



Full wwPDB EM Validation Report ⓘ

Apr 15, 2026 – 11:39 AM UTC

PDB ID : 9Y49 / pdb_00009y49
EMDB ID : EMD-72475
Title : Structure of tuco-tuco ribosome with P/E tRNA and eEF2 (rotated)
Authors : Gutierrez-Vargas, C.; De, S.; Maji, S.; Liu, Z.; Nieb, M.; Seluanov, A.; Gorbunova, V.; Frank, J.
Deposited on : 2025-09-02
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

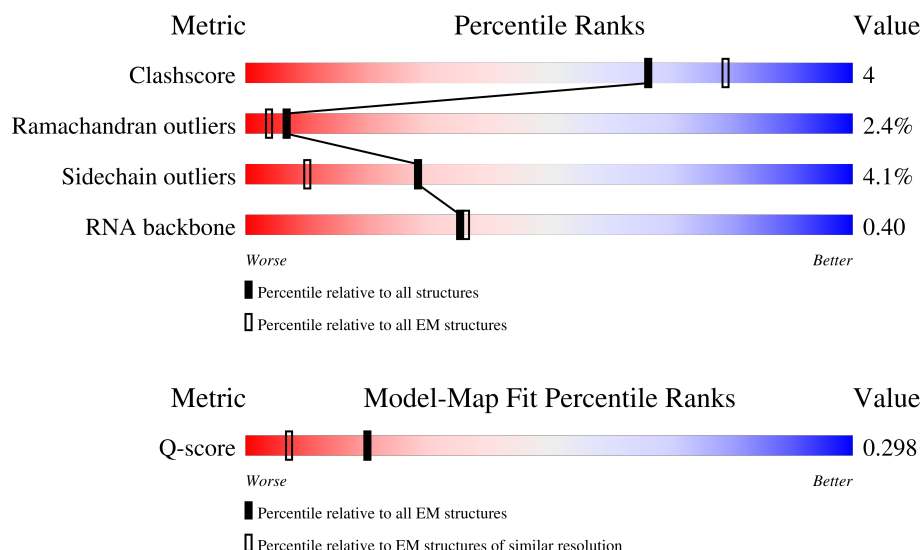
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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.






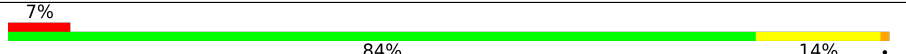
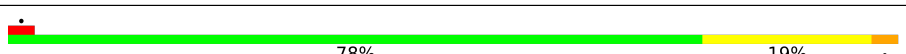
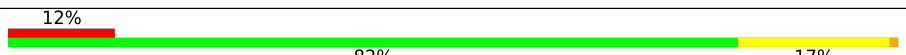
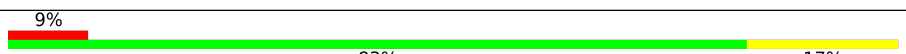
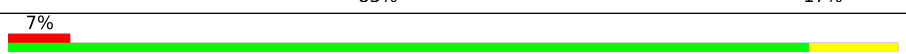
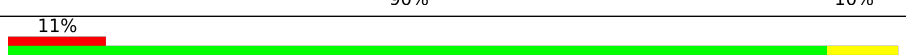
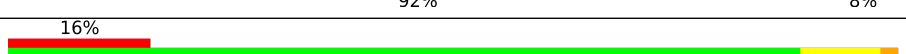
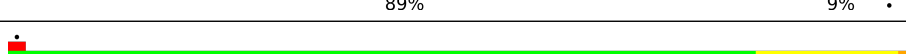

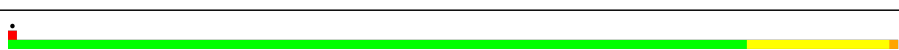
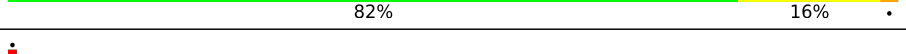





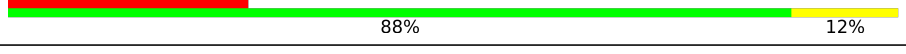

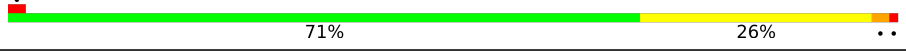



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	tR	77	
2	Ct	847	
3	AO	136	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	AX	139	
5	AN	149	
6	AL	157	
7	AB	212	
8	AA	208	
9	AV	82	
10	AY	126	
11	Aa	102	
12	Ab	84	
13	Ae	57	
14	AJ	178	
15	AE	262	
16	AC	220	
17	AG	237	
18	AH	189	
19	AW	129	
20	AI	206	
21	B2	1786	
22	CW	124	
23	Ag	313	
24	AU	104	
25	AK	98	
26	AM	122	
27	AS	137	
28	Ad	53	




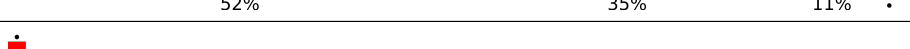
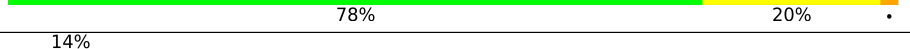
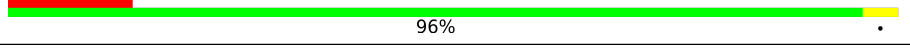


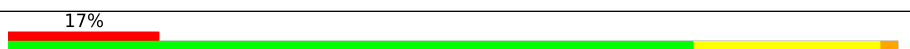
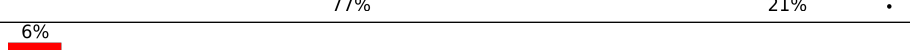
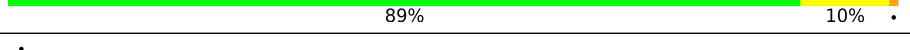
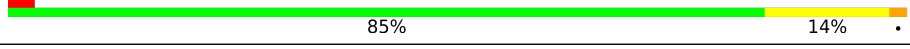



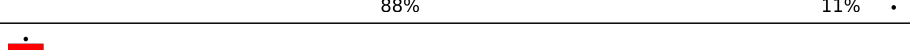
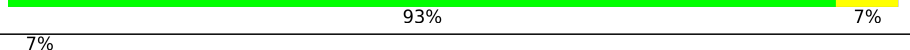
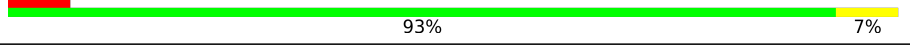
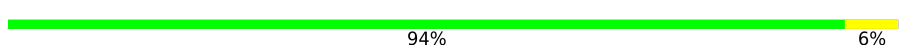
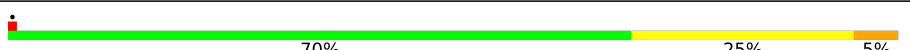

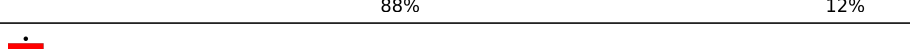
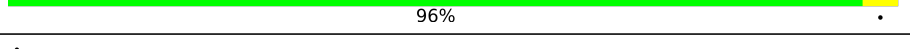
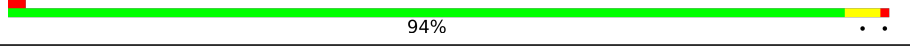

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	AR	126	
30	AP	124	
31	AT	141	
32	AZ	75	
33	Ac	64	
34	AD	227	
35	Af	71	
36	AF	188	
37	AQ	141	
38	Cz	207	
39	CO	199	
40	CL	208	
41	CV	132	
42	CM	139	
43	Ca	147	
44	CN	203	
45	CI	207	
46	CD	289	
47	CQ	188	
48	CA	255	
49	CS	175	
50	CT	159	
51	CP	152	
52	CU	110	
53	CX	121	





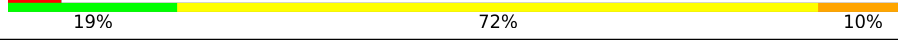
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	CY	133	
55	CZ	135	
56	Cr	137	
57	Ch	123	
58	Cb	73	
59	CB	395	
60	CF	229	
61	Cc	100	
62	Cd	113	
63	Ce	130	
64	Cf	109	
65	Cg	114	
66	Ci	103	
67	Cj	89	
68	Ck	68	
69	Cl	49	
70	CC	365	
71	Cm	50	
72	Cn	24	
73	Cp	89	
74	Co	104	
75	CJ	168	
76	CH	191	
77	CE	254	
78	CG	246	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
79	A5	1722	
80	A7	121	
81	A8	157	
82	A6	2069	
83	CR	189	

2 Entry composition [i](#)

There are 83 unique types of molecules in this entry. The entry contains 392048 atoms, of which 166649 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called tRNA (77-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
1	tR	77	Total	C	H	N	O	P	0	0
			2477	732	833	298	537	77		

- Molecule 2 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	Ct	847	Total	C	H	N	O	S	0	0
			13315	4202	6696	1137	1236	44		

- Molecule 3 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	AO	136	Total	C	H	N	O	S	0	0
			2040	618	1028	198	190	6		

- Molecule 4 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	AX	139	Total	C	H	N	O	S	0	0
			2235	685	1150	216	181	3		

- Molecule 5 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	AN	149	Total	C	H	N	O	S	0	0
			2491	770	1289	228	203	1		

- Molecule 6 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	AL	157	Total	C	H	N	O	S	0	0
			2647	822	1359	240	220	6		

- Molecule 7 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	AB	212	Total	C	H	N	O	S	0	0
			3532	1099	1805	309	305	14		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
8	AA	208	Total	C	H	N	O	S	0	0
			3284	1045	1642	289	300	8		

- Molecule 9 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	AV	82	Total	C	H	N	O	S	0	0
			1250	384	625	116	120	5		

- Molecule 10 is a protein called 40S ribosomal protein S24.

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

- Molecule 11 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	Aa	102	Total	C	H	N	O	S	0	0
			1695	512	874	171	133	5		

- Molecule 12 is a protein called 40S ribosomal protein S27.

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

- Molecule 13 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	Ae	57	Total	C	H	N	O	S	0	0
			946	281	494	99	71	1		

- Molecule 14 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AJ	178	Total	C	H	N	O	S	0	0
			3063	942	1583	296	240	2		

- Molecule 15 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	AE	262	Total	C	H	N	O	S	0	0
			4265	1327	2186	386	357	9		

- Molecule 16 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace	
16	AC	220	Total	C	H	N	O	S	0	0
			3496	1105	1787	292	302	10		

- Molecule 17 is a protein called 40S ribosomal protein S6.

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

- Molecule 18 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace	
18	AH	189	Total	C	H	N	O	S	0	0
			3134	969	1613	280	271	1		

- Molecule 19 is a protein called 40S ribosomal protein S15a.

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

- Molecule 20 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	AI	206	Total	C	H	N	O	S	0	0
			3456	1058	1770	332	291	5		

- Molecule 21 is a RNA chain called 18S rRNA (1786-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
21	B2	1786	Total	C	H	N	O	P	0	0
			56628	16798	18952	6720	12373	1785		

- Molecule 22 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	CW	124	Total	C	H	N	O	S	0	0
			2085	634	1070	207	170	4		

- Molecule 23 is a protein called Guanine nucleotide-binding protein subunit beta-2-like 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	Ag	313	Total	C	H	N	O	S	0	0
			4824	1535	2388	424	465	12		

- Molecule 24 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	AU	104	Total	C	H	N	O	S	0	0
			1708	514	886	156	148	4		

- Molecule 25 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	AK	98	Total	C	H	N	O	S	0	0
			1680	539	853	148	134	6		

- Molecule 26 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	AM	122	Total	C	H	N	O	S	0	0
			1903	588	962	167	178	8		

- Molecule 27 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	AS	137	Total	C	H	N	O	S	0	0
			2326	714	1187	231	193	1		

- Molecule 28 is a protein called 40S ribosomal protein S29.

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

- Molecule 29 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	AR	126	Total	C	H	N	O	S	0	0
			2089	639	1070	188	187	5		

- Molecule 30 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	AP	124	Total	C	H	N	O	S	0	0
			2135	660	1098	194	176	7		

- Molecule 31 is a protein called 40S ribosomal protein S19.

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

- Molecule 32 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	AZ	75	Total	C	H	N	O	S	0	0
			1250	382	652	111	104	1		

- Molecule 33 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	Ac	64	Total	C	H	N	O	S	0	0
			1042	308	536	102	94	2		

- Molecule 34 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	AD	227	Total	C	H	N	O	S	0	0
			3620	1125	1855	317	315	8		

- Molecule 35 is a protein called 40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	Af	71	Total	C	H	N	O	S	0	0
			1179	367	598	109	98	7		

- Molecule 36 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	AF	188	Total	C	H	N	O	S	0	0
			3038	934	1545	283	269	7		

- Molecule 37 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	AQ	141	Total	C	H	N	O	S	0	0
			2317	715	1193	212	194	3		

- Molecule 38 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	Cz	207	Total	C	H	N	O	S	0	0
			3434	1068	1769	298	291	8		

- Molecule 39 is a protein called 60S ribosomal protein L13a.

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

- Molecule 40 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	CL	208	Total	C	H	N	O	S	0	0
			3471	1052	1789	348	278	4		

- Molecule 41 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	CV	132	Total	C	H	N	O	S	0	0
			2022	620	1039	185	173	5		

- Molecule 42 is a protein called 60S ribosomal protein L14.

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

- Molecule 43 is a protein called 60S ribosomal protein L27a.

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

- Molecule 44 is a protein called 60S ribosomal protein L15.

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

- Molecule 45 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	CI	207	Total	C	H	N	O	S	0	0
			3383	1061	1711	320	277	14		

- Molecule 46 is a protein called 60S ribosomal protein L5.

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

- Molecule 47 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	CQ	188	Total	C	H	N	O	S	0	0
			3161	949	1640	315	251	6		

- Molecule 48 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	CA	255	Total	C	H	N	O	S	0	0
			4009	1225	2052	399	327	6		

- Molecule 49 is a protein called 60S ribosomal protein L18a.

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

- Molecule 50 is a protein called 60S ribosomal protein L21.

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

- Molecule 51 is a protein called 60S ribosomal protein L17.

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

- Molecule 52 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	CU	110	Total	C	H	N	O	S	0	0
			1804	571	904	155	172	2		

- Molecule 53 is a protein called 60S ribosomal protein L23a.

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

- Molecule 54 is a protein called 60S ribosomal protein L26.

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

- Molecule 55 is a protein called 60S ribosomal protein L27.

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

- Molecule 56 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	Cr	137	Total	C	H	N	O	S	0	0
			2288	682	1184	231	185	6		

- Molecule 57 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	Ch	123	Total	C	H	N	O	S	0	0
			2182	646	1159	206	169	2		

- Molecule 58 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	Cb	73	Total	C	H	N	O	S	0	0
			1225	367	630	128	97	3		

- Molecule 59 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	CB	395	Total	C	H	N	O	S	0	0
			6505	2030	3316	600	545	14		

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

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

- Molecule 61 is a protein called 60S ribosomal protein L30.

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

- Molecule 62 is a protein called 60S ribosomal protein L31.

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

- Molecule 63 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	Ce	130	Total	C	H	N	O	S	0	0
			2235	676	1165	221	168	5		

- Molecule 64 is a protein called 60S ribosomal protein L35a.

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

- Molecule 65 is a protein called 60S ribosomal protein L34.

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

- Molecule 66 is a protein called 60S ribosomal protein L36.

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

- Molecule 67 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms						AltConf	Trace
67	Cj	89	Total	C	H	N	O	S	0	0
			1490	446	764	161	114	5		

- Molecule 68 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms						AltConf	Trace
68	Ck	68	Total	C	H	N	O	S	0	0
			1183	360	624	101	97	1		

- Molecule 69 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms						AltConf	Trace
69	Cl	49	Total	C	H	N	O	S	0	0
			907	275	472	97	62	1		

- Molecule 70 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
70	CC	365	Total	C	H	N	O	S	0	0
			5982	1829	3074	580	486	13		

- Molecule 71 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms						AltConf	Trace
71	Cm	50	Total	C	H	N	O	S	0	0
			857	254	446	87	64	6		

- Molecule 72 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms						AltConf	Trace
72	Cn	24	Total	C	H	N	O	S	0	0
			504	139	274	62	26	3		

- Molecule 73 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms						AltConf	Trace
73	Cp	89	Total	C	H	N	O	S	0	0
			1440	437	747	133	116	7		

- Molecule 74 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms						AltConf	Trace
74	Co	104	Total	C	H	N	O	S	0	0
			1772	533	921	174	138	6		

- Molecule 75 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms						AltConf	Trace
75	CJ	168	Total	C	H	N	O	S	0	0
			2731	853	1382	251	239	6		

- Molecule 76 is a protein called 60S ribosomal protein L9.

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

- Molecule 77 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
77	CE	254	Total	C	H	N	O	S	0	0
			4290	1317	2240	389	340	4		

- Molecule 78 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms						AltConf	Trace
78	CG	246	Total	C	H	N	O	S	0	0
			4096	1256	2123	379	334	4		

- Molecule 79 is a RNA chain called LSU-alpha rRNA (1722-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
79	A5	1715	Total	C	H	N	O	P	0	0
			54360	16069	18197	6597	11783	1714		

- Molecule 80 is a RNA chain called 5S rRNA (121-MER).

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

- Molecule 81 is a RNA chain called 5.8S rRNA (157-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
81	A8	157	Total	C	H	N	O	P	0	0
			5027	1489	1693	587	1102	156		

- Molecule 82 is a RNA chain called LSU-beta rRNA (2069-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
82	A6	2069	Total	C	H	N	O	P	0	0
			65289	19344	21793	7815	14268	2069		

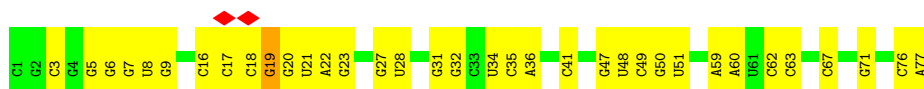
- Molecule 83 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms						AltConf	Trace
83	CR	189	Total	C	N	O	S		0	0
			1580	979	338	253	10			

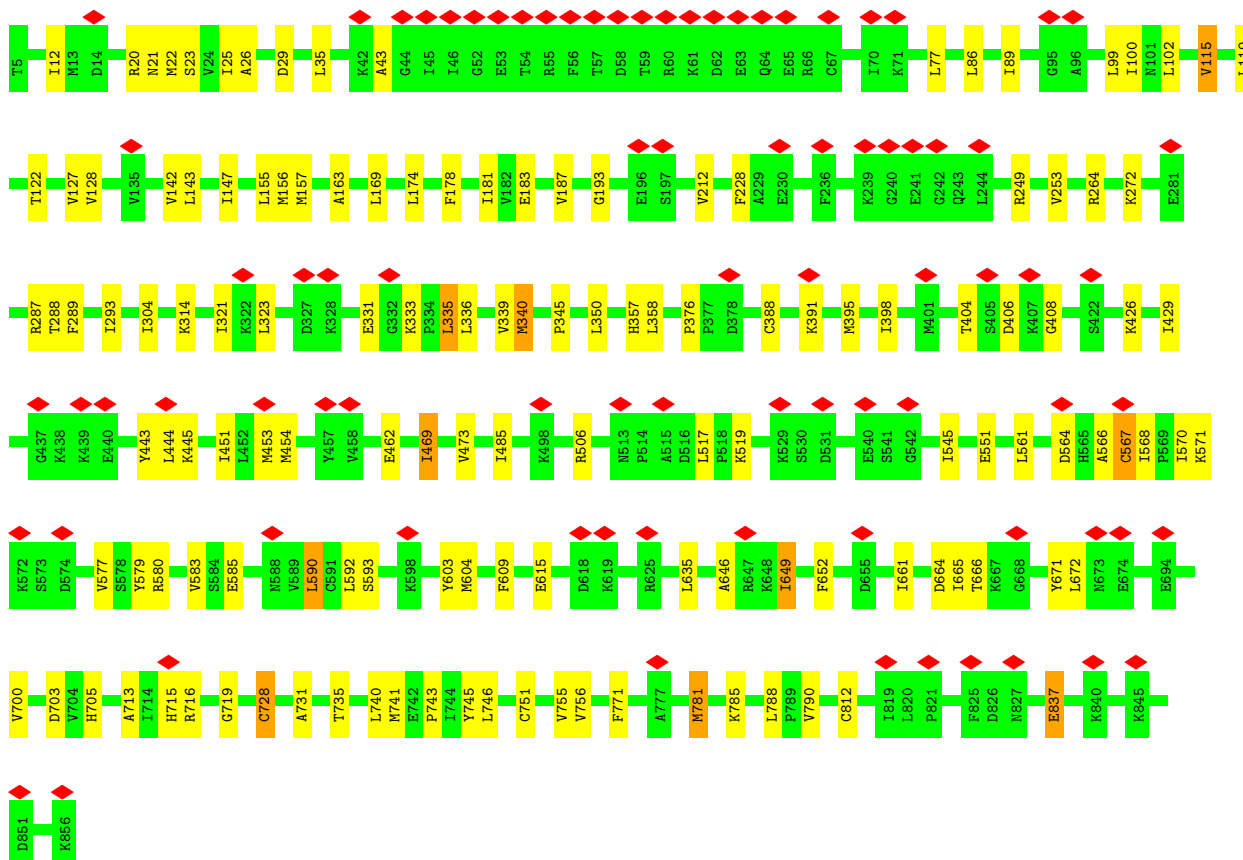
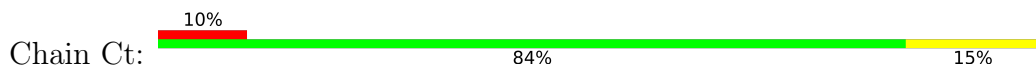
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

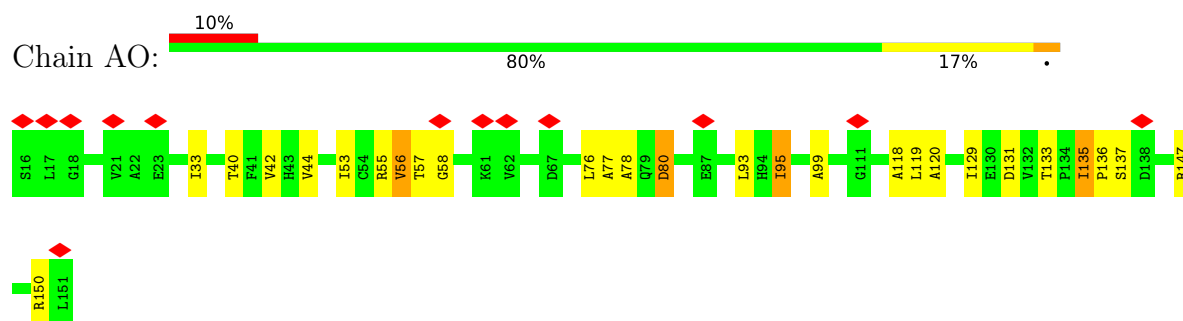
- Molecule 1: tRNA (77-MER)



