



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 06:56 PM UTC

PDB ID : 7OQC / pdb_00007oqc
EMDB ID : EMD-13029
Title : The U1 part of *Saccharomyces cerevisiae* spliceosomal pre-A complex (delta BS-A ACT1)
Authors : Zhang, Z.; Rigo, N.; Dybkov, O.; Fourmann, J.; Will, C.L.; Kumar, V.; Urlaub, H.; Stark, H.; Luehrmann, R.
Deposited on : 2021-06-03
Resolution : 4.10 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

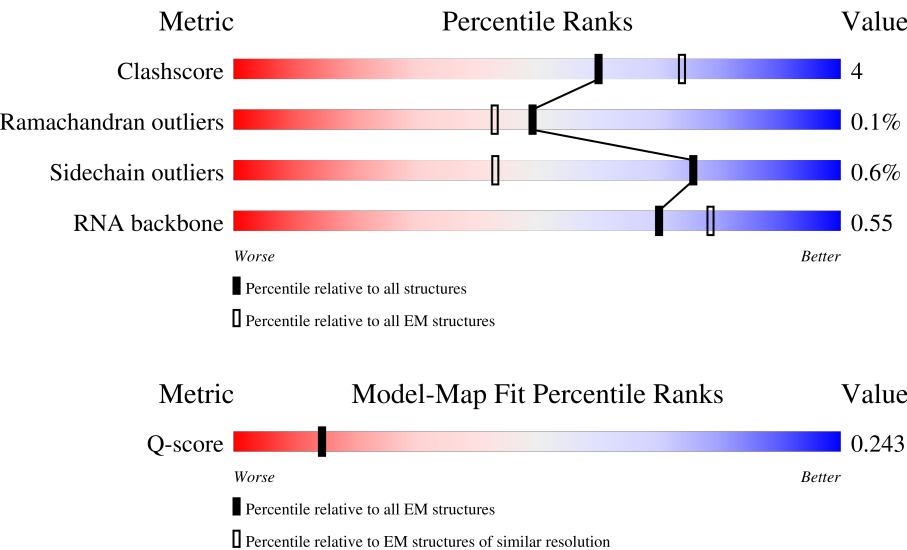
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.10 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	6458 (3.60 - 4.60)

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	F	523	
2	I	371	
3	E	544	

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Mol	Chain	Length	Quality of chain
4	J	620	
5	1	568	
6	G	492	
7	A	298	
8	C	231	
9	b	196	
10	d	101	
11	e	94	
12	f	86	
13	g	77	
14	h	146	
15	i	110	
16	H	261	
17	D	629	
18	B	300	

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 35050 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Protein NAM8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	F	267	Total	C	N	O	S	0	0
			1758	1091	316	341	10		

- Molecule 2 is a RNA chain called ACT1 pre-mRNA (delta BS-A),ACT1 pre-mRNA (delta BS-A),ACT1 pre-mRNA (delta BS-A),ACT1 pre-mRNA (delta BS-A),ACT1 pre-mRNA (delta BS-A),ACT1 pre-mRNA (delta BS-A),ACT1 pre-mRNA (delta BS-A),ACT1 pre-mRNA (delta BS-A),ACT1 pre-mRNA (delta BS-A).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	63	Total	C	N	O	P	0	0
			847	359	33	392	63		

- Molecule 3 is a protein called U1 small nuclear ribonucleoprotein component PRP42.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	544	Total	C	N	O	S	0	0
			4561	2990	723	828	20		

- Molecule 4 is a protein called U1 small nuclear ribonucleoprotein component SNU71.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	105	Total	C	N	O	S	0	0
			687	427	127	132	1		

- Molecule 5 is a RNA chain called U1 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1	558	Total	C	N	O	P	0	0
			11822	5287	2003	3974	558		

- Molecule 6 is a protein called 56 kDa U1 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	239	Total	C	N	O	S	0	0
			1954	1267	321	354	12		

- Molecule 7 is a protein called U1 small nuclear ribonucleoprotein A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	132	Total	C	N	O	S	0	0
			1058	674	193	187	4		

- Molecule 8 is a protein called U1 small nuclear ribonucleoprotein C.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	195	Total	C	N	O	S	0	0
			1570	976	301	288	5		

- Molecule 9 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	b	121	Total	C	N	O	S	0	0
			972	613	183	173	3		

- Molecule 10 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	d	93	Total	C	N	O	S	0	0
			714	453	125	133	3		

- Molecule 11 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	e	77	Total	C	N	O	S	0	0
			600	395	96	106	3		

- Molecule 12 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	f	73	Total	C	N	O	S	0	0
			585	376	102	106	1		

- Molecule 13 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	g	72	Total	C	N	O	S	0	0
			556	352	97	105	2		

- Molecule 14 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	h	107	Total	C	N	O	S	0	0
			771	487	138	143	3		

- Molecule 15 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	i	99	Total	C	N	O	S	0	0
			805	514	148	139	4		

- Molecule 16 is a protein called Protein LUC7.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	192	Total	C	N	O	S	0	0
			1201	740	226	228	7		

- Molecule 17 is a protein called Pre-mRNA-processing factor 39.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	D	576	Total	C	N	O	S	0	0
			3530	2204	642	680	4		

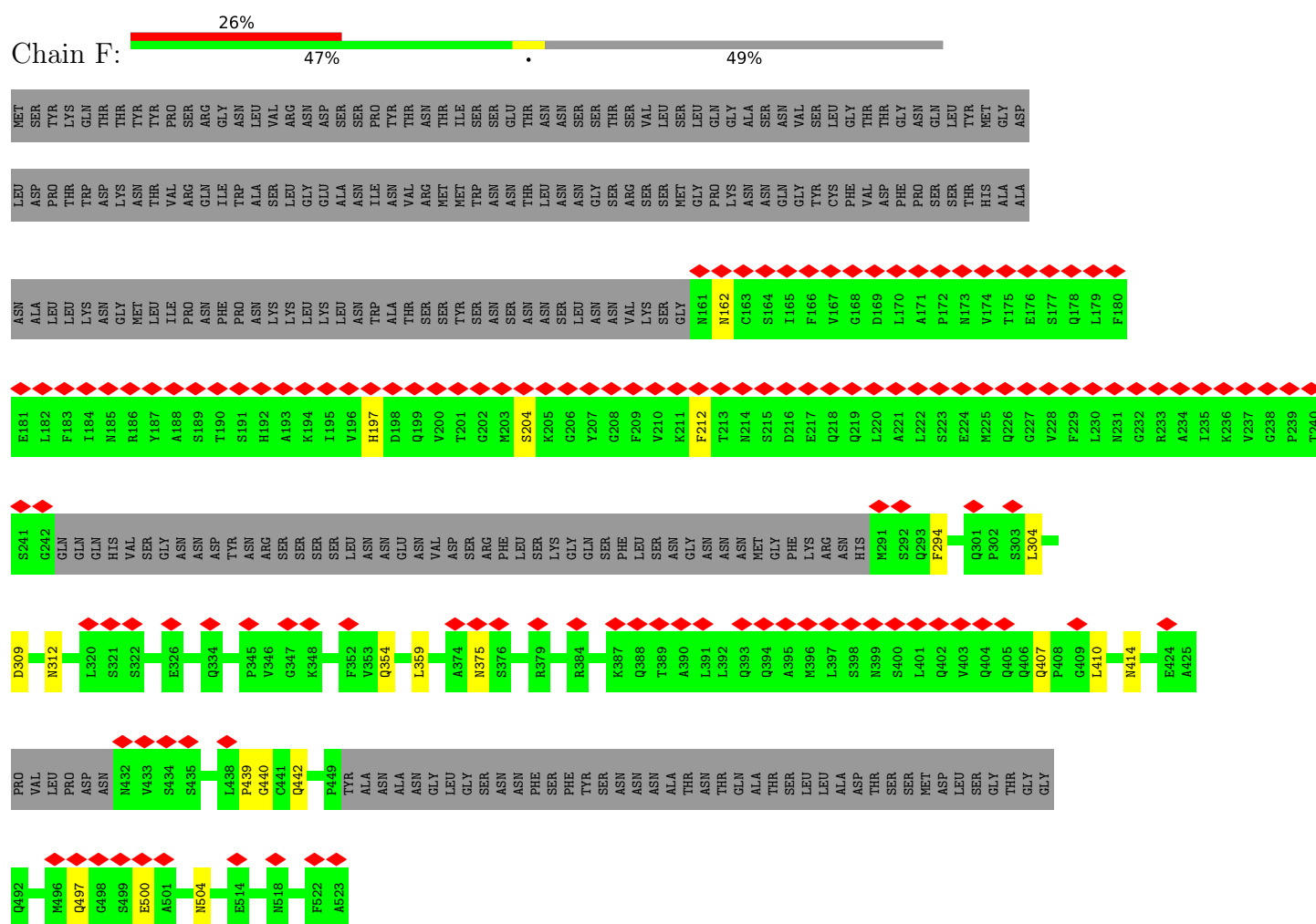
- Molecule 18 is a protein called U1 small nuclear ribonucleoprotein 70 kDa homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	B	186	Total	C	N	O		0	0
			1059	647	206	206			

3 Residue-property plots

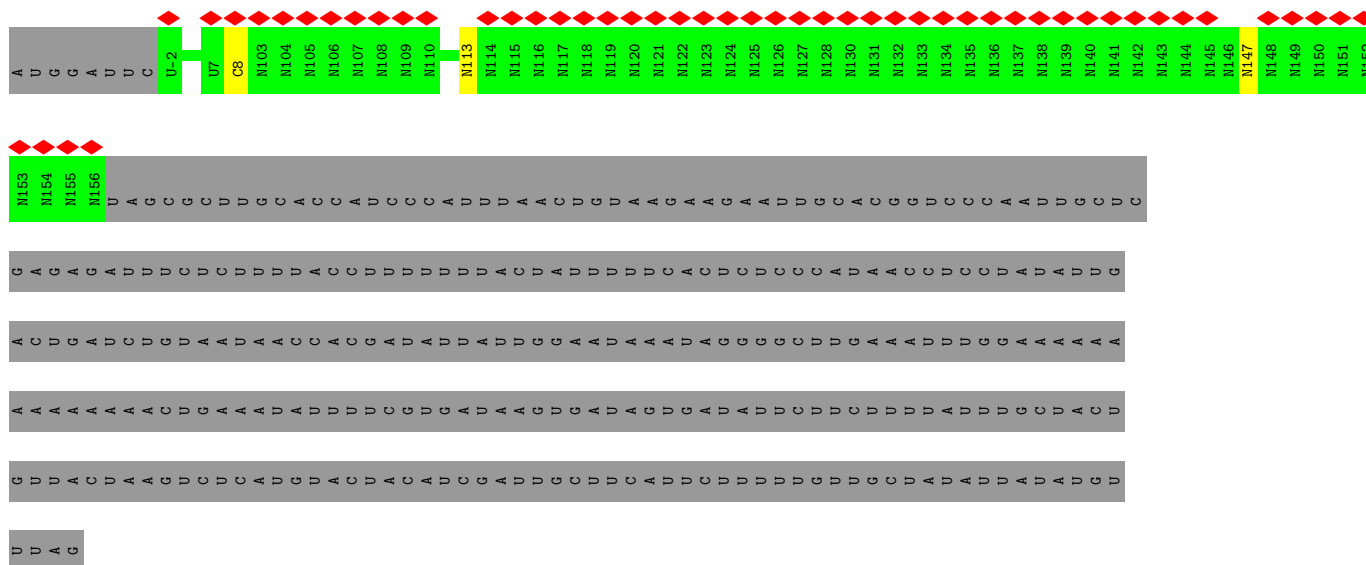
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Protein NAM8

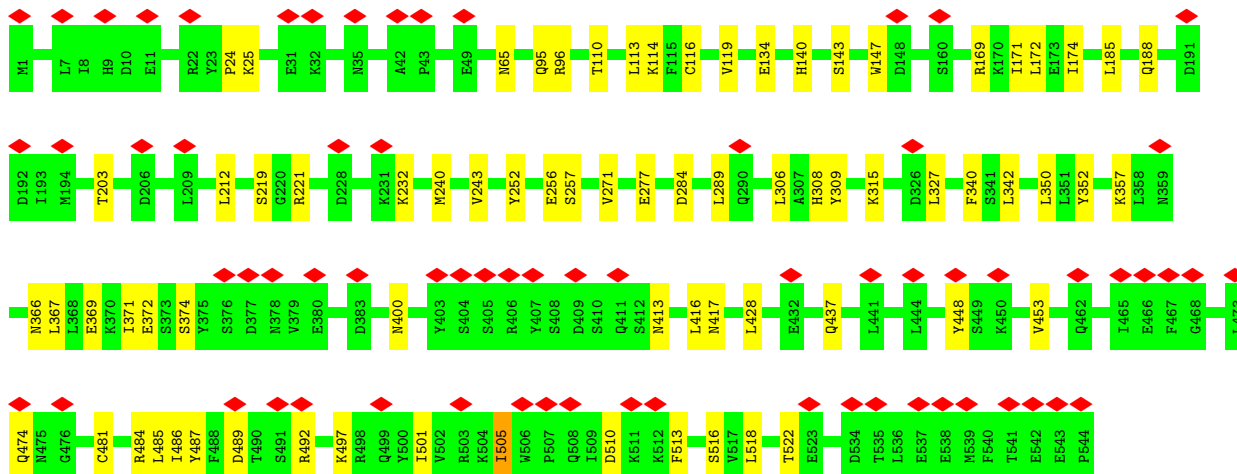
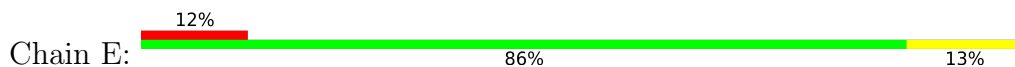


