



wwPDB EM Validation Summary Report ⓘ

Jan 3, 2023 – 10:30 AM EST

PDB ID : 7TZO
EMDB ID : EMD-26213
Title : The apo structure of human mTORC2 complex
Authors : Yu, Z.; Chen, J.; Pearce, D.
Deposited on : 2022-02-16
Resolution : 3.28 Å (reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

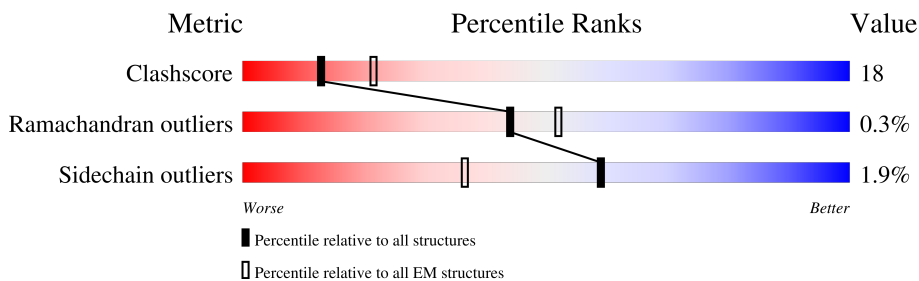
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance

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

The reported resolution of this entry is 3.28 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2674	
1	B	2674	
2	C	347	
2	D	347	
3	E	1720	
3	F	1720	
4	G	538	
4	H	538	

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 57117 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 Serine/threonine-protein kinase mTOR.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	2184	16337	10356	2906	2977	98	0	0
1	B	2185	16304	10330	2904	2972	98	0	0

There are 250 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-124	MET	-	initiating methionine	UNP P42345
A	-123	VAL	-	expression tag	UNP P42345
A	-122	THR	-	expression tag	UNP P42345
A	-121	THR	-	expression tag	UNP P42345
A	-120	LEU	-	expression tag	UNP P42345
A	-119	SER	-	expression tag	UNP P42345
A	-118	GLY	-	expression tag	UNP P42345
A	-117	LEU	-	expression tag	UNP P42345
A	-116	SER	-	expression tag	UNP P42345
A	-115	GLY	-	expression tag	UNP P42345
A	-114	GLU	-	expression tag	UNP P42345
A	-113	GLN	-	expression tag	UNP P42345
A	-112	GLY	-	expression tag	UNP P42345
A	-111	PRO	-	expression tag	UNP P42345
A	-110	SER	-	expression tag	UNP P42345
A	-109	GLY	-	expression tag	UNP P42345
A	-108	ASP	-	expression tag	UNP P42345
A	-107	MET	-	expression tag	UNP P42345
A	-106	THR	-	expression tag	UNP P42345
A	-105	THR	-	expression tag	UNP P42345
A	-104	GLU	-	expression tag	UNP P42345
A	-103	GLU	-	expression tag	UNP P42345
A	-102	ASP	-	expression tag	UNP P42345
A	-101	SER	-	expression tag	UNP P42345
A	-100	ALA	-	expression tag	UNP P42345
A	-99	THR	-	expression tag	UNP P42345

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-98	HIS	-	expression tag	UNP P42345
A	-97	ILE	-	expression tag	UNP P42345
A	-96	LYS	-	expression tag	UNP P42345
A	-95	PHE	-	expression tag	UNP P42345
A	-94	SER	-	expression tag	UNP P42345
A	-93	LYS	-	expression tag	UNP P42345
A	-92	ARG	-	expression tag	UNP P42345
A	-91	ASP	-	expression tag	UNP P42345
A	-90	GLU	-	expression tag	UNP P42345
A	-89	ASP	-	expression tag	UNP P42345
A	-88	GLY	-	expression tag	UNP P42345
A	-87	ARG	-	expression tag	UNP P42345
A	-86	GLU	-	expression tag	UNP P42345
A	-85	LEU	-	expression tag	UNP P42345
A	-84	ALA	-	expression tag	UNP P42345
A	-83	GLY	-	expression tag	UNP P42345
A	-82	ALA	-	expression tag	UNP P42345
A	-81	THR	-	expression tag	UNP P42345
A	-80	MET	-	expression tag	UNP P42345
A	-79	GLU	-	expression tag	UNP P42345
A	-78	LEU	-	expression tag	UNP P42345
A	-77	ARG	-	expression tag	UNP P42345
A	-76	ASP	-	expression tag	UNP P42345
A	-75	SER	-	expression tag	UNP P42345
A	-74	SER	-	expression tag	UNP P42345
A	-73	GLY	-	expression tag	UNP P42345
A	-72	LYS	-	expression tag	UNP P42345
A	-71	THR	-	expression tag	UNP P42345
A	-70	ILE	-	expression tag	UNP P42345
A	-69	SER	-	expression tag	UNP P42345
A	-68	THR	-	expression tag	UNP P42345
A	-67	TRP	-	expression tag	UNP P42345
A	-66	ILE	-	expression tag	UNP P42345
A	-65	SER	-	expression tag	UNP P42345
A	-64	ASP	-	expression tag	UNP P42345
A	-63	GLY	-	expression tag	UNP P42345
A	-62	HIS	-	expression tag	UNP P42345
A	-61	VAL	-	expression tag	UNP P42345
A	-60	LYS	-	expression tag	UNP P42345
A	-59	ASP	-	expression tag	UNP P42345
A	-58	PHE	-	expression tag	UNP P42345
A	-57	TYR	-	expression tag	UNP P42345

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-56	LEU	-	expression tag	UNP P42345
A	-55	TYR	-	expression tag	UNP P42345
A	-54	PRO	-	expression tag	UNP P42345
A	-53	GLY	-	expression tag	UNP P42345
A	-52	LYS	-	expression tag	UNP P42345
A	-51	TYR	-	expression tag	UNP P42345
A	-50	THR	-	expression tag	UNP P42345
A	-49	PHE	-	expression tag	UNP P42345
A	-48	VAL	-	expression tag	UNP P42345
A	-47	GLU	-	expression tag	UNP P42345
A	-46	THR	-	expression tag	UNP P42345
A	-45	ALA	-	expression tag	UNP P42345
A	-44	ALA	-	expression tag	UNP P42345
A	-43	PRO	-	expression tag	UNP P42345
A	-42	ASP	-	expression tag	UNP P42345
A	-41	GLY	-	expression tag	UNP P42345
A	-40	TYR	-	expression tag	UNP P42345
A	-39	GLU	-	expression tag	UNP P42345
A	-38	VAL	-	expression tag	UNP P42345
A	-37	ALA	-	expression tag	UNP P42345
A	-36	THR	-	expression tag	UNP P42345
A	-35	PRO	-	expression tag	UNP P42345
A	-34	ILE	-	expression tag	UNP P42345
A	-33	GLU	-	expression tag	UNP P42345
A	-32	PHE	-	expression tag	UNP P42345
A	-31	THR	-	expression tag	UNP P42345
A	-30	VAL	-	expression tag	UNP P42345
A	-29	ASN	-	expression tag	UNP P42345
A	-28	GLU	-	expression tag	UNP P42345
A	-27	ASP	-	expression tag	UNP P42345
A	-26	GLY	-	expression tag	UNP P42345
A	-25	GLN	-	expression tag	UNP P42345
A	-24	VAL	-	expression tag	UNP P42345
A	-23	THR	-	expression tag	UNP P42345
A	-22	VAL	-	expression tag	UNP P42345
A	-21	ASP	-	expression tag	UNP P42345
A	-20	GLY	-	expression tag	UNP P42345
A	-19	GLU	-	expression tag	UNP P42345
A	-18	ALA	-	expression tag	UNP P42345
A	-17	THR	-	expression tag	UNP P42345
A	-16	GLU	-	expression tag	UNP P42345
A	-15	GLY	-	expression tag	UNP P42345

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	ASP	-	expression tag	UNP P42345
A	-13	ALA	-	expression tag	UNP P42345
A	-12	HIS	-	expression tag	UNP P42345
A	-11	THR	-	expression tag	UNP P42345
A	-10	GLY	-	expression tag	UNP P42345
A	-9	SER	-	expression tag	UNP P42345
A	-8	SER	-	expression tag	UNP P42345
A	-7	GLY	-	expression tag	UNP P42345
A	-6	SER	-	expression tag	UNP P42345
A	-5	GLY	-	expression tag	UNP P42345
A	-4	SER	-	expression tag	UNP P42345
A	-3	GLY	-	expression tag	UNP P42345
A	-2	THR	-	expression tag	UNP P42345
A	-1	GLY	-	expression tag	UNP P42345
A	0	SER	-	expression tag	UNP P42345
B	-124	MET	-	initiating methionine	UNP P42345
B	-123	VAL	-	expression tag	UNP P42345
B	-122	THR	-	expression tag	UNP P42345
B	-121	THR	-	expression tag	UNP P42345
B	-120	LEU	-	expression tag	UNP P42345
B	-119	SER	-	expression tag	UNP P42345
B	-118	GLY	-	expression tag	UNP P42345
B	-117	LEU	-	expression tag	UNP P42345
B	-116	SER	-	expression tag	UNP P42345
B	-115	GLY	-	expression tag	UNP P42345
B	-114	GLU	-	expression tag	UNP P42345
B	-113	GLN	-	expression tag	UNP P42345
B	-112	GLY	-	expression tag	UNP P42345
B	-111	PRO	-	expression tag	UNP P42345
B	-110	SER	-	expression tag	UNP P42345
B	-109	GLY	-	expression tag	UNP P42345
B	-108	ASP	-	expression tag	UNP P42345
B	-107	MET	-	expression tag	UNP P42345
B	-106	THR	-	expression tag	UNP P42345
B	-105	THR	-	expression tag	UNP P42345
B	-104	GLU	-	expression tag	UNP P42345
B	-103	GLU	-	expression tag	UNP P42345
B	-102	ASP	-	expression tag	UNP P42345
B	-101	SER	-	expression tag	UNP P42345
B	-100	ALA	-	expression tag	UNP P42345
B	-99	THR	-	expression tag	UNP P42345
B	-98	HIS	-	expression tag	UNP P42345

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-97	ILE	-	expression tag	UNP P42345
B	-96	LYS	-	expression tag	UNP P42345
B	-95	PHE	-	expression tag	UNP P42345
B	-94	SER	-	expression tag	UNP P42345
B	-93	LYS	-	expression tag	UNP P42345
B	-92	ARG	-	expression tag	UNP P42345
B	-91	ASP	-	expression tag	UNP P42345
B	-90	GLU	-	expression tag	UNP P42345
B	-89	ASP	-	expression tag	UNP P42345
B	-88	GLY	-	expression tag	UNP P42345
B	-87	ARG	-	expression tag	UNP P42345
B	-86	GLU	-	expression tag	UNP P42345
B	-85	LEU	-	expression tag	UNP P42345
B	-84	ALA	-	expression tag	UNP P42345
B	-83	GLY	-	expression tag	UNP P42345
B	-82	ALA	-	expression tag	UNP P42345
B	-81	THR	-	expression tag	UNP P42345
B	-80	MET	-	expression tag	UNP P42345
B	-79	GLU	-	expression tag	UNP P42345
B	-78	LEU	-	expression tag	UNP P42345
B	-77	ARG	-	expression tag	UNP P42345
B	-76	ASP	-	expression tag	UNP P42345
B	-75	SER	-	expression tag	UNP P42345
B	-74	SER	-	expression tag	UNP P42345
B	-73	GLY	-	expression tag	UNP P42345
B	-72	LYS	-	expression tag	UNP P42345
B	-71	THR	-	expression tag	UNP P42345
B	-70	ILE	-	expression tag	UNP P42345
B	-69	SER	-	expression tag	UNP P42345
B	-68	THR	-	expression tag	UNP P42345
B	-67	TRP	-	expression tag	UNP P42345
B	-66	ILE	-	expression tag	UNP P42345
B	-65	SER	-	expression tag	UNP P42345
B	-64	ASP	-	expression tag	UNP P42345
B	-63	GLY	-	expression tag	UNP P42345
B	-62	HIS	-	expression tag	UNP P42345
B	-61	VAL	-	expression tag	UNP P42345
B	-60	LYS	-	expression tag	UNP P42345
B	-59	ASP	-	expression tag	UNP P42345
B	-58	PHE	-	expression tag	UNP P42345
B	-57	TYR	-	expression tag	UNP P42345
B	-56	LEU	-	expression tag	UNP P42345