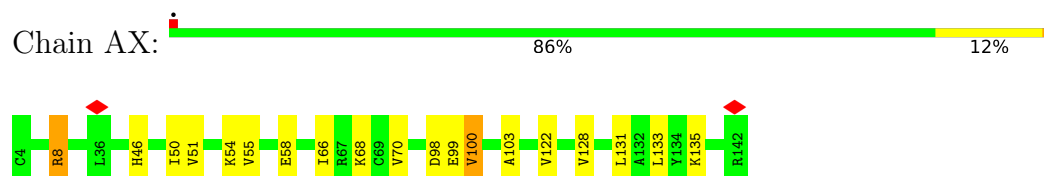
- Molecule 2: Elongation factor 2



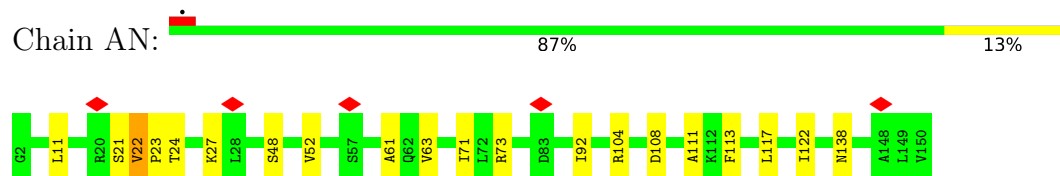
- Molecule 3: 40S ribosomal protein S14



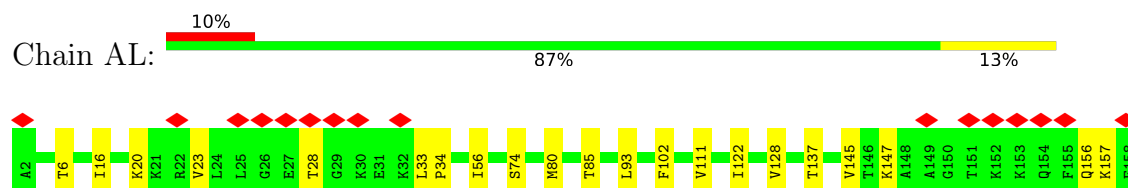
- Molecule 4: 40S ribosomal protein S23



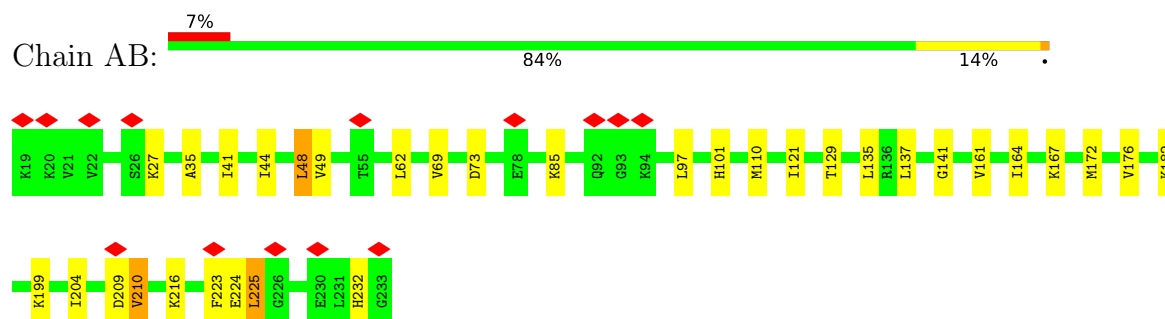
- Molecule 5: 40S ribosomal protein S13



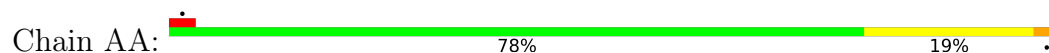
- Molecule 6: 40S ribosomal protein S11

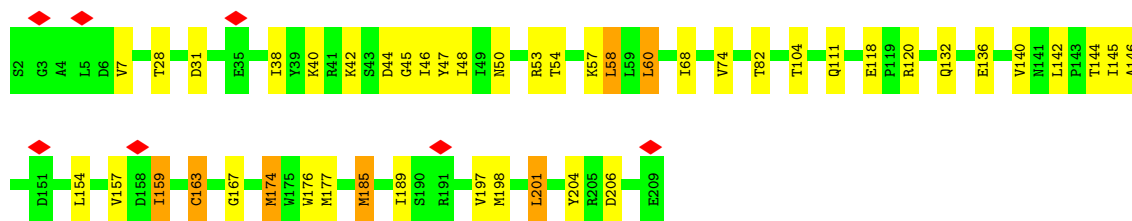


- Molecule 7: 40S ribosomal protein S3a

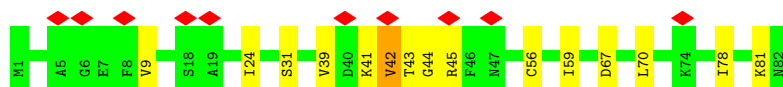
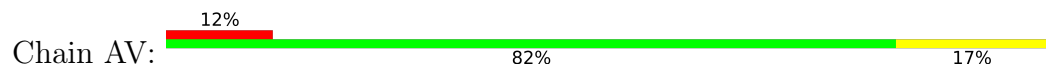


- Molecule 8: 40S ribosomal protein SA

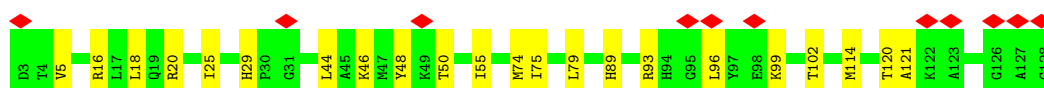
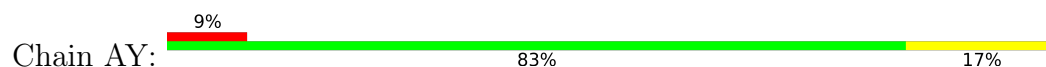




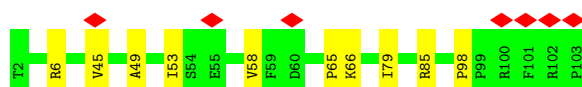
• Molecule 9: 40S ribosomal protein S21



• Molecule 10: 40S ribosomal protein S24



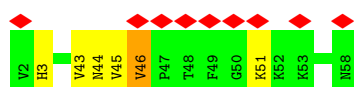
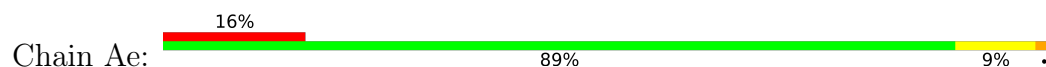
• Molecule 11: 40S ribosomal protein S26



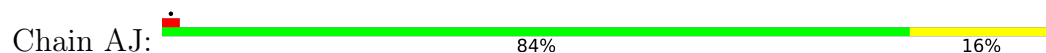
• Molecule 12: 40S ribosomal protein S27



• Molecule 13: 40S ribosomal protein S30

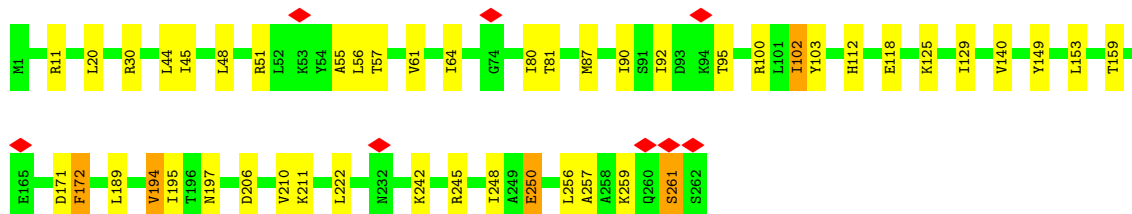
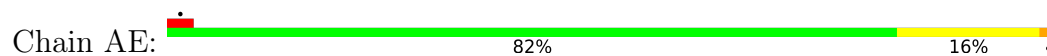


• Molecule 14: 40S ribosomal protein S9

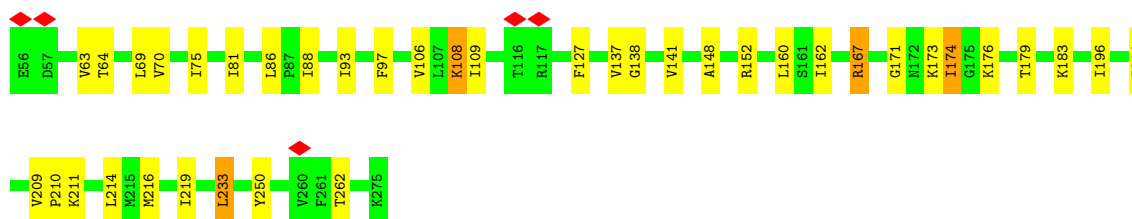
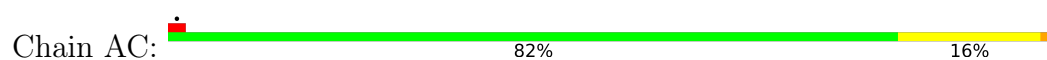




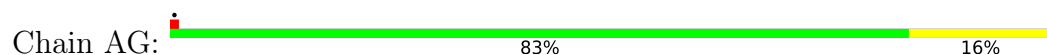
- Molecule 15: 40S ribosomal protein S4, X isoform



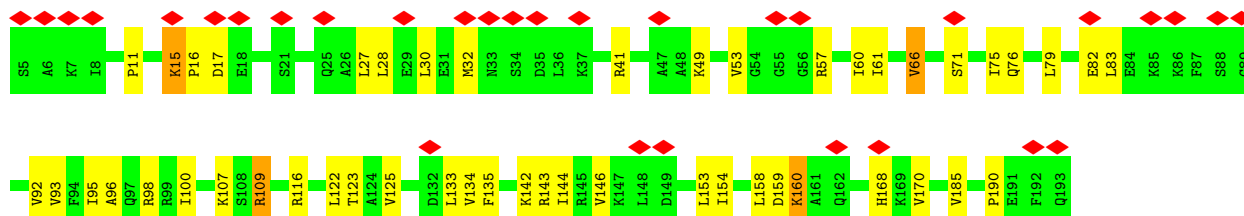
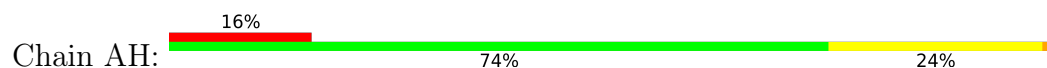
- Molecule 16: 40S ribosomal protein S2




- Molecule 17: 40S ribosomal protein S6

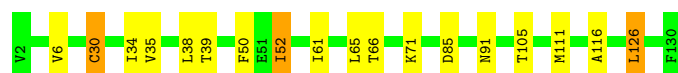


- Molecule 18: 40S ribosomal protein S7



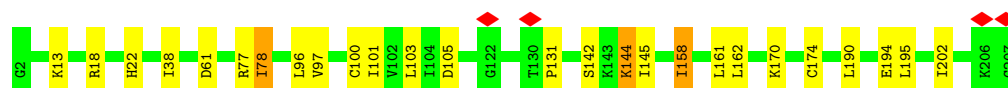
- Molecule 19: 40S ribosomal protein S15a

Chain AW:  86% 12%



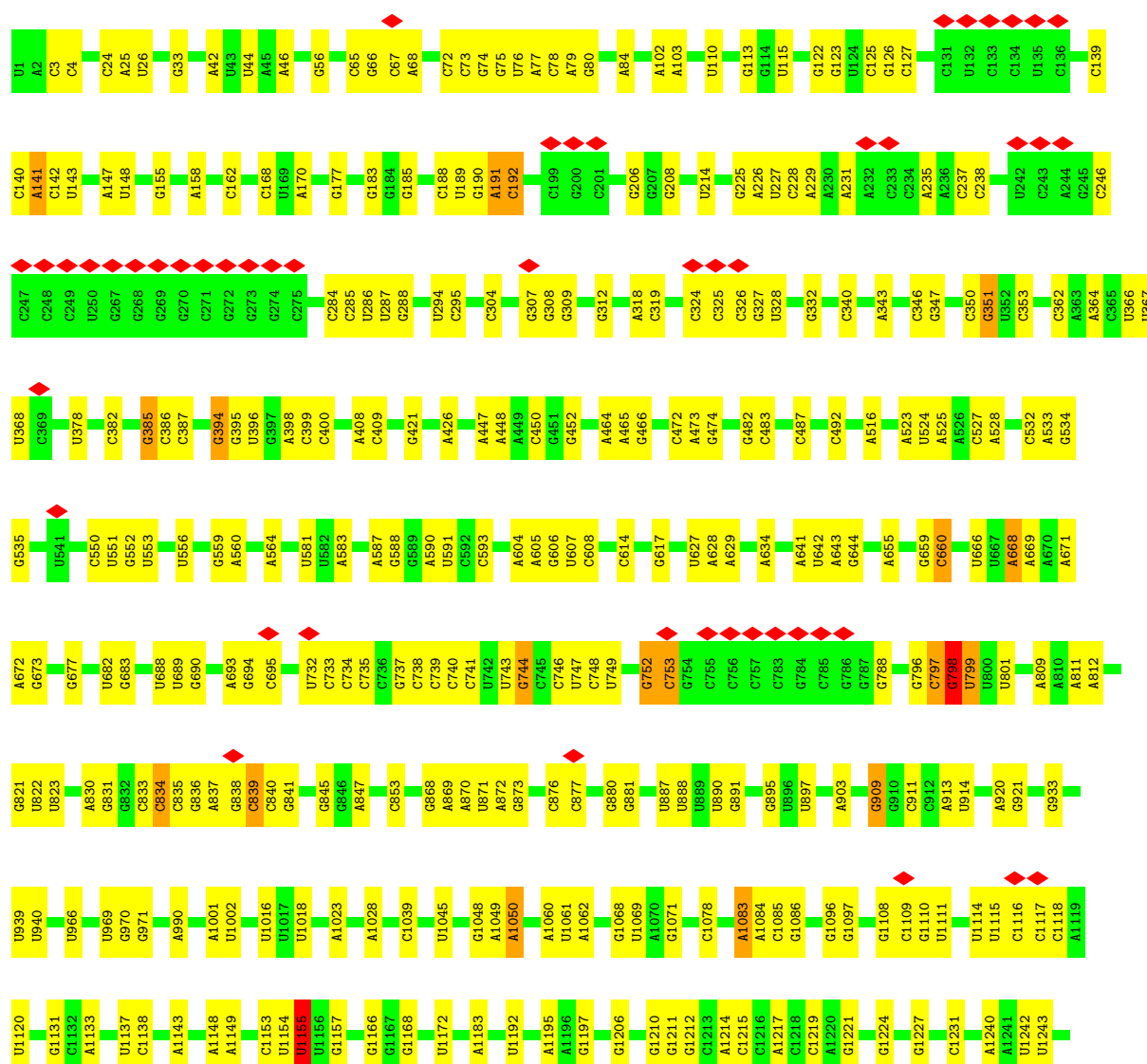
- Molecule 20: 40S ribosomal protein S8

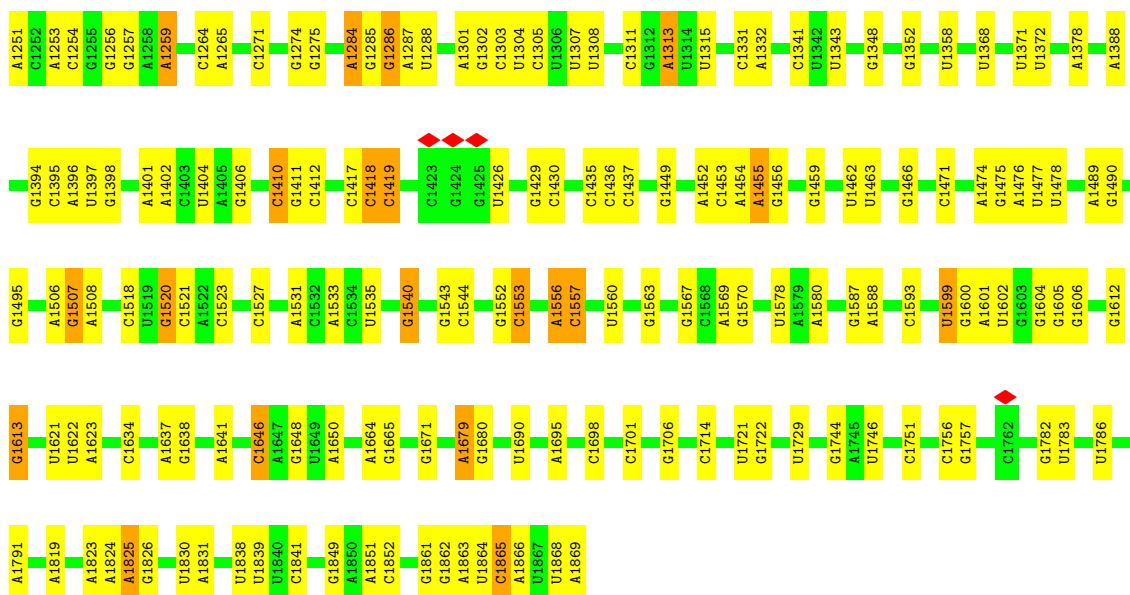
Chain AI:  87% 11%



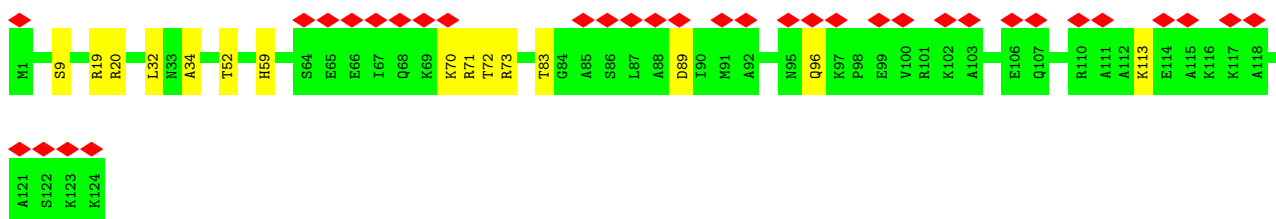
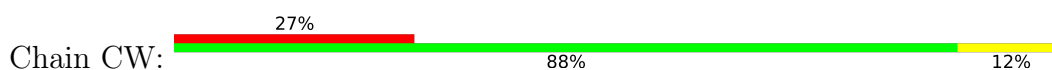
- Molecule 21: 18S rRNA (1786-MER)

Chain B2:  72% 26%

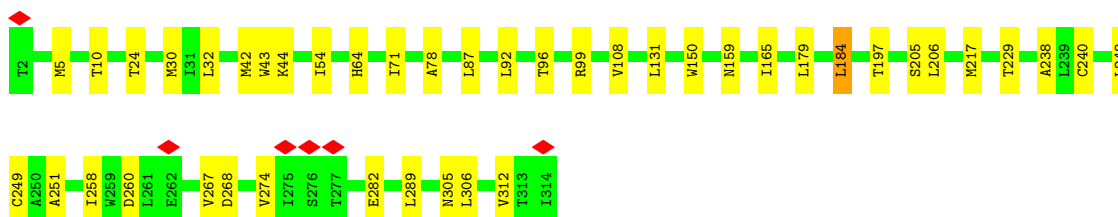




• Molecule 22: 60S ribosomal protein L24



• Molecule 23: Guanine nucleotide-binding protein subunit beta-2-like 1



• Molecule 24: 40S ribosomal protein S20




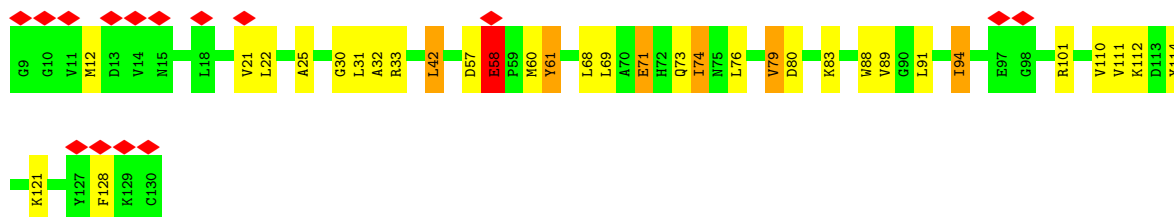
• Molecule 25: 40S ribosomal protein S10

Chain AK:  69% 29% .




- Molecule 26: 40S ribosomal protein S12

Chain AM:  12% 73% 21% 5% .



- Molecule 27: 40S ribosomal protein S18

Chain AS:  84% 15% ..




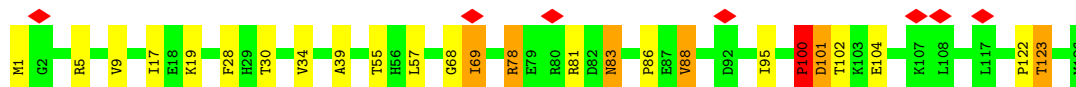
- Molecule 28: 40S ribosomal protein S29

Chain Ad:  92% 8%




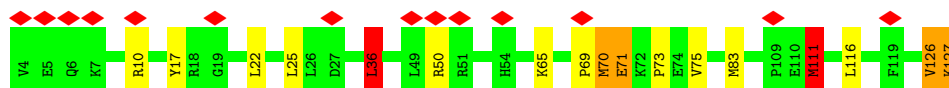
- Molecule 29: 40S ribosomal protein S17

Chain AR:  6% 80% 14% 5% .



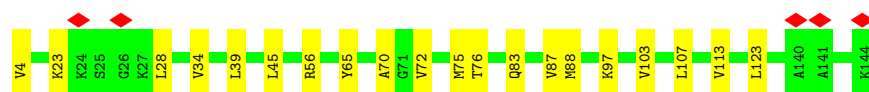
- Molecule 30: 40S ribosomal protein S15

Chain AP:  11% 86% 9% ..

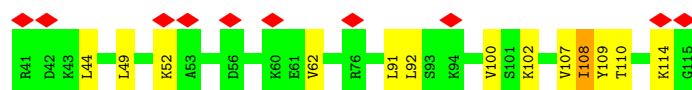
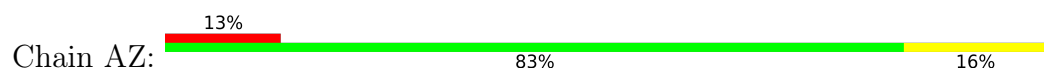


- Molecule 31: 40S ribosomal protein S19

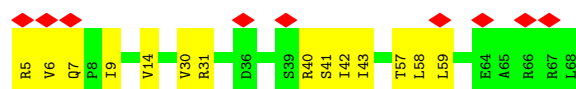
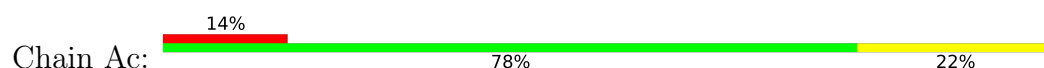
Chain AT:  86% 14%



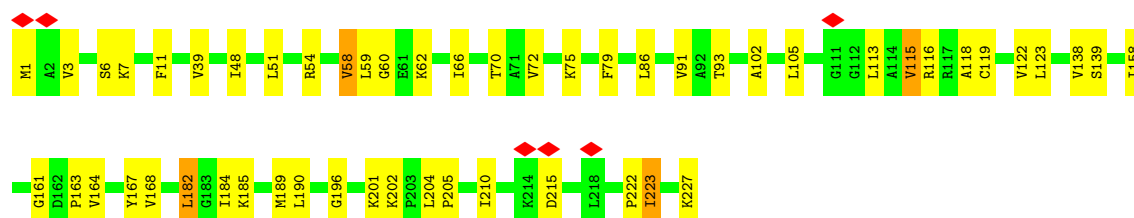
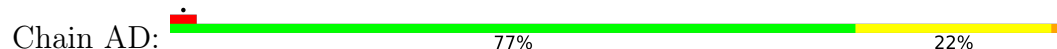
- Molecule 32: 40S ribosomal protein S25



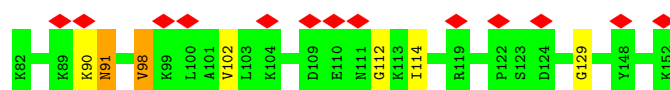
- Molecule 33: 40S ribosomal protein S28



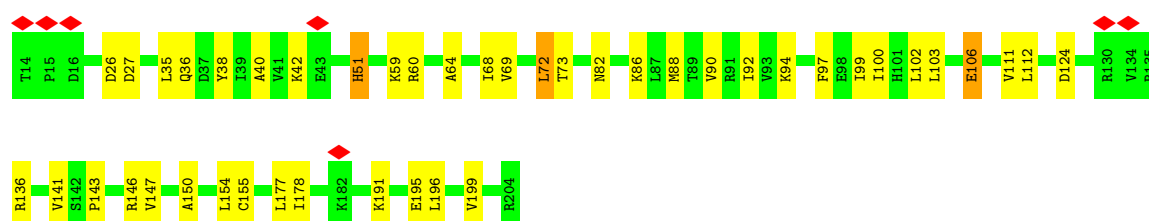
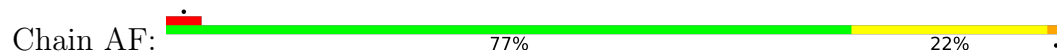
- Molecule 34: 40S ribosomal protein S3




- Molecule 35: 40S ribosomal protein S27a

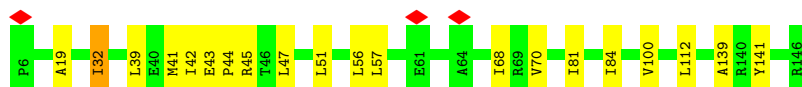


- Molecule 36: 40S ribosomal protein S5




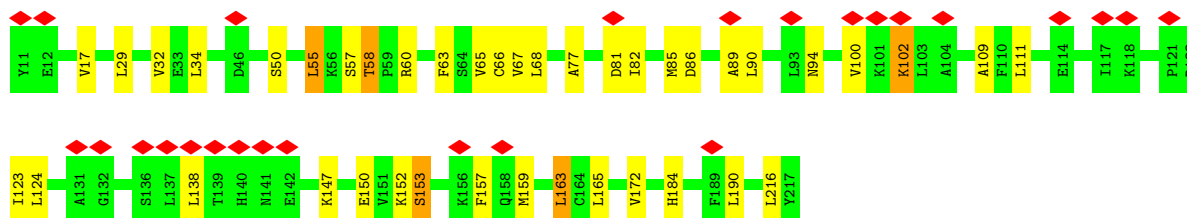
- Molecule 37: 40S ribosomal protein S16

