



## wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 09:03 AM UTC

PDB ID : 7TM3 / pdb\_00007tm3  
EMDB ID : EMD-25994  
Title : Structure of the rabbit 80S ribosome stalled on a 2-TMD Rhodopsin intermediate in complex with the multipass translocon  
Authors : Kim, M.K.; Lewis, A.J.O.; Keenan, R.J.; Hegde, R.S.  
Deposited on : 2022-01-19  
Resolution : 3.25 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](mailto: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>.

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

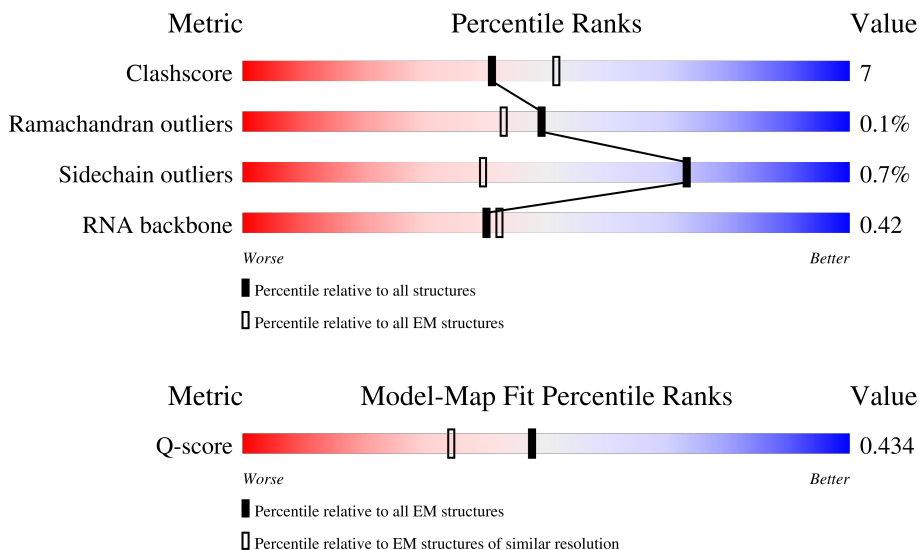
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 3.25 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.









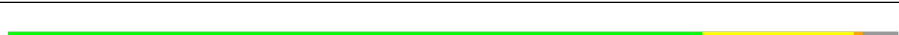
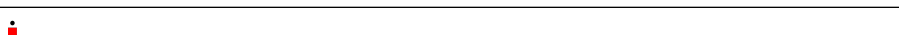
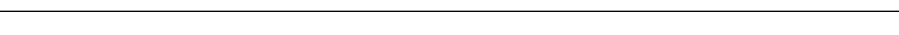
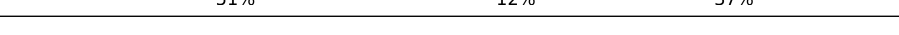
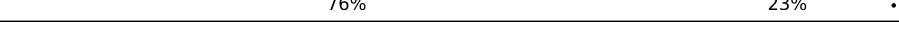
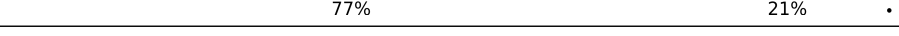













Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14599 ( 2.75 - 3.75 )

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  $\geq 3$ , 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	257	
2	B	229	
3	C	425	

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Mol	Chain	Length	Quality of chain
4	D	297	 80% 18%
5	E	291	 58% 21% 20%
6	F	247	 72% 18% 9%
7	G	319	 59% 14% 27%
8	H	192	 79% 20%
9	I	214	 80% 15%
10	J	178	 78% 17%
11	L	211	 80% 20%
12	M	218	 51% 12% 37%
13	N	204	 76% 23%
14	O	203	 77% 21%
15	P	184	 64% 19% 17%
16	Q	188	 83% 16%
17	R	196	 64% 15% 21%
18	S	176	 76% 24%
19	T	160	 81% 18%
20	U	128	 65% 15% 20%
21	V	140	 81% 11% 6%
22	W	157	 36% 60%
23	X	156	 56% 19% 24%
24	Y	145	 68% 25% 8%
25	Z	136	 75% 24%
26	a	148	 75% 24%
27	b	226	 38% 8% 54%
28	c	115	 69% 17% 15%


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Mol	Chain	Length	Quality of chain
29	d	125	72% 14% 14%
30	e	135	84% 10% 5%
31	f	110	77% 22%
32	g	116	81% 17%
33	h	123	85% 15%
34	i	105	81% 16%
35	j	97	67% 21% 11%
36	k	70	84% 14%
37	l	51	73% 25%
38	m	102	38% 13% 49%
39	n	25	72% 28%
40	o	106	85% 13%
41	p	92	75% 22%
42	q	77	69% 22% 8%
43	r	137	67% 23% 9%
44	u	120	62% 34%
45	v	156	56% 33% 10%
46	w	403	80% 17%
47	1	476	86% 12%
48	2	96	30% 70%
49	3	68	87% 13%
50	4	483	61% 10% 29%
51	5	106	6% 81% 15%
52	7	563	51% 86% 7% 7%
53	6	224	91% 9%

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Mol	Chain	Length	Quality of chain
54	K	3543	 54% 36% 10%

## 2 Entry composition [i](#)

There are 56 unique types of molecules in this entry. The entry contains 261738 atoms, of which 111794 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 uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	A	248	3891	1189	1993	389	314	6	0	0

- Molecule 2 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
2	B	27	351	112	171	31	36	1	0	0

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
3	C	362	5936	1812	3053	577	480	14	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	378	LYS	-	insertion	UNP G1SVW5
C	379	VAL	-	insertion	UNP G1SVW5
C	380	LYS	-	insertion	UNP G1SVW5
C	381	LYS	-	insertion	UNP G1SVW5
C	382	PRO	-	insertion	UNP G1SVW5
C	383	ARG	-	insertion	UNP G1SVW5
C	384	ALA	-	insertion	UNP G1SVW5
C	385	VAL	-	insertion	UNP G1SVW5
C	386	GLY	-	insertion	UNP G1SVW5
C	387	ILE	-	insertion	UNP G1SVW5
C	388	LYS	-	insertion	UNP G1SVW5
C	389	GLN	-	insertion	UNP G1SVW5

- Molecule 4 is a protein called uL18.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	D	293	4815	1512	2424	438	427	14	0	0

- Molecule 5 is a protein called eL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	E	233	3908	1206	2031	357	311	3	0	0

- Molecule 6 is a protein called uL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
6	F	225	3870	1205	1995	358	303	9	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	61	ARG	GLY	conflict	UNP G1TUB1
F	93	ARG	GLY	conflict	UNP G1TUB1
F	131	MET	VAL	conflict	UNP G1TUB1
F	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
7	G	233	3906	1199	2027	361	315	4	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 8 is a protein called uL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
8	H	190	3113	954	1597	284	272	6	0	0

- Molecule 9 is a protein called uL16.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
9	I	205	3376	1056	1712	321	274	13	0	0

- Molecule 10 is a protein called uL5.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
10	J	170	2761	861	1399	254	241	6	0	0

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
11	L	210	3522	1065	1820	354	279	4	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	46	ILE	-	insertion	UNP G1TPV0
L	47	ALA	-	insertion	UNP G1TPV0
L	48	PRO	-	insertion	UNP G1TPV0
L	49	ARG	-	insertion	UNP G1TPV0
L	50	PRO	-	insertion	UNP G1TPV0
L	51	ALA	-	insertion	UNP G1TPV0
L	52	ALA	-	insertion	UNP G1TPV0
L	53	GLY	-	insertion	UNP G1TPV0
L	54	PRO	-	insertion	UNP G1TPV0

- Molecule 12 is a protein called eL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
12	M	138	2348	727	1211	221	182	7	0	0

- Molecule 13 is a protein called eL15.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
13	N	202	3440	1069	1744	358	265	4	0	0

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
14	O	199	3408	1051	1778	319	255	5	0	0

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
15	P	153	2516	777	1274	241	215	9	0	0

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
16	Q	187	3148	946	1634	315	249	4	0	0

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
17	R	155	2728	808	1434	278	199	9	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	38	ARG	CYS	conflict	UNP G1TJR3
R	64	ARG	GLN	conflict	UNP G1TJR3
R	94	THR	LYS	conflict	UNP G1TJR3

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
18	S	176	2970	930	1508	285	236	11	0	0

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
19	T	159	2665	823	1367	252	217	6	0	0

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
20	U	102	1692	534	858	146	152	2	0	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	18	LEU	VAL	conflict	UNP G1TSG1
U	32	GLY	ARG	conflict	UNP G1TSG1
U	36	ALA	GLU	conflict	UNP G1TSG1
U	39	PHE	SER	conflict	UNP G1TSG1
U	54	GLY	ARG	conflict	UNP G1TSG1
U	60	VAL	ALA	conflict	UNP G1TSG1
U	62	SER	THR	conflict	UNP G1TSG1
U	63	LEU	ILE	conflict	UNP G1TSG1
U	97	ARG	HIS	conflict	UNP G1TSG1
U	106	THR	SER	conflict	UNP G1TSG1
U	126	GLU	ASP	conflict	UNP G1TSG1

- Molecule 21 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
21	V	131	2018	618	1039	184	172	5	0	0

- Molecule 22 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
22	W	63	1069	337	541	103	85	3	0	0

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
23	X	118	2007	618	1040	181	167	1	0	0

- Molecule 24 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
24	Y	134	2320	700	1205	226	186	3	0	0

- Molecule 25 is a protein called eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
25	Z	135	2289	714	1182	208	182	3	0	0

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
26	a	147	2371	734	1209	239	185	4	0	0

- Molecule 27 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
27	b	104	1768	527	920	189	129	3	0	0

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
28	c	98	1555	481	794	134	140	6	0	0

- Molecule 29 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
29	d	107	1818	560	930	171	155	2	0	0

- Molecule 30 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
30	e	128	2200	667	1147	216	165	5	0	0

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
31	f	109	1788	555	912	174	143	4	0	0

- Molecule 32 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace	
32	g	114	Total	C	H	N	O	S	0	0
			1904	566	998	187	147	6		

- Molecule 33 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace	
33	h	122	Total	C	H	N	O	S	0	0
			2145	637	1136	203	168	1		

- Molecule 34 is a protein called eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace	
34	i	102	Total	C	H	N	O	S	0	0
			1746	520	916	176	129	5		

- Molecule 35 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace	
35	j	86	Total	C	H	N	O	S	0	0
			1442	434	737	155	111	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace	
36	k	69	Total	C	H	N	O	S	0	0
			1206	366	637	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	24	LYS	ASN	conflict	UNP G1U001

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace	
37	l	50	Total	C	H	N	O	S	0	0
			927	286	480	96	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
38	m	52	895	266	466	90	67	6	0	0

- Molecule 39 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
39	n	25	528	145	289	64	27	3	0	0

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
40	o	104	1773	533	922	174	138	6	0	0

- Molecule 41 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
41	p	91	1465	445	757	136	120	7	0	0

- Molecule 42 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
42	q	76	2439	723	823	291	527	75	0	0

- Molecule 43 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
43	r	124	2045	616	1051	205	167	6	0	0

- Molecule 44 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
44	u	120	3854	1141	1296	456	842	119	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	2	U	N	conflict	GB X06789.1
u	36	C	N	conflict	GB X06789.1
u	102	U	N	conflict	GB X06789.1
u	112	U	N	conflict	GB X06789.1
u	114	U	N	conflict	GB X06789.1
u	119	U	C	conflict	GB X06789.1
u	120	U	N	conflict	GB X06789.1

- Molecule 45 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O	P		
45	v	156	4997	1480	1683	585	1094	155	0	0

- Molecule 46 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O	S		
46	w	394	6482	2020	3310	597	542	13	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w	1	MET	-	insertion	UNP G1TL06

- Molecule 47 is a protein called Protein transport protein Sec61 subunit alpha isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O	S		
47	1	465	7320	2360	3722	580	634	24	0	0

- Molecule 48 is a protein called Protein transport protein Sec61 subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O	S		
48	2	29	475	157	245	36	35	2	0	0

- Molecule 49 is a protein called Protein transport protein Sec61 gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O	S		
49	3	68	1120	355	577	94	89	5	0	0

- Molecule 50 is a protein called Coiled-coil domain containing 47.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
50	4	342	5597	1738	2819	495	522	23	0	0

- Molecule 51 is a protein called PAT complex subunit Asterix.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
51	5	90	1421	456	710	115	128	12	0	0

- Molecule 52 is a protein called Nicalin.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
52	7	521	8260	2625	4121	726	771	17	0	0

- Molecule 53 is a protein called Transmembrane protein 147.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
53	6	224	3575	1190	1792	277	300	16	0	0

- Molecule 54 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
54	K	3543	114330	33833	38358	13910	24686	3543	0	0

- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
55	P	2	Total	Mg	0
			2	2	
55	V	1	Total	Mg	0
			1	1	
55	a	1	Total	Mg	0
			1	1	
55	g	1	Total	Mg	0
			1	1	
55	j	1	Total	Mg	0
			1	1	