• Molecule 2: ACT1 pre-mRNA (delta BS-A),ACT1 pre-mRNA (delta BS-A),ACT1 pre-mRNA (delta BS-A),ACT1 pre-mRNA (delta BS-A),ACT1 pre-mRNA (delta BS-A),ACT1 pre-mRNA (delta BS-A),ACT1 pre-mRNA (delta BS-A),ACT1 pre-mRNA (delta BS-A)

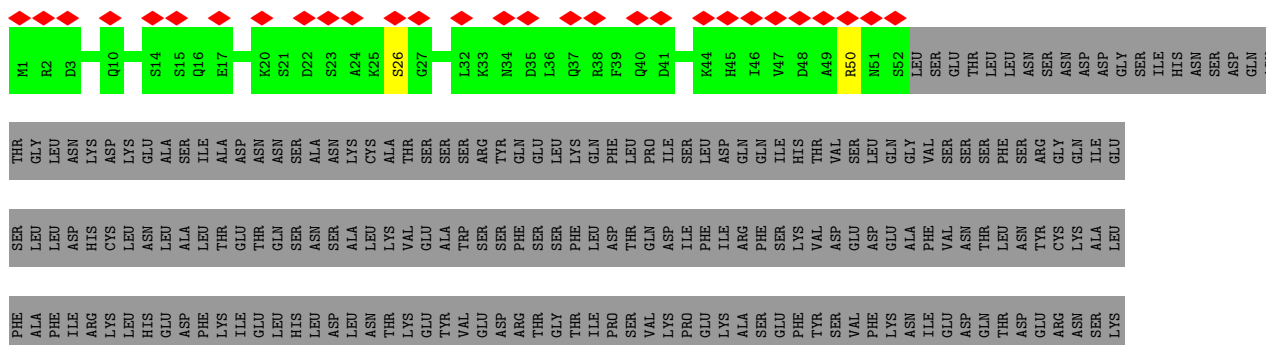




• Molecule 3: U1 small nuclear ribonucleoprotein component PRP42



• Molecule 4: U1 small nuclear ribonucleoprotein component SNU71



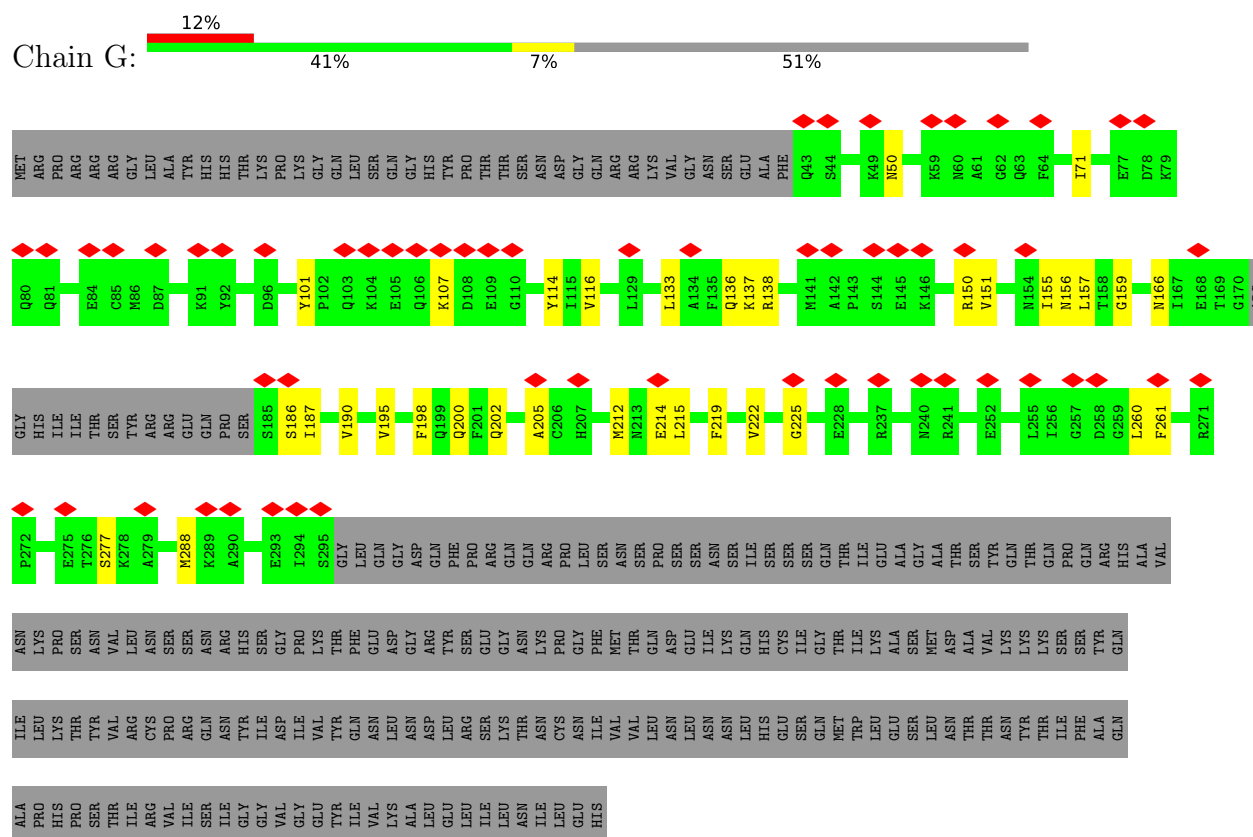
GLU PHE ARG LEU GLY THR	GLU SER ARG TYR VAL ASP	GLU SER VAL GLU PHE ASP	HIS VAL LYS ILE LYS PHE ASP	GLU GLU ARG ASP GLU
--	--	--	---	---

● Molecule 5: U1 snRNA

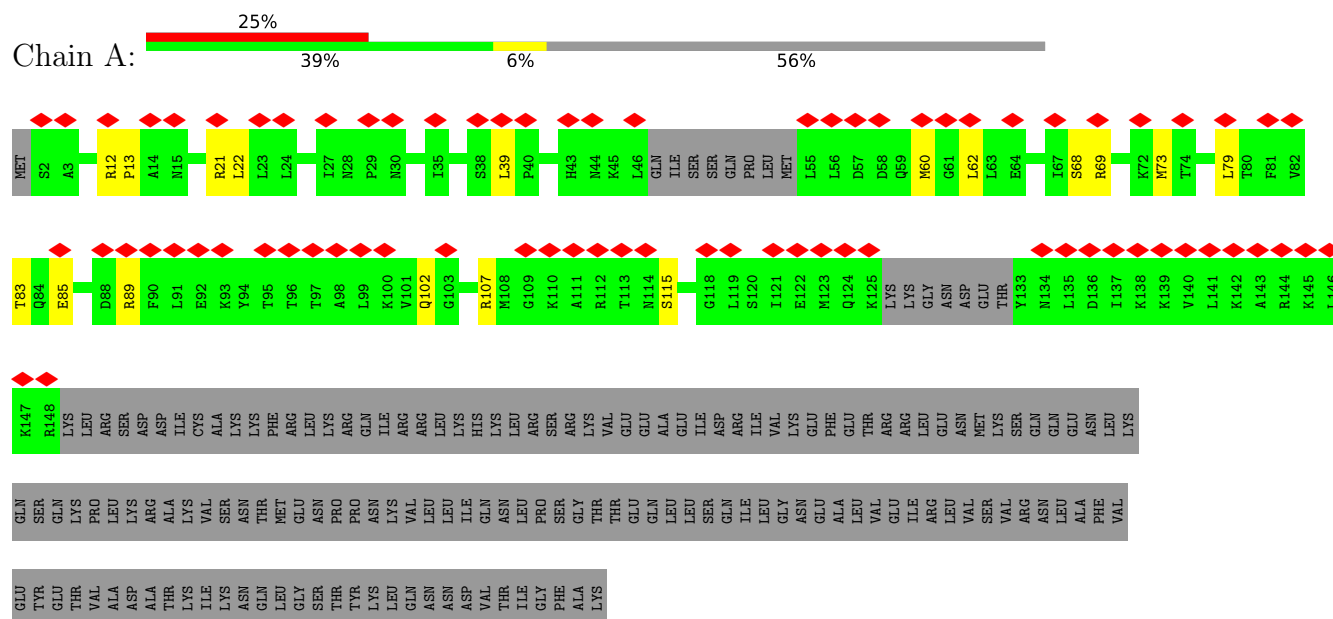
Chain 1: 57% 57% 37%

U504	U505	A506	U507	G508	G509	G510	A511	A512	A513	A514	A515	U516	U517	U518	U519	G520	G521	A522	A523	G524	G525	U529	G530	G535	A536	A537	C538	G539	G540	G541	U542	C547	U551	A552	A553	U554	U555	U556	U557	U558	G559	A560	U561	U562	U563	A564	U565	U	U	U									
G444	G445	U446	C447	G448	G449	G450	A451	A452	U453	G454	U455	A456	G457	U458	U459	U460	G461	A462	A463	G464	A465	U466	G467	U468	G469	C470	U471	C472	U473	U474	U475	U476	G477	A478	G479	C480	A481	G482	U483	C484	U485	C486	A487	A488	C489	U490	U491	U492	G493	C494	U495	C496	G497	U498	U499	C500	C501	C502	G503
U384	U385	G386	A387	G388	G389	G390	C391	A392	C393	A394	U395	U396	C397	G398	A399	A400	U401	G402	A403	A404	C405	U406	U407	A408	A409	G410	U411	U412	U413	A414	U415	G416	A417	U418	G419	A420	A421	G422	G423	U424	A425	U426	G427	G428	C429	U430	G431	U432	U433	G434	A435	A436	G437	U438	U439	A440	U441	U442	U443
A324	A325	G326	A327	G328	A329	G330	C331	U332	U333	U334	G335	U336	A337	G338	A339	G340	G341	C342	A343	U344	U345	C346	U347	U348	U349	U350	U351	G352	A353	C354	U355	A356	C357	U358	U359	U360	U361	C362	U363	C364	U365	A366	G367	C368	G369	U370	G371	C372	C373	A374	U375	U376	U377	U378	A379	G380	U381	U382	U383
U234	A235	A236	A237	C238	U239	G240	A241	U242	U243	U244	U245	G249	G250	U254	U255	U256	G257	U258	U259	U260	C268	U269	G270	G271	A272	U277	U278	U279	G280	A287	A288	U289	U290	C291	A292	A293	A294	U295	U299	G307	A308	G313	G314	C317	U318	U319	C321	A322	A323										
G170	A171	U174	U175	U176	C177	A178	U179	U180	C182	U186	G187	U188	C191	A192	A193	U194	C195	A196	U197	U198	G199	G200	U201	U202	A203	A204	U205	C206	C207	C208	U209	U210	G211	A212	U213	U214	C215	C216	U217	U218	U219	C220	G221	G222	A224	U225	U226	U227	U228	U229	G230	G231	G232	U233					
U91	G92	A93	A94	C95	U96	A97	U98	A99	A100	U101	U102	G103	U104	U105	C106	A107	U108	U109	G110	A111	A112	G113	U114	C115	A116	U117	U121	A125	A126	G133	G134	C140	A141	C142	A143	C144	A145	U146	A147	C148	G149	G150	C151	G152	C153	G154	G158	G159	U162	G163	G167								
A1	U2	U6	A7	U10	U11	A12	G21	A22	G23	G24	A25	G26	A	U	C	A	A	G	A	A34	A40	C41	U42	G43	C46	A47	U52	G53	C54	G55	C56	A62	U63	A64	G65	U66	A67	A73	C74	G75	A78	A79	G80	U85	A86	U87	C88	A89	U90										

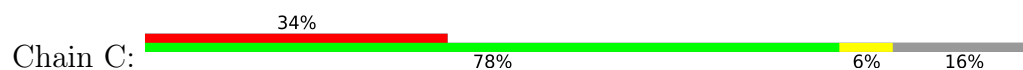
• Molecule 6: 56 kDa U1 small nuclear ribonucleoprotein component

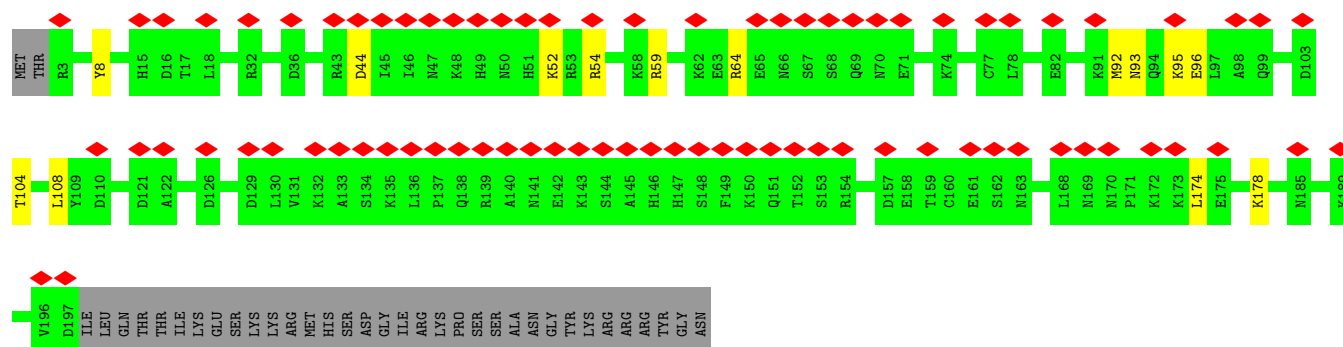


• Molecule 7: U1 small nuclear ribonucleoprotein A

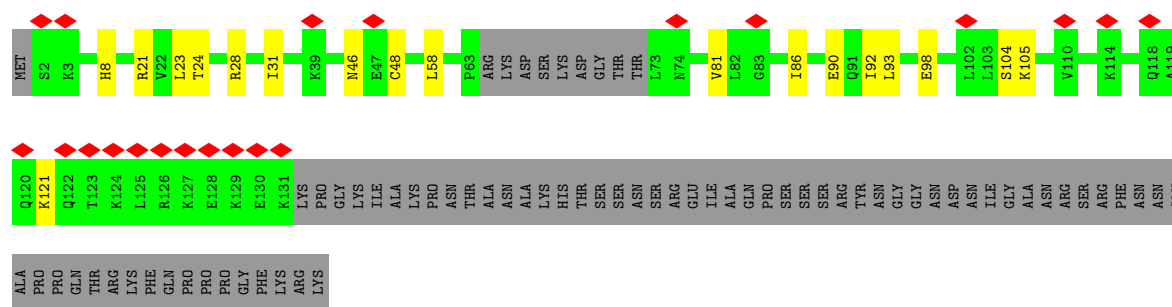


• Molecule 8: U1 small nuclear ribonucleoprotein C

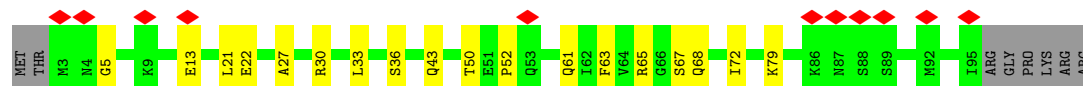
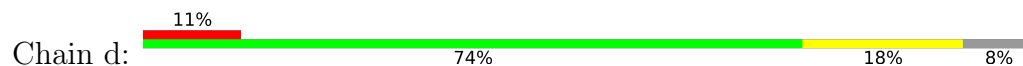