Chain AQ:  86% 13%




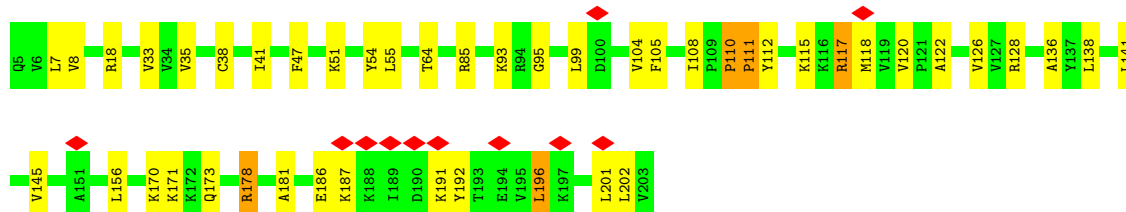
- Molecule 38: 60S ribosomal protein L10a

Chain Cz:  13% 80% 17%



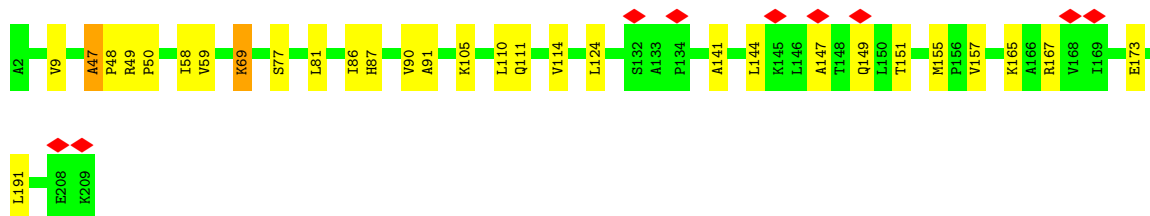
- Molecule 39: 60S ribosomal protein L13a

Chain CO:  6% 77% 21%

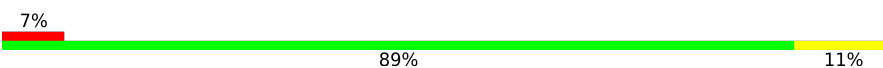


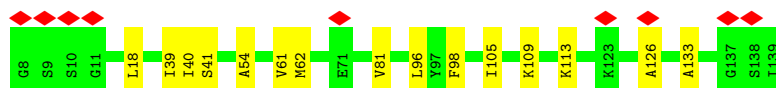
- Molecule 40: 60S ribosomal protein L13

Chain CL:  86% 13%




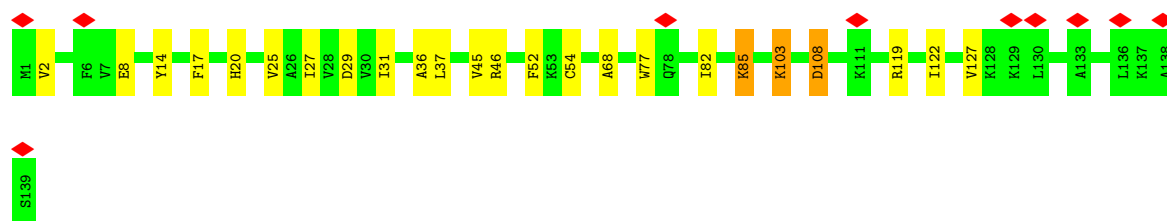
- Molecule 41: 60S ribosomal protein L23

Chain CV:  7% 89% 11%

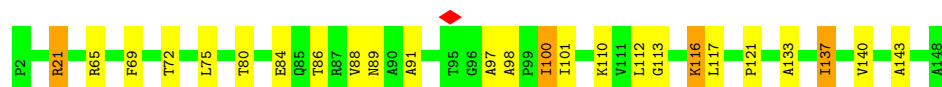
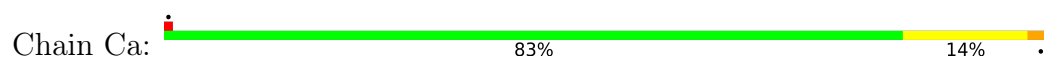


- Molecule 42: 60S ribosomal protein L14

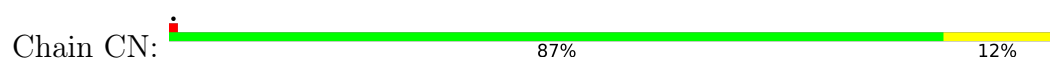
Chain CM:  7% 83% 15%



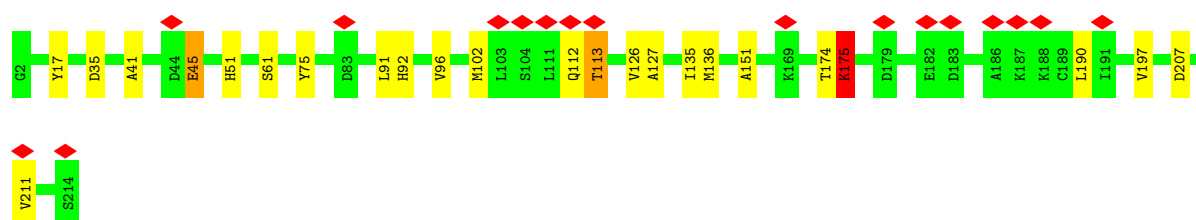
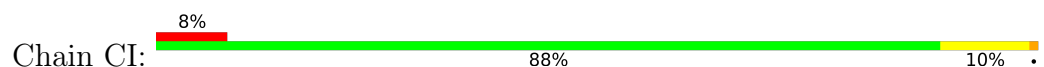
- Molecule 43: 60S ribosomal protein L27a



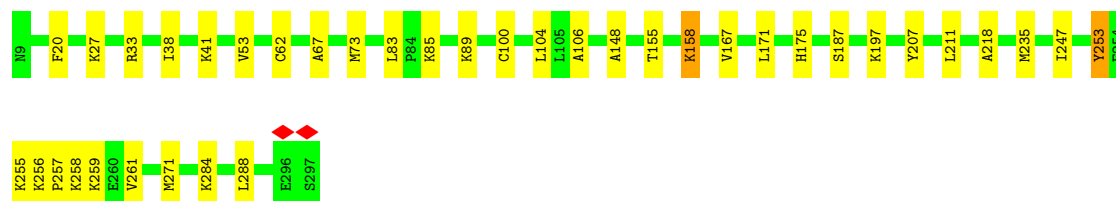
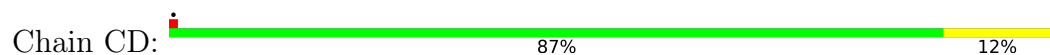
- Molecule 44: 60S ribosomal protein L15



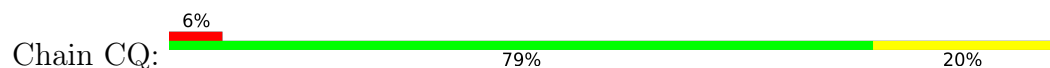
- Molecule 45: 60S ribosomal protein L10-like

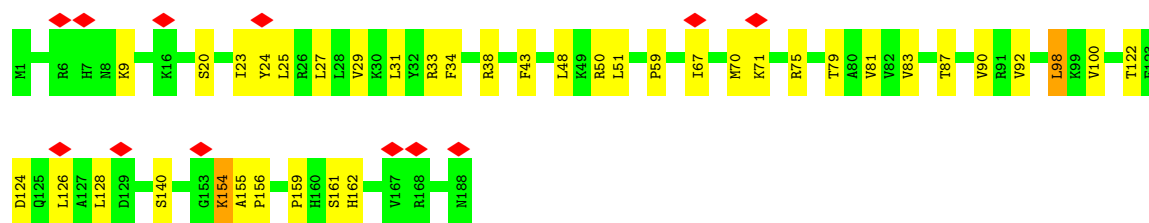


- Molecule 46: 60S ribosomal protein L5

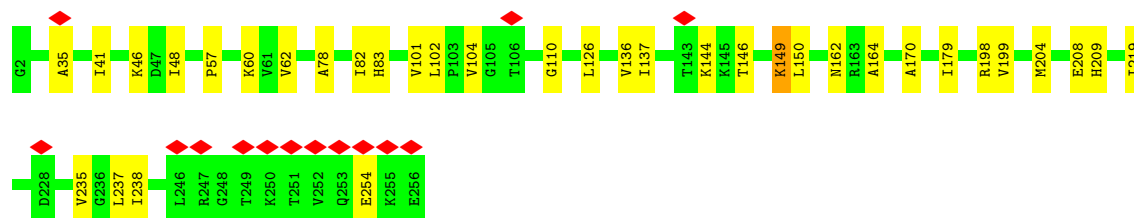
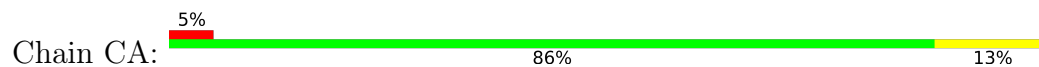


- Molecule 47: 60S ribosomal protein L18

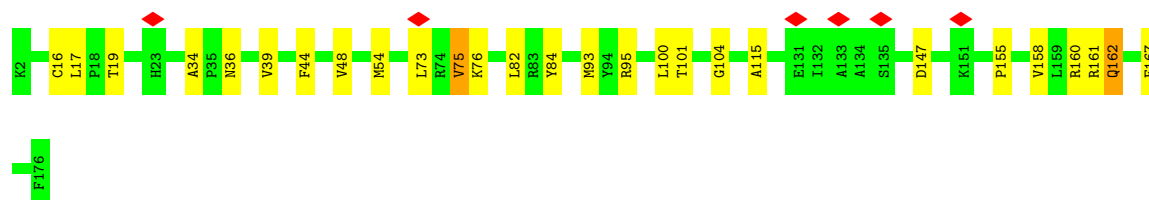
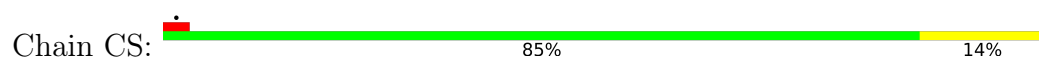




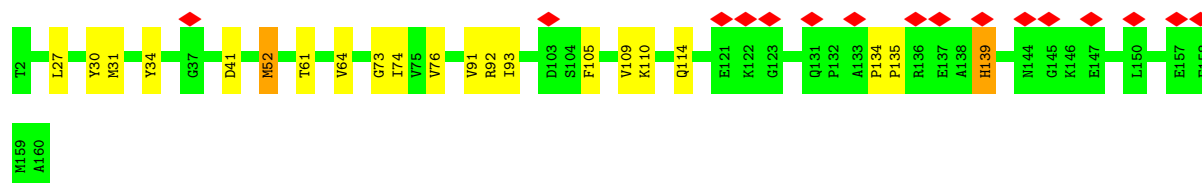
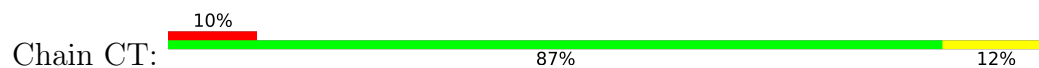
- Molecule 48: 60S ribosomal protein L8



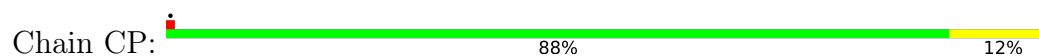
- Molecule 49: 60S ribosomal protein L18a



- Molecule 50: 60S ribosomal protein L21

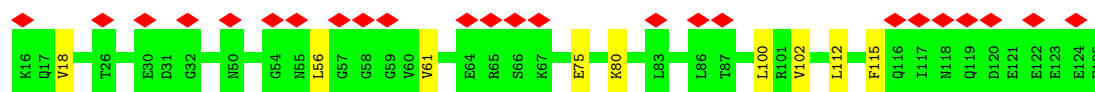


- Molecule 51: 60S ribosomal protein L17

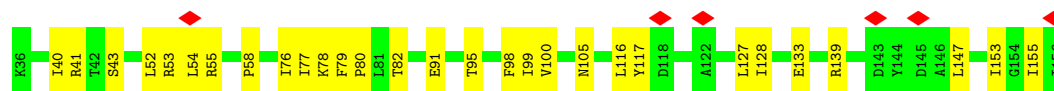
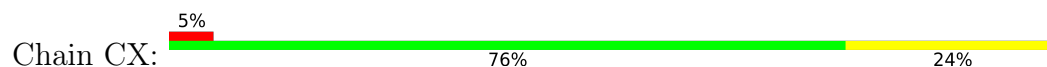


- Molecule 52: 60S ribosomal protein L22

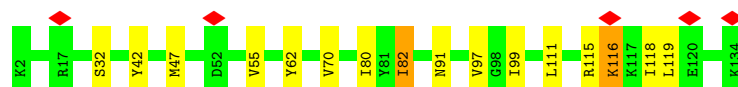




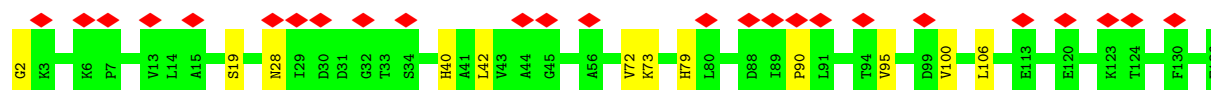
- Molecule 53: 60S ribosomal protein L23a



- Molecule 54: 60S ribosomal protein L26



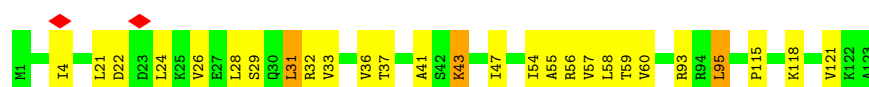
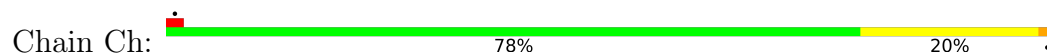
- Molecule 55: 60S ribosomal protein L27



- Molecule 56: 60S ribosomal protein L28

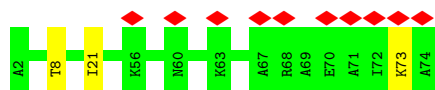


- Molecule 57: 60S ribosomal protein L35



- Molecule 58: 60S ribosomal protein L29





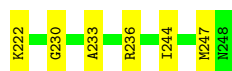
- Molecule 59: 60S ribosomal protein L3

Chain CB: 88% 11%



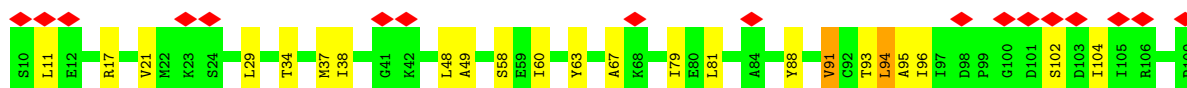
- Molecule 60: 60S ribosomal protein L7

Chain CF: 83% 16%



- Molecule 61: 60S ribosomal protein L30

Chain Cc: 17% 77% 21%



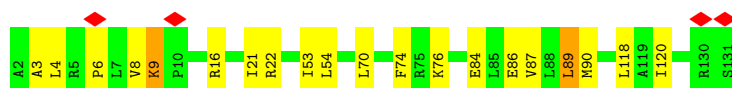
- Molecule 62: 60S ribosomal protein L31

Chain Cd: 6% 89% 10%



- Molecule 63: 60S ribosomal protein L32

Chain Ce: 85% 14%

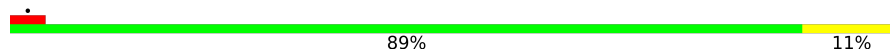


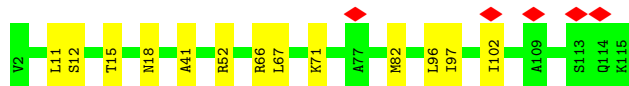
- Molecule 64: 60S ribosomal protein L35a

Chain Cf:  57% 37% 6%




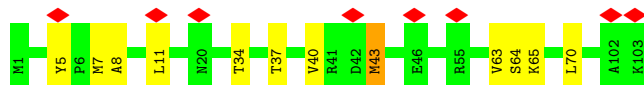
- Molecule 65: 60S ribosomal protein L34

Chain Cg:  89% 11%



- Molecule 66: 60S ribosomal protein L36

Chain Ci:  8% 88% 11%



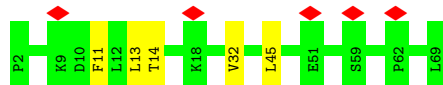
- Molecule 67: 60S ribosomal protein L37

Chain Cj:  93% 7%



- Molecule 68: 60S ribosomal protein L38

Chain Ck:  7% 93% 7%



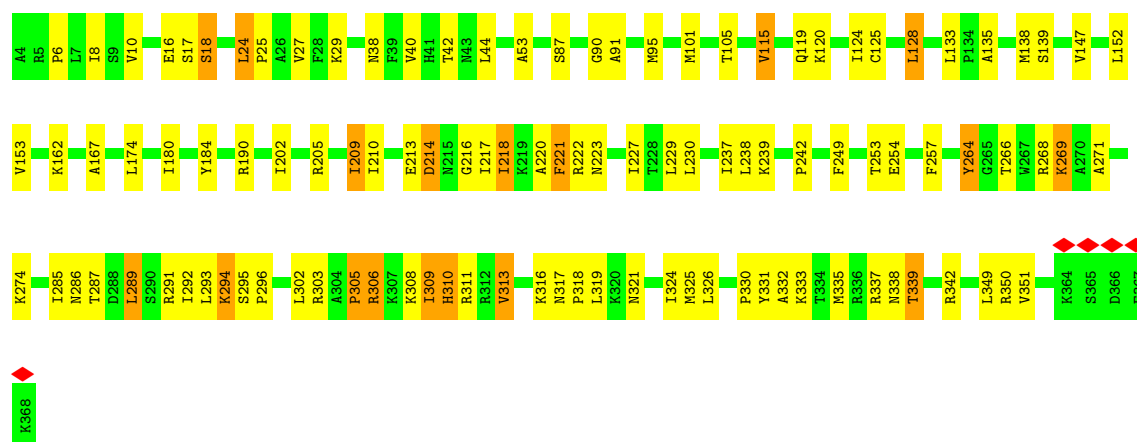
- Molecule 69: 60S ribosomal protein L39

Chain Cl:  94% 6%

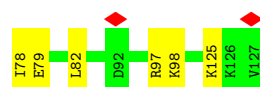
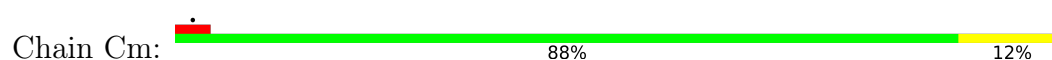


- Molecule 70: 60S ribosomal protein L4

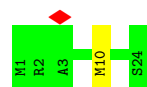
Chain CC:  70% 25% 5%



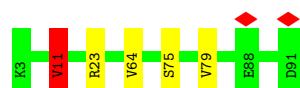
- Molecule 71: 60S ribosomal protein L40



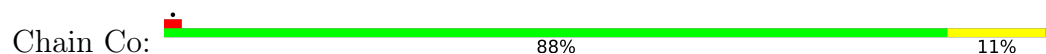
- Molecule 72: 60S ribosomal protein L41



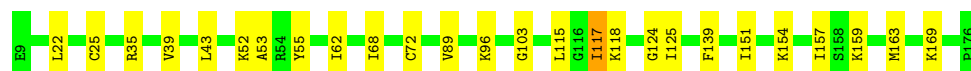
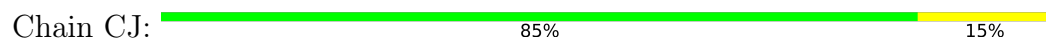
- Molecule 73: 60S ribosomal protein L37a



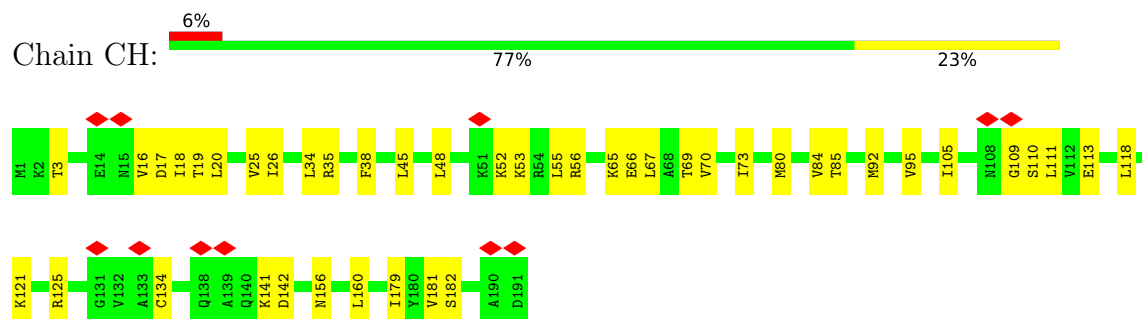
- Molecule 74: 60S ribosomal protein L36a



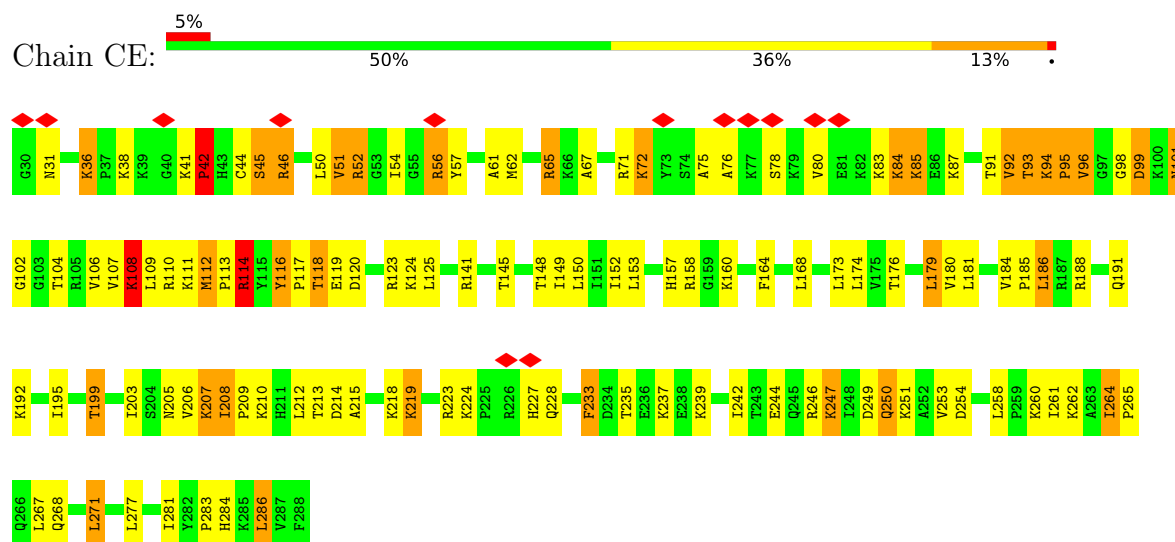
- Molecule 75: 60S ribosomal protein L11



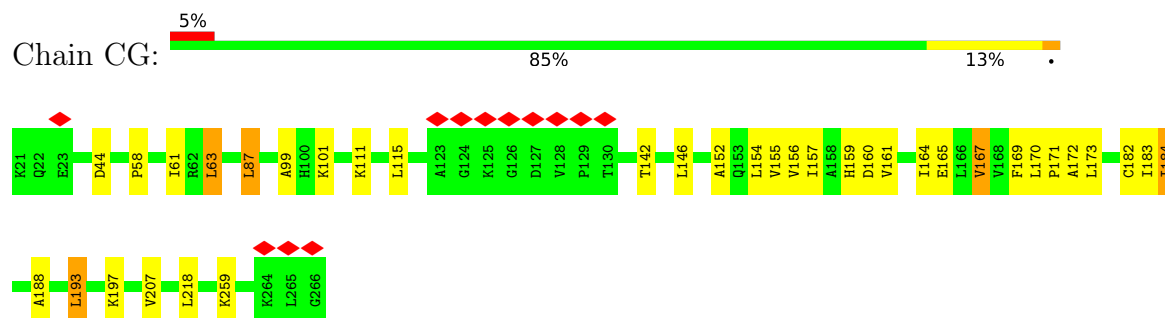
- Molecule 76: 60S ribosomal protein L9



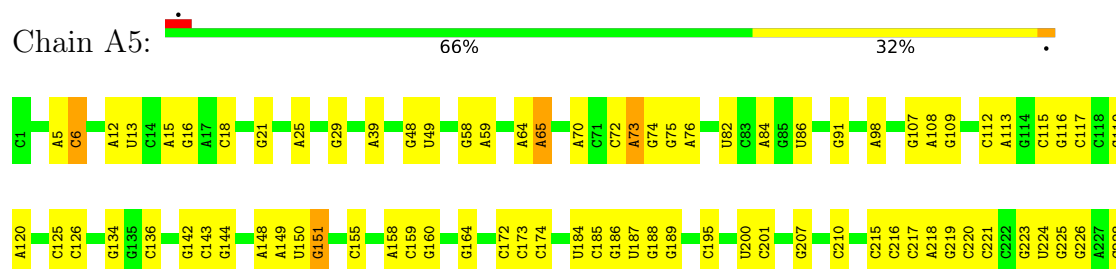
- Molecule 77: 60S ribosomal protein L6



- Molecule 78: 60S ribosomal protein L7a




- Molecule 79: LSU-alpha rRNA (1722-MER)






