



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 09:39 PM UTC

PDB ID : 7YEV / pdb_00007yev
EMDB ID : EMD-33778
Title : In situ structure of polymerase complex of mammalian reovirus in the pre-elongation state
Authors : Bao, K.Y.; Zhang, X.L.; Li, D.Y.; Zhu, P.
Deposited on : 2022-07-06
Resolution : 3.60 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

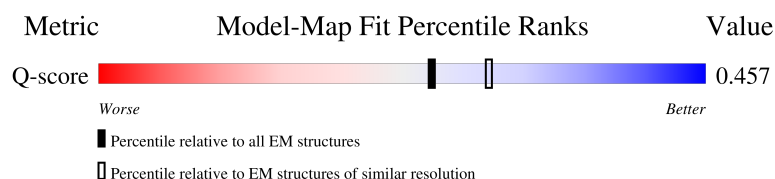
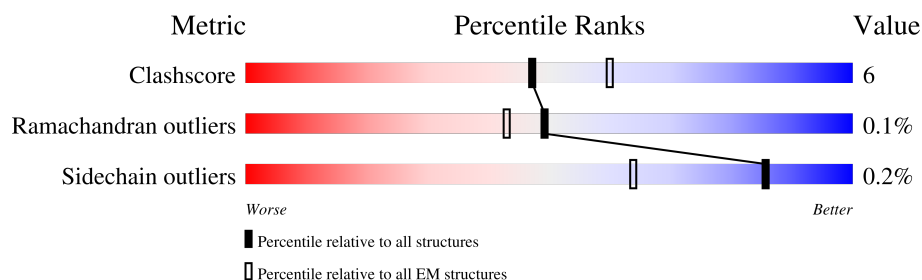
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.60 Å.

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



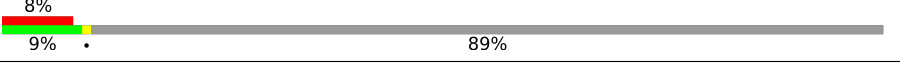
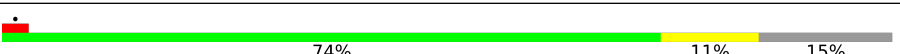
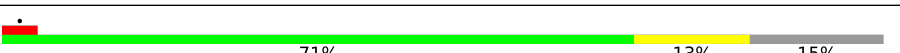
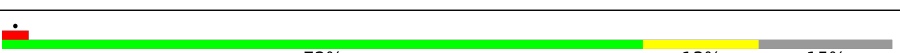
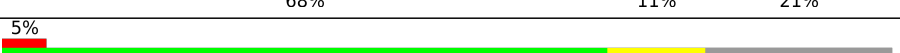
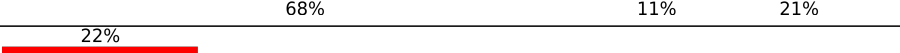
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	12797 (3.10 - 4.10)

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

Mol	Chain	Length	Quality of chain
1	1	1275	
1	2	1275	
1	3	1275	
1	4	1275	

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Mol	Chain	Length	Quality of chain
1	5	1275	
1	A	1275	
1	B	1275	
1	C	1275	
1	D	1275	
1	E	1275	
1	a	1275	
1	b	1275	
1	c	1275	
1	d	1275	
1	e	1275	
2	H	1289	
2	I	1289	
2	J	1289	
2	K	1289	
2	L	1289	
3	R	1267	
4	U	736	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	SAM	H	1301	-	-	X	-
6	SAM	H	1302	-	-	X	-
6	SAM	I	1301	-	-	X	-
6	SAM	I	1302	-	-	X	-
6	SAM	J	1301	-	-	X	-
6	SAM	J	1302	-	-	X	-
6	SAM	K	1301	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	SAM	K	1302	-	-	X	-
6	SAM	L	1301	-	-	X	-
6	SAM	L	1302	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 146613 atoms, of which 220 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 RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	140	Total	C	N	O	S	0	0
			1041	619	198	221	3		
1	2	139	Total	C	N	O	S	0	0
			1035	616	197	219	3		
1	3	138	Total	C	N	O	S	0	0
			1030	613	196	218	3		
1	4	131	Total	C	N	O	S	0	0
			967	574	183	207	3		
1	5	140	Total	C	N	O	S	0	0
			1041	619	198	221	3		
1	A	1128	Total	C	N	O	S	0	0
			8868	5654	1510	1651	53		
1	B	1073	Total	C	N	O	S	0	0
			8442	5389	1431	1571	51		
1	C	1088	Total	C	N	O	S	0	0
			8583	5480	1454	1598	51		
1	D	1050	Total	C	N	O	S	0	0
			8300	5306	1403	1542	49		
1	E	1061	Total	C	N	O	S	0	0
			8385	5356	1420	1560	49		
1	a	1087	Total	C	N	O	S	0	0
			8571	5473	1455	1592	51		
1	b	1087	Total	C	N	O	S	0	0
			8571	5473	1455	1592	51		
1	c	1082	Total	C	N	O	S	0	0
			8539	5455	1452	1581	51		
1	d	1087	Total	C	N	O	S	0	0
			8571	5473	1455	1592	51		
1	e	1087	Total	C	N	O	S	0	0
			8571	5473	1455	1592	51		

- Molecule 2 is a protein called Lambda-2 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	1024	Total	C	N	O	S	0	0
			8073	5150	1375	1519	29		
2	I	1024	Total	C	N	O	S	0	0
			8073	5150	1375	1519	29		
2	J	1024	Total	C	N	O	S	0	0
			8073	5150	1375	1519	29		
2	K	1024	Total	C	N	O	S	0	0
			8073	5150	1375	1519	29		
2	L	1024	Total	C	N	O	S	0	0
			8073	5150	1375	1519	29		

- Molecule 3 is a protein called RNA-directed RNA polymerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	R	1253	Total	C	N	O	S	0	0
			9913	6327	1697	1824	65		

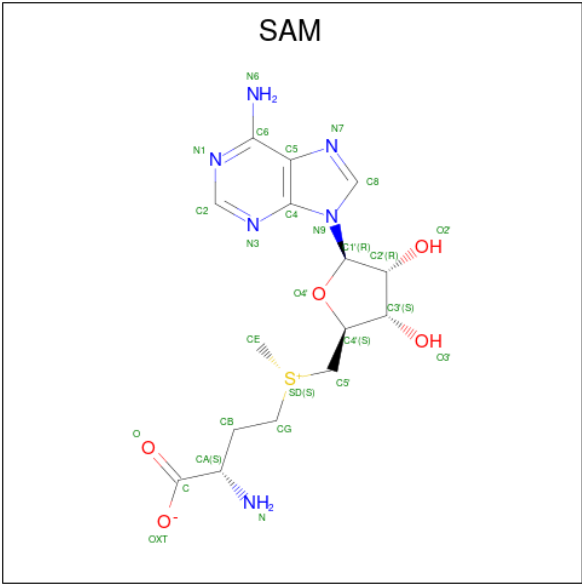
- Molecule 4 is a protein called Mu-2 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	U	668	Total	C	N	O	S	0	0
			5322	3413	901	979	29		

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
5	A	1	Total	Zn	0
			1	1	
5	B	1	Total	Zn	0
			1	1	
5	C	1	Total	Zn	0
			1	1	
5	a	1	Total	Zn	0
			1	1	
5	b	1	Total	Zn	0
			1	1	
5	c	1	Total	Zn	0
			1	1	
5	d	1	Total	Zn	0
			1	1	
5	e	1	Total	Zn	0
			1	1	

- Molecule 6 is S-ADENOSYLMETHIONINE (CCD ID: SAM) (formula: C₁₅H₂₂N₆O₅S).

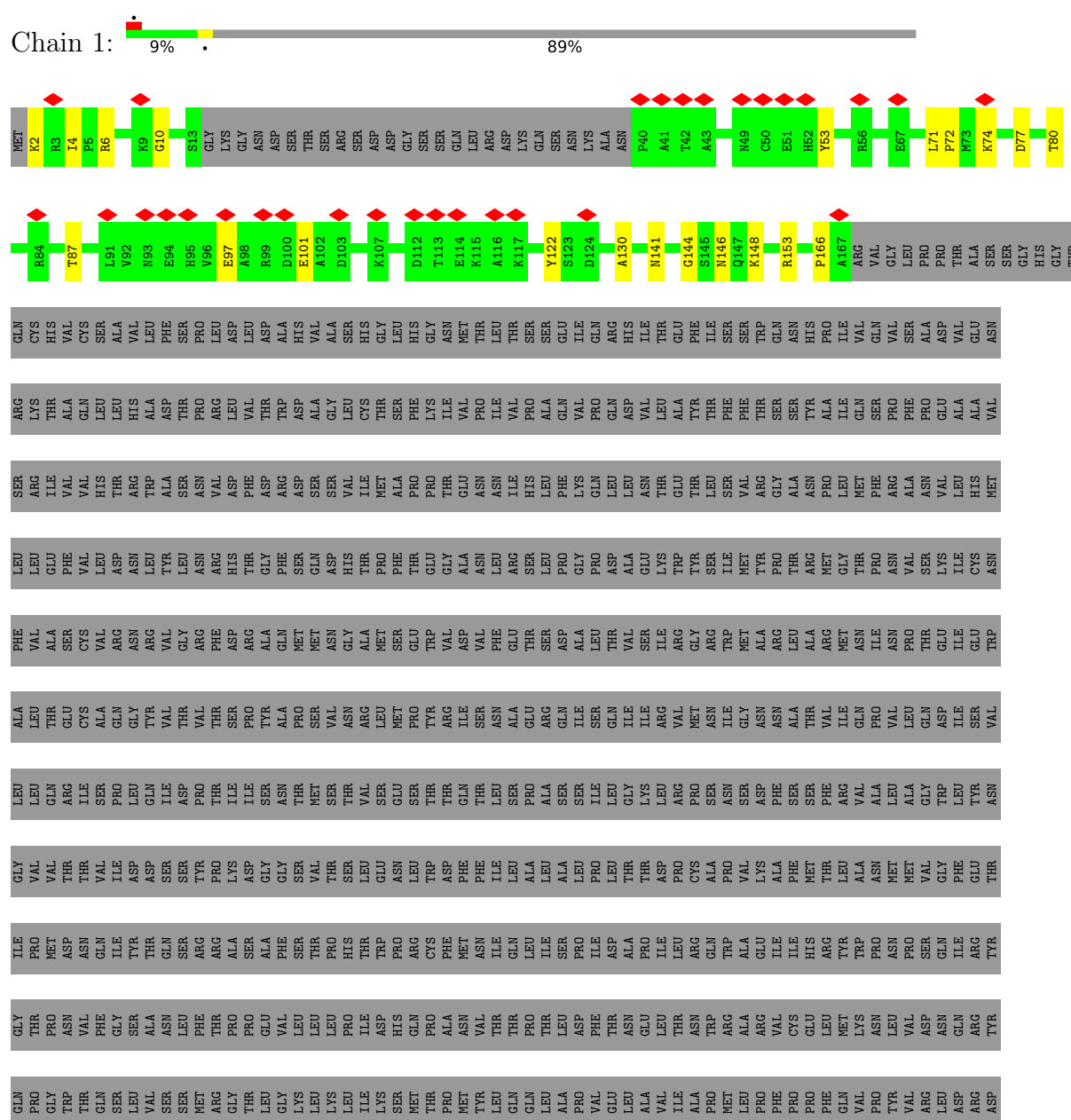


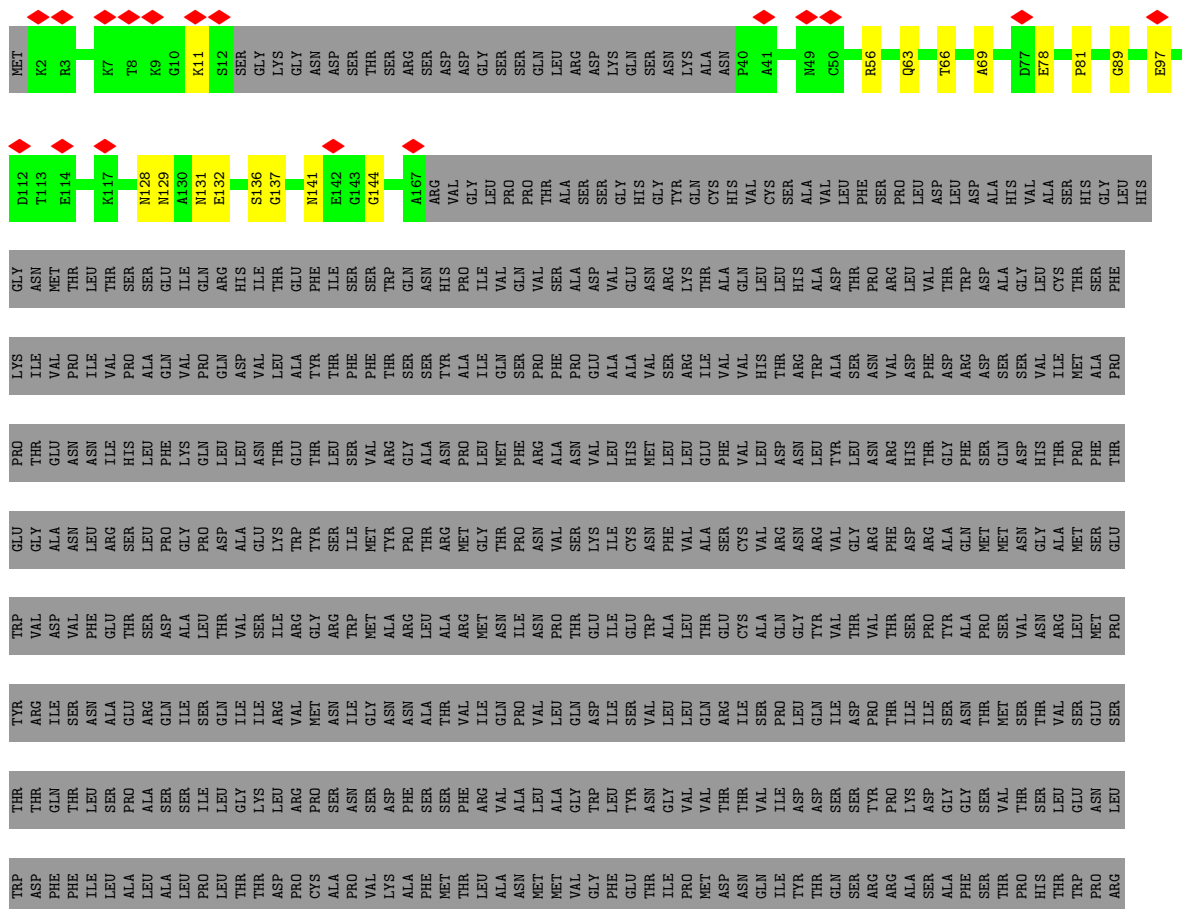
Mol	Chain	Residues	Atoms					AltConf
6	H	1	Total	C	H	N	O	S
			49	15	22	6	5	1
6	H	1	Total	C	H	N	O	S
			49	15	22	6	5	1
6	I	1	Total	C	H	N	O	S
			49	15	22	6	5	1
6	I	1	Total	C	H	N	O	S
			49	15	22	6	5	1
6	J	1	Total	C	H	N	O	S
			49	15	22	6	5	1
6	J	1	Total	C	H	N	O	S
			49	15	22	6	5	1
6	K	1	Total	C	H	N	O	S
			49	15	22	6	5	1
6	K	1	Total	C	H	N	O	S
			49	15	22	6	5	1
6	L	1	Total	C	H	N	O	S
			49	15	22	6	5	1
6	L	1	Total	C	H	N	O	S
			49	15	22	6	5	1

