



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 08:52 AM UTC

PDB ID : 3JD5 / pdb_00003jd5
EMDB ID : EMD-5941
Title : Cryo-EM structure of the small subunit of the mammalian mitochondrial ribosome
Authors : Kaushal, P.S.; Sharma, M.R.; Booth, T.M.; Haque, E.M.; Tung, C.S.; Sanbonmatsu, K.Y.; Spremulli, L.L.; Agrawal, R.K.
Deposited on : 2016-04-08
Resolution : 7.00 Å(reported)
Based on initial models : 5AJ3, 3J9M

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

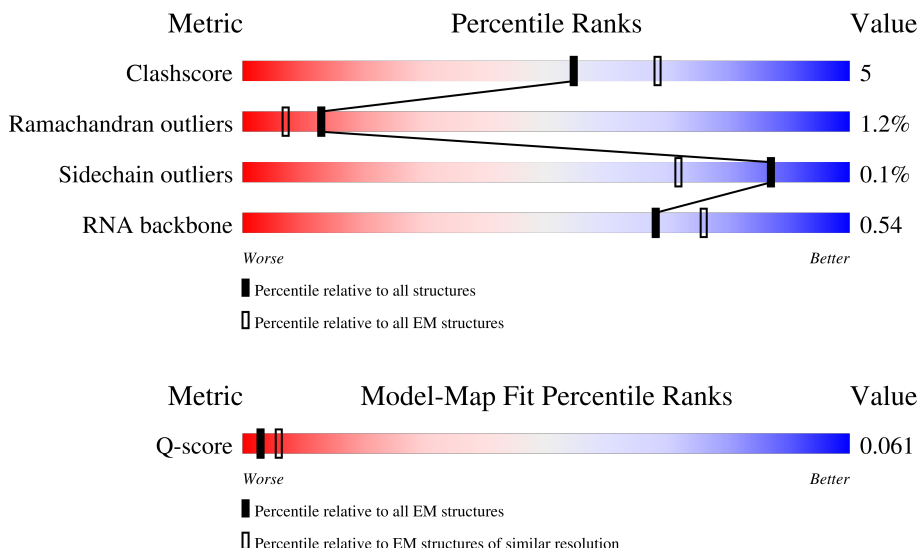
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.00 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	483 (6.50 - 7.50)

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

Mol	Chain	Length	Quality of chain
1	A	955	 10% 62% 33% 5%
2	B	293	 16% 64% 10% 26%
3	C	167	 16% 64% 15% 21%

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Mol	Chain	Length	Quality of chain
4	E	430	
5	F	124	
6	G	242	
7	I	396	
8	J	201	
9	K	197	
10	L	139	
11	N	128	
12	O	256	
13	P	135	
14	Q	130	
15	R	143	
16	U	87	
17	a	359	
18	b	190	
19	c	173	
20	d	205	
21	e	415	
22	f	189	
23	g	397	
24	h	386	
25	i	106	
26	j	218	
27	k	325	
28	m	118	

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Mol	Chain	Length	Quality of chain
29	n	199	5% 31% 5% 64%
30	o	575	50% 73% 7% 20%
31	p	258	7% 64% 8% 28%
32	s	17	65% 94% 6%
32	z	17	6% 100%

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 64319 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 RNA chain called 28S ribosomal RNA, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	952	Total	C	N	O	P	0	0
			20256	9090	3685	6529	952		

- Molecule 2 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	217	Total	C	N	O	S	0	0
			1726	1102	319	298	7		

- Molecule 3 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	132	Total	C	N	O	S	0	0
			1072	692	197	179	4		

- Molecule 4 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	328	Total	C	N	O	S	0	0
			2613	1634	494	474	11		

- Molecule 5 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	124	Total	C	N	O	S	0	0
			991	627	179	179	6		

- Molecule 6 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	208	Total	C	N	O	S	0	0
			1720	1093	313	301	13		

- Molecule 7 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	311	Total	C	N	O	S	0	0
			2541	1608	454	467	12		

- Molecule 8 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	128	Total	C	N	O	S	0	0
			1049	676	180	190	3		

- Molecule 9 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	136	Total	C	N	O	S	0	0
			1001	628	193	177	3		

- Molecule 10 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	109	Total	C	N	O	S	0	0
			853	534	175	140	4		

- Molecule 11 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	101	Total	C	N	O	S	0	0
			861	538	178	140	5		

- Molecule 12 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	O	173	Total	C	N	O	S	0	0
			1421	904	258	250	9		

- Molecule 13 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	P	116	Total	C	N	O	S	0	0
			916	580	180	151	5		

- Molecule 14 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	109	Total	C	N	O	S	0	0
			857	555	153	145	4		

- Molecule 15 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	97	Total	C	N	O	S	0	0
			788	507	136	138	7		

- Molecule 16 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	U	86	Total	C	N	O	S	0	0
			737	457	148	124	8		

- Molecule 17 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	a	289	Total	C	N	O	S	0	0
			2356	1505	400	443	8		

- Molecule 18 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	b	135	Total	C	N	O	S	0	0
			1108	717	195	194	2		

- Molecule 19 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	c	168	Total	C	N	O	S	0	0
			1374	878	246	241	9		

- Molecule 20 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	d	176	Total	C	N	O	S	0	0
			1463	899	290	272	2		

- Molecule 21 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	e	344	Total	C	N	O	S	0	0
			2822	1804	476	529	13		

- Molecule 22 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	f	98	Total	C	N	O	S	0	0
			775	493	135	143	4		

- Molecule 23 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	g	338	Total	C	N	O	S	0	0
			2754	1774	482	488	10		

- Molecule 24 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	h	103	Total	C	N	O	S	0	0
			871	566	141	161	3		

- Molecule 25 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	i	98	Total	C	N	O	S	0	0
			818	519	153	143	3		

- Molecule 26 is a protein called 28S ribosomal protein S34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	j	213	Total	C	N	O	S	0	0
			1792	1132	346	309	5		

- Molecule 27 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	k	275	Total	C	N	O	S	0	0
			2227	1418	377	421	11		

- Molecule 28 is a protein called Coiled-coil-helix-coiled-coil-helix domain containing 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	m	118	Total	C	N	O	S	0	0
			945	587	185	164	9		

- Molecule 29 is a protein called Aurora kinase A interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	n	72	Total	C	N	O	S	0	0
			642	409	142	89	2		

- Molecule 30 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	o	461	Total	C	N	O	S	0	0
			3273	2082	573	605	13		

- Molecule 31 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	p	187	Total	C	N	O	S	0	0
			1531	968	288	267	8		

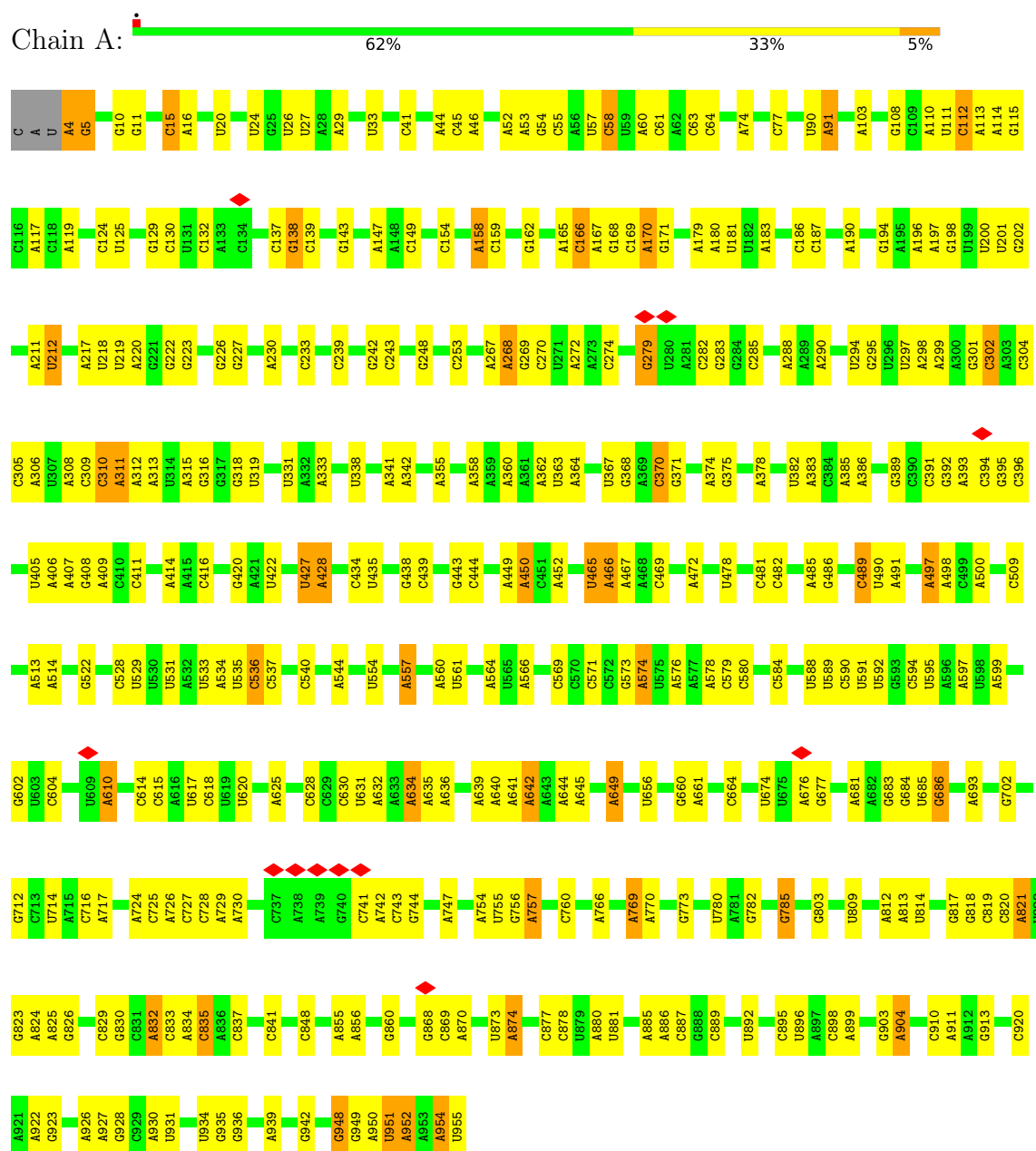
- Molecule 32 is a protein called unknown.

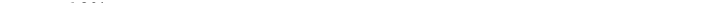
Mol	Chain	Residues	Atoms				AltConf	Trace
32	s	16	Total	C	N	O	0	0
			80	48	16	16		
32	z	17	Total	C	N	O	0	0
			86	51	17	18		

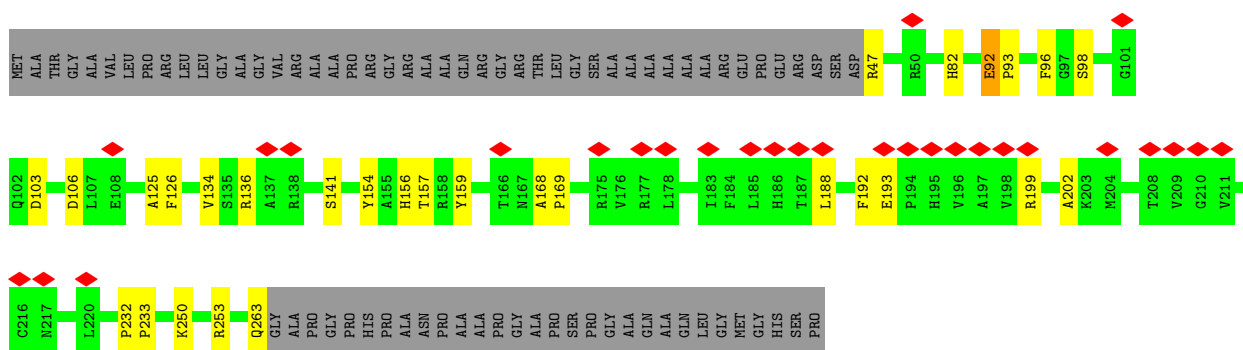
3 Residue-property plots

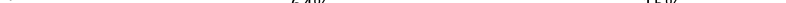
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

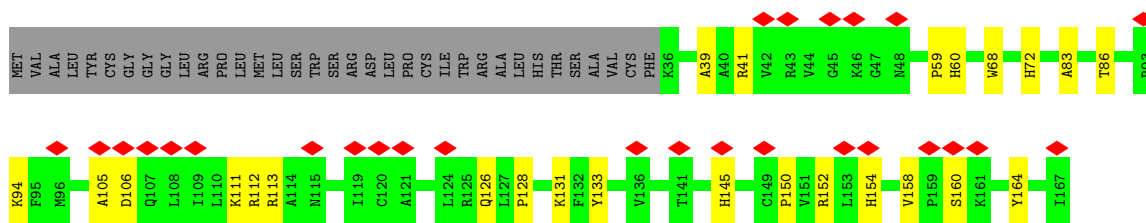
- Molecule 1: 28S ribosomal RNA, mitochondrial

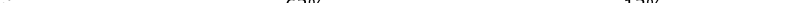


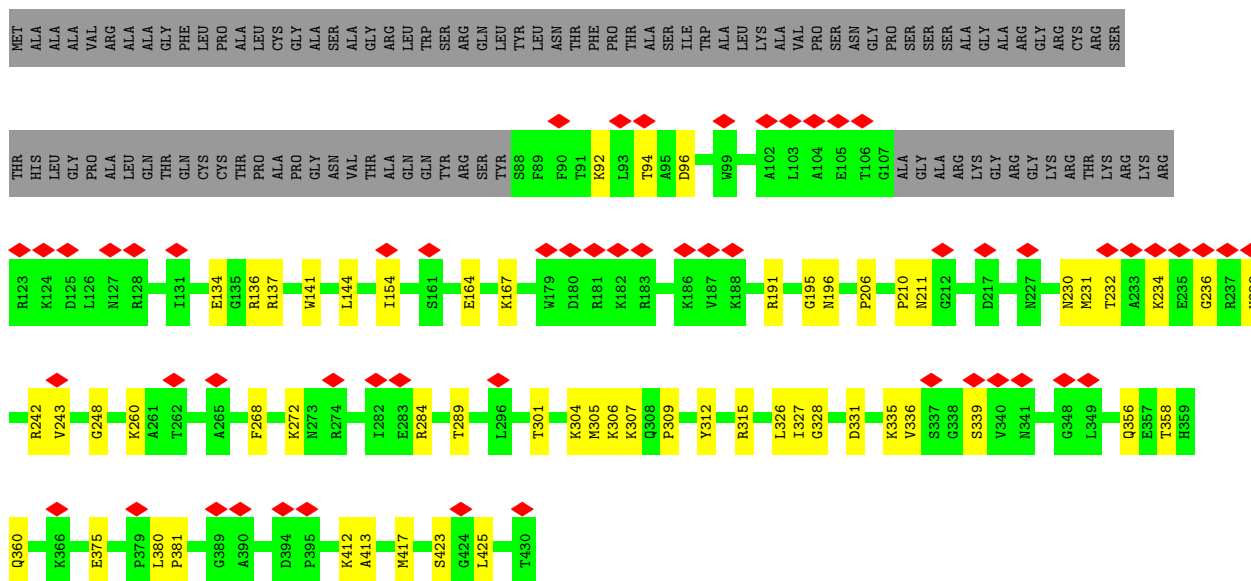
- Chain B:  10% 64% 10% 26%

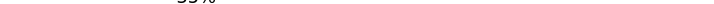


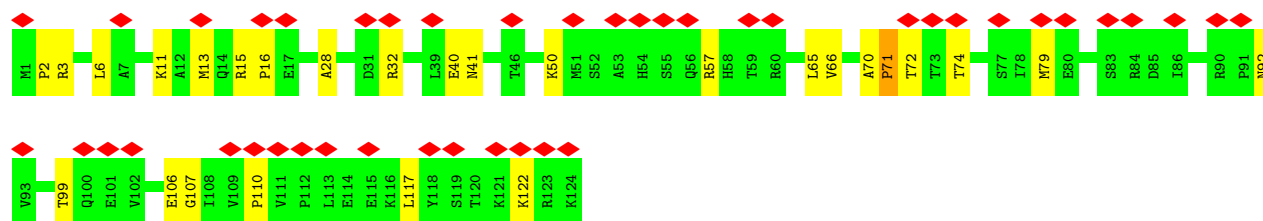
- Chain C:  16% 64% 15% 21%



- Chain E: 