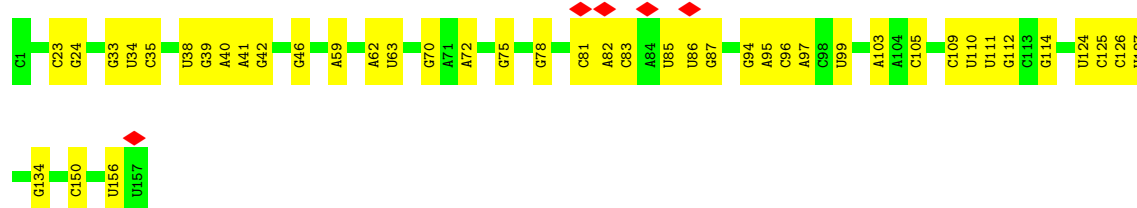
- Molecule 80: 5S rRNA (121-MER)

Chain A7:  77% 22%




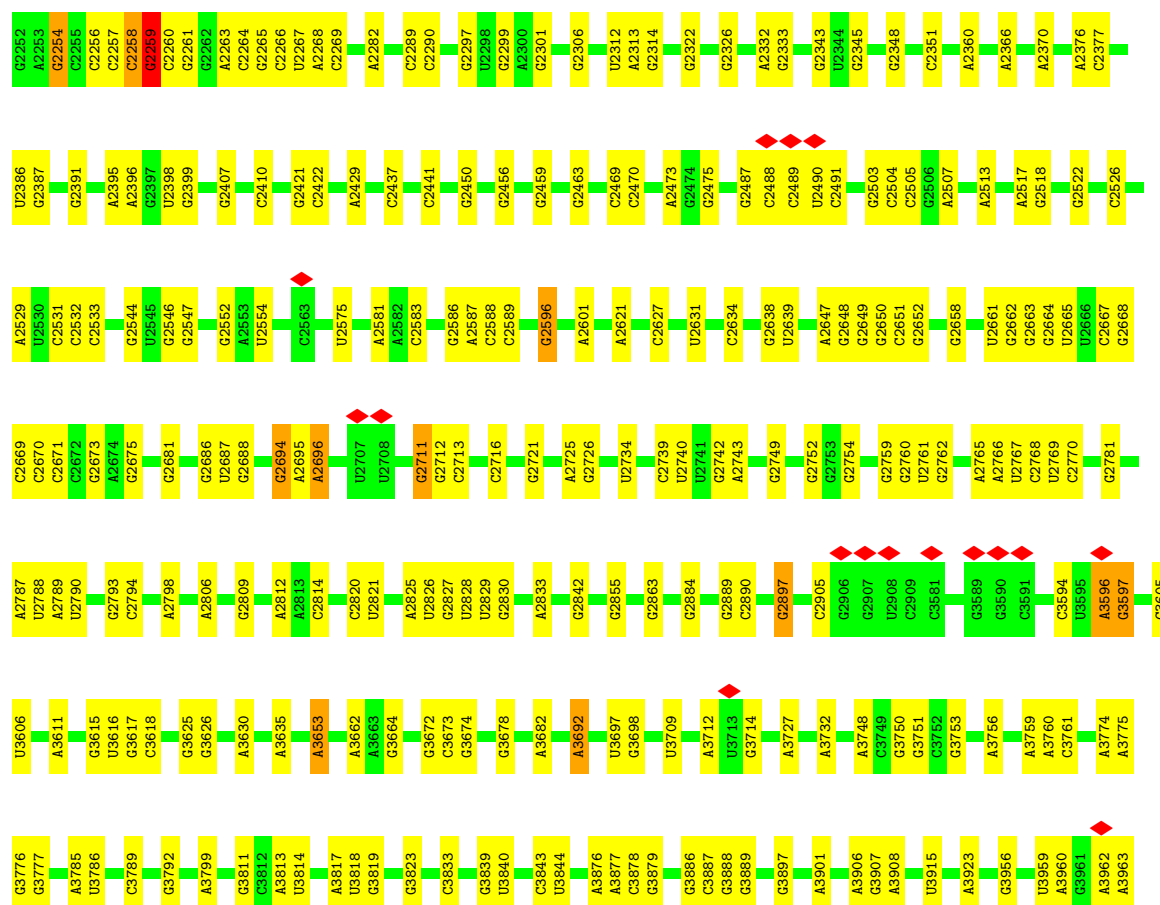
- Molecule 81: 5.8S rRNA (157-MER)

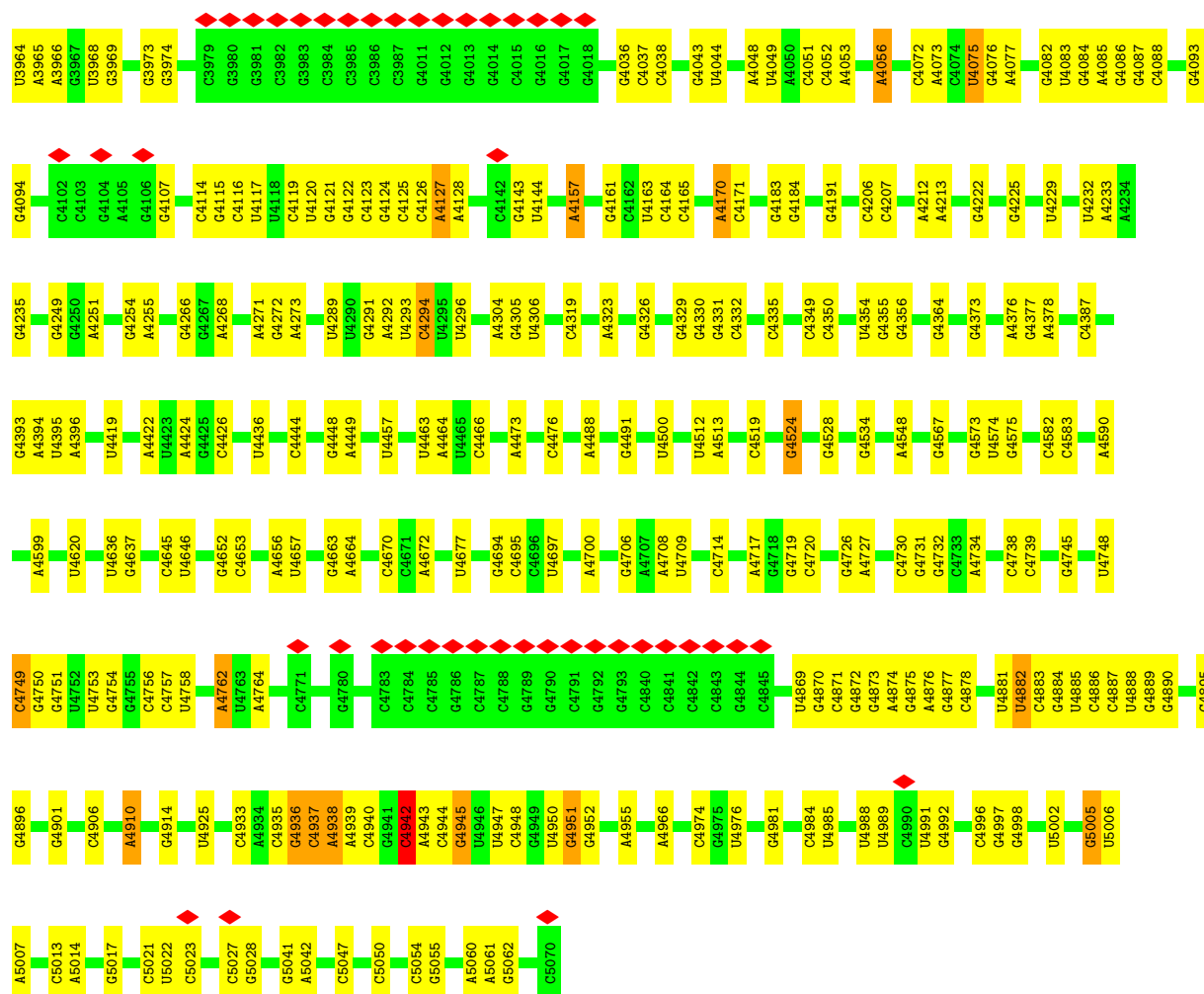
Chain A8:  73% 27%



- Molecule 82: LSU-beta rRNA (2069-MER)

Chain A6:  75% 24%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	295008	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.044	Depositor
Minimum map value	-0.015	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.006	Depositor
Map size (Å)	417.99997, 417.99997, 417.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: DDE

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	tR	0.15	0/1836	0.35	0/2859
2	Ct	0.32	1/6726 (0.0%)	0.64	8/9082 (0.1%)
3	AO	0.25	0/1025	0.58	0/1376
4	AX	0.26	0/1103	0.66	0/1474
5	AN	0.32	0/1226	0.66	0/1649
6	AL	0.30	0/1311	0.63	0/1751
7	AB	0.32	0/1753	0.69	1/2342 (0.0%)
8	AA	0.31	0/1679	0.74	1/2283 (0.0%)
9	AV	0.36	0/631	0.83	0/844
10	AY	0.24	0/1040	0.62	0/1382
11	Aa	0.22	0/836	0.50	0/1121
12	Ab	0.23	0/673	0.59	0/902
13	Ae	0.29	0/458	0.72	0/604
14	AJ	0.28	0/1504	0.63	0/2007
15	AE	0.34	1/2121 (0.0%)	0.62	2/2854 (0.1%)
16	AC	0.28	0/1745	0.62	0/2356
17	AG	0.25	0/1946	0.60	1/2590 (0.0%)
18	AH	0.27	0/1544	0.66	0/2068
19	AW	0.39	1/1051 (0.1%)	0.75	0/1406
20	AI	0.29	0/1715	0.67	2/2287 (0.1%)
21	B2	0.16	0/42094	0.40	9/65553 (0.0%)
22	CW	0.32	0/1030	0.65	0/1364
23	Ag	0.20	0/2493	0.48	0/3394
24	AU	0.37	0/832	0.84	1/1117 (0.1%)
25	AK	0.38	0/851	0.84	2/1147 (0.2%)
26	AM	0.31	0/951	0.70	1/1278 (0.1%)
27	AS	0.27	0/1157	0.66	1/1548 (0.1%)
28	Ad	0.27	0/455	0.59	0/603
29	AR	0.40	0/1031	0.83	2/1383 (0.1%)
30	AP	0.32	0/1055	0.79	3/1406 (0.2%)
31	AT	0.21	0/1119	0.54	0/1499
32	AZ	0.30	0/604	0.52	0/810

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Ac	0.25	0/508	0.55	0/680
34	AD	0.32	0/1793	0.72	2/2414 (0.1%)
35	Af	0.28	0/593	0.67	0/786
36	AF	0.31	0/1514	0.71	2/2034 (0.1%)
37	AQ	0.30	0/1142	0.62	0/1528
38	Cz	0.30	0/1693	0.66	0/2270
39	CO	0.33	0/1666	0.73	2/2228 (0.1%)
40	CL	0.31	0/1713	0.71	1/2293 (0.0%)
41	CV	0.26	0/997	0.67	0/1338
42	CM	0.29	0/1161	0.69	0/1552
43	Ca	0.28	0/1191	0.62	0/1591
44	CN	0.36	0/1746	0.69	0/2338
45	CI	0.30	0/1711	0.71	1/2285 (0.0%)
46	CD	0.26	0/2398	0.65	2/3210 (0.1%)
47	CQ	0.36	1/1545 (0.1%)	0.80	2/2062 (0.1%)
48	CA	0.31	0/1995	0.69	2/2674 (0.1%)
49	CS	0.30	0/1493	0.68	2/2003 (0.1%)
50	CT	0.32	0/1326	0.73	1/1770 (0.1%)
51	CP	0.28	0/1259	0.65	0/1689
52	CU	0.26	0/914	0.62	0/1226
53	CX	0.33	0/1011	0.71	0/1356
54	CY	0.30	0/1124	0.64	0/1494
55	CZ	0.22	0/1130	0.50	0/1507
56	Cr	0.65	0/1120	1.31	8/1497 (0.5%)
57	Ch	0.40	0/1031	0.76	0/1361
58	Cb	0.27	0/605	0.64	0/798
59	CB	0.28	0/3257	0.64	2/4359 (0.0%)
60	CF	0.32	0/1945	0.68	0/2589
61	Cc	0.30	0/787	0.68	0/1057
62	Cd	0.34	0/946	0.71	1/1272 (0.1%)
63	Ce	0.42	0/1088	0.73	0/1451
64	Cf	0.61	0/895	1.10	4/1198 (0.3%)
65	Cg	0.26	0/916	0.63	0/1220
66	Ci	0.31	0/851	0.75	0/1125
67	Cj	0.25	0/741	0.57	0/980
68	Ck	0.26	0/565	0.58	0/750
69	Cl	0.26	0/445	0.59	0/588
70	CC	0.52	0/2962	0.96	3/3977 (0.1%)
71	Cm	0.26	0/417	0.58	0/553
72	Cn	0.31	0/231	0.75	0/294
73	Cp	0.23	0/703	0.62	0/934
74	Co	0.37	0/864	0.77	1/1140 (0.1%)
75	CJ	0.26	0/1372	0.60	0/1836

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	CH	0.26	0/1545	0.58	0/2077
77	CE	0.60	0/2088	1.20	5/2792 (0.2%)
78	CG	0.28	0/2006	0.65	0/2697
79	A5	0.40	5/40404 (0.0%)	0.46	13/62957 (0.0%)
80	A7	0.16	0/2880	0.37	0/4489
81	A8	0.17	0/3723	0.41	0/5800
82	A6	0.40	1/48600 (0.0%)	0.40	4/75715 (0.0%)
83	CR	0.46	0/1596	1.06	7/2109 (0.3%)
All	All	0.33	10/241801 (0.0%)	0.55	99/354282 (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
3	AO	0	1
4	AX	0	2
8	AA	0	2
15	AE	0	1
16	AC	0	1
18	AH	0	3
22	CW	0	1
23	Ag	0	1
24	AU	0	2
25	AK	0	2
27	AS	0	1
29	AR	0	3
30	AP	0	3
34	AD	0	1
37	AQ	0	1
39	CO	0	3
42	CM	0	1
43	Ca	0	1
44	CN	0	1
47	CQ	0	1
48	CA	0	1
53	CX	0	1
56	Cr	0	9
64	Cf	0	2
67	Cj	0	1
70	CC	0	3

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
73	Cp	0	1
75	CJ	0	1
76	CH	0	2
77	CE	0	12
All	All	0	65

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	A6	2259	G	O5'-C5'	79.44	3.02	1.43
79	A5	2090	U	O4'-C1'	37.83	2.17	1.41
79	A5	2090	U	C4'-O4'	36.26	2.17	1.45
79	A5	2090	U	C2'-C1'	28.51	2.10	1.53
79	A5	2090	U	C3'-C2'	27.69	2.08	1.53
79	A5	2090	U	C4'-C3'	25.14	2.02	1.52
2	Ct	376	PRO	CA-C	-10.94	1.45	1.51
15	AE	149	TYR	C-O	9.12	1.28	1.23
19	AW	85	ASP	CG-OD2	5.43	1.35	1.25
47	CQ	59	PRO	CA-C	5.23	1.55	1.52

All (99) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	A5	1702	C	O5'-C5'-C4'	-18.76	82.66	110.80
21	B2	246	C	O5'-C5'-C4'	-18.66	82.82	110.80
82	A6	2259	G	P-O5'-C5'	12.48	158.33	120.90
82	A6	2259	G	O5'-C5'-C4'	10.25	131.00	110.50
2	Ct	837	GLU	CA-CB-CG	9.83	133.75	114.10
36	AF	36	GLN	CA-C-N	8.38	137.55	121.54
36	AF	36	GLN	C-N-CA	8.38	137.55	121.54
46	CD	89	LYS	CD-CE-NZ	8.33	138.56	111.90
24	AU	82	MET	CA-CB-CG	8.14	130.38	114.10
34	AD	196	GLY	N-CA-C	8.11	132.39	113.18
2	Ct	376	PRO	O-C-N	-8.06	117.60	121.31
26	AM	58	GLU	CA-CB-CG	7.99	130.08	114.10
79	A5	2090	U	N1-C1'-C2'	7.78	135.75	112.40
29	AR	100	PRO	CA-C-N	7.65	136.16	121.54
29	AR	100	PRO	C-N-CA	7.65	136.16	121.54
82	A6	4942	C	N1-C1'-C2'	6.99	124.49	114.00
21	B2	1418	C	N1-C1'-C2'	6.94	124.41	114.00
70	CC	305	PRO	CA-C-N	6.88	134.67	121.54
70	CC	305	PRO	C-N-CA	6.88	134.67	121.54

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	Cr	108	MET	N-CA-CB	6.73	120.12	110.16
15	AE	250	GLU	CA-CB-CG	6.67	127.44	114.10
8	AA	189	ILE	N-CA-C	-6.57	106.43	111.62
39	CO	118	MET	CA-CB-CG	6.51	127.11	114.10
83	CR	71	ARG	CB-CG-CD	-6.47	96.41	111.30
79	A5	969	C	C2'-C3'-O3'	6.42	123.33	113.70
64	Cf	31	GLU	CA-CB-CG	6.38	126.85	114.10
70	CC	268	ARG	CA-CB-CG	6.29	126.68	114.10
83	CR	135	LYS	CB-CG-CD	-6.24	96.94	111.30
21	B2	1155	U	N1-C1'-C2'	6.23	123.35	114.00
79	A5	2090	U	C3'-C2'-O2'	6.22	128.47	109.80
2	Ct	837	GLU	CB-CG-CD	6.21	123.15	112.60
27	AS	118	ARG	CA-CB-CG	6.15	126.40	114.10
56	Cr	8	MET	CA-CB-CG	6.10	126.30	114.10
21	B2	1155	U	O4'-C1'-N1	6.09	117.33	108.20
77	CE	114	ARG	CA-CB-CG	6.02	126.14	114.10
79	A5	966	A	C3'-C2'-O2'	5.96	123.55	114.60
39	CO	178	ARG	CB-CG-CD	5.94	124.95	111.30
21	B2	1507	G	O4'-C1'-N9	5.91	117.07	108.20
77	CE	42	PRO	N-CA-C	5.90	124.63	112.47
74	Co	97	LYS	CB-CG-CD	5.90	124.86	111.30
2	Ct	454	MET	CB-CG-SD	5.82	130.17	112.70
56	Cr	103	ARG	CG-CD-NE	5.82	124.81	112.00
7	AB	172	MET	CA-CB-CG	5.76	125.63	114.10
79	A5	1409	C	C3'-C2'-O2'	5.76	123.25	114.60
79	A5	1974	U	C5'-C4'-C3'	5.73	123.80	115.20
79	A5	969	C	C4'-C3'-O3'	5.69	121.53	113.00
21	B2	798	G	C5'-C4'-C3'	5.69	123.73	115.20
79	A5	1422	G	C5'-C4'-C3'	5.68	124.52	116.00
30	AP	111	MET	CA-CB-CG	5.66	125.41	114.10
21	B2	1507	G	N9-C1'-C2'	5.65	122.48	114.00
25	AK	1	MET	CA-C-N	5.65	131.87	121.70
25	AK	1	MET	C-N-CA	5.65	131.87	121.70
47	CQ	154	LYS	CA-C-N	5.65	131.87	121.70
47	CQ	154	LYS	C-N-CA	5.65	131.87	121.70
49	CS	147	ASP	CA-C-N	5.65	131.86	121.70
49	CS	147	ASP	C-N-CA	5.65	131.86	121.70
83	CR	71	ARG	CG-CD-NE	-5.60	99.68	112.00
79	A5	966	A	C1'-C2'-O2'	5.58	120.17	111.80
79	A5	1470	G	C5'-C4'-C3'	5.56	124.34	116.00
45	CI	175	LYS	CA-CB-CG	5.56	125.22	114.10
59	CB	389	MET	CB-CG-SD	5.55	129.35	112.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	Cr	108	MET	CA-CB-CG	-5.51	103.07	114.10
50	CT	52	MET	CB-CG-SD	5.50	129.19	112.70
56	Cr	113	ARG	CG-CD-NE	5.50	124.10	112.00
2	Ct	453	MET	CB-CG-SD	5.49	129.17	112.70
83	CR	31	GLU	CA-CB-CG	5.46	125.03	114.10
56	Cr	42	GLY	N-CA-C	-5.45	105.56	112.54
83	CR	96	MET	CA-C-N	5.44	127.51	120.44
83	CR	96	MET	C-N-CA	5.44	127.51	120.44
20	AI	144	LYS	CA-C-N	5.42	131.72	121.97
20	AI	144	LYS	C-N-CA	5.42	131.72	121.97
21	B2	1418	C	O4'-C1'-N1	5.41	116.31	108.20
48	CA	254	GLU	CA-C-N	5.41	131.43	121.70
48	CA	254	GLU	C-N-CA	5.41	131.43	121.70
56	Cr	108	MET	CB-CA-C	-5.39	101.68	110.85
79	A5	1409	C	C1'-C2'-O2'	5.39	119.89	111.80
21	B2	798	G	C5'-C4'-O4'	5.39	117.19	109.10
34	AD	223	ILE	CA-CB-CG1	5.38	119.55	110.40
79	A5	1470	G	C5'-C4'-O4'	5.33	117.79	109.80
2	Ct	615	GLU	CA-CB-CG	5.29	124.69	114.10
82	A6	4942	C	O4'-C1'-N1	5.29	116.14	108.20
40	CL	69	LYS	CB-CG-CD	5.29	123.46	111.30
64	Cf	104	MET	CB-CG-SD	5.26	128.48	112.70
77	CE	112	MET	CA-CB-CG	5.22	124.55	114.10
77	CE	264	ILE	N-CA-C	-5.21	104.18	109.02
15	AE	250	GLU	CB-CG-CD	5.21	121.45	112.60
2	Ct	741	MET	CB-CG-SD	5.17	128.19	112.70
56	Cr	64	ILE	CA-CB-CG1	5.16	119.17	110.40
64	Cf	56	ASN	CA-C-N	5.15	131.37	121.54
64	Cf	56	ASN	C-N-CA	5.15	131.37	121.54
17	AG	217	MET	CB-CG-SD	5.15	128.14	112.70
2	Ct	395	MET	CB-CG-SD	5.10	128.01	112.70
30	AP	70	MET	CA-C-N	5.07	131.22	121.54
30	AP	70	MET	C-N-CA	5.07	131.22	121.54
77	CE	42	PRO	CA-N-CD	-5.05	104.93	112.00
83	CR	76	MET	CB-CG-SD	5.04	127.81	112.70
59	CB	382	MET	CB-CG-SD	5.03	127.80	112.70
46	CD	235	MET	CA-CB-CG	5.02	124.14	114.10
62	Cd	19	GLU	CB-CG-CD	5.02	121.14	112.60

There are no chirality outliers.