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: RNA helicase

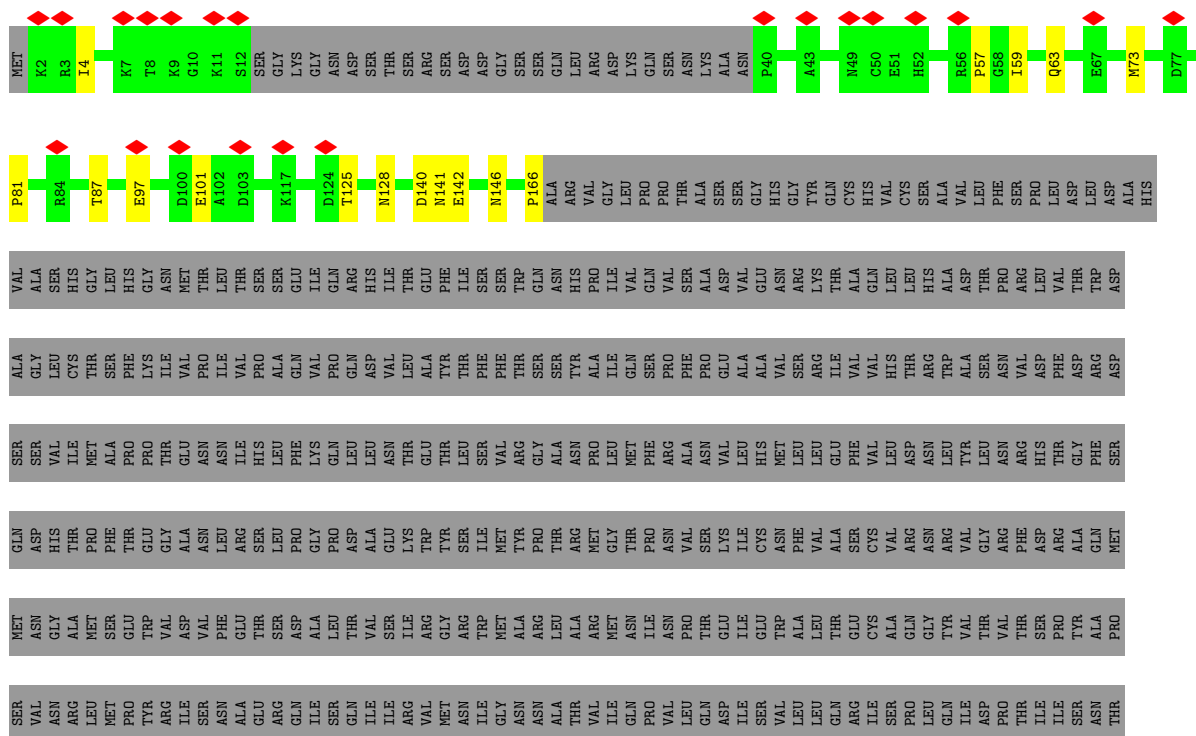




[illegible]

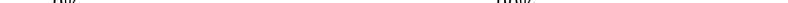
- Molecule 1: RNA helicase

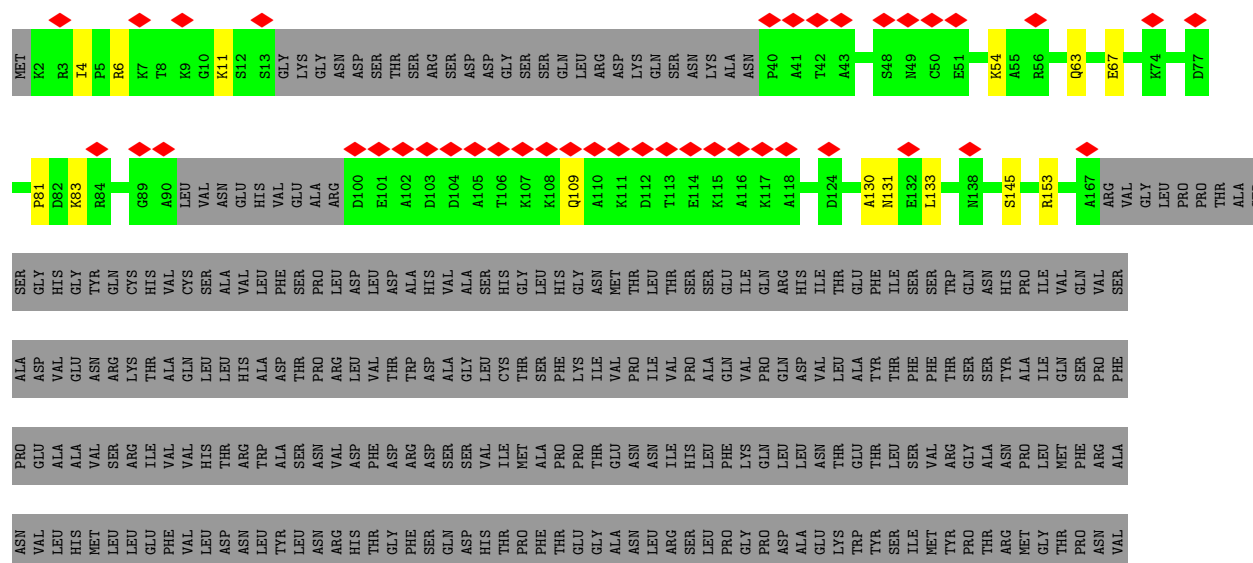
Chain 3: 10% 89%



[illegible]

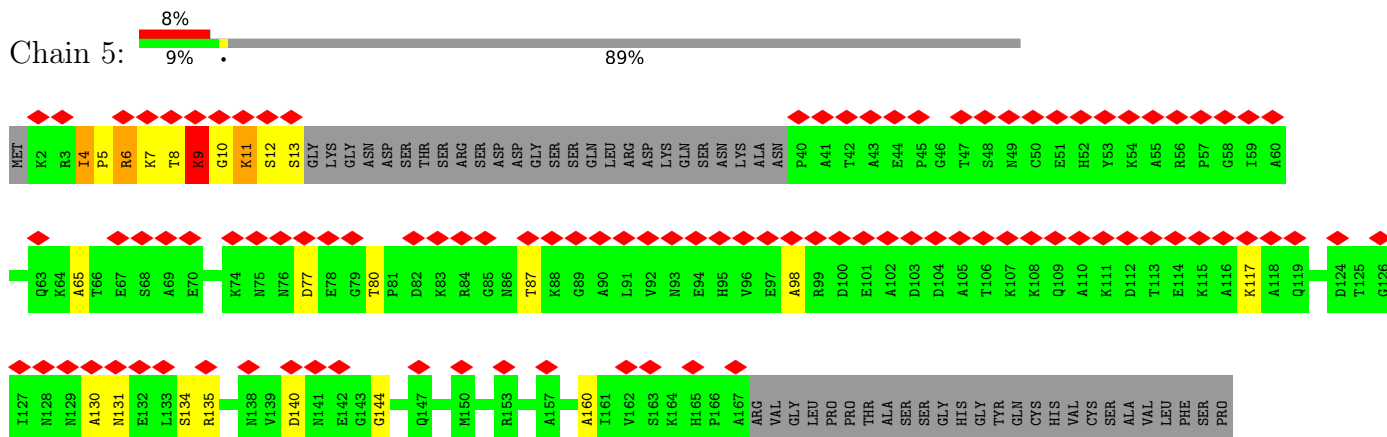
- Molecule 1: RNA helicase

Chain 4:  9% 90%

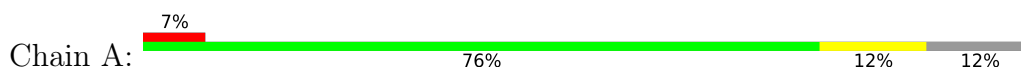


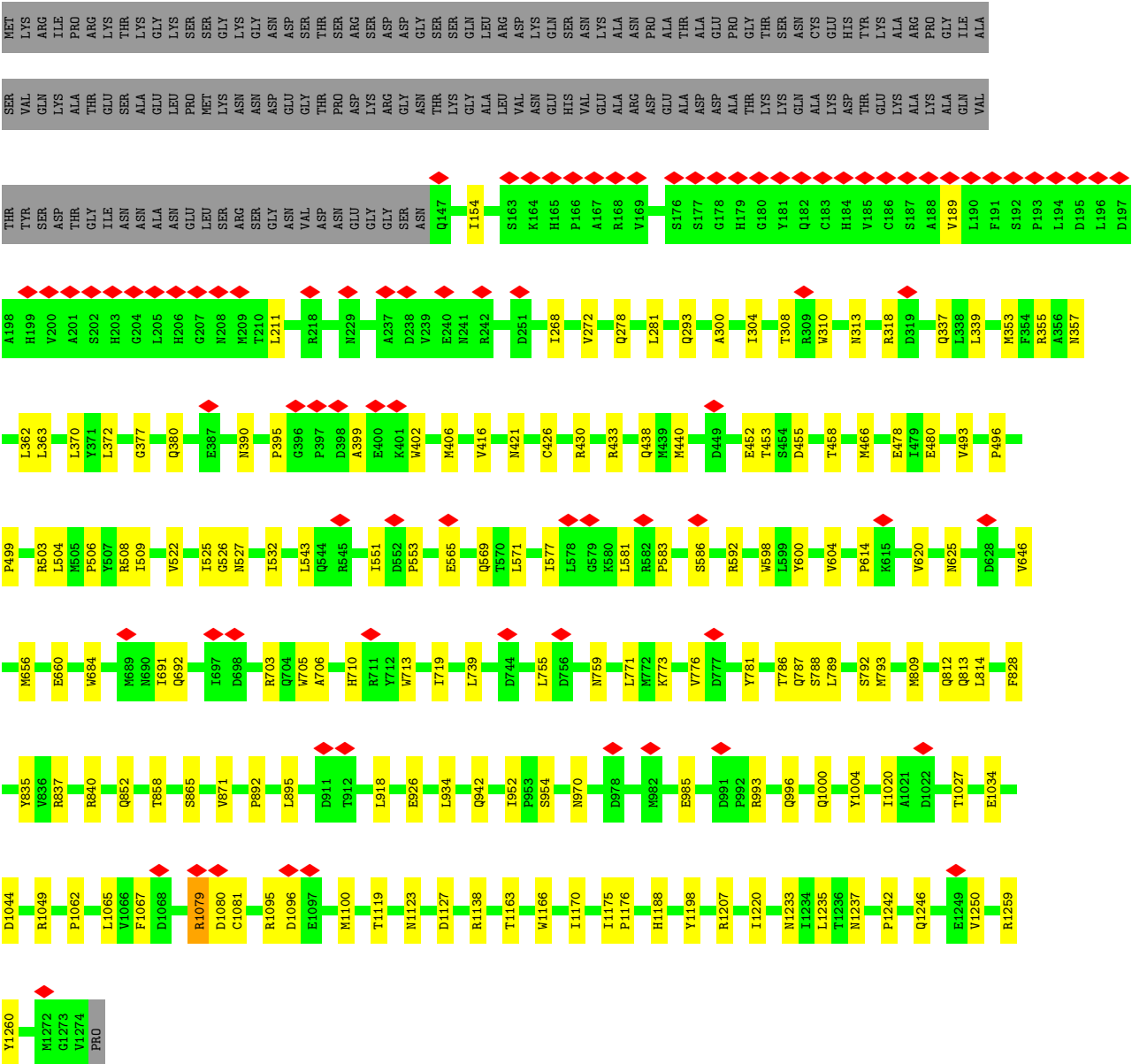
[illegible]