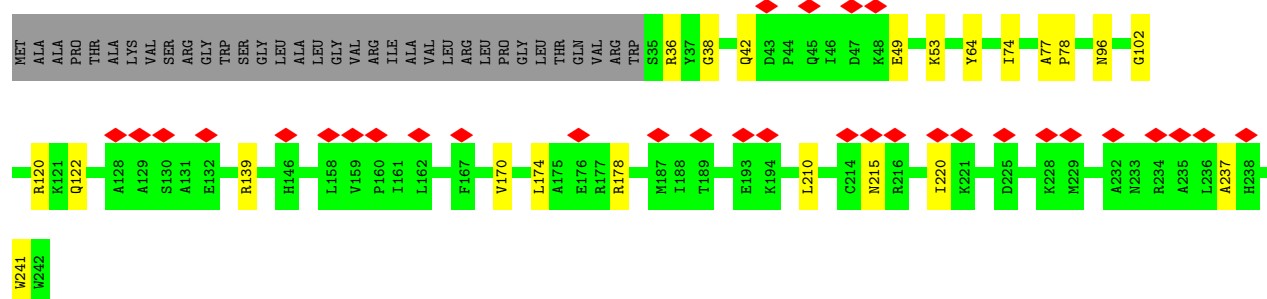


- Chain F:  35% 78% 21%



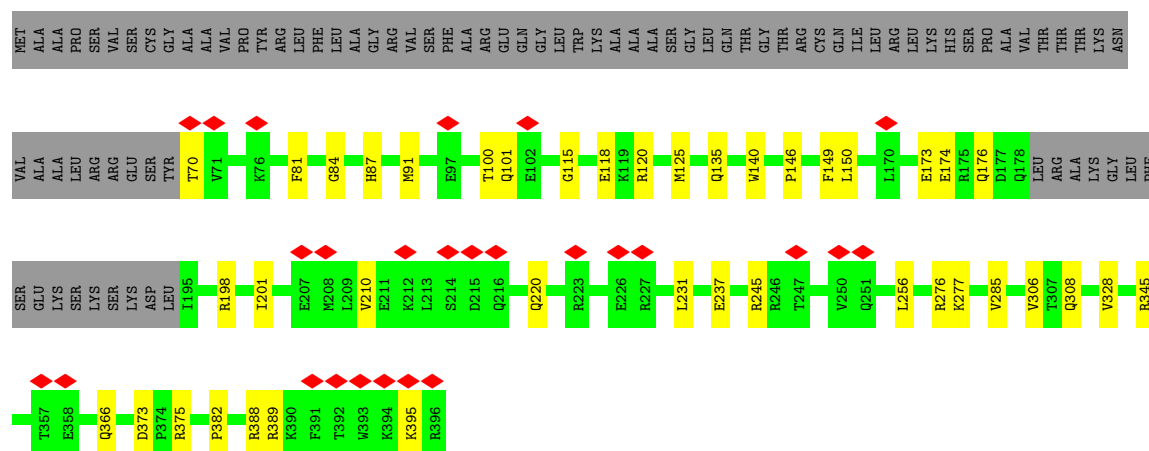
- Molecule 6: 28S ribosomal protein S7, mitochondrial

Chain G:



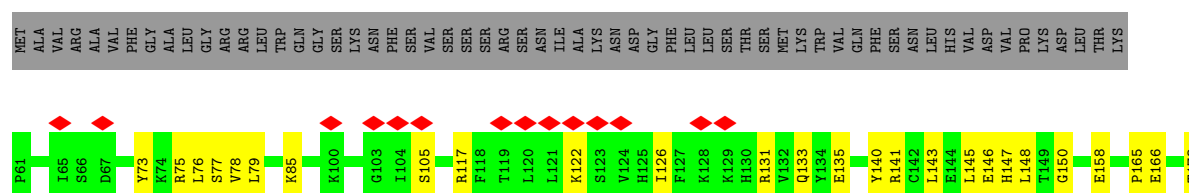
- Molecule 7: 28S ribosomal protein S9, mitochondrial

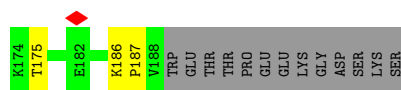
Chain I:



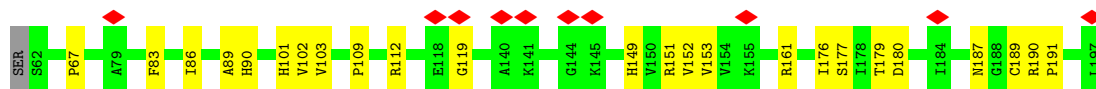
- Molecule 8: 28S ribosomal protein S10, mitochondrial

Chain J:

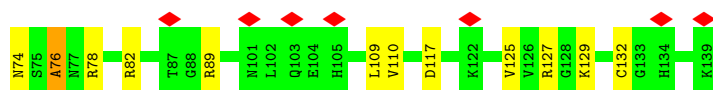
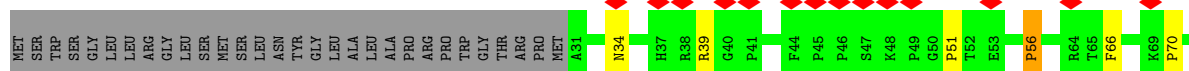




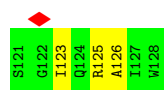
- Molecule 9: 28S ribosomal protein S11, mitochondrial



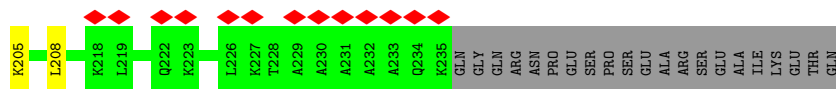
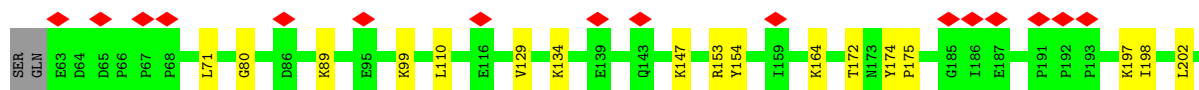
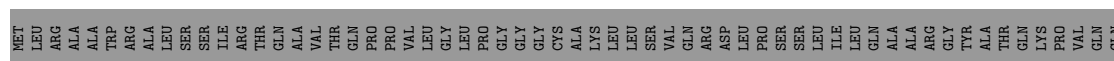
- Molecule 10: 28S ribosomal protein S12, mitochondrial



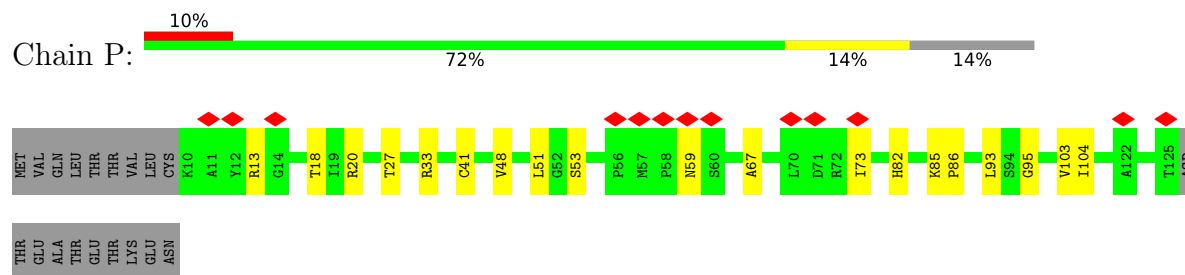
- Molecule 11: 28S ribosomal protein S14, mitochondrial



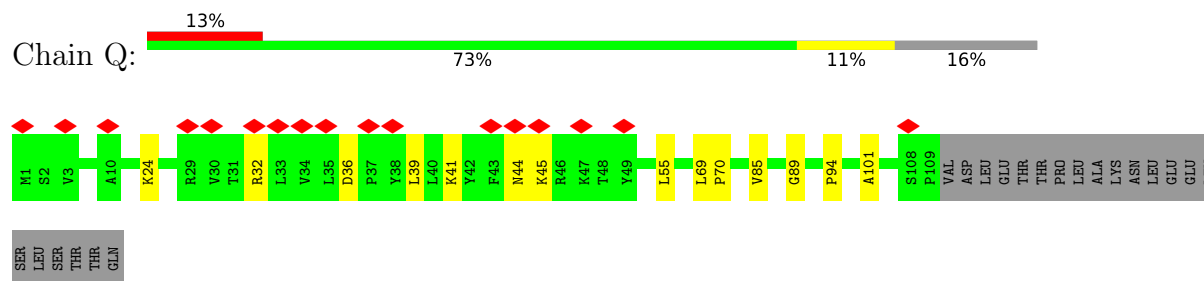
- Molecule 12: 28S ribosomal protein S15, mitochondrial



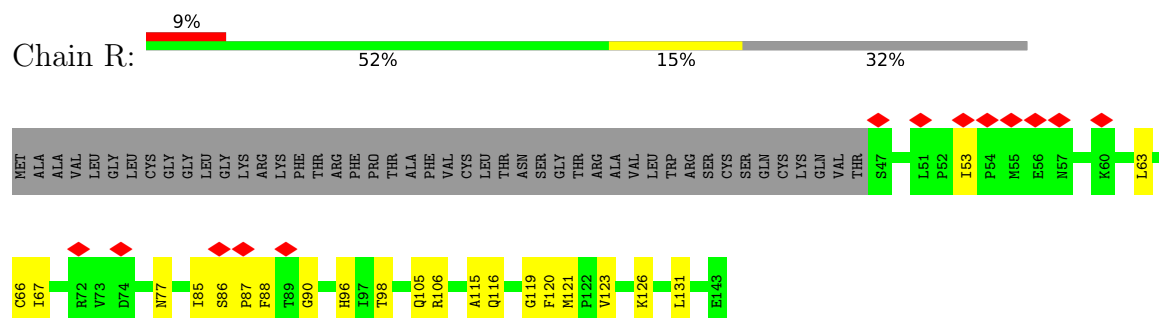
- Molecule 13: 28S ribosomal protein S16, mitochondrial



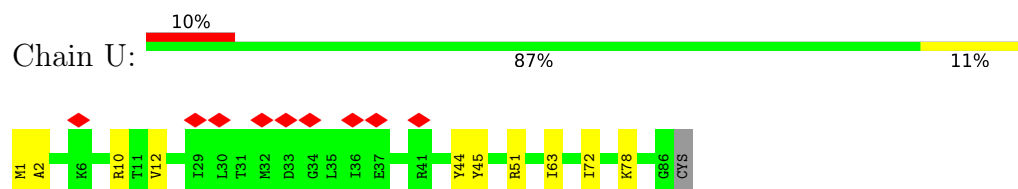
- Molecule 14: 28S ribosomal protein S17, mitochondrial



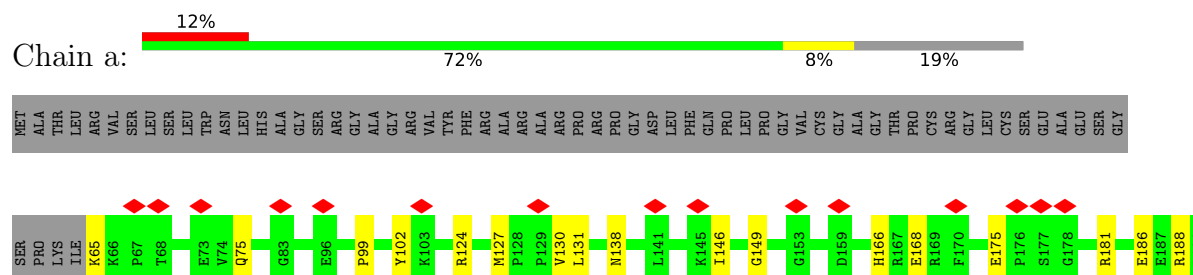
- Molecule 15: 28S ribosomal protein S18c, mitochondrial

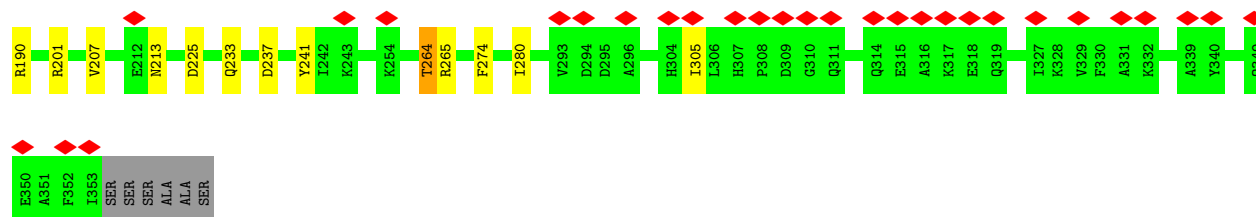


- Molecule 16: 28S ribosomal protein S21, mitochondrial

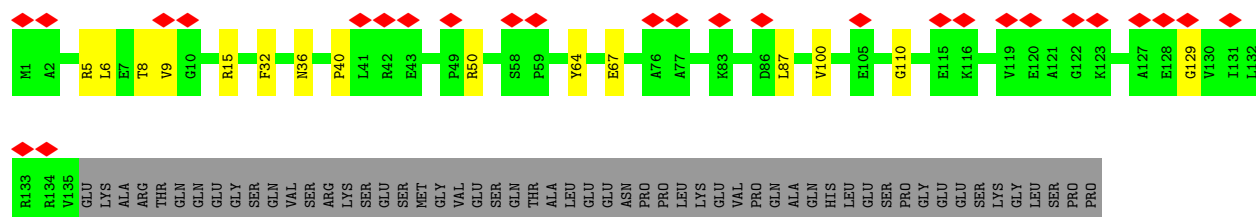


- Molecule 17: 28S ribosomal protein S22, mitochondrial

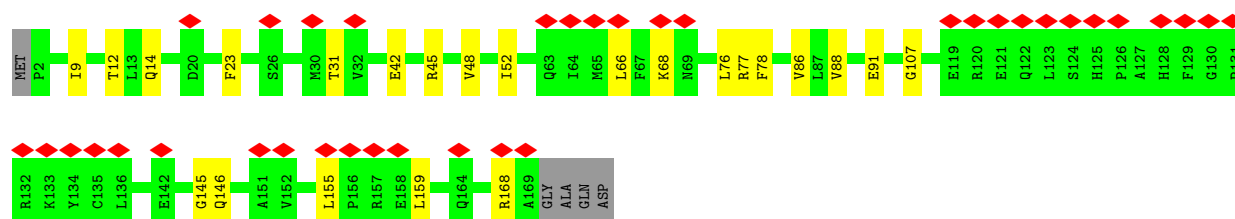
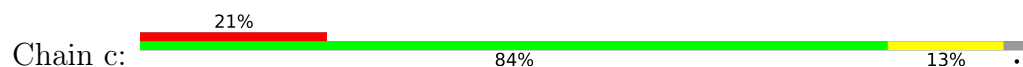




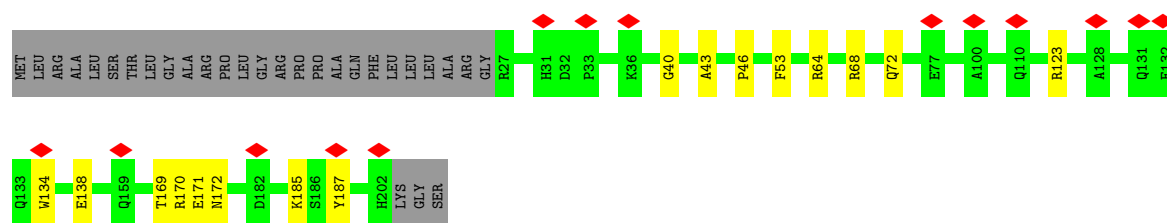
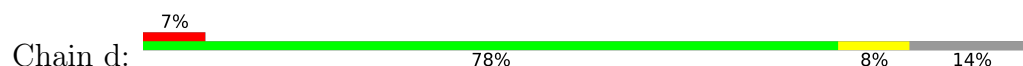
- Molecule 18: 28S ribosomal protein S23, mitochondrial



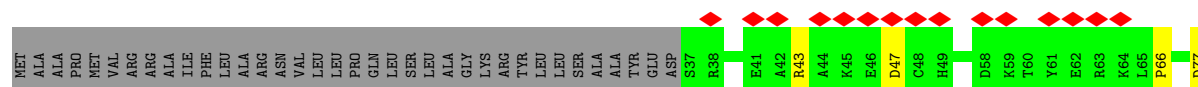
- Molecule 19: 28S ribosomal protein S25, mitochondrial

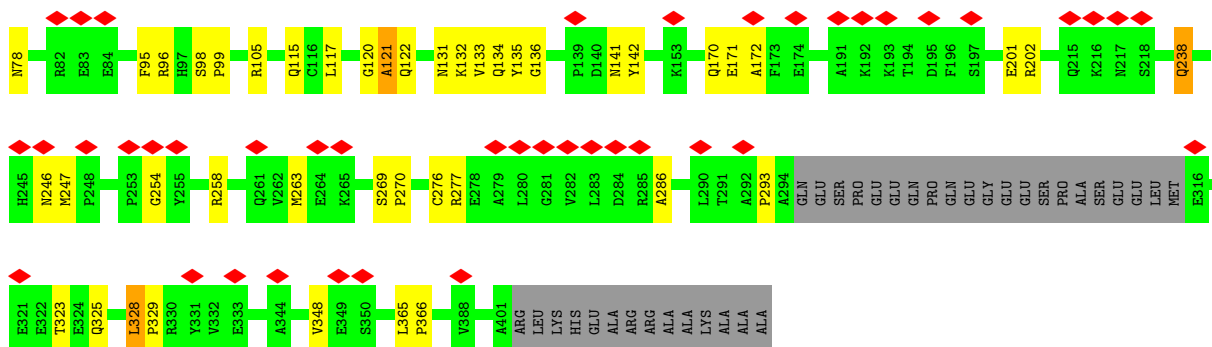


- Molecule 20: 28S ribosomal protein S26, mitochondrial

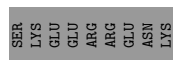
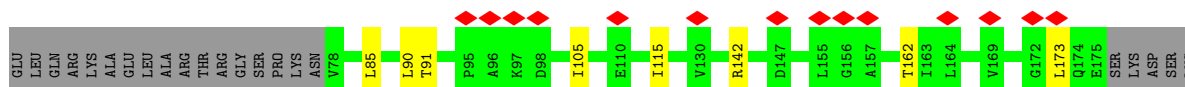