All (65) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	AA	185	MET	Peptide
8	AA	31	ASP	Peptide
16	AC	167	ARG	Sidechain
34	AD	6	SER	Peptide
15	AE	172	PHE	Peptide
18	AH	107	LYS	Peptide
18	AH	15	LYS	Peptide
18	AH	17	ASP	Peptide
25	AK	1	MET	Peptide
25	AK	29	MET	Peptide
3	AO	137	SER	Peptide
30	AP	36	LEU	Peptide
30	AP	50	ARG	Peptide
30	AP	69	PRO	Peptide
37	AQ	43	GLU	Peptide
29	AR	101	ASP	Peptide
29	AR	78	ARG	Sidechain
29	AR	81	ARG	Sidechain
27	AS	118	ARG	Sidechain
24	AU	50	VAL	Peptide
24	AU	81	GLN	Peptide
4	AX	8	ARG	Sidechain
4	AX	98	ASP	Peptide
23	Ag	99	ARG	Sidechain
48	CA	198	ARG	Sidechain
70	CC	213	GLU	Peptide
70	CC	291	ARG	Sidechain
70	CC	342	ARG	Sidechain
77	CE	101	ASN	Peptide
77	CE	123	ARG	Sidechain
77	CE	286	LEU	Peptide
77	CE	36	LYS	Peptide
77	CE	42	PRO	Peptide
77	CE	51	VAL	Peptide
77	CE	52	ARG	Sidechain
77	CE	75	ALA	Peptide
77	CE	78	SER	Peptide
77	CE	83	LYS	Peptide
77	CE	92	VAL	Peptide
77	CE	98	GLY	Peptide
76	CH	109	GLY	Peptide
76	CH	52	LYS	Peptide
75	CJ	154	LYS	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
42	CM	68	ALA	Peptide
44	CN	178	HIS	Peptide
39	CO	110	PRO	Peptide
39	CO	117	ARG	Peptide
39	CO	178	ARG	Sidechain
47	CQ	122	THR	Peptide
22	CW	19	ARG	Sidechain
53	CX	55	ARG	Sidechain
43	Ca	21	ARG	Sidechain
64	Cf	109	ARG	Peptide
64	Cf	61	GLY	Peptide
67	Cj	10	LYS	Peptide
73	Cp	11	VAL	Peptide
56	Cr	103	ARG	Sidechain
56	Cr	112	ARG	Sidechain
56	Cr	119	ARG	Sidechain,Peptide
56	Cr	43	LEU	Peptide
56	Cr	53	PRO	Peptide
56	Cr	55	ALA	Peptide
56	Cr	57	GLY	Peptide
56	Cr	75	THR	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	tR	1644	833	837	1	0
2	Ct	6619	6696	6701	64	0
3	AO	1012	1028	1028	17	0
4	AX	1085	1150	1151	12	0
5	AN	1202	1289	1289	11	0
6	AL	1288	1359	1362	13	0
7	AB	1727	1805	1810	18	0
8	AA	1642	1642	1646	30	0
9	AV	625	625	628	12	0
10	AY	1023	1088	1090	14	0
11	Aa	821	874	872	5	0
12	Ab	659	680	683	3	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	Ae	452	494	498	1	0
14	AJ	1480	1583	1592	13	0
15	AE	2079	2186	2186	29	0
16	AC	1709	1787	1793	24	0
17	AG	1923	2085	2089	18	0
18	AH	1521	1613	1616	22	0
19	AW	1034	1079	1080	10	0
20	AI	1686	1770	1772	13	0
21	B2	37676	18952	18977	60	0
22	CW	1015	1070	1079	4	0
23	Ag	2436	2388	2393	26	0
24	AU	822	886	887	18	0
25	AK	827	853	854	14	0
26	AM	941	962	963	20	0
27	AS	1139	1187	1191	11	0
28	Ad	445	442	442	4	0
29	AR	1019	1070	1075	17	0
30	AP	1037	1098	1098	5	0
31	AT	1101	1135	1135	13	0
32	AZ	598	652	656	11	0
33	Ac	506	536	536	10	0
34	AD	1765	1855	1865	34	0
35	Af	581	598	599	2	0
36	AF	1493	1545	1547	25	0
37	AQ	1124	1193	1193	10	0
38	Cz	1665	1769	1770	25	0
39	CO	1634	1776	1779	25	0
40	CL	1682	1789	1792	17	0
41	CV	983	1039	1042	14	0
42	CM	1139	1209	1209	18	0
43	Ca	1162	1210	1213	21	0
44	CN	1701	1747	1749	19	0
45	CI	1672	1711	1713	16	0
46	CD	2353	2370	2372	18	0
47	CQ	1521	1640	1640	29	0
48	CA	1957	2052	2055	19	0
49	CS	1453	1485	1490	14	0
50	CT	1298	1363	1366	12	0
51	CP	1233	1260	1263	12	0
52	CU	900	904	905	4	0
53	CX	994	1078	1079	14	0
54	CY	1107	1193	1193	9	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	CZ	1107	1182	1182	6	0
56	Cr	1104	1184	1189	53	0
57	Ch	1023	1159	1160	23	0
58	Cb	595	630	630	0	0
59	CB	3189	3316	3327	29	0
60	CF	1910	2046	2048	18	0
61	Cc	776	812	812	18	0
62	Cd	931	979	980	6	0
63	Ce	1070	1165	1165	11	0
64	Cf	876	910	912	25	0
65	Cg	906	999	999	9	0
66	Ci	840	925	929	5	0
67	Cj	726	764	764	2	0
68	Ck	559	624	624	2	0
69	Cl	435	472	472	2	0
70	CC	2908	3074	3082	74	0
71	Cm	411	446	445	3	0
72	Cn	230	274	276	3	0
73	Cp	693	747	747	3	0
74	Co	851	921	922	7	0
75	CJ	1349	1382	1383	11	0
76	CH	1526	1603	1605	21	0
77	CE	2050	2240	2244	90	0
78	CG	1973	2123	2128	23	0
79	A5	36163	18197	18215	86	0
80	A7	2578	1306	1306	3	0
81	A8	3334	1693	1693	3	0
82	A6	43496	21793	21810	107	0
83	CR	1580	0	1746	254	0
All	All	225399	166649	168638	1524	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (1524) 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)
79:A5:2090:U:C4'	79:A5:2090:U:C3'	2.02	1.34
79:A5:2090:U:C3'	79:A5:2090:U:C2'	2.08	1.30
79:A5:2090:U:C2'	79:A5:2090:U:C1'	2.10	1.28
83:CR:78:ILE:HA	83:CR:81:ARG:HD2	1.40	1.02