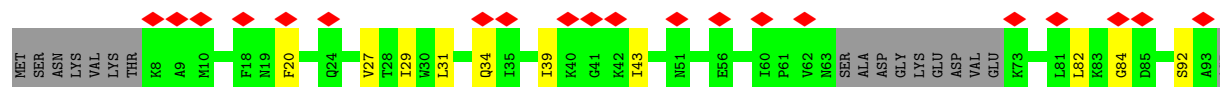
• Molecule 9: Small nuclear ribonucleoprotein-associated protein B



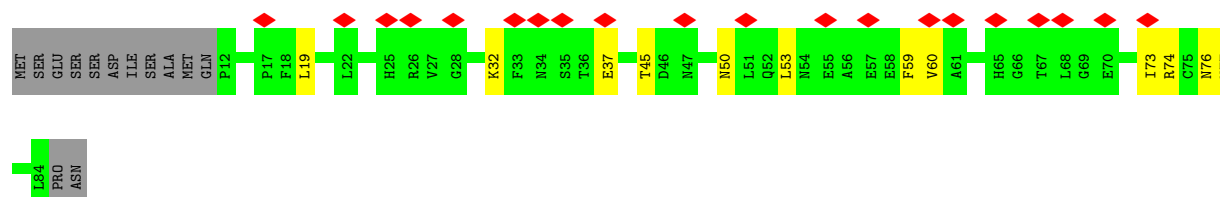
• Molecule 10: Small nuclear ribonucleoprotein Sm D3



• Molecule 11: Small nuclear ribonucleoprotein E

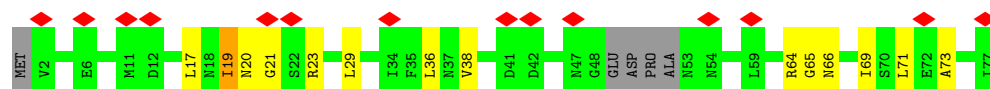


• Molecule 12: Small nuclear ribonucleoprotein F



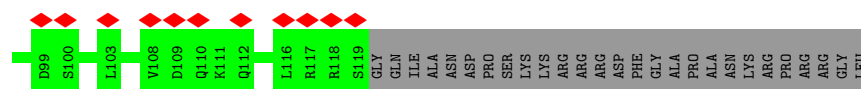
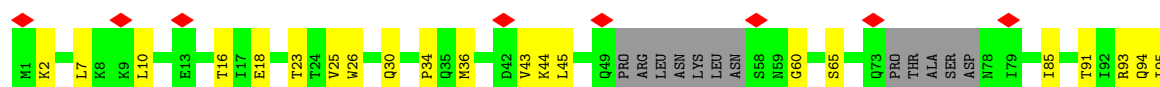
- Molecule 13: Small nuclear ribonucleoprotein G

Chain g: 



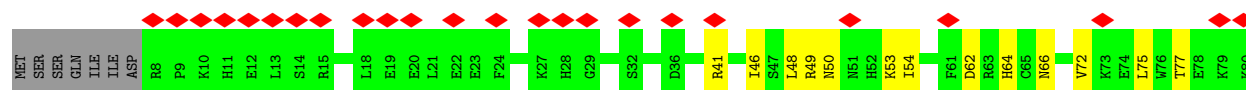
- Molecule 14: Small nuclear ribonucleoprotein Sm D1

Chain h: 



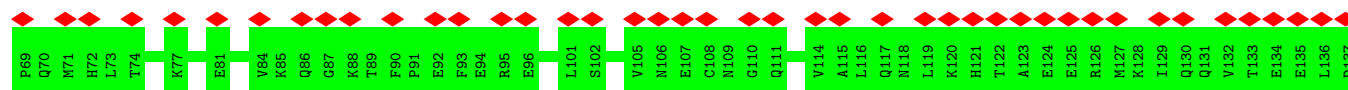
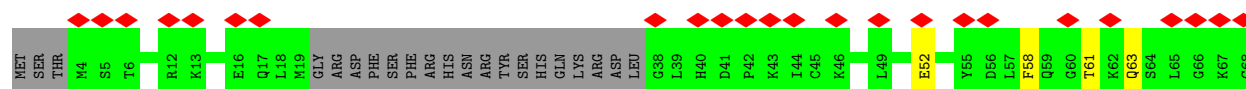
- Molecule 15: Small nuclear ribonucleoprotein Sm D2

Chain i: 

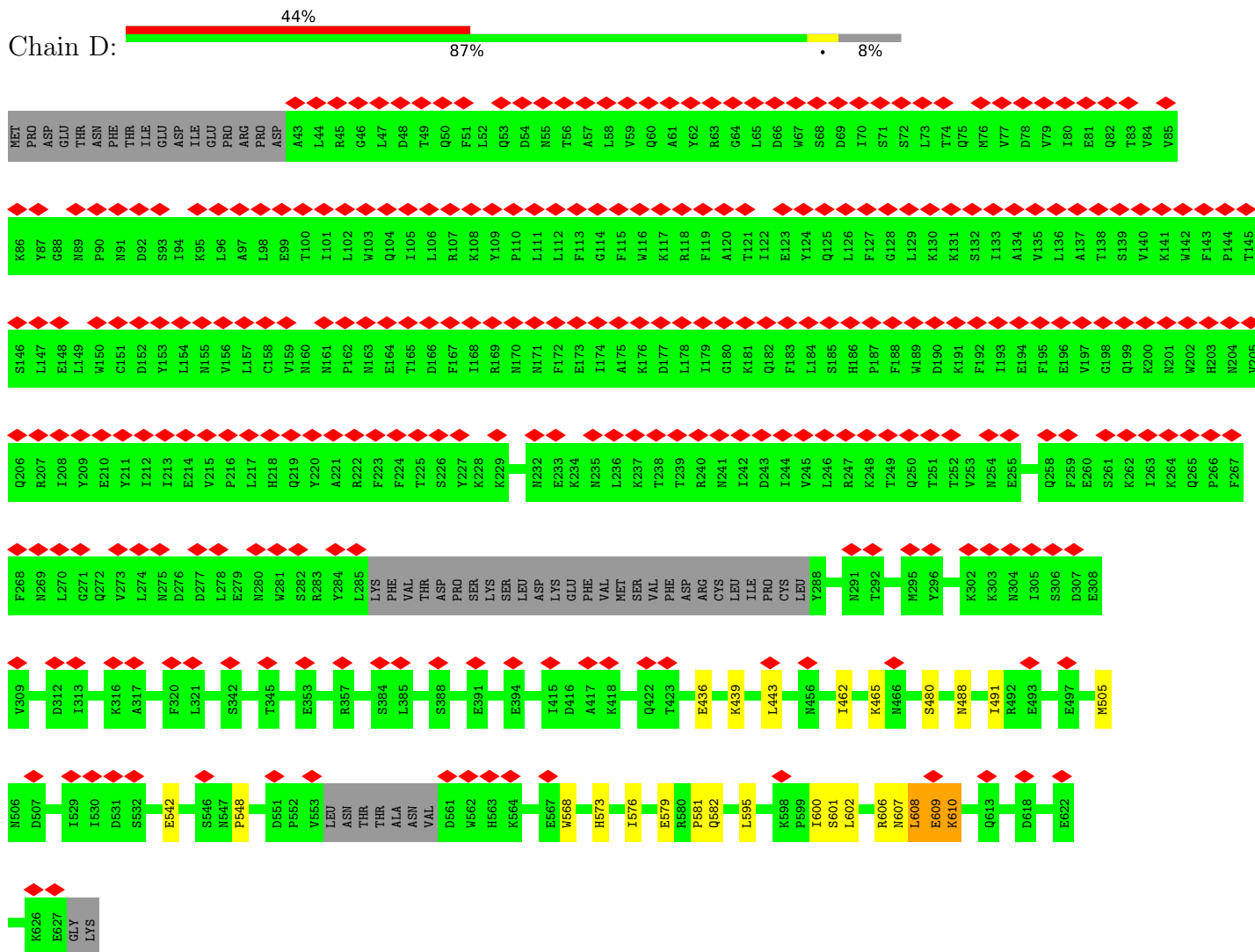


- Molecule 16: Protein LUC7

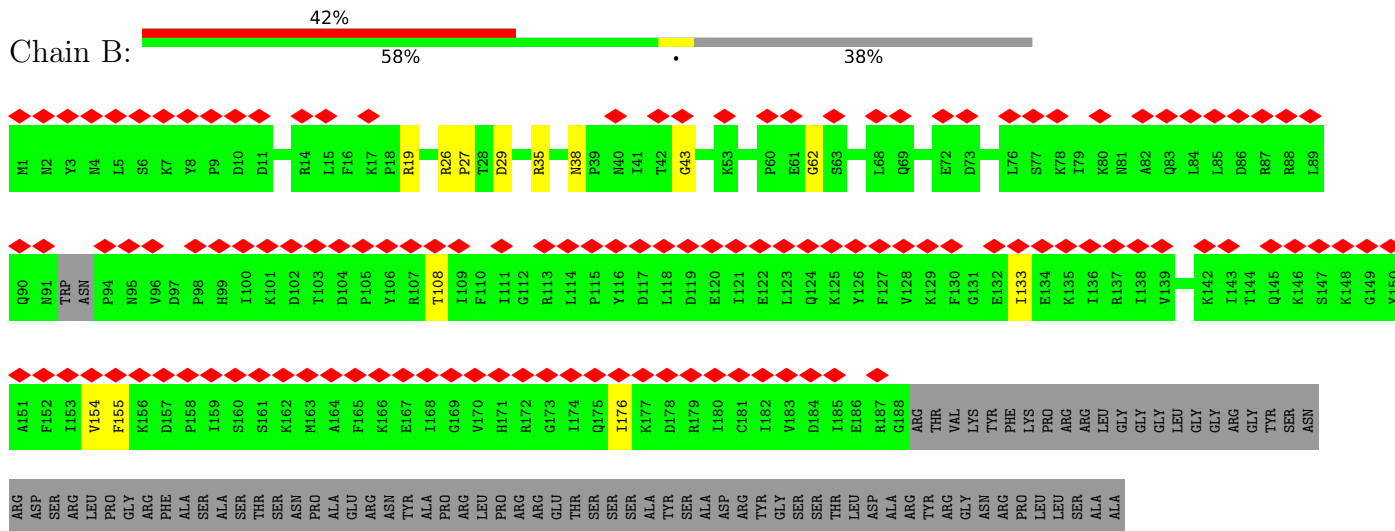
Chain H: 



Chain D:



Chain B:



THR
PRO
THR
ALA
ALA
VAL
THR
SER
VAL
TYR
LYS
SER
ARG
ASN
SER
ARG
THR
ARG
GLU
SER
GLN
PRO
ALA
PRO
LYS
GLU
ALA
PRO
ASP
TYR

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	217460	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 ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.188	Depositor
Minimum map value	-0.117	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.042	Depositor
Map size (Å)	464.0, 464.0, 464.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	F	0.17	0/1784	0.49	0/2436
2	I	0.12	0/234	0.25	0/362
3	E	0.18	0/4676	0.45	0/6320
4	J	0.24	0/695	0.67	1/948 (0.1%)
5	1	0.29	1/13201 (0.0%)	0.34	2/20553 (0.0%)
6	G	0.18	0/1996	0.48	0/2682
7	A	0.17	0/1072	0.56	0/1437
8	C	0.18	0/1601	0.48	0/2154
9	b	0.19	0/978	0.56	0/1306
10	d	0.23	0/726	0.60	2/984 (0.2%)
11	e	0.20	0/610	0.56	0/826
12	f	0.21	0/597	0.55	0/807
13	g	0.15	0/559	0.55	2/751 (0.3%)
14	h	0.16	0/776	0.45	0/1053
15	i	0.17	0/818	0.49	0/1099
16	H	0.13	0/1212	0.36	0/1652
17	D	0.17	0/3570	0.40	0/4924
18	B	0.16	0/1071	0.45	0/1482
All	All	0.22	1/36176 (0.0%)	0.43	7/51776 (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
7	A	0	1
13	g	0	1
18	B	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	1	325	A	O3'-P	-27.08	1.20	1.61

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	J	274	PRO	CA-N-CD	-8.88	99.56	112.00
5	1	442	U	OP2-P-O3'	-8.61	82.18	108.00
5	1	442	U	OP1-P-O3'	-8.59	82.24	108.00
10	d	5	GLY	CA-C-N	6.01	124.02	120.24
10	d	5	GLY	C-N-CA	6.01	124.02	120.24
13	g	19	ILE	CA-C-N	5.21	131.49	121.54
13	g	19	ILE	C-N-CA	5.21	131.49	121.54

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	A	12	ARG	Peptide
18	B	176	ILE	Peptide
13	g	20	ASN	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	F	1758	0	1443	14	0
2	I	847	0	532	11	0
3	E	4561	0	4549	45	0
4	J	687	0	534	12	0
5	1	11822	0	5940	96	0
6	G	1954	0	1961	23	0
7	A	1058	0	1118	10	0
8	C	1570	0	1555	11	0
9	b	972	0	1048	14	0
10	d	714	0	738	16	0
11	e	600	0	634	6	0
12	f	585	0	587	8	0
13	g	556	0	583	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	h	771	0	751	15	0
15	i	805	0	834	16	0
16	H	1201	0	902	4	0
17	D	3530	0	2469	25	0
18	B	1059	0	651	10	0
All	All	35050	0	26829	275	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 4.

