



wwPDB EM Validation Summary Report ⓘ

Aug 13, 2025 – 04:46 pm BST

PDB ID : 9I5X / pdb_00009i5x
EMDB ID : EMD-52641
Title : Porphyromonas gingivalis 70S ribosome (W83 Strain)
Authors : Hiregange, D.G.; Bashan, A.; Yonath, A.
Deposited on : 2025-01-28
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev126
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

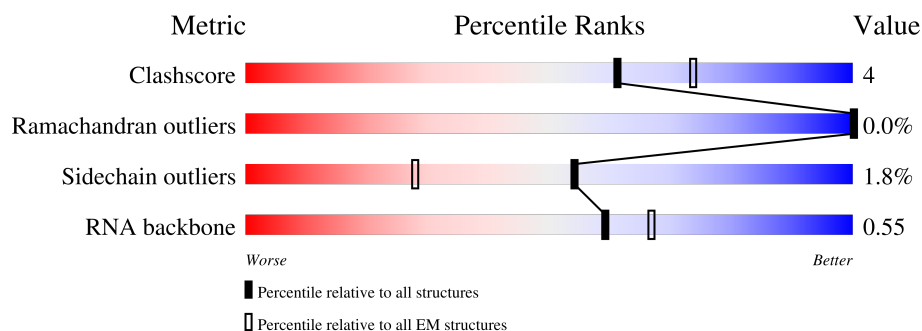
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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.









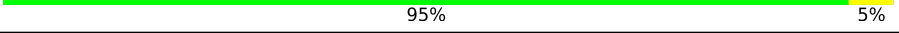



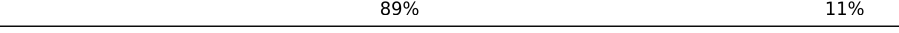
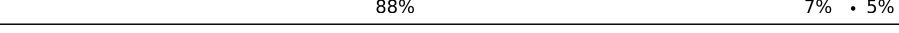
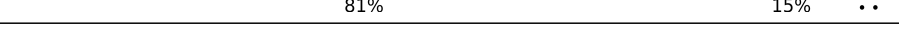


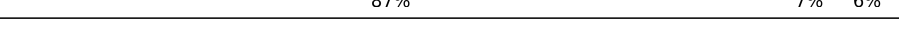
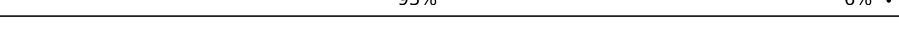








Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	p	89	
2	0	79	
3	1	64	
4	2	58	
5	4	61	
6	5	62	
7	6	50	




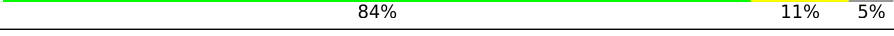
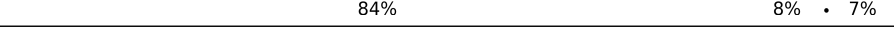

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	7	65	
9	8	38	
10	A	2889	
11	B	109	
12	D	274	
13	E	205	
14	F	209	
15	K	101	
16	L	128	
17	M	151	
18	N	121	
19	O	148	
20	P	144	
21	Q	160	
22	R	114	
23	S	121	
24	T	115	
25	U	105	
26	V	134	
27	W	97	
28	X	106	
29	Z	85	
30	a	1534	
31	b	117	
32	c	192	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
33	d	84	
34	e	84	
35	f	89	
36	g	89	
37	h	179	
38	i	126	
39	j	134	
40	k	246	
41	l	201	
42	m	158	
43	n	172	
44	Y	192	
45	o	131	
46	10	30	
47	J	128	
48	I	90	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 116574 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 Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	p	71	Total	C	N	O	S	0	0
			510	325	95	88	2		

- Molecule 2 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	0	77	Total	C	N	O	S	0	0
			608	390	118	97	3		

- Molecule 3 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1	63	Total	C	N	O	S	0	0
			450	281	87	79	3		

- Molecule 4 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	2	56	Total	C	N	O	S	0	0
			437	276	89	70	2		

- Molecule 5 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	56	Total	C	N	O	S	0	0
			427	265	89	69	4		

- Molecule 6 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	47	Total	C	N	O	S	0	0
			342	213	62	66	1		

- Molecule 7 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	48	Total	C	N	O	S	0	0
			391	237	89	63	2		

- Molecule 8 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	64	Total	C	N	O	S	0	0
			456	289	91	75	1		

- Molecule 9 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	35	Total	C	N	O	S	0	0
			262	164	53	43	2		

- Molecule 10 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A	2344	Total	C	N	O	P	0	0
			50306	22463	9275	16224	2344		

- Molecule 11 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B	100	Total	C	N	O	P	0	0
			2142	955	391	696	100		

- Molecule 12 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	272	Total	C	N	O	S	0	0
			2058	1282	403	365	8		

- Molecule 13 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	204	Total	C	N	O	S	0	0
			1512	963	273	269	7		

- Molecule 14 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	209	Total	C	N	O	S	0	0
			1624	1029	295	298	2		

- Molecule 15 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	K	71	Total	C	N	O	0	0
			511	330	91	90		

- Molecule 16 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	95	Total	C	N	O	S	0	0
			550	331	113	105	1		

- Molecule 17 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	150	Total	C	N	O	S	0	0
			1178	751	217	204	6		

- Molecule 18 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	121	Total	C	N	O	S	0	0
			904	565	173	162	4		

- Molecule 19 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	141	Total	C	N	O	S	0	0
			991	620	189	180	2		

- Molecule 20 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	141	Total	C	N	O	S	0	0
			1089	699	201	186	3		

- Molecule 21 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	123	Total	C	N	O	S	0	0
			989	630	184	169	6		

- Molecule 22 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	107	Total	C	N	O	S	0	0
			739	460	147	132			

- Molecule 23 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	114	Total	C	N	O	S	0	0
			945	602	178	164	1		

- Molecule 24 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	114	Total	C	N	O	S	0	0
			919	581	189	146	3		

- Molecule 25 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	104	Total	C	N	O	S	0	0
			824	526	150	145	3		

- Molecule 26 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	128	Total	C	N	O	S	0	0
			1023	634	203	181	5		

- Molecule 27 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	90	Total	C	N	O	S	0	0
			683	434	122	124	3		

- Molecule 28 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	102	Total	C	N	O	S	0	0
			732	458	144	128	2		

- Molecule 29 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	77	Total	C	N	O	S	0	0
			570	352	113	104	1		

- Molecule 30 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	1326	Total	C	N	O	P	0	0
			28463	12702	5226	9209	1326		

- Molecule 31 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	b	98	Total	C	N	O	0	0
			696	445	128	123		

- Molecule 32 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	c	97	Total	C	N	O	S	0	0
			712	446	135	130	1		

- Molecule 33 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	76	Total	C	N	O	S	0	0
			591	367	123	100	1		

- Molecule 34 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	e	81	Total	C	N	O	S	0	0
			639	403	124	109	3		

- Molecule 35 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	f	89	Total	C	N	O	S	0	0
			671	426	124	119	2		

- Molecule 36 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	88	Total	C	N	O	S	0	0
			659	415	132	107	5		

- Molecule 37 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	h	55	Total	C	N	O	S	0	0
			415	263	76	75	1		

- Molecule 38 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	i	82	Total	C	N	O	S	0	0
			616	392	114	109	1		

- Molecule 39 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	120	Total	C	N	O	S	0	0
			849	521	178	148	2		

- Molecule 40 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	106	Total	C	N	O	S	0	0
			691	433	123	131	4		

- Molecule 41 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	191	Total	C	N	O	S	0	0
			1383	889	250	243	1		

- Molecule 42 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	105	Total	C	N	O	S	0	0
			714	456	123	133	2		

- Molecule 43 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	160	Total	C	N	O	S	0	0
			1032	648	191	191	2		

- Molecule 44 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Y	128	Total	C	N	O	S	0	0
			851	549	152	149	1		

- Molecule 45 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	129	Total	C	N	O	S	0	0
			964	623	167	169	5		

- Molecule 46 is a protein called AURKAIP1/COX24 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	10	27	Total	C	N	O	S	0	0
			219	132	56	30	1		

- Molecule 47 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	J	124	Total	C	N	O		0	0
			827	528	162	137			

- Molecule 48 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	I	51	Total	C	N	O		0	0
			369	239	73	57			

- Molecule 49 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
49	4	1	Total 1	Mg 1	0
49	A	119	Total 119	Mg 119	0
49	F	1	Total 1	Mg 1	0
49	T	1	Total 1	Mg 1	0
49	V	2	Total 2	Mg 2	0
49	a	4	Total 4	Mg 4	0

- Molecule 50 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
50	4	1	Total 1	Zn 1	0

- Molecule 51 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
51	A	31	Total 31	K 31	0
51	B	1	Total 1	K 1	0
51	W	1	Total 1	K 1	0
51	X	1	Total 1	K 1	0
51	a	9	Total 9	K 9	0

- Molecule 52 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
52	A	12	Total 12	Na 12	0
52	B	2	Total 2	Na 2	0

- Molecule 53 is water.

Mol	Chain	Residues	Atoms		AltConf
53	4	2	Total 2	O 2	0
53	A	741	Total 741	O 741	0
53	B	6	Total 6	O 6	0
53	D	4	Total 4	O 4	0
53	E	10	Total 10	O 10	0
53	F	4	Total 4	O 4	0
53	M	2	Total 2	O 2	0
53	O	13	Total 13	O 13	0
53	Q	8	Total 8	O 8	0
53	T	10	Total 10	O 10	0
53	U	8	Total 8	O 8	0
53	V	6	Total 6	O 6	0
53	Z	1	Total 1	O 1	0
53	a	40	Total 40	O 40	0

3 Residue-property plots [i](#)

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: Small ribosomal subunit protein uS19

Chain p: 




- Molecule 2: Large ribosomal subunit protein bL28

Chain 0: 




- Molecule 3: Large ribosomal subunit protein uL29

Chain 1: 




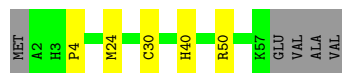
- Molecule 4: Large ribosomal subunit protein uL30

Chain 2: 



- Molecule 5: Large ribosomal subunit protein bL32

Chain 4: 



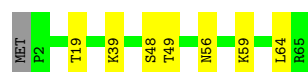
- Molecule 6: Large ribosomal subunit protein bL33

Met	ALA	LYS	LYS	VAL	LYS	GLY	ASN	ARG	VAL	GLN	VAL	ILE	L14	T17	K20	N24	PR0	G26	T32	T33	K34	L43	K46	K47	Y48	N49	R53	R54	R55	T56	L57	I61	LYS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Chain 6: 92% . .