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-55	TYR	-	expression tag	UNP P42345
B	-54	PRO	-	expression tag	UNP P42345
B	-53	GLY	-	expression tag	UNP P42345
B	-52	LYS	-	expression tag	UNP P42345
B	-51	TYR	-	expression tag	UNP P42345
B	-50	THR	-	expression tag	UNP P42345
B	-49	PHE	-	expression tag	UNP P42345
B	-48	VAL	-	expression tag	UNP P42345
B	-47	GLU	-	expression tag	UNP P42345
B	-46	THR	-	expression tag	UNP P42345
B	-45	ALA	-	expression tag	UNP P42345
B	-44	ALA	-	expression tag	UNP P42345
B	-43	PRO	-	expression tag	UNP P42345
B	-42	ASP	-	expression tag	UNP P42345
B	-41	GLY	-	expression tag	UNP P42345
B	-40	TYR	-	expression tag	UNP P42345
B	-39	GLU	-	expression tag	UNP P42345
B	-38	VAL	-	expression tag	UNP P42345
B	-37	ALA	-	expression tag	UNP P42345
B	-36	THR	-	expression tag	UNP P42345
B	-35	PRO	-	expression tag	UNP P42345
B	-34	ILE	-	expression tag	UNP P42345
B	-33	GLU	-	expression tag	UNP P42345
B	-32	PHE	-	expression tag	UNP P42345
B	-31	THR	-	expression tag	UNP P42345
B	-30	VAL	-	expression tag	UNP P42345
B	-29	ASN	-	expression tag	UNP P42345
B	-28	GLU	-	expression tag	UNP P42345
B	-27	ASP	-	expression tag	UNP P42345
B	-26	GLY	-	expression tag	UNP P42345
B	-25	GLN	-	expression tag	UNP P42345
B	-24	VAL	-	expression tag	UNP P42345
B	-23	THR	-	expression tag	UNP P42345
B	-22	VAL	-	expression tag	UNP P42345
B	-21	ASP	-	expression tag	UNP P42345
B	-20	GLY	-	expression tag	UNP P42345
B	-19	GLU	-	expression tag	UNP P42345
B	-18	ALA	-	expression tag	UNP P42345
B	-17	THR	-	expression tag	UNP P42345
B	-16	GLU	-	expression tag	UNP P42345
B	-15	GLY	-	expression tag	UNP P42345
B	-14	ASP	-	expression tag	UNP P42345

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-13	ALA	-	expression tag	UNP P42345
B	-12	HIS	-	expression tag	UNP P42345
B	-11	THR	-	expression tag	UNP P42345
B	-10	GLY	-	expression tag	UNP P42345
B	-9	SER	-	expression tag	UNP P42345
B	-8	SER	-	expression tag	UNP P42345
B	-7	GLY	-	expression tag	UNP P42345
B	-6	SER	-	expression tag	UNP P42345
B	-5	GLY	-	expression tag	UNP P42345
B	-4	SER	-	expression tag	UNP P42345
B	-3	GLY	-	expression tag	UNP P42345
B	-2	THR	-	expression tag	UNP P42345
B	-1	GLY	-	expression tag	UNP P42345
B	0	SER	-	expression tag	UNP P42345

- Molecule 2 is a protein called Target of rapamycin complex subunit LST8.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	319	Total	C	N	O	S	0	0
			2465	1533	437	477	18		
2	D	319	Total	C	N	O	S	0	0
			2465	1533	437	477	18		

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-20	MET	-	initiating methionine	UNP Q9BVC4
C	-19	GLY	-	expression tag	UNP Q9BVC4
C	-18	TYR	-	expression tag	UNP Q9BVC4
C	-17	PRO	-	expression tag	UNP Q9BVC4
C	-16	TYR	-	expression tag	UNP Q9BVC4
C	-15	ASP	-	expression tag	UNP Q9BVC4
C	-14	VAL	-	expression tag	UNP Q9BVC4
C	-13	PRO	-	expression tag	UNP Q9BVC4
C	-12	ASP	-	expression tag	UNP Q9BVC4
C	-11	TYR	-	expression tag	UNP Q9BVC4
C	-10	ALA	-	expression tag	UNP Q9BVC4
C	-9	ASP	-	expression tag	UNP Q9BVC4
C	-8	LEU	-	expression tag	UNP Q9BVC4
C	-7	ASN	-	expression tag	UNP Q9BVC4
C	-6	GLY	-	expression tag	UNP Q9BVC4
C	-5	GLY	-	expression tag	UNP Q9BVC4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	GLY	-	expression tag	UNP Q9BVC4
C	-3	GLY	-	expression tag	UNP Q9BVC4
C	-2	GLY	-	expression tag	UNP Q9BVC4
C	-1	SER	-	expression tag	UNP Q9BVC4
C	0	THR	-	expression tag	UNP Q9BVC4
D	-20	MET	-	initiating methionine	UNP Q9BVC4
D	-19	GLY	-	expression tag	UNP Q9BVC4
D	-18	TYR	-	expression tag	UNP Q9BVC4
D	-17	PRO	-	expression tag	UNP Q9BVC4
D	-16	TYR	-	expression tag	UNP Q9BVC4
D	-15	ASP	-	expression tag	UNP Q9BVC4
D	-14	VAL	-	expression tag	UNP Q9BVC4
D	-13	PRO	-	expression tag	UNP Q9BVC4
D	-12	ASP	-	expression tag	UNP Q9BVC4
D	-11	TYR	-	expression tag	UNP Q9BVC4
D	-10	ALA	-	expression tag	UNP Q9BVC4
D	-9	ASP	-	expression tag	UNP Q9BVC4
D	-8	LEU	-	expression tag	UNP Q9BVC4
D	-7	ASN	-	expression tag	UNP Q9BVC4
D	-6	GLY	-	expression tag	UNP Q9BVC4
D	-5	GLY	-	expression tag	UNP Q9BVC4
D	-4	GLY	-	expression tag	UNP Q9BVC4
D	-3	GLY	-	expression tag	UNP Q9BVC4
D	-2	GLY	-	expression tag	UNP Q9BVC4
D	-1	SER	-	expression tag	UNP Q9BVC4
D	0	THR	-	expression tag	UNP Q9BVC4

- Molecule 3 is a protein called Rapamycin-insensitive companion of mTOR.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	1117	Total	C	N	O	S	0	0
			8931	5689	1584	1611	47		
3	F	1117	Total	C	N	O	S	0	0
			8931	5689	1584	1611	47		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-11	MET	-	initiating methionine	UNP Q6R327
E	-10	ASP	-	expression tag	UNP Q6R327
E	-9	TYR	-	expression tag	UNP Q6R327
E	-8	LYS	-	expression tag	UNP Q6R327

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-7	ASP	-	expression tag	UNP Q6R327
E	-6	ASP	-	expression tag	UNP Q6R327
E	-5	ASP	-	expression tag	UNP Q6R327
E	-4	ASP	-	expression tag	UNP Q6R327
E	-3	LYS	-	expression tag	UNP Q6R327
E	-2	GLY	-	expression tag	UNP Q6R327
E	-1	SER	-	expression tag	UNP Q6R327
E	0	THR	-	expression tag	UNP Q6R327
F	-11	MET	-	initiating methionine	UNP Q6R327
F	-10	ASP	-	expression tag	UNP Q6R327
F	-9	TYR	-	expression tag	UNP Q6R327
F	-8	LYS	-	expression tag	UNP Q6R327
F	-7	ASP	-	expression tag	UNP Q6R327
F	-6	ASP	-	expression tag	UNP Q6R327
F	-5	ASP	-	expression tag	UNP Q6R327
F	-4	ASP	-	expression tag	UNP Q6R327
F	-3	LYS	-	expression tag	UNP Q6R327
F	-2	GLY	-	expression tag	UNP Q6R327
F	-1	SER	-	expression tag	UNP Q6R327
F	0	THR	-	expression tag	UNP Q6R327

- Molecule 4 is a protein called Target of rapamycin complex 2 subunit MAPKAP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	120	Total	C	N	O	S	0	0
			842	518	158	162	4		
4	H	120	Total	C	N	O	S	0	0
			842	518	158	162	4		

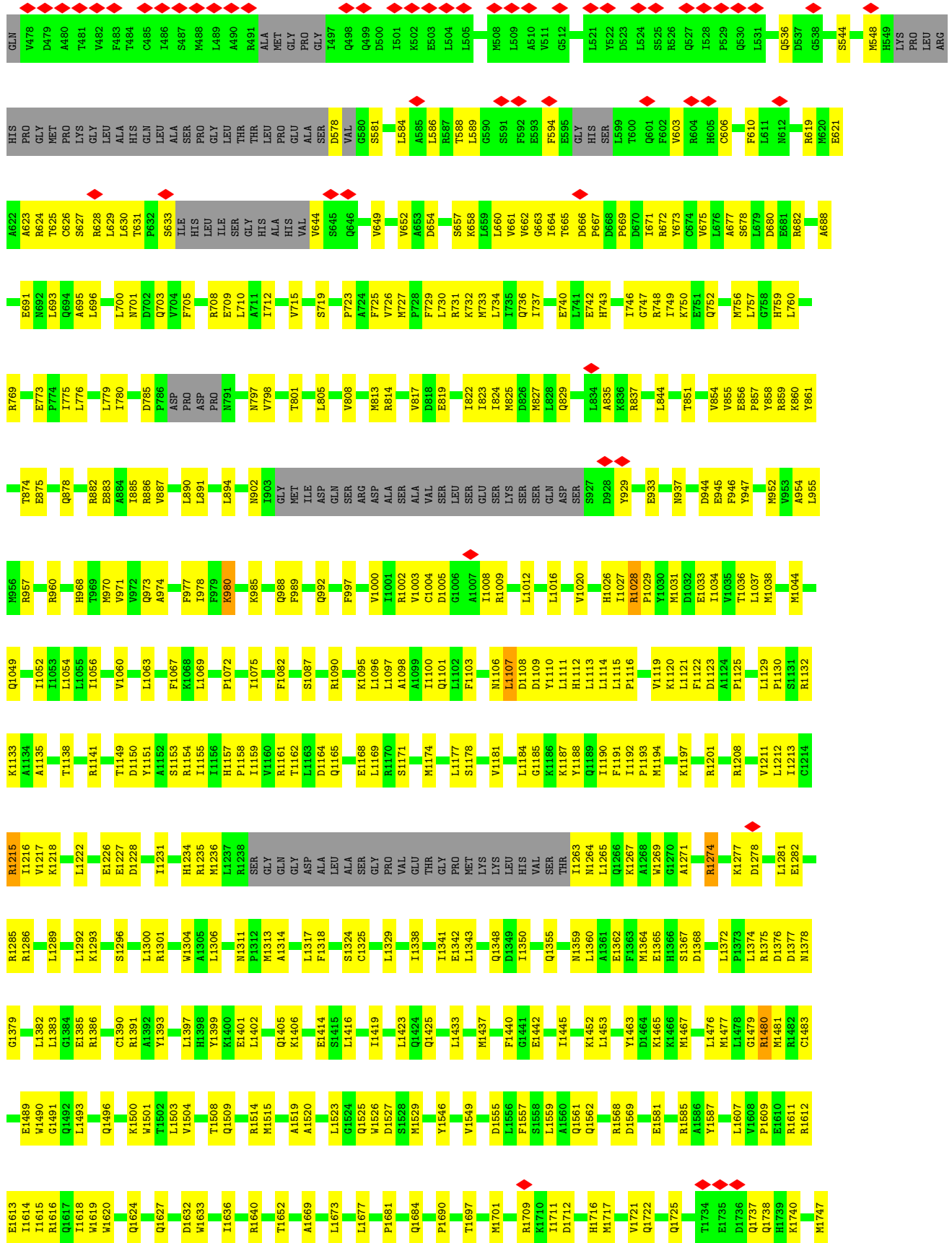
There are 32 discrepancies between the modelled and reference sequences:

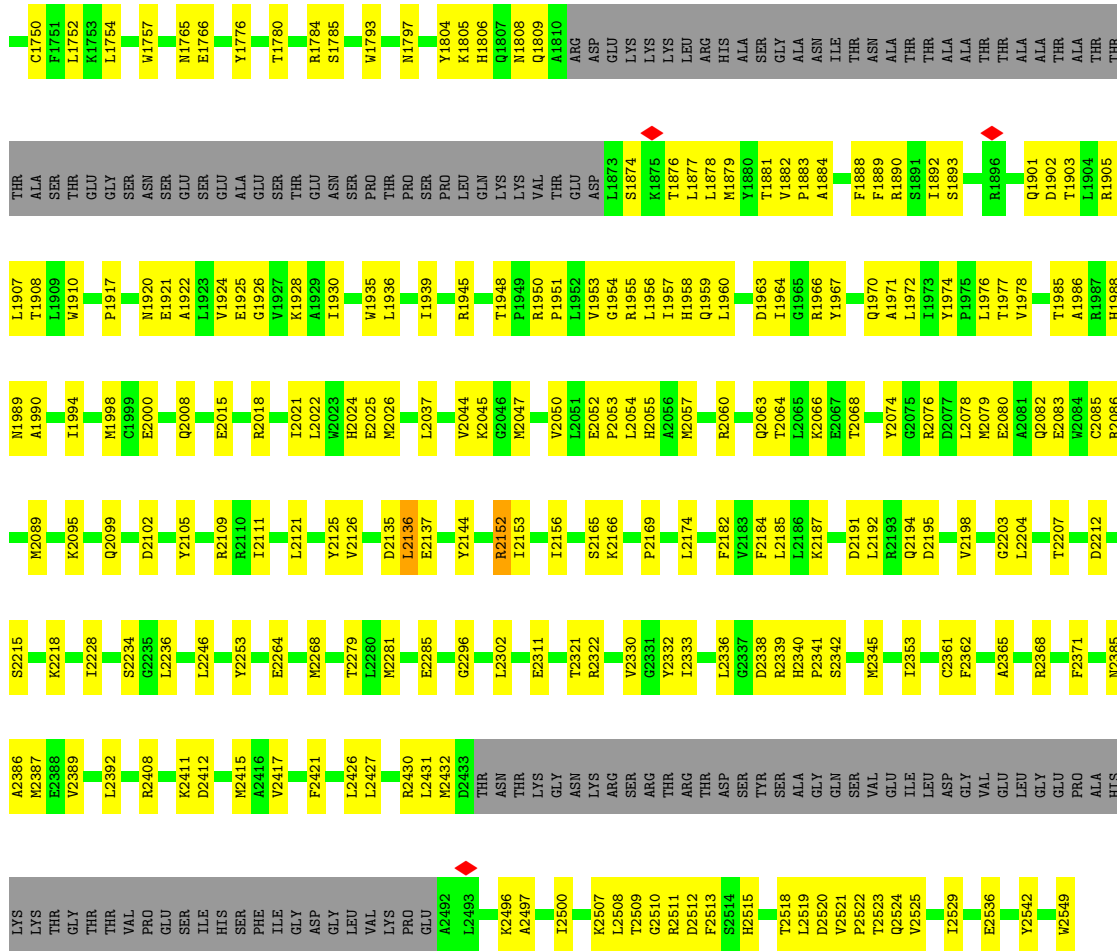
Chain	Residue	Modelled	Actual	Comment	Reference
G	523	ALA	-	expression tag	UNP Q9BPZ7
G	524	ALA	-	expression tag	UNP Q9BPZ7
G	525	ALA	-	expression tag	UNP Q9BPZ7
G	526	GLY	-	expression tag	UNP Q9BPZ7
G	527	GLY	-	expression tag	UNP Q9BPZ7
G	528	GLY	-	expression tag	UNP Q9BPZ7
G	529	GLY	-	expression tag	UNP Q9BPZ7
G	530	TYR	-	expression tag	UNP Q9BPZ7
G	531	PRO	-	expression tag	UNP Q9BPZ7
G	532	TYR	-	expression tag	UNP Q9BPZ7

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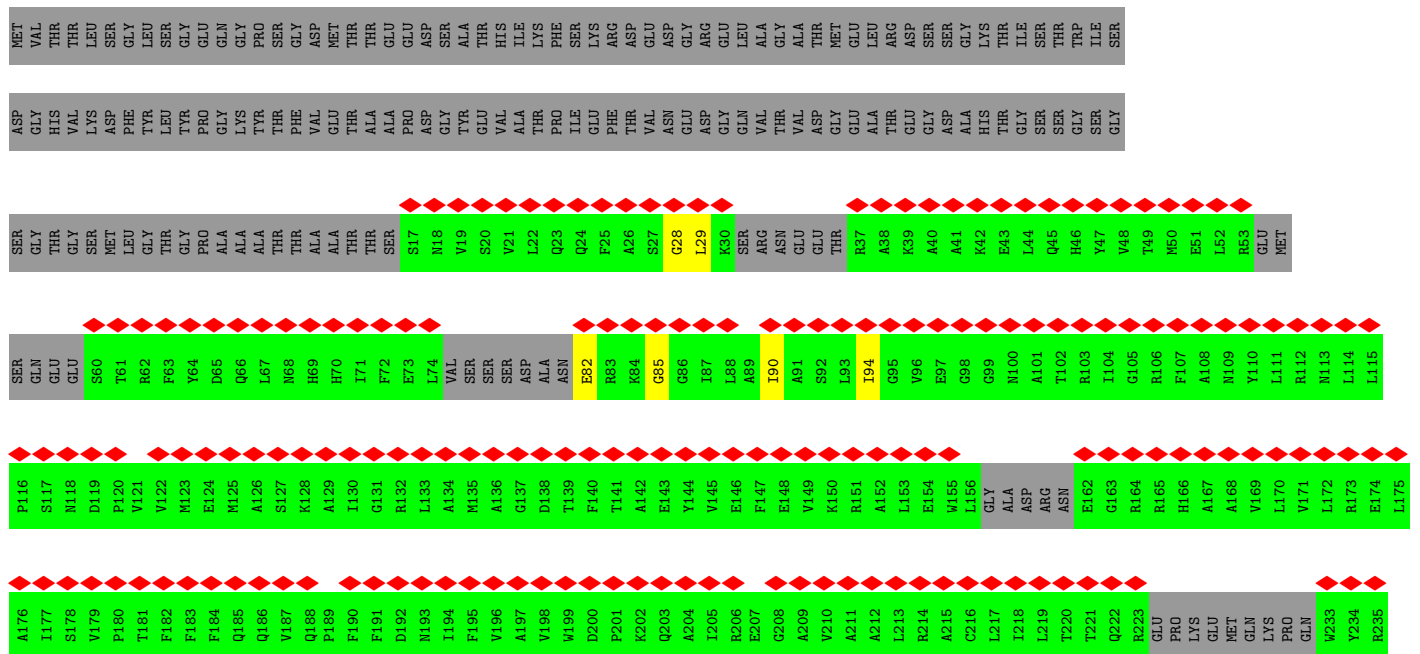
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Chain	Residue	Modelled	Actual	Comment	Reference
G	533	ASP	-	expression tag	UNP Q9BPZ7
G	534	VAL	-	expression tag	UNP Q9BPZ7
G	535	PRO	-	expression tag	UNP Q9BPZ7
G	536	ASP	-	expression tag	UNP Q9BPZ7
G	537	TYR	-	expression tag	UNP Q9BPZ7
G	538	ALA	-	expression tag	UNP Q9BPZ7
H	523	ALA	-	expression tag	UNP Q9BPZ7
H	524	ALA	-	expression tag	UNP Q9BPZ7
H	525	ALA	-	expression tag	UNP Q9BPZ7
H	526	GLY	-	expression tag	UNP Q9BPZ7
H	527	GLY	-	expression tag	UNP Q9BPZ7
H	528	GLY	-	expression tag	UNP Q9BPZ7
H	529	GLY	-	expression tag	UNP Q9BPZ7
H	530	TYR	-	expression tag	UNP Q9BPZ7
H	531	PRO	-	expression tag	UNP Q9BPZ7
H	532	TYR	-	expression tag	UNP Q9BPZ7
H	533	ASP	-	expression tag	UNP Q9BPZ7
H	534	VAL	-	expression tag	UNP Q9BPZ7
H	535	PRO	-	expression tag	UNP Q9BPZ7
H	536	ASP	-	expression tag	UNP Q9BPZ7
H	537	TYR	-	expression tag	UNP Q9BPZ7
H	538	ALA	-	expression tag	UNP Q9BPZ7