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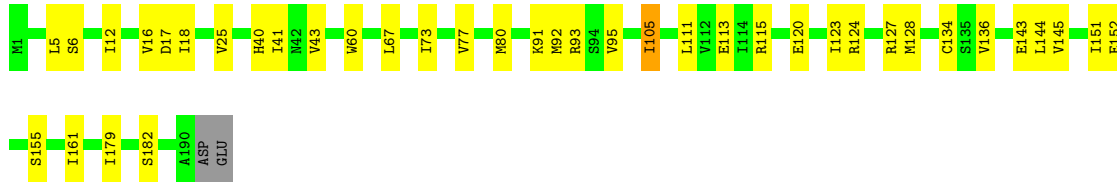
Mol	Chain	Residues	Atoms		AltConf
55	u	7	Total 7	Mg 7	0
55	v	6	Total 6	Mg 6	0
55	K	201	Total 201	Mg 201	0

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

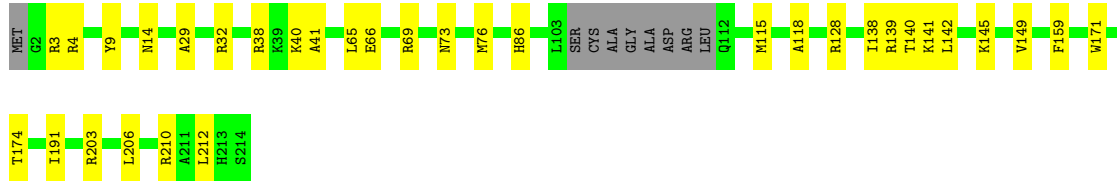
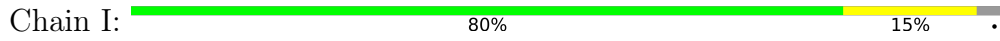
Mol	Chain	Residues	Atoms		AltConf
56	g	1	Total 1	Zn 1	0
56	j	1	Total 1	Zn 1	0
56	m	1	Total 1	Zn 1	0
56	o	1	Total 1	Zn 1	0
56	p	1	Total 1	Zn 1	0



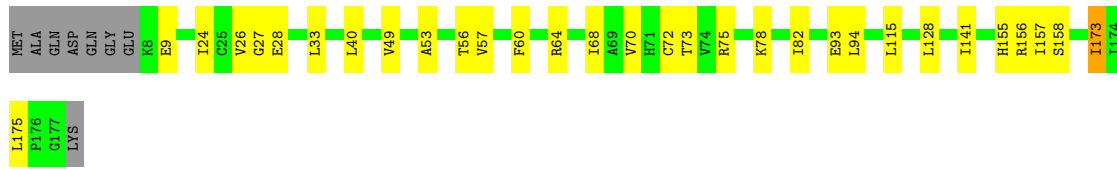
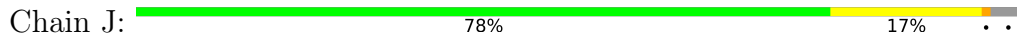




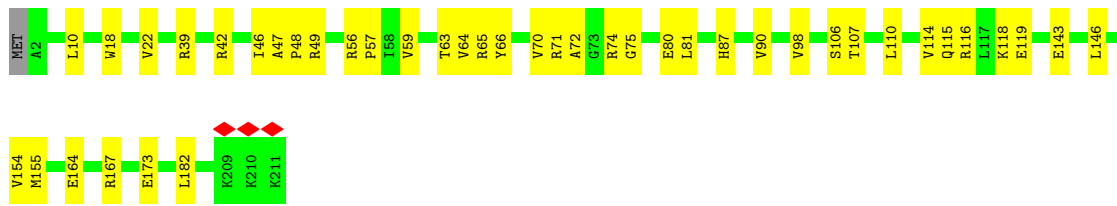
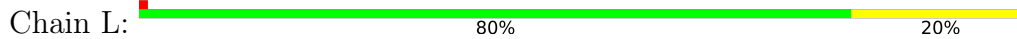
• Molecule 9: uL16



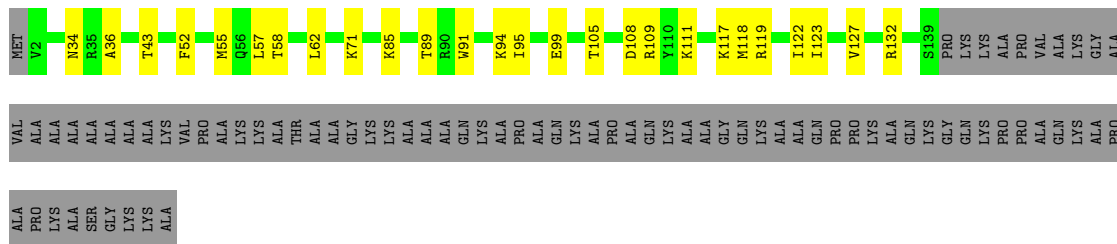
• Molecule 10: uL5



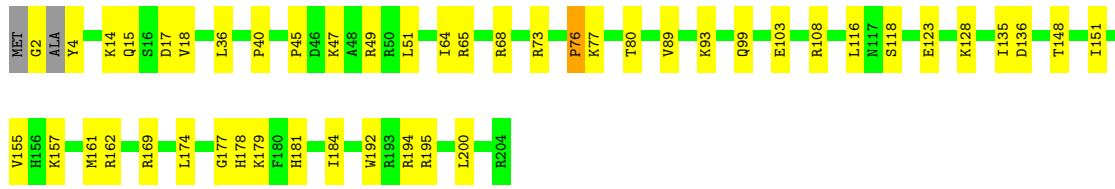
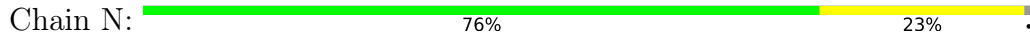
• Molecule 11: eL13



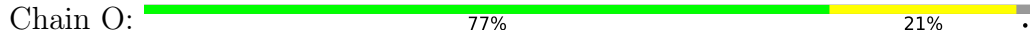
• Molecule 12: eL14



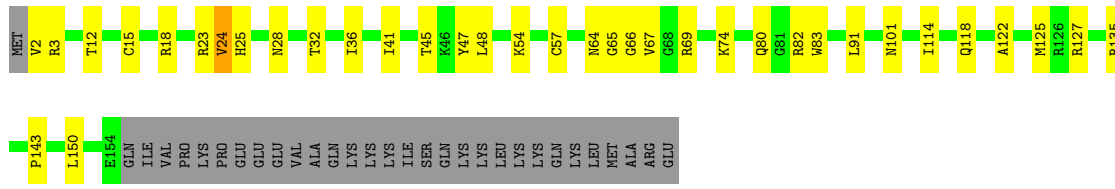
• Molecule 13: eL15



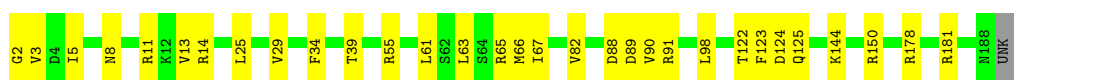
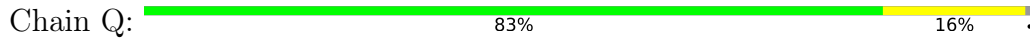
• Molecule 14: uL13



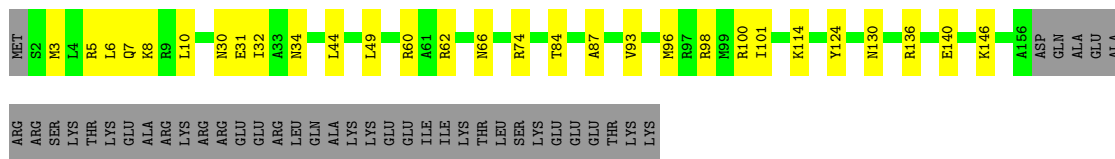
• Molecule 15: uL22



• Molecule 16: eL18

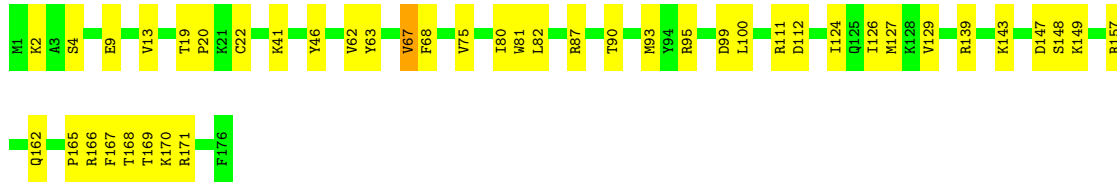


• Molecule 17: eL19

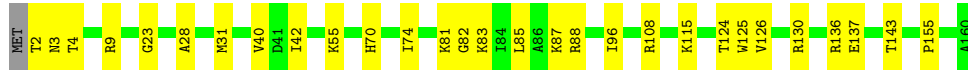
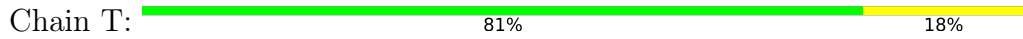


• Molecule 18: eL20

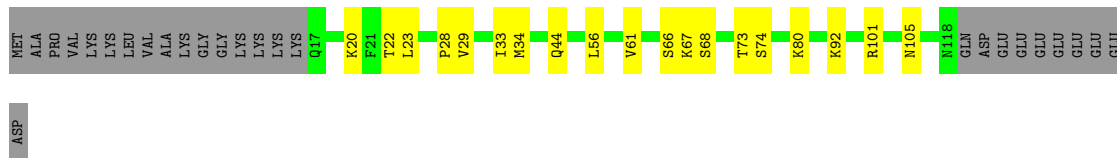




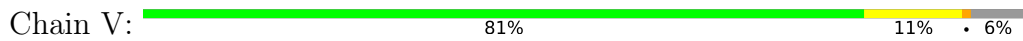
• Molecule 19: eL21



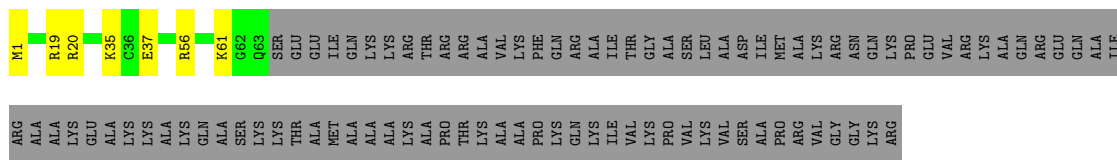
• Molecule 20: eL22



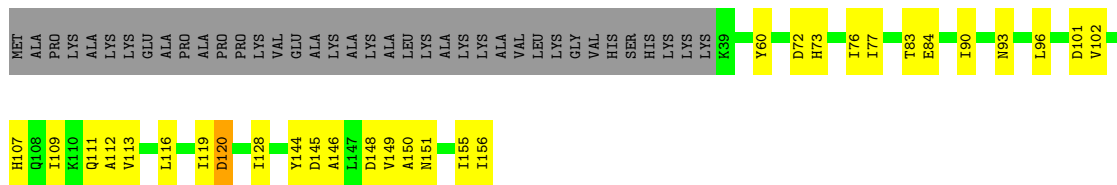
• Molecule 21: uL14



• Molecule 22: eL24



• Molecule 23: uL23



• Molecule 24: uL24







- Molecule 30: eL32

Chain e: 84% 10% 5%



- Molecule 31: eL33

Chain f: 77% 22%



- Molecule 32: eL34

Chain g: 81% 17%



- Molecule 33: uL29

Chain h: 85% 15%



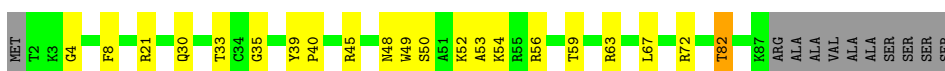
- Molecule 34: eL36

Chain i: 81% 16%



- Molecule 35: eL37

Chain j: 67% 21% 11%



- Molecule 36: eL38

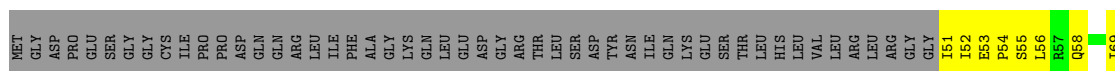
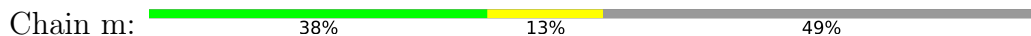
Chain k: 84% 14%