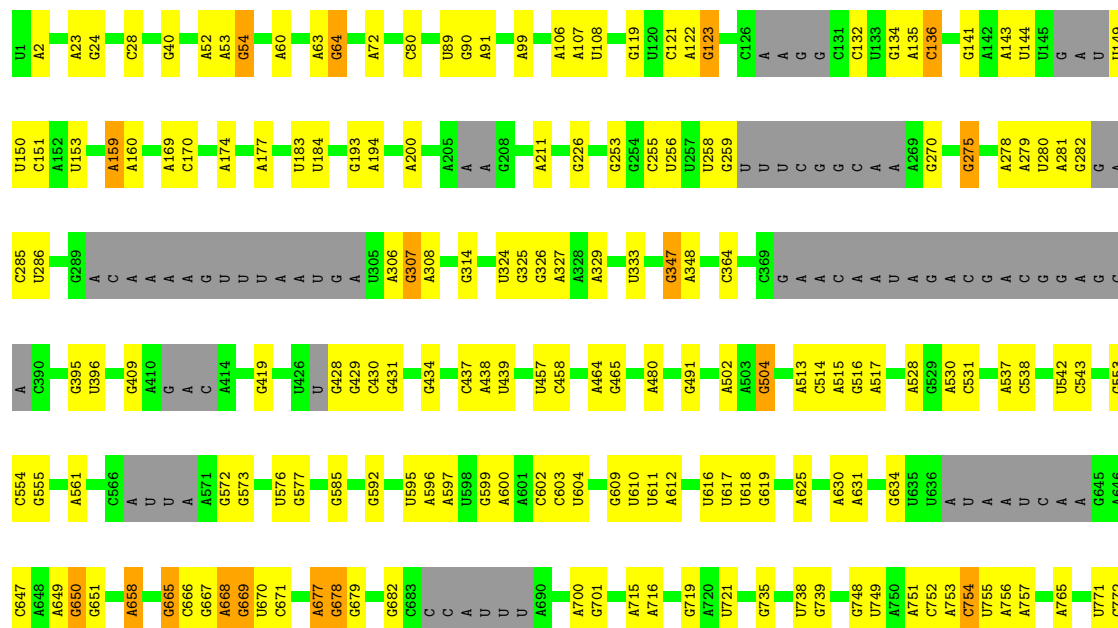
- Chain 7: 88% 11%



- Chain 8: 82% 11% 8%



- Chain A: 60% 19% • 19%



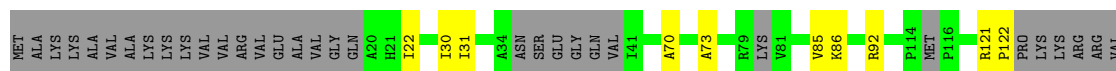


Chain K:  64% 5% 30%




- Molecule 16: Small ribosomal subunit protein uS11

Chain L:  66% 8% 26%



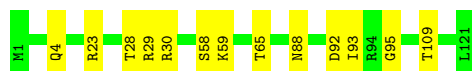
- Molecule 17: Large ribosomal subunit protein uL13

Chain M:  89% 11%




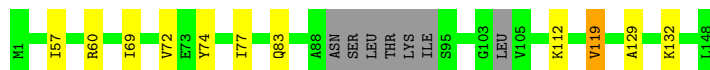
- Molecule 18: Large ribosomal subunit protein uL14

Chain N:  89% 11%




- Molecule 19: Large ribosomal subunit protein uL15

Chain O:  88% 7% 5%



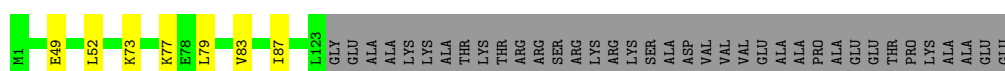
- Molecule 20: Large ribosomal subunit protein uL16

Chain P:  81% 15% 2%




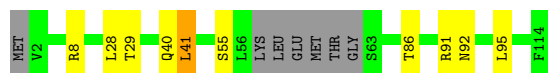
- Molecule 21: Large ribosomal subunit protein bL17

Chain Q:  72% 23%




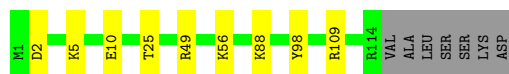
- Molecule 22: Large ribosomal subunit protein uL18

Chain R:  85% 8% 6%



- Molecule 23: Large ribosomal subunit protein bL19

Chain S:  87% 7% 6%




- Molecule 24: Large ribosomal subunit protein bL20

Chain T:  93% 6% .




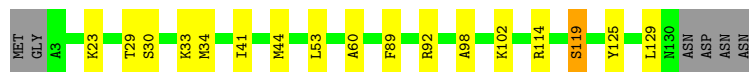
- Molecule 25: Large ribosomal subunit protein bL21

Chain U:  89% 10% ..



- Molecule 26: Large ribosomal subunit protein uL22

Chain V:  83% 12% . .



- Molecule 27: Large ribosomal subunit protein uL23

Chain W:  73% 20% 7%




- Molecule 28: Large ribosomal subunit protein uL24

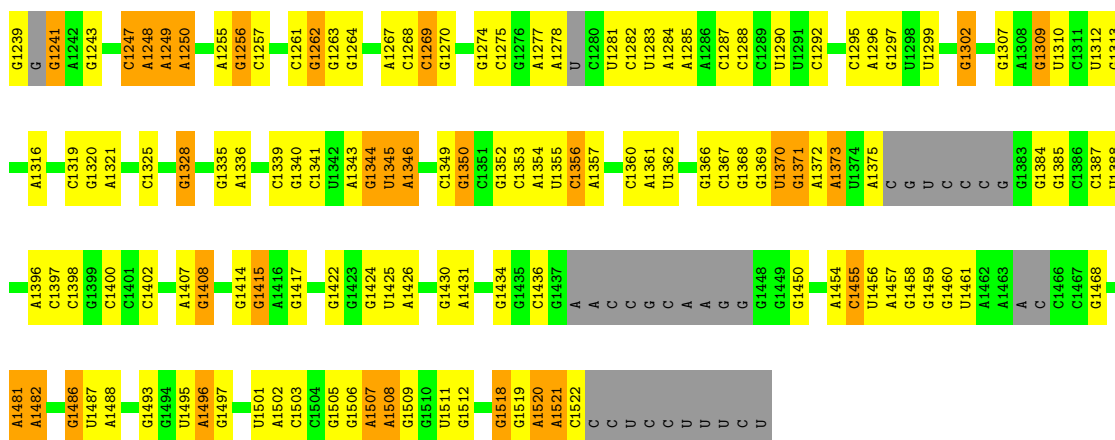
Chain X:  92% 5% .