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:CR:24:LEU:HD12	83:CR:32:ILE:HG21	1.43	1.00
79:A5:65:A:N6	79:A5:75:G:N3	2.08	0.99
83:CR:123:LEU:HA	83:CR:126:LYS:HG3	1.44	0.96
59:CB:76:VAL:HG22	59:CB:332:MET:HE2	1.48	0.94
79:A5:2090:U:C1'	79:A5:2090:U:O4'	2.17	0.93
83:CR:90:PRO:HB2	83:CR:93:VAL:HG12	1.47	0.93
79:A5:2090:U:O4'	82:A6:2259:G:O5'	1.87	0.93
38:Cz:67:VAL:HG23	38:Cz:82:ILE:HD13	1.49	0.93
83:CR:103:ARG:HB3	83:CR:107:ARG:HH12	1.32	0.92
79:A5:2090:U:C4'	82:A6:2259:G:O5'	2.18	0.92
79:A5:2090:U:C4'	79:A5:2090:U:O4'	2.17	0.92
31:AT:70:ALA:HB1	31:AT:75:MET:HE1	1.53	0.89
83:CR:182:GLU:HA	83:CR:185:ILE:HD12	1.54	0.89
77:CE:153:LEU:HD11	77:CE:195:ILE:HD13	1.55	0.89
79:A5:2090:U:C1'	82:A6:2259:G:O5'	2.21	0.89
83:CR:89:MET:HE2	83:CR:89:MET:HA	1.55	0.88
83:CR:173:ARG:HA	83:CR:176:ARG:HD2	1.53	0.87
83:CR:93:VAL:HA	83:CR:96:MET:HB2	1.55	0.86
56:Cr:43:LEU:HD22	70:CC:135:ALA:HB1	1.56	0.86
83:CR:45:ILE:HB	83:CR:50:ILE:HD11	1.55	0.85
36:AF:103:LEU:HD23	36:AF:178:ILE:HD13	1.57	0.85
79:A5:2090:U:C1'	82:A6:2259:G:C5'	2.55	0.85
42:CM:27:ILE:HD13	42:CM:36:ALA:HB1	1.59	0.84
83:CR:181:LYS:HA	83:CR:184:ILE:HD12	1.60	0.84
18:AH:66:VAL:HG22	18:AH:96:ALA:HB1	1.60	0.84
54:CY:55:VAL:HG21	54:CY:70:VAL:HG23	1.59	0.84
79:A5:2090:U:O4'	82:A6:2259:G:C5'	2.26	0.83
83:CR:170:ARG:HH21	83:CR:173:ARG:HG3	1.44	0.83
16:AC:63:VAL:HG23	16:AC:64:THR:HG23	1.59	0.83
83:CR:177:LEU:HA	83:CR:180:LYS:HD3	1.62	0.81
70:CC:209:ILE:HD11	70:CC:227:ILE:HG22	1.61	0.81
83:CR:10:LEU:HB3	83:CR:41:ILE:HD12	1.63	0.80
79:A5:2090:U:C2'	82:A6:2259:G:O5'	2.30	0.80
61:Cc:48:LEU:HD21	61:Cc:60:ILE:HG21	1.63	0.79
49:CS:34:ALA:HB1	49:CS:39:VAL:HG23	1.65	0.79
79:A5:2090:U:C3'	82:A6:2259:G:O5'	2.31	0.78
77:CE:91:THR:HG21	77:CE:106:VAL:HG22	1.66	0.78
79:A5:2090:U:C4'	82:A6:2259:G:C5'	2.61	0.78
83:CR:8:LYS:HE2	83:CR:22:VAL:HG23	1.65	0.78
83:CR:104:ARG:O	83:CR:108:ARG:HG2	1.84	0.77
9:AV:42:VAL:HG12	9:AV:43:THR:HG22	1.66	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:Ch:31:LEU:HD21	57:Ch:47:ILE:HG22	1.65	0.77
16:AC:209:VAL:HG21	16:AC:233:LEU:HD21	1.64	0.77
51:CP:36:ILE:HD11	51:CP:44:ALA:HB1	1.65	0.76
21:B2:366:U:O2	21:B2:394:G:O6	2.03	0.76
83:CR:70:ARG:HE	83:CR:75:HIS:HB2	1.50	0.76
83:CR:24:LEU:CB	83:CR:50:ILE:HG22	2.14	0.76
64:Cf:50:VAL:HG12	64:Cf:69:VAL:HG22	1.68	0.75
77:CE:186:LEU:HD21	77:CE:253:VAL:HG21	1.68	0.75
83:CR:3:MET:HE2	83:CR:3:MET:HA	1.68	0.75
26:AM:21:VAL:HG12	26:AM:111:VAL:HG11	1.68	0.75
3:AO:95:ILE:HD11	3:AO:129:ILE:HD12	1.69	0.75
83:CR:120:TYR:CE1	83:CR:124:TYR:HB2	2.22	0.75
83:CR:31:GLU:HA	83:CR:34:ASN:OD1	1.87	0.74
18:AH:133:LEU:HD12	18:AH:134:VAL:HG13	1.70	0.74
43:Ca:75:LEU:HD23	43:Ca:117:LEU:HD21	1.70	0.74
37:AQ:81:ILE:HD12	37:AQ:84:ILE:HD11	1.70	0.73
77:CE:219:LYS:HZ1	79:A5:1291:G:H5''	1.54	0.73
55:CZ:42:LEU:HD11	55:CZ:72:VAL:HG22	1.70	0.73
2:Ct:25:ILE:HD11	2:Ct:127:VAL:HG12	1.69	0.73
79:A5:86:U:O2	79:A5:98:A:N7	2.21	0.73
77:CE:174:LEU:HD11	77:CE:186:LEU:HD12	1.71	0.73
83:CR:167:LYS:O	83:CR:171:LYS:HG3	1.88	0.72
5:AN:92:ILE:HD13	5:AN:122:ILE:HD11	1.72	0.72
63:Ce:89:LEU:HD22	63:Ce:118:LEU:HD21	1.70	0.72
82:A6:3596:A:H5'	83:CR:146:LYS:HD3	1.70	0.72
83:CR:136:ARG:HA	83:CR:139:MET:HE3	1.70	0.72
44:CN:22:LEU:HD11	78:CG:164:ILE:HD11	1.71	0.72
79:A5:2090:U:C3'	82:A6:2259:G:C5'	2.68	0.72
44:CN:176:LYS:HA	44:CN:184:ILE:HD11	1.72	0.72
83:CR:174:GLU:HA	83:CR:177:LEU:HG	1.72	0.72
83:CR:133:LYS:H	83:CR:137:ILE:HG21	1.55	0.71
49:CS:44:PHE:O	49:CS:48:VAL:HG12	1.90	0.71
83:CR:126:LYS:HE2	83:CR:131:VAL:HG11	1.72	0.71
38:Cz:67:VAL:HG13	38:Cz:111:LEU:HD23	1.73	0.71
70:CC:316:LYS:HB2	70:CC:324:ILE:HD11	1.73	0.70
57:Ch:55:ALA:O	57:Ch:59:THR:HG23	1.91	0.70
83:CR:1:MET:HE3	83:CR:2:SER:H	1.57	0.70
83:CR:71:ARG:HE	83:CR:71:ARG:HA	1.56	0.70
10:AY:18:LEU:HD11	15:AE:64:ILE:HD11	1.72	0.70
70:CC:44:LEU:HD21	70:CC:115:VAL:HG22	1.73	0.70
83:CR:24:LEU:HB3	83:CR:50:ILE:HG22	1.73	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:CG:146:LEU:HD12	78:CG:152:ALA:HB2	1.73	0.70
83:CR:178:GLN:HA	83:CR:181:LYS:HD2	1.72	0.70
21:B2:1714:C:H42	21:B2:1819:A:H61	1.39	0.70
77:CE:153:LEU:HD11	77:CE:195:ILE:CD1	2.22	0.69
30:AP:22:LEU:HD23	30:AP:25:LEU:HD12	1.75	0.69
47:CQ:31:LEU:HD11	70:CC:292:ILE:HD12	1.75	0.68
83:CR:50:ILE:HD12	83:CR:50:ILE:O	1.94	0.68
21:B2:185:G:O6	21:B2:214:U:O2	2.11	0.68
9:AV:24:ILE:HG22	9:AV:56:CYS:HB3	1.74	0.67
83:CR:126:LYS:HB3	83:CR:131:VAL:HG11	1.76	0.67
83:CR:105:LEU:HD22	83:CR:138:LEU:HD12	1.76	0.67
83:CR:68:LEU:O	83:CR:71:ARG:HB2	1.94	0.67
45:CI:61:SER:HA	45:CI:126:VAL:HG22	1.77	0.67
83:CR:6:LEU:HD12	83:CR:10:LEU:HD13	1.77	0.67
83:CR:50:ILE:O	83:CR:51:ILE:HD13	1.94	0.67
7:AB:121:ILE:HD11	7:AB:161:VAL:HG22	1.77	0.66
47:CQ:124:ASP:O	47:CQ:128:LEU:HD23	1.95	0.66
83:CR:141:HIS:CE1	83:CR:145:LEU:HD21	2.30	0.66
59:CB:160:ILE:HD11	59:CB:190:VAL:HG13	1.78	0.66
70:CC:124:ILE:HD13	70:CC:237:ILE:HD12	1.77	0.66
26:AM:25:ALA:HB2	26:AM:111:VAL:HG13	1.77	0.66
79:A5:2090:U:C2'	82:A6:2259:G:C5'	2.73	0.66
80:A7:66:G:O6	80:A7:109:U:O2	2.12	0.66
29:AR:19:LYS:HZ2	34:AD:210:ILE:HG22	1.60	0.66
70:CC:147:VAL:HG13	70:CC:152:LEU:HD22	1.76	0.66
19:AW:105:THR:HB	19:AW:126:LEU:HD21	1.78	0.66
40:CL:47:ALA:HB1	40:CL:48:PRO:HD2	1.78	0.65
83:CR:42:ARG:HA	83:CR:45:ILE:HG22	1.77	0.65
83:CR:95:TRP:NE1	83:CR:99:MET:HG2	2.10	0.65
83:CR:184:ILE:HA	83:CR:187:THR:HG23	1.79	0.65
25:AK:40:VAL:HG22	25:AK:45:VAL:HG23	1.79	0.65
52:CU:56:LEU:HD13	52:CU:61:VAL:HG21	1.77	0.65
82:A6:3596:A:H4'	83:CR:146:LYS:HZ3	1.60	0.65
83:CR:116:ASP:OD1	83:CR:119:MET:HG3	1.96	0.65
77:CE:94:LYS:HD3	77:CE:107:VAL:HG23	1.78	0.65
83:CR:23:TRP:CH2	83:CR:25:ASP:HB2	2.32	0.65
83:CR:24:LEU:HB2	83:CR:50:ILE:HG22	1.78	0.65
49:CS:101:THR:HG23	49:CS:104:GLY:H	1.61	0.65
2:Ct:649:ILE:HG13	2:Ct:661:ILE:HD11	1.78	0.65
8:AA:42:LYS:NZ	29:AR:102:THR:HG23	2.12	0.64
83:CR:175:GLU:HA	83:CR:178:GLN:HG3	1.79	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:AM:42:LEU:HD21	26:AM:69:LEU:HD23	1.80	0.64
21:B2:909:G:H5'	83:CR:173:ARG:HB3	1.80	0.64
34:AD:70:THR:HG22	34:AD:86:LEU:HD13	1.79	0.64
19:AW:71:LYS:HD3	21:B2:1155:U:H1'	1.80	0.64
83:CR:78:ILE:HA	83:CR:81:ARG:CD	2.23	0.64
83:CR:93:VAL:HA	83:CR:96:MET:CB	2.27	0.64
82:A6:3692:A:H62	82:A6:3823:G:H21	1.45	0.64
82:A6:2634:C:H5'	83:CR:59:SER:HB2	1.81	0.63
29:AR:19:LYS:NZ	34:AD:210:ILE:HG22	2.13	0.63
38:Cz:65:VAL:HG22	38:Cz:109:ALA:HB3	1.79	0.63
57:Ch:29:SER:O	57:Ch:33:VAL:HG23	1.98	0.63
2:Ct:43:ALA:HB1	2:Ct:77:LEU:HD21	1.80	0.63
82:A6:3596:A:C5'	83:CR:146:LYS:HD3	2.27	0.63
53:CX:82:THR:HG22	57:Ch:36:VAL:HG12	1.79	0.63
79:A5:2090:U:C4'	82:A6:2259:G:H5'	2.28	0.63
43:Ca:80:THR:HG22	47:CQ:90:VAL:HG21	1.81	0.63
53:CX:99:ILE:HG23	53:CX:133:GLU:OE2	1.99	0.63
79:A5:516:G:H22	79:A5:645:G:H22	1.47	0.63
82:A6:4745:G:N2	82:A6:4955:A:H62	1.97	0.63
2:Ct:746:LEU:HD11	2:Ct:785:LYS:HB3	1.80	0.62
61:Cc:37:MET:HE1	61:Cc:95:ALA:HB3	1.80	0.62
83:CR:143:HIS:HA	83:CR:146:LYS:NZ	2.14	0.62
29:AR:28:PHE:HA	29:AR:55:THR:HG21	1.81	0.62
83:CR:96:MET:HE2	83:CR:96:MET:HA	1.81	0.62
56:Cr:89:THR:HG23	77:CE:110:ARG:HE	1.63	0.62
83:CR:32:ILE:HD12	83:CR:44:LEU:HD23	1.80	0.62
47:CQ:50:ARG:HG2	47:CQ:83:VAL:HG11	1.81	0.62
50:CT:61:THR:HG21	79:A5:1799:G:H21	1.63	0.62
77:CE:72:LYS:HA	77:CE:72:LYS:HE2	1.81	0.62
39:CO:54:TYR:CE1	39:CO:145:VAL:HG11	2.35	0.62
83:CR:98:ARG:NH1	83:CR:133:LYS:HA	2.15	0.62
4:AX:54:LYS:HE3	4:AX:70:VAL:HG22	1.80	0.62
60:CF:155:TYR:CE2	70:CC:325:MET:HE1	2.35	0.62
77:CE:87:LYS:HA	77:CE:92:VAL:HG13	1.82	0.62
18:AH:79:LEU:HD13	18:AH:83:LEU:HD23	1.82	0.62
2:Ct:756:VAL:HG23	79:A5:2009:A:H5''	1.80	0.61
13:Ae:44:ASN:O	13:Ae:46:VAL:HG13	1.99	0.61
60:CF:155:TYR:HE2	70:CC:325:MET:HE1	1.63	0.61
53:CX:80:PRO:CD	57:Ch:33:VAL:HG22	2.29	0.61
78:CG:99:ALA:HB1	78:CG:193:LEU:HD11	1.82	0.61
83:CR:8:LYS:HG3	83:CR:22:VAL:HG21	1.82	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AK:15:LEU:HD21	25:AK:49:MET:HE2	1.83	0.61
34:AD:113:LEU:HD12	34:AD:118:ALA:HB2	1.82	0.61
44:CN:193:ARG:O	44:CN:197:THR:HG23	2.00	0.61
70:CC:152:LEU:HD21	70:CC:174:LEU:HB3	1.82	0.61
83:CR:138:LEU:HD13	83:CR:142:ILE:HD13	1.82	0.61
70:CC:40:VAL:HG12	70:CC:115:VAL:HG21	1.81	0.61
77:CE:206:VAL:HG13	77:CE:208:ILE:HD13	1.82	0.61
83:CR:148:ASP:O	83:CR:152:LYS:HG2	2.01	0.61
83:CR:151:ARG:O	83:CR:155:LEU:HG	2.00	0.61
26:AM:42:LEU:HD11	26:AM:69:LEU:HG	1.83	0.61
36:AF:195:GLU:O	36:AF:199:VAL:HG23	2.01	0.61
83:CR:23:TRP:CE3	83:CR:51:ILE:HG12	2.35	0.61
4:AX:51:VAL:HG22	4:AX:70:VAL:HG11	1.81	0.61
8:AA:50:ASN:O	8:AA:54:THR:HG23	2.01	0.61
56:Cr:119:ARG:NH2	77:CE:112:MET:HE2	2.16	0.61
60:CF:54:ALA:HB3	70:CC:331:TYR:CE1	2.36	0.61
3:AO:53:ILE:HD12	3:AO:53:ILE:O	2.01	0.61
59:CB:76:VAL:HG23	59:CB:334:LYS:HA	1.82	0.61
37:AQ:70:VAL:HG11	37:AQ:84:ILE:HG22	1.82	0.61
66:CI:43:MET:HE1	78:CG:169:PHE:CZ	2.36	0.61
82:A6:2526:C:H4'	83:CR:10:LEU:HD21	1.83	0.61
26:AM:79:VAL:HG12	26:AM:80:ASP:H	1.66	0.60
79:A5:1550:G:OP1	83:CR:84:THR:HG21	2.00	0.60
2:Ct:426:LYS:HZ2	2:Ct:444:LEU:HD12	1.65	0.60
21:B2:1286:G:H21	21:B2:1313:A:N6	1.99	0.60
51:CP:41:ILE:HD12	51:CP:112:LEU:HB2	1.84	0.60
56:Cr:43:LEU:HD22	70:CC:135:ALA:CB	2.28	0.60
82:A6:2526:C:H5'	83:CR:37:SER:HA	1.83	0.60
70:CC:209:ILE:HD11	70:CC:229:LEU:HD12	1.84	0.60
78:CG:169:PHE:CE2	78:CG:172:ALA:HB3	2.37	0.60
8:AA:154:LEU:O	8:AA:157:VAL:HG12	2.01	0.60
18:AH:49:LYS:O	18:AH:60:ILE:HD12	2.01	0.60
57:Ch:33:VAL:O	57:Ch:37:THR:HG23	2.01	0.60
77:CE:125:LEU:HD13	79:A5:958:G:N3	2.17	0.60
83:CR:55:VAL:HG22	83:CR:56:THR:O	2.01	0.60
7:AB:121:ILE:HD12	7:AB:161:VAL:HG13	1.84	0.60
38:Cz:34:LEU:HD21	38:Cz:190:LEU:HD11	1.84	0.60
41:CV:105:ILE:HD11	41:CV:113:LYS:HB3	1.84	0.60
9:AV:24:ILE:HG22	9:AV:56:CYS:CB	2.32	0.60
19:AW:30:CYS:HA	19:AW:61:ILE:HD11	1.84	0.60
42:CM:36:ALA:HB2	42:CM:52:PHE:HE1	1.67	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:CC:349:LEU:HD12	70:CC:350:ARG:HH12	1.67	0.60
59:CB:252:ALA:HB3	82:A6:4457:U:O2	2.01	0.59
70:CC:190:ARG:HD2	70:CC:202:ILE:HD11	1.83	0.59
82:A6:4127:A:H62	82:A6:4157:A:H62	1.49	0.59
77:CE:249:ASP:O	77:CE:253:VAL:HG23	2.01	0.59
46:CD:38:ILE:HD12	46:CD:38:ILE:O	2.02	0.59
49:CS:82:LEU:HD23	49:CS:95:ARG:HD3	1.83	0.59
56:Cr:125:MET:HG2	56:Cr:126:VAL:HG23	1.85	0.59
60:CF:222:LYS:HA	60:CF:222:LYS:HE2	1.84	0.59
79:A5:1724:G:N1	79:A5:1838:A:C2	2.70	0.59
54:CY:62:TYR:OH	54:CY:97:VAL:HG21	2.02	0.59
83:CR:113:LYS:N	83:CR:113:LYS:HE2	2.17	0.59
16:AC:179:THR:C	16:AC:219:ILE:HD11	2.27	0.59
16:AC:183:LYS:HD3	16:AC:196:ILE:HG23	1.85	0.59
21:B2:1455:A:H61	21:B2:1471:C:H42	1.50	0.59
40:CL:86:ILE:HG23	40:CL:90:VAL:HG23	1.83	0.59
41:CV:40:ILE:HD11	82:A6:3799:A:C5	2.37	0.59
79:A5:1101:C:H42	79:A5:1195:G:H21	1.51	0.59
27:AS:117:ILE:HD11	30:AP:111:MET:SD	2.43	0.59
32:AZ:110:THR:HG21	36:AF:102:LEU:HD22	1.84	0.59
23:Ag:32:LEU:HD13	23:Ag:92:LEU:HD11	1.84	0.59
46:CD:106:ALA:HB1	46:CD:171:LEU:HD23	1.83	0.59
60:CF:190:LEU:HD21	60:CF:208:LEU:HD21	1.85	0.59
70:CC:218:ILE:HD12	70:CC:229:LEU:HD23	1.85	0.59
15:AE:80:ILE:HG23	15:AE:81:THR:HG23	1.83	0.59
31:AT:87:VAL:HG13	31:AT:88:MET:CE	2.32	0.59
57:Ch:28:LEU:HD23	57:Ch:31:LEU:HD22	1.85	0.59
17:AG:57:ASP:HA	17:AG:106:LEU:HD13	1.85	0.59
21:B2:1172:U:C5'	72:Cn:10:MET:HE1	2.33	0.59
83:CR:120:TYR:O	83:CR:124:TYR:HB3	2.02	0.59
70:CC:209:ILE:HD13	70:CC:221:PHE:CZ	2.38	0.58
82:A6:2725:A:O4'	83:CR:93:VAL:HG21	2.03	0.58
56:Cr:40:TYR:CE2	56:Cr:106:LEU:HD12	2.38	0.58
56:Cr:54:ALA:HA	56:Cr:60:VAL:HG13	1.86	0.58
70:CC:53:ALA:HB1	70:CC:105:THR:O	2.03	0.58
17:AG:141:ILE:HD13	17:AG:153:VAL:HG13	1.85	0.58
34:AD:189:MET:HA	34:AD:189:MET:HE2	1.84	0.58
53:CX:79:PHE:CZ	53:CX:99:ILE:HG21	2.39	0.58
70:CC:124:ILE:HG21	70:CC:264:TYR:OH	2.03	0.58
83:CR:14:VAL:HG11	83:CR:41:ILE:CG2	2.32	0.58
83:CR:77:GLY:O	83:CR:81:ARG:HG3	2.03	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:CR:99:MET:O	83:CR:103:ARG:HG3	2.02	0.58
2:Ct:86:LEU:O	2:Ct:89:ILE:HG22	2.02	0.58
38:Cz:94:ASN:CG	38:Cz:123:ILE:HG23	2.28	0.58
83:CR:10:LEU:O	83:CR:14:VAL:HG12	2.02	0.58
4:AX:100:VAL:HG23	4:AX:122:VAL:HG23	1.85	0.58
7:AB:167:LYS:HE2	7:AB:204:ILE:HD13	1.86	0.58
59:CB:252:ALA:HB1	82:A6:4524:G:N3	2.18	0.58
59:CB:282:LYS:HB2	59:CB:333:LEU:HD21	1.85	0.58
64:Cf:109:ARG:HH21	79:A5:951:G:H2'	1.69	0.58
40:CL:58:ILE:HG22	40:CL:157:VAL:HG13	1.86	0.58
2:Ct:183:GLU:O	2:Ct:187:VAL:HG23	2.04	0.58
79:A5:86:U:C2	79:A5:98:A:N7	2.72	0.58
83:CR:32:ILE:HA	83:CR:44:LEU:HD21	1.86	0.58
76:CH:65:LYS:O	76:CH:69:THR:HG23	2.01	0.58
83:CR:106:LEU:HD23	83:CR:120:TYR:CD1	2.39	0.58
53:CX:78:LYS:HB2	53:CX:99:ILE:HG22	1.86	0.58
2:Ct:665:ILE:HD11	2:Ct:703:ASP:HB3	1.85	0.57
39:CO:54:TYR:CD2	39:CO:141:LEU:HD11	2.39	0.57
40:CL:87:HIS:HB3	40:CL:90:VAL:HG22	1.85	0.57
59:CB:252:ALA:HB1	82:A6:4524:G:C2	2.39	0.57
82:A6:2725:A:N7	83:CR:89:MET:HE1	2.19	0.57
20:AI:103:LEU:HD22	20:AI:170:LYS:HB2	1.86	0.57
36:AF:124:ASP:OD1	36:AF:141:VAL:HG11	2.04	0.57
75:CJ:53:ALA:HB2	75:CJ:68:ILE:HD11	1.86	0.57
59:CB:154:LYS:HZ1	59:CB:190:VAL:HG12	1.69	0.57
74:Co:97:LYS:HE3	74:Co:97:LYS:HA	1.86	0.57
23:Ag:150:TRP:HH2	29:AR:34:VAL:HG22	1.68	0.57
24:AU:29:VAL:HG22	24:AU:85:HIS:CD2	2.39	0.57
23:Ag:240:CYS:O	23:Ag:248:LEU:HD12	2.05	0.57
56:Cr:113:ARG:HD2	63:Ce:90:MET:HE2	1.87	0.57
83:CR:136:ARG:O	83:CR:140:GLU:HG3	2.02	0.57
79:A5:86:U:N3	79:A5:98:A:C8	2.73	0.57
36:AF:35:LEU:HD21	36:AF:146:ARG:CZ	2.35	0.57
83:CR:14:VAL:HG11	83:CR:41:ILE:HG21	1.87	0.57
24:AU:84:ILE:HD11	34:AD:11:PHE:CZ	2.40	0.57
52:CU:18:VAL:HG22	52:CU:75:GLU:OE2	2.05	0.57
78:CG:58:PRO:CG	78:CG:61:ILE:HD12	2.35	0.57
79:A5:1558:A:H5'	83:CR:125:LEU:HD22	1.87	0.57
16:AC:138:GLY:HA3	16:AC:162:ILE:HD13	1.85	0.57
39:CO:7:LEU:HD11	39:CO:33:VAL:HG12	1.86	0.57
49:CS:160:ARG:HH22	79:A5:1920:C:H3'	1.70	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Ct:561:LEU:O	2:Ct:566:ALA:HB3	2.05	0.56
16:AC:81:ILE:HG13	16:AC:86:LEU:HD12	1.87	0.56
24:AU:20:ILE:HD11	24:AU:114:VAL:CG1	2.35	0.56
39:CO:156:LEU:HD13	82:A6:4910:A:C6	2.40	0.56
48:CA:137:ILE:HD11	48:CA:149:LYS:HB3	1.85	0.56
56:Cr:6:GLN:CB	56:Cr:43:LEU:HD13	2.34	0.56
56:Cr:51:VAL:HB	56:Cr:113:ARG:HB2	1.87	0.56
73:Cp:11:VAL:HG11	73:Cp:23:ARG:O	2.05	0.56
76:CH:38:PHE:CE2	76:CH:73:ILE:HG23	2.40	0.56
82:A6:2312:U:O2	82:A6:2326:G:O6	2.22	0.56
3:AO:131:ASP:OD1	3:AO:133:THR:HG23	2.05	0.56
16:AC:106:VAL:HG21	16:AC:109:ILE:HD11	1.86	0.56
44:CN:143:ARG:NE	57:Ch:95:LEU:HD12	2.20	0.56
59:CB:76:VAL:HG22	59:CB:332:MET:CE	2.29	0.56
2:Ct:404:THR:HG23	2:Ct:406:ASP:H	1.70	0.56
24:AU:24:LEU:HD23	24:AU:112:VAL:HG22	1.88	0.56
43:Ca:80:THR:CG2	47:CQ:90:VAL:HG21	2.34	0.56
77:CE:239:LYS:O	77:CE:242:ILE:HG22	2.05	0.56
83:CR:107:ARG:O	83:CR:111:GLU:HG3	2.06	0.56
2:Ct:155:LEU:HD12	2:Ct:212:VAL:HG23	1.87	0.56
29:AR:30:THR:O	29:AR:34:VAL:HG23	2.06	0.56
40:CL:105:LYS:HE2	79:A5:73:A:H5''	1.87	0.56
45:CI:91:LEU:HD11	45:CI:127:ALA:CB	2.36	0.56
76:CH:48:LEU:HD21	76:CH:56:ARG:HB2	1.87	0.56
82:A6:2387:G:OP1	83:CR:24:LEU:HD23	2.05	0.56
82:A6:2725:A:H1'	83:CR:93:VAL:HG11	1.88	0.56
20:AI:103:LEU:HD22	20:AI:170:LYS:CB	2.35	0.56
64:Cf:9:ALA:HB3	64:Cf:101:ILE:O	2.06	0.56
70:CC:167:ALA:HB1	70:CC:221:PHE:HB3	1.88	0.56
41:CV:39:ILE:HG12	41:CV:61:VAL:HG11	1.87	0.56
41:CV:126:ALA:HB1	41:CV:133:ALA:HB2	1.86	0.56
62:Cd:77:ILE:HD11	82:A6:2370:A:C6	2.41	0.56
64:Cf:95:LYS:HZ1	79:A5:1308:C:H4'	1.71	0.56
77:CE:168:LEU:HD11	77:CE:214:ASP:N	2.20	0.56
82:A6:4745:G:H21	82:A6:4955:A:H62	1.53	0.56
83:CR:78:ILE:HD12	83:CR:79:GLY:N	2.20	0.56
17:AG:3:LEU:HD13	17:AG:109:LEU:HD23	1.87	0.56
56:Cr:103:ARG:HD3	56:Cr:103:ARG:N	2.20	0.56
63:Ce:70:LEU:HD23	63:Ce:74:PHE:O	2.06	0.56
64:Cf:33:VAL:HA	77:CE:284:HIS:HE1	1.71	0.56
66:CI:43:MET:HE1	78:CG:169:PHE:CE2	2.41	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:CC:180:ILE:CG2	70:CC:227:ILE:HD11	2.34	0.56
70:CC:349:LEU:HD12	70:CC:350:ARG:NH1	2.21	0.56
24:AU:50:VAL:HG13	24:AU:51:LYS:H	1.71	0.56
82:A6:2526:C:OP2	83:CR:38:ARG:HG2	2.04	0.56
82:A6:2897:G:H5'	83:CR:101:ILE:HD12	1.88	0.56
17:AG:1:MET:SD	17:AG:109:LEU:HD21	2.45	0.56
77:CE:247:LYS:HA	77:CE:247:LYS:HE3	1.88	0.56
77:CE:261:ILE:HA	77:CE:267:LEU:HD23	1.88	0.56
83:CR:63:CYS:O	83:CR:67:THR:HG22	2.06	0.56
29:AR:5:ARG:HG2	29:AR:9:VAL:HG11	1.88	0.55
34:AD:138:VAL:HG13	34:AD:182:LEU:HD11	1.88	0.55
39:CO:64:THR:HG21	59:CB:261:ARG:HG3	1.88	0.55
48:CA:209:HIS:CE1	48:CA:235:VAL:HG11	2.41	0.55
83:CR:172:ARG:HA	83:CR:175:GLU:OE2	2.06	0.55
32:AZ:62:VAL:HG11	32:AZ:91:LEU:HD12	1.88	0.55
64:Cf:15:LYS:HA	64:Cf:27:LEU:HD11	1.88	0.55
2:Ct:339:VAL:HG13	2:Ct:340:MET:SD	2.46	0.55
45:CI:75:TYR:CE2	45:CI:151:ALA:HB2	2.42	0.55
77:CE:152:ILE:HD12	77:CE:153:LEU:H	1.71	0.55
82:A6:2667:C:C1'	83:CR:96:MET:HE1	2.36	0.55
83:CR:137:ILE:HD12	83:CR:140:GLU:OE1	2.06	0.55
6:AL:80:MET:HE1	6:AL:122:ILE:HD13	1.87	0.55
14:AJ:56:ALA:O	14:AJ:60:LEU:HD23	2.06	0.55
44:CN:103:GLU:HA	44:CN:132:VAL:HG21	1.87	0.55
82:A6:2863:G:O2'	83:CR:82:LYS:HG3	2.05	0.55
83:CR:132:PHE:CD1	83:CR:138:LEU:HA	2.42	0.55