● Molecule 1: Serine/threonine-protein kinase mTOR



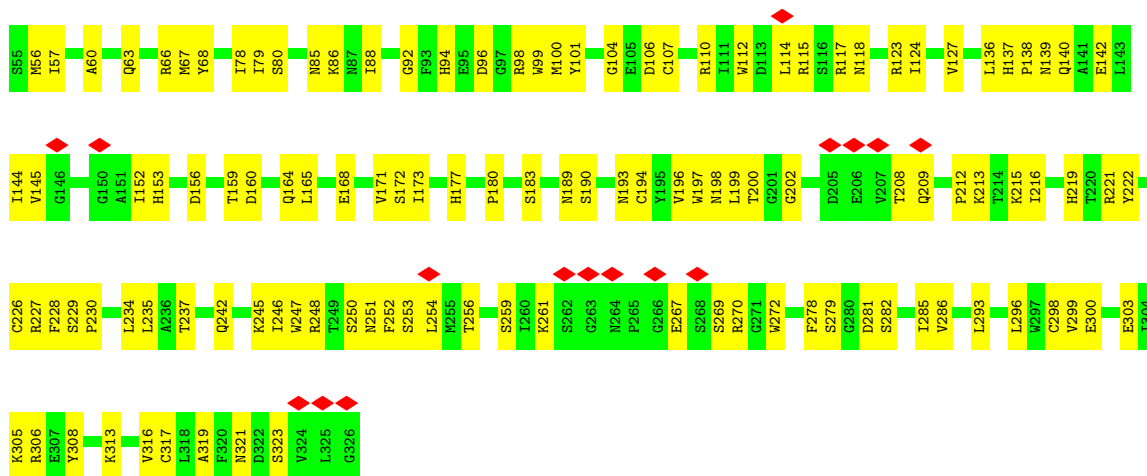
H236	H237	F238	E239	E240	A241	E242	K243	G244	F245	D246	GLU	THR	LEU	LEU	ALA	LYS	GLU	LYS	GLY	MET	ASN	ARG	D258	D259	R260	I261	H262	G263	A264	L265	L266	L267	L268	N269	E270	L271	V272	R273	I274	S275	S276	M277	E278	C279	E280	R281	L282	R283	E284	E285	M286	E287	E288	I289	THR	GLN	GLN	GLN	LEU	VAL									
HIS	ASP	LYS	TYR	CYS	LYS	ASP	LEU	MET	GLY	PHE	GLY	THR	LYS	PRO	ARG	HIS	ILE	THR	PRO	PHE	THR	SER	PHE	GLN	ALA	VAL	GLN	PRO	GLN	GLN	SER	ASN	ALA	LEU	LEU	VAL	GLY	LEU	LEU	GLY	TYR	SER	SER	HIS	GLN	GLY	I274	MET	GLY	L396	P397	THR	SER	PRO	SER	PRO	ALA	ALA	LYS	LYS	THR	ASP	THR	T410	Q411	Y412	L413	Q414	D415
L356	V357	E358	S359	C360	C362	D364	L365	K366	E367	E368	K369	F370	D371	Q372	Q373	C374	K376	V377	L378	C380	ARG	ASN	SER	LYS	ASN	S386	L387	I388	Q389	K390	T391	I392	L393	N394	L395	L396	P397	R398	L399	A400	A401	F402	R403	P404	ASP	ALA	ALA	THR	THR	ASP	T410	Q411	Y412	L413	Q414	D415													
T416	M417	M418	H419	V420	L421	S422	C423	V424	K425	K426	E427	E428	R430	T431	A432	A433	F434	Q435	Q436	L437	G438	L439	L440	S441	V442	A443	Y444	R445	S446	E447	F448	K449	L452	F453	L454	R455	L456	D457	R460	A461	A462	L463	P464	P465	K466	ASP	PHE	ALA	ALA	HIS	HIS	LYS	ARG	GLN	LYS	LYS	ALA	ALA	GLN										
V478	D479	A480	T481	V482	L484	C485	L486	S487	M488	L489	A490	K491	ALA	GLY	PRO	GLY	L497	Q498	Q499	D500	L501	K502	E503	L504	L505	A506	L509	A510	V511	Q512	Y522	D523	L524	S525	R526	Q527	L528	P529	Q530	G538	A461	A462	L463	P464	H549	L549	PRO	LEU	ARG	HIS	PRO	GLY	MET	PRO	GLN	LYS	GLY												
LEU	ALA	HIS	GLN	LEU	ALA	SER	PRO	GLY	LEU	THR	LEU	PRO	ALA	ALA	D578	A585	G590	S591	F592	E595	GLY	HIS	SER	L599	T600	Q601	R604	F610	L611	N612	S613	E614	E617	T618	R619	M620	R624	R628	S633	ILE	LEU	LEU	ILE	SER	GLY	HIS	ALA	HIS																					
VAL	V644	S645	Q646	V652	F653	D654	V655	L656	S657	K658	L659	V662	G663	D666	P667	I671	G672	V675	L676	A677	D680	E681	R682	F683	D684	A685	H686	Q689	A690	E691	N692	L693	Q694	N701	D702	Q703	V704	F705	E706	I707	R708	E709	L710	A711	I712	G713	T714	R717	M733																				
Q736	I737	L738	E740	L741	E742	H743	G747	K750	E751	Q752	H759	L760	M763	R769	M772	F773	P774	I775	L776	K777	E782	E783	A784	I785	R786	ASP	PRO	ASP	PRO	N791	V794	I795	V798	A806	G810	L811	E812	M813	R814	E819	R820	F821	I822	R823	I824																								
M825	L834	A835	K836	R837	Q838	V839	T843	L844	V854	V855	E856	P857	K860	L869	L872	Q876	M877	Q878	R881	R882	E883	A884	I885	R886	V887	L903	GLY	MET	ILE	ASP	GLN	SER	ARG	ASP	ALA	SER	ALA	I1000	I1001	SER	LEU	SER	GLU	LYS	SER	R1009	SER	GLN	ASP	SER	I1027																		
D928	Y929	S930	I931	L935	V936	N937	H938	I941	L943	D944	F945	Y946	P948	N952	A954	R957	H967	R970	V971	V972	A974	I975	I978	F979	K980	Q988	F989	M994	L998	N999	V1000	I1001	R1002	C1004	D1005	I1008	R1009	SER	SER	V1020	S1021	F1022	I1027																										
Y1030	M1031	I1034	M1044	N1045	S1047	I1048	Q1049	I1053	I1056	I1057	Q1058	I1059	V1060	L1069	P1072	I1075	L1079	M1083	S1087	R1090	K1095	L1096	L1097	A1098	I1100	Q1101	L1102	F1103	L1107	D1108	I1109	Y1110	L1111	H1112	L1113	L1114	L1115	P1116	P1117	I1118	V1119	K1120	L1121																										
F1122	D1123	A1124	P1125	L1129	R1132	K1133	A1134	A1135	L1136	E1137	T1138	V1139	D1140	R1141	L1142	Y1151	A1152	S1153	R1154	I1155	I1156	H1157	P1158	R1161	D1164	Q1165	L1169	A1173	T1176	L1177	S1178	V1181	L1184	Y1188	I1192	P1193	M1194	V1195	M1196	K1197	V1200	R1201	H1202	R1203	Q1207																								
R1208	I1209	D1210	V1211	L1212	C1214	R1215	I1216	V1217	K1218	G1219	E1220	T1221	L1222	E1225	E1226	H1234	R1235	M1236	L1237	R1238	SER	GLY	GLN	GLY	ASP	ALA	LEU	ALA	SER	GLY	VAL	GLU	THR	GLY	MET	LYS	LEU	HIS	VAL	SER	I1263	N1264	L1265	Q1266	K1267	A1268	M1269	G1270	A1271	R1274	V1275																		
S1276	K1277	D1278	L1279	M1280	L1281	E1282	R1285	R1286	L1292	K1293	D1294	S1295	S1296	R1301	M1304	N1311	P1312	M1313	A1314	R1315	D1316	L1317	F1318	F1322	V1323	S1324	C1325	M1326	L1329	M1330	Q1333	Q1334	I1338	R1339	S1340	L1343	A1344	L1345	T1346	S1347	O1348	D1349	E1352	G1270	L1357	L1360	A1361																						

L1476	M1477	L1478	G1479	R1480	C1483	I1618	W1619	W1620	E1499	K1500	M1505	D1506	E1507	T1508	M1512	M1515	A1519	A1520	W1526	D1527	S1528	M1529	Y1532	M1535	I1536	P1537	R1538	H1541	D1542	G1543	F1440	G1441	E1442	L1443	E1444	T1445	Q1446	K1452	L1453	V1461	A1462	R1568	D1569	L1570	L1571	D1572	M1578				
E1362	L1372	P1373	L1374	M1378	L1382	E1385	R1386	K1389	C1390	L1391	K1395	E1401	L1402	Q1405	E1414	S1415	L1416	I1417	M1420	L1423	Q1424	Q1425	L1433	M1437	F1440	G1441	E1442	L1443	E1444	T1445	Q1446	K1452	L1453	V1461	A1462	R1568	D1569	L1570	L1571	D1572	M1578										
R1585	M1595	I1614	I1615	I1618	W1619	W1620	Q1624	V1630	W1633	I1636	L1637	M1638	R1640	S1645	H1647	E1648	W1653	L1654	L1659	A1669	L1673	L1676	L1677	P1681	Q1684	L1685	D1686	L1687	P1690	T1691	V1696	T1697	M1701	M1701	M1701	M1701	M1797	M1797	M1798	M1798	M1798	L1802	A1810	R1709							
K1710	I1711	D1712	L1716	M1717	F1720	H1723	M1724	Q1725	Q1729	E1735	D1736	Q1737	Q1738	H1738	K1740	L1752	K1753	L1754	G1755	E1756	W1757	Q1758	L1759	L1764	M1765	L1768	I1769	V1772	Y1776	S1777	A1778	A1778	T1780	E1781	R1784	P1690	T1691	Y1787	K1788	W1793	M1797	M1798	L1802	A1810	R1709						
ASP	GLU	LYS	LYS	LEU	ARG	HIS	ALA	SER	GLY	ALA	ASN	THR	ALA	ALA	THR	THR	THR	ALA	THR	THR	THR	THR	ALA	THR	THR	GLY	GLY	ASN	SER	GLU	SER	GLU	GLU	ALA	GLU	SER	GLU	ASN	PRO	THR	PRO	SER	PRO	LEU	GLN	LYS	LYS	VAL	THR	GLU	ARG
L1873	S1874	K1875	L1876	L1877	L1878	T1881	P1882	P1883	A1884	F1888	F1889	R1890	S1891	S1895	R1896	L1900	Q1901	D1902	T1903	L1904	R1905	E1906	L1907	T1908	L1909	F1911	D1912	Y1913	W1916	P1917	D1918	V1919	M1920	E1921	A1922	L1923	V1924	E1925	G1926	W1927	K1928	W1935	D1947	T1948	F1949	R1950	P1951	L1953	G1954		
R1955	L1956	I1957	H1958	Q1959	L1960	I1964	Q1970	A1971	L1972	I1973	Y1974	P1975	L1976	T1977	V1978	T1985	A1986	H1987	N1989	A1990	E2000	E2015	R2018	L2022	W2023	H2024	E2025	W2026	W2027	R2036	L2037	E1921	A1922	L1923	V1924	E1925	G1926	W1927	K1928	W1935	D1947	T1948	F1949	R1950	P1951	L1953	G1954				
Q2082	N2093	W2094	K2095	T2098	Q2099	L2103	A1971	Y2105	R2109	R2110	I2111	L2121	F2122	L2123	V2126	S2127	L2131	M2132	C2133	R2134	D2135	L2136	E2137	Y2144	R2152	I2153	L2160	Q2161	V2162	S2165	K2166	P2169	R2170	K2171	H2055	A2056	W2057	R2060	Q2063	Q2072	L2078	W2079	E2080	V1953	L1953	G1954					
D2195	W2199	L2204	T2207	L2208	L2209	K2218	W2219	L2220	Y2225	S2234	C2243	D2244	L2246	L2249	Y2253	L2263	E2264	H2265	R2266	L2267	M2268	D2274	Y2275	D2276	T2279	L2280	W2281	E2285	Y2286	F2287	D2298	L2302	K2306	S2307	P2308	H2189	E2311	V2312	R2316	R2317	T2433	THR	ASN	THR	THR						
T2318	T2321	R2322	M2329	Y2332	L2336	G2337	D2338	R2339	H2340	P2341	S2342	M2345	L2349	F2358	F2362	F2371	R2378	M2382	M2387	E2388	V2389	L2392	R2397	M2404	R2408	K2411	M2415	A2416	V2417	L2418	E2419	L2426	W2429	R2430	D2433	THR	ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR				
LYS	GLY	ASN	LYS	ARG	ARG	THR	THR	ASP	SER	TYR	SER	ALA	ALA	GLY	GLN	SER	VAL	GLU	ILE	LEU	ASP	ASP	THR	VAL	PRO	GLU	SER	ILE	HIS	SER	PHE	ILE	GLY	ASP	GLY	LEU	VAL	LYS	PRO	GLU	R2430	D2433	THR	ASN	THR	THR	THR				
I2501	K2507	L2508	T2509	G2510	R2511	D2512	F2513	S2514	H2515	D2516	L2519	D2520	V2521	P2522	T2523	E2526	L2527	S2534	H2535	E2536	M2537	L2538	Y2542	W2549	D11	P12	V13	I14	G19	Y20	W27	Q28	A29	H30	C34	Q39	H40	A47	L48	E49	S43	Q44	W45	M46	A47	L48	E49	T51	P52	D53	R54

