



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 03:47 AM UTC

PDB ID : 9Y4H / pdb_00009y4h
EMDB ID : EMD-72483
Title : Structure of guinea pig ribosome with P/E-tRNA and mRNA
Authors : Gutierrez-Vargas, C.; De, S.; Maji, S.; Liu, Z.; Nieb, M.; Seluanov, A.; Gorbunova, V.; Frank, J.
Deposited on : 2025-09-03
Resolution : 4.70 Å(reported)
Based on initial model : 4V6X

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

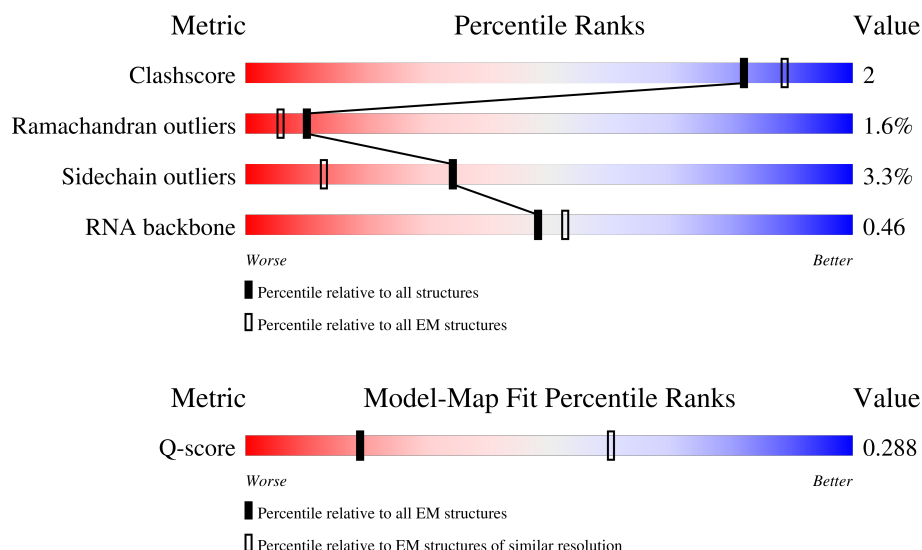
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.70 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.









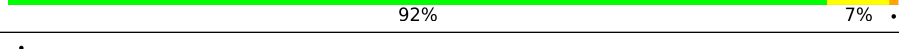
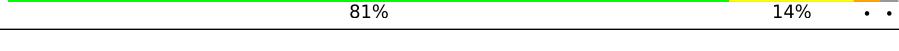
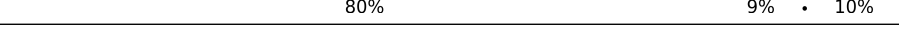
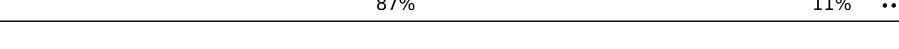
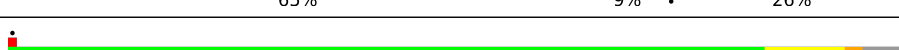

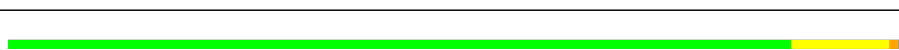

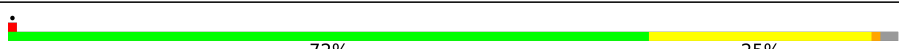



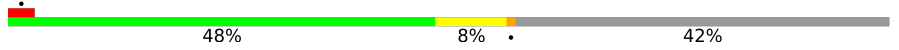

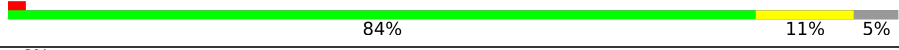
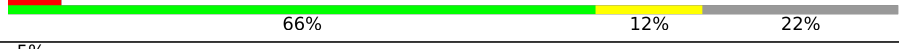



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1989 (4.20 - 5.20)

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	AO	151	
2	AX	143	
3	AN	151	



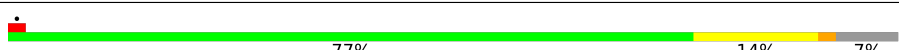
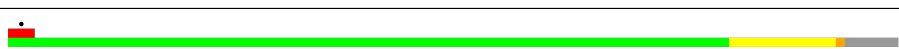

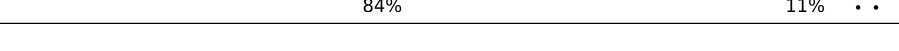
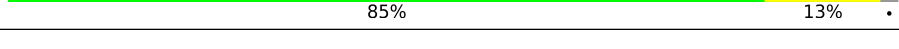



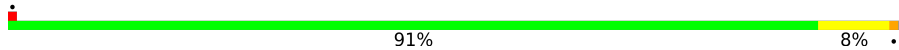

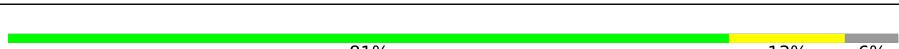


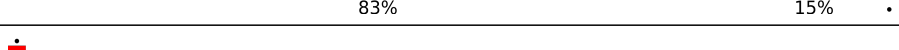


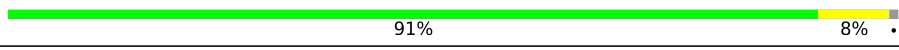





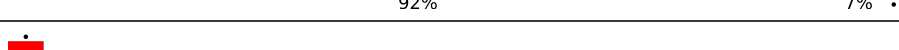
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Mol	Chain	Length	Quality of chain
4	AL	158	
5	AB	264	
6	AA	295	
7	AV	83	
8	AY	133	
9	Aa	115	
10	Ab	84	
11	Ae	59	
12	AJ	194	
13	AE	263	
14	AC	293	
15	AG	249	
16	AH	194	
17	AW	130	
18	AI	208	
19	B2	1803	
20	CW	157	
21	Ag	317	
22	AU	119	
23	AK	165	
24	AS	152	
25	Ad	56	
26	AR	135	
27	AP	145	
28	AT	145	


























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Mol	Chain	Length	Quality of chain
29	AZ	125	
30	Ac	69	
31	AD	243	
32	AF	204	
33	AQ	146	
34	CO	203	
35	CL	211	
36	CV	140	
37	CM	215	
38	Ca	148	
39	CN	204	
40	CI	214	
41	CD	297	
42	CQ	188	
43	CA	257	
44	CS	176	
45	CT	160	
46	CP	184	
47	CU	128	
48	CX	156	
49	CY	145	
50	CZ	136	
51	Cr	137	
52	Ch	123	
53	Cb	159	

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Mol	Chain	Length	Quality of chain
54	CB	403	
55	CF	248	
56	Cc	115	
57	Cd	125	
58	Ce	135	
59	Cf	110	
60	Cg	117	
61	Ci	105	
62	Cj	97	
63	Ck	70	
64	Cl	51	
65	CC	427	
66	Cm	52	
67	Cn	25	
68	Cp	92	
69	Co	106	
70	CJ	178	
71	CH	192	
72	CE	288	
73	CG	266	
74	A5	4010	
75	A7	121	
76	A8	157	
77	Cw	77	
78	Dd	7	

2 Entry composition [i](#)

There are 79 unique types of molecules in this entry. The entry contains 371528 atoms, of which 156643 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 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	AO	126	Total	C	H	N	O	S	0	0
			1921	580	973	188	174	6		

- Molecule 2 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	AX	140	Total	C	H	N	O	S	0	0
			2257	691	1163	218	182	3		

- Molecule 3 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	AN	150	Total	C	H	N	O	S	0	0
			2502	773	1294	229	205	1		

- Molecule 4 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	AL	147	Total	C	H	N	O	S	0	0
			2495	777	1279	226	207	6		

- Molecule 5 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	AB	215	Total	C	H	N	O	S	0	0
			3567	1110	1820	313	310	14		

- Molecule 6 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	AA	206	Total	C	H	N	O	S	0	0
			3250	1035	1626	287	294	8		

- Molecule 7 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	AV	81	Total	C	H	N	O	S	0	0
			1232	379	615	115	119	4		

- Molecule 8 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	AY	126	Total	C	H	N	O	S	0	0
			2111	646	1088	200	172	5		

- Molecule 9 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	Aa	98	Total	C	H	N	O	S	0	0
			1613	486	832	161	129	5		

- Molecule 10 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	Ab	84	Total	C	H	N	O	S	0	0
			1339	413	680	122	116	8		

- Molecule 11 is a protein called FAU ubiquitin like and ribosomal protein S30 fusion.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	Ae	58	Total	C	H	N	O	S	0	0
			972	287	511	101	72	1		

- Molecule 12 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	AJ	174	Total	C	H	N	O	S	0	0
			3025	931	1566	291	235	2		

- Molecule 13 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AE	261	Total	C	H	N	O	S	0	0
			4254	1324	2181	385	355	9		

- Molecule 14 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AC	218	Total	C	H	N	O	S	0	0
			3469	1096	1777	290	296	10		

- Molecule 15 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	AG	237	Total	C	H	N	O	S	0	0
			4008	1200	2085	387	329	7		

- Molecule 16 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	AH	179	Total	C	H	N	O	S	0	0
			2983	924	1534	266	258	1		

- Molecule 17 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	AW	129	Total	C	H	N	O	S	0	0
			2113	659	1079	193	176	6		

- Molecule 18 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	AI	200	Total	C	H	N	O	S	0	0
			3364	1031	1720	324	284	5		

- Molecule 19 is a RNA chain called 18S rRNA (1803-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
19	B2	1773	Total	C	H	N	O	P	0	0
			56567	16783	18948	6729	12335	1772		

- Molecule 20 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	CW	118	Total	C	H	N	O	S	0	0
			1988	604	1023	199	158	4		

- Molecule 21 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	Ag	299	Total	C	H	N	O	S	0	0
			4623	1474	2289	408	440	12		

- Molecule 22 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	AU	103	Total	C	H	N	O	S	0	0
			1699	511	882	155	147	4		

- Molecule 23 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	AK	95	Total	C	H	N	O	S	0	0
			1621	524	822	139	130	6		

- Molecule 24 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	AS	137	Total	C	H	N	O	S	0	0
			2327	714	1188	231	193	1		

- Molecule 25 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Ad	53	Total	C	H	N	O	S	0	0
			887	278	442	90	72	5		

- Molecule 26 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	AR	105	Total	C	H	N	O	S	0	0
			1768	538	910	164	151	5		

- Molecule 27 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	AP	124	Total	C	H	N	O	S	0	0
			2136	659	1099	198	173	7		

- Molecule 28 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	AT	141	Total	C	H	N	O	S	0	0
			2236	690	1135	212	196	3		

- Molecule 29 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	AZ	74	Total	C	H	N	O	S	0	0
			1243	380	649	110	103	1		

- Molecule 30 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	Ac	64	Total	C	H	N	O	S	0	0
			1041	308	535	102	94	2		

- Molecule 31 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	AD	227	Total	C	H	N	O	S	0	0
			3622	1125	1857	317	315	8		

- Molecule 32 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	AF	191	Total	C	H	N	O	S	0	0
			3067	943	1558	286	273	7		

- Molecule 33 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	AQ	141	Total	C	H	N	O	S	0	0
			2316	715	1192	212	194	3		

- Molecule 34 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	CO	199	Total	C	H	N	O	S	0	0
			3410	1053	1776	319	257	5		

- Molecule 35 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	CL	204	Total	C	H	N	O	S	0	0
			3406	1032	1757	343	270	4		

- Molecule 36 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	CV	129	Total	C	H	N	O	S	0	0
			1999	613	1030	182	169	5		

- Molecule 37 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	CM	139	Total	C	H	N	O	S	0	0
			2348	730	1209	218	183	8		

- Molecule 38 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	Ca	147	Total	C	H	N	O	S	0	0
			2372	736	1210	237	186	3		

- Molecule 39 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	CN	203	Total	C	H	N	O	S	0	0
			3448	1072	1747	359	266	4		

- Molecule 40 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	CI	202	Total	C	H	N	O	S	0	0
			3300	1037	1666	314	269	14		

- Molecule 41 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	CD	289	Total	C	H	N	O	S	0	0
			4723	1483	2370	429	427	14		

- Molecule 42 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	CQ	187	Total	C	H	N	O	S	0	0
			3142	944	1629	314	250	5		

- Molecule 43 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	CA	255	Total	C	H	N	O	S	0	0
			4008	1225	2051	399	327	6		

- Molecule 44 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	CS	175	Total	C	H	N	O	S	0	0
			2938	925	1485	283	235	10		

- Molecule 45 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	CT	159	Total	C	H	N	O	S	0	0
			2661	823	1363	252	217	6		

- Molecule 46 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	CP	152	Total	C	H	N	O	S	0	0
			2493	771	1260	240	213	9		

- Molecule 47 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	CU	102	Total	C	H	N	O	S	0	0
			1698	535	863	147	151	2		

- Molecule 48 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	CX	121	Total	C	H	N	O	S	0	0
			2072	636	1078	187	170	1		

- Molecule 49 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	CY	133	Total	C	H	N	O	S	0	0
			2300	695	1193	225	185	2		

- Molecule 50 is a protein called 60S ribosomal protein L27.

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

- Molecule 51 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	Cr	134	Total	C	H	N	O	S	0	0
			2247	670	1164	227	180	6		

- Molecule 52 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	Ch	123	Total	C	H	N	O	S	0	0
			2183	646	1160	206	169	2		

- Molecule 53 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	Cb	68	Total	C	H	N	O	S	0	0
			1149	344	590	122	90	3		

- Molecule 54 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	CB	394	Total	C	H	N	O	S	0	0
			6484	2024	3306	596	544	14		

- Molecule 55 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	CF	229	Total	C	H	N	O	S	0	0
			3956	1226	2046	370	305	9		

- Molecule 56 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	Cc	100	Total	C	H	N	O	S	0	0
			1588	492	812	136	141	7		

- Molecule 57 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	Cd	113	Total	C	H	N	O	S	0	0
			1910	586	979	181	162	2		

- Molecule 58 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	Ce	129	Total	C	H	N	O	S	0	0
			2219	672	1158	217	166	6		

- Molecule 59 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	Cf	109	Total	C	H	N	O	S	0	0
			1786	555	910	174	144	3		

- Molecule 60 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	Cg	114	Total	C	H	N	O	S	0	0
			1905	566	999	187	147	6		

- Molecule 61 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	Ci	103	Total	C	H	N	O	S	0	0
			1765	526	925	178	130	6		

- Molecule 62 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	Cj	87	Total	C	H	N	O	S	0	0
			1470	440	754	159	112	5		

- Molecule 63 is a protein called Large ribosomal subunit protein eL38.

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

- Molecule 64 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	Cl	48	Total	C	H	N	O	S	0	0
			900	273	469	96	61	1		

- Molecule 65 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	CC	360	Total	C	H	N	O	S	0	0
			5900	1805	3033	573	476	13		

- Molecule 66 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
66	Cm	51	Total	C	H	N	O	S	0	0
			875	260	456	88	65	6		

- Molecule 67 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms						AltConf	Trace
67	Cn	25	Total	C	H	N	O	S	0	0
			529	145	289	64	28	3		

- Molecule 68 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms						AltConf	Trace
68	Cp	90	Total	C	H	N	O	S	0	0
			1458	442	755	135	119	7		

- Molecule 69 is a protein called Ribosomal protein L36a.

Mol	Chain	Residues	Atoms						AltConf	Trace
69	Co	101	Total	C	H	N	O	S	0	0
			1720	517	893	170	134	6		

- Molecule 70 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms						AltConf	Trace
70	CJ	168	Total	C	H	N	O	S	0	0
			2732	853	1383	251	239	6		

- Molecule 71 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
71	CH	191	Total	C	H	N	O	S	0	0
			3129	960	1603	285	275	6		

- Molecule 72 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
72	CE	252	Total	C	H	N	O	S	0	0
			4253	1307	2217	387	338	4		

- Molecule 73 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms						AltConf	Trace
73	CG	246	Total	C	H	N	O	S	0	0
			4093	1256	2120	379	334	4		

- Molecule 74 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
74	A5	3875	Total	C	H	N	O	P	0	0
			122271	36174	40870	14718	26635	3874		

- Molecule 75 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
75	A7	121	Total	C	H	N	O	P	0	0
			3884	1150	1306	458	850	120		

- Molecule 76 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
76	A8	156	Total	C	H	N	O	P	0	0
			4996	1480	1682	585	1094	155		

- Molecule 77 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
77	Cw	77	Total	C	H	N	O	P	0	0
			2481	732	837	298	537	77		

- Molecule 78 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
78	Dd	7	Total	C	H	N	O	P	0	0
			209	63	69	14	56	7		

- Molecule 79 is water.

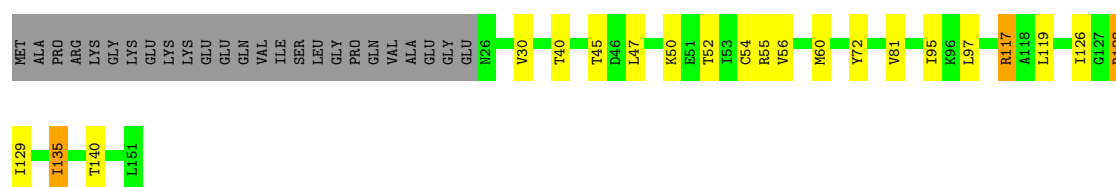
Mol	Chain	Residues	Atoms		AltConf
79	B2	2	Total	O	0
			2	2	
79	Cw	4	Total	O	0
			4	4	
79	Dd	1	Total	O	0
			1	1	

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: 40S ribosomal protein S14

Chain AO: 



- Molecule 2: Small ribosomal subunit protein uS12

Chain AX: 




- Molecule 3: 40S ribosomal protein S13

Chain AN: 



- Molecule 4: Small ribosomal subunit protein uS17

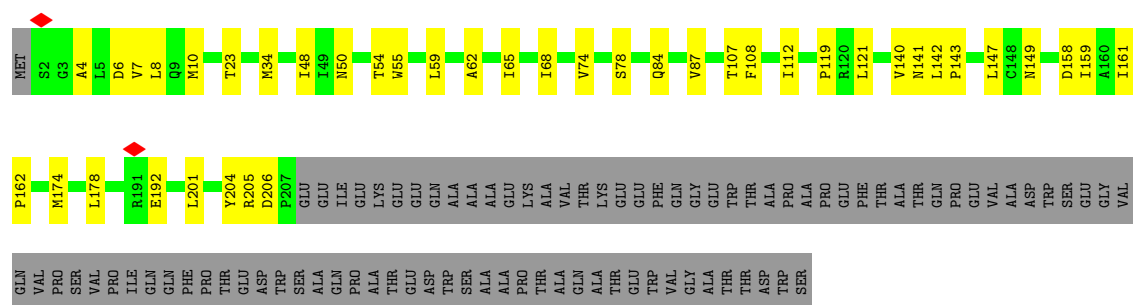
Chain AL: 



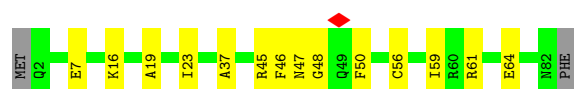
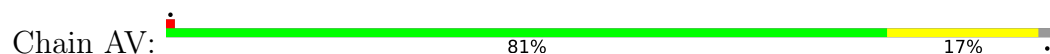
- Molecule 5: Small ribosomal subunit protein eS1

Chain AB: 

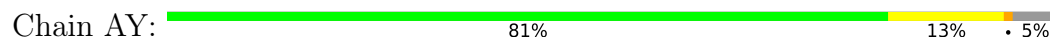
- Molecule 6: 40S ribosomal protein SA



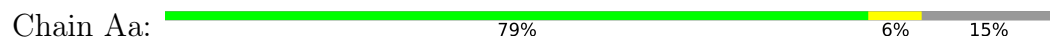
- Molecule 7: 40S ribosomal protein S21



- Molecule 8: 40S ribosomal protein S24



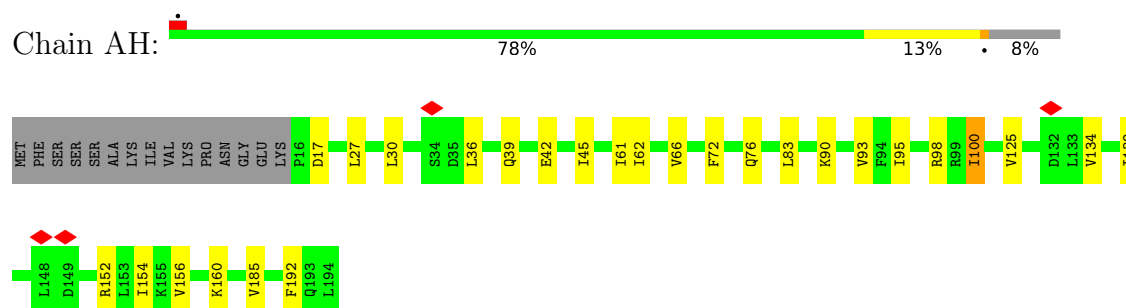
- Molecule 9: 40S ribosomal protein S26



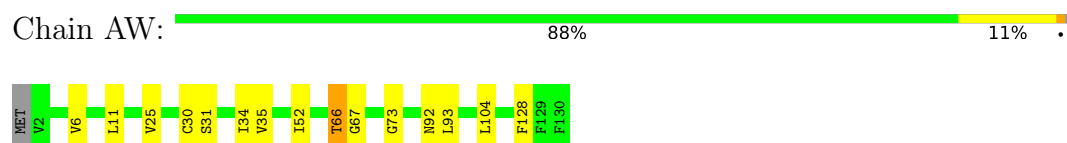
- Molecule 10: 40S ribosomal protein S27



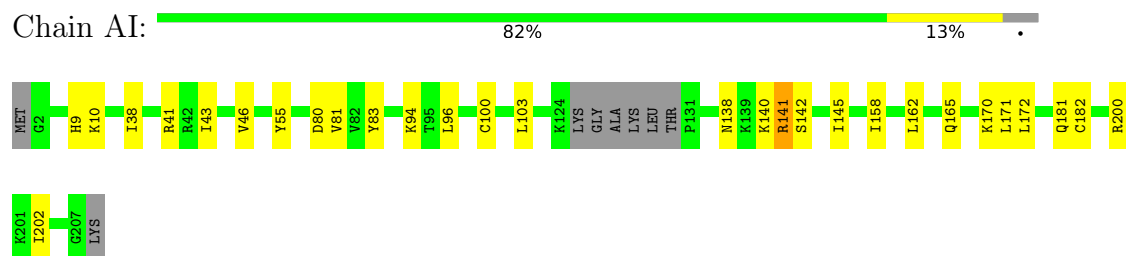
- Molecule 16: 40S ribosomal protein S7



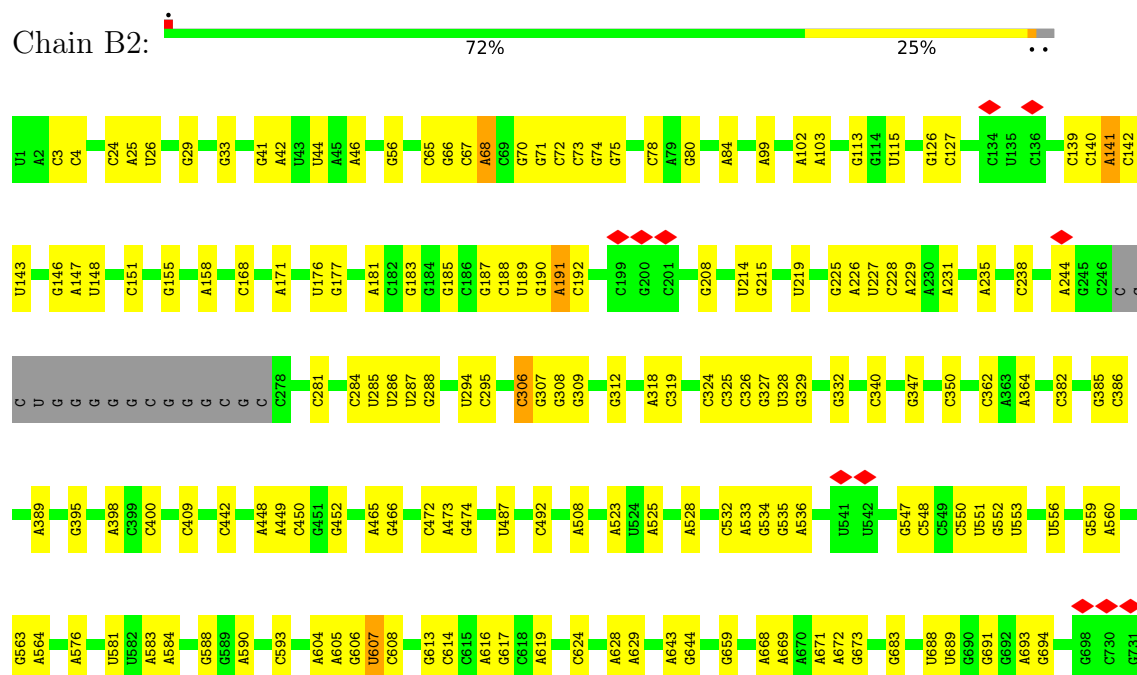
- Molecule 17: Small ribosomal subunit protein uS8

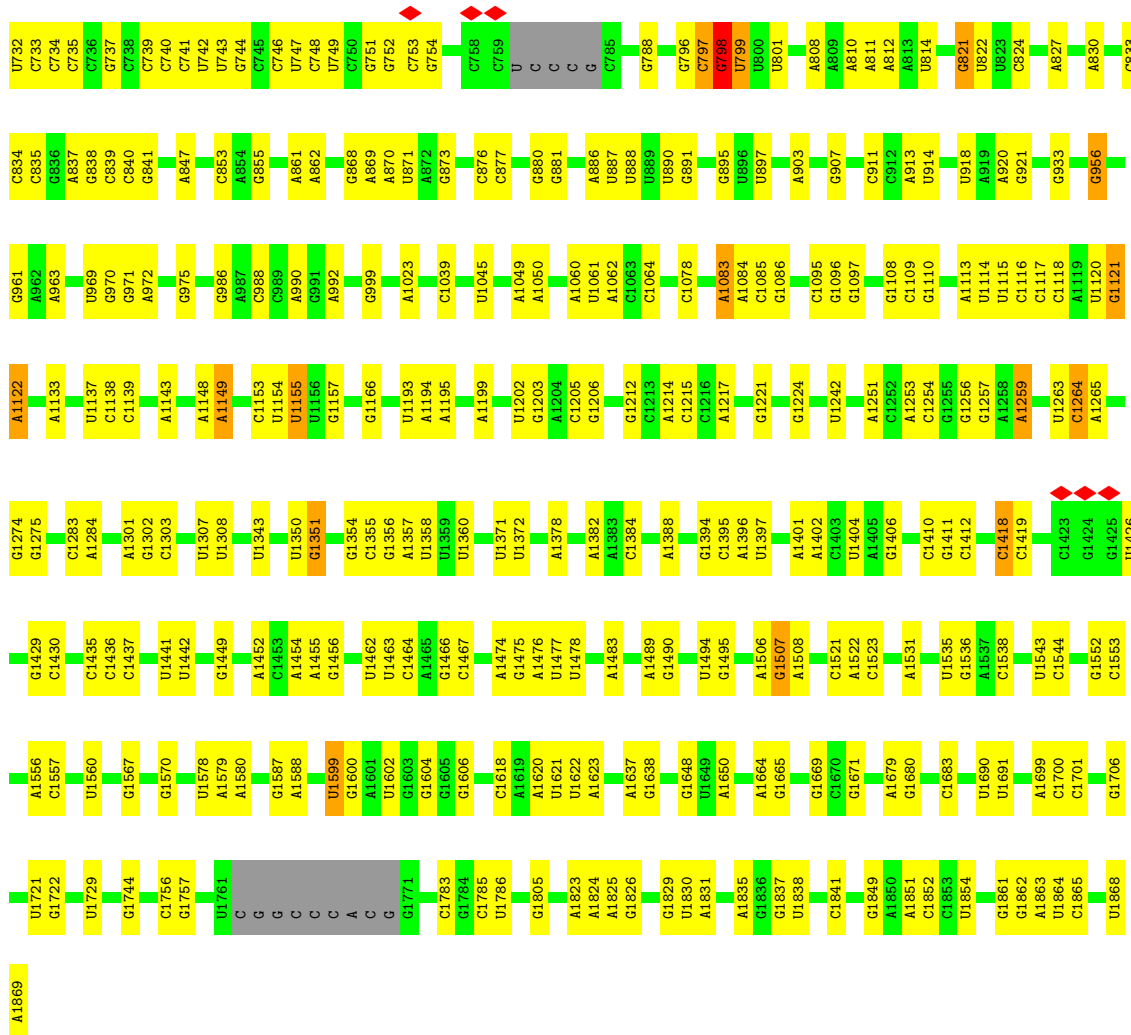


- Molecule 18: 40S ribosomal protein S8

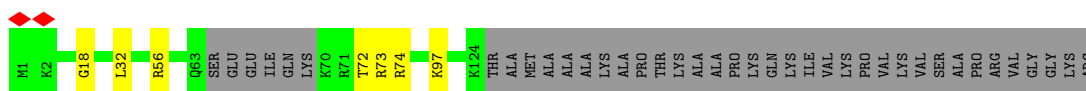
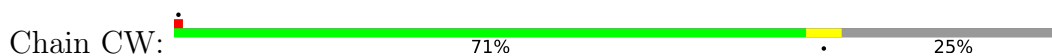


- Molecule 19: 18S rRNA (1803-MER)

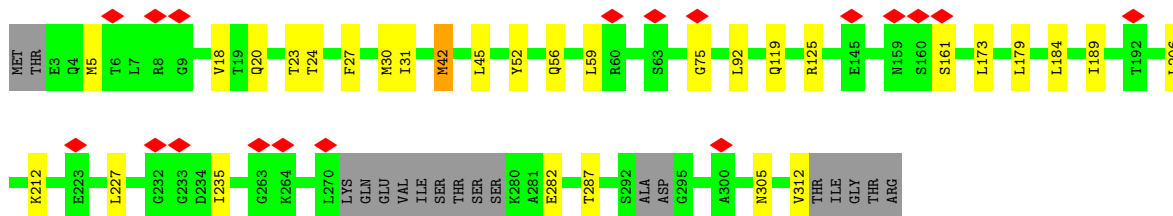
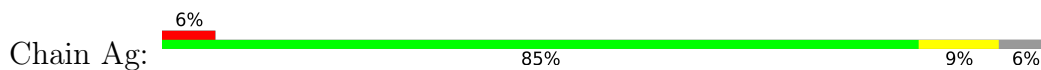




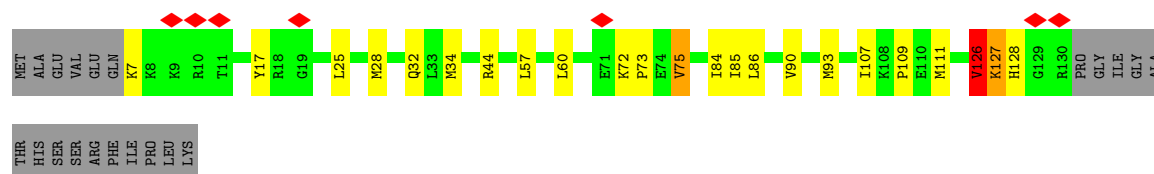
- Molecule 20: Large ribosomal subunit protein eL24



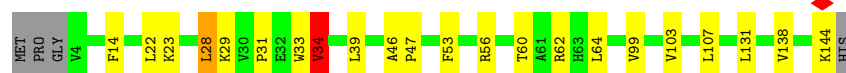
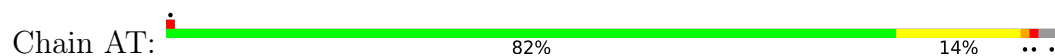
- Molecule 21: Small ribosomal subunit protein RACK1



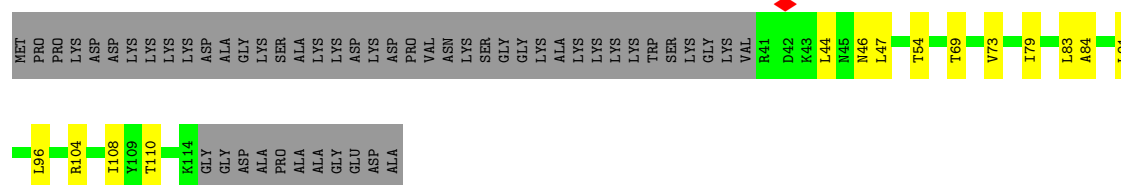
- Molecule 22: Small ribosomal subunit protein uS10



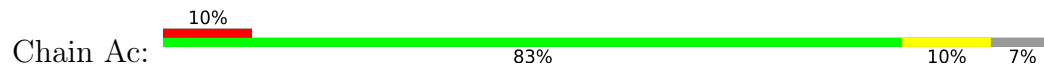
- Molecule 28: Small ribosomal subunit protein eS19