36:AF:51:HIS:HB2	36:AF:90:VAL:HG21	1.89	0.55
83:CR:1:MET:HE3	83:CR:2:SER:N	2.21	0.55
83:CR:28:GLU:O	83:CR:32:ILE:HG12	2.07	0.55
8:AA:136:GLU:O	8:AA:140:VAL:HG22	2.06	0.55
36:AF:38:TYR:HA	36:AF:64:ALA:HB1	1.88	0.55
37:AQ:42:ILE:HD13	37:AQ:51:LEU:HD21	1.89	0.55
47:CQ:50:ARG:CG	47:CQ:83:VAL:HG11	2.36	0.55
47:CQ:70:MET:HE1	47:CQ:75:ARG:O	2.07	0.55
77:CE:207:LYS:N	77:CE:208:ILE:HD12	2.22	0.55
77:CE:264:ILE:HG21	77:CE:267:LEU:HD22	1.88	0.55
34:AD:66:ILE:O	34:AD:70:THR:HG23	2.06	0.55
43:Ca:110:LYS:HG3	43:Ca:112:LEU:HD12	1.87	0.55
46:CD:83:LEU:HD21	46:CD:100:CYS:HB2	1.89	0.55
83:CR:69:ALA:HB1	83:CR:74:ARG:HB2	1.89	0.55
19:AW:6:VAL:HG23	19:AW:34:ILE:HD11	1.88	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:B2:1050:A:H62	21:B2:1068:G:H21	1.55	0.55
26:AM:69:LEU:HD13	26:AM:76:LEU:HD13	1.88	0.55
83:CR:121:HIS:O	83:CR:125:LEU:HB2	2.07	0.55
3:AO:99:ALA:H	3:AO:133:THR:HG22	1.71	0.55
6:AL:80:MET:HE1	6:AL:122:ILE:CD1	2.37	0.55
56:Cr:90:LEU:HD11	77:CE:112:MET:CA	2.37	0.55
5:AN:48:SER:O	5:AN:52:VAL:HG23	2.07	0.55
8:AA:42:LYS:HZ3	29:AR:102:THR:HG23	1.71	0.55
8:AA:198:MET:HE3	29:AR:88:VAL:HG22	1.87	0.55
56:Cr:93:ILE:HD11	56:Cr:118:LEU:HD11	1.88	0.55
7:AB:41:ILE:HD11	7:AB:73:ASP:O	2.07	0.54
15:AE:87:MET:HE2	15:AE:87:MET:HA	1.89	0.54
25:AK:40:VAL:HG23	25:AK:44:HIS:HB3	1.88	0.54
38:Cz:100:VAL:HG23	38:Cz:102:LYS:HG3	1.88	0.54
44:CN:118:SER:HB3	44:CN:132:VAL:HG22	1.87	0.54
47:CQ:25:LEU:O	47:CQ:29:VAL:HG23	2.07	0.54
83:CR:19:LYS:O	83:CR:22:VAL:HG22	2.06	0.54
83:CR:141:HIS:O	83:CR:145:LEU:HD22	2.07	0.54
14:AJ:113:GLN:HG3	14:AJ:149:VAL:HG11	1.89	0.54
15:AE:103:TYR:CE1	15:AE:189:LEU:HD11	2.42	0.54
56:Cr:127:LYS:HE2	56:Cr:131:THR:HG21	1.89	0.54
82:A6:2821:U:OP1	83:CR:55:VAL:HG23	2.07	0.54
82:A6:2897:G:OP1	83:CR:101:ILE:HG21	2.06	0.54
21:B2:1231:C:H42	21:B2:1527:C:H42	1.55	0.54
49:CS:36:ASN:OD1	49:CS:39:VAL:HG22	2.07	0.54
51:CP:41:ILE:HD12	51:CP:112:LEU:CB	2.37	0.54
21:B2:668:A:H1'	21:B2:1197:G:H21	1.72	0.54
63:Ce:16:ARG:HH11	63:Ce:54:LEU:HD22	1.73	0.54
83:CR:180:LYS:O	83:CR:184:ILE:HG13	2.07	0.54
40:CL:167:ARG:NE	43:Ca:97:ALA:HB3	2.22	0.54
45:CI:91:LEU:HD13	45:CI:92:HIS:N	2.22	0.54
53:CX:77:ILE:HD13	53:CX:116:LEU:HD12	1.88	0.54
64:Cf:11:PHE:CE1	64:Cf:26:ALA:HB1	2.42	0.54
77:CE:124:LYS:HZ3	79:A5:959:G:H1	1.53	0.54
10:AY:18:LEU:CD1	15:AE:64:ILE:HD11	2.38	0.54
56:Cr:4:HIS:CG	70:CC:289:LEU:HD22	2.43	0.54
15:AE:129:ILE:HD12	15:AE:129:ILE:O	2.07	0.54
24:AU:80:PHE:HB2	28:Ad:52:PHE:CD1	2.43	0.54
61:Cc:29:LEU:HD13	61:Cc:91:VAL:HG11	1.90	0.54
2:Ct:429:ILE:HD11	2:Ct:445:LYS:HB3	1.89	0.54
18:AH:143:ARG:O	18:AH:154:ILE:HD12	2.07	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AT:87:VAL:HG13	31:AT:88:MET:HE2	1.90	0.54
83:CR:163:ARG:HA	83:CR:166:THR:HG23	1.90	0.54
2:Ct:646:ALA:HA	2:Ct:649:ILE:HD13	1.89	0.53
38:Cz:65:VAL:HG21	38:Cz:150:GLU:HB3	1.90	0.53
77:CE:91:THR:HG21	77:CE:106:VAL:CG2	2.37	0.53
83:CR:107:ARG:HG2	83:CR:110:ARG:NH2	2.23	0.53
15:AE:57:THR:O	15:AE:61:VAL:HG23	2.08	0.53
48:CA:35:ALA:HB1	48:CA:41:ILE:CG2	2.38	0.53
83:CR:25:ASP:HB3	83:CR:28:GLU:HG2	1.91	0.53
83:CR:110:ARG:N	83:CR:115:ILE:HG22	2.24	0.53
24:AU:20:ILE:HD12	24:AU:115:THR:O	2.08	0.53
45:CI:190:LEU:HD22	45:CI:197:VAL:HG22	1.91	0.53
49:CS:100:LEU:HG	49:CS:101:THR:HG22	1.90	0.53
60:CF:90:ALA:HB2	60:CF:125:LEU:HD21	1.91	0.53
26:AM:71:GLU:HB3	35:Af:114:ILE:HD11	1.90	0.53
78:CG:87:LEU:HD23	78:CG:184:ILE:HA	1.88	0.53
79:A5:516:G:H22	79:A5:645:G:H1	1.56	0.53
17:AG:75:LEU:HD21	21:B2:1791:A:C5'	2.39	0.53
17:AG:75:LEU:HD21	21:B2:1791:A:H5''	1.89	0.53
38:Cz:123:ILE:HG22	38:Cz:124:LEU:HD22	1.91	0.53
83:CR:76:MET:HE3	83:CR:76:MET:O	2.08	0.53
36:AF:68:ILE:HD12	36:AF:68:ILE:H	1.74	0.53
46:CD:284:LYS:O	46:CD:288:LEU:HD23	2.09	0.53
49:CS:162:GLN:NE2	79:A5:1919:G:O4'	2.42	0.53
59:CB:292:LEU:HD23	59:CB:299:ILE:HG13	1.90	0.53
62:Cd:87:ARG:HH21	62:Cd:122:VAL:HG11	1.73	0.53
70:CC:10:VAL:HA	70:CC:153:VAL:HG13	1.90	0.53
83:CR:100:ARG:O	83:CR:104:ARG:HG3	2.08	0.53
83:CR:110:ARG:HA	83:CR:115:ILE:O	2.08	0.53
7:AB:110:MET:HE3	7:AB:110:MET:O	2.09	0.53
34:AD:119:CYS:O	34:AD:123:LEU:HD23	2.09	0.53
57:Ch:32:ARG:O	57:Ch:36:VAL:HG23	2.09	0.53
70:CC:40:VAL:O	70:CC:44:LEU:HD23	2.09	0.53
70:CC:124:ILE:HG22	70:CC:128:LEU:CD2	2.38	0.53
70:CC:209:ILE:HD11	70:CC:227:ILE:CG2	2.36	0.53
21:B2:191:A:H62	21:B2:208:G:H21	1.57	0.53
44:CN:179:LYS:HE2	44:CN:179:LYS:HA	1.91	0.53
50:CT:34:TYR:CE1	50:CT:93:ILE:HG23	2.44	0.53
64:Cf:57:THR:OG1	64:Cf:58:VAL:HG23	2.08	0.53
77:CE:247:LYS:NZ	82:A6:4936:G:H22	2.05	0.53
78:CG:159:HIS:HA	78:CG:183:ILE:HD11	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:AW:35:VAL:O	19:AW:39:THR:HG23	2.08	0.53
6:AL:111:VAL:HG11	6:AL:128:VAL:CG1	2.39	0.53
21:B2:1227:G:O6	21:B2:1531:A:N1	2.42	0.53
23:Ag:30:MET:HE2	23:Ag:42:MET:SD	2.48	0.53
55:CZ:100:VAL:HG22	55:CZ:106:LEU:HD11	1.91	0.53
82:A6:5005:G:H1'	82:A6:5042:A:H61	1.73	0.53
83:CR:50:ILE:C	83:CR:51:ILE:HD13	2.34	0.53
83:CR:184:ILE:HA	83:CR:187:THR:CG2	2.39	0.53
6:AL:93:LEU:HD12	6:AL:102:PHE:HB3	1.91	0.52
34:AD:115:VAL:HG13	34:AD:138:VAL:HG11	1.90	0.52
76:CH:69:THR:HG22	82:A6:4700:A:H2	1.74	0.52
16:AC:209:VAL:HG21	16:AC:233:LEU:CD2	2.36	0.52
21:B2:1286:G:H21	21:B2:1313:A:H62	1.55	0.52
23:Ag:251:ALA:HB2	23:Ag:289:LEU:HD23	1.91	0.52
25:AK:15:LEU:HD22	25:AK:21:MET:HE2	1.90	0.52
56:Cr:1:MET:N	56:Cr:5:LEU:HD23	2.25	0.52
64:Cf:8:LYS:HB2	64:Cf:31:GLU:HB2	1.91	0.52
75:CJ:62:ILE:HD12	75:CJ:62:ILE:O	2.09	0.52
71:Cm:82:LEU:HD11	76:CH:95:VAL:HB	1.92	0.52
77:CE:61:ALA:HA	77:CE:65:ARG:HB3	1.90	0.52
10:AY:114:MET:HE3	10:AY:114:MET:O	2.10	0.52
34:AD:102:ALA:HB1	34:AD:184:ILE:HD11	1.91	0.52
83:CR:115:ILE:CD1	83:CR:119:MET:HE2	2.40	0.52
83:CR:133:LYS:H	83:CR:137:ILE:CG2	2.21	0.52
80:A7:66:G:O6	80:A7:109:U:C2	2.62	0.52
82:A6:2820:C:C4'	83:CR:58:HIS:HB2	2.39	0.52
83:CR:98:ARG:HH11	83:CR:133:LYS:HA	1.75	0.52
20:AI:161:LEU:HB3	20:AI:195:LEU:HD12	1.92	0.52
21:B2:1540:G:OP1	31:AT:39:LEU:HD23	2.09	0.52
33:Ac:9:ILE:HD11	33:Ac:57:THR:CG2	2.40	0.52
70:CC:210:ILE:O	70:CC:253:THR:HG23	2.09	0.52
70:CC:285:ILE:HD12	70:CC:286:ASN:N	2.25	0.52
83:CR:159:ALA:HA	83:CR:162:ARG:HB3	1.91	0.52
12:Ab:81:ARG:HB3	12:Ab:82:LYS:HA	1.91	0.52
4:AX:8:ARG:HG3	6:AL:93:LEU:HD11	1.90	0.52
9:AV:67:ASP:HA	9:AV:70:LEU:HD12	1.92	0.52
31:AT:76:THR:HG21	31:AT:97:LYS:HB3	1.90	0.52
77:CE:247:LYS:HZ1	82:A6:4936:G:H22	1.57	0.52
83:CR:172:ARG:HA	83:CR:175:GLU:CD	2.34	0.52
83:CR:173:ARG:O	83:CR:177:LEU:HG	2.10	0.52
3:AO:33:ILE:HD13	3:AO:42:VAL:HG12	1.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:Ca:121:PRO:HA	43:Ca:140:VAL:HG12	1.92	0.52
83:CR:75:HIS:C	83:CR:80:LYS:HD3	2.35	0.52
83:CR:133:LYS:NZ	83:CR:134:ASN:HD22	2.08	0.52
34:AD:39:VAL:HG12	34:AD:48:ILE:HD13	1.91	0.51
42:CM:82:ILE:HD12	42:CM:85:LYS:HZ3	1.75	0.51
45:CI:17:TYR:O	45:CI:96:VAL:HG12	2.10	0.51
61:Cc:95:ALA:C	61:Cc:96:ILE:HD12	2.35	0.51
83:CR:42:ARG:HA	83:CR:45:ILE:CG2	2.40	0.51
83:CR:98:ARG:O	83:CR:102:LEU:HD22	2.10	0.51
47:CQ:98:LEU:CD1	47:CQ:100:VAL:HG23	2.40	0.51
56:Cr:98:ARG:HB2	56:Cr:111:ILE:HD11	1.92	0.51
59:CB:49:TYR:HE1	59:CB:344:VAL:HG12	1.75	0.51
76:CH:55:LEU:HD13	76:CH:56:ARG:N	2.25	0.51
5:AN:71:ILE:HG12	21:B2:1018:U:H5''	1.92	0.51
15:AE:45:ILE:HA	15:AE:61:VAL:HG11	1.92	0.51
16:AC:70:VAL:HG22	16:AC:97:PHE:HE2	1.76	0.51
32:AZ:110:THR:CG2	36:AF:102:LEU:HD22	2.41	0.51
38:Cz:85:MET:CB	38:Cz:89:ALA:HB2	2.39	0.51
56:Cr:10:VAL:HG13	70:CC:139:SER:OG	2.11	0.51
59:CB:292:LEU:HD23	59:CB:299:ILE:CG1	2.41	0.51
77:CE:213:THR:HG23	77:CE:215:ALA:H	1.74	0.51
78:CG:169:PHE:HE2	78:CG:172:ALA:HB3	1.74	0.51
82:A6:3692:A:H62	82:A6:3823:G:N2	2.08	0.51
83:CR:161:ALA:HA	83:CR:164:SER:OG	2.10	0.51
8:AA:57:LYS:CE	9:AV:70:LEU:HD11	2.41	0.51
18:AH:61:ILE:HD12	18:AH:93:VAL:O	2.10	0.51
39:CO:181:ALA:CB	42:CM:127:VAL:HG22	2.41	0.51
60:CF:190:LEU:HD21	60:CF:208:LEU:CD2	2.39	0.51
62:Cd:105:LEU:HD13	62:Cd:106:VAL:N	2.26	0.51
77:CE:93:THR:HG22	77:CE:95:PRO:HD2	1.91	0.51
83:CR:37:SER:OG	83:CR:40:GLN:HG2	2.11	0.51
83:CR:70:ARG:NE	83:CR:75:HIS:HB2	2.21	0.51
15:AE:103:TYR:CZ	15:AE:189:LEU:HD11	2.46	0.51
39:CO:35:VAL:HB	39:CO:104:VAL:HG12	1.91	0.51
48:CA:179:ILE:HD11	82:A6:3653:A:H5''	1.92	0.51
11:Aa:45:VAL:HG12	11:Aa:53:ILE:HD13	1.93	0.51
21:B2:1172:U:H4'	72:Cn:10:MET:HE1	1.93	0.51
45:CI:207:ASP:O	45:CI:211:VAL:HG23	2.09	0.51
54:CY:55:VAL:HG21	54:CY:70:VAL:CG2	2.37	0.51
61:Cc:17:ARG:O	61:Cc:21:VAL:HG23	2.10	0.51
83:CR:169:ALA:O	83:CR:173:ARG:HG2	2.10	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:AU:20:ILE:HD11	24:AU:114:VAL:HG12	1.92	0.51
47:CQ:29:VAL:HG22	47:CQ:51:LEU:HD13	1.93	0.51
56:Cr:6:GLN:HB2	56:Cr:43:LEU:HD13	1.92	0.51
65:Cg:67:LEU:HD13	65:Cg:71:LYS:HB2	1.91	0.51
70:CC:27:VAL:HG23	70:CC:125:CYS:HB3	1.93	0.51
38:Cz:157:PHE:HB2	38:Cz:165:LEU:HD21	1.92	0.51
47:CQ:33:ARG:HA	47:CQ:48:LEU:HD22	1.93	0.51
59:CB:305:THR:HG21	59:CB:365:LEU:O	2.11	0.51
61:Cc:102:SER:HB2	61:Cc:104:ILE:HD12	1.93	0.51
83:CR:12:SER:HB2	83:CR:17:CYS:O	2.09	0.51
17:AG:45:TRP:HZ2	17:AG:113:ILE:HD11	1.75	0.51
20:AI:38:ILE:HD12	20:AI:38:ILE:O	2.11	0.51
83:CR:133:LYS:O	83:CR:133:LYS:HG2	2.09	0.51
9:AV:59:ILE:HD12	9:AV:59:ILE:H	1.76	0.51
82:A6:2889:G:P	83:CR:80:LYS:HD2	2.50	0.51
83:CR:175:GLU:CB	83:CR:178:GLN:HE21	2.24	0.51
8:AA:68:ILE:HG23	8:AA:120:ARG:HG3	1.92	0.50
21:B2:834:C:H42	21:B2:839:C:H41	1.59	0.50
25:AK:15:LEU:HD21	25:AK:49:MET:CE	2.40	0.50
26:AM:25:ALA:HB1	26:AM:30:GLY:O	2.09	0.50
33:Ac:40:ARG:CZ	33:Ac:42:ILE:HD13	2.41	0.50
46:CD:211:LEU:HD22	46:CD:218:ALA:HB3	1.93	0.50
51:CP:149:ILE:HD12	51:CP:149:ILE:O	2.12	0.50
56:Cr:64:ILE:HB	56:Cr:81:THR:HG23	1.94	0.50
4:AX:66:ILE:O	4:AX:66:ILE:HD12	2.11	0.50
7:AB:135:LEU:HD13	7:AB:216:LYS:O	2.10	0.50
10:AY:20:ARG:CD	10:AY:74:MET:HE2	2.40	0.50
56:Cr:42:GLY:O	56:Cr:43:LEU:HG	2.11	0.50
82:A6:4235:G:O6	82:A6:4289:U:O2	2.29	0.50
2:Ct:228:PHE:CD2	2:Ct:293:ILE:HG23	2.47	0.50
20:AI:78:ILE:HD12	20:AI:78:ILE:O	2.12	0.50
31:AT:70:ALA:HB1	31:AT:75:MET:CE	2.32	0.50
34:AD:161:GLY:O	34:AD:164:VAL:HG22	2.12	0.50
42:CM:36:ALA:HB2	42:CM:52:PHE:CE1	2.47	0.50
45:CI:41:ALA:HB1	45:CI:45:GLU:CD	2.36	0.50
51:CP:30:ARG:HA	51:CP:119:VAL:HG11	1.93	0.50
56:Cr:9:VAL:HG13	56:Cr:10:VAL:HG23	1.93	0.50
61:Cc:93:THR:C	61:Cc:94:LEU:HD13	2.37	0.50
23:Ag:258:ILE:HD11	23:Ag:268:ASP:HB3	1.93	0.50
34:AD:59:LEU:HD12	34:AD:60:GLY:O	2.11	0.50
53:CX:155:ILE:CD1	57:Ch:37:THR:HG22	2.41	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:CF:166:ARG:C	60:CF:167:ILE:HD12	2.35	0.50
70:CC:101:MET:HE1	82:A6:2343:G:C4	2.46	0.50
82:A6:4645:C:OP2	83:CR:62:ARG:HD2	2.12	0.50
41:CV:18:LEU:HD21	41:CV:54:ALA:CB	2.42	0.50
43:Ca:97:ALA:HB1	43:Ca:121:PRO:CG	2.41	0.50
78:CG:87:LEU:HD22	78:CG:182:CYS:SG	2.52	0.50
3:AO:55:ARG:O	3:AO:56:VAL:HG12	2.11	0.50
76:CH:92:MET:HE2	76:CH:92:MET:N	2.27	0.50
83:CR:148:ASP:O	83:CR:152:LYS:HE2	2.12	0.50
14:AJ:94:LEU:HD23	14:AJ:94:LEU:H	1.77	0.50
14:AJ:108:ARG:NH1	14:AJ:149:VAL:HG13	2.27	0.50
57:Ch:22:ASP:O	57:Ch:26:VAL:HG23	2.11	0.50
2:Ct:147:ILE:HD13	2:Ct:193:GLY:HA3	1.94	0.50
26:AM:22:LEU:HD13	26:AM:89:VAL:HG22	1.94	0.50
44:CN:32:GLN:HB3	78:CG:63:LEU:HD21	1.93	0.50
44:CN:118:SER:CB	44:CN:132:VAL:HG22	2.42	0.50
46:CD:67:ALA:C	50:CT:31:MET:HE1	2.37	0.50
48:CA:104:VAL:HG23	48:CA:162:ASN:O	2.12	0.50
57:Ch:31:LEU:HD23	57:Ch:32:ARG:N	2.26	0.50
82:A6:2377:C:O4'	83:CR:1:MET:HE2	2.12	0.50
82:A6:2890:C:H3'	83:CR:74:ARG:HH22	1.77	0.50
83:CR:126:LYS:HB3	83:CR:131:VAL:CG1	2.42	0.50
83:CR:164:SER:HA	83:CR:167:LYS:CE	2.42	0.50
82:A6:2665:U:OP2	83:CR:120:TYR:HE2	1.95	0.50
41:CV:18:LEU:HD11	41:CV:54:ALA:CB	2.42	0.49
45:CI:190:LEU:HD22	45:CI:197:VAL:CG2	2.42	0.49
56:Cr:75:THR:HG23	70:CC:147:VAL:O	2.12	0.49
83:CR:175:GLU:HA	83:CR:178:GLN:CG	2.42	0.49
30:AP:126:VAL:HG12	30:AP:127:LYS:H	1.77	0.49
38:Cz:50:SER:HB3	38:Cz:138:LEU:HD13	1.94	0.49
38:Cz:85:MET:HB3	38:Cz:89:ALA:HB2	1.94	0.49
42:CM:25:VAL:HG11	42:CM:45:VAL:HG11	1.94	0.49
62:Cd:88:LEU:HG	62:Cd:106:VAL:HG13	1.93	0.49
11:Aa:85:ARG:HB3	21:B2:1866:A:H61	1.77	0.49
15:AE:48:LEU:HD12	15:AE:61:VAL:HG22	1.94	0.49
18:AH:79:LEU:CD1	18:AH:83:LEU:HD23	2.41	0.49
33:Ac:41:SER:C	33:Ac:42:ILE:HD12	2.38	0.49
34:AD:167:TYR:CB	34:AD:189:MET:HE1	2.42	0.49
47:CQ:154:LYS:HA	47:CQ:155:ALA:HB3	1.94	0.49
47:CQ:155:ALA:HB2	47:CQ:159:PRO:HG3	1.94	0.49
57:Ch:56:ARG:O	57:Ch:60:VAL:HG23	2.12	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:CC:321:ASN:HB3	70:CC:324:ILE:HD12	1.93	0.49
83:CR:98:ARG:O	83:CR:101:ILE:HB	2.12	0.49
83:CR:105:LEU:CD2	83:CR:138:LEU:HD12	2.41	0.49
83:CR:123:LEU:O	83:CR:126:LYS:HB2	2.12	0.49
83:CR:177:LEU:HA	83:CR:180:LYS:CD	2.39	0.49
17:AG:3:LEU:CD1	17:AG:109:LEU:HD23	2.41	0.49
21:B2:677:G:H21	21:B2:1028:A:H62	1.61	0.49
25:AK:22:VAL:HG13	34:AD:75:LYS:CE	2.43	0.49
44:CN:22:LEU:CD1	78:CG:164:ILE:HD11	2.40	0.49
57:Ch:54:ILE:HD12	57:Ch:55:ALA:N	2.27	0.49
60:CF:50:ILE:HG21	70:CC:330:PRO:HD2	1.94	0.49
82:A6:2663:G:H5''	83:CR:118:HIS:HA	1.94	0.49
83:CR:136:ARG:CA	83:CR:139:MET:HE3	2.41	0.49
8:AA:60:LEU:HD12	8:AA:159:ILE:HD12	1.93	0.49
21:B2:1553:C:OP2	34:AD:3:VAL:HG22	2.12	0.49
40:CL:167:ARG:CZ	43:Ca:97:ALA:HB3	2.43	0.49
41:CV:41:SER:O	41:CV:61:VAL:HG13	2.11	0.49
47:CQ:155:ALA:HB1	47:CQ:156:PRO:HA	1.94	0.49
59:CB:325:GLU:O	59:CB:326:VAL:HG13	2.12	0.49
69:Cl:13:LEU:HD12	82:A6:2407:G:O2'	2.12	0.49
70:CC:271:ALA:HB1	70:CC:274:LYS:HB2	1.95	0.49
76:CH:105:ILE:HD11	76:CH:110:SER:OG	2.13	0.49
2:Ct:147:ILE:HD13	2:Ct:193:GLY:CA	2.43	0.49
8:AA:144:THR:HG22	8:AA:145:ILE:O	2.12	0.49
29:AR:39:ALA:HB2	34:AD:210:ILE:HG23	1.94	0.49
39:CO:95:GLY:O	39:CO:99:LEU:HD23	2.12	0.49
56:Cr:61:VAL:HG22	56:Cr:86:ALA:HB3	1.94	0.49
77:CE:186:LEU:HD23	77:CE:250:GLN:HG2	1.94	0.49
79:A5:2085:G:H2'	79:A5:2086:G:O4'	2.12	0.49
18:AH:41:ARG:HG3	83:CR:188:LEU:HG	1.95	0.49
26:AM:31:LEU:HD12	26:AM:31:LEU:O	2.13	0.49
33:Ac:5:ARG:CD	33:Ac:6:VAL:HG12	2.43	0.49
43:Ca:84:GLU:O	43:Ca:88:VAL:HG22	2.12	0.49
46:CD:158:LYS:HD3	46:CD:158:LYS:N	2.27	0.49
77:CE:203:ILE:HD12	77:CE:203:ILE:O	2.13	0.49
79:A5:1557:C:O3'	83:CR:125:LEU:HD21	2.12	0.49
39:CO:122:ALA:HA	49:CS:161:ARG:HD3	1.94	0.49
49:CS:93:MET:HE3	79:A5:1952:G:O2'	2.13	0.49
61:Cc:58:SER:OG	65:Cg:96:LEU:HD22	2.13	0.49
83:CR:64:ARG:HA	83:CR:67:THR:HG22	1.95	0.49
83:CR:115:ILE:HD11	83:CR:119:MET:HB2	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:Cr:117:ILE:O	56:Cr:121:GLN:HG3	2.13	0.49
64:Cf:50:VAL:HG12	64:Cf:69:VAL:CG2	2.41	0.49
70:CC:326:LEU:HD23	70:CC:332:ALA:HB3	1.94	0.49
75:CJ:96:LYS:HD2	75:CJ:163:MET:HE2	1.94	0.49
6:AL:111:VAL:HG11	6:AL:128:VAL:HG11	1.95	0.49
18:AH:154:ILE:O	18:AH:185:VAL:HG23	2.13	0.49
31:AT:56:ARG:HG3	31:AT:103:VAL:HG21	1.95	0.49
34:AD:204:LEU:HD22	34:AD:205:PRO:HD2	1.94	0.49
39:CO:202:LEU:HD21	42:CM:108:ASP:HB2	1.95	0.49
56:Cr:90:LEU:HD23	77:CE:110:ARG:HH22	1.77	0.49
77:CE:180:VAL:HG21	77:CE:258:LEU:HD11	1.95	0.49
82:A6:3597:G:OP1	83:CR:146:LYS:HE2	2.13	0.49
8:AA:140:VAL:HG23	8:AA:142:LEU:HD13	1.95	0.48
14:AJ:110:LEU:O	14:AJ:114:VAL:HG23	2.13	0.48
15:AE:44:LEU:HD12	15:AE:44:LEU:O	2.13	0.48
16:AC:204:ILE:HD12	16:AC:204:ILE:O	2.12	0.48
21:B2:141:A:H61	21:B2:177:G:H21	1.59	0.48
21:B2:1083:A:H62	21:B2:1841:C:H1'	1.78	0.48
53:CX:155:ILE:HD13	57:Ch:37:THR:HG22	1.95	0.48
57:Ch:24:LEU:HD11	57:Ch:54:ILE:HG22	1.94	0.48
79:A5:516:G:N2	79:A5:645:G:H22	2.11	0.48
3:AO:56:VAL:HG11	3:AO:80:ASP:OD2	2.14	0.48
22:CW:9:SER:HA	22:CW:52:THR:HG22	1.93	0.48
61:Cc:29:LEU:HD22	61:Cc:94:LEU:HD12	1.94	0.48
71:Cm:82:LEU:HD13	71:Cm:82:LEU:O	2.13	0.48
77:CE:168:LEU:HD22	77:CE:188:ARG:NE	2.28	0.48
82:A6:2863:G:H1'	83:CR:82:LYS:HD3	1.95	0.48
83:CR:26:PRO:O	83:CR:29:THR:HG23	2.13	0.48
83:CR:45:ILE:HB	83:CR:50:ILE:CD1	2.35	0.48
3:AO:95:ILE:CD1	3:AO:129:ILE:HD12	2.42	0.48
7:AB:49:VAL:HG21	7:AB:62:LEU:HD13	1.94	0.48
20:AI:101:ILE:HD12	20:AI:190:LEU:HD11	1.95	0.48
70:CC:230:LEU:HD21	70:CC:239:LYS:HG3	1.95	0.48
82:A6:2711:G:N2	83:CR:39:GLN:HB2	2.28	0.48
83:CR:68:LEU:HA	83:CR:71:ARG:HG3	1.95	0.48
7:AB:141:GLY:HA2	7:AB:210:VAL:HG22	1.95	0.48
47:CQ:24:TYR:CE1	56:Cr:5:LEU:HD22	2.49	0.48
70:CC:124:ILE:HD13	70:CC:237:ILE:CD1	2.42	0.48
83:CR:1:MET:HE3	83:CR:2:SER:HA	1.95	0.48
15:AE:194:VAL:HG22	15:AE:211:LYS:O	2.14	0.48
17:AG:45:TRP:CZ2	17:AG:113:ILE:HD11	2.48	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:AU:30:LYS:H	24:AU:30:LYS:HE2	1.78	0.48
40:CL:59:VAL:HG13	79:A5:74:G:H5''	1.94	0.48
51:CP:53:LEU:HD13	51:CP:53:LEU:O	2.13	0.48
57:Ch:41:ALA:HB1	81:A8:78:G:H5'	1.94	0.48
64:Cf:35:ALA:HB3	64:Cf:38:GLU:OE2	2.13	0.48
79:A5:1550:G:OP1	83:CR:86:ASN:HB3	2.13	0.48
83:CR:130:ASN:C	83:CR:132:PHE:H	2.21	0.48
21:B2:1419:C:HO2'	31:AT:4:VAL:N	2.11	0.48
48:CA:46:LYS:HE2	48:CA:62:VAL:HG21	1.95	0.48
56:Cr:64:ILE:HD12	56:Cr:64:ILE:O	2.13	0.48
64:Cf:56:ASN:HD21	82:A6:4945:G:H22	1.61	0.48
77:CE:41:LYS:HB2	77:CE:42:PRO:HD2	1.95	0.48
82:A6:3692:A:N6	82:A6:3823:G:H21	2.09	0.48
83:CR:115:ILE:CD1	83:CR:119:MET:HB2	2.44	0.48
83:CR:179:ALA:O	83:CR:182:GLU:HG3	2.14	0.48