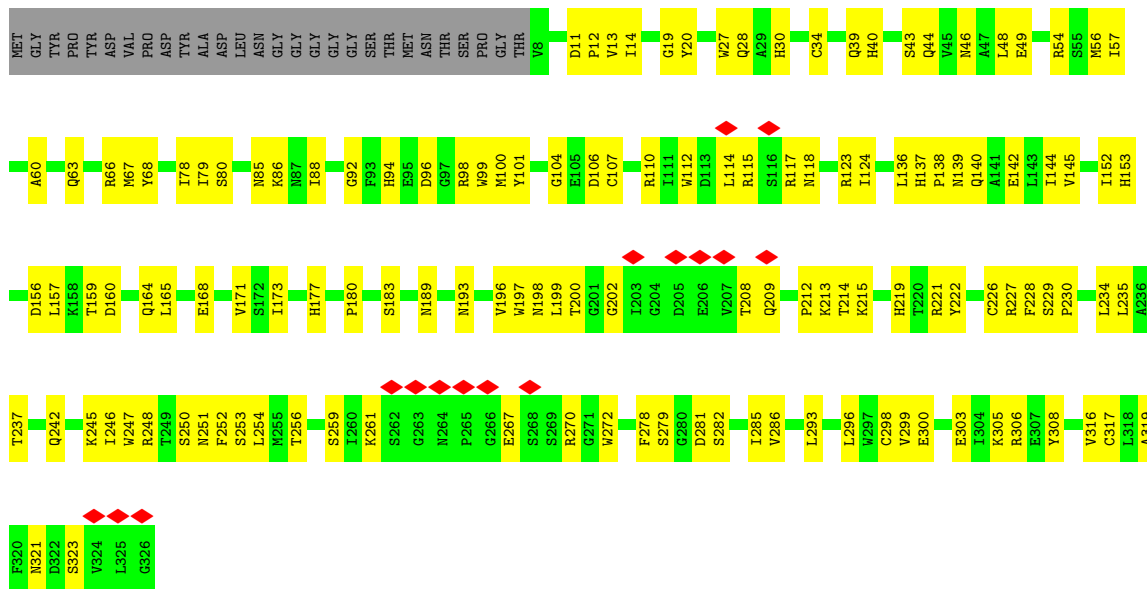
• Molecule 2: Target of rapamycin complex subunit LST8



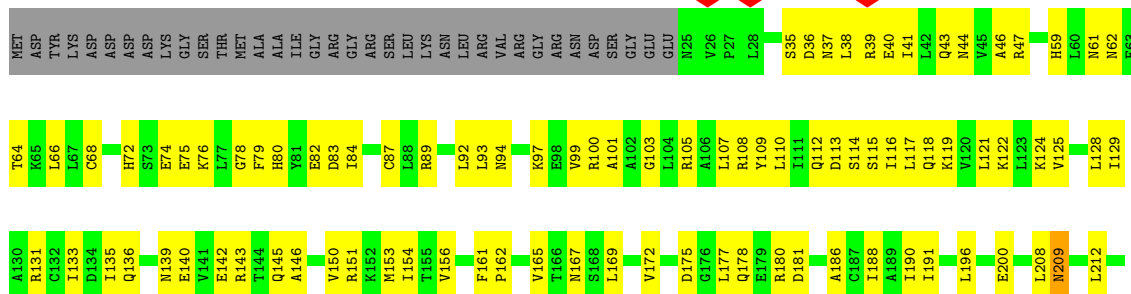
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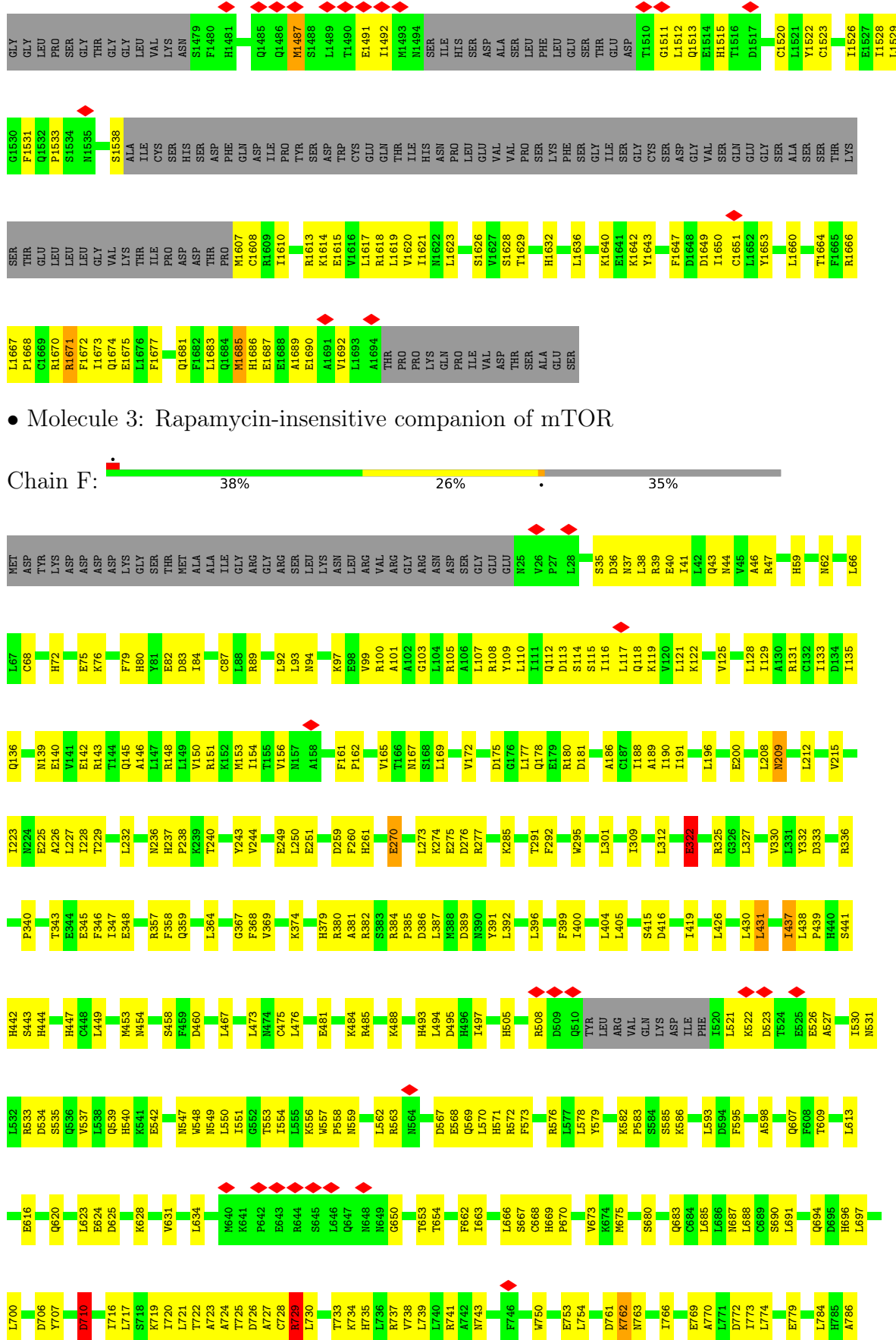