- Molecule 29: Large ribosomal subunit protein bL27

Chain Z:  87% 9%

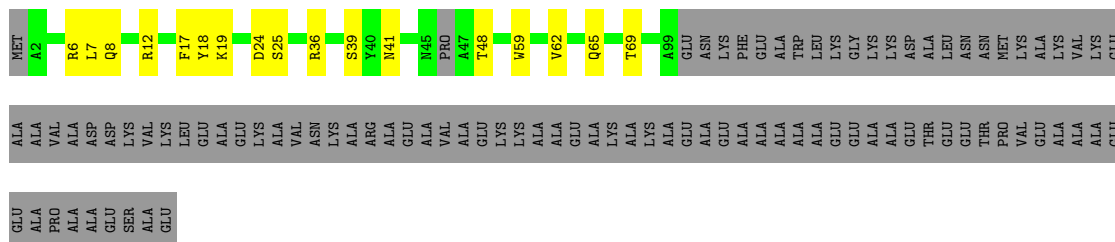
MET
 ALA
 HIS
 LYS
 LYS
 GLY
 VAL
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525
 526
 527
 528
 529
 530
 531
 532
 533
 534
 535
 536
 537
 538
 539
 540
 541
 542
 543
 544
 545
 546
 547
 548
 549
 550
 551
 552
 553
 554
 555
 556
 557
 558
 559
 560
 561
 562
 563
 564
 565
 566
 567
 568
 569
 570
 571
 572
 573
 574
 575
 576
 577
 578
 579
 580
 581
 582
 583
 584
 585
 586
 587
 588
 589
 590
 591
 592
 593
 594
 595
 596
 597
 598
 599
 600
 601
 602
 603
 604
 605
 606
 607
 608
 609
 610
 611
 612
 613
 614
 615
 616
 617
 618
 619
 620
 621
 622
 623
 624
 625
 626
 627
 628
 629
 630
 631
 632
 633
 634
 635
 636
 637
 638
 639
 640
 641
 642
 643
 644
 645
 646
 647
 648
 649
 650
 651
 652
 653
 654
 655
 656
 657
 658
 659
 660
 661
 662
 663
 664
 665
 666
 667
 668
 669
 670
 671
 672
 673
 674
 675
 676
 677
 678
 679
 680
 681
 682
 683
 684
 685
 686
 687
 688
 689
 690
 691
 692
 693
 694
 695
 696
 697
 698
 699
 700
 701
 702
 703
 704
 705
 706
 707
 708
 709
 710
 711
 712
 713
 714
 715
 716
 717
 718
 719
 720
 721
 722
 723
 724
 725
 726
 727
 728
 729
 730
 731
 732
 733
 734
 735
 736
 737
 738
 739
 740
 741
 742
 743
 744
 745
 746
 747
 748
 749
 750
 751
 752
 753
 754
 755
 756
 757
 758
 759
 760
 761
 762
 763
 764
 765
 766
 767
 768
 769
 770
 771
 772
 773
 774
 775
 776
 777
 778
 779
 780
 781
 782
 783
 784
 785
 786
 787
 788
 789
 790
 791
 792
 793
 794
 795
 796
 797
 798
 799
 800
 801
 802
 803
 804
 805
 806
 807
 808
 809
 810
 811
 812
 813
 814
 815
 816
 817
 818
 819
 820
 821
 822
 823
 824
 825
 826
 827
 828
 829
 830
 831
 832
 833
 834
 835
 836
 837
 838
 839
 840
 841
 842
 843
 844
 845
 846
 847
 848
 849
 850
 851
 852
 853
 854
 855
 856
 857
 858
 859
 860
 861
 862
 863
 864
 865
 866
 867
 868
 869
 870
 871
 872
 873
 874
 875
 876
 877
 878
 879
 880
 881
 882
 883
 884
 885
 886
 887
 888
 889
 890
 891
 892
 893
 894
 895
 896
 897
 898
 899
 900
 901
 902
 903
 904
 905
 906
 907
 908
 909
 910
 911
 912
 913
 914
 915
 916
 917
 918
 919
 920
 921
 922
 923
 924
 925
 926
 927
 928
 929
 930
 931
 932
 933
 934
 935
 936
 937
 938
 939
 940
 941
 942
 943
 944
 945
 946
 947
 948
 949
 950
 951
 952
 953
 954
 955
 956
 957
 958
 959
 960
 961
 962
 963
 964
 965
 966
 967
 968
 969
 970
 971
 972
 973
 974
 975
 976
 977
 978
 979
 980
 981
 982
 983
 984
 985
 986
 987
 988
 989
 990
 991
 992
 993
 994
 995
 996
 997
 998
 999
 1000
 1001
 1002
 1003
 1004
 1005
 1006
 1007
 1008
 1009
 1010
 1011
 1012
 1013
 1014
 1015
 1016
 1017
 1018
 1019
 1020
 1021
 1022
 1023
 1024
 1025
 1026
 1027
 1028
 1029
 1030
 1031
 1032
 1033
 1034
 1035
 1036
 1037
 1038
 1039
 1040
 1041
 1042
 1043
 1044
 1045
 1046
 1047
 1048
 1049
 1050
 1051
 1052
 1053
 1054
 1055
 1056
 1057
 1058
 1059
 1060
 1061
 1062
 1063
 1064
 1065
 1066
 1067
 1068
 1069
 1070
 1071
 1072
 1073
 1074
 1075
 1076
 1077
 1078
 1079
 1080
 1081
 1082
 1083
 1084
 1085
 1086
 1087
 1088
 1089
 1090
 1091
 1092
 1093
 1094
 1095
 1096
 1097
 1098
 1099
 1100
 1101
 1102
 1103
 1104
 1105
 1106
 1107
 1108
 1109
 1110
 1111
 1112
 1113
 1114
 1115
 1116
 1117
 1118
 1119
 1120
 1121
 1122
 1123
 1124
 1125
 1126
 1127
 1128
 1129
 1130
 1131
 1132
 1133
 1134
 1135
 1136
 1137
 1138
 1139
 1140
 1141
 1142
 1143
 1144
 1145
 1146
 1147
 1148
 1149
 1150
 1151
 1152
 1153
 1154
 1155
 1156
 1157
 1158
 1159
 1160
 1161
 1162
 1163
 1164
 1165
 1166
 1167
 1168
 1169
 1170
 1171
 1172
 1173
 1174
 1175
 1176
 1177
 1178
 1179
 1180
 1181
 1182
 1183
 1184
 1185
 1186
 1187
 1188
 1189
 1190
 1191
 1192
 1193
 1194
 1195
 1196
 1197
 1198
 1199
 1200
 1201
 1202
 1203
 1204
 1205
 1206
 1207
 1208
 1209
 1210
 1211
 1212
 1213
 1214
 1215
 1216
 1217
 1218
 1219
 1220
 1221
 1222
 1223
 1224
 1225
 1226
 1227
 1228
 1229
 1230
 1231
 1232
 1233
 1234
 1235
 1236
 1237
 1238
 1239
 1240
 1241
 1242
 1243
 1244
 1245
 1246
 1247
 1248
 1249
 1250
 1251
 1252
 1253
 1254
 1255
 1256
 1257
 1258
 1259
 1260
 1261
 1262
 1263
 1264
 1265
 1266
 1267
 1268
 1269
 1270
 1271
 1272
 1273
 1274
 1275
 1276
 1277
 1278
 1279
 1280
 1281
 1282
 1283
 1284
 1285
 1286
 1287
 1288
 1289
 1290
 1291
 1292
 1293
 1294
 1295
 1296
 1297
 1298
 1299
 1300
 1301
 1302
 1303
 1304
 1305
 1306
 1307
 1308
 1309
 1310
 1311
 1312
 1313
 1314
 1315
 1316
 1317
 1318
 1319
 1320
 1321
 1322
 1323
 1324
 1325
 1326
 1327
 1328
 1329
 1330
 1331
 1332
 1333
 1334
 1335
 1336
 1337
 1338
 1339
 1340
 1341
 1342
 1343
 1344
 1345
 1346
 1347
 1348
 1349
 1350
 1351
 1352
 1353
 1354
 1355
 1356
 1357
 1358
 1359
 1360
 1361
 1362
 1363
 1364
 1365
 1366
 1367
 1368
 1369
 1370
 1371
 1372
 1373
 1374
 1375
 1376
 1377
 1378
 1379
 1380
 1381
 1382
 1383
 1384
 1385
 1386
 1387
 1388
 1389
 1390
 1391
 1392
 1393
 1394
 1395
 1396
 1397
 1398
 1399
 1400
 1401
 1402
 1403
 1404
 1405
 1406
 1407
 1408
 1409
 1410
 1411
 1412
 1413
 1414
 1415
 1416
 1417
 1418
 1419
 1420
 1421
 1422
 1423
 1424
 1425
 1426
 1427
 1428
 1429
 1430
 1431
 1432
 1433
 1434
 1435
 1436
 1437
 1438
 1439
 1440
 1441
 1442
 1443
 1444
 1445
 1446
 1447
 1448
 1449
 1450
 1451
 1452
 1453
 1454
 1455
 1456
 1457
 1458
 1459
 1460
 1461
 1462
 1463
 1464
 1465
 1466
 1467
 1468
 1469
 1470
 1471
 1472
 1473
 1474
 1475
 1476
 1477
 1478
 1479
 1480
 1481
 1482
 1483
 1484
 1485
 1486
 1487
 1488
 1489
 1490
 1491
 1492
 1493
 1494
 1495
 1496
 1497
 1498
 1499
 1500
 1501
 1502
 1503
 1504
 1505
 1506
 1507
 1508
 1509
 1510
 1511
 1512
 1513
 1514
 1515
 1516
 1517
 1518
 1519
 1520
 1521
 1522
 1523
 1524
 1525
 1526
 1527
 1528
 1529
 1530
 1531
 1532
 1533
 1534
 1535
 1536



- Molecule 31: Small ribosomal subunit protein bS6



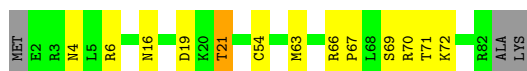
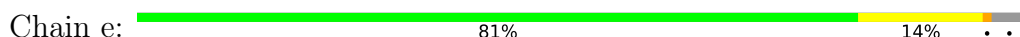
- Molecule 32: Small ribosomal subunit protein bS16



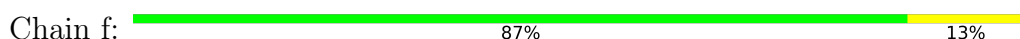
- Molecule 33: Small ribosomal subunit protein bS20



- Molecule 34: Small ribosomal subunit protein uS17



- Molecule 35: Small ribosomal subunit protein uS15





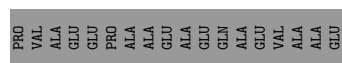
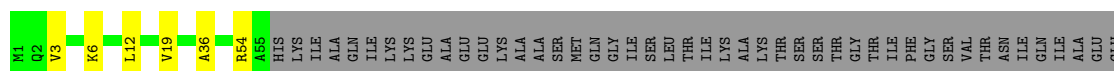
- Molecule 36: Small ribosomal subunit protein uS14

Chain g: 93% 6%



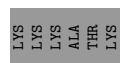
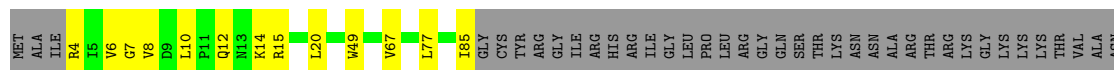
- Molecule 37: Large ribosomal subunit protein bL9

Chain h: 27% 69%



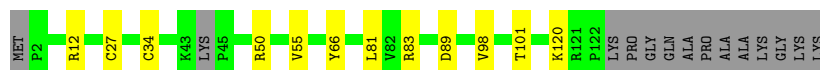
- Molecule 38: Small ribosomal subunit protein uS13

Chain i: 55% 10% 35%



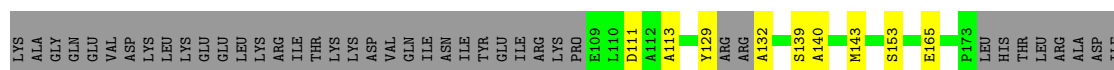
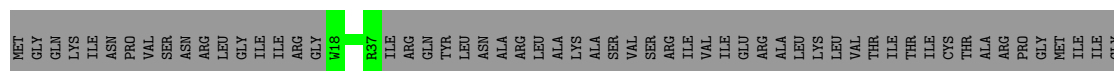
- Molecule 39: Small ribosomal subunit protein uS12

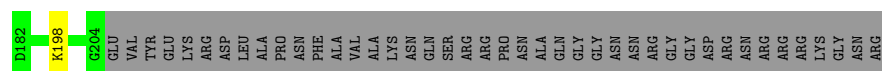
Chain j: 81% 9% 10%



- Molecule 40: Small ribosomal subunit protein uS3

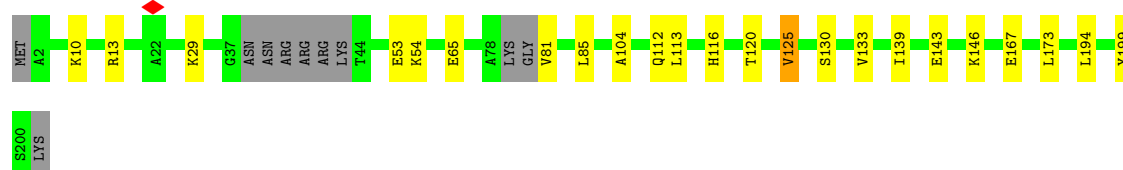
Chain k: 39% 57%





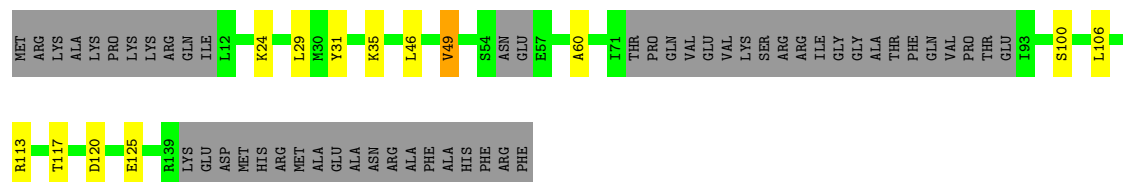
- Molecule 41: Small ribosomal subunit protein uS4