- Molecule 21: 28S ribosomal protein S27, mitochondrial

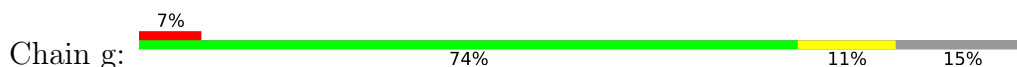




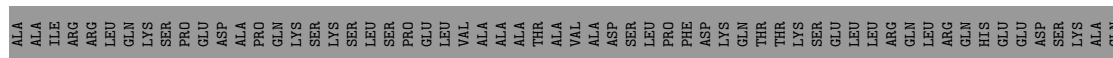
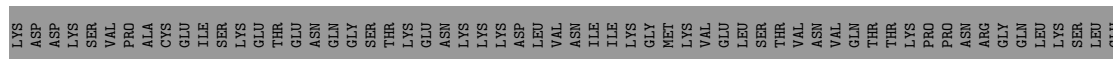
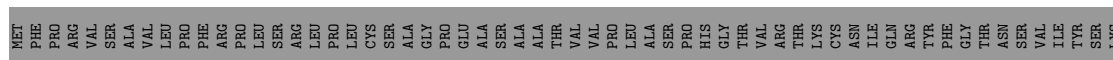
- Molecule 22: 28S ribosomal protein S28, mitochondrial

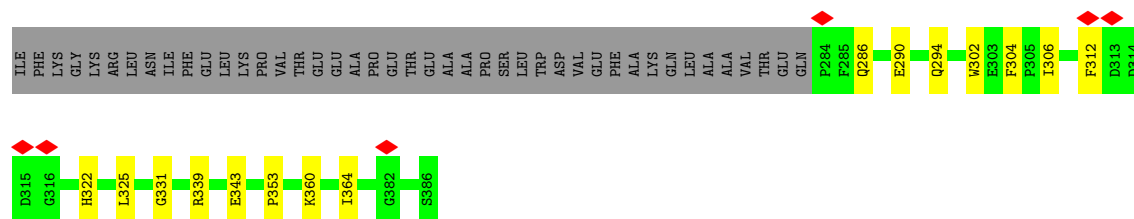


- Molecule 23: 28S ribosomal protein S29, mitochondrial

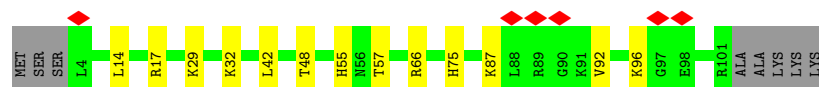
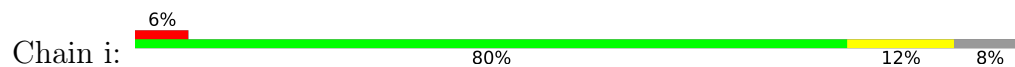


- Molecule 24: 28S ribosomal protein S31, mitochondrial

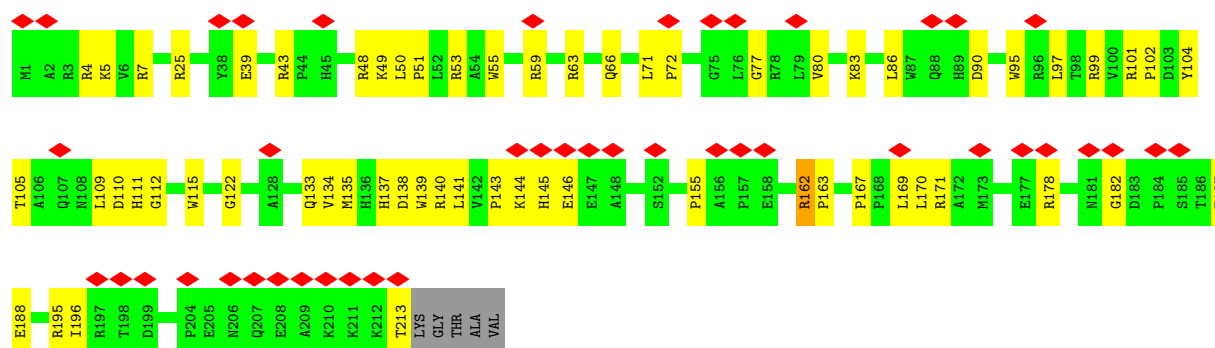




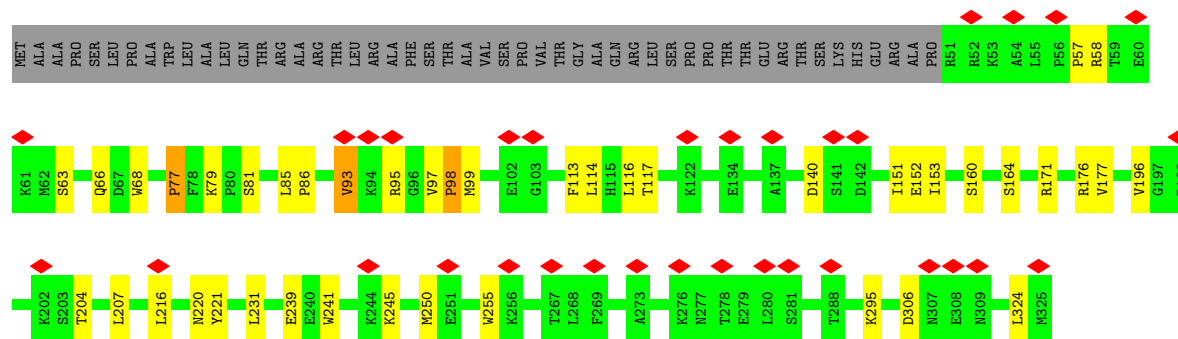
- Molecule 25: 28S ribosomal protein S33, mitochondrial



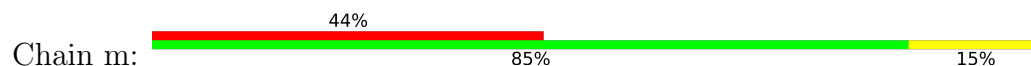
- Molecule 26: 28S ribosomal protein S34, mitochondrial

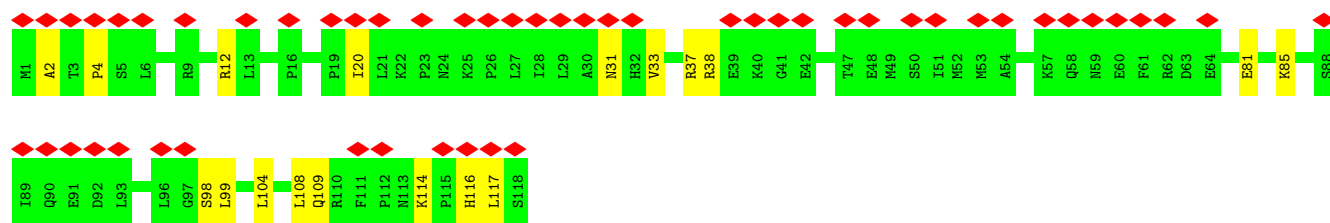


- Molecule 27: 28S ribosomal protein S35, mitochondrial

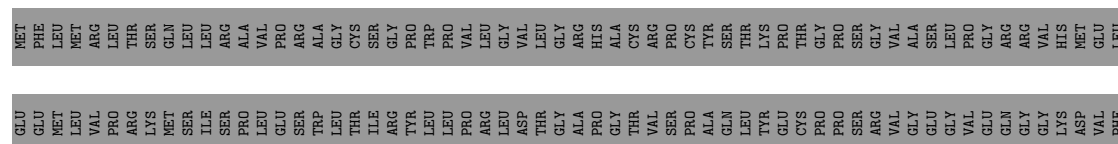


- Molecule 28: Coiled-coil-helix-coiled-coil-helix domain containing 1

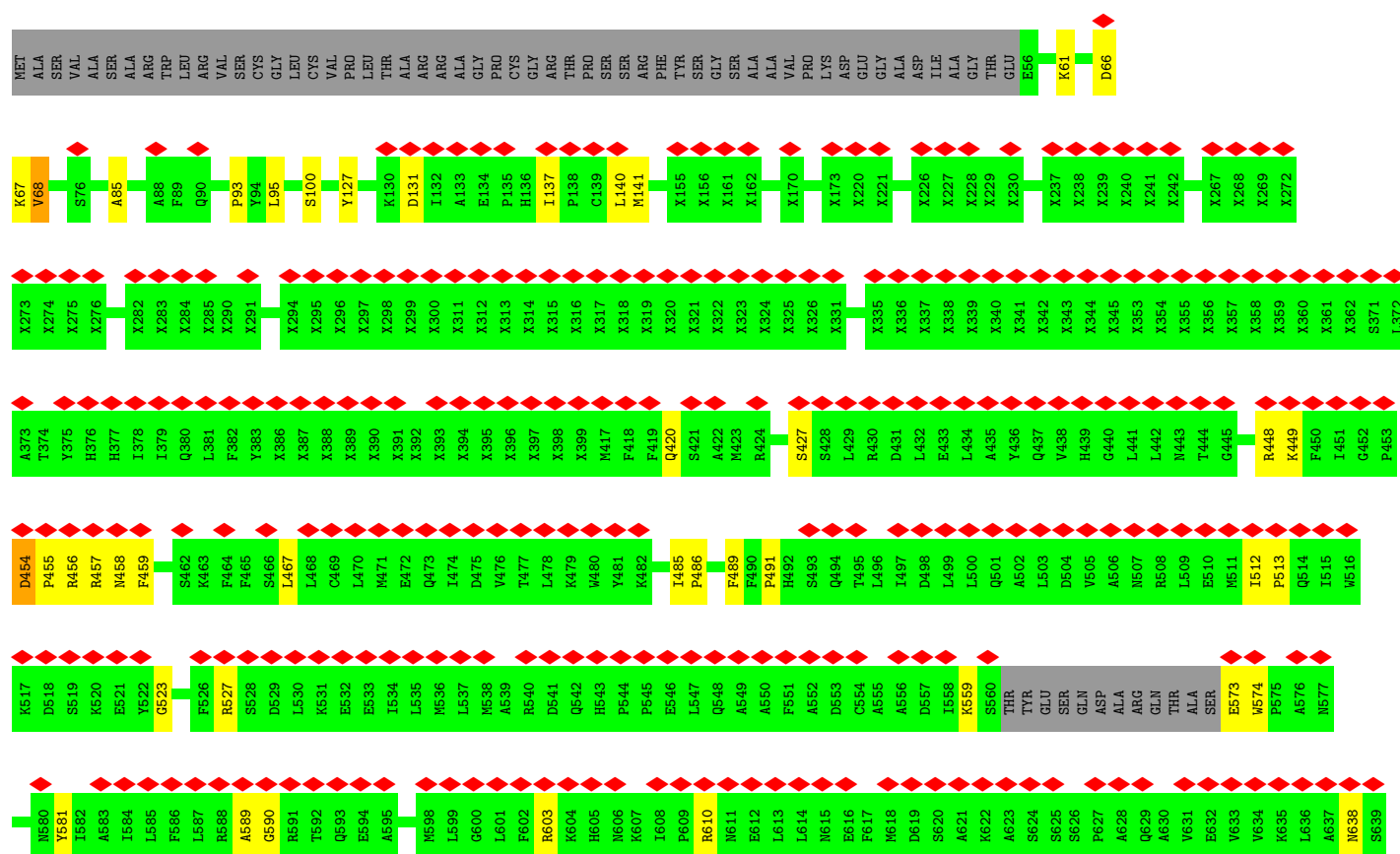
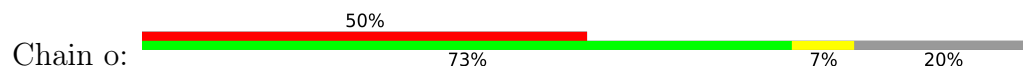


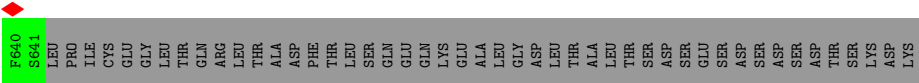


• Molecule 29: Aurora kinase A interacting protein 1

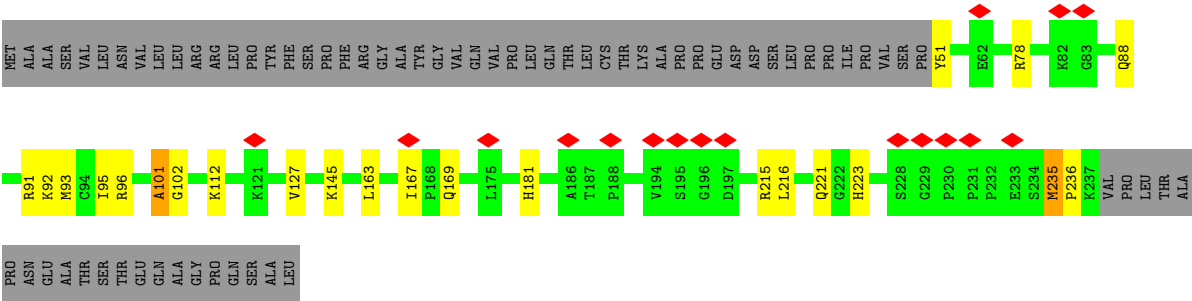


• Molecule 30: Pentatricopeptide repeat domain-containing protein 3, mitochondrial

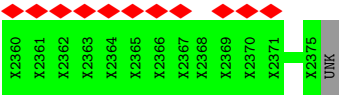
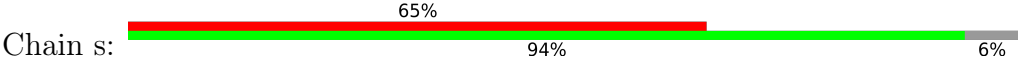




• Molecule 31: 28S ribosomal protein S18b, mitochondrial



• Molecule 32: unknown



• Molecule 32: unknown



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	307556	Depositor
Resolution determination method	Not provided	
CTF correction method	CTFFIND3	Depositor
Microscope	JEOL 3200FS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	9.0	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	59717	Depositor
Image detector	GATAN ULTRASCAN 1000 (2k x 2k)	Depositor
Maximum map value	0.001	Depositor
Minimum map value	-0.000	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.00017	Depositor
Map size ($\text{\AA}$)	438.74997, 438.74997, 438.74997	wwPDB
Map dimensions	375, 375, 375	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.17, 1.17, 1.17	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.04	0/22681	0.07	0/35318
2	B	0.09	0/1766	0.25	0/2392
3	C	0.08	0/1100	0.24	0/1487
4	E	0.09	0/2664	0.26	0/3578
5	F	0.09	0/1009	0.24	0/1362
6	G	0.08	0/1760	0.25	0/2366
7	I	0.08	0/2598	0.24	0/3490
8	J	0.08	0/1071	0.23	0/1447
9	K	0.09	0/1021	0.26	0/1380
10	L	0.08	0/872	0.26	0/1171
11	N	0.09	0/878	0.28	0/1179
12	O	0.06	0/1443	0.20	0/1927
13	P	0.08	0/937	0.26	0/1262
14	Q	0.07	0/874	0.22	0/1183
15	R	0.08	0/805	0.24	0/1082
16	U	0.08	0/748	0.26	0/995
17	a	0.07	0/2403	0.23	0/3246
18	b	0.08	0/1135	0.26	0/1528
19	c	0.08	0/1406	0.24	0/1894
20	d	0.08	0/1489	0.25	0/2008
21	e	0.08	0/2881	0.25	0/3893
22	f	0.07	0/787	0.22	0/1059
23	g	0.08	0/2819	0.24	0/3814
24	h	0.09	0/899	0.20	0/1209
25	i	0.07	0/834	0.24	0/1112
26	j	0.10	0/1841	0.30	0/2493
27	k	0.07	0/2275	0.21	0/3075
28	m	0.10	0/961	0.30	0/1284
29	n	0.10	0/654	0.34	0/862
30	o	0.09	0/2605	0.25	0/3526
31	p	0.08	0/1583	0.25	0/2149
All	All	0.07	0/66799	0.20	0/94771

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	A	20256	0	10258	176	0
2	B	1726	0	1747	18	0
3	C	1072	0	1091	19	0
4	E	2613	0	2638	37	0
5	F	991	0	1034	17	0
6	G	1720	0	1751	16	0
7	I	2541	0	2499	33	0
8	J	1049	0	1088	17	0
9	K	1001	0	1041	15	0
10	L	853	0	904	11	0
11	N	861	0	890	17	0
12	O	1421	0	1526	15	0
13	P	916	0	944	12	0
14	Q	857	0	920	9	0
15	R	788	0	823	20	0
16	U	737	0	759	9	0
17	a	2356	0	2371	19	0
18	b	1108	0	1124	9	0
19	c	1374	0	1395	14	0
20	d	1463	0	1438	15	0
21	e	2822	0	2816	26	0
22	f	775	0	793	6	0
23	g	2754	0	2793	26	0
24	h	871	0	814	8	0
25	i	818	0	845	9	0
26	j	1792	0	1810	44	0
27	k	2227	0	2267	28	0
28	m	945	0	984	13	0
29	n	642	0	718	7	0
30	o	3273	0	2695	22	0
31	p	1531	0	1495	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	s	80	0	18	0	0
32	z	86	0	19	0	0
All	All	64319	0	54308	546	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 5.