All (275) 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)
5:1:384:U:H3	5:1:434:G:H1	1.01	0.97
5:1:380:G:H1	5:1:438:U:H3	1.07	0.96
4:J:272:ASP:C	4:J:274:PRO:HD3	1.97	0.88
4:J:273:LEU:N	4:J:274:PRO:HD3	1.89	0.87
5:1:389:G:H1	5:1:430:U:H3	0.86	0.85
1:F:162:ASN:HA	1:F:212:PHE:O	1.80	0.81
2:I:8:C:N4	5:1:1:A:N6	2.34	0.75
4:J:272:ASP:CB	4:J:274:PRO:HD3	2.22	0.70
13:g:19:ILE:HB	13:g:23:ARG:HB2	1.74	0.70
4:J:273:LEU:N	4:J:274:PRO:CD	2.56	0.69
5:1:512:A:H3'	5:1:513:A:H4'	1.75	0.68
5:1:425:A:H2'	5:1:426:U:H4'	1.76	0.67
2:I:113:N:H4'	17:D:606:ARG:HA	1.77	0.67
2:I:113:N:H4'	17:D:607:ASN:H	1.60	0.66
5:1:386:G:H1	5:1:433:U:H3	1.45	0.65
6:G:101:TYR:HB2	6:G:114:TYR:HB2	1.78	0.64
10:d:65:ARG:HD3	10:d:67:SER:H	1.62	0.64
14:h:36:MET:SD	15:i:97:ARG:NH2	2.72	0.63
3:E:140:HIS:HB3	3:E:143:SER:HB3	1.79	0.63
11:e:27:VAL:HG21	11:e:43:ILE:HG12	1.81	0.62
12:f:37:GLU:HB2	12:f:59:PHE:HB2	1.82	0.61
5:1:188:U:H3	5:1:250:G:H1	1.48	0.61
17:D:582:GLN:HE21	17:D:606:ARG:HD2	1.65	0.61
14:h:2:LYS:HE2	15:i:64:HIS:HE1	1.66	0.61
5:1:342:C:H2'	5:1:343:A:H4'	1.82	0.60
5:1:199:G:H1	5:1:239:U:H3	1.46	0.60
1:F:309:ASP:HB3	1:F:312:ASN:HB2	1.83	0.59
1:F:440:GLY:HA3	3:E:342:LEU:HB2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:147:N:HI'2	17:D:609:GLU:HB3	1.84	0.59
10:d:27:ALA:HA	10:d:50:THR:O	2.02	0.59
15:i:46:ILE:HG12	15:i:104:VAL:HG22	1.85	0.59
12:f:77:ASN:OD1	15:i:49:ARG:NH1	2.35	0.59
6:G:71:ILE:HG12	6:G:116:VAL:HG22	1.86	0.58
4:J:272:ASP:C	4:J:274:PRO:CD	2.73	0.58
11:e:84:GLY:O	13:g:64:ARG:NH1	2.34	0.58
5:1:85:U:H3	5:1:117:U:H3	1.52	0.58
3:E:400:ASN:ND2	3:E:413:ASN:O	2.37	0.57
5:1:10:U:H5''	5:1:11:U:H5'	1.85	0.57
1:F:442:GLN:HB3	1:F:497:GLN:HG2	1.86	0.57
3:E:185:LEU:HD13	3:E:188:GLN:HE21	1.70	0.57
5:1:144:C:H41	7:A:115:SER:HA	1.70	0.57
5:1:254:U:HI'	8:C:54:ARG:HH11	1.70	0.57
3:E:501:ILE:HA	3:E:505:ILE:HD13	1.87	0.56
4:J:274:PRO:HD2	4:J:275:SER:N	2.19	0.56
12:f:74:ARG:HG3	12:f:76:ASN:H	1.70	0.56
2:I:113:N:H4'	17:D:606:ARG:CA	2.35	0.56
10:d:68:GLN:HG2	13:g:69:ILE:HG12	1.87	0.56
5:1:391:C:N4	5:1:423:G:O2'	2.37	0.56
7:A:62:LEU:HG	7:A:79:LEU:HD21	1.88	0.56
5:1:140:C:O2'	7:A:107:ARG:NH1	2.37	0.55
3:E:481:CYS:SG	3:E:484:ARG:NH1	2.76	0.55
4:J:272:ASP:CA	4:J:274:PRO:HD3	2.36	0.55
15:i:54:ILE:HG23	15:i:72:VAL:HG13	1.88	0.55
3:E:212:LEU:O	3:E:232:LYS:NZ	2.37	0.55
5:1:384:U:O4	5:1:434:G:O6	2.25	0.55
5:1:448:G:H2'	5:1:449:G:H8	1.72	0.55
7:A:68:SER:OG	7:A:73:MET:SD	2.65	0.55
7:A:21:ARG:NH2	7:A:39:LEU:O	2.40	0.55
5:1:217:U:O2	5:1:220:G:O6	2.25	0.55
8:C:52:LYS:O	8:C:54:ARG:NH2	2.40	0.55
15:i:48:LEU:HD21	15:i:96:LEU:HD21	1.89	0.54
5:1:502:C:H2'	5:1:503:G:H8	1.71	0.54
2:I:113:N:C5'	17:D:606:ARG:HA	2.37	0.54
3:E:252:TYR:HA	3:E:256:GLU:HB2	1.90	0.54
6:G:187:ILE:HD11	6:G:215:LEU:HD22	1.88	0.54
17:D:462:ILE:HA	17:D:465:LYS:HE3	1.90	0.54
5:1:313:G:H2'	5:1:314:G:H8	1.73	0.53
2:I:113:N:C4'	17:D:606:ARG:HA	2.37	0.53
9:b:21:ARG:HB2	9:b:98:GLU:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:272:ASP:CB	4:J:274:PRO:CD	2.86	0.53
3:E:428:LEU:HA	3:E:437:GLN:HE22	1.73	0.53
13:g:17:LEU:HD23	13:g:71:LEU:HB3	1.90	0.53
14:h:43:VAL:HG11	14:h:85:ILE:HD12	1.90	0.53
9:b:28:ARG:NH1	10:d:22:GLU:OE2	2.42	0.53
10:d:30:ARG:NH1	18:B:19:ARG:O	2.42	0.53
1:F:294:PHE:HB3	8:C:178:LYS:HD2	1.91	0.52
6:G:166:ASN:ND2	6:G:225:GLY:O	2.43	0.52
17:D:436:GLU:OE1	17:D:439:LYS:NZ	2.42	0.52
5:1:6:U:O2	16:H:216:ARG:NH2	2.43	0.52
1:F:500:GLU:O	1:F:504:ASN:ND2	2.42	0.52
2:I:8:C:N3	5:1:1:A:N1	2.57	0.52
5:1:158:G:H2'	5:1:159:G:H8	1.74	0.52
10:d:65:ARG:NH1	13:g:65:GLY:O	2.42	0.52
17:D:439:LYS:HG3	17:D:443:LEU:HD12	1.91	0.52
11:e:29:ILE:HG23	11:e:39:ILE:HB	1.92	0.51
3:E:24:PRO:HD2	6:G:260:LEU:HB2	1.92	0.51
3:E:374:SER:O	4:J:50:ARG:NH2	2.44	0.51
5:1:439:U:H2'	5:1:440:A:C8	2.46	0.51
3:E:65:ASN:ND2	4:J:26:SER:OG	2.44	0.51
3:E:171:ILE:HD13	3:E:174:ILE:HD12	1.92	0.51
3:E:489:ASP:OD2	3:E:492:ARG:NH2	2.44	0.51
5:1:511:A:H2'	5:1:512:A:C8	2.46	0.51
5:1:516:U:H6	5:1:516:U:O5'	1.94	0.51
13:g:64:ARG:HG3	13:g:66:ASN:H	1.75	0.50
3:E:169:ARG:NH2	17:D:601:SER:O	2.42	0.50
9:b:23:LEU:HD21	14:h:65:SER:HB3	1.92	0.50
11:e:31:LEU:HD21	11:e:82:LEU:HD21	1.94	0.50
14:h:23:THR:HG21	14:h:45:LEU:HD12	1.93	0.50
15:i:41:ARG:NH2	18:B:62:GLY:O	2.44	0.50
3:E:221:ARG:NH2	5:1:268:C:N3	2.49	0.50
6:G:186:SER:HB3	6:G:214:GLU:HG2	1.94	0.50
1:F:410:LEU:HD21	1:F:414:ASN:HD22	1.77	0.50
18:B:133:ILE:HA	18:B:155:PHE:HA	1.94	0.49
9:b:86:ILE:HG23	10:d:72:ILE:HG23	1.94	0.49
5:1:547:C:H5''	14:h:34:PRO:HG2	1.94	0.49
15:i:53:LYS:NZ	18:B:43:GLY:O	2.44	0.49
15:i:97:ARG:HG2	15:i:99:ASP:H	1.77	0.49
5:1:401:U:H2'	5:1:402:G:H8	1.78	0.49
14:h:16:THR:HA	14:h:25:VAL:O	2.13	0.49
10:d:21:LEU:HD23	10:d:72:ILE:HB	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1:78:A:H4'	5:1:79:A:H3'	1.95	0.48
5:1:389:G:O6	5:1:430:U:O4	2.30	0.48
9:b:24:THR:HG22	9:b:92:ILE:HG22	1.95	0.48
12:f:77:ASN:HD22	15:i:102:ILE:HA	1.77	0.48
6:G:50:ASN:HB3	6:G:212:MET:HG3	1.96	0.48
3:E:243:VAL:HG22	17:D:581:PRO:HB2	1.94	0.48
6:G:133:LEU:HB3	6:G:157:LEU:HD22	1.95	0.48
9:b:58:LEU:HD21	14:h:60:GLY:HA3	1.95	0.48
5:1:162:U:H2'	5:1:163:G:H8	1.79	0.48
3:E:453:VAL:HG13	3:E:485:LEU:HG	1.95	0.48
5:1:6:U:H2'	5:1:7:A:H8	1.78	0.48
5:1:392:A:N6	5:1:424:U:O3'	2.46	0.48
8:C:8:TYR:OH	10:d:13:GLU:OE2	2.31	0.48
8:C:104:THR:O	8:C:108:LEU:HB2	2.14	0.48
3:E:474:GLN:O	3:E:516:SER:OG	2.32	0.48
5:1:497:G:N2	5:1:498:U:O4	2.46	0.48
4:J:274:PRO:CD	4:J:275:SER:N	2.77	0.47
5:1:170:G:H2'	5:1:171:A:H8	1.79	0.47
10:d:63:PHE:HE2	13:g:36:LEU:HD11	1.79	0.47
14:h:93:ARG:NH1	15:i:50:ASN:OD1	2.47	0.47
5:1:250:G:O3'	8:C:64:ARG:NH2	2.47	0.47
5:1:560:A:N6	12:f:32:LYS:O	2.47	0.47
9:b:8:HIS:O	14:h:30:GLN:NE2	2.47	0.47
14:h:95:ILE:HG23	15:i:95:PHE:HB3	1.95	0.47
17:D:505:MET:HE1	17:D:548:PRO:HA	1.96	0.47
5:1:552:A:N1	12:f:50:ASN:ND2	2.54	0.47
15:i:50:ASN:HA	18:B:38:ASN:HD21	1.80	0.47
15:i:77:THR:OG1	15:i:86:ASN:ND2	2.48	0.47
2:I:113:N:H5'	17:D:606:ARG:HA	1.97	0.47
3:E:172:LEU:HB3	3:E:240:MET:HE3	1.96	0.47
3:E:110:THR:HG22	3:E:114:LYS:HE2	1.96	0.47
5:1:198:U:H2'	5:1:199:G:H8	1.80	0.47
3:E:65:ASN:OD1	3:E:96:ARG:NH2	2.48	0.46
5:1:249:G:H2'	5:1:250:G:H8	1.80	0.46
5:1:424:U:H2'	5:1:425:A:C8	2.50	0.46
17:D:573:HIS:HD2	17:D:576:ILE:HB	1.80	0.46
5:1:342:C:N4	5:1:480:C:OP2	2.48	0.46
3:E:366:ASN:HD21	6:G:107:LYS:HG2	1.80	0.46
1:F:414:ASN:OD1	6:G:277:SER:OG	2.34	0.46
5:1:46:C:H2'	5:1:47:A:H8	1.81	0.46
1:F:407:GLN:HE21	6:G:288:MET:HE1	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1:299:U:O2'	8:C:44:ASP:OD2	2.29	0.46
9:b:46:ASN:HD21	10:d:79:LYS:HE3	1.81	0.46
11:e:27:VAL:HG11	11:e:43:ILE:HD11	1.98	0.46
17:D:579:GLU:OE1	17:D:610:LYS:HE2	2.15	0.46
6:G:156:ASN:HB3	6:G:205:ALA:HA	1.97	0.46
5:1:191:C:H2'	5:1:192:A:H8	1.81	0.46
5:1:529:U:H2'	5:1:530:G:H8	1.81	0.46
5:1:486:C:H2'	5:1:487:A:C8	2.51	0.45
5:1:535:G:H2'	5:1:536:A:H8	1.81	0.45
3:E:369:GLU:HA	3:E:372:GLU:HG2	1.99	0.45
6:G:137:LYS:HB3	6:G:155:ILE:HD11	1.97	0.45
3:E:95:GLN:NE2	5:1:116:A:OP1	2.47	0.45
10:d:27:ALA:HB2	10:d:52:PRO:HD3	1.98	0.45
10:d:65:ARG:HD2	10:d:68:GLN:HE22	1.81	0.45
9:b:93:LEU:HA	14:h:91:THR:HG21	1.99	0.45
5:1:429:C:H2'	5:1:430:U:H6	1.81	0.45
5:1:455:U:H2'	5:1:456:A:H8	1.82	0.45
5:1:538:C:H2'	5:1:539:G:C8	2.52	0.45
9:b:104:SER:OG	9:b:105:LYS:N	2.48	0.45
15:i:75:LEU:HD11	15:i:86:ASN:HB3	1.98	0.45
5:1:280:G:O6	9:b:121:LYS:NZ	2.40	0.45
9:b:81:VAL:O	18:B:19:ARG:NH1	2.50	0.45
5:1:334:U:H2'	5:1:335:G:C8	2.52	0.44
3:E:487:TYR:HA	3:E:497:LYS:HD3	1.98	0.44
5:1:328:G:H2'	5:1:329:A:H8	1.83	0.44
5:1:403:A:H2'	5:1:404:A:H8	1.81	0.44
6:G:187:ILE:HA	6:G:202:GLN:O	2.17	0.44
5:1:380:G:O6	5:1:438:U:O4	2.36	0.44
6:G:138:ARG:HH12	6:G:151:VAL:HA	1.83	0.44
13:g:29:LEU:HD13	13:g:38:VAL:HG13	2.00	0.44
9:b:31:ILE:O	9:b:48:CYS:HA	2.17	0.44
5:1:478:A:H2'	5:1:479:G:H8	1.81	0.44
6:G:133:LEU:HD13	6:G:136:GLN:HE21	1.82	0.44
7:A:83:THR:HG23	7:A:85:GLU:H	1.82	0.44
14:h:18:GLU:OE1	14:h:94:GLN:NE2	2.42	0.44
5:1:73:A:O2'	5:1:75:G:OP1	2.28	0.44
5:1:73:A:H2'	5:1:75:G:C8	2.53	0.43
5:1:94:A:N6	5:1:105:U:O4	2.51	0.43
5:1:307:G:H2'	5:1:308:A:H8	1.84	0.43
6:G:138:ARG:NH1	6:G:150:ARG:O	2.50	0.43
3:E:289:LEU:HA	17:D:568:TRP:HZ3	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1:521:G:H2'	5:1:522:A:H8	1.83	0.43
14:h:7:LEU:HA	14:h:10:LEU:HD12	2.00	0.43
5:1:396:U:H5	5:1:416:G:H1	1.65	0.43
11:e:20:PHE:HE1	11:e:92:SER:HB2	1.84	0.43
12:f:53:LEU:HD13	12:f:73:ILE:HD12	2.00	0.43
5:1:192:A:H2'	5:1:193:A:H8	1.83	0.43
7:A:21:ARG:HH22	7:A:39:LEU:H	1.67	0.43
5:1:64:A:N6	5:1:140:C:O2	2.52	0.43
14:h:26:TRP:HE3	14:h:44:LYS:HG2	1.83	0.43
16:H:52:GLU:HG2	16:H:231:LYS:HG2	2.00	0.43
6:G:219:PHE:HA	6:G:222:VAL:HG12	2.00	0.43
3:E:134:GLU:HG3	3:E:147:TRP:HH2	1.84	0.43
5:1:350:U:H1'	5:1:351:U:H5	1.84	0.43
5:1:556:U:H3'	5:1:557:U:H2'	2.00	0.43
18:B:29:ASP:OD2	18:B:35:ARG:NH2	2.49	0.43
1:F:354:GLN:NE2	6:G:288:MET:SD	2.92	0.42
3:E:308:HIS:ND1	3:E:340:PHE:O	2.46	0.42
5:1:328:G:H2'	5:1:329:A:C8	2.55	0.42
3:E:352:TYR:HE1	3:E:367:LEU:HD12	1.84	0.42
1:F:197:HIS:HA	1:F:204:SER:HA	2.01	0.42
5:1:171:A:H61	5:1:540:G:H1	1.67	0.42
5:1:321:C:H2'	5:1:322:A:H8	1.84	0.42
5:1:418:U:H2'	5:1:419:G:C8	2.55	0.42
6:G:190:VAL:HG21	6:G:200:GLN:HB3	2.01	0.42
1:F:375:ASN:ND2	17:D:462:ILE:O	2.51	0.42
3:E:510:ASP:HB3	3:E:513:PHE:HB2	2.01	0.42
5:1:403:A:H2'	5:1:404:A:C8	2.55	0.42
7:A:13:PRO:O	7:A:69:ARG:NH1	2.42	0.42
18:B:108:THR:HA	18:B:154:VAL:HA	2.00	0.42
5:1:337:A:H2'	5:1:338:G:H8	1.84	0.42
5:1:52:U:H2'	5:1:53:G:C8	2.55	0.42
5:1:444:G:H2'	5:1:445:G:C8	2.55	0.42
5:1:121:U:H5'	18:B:26:ARG:HH22	1.84	0.42
7:A:22:LEU:HD21	7:A:102:GLN:HG2	2.02	0.42
8:C:93:ASN:HA	8:C:96:GLU:HG2	2.02	0.42
10:d:33:LEU:HD21	10:d:36:SER:HB2	2.01	0.42
10:d:61:GLN:HB3	13:g:73:ALA:HB3	2.02	0.42
1:F:359:LEU:HB2	3:E:277:GLU:HG3	2.02	0.41
3:E:113:LEU:HD23	3:E:113:LEU:HA	1.94	0.41
5:1:443:U:H2'	5:1:444:G:H8	1.84	0.41
10:d:43:GLN:HB2	10:d:63:PHE:HD1	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:608:LEU:HD13	17:D:608:LEU:HA	1.79	0.41
3:E:271:VAL:HB	3:E:309:TYR:HE2	1.85	0.41
16:H:61:THR:HG23	16:H:63:GLN:H	1.84	0.41
3:E:25:LYS:HD2	6:G:261:PHE:HE1	1.85	0.41
3:E:257:SER:HA	8:C:174:LEU:HD21	2.01	0.41
5:1:21:G:H2'	5:1:22:A:H8	1.86	0.41
5:1:413:U:H2'	5:1:414:A:C8	2.56	0.41
5:1:91:U:H2'	5:1:92:G:C8	2.56	0.41
5:1:389:G:N2	5:1:430:U:O2	2.33	0.41
5:1:444:G:H2'	5:1:445:G:H8	1.86	0.41
5:1:498:U:H1'	5:1:514:A:N1	2.35	0.41
5:1:443:U:H2'	5:1:444:G:C8	2.55	0.41
15:i:62:ASP:HB3	15:i:66:ASN:H	1.85	0.41
17:D:488:ASN:HA	17:D:491:ILE:HG12	2.02	0.41
5:1:438:U:H2'	5:1:439:U:C6	2.56	0.41
5:1:453:U:H2'	5:1:454:G:C8	2.56	0.41
3:E:116:CYS:HA	3:E:119:VAL:HG22	2.01	0.41
5:1:195:C:H42	5:1:243:U:H3	1.68	0.41
3:E:284:ASP:OD1	3:E:315:LYS:NZ	2.38	0.41
3:E:327:LEU:HD13	3:E:357:LYS:HD2	2.03	0.41
4:J:274:PRO:HD2	4:J:275:SER:H	1.84	0.41
18:B:26:ARG:HA	18:B:27:PRO:HD3	1.97	0.41
2:I:113:N:H4'	17:D:607:ASN:N	2.31	0.41
3:E:350:LEU:HD13	17:D:542:GLU:HG2	2.03	0.41
5:1:510:G:H2'	5:1:511:A:C8	2.56	0.41
5:1:454:G:H2'	5:1:455:U:H6	1.86	0.40
17:D:595:LEU:HB3	17:D:600:ILE:HD11	2.02	0.40
3:E:219:SER:O	8:C:59:ARG:NH1	2.55	0.40
5:1:125:A:H2'	5:1:126:A:C8	2.56	0.40
5:1:416:G:H4'	5:1:417:A:H5'	2.03	0.40
6:G:133:LEU:HD11	6:G:159:GLY:HA3	2.02	0.40
3:E:448:TYR:HD2	17:D:480:SER:HA	1.86	0.40
3:E:518:LEU:O	3:E:522:THR:OG1	2.33	0.40
7:A:60:MET:HG3	7:A:89:ARG:HH12	1.86	0.40
8:C:92:MET:HA	8:C:95:LYS:HG2	2.02	0.40
12:f:19:LEU:HD21	12:f:45:THR:HG21	2.02	0.40
2:I:8:C:C4	5:1:1:A:N6	2.89	0.40
1:F:439:PRO:HB2	3:E:309:TYR:HE1	1.86	0.40
3:E:203:THR:HG21	17:D:602:LEU:HD22	2.03	0.40
5:1:556:U:H1'	9:b:90:GLU:HB2	2.04	0.40
6:G:195:VAL:HG12	6:G:198:PHE:H	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:H:58:PHE:HE1	16:H:225:ILE:HG23	1.86	0.40