- Molecule 1: RNA helicase

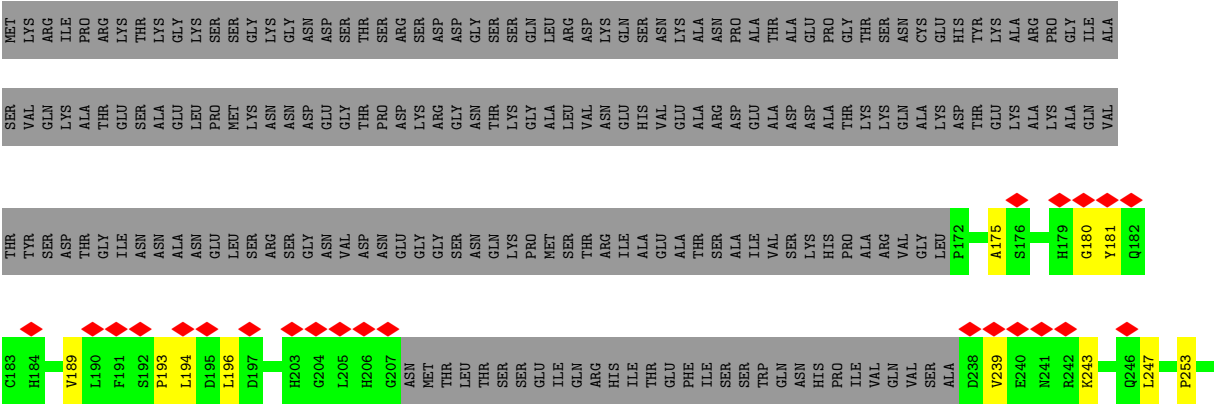


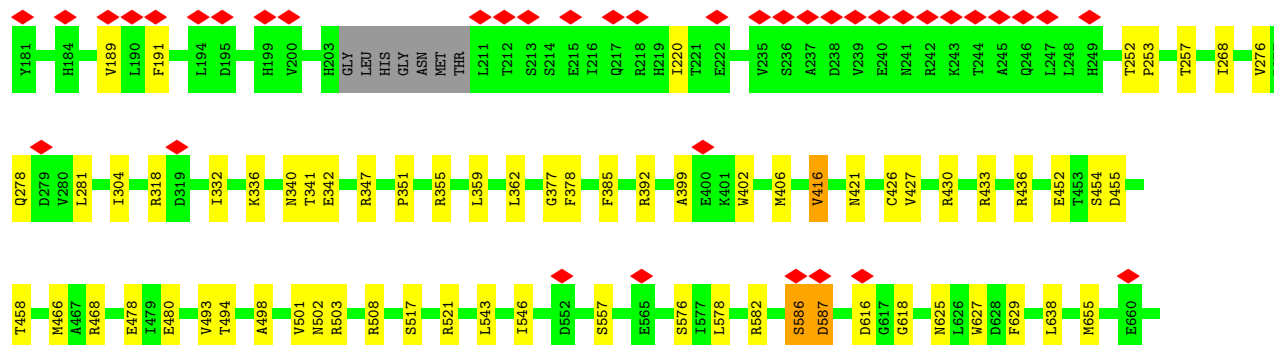
- Molecule 1: RNA helicase



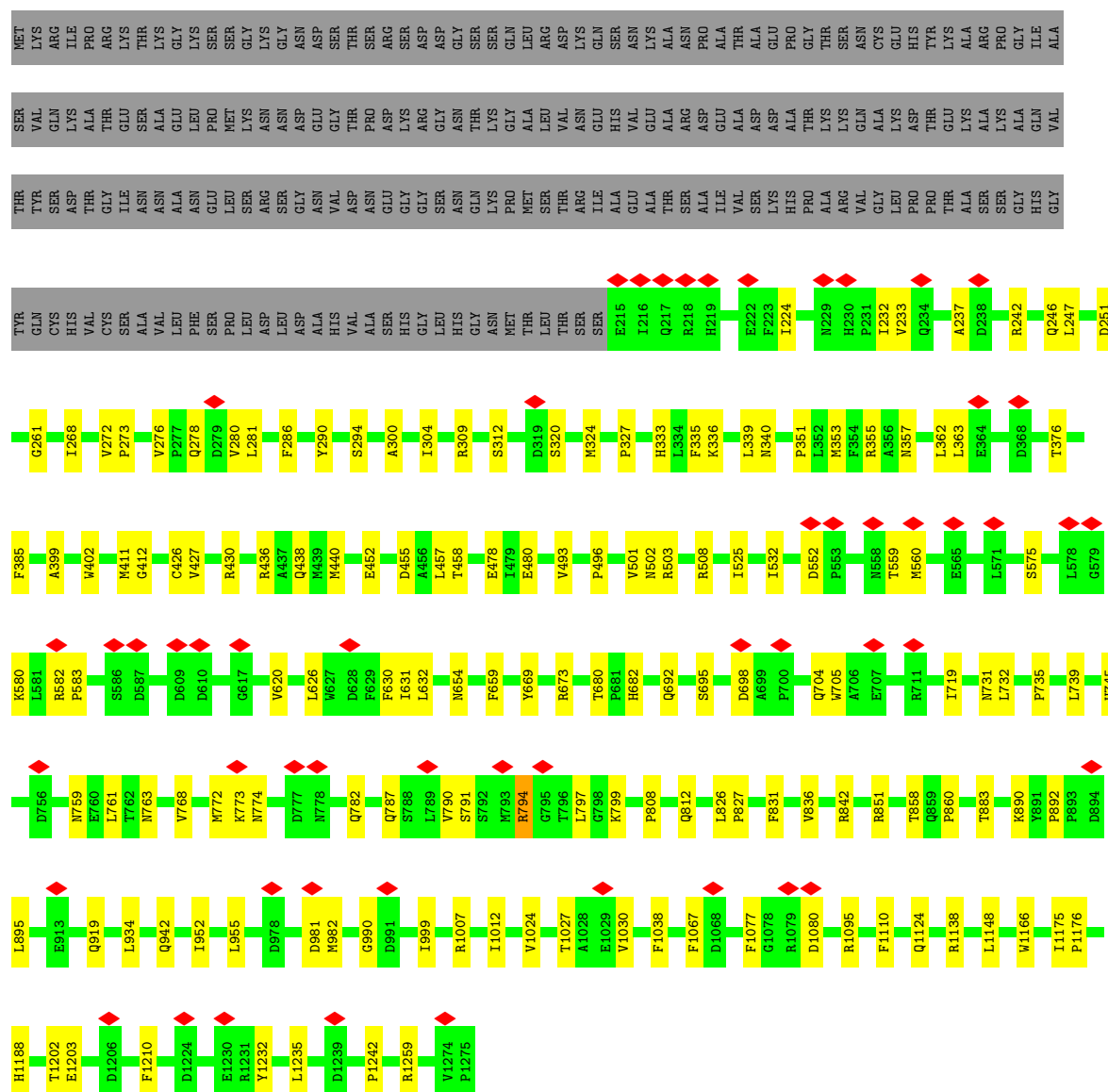


● Molecule 1: RNA helicase



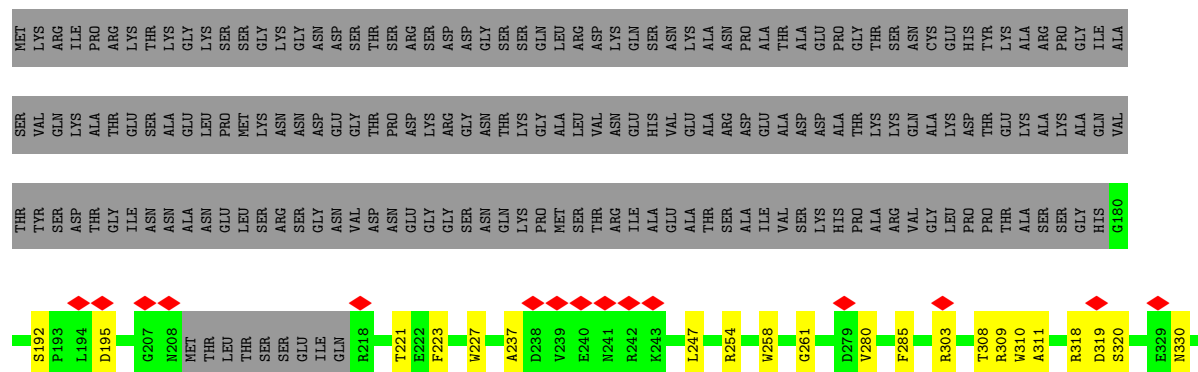


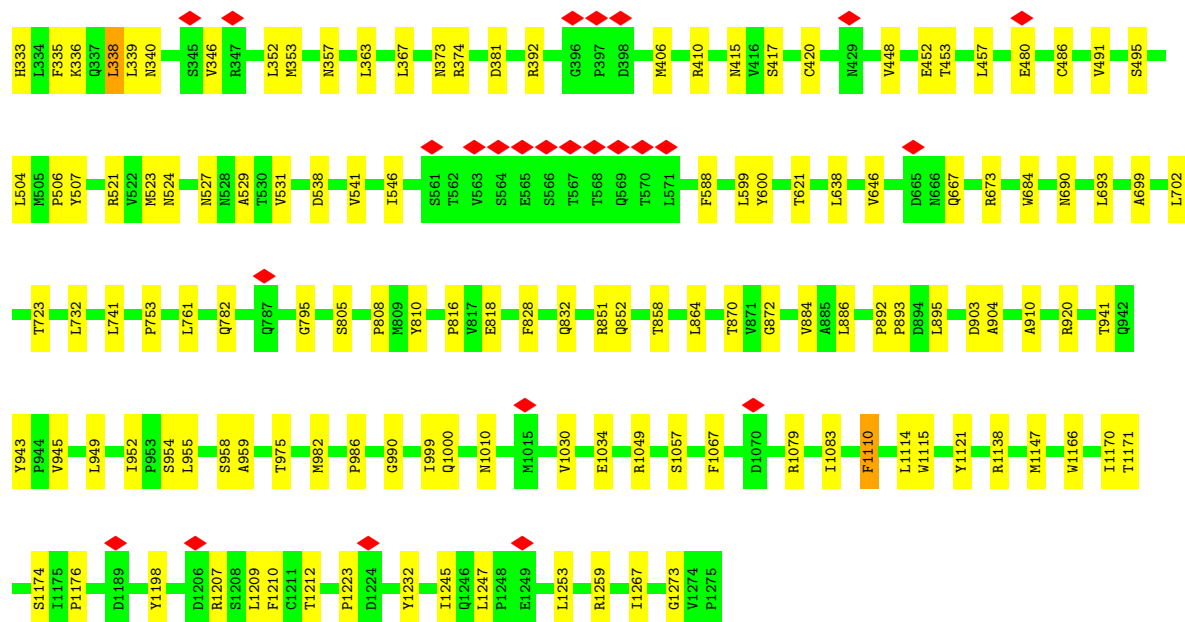
Chain E:  71% 12% 17%



• Molecule 1: RNA helicase

Chain a:  73% 12% 15%





- Molecule 1: RNA helicase

Chain b:



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

Amino Acid	Frequency (%)
S187	~1
L194	~15
D195	~11
V200	~2
L205	~2
H208	~1
ME1	~1
THR	~12
LEU	~12
THR	~12
THR	~12
SER	~12
GLU	~12
ILE	~12
GLN	~12
R218	~1
T221	~2
D238	~1
V239	~1
E240	~1
Q246	~2
F266	~2
V272	~2
V280	~2
F285	~1
A300	~2
V301	~2
D319	~1
H333	~2
K336	~2
K337	~2
L338	~2
L339	~2
L344	~1
S345	~2
V346	~2
R347	~1
L352	~2
N373	~2
F376	~2

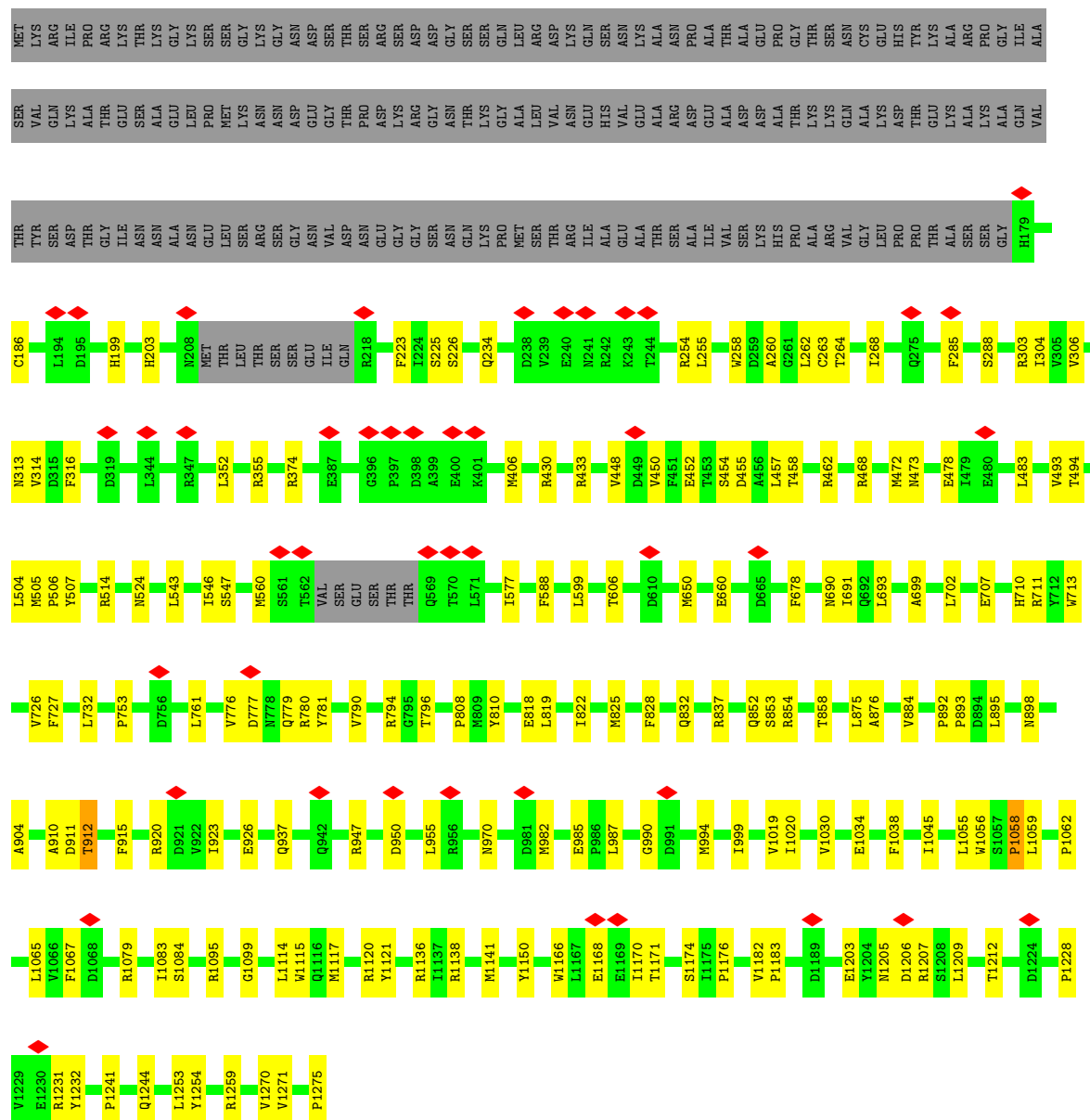
Year	Value	Category
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1902	1.0	Low
1903	1.0	Low
1904	1.0	Low
1905	1.0	Low
1906	1.0	Low
1907	1.0	Low
1908	1.0	Low
1909	1.0	Low
1910	1.0	Low
1911	1.0	Low
1912	1.0	Low
1913	1.0	Low
1914	1.0	Low
1915	1.0	Low
1916	1.0	Low
1917	1.0	Low
1918	1.0	Low
1919	1.0	Low
1920	1.0	Low
1921	1.0	Low
1922	1.0	Low
1923	1.0	Low
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1983	1.0	Low
1984	1.0	Low
1985	1.0	Low
1986	1.0	Low
1987	1.0	Low
1988	1.0	Low
1989	1.0	Low
1990	1.0	Low

Year	Number of Publications
1994	10
1998	10
1999	10
2019	10
2024	10
2034	10
2044	10
2049	10
2057	10
2068	10
2079	10
2080	10
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2082	10
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2084	10
2095	10
2099	10
2110	10
2115	10
2116	10
2117	10
2118	10
2121	10
2131	10
2138	10
2155	10
2166	10
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2176	10
2206	10
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2209	10
2212	10