• Molecule 2: Target of rapamycin complex subunit LST8



• Molecule 3: Rapamycin-insensitive companion of mTOR

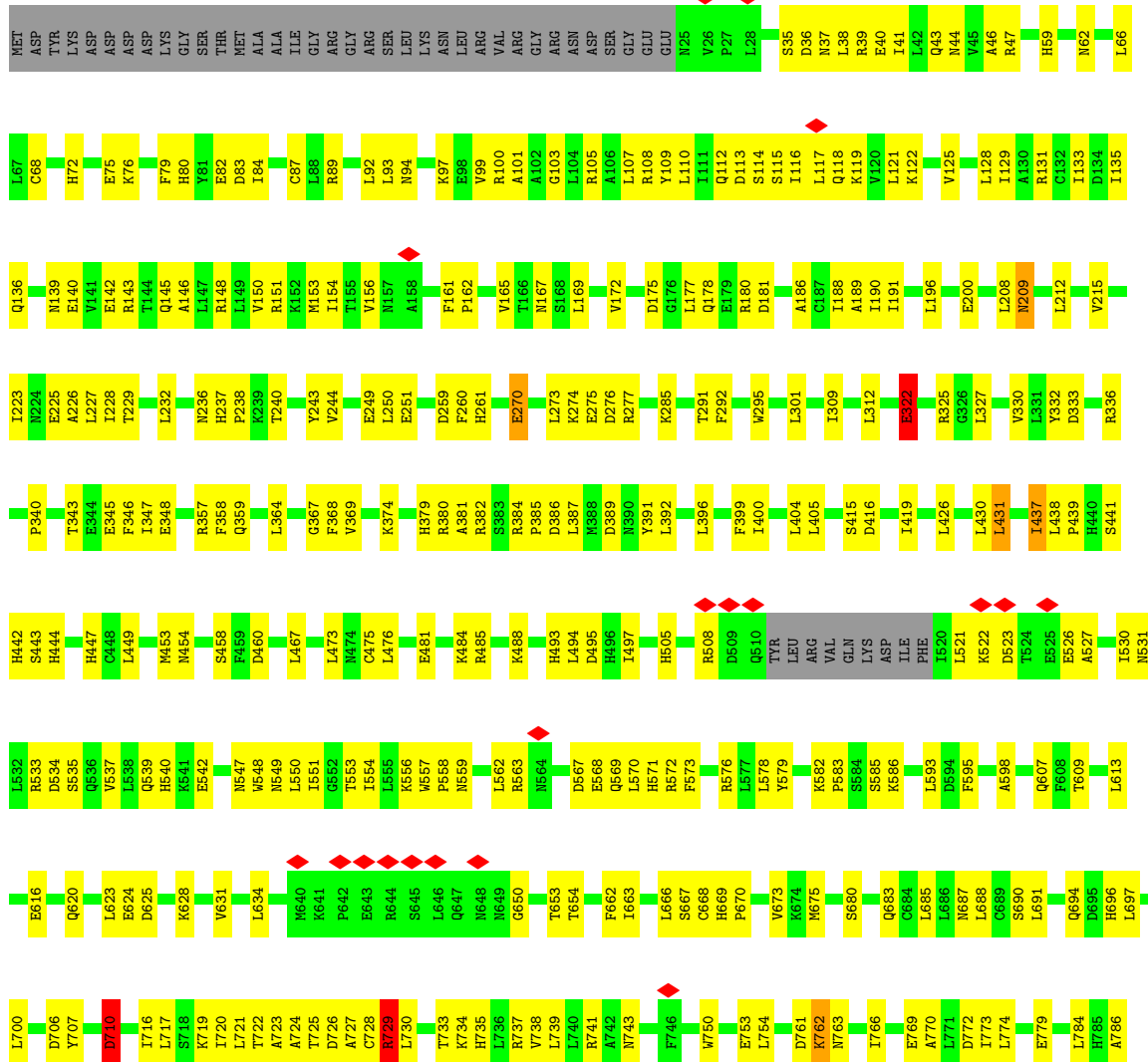


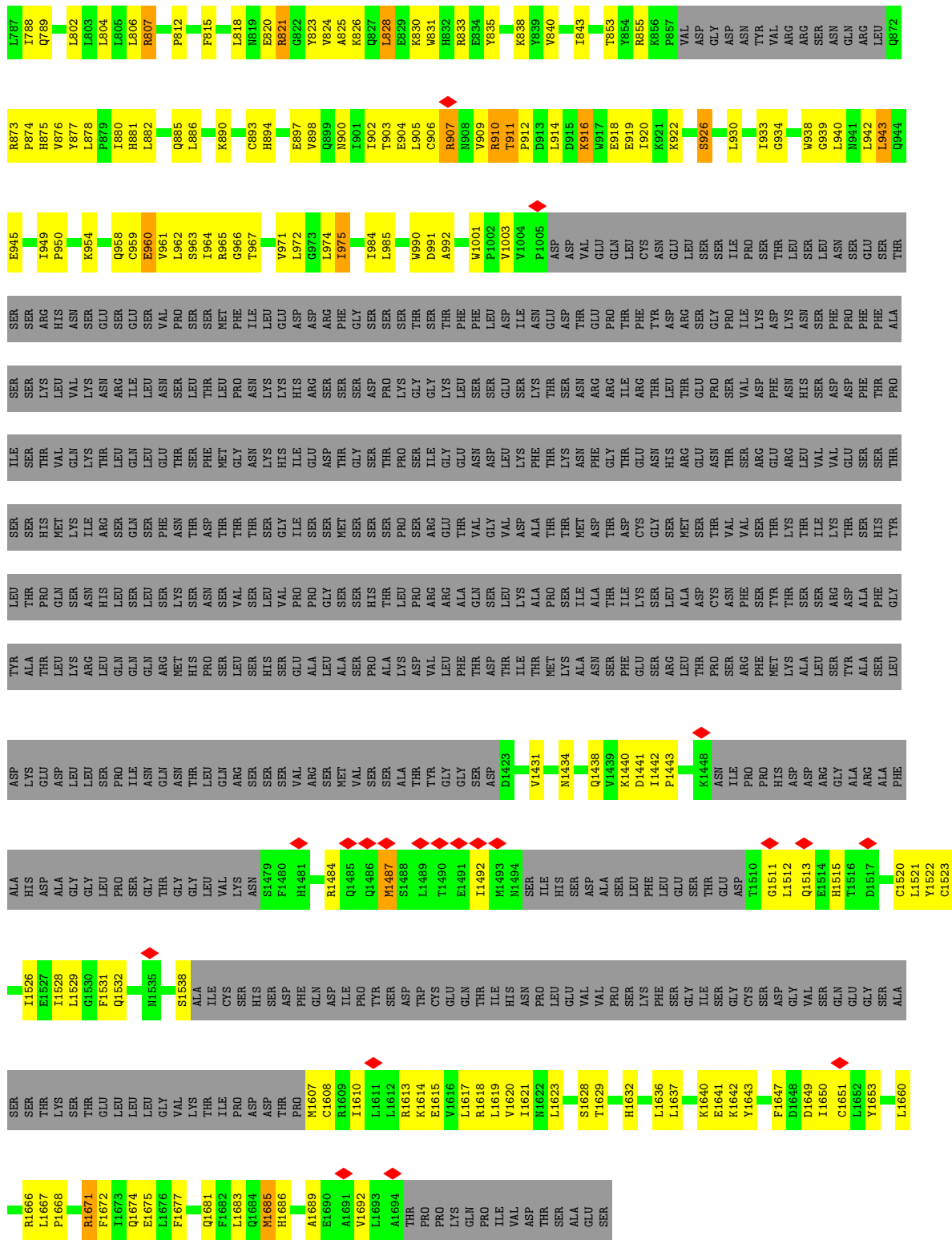


● Molecule 3: Rapamycin-insensitive companion of mTOR



Chain F:





● Molecule 4: Target of rapamycin complex 2 subunit MAPKAP1



LYS
LYS
SER
GLY
GLN
GLN
ALA
ALA
ALA
GLY
GLY
GLY
GLY
TYR
PRO
TYR
TYR
ASP
VAL
PRO
ASP
TYR
ALA

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	288538	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	22.607	Depositor
Minimum map value	-11.647	Depositor
Average map value	0.026	Depositor
Map value standard deviation	1.029	Depositor
Recommended contour level	2.64	Depositor
Map size (\AA)	356.4, 356.4, 356.4	wwPDB
Map dimensions	324, 324, 324	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1, 1.1, 1.1	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.31	0/16632	0.50	3/22593 (0.0%)
1	B	0.31	0/16598	0.50	3/22552 (0.0%)
2	C	0.28	0/2523	0.54	0/3438
2	D	0.28	0/2523	0.54	0/3438
3	E	0.31	1/9092 (0.0%)	0.54	8/12300 (0.1%)
3	F	0.31	1/9092 (0.0%)	0.54	8/12300 (0.1%)
4	G	1.95	39/852 (4.6%)	2.07	51/1161 (4.4%)
4	H	1.95	39/852 (4.6%)	2.07	51/1161 (4.4%)
All	All	0.45	80/58164 (0.1%)	0.62	124/78943 (0.2%)

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
3	E	0	1
3	F	0	1
4	G	2	6
4	H	2	6
All	All	4	14

The worst 5 of 80 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	77	ASP	CB-CG	-11.57	1.27	1.51
4	H	77	ASP	CB-CG	-11.54	1.27	1.51
4	G	86	THR	C-O	11.16	1.44	1.23
4	H	86	THR	C-O	11.13	1.44	1.23
4	H	88	GLN	CG-CD	-10.90	1.25	1.51

The worst 5 of 124 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	35	ASP	CB-CG-OD1	19.25	135.62	118.30
4	H	35	ASP	CB-CG-OD1	19.16	135.54	118.30
4	H	77	ASP	N-CA-C	16.71	156.12	111.00
4	G	77	ASP	N-CA-C	16.70	156.08	111.00
4	G	77	ASP	CB-CA-C	-16.17	78.05	110.40

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	G	80	ILE	CA
4	G	85	ASN	CA
4	H	80	ILE	CA
4	H	85	ASN	CA

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	E	367	GLY	Peptide
3	F	367	GLY	Peptide
4	G	34	HIS	Mainchain
4	G	36	VAL	Mainchain
4	G	69	SER	Mainchain

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	A	16337	0	15369	521	0
1	B	16304	0	15298	477	0
2	C	2465	0	2351	106	0
2	D	2465	0	2351	105	0
3	E	8931	0	9083	369	0
3	F	8931	0	9083	382	0
4	G	842	0	695	83	0
4	H	842	0	695	96	0
All	All	57117	0	54925	2072	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 18.

The worst 5 of 2072 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)
4:H:67:ALA:O	4:H:68:GLN:CG	1.78	1.31
4:G:67:ALA:O	4:G:68:GLN:CG	1.78	1.30
4:H:87:ALA:O	4:H:90:LEU:N	1.71	1.21
4:G:87:ALA:O	4:G:90:LEU:N	1.71	1.21
4:G:32:ILE:HD12	4:G:34:HIS:CD2	1.79	1.17

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	A	2143/2674 (80%)	2026 (94%)	117 (6%)	0	100	100
1	B	2145/2674 (80%)	2012 (94%)	133 (6%)	0	100	100
2	C	317/347 (91%)	292 (92%)	25 (8%)	0	100	100
2	D	317/347 (91%)	292 (92%)	25 (8%)	0	100	100
3	E	1103/1720 (64%)	1027 (93%)	76 (7%)	0	100	100
3	F	1103/1720 (64%)	1027 (93%)	76 (7%)	0	100	100
4	G	116/538 (22%)	87 (75%)	17 (15%)	12 (10%)	0	3
4	H	116/538 (22%)	87 (75%)	17 (15%)	12 (10%)	0	3
All	All	7360/10558 (70%)	6850 (93%)	486 (7%)	24 (0%)	44	72

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	G	35	ASP
4	G	37	ASP

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Mol	Chain	Res	Type
4	G	72	ILE
4	G	74	SER
4	G	78	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	A	1563/2319 (67%)	1554 (99%)	9 (1%)	86	91
1	B	1552/2319 (67%)	1546 (100%)	6 (0%)	91	95
2	C	269/290 (93%)	266 (99%)	3 (1%)	73	85
2	D	269/290 (93%)	266 (99%)	3 (1%)	73	85
3	E	987/1550 (64%)	957 (97%)	30 (3%)	41	68
3	F	987/1550 (64%)	957 (97%)	30 (3%)	41	68
4	G	70/479 (15%)	57 (81%)	13 (19%)	1	7
4	H	70/479 (15%)	57 (81%)	13 (19%)	1	7
All	All	5767/9276 (62%)	5660 (98%)	107 (2%)	59	77

5 of 107 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	333	ASP
3	F	910	ARG
4	H	70	VAL
3	F	430	LEU
3	F	821	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	94	ASN
3	F	1438	GLN

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Mol	Chain	Res	Type
3	F	607	GLN
4	G	34	HIS
1	B	1049	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	G	1
4	H	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	G	85:ASN	C	86:THR	N	1.20
1	H	85:ASN	C	86:THR	N	1.20

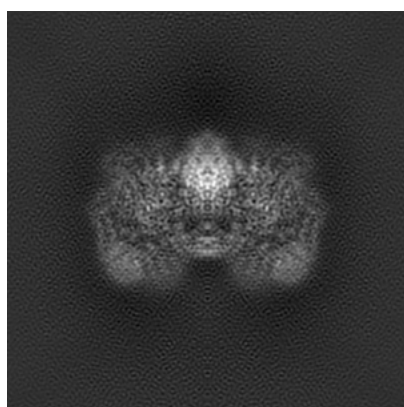
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26213. These allow visual inspection of the internal detail of the map and identification of artifacts.

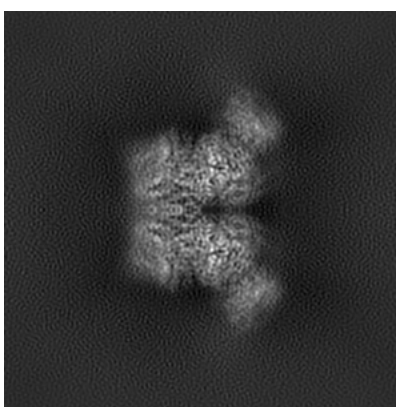
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

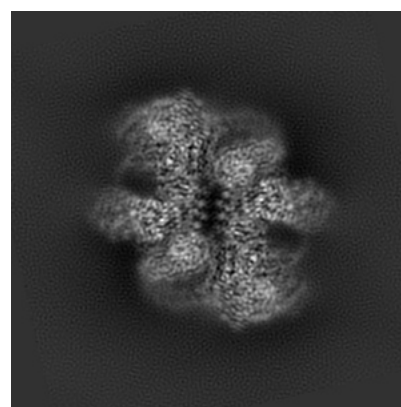
6.1.1 Primary map



X



Y

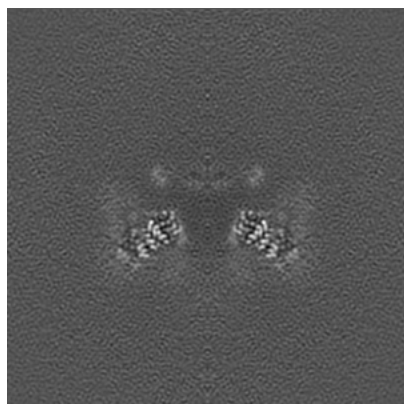


Z

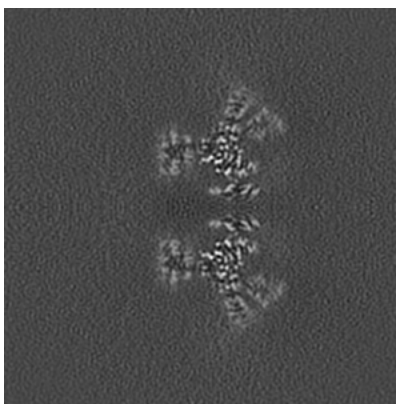
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

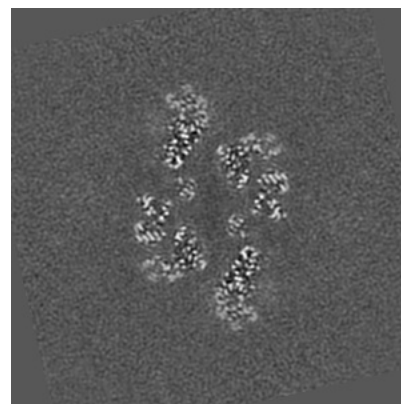
6.2.1 Primary map



X Index: 162



Y Index: 162

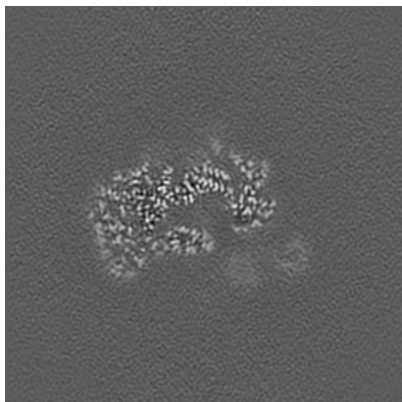


Z Index: 162

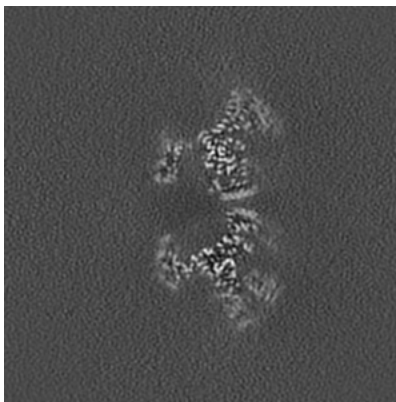
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