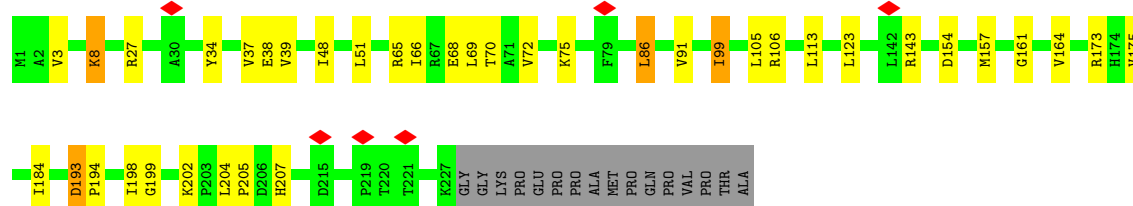
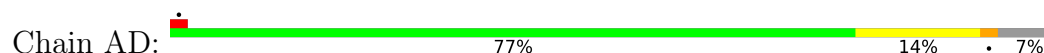
- Molecule 29: 40S ribosomal protein S25



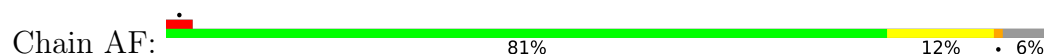
- Molecule 30: 40S ribosomal protein S28

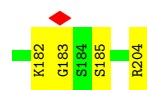


- Molecule 31: 40S ribosomal protein S3

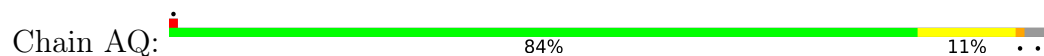


- Molecule 32: Small ribosomal subunit protein uS7

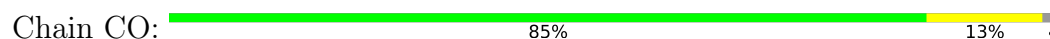




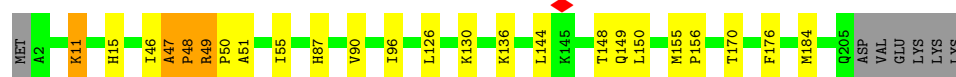
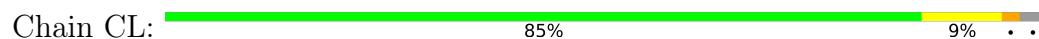
- Molecule 33: Small ribosomal subunit protein uS9



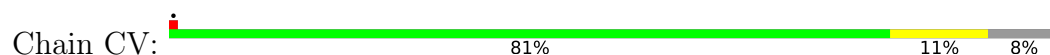
- Molecule 34: 60S ribosomal protein L13a



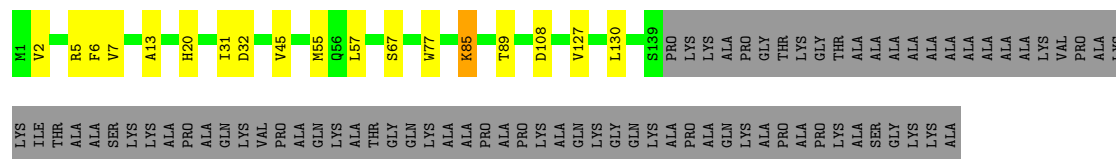
- Molecule 35: 60S ribosomal protein L13



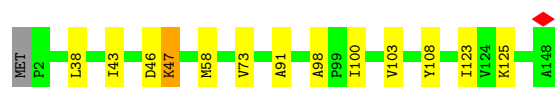
- Molecule 36: Large ribosomal subunit protein uL14



- Molecule 37: 60S ribosomal protein L14

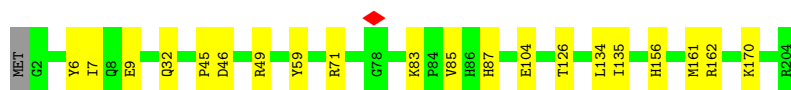


- Molecule 38: 60S ribosomal protein L27a




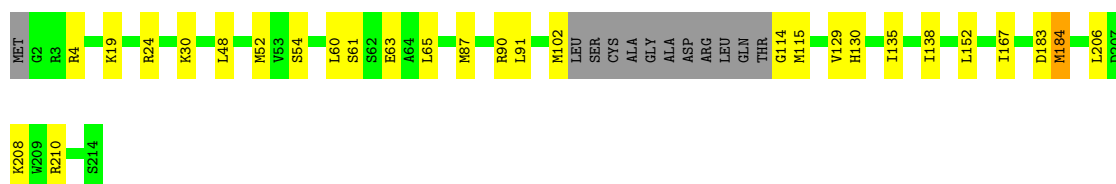
- Molecule 39: Ribosomal protein L15

Chain CN:  90% 10%




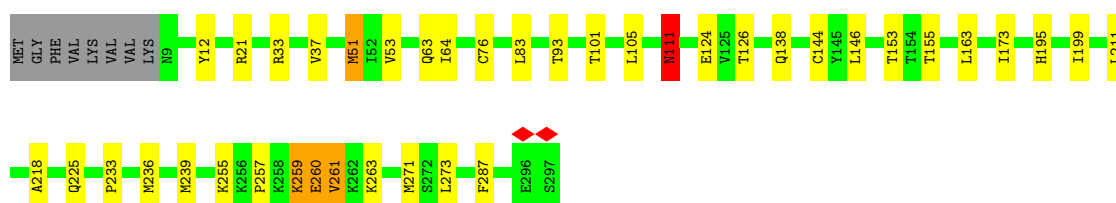
- Molecule 40: 60S ribosomal protein L10-like

Chain CI:  81% 13% 6%




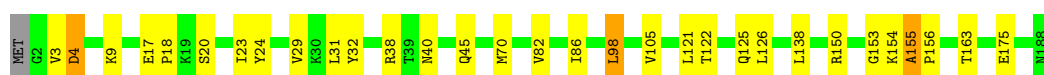
- Molecule 41: 60S ribosomal protein L5

Chain CD:  84% 12% ..



- Molecule 42: 60S ribosomal protein L18

Chain CQ:  83% 15% ..




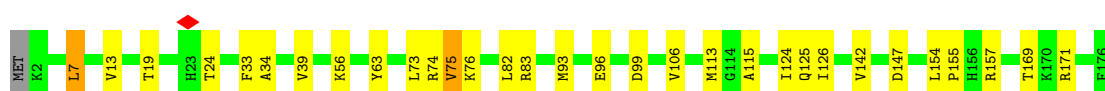
- Molecule 43: Large ribosomal subunit protein uL2

Chain CA:  89% 10% .



- Molecule 44: 60S ribosomal protein L18a

Chain CS:  82% 16% ..



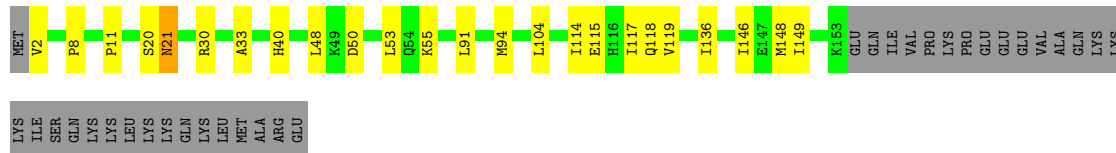
- Molecule 45: Large ribosomal subunit protein eL21

Chain CT:  91% 8%



- Molecule 46: 60S ribosomal protein L17

Chain CP:  70% 12% 17%



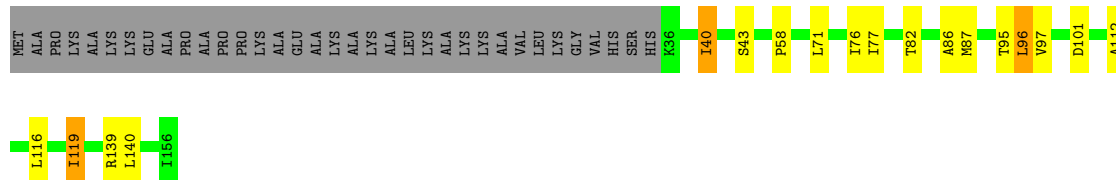
- Molecule 47: 60S ribosomal protein L22

Chain CU:  69% 11% 20%




- Molecule 48: 60S ribosomal protein L23a

Chain CX:  66% 10% 22%



- Molecule 49: Large ribosomal subunit protein uL24

Chain CY:  85% 6% 8%

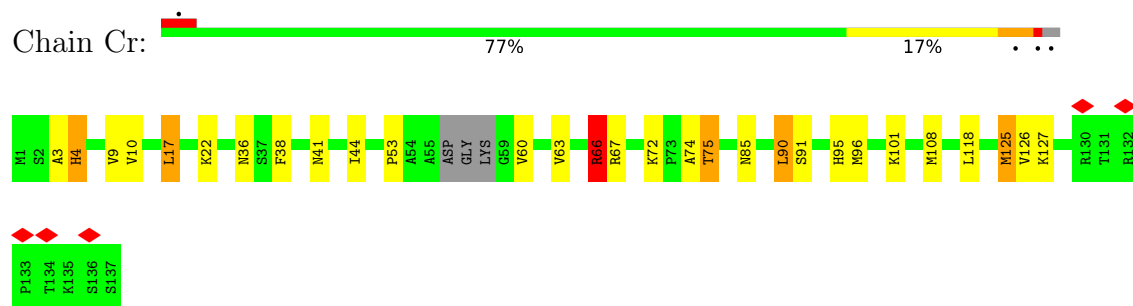


- Molecule 50: 60S ribosomal protein L27

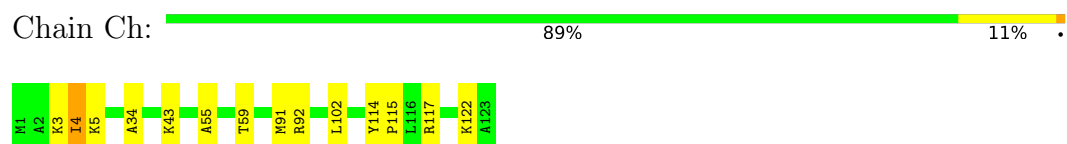
Chain CZ:  92% 7%



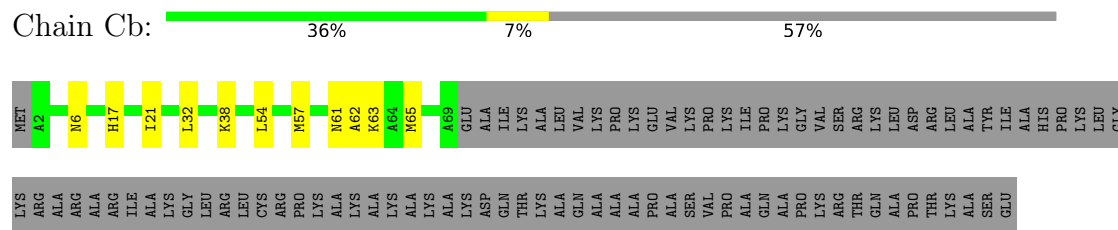
- Molecule 51: Large ribosomal subunit protein eL28



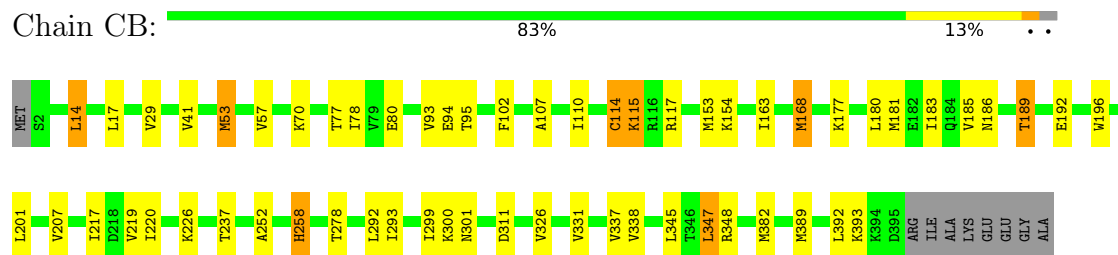
- Molecule 52: 60S ribosomal protein L35



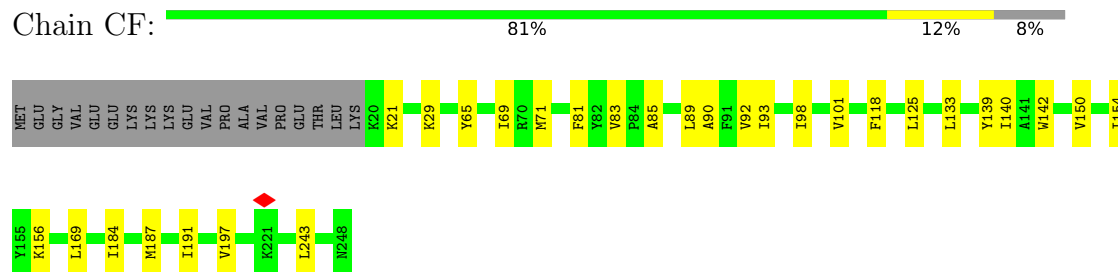
- Molecule 53: 60S ribosomal protein L29



- Molecule 54: 60S ribosomal protein L3




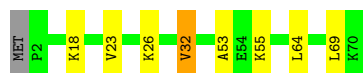
- Molecule 55: 60S ribosomal protein L7




- Molecule 56: Large ribosomal subunit protein eL30



Chain Ck:  87% 10% ..



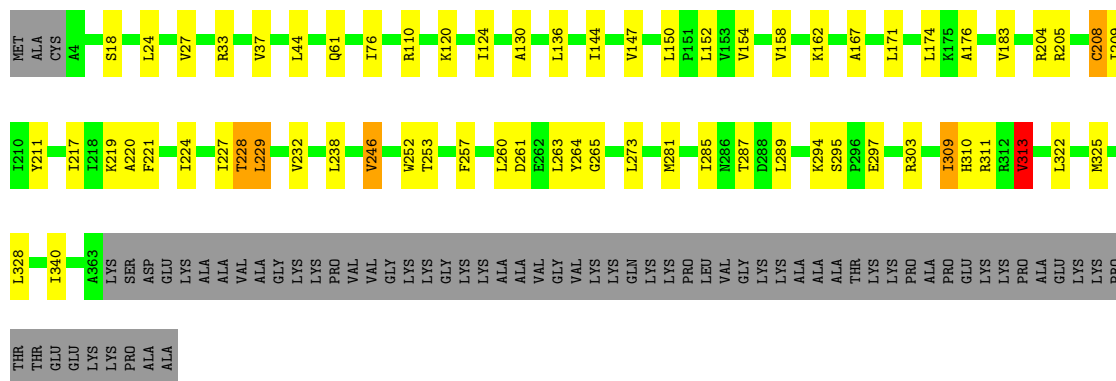
- Molecule 64: 60S ribosomal protein L39

Chain Cl:  82% 10% • 6%




- Molecule 65: 60S ribosomal protein L4

Chain CC:  69% 14% • 16%



- Molecule 66: Ubiquitin-ribosomal protein eL40 fusion protein

Chain Cm:  75% 23% •




- Molecule 67: 60S ribosomal protein L41

Chain Cn:  96% •




- Molecule 68: Large ribosomal subunit protein eL43

Chain Cp:  85% 12% ..




- Molecule 69: Ribosomal protein L36a

Chain Co:  81% 13% • 5%



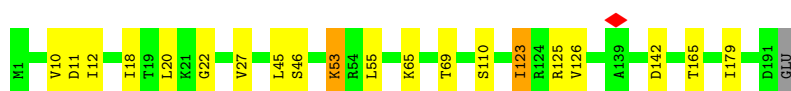
- Molecule 70: Large ribosomal subunit protein uL5

Chain CJ:  80% 13% • 6%



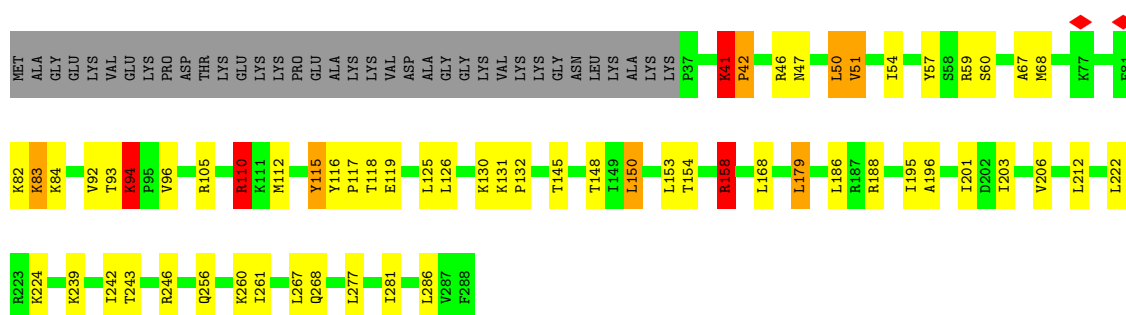
- Molecule 71: 60S ribosomal protein L9

Chain CH:  89% 9% ••




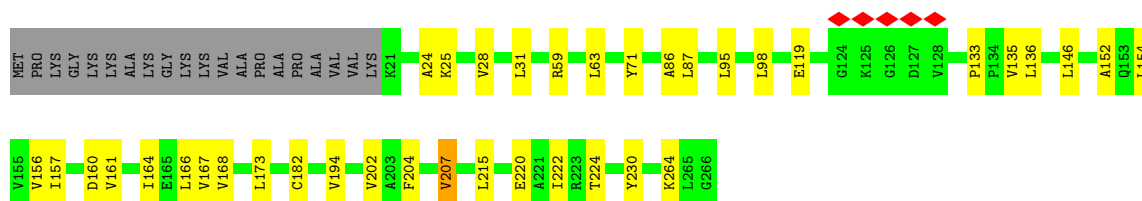
- Molecule 72: 60S ribosomal protein L6

Chain CE:  66% 18% •• 12%




- Molecule 73: 60S ribosomal protein L7a

Chain CG:  78% 14% 8%

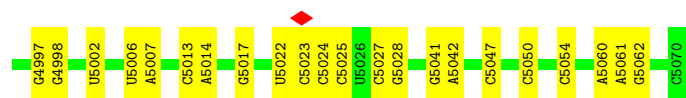


- Molecule 74: 28S ribosomal RNA

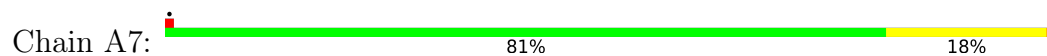
Chain A5:  72% 24% ••



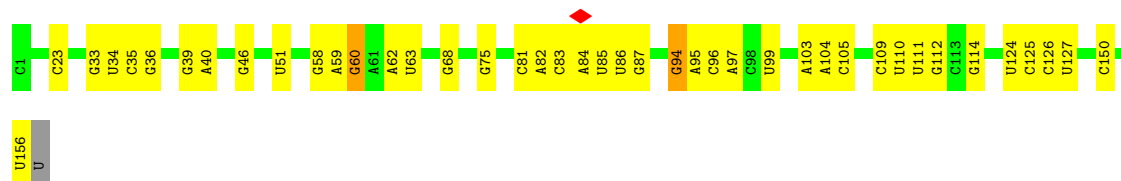
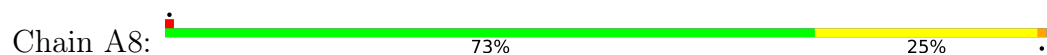
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U4512	A4513	G4524	G4527	G4534	A4548	U4556	U4557	G4567	A4568	U4569	U4574	G4575	A4584	U4588	A4589	A4590	G4591	G4592	A4599	A4616	A4626	U4627	G4633	U4634	G4637	G4652	A4656	U4657	A4664	G4670	C4671	A4672	U4677	A4687	G4694	G4695	G4696	A4871	G4872	A4873	A4874	G4875	U4876																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
C4335	A4336	C4337	C4341	C4349	C4350	U4354	G4355	G4356	G4373	A4376	C4377	A4378	A4381	C4387	G4393	A4394	U4395	A4396	G4405	U4419	A4422	C4426	U4436	U4437	U4438	C4444	C4448	A4449	U4452	U4457	U4463	A4464	A4473	C4476	U4500	C4508																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
A4157	C4158	C4159	C4161	C4162	U4163	C4164	C4165	A4170	C4171	U4174	G4183	G4184	G4191	G4196	G4217	G4222	U4229	U4232	A4233	A4254	G4267	G4268	A4271	A4272	A4273	C4284	U4295	U4296	U4299	A4304	G4305	U4306	G4326	G4329	G4330	G4331	G4332																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
G	G4028	G4036	G4037	G4038	G4041	G4042	G4043	A4047	A4048	U4049	A4053	G4054	U4055	C4072	A4073	U4075	A4076	A4077	G4082	U4083	G4084	A4085	G4086	G4087	G4088	G4093	G4094	G4107	C4114	C4115	U4117	U4118	C4119	U4120	G4121	C4122	C4123	G4124	C4125	C4126	A4127	A4128	G4143	C4144	G4150																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
A4157	C4158	C4159	C4161	C4162	U4163	C4164	C4165	A4170	C4171	U4174	G4183	G4184	G4191	G4196	G4217	G4222	U4229	U4232	A4233	A4254	G4267	G4268	A4271	A4272	A4273	C4284	U4295	U4296	U4299	A4304	G4305	U4306	G4326	G4329	G4330	G4331	G4332																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
C4335	A4336	C4337	C4341	C4349	C4350	U4354	G4355	G4356	G4373	A4376	C4377	A4378	A4381	C4387	G4393	A4394	U4395	A4396	G4405	U4419	A4422	C4426	U4436	U4437	U4438	C4444	C4448	A4449	U4452	U4457	U4463	A4464	A4473	C4476	U4500	C4508																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
U4700	A4708	U4709	G4713	C4714	G4719	C4720	G4730	G4731	G4732	G4733	A4734	G4738	C4739	C4747	U4748	G4749	G4750	G4751	U4752	G4753	G4754	G4755	G4756	G4757	U4758	A4764	C4767	C4771	G4789	G4790	G4791	G4794	C4795	G4837	U4838	G4839	C4843	U4869	G4870	G4871	G4872	G4873	A4874	G4875	U4876																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
G2116	G2117	G2118	G2119	G2122	C2123	G2124	G2125	G2126	G2127	G2133	G2241	G2242	G2246	C2247	C2248	G2249	C2250	G2251	G2252	G2253	G2254	C2255	C2256	C2257	G2258	A2259	C2260	G2261	A2263	C2264	G2265	C2266	U2267	A2268	C2269	G2270	C2271	C2272	G2273	C2289	C2290	A2300	G2301	G2306	U2312	A2313	G2314	C2326																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
G2331	A2332	G2333	G2345	G2346	A2347	G2348	G2349	C2351	A2360	A2370	A2395	A2396	G2397	U2398	G2399	A2401	G2407	U2408	U2409	C2410	G2416	A2417	A2418	C2419	A2420	G2421	C2422	C2430	C2437	C2441	G2442	G2449	G2463	C2470	G2471	A2472	G2475	G2476	G2487	C2488	C2489	U2490	C2491																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
C2504	C2505	G2506	A2507	A2513	A2517	A2529	U2530	C2531	C2532	G2544	U2545	G2546	G2547	G2552	U2553	U2554	G2564	U2575	U2581	A2582	C2583	G2586	A2587	G2588	C2589	A2601	A2602	A2621	C2627	G2638	U2639	A2647	G2648	G2652	G2658	U2661	C2662	C2669	C2670	C2671																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
G2681	C2685	G2686	G2687	G2688	A2695	A2696	U2707	G2711	G2712	G2713	C2716	C2719	G2720	G2721	A2725	G2726	U2734	U2740	U2741	G2742	A2743	C2748	C2749	G2752	G2753	G2754	G2759	G2760	U2761	G2762	A2766	U2767	C2768	U2769	C2770	G2778	G2781	A2787	U2788	C2789	U2790																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
G2793	C2794	A2798	U2803	A2806	C2814	A2825	U2826	G2827	U2828	U2829	G2842	G2855	C2890	U2900	G2901	C2902	G2903	U2904	C2905	G2918	C	G	C	C	A	A	U	G	A	U3272	C3273	G3274	C3275	C3276	C3277	C3281	U3282	G3290	C3291	G3292	G3293	G3294	G3295	G3296	G3297	G3298	G3299	G3300	G3301	G3302	G3303	G3304	G3305	G3306	G3307	G3308	G3309	G3310	G3311	G3312	G3313	G3314	G3315	G3316	G3317	G3318	G3319	G3320	G3321	G3322	G3323	G3324	G3325	G3326	G3327	G3328	G3329	G3330	G3331	G3332	G3333	G3334	G3335	G3336	G3337	G3338	G3339	G3340	G3341	G3342	G3343	G3344	G3345	G3346	G3347	G3348	G3349	G3350	G3351	G3352	G3353	G3354	G3355	G3356	G3357	G3358	G3359	G3360	G3361	G3362	G3363	G3364	G3365	G3366	G3367	G3368	G3369	G3370	G3371	G3372	G3373	G3374	G3375	G3376	G3377	G3378	G3379	G3380	G3381	G3382	G3383	G3384	G3385	G3386	G3387	G3388	G3389	G3390	G3391	G3392	G3393	G3394	G3395	G3396	G3397	G3398	G3399	G3400	G3401	G3402	G3403	G3404	G3405	G3406	G3407	G3408	G3409	G3410	G3411	G3412	G3413	G3414	G3415	G3416	G3417	G3418	G3419	G3420	G3421	G3422	G3423	G3424	G3425	G3426	G3427	G3428	G3429	G3430	G3431	G3432	G3433	G3434	G3435	G3436	G3437	G3438	G3439	G3440	G3441	G3442	G3443	G3444	G3445	G3446	G3447	G3448	G3449	G3450	G3451	G3452	G3453	G3454	G3455	G3456	G3457	G3458	G3459	G3460	G3461	G3462	G3463	G3464	G3465	G3466	G3467	G3468	G3469	G3470	G3471	G3472	G3473	G3474	G3475	G3476	G3477	G3478	G3479	G3480	G3481	G3482	G3483	G3484	G3485	G3486	G3487	G3488	G3489	G3490	G3491	G3492	G3493	G3494	G3495	G3496	G3497	G3498	G3499	G3500	G3501	G3502	G3503	G3504	G3505	G3506	G3507	G3508	G3509	G3510	G3511	G3512	G3513	G3514	G3515	G3516	G3517	G3518	G3519	G3520	G3521	G3522	G3523	G3524	G3525	G3526	G3527	G3528	G3529	G3530	G3531	G3532	G3533	G3534	G3535	G3536	G3537	G3538	G3539	G3540	G3541	G3542	G3543	G3544	G3545	G3546	G3547	G3548	G3549	G3550	G3551	G3552	G3553	G3554	G3555	G3556	G3557	G3558	G3559	G3560	G3561	G3562	G3563	G3564	G3565	G3566	G3567	G3568	G3569	G3570	G3571	G3572	G3573	G3574	G3575	G3576	G3577	G3578	G3579	G3580	G3581	G3582	G3583	G3584	G3585	G3586	G3587	G3588	G3589	G3590	G3591	G3592	G3593	G3594	G3595	G3596	G3597	G3598	G3599	G3600	G3601	G3602	G3603	G3604	G3605	G3606	G3607	G3608	G3609	G3610	G3611	G3612	G3613	G3614	G3615	G3616	G3617	G3618	G3619	G3620	G3621	G3622	G3623	G3624	G3625	G3626	G3627	G3628	G3629	G3630	G3631	G3632	G3633	G3634	G3635	G3636	G3637	G3638	G3639	G3640	G3641	G3642	G3643	G3644	G3645	G3646	G3647	G3648	G3649	G3650	G3651	G3652	G3653	G3654	G3655	G3656	G3657	G3658	G3659	G3660	G3661	G3662	G3663	G3664	G3665	G3666	G3667	G3668	G3669	G3670	G3671	G3672	G3673	G3674	G3675	G3676	G3677	G3678	G3679	G3680	G3681	G3682	G3683	G3684	G3685	G3686	G3687	G3688	G3689	G3690	G3691	G3692	G3693	G3694	G3695	G3696	G3697	G3698	G3699	G3700	G3701	G3702	G3703	G3704	G3705	G3706	G3707	G3708	G3709	G3710	G3711	G3712	G3713	G3714	G3715	G3716	G3717	G3718	G3719	G3720	G3721	G3722	G3723	G3724	G3725	G3726	G3727	G3728	G3729	G3730	G3731	G3732	G3733	G3734	G3735	G3736	G3737	G3738	G3739	G3740	G3741	G3742	G3743	G3744	G3745	G3746	G3747	G3748	G3749	G3750	G3751	G3752	G3753	G3754	G3755	G3756	G3757	G3758	G3759	G3760	G3761	G3762	G3763	G3764	G3765	G3766	G3767	G3768	G3769	G3770	G3771	G3772	G3773	G3774	G3775	G3776	G3777	G3778	G3779	G3780	G3781	G3782	G3783	G3784	G3785	G3786	G3787	G3788	G3789	G3790	G3791	G3792	G3793	G3794	G3795	G3796	G3797	G3798	G3799	G3800	G3801	G3802	G3803	G3804	G3805	G3806	G3807	G3808	G3809	G3810	G3811	G3812	G3813	G3814	G3815	G3816	G3817	G3818	G3819	G3820	G3821	G3822	G3823	G3824	G3825	G3826	G3827	G3828	G3829	G3830	G3831	G3832	G3833	G3834	G3835	G3836	G3837	G3838	G3839	G3840	G3841	G3842	G3843	G3844	G3845	G3846	G3847	G3848	G3849	G3850	G3851	G3852	G3853	G3854	G3855	G3856	G3857	G3858	G3859	G3860	G3861	G3862	G3863	G3864	G3865	G3866	G3867	G3868	G3869	G3870	G3871	G3872	G3873	G3874	G3875	G3876	G3877	G3878	G3879	G3880	G3881	G3882	G3883	G3884	G3885	G3886	G3887	G3888	G3889	G3890	G3891	G3892	G3893	G3894	G3895	G3896	G3897	G3898	G3899	G3900	G3901	G3902	G3903	G3904	G3905	G3906	G3907	G3908	G3909	G3910	G3911	G3912	G3913	G3914	G3915	G3916	G3917	G3918	G3919	G3920	G3921	G3922	G3923	G3924	G3925	G3926	G3927	G3928	G3929	G3930	G3931	G3932	G3933	G3934	G3935	G3936	G3937	G3938	G3939	G3940	G3941	G3942	G3943	G3944	G3945	G3946	G3947	G3948	G3949	G3950	G3951	G3952	G3953	G3954	G3955	G3956	G3957	G3958	G3959	G3960	G3961	G3962	G3963	G3964	G3965	G3966	G3967	G3968	G3969	G3970	G3971	G3972	G3973	G3974	G3975	G3976	G3977	G3978	G3979	G3980	G3981	G3982	G3983	G3984	G3985	G3986	G3987	G3988	G3989	G3990	G3991	G3992	G3993	G3994	G3995	G3996	G3997	G3998	G3999	G4000	G4001	G4002	G4003	G4004	G4005	G4006	G4007	G4008	G4009	G4010	G4011	G4012	G4013	G4014	G4015	G4016	G4017	G4018	G4019	G4020	G4021	G4022	G4023	G4024	G4025	G4026	G4027	G4028	G4029	G4030	G4031	G4032	G4033	G4034	G4035	G4036	G4037	G4038	G4039	G4040	G4041	G4042	G4043	G4044	G4045	G4046	G4047	G4048	G4049	G4050	G4051	G4052	G4053	G4054	G4055	G4056	G4057	G4058	G4059	G4060	G4061	G4062	G4063	G4064	G4065	G4066	G4067	G4068	G4069	G4070	G4071	G4072	G4073	G4074	G4075	G407



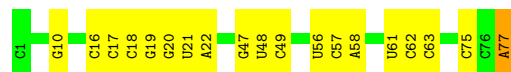
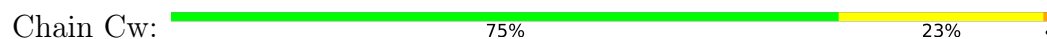
- Molecule 75: 5S ribosomal RNA