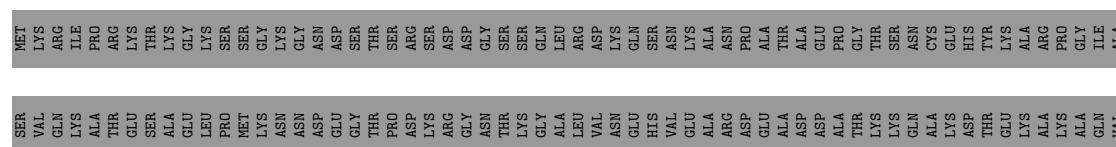
• Molecule 1: RNA helicase

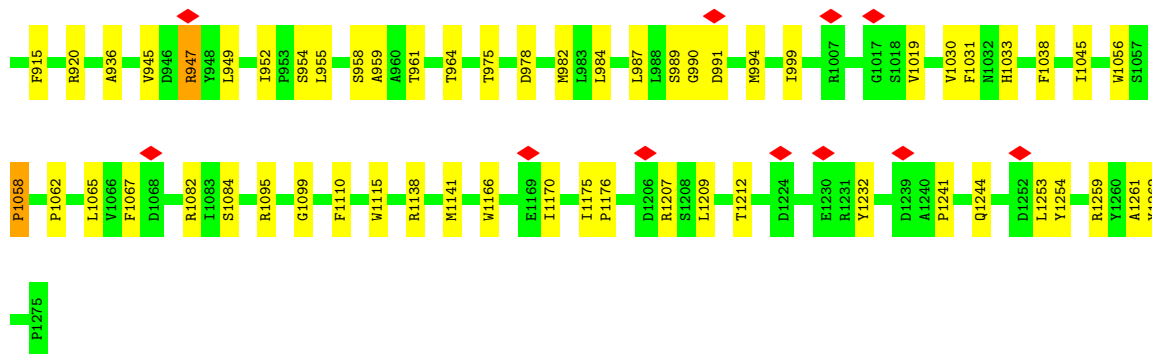
Chain c: 71% 13% 15%



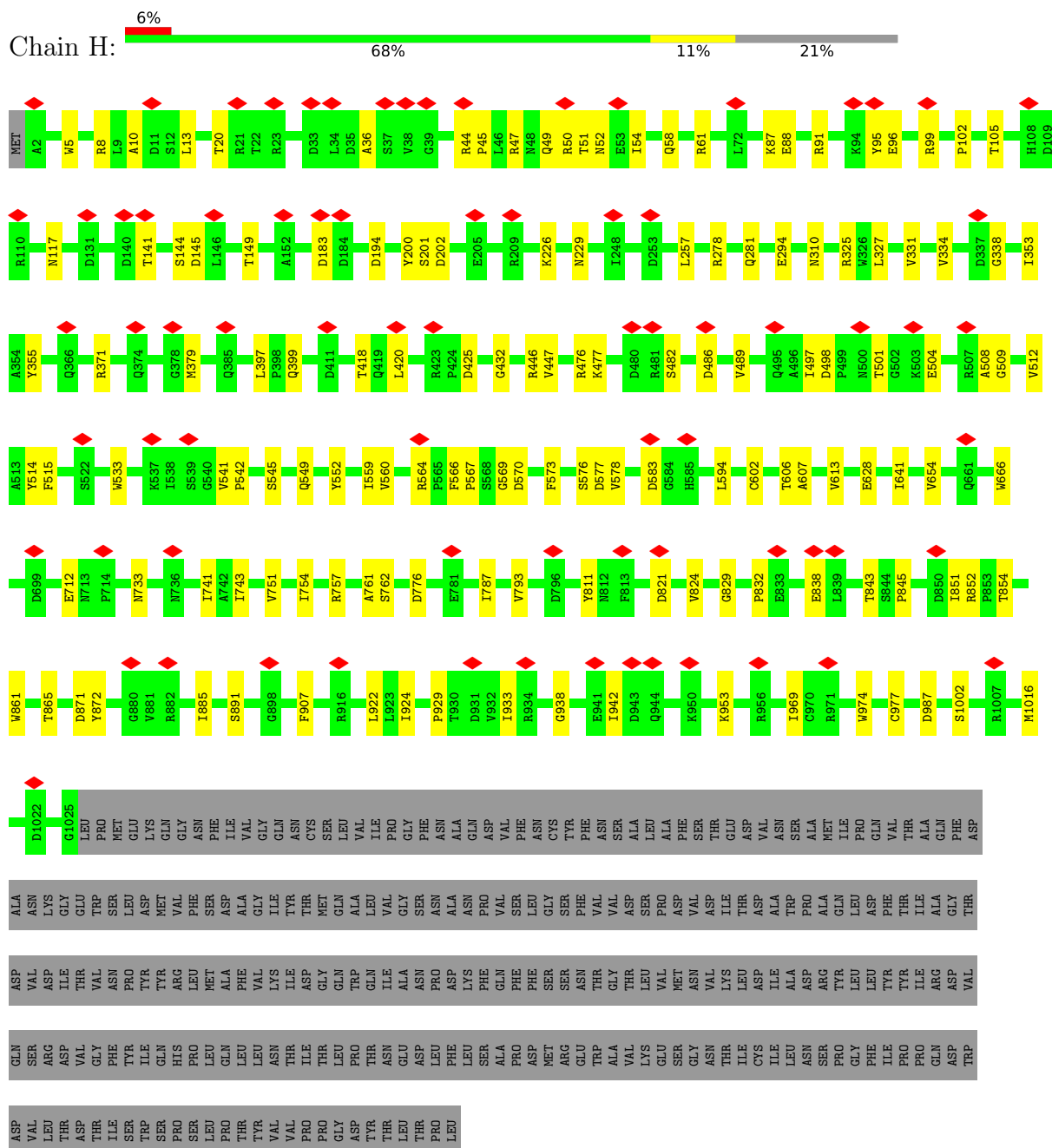
• Molecule 1: RNA helicase

Chain d: 74% 11% 15%

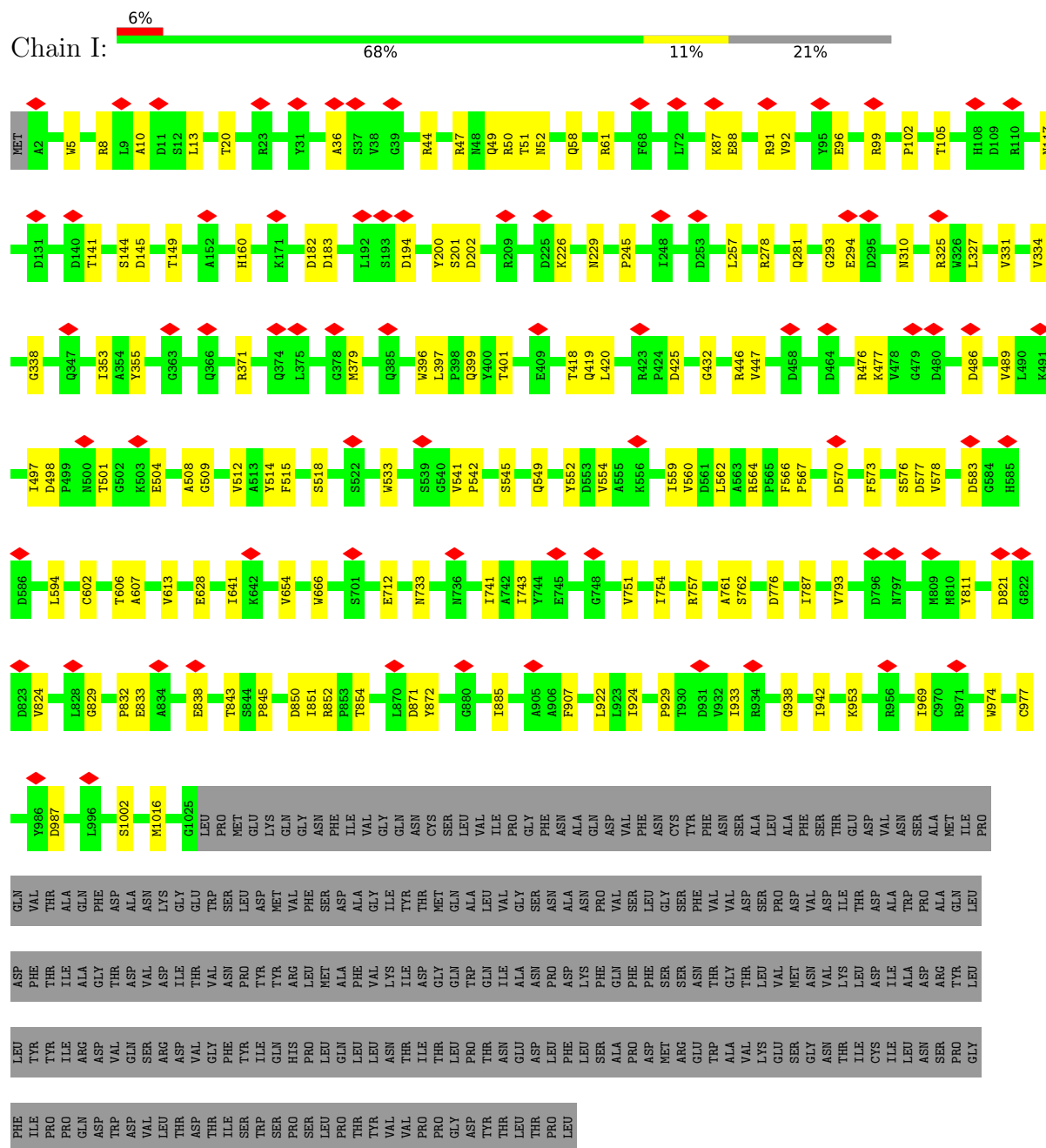




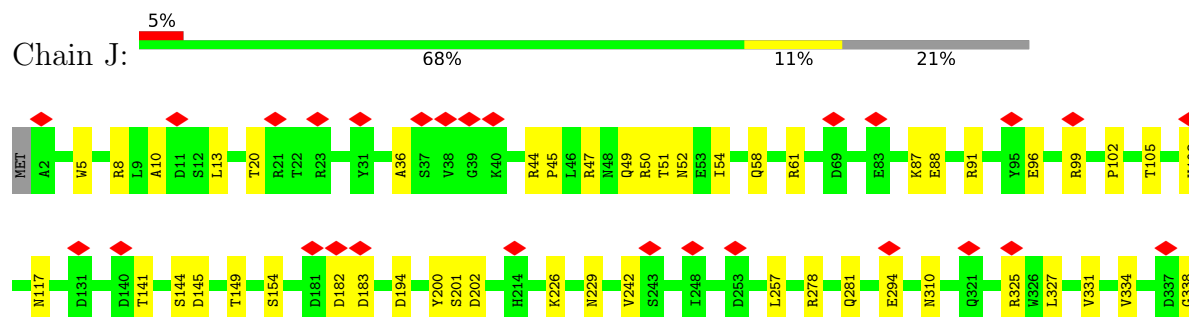
• Molecule 2: Lambda-2 protein



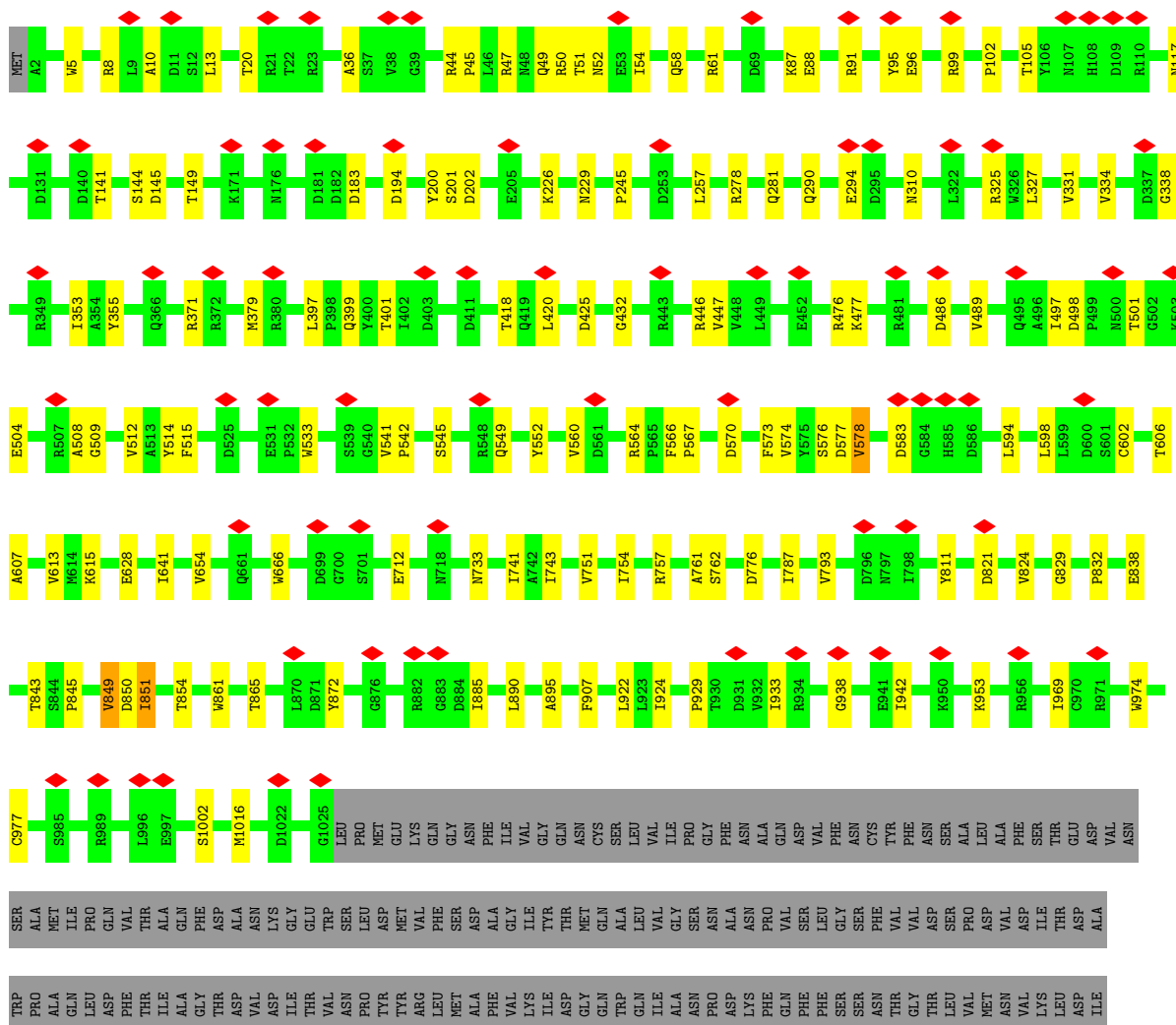
- Molecule 2: Lambda-2 protein



- Molecule 2: Lambda-2 protein

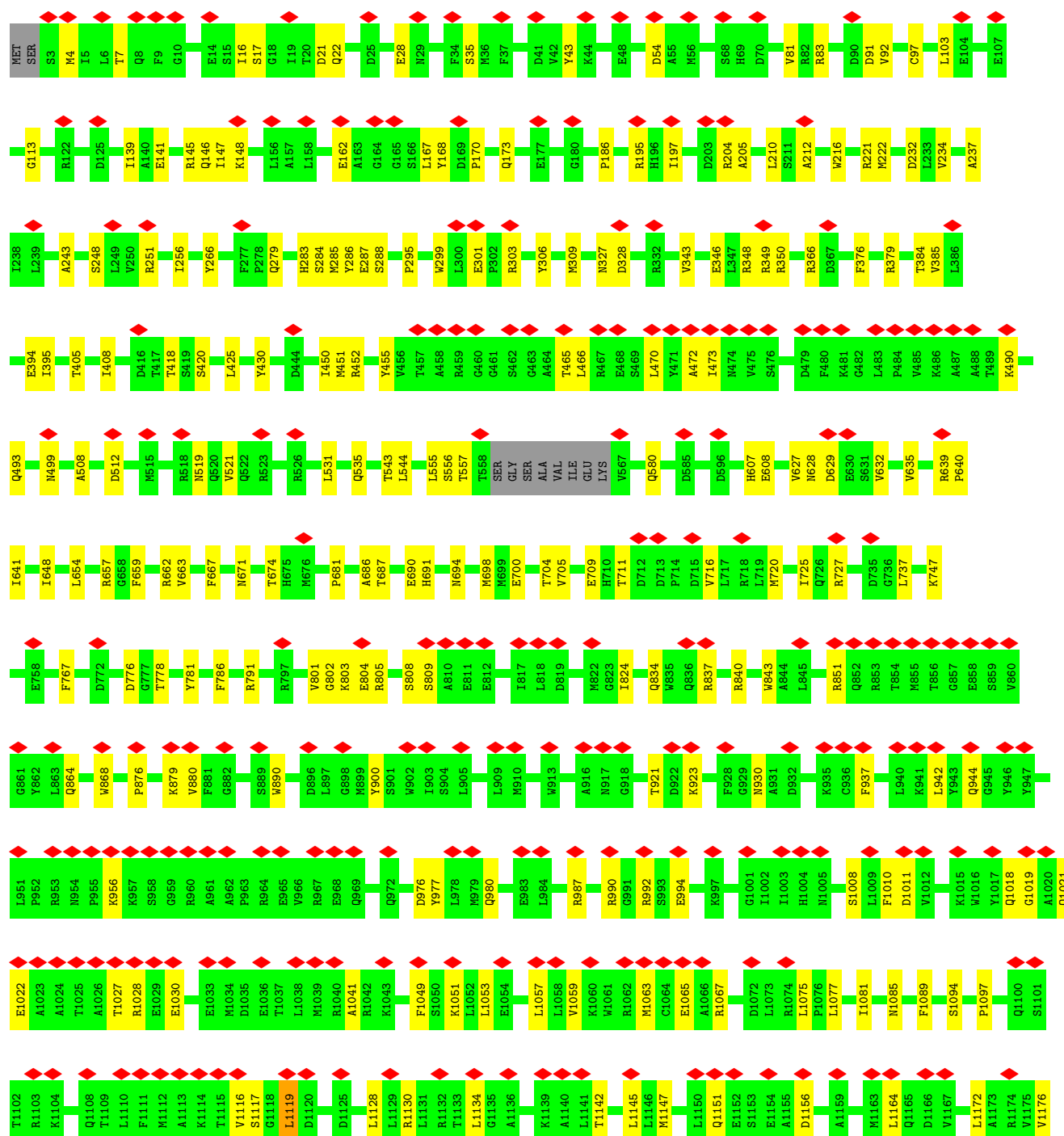
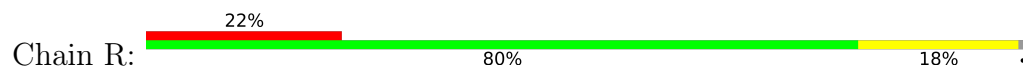