• Molecule 37: eL39



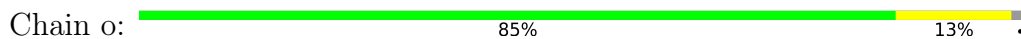
• Molecule 38: eL40



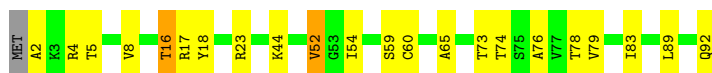
• Molecule 39: eL41



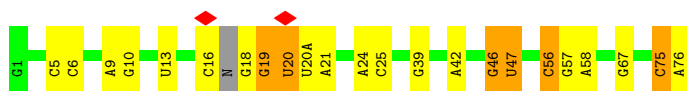
• Molecule 40: eL42



• Molecule 41: eL43

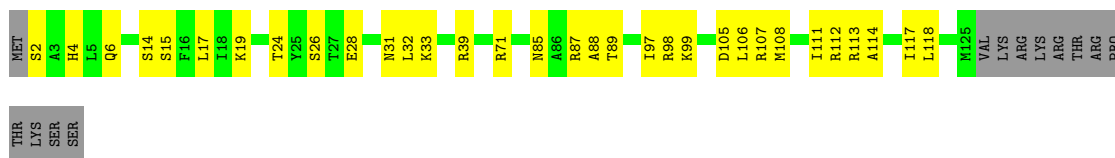


• Molecule 42: P-site tRNA



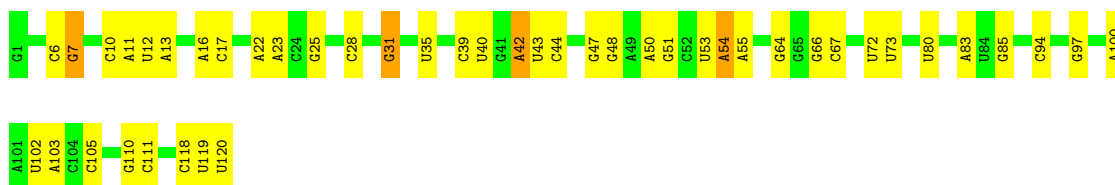
• Molecule 43: eL28

Chain r: 



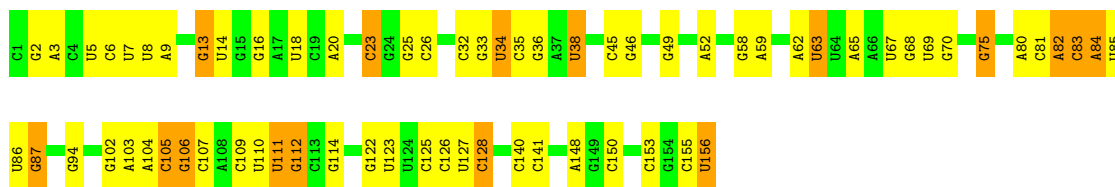
• Molecule 44: 5S ribosomal RNA

Chain u: 




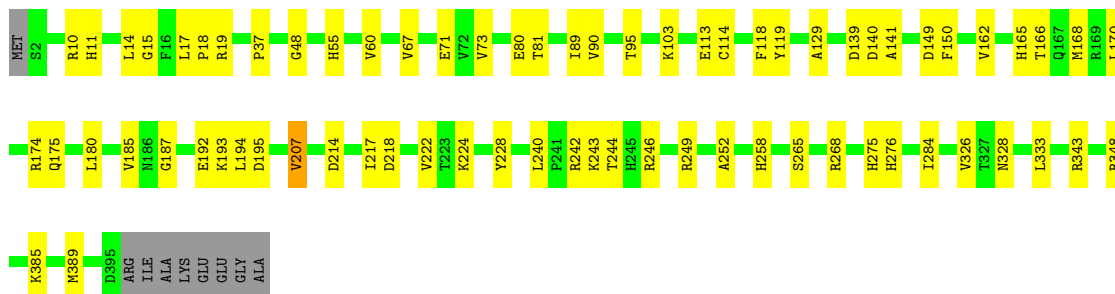
• Molecule 45: 5.8S ribosomal RNA

Chain v: 




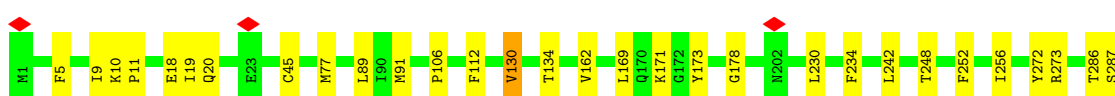
• Molecule 46: uL3

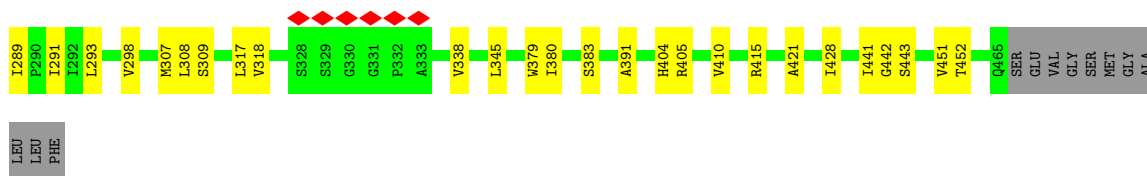
Chain w: 



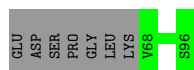
• Molecule 47: Protein transport protein Sec61 subunit alpha isoform 1

Chain 1: 

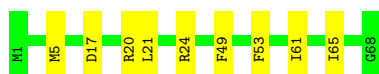
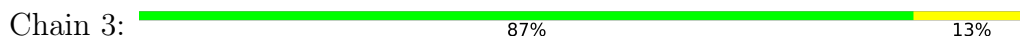




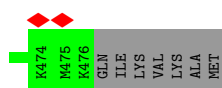
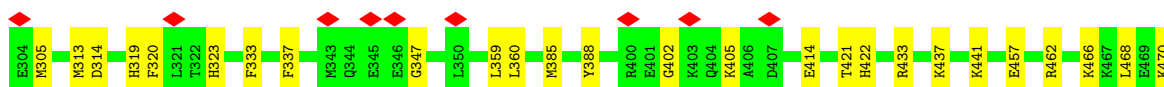
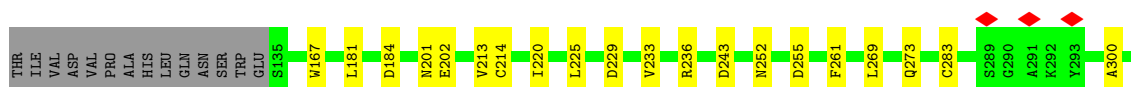
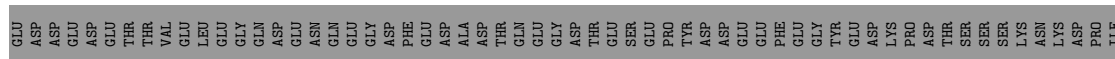
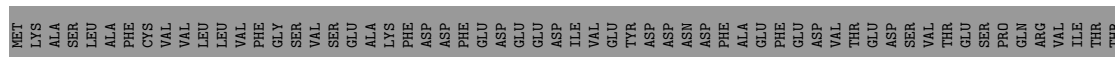
• Molecule 48: Protein transport protein Sec61 subunit beta



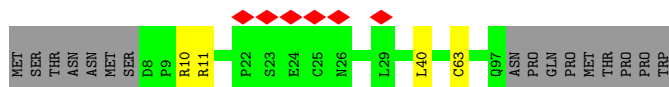
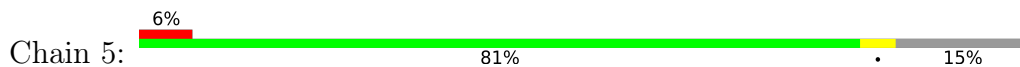
• Molecule 49: Protein transport protein Sec61 gamma



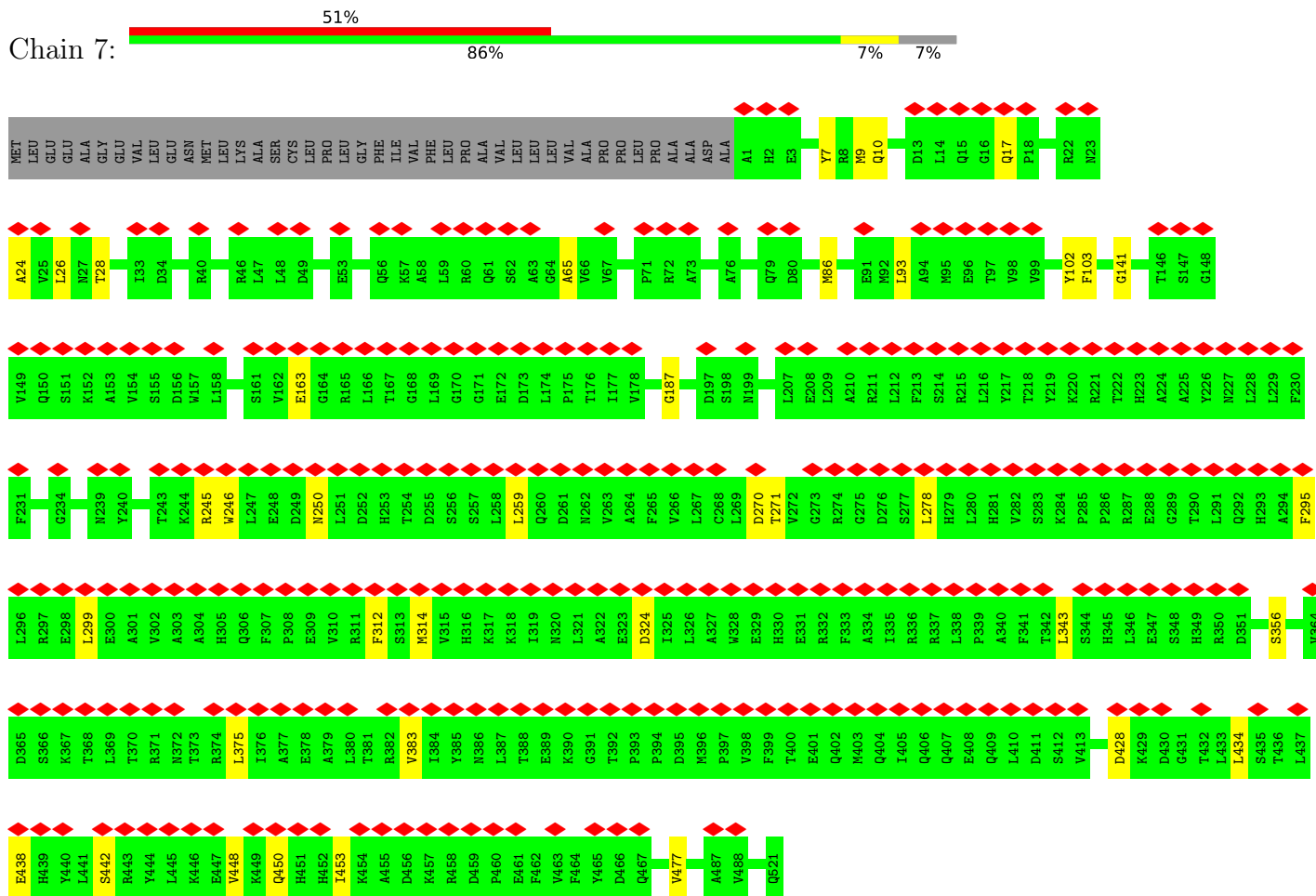
• Molecule 50: Coiled-coil domain containing 47



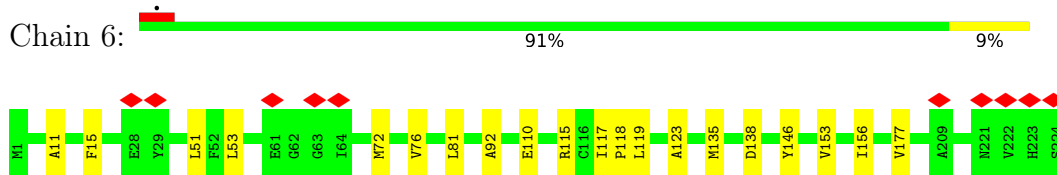
• Molecule 51: PAT complex subunit Asterix