Chain l: 84% 11% 5%



- Molecule 42: Small ribosomal subunit protein uS7

Chain m: 58% 8% 34%



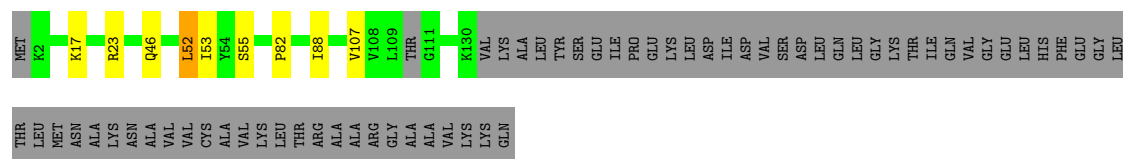
- Molecule 43: Small ribosomal subunit protein uS5

Chain n: 84% 8% 7%



- Molecule 44: Large ribosomal subunit protein bL25

Chain Y: 62% 33%



- Molecule 45: Small ribosomal subunit protein uS8

Chain o: 89% 9% 2%

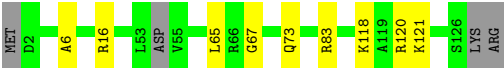
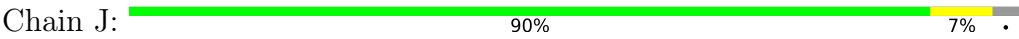


- Molecule 46: AURKAIP1/COX24 domain-containing protein

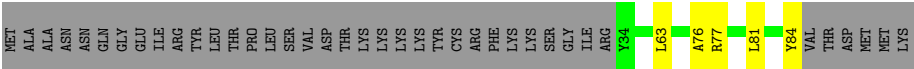
Chain 10: 73% 17% 10%



- Molecule 47: Small ribosomal subunit protein uS9



- Molecule 48: Small ribosomal subunit protein bS18



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	129576	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.0	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.182	Depositor
Minimum map value	-0.077	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	370.48, 370.48, 370.48	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.842, 0.842, 0.842	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: PSU, MG, 2MA, 5MC, 5MU, 4OC, K, NA, UR3, ZN, MA6, OMG, 2MG, OMU, 7MG, 5OC, H2U

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	p	0.13	0/522	0.30	0/708
2	0	0.16	0/617	0.31	0/825
3	1	0.14	0/454	0.26	0/615
4	2	0.19	0/440	0.35	0/591
5	4	0.19	0/438	0.34	0/592
6	5	0.17	0/344	0.39	0/464
7	6	0.18	0/395	0.35	0/521
8	7	0.16	0/461	0.44	0/617
9	8	0.10	0/263	0.25	0/347
10	A	0.23	0/56035	0.35	5/87314 (0.0%)
11	B	0.15	0/2393	0.27	0/3723
12	D	0.19	0/2097	0.37	1/2814 (0.0%)
13	E	0.18	0/1541	0.39	0/2071
14	F	0.18	0/1647	0.34	0/2219
15	K	0.14	0/518	0.38	0/703
16	L	0.09	0/553	0.23	0/750
17	M	0.18	0/1203	0.31	0/1622
18	N	0.17	0/911	0.34	0/1225
19	O	0.16	0/1001	0.37	0/1341
20	P	0.17	0/1112	0.39	0/1495
21	Q	0.18	0/1006	0.36	0/1347
22	R	0.13	0/745	0.30	0/1000
23	S	0.15	0/960	0.26	0/1275
24	T	0.21	0/936	0.35	0/1252
25	U	0.20	0/834	0.44	0/1118
26	V	0.18	0/1036	0.33	0/1385
27	W	0.18	0/690	0.37	0/924
28	X	0.14	0/738	0.31	0/988
29	Z	0.16	0/577	0.29	0/772
30	a	0.15	0/31641	0.30	0/49284
31	b	0.10	0/708	0.30	0/967
32	c	0.14	0/723	0.32	0/977

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	d	0.16	0/597	0.37	0/799
34	e	0.11	0/650	0.28	0/872
35	f	0.15	0/680	0.34	0/914
36	g	0.11	0/670	0.27	0/897
37	h	0.20	0/417	0.54	0/559
38	i	0.13	0/622	0.32	0/839
39	j	0.10	0/860	0.30	0/1167
40	k	0.12	0/694	0.34	0/936
41	l	0.14	0/1412	0.38	0/1922
42	m	0.15	0/722	0.36	0/981
43	n	0.10	0/1043	0.28	0/1425
44	Y	0.15	0/863	0.38	0/1178
45	o	0.13	0/977	0.31	0/1317
46	10	0.10	0/222	0.23	0/289
47	J	0.12	0/838	0.30	0/1141
48	I	0.12	0/376	0.27	0/511
All	All	0.19	0/125182	0.33	6/187593 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	2672	U	OP1-P-OP2	-13.12	80.23	119.60
10	A	2671	G	OP2-P-O3'	-12.05	71.84	108.00
10	A	2672	U	O5'-P-OP1	-10.34	76.98	108.00
10	A	2672	U	O5'-P-OP2	8.86	134.59	108.00
10	A	2671	G	OP1-P-O3'	8.36	133.08	108.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	p	510	0	465	4	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	0	608	0	643	1	0
3	1	450	0	427	4	0
4	2	437	0	484	7	0
5	4	427	0	413	4	0
6	5	342	0	319	8	0
7	6	391	0	418	2	0
8	7	456	0	448	5	0
9	8	262	0	264	4	0
10	A	50306	0	25356	260	0
11	B	2142	0	1085	10	0
12	D	2058	0	2134	14	0
13	E	1512	0	1548	12	0
14	F	1624	0	1692	7	0
15	K	511	0	458	6	0
16	L	550	0	401	7	0
17	M	1178	0	1208	11	0
18	N	904	0	969	7	0
19	O	991	0	1005	5	0
20	P	1089	0	1108	15	0
21	Q	989	0	1035	4	0
22	R	739	0	692	5	0
23	S	945	0	998	6	0
24	T	919	0	964	5	0
25	U	824	0	869	5	0
26	V	1023	0	1065	9	0
27	W	683	0	709	12	0
28	X	732	0	756	3	0
29	Z	570	0	574	1	0
30	a	28463	0	14367	256	0
31	b	696	0	618	9	0
32	c	712	0	676	10	0
33	d	591	0	608	9	0
34	e	639	0	644	10	0
35	f	671	0	645	9	0
36	g	659	0	676	4	0
37	h	415	0	443	4	0
38	i	616	0	633	8	0
39	j	849	0	810	8	0
40	k	691	0	604	7	0
41	l	1383	0	1297	18	0
42	m	714	0	628	9	0
43	n	1032	0	952	7	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	Y	851	0	777	6	0
45	o	964	0	983	8	0
46	10	219	0	228	4	0
47	J	827	0	751	9	0
48	I	369	0	347	3	0
49	4	1	0	0	0	0
49	A	119	0	0	0	0
49	F	1	0	0	0	0
49	T	1	0	0	0	0
49	V	2	0	0	0	0
49	a	4	0	0	0	0
50	4	1	0	0	0	0
51	A	31	0	0	0	0
51	B	1	0	0	0	0
51	W	1	0	0	0	0
51	X	1	0	0	0	0
51	a	9	0	0	0	0
52	A	12	0	0	0	0
52	B	2	0	0	0	0
53	4	2	0	0	0	0
53	A	741	0	0	13	0
53	B	6	0	0	1	0
53	D	4	0	0	0	0
53	E	10	0	0	0	0
53	F	4	0	0	0	0
53	M	2	0	0	1	0
53	O	13	0	0	0	0
53	Q	8	0	0	0	0
53	T	10	0	0	0	0
53	U	8	0	0	0	0
53	V	6	0	0	0	0
53	Z	1	0	0	0	0
53	a	40	0	0	3	0
All	All	116574	0	75194	748	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.

The worst 5 of 748 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)
10:A:1949:5MU:C5	10:A:1949:5MU:C4	1.79	1.68
30:a:1426:A:H2	30:a:1459:G:H1	1.31	0.79
10:A:1436:G:H1	10:A:1632:U:H3	1.29	0.78
30:a:1117:G:H1	30:a:1148:U:H3	1.33	0.77
10:A:253:G:H22	10:A:275:G:H1	1.31	0.76