All (546) 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)
1:A:29:A:H61	1:A:270:C:H42	1.41	0.67
17:a:175:GLU:OE2	17:a:181:ARG:NH1	2.30	0.64
23:g:347:TYR:HB2	23:g:385:ARG:HB2	1.79	0.64
8:J:76:LEU:HB2	8:J:145:LEU:HB2	1.79	0.64
15:R:116:GLN:HE21	15:R:121:MET:HE3	1.62	0.64
1:A:190:A:H5'	13:P:20:ARG:HB2	1.79	0.64
1:A:299:A:H62	1:A:392:G:H21	1.45	0.64
27:k:68:TRP:HE1	27:k:114:LEU:HB3	1.63	0.63
1:A:416:C:N4	1:A:434:C:N3	2.46	0.63
30:o:67:LYS:HG2	30:o:68:VAL:HG23	1.80	0.62
23:g:265:ASN:HB3	23:g:317:LYS:HE3	1.81	0.62
26:j:83:LYS:HE2	26:j:140:ARG:HH21	1.64	0.62
26:j:144:LYS:O	26:j:145:HIS:ND1	2.32	0.62
8:J:77:SER:HB2	8:J:173:THR:HB	1.82	0.62
26:j:102:PRO:HA	26:j:112:GLY:HA3	1.83	0.61
14:Q:44:ASN:HD21	19:c:66:LEU:HD12	1.66	0.61
12:O:198:ILE:HA	12:O:202:LEU:HD23	1.83	0.61
1:A:528:C:H42	1:A:826:G:H1	1.49	0.60
21:e:323:THR:HG22	21:e:325:GLN:H	1.66	0.60
28:m:31:ASN:HB3	28:m:109:GLN:HG2	1.84	0.60
1:A:628:C:H4'	4:E:210:PRO:HG3	1.83	0.60
26:j:63:ARG:NH1	26:j:135:MET:SD	2.74	0.60
1:A:295:G:O2'	12:O:153:ARG:NH2	2.34	0.60
26:j:43:ARG:HD3	26:j:48:ARG:HD2	1.84	0.60
1:A:309:C:N4	1:A:385:A:N1	2.49	0.60
7:I:173:GLU:HB2	7:I:231:LEU:HB2	1.84	0.59
1:A:395:G:H5''	12:O:197:LYS:HB2	1.84	0.59
21:e:66:PRO:HB3	21:e:99:PRO:HD2	1.85	0.59
13:P:33:ARG:HA	13:P:53:SER:HA	1.84	0.59
3:C:72:HIS:HE1	11:N:120:LEU:HA	1.66	0.59
15:R:86:SER:HB3	15:R:90:GLY:H	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:531:U:H3	1:A:823:G:H1	1.51	0.59
1:A:757:A:N1	11:N:80:ARG:NH2	2.51	0.58
2:B:126:PHE:O	2:B:253:ARG:NH1	2.36	0.58
1:A:597:A:N3	4:E:136:ARG:NH2	2.51	0.58
5:F:40:GLU:HB2	5:F:65:LEU:HB2	1.83	0.58
2:B:96:PHE:HB2	2:B:106:ASP:HB2	1.84	0.58
4:E:412:LYS:HG3	4:E:417:MET:HB2	1.85	0.58
13:P:20:ARG:NH2	13:P:41:CYS:SG	2.76	0.58
20:d:68:ARG:HH11	26:j:196:ILE:HG22	1.68	0.58
4:E:425:LEU:HB3	31:p:88:GLN:HE22	1.69	0.58
26:j:162:ARG:H	26:j:163:PRO:HD2	1.67	0.58
1:A:531:U:OP2	1:A:819:C:N4	2.37	0.58
18:b:6:LEU:H	18:b:15:ARG:HH11	1.52	0.58
26:j:77:GLY:HA3	26:j:97:LEU:HB2	1.85	0.58
11:N:60:ASN:HD22	11:N:63:LEU:H	1.51	0.58
3:C:86:THR:HG21	11:N:106:LEU:HD21	1.86	0.57
30:o:455:PRO:HG2	30:o:458:ASN:HD21	1.69	0.57
6:G:215:ASN:HA	6:G:220:ILE:HG13	1.86	0.57
9:K:153:VAL:HG12	9:K:179:THR:HB	1.87	0.57
1:A:642:A:N6	16:U:78:LYS:O	2.37	0.57
7:I:198:ARG:HH22	7:I:201:ILE:HD11	1.70	0.57
1:A:285:C:OP1	1:A:466:A:N6	2.38	0.57
15:R:116:GLN:HB3	15:R:123:VAL:HG22	1.87	0.57
1:A:331:U:O2'	9:K:112:ARG:NH2	2.37	0.56
4:E:230:ASN:HB3	4:E:238:LYS:HB3	1.86	0.56
24:h:339:ARG:NH1	24:h:343:GLU:OE2	2.38	0.56
26:j:53:ARG:HH21	31:p:223:HIS:HB2	1.69	0.56
1:A:360:A:O2'	16:U:51:ARG:NH1	2.38	0.56
1:A:610:A:H61	1:A:685:U:H3	1.53	0.56
1:A:880:A:O3'	26:j:99:ARG:NH2	2.38	0.56
11:N:91:CYS:SG	11:N:92:VAL:N	2.75	0.56
17:a:207:VAL:O	17:a:213:ASN:ND2	2.37	0.56
23:g:103:PRO:HG2	23:g:344:VAL:HG13	1.87	0.56
30:o:523:GLY:O	30:o:527:ARG:NH1	2.37	0.56
27:k:152:GLU:HB2	27:k:176:ARG:HB2	1.87	0.56
3:C:111:LYS:HB3	8:J:166:GLU:HG2	1.88	0.56
7:I:276:ARG:HA	7:I:373:ASP:HB3	1.88	0.56
21:e:131:ASN:O	21:e:133:VAL:N	2.39	0.56
1:A:168:G:N2	1:A:202:G:O2'	2.38	0.56
2:B:202:ALA:O	18:b:15:ARG:NH2	2.39	0.56
20:d:40:GLY:O	26:j:49:LYS:NZ	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:h:353:PRO:O	27:k:171:ARG:NH1	2.39	0.56
1:A:112:C:N3	1:A:137:C:N4	2.43	0.56
1:A:529:U:OP1	28:m:37:ARG:NH1	2.39	0.55
27:k:239:GLU:OE1	27:k:241:TRP:NE1	2.39	0.55
11:N:96:ARG:NH1	11:N:98:ARG:O	2.39	0.55
1:A:63:C:OP1	13:P:13:ARG:NH1	2.40	0.55
1:A:414:A:N6	1:A:435:U:OP2	2.39	0.55
9:K:89:ALA:HB3	9:K:152:VAL:HA	1.88	0.55
1:A:115:G:OP1	12:O:205:LYS:NZ	2.40	0.55
8:J:147:HIS:HE1	27:k:140:ASP:HA	1.72	0.55
18:b:32:PHE:O	18:b:36:ASN:ND2	2.36	0.55
1:A:465:U:OP2	18:b:50:ARG:NH2	2.38	0.55
24:h:312:PHE:HD2	27:k:216:LEU:HD13	1.72	0.55
1:A:243:C:H41	10:L:78:ARG:HH21	1.55	0.55
1:A:664:C:H1'	6:G:38:GLY:HA2	1.89	0.55
3:C:145:HIS:HA	30:o:140:LEU:HD13	1.89	0.55
15:R:87:PRO:HA	15:R:126:LYS:HZ1	1.71	0.55
30:o:448:ARG:HE	30:o:457:ARG:HB3	1.72	0.55
1:A:138:G:OP2	26:j:4:ARG:NH2	2.40	0.54
4:E:304:LYS:HB3	4:E:335:LYS:HB3	1.90	0.54
4:E:134:GLU:O	25:i:66:ARG:NH1	2.40	0.54
5:F:6:LEU:HB3	5:F:66:VAL:HB	1.88	0.54
6:G:139:ARG:NH2	23:g:363:ASN:O	2.40	0.54
21:e:254:GLY:O	21:e:258:ARG:NH1	2.41	0.54
1:A:744:G:N1	1:A:770:A:OP2	2.41	0.54
15:R:66:CYS:SG	15:R:67:ILE:N	2.80	0.54
1:A:743:C:OP2	1:A:769:A:N6	2.41	0.54
2:B:169:PRO:HG3	4:E:211:ASN:HA	1.89	0.54
4:E:307:LYS:NZ	17:a:102:TYR:OH	2.40	0.54
1:A:166:C:O2	1:A:169:C:N4	2.40	0.54
1:A:756:G:OP2	25:i:32:LYS:NZ	2.41	0.54
16:U:72:ILE:HG12	28:m:108:LEU:HD21	1.88	0.54
17:a:65:LYS:N	17:a:305:ILE:O	2.41	0.54
29:n:189:TRP:NE1	29:n:191:THR:OG1	2.40	0.54
1:A:154:C:OP1	1:A:158:A:N6	2.35	0.54
1:A:486:G:H1	1:A:509:C:H42	1.56	0.54
20:d:134:TRP:NE1	20:d:138:GLU:OE2	2.41	0.54
7:I:285:VAL:HG22	7:I:328:VAL:HG22	1.90	0.54
1:A:617:U:H3	1:A:674:U:H3	1.55	0.53
1:A:834:A:H5''	1:A:835:C:H2'	1.91	0.53
6:G:120:ARG:NH1	23:g:88:MET:SD	2.80	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:I:328:VAL:HG11	7:I:348:MET:HE2	1.90	0.53
10:L:51:PRO:O	10:L:89:ARG:NH2	2.41	0.53
1:A:183:A:OP2	1:A:202:G:N1	2.38	0.53
7:I:382:PRO:HB2	8:J:131:ARG:HB2	1.89	0.53
1:A:382:U:H4'	5:F:72:THR:HG23	1.89	0.53
31:p:95:ILE:O	31:p:145:LYS:NZ	2.41	0.53
1:A:385:A:OP1	12:O:134:LYS:NZ	2.42	0.53
6:G:77:ALA:O	7:I:345:ARG:NH2	2.41	0.53
1:A:952:A:H5'	1:A:955:U:H3	1.72	0.53
9:K:102:VAL:H	9:K:112:ARG:HG2	1.74	0.53
27:k:58:ARG:HH21	30:o:85:ALA:HB3	1.73	0.53
1:A:873:U:H2'	1:A:874:A:H4'	1.91	0.53
17:a:201:ARG:HG2	17:a:233:GLN:HA	1.90	0.53
21:e:293:PRO:HB3	31:p:221:GLN:HE22	1.74	0.53
1:A:642:A:OP1	7:I:220:GLN:NE2	2.42	0.53
6:G:64:TYR:HB2	7:I:366:GLN:HE22	1.74	0.53
26:j:39:GLU:O	26:j:59:ARG:NH2	2.42	0.53
30:o:61:LYS:H	30:o:61:LYS:HD3	1.74	0.53
1:A:115:G:H1	1:A:130:C:H42	1.55	0.52
8:J:133:GLN:HB2	11:N:126:ALA:HB2	1.90	0.52
13:P:59:ASN:ND2	19:c:146:GLN:OE1	2.41	0.52
17:a:138:ASN:HB3	17:a:181:ARG:HD2	1.91	0.52
1:A:267:A:H4'	1:A:269:G:H4'	1.90	0.52
27:k:255:TRP:HB3	27:k:295:LYS:HE3	1.91	0.52
13:P:95:GLY:HA3	26:j:169:LEU:HB3	1.92	0.52
24:h:325:LEU:HD13	24:h:364:ILE:HD11	1.92	0.52
4:E:289:THR:HG22	4:E:331:ASP:HB2	1.90	0.52
4:E:380:LEU:HD12	4:E:381:PRO:HD2	1.90	0.52
31:p:235:MET:H	31:p:236:PRO:HD2	1.74	0.52
1:A:318:G:O2'	5:F:79:MET:SD	2.68	0.52
19:c:42:GLU:OE1	19:c:45:ARG:NH2	2.43	0.52
26:j:86:LEU:O	31:p:215:ARG:NH1	2.43	0.52
1:A:579:C:H42	11:N:85:VAL:HB	1.73	0.52
1:A:196:A:OP1	20:d:64:ARG:NH2	2.43	0.52
1:A:832:A:O2'	1:A:920:C:O2	2.28	0.52
2:B:136:ARG:HH21	2:B:159:TYR:HD1	1.58	0.52
1:A:5:G:H1	1:A:20:U:H3	1.57	0.52
10:L:34:ASN:OD1	14:Q:41:LYS:NZ	2.42	0.51
10:L:74:ASN:ND2	10:L:117:ASP:OD1	2.44	0.51
22:f:142:ARG:NH1	22:f:173:LEU:O	2.43	0.51
9:K:191:PRO:HD2	16:U:45:TYR:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:573:G:O3'	11:N:108:ARG:NH2	2.42	0.51
1:A:809:U:OP2	7:I:277:LYS:NZ	2.43	0.51
7:I:176:GLN:OE1	7:I:245:ARG:NH2	2.43	0.51
19:c:23:PHE:HA	19:c:107:GLY:HA2	1.92	0.51
4:E:243:VAL:HG11	4:E:268:PHE:HE1	1.76	0.51
9:K:90:HIS:HB2	9:K:101:HIS:HB2	1.92	0.51
22:f:105:ILE:HG12	22:f:115:ILE:HG12	1.91	0.51
5:F:3:ARG:NH1	5:F:70:ALA:O	2.44	0.51
27:k:63:SER:HB2	27:k:66:GLN:HB2	1.93	0.51
11:N:29:TYR:HD1	25:i:55:HIS:HB2	1.76	0.51
14:Q:69:LEU:HD12	14:Q:70:PRO:HD2	1.92	0.51
1:A:90:U:OP1	20:d:72:GLN:NE2	2.44	0.51
1:A:194:G:N2	1:A:197:A:OP2	2.44	0.51
1:A:930:A:N6	1:A:942:G:O6	2.43	0.51
12:O:110:LEU:HD23	12:O:129:VAL:HG13	1.93	0.51
15:R:53:ILE:O	18:b:64:TYR:OH	2.27	0.51
18:b:67:GLU:HG2	18:b:100:VAL:HG11	1.93	0.51
19:c:31:THR:HB	19:c:77:ARG:HB2	1.93	0.51
1:A:880:A:H2	26:j:101:ARG:HA	1.75	0.51
7:I:118:GLU:HG3	7:I:120:ARG:H	1.76	0.51
12:O:208:LEU:HD23	29:n:173:LEU:HD22	1.92	0.51
21:e:201:GLU:OE1	21:e:238:GLN:NE2	2.42	0.51
24:h:290:GLU:O	24:h:294:GLN:NE2	2.35	0.51
1:A:227:G:OP1	4:E:196:ASN:ND2	2.44	0.51
1:A:841:C:O2'	29:n:134:ARG:NH2	2.37	0.51
1:A:308:A:H2'	1:A:309:C:H4'	1.93	0.50
4:E:284:ARG:NH1	4:E:327:ILE:O	2.44	0.50
7:I:84:GLY:HA2	7:I:87:HIS:HD2	1.76	0.50
9:K:103:VAL:HA	9:K:109:PRO:HA	1.93	0.50
14:Q:94:PRO:HG3	19:c:77:ARG:HH21	1.76	0.50
30:o:581:TYR:OH	30:o:610:ARG:NH1	2.44	0.50
4:E:136:ARG:HG3	4:E:137:ARG:HG2	1.93	0.50
5:F:28:ALA:O	5:F:32:ARG:NH1	2.44	0.50
26:j:133:GLN:HB2	26:j:139:TRP:HE1	1.76	0.50
30:o:573:GLU:HG2	30:o:574:TRP:HD1	1.76	0.50
1:A:26:U:OP1	1:A:212:U:O2'	2.27	0.50
1:A:319:U:H3	1:A:378:A:H61	1.59	0.50
3:C:83:ALA:HB2	11:N:105:ARG:HB2	1.93	0.50
7:I:174:GLU:HG2	7:I:237:GLU:HB3	1.94	0.50
19:c:76:LEU:HB2	19:c:88:VAL:HB	1.93	0.50
23:g:267:LEU:O	23:g:293:ARG:NH2	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:h:322:HIS:O	24:h:360:LYS:NZ	2.42	0.50
1:A:481:C:N3	10:L:39:ARG:NH2	2.59	0.50
3:C:164:TYR:HB2	27:k:99:MET:HE2	1.93	0.50
1:A:904:A:H1'	29:n:153:LEU:HD22	1.93	0.50
21:e:270:PRO:HA	21:e:348:VAL:HG11	1.92	0.50
23:g:367:HIS:HB3	23:g:370:ALA:HB2	1.94	0.50
1:A:780:U:O2	7:I:389:ARG:NH1	2.39	0.50
6:G:42:GLN:HB2	6:G:74:ILE:HG22	1.93	0.50
28:m:37:ARG:NH1	28:m:38:ARG:O	2.45	0.50
17:a:168:GLU:HA	31:p:181:HIS:HE1	1.75	0.49
19:c:12:THR:HG22	19:c:14:GLN:H	1.77	0.49
1:A:77:C:OP1	1:A:149:C:O2'	2.25	0.49
4:E:242:ARG:HB3	4:E:260:LYS:HG2	1.94	0.49
4:E:284:ARG:HH11	4:E:328:GLY:HA3	1.76	0.49
7:I:149:PHE:HD1	7:I:150:LEU:HG	1.77	0.49
1:A:230:A:OP1	4:E:195:GLY:N	2.40	0.49
2:B:47:ARG:NH1	2:B:263:GLN:O	2.46	0.49
6:G:49:GLU:HB3	6:G:53:LYS:HE2	1.94	0.49
15:R:98:THR:OG1	15:R:105:GLN:OE1	2.26	0.49
18:b:8:THR:HG22	18:b:9:VAL:HG13	1.94	0.49
3:C:60:HIS:HB3	11:N:125:ARG:HD2	1.94	0.49
27:k:216:LEU:O	27:k:220:ASN:ND2	2.45	0.49
1:A:374:A:H4'	1:A:450:A:H1'	1.94	0.49
11:N:34:MET:HE3	11:N:95:SER:HB3	1.95	0.49
1:A:91:A:H61	26:j:213:THR:HB	1.78	0.49
1:A:443:G:OP2	12:O:147:LYS:NZ	2.45	0.49
6:G:36:ARG:HG3	7:I:375:ARG:HA	1.95	0.49
17:a:264:THR:HG22	17:a:265:ARG:H	1.76	0.49
31:p:127:VAL:HG21	31:p:163:LEU:HD21	1.93	0.49
14:Q:36:ASP:OD2	14:Q:39:LEU:N	2.45	0.49
1:A:391:C:O2'	1:A:478:U:O2	2.31	0.49
1:A:485:A:O2'	1:A:514:A:O2'	2.29	0.49
1:A:594:C:H41	1:A:602:G:H5''	1.78	0.49
3:C:133:TYR:OH	30:o:95:LEU:O	2.26	0.49
8:J:79:LEU:HD11	8:J:140:TYR:HB3	1.94	0.49
30:o:603:ARG:NH2	30:o:638:ASN:OD1	2.45	0.49
23:g:259:VAL:HB	23:g:305:ILE:HA	1.95	0.49
1:A:358:A:OP1	1:A:439:C:O2'	2.31	0.48
5:F:79:MET:HE2	5:F:92:ASN:HA	1.94	0.48
20:d:53:PHE:HB3	31:p:216:LEU:HD21	1.94	0.48
5:F:50:LYS:HG3	5:F:57:ARG:HH21	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:N:63:LEU:HB3	11:N:67:LEU:HD12	1.94	0.48
1:A:55:C:O2'	1:A:198:G:N2	2.46	0.48
1:A:630:C:OP1	18:b:5:ARG:NH1	2.45	0.48
3:C:68:TRP:HH2	7:I:115:GLY:HA3	1.78	0.48
5:F:117:LEU:HA	28:m:12:ARG:HE	1.79	0.48
1:A:297:U:H5''	12:O:164:LYS:HD2	1.95	0.48
1:A:580:C:H1'	11:N:86:ARG:HG2	1.94	0.48
6:G:170:VAL:HG12	6:G:237:ALA:HA	1.94	0.48
7:I:91:MET:O	27:k:117:THR:OG1	2.31	0.48
20:d:171:GLU:N	20:d:171:GLU:OE1	2.45	0.48
21:e:117:LEU:HA	21:e:121:ALA:HB2	1.93	0.48
26:j:167:PRO:HG2	26:j:170:LEU:HD12	1.94	0.48
1:A:950:A:H5''	1:A:951:U:H5	1.78	0.48
7:I:125:MET:HE3	27:k:86:PRO:HD2	1.95	0.48
4:E:358:THR:HG22	4:E:360:GLN:H	1.79	0.48
24:h:302:TRP:HE3	24:h:306:ILE:HD13	1.79	0.48
27:k:93:VAL:HG23	27:k:95:ARG:H	1.77	0.48
1:A:61:C:N3	26:j:48:ARG:NH2	2.60	0.48
26:j:71:LEU:HD21	26:j:141:LEU:HD21	1.95	0.48
26:j:80:VAL:HB	26:j:95:TRP:HB3	1.95	0.48
4:E:164:GLU:HA	4:E:167:LYS:HE2	1.96	0.48
26:j:80:VAL:O	26:j:95:TRP:N	2.42	0.48
9:K:189:CYS:SG	9:K:190:ARG:N	2.86	0.48
1:A:111:U:H3	1:A:491:A:H61	1.61	0.48
1:A:383:A:H5''	12:O:99:LYS:HD2	1.96	0.48
4:E:309:PRO:HD3	17:a:99:PRO:HG3	1.94	0.48
5:F:106:GLU:HG3	15:R:63:LEU:HB2	1.96	0.48
9:K:83:PHE:O	9:K:151:ARG:NH1	2.46	0.48
21:e:365:LEU:HB2	21:e:366:PRO:HD3	1.96	0.48
1:A:15:C:OP1	4:E:339:SER:OG	2.32	0.47
1:A:903:G:H2'	1:A:904:A:H8	1.79	0.47
1:A:27:U:H3	1:A:272:A:H61	1.60	0.47
1:A:574:A:N3	1:A:576:A:O2'	2.47	0.47
7:I:70:THR:HG21	7:I:135:GLN:HG3	1.96	0.47
1:A:367:U:O2	15:R:106:ARG:NH2	2.47	0.47
2:B:82:HIS:HD2	22:f:162:THR:HG21	1.80	0.47
27:k:77:PRO:HD2	27:k:79:LYS:HE3	1.96	0.47
1:A:877:C:H5'	21:e:105:ARG:HH12	1.79	0.47
17:a:75:GLN:HE22	17:a:127:MET:HB2	1.79	0.47
17:a:130:VAL:HG12	17:a:241:TYR:HE2	1.79	0.47
21:e:99:PRO:HA	26:j:104:TYR:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:k:68:TRP:HZ2	27:k:114:LEU:HD13	1.79	0.47
1:A:360:A:H2'	9:K:187:ASN:HD22	1.79	0.47
19:c:155:LEU:HD13	19:c:159:LEU:HD12	1.97	0.47
1:A:362:A:H62	15:R:123:VAL:HG12	1.80	0.47
1:A:489:C:N4	1:A:931:U:OP2	2.44	0.47
1:A:820:C:H1'	6:G:241:TRP:HZ2	1.80	0.47
6:G:42:GLN:H	6:G:74:ILE:HA	1.78	0.47
6:G:174:LEU:HD22	6:G:178:ARG:HG2	1.97	0.47
17:a:149:GLY:HA2	31:p:235:MET:HE1	1.95	0.47
23:g:265:ASN:HD21	23:g:309:VAL:HB	1.79	0.47
1:A:630:C:HO2'	2:B:199:ARG:HH22	1.60	0.47
1:A:634:A:H1'	4:E:260:LYS:HD3	1.97	0.47
1:A:656:U:O2'	7:I:118:GLU:OE1	2.33	0.47
15:R:115:ALA:HB1	15:R:120:PHE:HB2	1.96	0.47