- Molecule 76: 5.8S ribosomal RNA



- Molecule 77: tRNA



- Molecule 78: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	42298	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.028	Depositor
Minimum map value	-0.008	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	392.0, 392.0, 392.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.98, 0.98, 0.98	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	AO	0.25	0/960	0.62	0/1286
2	AX	0.26	0/1112	0.59	0/1485
3	AN	0.26	0/1232	0.61	0/1656
4	AL	0.21	0/1238	0.50	0/1652
5	AB	0.24	0/1774	0.57	0/2372
6	AA	0.30	0/1661	0.66	0/2259
7	AV	0.30	0/623	0.76	0/834
8	AY	0.25	0/1040	0.61	0/1382
9	Aa	0.21	0/794	0.48	0/1065
10	Ab	0.24	0/673	0.59	0/902
11	Ae	0.29	0/467	0.73	0/615
12	AJ	0.22	0/1483	0.50	0/1980
13	AE	0.23	0/2115	0.54	0/2846
14	AC	0.26	0/1728	0.61	0/2333
15	AG	0.23	0/1946	0.49	0/2590
16	AH	0.28	0/1471	0.65	0/1969
17	AW	0.26	0/1051	0.60	0/1406
18	AI	0.25	0/1672	0.61	0/2228
19	B2	0.15	0/42050	0.37	10/65520 (0.0%)
20	CW	0.26	0/979	0.60	0/1295
21	Ag	0.22	0/2389	0.49	0/3249
22	AU	0.26	0/827	0.58	0/1110
23	AK	0.35	0/823	0.76	2/1111 (0.2%)
24	AS	0.24	0/1157	0.58	0/1548
25	Ad	0.27	0/455	0.61	0/603
26	AR	0.27	0/866	0.60	1/1154 (0.1%)
27	AP	0.25	0/1056	0.58	0/1406
28	AT	0.23	0/1119	0.56	0/1499
29	AZ	0.25	0/600	0.56	0/805
30	Ac	0.22	0/508	0.55	0/680
31	AD	0.29	0/1793	0.57	0/2414
32	AF	0.22	0/1531	0.50	0/2059
33	AQ	0.26	0/1142	0.54	0/1528
34	CO	0.30	0/1666	0.64	0/2228

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	CL	0.32	1/1680 (0.1%)	0.65	0/2249
36	CV	0.26	0/983	0.61	0/1319
37	CM	0.24	0/1161	0.59	0/1552
38	Ca	0.23	0/1191	0.61	0/1591
39	CN	0.25	0/1746	0.52	0/2338
40	CI	0.32	0/1673	0.76	3/2233 (0.1%)
41	CD	0.29	0/2398	0.66	5/3210 (0.2%)
42	CQ	0.27	0/1537	0.64	0/2052
43	CA	0.25	0/1995	0.61	2/2674 (0.1%)
44	CS	0.28	0/1493	0.70	2/2003 (0.1%)
45	CT	0.25	0/1326	0.58	0/1770
46	CP	0.26	0/1259	0.56	0/1689
47	CU	0.23	0/849	0.57	0/1137
48	CX	0.28	0/1011	0.61	0/1356
49	CY	0.21	0/1124	0.49	0/1494
50	CZ	0.22	0/1130	0.50	0/1507
51	Cr	0.35	0/1098	0.89	1/1467 (0.1%)
52	Ch	0.25	0/1031	0.62	2/1361 (0.1%)
53	Cb	0.27	0/569	0.64	0/750
54	CB	0.25	0/3246	0.62	0/4345
55	CF	0.25	0/1945	0.58	0/2589
56	Cc	0.30	0/787	0.65	0/1057
57	Cd	0.24	0/946	0.60	0/1272
58	Ce	0.25	0/1079	0.60	0/1439
59	Cf	0.28	0/895	0.68	0/1198
60	Cg	0.29	0/916	0.64	1/1220 (0.1%)
61	Ci	0.26	0/851	0.61	0/1125
62	Cj	0.29	0/731	0.62	0/966
63	Ck	0.23	0/575	0.51	0/761
64	Cl	0.28	0/441	0.62	0/583
65	CC	0.28	0/2921	0.67	1/3924 (0.0%)
66	Cm	0.26	0/425	0.63	0/564
67	Cn	0.17	0/241	0.44	0/305
68	Cp	0.25	0/713	0.60	0/946
69	Co	0.30	0/840	0.69	0/1107
70	CJ	0.27	0/1372	0.58	0/1836
71	CH	0.23	0/1545	0.54	0/2077
72	CE	0.35	0/2076	0.81	6/2778 (0.2%)
73	CG	0.25	0/2006	0.55	0/2697
74	A5	0.15	0/90934	0.38	6/141664 (0.0%)
75	A7	0.14	0/2880	0.32	0/4489
76	A8	0.16	0/3701	0.38	0/5766
77	Cw	0.13	0/1836	0.28	0/2859

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	Dd	0.15	0/153	0.36	0/234
All	All	0.20	1/231310 (0.0%)	0.47	42/340622 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	AL	0	1
7	AV	0	2
11	Ae	0	1
12	AJ	0	1
20	CW	0	2
22	AU	0	1
23	AK	0	1
34	CO	0	1
40	CI	0	1
42	CQ	0	2
51	Cr	0	2
54	CB	0	2
59	Cf	0	1
62	Cj	0	2
70	CJ	0	2
72	CE	0	9
74	A5	1	0
All	All	1	31

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	CL	11	LYS	C-N	7.17	1.42	1.33

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	CI	114	GLY	CA-C-N	10.87	140.11	123.05
40	CI	114	GLY	C-N-CA	10.87	140.11	123.05
74	A5	2097	U	O4'-C1'-N1	8.32	120.69	108.20
74	A5	2097	U	N1-C1'-C2'	8.19	126.28	114.00
74	A5	4942	C	N1-C1'-C2'	7.84	125.77	114.00
23	AK	1	MET	CA-C-N	6.83	134.00	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AK	1	MET	C-N-CA	6.83	134.00	121.70
41	CD	259	LYS	CA-C-N	6.79	134.50	121.54
41	CD	259	LYS	C-N-CA	6.79	134.50	121.54
74	A5	2126	G	N9-C1'-C2'	6.68	122.02	112.00
19	B2	1507	G	O4'-C1'-N9	6.59	118.09	108.20
19	B2	607	U	N1-C1'-C2'	6.56	121.84	112.00
19	B2	1418	C	N1-C1'-C2'	6.48	123.72	114.00
74	A5	2126	G	O4'-C1'-N9	6.45	118.18	108.50
19	B2	1155	U	N1-C1'-C2'	6.36	123.54	114.00
19	B2	1507	G	N9-C1'-C2'	6.14	123.21	114.00
44	CS	147	ASP	CA-C-N	6.09	132.66	121.70
44	CS	147	ASP	C-N-CA	6.09	132.66	121.70
19	B2	607	U	O4'-C1'-N1	6.05	117.58	108.50
51	Cr	90	LEU	CA-CB-CG	6.03	137.41	116.30
72	CE	42	PRO	N-CA-C	6.03	124.88	112.47
43	CA	254	GLU	CA-C-N	5.98	132.46	121.70
43	CA	254	GLU	C-N-CA	5.98	132.46	121.70
65	CC	340	ILE	N-CA-C	-5.90	106.48	111.56
41	CD	111	ASN	CA-CB-CG	5.87	118.47	112.60
19	B2	798	G	C5'-C4'-C3'	5.63	123.65	115.20
72	CE	110	ARG	CA-CB-CG	5.61	125.31	114.10
40	CI	184	MET	CB-CG-SD	5.49	129.17	112.70
60	Cg	52	ARG	CG-CD-NE	5.48	124.06	112.00
72	CE	158	ARG	CD-NE-CZ	5.42	131.99	124.40
19	B2	1155	U	O4'-C1'-N1	5.39	116.29	108.20
72	CE	110	ARG	CB-CA-C	5.39	119.31	110.95
72	CE	83	LYS	CA-C-N	5.37	131.37	121.70
72	CE	83	LYS	C-N-CA	5.37	131.37	121.70
26	AR	80	ARG	CB-CG-CD	5.36	123.62	111.30
19	B2	798	G	C5'-C4'-O4'	5.33	117.09	109.10
19	B2	1418	C	O4'-C1'-N1	5.19	115.99	108.20
41	CD	51	MET	CA-CB-CG	5.18	124.46	114.10
74	A5	4942	C	O4'-C1'-N1	5.17	115.96	108.20
41	CD	260	GLU	CA-CB-CG	5.09	124.28	114.10
52	Ch	3	LYS	CA-C-N	5.06	131.08	121.97
52	Ch	3	LYS	C-N-CA	5.06	131.08	121.97

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
74	A5	2126	G	C1'

All (31) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	AJ	38	ARG	Sidechain
23	AK	29	MET	Peptide
4	AL	151	THR	Peptide
22	AU	81	GLN	Peptide
7	AV	48	GLY	Peptide
7	AV	61	ARG	Sidechain
11	Ae	46	VAL	Peptide
54	CB	17	LEU	Peptide
54	CB	258	HIS	Peptide
72	CE	110	ARG	Sidechain
72	CE	115	TYR	Peptide
72	CE	116	TYR	Peptide
72	CE	118	THR	Peptide
72	CE	158	ARG	Sidechain
72	CE	41	LYS	Peptide
72	CE	57	TYR	Peptide
72	CE	59	ARG	Peptide
72	CE	94	LYS	Peptide
40	CI	210	ARG	Sidechain
70	CJ	71	HIS	Peptide
70	CJ	72	CYS	Peptide
34	CO	110	PRO	Peptide
42	CQ	153	GLY	Peptide
42	CQ	154	LYS	Peptide
20	CW	56	ARG	Sidechain
20	CW	97	LYS	Peptide
59	Cf	54	LYS	Peptide
62	Cj	39	TYR	Peptide
62	Cj	43	ARG	Sidechain
51	Cr	66	ARG	Peptide
51	Cr	75	THR	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AO	948	973	976	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	AX	1094	1163	1164	13	0
3	AN	1208	1294	1294	7	0
4	AL	1216	1279	1280	6	0
5	AB	1747	1820	1829	24	0
6	AA	1624	1626	1632	21	0
7	AV	617	615	614	5	0
8	AY	1023	1088	1090	14	0
9	Aa	781	832	830	6	0
10	Ab	659	680	683	3	0
11	Ae	461	511	514	4	0
12	AJ	1459	1566	1575	8	0
13	AE	2073	2181	2181	18	0
14	AC	1692	1777	1783	15	0
15	AG	1923	2085	2089	16	0
16	AH	1449	1534	1537	15	0
17	AW	1034	1079	1080	6	0
18	AI	1644	1720	1718	11	0
19	B2	37619	18948	18979	47	0
20	CW	965	1023	1029	1	0
21	Ag	2334	2289	2288	16	0
22	AU	817	882	882	10	0
23	AK	799	822	823	9	0
24	AS	1139	1188	1191	8	0
25	Ad	445	442	442	7	0
26	AR	858	910	917	12	0
27	AP	1037	1099	1098	12	0
28	AT	1101	1135	1135	13	0
29	AZ	594	649	653	12	0
30	Ac	506	535	536	6	0
31	AD	1765	1857	1865	28	0
32	AF	1509	1558	1563	15	0
33	AQ	1124	1192	1193	8	0
34	CO	1634	1776	1779	17	0
35	CL	1649	1757	1760	15	0
36	CV	969	1030	1031	7	0
37	CM	1139	1209	1209	10	0
38	Ca	1162	1210	1213	8	0
39	CN	1701	1747	1749	17	0
40	CI	1634	1666	1671	13	0
41	CD	2353	2370	2372	23	0
42	CQ	1513	1629	1628	17	0
43	CA	1957	2051	2055	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	CS	1453	1485	1490	21	0
45	CT	1298	1363	1366	10	0
46	CP	1233	1260	1263	15	0
47	CU	835	863	865	10	0
48	CX	994	1078	1079	10	0
49	CY	1107	1193	1193	6	0
50	CZ	1107	1182	1182	9	0
51	Cr	1083	1164	1168	19	0
52	Ch	1023	1160	1160	9	0
53	Cb	559	590	590	9	0
54	CB	3178	3306	3314	31	0
55	CF	1910	2046	2048	18	0
56	Cc	776	812	812	12	0
57	Cd	931	979	980	6	0
58	Ce	1061	1158	1159	12	0
59	Cf	876	910	912	8	0
60	Cg	906	999	999	4	0
61	Ci	840	925	929	9	0
62	Cj	716	754	750	9	0
63	Ck	569	637	637	4	0
64	Cl	431	469	469	2	0
65	CC	2867	3033	3039	43	0
66	Cm	419	456	452	5	0
67	Cn	240	289	289	1	0
68	Cp	703	755	755	8	0
69	Co	827	893	892	6	0
70	CJ	1349	1383	1381	12	0
71	CH	1526	1603	1605	10	0
72	CE	2036	2217	2222	32	0
73	CG	1973	2120	2128	25	0
74	A5	81401	40870	40887	101	0
75	A7	2578	1306	1306	6	0
76	A8	3314	1682	1683	3	0
77	Cw	1644	837	837	1	0
78	Dd	140	69	71	0	0
79	B2	2	0	0	0	0
79	Cw	4	0	0	0	0
79	Dd	1	0	0	0	0
All	All	214885	156643	156842	891	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 2.