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	p	67/89 (75%)	65 (97%)	2 (3%)	0	100	100
2	0	75/79 (95%)	75 (100%)	0	0	100	100
3	1	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
4	2	54/58 (93%)	53 (98%)	1 (2%)	0	100	100
5	4	54/61 (88%)	53 (98%)	1 (2%)	0	100	100
6	5	43/62 (69%)	33 (77%)	10 (23%)	0	100	100
7	6	46/50 (92%)	46 (100%)	0	0	100	100
8	7	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
9	8	31/38 (82%)	29 (94%)	2 (6%)	0	100	100
12	D	270/274 (98%)	264 (98%)	6 (2%)	0	100	100
13	E	202/205 (98%)	193 (96%)	9 (4%)	0	100	100
14	F	207/209 (99%)	196 (95%)	11 (5%)	0	100	100
15	K	65/101 (64%)	63 (97%)	2 (3%)	0	100	100
16	L	87/128 (68%)	77 (88%)	10 (12%)	0	100	100
17	M	148/151 (98%)	145 (98%)	3 (2%)	0	100	100
18	N	119/121 (98%)	113 (95%)	6 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	O	135/148 (91%)	127 (94%)	8 (6%)	0	100	100
20	P	139/144 (96%)	133 (96%)	6 (4%)	0	100	100
21	Q	121/160 (76%)	118 (98%)	3 (2%)	0	100	100
22	R	103/114 (90%)	95 (92%)	8 (8%)	0	100	100
23	S	112/121 (93%)	108 (96%)	4 (4%)	0	100	100
24	T	112/115 (97%)	109 (97%)	3 (3%)	0	100	100
25	U	102/105 (97%)	96 (94%)	6 (6%)	0	100	100
26	V	126/134 (94%)	124 (98%)	2 (2%)	0	100	100
27	W	88/97 (91%)	86 (98%)	2 (2%)	0	100	100
28	X	98/106 (92%)	91 (93%)	7 (7%)	0	100	100
29	Z	75/85 (88%)	72 (96%)	3 (4%)	0	100	100
31	b	96/117 (82%)	95 (99%)	1 (1%)	0	100	100
32	c	93/192 (48%)	85 (91%)	8 (9%)	0	100	100
33	d	74/84 (88%)	73 (99%)	1 (1%)	0	100	100
34	e	79/84 (94%)	73 (92%)	6 (8%)	0	100	100
35	f	87/89 (98%)	81 (93%)	6 (7%)	0	100	100
36	g	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
37	h	53/179 (30%)	48 (91%)	5 (9%)	0	100	100
38	i	80/126 (64%)	75 (94%)	4 (5%)	1 (1%)	10	39
39	j	116/134 (87%)	110 (95%)	6 (5%)	0	100	100
40	k	98/246 (40%)	91 (93%)	7 (7%)	0	100	100
41	l	185/201 (92%)	172 (93%)	13 (7%)	0	100	100
42	m	99/158 (63%)	94 (95%)	5 (5%)	0	100	100
43	n	156/172 (91%)	151 (97%)	5 (3%)	0	100	100
44	Y	124/192 (65%)	110 (89%)	14 (11%)	0	100	100
45	o	125/131 (95%)	122 (98%)	3 (2%)	0	100	100
46	10	25/30 (83%)	24 (96%)	1 (4%)	0	100	100
47	J	120/128 (94%)	116 (97%)	4 (3%)	0	100	100
48	I	49/90 (54%)	47 (96%)	2 (4%)	0	100	100
All	All	4547/5526 (82%)	4331 (95%)	215 (5%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
38	i	7	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	p	46/75 (61%)	46 (100%)	0	100	100
2	0	62/66 (94%)	61 (98%)	1 (2%)	58	82
3	1	38/56 (68%)	38 (100%)	0	100	100
4	2	48/53 (91%)	48 (100%)	0	100	100
5	4	40/50 (80%)	39 (98%)	1 (2%)	42	73
6	5	33/58 (57%)	30 (91%)	3 (9%)	7	30
7	6	39/40 (98%)	39 (100%)	0	100	100
8	7	40/58 (69%)	40 (100%)	0	100	100
9	8	24/35 (69%)	24 (100%)	0	100	100
12	D	213/218 (98%)	206 (97%)	7 (3%)	33	67
13	E	157/163 (96%)	152 (97%)	5 (3%)	34	67
14	F	174/177 (98%)	174 (100%)	0	100	100
15	K	45/92 (49%)	44 (98%)	1 (2%)	47	76
16	L	28/102 (28%)	28 (100%)	0	100	100
17	M	124/128 (97%)	124 (100%)	0	100	100
18	N	97/100 (97%)	95 (98%)	2 (2%)	48	77
19	O	95/117 (81%)	91 (96%)	4 (4%)	25	59
20	P	107/118 (91%)	105 (98%)	2 (2%)	52	79
21	Q	102/129 (79%)	101 (99%)	1 (1%)	73	88
22	R	57/90 (63%)	53 (93%)	4 (7%)	12	41
23	S	101/107 (94%)	101 (100%)	0	100	100
24	T	89/93 (96%)	89 (100%)	0	100	100
25	U	91/92 (99%)	89 (98%)	2 (2%)	47	76

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	V	107/113 (95%)	105 (98%)	2 (2%)	52	79
27	W	70/85 (82%)	70 (100%)	0	100	100
28	X	72/89 (81%)	72 (100%)	0	100	100
29	Z	58/69 (84%)	56 (97%)	2 (3%)	32	66
31	b	55/101 (54%)	54 (98%)	1 (2%)	54	80
32	c	63/137 (46%)	60 (95%)	3 (5%)	21	55
33	d	55/69 (80%)	54 (98%)	1 (2%)	54	80
34	e	65/77 (84%)	64 (98%)	1 (2%)	60	83
35	f	61/79 (77%)	61 (100%)	0	100	100
36	g	60/69 (87%)	60 (100%)	0	100	100
37	h	43/146 (30%)	43 (100%)	0	100	100
38	i	60/102 (59%)	58 (97%)	2 (3%)	33	67
39	j	76/111 (68%)	76 (100%)	0	100	100
40	k	48/197 (24%)	48 (100%)	0	100	100
41	l	125/174 (72%)	124 (99%)	1 (1%)	79	90
42	m	56/132 (42%)	52 (93%)	4 (7%)	12	40
43	n	81/130 (62%)	78 (96%)	3 (4%)	29	63
44	Y	68/159 (43%)	65 (96%)	3 (4%)	24	58
45	o	95/112 (85%)	93 (98%)	2 (2%)	48	77
46	10	20/28 (71%)	20 (100%)	0	100	100
47	J	58/106 (55%)	58 (100%)	0	100	100
48	I	29/80 (36%)	29 (100%)	0	100	100
All	All	3275/4582 (72%)	3217 (98%)	58 (2%)	54	80

5 of 58 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	R	41	LEU
44	Y	107	VAL
29	Z	9	SER
44	Y	52	LEU
42	m	100	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
41	l	73	HIS
41	l	137	GLN
48	I	71	GLN
21	Q	31	HIS
20	P	135	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	2306/2889 (79%)	292 (12%)	10 (0%)
11	B	96/109 (88%)	22 (22%)	1 (1%)
30	a	1297/1534 (84%)	270 (20%)	0
All	All	3699/4532 (81%)	584 (15%)	11 (0%)

5 of 584 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
10	A	2	A
10	A	23	A
10	A	24	G
10	A	28	C
10	A	40	G

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	A	2670	U
10	A	2671	G
11	B	61	A
10	A	2852	A
10	A	1255	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

20 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection.

RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	H2U	A	2620	10	18,21,22	0.43	0	21,30,33	0.37	0
30	5OC	a	276	30	18,21,22	4.40	13 (72%)	25,30,33	1.18	1 (4%)
10	5MU	A	1949	10	19,22,23	7.25	8 (42%)	28,32,35	3.41	10 (35%)
10	5MC	A	1972	10	18,22,23	3.67	7 (38%)	26,32,35	1.00	2 (7%)
30	7MG	a	821	30	22,26,27	3.70	10 (45%)	29,39,42	2.04	9 (31%)
10	OMG	A	2252	10	18,26,27	2.51	8 (44%)	19,38,41	1.49	4 (21%)
30	4OC	a	1400	30	20,23,24	3.14	8 (40%)	26,32,35	0.90	1 (3%)
10	H2U	A	781	10	18,21,22	0.31	0	21,30,33	0.50	0
10	5OC	A	2502	10,51	18,21,22	4.26	13 (72%)	25,30,33	1.17	3 (12%)
10	2MA	A	2504	10,51,49	19,25,26	3.59	6 (31%)	21,37,40	2.51	4 (19%)
30	2MG	a	1408	30	18,26,27	2.50	7 (38%)	16,38,41	1.36	3 (18%)
10	PSU	A	2606	10	18,21,22	1.01	1 (5%)	22,30,33	1.73	4 (18%)
30	MA6	a	1508	30	18,26,27	1.04	2 (11%)	19,38,41	4.07	2 (10%)
30	MA6	a	1507	30	18,26,27	1.02	2 (11%)	19,38,41	4.21	3 (15%)
10	PSU	A	2581	10	18,21,22	1.10	2 (11%)	22,30,33	1.88	5 (22%)
30	5MC	a	1402	30	18,22,23	3.72	7 (38%)	26,32,35	0.98	1 (3%)
10	H2U	A	876	10	18,21,22	0.40	0	21,30,33	0.39	0
10	OMU	A	2450	10	19,22,23	2.98	8 (42%)	26,31,34	1.74	5 (19%)
10	2MG	A	2446	10	18,26,27	2.42	7 (38%)	16,38,41	1.35	3 (18%)
30	UR3	a	1487	30	19,22,23	3.21	8 (42%)	26,32,35	1.30	2 (7%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	H2U	A	2620	10	-	0/7/38/39	0/2/2/2
30	5OC	a	276	30	-	1/7/21/22	0/2/2/2
10	5MU	A	1949	10	-	0/7/25/26	0/2/2/2
10	5MC	A	1972	10	-	0/7/25/26	0/2/2/2
30	7MG	a	821	30	-	0/7/37/38	0/3/3/3
10	OMG	A	2252	10	-	1/5/27/28	0/3/3/3
30	4OC	a	1400	30	-	0/9/29/30	0/2/2/2
10	H2U	A	781	10	-	0/7/38/39	0/2/2/2
10	5OC	A	2502	10,51	-	5/7/21/22	0/2/2/2
10	2MA	A	2504	10,51,49	-	1/3/25/26	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
30	2MG	a	1408	30	-	0/5/27/28	0/3/3/3
10	PSU	A	2606	10	-	0/7/25/26	0/2/2/2
30	MA6	a	1508	30	-	5/7/29/30	0/3/3/3
30	MA6	a	1507	30	-	3/7/29/30	0/3/3/3
10	PSU	A	2581	10	-	0/7/25/26	0/2/2/2
30	5MC	a	1402	30	-	0/7/25/26	0/2/2/2
10	H2U	A	876	10	-	0/7/38/39	0/2/2/2
10	OMU	A	2450	10	-	0/9/27/28	0/2/2/2
10	2MG	A	2446	10	-	2/5/27/28	0/3/3/3
30	UR3	a	1487	30	-	0/7/25/26	0/2/2/2

The worst 5 of 117 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	1949	5MU	C4-C5	21.01	1.79	1.44
10	A	1949	5MU	C6-N1	15.49	1.64	1.38
10	A	1949	5MU	C6-C5	-11.72	1.15	1.34
10	A	1949	5MU	C4-N3	-11.71	1.17	1.38
30	a	1402	5MC	C6-C5	9.37	1.50	1.34

The worst 5 of 62 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	a	1507	MA6	N1-C6-N6	-17.14	99.02	117.06
30	a	1508	MA6	N1-C6-N6	-16.56	99.63	117.06
10	A	1949	5MU	C5-C4-N3	10.60	124.36	115.31
10	A	1949	5MU	C5-C6-N1	-8.70	114.39	123.34
10	A	2504	2MA	C2-N3-C4	7.76	121.83	115.52

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	A	2252	OMG	C1'-C2'-O2'-CM2
30	a	1507	MA6	C5-C6-N6-C9
30	a	1507	MA6	C5-C6-N6-C10
30	a	1508	MA6	C5-C6-N6-C10
30	a	1508	MA6	O4'-C4'-C5'-O5'

There are no ring outliers.