20:d:169:THR:HG22	20:d:170:ARG:H	1.80	0.47
1:A:954:A:H3'	1:A:955:U:H5'	1.97	0.47
1:A:742:A:H61	1:A:773:G:H1	1.62	0.47
1:A:754:A:OP2	25:i:29:LYS:NZ	2.48	0.47
14:Q:24:LYS:HE2	14:Q:55:LEU:HA	1.97	0.47
30:o:420:GLN:NE2	30:o:459:PHE:O	2.41	0.47
1:A:414:A:O2'	1:A:942:G:O2'	2.32	0.46
4:E:306:LYS:NZ	4:E:413:ALA:O	2.46	0.46
10:L:76:ALA:HB3	10:L:78:ARG:HH12	1.80	0.46
15:R:85:ILE:HD11	15:R:126:LYS:HD3	1.96	0.46
21:e:202:ARG:HB3	21:e:247:MET:HG3	1.96	0.46
26:j:178:ARG:HH12	26:j:187:GLU:H	1.63	0.46
1:A:631:U:O4	1:A:634:A:N6	2.49	0.46
16:U:1:MET:HA	16:U:2:ALA:HA	1.64	0.46
28:m:116:HIS:CD2	28:m:117:LEU:HG	2.50	0.46
1:A:217:A:H61	1:A:268:A:H5'	1.80	0.46
1:A:283:G:H1	1:A:290:A:H2	1.63	0.46
23:g:210:ASN:HD21	23:g:234:ASN:HD21	1.63	0.46
23:g:323:LEU:HD13	27:k:306:ASP:HB2	1.97	0.46
1:A:625:A:O2'	1:A:649:A:N6	2.48	0.46
3:C:152:ARG:HB3	3:C:154:HIS:HE1	1.81	0.46
4:E:284:ARG:HD3	4:E:327:ILE:HG22	1.96	0.46
9:K:161:ARG:NH2	9:K:180:ASP:OD1	2.47	0.46
13:P:51:LEU:HD13	13:P:73:ILE:HG12	1.98	0.46
20:d:46:PRO:O	26:j:53:ARG:NH2	2.48	0.46
23:g:144:CYS:HB3	23:g:149:TRP:CG	2.51	0.46
5:F:2:PRO:O	5:F:99:THR:OG1	2.34	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:K:67:PRO:HB3	15:R:131:LEU:HD23	1.98	0.46
26:j:144:LYS:C	26:j:146:GLU:H	2.23	0.46
1:A:615:C:H5'	8:J:122:LYS:HE2	1.98	0.46
1:A:712:G:O2'	1:A:803:G:OP1	2.31	0.46
7:I:125:MET:HE1	27:k:85:LEU:HD22	1.96	0.46
26:j:122:GLY:HA3	26:j:155:PRO:HD2	1.97	0.46
1:A:301:G:O2'	1:A:478:U:OP1	2.26	0.46
1:A:368:G:H1	28:m:20:ILE:HG13	1.79	0.46
1:A:544:A:O2'	1:A:712:G:OP2	2.33	0.46
8:J:85:LYS:HZ1	8:J:141:ARG:HE	1.62	0.46
8:J:186:LYS:HB2	8:J:187:PRO:HD3	1.98	0.46
13:P:85:LYS:HB2	13:P:86:PRO:HD3	1.96	0.46
18:b:87:LEU:HD22	22:f:90:LEU:HD23	1.98	0.46
3:C:41:ARG:HE	3:C:59:PRO:HD2	1.80	0.46
3:C:94:LYS:NZ	4:E:94:THR:OG1	2.49	0.46
8:J:75:ARG:HG3	8:J:146:GLU:HG2	1.97	0.46
27:k:196:VAL:HG21	27:k:207:LEU:HD11	1.97	0.46
31:p:92:LYS:HE2	31:p:93:MET:HE3	1.97	0.46
2:B:168:ALA:H	2:B:169:PRO:HD2	1.81	0.46
4:E:301:THR:HG23	4:E:336:VAL:HG23	1.98	0.46
31:p:91:ARG:HH22	31:p:102:GLY:HA3	1.81	0.46
1:A:358:A:H1'	1:A:411:C:H42	1.81	0.46
26:j:105:THR:HG23	26:j:109:LEU:HA	1.98	0.46
5:F:107:GLY:HA3	15:R:63:LEU:HB3	1.97	0.45
12:O:174:TYR:HB3	12:O:175:PRO:HD3	1.98	0.45
21:e:263:MET:HB2	21:e:269:SER:HB2	1.98	0.45
3:C:113:ARG:HH21	8:J:165:PRO:HA	1.82	0.45
7:I:373:ASP:OD1	7:I:375:ARG:NE	2.49	0.45
21:e:96:ARG:NH2	21:e:136:GLY:O	2.49	0.45
22:f:173:LEU:HD23	22:f:173:LEU:H	1.81	0.45
10:L:110:VAL:HG12	10:L:125:VAL:HG22	1.98	0.45
21:e:171:GLU:H	26:j:72:PRO:HD3	1.81	0.45
23:g:108:LEU:HD13	23:g:140:ILE:HG23	1.97	0.45
27:k:245:LYS:HE2	27:k:250:MET:HG2	1.98	0.45
1:A:297:U:H2'	1:A:298:A:H8	1.82	0.45
1:A:685:U:H2'	1:A:686:G:H8	1.82	0.45
13:P:104:ILE:HG12	17:a:146:ILE:HG21	1.99	0.45
17:a:225:ASP:HB3	31:p:167:ILE:HD12	1.97	0.45
1:A:338:U:OP1	16:U:44:TYR:OH	2.33	0.45
11:N:91:CYS:HB3	11:N:96:ARG:H	1.81	0.45
13:P:93:LEU:HD21	13:P:103:VAL:HG11	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:127:ARG:HD2	10:L:132:CYS:HB3	1.98	0.45
26:j:90:ASP:OD2	31:p:215:ARG:NE	2.50	0.45
1:A:274:C:H1'	10:L:56:PRO:HG3	1.99	0.45
1:A:534:A:H61	1:A:540:C:H1'	1.81	0.45
3:C:150:PRO:HB2	3:C:152:ARG:HH12	1.82	0.45
8:J:158:GLU:HG3	24:h:304:PHE:HB3	1.99	0.45
3:C:145:HIS:ND1	30:o:140:LEU:O	2.48	0.45
10:L:109:LEU:HD22	10:L:129:LYS:HD3	1.98	0.45
1:A:557:A:N6	1:A:702:G:O2'	2.50	0.45
2:B:92:GLU:HB2	2:B:93:PRO:HD3	1.97	0.45
2:B:125:ALA:HB1	2:B:250:LYS:HE2	1.98	0.45
16:U:63:ILE:HG12	28:m:4:PRO:HG2	1.99	0.45
23:g:121:VAL:HG21	27:k:324:LEU:HD11	1.99	0.45
26:j:63:ARG:HE	26:j:66:GLN:HG3	1.82	0.45
1:A:58:C:H4'	26:j:50:LEU:HD22	1.98	0.45
1:A:310:C:O3'	15:R:106:ARG:NH1	2.47	0.45
1:A:443:G:O2'	1:A:497:A:N6	2.50	0.45
7:I:100:THR:HG22	7:I:101:GLN:H	1.81	0.45
1:A:486:G:OP1	29:n:135:ARG:NH2	2.50	0.44
17:a:274:PHE:HB3	17:a:280:ILE:HA	1.99	0.44
21:e:47:ASP:O	21:e:78:ASN:ND2	2.43	0.44
1:A:614:C:H5'	3:C:39:ALA:HB2	1.99	0.44
2:B:193:GLU:OE2	28:m:114:LYS:NZ	2.48	0.44
19:c:48:VAL:HG13	19:c:52:ILE:HD12	1.99	0.44
27:k:153:ILE:HD13	27:k:221:TYR:HE1	1.82	0.44
27:k:160:SER:OG	27:k:164:SER:O	2.36	0.44
31:p:51:TYR:HB2	31:p:112:LYS:HE2	1.98	0.44
5:F:15:ARG:HB3	5:F:16:PRO:HD3	2.00	0.44
17:a:186:GLU:O	17:a:190:ARG:NH1	2.49	0.44
27:k:81:SER:HB3	30:o:93:PRO:HD3	1.98	0.44
1:A:560:A:O2'	1:A:584:C:O2	2.34	0.44
1:A:785:G:N2	1:A:812:A:O5'	2.46	0.44
23:g:82:LEU:HD23	23:g:87:VAL:HG22	1.98	0.44
23:g:102:LYS:HB2	23:g:103:PRO:HD3	1.99	0.44
25:i:42:LEU:O	25:i:48:THR:OG1	2.26	0.44
30:o:420:GLN:HB2	30:o:449:LYS:HG3	2.00	0.44
1:A:469:C:OP1	5:F:122:LYS:NZ	2.48	0.44
1:A:566:A:O2'	7:I:395:LYS:O	2.36	0.44
1:A:54:G:H4'	1:A:200:U:H1'	1.99	0.44
1:A:113:A:N1	1:A:132:C:O2'	2.43	0.44
4:E:248:GLY:HA3	4:E:326:LEU:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:78:PRO:HA	7:I:276:ARG:HH22	1.83	0.44
15:R:96:HIS:HB2	28:m:2:ALA:HB1	1.99	0.44
2:B:141:SER:HA	2:B:157:THR:HG21	1.99	0.44
11:N:115:ALA:HB1	11:N:123:ILE:HG21	2.00	0.44
23:g:364:TRP:NE1	23:g:394:CYS:O	2.48	0.44
30:o:454:ASP:HB3	30:o:455:PRO:HD3	2.00	0.44
1:A:267:A:H62	31:p:101:ALA:HA	1.83	0.43
1:A:724:A:O2'	23:g:317:LYS:O	2.33	0.43
2:B:98:SER:HA	2:B:103:ASP:HA	2.00	0.43
29:n:128:ARG:HG2	29:n:130:VAL:H	1.83	0.43
1:A:311:A:OP2	15:R:106:ARG:NH2	2.36	0.43
2:B:188:LEU:HB3	2:B:192:PHE:HA	2.00	0.43
23:g:74:LEU:HD21	23:g:90:VAL:HG21	1.99	0.43
1:A:154:C:N3	1:A:162:G:N1	2.66	0.43
4:E:94:THR:HG22	4:E:96:ASP:H	1.84	0.43
1:A:406:A:H2'	1:A:407:A:C8	2.54	0.43
21:e:328:LEU:H	21:e:329:PRO:HD2	1.83	0.43
1:A:187:C:H4'	19:c:168:ARG:HH12	1.84	0.43
12:O:71:LEU:HD21	12:O:89:LYS:HE3	2.00	0.43
1:A:370:C:N4	1:A:371:G:O6	2.52	0.43
7:I:81:PHE:HZ	7:I:101:GLN:HE22	1.65	0.43
3:C:72:HIS:HA	3:C:112:ARG:HD3	2.01	0.43
26:j:99:ARG:O	26:j:115:TRP:N	2.43	0.43
1:A:885:A:C5	26:j:25:ARG:HG2	2.54	0.43
2:B:134:VAL:HG13	2:B:156:HIS:HD2	1.84	0.43
21:e:120:GLY:O	21:e:122:GLN:N	2.52	0.43
25:i:57:THR:HG22	30:o:127:TYR:HA	2.01	0.43
26:j:50:LEU:HB2	26:j:55:TRP:HE1	1.83	0.43
1:A:554:U:OP1	1:A:564:A:N6	2.52	0.42
7:I:140:TRP:HA	7:I:146:PRO:HA	2.01	0.42
17:a:166:HIS:O	17:a:188:ARG:NH2	2.50	0.42
19:c:91:GLU:OE2	20:d:123:ARG:NH2	2.52	0.42
21:e:43:ARG:HH12	21:e:115:GLN:HE21	1.67	0.42
26:j:171:ARG:HH12	26:j:188:GLU:HG2	1.84	0.42
28:m:33:VAL:HG11	28:m:104:LEU:HB2	2.01	0.42
1:A:522:G:H21	1:A:837:C:H41	1.66	0.42
21:e:202:ARG:HH12	21:e:246:ASN:H	1.66	0.42
1:A:311:A:P	15:R:106:ARG:HH12	2.43	0.42
1:A:536:C:H2'	1:A:821:A:H2	1.85	0.42
1:A:898:C:H2'	1:A:899:A:C8	2.54	0.42
5:F:41:ASN:O	20:d:185:LYS:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:a:124:ARG:HB3	31:p:169:GLN:HE22	1.84	0.42
27:k:98:PRO:HB2	27:k:99:MET:H	1.66	0.42
1:A:52:A:H5''	1:A:201:U:H4'	2.00	0.42
1:A:405:U:H2'	1:A:406:A:C8	2.53	0.42
1:A:683:G:H2'	1:A:684:G:C8	2.55	0.42
10:L:66:PHE:HE2	10:L:82:ARG:HB2	1.85	0.42
22:f:85:LEU:O	22:f:91:THR:OG1	2.32	0.42
23:g:79:PRO:HG3	23:g:193:ALA:HB2	2.00	0.42
1:A:408:G:H2'	1:A:409:A:H8	1.84	0.42
1:A:755:U:H2'	1:A:756:G:C8	2.54	0.42
1:A:785:G:H22	1:A:812:A:P	2.43	0.42
2:B:154:TYR:OH	7:I:146:PRO:O	2.33	0.42
14:Q:32:ARG:O	14:Q:45:LYS:N	2.48	0.42
28:m:98:SER:OG	28:m:99:LEU:N	2.51	0.42
30:o:131:ASP:HB3	30:o:141:MET:HE1	2.02	0.42
15:R:77:ASN:ND2	20:d:187:TYR:O	2.52	0.42
30:o:427:SER:HA	30:o:467:LEU:HD21	2.00	0.42
1:A:427:U:O2	1:A:935:G:O2'	2.30	0.42
5:F:71:PRO:HD2	5:F:74:THR:HB	2.02	0.42
1:A:4:A:O2'	1:A:5:G:OP1	2.35	0.42
1:A:295:G:O6	1:A:396:C:N4	2.52	0.42
1:A:371:G:O3'	12:O:154:TYR:OH	2.37	0.42
1:A:422:U:O2	1:A:428:A:N6	2.53	0.42
1:A:590:C:N4	1:A:591:U:O4	2.53	0.42
8:J:117:ARG:HG2	8:J:135:GLU:HG2	2.02	0.42
19:c:78:PHE:HB2	19:c:86:VAL:HB	2.02	0.42
1:A:302:C:H5	19:c:68:LYS:HD2	1.85	0.42
1:A:342:A:N3	1:A:420:G:O2'	2.40	0.42
1:A:490:U:H2'	1:A:491:A:H8	1.85	0.42
8:J:78:VAL:O	8:J:143:LEU:N	2.45	0.42
21:e:277:ARG:HG2	21:e:286:ALA:HB2	2.02	0.42
23:g:82:LEU:HD12	23:g:83:PRO:HD2	2.01	0.42
1:A:294:U:H2'	1:A:295:G:C8	2.55	0.42
1:A:785:G:O6	7:I:276:ARG:NH2	2.53	0.42
1:A:934:U:H2'	1:A:935:G:C8	2.55	0.42
3:C:128:PRO:HD2	3:C:131:LYS:HD2	2.01	0.42
4:E:312:TYR:HE2	4:E:315:ARG:HB2	1.85	0.42
9:K:86:ILE:HD13	9:K:176:ILE:HG13	2.01	0.42
21:e:141:ASN:HB3	21:e:142:TYR:H	1.70	0.42
26:j:111:HIS:HA	26:j:135:MET:HE1	2.01	0.42
1:A:11:G:H1'	4:E:231:MET:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:589:U:H2'	1:A:590:C:C6	2.55	0.41
1:A:782:G:H5'	7:I:388:ARG:HB3	2.02	0.41
1:A:813:A:OP1	6:G:96:ASN:ND2	2.46	0.41
6:G:122:GLN:HE21	6:G:210:LEU:HD13	1.85	0.41
30:o:485:ILE:HB	30:o:486:PRO:HD3	2.02	0.41
20:d:43:ALA:HB3	26:j:51:PRO:HB3	2.03	0.41
26:j:5:LYS:HE2	26:j:7:ARG:HG3	2.02	0.41
1:A:4:A:H62	1:A:279:G:H5'	1.84	0.41
4:E:141:TRP:CD1	4:E:144:LEU:HD12	2.55	0.41
13:P:18:THR:HG23	13:P:82:HIS:HB2	2.01	0.41
25:i:87:LYS:HE3	25:i:92:VAL:HG23	2.01	0.41
30:o:512:ILE:HB	30:o:513:PRO:HD3	2.03	0.41
21:e:131:ASN:HB3	21:e:134:GLN:HB2	2.02	0.41
30:o:100:SER:HB3	30:o:491:PRO:HD2	2.02	0.41
1:A:170:A:O2'	1:A:202:G:N2	2.52	0.41
12:O:174:TYR:HB2	14:Q:89:GLY:HA3	2.01	0.41
1:A:108:G:H1	1:A:139:C:H42	1.69	0.41
1:A:829:C:H2'	1:A:830:G:C8	2.55	0.41
4:E:92:LYS:HD3	25:i:75:HIS:HB3	2.03	0.41
9:K:149:HIS:HB3	9:K:176:ILE:HD11	2.02	0.41
23:g:386:ASN:HB3	23:g:389:LEU:HB2	2.03	0.41
1:A:716:C:H3'	1:A:717:A:H5'	2.02	0.41
4:E:191:ARG:O	31:p:78:ARG:NH1	2.41	0.41
9:K:177:SER:OG	16:U:12:VAL:O	2.35	0.41
23:g:154:ILE:HD12	23:g:261:VAL:HG22	2.02	0.41
27:k:151:ILE:HG12	27:k:177:VAL:HG22	2.02	0.41
1:A:45:C:H2'	1:A:46:A:C8	2.56	0.41
1:A:220:A:H62	31:p:96:ARG:HD3	1.86	0.41
1:A:220:A:N6	1:A:268:A:OP2	2.49	0.41
1:A:315:A:H2'	1:A:316:G:C8	2.56	0.41
1:A:948:G:C8	29:n:129:ASN:HB3	2.55	0.41
4:E:232:THR:HG22	4:E:234:LYS:H	1.86	0.41
17:a:131:LEU:HD12	17:a:237:ASP:HB3	2.02	0.41
26:j:110:ASP:OD1	26:j:110:ASP:N	2.53	0.41
31:p:91:ARG:HH12	31:p:102:GLY:H	1.69	0.41
1:A:766:A:H5''	23:g:278:LYS:HE3	2.02	0.41
21:e:43:ARG:NH1	21:e:77:ASP:OD1	2.54	0.41
27:k:196:VAL:HG22	27:k:231:LEU:HD13	2.03	0.41
1:A:154:C:H4'	1:A:167:A:H61	1.85	0.40
2:B:232:PRO:HB2	2:B:233:PRO:HD3	2.03	0.40
3:C:158:VAL:HG12	3:C:160:SER:H	1.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:11:LYS:HB3	5:F:13:MET:HE3	2.02	0.40
13:P:53:SER:H	13:P:67:ALA:HB3	1.86	0.40
21:e:95:PHE:O	21:e:98:SER:OG	2.37	0.40
25:i:14:LEU:HD13	25:i:17:ARG:HH21	1.85	0.40
1:A:171:G:OP1	1:A:180:A:O2'	2.34	0.40
8:J:76:LEU:HD12	8:J:148:LEU:HD22	2.02	0.40
15:R:88:PHE:HB3	16:U:10:ARG:HA	2.03	0.40
21:e:170:GLN:HB3	26:j:72:PRO:HB3	2.03	0.40
23:g:198:LEU:HB3	23:g:222:ALA:HB2	2.03	0.40
1:A:358:A:O2'	1:A:438:G:N1	2.51	0.40
26:j:63:ARG:HB3	26:j:137:HIS:HA	2.04	0.40
27:k:113:PHE:HD2	27:k:116:LEU:HD12	1.86	0.40
4:E:206:PRO:HA	4:E:272:LYS:HZ2	1.86	0.40
4:E:305:MET:HE1	4:E:356:GLN:HE21	1.86	0.40
7:I:306:VAL:HG12	7:I:308:GLN:H	1.87	0.40
8:J:73:TYR:HE2	8:J:150:GLY:HA2	1.86	0.40
20:d:169:THR:H	20:d:172:ASN:HB2	1.87	0.40
1:A:222:G:H2'	1:A:223:G:C8	2.56	0.40
1:A:824:A:H2'	1:A:825:A:C8	2.57	0.40
12:O:172:THR:HB	14:Q:101:ALA:HB1	2.04	0.40
20:d:68:ARG:NH1	26:j:195:ARG:O	2.55	0.40
23:g:167:LEU:HG	23:g:179:GLN:HE22	1.87	0.40
28:m:81:GLU:HG2	28:m:85:LYS:HE3	2.04	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
2	B	215/293 (73%)	197 (92%)	17 (8%)	1 (0%)	24 63
3	C	130/167 (78%)	108 (83%)	19 (15%)	3 (2%)	5 28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	E	326/430 (76%)	280 (86%)	43 (13%)	3 (1%)	14	51
5	F	122/124 (98%)	106 (87%)	14 (12%)	2 (2%)	7	38
6	G	206/242 (85%)	188 (91%)	17 (8%)	1 (0%)	24	63
7	I	309/396 (78%)	277 (90%)	31 (10%)	1 (0%)	36	72
8	J	126/201 (63%)	105 (83%)	19 (15%)	2 (2%)	7	38
9	K	134/197 (68%)	119 (89%)	14 (10%)	1 (1%)	18	56
10	L	107/139 (77%)	86 (80%)	18 (17%)	3 (3%)	4	24
11	N	99/128 (77%)	89 (90%)	9 (9%)	1 (1%)	12	48
12	O	171/256 (67%)	158 (92%)	12 (7%)	1 (1%)	21	59
13	P	114/135 (84%)	101 (89%)	11 (10%)	2 (2%)	6	34
14	Q	107/130 (82%)	92 (86%)	14 (13%)	1 (1%)	14	51
15	R	95/143 (66%)	85 (90%)	9 (10%)	1 (1%)	11	46
16	U	84/87 (97%)	80 (95%)	4 (5%)	0	100	100
17	a	287/359 (80%)	260 (91%)	27 (9%)	0	100	100
18	b	133/190 (70%)	120 (90%)	10 (8%)	3 (2%)	5	28
19	c	166/173 (96%)	148 (89%)	16 (10%)	2 (1%)	10	44
20	d	174/205 (85%)	166 (95%)	8 (5%)	0	100	100
21	e	340/415 (82%)	287 (84%)	46 (14%)	7 (2%)	5	30
22	f	96/189 (51%)	93 (97%)	3 (3%)	0	100	100
23	g	334/397 (84%)	302 (90%)	29 (9%)	3 (1%)	14	51
24	h	101/386 (26%)	90 (89%)	9 (9%)	2 (2%)	6	31
25	i	96/106 (91%)	89 (93%)	6 (6%)	1 (1%)	12	48
26	j	211/218 (97%)	173 (82%)	33 (16%)	5 (2%)	4	27
27	k	273/325 (84%)	243 (89%)	26 (10%)	4 (2%)	8	40
28	m	116/118 (98%)	94 (81%)	22 (19%)	0	100	100
29	n	70/199 (35%)	66 (94%)	2 (3%)	2 (3%)	3	23
30	o	306/575 (53%)	273 (89%)	24 (8%)	9 (3%)	3	23
31	p	185/258 (72%)	154 (83%)	29 (16%)	2 (1%)	11	46
All	All	5233/7181 (73%)	4629 (88%)	541 (10%)	63 (1%)	13	44