All (891) 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)
74:A5:3653:A:N6	74:A5:3691:G:C2	2.17	1.13
19:B2:191:A:H62	19:B2:208:G:H21	1.12	0.98
74:A5:664:G:N2	74:A5:667:A:C2	2.37	0.92
74:A5:3653:A:N6	74:A5:3691:G:N3	2.16	0.92
70:CJ:24:ILE:HD11	74:A5:4251:A:H62	1.37	0.87
32:AF:103:LEU:HD23	32:AF:178:ILE:HD13	1.60	0.84
19:B2:1095:C:N3	19:B2:1149:A:N1	2.27	0.83
18:AI:38:ILE:HD11	18:AI:81:VAL:HG23	1.61	0.82
46:CP:48:LEU:HD21	46:CP:91:LEU:HD11	1.62	0.81
63:Ck:23:VAL:HG21	63:Ck:64:LEU:HD21	1.61	0.80
35:CL:55:ILE:HD12	35:CL:96:ILE:HD11	1.64	0.80
19:B2:191:A:H62	19:B2:208:G:N2	1.78	0.80
8:AY:18:LEU:HD11	13:AE:64:ILE:HD11	1.63	0.79
5:AB:123:ALA:HB1	5:AB:169:MET:HE2	1.63	0.79
5:AB:121:ILE:HD12	5:AB:161:VAL:HG13	1.65	0.79
39:CN:46:ASP:O	39:CN:49:ARG:O	2.02	0.78
19:B2:191:A:N6	19:B2:208:G:H21	1.83	0.77
11:Ae:45:VAL:HG22	11:Ae:47:PRO:HD3	1.65	0.77
74:A5:3927:U:O2	74:A5:4184:G:O6	2.03	0.75
55:CF:92:VAL:HG13	55:CF:140:ILE:HD13	1.66	0.75
73:CG:95:LEU:HD21	73:CG:156:VAL:HG11	1.69	0.74
36:CV:39:ILE:HD12	36:CV:61:VAL:HG11	1.69	0.73
44:CS:75:VAL:O	44:CS:99:ASP:O	2.07	0.73
56:Cc:18:LEU:HD11	56:Cc:84:ALA:HB1	1.73	0.70
19:B2:1095:C:H42	19:B2:1149:A:H2	1.41	0.69
74:A5:2312:U:O2	74:A5:2326:G:O6	2.11	0.69
65:CC:27:VAL:HG21	65:CC:264:TYR:HD1	1.56	0.69
6:AA:7:VAL:HG13	6:AA:8:LEU:HD12	1.75	0.69
1:AO:60:MET:HE3	1:AO:60:MET:HA	1.76	0.68
26:AR:58:MET:HE3	26:AR:58:MET:O	1.93	0.68
41:CD:239:MET:HE3	41:CD:239:MET:O	1.93	0.68
25:Ad:38:MET:HE3	25:Ad:38:MET:HA	1.76	0.67
72:CE:242:ILE:HD13	74:A5:4939:C:H1'	1.76	0.67
70:CJ:167:GLN:O	70:CJ:171:ASP:HA	1.94	0.67
72:CE:153:LEU:HD12	72:CE:195:ILE:HD13	1.76	0.67
33:AQ:89:SER:O	33:AQ:93:VAL:HG23	1.95	0.67
51:Cr:17:LEU:HD21	51:Cr:36:ASN:HD22	1.59	0.67
74:A5:1724:G:N1	74:A5:1838:A:C2	2.63	0.67
65:CC:158:VAL:HG21	65:CC:253:THR:HG22	1.77	0.67
65:CC:147:VAL:HG13	65:CC:152:LEU:HD12	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:Ch:55:ALA:O	52:Ch:59:THR:HG23	1.96	0.66
74:A5:664:G:C2	74:A5:667:A:N1	2.63	0.66
21:Ag:30:MET:HE2	21:Ag:92:LEU:HD21	1.75	0.66
39:CN:9:GLU:OE2	61:Ci:44:ILE:HG21	1.95	0.66
47:CU:43:LEU:O	47:CU:47:ILE:HG22	1.97	0.65
39:CN:7:ILE:HD11	73:CG:166:LEU:HA	1.78	0.65
41:CD:51:MET:HE1	41:CD:53:VAL:HG23	1.79	0.65
51:Cr:96:MET:HE1	74:A5:678:C:H5'	1.78	0.65
59:Cf:50:VAL:HG12	59:Cf:69:VAL:HG22	1.79	0.64
71:CH:165:THR:HG21	71:CH:179:ILE:HG22	1.79	0.64
5:AB:38:MET:H	5:AB:38:MET:HE2	1.62	0.64
62:Cj:15:THR:HG23	74:A5:1534:A:C8	2.32	0.64
22:AU:39:LEU:HD22	22:AU:101:ILE:HG22	1.80	0.64
59:Cf:28:LEU:HD12	59:Cf:101:ILE:HD11	1.80	0.64
54:CB:189:THR:HG23	54:CB:192:GLU:HB3	1.79	0.63
70:CJ:128:LEU:HD13	70:CJ:129:ASP:N	2.13	0.63
75:A7:66:G:O6	75:A7:109:U:O2	2.17	0.63
24:AS:71:MET:SD	24:AS:99:LEU:HD13	2.38	0.63
31:AD:105:LEU:HD12	31:AD:184:ILE:HG21	1.80	0.63
54:CB:110:ILE:HD13	54:CB:115:LYS:HG2	1.80	0.63
65:CC:325:MET:HE2	65:CC:325:MET:HA	1.81	0.63
65:CC:313:VAL:HG21	74:A5:1283:G:O2'	1.98	0.62
19:B2:1410:C:H42	19:B2:1436:C:H42	1.48	0.62
6:AA:121:LEU:HD12	6:AA:143:PRO:O	1.99	0.62
22:AU:84:ILE:HG21	31:AD:8:LYS:NZ	2.15	0.62
50:CZ:81:MET:HA	50:CZ:81:MET:HE3	1.82	0.62
19:B2:185:G:O6	19:B2:214:U:O2	2.17	0.61
35:CL:46:ILE:HG22	35:CL:49:ARG:HG3	1.81	0.61
44:CS:75:VAL:C	44:CS:99:ASP:O	2.42	0.61
12:AJ:35:TYR:HD2	12:AJ:112:THR:HG21	1.64	0.61
42:CQ:155:ALA:HB1	42:CQ:156:PRO:HA	1.81	0.61
73:CG:164:ILE:O	73:CG:168:VAL:HG23	2.01	0.61
35:CL:170:THR:HG22	38:Ca:123:ILE:HD11	1.82	0.61
57:Cd:27:ILE:HD13	57:Cd:29:ILE:HD11	1.82	0.61
59:Cf:35:ALA:O	59:Cf:39:THR:HG23	2.00	0.61
10:Ab:62:VAL:HG12	10:Ab:74:THR:HG21	1.82	0.61
42:CQ:31:LEU:HD21	65:CC:289:LEU:HD23	1.82	0.61
47:CU:56:LEU:HB2	47:CU:61:VAL:HG21	1.83	0.61
23:AK:49:MET:HE2	23:AK:69:TRP:CD1	2.36	0.60
54:CB:41:VAL:HG13	54:CB:185:VAL:HG13	1.83	0.60
71:CH:65:LYS:O	71:CH:69:THR:HG23	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AG:32:MET:HE3	15:AG:33:ALA:H	1.65	0.60
65:CC:322:LEU:HD21	74:A5:1281:G:C8	2.36	0.60
9:Aa:41:ILE:HG23	9:Aa:68:TYR:HD1	1.67	0.60
65:CC:221:PHE:HB3	65:CC:229:LEU:HD22	1.84	0.60
36:CV:82:ILE:HD12	36:CV:121:VAL:HG23	1.82	0.60
47:CU:34:MET:HE3	47:CU:34:MET:HA	1.83	0.60
43:CA:199:VAL:HG21	74:A5:1631:A:N7	2.16	0.60
24:AS:42:HIS:CE1	28:AT:46:ALA:HB3	2.37	0.59
47:CU:55:ASN:C	47:CU:56:LEU:HD23	2.27	0.59
74:A5:1290:G:H1'	74:A5:4942:C:H42	1.67	0.59
25:Ad:47:ALA:HB1	25:Ad:52:PHE:CB	2.32	0.59
65:CC:183:VAL:HG13	65:CC:204:ARG:HB2	1.82	0.59
34:CO:41:ILE:HD11	34:CO:138:LEU:HD12	1.85	0.59
5:AB:62:LEU:HD11	5:AB:91:VAL:CG2	2.32	0.59
73:CG:24:ALA:O	73:CG:28:VAL:HG13	2.01	0.59
28:AT:60:THR:HG23	28:AT:107:LEU:HD11	1.85	0.59
73:CG:207:VAL:HG11	73:CG:215:LEU:CD1	2.33	0.58
66:Cm:103:LEU:HD12	66:Cm:107:ALA:HB3	1.84	0.58
5:AB:71:LEU:HD13	5:AB:84:PHE:CE1	2.38	0.58
54:CB:107:ALA:HB2	54:CB:201:LEU:HD12	1.84	0.58
66:Cm:104:HIS:NE2	66:Cm:107:ALA:HB2	2.18	0.58
26:AR:11:LYS:O	26:AR:15:VAL:HG23	2.03	0.58
6:AA:6:ASP:OD2	6:AA:7:VAL:HG12	2.03	0.58
30:Ac:59:LEU:HD11	32:AF:123:GLU:OE1	2.03	0.58
54:CB:114:CYS:HB3	54:CB:180:LEU:HD11	1.84	0.58
28:AT:14:PHE:HA	28:AT:138:VAL:HG21	1.85	0.58
70:CJ:15:LEU:HD23	70:CJ:165:TRP:CG	2.39	0.58
14:AC:209:VAL:CG2	14:AC:233:LEU:HD23	2.34	0.58
46:CP:114:ILE:HD12	46:CP:114:ILE:O	2.04	0.58
70:CJ:74:VAL:HG11	70:CJ:82:ILE:HD13	1.85	0.58
70:CJ:99:PHE:CD2	70:CJ:163:MET:HE1	2.39	0.58
21:Ag:45:LEU:HD22	21:Ag:52:TYR:CD2	2.39	0.58
30:Ac:46:VAL:CG2	30:Ac:56:LEU:HD21	2.34	0.58
44:CS:34:ALA:HB1	44:CS:39:VAL:HG23	1.85	0.58
72:CE:158:ARG:HE	74:A5:4948:C:N4	2.01	0.58
55:CF:65:TYR:CE2	55:CF:69:ILE:HD11	2.39	0.57
44:CS:33:PHE:CD2	44:CS:106:VAL:HG21	2.39	0.57
54:CB:53:MET:HE2	74:A5:4626:A:H4'	1.85	0.57
73:CG:136:LEU:HD21	73:CG:204:PHE:CE2	2.39	0.57
58:Ce:70:LEU:HD12	58:Ce:123:THR:HG21	1.87	0.57
18:AI:83:TYR:HB2	18:AI:202:ILE:HD11	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AL:35:ARG:NH2	4:AL:63:THR:HG21	2.19	0.57
23:AK:49:MET:HE2	23:AK:69:TRP:NE1	2.19	0.57
31:AD:70:THR:HG22	31:AD:86:LEU:HD12	1.87	0.57
63:Ck:26:LYS:HD2	63:Ck:69:LEU:HD12	1.87	0.56
50:CZ:42:LEU:HD11	50:CZ:72:VAL:HG22	1.88	0.56
70:CJ:128:LEU:HD12	70:CJ:130:PHE:CE1	2.39	0.56
3:AN:25:TRP:CH2	10:Ab:45:THR:HG21	2.39	0.56
14:AC:69:LEU:HD23	14:AC:273:LEU:HD21	1.87	0.56
34:CO:202:LEU:HD13	37:CM:108:ASP:OD1	2.06	0.56
37:CM:31:ILE:HG22	37:CM:32:ASP:OD1	2.04	0.56
41:CD:211:LEU:HD11	41:CD:218:ALA:HB3	1.87	0.56
54:CB:41:VAL:HG11	54:CB:196:TRP:CE3	2.40	0.56
54:CB:77:THR:HG21	54:CB:337:VAL:HG22	1.87	0.56
12:AJ:94:LEU:HD23	12:AJ:94:LEU:H	1.70	0.56
35:CL:49:ARG:HB3	35:CL:51:ALA:HB2	1.88	0.56
43:CA:101:VAL:HG23	43:CA:164:ALA:C	2.30	0.56
8:AY:15:ASN:HD21	8:AY:18:LEU:HD12	1.71	0.56
18:AI:103:LEU:HD22	18:AI:170:LYS:HB3	1.87	0.56
47:CU:34:MET:SD	47:CU:96:LEU:HD13	2.45	0.56
62:Cj:50:SER:OG	62:Cj:53:ALA:HB3	2.05	0.56
18:AI:43:ILE:CG2	19:B2:306:C:H41	2.17	0.56
31:AD:99:ILE:HD13	31:AD:173:ARG:NH2	2.20	0.56
40:CI:87:MET:HB3	40:CI:138:ILE:HG22	1.88	0.56
56:Cc:17:ARG:O	56:Cc:21:VAL:HG23	2.06	0.56
31:AD:34:TYR:O	31:AD:99:ILE:HD11	2.06	0.56
39:CN:156:HIS:HA	39:CN:162:ARG:HH22	1.70	0.56
41:CD:273:LEU:HD21	75:A7:107:G:OP1	2.05	0.56
51:Cr:96:MET:HE1	74:A5:678:C:C5'	2.36	0.56
72:CE:203:ILE:HD13	72:CE:206:VAL:HG23	1.87	0.56
6:AA:7:VAL:HG11	6:AA:192:GLU:OE2	2.05	0.55
60:Cg:5:LEU:HD13	60:Cg:32:TYR:CE2	2.41	0.55
22:AU:61:LEU:HD11	31:AD:8:LYS:HE3	1.88	0.55
40:CI:54:SER:HB2	40:CI:135:ILE:HD11	1.88	0.55
2:AX:94:ILE:HD12	2:AX:94:ILE:O	2.07	0.55
5:AB:41:ILE:HD11	5:AB:73:ASP:O	2.07	0.55
6:AA:112:ILE:HD13	19:B2:1350:U:H4'	1.89	0.55
6:AA:141:ASN:O	6:AA:142:LEU:HD23	2.05	0.55
65:CC:228:THR:C	65:CC:229:LEU:HD23	2.31	0.55
19:B2:1351:G:O6	19:B2:1360:U:O4	2.25	0.55
72:CE:186:LEU:HD23	72:CE:212:LEU:HD23	1.88	0.55
15:AG:141:ILE:HG21	15:AG:153:VAL:HG13	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:AW:6:VAL:HG23	17:AW:34:ILE:HD11	1.87	0.55
37:CM:13:ALA:HB2	37:CM:57:LEU:HD12	1.88	0.55
44:CS:154:LEU:HD21	44:CS:157:ARG:HD2	1.89	0.55
31:AD:68:GLU:O	31:AD:72:VAL:HG23	2.06	0.55
71:CH:45:LEU:HD11	71:CH:55:LEU:HD22	1.89	0.55
42:CQ:86:ILE:HB	42:CQ:105:VAL:HG22	1.89	0.55
5:AB:208:HIS:O	5:AB:210:VAL:HG23	2.07	0.55
7:AV:23:ILE:HD11	14:AC:249:SER:HA	1.88	0.55
57:CD:54:MET:HE2	57:CD:54:MET:HA	1.88	0.55
20:CW:18:GLY:HA2	20:CW:32:LEU:O	2.07	0.55
37:CM:85:LYS:O	37:CM:89:THR:HG23	2.07	0.54
53:Cb:65:MET:HE2	74:A5:1810:G:O2'	2.06	0.54
54:CB:78:ILE:O	54:CB:78:ILE:HD12	2.06	0.54
65:CC:261:ASP:O	65:CC:265:GLY:HA2	2.07	0.54
74:A5:4888:U:O2	74:A5:4931:G:N2	2.40	0.54
42:CQ:82:VAL:HG21	42:CQ:86:ILE:HD11	1.88	0.54
21:Ag:45:LEU:HD22	21:Ag:52:TYR:HD2	1.72	0.54
57:CD:27:ILE:HD13	57:CD:29:ILE:CD1	2.37	0.54
63:Ck:69:LEU:HD11	74:A5:2696:A:O4'	2.07	0.54
3:AN:40:LEU:HB3	3:AN:45:LEU:HD12	1.90	0.54
6:AA:119:PRO:O	6:AA:142:LEU:HD22	2.07	0.54
55:CF:150:VAL:HG12	55:CF:154:ILE:HD11	1.89	0.54
39:CN:59:TYR:CE2	39:CN:135:ILE:HD12	2.42	0.54
39:CN:85:VAL:HG21	74:A5:44:A:OP2	2.07	0.54
71:CH:18:ILE:HG22	71:CH:27:VAL:HG13	1.89	0.54
6:AA:68:ILE:HG21	6:AA:74:VAL:HG22	1.89	0.54
16:AH:98:ARG:CZ	16:AH:125:VAL:HG22	2.38	0.54
39:CN:6:TYR:HE2	73:CG:173:LEU:HD21	1.71	0.54
40:CI:206:LEU:HD13	40:CI:206:LEU:O	2.08	0.54
59:Cf:74:VAL:HG13	59:Cf:84:VAL:HG13	1.89	0.54
19:B2:1351:G:O6	19:B2:1360:U:C4	2.60	0.54
25:Ad:47:ALA:HA	25:Ad:50:ILE:HD12	1.88	0.54
34:CO:58:LEU:HD11	34:CO:145:VAL:CG1	2.38	0.54
6:AA:54:THR:HG22	6:AA:162:PRO:HB2	1.88	0.54
27:AP:17:TYR:HB2	27:AP:25:LEU:HD11	1.88	0.54
42:CQ:121:LEU:HD13	42:CQ:125:GLN:OE1	2.08	0.54
43:CA:94:ALA:HB3	43:CA:102:LEU:CD2	2.37	0.54
65:CC:257:PHE:HA	65:CC:260:LEU:HD12	1.89	0.54
67:Cn:1:MET:HE3	67:Cn:1:MET:HA	1.88	0.54
28:AT:56:ARG:O	28:AT:60:THR:HG22	2.07	0.54
15:AG:5:ILE:HG22	15:AG:111:LEU:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:AU:84:ILE:HG21	31:AD:8:LYS:HZ1	1.73	0.53
31:AD:39:VAL:HA	31:AD:48:ILE:HD12	1.88	0.53
16:AH:61:ILE:HD11	16:AH:95:ILE:HD12	1.91	0.53
8:AY:29:HIS:CE1	8:AY:69:THR:HG23	2.43	0.53
41:CD:195:HIS:CE1	41:CD:199:ILE:HD11	2.42	0.53
71:CH:123:ILE:HG23	71:CH:125:ARG:HH21	1.73	0.53
58:Ce:77:PHE:CD1	58:Ce:88:LEU:HD21	2.42	0.53
71:CH:46:SER:O	71:CH:55:LEU:HD23	2.08	0.53
16:AH:61:ILE:HD12	16:AH:93:VAL:HG13	1.91	0.53
19:B2:141:A:H61	19:B2:177:G:H21	1.56	0.53
25:Ad:53:ILE:HD12	25:Ad:53:ILE:O	2.09	0.53
31:AD:99:ILE:HD13	31:AD:173:ARG:HH21	1.74	0.53
32:AF:76:MET:HE1	32:AF:155:CYS:HA	1.89	0.53
23:AK:49:MET:C	23:AK:49:MET:HE3	2.34	0.53
69:Co:85:ILE:HD12	69:Co:86:LYS:O	2.09	0.53
5:AB:78:GLU:OE1	5:AB:79:VAL:HG13	2.09	0.53
6:AA:161:ILE:HD12	6:AA:161:ILE:O	2.09	0.53
46:CP:94:MET:HE1	46:CP:146:ILE:HG23	1.91	0.53
33:AQ:12:VAL:HG11	33:AQ:90:LYS:HB3	1.91	0.53
40:CI:102:MET:HE2	40:CI:102:MET:HA	1.91	0.53
19:B2:1384:C:O2'	31:AD:157:MET:HE1	2.10	0.52
62:Cj:15:THR:HG23	74:A5:1534:A:H8	1.72	0.52
8:AY:29:HIS:HE1	8:AY:69:THR:HG23	1.73	0.52
9:Aa:41:ILE:HG23	9:Aa:68:TYR:CD1	2.44	0.52
16:AH:100:ILE:HG13	16:AH:125:VAL:HG21	1.90	0.52
31:AD:51:LEU:HG	31:AD:91:VAL:HG22	1.90	0.52
35:CL:49:ARG:CB	35:CL:51:ALA:HB2	2.38	0.52
55:CF:133:LEU:CD2	55:CF:140:ILE:HD11	2.40	0.52
12:AJ:8:VAL:HG21	19:B2:814:U:H5''	1.92	0.52
15:AG:162:LEU:HD13	19:B2:68:A:OP2	2.09	0.52
39:CN:32:GLN:HB3	73:CG:63:LEU:HD11	1.90	0.52
72:CE:168:LEU:HD12	72:CE:188:ARG:HG2	1.91	0.52
16:AH:61:ILE:CD1	16:AH:95:ILE:HD12	2.40	0.52
48:CX:87:MET:HE3	48:CX:87:MET:N	2.25	0.52
40:CI:52:MET:HG3	40:CI:152:LEU:HD22	1.90	0.52
41:CD:273:LEU:HD22	75:A7:108:G:P	2.50	0.52
54:CB:252:ALA:HB1	74:A5:4524:G:N3	2.24	0.52
13:AE:55:ALA:O	13:AE:56:LEU:HD23	2.10	0.52
31:AD:69:LEU:HB3	31:AD:86:LEU:HD13	1.92	0.52
32:AF:162:ALA:HB2	32:AF:172:CYS:SG	2.50	0.52
73:CG:157:ILE:HG23	73:CG:167:VAL:HG11	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:60:MET:HE1	19:B2:956:G:O5'	2.09	0.52
6:AA:4:ALA:HB3	6:AA:8:LEU:HB2	1.90	0.52
42:CQ:23:ILE:HD12	42:CQ:24:TYR:N	2.25	0.52
44:CS:93:MET:HA	44:CS:93:MET:HE3	1.91	0.52
48:CX:95:THR:HG22	48:CX:139:ARG:HA	1.91	0.52
55:CF:133:LEU:HD11	55:CF:142:TRP:NE1	2.24	0.52
65:CC:167:ALA:HB2	65:CC:220:ALA:HB1	1.91	0.52
26:AR:31:ASN:HD22	26:AR:55:THR:HG22	1.75	0.52
61:CI:44:ILE:HA	61:CI:47:VAL:HG12	1.90	0.52
19:B2:1467:C:H5''	26:AR:1:MET:HE1	1.91	0.52
27:AP:17:TYR:CB	27:AP:25:LEU:HD11	2.40	0.52
44:CS:82:LEU:HD21	44:CS:124:ILE:HG22	1.92	0.52
61:CI:69:ALA:O	61:CI:73:ILE:HG22	2.09	0.52
69:Co:93:LEU:O	69:Co:93:LEU:HD23	2.10	0.52
1:AO:95:ILE:HD11	1:AO:119:LEU:HD21	1.92	0.51
14:AC:127:PHE:HE2	14:AC:141:VAL:HG13	1.75	0.51
40:CI:54:SER:CB	40:CI:135:ILE:HD11	2.40	0.51
16:AH:139:ILE:HG23	16:AH:156:VAL:HG13	1.91	0.51
17:AW:6:VAL:CG2	17:AW:34:ILE:HD11	2.40	0.51
43:CA:104:VAL:HG23	43:CA:162:ASN:O	2.10	0.51
44:CS:33:PHE:CE2	44:CS:106:VAL:HG21	2.45	0.51
65:CC:27:VAL:HG21	65:CC:264:TYR:CD1	2.42	0.51
51:Cr:4:HIS:HD2	65:CC:289:LEU:HD22	1.76	0.51
8:AY:16:ARG:HB2	13:AE:95:THR:HG22	1.91	0.51
21:Ag:173:LEU:HD22	21:Ag:189:ILE:HG12	1.93	0.51
38:Ca:43:ILE:HD11	74:A5:4304:A:N1	2.25	0.51
42:CQ:4:ASP:OD2	55:CF:98:ILE:HG21	2.10	0.51
54:CB:338:VAL:O	54:CB:345:LEU:HD21	2.10	0.51
74:A5:3653:A:C6	74:A5:3691:G:N3	2.78	0.51
2:AX:131:LEU:HD11	19:B2:29:G:O2'	2.10	0.51
61:CI:81:ILE:HD12	61:CI:81:ILE:H	1.75	0.51
65:CC:152:LEU:HD21	65:CC:154:VAL:HG23	1.92	0.51
72:CE:261:ILE:HD13	72:CE:268:GLN:HG2	1.91	0.51
46:CP:20:SER:C	46:CP:21:ASN:HD22	2.19	0.51
72:CE:96:VAL:HG21	74:A5:470:A:C2	2.45	0.51
1:AO:135:ILE:HD11	19:B2:986:G:N3	2.25	0.51
18:AI:38:ILE:HD13	18:AI:80:ASP:HA	1.93	0.51
19:B2:536:A:H62	19:B2:547:G:H21	1.59	0.51
45:CT:143:THR:HG21	55:CF:81:PHE:CZ	2.46	0.51
72:CE:150:LEU:HD12	72:CE:196:ALA:HA	1.92	0.51
74:A5:664:G:C2	74:A5:667:A:C2	2.99	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:AI:38:ILE:HG12	18:AI:96:LEU:HD21	1.93	0.51
35:CL:150:LEU:HD22	52:Ch:122:LYS:HB2	1.92	0.51
37:CM:55:MET:HA	37:CM:55:MET:HE2	1.92	0.51
49:CY:25:ILE:HD12	49:CY:25:ILE:H	1.75	0.51
54:CB:41:VAL:HG13	54:CB:185:VAL:CG1	2.41	0.51
58:Ce:31:ILE:HD11	74:A5:2347:A:C6	2.46	0.51
16:AH:61:ILE:HD12	16:AH:93:VAL:CG1	2.40	0.51
8:AY:9:THR:HG21	8:AY:48:TYR:HE2	1.74	0.51
43:CA:250:LYS:CG	43:CA:252:VAL:HG23	2.41	0.51
74:A5:1874:A:H4'	74:A5:4217:G:H22	1.75	0.51
6:AA:55:TRP:NE1	6:AA:59:LEU:HD11	2.26	0.50
22:AU:89:ILE:HG22	22:AU:91:LEU:HD11	1.93	0.50
48:CX:77:ILE:HD12	48:CX:116:LEU:HD12	1.92	0.50
51:Cr:3:ALA:HB1	51:Cr:44:ILE:HD13	1.92	0.50
54:CB:252:ALA:HB1	74:A5:4524:G:C2	2.46	0.50
62:Cj:56:ARG:O	62:Cj:61:THR:HG21	2.11	0.50
5:AB:110:MET:O	5:AB:114:VAL:HG23	2.12	0.50
14:AC:240:THR:O	14:AC:244:ILE:HG23	2.11	0.50
44:CS:115:ALA:HB1	74:A5:1925:G:N3	2.26	0.50
5:AB:123:ALA:HB3	5:AB:168:MET:HE2	1.92	0.50
5:AB:188:LEU:O	5:AB:188:LEU:HD13	2.11	0.50
9:Aa:44:ILE:HD12	9:Aa:44:ILE:H	1.76	0.50
18:AI:141:ARG:NH2	19:B2:208:G:H22	2.08	0.50
62:Cj:5:THR:HG22	74:A5:2793:G:O2'	2.12	0.50
8:AY:62:THR:HA	8:AY:69:THR:HG22	1.92	0.50
27:AP:75:VAL:HG22	27:AP:93:MET:HG3	1.93	0.50
51:Cr:9:VAL:HG23	51:Cr:10:VAL:HG23	1.93	0.50
1:AO:30:VAL:HG13	1:AO:47:LEU:HD23	1.94	0.50
14:AC:204:ILE:HG21	14:AC:211:LYS:HA	1.94	0.50
27:AP:85:ILE:HG23	27:AP:107:ILE:HD12	1.93	0.50
51:Cr:17:LEU:HD21	51:Cr:36:ASN:ND2	2.24	0.50
55:CF:89:LEU:HD13	55:CF:90:ALA:N	2.26	0.50
59:Cf:5:LEU:H	72:CE:277:LEU:HD23	1.76	0.50
30:Ac:46:VAL:HG22	30:Ac:56:LEU:HD21	1.93	0.50
72:CE:222:LEU:HD12	72:CE:222:LEU:O	2.11	0.50
2:AX:91:LEU:HD22	2:AX:94:ILE:HD11	1.93	0.50
19:B2:798:G:H4'	19:B2:799:U:OP2	2.11	0.50
26:AR:28:PHE:HA	26:AR:55:THR:HG21	1.94	0.50
31:AD:193:ASP:OD1	31:AD:204:LEU:HD11	2.12	0.50
34:CO:87:MET:HE1	74:A5:2051:C:O2	2.12	0.50
44:CS:13:VAL:HG12	44:CS:63:TYR:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:CS:82:LEU:HD21	44:CS:124:ILE:CG2	2.41	0.50
44:CS:82:LEU:HD22	44:CS:83:ARG:H	1.77	0.50
51:Cr:74:ALA:O	65:CC:150:LEU:HD12	2.12	0.50
70:CJ:78:LYS:O	70:CJ:82:ILE:HD12	2.11	0.50
72:CE:242:ILE:HD13	74:A5:4939:C:C1'	2.42	0.50
5:AB:41:ILE:HD12	5:AB:41:ILE:O	2.11	0.50
21:Ag:5:MET:HE1	21:Ag:312:VAL:HG22	1.94	0.50
54:CB:252:ALA:HB3	74:A5:4457:U:O2	2.11	0.50
56:Cc:94:LEU:HD23	56:Cc:95:ALA:N	2.27	0.50
4:AL:71:ARG:HD3	4:AL:73:LEU:HD21	1.94	0.50
13:AE:176:ASP:O	13:AE:195:ILE:HD12	2.12	0.50
17:AW:11:LEU:HD13	17:AW:73:GLY:C	2.37	0.50
18:AI:38:ILE:HD12	18:AI:94:LYS:HB3	1.94	0.50
28:AT:46:ALA:HB1	28:AT:47:PRO:HD2	1.94	0.49
41:CD:64:ILE:HD13	41:CD:105:LEU:CD2	2.42	0.49
1:AO:119:LEU:HD13	1:AO:126:ILE:CD1	2.43	0.49
6:AA:108:PHE:HB2	6:AA:140:VAL:HG21	1.93	0.49
49:CY:55:VAL:HG23	49:CY:104:VAL:HG13	1.93	0.49
6:AA:34:MET:HE3	6:AA:149:ASN:O	2.12	0.49
19:B2:693:A:C2	19:B2:737:G:N1	2.80	0.49
24:AS:42:HIS:HE1	28:AT:46:ALA:HB3	1.77	0.49
31:AD:72:VAL:HG22	31:AD:75:LYS:NZ	2.26	0.49
42:CQ:70:MET:HG3	42:CQ:98:LEU:HD21	1.93	0.49
48:CX:71:LEU:HD12	48:CX:76:ILE:HG23	1.94	0.49
65:CC:211:TYR:O	65:CC:232:VAL:HG23	2.12	0.49
69:Co:6:LYS:O	69:Co:23:VAL:HG12	2.11	0.49
13:AE:62:LYS:HD3	13:AE:80:ILE:HD11	1.94	0.49
33:AQ:112:LEU:HD22	33:AQ:119:LEU:HD22	1.94	0.49
35:CL:55:ILE:HD12	35:CL:96:ILE:CD1	2.37	0.49
50:CZ:42:LEU:HD11	50:CZ:72:VAL:CG2	2.41	0.49
32:AF:72:LEU:HD21	32:AF:154:LEU:HD11	1.94	0.49
14:AC:106:VAL:HG22	14:AC:128:VAL:HG22	1.93	0.49
19:B2:796:G:H3'	19:B2:797:C:H5'	1.95	0.49
56:Cc:38:ILE:HD11	56:Cc:67:ALA:HB3	1.94	0.49
74:A5:2266:C:H5'	74:A5:2270:G:H21	1.78	0.49
74:A5:2890:C:H42	74:A5:3611:A:H61	1.59	0.49
15:AG:162:LEU:HD13	19:B2:68:A:P	2.53	0.49
19:B2:1083:A:H62	19:B2:1841:C:H1'	1.78	0.49
70:CJ:24:ILE:HD13	70:CJ:128:LEU:HA	1.94	0.49
13:AE:146:THR:O	13:AE:147:ILE:HD13	2.12	0.49
29:AZ:47:LEU:CD2	29:AZ:54:THR:HG21	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:CS:96:GLU:HB2	44:CS:142:VAL:HG21	1.94	0.49
55:CF:156:LYS:HE3	55:CF:156:LYS:HA	1.95	0.49
75:A7:66:G:O6	75:A7:109:U:C2	2.65	0.49
1:AO:45:THR:HG22	1:AO:52:THR:HA	1.95	0.49
29:AZ:79:ILE:HG23	29:AZ:84:ALA:HB2	1.94	0.49
55:CF:133:LEU:HD21	55:CF:140:ILE:HD11	1.94	0.49
65:CC:147:VAL:CG1	65:CC:152:LEU:HD12	2.43	0.49
65:CC:152:LEU:HD11	65:CC:174:LEU:HD13	1.95	0.49
19:B2:693:A:N1	19:B2:737:G:O6	2.46	0.48
21:Ag:119:GLN:NE2	21:Ag:179:LEU:HD13	2.27	0.48
46:CP:33:ALA:HB1	46:CP:117:ILE:HD13	1.95	0.48
58:Ce:70:LEU:CD1	58:Ce:123:THR:HG21	2.43	0.48
73:CG:136:LEU:HD22	73:CG:202:VAL:HG12	1.94	0.48
35:CL:184:MET:HE2	74:A5:1482:G:N2	2.28	0.48
54:CB:181:MET:HE1	54:CB:183:ILE:HD11	1.94	0.48
13:AE:151:ASP:H	13:AE:154:ILE:HD12	1.77	0.48
19:B2:1388:A:H2'	31:AD:205:PRO:HB3	1.95	0.48
33:AQ:13:PHE:HB3	33:AQ:22:VAL:HG22	1.94	0.48
43:CA:182:ALA:HB2	74:A5:3652:A:O2'	2.13	0.48
62:Cj:66:HIS:O	62:Cj:70:VAL:HG13	2.12	0.48
74:A5:3973:G:H1	74:A5:4038:C:H42	1.61	0.48
32:AF:100:ILE:HD13	32:AF:177:LEU:HD22	1.95	0.48
50:CZ:11:VAL:HG21	50:CZ:25:ILE:HD11	1.95	0.48
73:CG:136:LEU:HD22	73:CG:202:VAL:CG1	2.43	0.48
6:AA:78:SER:HB3	6:AA:87:VAL:HG21	1.95	0.48
15:AG:5:ILE:HD11	15:AG:14:LYS:HG2	1.96	0.48
31:AD:38:GLU:OE2	31:AD:51:LEU:HD22	2.13	0.48
41:CD:83:LEU:HD11	41:CD:101:THR:OG1	2.14	0.48
41:CD:239:MET:HE3	41:CD:239:MET:C	2.38	0.48
46:CP:53:LEU:HD23	46:CP:53:LEU:O	2.14	0.48
69:Co:66:ILE:HG12	69:Co:85:ILE:HD11	1.96	0.48
15:AG:63:MET:N	15:AG:63:MET:HE3	2.28	0.48
21:Ag:125:ARG:HH22	26:AR:30:THR:HG22	1.78	0.48
34:CO:194:GLU:CD	34:CO:195:VAL:HG13	2.37	0.48
43:CA:40:TYR:CB	43:CA:94:ALA:HB2	2.44	0.48
51:Cr:4:HIS:CD2	65:CC:289:LEU:HD22	2.49	0.48
58:Ce:9:LYS:HD2	58:Ce:12:ILE:HD11	1.96	0.48
65:CC:171:LEU:CD1	65:CC:176:ALA:HB3	2.43	0.48
23:AK:89:ILE:HG23	23:AK:89:ILE:O	2.13	0.48
55:CF:93:ILE:HD11	55:CF:118:PHE:HA	1.94	0.48
13:AE:129:ILE:HG13	13:AE:139:LEU:HD22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CP:104:LEU:HD11	74:A5:392:U:H1'	1.95	0.48
74:A5:3692:A:H62	74:A5:3823:G:H21	1.62	0.48
21:Ag:18:VAL:O	21:Ag:287:THR:HG23	2.14	0.48
28:AT:28:LEU:HD13	28:AT:28:LEU:O	2.13	0.48
12:AJ:130:ILE:HG21	12:AJ:145:PRO:HA	1.96	0.48
15:AG:5:ILE:O	15:AG:5:ILE:HD12	2.14	0.48
39:CN:161:MET:HE1	74:A5:55:G:O4'	2.14	0.48
56:Cc:49:ALA:HB2	56:Cc:81:LEU:CD1	2.43	0.48
58:Ce:103:VAL:HG22	58:Ce:107:ASN:HB2	1.95	0.48
2:AX:46:HIS:HB3	2:AX:101:LEU:HD21	1.96	0.47
16:AH:30:LEU:O	16:AH:36:LEU:HD12	2.14	0.47
19:B2:1259:A:H1'	19:B2:1264:C:H42	1.78	0.47
36:CV:16:ILE:HD11	36:CV:56:GLY:HA3	1.96	0.47
58:Ce:41:ILE:HD12	74:A5:1317:U:OP2	2.14	0.47
30:Ac:9:ILE:HD12	30:Ac:9:ILE:O	2.14	0.47
38:Ca:103:VAL:HG12	38:Ca:108:TYR:O	2.14	0.47
44:CS:169:THR:HG21	74:A5:4875:G:O4'	2.13	0.47
48:CX:86:ALA:HB1	48:CX:97:VAL:HG21	1.96	0.47
49:CY:80:ILE:HD12	49:CY:80:ILE:O	2.14	0.47
73:CG:146:LEU:HD12	73:CG:152:ALA:HB2	1.96	0.47
2:AX:111:ALA:HB3	19:B2:1193:U:OP2	2.14	0.47
19:B2:821:G:H21	19:B2:824:C:H5''	1.79	0.47
32:AF:39:ILE:HG23	32:AF:68:ILE:HG21	1.96	0.47
32:AF:39:ILE:HG21	32:AF:113:VAL:HG23	1.96	0.47
73:CG:220:GLU:O	73:CG:224:THR:HG23	2.14	0.47
74:A5:4075:U:H3	74:A5:4170:A:H62	1.62	0.47
12:AJ:87:LEU:HD13	12:AJ:97:ILE:CD1	2.45	0.47
14:AC:88:ILE:HD11	14:AC:94:ILE:HD11	1.95	0.47
16:AH:45:ILE:HD12	16:AH:62:ILE:CG2	2.45	0.47
19:B2:1538:C:H42	29:AZ:104:ARG:NH2	2.11	0.47
26:AR:31:ASN:ND2	26:AR:55:THR:HG22	2.29	0.47
62:Cj:83:THR:HG22	76:A8:94:G:O6	2.14	0.47
8:AY:120:THR:HG22	19:B2:151:C:OP1	2.14	0.47
34:CO:152:VAL:HG22	54:CB:94:GLU:OE2	2.13	0.47
46:CP:30:ARG:HA	46:CP:119:VAL:HG21	1.96	0.47
5:AB:84:PHE:HZ	5:AB:188:LEU:HD12	1.79	0.47
19:B2:442:C:H42	19:B2:449:A:H62	1.62	0.47
43:CA:199:VAL:HG21	74:A5:1631:A:C8	2.49	0.47
52:Ch:59:THR:HG22	76:A8:60:G:C2	2.50	0.47
54:CB:80:GLU:OE1	54:CB:326:VAL:HG13	2.15	0.47
7:AV:59:ILE:HG23	7:AV:64:GLU:OE2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AY:18:LEU:HD13	8:AY:20:ARG:HH21	1.80	0.47
16:AH:134:VAL:HG23	16:AH:134:VAL:O	2.14	0.47
32:AF:76:MET:HE3	32:AF:76:MET:HA	1.97	0.47
32:AF:169:ILE:HG22	32:AF:173:LEU:HD22	1.96	0.47
34:CO:34:VAL:HG11	34:CO:112:TYR:CE2	2.49	0.47
34:CO:102:LEU:HD11	34:CO:104:VAL:HG23	1.96	0.47
37:CM:20:HIS:CD2	37:CM:45:VAL:HG13	2.49	0.47
40:CI:61:SER:O	40:CI:65:LEU:HD22	2.15	0.47
50:CZ:11:VAL:HG11	50:CZ:80:LEU:HB2	1.96	0.47
55:CF:90:ALA:HB2	55:CF:125:LEU:HD11	1.97	0.47
58:Ce:9:LYS:HD3	58:Ce:69:MET:HE2	1.96	0.47
65:CC:309:ILE:HG23	65:CC:310:HIS:N	2.30	0.47
69:Co:63:THR:HG21	69:Co:87:ARG:HB3	1.97	0.47
71:CH:12:ILE:HD12	71:CH:53:LYS:O	2.15	0.47
74:A5:708:G:N2	74:A5:4942:C:H41	2.13	0.47
23:AK:63:ALA:HB3	23:AK:68:TYR:CE1	2.49	0.47
28:AT:99:VAL:O	28:AT:103:VAL:HG23	2.15	0.47
49:CY:73:VAL:HA	49:CY:80:ILE:HG22	1.97	0.47
65:CC:263:LEU:HD22	65:CC:273:LEU:HD23	1.95	0.47
68:Cp:29:ILE:HD11	68:Cp:69:TRP:CE3	2.50	0.47
74:A5:4341:C:H42	77:Cw:77:A:H8	1.62	0.47
26:AR:51:ALA:O	26:AR:55:THR:HG23	2.14	0.47
29:AZ:47:LEU:HD23	29:AZ:54:THR:HG21	1.97	0.47
31:AD:123:LEU:HD21	31:AD:154:ASP:HB2	1.96	0.47
60:Cg:59:VAL:HG22	60:Cg:60:ARG:H	1.78	0.47
9:Aa:44:ILE:HD13	9:Aa:65:PRO:HG2	1.97	0.47
21:Ag:24:THR:HG21	21:Ag:75:GLY:HA3	1.97	0.47
21:Ag:42:MET:HE2	21:Ag:56:GLN:CG	2.45	0.47
46:CP:53:LEU:HD22	46:CP:55:LYS:HB2	1.96	0.47
47:CU:100:LEU:HD22	47:CU:112:LEU:HB3	1.97	0.47
65:CC:158:VAL:O	65:CC:217:ILE:HD13	2.15	0.47
5:AB:103:MET:HE3	5:AB:215:VAL:HG23	1.97	0.46
5:AB:135:LEU:HD12	5:AB:215:VAL:CG1	2.45	0.46
34:CO:119:VAL:HG21	44:CS:171:ARG:HD2	1.97	0.46
36:CV:82:ILE:HG22	36:CV:83:ARG:HG3	1.97	0.46
39:CN:9:GLU:CD	61:Ci:44:ILE:HG21	2.39	0.46