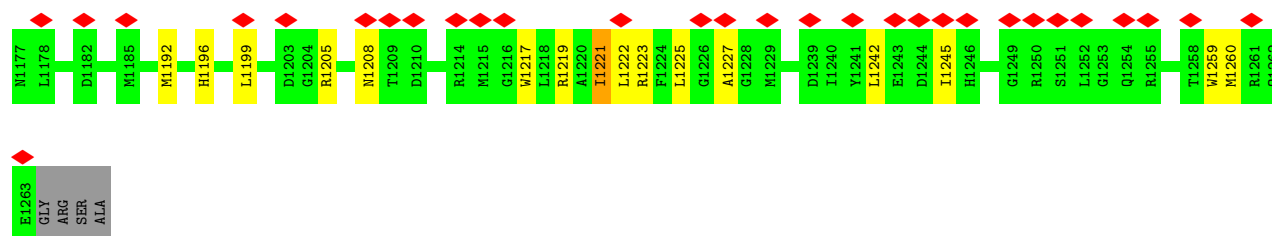
- Molecule 2: Lambda-2 protein



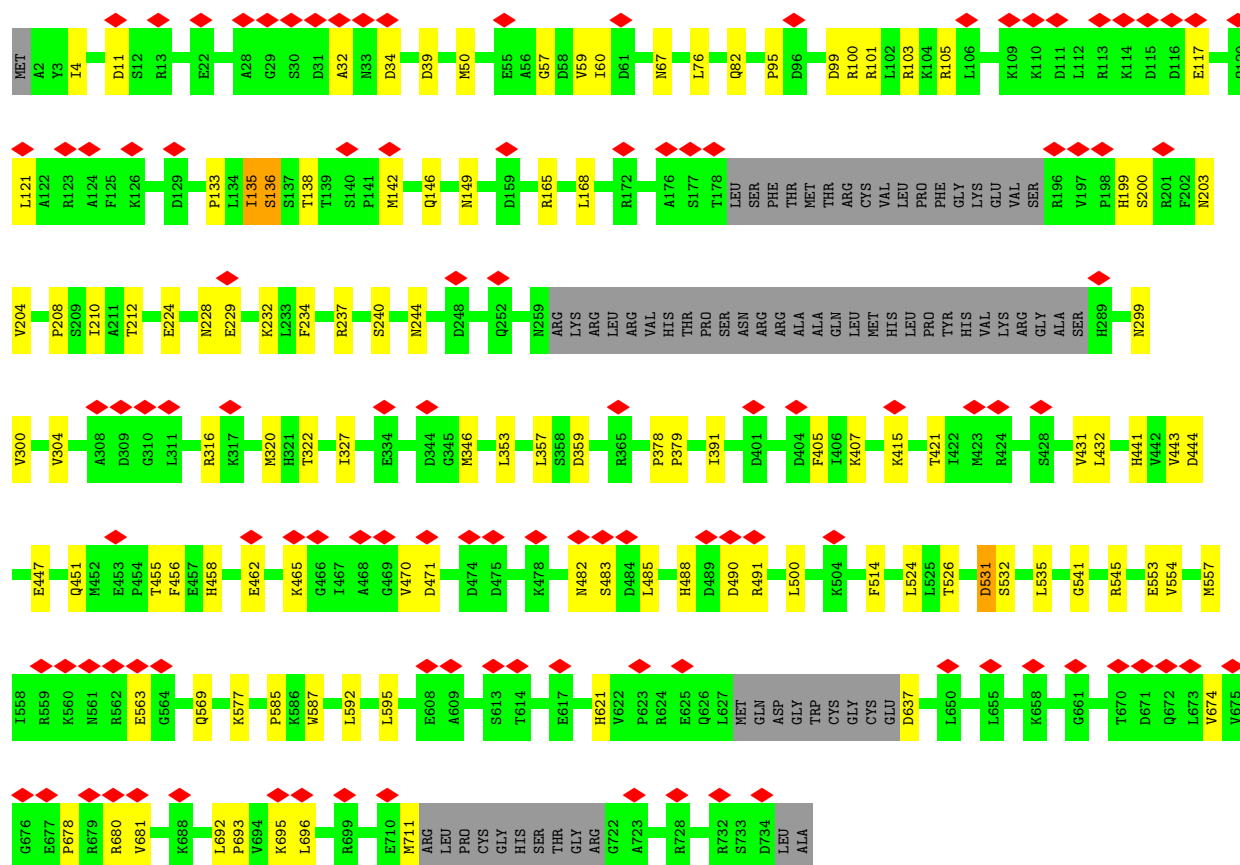
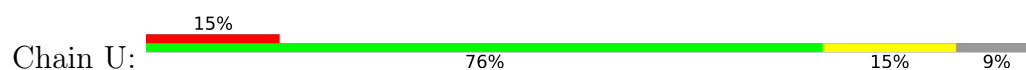
ALA	ASP	ARG	TYR	LEU	LEU	TYR	TYR	ILE	ARG	ASP	VAL	GLN	SER	ASP	VAL	ASP	VAL	GLY	PHE	TYR	ILE	THR	GLN	HIS	PRO	SER	PRO	LEU	GLN	LEU	LEU	ASN	THR	THR	ILE	THR	THR	GLY	ASP	PRO	ASN	GLU	ASP	PHE	LEU	SER	SER	ALA	PRO	ASP	MET	ARG	GLU	TRP	ALA	VAL	LYS	GLU	SER	GLY	ASN	THR	ILE	CYS	ILE			
LEU	ASN	SER	PRO	GLY	PHE	ILE	PRO	PRO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

• Molecule 3: RNA-directed RNA polymerase





• Molecule 4: Mu-2 protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45544	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.634	Depositor
Minimum map value	-1.369	Depositor
Average map value	0.035	Depositor
Map value standard deviation	0.179	Depositor
Recommended contour level	0.6	Depositor
Map size (Å)	435.2, 435.2, 435.2	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.36, 1.36, 1.36	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.24	0/1052	0.55	0/1413
1	2	0.22	0/1046	0.52	0/1405
1	3	0.25	0/1041	0.56	0/1398
1	4	0.24	0/976	0.60	0/1308
1	5	0.31	0/1052	0.81	6/1413 (0.4%)
1	A	0.28	0/9107	0.59	7/12474 (0.1%)
1	B	0.28	0/8671	0.59	2/11878 (0.0%)
1	C	0.28	0/8814	0.58	1/12074 (0.0%)
1	D	0.27	0/8526	0.57	4/11680 (0.0%)
1	E	0.27	0/8612	0.57	0/11798
1	a	0.27	0/8804	0.58	2/12061 (0.0%)
1	b	0.25	0/8804	0.53	0/12061
1	c	0.27	0/8772	0.55	0/12015
1	d	0.26	1/8804 (0.0%)	0.53	0/12061
1	e	0.26	0/8804	0.56	0/12061
2	H	0.22	0/8275	0.55	2/11284 (0.0%)
2	I	0.22	0/8275	0.55	2/11284 (0.0%)
2	J	0.22	0/8275	0.56	2/11284 (0.0%)
2	K	0.22	0/8275	0.55	2/11284 (0.0%)
2	L	0.24	0/8275	0.57	3/11284 (0.0%)
3	R	0.28	0/10166	0.65	6/13806 (0.0%)
4	U	0.30	0/5439	0.69	10/7385 (0.1%)
All	All	0.26	1/149865 (0.0%)	0.57	49/204711 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
1	E	0	2
1	a	0	3
1	b	0	2
1	c	0	1
1	d	0	4
1	e	0	2
2	H	0	1
2	I	0	1
2	J	0	1
2	K	0	1
2	L	0	1
3	R	0	3
4	U	0	3
All	All	0	27

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	d	242	ARG	CA-CB	5.12	1.62	1.53

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	9	LYS	N-CA-C	10.83	123.09	111.28
4	U	210	ILE	N-CA-C	-9.43	103.21	112.17
1	5	4	ILE	CA-C-N	8.50	128.94	120.52
1	5	4	ILE	C-N-CA	8.50	128.94	120.52
3	R	1011	ASP	CA-C-N	7.75	125.12	120.24

There are no chirality outliers.

5 of 27 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	793	MET	Peptide
1	C	276	VAL	Peptide
1	E	376	THR	Peptide
1	E	981	ASP	Peptide
2	H	1002	SER	Peptide

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	1041	0	1024	16	0
1	2	1035	0	1019	15	0
1	3	1030	0	1014	13	0
1	4	967	0	951	13	0
1	5	1041	0	1024	44	0
1	A	8868	0	8762	94	0
1	B	8442	0	8328	106	0
1	C	8583	0	8470	83	0
1	D	8300	0	8200	88	0
1	E	8385	0	8286	99	0
1	a	8571	0	8453	92	0
1	b	8571	0	8453	79	0
1	c	8539	0	8421	99	0
1	d	8571	0	8453	84	0
1	e	8571	0	8453	120	0
2	H	8073	0	7925	146	0
2	I	8073	0	7925	141	0
2	J	8073	0	7925	126	0
2	K	8073	0	7925	147	0
2	L	8073	0	7925	118	0
3	R	9913	0	9836	138	0
4	U	5322	0	5341	59	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	a	1	0	0	0	0
5	b	1	0	0	0	0
5	c	1	0	0	0	0
5	d	1	0	0	0	0
5	e	1	0	0	0	0
6	H	54	44	41	66	0
6	I	54	44	42	55	0
6	J	54	44	44	43	0
6	K	54	44	44	65	0
6	L	54	44	44	37	0
All	All	146393	220	144328	1747	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 6.

The worst 5 of 1747 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:I:851:ILE:HG23	6:I:1301:SAM:C2	1.44	1.43
2:H:577:ASP:O	6:H:1301:SAM:CE	1.66	1.41
2:I:552:TYR:CE2	6:I:1302:SAM:C5	2.05	1.40
2:H:552:TYR:HB2	6:H:1301:SAM:O2'	1.21	1.33
2:K:872:TYR:CE1	6:K:1302:SAM:C2	2.11	1.33

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	1	136/1275 (11%)	123 (90%)	13 (10%)	0	100	100
1	2	135/1275 (11%)	125 (93%)	10 (7%)	0	100	100
1	3	134/1275 (10%)	124 (92%)	10 (8%)	0	100	100
1	4	125/1275 (10%)	115 (92%)	10 (8%)	0	100	100
1	5	136/1275 (11%)	126 (93%)	10 (7%)	0	100	100
1	A	1126/1275 (88%)	1045 (93%)	80 (7%)	1 (0%)	48	79
1	B	1069/1275 (84%)	991 (93%)	76 (7%)	2 (0%)	43	72
1	C	1084/1275 (85%)	1016 (94%)	67 (6%)	1 (0%)	48	79
1	D	1046/1275 (82%)	974 (93%)	72 (7%)	0	100	100
1	E	1059/1275 (83%)	992 (94%)	66 (6%)	1 (0%)	48	79
1	a	1083/1275 (85%)	1002 (92%)	79 (7%)	2 (0%)	43	72
1	b	1083/1275 (85%)	1015 (94%)	68 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	c	1076/1275 (84%)	1016 (94%)	59 (6%)	1 (0%)	48	79
1	d	1083/1275 (85%)	1017 (94%)	66 (6%)	0	100	100
1	e	1083/1275 (85%)	1002 (92%)	80 (7%)	1 (0%)	48	79
2	H	1022/1289 (79%)	950 (93%)	72 (7%)	0	100	100
2	I	1022/1289 (79%)	950 (93%)	72 (7%)	0	100	100
2	J	1022/1289 (79%)	949 (93%)	73 (7%)	0	100	100
2	K	1022/1289 (79%)	950 (93%)	72 (7%)	0	100	100
2	L	1022/1289 (79%)	946 (93%)	76 (7%)	0	100	100
3	R	1249/1267 (99%)	1166 (93%)	82 (7%)	1 (0%)	48	79
4	U	658/736 (89%)	591 (90%)	60 (9%)	7 (1%)	11	43
All	All	18475/27573 (67%)	17185 (93%)	1273 (7%)	17 (0%)	49	79

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	310	TRP
1	B	310	TRP
3	R	287	GLU
1	a	310	TRP
1	B	1214	SER

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	112/1113 (10%)	112 (100%)	0	100	100
1	2	111/1113 (10%)	111 (100%)	0	100	100
1	3	111/1113 (10%)	111 (100%)	0	100	100
1	4	104/1113 (9%)	104 (100%)	0	100	100
1	5	112/1113 (10%)	109 (97%)	3 (3%)	39	61
1	A	994/1113 (89%)	993 (100%)	1 (0%)	88	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	945/1113 (85%)	942 (100%)	3 (0%)	86	83
1	C	963/1113 (86%)	962 (100%)	1 (0%)	88	87
1	D	931/1113 (84%)	930 (100%)	1 (0%)	88	87
1	E	940/1113 (84%)	939 (100%)	1 (0%)	88	87
1	a	960/1113 (86%)	959 (100%)	1 (0%)	88	87
1	b	960/1113 (86%)	960 (100%)	0	100	100
1	c	955/1113 (86%)	954 (100%)	1 (0%)	88	87
1	d	960/1113 (86%)	959 (100%)	1 (0%)	88	87
1	e	960/1113 (86%)	958 (100%)	2 (0%)	87	85
2	H	884/1118 (79%)	883 (100%)	1 (0%)	88	87
2	I	884/1118 (79%)	883 (100%)	1 (0%)	88	87
2	J	884/1118 (79%)	882 (100%)	2 (0%)	87	85
2	K	884/1118 (79%)	883 (100%)	1 (0%)	88	87
2	L	884/1118 (79%)	879 (99%)	5 (1%)	78	79
3	R	1074/1084 (99%)	1071 (100%)	3 (0%)	86	83
4	U	592/650 (91%)	591 (100%)	1 (0%)	87	85
All	All	16204/24019 (68%)	16175 (100%)	29 (0%)	85	85

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	K	969	ILE
1	e	480	GLU
2	L	849	VAL
1	a	338	LEU
2	L	578	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 261 such sidechains are listed below:

Mol	Chain	Res	Type
1	c	1033	HIS
1	d	537	GLN
1	e	1213	ASN
1	E	690	ASN
1	E	357	ASN

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 ⓘ

Of 18 ligands modelled in this entry, 8 are monoatomic - leaving 10 for Mogul analysis.

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$
6	SAM	K	1301	-	27,29,29	1.47	6 (22%)	34,42,42	2.16	8 (23%)
6	SAM	I	1301	-	27,29,29	1.44	5 (18%)	34,42,42	2.16	12 (35%)
6	SAM	J	1302	-	27,29,29	1.45	6 (22%)	34,42,42	2.14	10 (29%)
6	SAM	H	1302	-	27,29,29	1.45	6 (22%)	34,42,42	2.06	11 (32%)
6	SAM	L	1302	-	27,29,29	1.47	5 (18%)	34,42,42	1.95	10 (29%)
6	SAM	J	1301	-	27,29,29	1.45	6 (22%)	34,42,42	2.16	10 (29%)
6	SAM	K	1302	-	27,29,29	1.42	5 (18%)	34,42,42	2.17	10 (29%)
6	SAM	H	1301	-	27,29,29	1.44	6 (22%)	34,42,42	2.10	12 (35%)
6	SAM	L	1301	-	27,29,29	1.45	6 (22%)	34,42,42	2.15	13 (38%)
6	SAM	I	1302	-	27,29,29	1.46	6 (22%)	34,42,42	2.07	12 (35%)

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
6	SAM	K	1301	-	-	8/17/33/33	0/3/3/3
6	SAM	I	1301	-	-	0/17/33/33	0/3/3/3
6	SAM	J	1302	-	-	8/17/33/33	0/3/3/3
6	SAM	H	1302	-	-	6/17/33/33	0/3/3/3
6	SAM	L	1302	-	-	4/17/33/33	0/3/3/3
6	SAM	J	1301	-	-	6/17/33/33	0/3/3/3
6	SAM	K	1302	-	-	2/17/33/33	0/3/3/3
6	SAM	H	1301	-	-	4/17/33/33	0/3/3/3
6	SAM	L	1301	-	-	6/17/33/33	0/3/3/3
6	SAM	I	1302	-	-	8/17/33/33	0/3/3/3

The worst 5 of 57 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	K	1301	SAM	C5-C4	4.44	1.47	1.39
6	L	1302	SAM	C5-C4	4.36	1.46	1.39
6	J	1301	SAM	C5-C4	4.30	1.46	1.39
6	I	1301	SAM	C5-C4	4.23	1.46	1.39
6	L	1301	SAM	C5-C4	4.22	1.46	1.39

The worst 5 of 108 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	K	1301	SAM	C5-C4-N3	-6.57	117.66	126.72
6	J	1302	SAM	C5-C4-N3	-6.05	118.39	126.72
6	J	1301	SAM	C5-C4-N3	-6.03	118.42	126.72
6	I	1302	SAM	C5-C4-N3	-5.87	118.63	126.72
6	K	1302	SAM	C5-C4-N3	-5.78	118.75	126.72

There are no chirality outliers.