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	F	259/523 (50%)	251 (97%)	8 (3%)	0	100	100
3	E	542/544 (100%)	521 (96%)	21 (4%)	0	100	100
4	J	101/620 (16%)	92 (91%)	8 (8%)	1 (1%)	12	46
6	G	235/492 (48%)	222 (94%)	13 (6%)	0	100	100
7	A	126/298 (42%)	116 (92%)	10 (8%)	0	100	100
8	C	193/231 (84%)	183 (95%)	10 (5%)	0	100	100
9	b	117/196 (60%)	110 (94%)	7 (6%)	0	100	100
10	d	91/101 (90%)	87 (96%)	4 (4%)	0	100	100
11	e	73/94 (78%)	67 (92%)	5 (7%)	1 (1%)	9	39
12	f	71/86 (83%)	69 (97%)	2 (3%)	0	100	100
13	g	68/77 (88%)	62 (91%)	5 (7%)	1 (2%)	8	39
14	h	101/146 (69%)	98 (97%)	3 (3%)	0	100	100
15	i	95/110 (86%)	91 (96%)	4 (4%)	0	100	100
16	H	186/261 (71%)	180 (97%)	6 (3%)	0	100	100
17	D	570/629 (91%)	554 (97%)	16 (3%)	0	100	100
18	B	182/300 (61%)	169 (93%)	13 (7%)	0	100	100
All	All	3010/4708 (64%)	2872 (95%)	135 (4%)	3 (0%)	49	81

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	J	274	PRO
11	e	34	GLN
13	g	21	GLY

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	F	138/451 (31%)	137 (99%)	1 (1%)	76	79
3	E	508/519 (98%)	502 (99%)	6 (1%)	63	73
4	J	49/568 (9%)	49 (100%)	0	100	100
6	G	218/448 (49%)	218 (100%)	0	100	100
7	A	117/273 (43%)	117 (100%)	0	100	100
8	C	171/214 (80%)	171 (100%)	0	100	100
9	b	108/176 (61%)	108 (100%)	0	100	100
10	d	81/89 (91%)	81 (100%)	0	100	100
11	e	68/83 (82%)	68 (100%)	0	100	100
12	f	65/77 (84%)	64 (98%)	1 (2%)	57	70
13	g	62/66 (94%)	62 (100%)	0	100	100
14	h	75/129 (58%)	75 (100%)	0	100	100
15	i	90/103 (87%)	89 (99%)	1 (1%)	65	74
16	H	72/234 (31%)	72 (100%)	0	100	100
17	D	193/603 (32%)	190 (98%)	3 (2%)	55	69
18	B	40/265 (15%)	40 (100%)	0	100	100
All	All	2055/4298 (48%)	2043 (99%)	12 (1%)	76	80

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	304	LEU
3	E	306	LEU

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Mol	Chain	Res	Type
3	E	371	ILE
3	E	416	LEU
3	E	417	ASN
3	E	486	ILE
3	E	505	ILE
12	f	60	VAL
15	i	103	VAL
17	D	608	LEU
17	D	609	GLU
17	D	610	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (42) such sidechains are listed below:

Mol	Chain	Res	Type
1	F	301	GLN
1	F	312	ASN
1	F	369	GLN
3	E	99	GLN
3	E	102	ASN
3	E	117	ASN
3	E	153	GLN
3	E	188	GLN
3	E	300	GLN
3	E	359	ASN
3	E	366	ASN
3	E	437	GLN
3	E	459	ASN
3	E	474	GLN
3	E	515	GLN
4	J	37	GLN
4	J	51	ASN
6	G	63	GLN
6	G	136	GLN
6	G	292	ASN
7	A	84	GLN
8	C	29	ASN
8	C	30	HIS
8	C	40	ASN
8	C	47	ASN
8	C	80	ASN
8	C	138	GLN
10	d	12	ASN

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Mol	Chain	Res	Type
10	d	68	GLN
12	f	76	ASN
13	g	55	HIS
14	h	12	ASN
14	h	78	ASN
15	i	86	ASN
16	H	17	GLN
16	H	63	GLN
17	D	450	GLN
17	D	466	ASN
17	D	533	ASN
17	D	573	HIS
17	D	582	GLN
17	D	617	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	I	9/371 (2%)	0	0
5	1	556/568 (97%)	117 (21%)	9 (1%)
All	All	565/939 (60%)	117 (20%)	9 (1%)