53:Cb:61:ASN:OD1	53:Cb:65:MET:HE3	2.15	0.46
60:Cg:65:MET:HE1	74:A5:2748:C:O3'	2.15	0.46
65:CC:144:ILE:CG1	65:CC:147:VAL:HG23	2.44	0.46
72:CE:239:LYS:O	72:CE:243:THR:HG23	2.15	0.46
14:AC:233:LEU:O	14:AC:233:LEU:HD22	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:AS:31:THR:HG22	24:AS:37:GLY:C	2.40	0.46
25:Ad:47:ALA:HB1	25:Ad:52:PHE:CG	2.50	0.46
25:Ad:48:LYS:HE2	25:Ad:48:LYS:HA	1.98	0.46
54:CB:389:MET:HE2	54:CB:392:LEU:HD11	1.97	0.46
60:Cg:6:THR:HG21	74:A5:2401:A:O2'	2.15	0.46
71:CH:165:THR:CG2	71:CH:179:ILE:HG22	2.45	0.46
74:A5:1318:C:H42	74:A5:1322:A:H8	1.63	0.46
14:AC:209:VAL:HG22	14:AC:233:LEU:HD23	1.97	0.46
54:CB:117:ARG:HG2	54:CB:180:LEU:HD13	1.97	0.46
58:Ce:85:LEU:HD21	58:Ce:118:LEU:HD23	1.98	0.46
74:A5:1804:A:H61	74:A5:1832:C:H2'	1.80	0.46
3:AN:99:ARG:NE	3:AN:115:LEU:HD11	2.31	0.46
34:CO:11:GLY:O	34:CO:41:ILE:HG22	2.16	0.46
43:CA:45:VAL:HG12	43:CA:86:GLN:O	2.15	0.46
3:AN:16:LEU:HD23	3:AN:16:LEU:H	1.81	0.46
31:AD:193:ASP:HB3	31:AD:194:PRO:CD	2.45	0.46
70:CJ:96:LYS:HE2	70:CJ:163:MET:HE2	1.98	0.46
72:CE:83:LYS:N	72:CE:84:LYS:HA	2.31	0.46
7:AV:56:CYS:SG	7:AV:59:ILE:HD13	2.56	0.46
12:AJ:92:MET:HE3	12:AJ:92:MET:O	2.15	0.46
28:AT:53:PHE:CE1	28:AT:103:VAL:HG22	2.50	0.46
46:CP:136:ILE:HD13	74:A5:2794:C:C4	2.51	0.46
65:CC:44:LEU:HD12	65:CC:238:LEU:HD21	1.96	0.46
72:CE:125:LEU:HD21	74:A5:1283:G:C6	2.51	0.46
72:CE:277:LEU:HB2	72:CE:281:ILE:HD11	1.98	0.46
73:CG:133:PRO:HB2	73:CG:135:VAL:HG23	1.97	0.46
74:A5:2417:A:H61	74:A5:2430:C:H1'	1.80	0.46
8:AY:62:THR:HG22	8:AY:69:THR:HG22	1.97	0.46
13:AE:129:ILE:CG1	13:AE:139:LEU:HD22	2.46	0.46
22:AU:24:LEU:HB2	22:AU:32:LEU:HD11	1.97	0.46
26:AR:1:MET:HE3	26:AR:1:MET:N	2.31	0.46
31:AD:72:VAL:HG22	31:AD:75:LYS:HZ2	1.80	0.46
74:A5:1380:G:H21	74:A5:1381:U:H5	1.64	0.46
74:A5:3967:G:N1	74:A5:4055:U:C2	2.83	0.46
74:A5:4127:A:H62	74:A5:4157:A:H62	1.64	0.46
10:Ab:12:PRO:C	10:Ab:16:LYS:HZ2	2.24	0.46
16:AH:45:ILE:HD11	16:AH:72:PHE:CE2	2.50	0.46
18:AI:165:GLN:OE1	18:AI:172:LEU:HD22	2.15	0.46
42:CQ:150:ARG:O	42:CQ:163:THR:HG23	2.15	0.46
15:AG:5:ILE:CG2	15:AG:111:LEU:HD12	2.46	0.46
19:B2:808:A:H2	19:B2:855:G:H22	1.62	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:CY:32:SER:OG	49:CY:49:ILE:HD11	2.16	0.46
53:Cb:62:ALA:HB3	53:Cb:63:LYS:HE2	1.98	0.46
56:Cc:48:LEU:HD21	56:Cc:60:ILE:HG21	1.97	0.46
73:CG:194:VAL:HG12	73:CG:194:VAL:O	2.15	0.46
74:A5:3751:G:H21	74:A5:3775:A:H8	1.63	0.46
8:AY:18:LEU:HB3	8:AY:20:ARG:HE	1.81	0.45
16:AH:154:ILE:HG23	16:AH:185:VAL:HG22	1.98	0.45
18:AI:41:ARG:CZ	19:B2:306:C:H42	2.29	0.45
24:AS:125:HIS:CE1	24:AS:131:VAL:HG21	2.51	0.45
31:AD:198:ILE:HD12	31:AD:199:GLY:N	2.31	0.45
34:CO:54:TYR:CE2	34:CO:145:VAL:HG11	2.50	0.45
66:Cm:95:ILE:HD13	74:A5:4473:A:H4'	1.98	0.45
72:CE:41:LYS:HE2	74:A5:983:C:H41	1.80	0.45
73:CG:207:VAL:HG11	73:CG:215:LEU:HD12	1.98	0.45
74:A5:58:G:H2'	76:A8:33:G:H2'	1.98	0.45
5:AB:137:LEU:CD1	5:AB:176:VAL:HG21	2.47	0.45
19:B2:1467:C:C5'	26:AR:1:MET:HE1	2.46	0.45
54:CB:207:VAL:HG21	54:CB:331:VAL:HG11	1.98	0.45
56:Cc:22:MET:HE2	56:Cc:22:MET:HA	1.98	0.45
64:Cl:13:LEU:HD22	74:A5:2407:G:H2'	1.98	0.45
22:AU:94:PRO:CG	22:AU:97:ILE:HD12	2.46	0.45
54:CB:217:ILE:HD12	54:CB:347:LEU:HB3	1.98	0.45
63:Ck:32:VAL:HG11	63:Ck:53:ALA:HB1	1.98	0.45
6:AA:84:GLN:O	6:AA:87:VAL:HG22	2.16	0.45
11:Ae:35:ARG:HB2	11:Ae:36:MET:HE3	1.97	0.45
14:AC:209:VAL:HG21	14:AC:233:LEU:HD23	1.97	0.45
40:CI:4:ARG:HE	74:A5:4405:G:H4'	1.81	0.45
43:CA:82:ILE:HG22	68:Cp:65:ALA:HB3	1.97	0.45
54:CB:219:VAL:CG1	54:CB:345:LEU:HD23	2.47	0.45
74:A5:4749:C:H42	74:A5:4951:G:H22	1.64	0.45
5:AB:172:MET:O	5:AB:176:VAL:HG23	2.16	0.45
8:AY:18:LEU:CD1	13:AE:64:ILE:HD11	2.39	0.45
40:CI:129:VAL:HG12	40:CI:130:HIS:O	2.17	0.45
44:CS:7:LEU:H	44:CS:7:LEU:HD22	1.81	0.45
56:Cc:28:VAL:HG11	56:Cc:33:GLN:HB3	1.98	0.45
61:Ci:73:ILE:HG23	61:Ci:83:ALA:HB1	1.99	0.45
62:Cj:17:THR:HG23	62:Cj:29:LEU:HD21	1.99	0.45
25:Ad:47:ALA:HB1	25:Ad:52:PHE:HB3	1.97	0.45
47:CU:82:TYR:CE2	47:CU:86:LEU:HD11	2.51	0.45
54:CB:14:LEU:HD13	74:A5:4588:U:C5'	2.47	0.45
54:CB:29:VAL:HG13	54:CB:348:ARG:HE	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:Cc:49:ALA:HB2	56:Cc:81:LEU:HD12	1.98	0.45
65:CC:130:ALA:CB	65:CC:246:VAL:HG12	2.47	0.45
15:AG:121:ILE:HD12	15:AG:121:ILE:O	2.17	0.45
19:B2:693:A:N1	19:B2:737:G:C6	2.85	0.45
31:AD:37:VAL:HB	31:AD:48:ILE:HD11	1.99	0.45
32:AF:100:ILE:CD1	32:AF:177:LEU:HD22	2.46	0.45
38:Ca:43:ILE:HD11	74:A5:4304:A:C6	2.51	0.45
51:Cr:91:SER:HB2	72:CE:110:ARG:NH1	2.32	0.45
57:Cd:83:ARG:C	57:Cd:84:ILE:HD12	2.42	0.45
65:CC:209:ILE:HG21	65:CC:221:PHE:CZ	2.52	0.45
74:A5:3653:A:C6	74:A5:3691:G:C2	3.01	0.45
1:AO:117:ARG:HH21	9:Aa:48:ALA:HB3	1.81	0.45
59:Cf:104:MET:HE2	59:Cf:104:MET:N	2.32	0.45
73:CG:59:ARG:O	73:CG:63:LEU:HD23	2.17	0.45
13:AE:68:ARG:NE	13:AE:76:VAL:HG11	2.32	0.45
13:AE:192:ILE:HD12	13:AE:242:LYS:O	2.16	0.45
39:CN:32:GLN:CB	73:CG:63:LEU:HD11	2.47	0.45
42:CQ:138:LEU:HD13	74:A5:1429:C:OP1	2.17	0.45
43:CA:179:ILE:HG21	43:CA:188:LYS:HE2	1.97	0.45
74:A5:741:C:H42	74:A5:923:C:H42	1.64	0.45
4:AL:72:ILE:O	4:AL:73:LEU:HD23	2.17	0.45
35:CL:47:ALA:HB1	35:CL:48:PRO:HD2	1.98	0.45
43:CA:29:LEU:HD21	43:CA:115:CYS:SG	2.57	0.45
51:Cr:9:VAL:CG2	65:CC:136:LEU:HD11	2.46	0.45
65:CC:124:ILE:HG21	65:CC:264:TYR:OH	2.16	0.45
1:AO:135:ILE:HD11	19:B2:986:G:C2	2.51	0.44
15:AG:213:LEU:HD12	15:AG:214:ALA:N	2.32	0.44
50:CZ:42:LEU:HD12	50:CZ:73:LYS:O	2.17	0.44
51:Cr:91:SER:O	51:Cr:95:HIS:HB3	2.17	0.44
55:CF:154:ILE:HD12	55:CF:191:ILE:HD12	1.98	0.44
65:CC:44:LEU:HD11	74:A5:1373:A:H5"	1.99	0.44
65:CC:281:MET:HE2	65:CC:281:MET:HA	1.99	0.44
38:Ca:58:MET:N	38:Ca:58:MET:HE2	2.32	0.44
43:CA:82:ILE:CG2	68:Cp:65:ALA:HB3	2.47	0.44
44:CS:82:LEU:HD22	44:CS:125:GLN:O	2.17	0.44
39:CN:46:ASP:O	39:CN:49:ARG:C	2.61	0.44
41:CD:33:ARG:HE	41:CD:37:VAL:HG11	1.82	0.44
45:CT:95:HIS:C	45:CT:96:ILE:HD12	2.43	0.44
53:Cb:32:LEU:HD23	53:Cb:32:LEU:H	1.82	0.44
55:CF:187:MET:CE	65:CC:328:LEU:HD22	2.47	0.44
56:Cc:12:GLU:CB	56:Cc:13:SER:HA	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AG:147:LEU:HD21	15:AG:156:TYR:CD2	2.52	0.44
27:AP:57:LEU:HA	27:AP:60:LEU:HD12	2.00	0.44
37:CM:7:VAL:O	37:CM:7:VAL:HG13	2.17	0.44
39:CN:6:TYR:CE2	73:CG:173:LEU:HD21	2.51	0.44
59:Cf:50:VAL:HG12	59:Cf:69:VAL:CG2	2.46	0.44
65:CC:208:CYS:C	65:CC:209:ILE:HD12	2.43	0.44
7:AV:37:ALA:HB1	7:AV:46:PHE:CD1	2.52	0.44
22:AU:84:ILE:HD13	31:AD:8:LYS:HZ3	1.82	0.44
29:AZ:69:THR:O	29:AZ:73:VAL:HG23	2.18	0.44
29:AZ:91:LEU:HD22	29:AZ:96:LEU:HD12	1.99	0.44
31:AD:65:ARG:O	31:AD:69:LEU:HD13	2.18	0.44
43:CA:207:VAL:HG12	74:A5:3919:C:C5'	2.48	0.44
48:CX:119:ILE:O	48:CX:119:ILE:HD12	2.18	0.44
53:Cb:17:HIS:ND1	53:Cb:21:ILE:HD11	2.32	0.44
68:Cp:47:MET:HE2	68:Cp:47:MET:HA	2.00	0.44
35:CL:184:MET:HE2	74:A5:1482:G:H22	1.83	0.44
48:CX:82:THR:HA	48:CX:87:MET:HE1	1.99	0.44
14:AC:127:PHE:CE2	14:AC:141:VAL:HG13	2.52	0.44
14:AC:216:MET:HE2	14:AC:216:MET:HA	1.99	0.44
23:AK:49:MET:SD	23:AK:58:VAL:HG11	2.58	0.44
64:Cl:5:LYS:HB2	64:Cl:9:ILE:HD11	2.00	0.44
72:CE:94:LYS:HG2	72:CE:105:ARG:H	1.81	0.44
74:A5:1436:C:H4'	74:A5:2119:C:H42	1.82	0.44
2:AX:50:ILE:HD11	2:AX:97:ASN:HA	2.00	0.44
4:AL:72:ILE:HD11	4:AL:127:THR:HG22	1.99	0.44
24:AS:117:ILE:HG22	24:AS:117:ILE:O	2.18	0.44
26:AR:41:ILE:HG21	26:AR:47:ARG:HB2	2.00	0.44
39:CN:126:THR:HG23	74:A5:4174:U:O2'	2.17	0.44
70:CJ:163:MET:HE3	70:CJ:174:ILE:HD13	1.98	0.44
71:CH:18:ILE:HD11	71:CH:55:LEU:CD1	2.48	0.44
13:AE:9:LEU:HD12	13:AE:30:ARG:HA	2.00	0.44
33:AQ:52:LEU:O	33:AQ:55:VAL:HG22	2.18	0.44
57:Cd:77:ILE:HD11	74:A5:2370:A:C6	2.52	0.44
13:AE:126:VAL:O	13:AE:126:VAL:HG23	2.18	0.43
26:AR:99:ASP:OD1	26:AR:119:VAL:HG13	2.17	0.43
51:Cr:101:LYS:O	51:Cr:101:LYS:HG3	2.18	0.43
68:Cp:22:LEU:O	68:Cp:26:VAL:HG23	2.18	0.43
72:CE:50:LEU:HD12	72:CE:51:VAL:HG23	1.98	0.43
72:CE:179:LEU:HD21	74:A5:4936:G:H21	1.82	0.43
13:AE:87:MET:HE1	13:AE:100:ARG:NE	2.32	0.43
21:Ag:5:MET:CE	21:Ag:312:VAL:HG22	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:AZ:79:ILE:HD11	29:AZ:83:LEU:HB3	2.00	0.43
35:CL:126:LEU:HD11	52:Ch:117:ARG:CD	2.48	0.43
36:CV:116:ALA:C	36:CV:117:ILE:HD12	2.43	0.43
41:CD:261:VAL:HG12	41:CD:263:LYS:HB2	2.00	0.43
2:AX:122:VAL:O	2:AX:122:VAL:HG13	2.18	0.43
27:AP:72:LYS:NZ	27:AP:75:VAL:HG23	2.32	0.43
28:AT:22:LEU:HD13	28:AT:28:LEU:HD21	2.00	0.43
35:CL:126:LEU:HD11	52:Ch:117:ARG:HD3	2.01	0.43
58:Ce:7:LEU:HD21	58:Ce:94:SER:HA	1.99	0.43
72:CE:158:ARG:HG3	72:CE:158:ARG:HH11	1.82	0.43
72:CE:195:ILE:N	72:CE:195:ILE:HD12	2.33	0.43
74:A5:2685:C:H1'	74:A5:2686:G:H5'	2.00	0.43
44:CS:33:PHE:HE1	44:CS:126:ILE:HD13	1.83	0.43
47:CU:47:ILE:HG23	47:CU:56:LEU:CD1	2.49	0.43
72:CE:125:LEU:HD21	74:A5:1283:G:O6	2.17	0.43
17:AW:93:LEU:HD21	17:AW:128:PHE:CD1	2.53	0.43
28:AT:39:LEU:HD12	28:AT:99:VAL:HG21	1.99	0.43
35:CL:126:LEU:HD12	35:CL:136:LYS:O	2.18	0.43
51:Cr:63:VAL:HG13	51:Cr:63:VAL:O	2.18	0.43
57:Cd:54:MET:O	57:Cd:58:GLY:HA2	2.18	0.43
70:CJ:94:LEU:HD21	70:CJ:107:PHE:HB3	2.00	0.43
72:CE:179:LEU:HD13	72:CE:179:LEU:O	2.19	0.43
72:CE:201:ILE:HD11	72:CE:260:LYS:HG3	2.01	0.43
23:AK:16:PHE:CE1	23:AK:89:ILE:HD12	2.54	0.43
40:CI:52:MET:CG	40:CI:152:LEU:HD22	2.48	0.43
52:Ch:34:ALA:HB3	52:Ch:43:LYS:HE3	2.01	0.43
73:CG:25:LYS:HA	73:CG:28:VAL:HG22	2.00	0.43
1:AO:50:LYS:HA	19:B2:975:G:H21	1.83	0.43
6:AA:108:PHE:CB	6:AA:140:VAL:HG21	2.48	0.43
17:AW:66:THR:HG23	17:AW:67:GLY:H	1.82	0.43
19:B2:1121:G:H2'	19:B2:1122:A:H5'	2.01	0.43
27:AP:28:MET:HE2	27:AP:32:GLN:HB3	2.00	0.43
51:Cr:38:PHE:O	51:Cr:44:ILE:HD11	2.19	0.43
54:CB:168:MET:HE3	54:CB:177:LYS:O	2.19	0.43
65:CC:287:THR:O	65:CC:287:THR:HG23	2.18	0.43
74:A5:2258:C:H1'	74:A5:2260:C:H41	1.83	0.43
5:AB:66:VAL:HG22	5:AB:87:ILE:HG22	2.01	0.43
9:Aa:2:THR:HG22	19:B2:1199:A:H5''	2.00	0.43
17:AW:31:SER:O	17:AW:35:VAL:HG23	2.19	0.43
23:AK:80:ARG:HH11	23:AK:89:ILE:HG21	1.83	0.43
44:CS:73:LEU:HD23	44:CS:74:ARG:HH22	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:CT:48:VAL:HG22	45:CT:50:LYS:H	1.84	0.43
72:CE:67:ALA:HB3	72:CE:68:MET:HE2	2.01	0.43
5:AB:134:LEU:HD12	5:AB:219:LYS:HB2	2.01	0.43
15:AG:1:MET:HE1	15:AG:3:LEU:HD13	2.00	0.43
31:AD:161:GLY:O	31:AD:164:VAL:HG12	2.18	0.43
36:CV:78:PRO:O	36:CV:105:ILE:HD12	2.19	0.43
46:CP:48:LEU:CD2	46:CP:91:LEU:HD11	2.43	0.43
48:CX:71:LEU:HD12	48:CX:76:ILE:CG2	2.48	0.43
52:Ch:102:LEU:O	52:Ch:102:LEU:HD12	2.18	0.43
53:Cb:54:LEU:HD22	74:A5:1812:C:H4'	2.00	0.43
54:CB:53:MET:HE1	74:A5:4627:U:OP1	2.19	0.43
1:AO:56:VAL:HG21	1:AO:81:VAL:HG22	2.00	0.43
13:AE:125:LYS:HA	13:AE:159:THR:HG22	2.01	0.43
27:AP:126:VAL:HG12	27:AP:127:LYS:H	1.83	0.43
37:CM:7:VAL:HB	37:CM:57:LEU:HD21	2.00	0.43
38:Ca:98:ALA:HB1	38:Ca:123:ILE:HG12	2.00	0.43
53:Cb:54:LEU:HD23	53:Cb:57:MET:SD	2.59	0.43
66:Cm:95:ILE:HD11	66:Cm:124:LYS:HG2	2.01	0.43
68:Cp:8:VAL:O	68:Cp:11:VAL:HG12	2.18	0.43
22:AU:24:LEU:CB	22:AU:32:LEU:HD11	2.49	0.42
27:AP:90:VAL:HG21	27:AP:109:PRO:HA	2.00	0.42
36:CV:39:ILE:CD1	36:CV:61:VAL:HG11	2.44	0.42
41:CD:233:PRO:HA	41:CD:236:MET:HE3	2.00	0.42
46:CP:148:MET:C	46:CP:148:MET:HE2	2.44	0.42
56:Cc:46:VAL:C	56:Cc:47:ILE:HD12	2.43	0.42
74:A5:930:G:H3'	74:A5:931:C:C5'	2.49	0.42
74:A5:4527:G:H22	74:A5:4556:U:H2'	1.84	0.42
14:AC:61:MET:HE3	14:AC:61:MET:O	2.18	0.42
33:AQ:115:TYR:HE2	33:AQ:119:LEU:HD21	1.84	0.42
42:CQ:122:THR:HG23	65:CC:285:ILE:HD11	2.01	0.42
66:Cm:96:CYS:HA	66:Cm:121:LEU:HD23	2.00	0.42
74:A5:3653:A:N6	74:A5:3691:G:N2	2.60	0.42
32:AF:179:ASN:O	32:AF:183:GLY:HA2	2.19	0.42
74:A5:1934:A:N1	74:A5:2052:G:O6	2.52	0.42
30:Ac:32:VAL:HG11	30:Ac:56:LEU:HD22	2.01	0.42
31:AD:39:VAL:CA	31:AD:48:ILE:HD12	2.49	0.42
34:CO:88:LEU:HD23	34:CO:98:ALA:HB3	2.01	0.42
39:CN:45:PRO:HG2	73:CG:166:LEU:HD21	2.00	0.42
62:Cj:66:HIS:O	62:Cj:69:ILE:HD12	2.20	0.42
1:AO:117:ARG:HH11	1:AO:117:ARG:HB2	1.84	0.42
19:B2:141:A:N6	19:B2:177:G:H21	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:CO:119:VAL:HG21	44:CS:171:ARG:CD	2.49	0.42
41:CD:211:LEU:HD11	41:CD:218:ALA:CB	2.49	0.42
47:CU:28:PRO:HB2	47:CU:34:MET:HG2	2.00	0.42
52:Ch:91:MET:HE3	52:Ch:92:ARG:N	2.35	0.42
55:CF:101:VAL:HG12	55:CF:139:TYR:CE2	2.54	0.42
69:Co:20:PRO:O	69:Co:73:VAL:HG13	2.19	0.42
13:AE:126:VAL:HG22	13:AE:158:ASP:O	2.20	0.42
16:AH:45:ILE:HD12	16:AH:62:ILE:HG22	2.01	0.42
43:CA:62:VAL:HG11	43:CA:71:LYS:HD3	2.02	0.42
65:CC:224:ILE:CG2	65:CC:227:ILE:HD12	2.50	0.42
73:CG:87:LEU:HD13	73:CG:182:CYS:SG	2.59	0.42
13:AE:87:MET:HE3	13:AE:87:MET:C	2.44	0.42
27:AP:44:ARG:NE	27:AP:84:ILE:HD13	2.35	0.42
38:Ca:73:VAL:HG21	38:Ca:108:TYR:CD1	2.54	0.42
41:CD:124:GLU:HG2	41:CD:126:THR:HG23	2.01	0.42
49:CY:30:MET:HA	49:CY:30:MET:HE2	2.01	0.42
51:Cr:91:SER:O	51:Cr:95:HIS:CB	2.68	0.42
53:Cb:54:LEU:HD23	53:Cb:57:MET:HB3	2.02	0.42
5:AB:167:LYS:HE2	5:AB:204:ILE:HD12	2.02	0.42
42:CQ:23:ILE:HD12	42:CQ:24:TYR:H	1.82	0.42
48:CX:95:THR:O	48:CX:96:LEU:HD22	2.19	0.42
59:Cf:105:LEU:HD12	59:Cf:106:TYR:N	2.34	0.42
2:AX:129:SER:O	2:AX:133:LEU:HD22	2.19	0.42
4:AL:86:ILE:CD1	4:AL:88:ILE:HG23	2.49	0.42
5:AB:105:LEU:HB2	5:AB:110:MET:HE2	2.01	0.42
16:AH:98:ARG:CB	16:AH:125:VAL:HG13	2.49	0.42
21:Ag:206:LEU:HD22	21:Ag:227:LEU:HD11	2.02	0.42
22:AU:59:LYS:HD2	22:AU:84:ILE:HG23	2.02	0.42
41:CD:155:THR:HG23	75:A7:36:C:C5'	2.50	0.42
41:CD:163:LEU:HD13	41:CD:173:ILE:HG21	2.00	0.42
42:CQ:32:TYR:OH	42:CQ:126:LEU:HD22	2.19	0.42
46:CP:148:MET:O	46:CP:149:ILE:HD13	2.20	0.42
3:AN:99:ARG:HE	3:AN:115:LEU:HD11	1.85	0.42
24:AS:27:ALA:O	24:AS:31:THR:HG23	2.19	0.42
34:CO:177:LEU:HD21	37:CM:130:LEU:HB3	2.02	0.42
35:CL:87:HIS:CE1	35:CL:90:VAL:HG23	2.55	0.42
56:Cc:28:VAL:C	56:Cc:29:LEU:HD23	2.45	0.42
21:Ag:212:LYS:HA	21:Ag:235:ILE:HG22	2.02	0.41
30:Ac:6:VAL:HG12	30:Ac:8:PRO:HD3	2.02	0.41
21:Ag:42:MET:HE2	21:Ag:56:GLN:HG2	2.01	0.41
31:AD:106:ARG:CD	31:AD:175:VAL:HG22	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:Ca:100:ILE:HG23	38:Ca:125:LYS:HG2	2.01	0.41
39:CN:9:GLU:OE1	61:CI:44:ILE:HD13	2.20	0.41
51:Cr:60:VAL:HG11	51:Cr:85:ASN:HB2	2.02	0.41
58:Ce:45:VAL:O	58:Ce:55:MET:HE2	2.20	0.41
73:CG:98:LEU:HD11	73:CG:215:LEU:HD21	2.03	0.41
2:AX:105:PHE:HB3	2:AX:112:VAL:HG21	2.02	0.41
5:AB:114:VAL:HG22	5:AB:142:PHE:HZ	1.85	0.41
19:B2:1650:A:H5''	33:AQ:139:ALA:HB2	2.03	0.41
41:CD:63:GLN:C	41:CD:64:ILE:HD12	2.44	0.41
41:CD:64:ILE:HD13	41:CD:105:LEU:HD22	2.02	0.41
43:CA:207:VAL:HG12	74:A5:3919:C:H5''	2.03	0.41
45:CT:151:LEU:HD12	45:CT:151:LEU:O	2.20	0.41
50:CZ:46:ILE:HD11	50:CZ:49:TYR:CE1	2.55	0.41
54:CB:392:LEU:HD12	74:A5:5042:A:P	2.61	0.41
1:AO:55:ARG:NH2	19:B2:972:A:H61	2.18	0.41
6:AA:62:ALA:HA	6:AA:65:ILE:HD12	2.02	0.41
19:B2:1599:U:O5'	29:AZ:44:LEU:HD12	2.20	0.41
39:CN:6:TYR:CE2	61:CI:40:VAL:HG23	2.56	0.41
41:CD:273:LEU:HD22	75:A7:108:G:OP2	2.19	0.41
45:CT:138:ALA:HB3	55:CF:85:ALA:HA	2.01	0.41
53:Cb:32:LEU:HD21	74:A5:1464:C:OP1	2.20	0.41
54:CB:70:LYS:HE2	54:CB:70:LYS:HA	2.01	0.41
54:CB:220:ILE:HG13	54:CB:278:THR:HG22	2.03	0.41
71:CH:20:LEU:HD11	71:CH:22:GLY:O	2.19	0.41
73:CG:154:LEU:HD11	73:CG:222:ILE:HD13	2.01	0.41
15:AG:181:THR:HG22	15:AG:183:ARG:H	1.85	0.41
34:CO:177:LEU:HD22	37:CM:127:VAL:HG13	2.02	0.41
40:CI:184:MET:HE3	40:CI:184:MET:HA	2.02	0.41
45:CT:138:ALA:HB1	55:CF:83:VAL:HG23	2.03	0.41
50:CZ:57:MET:HE1	74:A5:4150:G:OP1	2.20	0.41
54:CB:93:VAL:HG13	54:CB:102:PHE:HB2	2.02	0.41
32:AF:72:LEU:HD21	32:AF:154:LEU:CD1	2.51	0.41
41:CD:146:LEU:HD23	41:CD:163:LEU:HD22	2.03	0.41
47:CU:55:ASN:O	47:CU:56:LEU:HD23	2.20	0.41
74:A5:708:G:H21	74:A5:4942:C:H41	1.67	0.41
4:AL:35:ARG:HH21	4:AL:63:THR:HG21	1.83	0.41
29:AZ:44:LEU:HD11	29:AZ:46:ASN:ND2	2.36	0.41
33:AQ:85:ARG:HD3	33:AQ:119:LEU:HD23	2.02	0.41
65:CC:44:LEU:HD13	65:CC:44:LEU:O	2.21	0.41
65:CC:252:TRP:CZ3	65:CC:260:LEU:HD11	2.56	0.41
2:AX:66:ILE:HD12	2:AX:66:ILE:H	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AY:40:ILE:CD1	8:AY:57:VAL:HG11	2.51	0.41
40:CI:90:ARG:O	40:CI:91:LEU:HD22	2.21	0.41
42:CQ:18:PRO:HG3	42:CQ:29:VAL:HG21	2.02	0.41
46:CP:118:GLN:NE2	74:A5:423:G:H21	2.18	0.41
68:Cp:56:HIS:CD2	68:Cp:63:THR:HG22	2.56	0.41
74:A5:2902:G:N2	74:A5:3597:G:H22	2.19	0.41
74:A5:3927:U:C2	74:A5:4184:G:O6	2.71	0.41
8:AY:102:THR:HB	8:AY:103:SER:HA	2.02	0.41
27:AP:86:LEU:O	27:AP:90:VAL:HG23	2.21	0.41
28:AT:62:ARG:HA	28:AT:131:LEU:HD21	2.01	0.41
34:CO:138:LEU:HD23	34:CO:138:LEU:O	2.21	0.41
42:CQ:38:ARG:HA	65:CC:303:ARG:HE	1.85	0.41
45:CT:95:HIS:O	45:CT:96:ILE:HD12	2.21	0.41
74:A5:2250:C:H42	74:A5:2254:G:H21	1.69	0.41
6:AA:121:LEU:HD12	6:AA:143:PRO:C	2.44	0.41
11:Ae:12:VAL:HG11	19:B2:616:A:N3	2.36	0.41
21:Ag:23:THR:HG22	21:Ag:31:ILE:HD12	2.02	0.41
23:AK:63:ALA:HB2	31:AD:27:ARG:HD2	2.02	0.41
34:CO:19:LEU:O	34:CO:23:VAL:HG12	2.21	0.41
52:Ch:34:ALA:HB3	52:Ch:43:LYS:CE	2.50	0.41
72:CE:92:VAL:N	72:CE:93:THR:HA	2.35	0.41
74:A5:2890:C:H42	74:A5:3611:A:N6	2.18	0.41
1:AO:119:LEU:HD13	1:AO:126:ILE:HD12	2.04	0.40
3:AN:63:VAL:HG11	3:AN:71:ILE:HG22	2.02	0.40
5:AB:38:MET:HE3	5:AB:182:LYS:CD	2.51	0.40
48:CX:76:ILE:HD12	48:CX:112:ALA:HB2	2.03	0.40
50:CZ:80:LEU:HD12	50:CZ:80:LEU:O	2.20	0.40
51:Cr:91:SER:N	72:CE:110:ARG:HH12	2.19	0.40
54:CB:102:PHE:HB3	54:CB:153:MET:HE1	2.03	0.40
72:CE:246:ARG:HH12	74:A5:4936:G:H22	1.70	0.40
6:AA:23:THR:HG21	6:AA:174:MET:SD	2.60	0.40
12:AJ:130:ILE:HG22	12:AJ:143:ASN:O	2.21	0.40
14:AC:269:PHE:O	14:AC:273:LEU:HD23	2.21	0.40
21:Ag:23:THR:HG22	21:Ag:31:ILE:CD1	2.51	0.40
24:AS:117:ILE:HD12	27:AP:111:MET:HE1	2.03	0.40
32:AF:138:ALA:HB3	32:AF:204:ARG:HD3	2.03	0.40
40:CI:48:LEU:HD11	40:CI:167:ILE:HD12	2.03	0.40
41:CD:64:ILE:HD13	41:CD:105:LEU:HD21	2.02	0.40
41:CD:111:ASN:C	41:CD:111:ASN:HD22	2.29	0.40
42:CQ:175:GLU:HG2	74:A5:1497:A:H61	1.86	0.40
45:CT:62:GLY:C	45:CT:74:ILE:HD11	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:CT:72:VAL:HG23	45:CT:93:ILE:HD12	2.02	0.40
51:Cr:125:MET:O	51:Cr:126:VAL:HG23	2.21	0.40
58:Ce:28:TYR:HB2	58:Ce:31:ILE:HD12	2.04	0.40
72:CE:158:ARG:HE	74:A5:4948:C:H42	1.67	0.40
2:AX:85:VAL:HG21	2:AX:91:LEU:HD23	2.04	0.40
2:AX:107:ARG:HB2	2:AX:112:VAL:HG22	2.03	0.40
5:AB:91:VAL:HG11	73:CG:264:LYS:NZ	2.36	0.40
16:AH:93:VAL:HG22	16:AH:95:ILE:HG13	2.02	0.40
18:AI:43:ILE:HD11	18:AI:55:TYR:HB3	2.03	0.40
29:AZ:79:ILE:HD11	29:AZ:83:LEU:CB	2.51	0.40
29:AZ:91:LEU:HD22	29:AZ:96:LEU:CD1	2.52	0.40
29:AZ:110:THR:HG22	32:AF:102:LEU:CD1	2.52	0.40
35:CL:144:LEU:HD12	35:CL:148:THR:OG1	2.21	0.40
45:CT:72:VAL:HG23	45:CT:93:ILE:CD1	2.52	0.40
46:CP:50:ASP:HB3	46:CP:55:LYS:HB3	2.03	0.40
2:AX:66:ILE:HD13	11:Ae:8:ARG:HH22	1.86	0.40
3:AN:113:PHE:CE2	3:AN:117:LEU:HD11	2.56	0.40
6:AA:78:SER:CB	6:AA:87:VAL:HG21	2.52	0.40
7:AV:59:ILE:HD12	7:AV:59:ILE:N	2.36	0.40
12:AJ:32:ILE:HD11	12:AJ:37:LEU:O	2.21	0.40
15:AG:6:SER:OG	15:AG:112:VAL:HG12	2.21	0.40
15:AG:32:MET:HE3	15:AG:32:MET:HA	2.03	0.40
28:AT:33:TRP:O	28:AT:34:VAL:HG23	2.21	0.40
41:CD:287:PHE:CD1	41:CD:287:PHE:C	2.99	0.40
42:CQ:18:PRO:CG	42:CQ:29:VAL:HG21	2.51	0.40
44:CS:33:PHE:CE1	44:CS:126:ILE:HD13	2.57	0.40
55:CF:187:MET:HE2	65:CC:328:LEU:HD22	2.04	0.40
61:CI:40:VAL:O	61:CI:44:ILE:HG23	2.21	0.40
72:CE:145:THR:O	72:CE:148:THR:HG22	2.21	0.40
65:CC:33:ARG:O	65:CC:37:VAL:HG23	2.22	0.40
68:Cp:14:TYR:HE2	68:Cp:26:VAL:HG11	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	AO	124/151 (82%)	106 (86%)	15 (12%)	3 (2%)	4	27
2	AX	138/143 (96%)	121 (88%)	16 (12%)	1 (1%)	18	55
3	AN	148/151 (98%)	127 (86%)	19 (13%)	2 (1%)	9	39
4	AL	143/158 (90%)	123 (86%)	18 (13%)	2 (1%)	9	39
5	AB	213/264 (81%)	186 (87%)	23 (11%)	4 (2%)	6	32
6	AA	204/295 (69%)	177 (87%)	25 (12%)	2 (1%)	12	47
7	AV	79/83 (95%)	63 (80%)	13 (16%)	3 (4%)	2	19
8	AY	124/133 (93%)	108 (87%)	13 (10%)	3 (2%)	4	27
9	Aa	96/115 (84%)	80 (83%)	15 (16%)	1 (1%)	12	47
10	Ab	82/84 (98%)	71 (87%)	9 (11%)	2 (2%)	4	27
11	Ae	56/59 (95%)	46 (82%)	8 (14%)	2 (4%)	2	20
12	AJ	172/194 (89%)	161 (94%)	10 (6%)	1 (1%)	21	59
13	AE	259/263 (98%)	224 (86%)	30 (12%)	5 (2%)	6	32
14	AC	216/293 (74%)	199 (92%)	17 (8%)	0	100	100
15	AG	235/249 (94%)	217 (92%)	15 (6%)	3 (1%)	9	41
16	AH	177/194 (91%)	160 (90%)	13 (7%)	4 (2%)	5	28
17	AW	127/130 (98%)	111 (87%)	15 (12%)	1 (1%)	16	53
18	AI	196/208 (94%)	169 (86%)	20 (10%)	7 (4%)	2	20
20	CW	114/157 (73%)	98 (86%)	13 (11%)	3 (3%)	4	25
21	Ag	293/317 (92%)	253 (86%)	38 (13%)	2 (1%)	18	55
22	AU	101/119 (85%)	87 (86%)	13 (13%)	1 (1%)	12	47
23	AK	93/165 (56%)	67 (72%)	23 (25%)	3 (3%)	3	21
24	AS	135/152 (89%)	115 (85%)	18 (13%)	2 (2%)	8	38
25	Ad	51/56 (91%)	44 (86%)	7 (14%)	0	100	100
26	AR	99/135 (73%)	90 (91%)	9 (9%)	0	100	100
27	AP	122/145 (84%)	93 (76%)	26 (21%)	3 (2%)	4	26
28	AT	139/145 (96%)	126 (91%)	10 (7%)	3 (2%)	5	28
29	AZ	72/125 (58%)	57 (79%)	14 (19%)	1 (1%)	9	39
30	Ac	62/69 (90%)	53 (86%)	9 (14%)	0	100	100
31	AD	225/243 (93%)	185 (82%)	37 (16%)	3 (1%)	9	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	AF	189/204 (93%)	170 (90%)	19 (10%)	0	100	100
33	AQ	139/146 (95%)	120 (86%)	14 (10%)	5 (4%)	2	20
34	CO	197/203 (97%)	179 (91%)	15 (8%)	3 (2%)	8	38
35	CL	202/211 (96%)	169 (84%)	23 (11%)	10 (5%)	1	16
36	CV	127/140 (91%)	119 (94%)	7 (6%)	1 (1%)	16	53
37	CM	137/215 (64%)	121 (88%)	12 (9%)	4 (3%)	3	23
38	Ca	145/148 (98%)	120 (83%)	23 (16%)	2 (1%)	9	39
39	CN	201/204 (98%)	180 (90%)	21 (10%)	0	100	100
40	CI	198/214 (92%)	177 (89%)	21 (11%)	0	100	100
41	CD	287/297 (97%)	258 (90%)	24 (8%)	5 (2%)	7	35
42	CQ	185/188 (98%)	157 (85%)	25 (14%)	3 (2%)	7	37
43	CA	253/257 (98%)	231 (91%)	21 (8%)	1 (0%)	30	67
44	CS	173/176 (98%)	143 (83%)	27 (16%)	3 (2%)	7	35
45	CT	157/160 (98%)	143 (91%)	13 (8%)	1 (1%)	21	59
46	CP	150/184 (82%)	137 (91%)	11 (7%)	2 (1%)	9	41
47	CU	100/128 (78%)	86 (86%)	13 (13%)	1 (1%)	12	47
48	CX	119/156 (76%)	101 (85%)	15 (13%)	3 (2%)	4	26
49	CY	131/145 (90%)	118 (90%)	12 (9%)	1 (1%)	16	53
50	CZ	133/136 (98%)	121 (91%)	12 (9%)	0	100	100
51	Cr	130/137 (95%)	102 (78%)	24 (18%)	4 (3%)	3	21
52	Ch	121/123 (98%)	107 (88%)	11 (9%)	3 (2%)	4	26
53	Cb	66/159 (42%)	59 (89%)	7 (11%)	0	100	100
54	CB	392/403 (97%)	355 (91%)	32 (8%)	5 (1%)	9	41
55	CF	227/248 (92%)	208 (92%)	17 (8%)	2 (1%)	14	49
56	Cc	98/115 (85%)	90 (92%)	7 (7%)	1 (1%)	12	47
57	Cd	111/125 (89%)	95 (86%)	15 (14%)	1 (1%)	14	49
58	Ce	127/135 (94%)	112 (88%)	14 (11%)	1 (1%)	16	53
59	Cf	107/110 (97%)	88 (82%)	19 (18%)	0	100	100
60	Cg	112/117 (96%)	95 (85%)	16 (14%)	1 (1%)	14	49
61	Ci	101/105 (96%)	91 (90%)	8 (8%)	2 (2%)	6	31
62	Cj	85/97 (88%)	73 (86%)	11 (13%)	1 (1%)	10	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	Ck	67/70 (96%)	61 (91%)	5 (8%)	1 (2%)	8	38
64	Cl	46/51 (90%)	43 (94%)	3 (6%)	0	100	100
65	CC	358/427 (84%)	298 (83%)	53 (15%)	7 (2%)	6	31
66	Cm	49/52 (94%)	45 (92%)	3 (6%)	1 (2%)	6	31
67	Cn	23/25 (92%)	23 (100%)	0	0	100	100
68	Cp	88/92 (96%)	79 (90%)	9 (10%)	0	100	100
69	Co	99/106 (93%)	81 (82%)	13 (13%)	5 (5%)	1	15
70	CJ	166/178 (93%)	154 (93%)	9 (5%)	3 (2%)	6	33
71	CH	189/192 (98%)	173 (92%)	15 (8%)	1 (0%)	24	63
72	CE	250/288 (87%)	188 (75%)	49 (20%)	13 (5%)	1	15
73	CG	244/266 (92%)	211 (86%)	30 (12%)	3 (1%)	10	43
All	All	10774/12128 (89%)	9398 (87%)	1209 (11%)	167 (2%)	10	37