5 of 52 torsion outliers are listed below:

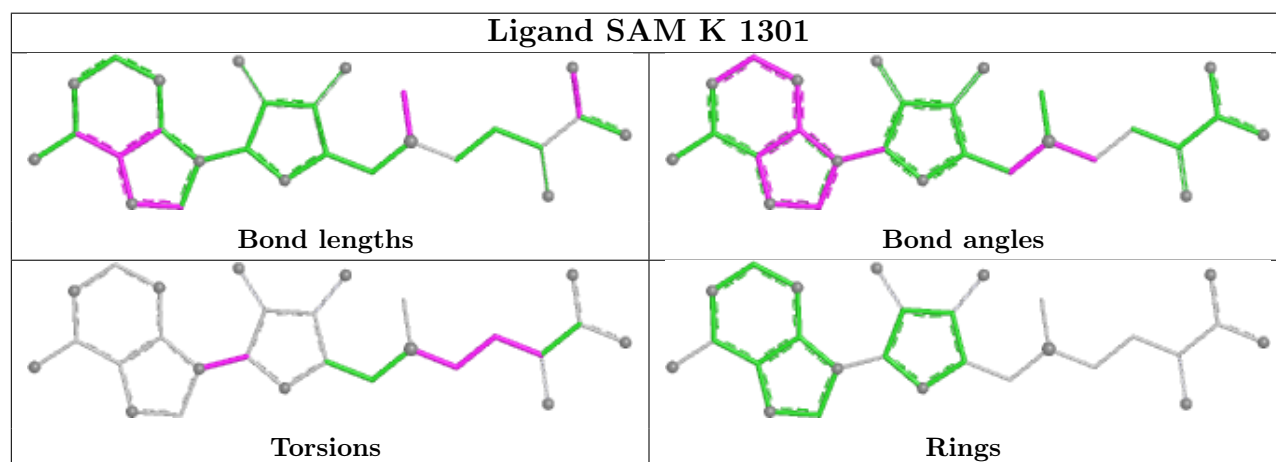
Mol	Chain	Res	Type	Atoms
6	H	1301	SAM	C4'-C5'-SD-CE
6	H	1302	SAM	C-CA-CB-CG
6	H	1302	SAM	CB-CG-SD-CE
6	H	1302	SAM	CB-CG-SD-C5'
6	H	1302	SAM	O4'-C4'-C5'-SD

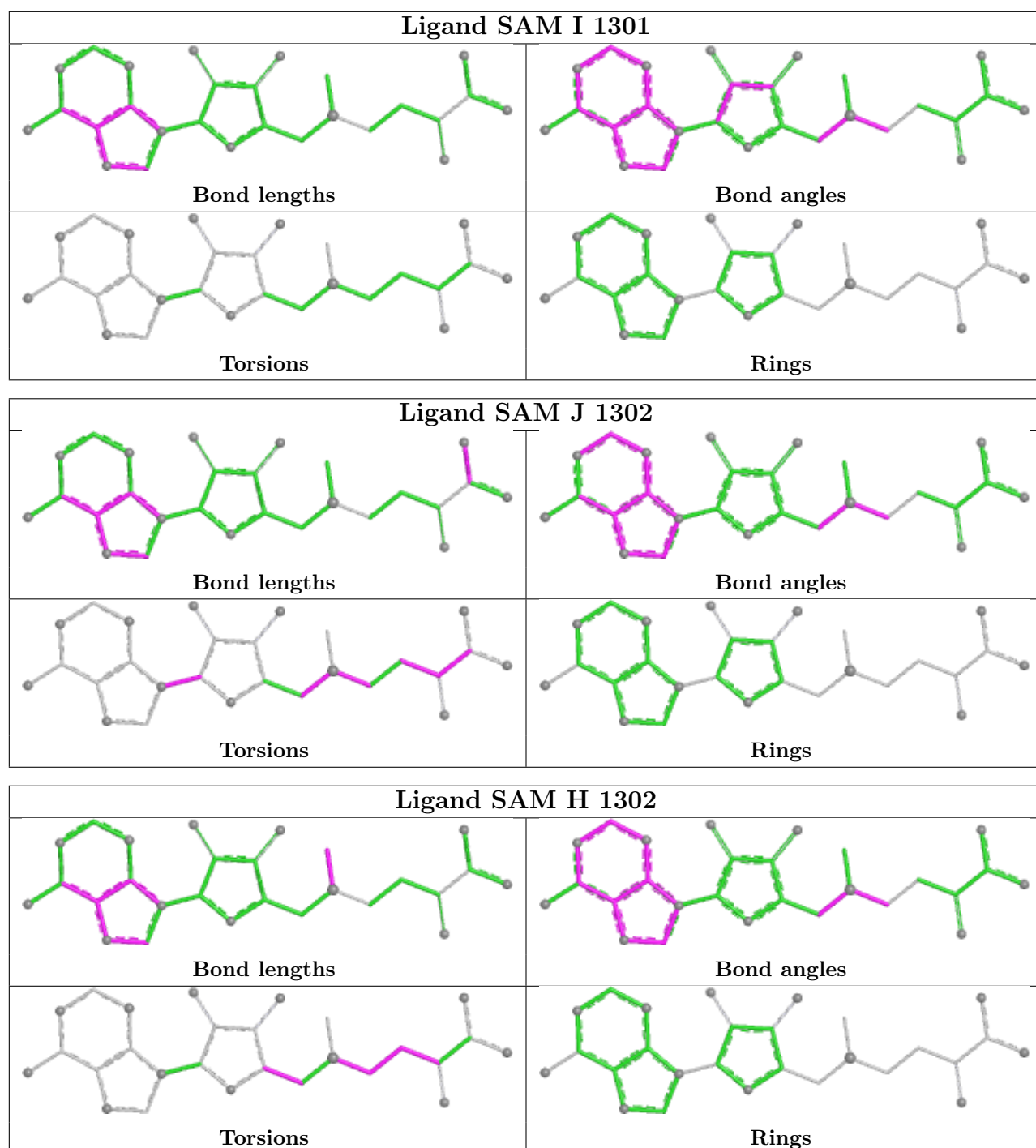
There are no ring outliers.

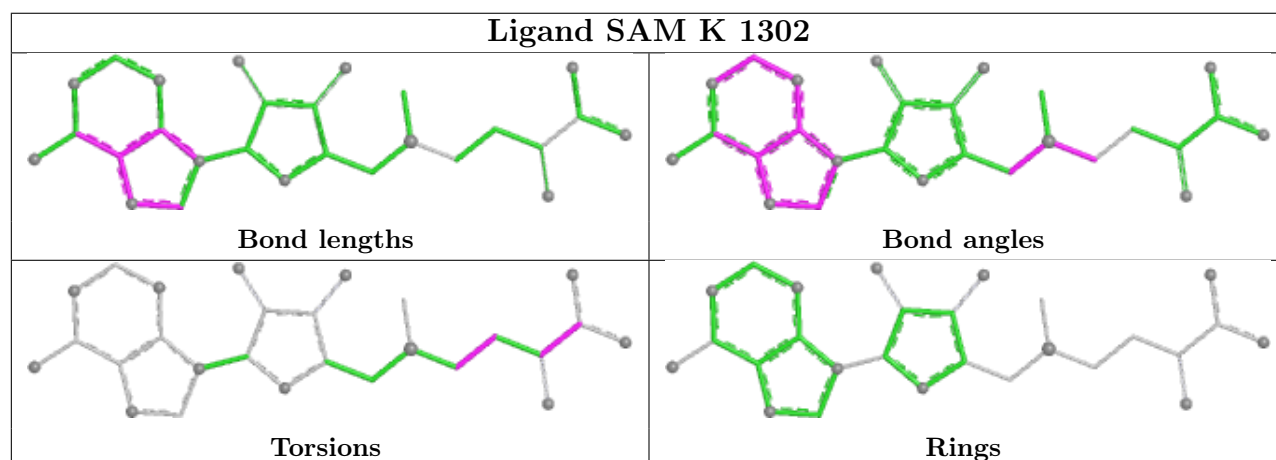
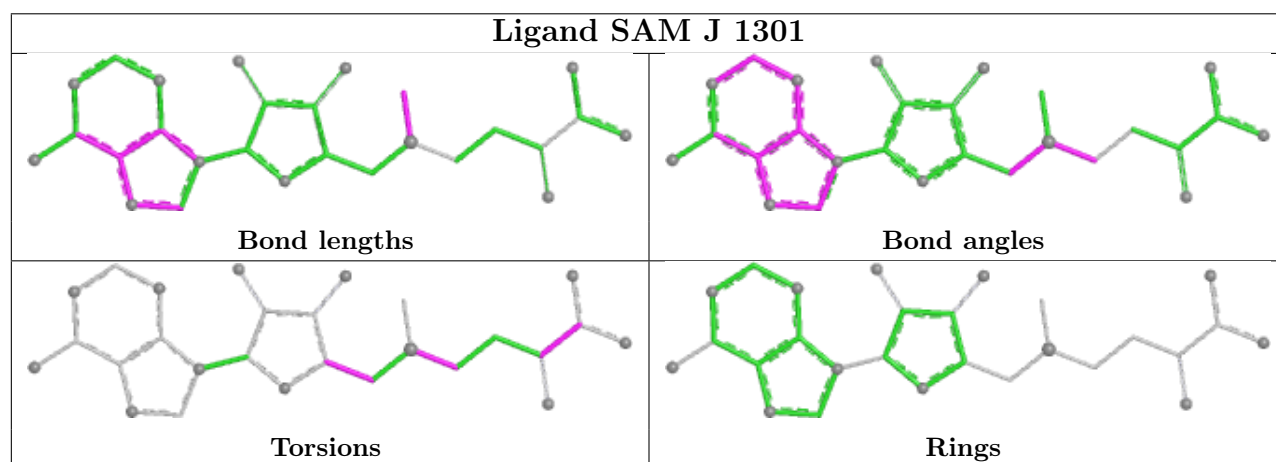
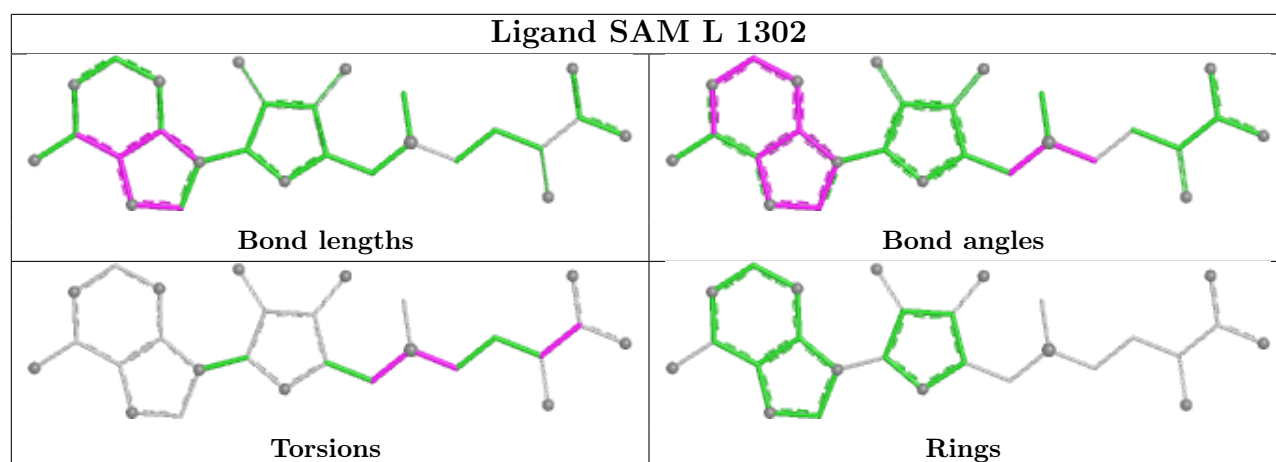
10 monomers are involved in 266 short contacts:

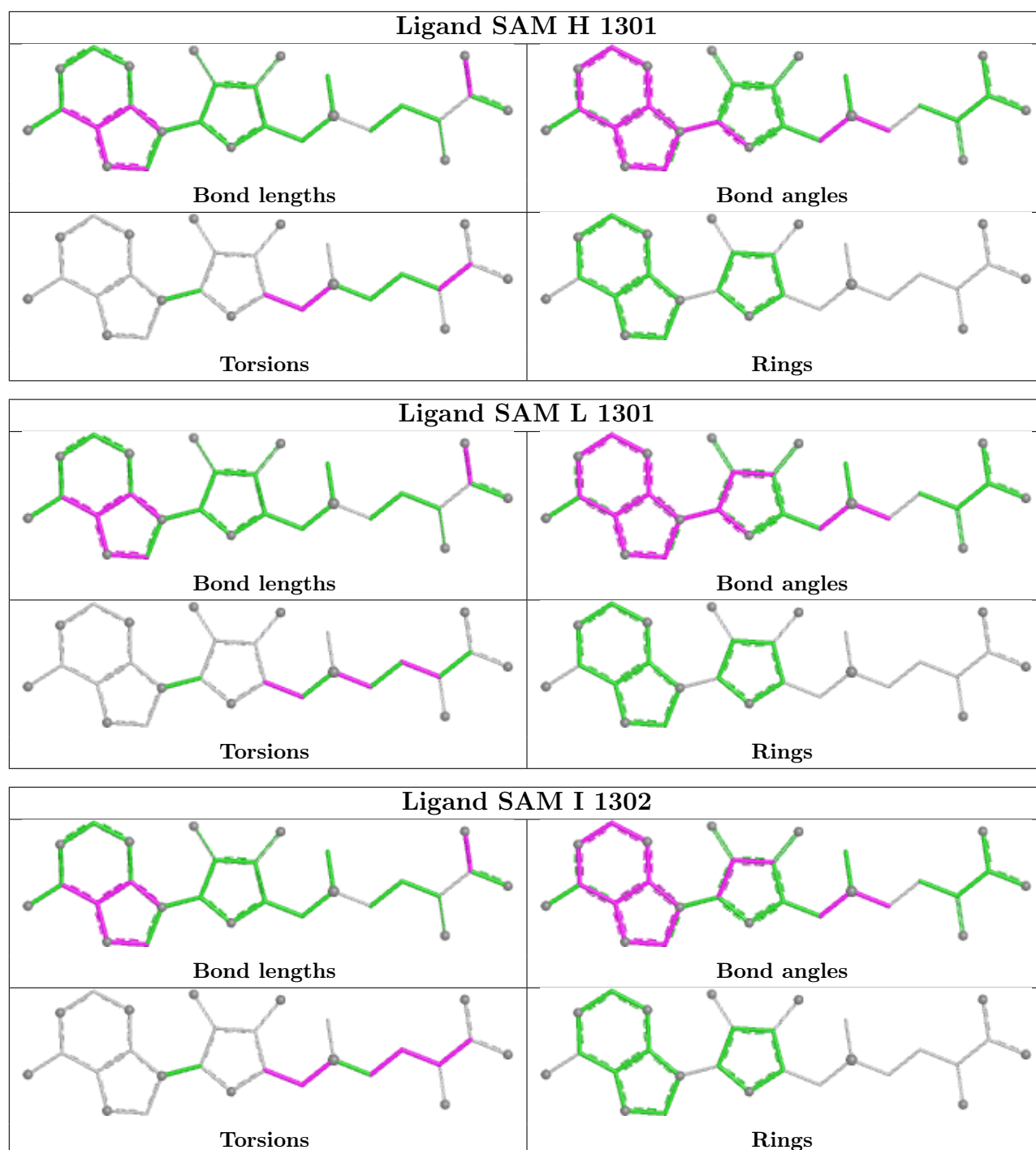
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	K	1301	SAM	33	0
6	I	1301	SAM	23	0
6	J	1302	SAM	30	0
6	H	1302	SAM	29	0
6	L	1302	SAM	25	0
6	J	1301	SAM	13	0
6	K	1302	SAM	32	0
6	H	1301	SAM	37	0
6	L	1301	SAM	12	0
6	I	1302	SAM	32	0

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.

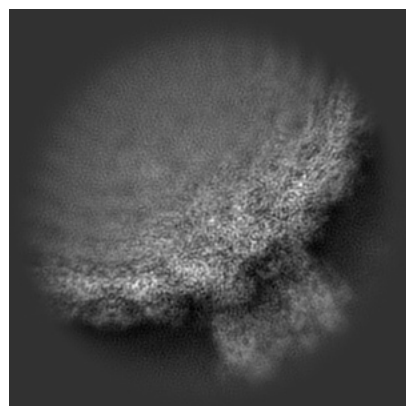
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33778. These allow visual inspection of the internal detail of the map and identification of artifacts.