All (117) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	1	11	U
5	1	12	A
5	1	40	A
5	1	41	C
5	1	55	G
5	1	56	C
5	1	62	A
5	1	63	U
5	1	64	A
5	1	65	G
5	1	66	U
5	1	67	A
5	1	74	C
5	1	75	G
5	1	79	A
5	1	80	G

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Mol	Chain	Res	Type
5	1	87	U
5	1	97	A
5	1	98	U
5	1	100	A
5	1	101	U
5	1	103	G
5	1	107	A
5	1	113	G
5	1	114	U
5	1	117	U
5	1	133	G
5	1	134	G
5	1	141	A
5	1	142	C
5	1	147	A
5	1	149	G
5	1	150	G
5	1	151	C
5	1	152	G
5	1	153	C
5	1	154	G
5	1	167	G
5	1	171	A
5	1	176	U
5	1	180	U
5	1	181	U
5	1	182	C
5	1	186	U
5	1	187	G
5	1	205	U
5	1	206	C
5	1	218	U
5	1	219	U
5	1	220	G
5	1	227	U
5	1	228	U
5	1	230	G
5	1	254	U
5	1	255	U
5	1	257	G
5	1	258	U
5	1	259	U

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Mol	Chain	Res	Type
5	1	260	U
5	1	269	U
5	1	270	G
5	1	271	G
5	1	272	A
5	1	278	U
5	1	279	U
5	1	280	G
5	1	287	A
5	1	290	U
5	1	327	A
5	1	328	G
5	1	343	A
5	1	352	G
5	1	365	U
5	1	369	G
5	1	377	U
5	1	378	U
5	1	385	U
5	1	386	G
5	1	389	G
5	1	393	G
5	1	394	A
5	1	395	U
5	1	399	A
5	1	400	A
5	1	407	U
5	1	409	A
5	1	416	G
5	1	418	U
5	1	422	G
5	1	424	U
5	1	426	U
5	1	427	G
5	1	443	U
5	1	460	U
5	1	466	U
5	1	468	U
5	1	477	G
5	1	482	G
5	1	493	G
5	1	504	U

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Mol	Chain	Res	Type
5	1	505	U
5	1	506	A
5	1	508	G
5	1	513	A
5	1	515	A
5	1	540	G
5	1	542	U
5	1	551	U
5	1	553	A
5	1	554	U
5	1	555	U
5	1	559	G
5	1	560	A
5	1	562	U
5	1	563	U
5	1	564	A
5	1	565	U

All (9) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	1	86	A
5	1	100	A
5	1	113	G
5	1	151	C
5	1	152	G
5	1	258	U
5	1	268	C
5	1	399	A
5	1	505	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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	I	2
5	1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	8:C	O3'	103:N	P	54.06
1	I	128:N	O3'	130:N	P	17.87
1	1	325:A	O3'	326:G	P	1.20

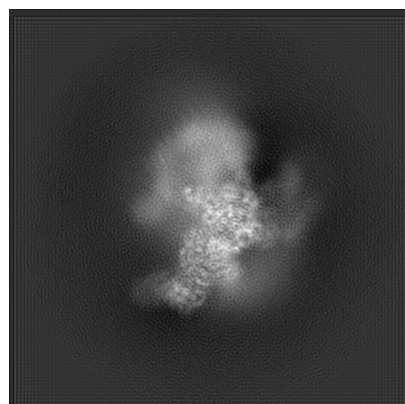
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13029. These allow visual inspection of the internal detail of the map and identification of artifacts.

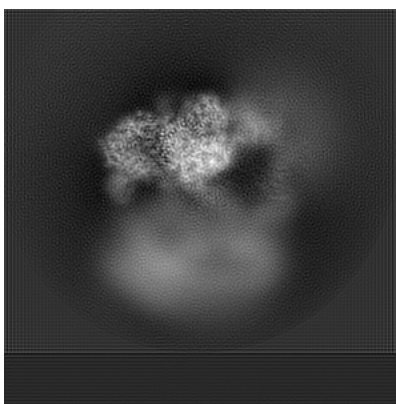
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

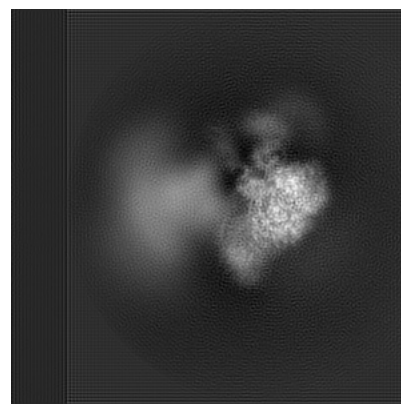
6.1.1 Primary map



X

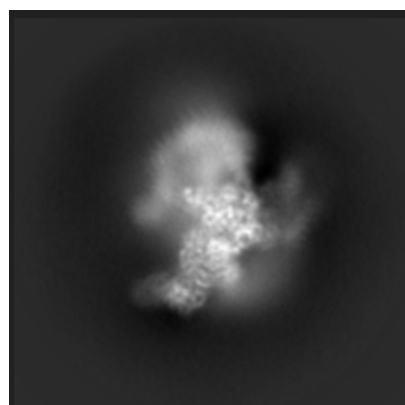


Y

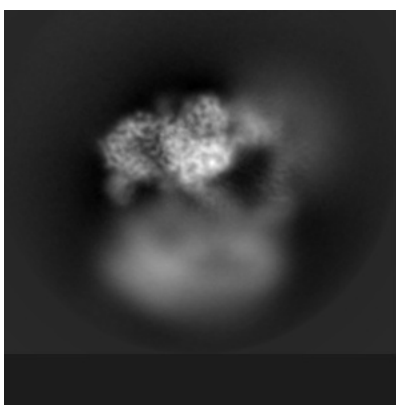


Z

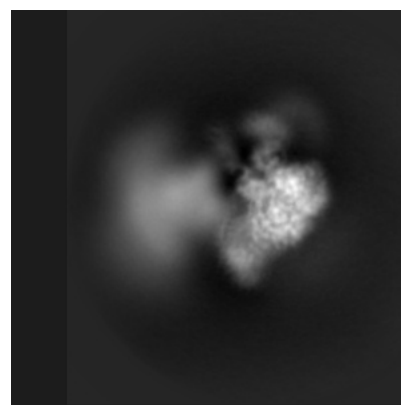
6.1.2 Raw map



X



Y

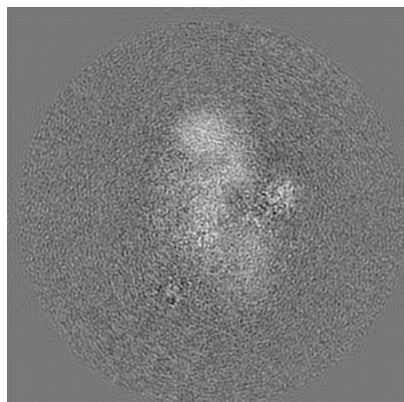


Z

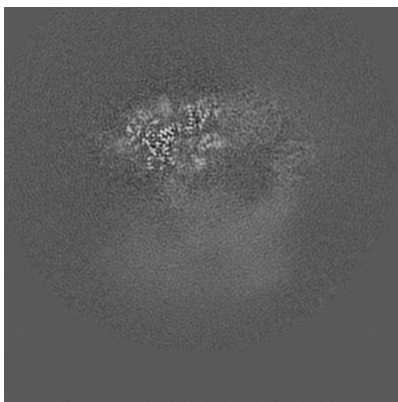
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

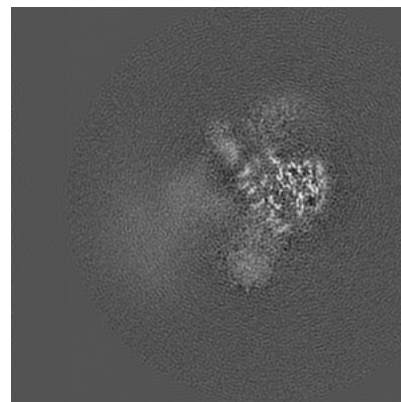
6.2.1 Primary map



X Index: 200

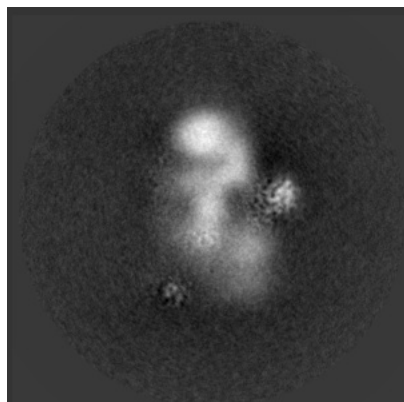


Y Index: 200

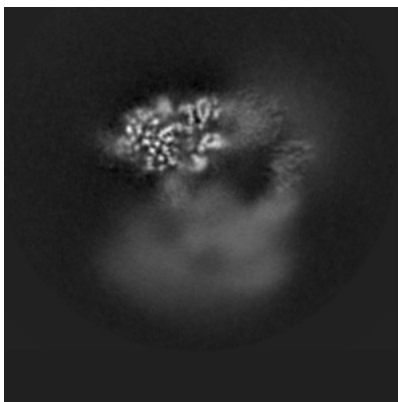


Z Index: 200

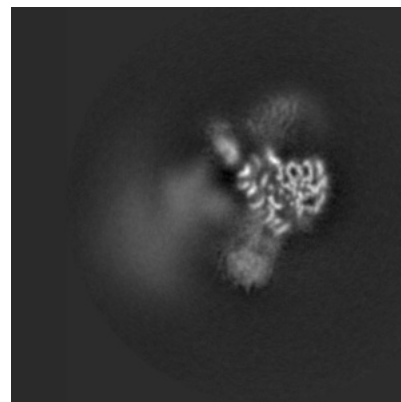
6.2.2 Raw map



X Index: 200



Y Index: 200

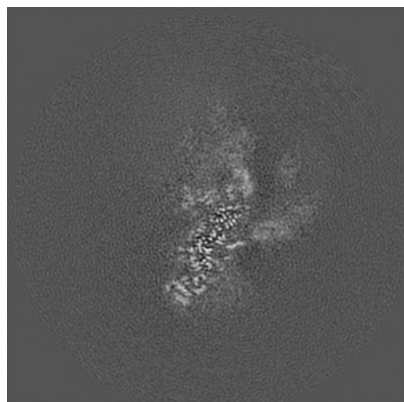


Z Index: 200

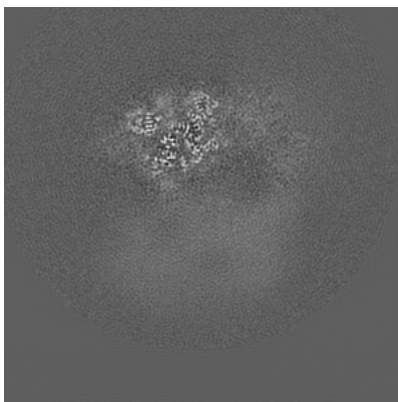
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

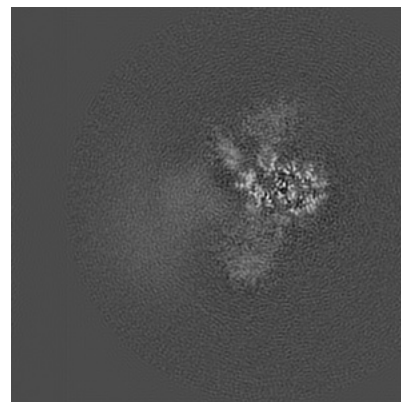
6.3.1 Primary map



X Index: 271

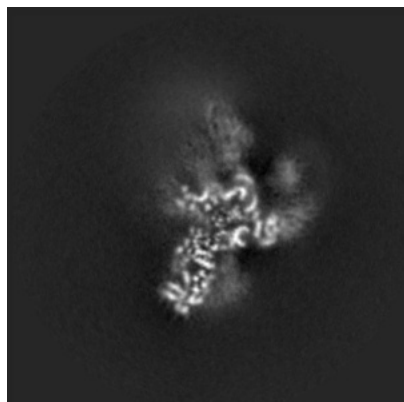


Y Index: 209

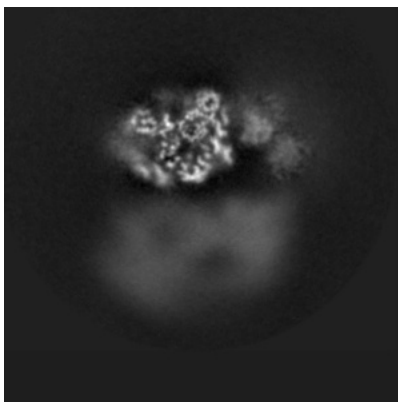


Z Index: 194

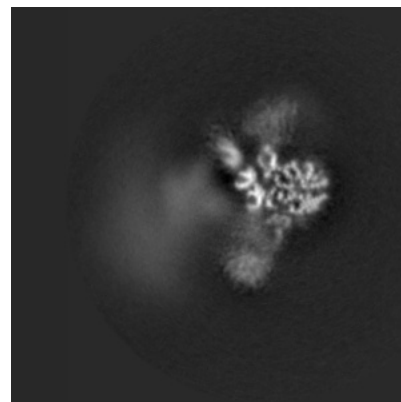
6.3.2 Raw map



X Index: 265



Y Index: 220

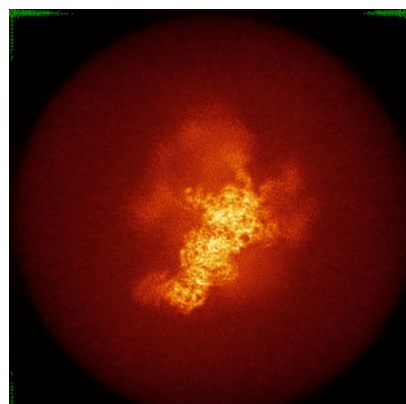


Z Index: 195

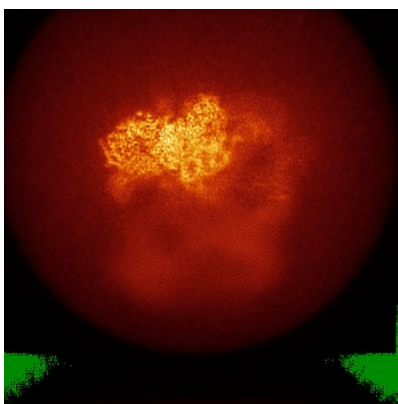
The images above show the largest variance slices of the map in three orthogonal directions.