All (63) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	N	97	PRO
5	F	71	PRO
5	F	110	PRO
6	G	102	GLY
10	L	56	PRO
15	R	119	GLY
23	g	193	ALA
27	k	77	PRO
27	k	98	PRO
29	n	181	GLY
30	o	489	PHE
30	o	559	LYS
31	p	101	ALA
3	C	105	ALA
10	L	70	PRO
13	P	27	THR
18	b	40	PRO
18	b	110	GLY
21	e	121	ALA
21	e	135	TYR
21	e	238	GLN
21	e	276	CYS
21	e	328	LEU
24	h	286	GLN
25	i	96	LYS
26	j	143	PRO
30	o	456	ARG
30	o	590	GLY
3	C	106	ASP
10	L	76	ALA
21	e	132	LYS
26	j	134	VAL
2	B	92	GLU
3	C	126	GLN
4	E	423	SER
8	J	105	SER
19	c	9	ILE
21	e	172	ALA
24	h	331	GLY
26	j	162	ARG
30	o	66	ASP
30	o	68	VAL
30	o	137	ILE

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Mol	Chain	Res	Type
30	o	454	ASP
31	p	235	MET
4	E	154	ILE
8	J	126	ILE
9	K	119	GLY
18	b	129	GLY
26	j	138	ASP
29	n	191	THR
30	o	589	ALA
13	P	48	VAL
23	g	132	GLY
23	g	337	ASP
4	E	236	GLY
7	I	210	VAL
12	O	80	GLY
27	k	93	VAL
14	Q	85	VAL
19	c	145	GLY
26	j	182	GLY
27	k	57	PRO