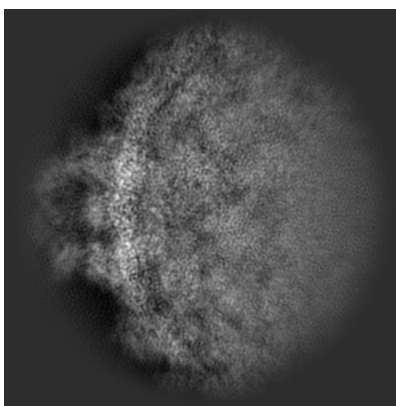
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

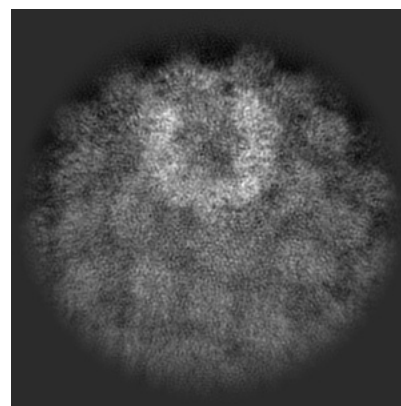
6.1.1 Primary map



X

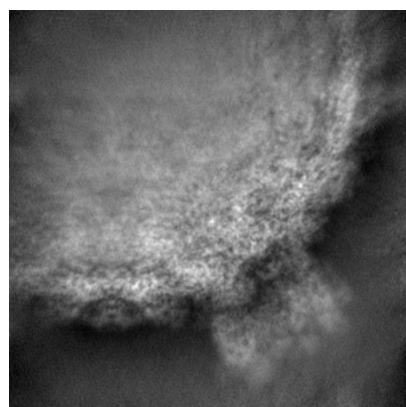


Y

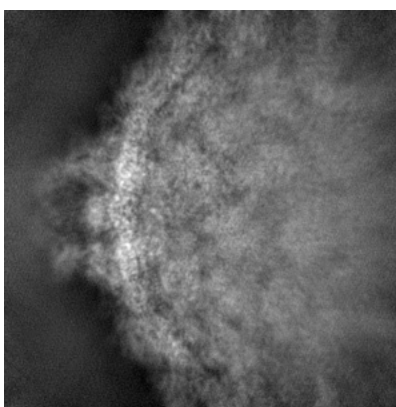


Z

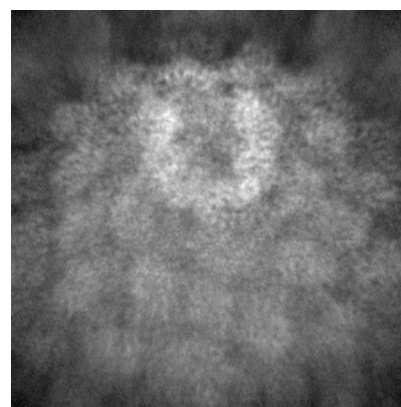
6.1.2 Raw map



X



Y

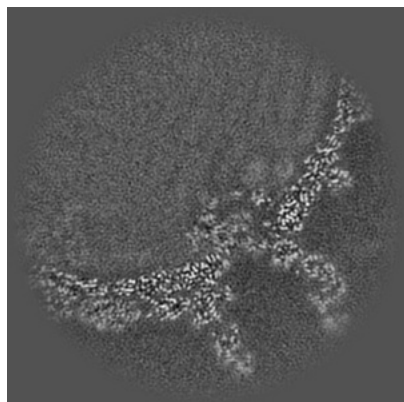


Z

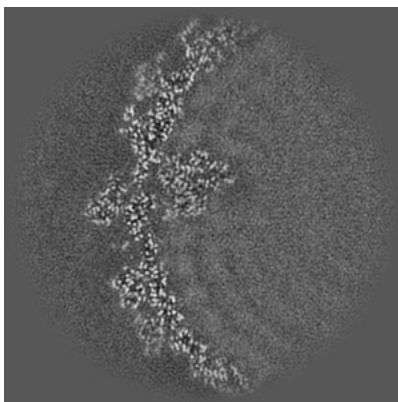
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

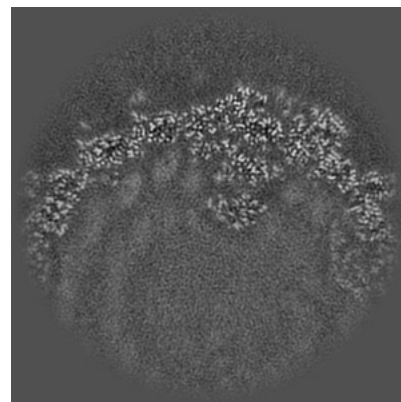
6.2.1 Primary map



X Index: 160

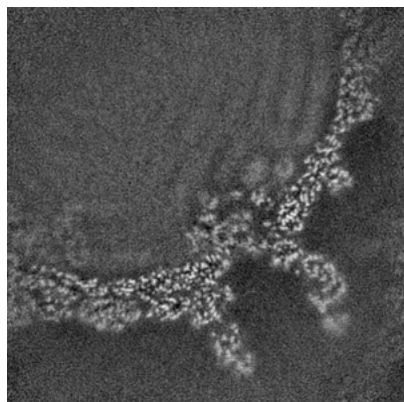


Y Index: 160

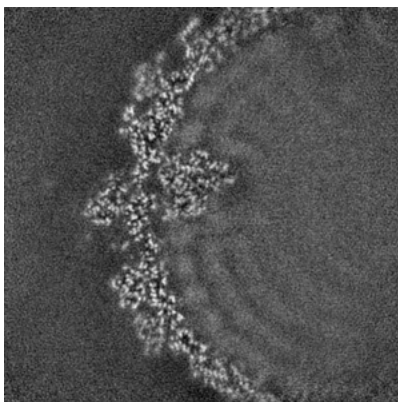


Z Index: 160

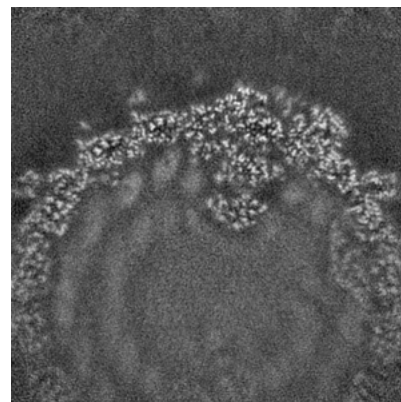
6.2.2 Raw map



X Index: 160



Y Index: 160

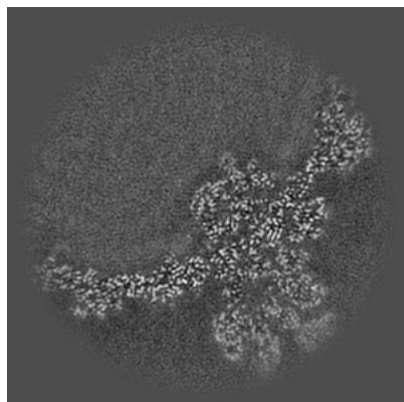


Z Index: 160

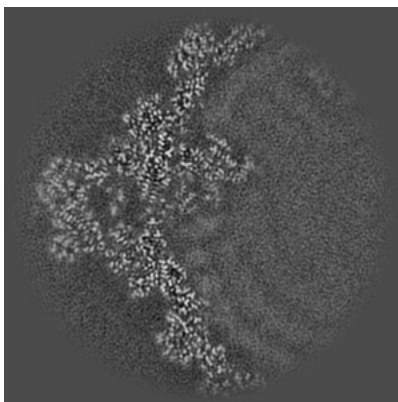
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

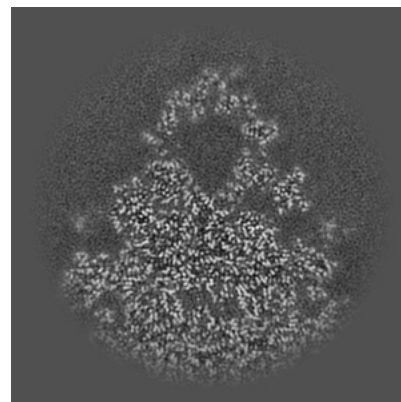
6.3.1 Primary map



X Index: 193

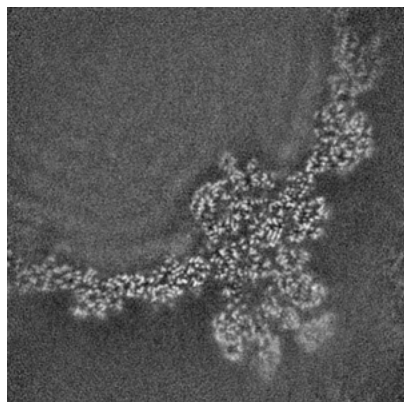


Y Index: 180

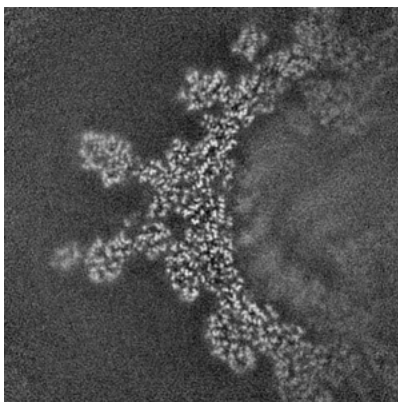


Z Index: 100

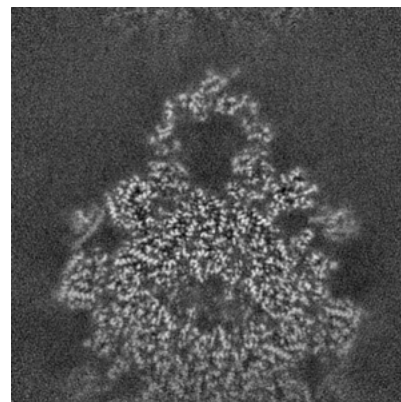
6.3.2 Raw map



X Index: 193



Y Index: 228

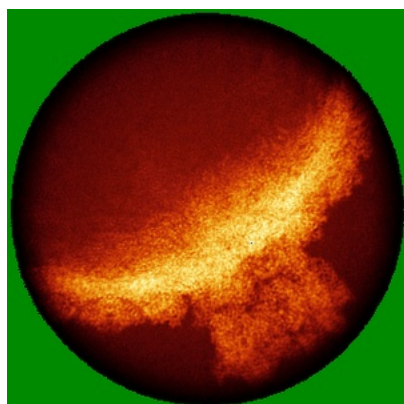


Z Index: 103

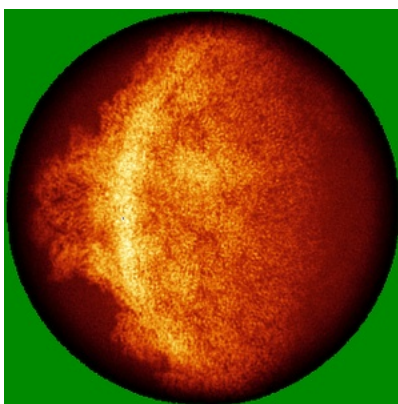
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

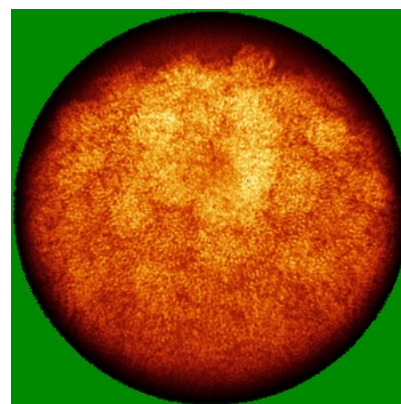
6.4.1 Primary map



X

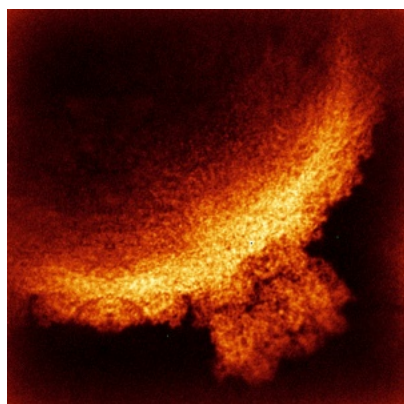


Y

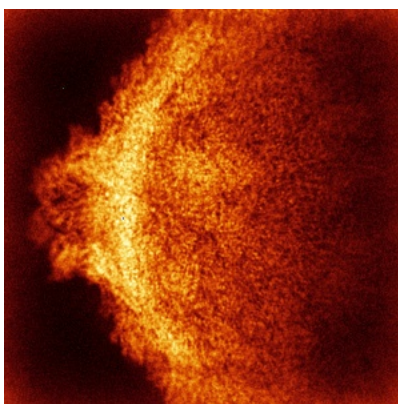


Z

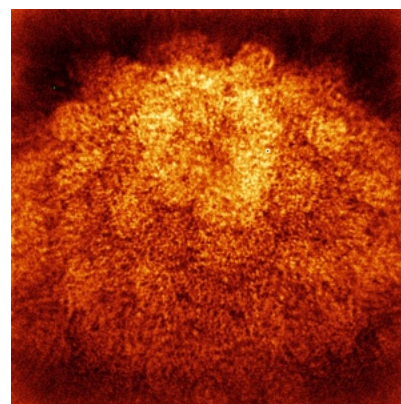
6.4.2 Raw map



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 0.6. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

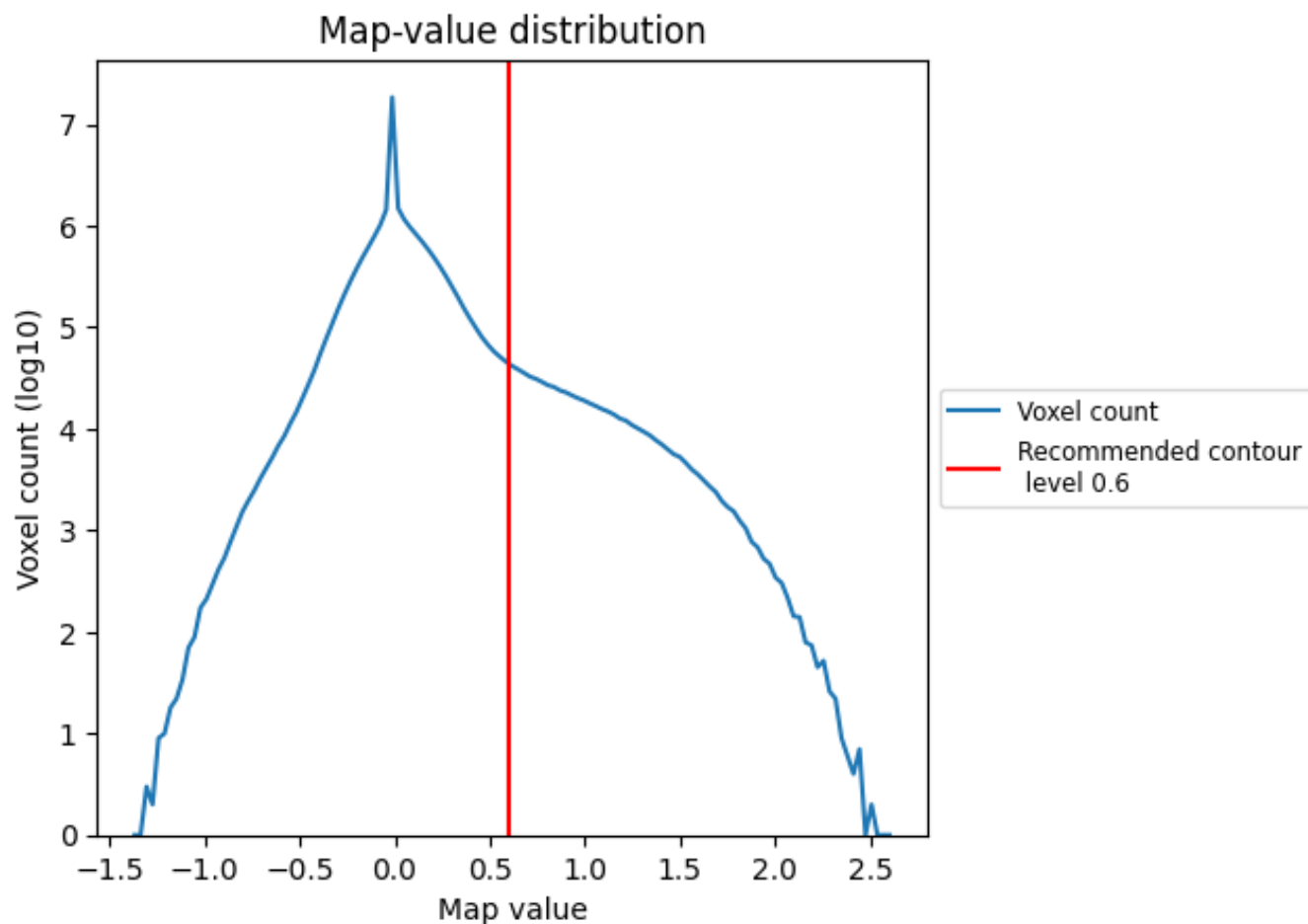
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

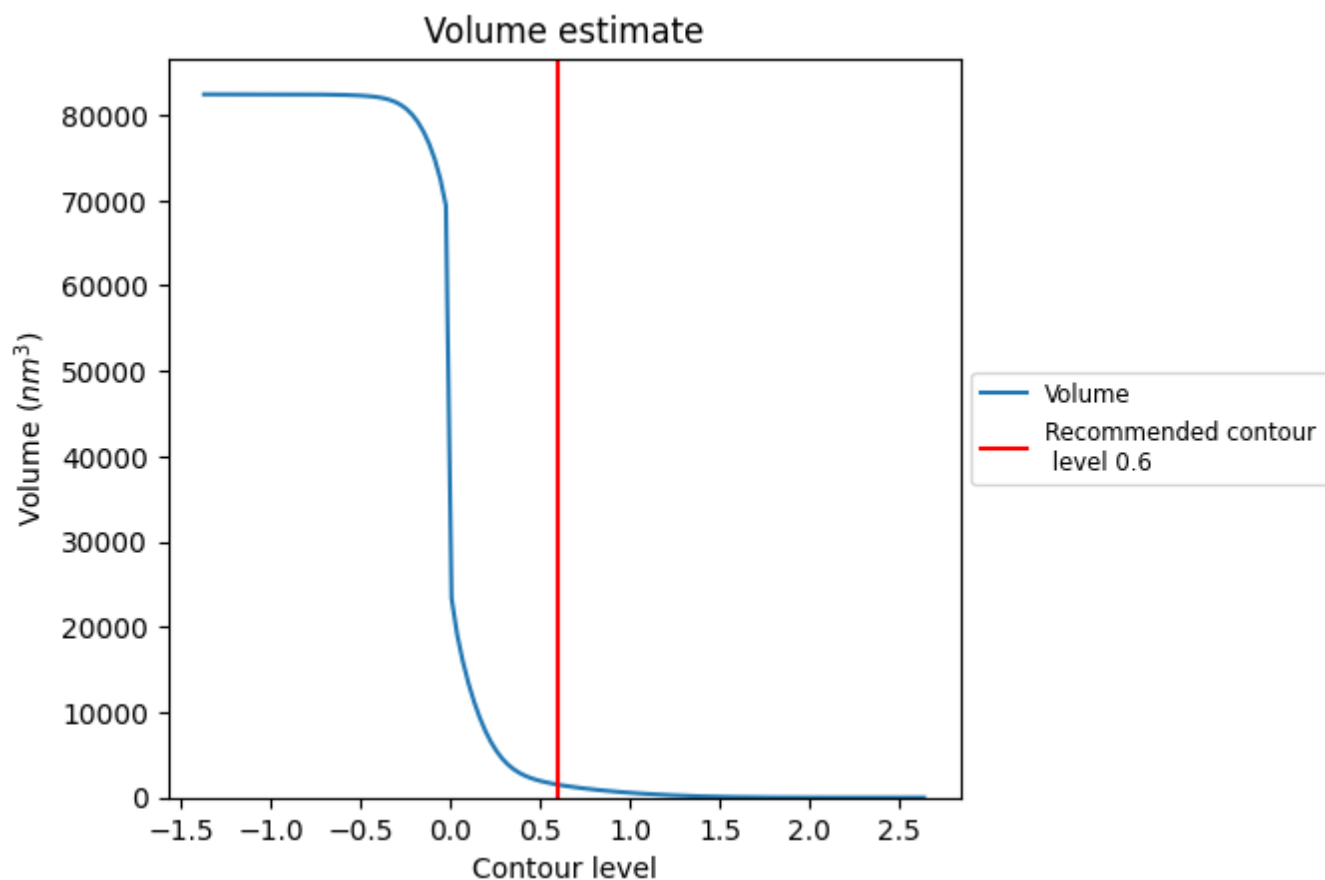
This section contains the results of statistical analysis of the map.