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

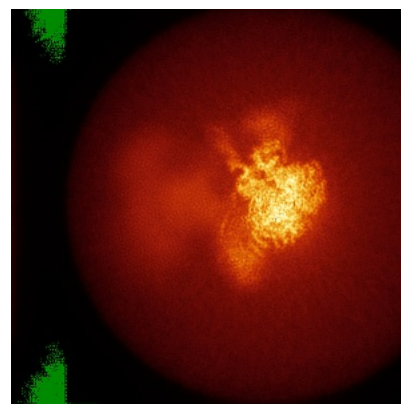
6.4.1 Primary map



X



Y

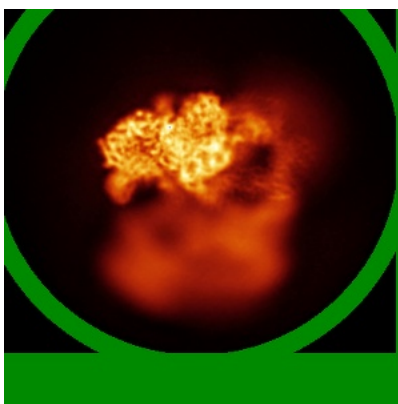


Z

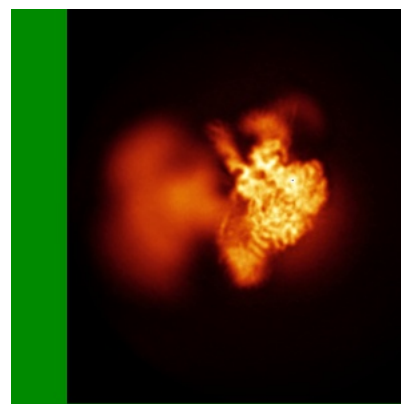
6.4.2 Raw map



X



Y

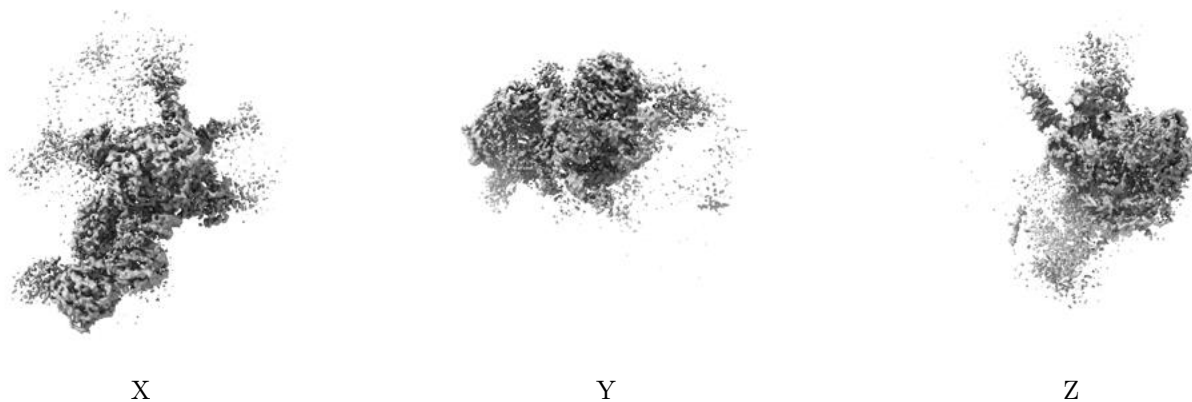


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.042. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

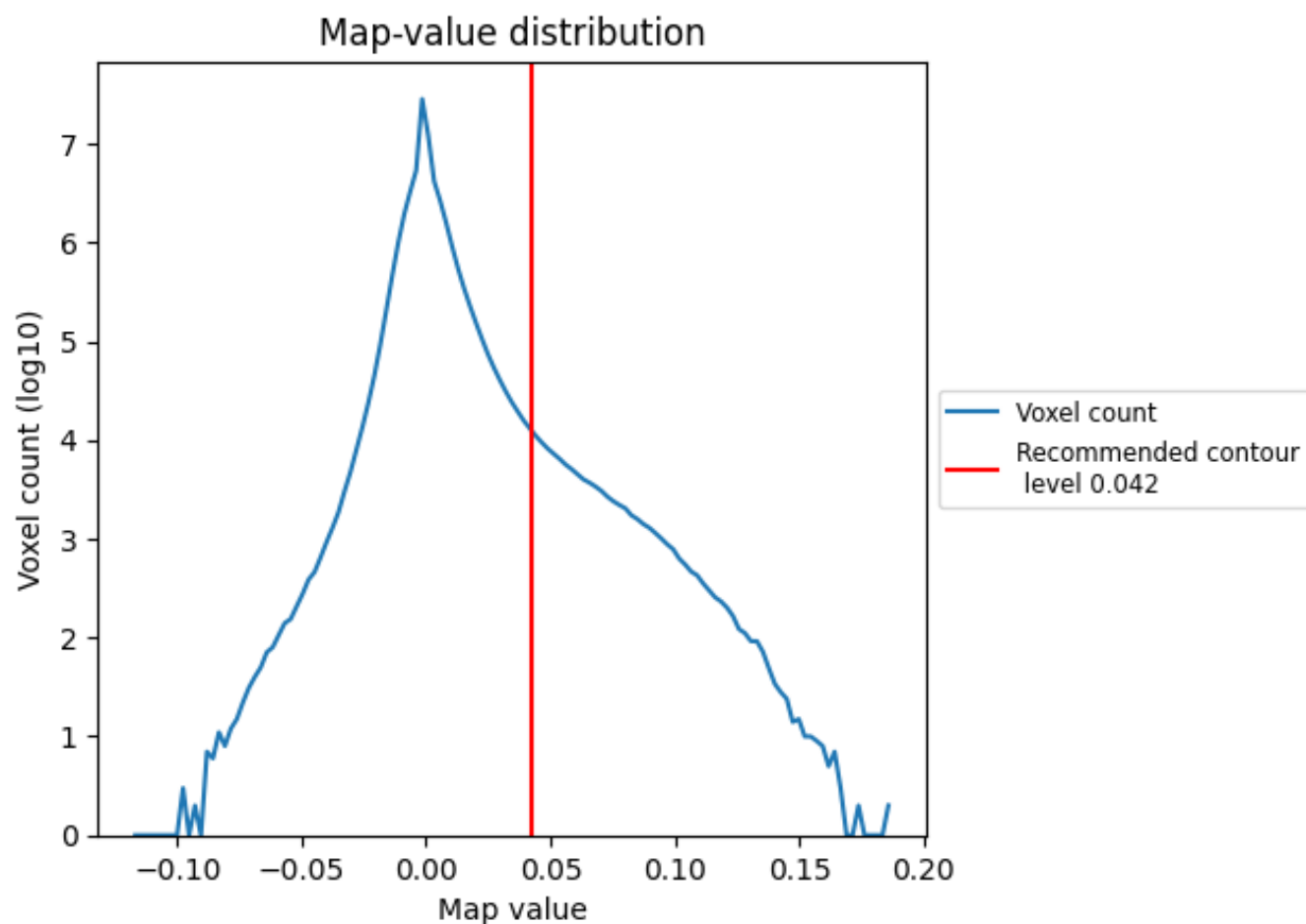
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

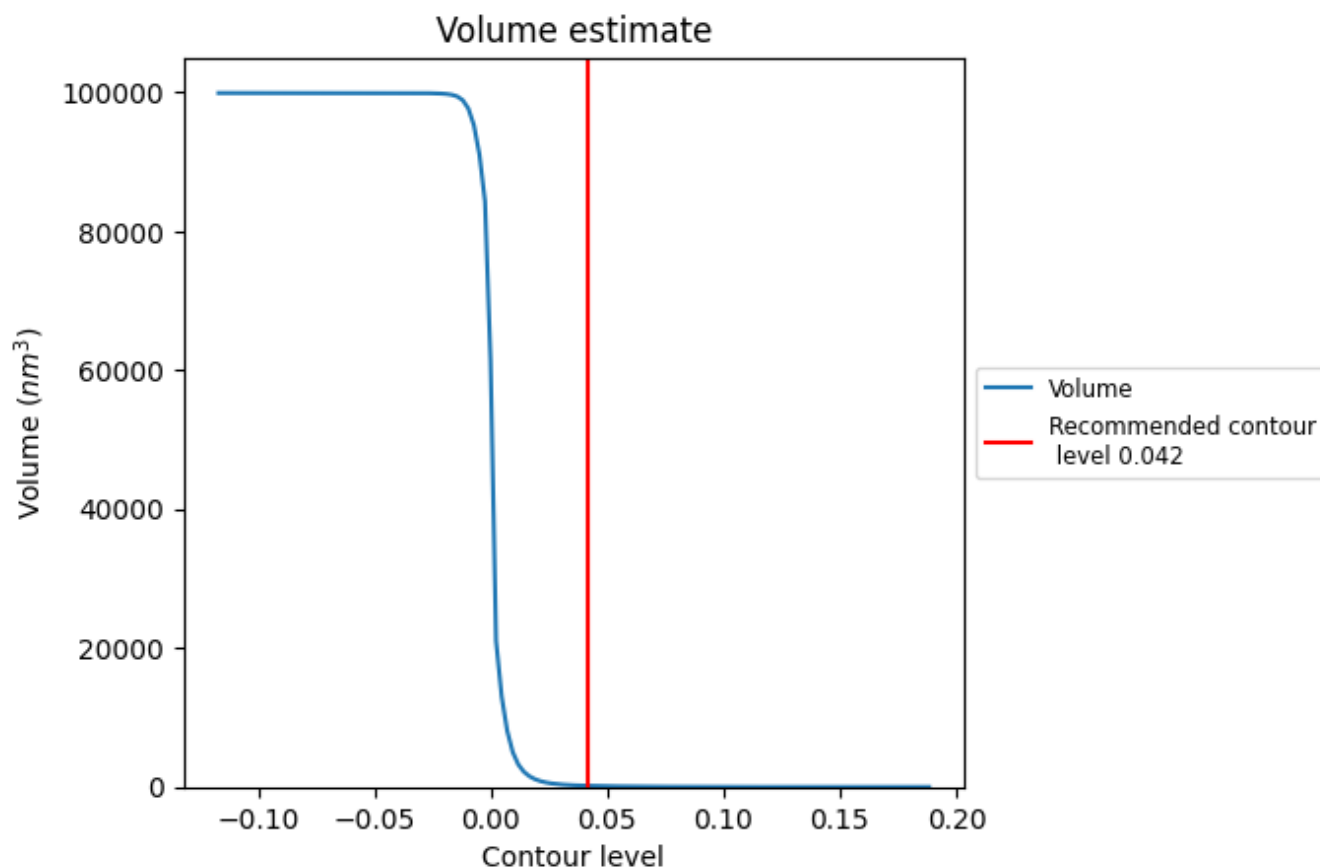
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

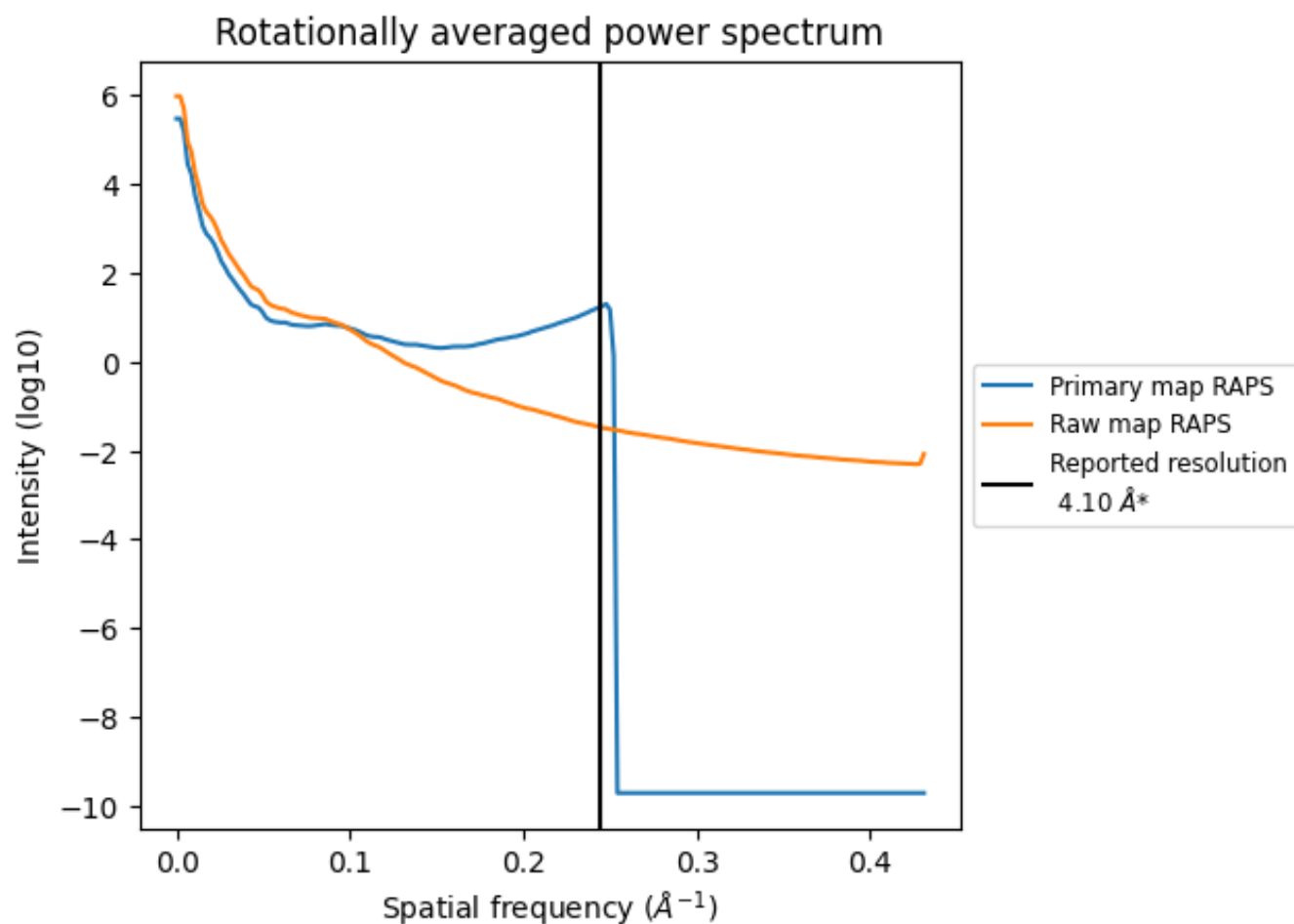
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 167 nm^3 ; this corresponds to an approximate mass of 151 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 ⓘ

