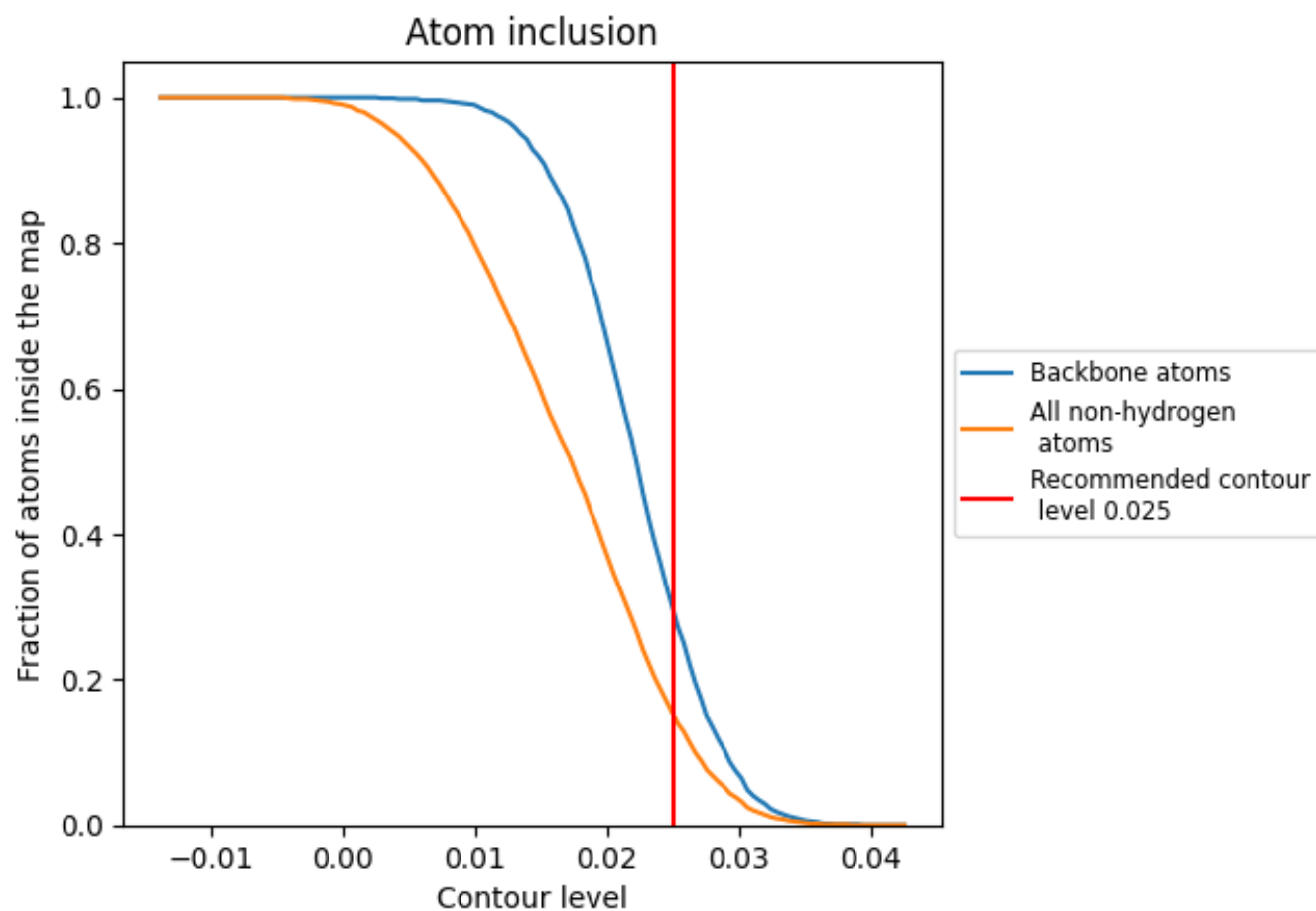
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 30% of all backbone atoms, 15% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.1530	0.2610
K	0.0540	0.2350
L	0.2000	0.2660
M	0.1310	0.2620
N	0.0960	0.2560