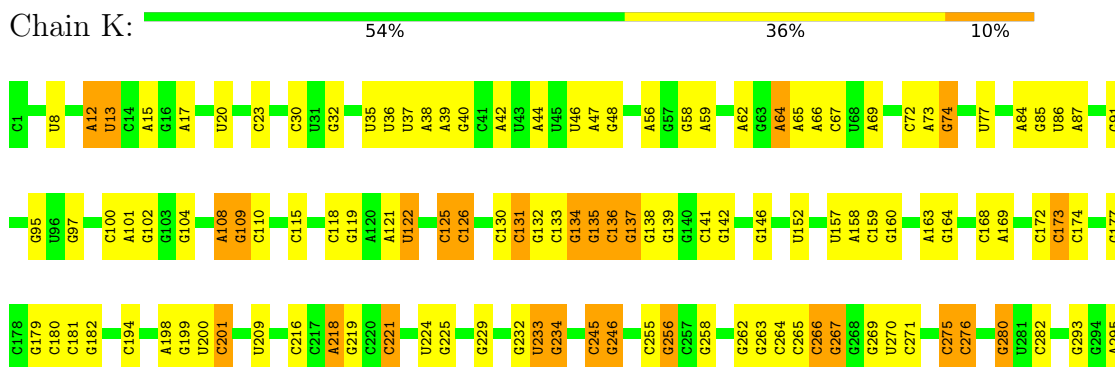
• Molecule 52: Nicalin



• Molecule 53: Transmembrane protein 147



• Molecule 54: 28S ribosomal RNA



A1942	A1943	A1944	A1945	A1946	A1947	A1948	A1949	A1950	A1951	A1952	U1957	A1958	A1959	A1960	A1961	A1962	C1963	A1964	A1965	A1966	A1967	A1968	A1969	U1971	U1974	A1975	A1976	A1977	C1977	C1978	A1979	U1980	U1981	A1982	A1983	A1984	G1985	U1986	C1987	A1988	A1989	A1990	A1991	U1997	A1998	G2000	G2001	A2002	G2003	G2004	G2005	U2006	G2007	U2008	A2010
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A1742	G1750	A1751	G1756	G1759	G1760	G1761	G1762	G1763	G1764	A1767	C1768	G1769	C1772	U1773	C1774	A1775	A1780	A1787	G1797	G1798	G1799	A1802	G1803	A1804	A1805	G1806	C1807	C1808	C1809	C1810	G1811	C1812	G1815	G1818	G1819	U1820	G1821	G1822	G1823	G1824	A1825	C1828	G1833	U1834	G1835	G1836									
A1621	U1622	A1623	G1624	G1625	G1626	G1627	G1628	A1631	A1632	G1633	A1634	A1637	A1638	U1639	C1640	C1645	C1646	C1651	G1654	C1655	G1658	U1659	C1660	C1661	C1666	A1669	G1670	U1671	C1676	U1677	A1682	U1683	A1684	G1688	G1689	C1690	C1696	U1727	G1731	G1732	G1733	G1741													
G1502	A1503	G1504	C1505	A1508	U1514	A1515	A1516	A1517	A1518	C1519	A1523	A1524	A1525	A1534	G1539	A1547	G1548	G1552	A1553	A1554	G1555	G1562	A1563	A1564	A1565	C1566	G1570	G1574	G1577	U1578	G1586	C1590	U1591	C1594	G1595	U1596	C1597	U1727	G1731	U1601	U1602	G1612	A1613												
A1420	G1421	G1426	G1430	G1431	G1432	A1433	G1434	G1435	G1436	G1437	U1438	U1440	C1441	C1442	A1443	G1444	U1445	U1446	G1447	G1448	G1449	C1450	G1451	G1455	C1456	G1457	G1458	A1459	C1460	C1464	G1465	G1467	C1468	C1469	C1474	G1475	C1476	C1477	C1478	C1481	G1482	C1483	G1484	G1489	C1490	G1493	A1497	G1498	C1499						
A1345	C1346	C1352	G1353	A1354	C1357	G1358	G1359	G1362	C1363	U1364	A1368	C1370	A1371	G1377	C1378	C1379	G1380	U1381	G1382	G1385	C1386	A1387	G1389	A1391	A1392	G1393	G1394	A1397	A1398	G1399	G1400	C1401	G1403	G1404	C1405	G1406	C1406A	G1406C	G1411A	C1411B	C1411C	A1330	C1331	G1412	C1413	G1414	G1415	G1419	G1419	G1420					
C1248	C1249	C1250	C1251	C1272	G1273	A1274	G1275	G1276	G1277	G1278	A1279	G1281	G1284	G1287	G1288	C1289	G1290	G1291	C1292	G1293	A1294	U1295	G1296	C1300	C1301	U1302	A1303	C1304	A1307	C1308	C1309	C1314	C1315	G1316	U1317	C1318	U1319	G1321	A1326	C1327	G1328	G1329	A1330	C1331	C1332	A1333	U1339	G1340							
G1175	C1076	A1077	C1079	G1080	C1081	C1082	G1090	G1091	G1095	G1096	U1100	G1168	G1169	G1170	G1171	C1172	A1173	U1174	A1175	C1176	U1177	G1178	U1179	U1186	C1187	G1188	G1189	C1192	C1193	G1194	G1195	G1196	C1197	G1198	G1199	G1202	G1203	C1210	G1211	G1212	G1215	C1216	G1217	G1218	G1219	C1233	G1234	G1235	C1236	C1237	G1272	G1273	C1239		
C924	C925	G926	A929	G930	C931	A932	G933	C934	A935	G935A	C936	U937	C938	G939	C940	C941	A944	U945	A956	G959	A960	C962	G963	A964	G965	A966	U950	C968	G969	G971A	C972	G973	C975	G976	C977	G978	C979	C983	C984	C985	C986	C987	C988	A915	C989	C990	C991	A916	C992A	C992B	C993				
A800	G401	A402	C403	C404	C405	A406	A407	A408	A409	A410	G411	G412	G413	G414	G415	G416	A420	U424	U425	A426	U427	G428	U432	A433	G438	G439	G442	C443	C446	G447	G448	C449	G450	A451	A452	G453	U454	C455	C456	G457	C458	C459	C460	A463	U467	U468	C469	A470	A471	U478	G479	C480	G481		
A396	U297	C303	C304	A305	A306	A307	G308	C309	G310	G311	G312	U313	G314	G315	U316	U321	C322	C323	A324	U325	C326	U327	A334	C340	G341	G342	C343	G346	C350	A363	G369	U370	A371	A372	G375	U381	A385	A386	G387	A388	U468	C469	A470	U392	U393	C394	A395	A396	G399						

C4294	C4199	G4087	C3893	A3774	C3885	G2896	A2798	U2708	G2616	G2518	U2440	C2011
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U4300	A4203	C4096	A3901	G4097	A3692	C3598	C2805	G2710	G2618	C2520	C2447	A2101
C4303	A4212	A4098	G3904	C3780	U3695	G3600	A2806	G2714	G2620	C2526	U2450	U2020
A4304	C4215	U4111	A3905	C3781	C3896	G3603	A2807	U2718	C2627	G2529	G2453	A2103
A4305	G4216	C4112	A3906	C3782	C3700	A3604	G2808	C2719	U2628	U2550	A2453	A2105
U4306	G4217	A3783	G3907	A3784	C3701	C3605	G2809	C3720	G2633	A2349	A2106	G2021
C4314	U4218	C4116	A3908	A3785	A3702	U3616	G2811	G2721	U2632	G2351	G2457	C2022
A4317	A4219	U4117	G3909	G3786	A3702	G3617	A2813	G2722	U2633	G2361	G2458	G2023
U4321	A4220	C4118	C3910	G3787	U3707	C3618	A2814	G2726	C2634	U2362	A2460	G2024
G4322	G4221	G4120	U3912	C3788	C3708	G3619	G2822	G2726	U2635	A2363	G2461	A2107
A4323	G4225	A4121	G3915	G3809	A3711	G3620	G2823	G2732	U2636	A2366	A2463	A2026
A4324	C4122	C4123	G3916	C3810	A3711	C3621	U2826	G2732	U2637	U2538	G2463	A2041
A4325	G4124	A4124	A3917	G3811	G3714	C3622	G2827	G2733	U2638	U2539	G2464	A2042
G4326	U4125	C4125	A3923	A3812	A3717	G3625	U2828	C2739	U2639	C2540	G2465	A2043
C4327	C4126	A4126	U3929	A3813	A3717	U3626	U2829	U2740	A2647	G2546	G2466	U2044
G4328	A4127	A4128	C3926	U3814	G3722	A3627	U2830	U2741	U2651	G2547	U2467	U2045
A4329	A4128	A4129	U3927	A3815	G3723	A3628	G2831	U2742	G2652	G2552	U2468	G2046
G4330	G4129	G3819	G3928	G3816	A3724	U3629	U2832	A2743	U2653	U2553	U2469	A2047
A4331	C4133	G3820	G3929	A3817	G3725	U3630	U2833	A2744	C2654	U2554	G2470	U2048
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A4333	G4135	G3823	C3931	G3819	U3729	U3641	U2835	A2748	G2656	C2561	G2476	C2053
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G4335	G4137	C3834	G3935	U3821	G3744	U3643	U2837	A2845	G2666	G2563	G2478	G2056
C4336	A4138	C3835	C3936	U3822	A3747	U3644	U2838	A2846	U2667	C2564	G2479	C2062
G4337	G4139	G3836	G3937	G3823	A3748	A3645	U2839	U2761	C2668	C2565	G2480	G2063
A4338	A4140	A3837	U3938	A3824	A3749	U3646	U2840	G2762	U2669	C2566	U2481	G2064
C4339	G4141	U3838	C3939	U3825	A3751	A3647	U2841	U2763	C2670	C2567	G2482	A2069
U4340	A4142	C3839	A3943	G3826	G3743	A3648	U2842	U2764	U2671	C2568	U2409	U2070
A4341	C4143	U3840	G3944	U3827	A3744	A3649	U2843	A2765	G2672	C2569	G2487	A2071
G4342	U4144	U3841	C3945	A3828	A3748	U3650	U2844	A2766	C2673	C2570	U2488	C2072
A4343	G4145	G3842	G3946	U3829	A3749	A3651	U2845	U2767	A2674	C2571	C2489	G2076
C4344	A4146	C3843	A3947	U3830	G3750	U3652	U2846	U2768	G2674	C2572	U2490	C2077
A4345	C4147	C3844	U3948	G3831	G3751	A3653	U2847	C2769	U2675	C2573	C2491	C2078
G4346	G4148	U3845	C3949	A3832	G3752	U3654	U2848	U2770	G2676	C2574	G2492	U2079
A4347	U4149	C3846	U3950	U3833	G3753	C3655	U2849	C2771	U2677	C2575	U2493	U2080
C4348	A4150	G3847	C3951	U3834	A3754	U3656	U2850	G2772	G2678	C2576	U2494	C2081
A4349	G4151	U3848	A3952	C3834	A3755	U3657	U2851	A2783	U2686	C2577	U2495	G2082
G4350	C4152	G3849	U3953	C3835	A3756	U3658	U2852	U2784	U2687	C2578	U2496	C2083
A4351	U4153	C3850	C3954	A3836	A3757	C3659	U2853	U2785	U2688	C2579	U2497	U2084
C4352	A4154	U3851	G3955	U3837	A3758	U3660	U2854	A2786	U2689	C2580	U2498	C2085
A4353	G4155	G3852	A3956	U3838	A3759	U3661	U2855	U2787	C2690	C2581	A2502	G2086
G4354	C4156	C3853	U3957	U3839	A3760	U3662	U2856	U2788	U2691	C2582	G2503	U2087
A4355	U4157	U3854	C3958	A3840	A3761	U3663	U2857	U2789	C2692	C2583	U2504	C2088
C4356	A4158	C3855	U3959	U3841	A3762	U3664	U2858	U2790	U2693	C2584	G2505	U2089
G4357	G4159	G3856	A3960	A3842	A3763	U3665	U2859	U2791	C2694	C2585	U2506	G2090
A4376	U4170	U3857	U3961	U3843	A3764	U3666	U2860	C2702	U2695	C2586	A2511	A2095
C4377	C4171	C3858	A3962	U3844	A3765	U3667	U2861	C2703	U2696	C2587	A2512	A2096
A4378	A4172	U3859	U3963	A3845	A3766	U3668	U2862	U2792	U2697	C2588	A2513	G2097
U4379	G4173	G3860	A3964	A3846	A3767	U3669	U2863	U2793	U2698	C2589	G2517	G2098
A4380	U4174	C3861	U3965	U3847	A3768	U3670	U2864	A2794	U2699	C2590	U2518	
U4384	A4182	A3872	G4075	A3876	A3769	U3671	U2865	U2795	U2700	A2696	U2519	
A4385	G4183	U3873	U4076	A3877	A3770	U3672	U2866	U2796	U2701	A2697	U2520	
C4386	A4184	C3874	A4077	A3878	A3771	U3673	U2867	U2797	U2702	U2698	U2521	
A4387	U4185	U3875	C4078	A3879	A3772	U3674	U2868	U2798	C2703	U2699	U2522	
C4388	G4186	G3876	C4079	A3880	A3773	U3675	U2869	U2799	U2704	U2700	U2523	
A4389	A4187	C3877	U4080	A3881	U3770	U3676	U2870	U2800	U2705	C2601	U2524	
A4390	U4188	U3878	C4081	A3882	U3771	U3677	U2871	U2801	U2706	C2602	U2525	
A4391	G4189	A3879	G4082	A3883	U3772	U3678	U2872	U2802	U2707	C2603	U2526	
A4292	U4191	C3880	U4083	A3884	U3773	U3679	U2873	U2803				
U4293	G4195	G3881	U4084	A3885			U2874	U2804				
		C3882	U4085	A3886			U2875	U2805				
		G3883	U4086	A3887			U2876	U2806				
		U3884	U4087	A3888			U2877	U2807				
		C3885	U4088	A3889			U2878	U2808				
		G3886	U4089	A3890			U2879	U2809				
		U3887	U4090	A3891			U2880	U2810				
		C3888	U4091	A3892			U2881	U2811				
		G3889	U4092	A3893			U2882	U2812				
		U3890	U4093	A3894			U2883	U2813				
		C3891	U4094	A3895			U2884	U2814				
		G3892	U4095	A3896			U2885	U2815				
		U3893	U4096	A3897			U2886	U2816				
		C3894	U4097	A3898			U2887	U2817				
		G3895	U4098	A3899			U2888	U2818				
		U3896	U4099	A3900			U2889	U2819				
		C3897	U4100	A3901			U2890	U2820				
		G3898	U4101	A3902			U2891	U2821				
		U3899	U4102	A3903			U2892	U2822				
		C3900	U4103	A3904			U2893	U2823				
		G3901	U4104	A3905			U2894	U2824				
		U3902	U4105	A3906			U2895	U2825				
		C3903	U4106	A3907			U2896	U2826				
		G3904	U4107	A3908			U2897	U2827				
		U3905	U4108	A3909			U2898	U2828				
		C3906	U4109	A3910			U2899	U2829				
		G3907	U4110	A3911			U2900	U2830				
		U3908	U4111	A3912			U2901	U2831				
		C3909	U4112	A3913			U2902	U2832				
		G3910	U4113	A3914			U2903	U2833				
		U3911	U4114	A3915			U2904	U2834				
		C3912	U4115	A3916			U2905	U2835				
		G3913	U4116	A3917			U2906	U2836				
		U3914	U4117	A3918			U2907	U2837				
		C3915	U4118	A3919			U2908	U2838				
		G3916	U4119	A3920			U2909	U2839				
		U3917	U4120	A3921			U2910	U2840				
		C3918	U4121	A3922			U2911	U2841				
		G3919	U4122	A3923			U2912	U2842				
		U3920	U4123	A3924			U2913	U2843				
		C3921	U4124	A3925			U2914	U2844				
		G3922	U4125	A3926			U2915	U2845				
		U3923	U4126	A3927			U2916	U2846				
		C3924	U4127	A3928			U2917	U2847				
		G3925	U4128	A3929			U2918	U2848				
		U3926	U4129	A3930			U2919	U2849				
		C3927	U4130	A3931			U2920	U2850				
		G3928	U4131	A3932			U2921	U2851				
		U3929	U4132	A3933			U2922	U2852				
		C3930	U4133	A3934			U2923	U2853				
		G3931	U4134	A3935			U2924	U2854				
		U3932	U4135	A3936			U2925	U2855				
		C3933	U4136	A3937			U2926	U2856				
		G3934	U4137	A3938			U2927	U2857				
		U3935	U4138	A3939			U2928	U2858				
		C3936	U4139	A3940			U2929	U2859				
		G3937	U4140	A3941								