All (167) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AN	138	ASN
7	AV	50	PHE
9	Aa	98	PRO
11	Ae	45	VAL
11	Ae	47	PRO
13	AE	196	THR
16	AH	66	VAL
16	AH	76	GLN
18	AI	100	CYS
21	Ag	161	SER
21	Ag	282	GLU
22	AU	107	GLU
23	AK	30	PRO
23	AK	44	HIS
27	AP	73	PRO
27	AP	126	VAL
28	AT	31	PRO
28	AT	34	VAL
31	AD	202	LYS
33	AQ	19	ALA
33	AQ	43	GLU
33	AQ	117	ARG

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Mol	Chain	Res	Type
34	CO	111	PRO
34	CO	191	LYS
35	CL	15	HIS
36	CV	45	ILE
41	CD	257	PRO
41	CD	271	MET
42	CQ	20	SER
42	CQ	155	ALA
44	CS	76	LYS
47	CU	60	VAL
48	CX	58	PRO
51	Cr	66	ARG
52	Ch	4	ILE
54	CB	189	THR
54	CB	293	ILE
54	CB	299	ILE
57	Cd	17	ILE
61	Ci	5	TYR
61	Ci	34	THR
65	CC	309	ILE
65	CC	313	VAL
66	Cm	78	ILE
69	Co	63	THR
70	CJ	72	CYS
70	CJ	117	ILE
71	CH	53	LYS
72	CE	42	PRO
72	CE	47	ASN
72	CE	94	LYS
72	CE	131	LYS
72	CE	132	PRO
72	CE	224	LYS
73	CG	86	ALA
73	CG	161	VAL
4	AL	57	ASP
6	AA	159	ILE
15	AG	154	ARG
18	AI	10	LYS
18	AI	140	LYS
18	AI	158	ILE
24	AS	12	ILE
27	AP	75	VAL

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Mol	Chain	Res	Type
35	CL	47	ALA
35	CL	156	PRO
41	CD	21	ARG
42	CQ	40	ASN
44	CS	75	VAL
46	CP	8	PRO
48	CX	40	ILE
51	Cr	127	LYS
52	Ch	115	PRO
65	CC	24	LEU
65	CC	294	LYS
69	Co	77	CYS
72	CE	41	LYS
72	CE	60	SER
73	CG	207	VAL
18	AI	142	SER
35	CL	155	MET
37	CM	6	PHE
38	Ca	47	LYS
41	CD	261	VAL
60	Cg	76	ARG
69	Co	65	LYS
69	Co	96	ASP
72	CE	117	PRO
3	AN	22	VAL
5	AB	223	PHE
8	AY	5	VAL
8	AY	60	PHE
12	AJ	148	ILE
15	AG	152	ASP
20	CW	73	ARG
31	AD	3	VAL
33	AQ	32	ILE
37	CM	5	ARG
38	Ca	91	ALA
46	CP	11	PRO
54	CB	258	HIS
54	CB	393	LYS
62	Cj	40	PRO
63	Ck	32	VAL
72	CE	51	VAL
5	AB	22	VAL

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Mol	Chain	Res	Type
10	Ab	62	VAL
13	AE	90	ILE
13	AE	150	PRO
16	AH	100	ILE
18	AI	141	ARG
20	CW	74	ARG
29	AZ	108	ILE
37	CM	67	SER
49	CY	67	ILE
52	Ch	5	LYS
56	Cc	11	LEU
1	AO	54	CYS
1	AO	128	ARG
1	AO	140	THR
2	AX	129	SER
4	AL	147	LYS
5	AB	106	THR
5	AB	210	VAL
7	AV	19	ALA
7	AV	45	ARG
8	AY	120	THR
13	AE	232	ASN
16	AH	17	ASP
17	AW	30	CYS
20	CW	72	THR
23	AK	36	ALA
24	AS	7	GLU
28	AT	29	LYS
35	CL	149	GLN
37	CM	2	VAL
41	CD	260	GLU
43	CA	180	LEU
44	CS	155	PRO
48	CX	43	SER
51	Cr	67	ARG
65	CC	18	SER
65	CC	311	ARG
70	CJ	111	GLU
72	CE	119	GLU
72	CE	154	THR
18	AI	145	ILE
35	CL	50	PRO

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Mol	Chain	Res	Type
72	CE	112	MET
31	AD	193	ASP
45	CT	135	PRO
65	CC	295	SER
13	AE	195	ILE
15	AG	153	VAL
34	CO	146	GLY
35	CL	11	LYS
35	CL	48	PRO
35	CL	49	ARG
51	Cr	53	PRO
55	CF	184	ILE
55	CF	197	VAL
69	Co	67	VAL
6	AA	206	ASP
10	Ab	37	CYS
33	AQ	42	ILE
35	CL	130	LYS
58	Ce	6	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	
1	AO	99/119 (83%)	92 (93%)	7 (7%)	13	36
2	AX	113/115 (98%)	107 (95%)	6 (5%)	20	42
3	AN	130/131 (99%)	128 (98%)	2 (2%)	57	71
4	AL	134/142 (94%)	130 (97%)	4 (3%)	36	57
5	AB	196/231 (85%)	191 (97%)	5 (3%)	40	61
6	AA	172/243 (71%)	162 (94%)	10 (6%)	18	40
7	AV	65/67 (97%)	62 (95%)	3 (5%)	24	46
8	AY	108/115 (94%)	106 (98%)	2 (2%)	50	66
9	Aa	85/98 (87%)	85 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	Ab	76/76 (100%)	75 (99%)	1 (1%)	61	72
11	Ae	47/48 (98%)	44 (94%)	3 (6%)	16	38
12	AJ	156/168 (93%)	151 (97%)	5 (3%)	34	56
13	AE	224/225 (100%)	222 (99%)	2 (1%)	70	77
14	AC	184/225 (82%)	172 (94%)	12 (6%)	15	38
15	AG	207/218 (95%)	200 (97%)	7 (3%)	32	55
16	AH	161/174 (92%)	153 (95%)	8 (5%)	22	43
17	AW	112/113 (99%)	107 (96%)	5 (4%)	24	47
18	AI	174/180 (97%)	166 (95%)	8 (5%)	24	46
20	CW	97/126 (77%)	97 (100%)	0	100	100
21	Ag	259/275 (94%)	253 (98%)	6 (2%)	44	64
22	AU	94/107 (88%)	89 (95%)	5 (5%)	20	42
23	AK	86/136 (63%)	82 (95%)	4 (5%)	23	45
24	AS	119/132 (90%)	117 (98%)	2 (2%)	53	68
25	Ad	47/49 (96%)	47 (100%)	0	100	100
26	AR	95/122 (78%)	93 (98%)	2 (2%)	47	65
27	AP	113/130 (87%)	108 (96%)	5 (4%)	25	47
28	AT	112/115 (97%)	107 (96%)	5 (4%)	24	47
29	AZ	66/103 (64%)	66 (100%)	0	100	100
30	Ac	57/62 (92%)	57 (100%)	0	100	100
31	AD	190/202 (94%)	183 (96%)	7 (4%)	30	51
32	AF	161/170 (95%)	154 (96%)	7 (4%)	26	48
33	AQ	117/121 (97%)	115 (98%)	2 (2%)	53	68
34	CO	171/174 (98%)	169 (99%)	2 (1%)	63	74
35	CL	170/177 (96%)	169 (99%)	1 (1%)	78	81
36	CV	100/107 (94%)	97 (97%)	3 (3%)	36	57
37	CM	118/161 (73%)	116 (98%)	2 (2%)	53	68
38	Ca	120/121 (99%)	117 (98%)	3 (2%)	42	62
39	CN	171/172 (99%)	165 (96%)	6 (4%)	32	54
40	CI	172/181 (95%)	164 (95%)	8 (5%)	23	45
41	CD	243/250 (97%)	233 (96%)	10 (4%)	27	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	CQ	164/165 (99%)	158 (96%)	6 (4%)	30	51
43	CA	197/199 (99%)	192 (98%)	5 (2%)	42	62
44	CS	156/157 (99%)	151 (97%)	5 (3%)	34	56
45	CT	139/140 (99%)	138 (99%)	1 (1%)	76	79
46	CP	133/163 (82%)	129 (97%)	4 (3%)	36	57
47	CU	92/115 (80%)	91 (99%)	1 (1%)	65	74
48	CX	109/133 (82%)	104 (95%)	5 (5%)	24	46
49	CY	123/135 (91%)	120 (98%)	3 (2%)	43	63
50	CZ	117/118 (99%)	117 (100%)	0	100	100
51	Cr	119/121 (98%)	108 (91%)	11 (9%)	8	27
52	Ch	110/110 (100%)	108 (98%)	2 (2%)	51	67
53	Cb	58/126 (46%)	56 (97%)	2 (3%)	32	55
54	CB	343/349 (98%)	325 (95%)	18 (5%)	21	43
55	CF	198/215 (92%)	193 (98%)	5 (2%)	42	62
56	Cc	85/97 (88%)	85 (100%)	0	100	100
57	Cd	102/110 (93%)	101 (99%)	1 (1%)	68	76
58	Ce	115/121 (95%)	109 (95%)	6 (5%)	21	43
59	Cf	88/89 (99%)	86 (98%)	2 (2%)	44	64
60	Cg	98/100 (98%)	95 (97%)	3 (3%)	35	56
61	Ci	87/89 (98%)	84 (97%)	3 (3%)	32	55
62	Cj	74/80 (92%)	71 (96%)	3 (4%)	27	49
63	Ck	64/65 (98%)	62 (97%)	2 (3%)	35	56
64	Cl	46/48 (96%)	42 (91%)	4 (9%)	9	29
65	CC	299/348 (86%)	286 (96%)	13 (4%)	26	48
66	Cm	47/48 (98%)	43 (92%)	4 (8%)	10	30
67	Cn	24/24 (100%)	24 (100%)	0	100	100
68	Cp	74/75 (99%)	72 (97%)	2 (3%)	39	60
69	Co	89/94 (95%)	88 (99%)	1 (1%)	65	74
70	CJ	142/149 (95%)	137 (96%)	5 (4%)	32	54
71	CH	170/171 (99%)	164 (96%)	6 (4%)	32	54
72	CE	224/252 (89%)	211 (94%)	13 (6%)	18	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	CG	209/223 (94%)	204 (98%)	5 (2%)	43	63
All	All	9416/10310 (91%)	9105 (97%)	311 (3%)	34	55

All (311) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AO	40	THR
1	AO	72	TYR
1	AO	97	LEU
1	AO	117	ARG
1	AO	128	ARG
1	AO	129	ILE
1	AO	135	ILE
2	AX	14	ARG
2	AX	41	PHE
2	AX	72	VAL
2	AX	77	ASN
2	AX	81	ILE
2	AX	115	ILE
3	AN	22	VAL
3	AN	78	LYS
4	AL	6	THR
4	AL	42	LEU
4	AL	102	PHE
4	AL	109	MET
5	AB	67	PHE
5	AB	79	VAL
5	AB	177	GLN
5	AB	179	ASN
5	AB	182	LYS
6	AA	10	MET
6	AA	48	ILE
6	AA	50	ASN
6	AA	107	THR
6	AA	147	LEU
6	AA	158	ASP
6	AA	178	LEU
6	AA	201	LEU
6	AA	204	TYR
6	AA	205	ARG
7	AV	7	GLU
7	AV	16	LYS

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Mol	Chain	Res	Type
7	AV	47	ASN
8	AY	75	ILE
8	AY	79	LEU
10	Ab	1	MET
11	Ae	5	SER
11	Ae	40	ARG
11	Ae	41	ARG
12	AJ	34	GLU
12	AJ	94	LEU
12	AJ	101	LYS
12	AJ	103	GLU
12	AJ	106	LEU
13	AE	9	LEU
13	AE	23	LEU
14	AC	73	MET
14	AC	74	LYS
14	AC	76	LYS
14	AC	132	ASP
14	AC	137	VAL
14	AC	211	LYS
14	AC	229	CYS
14	AC	233	LEU
14	AC	252	THR
14	AC	256	TRP
14	AC	258	GLU
14	AC	272	HIS
15	AG	14	LYS
15	AG	46	LYS
15	AG	63	MET
15	AG	79	LYS
15	AG	116	LYS
15	AG	124	LEU
15	AG	162	LEU
16	AH	27	LEU
16	AH	39	GLN
16	AH	42	GLU
16	AH	83	LEU
16	AH	90	LYS
16	AH	152	ARG
16	AH	160	LYS
16	AH	192	PHE
17	AW	25	VAL

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Mol	Chain	Res	Type
17	AW	52	ILE
17	AW	66	THR
17	AW	92	ASN
17	AW	104	LEU
18	AI	9	HIS
18	AI	46	VAL
18	AI	138	ASN
18	AI	162	LEU
18	AI	171	LEU
18	AI	181	GLN
18	AI	182	CYS
18	AI	200	ARG
21	Ag	20	GLN
21	Ag	27	PHE
21	Ag	42	MET
21	Ag	59	LEU
21	Ag	184	LEU
21	Ag	305	ASN
22	AU	28	ASN
22	AU	59	LYS
22	AU	82	MET
22	AU	87	ARG
22	AU	116	ILE
23	AK	1	MET
23	AK	3	MET
23	AK	46	MET
23	AK	89	ILE
24	AS	8	LYS
24	AS	59	LEU
26	AR	66	VAL
26	AR	78	ARG
27	AP	7	LYS
27	AP	34	MET
27	AP	126	VAL
27	AP	127	LYS
27	AP	128	HIS
28	AT	23	LYS
28	AT	28	LEU
28	AT	34	VAL
28	AT	64	LEU
28	AT	144	LYS
31	AD	8	LYS

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Mol	Chain	Res	Type
31	AD	66	ILE
31	AD	86	LEU
31	AD	99	ILE
31	AD	113	LEU
31	AD	143	ARG
31	AD	207	HIS
32	AF	52	SER
32	AF	71	ARG
32	AF	72	LEU
32	AF	136	ARG
32	AF	173	LEU
32	AF	182	LYS
32	AF	185	SER
33	AQ	90	LYS
33	AQ	115	TYR
34	CO	120	VAL
34	CO	188	LYS
35	CL	176	PHE
36	CV	25	VAL
36	CV	72	LEU
36	CV	77	HIS
37	CM	77	TRP
37	CM	85	LYS
38	Ca	38	LEU
38	Ca	46	ASP
38	Ca	47	LYS
39	CN	71	ARG
39	CN	83	LYS
39	CN	87	HIS
39	CN	104	GLU
39	CN	134	LEU
39	CN	170	LYS
40	CI	19	LYS
40	CI	24	ARG
40	CI	30	LYS
40	CI	60	LEU
40	CI	63	GLU
40	CI	115	MET
40	CI	183	ASP
40	CI	208	LYS
41	CD	12	TYR
41	CD	76	CYS

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Mol	Chain	Res	Type
41	CD	93	THR
41	CD	111	ASN
41	CD	138	GLN
41	CD	144	CYS
41	CD	153	THR
41	CD	225	GLN
41	CD	255	LYS
41	CD	259	LYS
42	CQ	3	VAL
42	CQ	4	ASP
42	CQ	9	LYS
42	CQ	17	GLU
42	CQ	45	GLN
42	CQ	98	LEU
43	CA	75	LEU
43	CA	237	LEU
43	CA	246	LEU
43	CA	251	THR
43	CA	254	GLU
44	CS	7	LEU
44	CS	19	THR
44	CS	24	THR
44	CS	56	LYS
44	CS	113	MET
45	CT	31	MET
46	CP	2	VAL
46	CP	21	ASN
46	CP	40	HIS
46	CP	115	GLU
47	CU	78	PHE
48	CX	40	ILE
48	CX	96	LEU
48	CX	101	ASP
48	CX	119	ILE
48	CX	140	LEU
49	CY	55	VAL
49	CY	104	VAL
49	CY	109	LEU
51	Cr	4	HIS
51	Cr	17	LEU
51	Cr	22	LYS
51	Cr	41	ASN

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Mol	Chain	Res	Type
51	Cr	66	ARG
51	Cr	72	LYS
51	Cr	75	THR
51	Cr	90	LEU
51	Cr	108	MET
51	Cr	118	LEU
51	Cr	125	MET
52	Ch	4	ILE
52	Ch	114	TYR
53	Cb	6	ASN
53	Cb	38	LYS
54	CB	14	LEU
54	CB	53	MET
54	CB	57	VAL
54	CB	95	THR
54	CB	114	CYS
54	CB	115	LYS
54	CB	154	LYS
54	CB	163	ILE
54	CB	168	MET
54	CB	186	ASN
54	CB	226	LYS
54	CB	237	THR
54	CB	292	LEU
54	CB	300	LYS
54	CB	301	ASN
54	CB	311	ASP
54	CB	347	LEU
54	CB	382	MET
55	CF	21	LYS
55	CF	29	LYS
55	CF	71	MET
55	CF	169	LEU
55	CF	243	LEU
57	Cd	27	ILE
58	Ce	69	MET
58	Ce	80	HIS
58	Ce	85	LEU
58	Ce	86	GLU
58	Ce	108	ARG
58	Ce	129	LEU
59	Cf	101	ILE

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Mol	Chain	Res	Type
59	Cf	105	LEU
60	Cg	5	LEU
60	Cg	40	LYS
60	Cg	107	LEU
61	Ci	76	ARG
61	Ci	80	HIS
61	Ci	94	LEU
62	Cj	2	THR
62	Cj	19	CYS
62	Cj	37	CYS
63	Ck	18	LYS
63	Ck	55	LYS
64	Cl	4	HIS
64	Cl	9	ILE
64	Cl	16	LYS
64	Cl	21	ARG
65	CC	61	GLN
65	CC	76	ILE
65	CC	110	ARG
65	CC	120	LYS
65	CC	162	LYS
65	CC	205	ARG
65	CC	208	CYS
65	CC	219	LYS
65	CC	228	THR
65	CC	229	LEU
65	CC	246	VAL
65	CC	297	GLU
65	CC	313	VAL
66	Cm	99	CYS
66	Cm	110	CYS
66	Cm	113	LYS
66	Cm	115	CYS
68	Cp	22	LEU
68	Cp	72	ASN
69	Co	15	CYS
70	CJ	33	LEU
70	CJ	56	THR
70	CJ	94	LEU
70	CJ	118	LYS
70	CJ	169	LYS
71	CH	10	VAL

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Mol	Chain	Res	Type
71	CH	11	ASP
71	CH	110	SER
71	CH	123	ILE
71	CH	126	VAL
71	CH	142	ASP
72	CE	46	ARG
72	CE	50	LEU
72	CE	54	ILE
72	CE	82	LYS
72	CE	110	ARG
72	CE	115	TYR
72	CE	126	LEU
72	CE	130	LYS
72	CE	150	LEU
72	CE	179	LEU
72	CE	256	GLN
72	CE	267	LEU
72	CE	286	LEU
73	CG	31	LEU
73	CG	71	TYR
73	CG	119	GLU
73	CG	160	ASP
73	CG	230	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
3	AN	101	HIS
5	AB	40	ASN
5	AB	118	GLN
5	AB	124	HIS
12	AJ	27	GLN
12	AJ	156	HIS
13	AE	142	HIS
13	AE	214	ASN
18	AI	146	GLN
24	AS	42	HIS
27	AP	98	ASN
27	AP	103	ASN
27	AP	114	HIS
28	AT	91	HIS
31	AD	226	GLN

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Mol	Chain	Res	Type
38	Ca	34	ASN
38	Ca	41	HIS
39	CN	8	GLN
40	CI	59	GLN
42	CQ	151	HIS
45	CT	95	HIS
46	CP	93	HIS
49	CY	43	ASN
51	Cr	4	HIS
51	Cr	36	ASN
54	CB	315	ASN
58	Ce	23	HIS
59	Cf	20	ASN
65	CC	48	ASN
70	CJ	104	ASN
72	CE	101	ASN
72	CE	279	ASN
72	CE	284	HIS
73	CG	236	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
19	B2	1752/1803 (97%)	410 (23%)	53 (3%)
74	A5	3736/4010 (93%)	878 (23%)	150 (4%)
75	A7	120/121 (99%)	18 (15%)	1 (0%)
76	A8	155/157 (98%)	39 (25%)	7 (4%)
77	Cw	76/77 (98%)	19 (25%)	0
78	Dd	6/7 (85%)	3 (50%)	0
All	All	5845/6175 (94%)	1367 (23%)	211 (3%)

All (1367) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
19	B2	3	C
19	B2	4	C
19	B2	25	A
19	B2	26	U
19	B2	33	G
19	B2	41	G
19	B2	42	A

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Mol	Chain	Res	Type
19	B2	44	U
19	B2	46	A
19	B2	56	G
19	B2	65	C
19	B2	66	G
19	B2	67	C
19	B2	68	A
19	B2	70	G
19	B2	71	G
19	B2	72	C
19	B2	73	C
19	B2	74	G
19	B2	75	G
19	B2	78	C
19	B2	80	G
19	B2	84	A
19	B2	99	A
19	B2	103	A
19	B2	113	G
19	B2	115	U
19	B2	126	G
19	B2	140	C
19	B2	141	A
19	B2	142	C
19	B2	143	U
19	B2	146	G
19	B2	147	A
19	B2	148	U
19	B2	155	G
19	B2	158	A
19	B2	168	C
19	B2	171	A
19	B2	176	U
19	B2	181	A
19	B2	183	G
19	B2	187	G
19	B2	188	C
19	B2	189	U
19	B2	190	G
19	B2	191	A
19	B2	192	C
19	B2	215	G

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Mol	Chain	Res	Type
19	B2	219	U
19	B2	226	A
19	B2	227	U
19	B2	228	C
19	B2	229	A
19	B2	231	A
19	B2	235	A
19	B2	238	C
19	B2	244	A
19	B2	281	C
19	B2	284	C
19	B2	285	U
19	B2	286	U
19	B2	287	U
19	B2	288	G
19	B2	294	U
19	B2	295	C
19	B2	306	C
19	B2	307	G
19	B2	308	G
19	B2	309	G
19	B2	312	G
19	B2	318	A
19	B2	319	C
19	B2	324	C
19	B2	325	C
19	B2	326	C
19	B2	328	U
19	B2	329	G
19	B2	332	G
19	B2	340	C
19	B2	347	G
19	B2	350	C
19	B2	362	C
19	B2	364	A
19	B2	382	C
19	B2	385	G
19	B2	386	C
19	B2	389	A
19	B2	395	G
19	B2	398	A
19	B2	400	C

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Mol	Chain	Res	Type
19	B2	409	C
19	B2	448	A
19	B2	450	C
19	B2	452	G
19	B2	466	G
19	B2	472	C
19	B2	473	A
19	B2	474	G
19	B2	487	U
19	B2	492	C
19	B2	508	A
19	B2	523	A
19	B2	525	A
19	B2	528	A
19	B2	532	C
19	B2	533	A
19	B2	535	G
19	B2	548	C
19	B2	550	C
19	B2	551	U
19	B2	552	G
19	B2	553	U
19	B2	556	U
19	B2	559	G
19	B2	560	A
19	B2	563	G
19	B2	564	A
19	B2	576	A
19	B2	581	U
19	B2	583	A
19	B2	584	A
19	B2	588	G
19	B2	590	A
19	B2	593	C
19	B2	604	A
19	B2	605	A
19	B2	606	G
19	B2	607	U
19	B2	608	C
19	B2	613	G
19	B2	614	C
19	B2	617	G

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Mol	Chain	Res	Type
19	B2	619	A
19	B2	624	C
19	B2	628	A
19	B2	629	A
19	B2	643	A
19	B2	644	G
19	B2	659	G
19	B2	668	A
19	B2	669	A
19	B2	671	A
19	B2	672	A
19	B2	673	G
19	B2	683	G
19	B2	688	U
19	B2	689	U
19	B2	691	G
19	B2	694	G
19	B2	733	C
19	B2	735	C
19	B2	739	C
19	B2	740	C
19	B2	741	C
19	B2	742	U
19	B2	743	U
19	B2	744	G
19	B2	747	U
19	B2	748	C
19	B2	749	U
19	B2	752	G
19	B2	753	C
19	B2	754	G
19	B2	788	G
19	B2	797	C
19	B2	798	G
19	B2	799	U
19	B2	801	U
19	B2	810	A
19	B2	811	A
19	B2	812	A
19	B2	821	G
19	B2	822	U
19	B2	827	A

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Mol	Chain	Res	Type
19	B2	830	A
19	B2	834	C
19	B2	835	C
19	B2	837	A
19	B2	838	G
19	B2	839	C
19	B2	840	C
19	B2	841	G
19	B2	847	A
19	B2	853	C
19	B2	862	A
19	B2	868	G
19	B2	870	A
19	B2	871	U
19	B2	873	G
19	B2	876	C
19	B2	877	C
19	B2	881	G
19	B2	886	A
19	B2	887	U
19	B2	888	U
19	B2	890	U
19	B2	891	G
19	B2	895	G
19	B2	897	U
19	B2	903	A
19	B2	907	G
19	B2	911	C
19	B2	913	A
19	B2	914	U
19	B2	918	U
19	B2	920	A
19	B2	921	G
19	B2	933	G
19	B2	956	G
19	B2	961	G
19	B2	963	A
19	B2	969	U
19	B2	970	G
19	B2	971	G
19	B2	988	C
19	B2	990	A

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Mol	Chain	Res	Type
19	B2	992	A
19	B2	999	G
19	B2	1023	A
19	B2	1039	C
19	B2	1045	U
19	B2	1049	A
19	B2	1050	A
19	B2	1060	A
19	B2	1061	U
19	B2	1062	A
19	B2	1064	C
19	B2	1078	C
19	B2	1083	A
19	B2	1084	A
19	B2	1085	C
19	B2	1086	G
19	B2	1096	G
19	B2	1097	G
19	B2	1109	C
19	B2	1110	G
19	B2	1113	A
19	B2	1114	U
19	B2	1115	U
19	B2	1116	C
19	B2	1117	C
19	B2	1118	C
19	B2	1120	U
19	B2	1121	G
19	B2	1122	A
19	B2	1133	A
19	B2	1138	C
19	B2	1139	C
19	B2	1143	A
19	B2	1148	A
19	B2	1149	A
19	B2	1153	C
19	B2	1154	U
19	B2	1155	U
19	B2	1157	G
19	B2	1166	G
19	B2	1194	A
19	B2	1195	A

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Mol	Chain	Res	Type
19	B2	1202	U
19	B2	1203	G
19	B2	1205	C
19	B2	1206	G
19	B2	1212	G
19	B2	1214	A
19	B2	1215	C
19	B2	1217	A
19	B2	1221	G
19	B2	1224	G
19	B2	1242	U
19	B2	1251	A
19	B2	1253	A
19	B2	1254	C
19	B2	1256	G
19	B2	1257	G
19	B2	1259	A
19	B2	1263	U
19	B2	1264	C
19	B2	1265	A
19	B2	1274	G
19	B2	1275	G
19	B2	1283	C
19	B2	1284	A
19	B2	1301	A
19	B2	1302	G
19	B2	1303	C
19	B2	1308	U
19	B2	1343	U
19	B2	1351	G
19	B2	1354	G
19	B2	1355	C
19	B2	1356	G
19	B2	1357	A
19	B2	1358	U
19	B2	1371	U
19	B2	1372	U
19	B2	1378	A
19	B2	1382	A
19	B2	1394	G
19	B2	1395	C
19	B2	1396	A

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Mol	Chain	Res	Type
19	B2	1397	U
19	B2	1401	A
19	B2	1402	A
19	B2	1404	U
19	B2	1406	G
19	B2	1411	G
19	B2	1412	C
19	B2	1418	C
19	B2	1419	C
19	B2	1426	U
19	B2	1430	C
19	B2	1435	C
19	B2	1437	C
19	B2	1441	U
19	B2	1442	U
19	B2	1449	G
19	B2	1452	A
19	B2	1454	A
19	B2	1455	A
19	B2	1456	G
19	B2	1462	U
19	B2	1463	U
19	B2	1464	C
19	B2	1466	G
19	B2	1475	G
19	B2	1476	A
19	B2	1477	U
19	B2	1478	U
19	B2	1483	A
19	B2	1489	A
19	B2	1490	G
19	B2	1494	U
19	B2	1495	G
19	B2	1506	A
19	B2	1507	G
19	B2	1508	A
19	B2	1521	C
19	B2	1522	A
19	B2	1523	C
19	B2	1531	A
19	B2	1535	U
19	B2	1536	G

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Mol	Chain	Res	Type
19	B2	1544	C
19	B2	1552	G
19	B2	1553	C
19	B2	1556	A
19	B2	1557	C
19	B2	1560	U
19	B2	1567	G
19	B2	1570	G
19	B2	1578	U
19	B2	1579	A
19	B2	1580	A
19	B2	1587	G
19	B2	1588	A
19	B2	1599	U
19	B2	1600	G
19	B2	1602	U
19	B2	1604	G
19	B2	1606	G
19	B2	1618	C
19	B2	1620	A
19	B2	1621	U
19	B2	1622	U
19	B2	1623	A
19	B2	1637	A
19	B2	1638	G
19	B2	1648	G
19	B2	1664	A
19	B2	1665	G
19	B2	1669	G
19	B2	1671	G
19	B2	1680	G
19	B2	1683	C
19	B2	1690	U
19	B2	1691	U
19	B2	1699	A
19	B2	1700	C
19	B2	1701	C
19	B2	1706	G
19	B2	1721	U
19	B2	1722	G
19	B2	1729	U
19	B2	1744	G

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Mol	Chain	Res	Type
19	B2	1757	G
19	B2	1783	C
19	B2	1785	C
19	B2	1786	U
19	B2	1805	G
19	B2	1823	A
19	B2	1824	A
19	B2	1825	A
19	B2	1826	G
19	B2	1829	G
19	B2	1831	A
19	B2	1835	A
19	B2	1837	G
19	B2	1838	U
19	B2	1849	G
19	B2	1851	A
19	B2	1852	C
19	B2	1854	U
19	B2	1861	G
19	B2	1862	G
19	B2	1863	A
19	B2	1864	U
19	B2	1865	C
19	B2	1868	U
19	B2	1869	A
74	A5	12	A
74	A5	13	U
74	A5	15	A
74	A5	19	G
74	A5	21	G
74	A5	25	A
74	A5	39	A
74	A5	40	G
74	A5	48	G
74	A5	49	U
74	A5	59	A
74	A5	64	A
74	A5	65	A
74	A5	73	A
74	A5	74	G
74	A5	75	G
74	A5	76	A

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Mol	Chain	Res	Type
74	A5	91	G
74	A5	108	A
74	A5	109	G
74	A5	112	C
74	A5	115	C
74	A5	116	G
74	A5	117	C
74	A5	119	G
74	A5	120	A
74	A5	126	C
74	A5	136	C
74	A5	142	G
74	A5	143	C
74	A5	144	G
74	A5	149	A
74	A5	150	U
74	A5	159	C
74	A5	160	G
74	A5	164	G
74	A5	170	C
74	A5	172	C
74	A5	177	G
74	A5	184	U
74	A5	185	C
74	A5	186	G
74	A5	187	U
74	A5	188	G
74	A5	189	G
74	A5	197	A
74	A5	200	U
74	A5	201	C
74	A5	207	G
74	A5	209	U
74	A5	210	C
74	A5	216	C
74	A5	217	C
74	A5	218	A
74	A5	219	G
74	A5	220	C
74	A5	221	C
74	A5	224	U
74	A5	226	G

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Mol	Chain	Res	Type
74	A5	227	A
74	A5	232	G
74	A5	233	U
74	A5	235	A
74	A5	243	A
74	A5	246	G
74	A5	265	C
74	A5	276	C
74	A5	277	G
74	A5	280	G
74	A5	294	G
74	A5	297	U
74	A5	305	A
74	A5	306	A
74	A5	309	C
74	A5	310	G
74	A5	315	G
74	A5	316	U
74	A5	322	C
74	A5	334	A
74	A5	336	A
74	A5	340	C
74	A5	350	C
74	A5	357	U
74	A5	361	C
74	A5	373	G
74	A5	379	G
74	A5	387	G
74	A5	406	C
74	A5	407	A
74	A5	408	A
74	A5	409	G
74	A5	410	A
74	A5	412	G
74	A5	413	G
74	A5	414	C
74	A5	415	G
74	A5	432	U
74	A5	433	A
74	A5	449	C
74	A5	452	A
74	A5	453	G

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Mol	Chain	Res	Type
74	A5	454	U
74	A5	455	C
74	A5	469	C
74	A5	485	C
74	A5	486	C
74	A5	487	G
74	A5	490	C
74	A5	498	C
74	A5	500	G
74	A5	502	C
74	A5	504	G
74	A5	505	G
74	A5	506	C
74	A5	509	A
74	A5	510	U
74	A5	514	U
74	A5	639	U
74	A5	640	C
74	A5	641	G
74	A5	649	A
74	A5	656	C
74	A5	659	G
74	A5	664	G
74	A5	665	C
74	A5	666	G
74	A5	667	A
74	A5	668	C
74	A5	669	C
74	A5	670	G
74	A5	685	C
74	A5	686	A
74	A5	687	U
74	A5	688	U
74	A5	689	U
74	A5	690	C
74	A5	696	C
74	A5	697	G
74	A5	704	C
74	A5	712	C
74	A5	720	G
74	A5	727	C
74	A5	728	U

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Mol	Chain	Res	Type
74	A5	729	G
74	A5	730	G
74	A5	734	G
74	A5	735	G
74	A5	737	C
74	A5	744	G
74	A5	746	A
74	A5	747	A
74	A5	748	G
74	A5	749	G
74	A5	912	G
74	A5	918	G
74	A5	926	G
74	A5	927	G
74	A5	928	C
74	A5	929	A
74	A5	931	C
74	A5	932	A
74	A5	933	G
74	A5	935	A
74	A5	936	C
74	A5	937	U
74	A5	938	C
74	A5	939	G
74	A5	944	A
74	A5	945	U
74	A5	946	C
74	A5	947	C
74	A5	952	G
74	A5	956	A
74	A5	957	G
74	A5	958	G
74	A5	959	G
74	A5	960	A
74	A5	961	G
74	A5	962	C
74	A5	963	G
74	A5	964	A
74	A5	966	A
74	A5	967	C
74	A5	968	C
74	A5	969	C