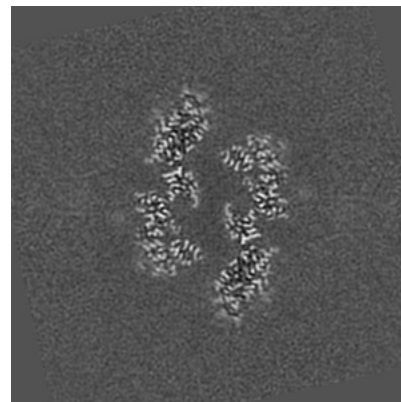
6.3.1 Primary map



X Index: 190



Y Index: 157

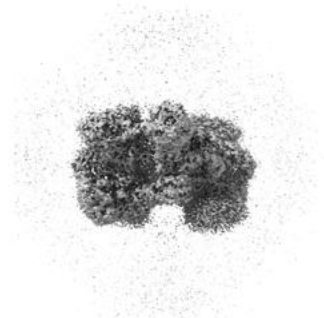


Z Index: 167

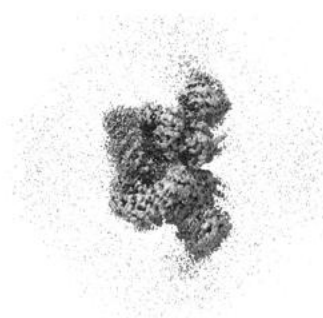
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

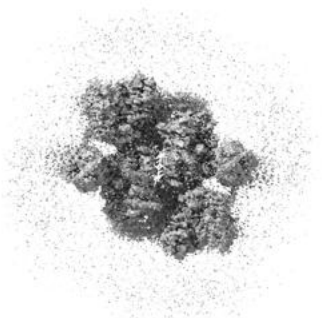
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.64. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

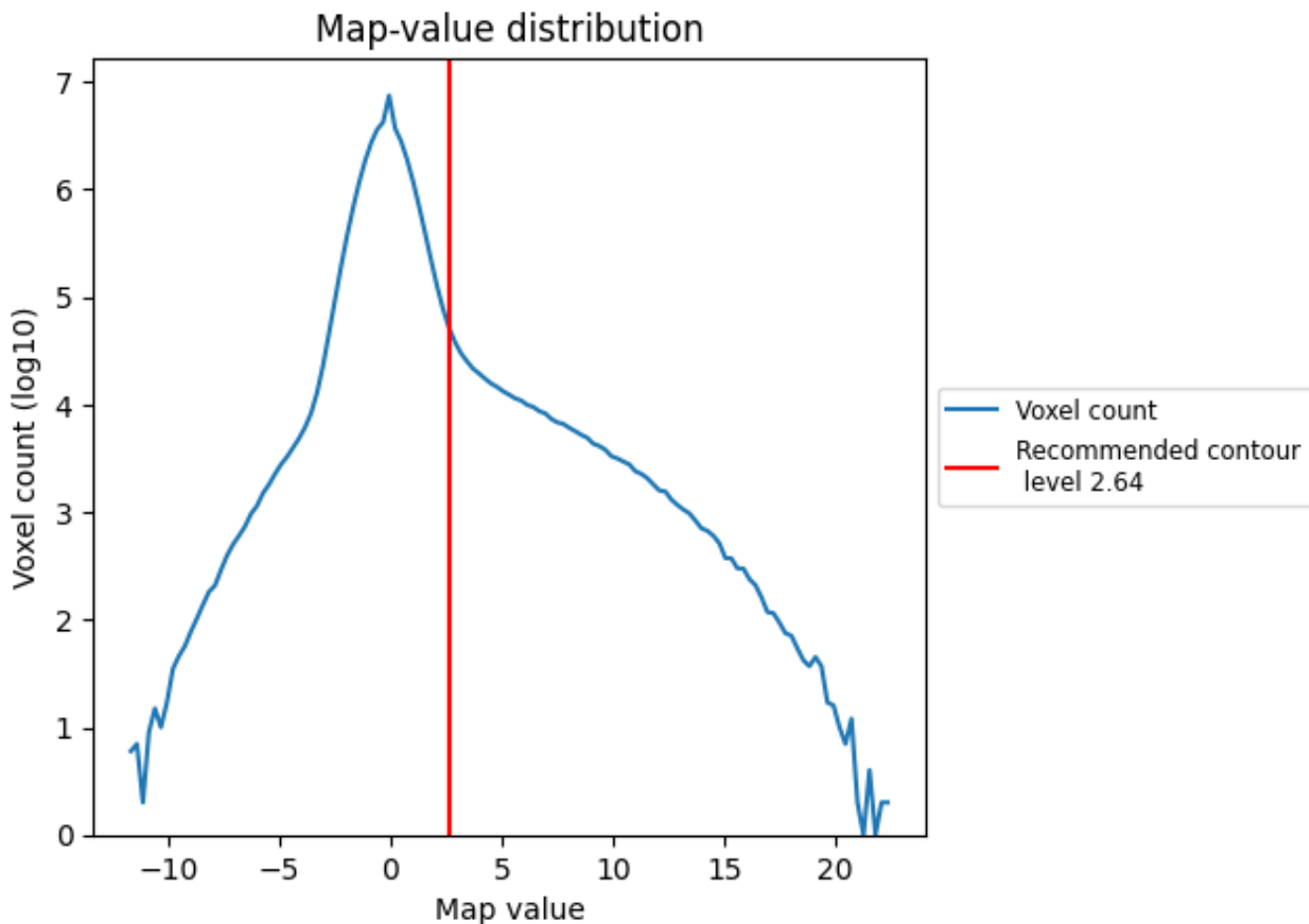
6.5 Mask visualisation

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

7 Map analysis [i](#)

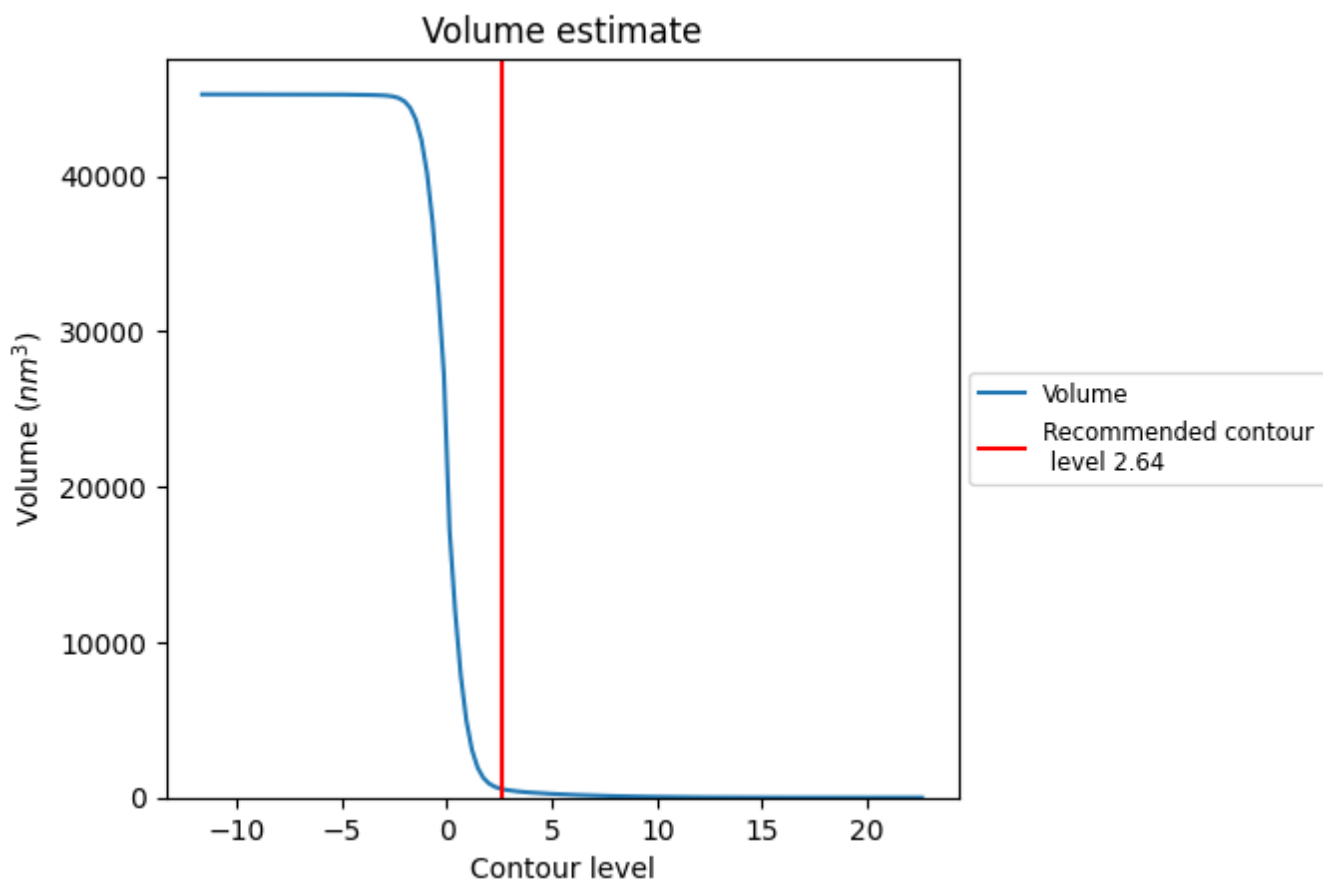
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