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.

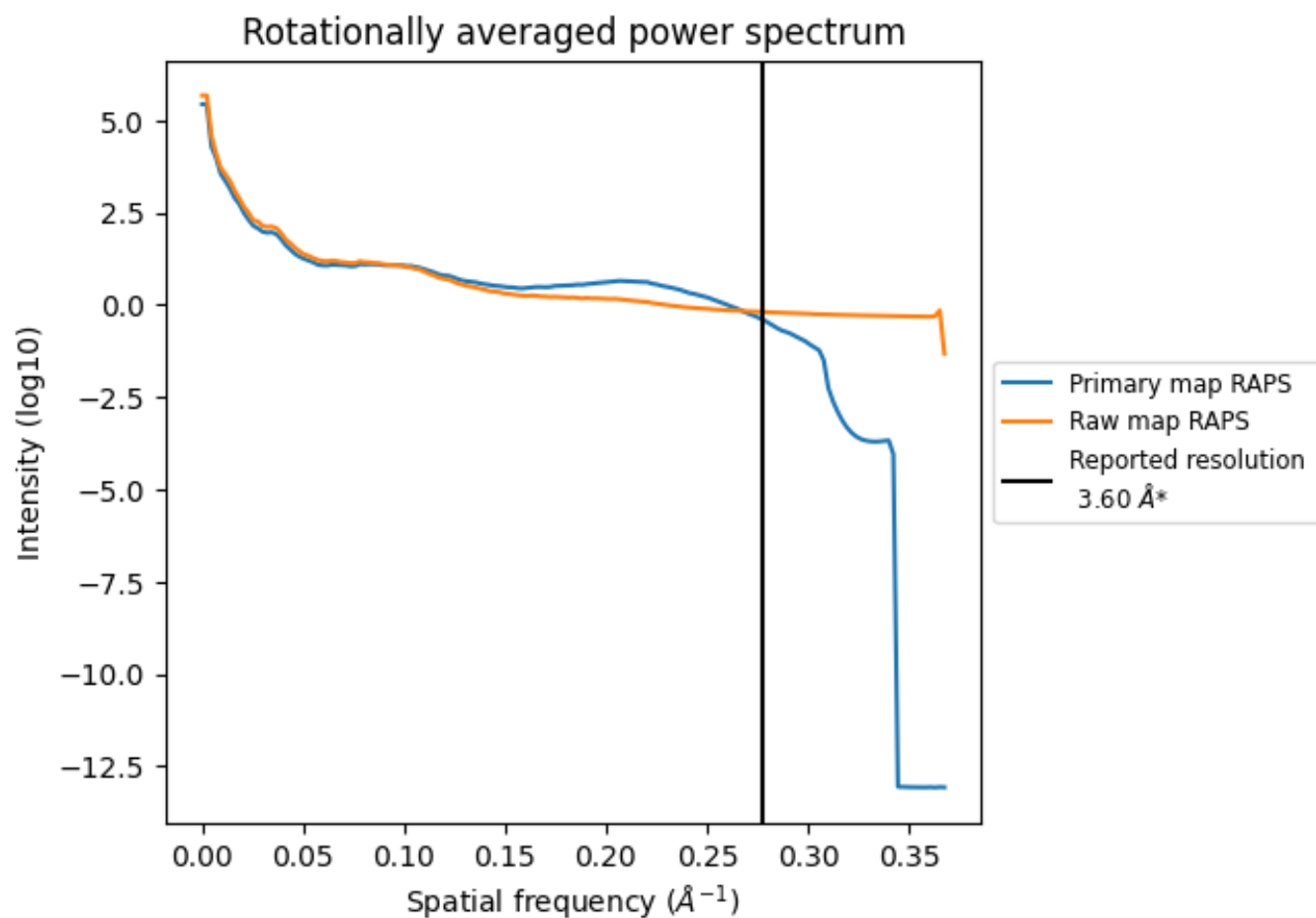
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1507 nm³; this corresponds to an approximate mass of 1361 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 ⓘ

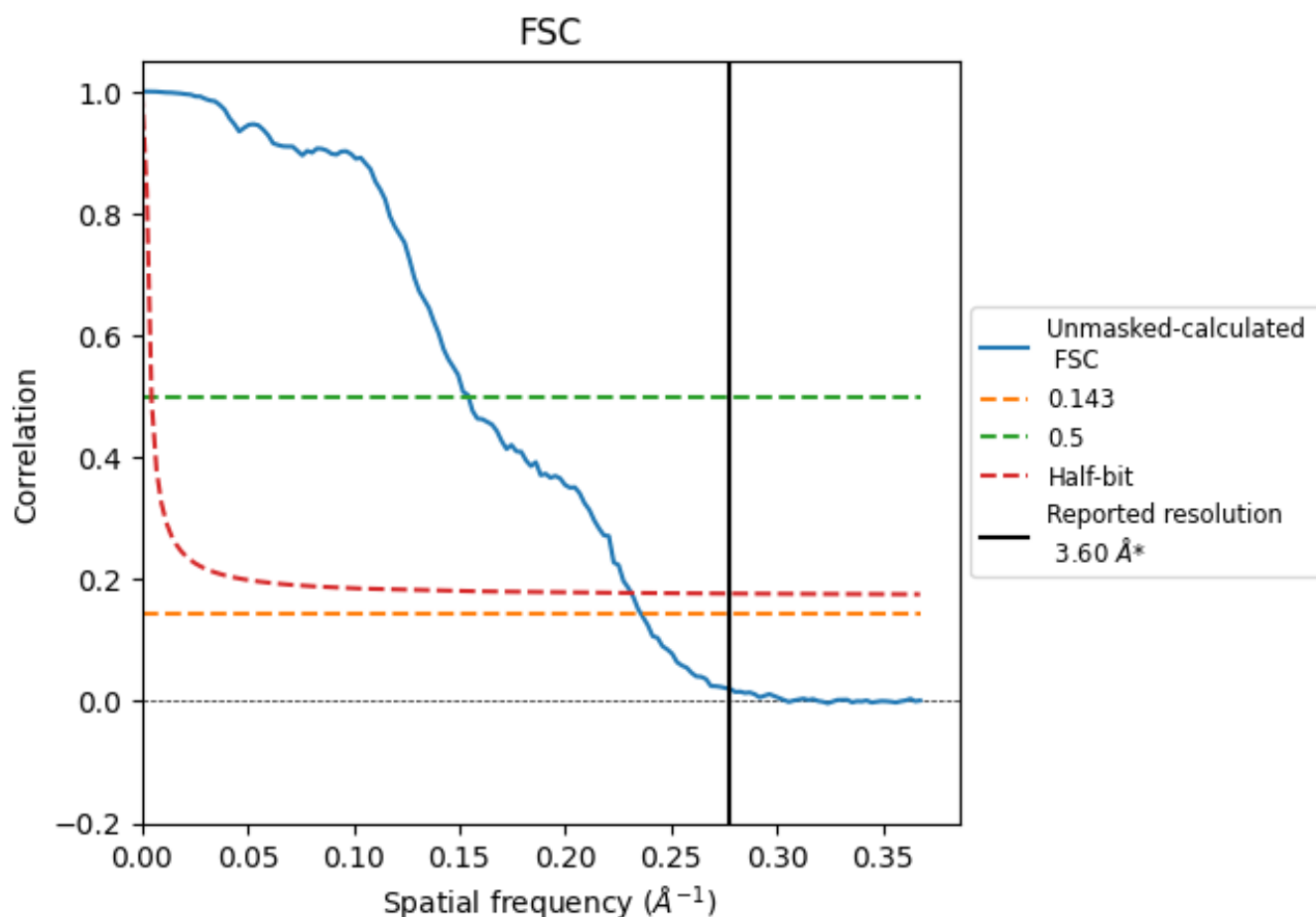


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.24	6.49	4.33

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.24 differs from the reported value 3.6 by more than 10 %

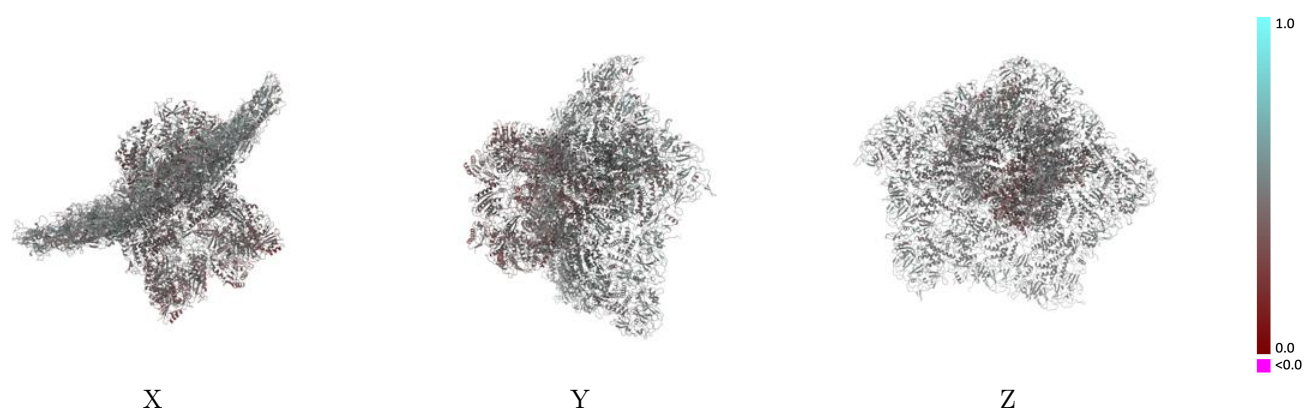
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-33778 and PDB model 7YEV. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)

This section was not generated.

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

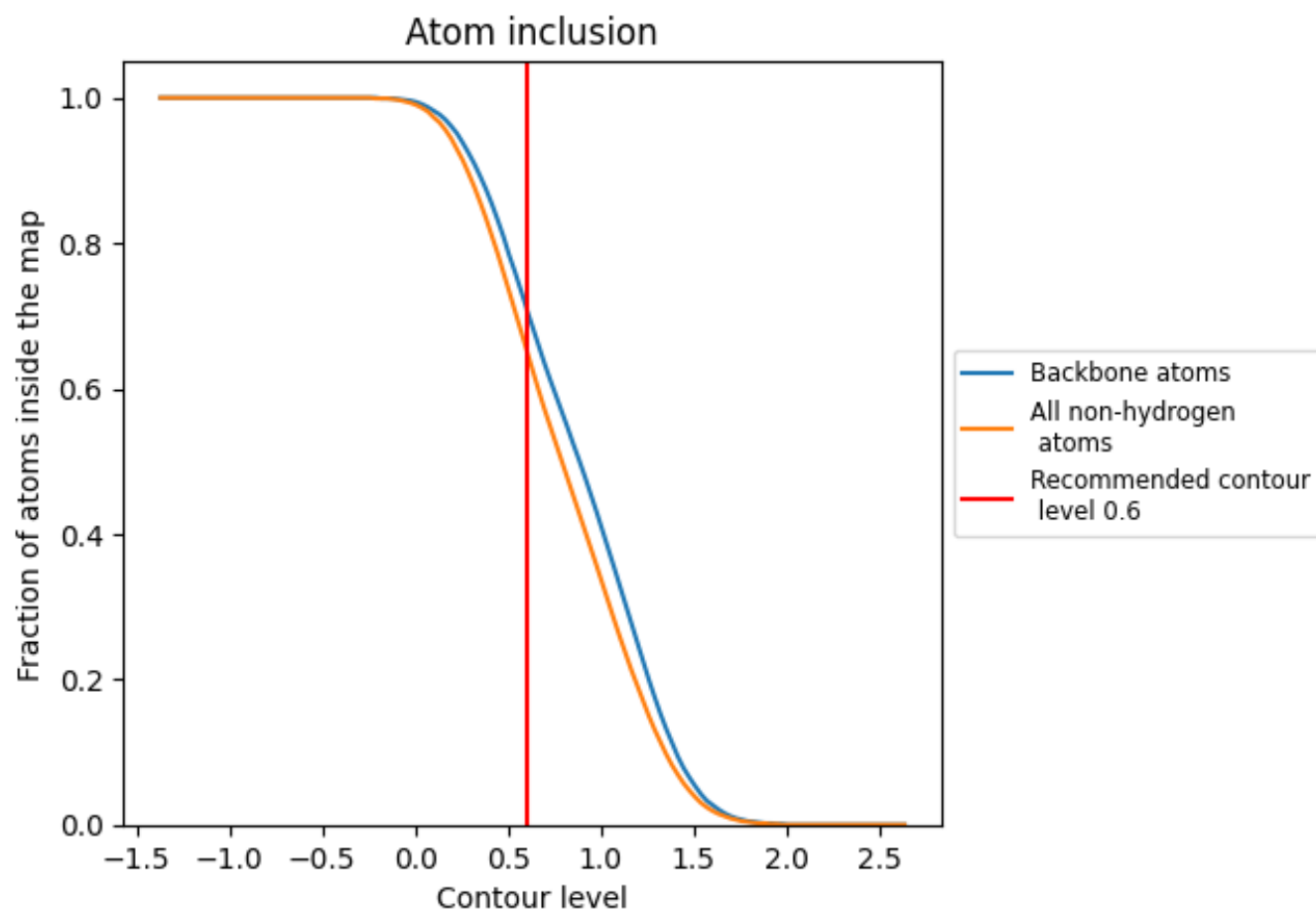


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 65% 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6530	 0.4570
1	 0.5300	 0.4540
2	 0.5980	 0.4660
3	 0.6020	 0.4560
4	 0.4770	 0.4560
5	 0.3040	 0.4250
A	 0.6740	 0.4720
B	 0.6850	 0.4730
C	 0.6880	 0.4730
D	 0.7050	 0.4810
E	 0.6890	 0.4790
H	 0.6450	 0.4230
I	 0.6430	 0.4230
J	 0.6500	 0.4270
K	 0.6550	 0.4260
L	 0.6500	 0.4310
R	 0.5440	 0.4260
U	 0.5810	 0.4500
a	 0.6960	 0.4780
b	 0.7050	 0.4790
c	 0.7030	 0.4800
d	 0.7030	 0.4780
e	 0.6900	 0.4760