C5008	C5009	A5014	G5015	A5016	G5017	C5018	A5019	C5020	C5021	U5022	G5028	C5029	A5034	U5035	U5040	G5041	A5042	A5043	A5044	C5047	A5048	G5049	C5050	C5051	C5052	U5053	C5054	G5055	A5056	C5057	A5058	A5059	A5060	A5061	G5062	G5068	U5069														
G4931	G4935	G4936	C4937	C4940	G4941	A4942	A4943	C4944	G4945	U4946	U4947	C4948	G4949	U4950	G4951	A4955	A4956	C4957	C4958	U4959	G4960	G4963	C4964	U4965	A4966	A4967	U4976	A4977	G4978	A4979	C4980	G4981	A4982	U4985	U4988	A4989	C4990	U4991	G4992	G4993	G4994	U4995	C4996	G5000	U5001	U5002	U5003	C5004	G5005	U5006	A5007
A4762	U4763	A4764	G4765	G4768	G4769	U4770	C4771	C4772	G4860	G4861	G4868	U4869	G4870	G4871	G4872	G4873	A4874	G4875	U4882	G4883	G4884	U4885	C4886	C4887	C4895	G4896	G4897	C4902	G4903	G4907	G4908	A4909	A4910	A4911	G4912	G4913	G4914	G4915	G4916	C4917	C4918	G4919	C4920	C4921	C4922	C4923	C4924	U4925	C4926	G4927	C4928
G4660	G4661	C4662	G4663	C4670	C4671	A4672	U4677	U4678	A4687	C4688	U4689	G4694	U4699	U4700	A4701	G4702	U4709	G4713	C4716	A4717	G4718	G4719	C4720	C4721	G4722	A4723	A4724	C4725	U4728	A4729	G4735	C4736	G4737	C4738	C4739	G4740	G4743	A4744	G4745	G4750	U4751	U4752	U4753	G4754	C4757	U4758	C4759	G4760	G4761		
G4392	G4393	A4394	U4395	C4398	U4399	G4400	C4401	C4402	U4403	U4406	G4407	C4412	C4413	A4414	U4419	U4420	A4421	A4422	U4423	A4424	C4429	G4430	U4431	C4432	G4433	C4434	U4437	U4438	U4442	C4443	C4444	U4445	G4448	A4449	U4452	C4453	G4454	U4457	C4458	U4459	U4460	C4461	C4462	U4463	A4464	U4465	C4466	A4467			
U4471	G4472	A4473	A4474	G4475	C4476	U4477	G4478	A4488	C4489	U4492	U4493	U4500	A4507	C4508	U4509	A4510	A4511	A4512	A4513	G4514	G4515	A4518	G4519	C4522	G4523	G4524	C4525	G4528	G4529	U4532	A4535	C4536	C4537	G4538	G4541	A4544	A4548	G4549	U4550	U4551	U4552	A4553	G4554	U4555	U4558	A4559					

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1665551	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 ( $e^-/\text{\AA}^2$ )	54	Depositor
Minimum defocus (nm)	1900	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.070	Depositor
Minimum map value	-0.021	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.007	Depositor
Map size ( $\text{\AA}$ )	552.0, 552.0, 552.0	wwPDB
Map dimensions	412, 412, 412	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.3398058, 1.3398058, 1.3398058	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, MG

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	0.12	0/1936	0.30	0/2596
2	B	0.14	0/186	0.36	0/254
3	C	0.13	0/2937	0.36	0/3946
4	D	0.14	0/2437	0.37	0/3264
5	E	0.13	0/1914	0.34	0/2566
6	F	0.14	0/1911	0.36	0/2549
7	G	0.14	0/1910	0.37	0/2569
8	H	0.13	0/1535	0.35	0/2063
9	I	0.12	0/1702	0.34	0/2272
10	J	0.13	0/1385	0.38	0/1852
11	L	0.13	0/1733	0.36	0/2316
12	M	0.15	0/1158	0.40	0/1547
13	N	0.15	0/1740	0.39	0/2328
14	O	0.15	0/1662	0.38	0/2222
15	P	0.19	0/1268	0.43	0/1700
16	Q	0.14	0/1538	0.35	0/2054
17	R	0.16	0/1310	0.41	0/1734
18	S	0.14	0/1501	0.36	0/2012
19	T	0.11	0/1326	0.30	0/1770
20	U	0.11	0/848	0.35	0/1138
21	V	0.12	0/993	0.34	1/1332 (0.1%)
22	W	0.13	0/541	0.35	0/720
23	X	0.14	0/984	0.37	0/1323
24	Y	0.12	0/1132	0.35	0/1504
25	Z	0.13	0/1130	0.32	0/1507
26	a	0.13	0/1191	0.32	0/1590
27	b	0.12	0/861	0.36	0/1138
28	c	0.13	0/771	0.34	0/1034
29	d	0.14	0/903	0.36	0/1216
30	e	0.13	0/1071	0.33	0/1429
31	f	0.13	0/895	0.33	0/1198
32	g	0.15	0/916	0.35	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	h	0.14	0/1017	0.40	0/1344
34	i	0.14	0/841	0.38	0/1112
35	j	0.11	0/720	0.30	0/952
36	k	0.13	0/575	0.34	0/761
37	l	0.14	0/459	0.37	0/608
38	m	0.13	0/435	0.33	0/575
39	n	0.16	0/240	0.45	0/305
40	o	0.11	0/864	0.32	0/1140
41	p	0.15	0/718	0.37	0/953
42	q	0.14	0/1805	0.38	0/2809
43	r	0.13	0/1010	0.37	0/1354
44	u	0.15	0/2858	0.34	0/4455
45	v	0.15	0/3701	0.37	0/5766
46	w	0.12	0/3240	0.30	0/4339
47	1	0.13	0/3677	0.37	0/4986
48	2	0.13	0/237	0.28	0/321
49	3	0.14	0/553	0.35	0/738
50	4	0.13	0/2819	0.35	0/3772
51	5	0.14	0/730	0.31	0/988
52	7	0.11	0/4224	0.30	0/5728
53	6	0.11	0/1835	0.30	0/2495
54	K	0.17	0/84978	0.42	0/132528
All	All	0.15	0/160861	0.39	1/235992 (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
13	N	0	1
50	4	0	1
54	K	0	1
All	All	0	3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	V	132	ILE	N-CA-C	-5.50	107.08	111.81

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
50	4	433	ARG	Sidechain
54	K	234	G	Sidechain
13	N	76	PRO	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1898	1993	1993	39	0
2	B	180	171	171	4	0
3	C	2883	3053	3053	52	0
4	D	2391	2424	2424	37	0
5	E	1877	2031	2031	58	0
6	F	1875	1995	1995	31	0
7	G	1879	2027	2027	29	0
8	H	1516	1597	1597	26	0
9	I	1664	1712	1712	20	0
10	J	1362	1399	1399	23	0
11	L	1702	1820	1820	28	0
12	M	1137	1211	1211	21	0
13	N	1696	1744	1743	37	0
14	O	1630	1778	1778	31	0
15	P	1242	1274	1274	34	0
16	Q	1514	1634	1634	25	0
17	R	1294	1434	1434	21	0
18	S	1462	1508	1508	34	0
19	T	1298	1367	1366	24	0
20	U	834	858	858	11	0
21	V	979	1039	1039	15	0
22	W	528	541	541	5	0
23	X	967	1040	1040	23	0
24	Y	1115	1205	1205	26	0
25	Z	1107	1182	1182	18	0
26	a	1162	1209	1209	26	0
27	b	848	920	920	18	0
28	c	761	794	794	12	0
29	d	888	930	930	9	0

*Continued on next page...*

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	e	1053	1147	1147	10	0
31	f	876	912	912	20	0
32	g	906	998	998	16	0
33	h	1009	1136	1136	14	0
34	i	830	916	916	11	0
35	j	705	737	737	14	0
36	k	569	637	637	7	0
37	l	447	480	480	12	0
38	m	429	466	466	9	0
39	n	239	289	289	5	0
40	o	851	922	922	11	0
41	p	708	757	757	18	0
42	q	1616	823	824	11	0
43	r	994	1051	1051	30	0
44	u	2558	1296	1296	29	0
45	v	3314	1683	1683	40	0
46	w	3172	3310	3310	58	0
47	1	3598	3722	3722	42	0
48	2	230	245	245	0	0
49	3	543	577	577	5	0
50	4	2778	2819	2819	35	0
51	5	711	710	710	2	0
52	7	4139	4121	4123	24	0
53	6	1783	1792	1792	11	0
54	K	75972	38358	38382	939	0
55	K	201	0	0	0	0
55	P	2	0	0	0	0
55	V	1	0	0	0	0
55	a	1	0	0	0	0
55	g	1	0	0	0	0
55	j	1	0	0	0	0
55	u	7	0	0	0	0
55	v	6	0	0	0	0
56	g	1	0	0	0	0
56	j	1	0	0	0	0
56	m	1	0	0	0	0
56	o	1	0	0	0	0
56	p	1	0	0	0	0
All	All	149944	111794	111819	1755	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 7.