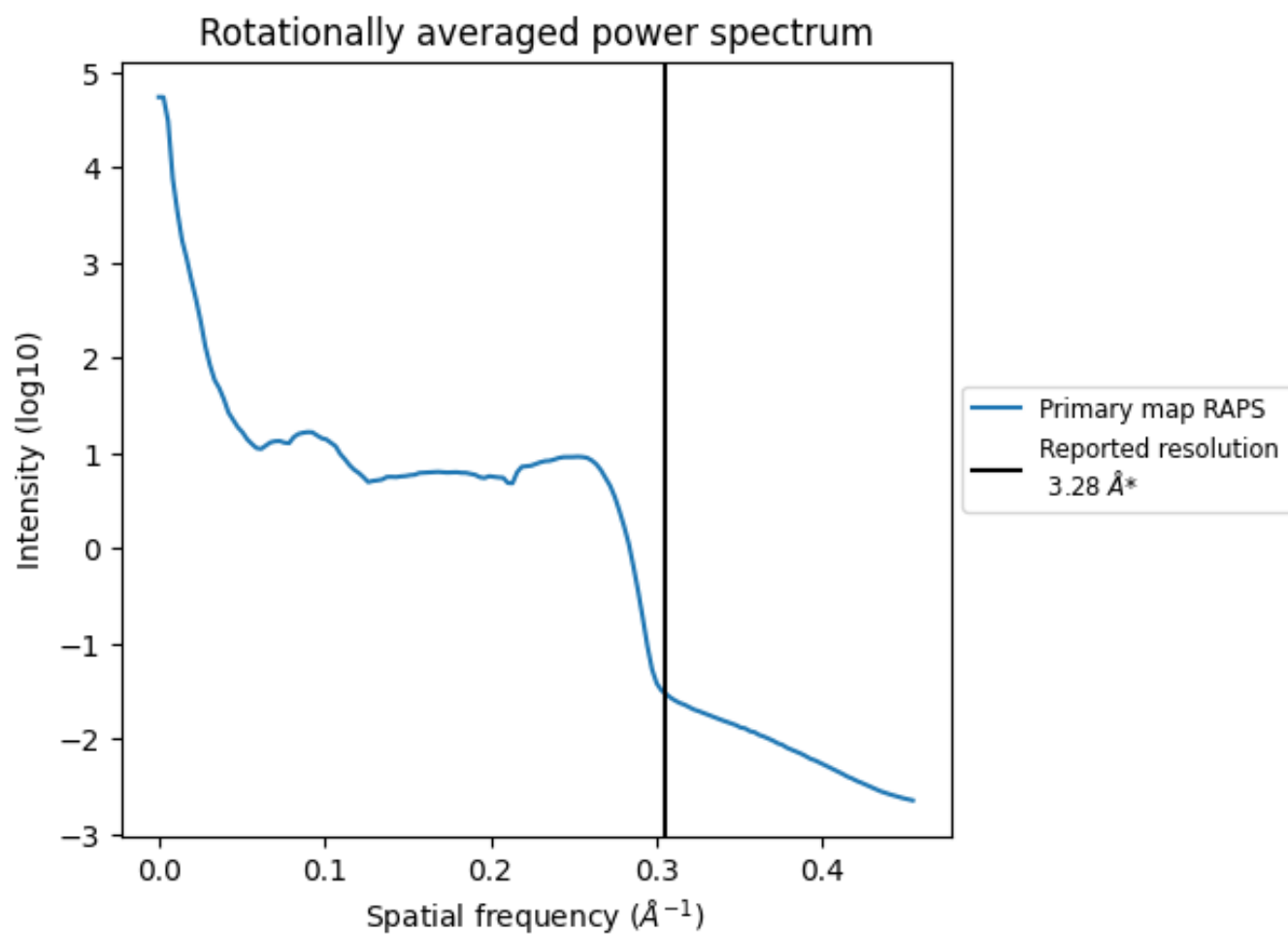
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 548 nm^3 ; this corresponds to an approximate mass of 495 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 0.305 Å⁻¹

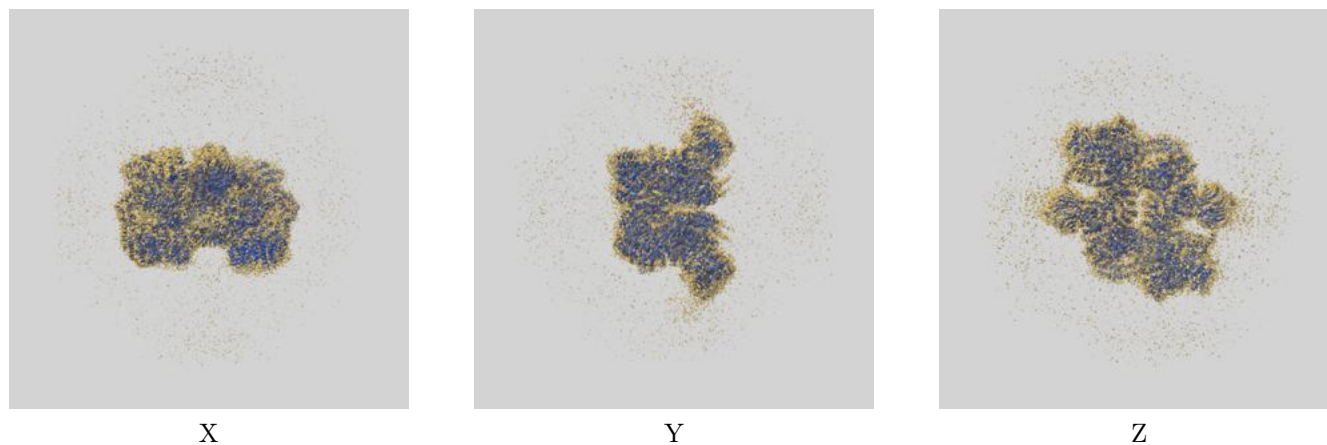
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

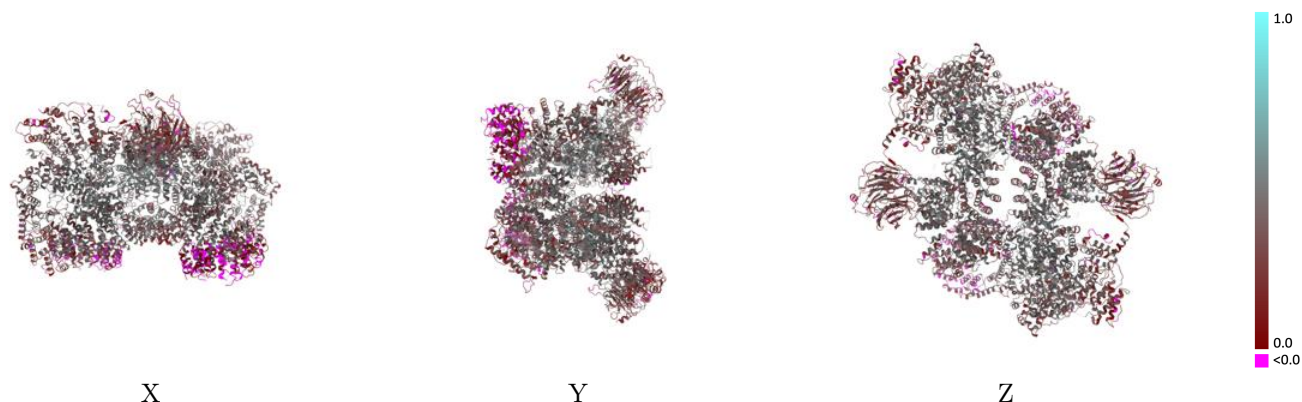
This section contains information regarding the fit between EMDB map EMD-26213 and PDB model 7TZO. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



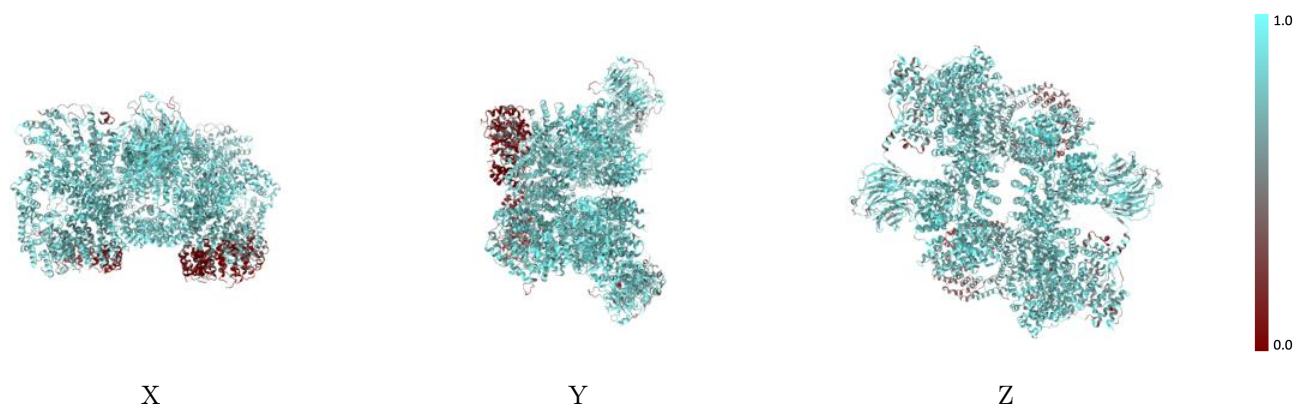
The images above show the 3D surface view of the map at the recommended contour level 2.64 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



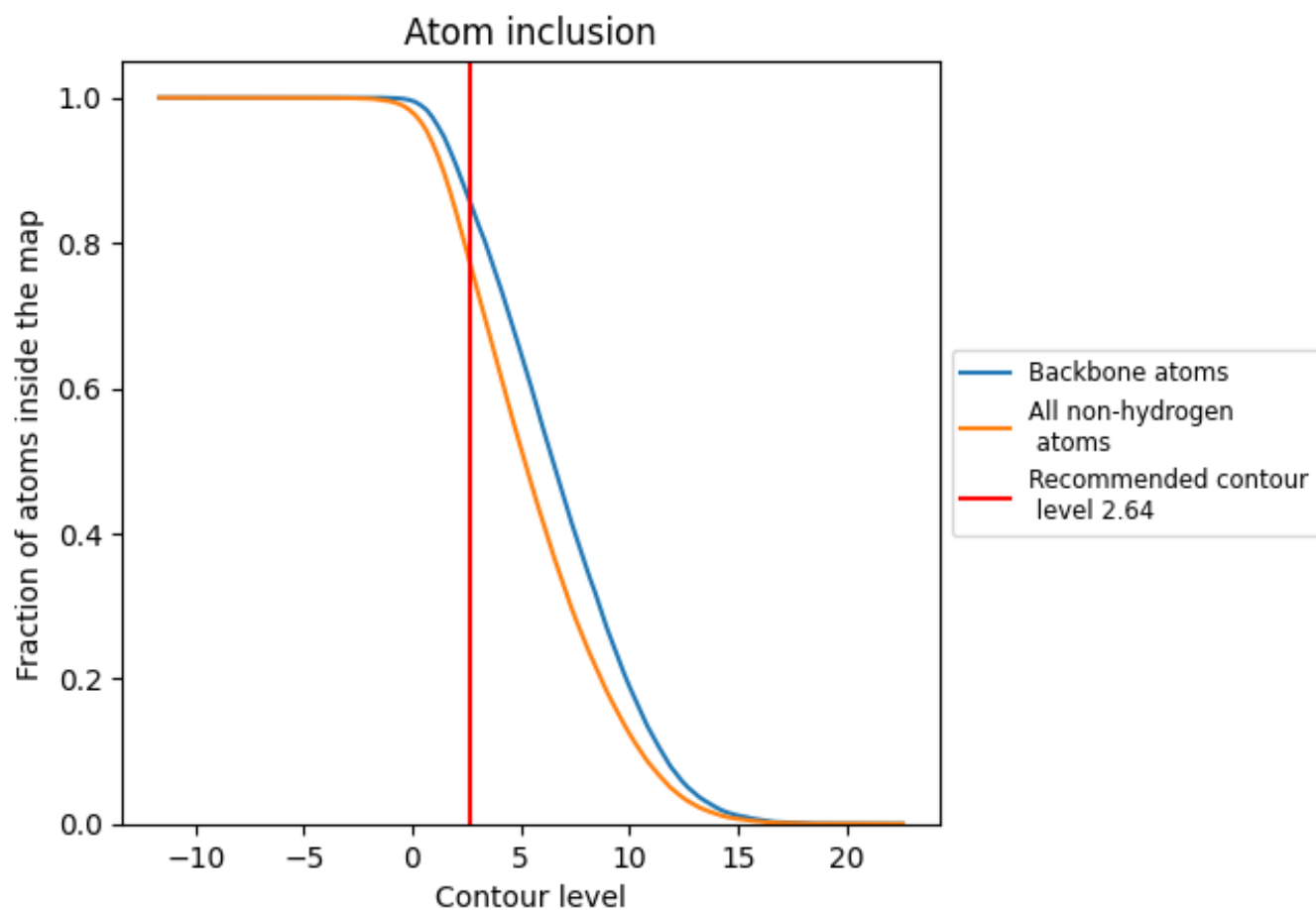
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.64).



















9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 77% 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 (2.64) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7741	 0.3530
A	 0.7622	 0.3570
B	 0.7660	 0.3630
C	 0.7690	 0.2750
D	 0.7724	 0.2860
E	 0.8006	 0.3650
F	 0.7980	 0.3600
G	 0.7112	 0.3150
H	 0.7100	 0.3180