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	
2	B	186/230 (81%)	186 (100%)	0	100	100
3	C	113/142 (80%)	113 (100%)	0	100	100
4	E	273/346 (79%)	272 (100%)	1 (0%)	84	84
5	F	109/109 (100%)	109 (100%)	0	100	100
6	G	183/208 (88%)	183 (100%)	0	100	100
7	I	267/333 (80%)	266 (100%)	1 (0%)	84	84
8	J	118/182 (65%)	117 (99%)	1 (1%)	73	80
9	K	102/151 (68%)	102 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	L	94/118 (80%)	94 (100%)	0	100	100
11	N	91/113 (80%)	91 (100%)	0	100	100
12	O	159/226 (70%)	159 (100%)	0	100	100
13	P	95/113 (84%)	95 (100%)	0	100	100
14	Q	95/115 (83%)	95 (100%)	0	100	100
15	R	89/126 (71%)	89 (100%)	0	100	100
16	U	77/78 (99%)	77 (100%)	0	100	100
17	a	255/307 (83%)	254 (100%)	1 (0%)	84	84
18	b	115/163 (71%)	115 (100%)	0	100	100
19	c	152/155 (98%)	152 (100%)	0	100	100
20	d	147/168 (88%)	147 (100%)	0	100	100
21	e	307/362 (85%)	307 (100%)	0	100	100
22	f	85/160 (53%)	85 (100%)	0	100	100
23	g	301/352 (86%)	301 (100%)	0	100	100
24	h	94/341 (28%)	94 (100%)	0	100	100
25	i	88/94 (94%)	88 (100%)	0	100	100
26	j	190/193 (98%)	190 (100%)	0	100	100
27	k	252/292 (86%)	250 (99%)	2 (1%)	73	80
28	m	102/102 (100%)	102 (100%)	0	100	100
29	n	66/173 (38%)	66 (100%)	0	100	100
30	o	277/369 (75%)	277 (100%)	0	100	100
31	p	166/226 (74%)	166 (100%)	0	100	100
All	All	4648/6047 (77%)	4642 (100%)	6 (0%)	87	89

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	E	375	GLU
7	I	256	LEU
8	J	175	THR
17	a	264	THR
27	k	97	VAL
27	k	204	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (110) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	63	ASN
2	B	119	ASN
2	B	123	HIS
2	B	139	GLN
2	B	142	HIS
2	B	167	ASN
2	B	186	HIS
2	B	243	GLN
2	B	255	GLN
3	C	57	HIS
3	C	72	HIS
3	C	81	HIS
3	C	107	GLN
3	C	154	HIS
4	E	130	GLN
4	E	155	GLN
4	E	356	GLN
5	F	58	HIS
5	F	100	GLN
6	G	122	GLN
6	G	224	HIS
6	G	227	HIS
7	I	87	HIS
7	I	101	GLN
7	I	127	HIS
7	I	163	HIS
7	I	178	GLN
7	I	220	GLN
7	I	255	HIS
7	I	296	ASN
7	I	366	GLN
7	I	384	GLN
8	J	147	HIS
8	J	163	ASN
9	K	99	GLN
9	K	101	HIS
9	K	132	GLN
9	K	149	HIS
10	L	106	HIS
11	N	60	ASN
11	N	68	GLN

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Mol	Chain	Res	Type
11	N	124	GLN
12	O	199	HIS
12	O	217	GLN
13	P	28	ASN
14	Q	44	ASN
14	Q	57	GLN
14	Q	76	HIS
14	Q	90	GLN
15	R	77	ASN
15	R	79	GLN
15	R	83	GLN
15	R	116	GLN
16	U	15	GLN
17	a	75	GLN
17	a	95	GLN
17	a	109	GLN
17	a	138	ASN
17	a	215	GLN
17	a	276	ASN
17	a	307	HIS
18	b	89	ASN
19	c	56	GLN
20	d	83	HIS
20	d	109	ASN
20	d	113	ASN
20	d	126	GLN
20	d	155	GLN
21	e	115	GLN
21	e	150	HIS
21	e	339	HIS
21	e	384	HIS
22	f	92	GLN
22	f	122	HIS
23	g	66	HIS
23	g	109	HIS
23	g	147	GLN
23	g	179	GLN
23	g	189	ASN
23	g	204	GLN
23	g	234	ASN
23	g	265	ASN
23	g	298	ASN

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Mol	Chain	Res	Type
23	g	346	ASN
23	g	366	GLN
24	h	286	GLN
24	h	287	ASN
25	i	56	ASN
26	j	24	GLN
26	j	45	HIS
26	j	89	HIS
26	j	179	GLN
27	k	167	ASN
27	k	220	ASN
27	k	263	ASN
27	k	270	GLN
27	k	307	ASN
28	m	24	ASN
28	m	31	ASN
29	n	140	HIS
29	n	178	GLN
30	o	458	ASN
31	p	68	ASN
31	p	88	GLN
31	p	146	GLN
31	p	169	GLN
31	p	181	HIS
31	p	207	GLN
31	p	221	GLN
31	p	223	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	952/955 (99%)	170 (17%)	3 (0%)

All (170) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	5	G
1	A	10	G
1	A	16	A
1	A	24	U
1	A	33	U

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Mol	Chain	Res	Type
1	A	41	C
1	A	44	A
1	A	53	A
1	A	57	U
1	A	58	C
1	A	60	A
1	A	64	C
1	A	74	A
1	A	91	A
1	A	103	A
1	A	110	A
1	A	112	C
1	A	114	A
1	A	117	A
1	A	119	A
1	A	124	C
1	A	125	U
1	A	129	G
1	A	138	G
1	A	143	G
1	A	147	A
1	A	158	A
1	A	159	C
1	A	165	A
1	A	166	C
1	A	170	A
1	A	179	A
1	A	181	U
1	A	186	C
1	A	211	A
1	A	212	U
1	A	218	U
1	A	219	U
1	A	226	G
1	A	233	C
1	A	239	C
1	A	242	G
1	A	248	G
1	A	253	C
1	A	268	A
1	A	279	G
1	A	282	C

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Mol	Chain	Res	Type
1	A	288	A
1	A	302	C
1	A	304	C
1	A	305	C
1	A	306	A
1	A	310	C
1	A	311	A
1	A	312	A
1	A	313	A
1	A	333	A
1	A	341	A
1	A	355	A
1	A	364	A
1	A	370	C
1	A	375	G
1	A	386	A
1	A	389	G
1	A	393	A
1	A	394	C
1	A	427	U
1	A	428	A
1	A	444	C
1	A	449	A
1	A	450	A
1	A	452	A
1	A	465	U
1	A	466	A
1	A	467	A
1	A	472	A
1	A	482	C
1	A	489	C
1	A	497	A
1	A	498	A
1	A	500	A
1	A	513	A
1	A	533	U
1	A	535	U
1	A	536	C
1	A	537	C
1	A	557	A
1	A	561	U
1	A	569	C

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Mol	Chain	Res	Type
1	A	571	C
1	A	574	A
1	A	578	A
1	A	588	U
1	A	592	U
1	A	595	U
1	A	599	A
1	A	604	C
1	A	610	A
1	A	618	C
1	A	620	U
1	A	632	A
1	A	634	A
1	A	635	A
1	A	636	A
1	A	639	A
1	A	640	A
1	A	641	A
1	A	642	A
1	A	644	A
1	A	645	A
1	A	649	A
1	A	660	G
1	A	661	A
1	A	676	A
1	A	677	G
1	A	681	A
1	A	686	G
1	A	693	A
1	A	714	U
1	A	725	C
1	A	726	A
1	A	727	C
1	A	728	C
1	A	729	A
1	A	730	A
1	A	741	C
1	A	747	A
1	A	757	A
1	A	760	C
1	A	769	A
1	A	785	G

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Mol	Chain	Res	Type
1	A	814	U
1	A	817	G
1	A	818	G
1	A	821	A
1	A	832	A
1	A	833	C
1	A	835	C
1	A	848	C
1	A	855	A
1	A	856	A
1	A	860	G
1	A	868	G
1	A	869	C
1	A	870	A
1	A	874	A
1	A	878	C
1	A	881	U
1	A	886	A
1	A	887	C
1	A	889	C
1	A	892	U
1	A	895	C
1	A	896	U
1	A	904	A
1	A	910	C
1	A	911	A
1	A	913	G
1	A	922	A
1	A	923	G
1	A	926	A
1	A	927	A
1	A	928	G
1	A	936	G
1	A	939	A
1	A	948	G
1	A	949	G
1	A	951	U
1	A	952	A
1	A	954	A

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	4	A
1	A	15	C
1	A	363	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
30	o	13
21	e	1
23	g	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	o	383:TYR	C	386:UNK	N	27.66
1	o	399:UNK	C	417:MET	N	21.54
1	o	143:GLU	C	145:UNK	N	20.88
1	e	291:THR	C	292:ALA	N	20.27
1	g	69:ILE	C	70:SER	N	20.27
1	o	173:UNK	C	220:UNK	N	14.26
1	o	285:UNK	C	290:UNK	N	13.31
1	o	300:UNK	C	311:UNK	N	13.28

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	o	362:UNK	C	371:SER	N	12.35
1	o	326:UNK	C	331:UNK	N	11.92
1	o	232:UNK	C	237:UNK	N	10.26
1	o	345:UNK	C	353:UNK	N	10.14
1	o	250:UNK	C	255:UNK	N	8.69
1	o	269:UNK	C	272:UNK	N	5.75
1	o	156:UNK	C	161:UNK	N	5.49

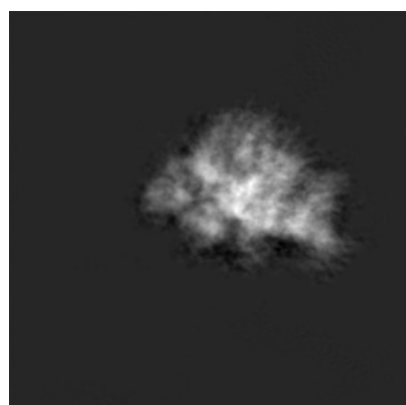
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5941. These allow visual inspection of the internal detail of the map and identification of artifacts.

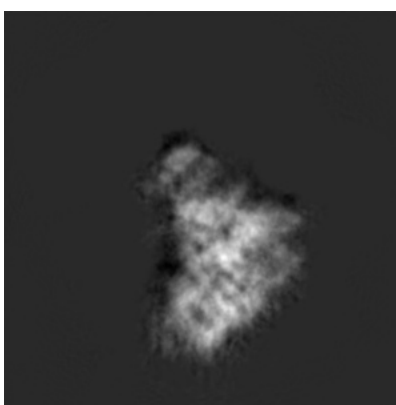
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

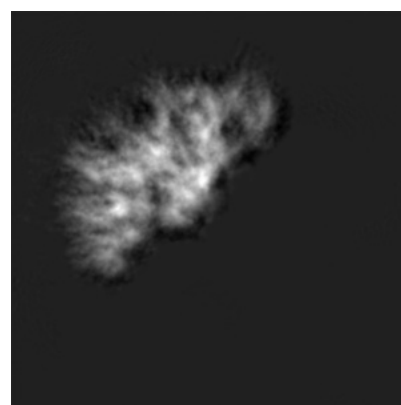
6.1.1 Primary map



X



Y

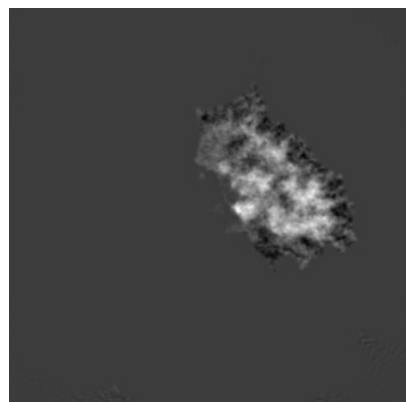


Z

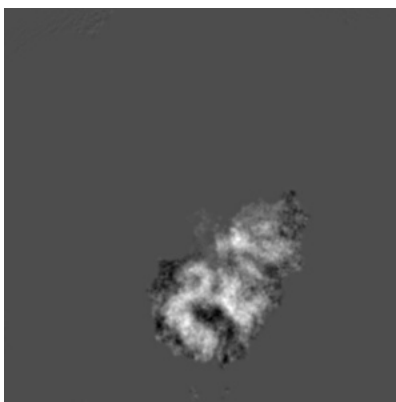
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

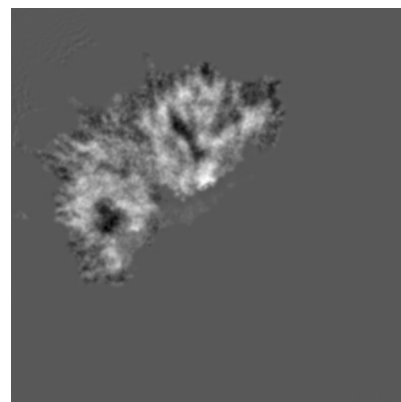
6.2.1 Primary map



X Index: 187



Y Index: 187

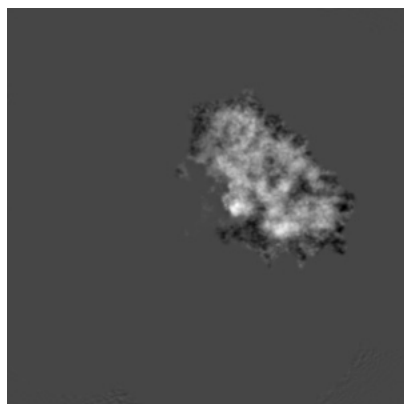


Z Index: 187

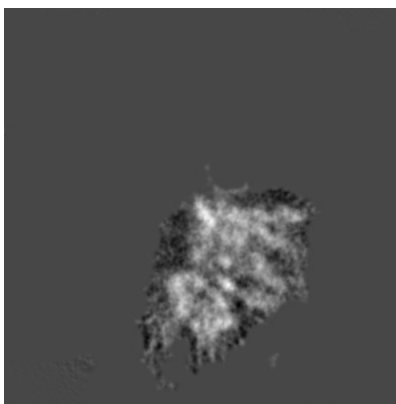
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

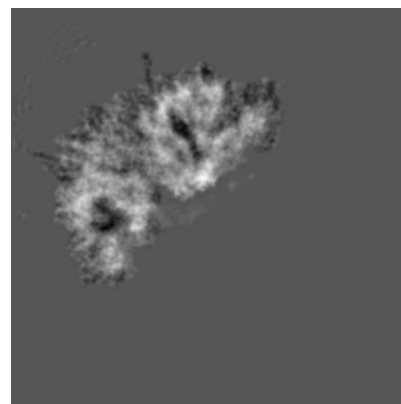
6.3.1 Primary map



X Index: 180



Y Index: 217

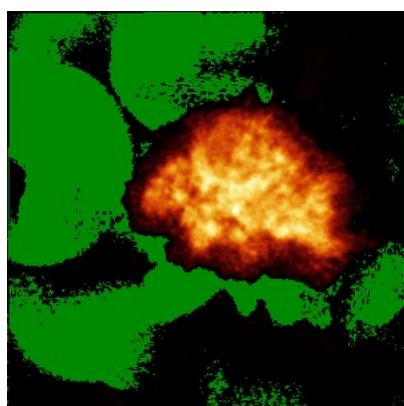


Z Index: 189

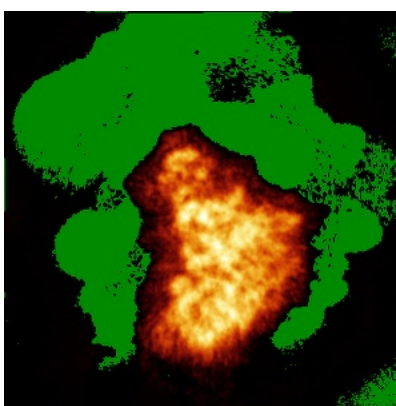
The images above show the largest variance slices of the map in three orthogonal directions.

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

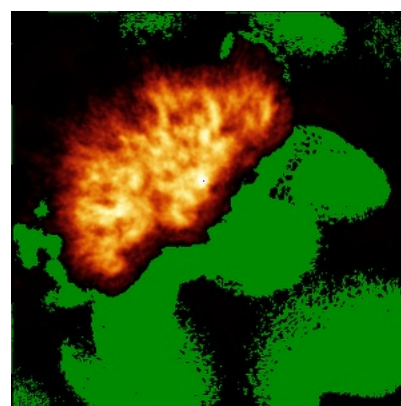
6.4.1 Primary map



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

This section was not generated.