9 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	A	2620	H2U	1	0
30	a	276	5OC	1	0
10	A	1949	5MU	2	0
30	a	821	7MG	1	0
10	A	2252	OMG	1	0
30	a	1408	2MG	2	0
30	a	1508	MA6	1	0
30	a	1507	MA6	1	0
10	A	876	H2U	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 186 ligands modelled in this entry, 186 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

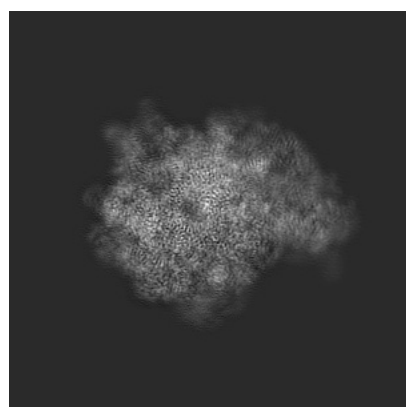
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52641. These allow visual inspection of the internal detail of the map and identification of artifacts.

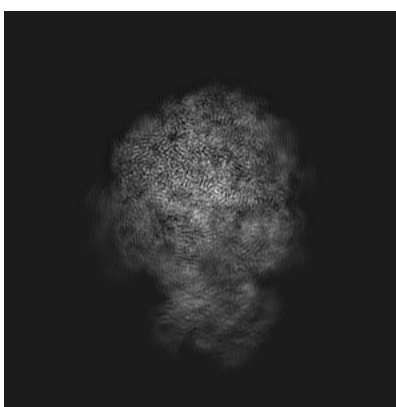
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

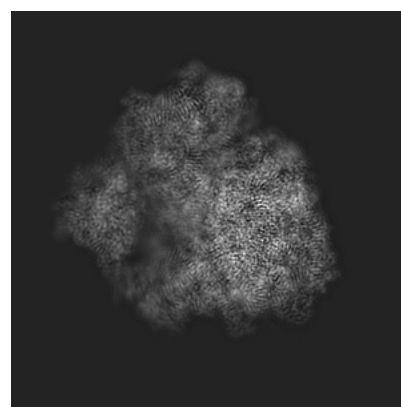
6.1.1 Primary map



X



Y

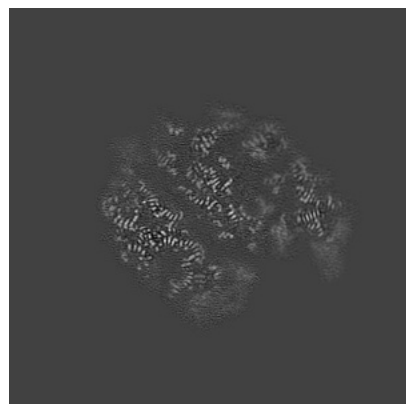


Z

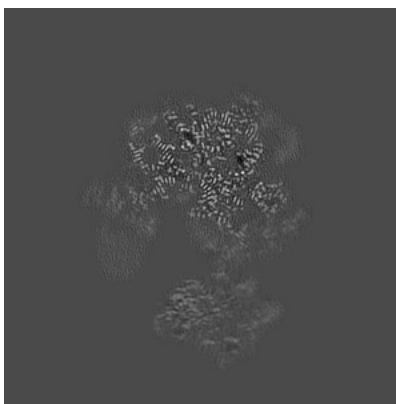
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

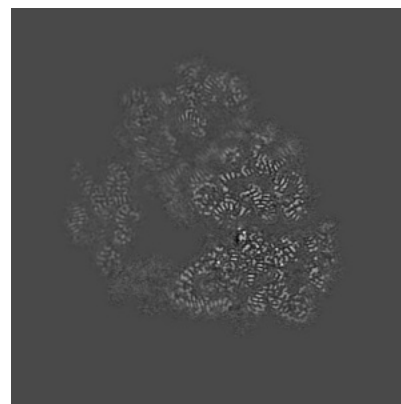
6.2.1 Primary map



X Index: 220



Y Index: 220

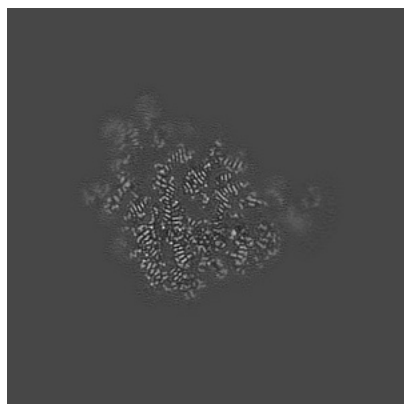


Z Index: 220

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

6.3 Largest variance slices [i](#)

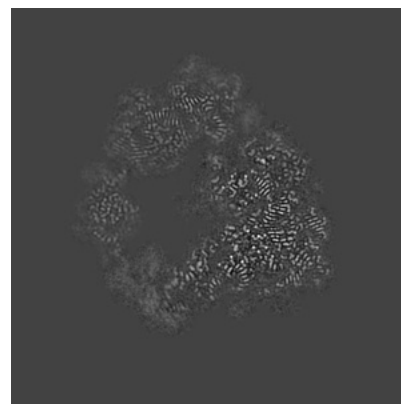
6.3.1 Primary map



X Index: 262



Y Index: 184

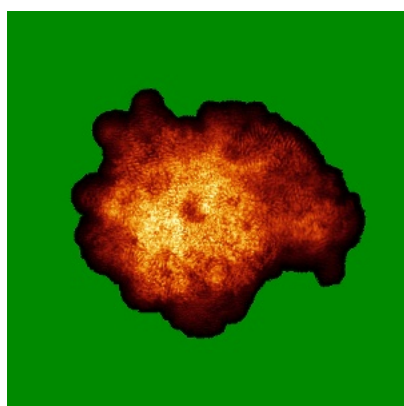


Z Index: 201

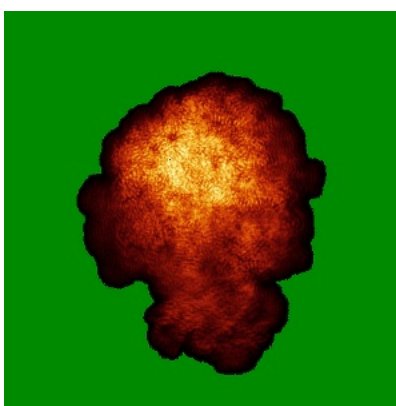
The images above show the largest variance slices of the map in three orthogonal directions.