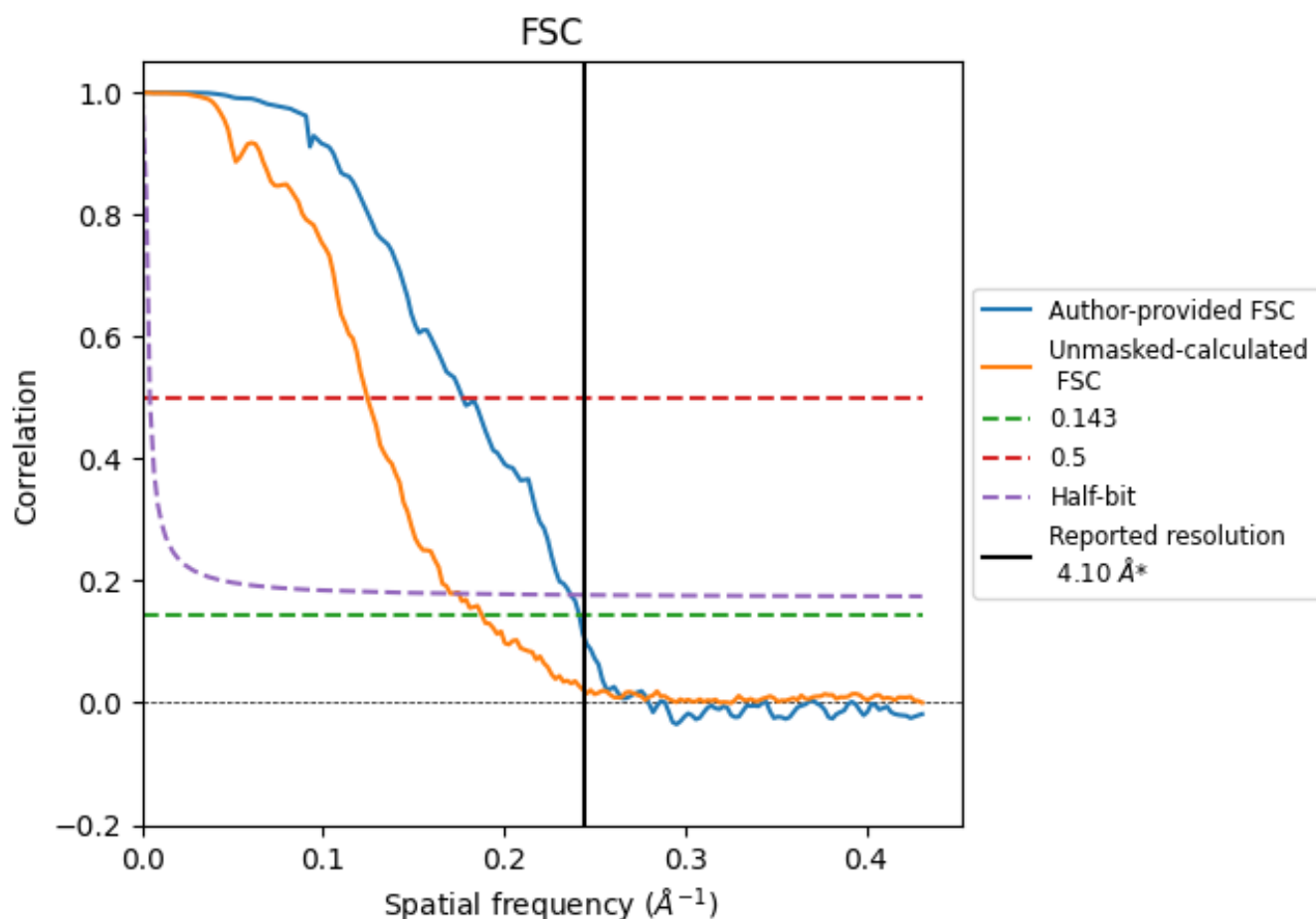


*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

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 0.244 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

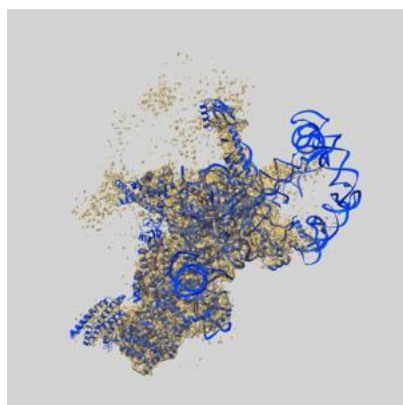
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.14	5.65	4.22
Unmasked-calculated*	5.33	8.04	5.72

*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 5.33 differs from the reported value 4.1 by more than 10 %

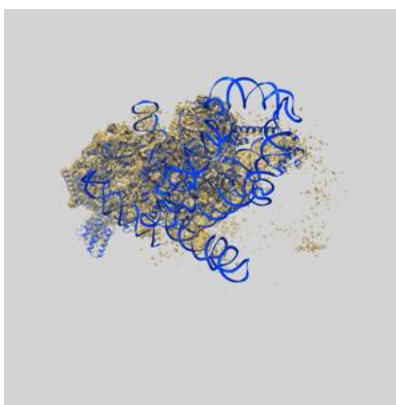
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13029 and PDB model 7OQC. Per-residue inclusion information can be found in section [3](#) on page [7](#).

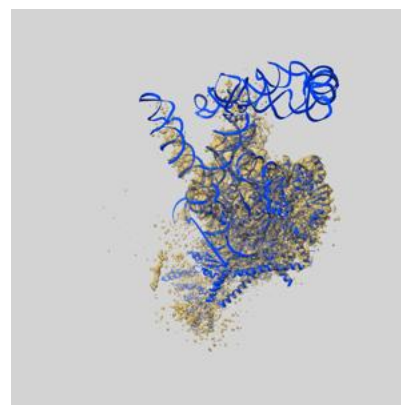
9.1 Map-model overlay [i](#)



X



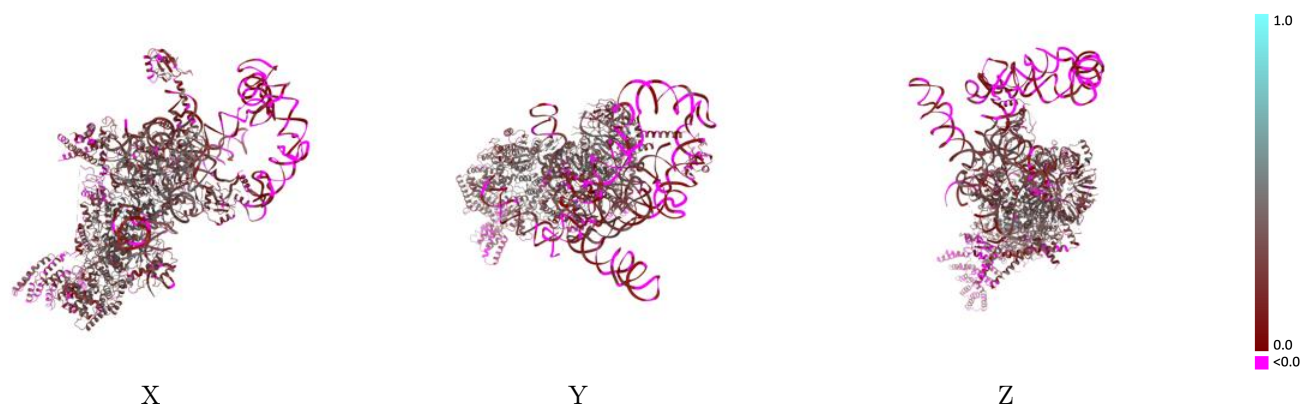
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.042 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](#)



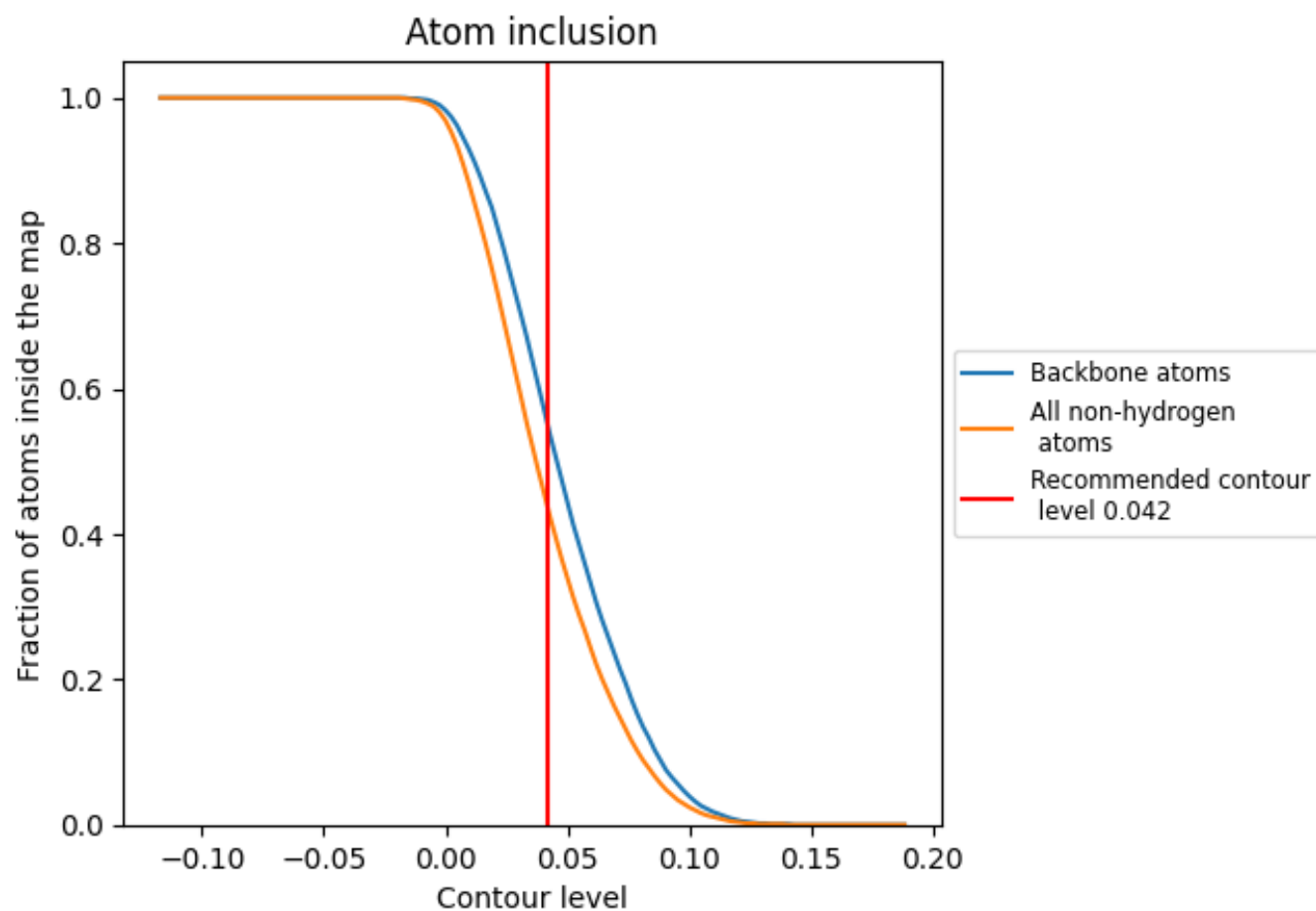
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.042).

9.4 Atom inclusion [i](#)



At the recommended contour level, 55% of all backbone atoms, 44% 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 (0.042) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4350	 0.2430
1	 0.3370	 0.1520
A	 0.3840	 0.2010
B	 0.3390	 0.2140
C	 0.4780	 0.3240
D	 0.4530	 0.2540
E	 0.6250	 0.3490
F	 0.4080	 0.2600
G	 0.5300	 0.3060
H	 0.3370	 0.2090
I	 0.2140	 0.1160
J	 0.3210	 0.2680
b	 0.5400	 0.3570
d	 0.5930	 0.3800
e	 0.5210	 0.2950
f	 0.5330	 0.2600
g	 0.5550	 0.3740
h	 0.5980	 0.3720
i	 0.5300	 0.2970