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Mol	Chain	Res	Type
74	A5	970	G
74	A5	971	U
74	A5	972	C
74	A5	974	C
74	A5	975	C
74	A5	982	U
74	A5	983	C
74	A5	1051	G
74	A5	1072	C
74	A5	1102	U
74	A5	1164	G
74	A5	1166	G
74	A5	1167	C
74	A5	1210	C
74	A5	1211	G
74	A5	1212	G
74	A5	1214	C
74	A5	1215	C
74	A5	1219	G
74	A5	1233	G
74	A5	1239	C
74	A5	1240	G
74	A5	1241	C
74	A5	1242	G
74	A5	1243	C
74	A5	1244	G
74	A5	1245	C
74	A5	1266	G
74	A5	1267	C
74	A5	1268	G
74	A5	1269	G
74	A5	1270	A
74	A5	1271	G
74	A5	1272	C
74	A5	1274	A
74	A5	1275	G
74	A5	1280	C
74	A5	1281	G
74	A5	1282	G
74	A5	1283	G
74	A5	1284	G
74	A5	1285	U

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Mol	Chain	Res	Type
74	A5	1288	G
74	A5	1289	C
74	A5	1294	A
74	A5	1295	C
74	A5	1296	G
74	A5	1297	U
74	A5	1301	C
74	A5	1302	U
74	A5	1303	A
74	A5	1304	C
74	A5	1308	C
74	A5	1314	C
74	A5	1326	A
74	A5	1344	C
74	A5	1354	A
74	A5	1357	C
74	A5	1358	G
74	A5	1359	G
74	A5	1361	G
74	A5	1365	C
74	A5	1366	G
74	A5	1367	C
74	A5	1368	A
74	A5	1370	G
74	A5	1371	A
74	A5	1372	A
74	A5	1377	G
74	A5	1378	C
74	A5	1379	C
74	A5	1380	G
74	A5	1381	U
74	A5	1387	A
74	A5	1394	G
74	A5	1397	A
74	A5	1398	A
74	A5	1399	G
74	A5	1408	G
74	A5	1420	A
74	A5	1428	U
74	A5	1429	C
74	A5	1437	C
74	A5	1440	U

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Mol	Chain	Res	Type
74	A5	1441	C
74	A5	1445	U
74	A5	1446	C
74	A5	1455	G
74	A5	1456	C
74	A5	1465	G
74	A5	1475	G
74	A5	1476	C
74	A5	1479	G
74	A5	1481	C
74	A5	1482	G
74	A5	1483	C
74	A5	1485	C
74	A5	1489	G
74	A5	1498	G
74	A5	1501	C
74	A5	1502	G
74	A5	1503	A
74	A5	1504	G
74	A5	1516	G
74	A5	1517	G
74	A5	1518	A
74	A5	1523	A
74	A5	1525	A
74	A5	1534	A
74	A5	1547	A
74	A5	1566	C
74	A5	1574	G
74	A5	1578	U
74	A5	1591	U
74	A5	1592	G
74	A5	1596	U
74	A5	1597	G
74	A5	1612	G
74	A5	1614	C
74	A5	1624	G
74	A5	1625	G
74	A5	1626	G
74	A5	1630	A
74	A5	1631	A
74	A5	1632	A
74	A5	1633	G

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Mol	Chain	Res	Type
74	A5	1634	A
74	A5	1637	A
74	A5	1638	A
74	A5	1639	U
74	A5	1640	C
74	A5	1646	A
74	A5	1654	G
74	A5	1661	C
74	A5	1676	C
74	A5	1677	U
74	A5	1691	G
74	A5	1694	C
74	A5	1697	G
74	A5	1698	C
74	A5	1699	A
74	A5	1700	G
74	A5	1719	A
74	A5	1725	U
74	A5	1731	C
74	A5	1742	A
74	A5	1750	G
74	A5	1751	A
74	A5	1752	G
74	A5	1754	U
74	A5	1755	C
74	A5	1756	U
74	A5	1758	G
74	A5	1760	G
74	A5	1761	G
74	A5	1764	G
74	A5	1769	G
74	A5	1776	A
74	A5	1777	C
74	A5	1781	U
74	A5	1787	A
74	A5	1789	C
74	A5	1803	G
74	A5	1804	A
74	A5	1805	A
74	A5	1806	G
74	A5	1812	C
74	A5	1818	G

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Mol	Chain	Res	Type
74	A5	1819	G
74	A5	1821	G
74	A5	1822	U
74	A5	1828	C
74	A5	1833	G
74	A5	1836	G
74	A5	1852	U
74	A5	1853	G
74	A5	1854	G
74	A5	1855	G
74	A5	1869	G
74	A5	1881	C
74	A5	1893	C
74	A5	1897	A
74	A5	1907	A
74	A5	1918	U
74	A5	1920	C
74	A5	1921	C
74	A5	1922	G
74	A5	1925	G
74	A5	1930	U
74	A5	1931	C
74	A5	1947	U
74	A5	1948	G
74	A5	1951	G
74	A5	1961	G
74	A5	1962	A
74	A5	1964	A
74	A5	1967	A
74	A5	1973	G
74	A5	1975	G
74	A5	1976	G
74	A5	1979	A
74	A5	1981	G
74	A5	1982	G
74	A5	1983	A
74	A5	1984	A
74	A5	1985	G
74	A5	1988	G
74	A5	1997	U
74	A5	1998	A
74	A5	2001	G

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Mol	Chain	Res	Type
74	A5	2002	A
74	A5	2003	G
74	A5	2004	U
74	A5	2008	U
74	A5	2009	A
74	A5	2010	A
74	A5	2016	C
74	A5	2024	G
74	A5	2025	A
74	A5	2026	A
74	A5	2047	A
74	A5	2048	U
74	A5	2052	G
74	A5	2056	G
74	A5	2069	A
74	A5	2084	C
74	A5	2085	G
74	A5	2089	G
74	A5	2090	U
74	A5	2091	C
74	A5	2093	A
74	A5	2094	G
74	A5	2095	A
74	A5	2097	U
74	A5	2098	G
74	A5	2100	A
74	A5	2105	A
74	A5	2107	C
74	A5	2108	G
74	A5	2109	G
74	A5	2111	G
74	A5	2112	G
74	A5	2113	G
74	A5	2114	G
74	A5	2115	G
74	A5	2116	C
74	A5	2117	G
74	A5	2118	G
74	A5	2119	C
74	A5	2123	C
74	A5	2124	G
74	A5	2125	C

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Mol	Chain	Res	Type
74	A5	2126	G
74	A5	2127	C
74	A5	2247	C
74	A5	2248	C
74	A5	2250	C
74	A5	2251	G
74	A5	2252	G
74	A5	2253	A
74	A5	2254	G
74	A5	2255	C
74	A5	2256	C
74	A5	2257	C
74	A5	2258	C
74	A5	2259	G
74	A5	2260	C
74	A5	2261	G
74	A5	2263	A
74	A5	2264	C
74	A5	2265	G
74	A5	2266	C
74	A5	2267	U
74	A5	2269	C
74	A5	2270	G
74	A5	2273	G
74	A5	2289	C
74	A5	2290	C
74	A5	2300	A
74	A5	2301	G
74	A5	2306	G
74	A5	2313	A
74	A5	2314	G
74	A5	2331	G
74	A5	2333	G
74	A5	2345	G
74	A5	2348	G
74	A5	2350	U
74	A5	2351	C
74	A5	2360	A
74	A5	2395	A
74	A5	2396	A
74	A5	2399	G
74	A5	2409	U

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Mol	Chain	Res	Type
74	A5	2410	C
74	A5	2416	G
74	A5	2419	C
74	A5	2421	G
74	A5	2422	C
74	A5	2437	C
74	A5	2441	C
74	A5	2442	G
74	A5	2459	G
74	A5	2463	G
74	A5	2470	C
74	A5	2471	G
74	A5	2472	A
74	A5	2475	G
74	A5	2476	G
74	A5	2487	G
74	A5	2488	C
74	A5	2489	C
74	A5	2490	U
74	A5	2491	C
74	A5	2504	C
74	A5	2505	C
74	A5	2507	A
74	A5	2513	A
74	A5	2517	A
74	A5	2529	A
74	A5	2531	C
74	A5	2532	C
74	A5	2544	G
74	A5	2546	G
74	A5	2547	G
74	A5	2552	G
74	A5	2554	U
74	A5	2564	G
74	A5	2575	U
74	A5	2581	A
74	A5	2583	C
74	A5	2586	G
74	A5	2587	A
74	A5	2589	C
74	A5	2600	A
74	A5	2601	A

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Mol	Chain	Res	Type
74	A5	2621	A
74	A5	2627	C
74	A5	2638	G
74	A5	2639	U
74	A5	2647	A
74	A5	2648	G
74	A5	2652	G
74	A5	2658	G
74	A5	2661	U
74	A5	2662	G
74	A5	2669	C
74	A5	2670	C
74	A5	2671	C
74	A5	2681	G
74	A5	2686	G
74	A5	2687	U
74	A5	2688	G
74	A5	2695	A
74	A5	2696	A
74	A5	2711	G
74	A5	2712	G
74	A5	2713	C
74	A5	2716	C
74	A5	2719	C
74	A5	2721	G
74	A5	2725	A
74	A5	2726	G
74	A5	2734	U
74	A5	2740	U
74	A5	2742	G
74	A5	2743	A
74	A5	2749	C
74	A5	2752	G
74	A5	2753	G
74	A5	2754	G
74	A5	2759	G
74	A5	2760	G
74	A5	2762	G
74	A5	2766	A
74	A5	2767	U
74	A5	2768	C
74	A5	2769	U

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Mol	Chain	Res	Type
74	A5	2770	C
74	A5	2778	G
74	A5	2781	G
74	A5	2787	A
74	A5	2788	U
74	A5	2790	U
74	A5	2798	A
74	A5	2803	U
74	A5	2806	A
74	A5	2814	C
74	A5	2825	A
74	A5	2826	U
74	A5	2828	U
74	A5	2829	U
74	A5	2842	G
74	A5	2855	G
74	A5	2900	U
74	A5	2902	G
74	A5	2904	U
74	A5	2905	C
74	A5	3594	C
74	A5	3596	A
74	A5	3597	G
74	A5	3605	C
74	A5	3606	U
74	A5	3615	G
74	A5	3617	G
74	A5	3618	C
74	A5	3625	G
74	A5	3626	G
74	A5	3635	A
74	A5	3646	A
74	A5	3653	A
74	A5	3656	A
74	A5	3662	A
74	A5	3664	G
74	A5	3673	C
74	A5	3674	G
74	A5	3678	G
74	A5	3691	G
74	A5	3692	A
74	A5	3698	G

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Mol	Chain	Res	Type
74	A5	3709	U
74	A5	3710	G
74	A5	3712	A
74	A5	3713	U
74	A5	3714	G
74	A5	3727	A
74	A5	3732	A
74	A5	3745	U
74	A5	3748	A
74	A5	3756	A
74	A5	3759	A
74	A5	3760	A
74	A5	3761	C
74	A5	3767	C
74	A5	3774	A
74	A5	3776	G
74	A5	3777	G
74	A5	3784	A
74	A5	3785	A
74	A5	3786	U
74	A5	3788	C
74	A5	3789	C
74	A5	3802	U
74	A5	3811	G
74	A5	3813	A
74	A5	3814	U
74	A5	3817	A
74	A5	3818	U
74	A5	3819	G
74	A5	3832	U
74	A5	3833	C
74	A5	3838	U
74	A5	3839	G
74	A5	3840	U
74	A5	3843	C
74	A5	3856	A
74	A5	3876	A
74	A5	3877	A
74	A5	3878	C
74	A5	3879	G
74	A5	3880	G
74	A5	3888	G

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Mol	Chain	Res	Type
74	A5	3889	G
74	A5	3897	G
74	A5	3901	A
74	A5	3906	A
74	A5	3907	G
74	A5	3908	A
74	A5	3915	U
74	A5	3922	G
74	A5	3923	A
74	A5	3959	U
74	A5	3960	A
74	A5	3961	G
74	A5	3962	A
74	A5	3963	A
74	A5	3964	U
74	A5	3965	A
74	A5	3966	A
74	A5	3968	U
74	A5	3969	G
74	A5	3973	G
74	A5	4037	C
74	A5	4038	C
74	A5	4041	C
74	A5	4043	G
74	A5	4047	A
74	A5	4048	A
74	A5	4049	U
74	A5	4053	A
74	A5	4073	A
74	A5	4076	G
74	A5	4077	A
74	A5	4083	U
74	A5	4084	G
74	A5	4085	A
74	A5	4088	C
74	A5	4093	G
74	A5	4094	G
74	A5	4107	G
74	A5	4114	C
74	A5	4115	G
74	A5	4117	U
74	A5	4119	C

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Mol	Chain	Res	Type
74	A5	4120	U
74	A5	4121	G
74	A5	4122	G
74	A5	4123	C
74	A5	4125	C
74	A5	4126	C
74	A5	4127	A
74	A5	4128	A
74	A5	4143	G
74	A5	4144	C
74	A5	4159	C
74	A5	4161	G
74	A5	4163	U
74	A5	4164	C
74	A5	4165	C
74	A5	4170	A
74	A5	4171	C
74	A5	4183	G
74	A5	4191	G
74	A5	4196	G
74	A5	4222	G
74	A5	4229	U
74	A5	4232	U
74	A5	4233	A
74	A5	4251	A
74	A5	4254	G
74	A5	4266	G
74	A5	4268	A
74	A5	4271	A
74	A5	4273	A
74	A5	4294	C
74	A5	4296	U
74	A5	4299	U
74	A5	4304	A
74	A5	4305	G
74	A5	4306	U
74	A5	4326	G
74	A5	4329	G
74	A5	4330	G
74	A5	4331	G
74	A5	4332	C
74	A5	4335	C

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Mol	Chain	Res	Type
74	A5	4337	C
74	A5	4349	C
74	A5	4350	C
74	A5	4354	U
74	A5	4356	G
74	A5	4373	G
74	A5	4376	A
74	A5	4377	G
74	A5	4378	A
74	A5	4381	A
74	A5	4387	C
74	A5	4393	G
74	A5	4394	A
74	A5	4395	U
74	A5	4396	A
74	A5	4419	U
74	A5	4422	A
74	A5	4426	C
74	A5	4436	U
74	A5	4438	U
74	A5	4444	C
74	A5	4449	A
74	A5	4452	U
74	A5	4463	U
74	A5	4464	A
74	A5	4473	A
74	A5	4476	C
74	A5	4500	U
74	A5	4508	C
74	A5	4512	U
74	A5	4513	A
74	A5	4524	G
74	A5	4534	G
74	A5	4548	A
74	A5	4557	U
74	A5	4567	G
74	A5	4569	U
74	A5	4574	U
74	A5	4575	G
74	A5	4584	A
74	A5	4590	A
74	A5	4592	C

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Mol	Chain	Res	Type
74	A5	4599	A
74	A5	4616	A
74	A5	4633	G
74	A5	4634	U
74	A5	4637	G
74	A5	4652	G
74	A5	4656	A
74	A5	4657	U
74	A5	4664	A
74	A5	4670	C
74	A5	4671	C
74	A5	4672	A
74	A5	4677	U
74	A5	4687	A
74	A5	4694	G
74	A5	4696	C
74	A5	4697	U
74	A5	4700	A
74	A5	4708	A
74	A5	4709	U
74	A5	4714	C
74	A5	4720	C
74	A5	4730	C
74	A5	4731	G
74	A5	4732	G
74	A5	4734	A
74	A5	4739	C
74	A5	4747	C
74	A5	4749	C
74	A5	4750	G
74	A5	4751	G
74	A5	4752	U
74	A5	4753	U
74	A5	4754	G
74	A5	4756	C
74	A5	4758	U
74	A5	4764	A
74	A5	4767	C
74	A5	4771	C
74	A5	4870	G
74	A5	4871	C
74	A5	4872	G

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Mol	Chain	Res	Type
74	A5	4873	G
74	A5	4874	A
74	A5	4875	G
74	A5	4876	U
74	A5	4877	G
74	A5	4882	U
74	A5	4883	C
74	A5	4884	G
74	A5	4885	U
74	A5	4886	C
74	A5	4888	U
74	A5	4889	G
74	A5	4890	G
74	A5	4893	A
74	A5	4895	C
74	A5	4896	G
74	A5	4900	C
74	A5	4901	G
74	A5	4910	G
74	A5	4911	A
74	A5	4915	G
74	A5	4925	U
74	A5	4937	C
74	A5	4938	A
74	A5	4939	C
74	A5	4940	C
74	A5	4941	G
74	A5	4943	A
74	A5	4944	C
74	A5	4945	G
74	A5	4946	U
74	A5	4948	C
74	A5	4950	U
74	A5	4951	G
74	A5	4952	G
74	A5	4966	A
74	A5	4967	A
74	A5	4976	U
74	A5	4985	U
74	A5	4986	G
74	A5	4988	U
74	A5	4989	U

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Mol	Chain	Res	Type
74	A5	4990	C
74	A5	4992	G
74	A5	4998	G
74	A5	5002	U
74	A5	5006	U
74	A5	5007	A
74	A5	5013	C
74	A5	5014	A
74	A5	5017	G
74	A5	5023	C
74	A5	5024	C
74	A5	5025	C
74	A5	5027	C
74	A5	5028	G
74	A5	5041	G
74	A5	5047	C
74	A5	5050	C
74	A5	5054	C
74	A5	5060	A
74	A5	5061	A
74	A5	5062	G
75	A7	11	A
75	A7	13	A
75	A7	14	C
75	A7	22	A
75	A7	27	G
75	A7	39	C
75	A7	41	G
75	A7	49	A
75	A7	63	C
75	A7	64	G
75	A7	66	G
75	A7	73	U
75	A7	85	G
75	A7	100	A
75	A7	106	G
75	A7	110	G
75	A7	115	A
75	A7	121	U
76	A8	23	C
76	A8	34	U
76	A8	35	C

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Mol	Chain	Res	Type
76	A8	36	G
76	A8	39	G
76	A8	40	A
76	A8	46	G
76	A8	51	U
76	A8	58	G
76	A8	59	A
76	A8	60	G
76	A8	62	A
76	A8	63	U
76	A8	68	G
76	A8	75	G
76	A8	81	C
76	A8	82	A
76	A8	83	C
76	A8	84	A
76	A8	85	U
76	A8	86	U
76	A8	87	G
76	A8	95	A
76	A8	96	C
76	A8	97	A
76	A8	99	U
76	A8	103	A
76	A8	104	A
76	A8	105	C
76	A8	109	C
76	A8	110	U
76	A8	111	U
76	A8	112	G
76	A8	114	G
76	A8	125	C
76	A8	126	C
76	A8	127	U
76	A8	150	C
76	A8	156	U
77	Cw	10	G
77	Cw	16	C
77	Cw	17	C
77	Cw	18	C
77	Cw	19	G
77	Cw	20	G

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Mol	Chain	Res	Type
77	Cw	21	U
77	Cw	22	A
77	Cw	47	G
77	Cw	48	U
77	Cw	49	C
77	Cw	56	U
77	Cw	57	C
77	Cw	58	A
77	Cw	61	U
77	Cw	62	C
77	Cw	63	C
77	Cw	75	C
77	Cw	77	A
78	Dd	20	U
78	Dd	22	U
78	Dd	24	U

All (211) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
19	B2	24	C
19	B2	72	C
19	B2	102	A
19	B2	127	C
19	B2	139	C
19	B2	140	C
19	B2	141	A
19	B2	190	G
19	B2	225	G
19	B2	228	C
19	B2	327	G
19	B2	465	A
19	B2	532	C
19	B2	534	G
19	B2	552	G
19	B2	604	A
19	B2	688	U
19	B2	732	U
19	B2	734	C
19	B2	746	C
19	B2	751	G
19	B2	752	G

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Mol	Chain	Res	Type
19	B2	797	C
19	B2	798	G
19	B2	821	G
19	B2	833	C
19	B2	839	C
19	B2	861	A
19	B2	869	A
19	B2	880	G
19	B2	970	G
19	B2	1108	G
19	B2	1114	U
19	B2	1120	U
19	B2	1137	U
19	B2	1202	U
19	B2	1214	A
19	B2	1253	A
19	B2	1283	C
19	B2	1307	U
19	B2	1394	G
19	B2	1401	A
19	B2	1429	G
19	B2	1474	A
19	B2	1543	U
19	B2	1556	A
19	B2	1637	A
19	B2	1679	A
19	B2	1756	C
19	B2	1823	A
19	B2	1825	A
19	B2	1830	U
19	B2	1868	U
74	A5	12	A
74	A5	48	G
74	A5	64	A
74	A5	125	C
74	A5	142	G
74	A5	184	U
74	A5	186	G
74	A5	187	U
74	A5	215	C
74	A5	220	C
74	A5	293	G

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Mol	Chain	Res	Type
74	A5	333	U
74	A5	406	C
74	A5	431	G
74	A5	451	C
74	A5	452	A
74	A5	486	C
74	A5	489	C
74	A5	497	G
74	A5	505	G
74	A5	648	G
74	A5	655	C
74	A5	666	G
74	A5	668	C
74	A5	685	C
74	A5	703	G
74	A5	727	C
74	A5	746	A
74	A5	911	U
74	A5	917	A
74	A5	926	G
74	A5	931	C
74	A5	936	C
74	A5	945	U
74	A5	955	G
74	A5	957	G
74	A5	958	G
74	A5	959	G
74	A5	969	C
74	A5	971	U
74	A5	974	C
74	A5	1163	G
74	A5	1210	C
74	A5	1211	G
74	A5	1232	G
74	A5	1238	A
74	A5	1239	C
74	A5	1268	G
74	A5	1269	G
74	A5	1284	G
74	A5	1287	G
74	A5	1288	G
74	A5	1293	G

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Mol	Chain	Res	Type
74	A5	1294	A
74	A5	1296	G
74	A5	1356	U
74	A5	1365	C
74	A5	1371	A
74	A5	1380	G
74	A5	1398	A
74	A5	1407	C
74	A5	1419	G
74	A5	1440	U
74	A5	1445	U
74	A5	1455	G
74	A5	1474	C
74	A5	1481	C
74	A5	1484	G
74	A5	1633	G
74	A5	1804	A
74	A5	1832	C
74	A5	1835	G
74	A5	1920	C
74	A5	2009	A
74	A5	2046	G
74	A5	2068	C
74	A5	2083	C
74	A5	2088	A
74	A5	2089	G
74	A5	2097	U
74	A5	2107	C
74	A5	2111	G
74	A5	2116	C
74	A5	2122	G
74	A5	2123	C
74	A5	2124	G
74	A5	2246	C
74	A5	2250	C
74	A5	2256	C
74	A5	2257	C
74	A5	2260	C
74	A5	2263	A
74	A5	2266	C
74	A5	2268	A
74	A5	2272	C

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Mol	Chain	Res	Type
74	A5	2313	A
74	A5	2395	A
74	A5	2398	U
74	A5	2487	G
74	A5	2490	U
74	A5	2531	C
74	A5	2661	U
74	A5	2670	C
74	A5	2695	A
74	A5	2753	G
74	A5	2761	U
74	A5	2766	A
74	A5	2769	U
74	A5	3605	C
74	A5	3616	U
74	A5	3672	G
74	A5	3697	U
74	A5	3876	A
74	A5	3887	C
74	A5	3888	G
74	A5	3959	U
74	A5	3963	A
74	A5	4036	G
74	A5	4072	C
74	A5	4075	U
74	A5	4082	G
74	A5	4087	G
74	A5	4093	G
74	A5	4119	C
74	A5	4121	G
74	A5	4127	A
74	A5	4163	U
74	A5	4164	C
74	A5	4170	A
74	A5	4232	U
74	A5	4448	G
74	A5	4656	A
74	A5	4713	G
74	A5	4719	G
74	A5	4738	C
74	A5	4749	C
74	A5	4869	U

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Mol	Chain	Res	Type
74	A5	4871	C
74	A5	4874	A
74	A5	4876	U
74	A5	4882	U
74	A5	4885	U
74	A5	4887	C
74	A5	4889	G
74	A5	4937	C
74	A5	4966	A
74	A5	4991	U
74	A5	4997	G
74	A5	5022	U
74	A5	5027	C
75	A7	72	U
76	A8	85	U
76	A8	94	G
76	A8	96	C
76	A8	109	C
76	A8	111	U
76	A8	124	U
76	A8	126	C

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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
74	A5	4
19	B2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B2	698:G	O3'	730:C	P	20.24
1	A5	3292:G	O3'	3572:G	P	18.88
1	A5	4795:C	O3'	4837:G	P	18.31
1	A5	763:C	O3'	886:C	P	18.27
1	A5	2133:C	O3'	2238:G	P	16.40

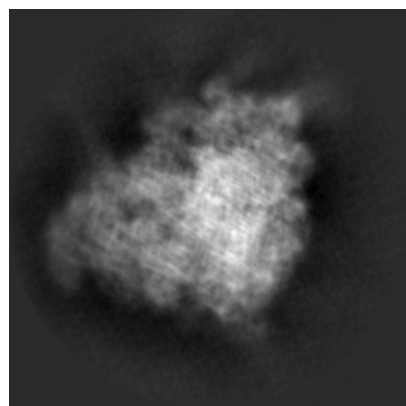
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72483. These allow visual inspection of the internal detail of the map and identification of artifacts.

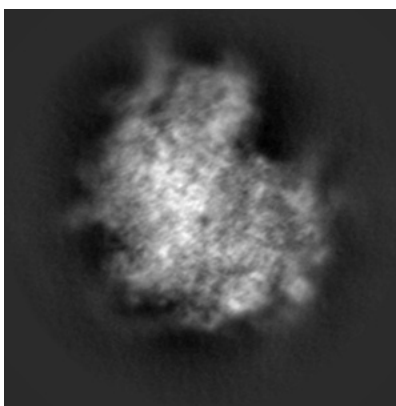
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

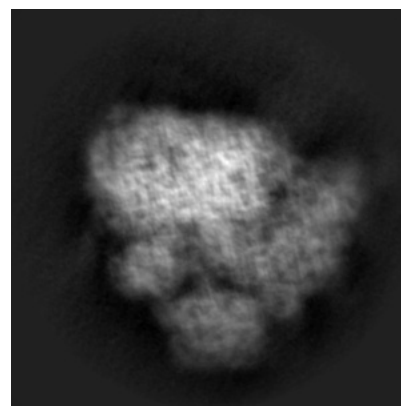
6.1.1 Primary map



X

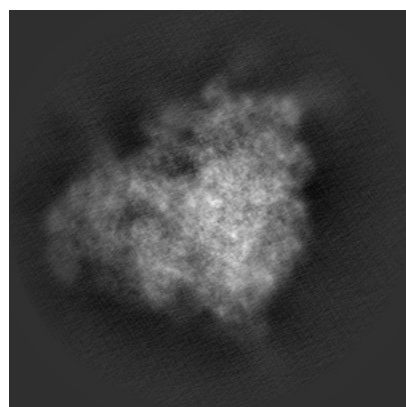


Y

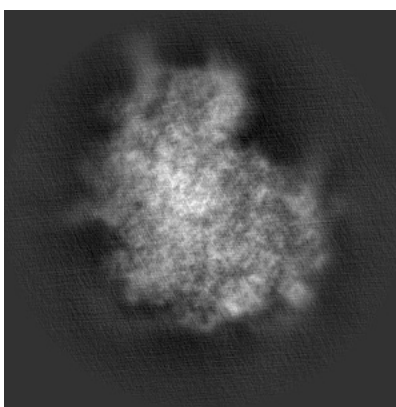


Z

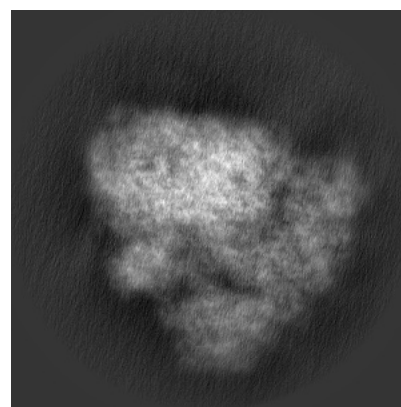
6.1.2 Raw map



X



Y

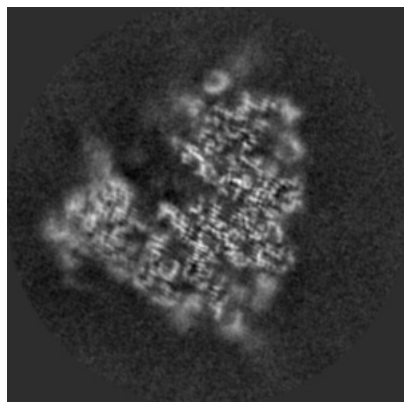


Z

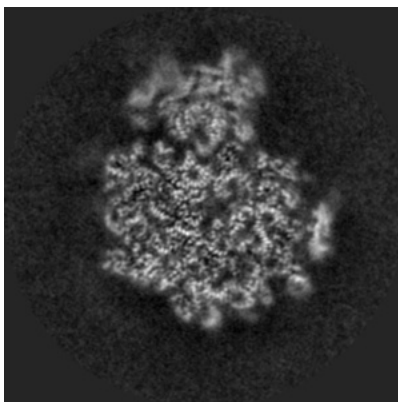
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

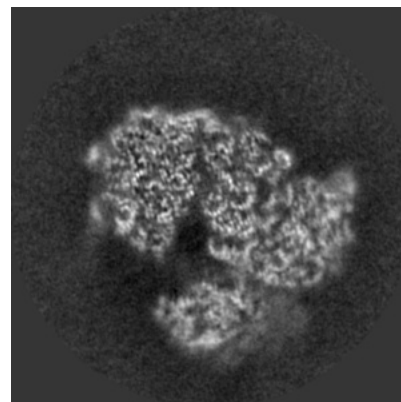
6.2.1 Primary map



X Index: 200

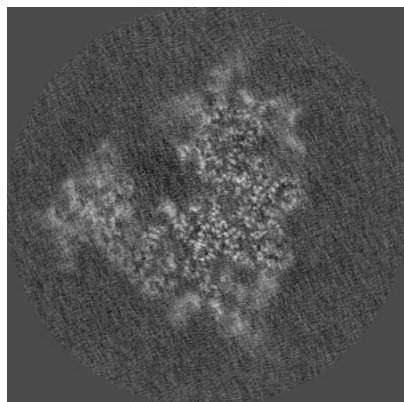


Y Index: 200

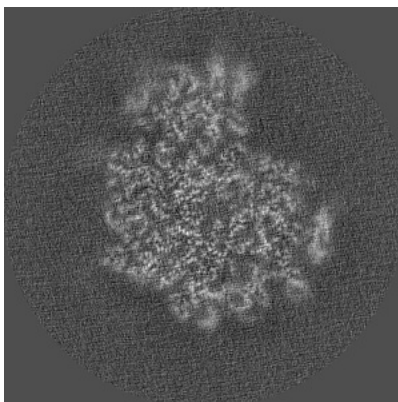


Z Index: 200

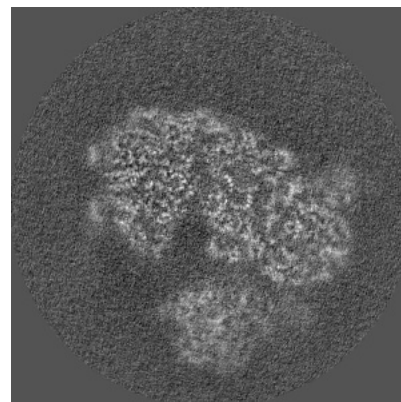
6.2.2 Raw map



X Index: 200



Y Index: 200

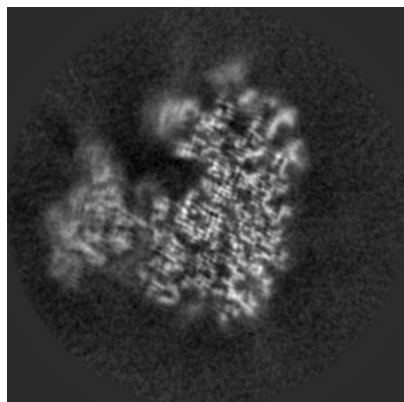


Z Index: 200

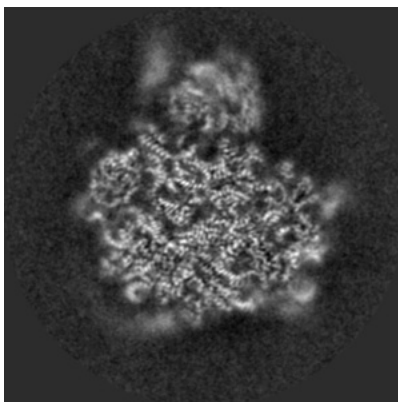
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

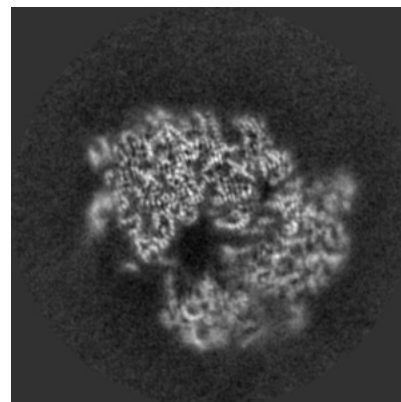
6.3.1 Primary map



X Index: 213

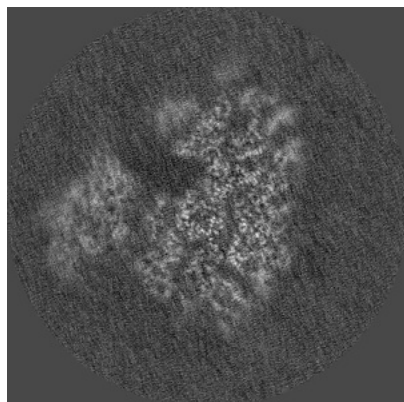


Y Index: 218

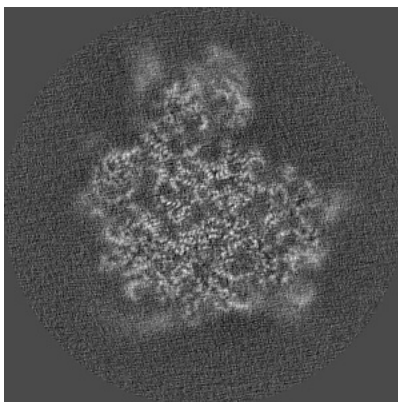


Z Index: 208

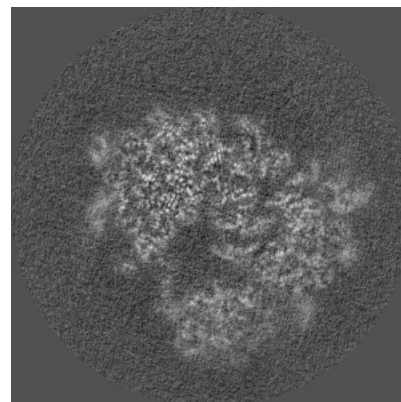
6.3.2 Raw map



X Index: 211



Y Index: 217

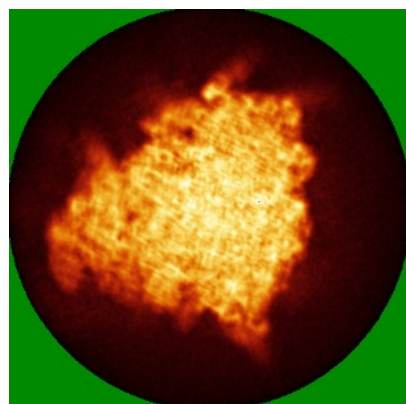


Z Index: 208

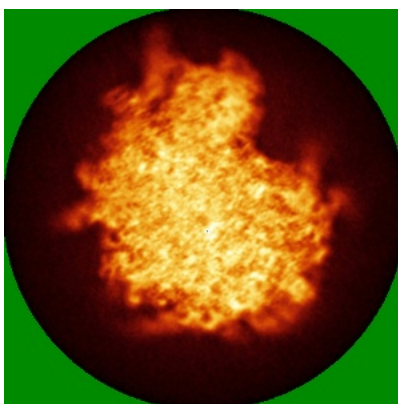
The images above show the largest variance slices of the map in three orthogonal directions.