The worst 5 of 1755 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)
54:K:1397:A:HO2'	54:K:1467:C:HO2'	1.00	0.92
54:K:2638:G:N2	54:K:2697:A:N1	2.16	0.92
21:V:50:ASN:ND2	54:K:4457:U:OP1	2.04	0.90
43:r:98:ARG:NH2	54:K:2262:G:OP2	2.05	0.89
42:q:10:G:N2	42:q:25:C:O2	2.04	0.89

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	246/257 (96%)	219 (89%)	27 (11%)	0	100	100
2	B	25/229 (11%)	22 (88%)	2 (8%)	1 (4%)	2	14
3	C	360/425 (85%)	335 (93%)	25 (7%)	0	100	100
4	D	291/297 (98%)	269 (92%)	22 (8%)	0	100	100
5	E	227/291 (78%)	217 (96%)	9 (4%)	1 (0%)	30	59
6	F	223/247 (90%)	205 (92%)	18 (8%)	0	100	100
7	G	229/319 (72%)	213 (93%)	16 (7%)	0	100	100
8	H	188/192 (98%)	176 (94%)	12 (6%)	0	100	100
9	I	201/214 (94%)	181 (90%)	20 (10%)	0	100	100
10	J	168/178 (94%)	158 (94%)	10 (6%)	0	100	100
11	L	208/211 (99%)	193 (93%)	14 (7%)	1 (0%)	24	55
12	M	136/218 (62%)	125 (92%)	11 (8%)	0	100	100
13	N	199/204 (98%)	183 (92%)	16 (8%)	0	100	100
14	O	197/203 (97%)	186 (94%)	11 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	P	151/184 (82%)	143 (95%)	8 (5%)	0	100	100
16	Q	185/188 (98%)	171 (92%)	14 (8%)	0	100	100
17	R	153/196 (78%)	144 (94%)	9 (6%)	0	100	100
18	S	174/176 (99%)	159 (91%)	15 (9%)	0	100	100
19	T	157/160 (98%)	139 (88%)	17 (11%)	1 (1%)	21	51
20	U	100/128 (78%)	90 (90%)	10 (10%)	0	100	100
21	V	129/140 (92%)	121 (94%)	8 (6%)	0	100	100
22	W	61/157 (39%)	55 (90%)	6 (10%)	0	100	100
23	X	116/156 (74%)	106 (91%)	10 (9%)	0	100	100
24	Y	132/145 (91%)	124 (94%)	8 (6%)	0	100	100
25	Z	133/136 (98%)	122 (92%)	11 (8%)	0	100	100
26	a	145/148 (98%)	132 (91%)	13 (9%)	0	100	100
27	b	100/226 (44%)	96 (96%)	4 (4%)	0	100	100
28	c	96/115 (84%)	90 (94%)	6 (6%)	0	100	100
29	d	105/125 (84%)	94 (90%)	11 (10%)	0	100	100
30	e	126/135 (93%)	118 (94%)	8 (6%)	0	100	100
31	f	107/110 (97%)	99 (92%)	8 (8%)	0	100	100
32	g	112/116 (97%)	104 (93%)	8 (7%)	0	100	100
33	h	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
34	i	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
35	j	84/97 (87%)	83 (99%)	1 (1%)	0	100	100
36	k	67/70 (96%)	63 (94%)	4 (6%)	0	100	100
37	l	48/51 (94%)	38 (79%)	10 (21%)	0	100	100
38	m	50/102 (49%)	46 (92%)	4 (8%)	0	100	100
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	102/106 (96%)	90 (88%)	12 (12%)	0	100	100
41	p	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
43	r	122/137 (89%)	112 (92%)	10 (8%)	0	100	100
46	w	392/403 (97%)	360 (92%)	32 (8%)	0	100	100
47	1	463/476 (97%)	460 (99%)	3 (1%)	0	100	100
48	2	27/96 (28%)	27 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	3	66/68 (97%)	66 (100%)	0	0	100	100
50	4	340/483 (70%)	338 (99%)	1 (0%)	1 (0%)	36	66
51	5	88/106 (83%)	87 (99%)	1 (1%)	0	100	100
52	7	519/563 (92%)	512 (99%)	7 (1%)	0	100	100
53	6	222/224 (99%)	222 (100%)	0	0	100	100
All	All	8102/9553 (85%)	7610 (94%)	487 (6%)	5 (0%)	49	76

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	L	64	VAL
50	4	347	GLY
2	B	42	PRO
5	E	228	PRO
19	T	82	GLY

### 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	190/199 (96%)	189 (100%)	1 (0%)	81	82
2	B	21/172 (12%)	21 (100%)	0	100	100
3	C	302/347 (87%)	302 (100%)	0	100	100
4	D	247/250 (99%)	247 (100%)	0	100	100
5	E	206/251 (82%)	203 (98%)	3 (2%)	57	71
6	F	196/215 (91%)	195 (100%)	1 (0%)	81	82
7	G	200/272 (74%)	199 (100%)	1 (0%)	81	82
8	H	169/171 (99%)	168 (99%)	1 (1%)	78	81
9	I	175/181 (97%)	174 (99%)	1 (1%)	78	81
10	J	143/149 (96%)	141 (99%)	2 (1%)	59	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	L	175/176 (99%)	172 (98%)	3 (2%)	53	69
12	M	117/161 (73%)	116 (99%)	1 (1%)	70	76
13	N	171/172 (99%)	170 (99%)	1 (1%)	78	81
14	O	171/173 (99%)	171 (100%)	0	100	100
15	P	134/163 (82%)	132 (98%)	2 (2%)	57	71
16	Q	164/164 (100%)	163 (99%)	1 (1%)	78	81
17	R	138/175 (79%)	138 (100%)	0	100	100
18	S	157/157 (100%)	155 (99%)	2 (1%)	61	73
19	T	139/140 (99%)	139 (100%)	0	100	100
20	U	92/114 (81%)	91 (99%)	1 (1%)	65	75
21	V	101/107 (94%)	100 (99%)	1 (1%)	68	75
22	W	55/126 (44%)	55 (100%)	0	100	100
23	X	106/134 (79%)	105 (99%)	1 (1%)	70	76
24	Y	124/135 (92%)	123 (99%)	1 (1%)	73	78
25	Z	117/118 (99%)	115 (98%)	2 (2%)	53	69
26	a	119/120 (99%)	118 (99%)	1 (1%)	73	78
27	b	84/172 (49%)	83 (99%)	1 (1%)	63	74
28	c	84/98 (86%)	83 (99%)	1 (1%)	63	74
29	d	98/110 (89%)	96 (98%)	2 (2%)	48	66
30	e	114/121 (94%)	114 (100%)	0	100	100
31	f	88/89 (99%)	88 (100%)	0	100	100
32	g	98/99 (99%)	98 (100%)	0	100	100
33	h	108/110 (98%)	107 (99%)	1 (1%)	70	76
34	i	86/89 (97%)	86 (100%)	0	100	100
35	j	73/80 (91%)	71 (97%)	2 (3%)	39	61
36	k	64/65 (98%)	64 (100%)	0	100	100
37	l	47/48 (98%)	47 (100%)	0	100	100
38	m	48/90 (53%)	48 (100%)	0	100	100
39	n	24/24 (100%)	24 (100%)	0	100	100
40	o	92/94 (98%)	92 (100%)	0	100	100
41	p	74/75 (99%)	72 (97%)	2 (3%)	39	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	r	108/121 (89%)	108 (100%)	0	100	100
46	w	342/348 (98%)	340 (99%)	2 (1%)	78	81
47	1	390/398 (98%)	386 (99%)	4 (1%)	68	75
48	2	26/74 (35%)	26 (100%)	0	100	100
49	3	59/59 (100%)	57 (97%)	2 (3%)	32	57
50	4	306/435 (70%)	304 (99%)	2 (1%)	76	79
51	5	83/99 (84%)	83 (100%)	0	100	100
52	7	443/476 (93%)	442 (100%)	1 (0%)	87	87
53	6	187/187 (100%)	186 (100%)	1 (0%)	81	82
All	All	7055/8103 (87%)	7007 (99%)	48 (1%)	73	79

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	c	91	VAL
41	p	52	VAL
29	d	22	THR
35	j	67	LEU
46	w	207	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
47	1	398	GLN
53	6	152	GLN
50	4	165	GLN
52	7	116	GLN
15	P	25	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
42	q	74/77 (96%)	15 (20%)	0
44	u	119/120 (99%)	14 (11%)	0
45	v	155/156 (99%)	37 (23%)	0
54	K	3520/3543 (99%)	822 (23%)	58 (1%)
All	All	3868/3896 (99%)	888 (22%)	58 (1%)

5 of 888 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
42	q	9	A
42	q	13	U
42	q	16	C
42	q	19	G
42	q	20	U

5 of 58 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	K	1455	G
54	K	4925	U
54	K	2266	C
54	K	4921	C
54	K	4354	U

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 225 ligands modelled in this entry, 225 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
54	K	25

The worst 5 of 25 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	K	2113:G	O3'	2258:C	P	40.63
1	K	1252:C	O3'	1271:G	P	36.90
1	K	1219:G	O3'	1233:G	P	19.23
1	K	3948:C	O3'	4065:G	P	18.79
1	K	4138:C	O3'	4146:G	P	18.12

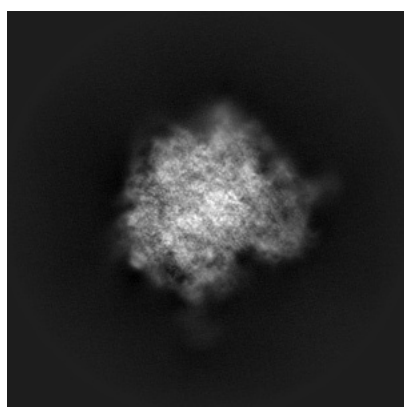
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25994. These allow visual inspection of the internal detail of the map and identification of artifacts.

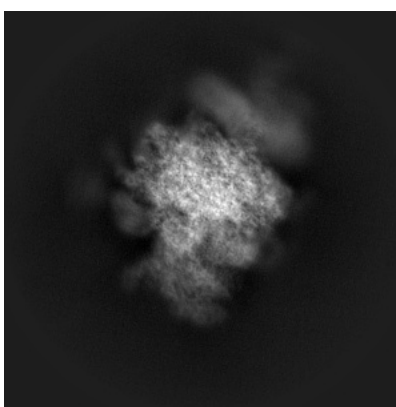
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

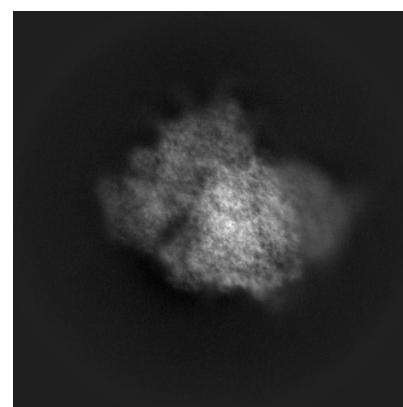
#### 6.1.1 Primary map



X



Y

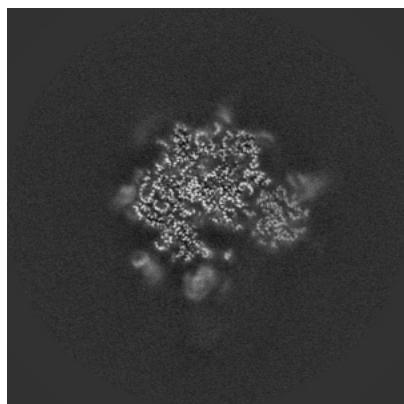


Z

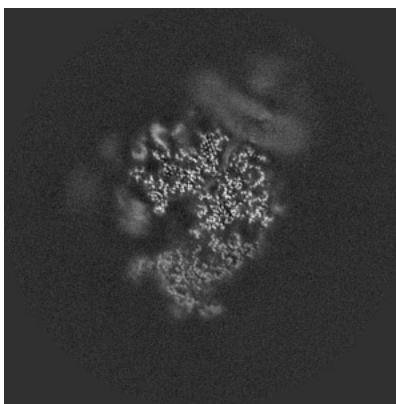
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

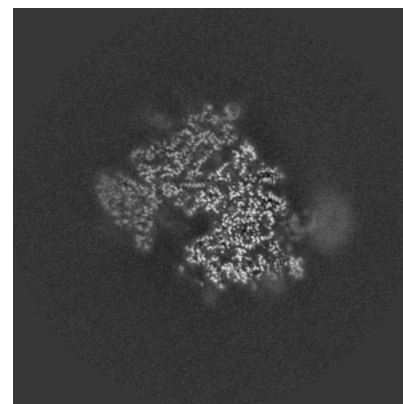
#### 6.2.1 Primary map



X Index: 206



Y Index: 206

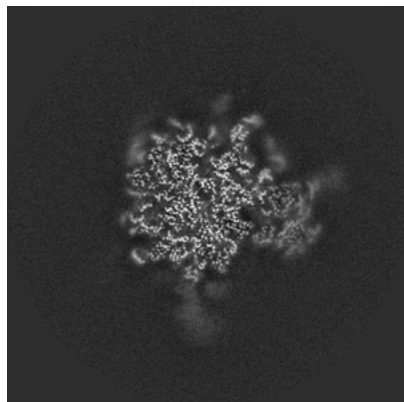


Z Index: 206

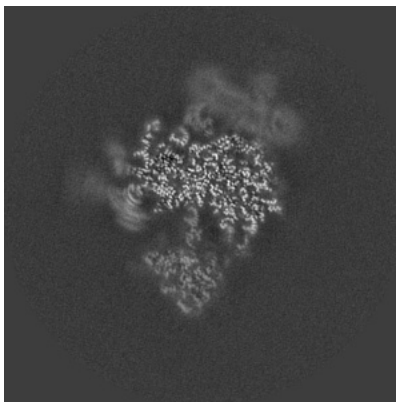
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

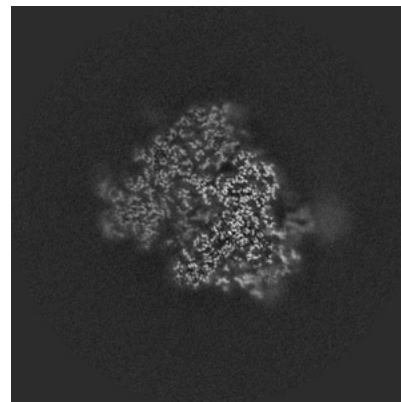
### 6.3.1 Primary map



X Index: 224



Y Index: 193

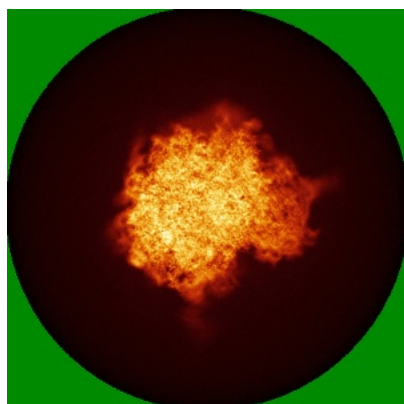


Z Index: 196

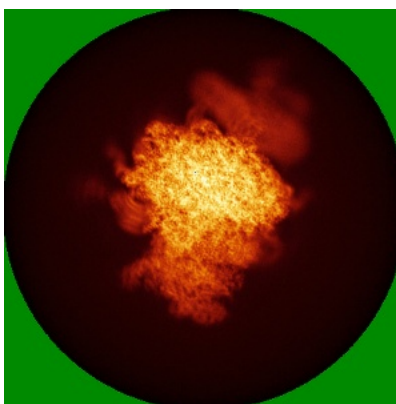
The images above show the largest variance slices of the map in three orthogonal directions.