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

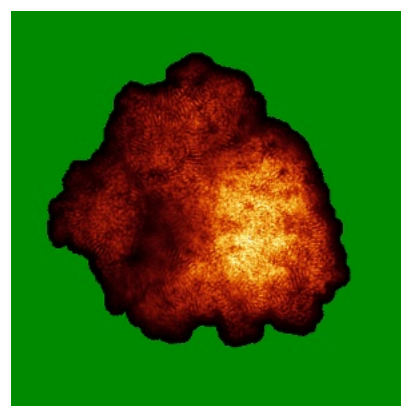
6.4.1 Primary map



X



Y

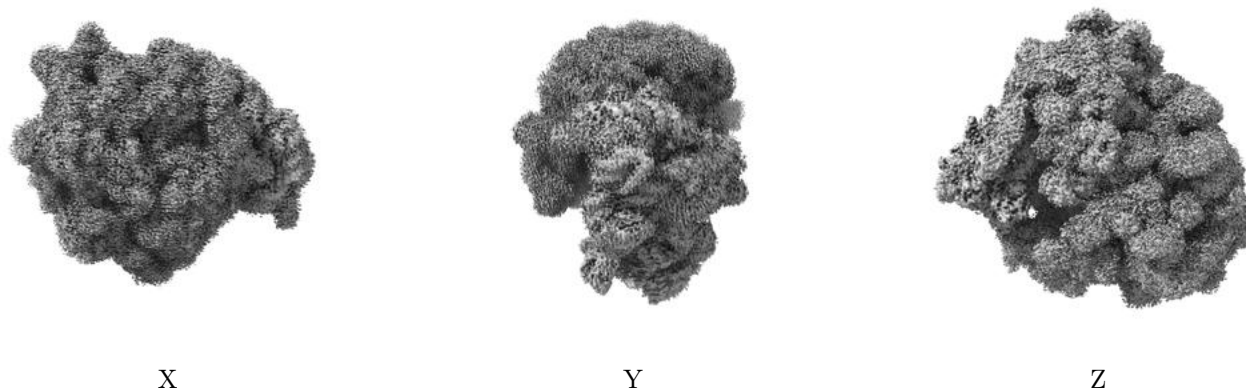


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

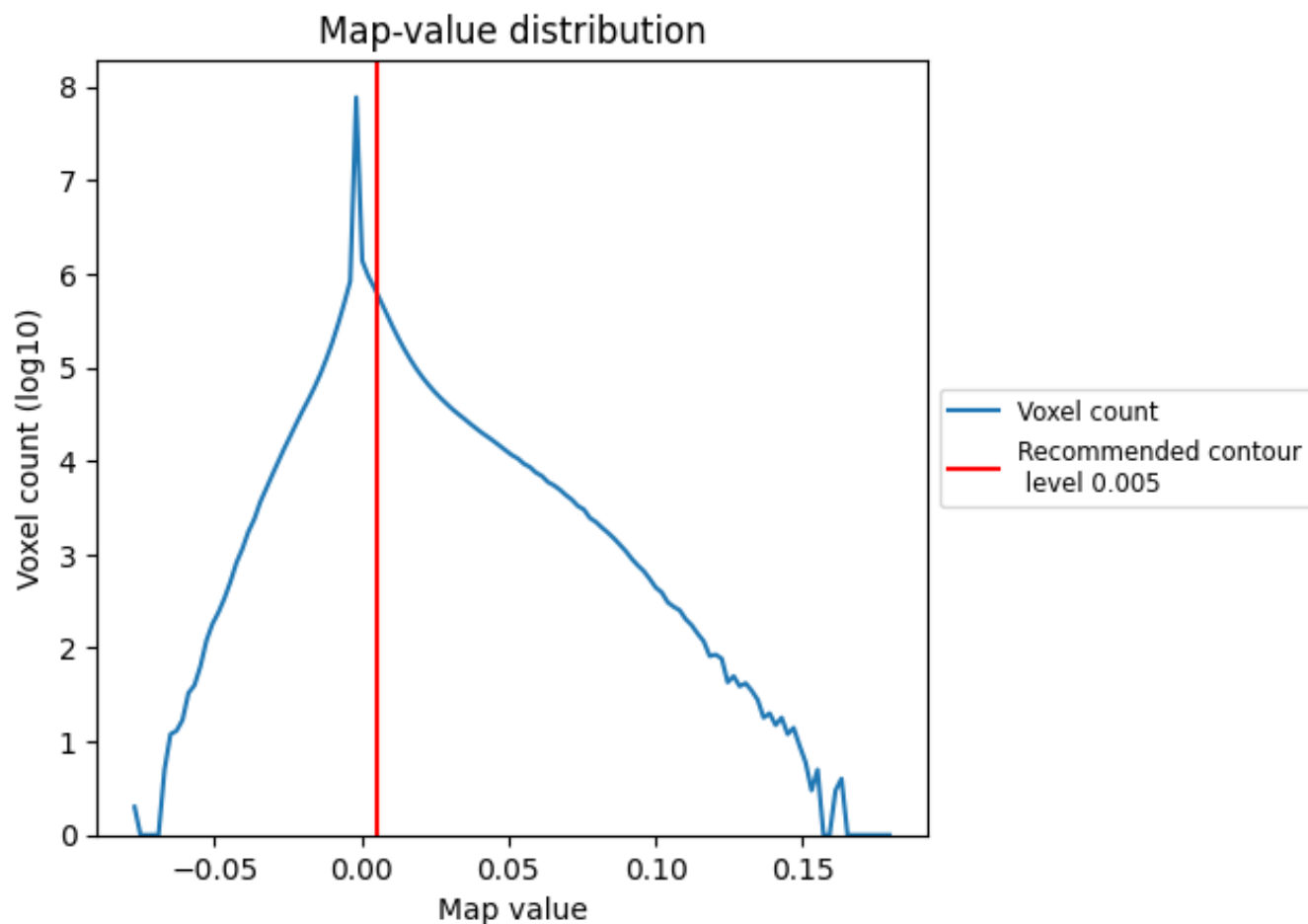
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

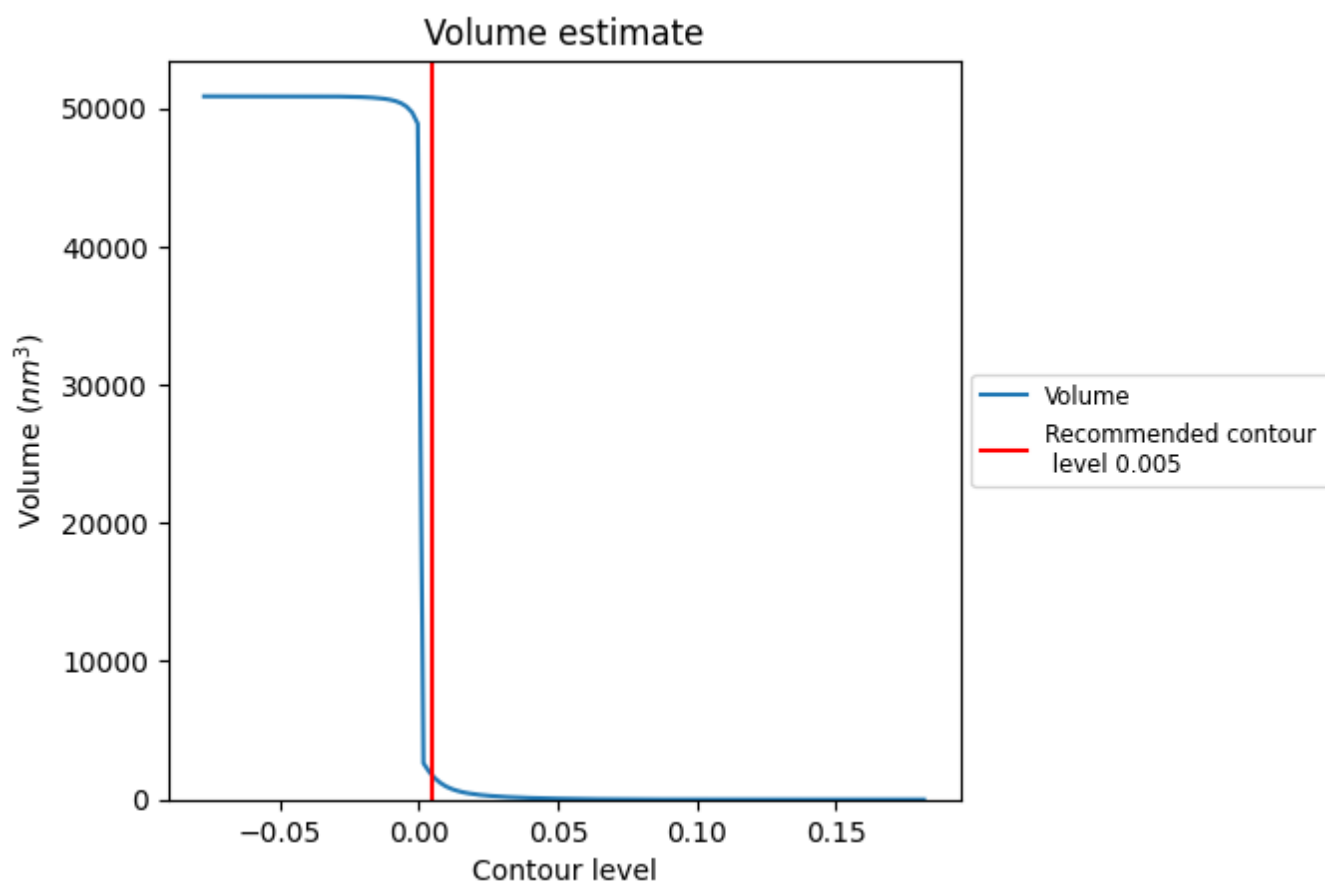
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

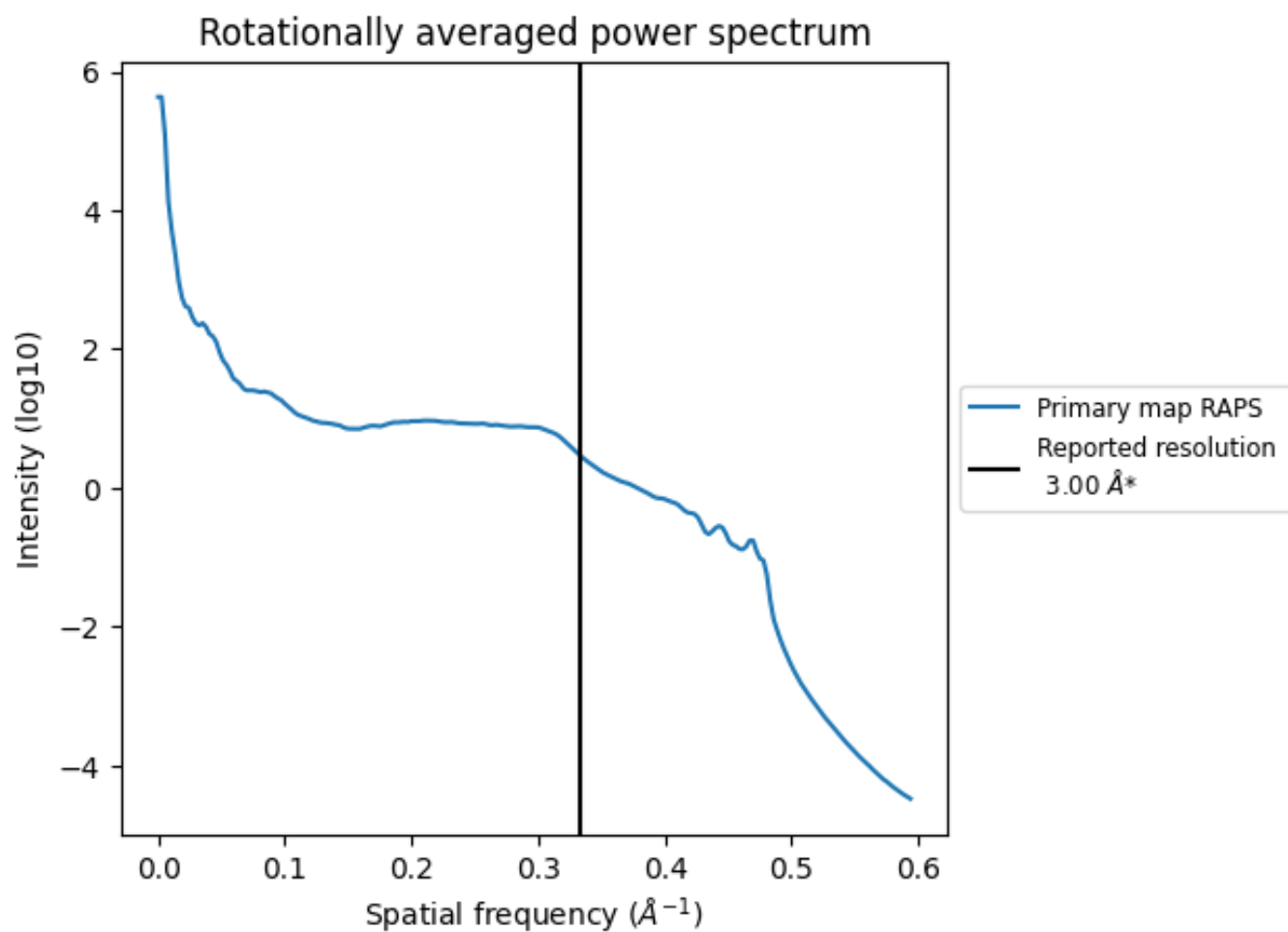
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1735 nm^3 ; this corresponds to an approximate mass of 1567 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 0.333 Å⁻¹

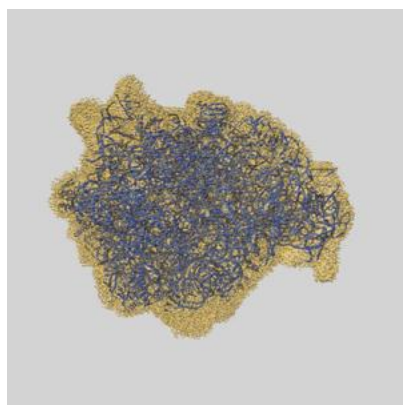
8 Fourier-Shell correlation

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

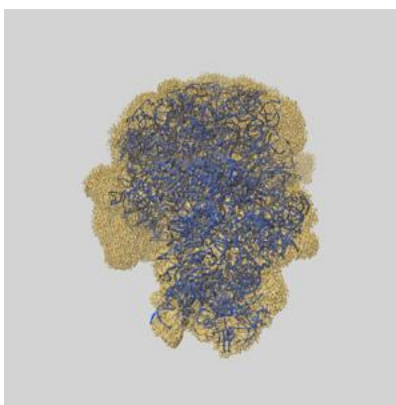
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-52641 and PDB model 9I5X. Per-residue inclusion information can be found in section 3 on page 14.