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

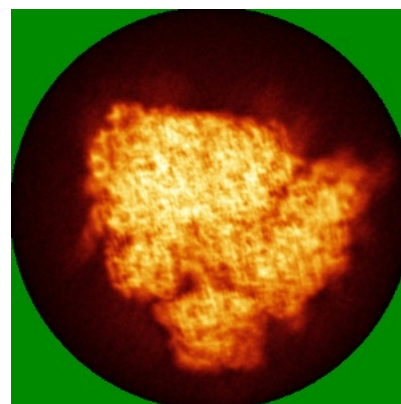
6.4.1 Primary map



X

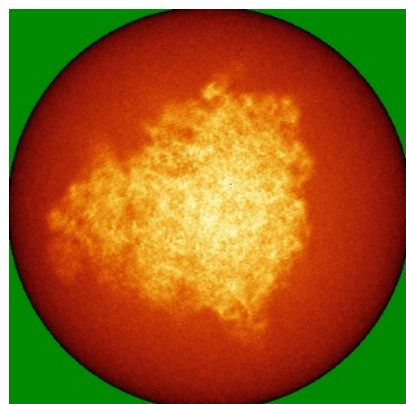


Y

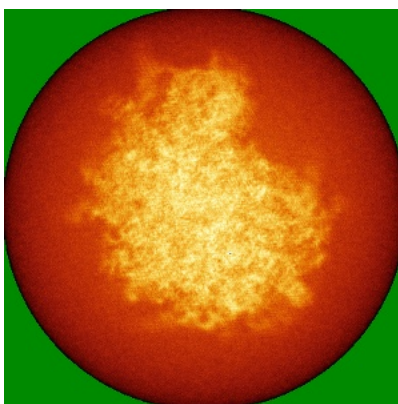


Z

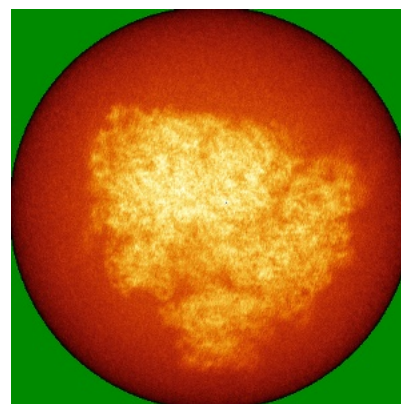
6.4.2 Raw map



X



Y

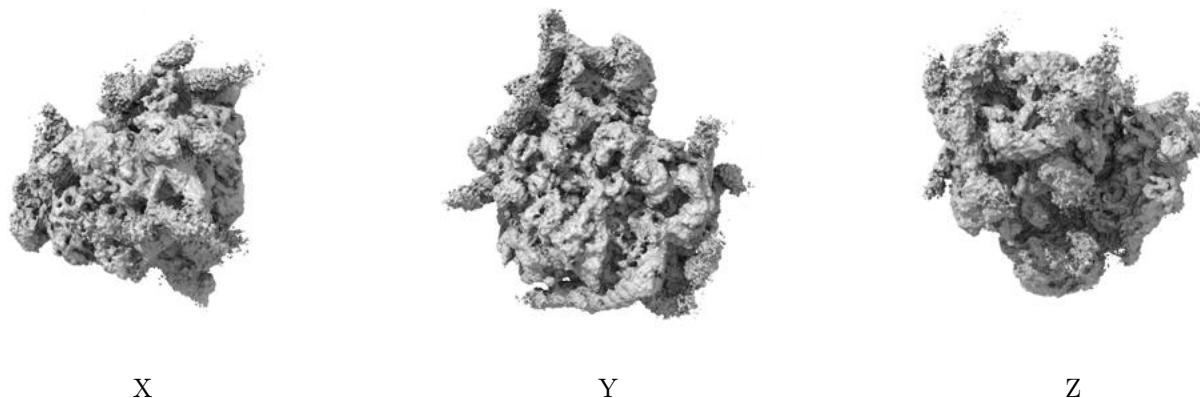


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.004. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

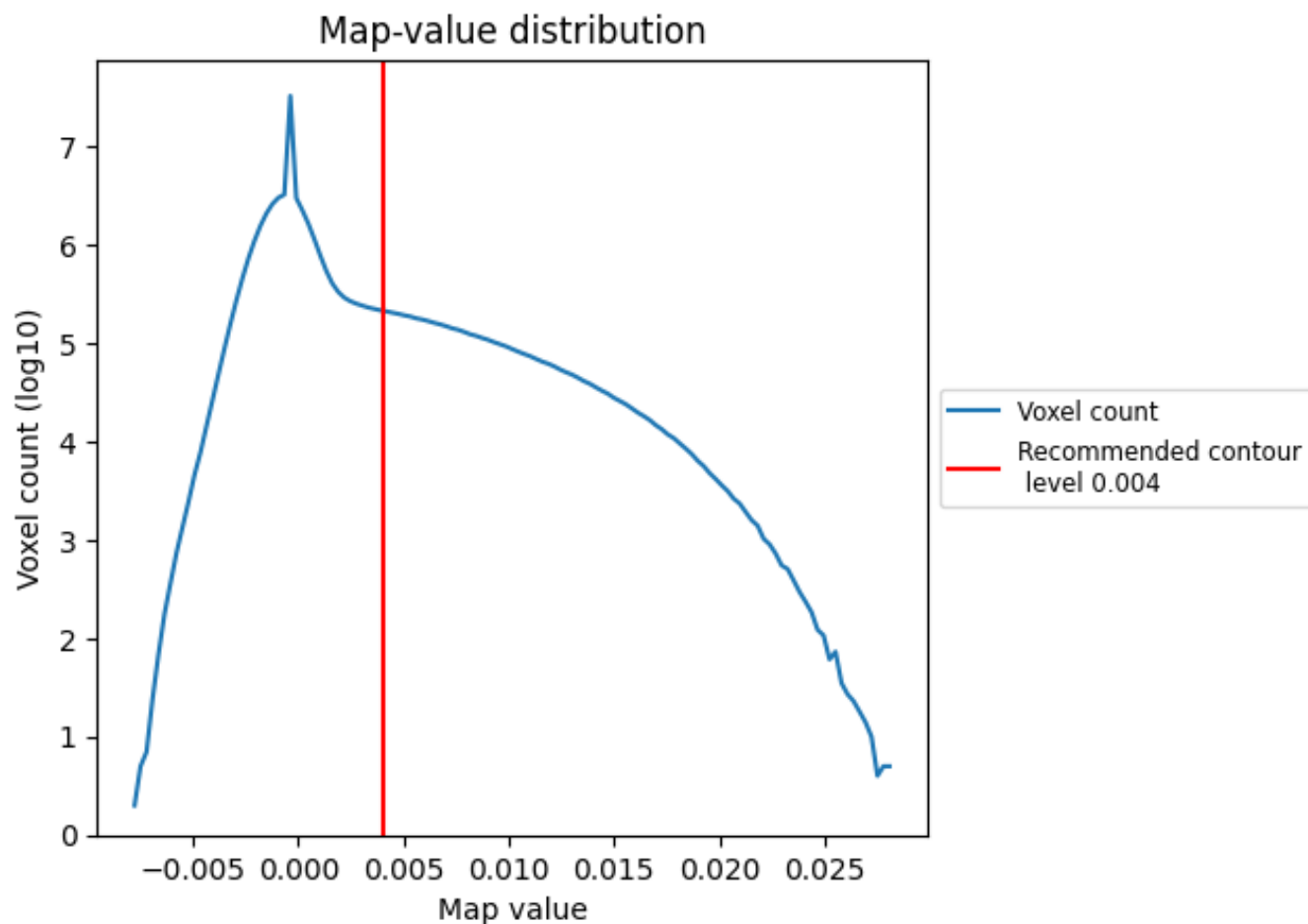
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

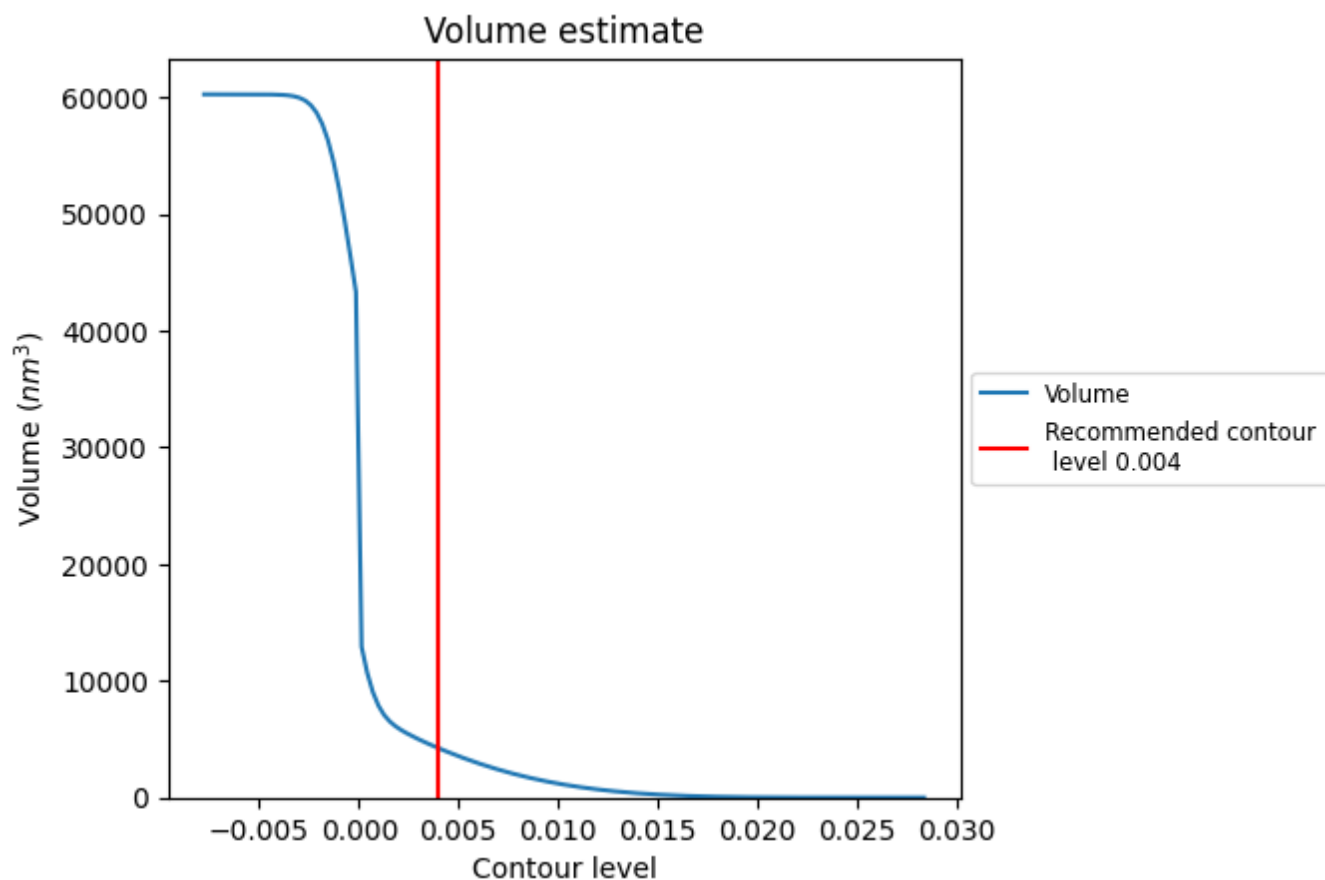
This section contains the results of statistical analysis of the map.

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.

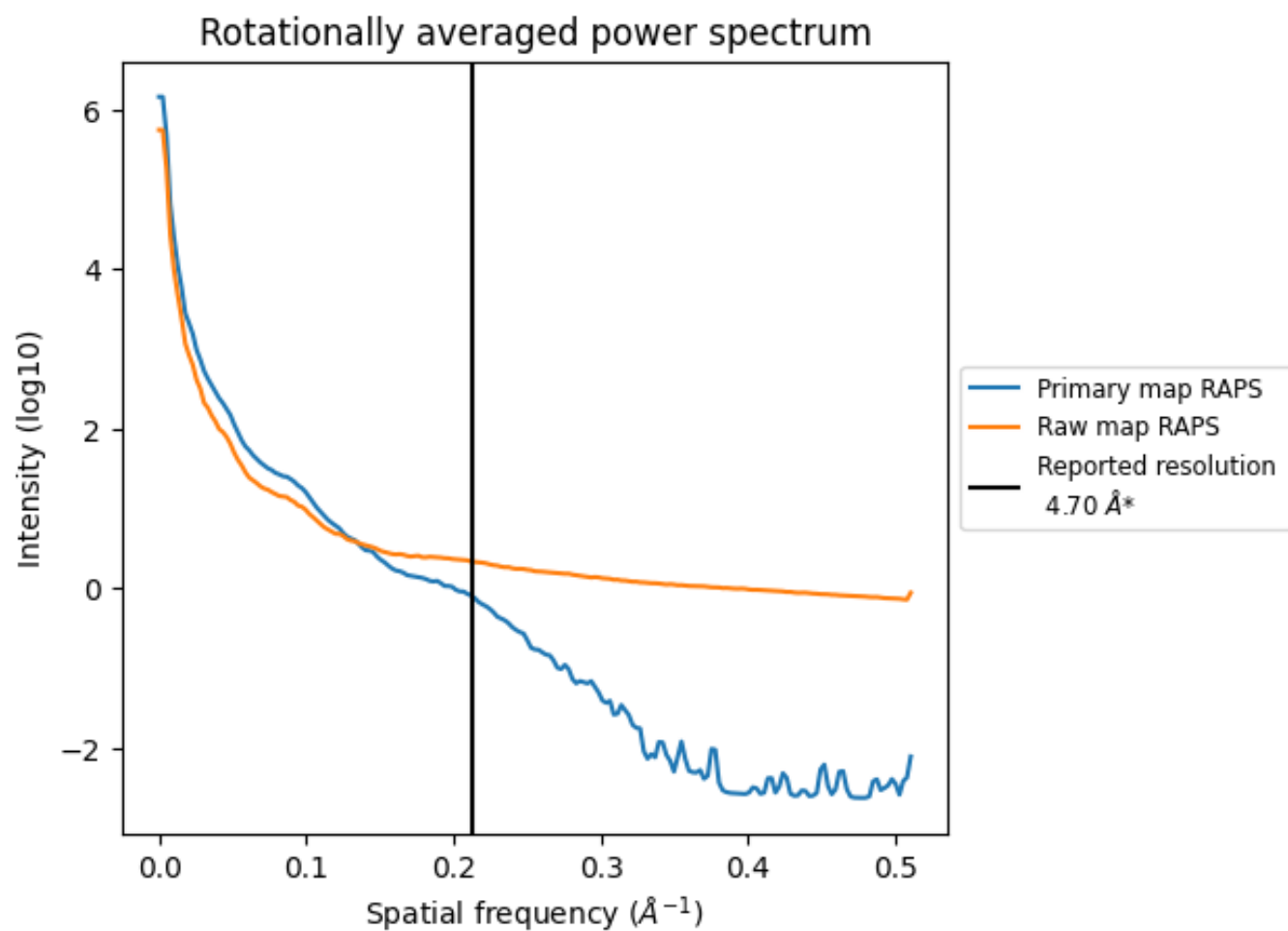
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4233 nm³; this corresponds to an approximate mass of 3824 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 ⓘ

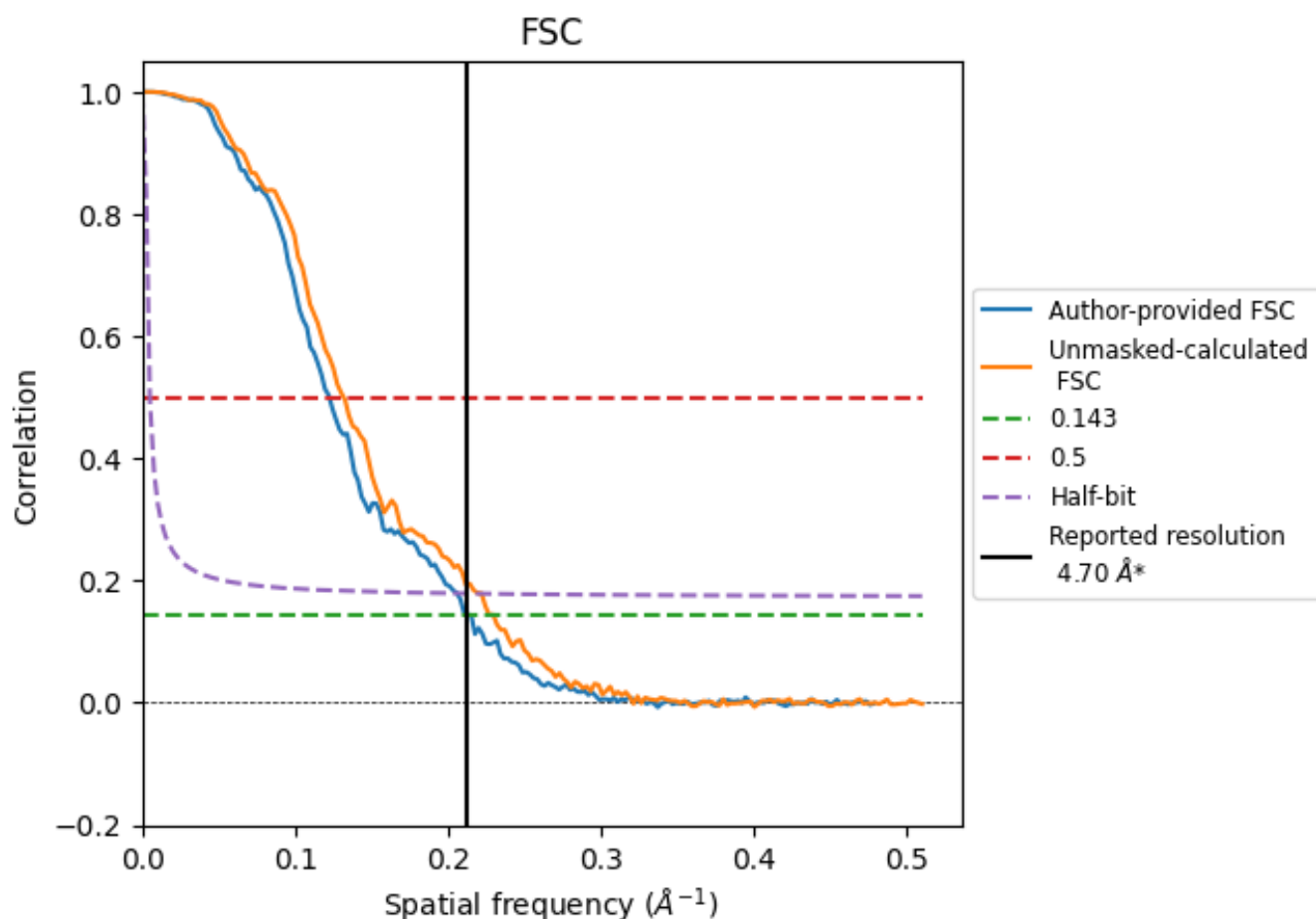


*Reported resolution corresponds to spatial frequency of 0.213 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.213 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.70	-	-
Author-provided FSC curve	4.66	8.17	4.85
Unmasked-calculated*	4.35	7.59	4.50

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

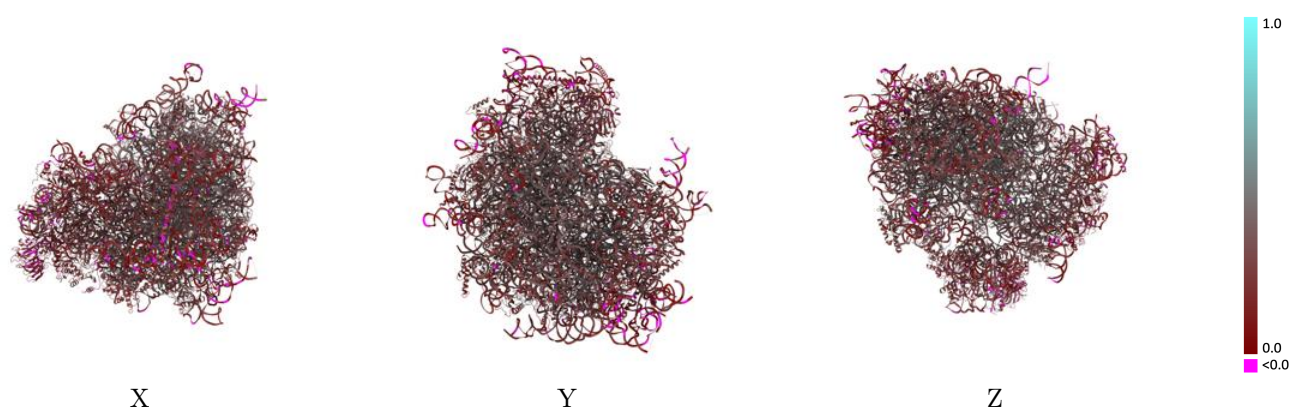
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-72483 and PDB model 9Y4H. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)

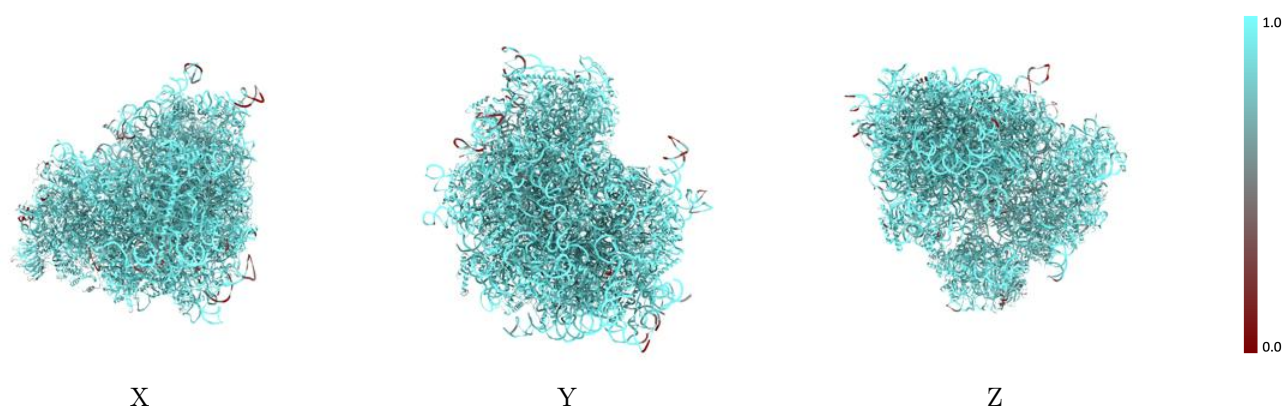
This section was not generated.

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



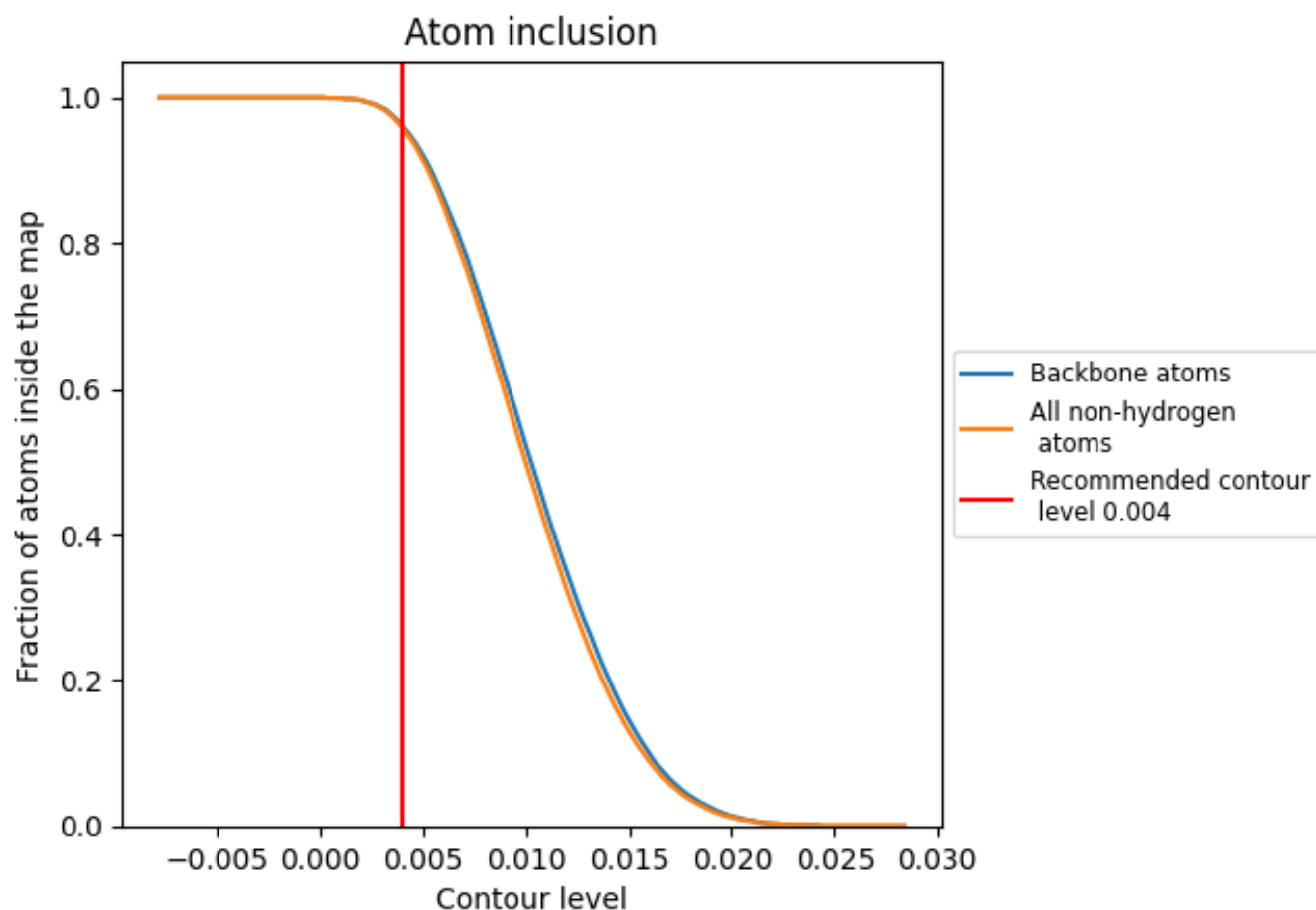
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (0.004).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9600	 0.2880
A5	 0.9810	 0.3090
A7	 0.9910	 0.3400
A8	 0.9920	 0.3110
AA	 0.9180	 0.2710
AB	 0.9440	 0.2740
AC	 0.9340	 0.2920
AD	 0.8660	 0.1960
AE	 0.9580	 0.2350
AF	 0.8900	 0.2040
AG	 0.9470	 0.1960
AH	 0.8950	 0.2840
AI	 0.9580	 0.2890
AJ	 0.9360	 0.1910
AK	 0.8460	 0.1660
AL	 0.9050	 0.2900
AN	 0.8980	 0.2930
AO	 0.9770	 0.3110
AP	 0.9220	 0.1830
AQ	 0.9160	 0.1550
AR	 0.8270	 0.1380
AS	 0.9650	 0.2010
AT	 0.9630	 0.1850
AU	 0.7940	 0.1750
AV	 0.9020	 0.2920
AW	 0.9390	 0.2850
AX	 0.9160	 0.3100
AY	 0.9690	 0.1890
AZ	 0.8890	 0.1760
Aa	 0.9570	 0.2950
Ab	 0.8980	 0.2650
Ac	 0.8150	 0.1860
Ad	 0.9560	 0.1780
Ae	 0.9010	 0.2420
Ag	 0.8700	 0.1470







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Chain	Atom inclusion	Q-score
B2	 0.9800	 0.2580
CA	 0.9220	 0.3560
CB	 0.9510	 0.3720
CC	 0.9630	 0.3360
CD	 0.9800	 0.3170
CE	 0.9610	 0.2480
CF	 0.9440	 0.3140
CG	 0.9340	 0.2720
CH	 0.9430	 0.3120
CI	 0.9520	 0.3500
CJ	 0.9580	 0.3050
CL	 0.9550	 0.2820
CM	 0.9740	 0.2830
CN	 0.9640	 0.3440
CO	 0.9370	 0.3530
CP	 0.9630	 0.3320
CQ	 0.9590	 0.3450
CS	 0.9560	 0.2930
CT	 0.9590	 0.3370
CU	 0.9560	 0.2410
CV	 0.8990	 0.3890
CW	 0.9140	 0.2580
CX	 0.9480	 0.2750
CY	 0.9700	 0.2700
CZ	 0.9660	 0.2860
Ca	 0.9670	 0.3480
Cb	 0.9740	 0.3480
Cc	 0.9620	 0.3060
Cd	 0.9200	 0.3170
Ce	 0.9430	 0.3570
Cf	 0.9390	 0.3170
Cg	 0.9690	 0.2920
Ch	 0.9750	 0.2650
Ci	 0.9520	 0.2660
Cj	 0.9790	 0.3530
Ck	 0.9190	 0.2730
Cl	 0.9980	 0.3510
Cm	 0.9630	 0.3570
Cn	 0.9220	 0.3220
Co	 0.9550	 0.3620
Cp	 0.9340	 0.3540
Cr	 0.8930	 0.2740

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Chain	Atom inclusion	Q-score
Cw	 0.9640	 0.2540
Dd	 0.9930	 0.2180