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

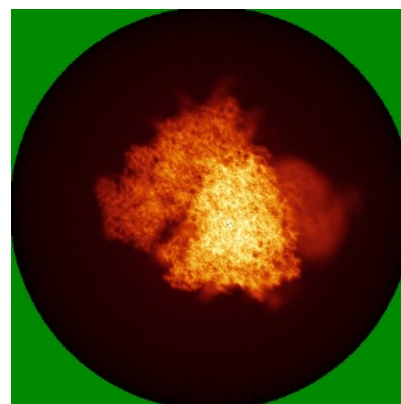
### 6.4.1 Primary map



X



Y

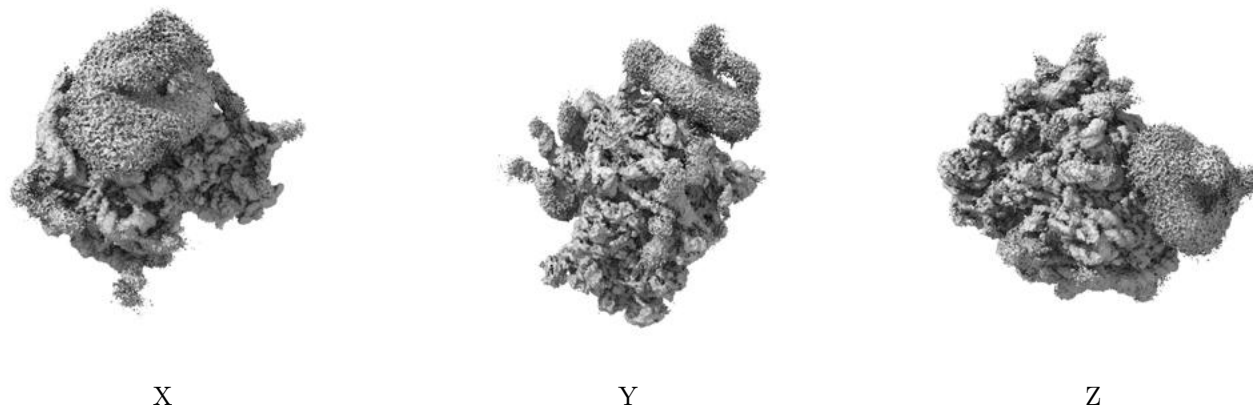


Z

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

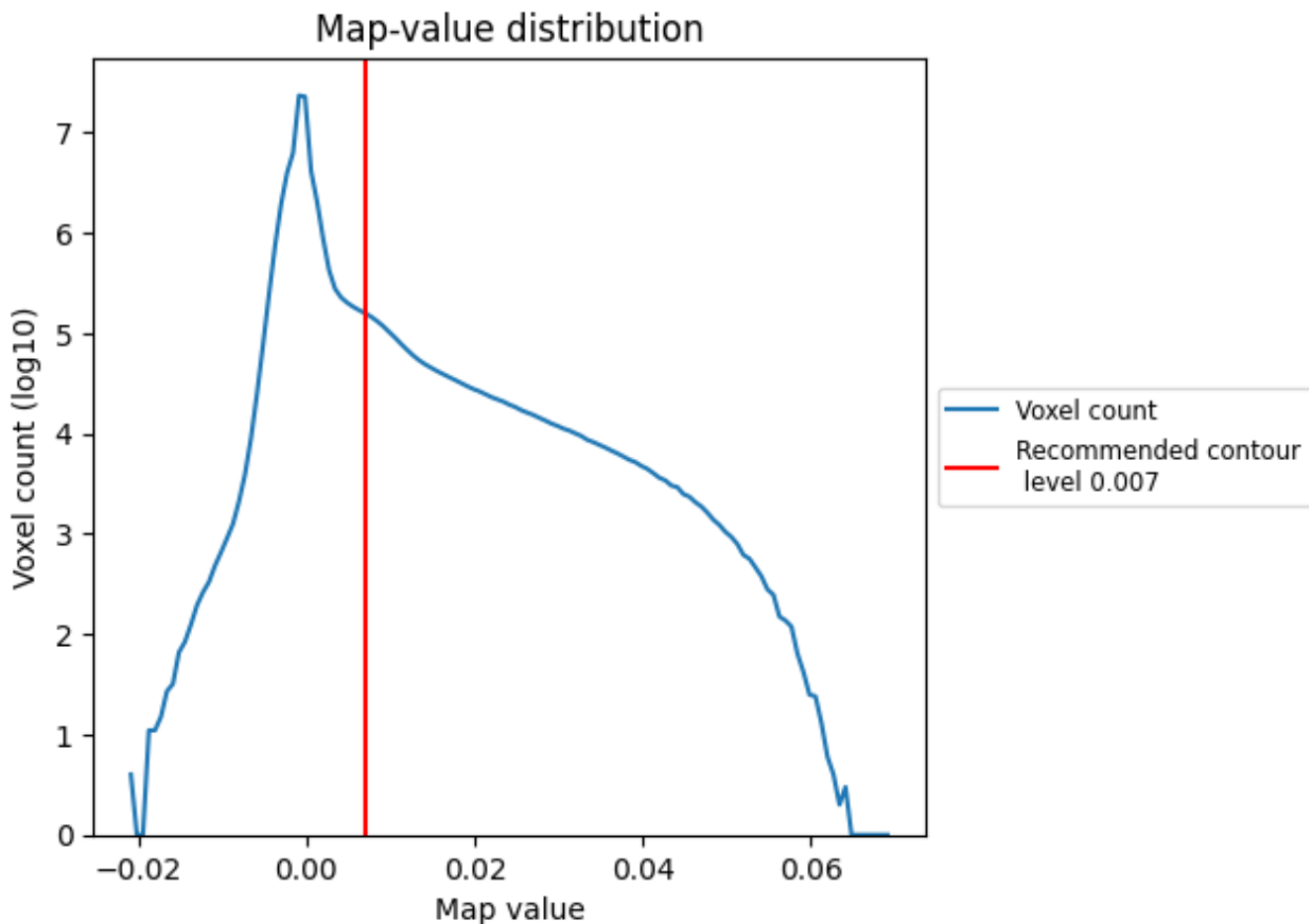
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

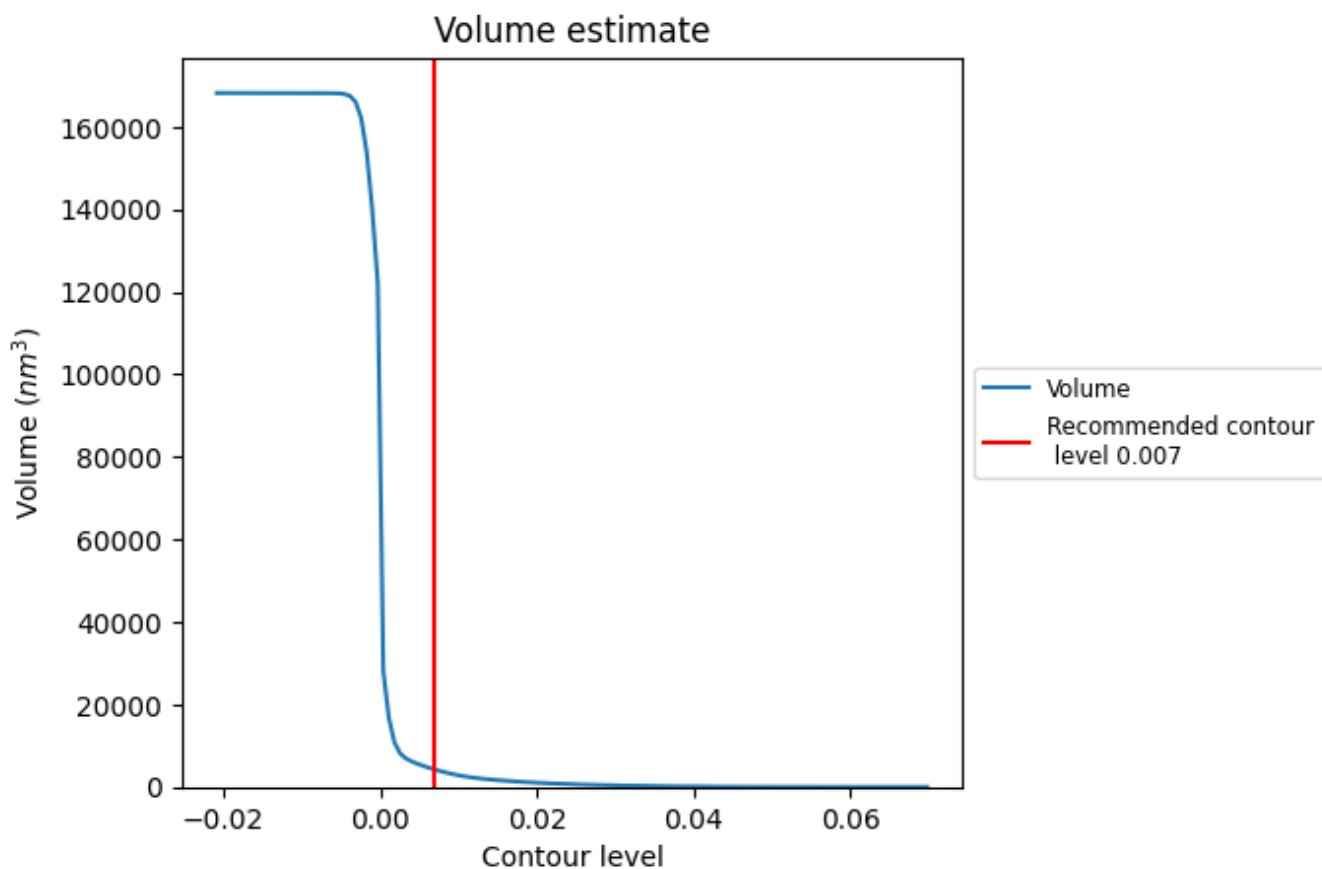
This section contains the results of statistical analysis of the map.

### 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.

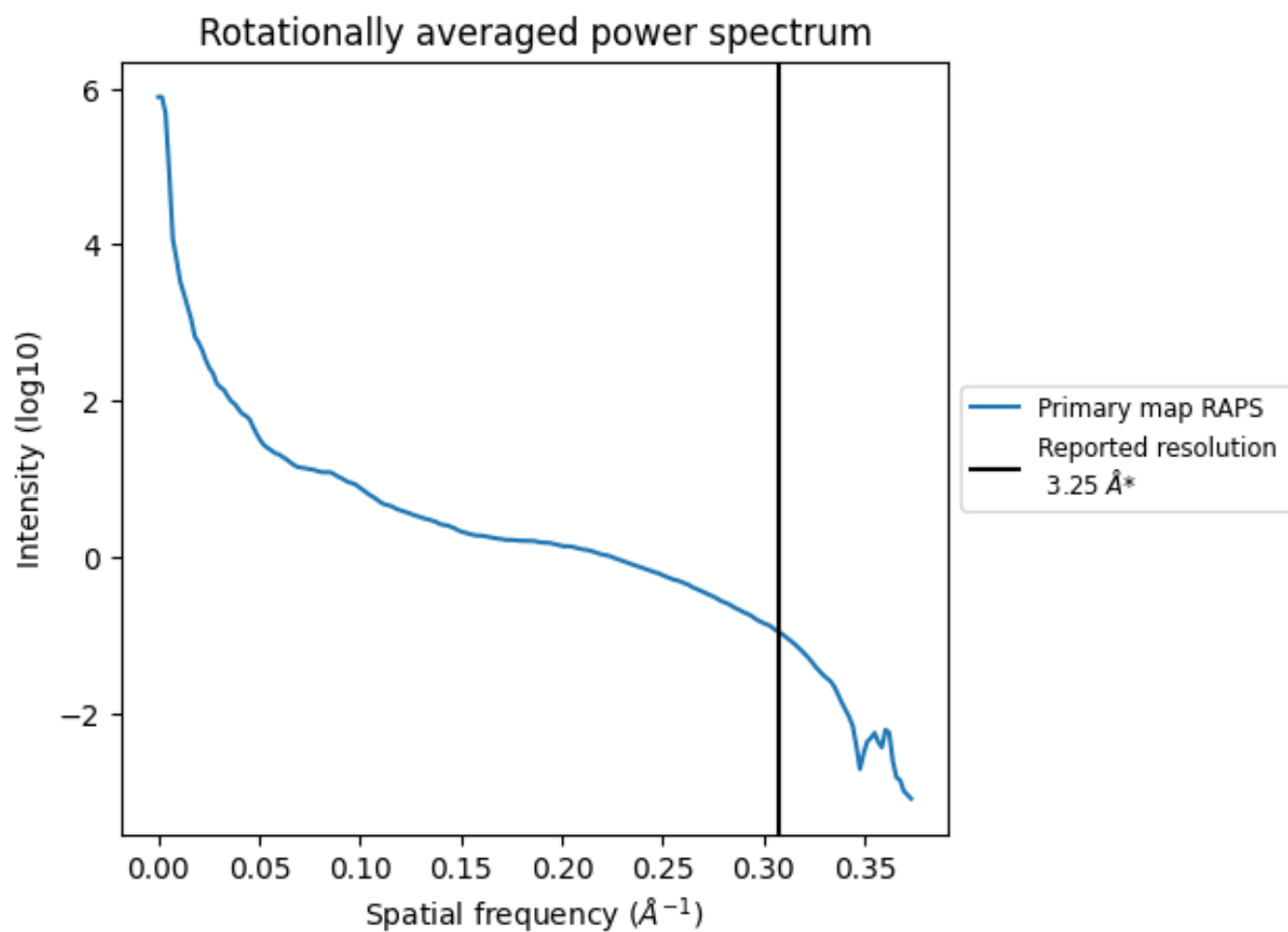
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 4210  $\text{nm}^3$ ; this corresponds to an approximate mass of 3803 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 0.308 Å<sup>-1</sup>