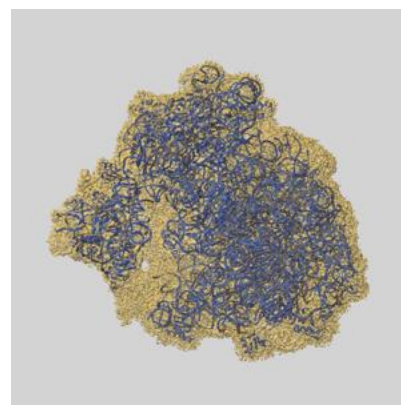
9.1 Map-model overlay [i](#)



X



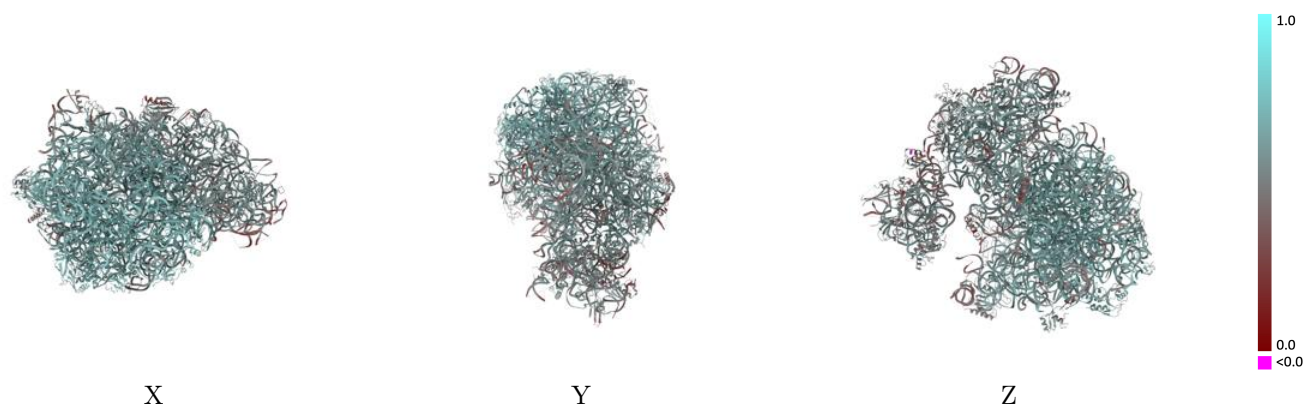
Y



Z

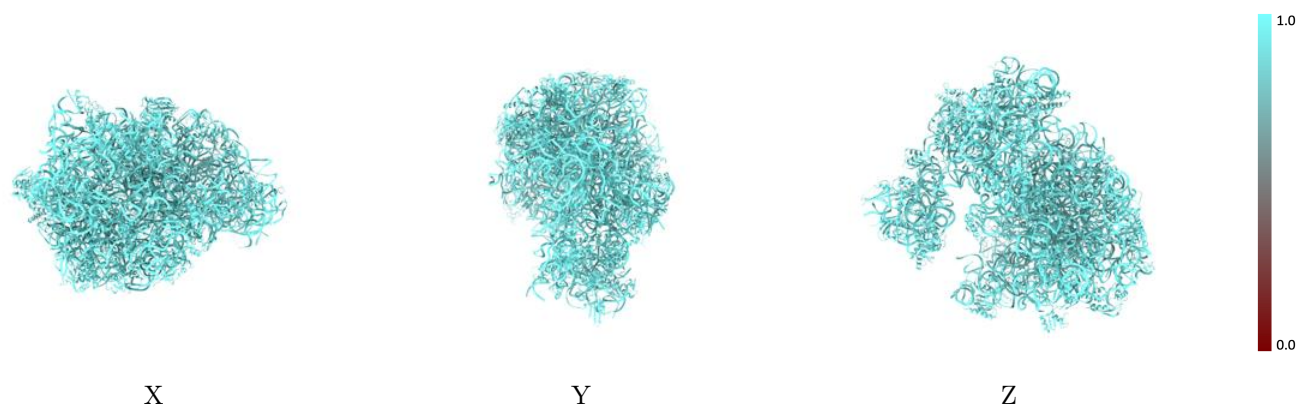
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



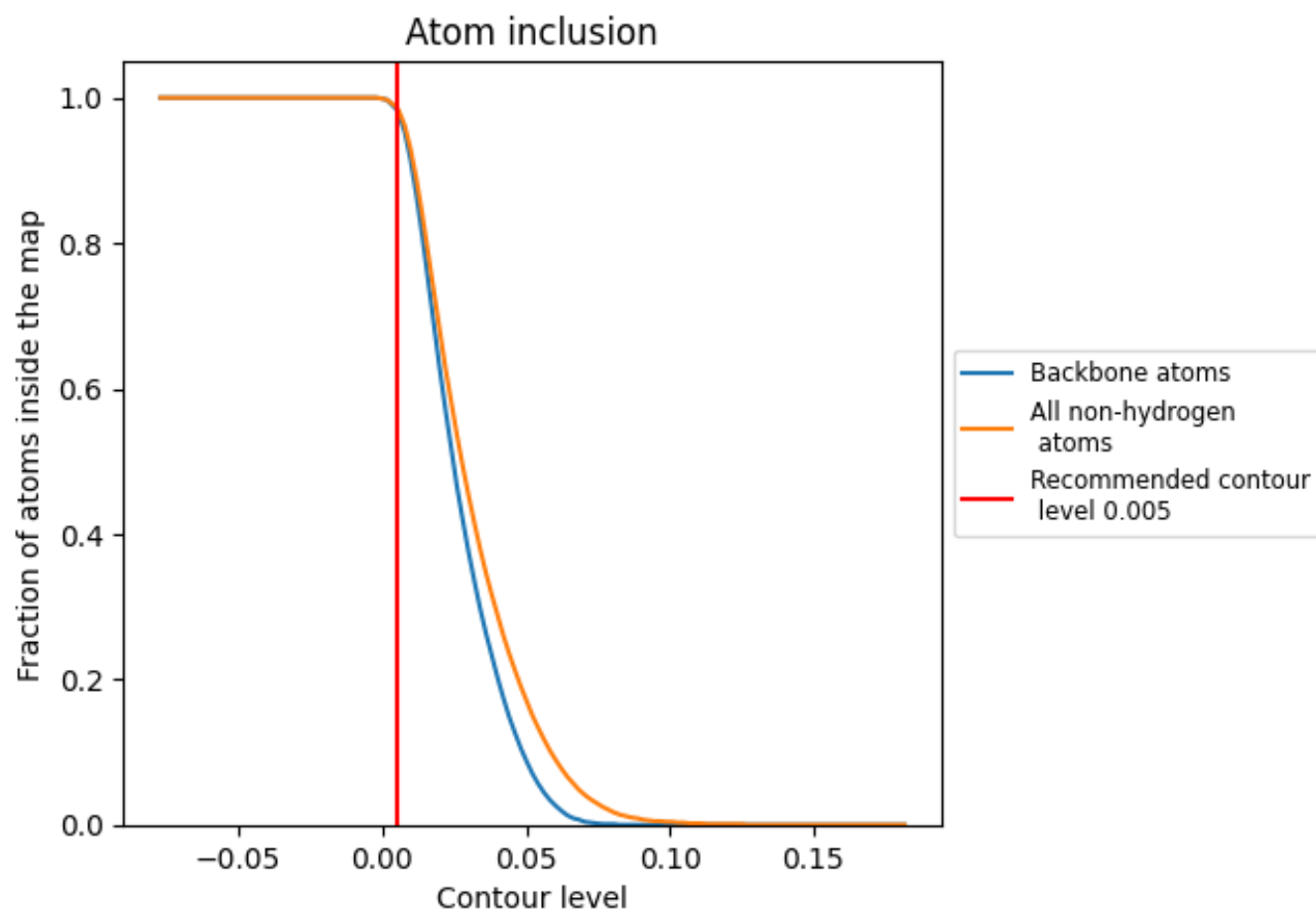
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 99% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9870	 0.5910
0	 0.9950	 0.6430
1	 0.9770	 0.5490
10	 0.9330	 0.5720
2	 0.9950	 0.6480
4	 0.9950	 0.6550
5	 0.9760	 0.5690
6	 0.9920	 0.6860
7	 0.9780	 0.6130
8	 0.9760	 0.5920
A	 0.9960	 0.6320
B	 0.9850	 0.4980
D	 0.9910	 0.6550
E	 0.9950	 0.6600
F	 0.9910	 0.6510
I	 0.9780	 0.5250
J	 0.9760	 0.5370
K	 0.9580	 0.5220
L	 0.9470	 0.4580
M	 0.9890	 0.6480
N	 0.9870	 0.6350
O	 0.9900	 0.6110
P	 0.9810	 0.6040
Q	 0.9960	 0.6640
R	 0.9750	 0.5130
S	 0.9900	 0.6260
T	 0.9970	 0.6810
U	 0.9890	 0.6440
V	 0.9950	 0.6680
W	 0.9840	 0.5970
X	 0.9900	 0.6140
Y	 0.9910	 0.5550
Z	 0.9960	 0.6660
a	 0.9820	 0.5240
b	 0.9570	 0.4690



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
c	 0.9740	 0.5530
d	 0.9720	 0.5450
e	 0.9840	 0.5630
f	 0.9660	 0.5330
g	 0.9690	 0.5530
h	 0.9490	 0.5170
i	 0.9770	 0.5210
j	 0.9530	 0.5570
k	 0.9430	 0.4990
l	 0.9680	 0.5060
m	 0.9530	 0.4960
n	 0.9650	 0.5290
o	 0.9840	 0.5680
p	 0.9860	 0.5570