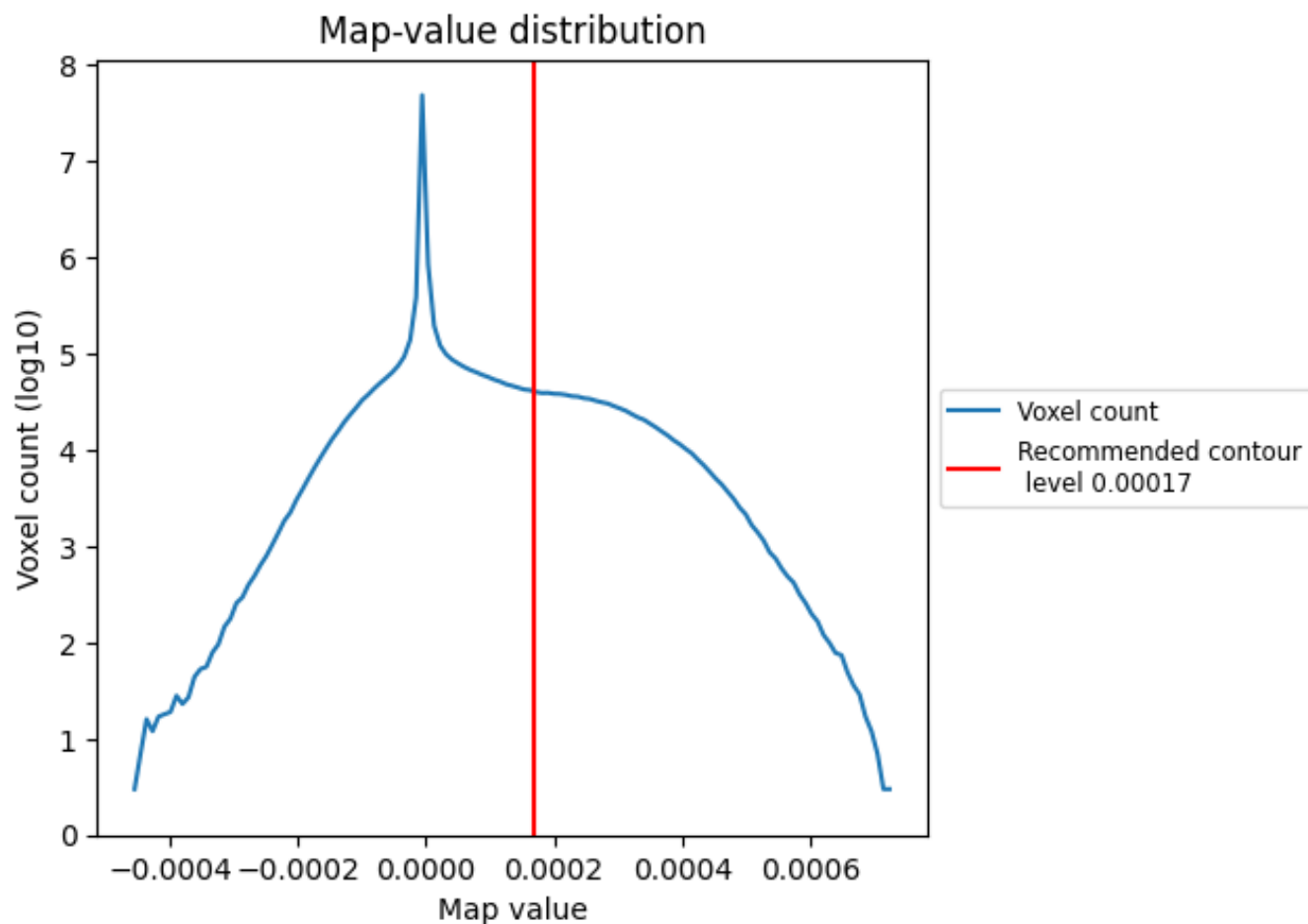
6.6 Mask visualisation

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

7 Map analysis [i](#)

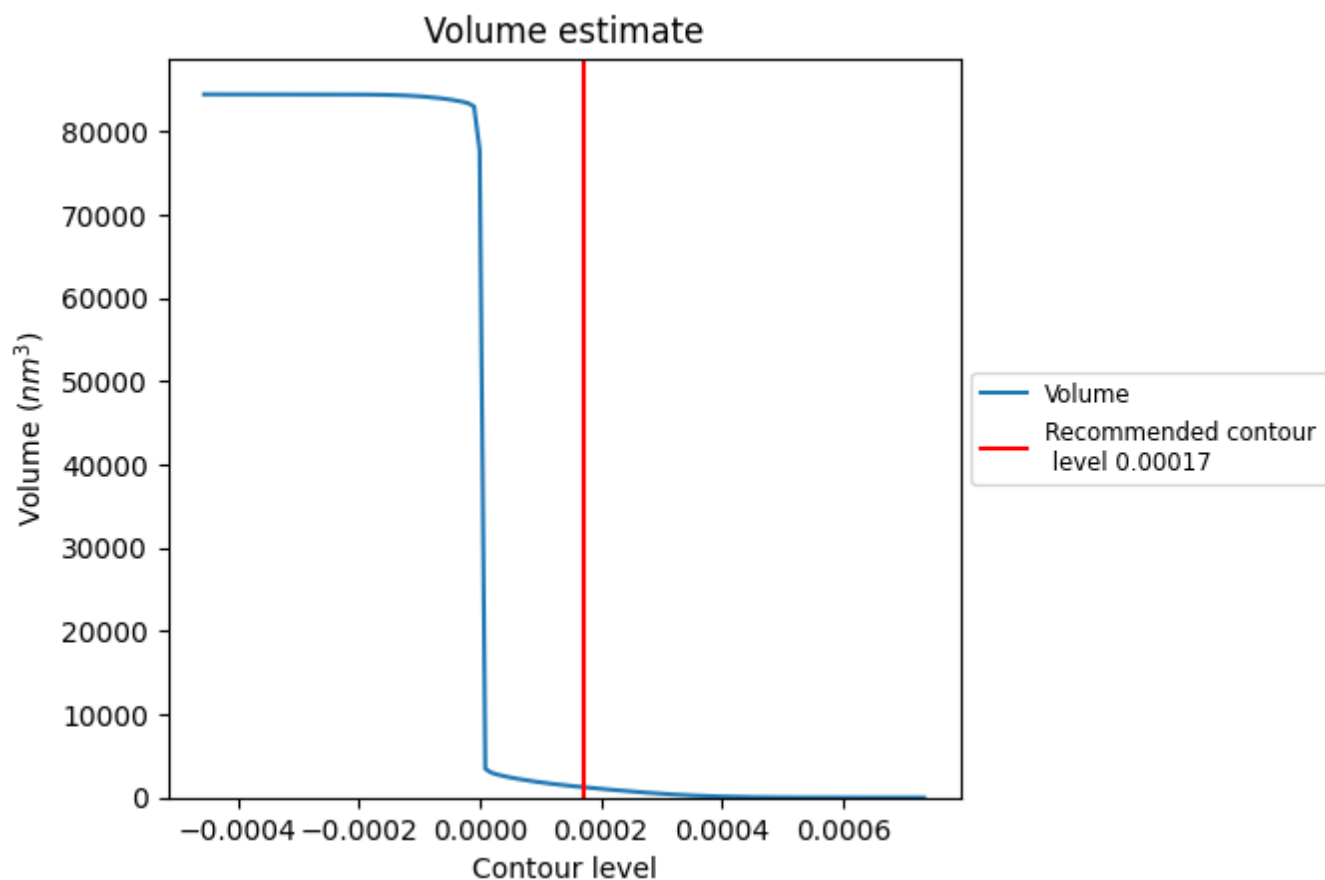
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

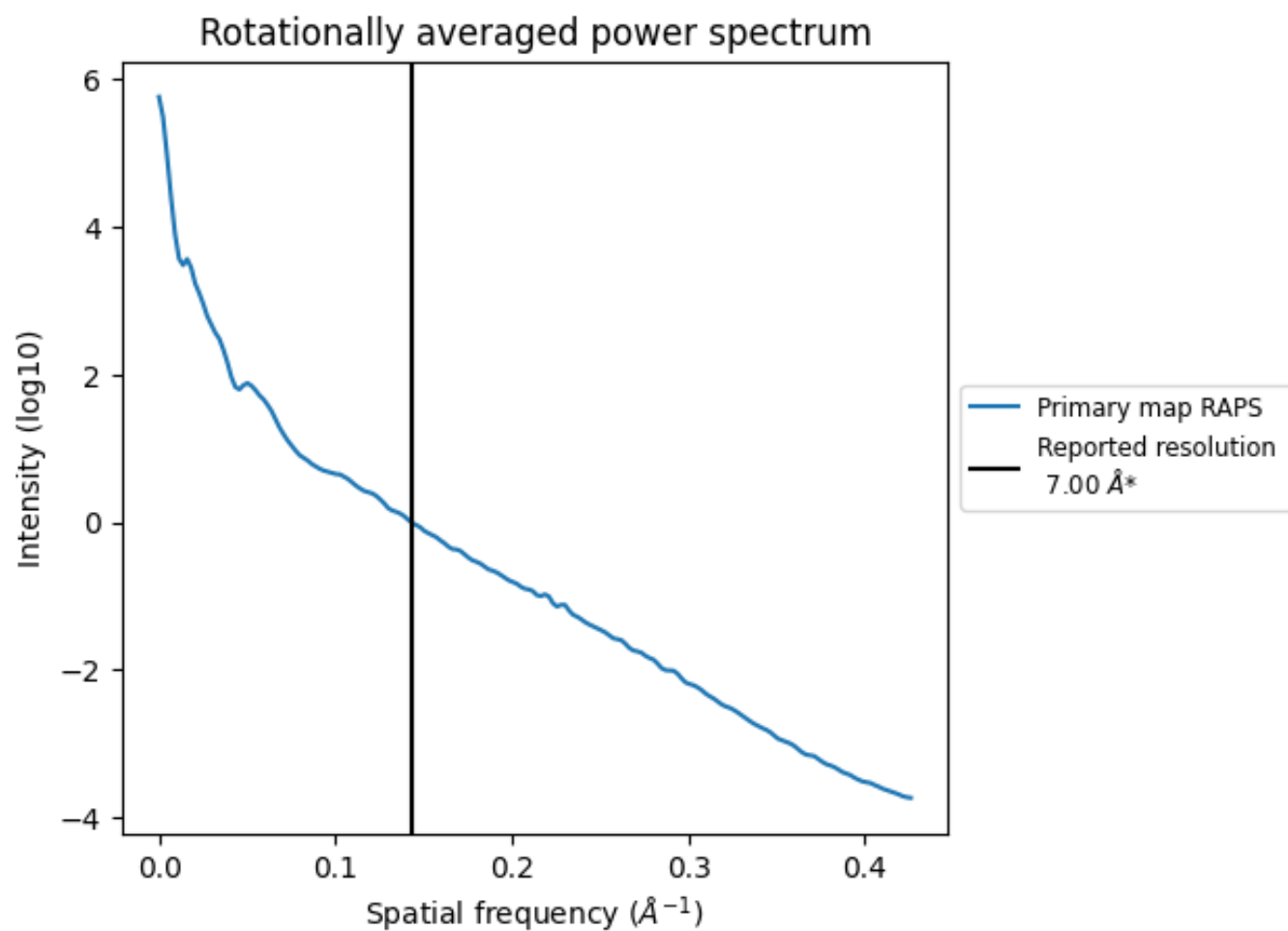
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1255 nm³; this corresponds to an approximate mass of 1134 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 0.143 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

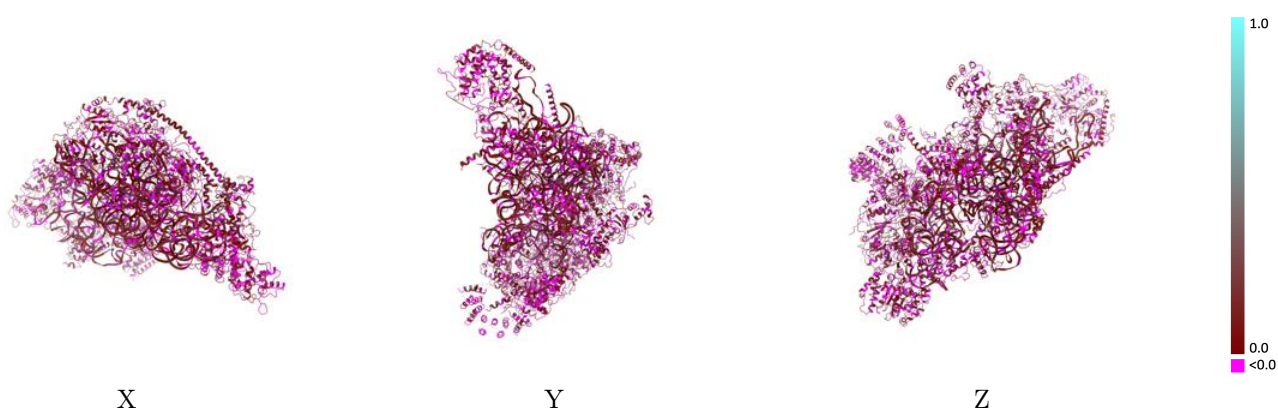
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5941 and PDB model 3JD5. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)

This section was not generated.

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

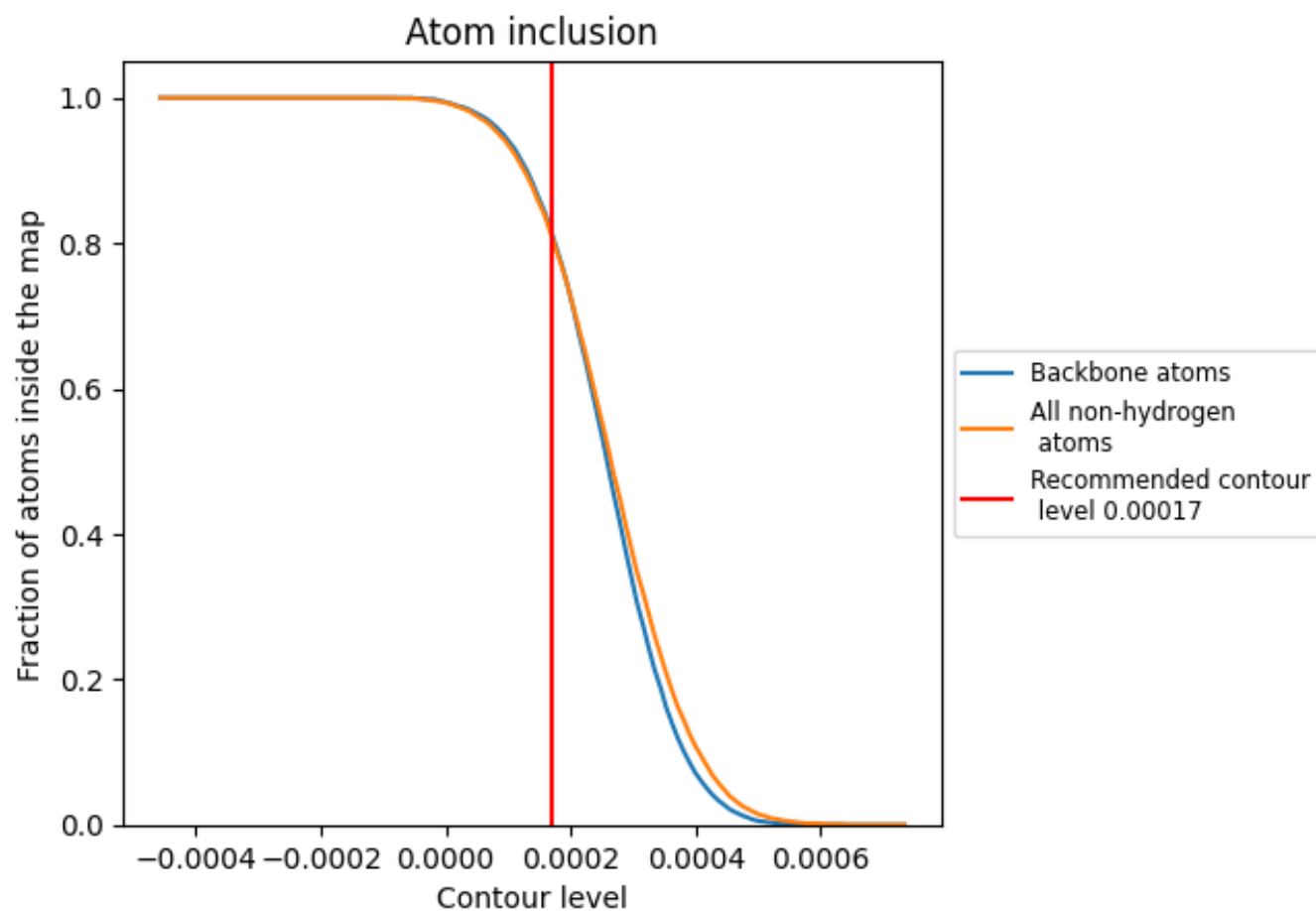


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 81% 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 (0.00017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8090	 0.0610
A	 0.9200	 0.0840
B	 0.8050	 0.0380
C	 0.7100	 0.0260
E	 0.7690	 0.0560
F	 0.5770	 0.0460
G	 0.7700	 0.0350
I	 0.8410	 0.0720
J	 0.8660	 0.0430
K	 0.8660	 0.0610
L	 0.7190	 0.0480
N	 0.9450	 0.0530
O	 0.7680	 0.0560
P	 0.8020	 0.0220
Q	 0.7590	 0.0430
R	 0.8100	 0.0690
U	 0.8320	 0.0960
a	 0.8000	 0.0620
b	 0.7120	 0.0460
c	 0.6950	 0.0530
d	 0.8530	 0.0880
e	 0.7710	 0.0360
f	 0.7920	 0.0330
g	 0.8740	 0.0490
h	 0.8870	 0.0910
i	 0.8960	 0.0640
j	 0.7220	 0.0540
k	 0.8170	 0.0410
m	 0.5200	 0.0330
n	 0.8010	 0.0430
o	 0.3520	 0.0210
p	 0.8460	 0.0590
s	 0.3000	 0.0650
z	 0.9540	 0.0690