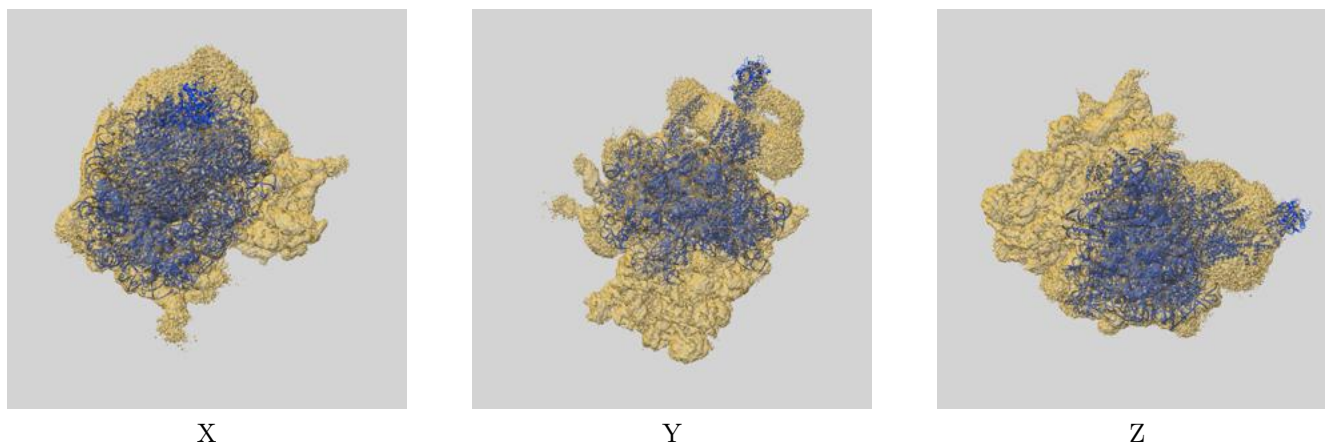
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

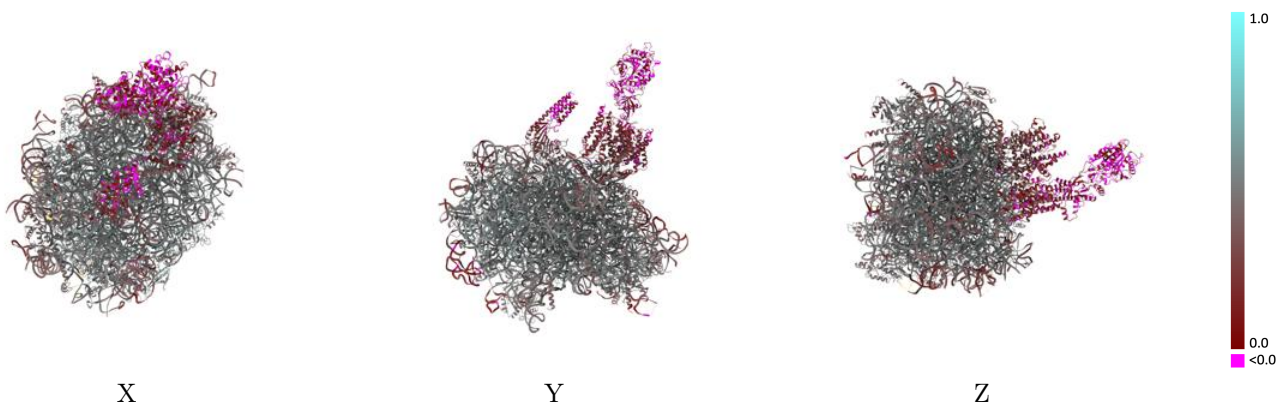
This section contains information regarding the fit between EMDB map EMD-25994 and PDB model 7TM3. Per-residue inclusion information can be found in section 3 on page 17.

### 9.1 Map-model overlay [i](#)



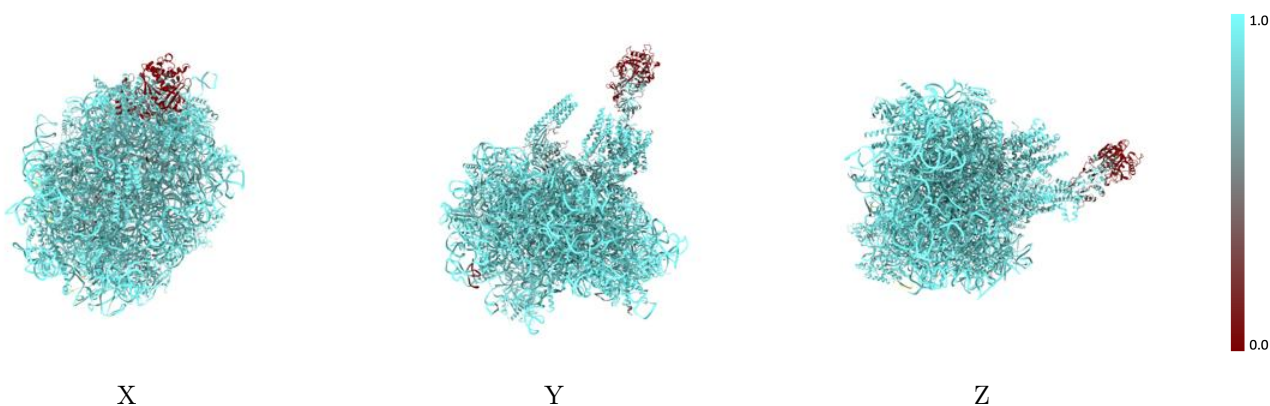
The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



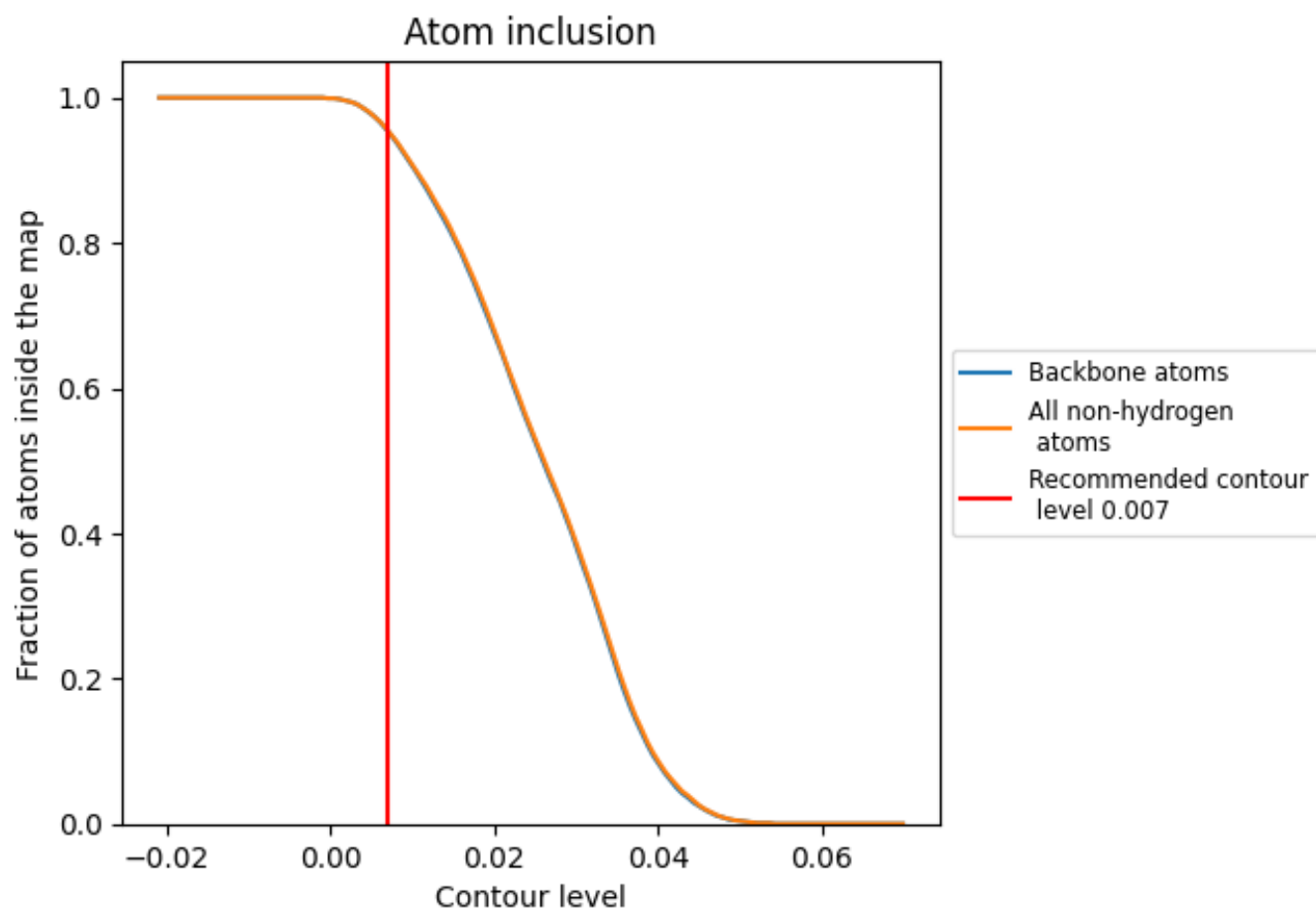
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.007).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 96% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9550	 0.4340
1	 0.8860	 0.2370
2	 0.9160	 0.1090
3	 0.8920	 0.2370
4	 0.7890	 0.2040
5	 0.8890	 0.0330
6	 0.8760	 0.1460
7	 0.3910	 0.0360
A	 0.9700	 0.5070
B	 0.9380	 0.3230
C	 0.9760	 0.4970
D	 0.9690	 0.4510
E	 0.9580	 0.4530
F	 0.9660	 0.4930
G	 0.9440	 0.4320
H	 0.9590	 0.4780
I	 0.9690	 0.4940
J	 0.9580	 0.4330
K	 0.9920	 0.4550
L	 0.9520	 0.4610
M	 0.9700	 0.4770
N	 0.9750	 0.5040
O	 0.9710	 0.4930
P	 0.9550	 0.4920
Q	 0.9770	 0.5040
R	 0.9560	 0.4660
S	 0.9760	 0.5050
T	 0.9620	 0.4830
U	 0.9350	 0.3940
V	 0.9680	 0.5100
W	 0.9610	 0.4900
X	 0.9490	 0.4690
Y	 0.9310	 0.4710
Z	 0.9680	 0.4620
a	 0.9810	 0.5030



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Chain	Atom inclusion	Q-score
b	 0.9460	 0.4210
c	 0.9490	 0.4500
d	 0.9460	 0.4690
e	 0.9710	 0.5100
f	 0.9790	 0.5240
g	 0.9530	 0.4730
h	 0.9340	 0.4560
i	 0.9520	 0.4510
j	 0.9810	 0.5080
k	 0.8890	 0.4190
l	 0.9650	 0.4830
m	 0.9710	 0.4900
n	 0.8990	 0.3970
o	 0.9650	 0.4910
p	 0.9550	 0.4660
q	 0.9480	 0.4000
r	 0.9750	 0.4960
u	 0.9970	 0.4790
v	 0.9970	 0.4530
w	 0.9720	 0.5050