7:AB:44:ILE:HG23	7:AB:69:VAL:HG21	1.96	0.48
23:Ag:184:LEU:HD11	34:AD:227:LYS:HB3	1.96	0.48
70:CC:218:ILE:HD12	70:CC:229:LEU:CD2	2.43	0.48
76:CH:3:THR:HG23	76:CH:67:LEU:HD11	1.96	0.48
77:CE:242:ILE:HG12	77:CE:246:ARG:CB	2.44	0.48
83:CR:106:LEU:HD23	83:CR:120:TYR:HD1	1.79	0.48
83:CR:178:GLN:O	83:CR:181:LYS:HG3	2.14	0.48
10:AY:16:ARG:NH2	15:AE:92:ILE:HG22	2.29	0.48
43:Ca:112:LEU:HD23	79:A5:1387:A:N6	2.29	0.48
57:Ch:93:ARG:HH12	79:A5:18:C:H5''	1.78	0.48
64:Cf:79:GLY:HA2	79:A5:1917:A:H4'	1.95	0.48
65:Cg:41:ALA:HB3	65:Cg:52:ARG:CG	2.44	0.48
67:Cj:64:MET:HE2	67:Cj:64:MET:N	2.29	0.48
75:CJ:35:ARG:O	75:CJ:39:VAL:HG23	2.14	0.48
82:A6:4646:U:H5''	83:CR:57:VAL:HG23	1.95	0.48
18:AH:53:VAL:HG22	18:AH:57:ARG:O	2.14	0.48
44:CN:113:LEU:CB	44:CN:134:LEU:HD12	2.44	0.48
57:Ch:21:LEU:HD23	57:Ch:57:VAL:CG2	2.44	0.48
59:CB:216:MET:HE2	59:CB:216:MET:HA	1.96	0.48
77:CE:152:ILE:HG23	77:CE:158:ARG:HA	1.95	0.48
77:CE:176:THR:CG2	77:CE:186:LEU:HD22	2.44	0.48
27:AS:90:VAL:HG12	27:AS:91:LYS:HE2	1.94	0.48
38:Cz:86:ASP:O	38:Cz:89:ALA:HB3	2.14	0.48
77:CE:67:ALA:HB1	77:CE:71:ARG:HH21	1.78	0.48
77:CE:91:THR:HG21	77:CE:106:VAL:HG13	1.94	0.48
10:AY:44:LEU:HB3	10:AY:55:ILE:HD13	1.95	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AC:148:ALA:HB1	16:AC:152:ARG:HH21	1.79	0.47
26:AM:79:VAL:HG11	26:AM:88:TRP:HZ3	1.78	0.47
34:AD:105:LEU:HD21	34:AD:122:VAL:HG11	1.96	0.47
43:Ca:97:ALA:HB1	43:Ca:121:PRO:HG3	1.97	0.47
47:CQ:23:ILE:HG21	56:Cr:5:LEU:CD1	2.44	0.47
53:CX:153:ILE:HD11	53:CX:155:ILE:HG22	1.96	0.47
56:Cr:90:LEU:HB2	56:Cr:118:LEU:HD12	1.96	0.47
59:CB:299:ILE:O	59:CB:299:ILE:HG22	2.13	0.47
83:CR:60:ARG:HB2	83:CR:63:CYS:HB3	1.96	0.47
2:Ct:99:LEU:HD13	2:Ct:100:ILE:N	2.29	0.47
2:Ct:128:VAL:HG23	2:Ct:156:MET:HG3	1.96	0.47
15:AE:195:ILE:HG22	15:AE:197:ASN:H	1.78	0.47
37:AQ:41:MET:C	37:AQ:42:ILE:HD12	2.39	0.47
56:Cr:64:ILE:CB	56:Cr:81:THR:HG23	2.44	0.47
63:Ce:21:ILE:HD12	63:Ce:22:ARG:O	2.14	0.47
70:CC:316:LYS:CB	70:CC:324:ILE:HD11	2.44	0.47
78:CG:164:ILE:HD12	78:CG:165:GLU:N	2.29	0.47
82:A6:2812:A:OP1	83:CR:88:ARG:HD2	2.14	0.47
83:CR:40:GLN:O	83:CR:44:LEU:HD12	2.14	0.47
21:B2:1410:C:H42	21:B2:1436:C:H42	1.60	0.47
21:B2:1599:U:O5'	32:AZ:44:LEU:HD11	2.15	0.47
34:AD:164:VAL:HA	34:AD:168:VAL:HG12	1.95	0.47
37:AQ:39:LEU:HA	37:AQ:42:ILE:HD11	1.97	0.47
47:CQ:34:PHE:CD2	70:CC:293:LEU:HD11	2.49	0.47
77:CE:148:THR:HG23	77:CE:150:LEU:HD21	1.95	0.47
77:CE:179:LEU:HD13	77:CE:180:VAL:N	2.29	0.47
82:A6:2386:U:OP1	83:CR:8:LYS:HD2	2.13	0.47
83:CR:144:LYS:HB3	83:CR:144:LYS:HZ2	1.79	0.47
83:CR:150:ALA:O	83:CR:153:LYS:HE3	2.14	0.47
2:Ct:451:ILE:HD11	2:Ct:473:VAL:HG13	1.96	0.47
16:AC:70:VAL:HG21	16:AC:93:ILE:CD1	2.45	0.47
23:Ag:78:ALA:HB2	23:Ag:92:LEU:HD13	1.96	0.47
55:CZ:106:LEU:HD12	55:CZ:106:LEU:O	2.15	0.47
56:Cr:94:ARG:HG2	56:Cr:111:ILE:HG23	1.96	0.47
77:CE:36:LYS:O	79:A5:980:U:H4'	2.15	0.47
77:CE:157:HIS:HB3	77:CE:184:VAL:HG22	1.97	0.47
77:CE:207:LYS:H	77:CE:208:ILE:HD12	1.78	0.47
8:AA:46:ILE:HG22	8:AA:47:TYR:H	1.79	0.47
14:AJ:35:TYR:CD2	14:AJ:106:LEU:HD23	2.50	0.47
54:CY:115:ARG:O	54:CY:119:LEU:HD23	2.14	0.47
61:Cc:37:MET:HE1	61:Cc:95:ALA:CB	2.44	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:CE:283:PRO:HA	77:CE:286:LEU:HB2	1.95	0.47
83:CR:8:LYS:HG2	83:CR:19:LYS:HB3	1.96	0.47
83:CR:164:SER:O	83:CR:167:LYS:HG2	2.14	0.47
2:Ct:506:ARG:HD2	2:Ct:545:ILE:HD13	1.97	0.47
8:AA:163:CYS:HB2	8:AA:174:MET:HE1	1.95	0.47
44:CN:21:PHE:CD1	44:CN:22:LEU:HD22	2.49	0.47
50:CT:105:PHE:O	50:CT:109:VAL:HG23	2.15	0.47
64:Cf:28:LEU:HD21	64:Cf:86:ALA:HB3	1.96	0.47
78:CG:188:ALA:HB2	79:A5:6:C:H1'	1.96	0.47
2:Ct:568:ILE:HD12	2:Ct:568:ILE:O	2.13	0.47
19:AW:111:MET:HE1	19:AW:116:ALA:HB2	1.97	0.47
20:AI:144:LYS:O	20:AI:145:ILE:HG12	2.15	0.47
36:AF:106:GLU:OE2	36:AF:111:VAL:HG23	2.15	0.47
38:Cz:29:LEU:CD2	38:Cz:172:VAL:HG22	2.44	0.47
38:Cz:67:VAL:HG23	38:Cz:82:ILE:CD1	2.34	0.47
41:CV:40:ILE:HD11	82:A6:3799:A:C6	2.49	0.47
43:Ca:75:LEU:HD13	43:Ca:113:GLY:HA2	1.95	0.47
46:CD:33:ARG:HG2	50:CT:27:LEU:HD11	1.96	0.47
49:CS:115:ALA:HB1	79:A5:1925:G:N3	2.28	0.47
61:Cc:38:ILE:HG21	61:Cc:63:TYR:HB3	1.97	0.47
63:Cc:16:ARG:NH1	63:Cc:54:LEU:HD22	2.29	0.47
77:CE:186:LEU:CD1	77:CE:212:LEU:HD21	2.45	0.47
83:CR:3:MET:C	83:CR:4:LEU:HD23	2.40	0.47
83:CR:84:THR:O	83:CR:88:ARG:HG2	2.14	0.47
83:CR:84:THR:CG2	83:CR:87:ALA:H	2.28	0.47
83:CR:93:VAL:O	83:CR:96:MET:HB3	2.15	0.47
27:AS:6:PRO:O	32:AZ:49:LEU:HD11	2.15	0.47
33:Ac:5:ARG:HD3	33:Ac:6:VAL:HG12	1.95	0.47
34:AD:167:TYR:HB2	34:AD:189:MET:HE1	1.97	0.47
41:CV:18:LEU:HD21	41:CV:54:ALA:HB3	1.96	0.47
47:CQ:98:LEU:HD13	47:CQ:100:VAL:HG23	1.97	0.47
77:CE:176:THR:OG1	77:CE:186:LEU:HD13	2.15	0.47
83:CR:4:LEU:HD22	83:CR:7:GLN:NE2	2.28	0.47
83:CR:108:ARG:HA	83:CR:111:GLU:HG3	1.97	0.47
17:AG:7:PHE:CE1	17:AG:9:ALA:HB3	2.49	0.47
38:Cz:63:PHE:O	38:Cz:65:VAL:HG23	2.14	0.47
39:CO:38:CYS:O	39:CO:41:ILE:HG22	2.15	0.47
78:CG:142:THR:HG23	79:A5:151:G:O6	2.15	0.47
2:Ct:592:LEU:HD23	2:Ct:603:TYR:CD2	2.50	0.47
6:AL:80:MET:N	6:AL:80:MET:HE2	2.30	0.47
20:AI:97:VAL:HG22	20:AI:100:CYS:SG	2.55	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:B2:385:G:C4'	21:B2:387:C:H41	2.28	0.47
31:AT:28:LEU:HD13	31:AT:28:LEU:O	2.15	0.47
61:Cc:48:LEU:HD21	61:Cc:60:ILE:CG2	2.40	0.47
78:CG:99:ALA:CB	78:CG:193:LEU:HD11	2.45	0.47
78:CG:146:LEU:HD13	78:CG:146:LEU:O	2.15	0.47
83:CR:1:MET:HE3	83:CR:2:SER:CA	2.45	0.47
83:CR:70:ARG:HE	83:CR:75:HIS:CB	2.25	0.47
83:CR:105:LEU:CD1	83:CR:135:LYS:HB3	2.45	0.47
14:AJ:60:LEU:HD21	14:AJ:73:GLU:HG3	1.97	0.46
20:AI:38:ILE:CG2	20:AI:96:LEU:HD21	2.45	0.46
25:AK:88:GLU:O	25:AK:89:ILE:HG22	2.15	0.46
32:AZ:108:ILE:HD11	36:AF:99:ILE:HD11	1.97	0.46
40:CL:86:ILE:CG2	40:CL:91:ALA:HB2	2.46	0.46
48:CA:60:LYS:HE2	48:CA:60:LYS:HA	1.97	0.46
48:CA:101:VAL:HG23	48:CA:164:ALA:C	2.39	0.46
60:CF:92:VAL:HG21	60:CF:133:LEU:HD22	1.96	0.46
70:CC:6:PRO:HD2	70:CC:24:LEU:HD21	1.97	0.46
83:CR:170:ARG:NH2	83:CR:173:ARG:HG3	2.22	0.46
83:CR:175:GLU:HB3	83:CR:178:GLN:HE21	1.80	0.46
2:Ct:287:ARG:HE	2:Ct:288:THR:HG22	1.80	0.46
3:AO:56:VAL:HG22	3:AO:57:THR:H	1.79	0.46
21:B2:1679:A:H3'	36:AF:60:ARG:HE	1.80	0.46
25:AK:19:GLY:C	25:AK:71:LEU:HD23	2.41	0.46
31:AT:65:TYR:HA	31:AT:123:LEU:HD13	1.98	0.46
48:CA:137:ILE:HD11	48:CA:149:LYS:CB	2.45	0.46
56:Cr:64:ILE:HB	56:Cr:81:THR:HA	1.98	0.46
79:A5:1550:G:P	83:CR:84:THR:HG21	2.55	0.46
83:CR:105:LEU:HG	83:CR:109:TYR:HE2	1.80	0.46
24:AU:50:VAL:HG22	24:AU:51:LYS:O	2.14	0.46
38:Cz:67:VAL:HG21	38:Cz:77:ALA:CB	2.45	0.46
39:CO:108:ILE:HG23	39:CO:108:ILE:O	2.15	0.46
41:CV:40:ILE:HD11	82:A6:3799:A:C4	2.50	0.46
46:CD:41:LYS:CE	50:CT:93:ILE:HD11	2.45	0.46
50:CT:30:TYR:HA	50:CT:93:ILE:HG21	1.97	0.46
50:CT:91:VAL:HG12	50:CT:92:ARG:H	1.79	0.46
70:CC:8:ILE:HG21	70:CC:257:PHE:HE2	1.81	0.46
70:CC:309:ILE:HG23	70:CC:310:HIS:H	1.81	0.46
77:CE:208:ILE:HG23	77:CE:212:LEU:CG	2.45	0.46
79:A5:2090:U:H2'	82:A6:2259:G:O4'	2.15	0.46
82:A6:2725:A:C8	83:CR:89:MET:HE1	2.50	0.46
82:A6:2890:C:H42	82:A6:3611:A:H61	1.63	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:AV:81:LYS:N	9:AV:81:LYS:HE2	2.31	0.46
34:AD:51:LEU:HD12	34:AD:91:VAL:HG22	1.97	0.46
36:AF:40:ALA:N	36:AF:68:ILE:HD11	2.31	0.46
56:Cr:126:VAL:HG12	56:Cr:127:LYS:N	2.31	0.46
61:Cc:79:ILE:HD12	61:Cc:79:ILE:H	1.80	0.46
71:Cm:78:ILE:HG13	71:Cm:82:LEU:HD12	1.98	0.46
75:CJ:96:LYS:CD	75:CJ:163:MET:HE2	2.46	0.46
5:AN:11:LEU:HD12	5:AN:11:LEU:O	2.16	0.46
18:AH:144:ILE:HD12	18:AH:153:LEU:O	2.15	0.46
41:CV:40:ILE:HG22	41:CV:62:MET:O	2.16	0.46
47:CQ:24:TYR:HE1	56:Cr:5:LEU:HD22	1.80	0.46
47:CQ:38:ARG:HB3	70:CC:302:LEU:HD22	1.96	0.46
47:CQ:43:PHE:CE1	47:CQ:81:VAL:HG11	2.51	0.46
47:CQ:79:THR:HG21	47:CQ:126:LEU:HD23	1.98	0.46
77:CE:111:LYS:O	77:CE:114:ARG:HG2	2.15	0.46
83:CR:143:HIS:HA	83:CR:146:LYS:HZ1	1.79	0.46
2:Ct:649:ILE:CG1	2:Ct:661:ILE:HD11	2.43	0.46
16:AC:173:LYS:O	16:AC:174:ILE:HG23	2.16	0.46
18:AH:60:ILE:HG23	18:AH:92:VAL:HG13	1.97	0.46
21:B2:110:U:O2	21:B2:351:G:N2	2.49	0.46
56:Cr:62:VAL:HG13	56:Cr:62:VAL:O	2.15	0.46
62:Cd:29:ILE:HD12	62:Cd:30:HIS:N	2.30	0.46
76:CH:156:ASN:O	76:CH:160:LEU:HD23	2.16	0.46
83:CR:145:LEU:HA	83:CR:148:ASP:OD1	2.16	0.46
83:CR:183:GLU:O	83:CR:187:THR:HG23	2.15	0.46
18:AH:75:ILE:HG23	18:AH:76:GLN:H	1.79	0.46
18:AH:146:VAL:HG21	19:AW:50:PHE:HE1	1.79	0.46
26:AM:32:ALA:HB3	26:AM:110:VAL:HB	1.97	0.46
27:AS:27:ALA:O	27:AS:31:THR:HG23	2.15	0.46
56:Cr:51:VAL:HB	56:Cr:113:ARG:CB	2.45	0.46
70:CC:115:VAL:HG23	70:CC:120:LYS:HG3	1.97	0.46
70:CC:294:LYS:HA	70:CC:294:LYS:HD3	1.65	0.46
77:CE:46:ARG:HE	77:CE:50:LEU:HD13	1.81	0.46
77:CE:85:LYS:HB3	77:CE:92:VAL:HG12	1.98	0.46
83:CR:82:LYS:HB2	83:CR:82:LYS:HE2	1.67	0.46
83:CR:124:TYR:O	83:CR:127:VAL:HG12	2.16	0.46
3:AO:129:ILE:HG23	11:Aa:65:PRO:HG3	1.98	0.46
8:AA:82:THR:HG21	8:AA:167:GLY:CA	2.46	0.46
34:AD:139:SER:O	34:AD:182:LEU:HD13	2.16	0.46
45:CI:41:ALA:HB1	45:CI:45:GLU:OE2	2.16	0.46
45:CI:112:GLN:O	45:CI:113:THR:HG23	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:Cf:74:VAL:HG13	64:Cf:84:VAL:HG13	1.97	0.46
77:CE:261:ILE:HD12	77:CE:262:LYS:N	2.30	0.46
78:CG:154:LEU:HD13	78:CG:155:VAL:N	2.31	0.46
79:A5:58:G:H2'	81:A8:33:G:H2'	1.98	0.46
83:CR:84:THR:HG23	83:CR:87:ALA:H	1.81	0.46
43:Ca:116:LYS:C	43:Ca:117:LEU:HD22	2.41	0.46
48:CA:110:GLY:H	48:CA:136:VAL:HG23	1.81	0.46
53:CX:80:PRO:HD3	57:Ch:33:VAL:HG22	1.98	0.46
77:CE:99:ASP:HA	77:CE:102:GLY:HA2	1.98	0.46
79:A5:113:A:N6	79:A5:158:A:H62	2.13	0.46
83:CR:4:LEU:HA	83:CR:7:GLN:OE1	2.16	0.46
83:CR:11:ALA:HA	83:CR:14:VAL:CG1	2.46	0.46
2:Ct:517:LEU:CD1	4:AX:50:ILE:HG21	2.46	0.46
14:AJ:118:GLY:O	14:AJ:119:LEU:HD23	2.15	0.46
20:AI:144:LYS:NZ	21:B2:208:G:H22	2.14	0.46
21:B2:796:G:H3'	21:B2:797:C:H5'	1.98	0.46
36:AF:86:LYS:O	36:AF:90:VAL:HG23	2.15	0.46
36:AF:150:ALA:O	36:AF:154:LEU:HD22	2.16	0.46
46:CD:148:ALA:HB2	82:A6:4323:A:N1	2.31	0.46
47:CQ:43:PHE:HE1	47:CQ:81:VAL:HG11	1.81	0.46
52:CU:100:LEU:HD22	52:CU:112:LEU:HB3	1.98	0.46
52:CU:102:VAL:HG22	52:CU:112:LEU:HD23	1.98	0.46
62:Cd:68:LEU:HD11	62:Cd:106:VAL:HG12	1.97	0.46
70:CC:180:ILE:HG22	70:CC:227:ILE:HD11	1.97	0.46
77:CE:108:LYS:CB	77:CE:114:ARG:HD3	2.46	0.46
83:CR:17:CYS:HB3	83:CR:52:ARG:NH2	2.30	0.46
32:AZ:108:ILE:CD1	36:AF:99:ILE:HD11	2.46	0.45
38:Cz:17:VAL:HG11	38:Cz:216:LEU:HD13	1.97	0.45
40:CL:86:ILE:HG22	40:CL:91:ALA:HB2	1.97	0.45
56:Cr:59:GLY:O	56:Cr:60:VAL:HB	2.15	0.45
59:CB:170:LEU:C	59:CB:171:LEU:HD23	2.41	0.45
64:Cf:106:TYR:HB2	77:CE:192:LYS:NZ	2.31	0.45
2:Ct:751:CYS:SG	2:Ct:755:VAL:HG23	2.55	0.45
8:AA:82:THR:HG22	8:AA:204:TYR:HB3	1.98	0.45
21:B2:1172:U:H5'	72:Cn:10:MET:HE1	1.98	0.45
24:AU:111:GLU:OE2	34:AD:11:PHE:HZ	1.99	0.45
30:AP:36:LEU:HD12	30:AP:36:LEU:O	2.16	0.45
41:CV:61:VAL:HG21	41:CV:81:VAL:HG23	1.98	0.45
44:CN:114:ARG:C	44:CN:134:LEU:HD13	2.42	0.45
48:CA:199:VAL:HG11	79:A5:1631:A:C5	2.52	0.45
51:CP:28:ASN:O	51:CP:32:THR:HG23	2.16	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:CP:33:ALA:HA	51:CP:36:ILE:HG22	1.98	0.45
63:Ce:84:GLU:O	63:Ce:87:VAL:HG12	2.16	0.45
76:CH:48:LEU:HD21	76:CH:56:ARG:CB	2.46	0.45
76:CH:92:MET:SD	76:CH:181:VAL:HG22	2.56	0.45
79:A5:2090:U:H3'	82:A6:2259:G:O4'	2.16	0.45
82:A6:2376:A:O2'	83:CR:1:MET:HE1	2.14	0.45
82:A6:2387:G:P	83:CR:24:LEU:HD23	2.56	0.45
83:CR:25:ASP:OD1	83:CR:27:ASN:HB3	2.16	0.45
83:CR:70:ARG:HA	83:CR:74:ARG:O	2.16	0.45
83:CR:109:TYR:C	83:CR:115:ILE:HG22	2.40	0.45
6:AL:16:ILE:HG22	6:AL:16:ILE:O	2.17	0.45
18:AH:142:LYS:HB2	18:AH:154:ILE:HD11	1.96	0.45
24:AU:88:LEU:C	24:AU:89:ILE:HD12	2.41	0.45
29:AR:78:ARG:HD3	29:AR:78:ARG:C	2.42	0.45
40:CL:77:SER:O	40:CL:81:LEU:HD22	2.15	0.45
42:CM:27:ILE:HD12	42:CM:37:LEU:O	2.15	0.45
44:CN:132:VAL:HG12	44:CN:134:LEU:CD2	2.45	0.45
77:CE:181:LEU:HD11	77:CE:268:GLN:HA	1.98	0.45
82:A6:2663:G:O3'	83:CR:117:ARG:HG2	2.17	0.45
82:A6:2668:G:OP1	83:CR:128:LYS:HE2	2.17	0.45
83:CR:174:GLU:HA	83:CR:177:LEU:CG	2.44	0.45
6:AL:157:LYS:HE2	83:CR:163:ARG:HE	1.82	0.45
8:AA:111:GLN:HB2	16:AC:63:VAL:HG21	1.97	0.45
15:AE:194:VAL:O	15:AE:210:VAL:HG13	2.16	0.45
23:Ag:197:THR:HG21	23:Ag:238:ALA:C	2.42	0.45
44:CN:55:ALA:HB1	79:A5:148:A:H4'	1.97	0.45
77:CE:149:ILE:HG22	77:CE:199:THR:O	2.17	0.45
77:CE:174:LEU:HD11	77:CE:186:LEU:CD1	2.43	0.45
2:Ct:21:ASN:HB3	2:Ct:122:THR:HG22	1.97	0.45
4:AX:51:VAL:HG13	4:AX:70:VAL:HG13	1.99	0.45
7:AB:49:VAL:CG2	7:AB:62:LEU:HD13	2.47	0.45
9:AV:43:THR:HG23	9:AV:44:GLY:H	1.81	0.45
16:AC:70:VAL:HG21	16:AC:93:ILE:HD12	1.98	0.45
21:B2:1650:A:H5''	37:AQ:139:ALA:HB2	1.98	0.45
25:AK:20:VAL:HG11	34:AD:72:VAL:CG2	2.46	0.45
32:AZ:100:VAL:HG21	36:AF:102:LEU:HD11	1.99	0.45
33:Ac:31:ARG:HA	33:Ac:43:ILE:HD13	1.98	0.45
42:CM:46:ARG:HH12	79:A5:934:C:H41	1.64	0.45
44:CN:113:LEU:HB2	44:CN:134:LEU:HD12	1.97	0.45
46:CD:104:LEU:HD23	46:CD:247:ILE:HG12	1.98	0.45
59:CB:219:VAL:HG11	59:CB:337:VAL:HG23	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:CF:122:PHE:HE2	60:CF:150:VAL:HG23	1.82	0.45
75:CJ:89:VAL:HG21	75:CJ:115:LEU:HB3	1.98	0.45
76:CH:38:PHE:HE2	76:CH:73:ILE:HG23	1.79	0.45
77:CE:44:CYS:HA	77:CE:54:ILE:HD11	1.99	0.45
83:CR:42:ARG:CA	83:CR:45:ILE:HG22	2.46	0.45
2:Ct:115:VAL:CG1	2:Ct:142:VAL:HG23	2.47	0.45
21:B2:1368:U:H5''	29:AR:1:MET:HE2	1.98	0.45
43:Ca:75:LEU:HB3	43:Ca:117:LEU:HD11	1.97	0.45
15:AE:140:VAL:HG21	21:B2:343:A:O2'	2.17	0.45
21:B2:1569:A:H1'	21:B2:1613:G:H21	1.82	0.45
26:AM:79:VAL:HG11	26:AM:88:TRP:CZ3	2.50	0.45
34:AD:116:ARG:HD3	34:AD:116:ARG:H	1.81	0.45
36:AF:88:MET:HE2	36:AF:92:ILE:HD11	1.98	0.45
39:CO:108:ILE:HD11	39:CO:112:TYR:O	2.17	0.45
43:Ca:21:ARG:HH21	82:A6:2282:A:H5''	1.81	0.45
51:CP:36:ILE:C	51:CP:39:MET:HE1	2.42	0.45
82:A6:4075:U:H3	82:A6:4170:A:H62	1.64	0.45
83:CR:106:LEU:CD1	83:CR:138:LEU:HD11	2.47	0.45
17:AG:18:VAL:HG13	17:AG:24:LEU:HD11	1.99	0.45
21:B2:1388:A:H61	34:AD:161:GLY:CA	2.30	0.45
59:CB:332:MET:HA	59:CB:332:MET:HE3	1.98	0.45
74:Co:55:ILE:HD11	74:Co:57:ARG:NH1	2.32	0.45
76:CH:34:LEU:HD13	76:CH:35:ARG:N	2.32	0.45
77:CE:208:ILE:HG23	77:CE:212:LEU:HG	1.98	0.45
83:CR:168:GLU:HA	83:CR:171:LYS:HD2	1.99	0.45
2:Ct:570:ILE:HD12	2:Ct:571:LYS:C	2.41	0.45
20:AI:158:ILE:HD11	20:AI:162:LEU:HB3	1.97	0.45
46:CD:211:LEU:HD22	46:CD:218:ALA:CB	2.47	0.45
60:CF:141:ALA:HB1	60:CF:236:ARG:NH1	2.31	0.45
70:CC:326:LEU:CD2	70:CC:332:ALA:HB3	2.47	0.45
73:Cp:75:SER:O	73:Cp:79:VAL:HG23	2.17	0.45
74:Co:55:ILE:HD11	74:Co:57:ARG:CZ	2.47	0.45
77:CE:125:LEU:HD12	79:A5:960:A:OP2	2.17	0.45
79:A5:1273:G:H3'	79:A5:1274:A:H5'	1.99	0.45
83:CR:152:LYS:HA	83:CR:155:LEU:HD12	1.99	0.45
2:Ct:321:ILE:HD13	2:Ct:323:LEU:HD23	1.98	0.45
22:CW:34:ALA:HB3	82:A6:4663:G:OP1	2.16	0.45
29:AR:68:GLY:C	29:AR:69:ILE:HD13	2.42	0.45
36:AF:100:ILE:HD11	36:AF:177:LEU:HD12	1.99	0.45
60:CF:213:LEU:HB3	60:CF:247:MET:HE3	1.99	0.45
5:AN:22:VAL:HA	5:AN:24:THR:HG23	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AB:121:ILE:HG13	7:AB:164:ILE:HD11	1.99	0.44
8:AA:58:LEU:HD13	8:AA:58:LEU:O	2.17	0.44
17:AG:106:LEU:HD12	17:AG:108:VAL:O	2.17	0.44
31:AT:72:VAL:HG22	31:AT:97:LYS:HB2	1.97	0.44
65:Cg:41:ALA:HB3	65:Cg:52:ARG:HG2	1.99	0.44
2:Ct:163:ALA:HB1	2:Ct:174:LEU:HD11	2.00	0.44
4:AX:128:VAL:HG13	4:AX:133:LEU:HD21	1.99	0.44
5:AN:108:ASP:HB3	5:AN:111:ALA:HB3	1.99	0.44
7:AB:129:THR:HG22	7:AB:176:VAL:O	2.17	0.44
9:AV:39:VAL:HG23	9:AV:41:LYS:H	1.83	0.44
24:AU:36:CYS:O	24:AU:40:ILE:HD12	2.16	0.44
26:AM:42:LEU:HD13	26:AM:68:LEU:HB2	1.98	0.44
46:CD:155:THR:HG23	80:A7:36:C:H5''	2.00	0.44
48:CA:78:ALA:HB1	48:CA:82:ILE:HD11	1.99	0.44
77:CE:157:HIS:CD2	77:CE:184:VAL:HG13	2.52	0.44
10:AY:16:ARG:HE	15:AE:95:THR:HG23	1.82	0.44
18:AH:134:VAL:HG11	18:AH:158:LEU:HD11	1.99	0.44
25:AK:43:LEU:O	25:AK:44:HIS:HB2	2.18	0.44
43:Ca:100:ILE:C	43:Ca:101:ILE:HD12	2.43	0.44
79:A5:1532:G:H21	79:A5:1637:A:P	2.40	0.44
2:Ct:115:VAL:HG11	2:Ct:142:VAL:HG23	1.99	0.44
2:Ct:719:GLY:HA3	21:B2:1825:A:H62	1.82	0.44
6:AL:33:LEU:HD13	6:AL:34:PRO:O	2.16	0.44
8:AA:197:VAL:HG13	8:AA:201:LEU:HD22	1.99	0.44
11:Aa:6:ARG:HB2	21:B2:1865:C:H41	1.83	0.44
77:CE:124:LYS:HD2	79:A5:959:G:C2	2.52	0.44
78:CG:111:LYS:O	78:CG:115:LEU:HD13	2.18	0.44
83:CR:153:LYS:O	83:CR:156:ALA:HB3	2.17	0.44
83:CR:170:ARG:HA	83:CR:173:ARG:HG2	2.00	0.44
15:AE:256:LEU:HD12	15:AE:257:ALA:N	2.32	0.44
16:AC:69:LEU:HD13	16:AC:75:ILE:HD11	1.98	0.44
17:AG:234:LEU:HA	17:AG:237:LEU:HD12	1.98	0.44
18:AH:30:LEU:HD22	18:AH:82:GLU:OE2	2.16	0.44
27:AS:125:HIS:NE2	27:AS:131:VAL:HG21	2.33	0.44
29:AR:100:PRO:O	29:AR:102:THR:N	2.51	0.44
53:CX:95:THR:HG22	53:CX:139:ARG:CG	2.47	0.44
57:Ch:24:LEU:HD11	57:Ch:54:ILE:CG2	2.48	0.44
59:CB:45:ALA:HB3	59:CB:183:ILE:HD12	2.00	0.44
75:CJ:103:GLY:C	75:CJ:157:ILE:HD12	2.43	0.44
82:A6:4974:C:H42	82:A6:4984:C:H42	1.65	0.44
21:B2:1286:G:H22	26:AM:33:ARG:NH1	2.14	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Ag:5:MET:SD	23:Ag:312:VAL:HG22	2.57	0.44
40:CL:69:LYS:HE2	40:CL:69:LYS:HA	1.99	0.44
56:Cr:6:GLN:OE1	70:CC:135:ALA:HB3	2.18	0.44
61:Cc:34:THR:HG22	61:Cc:95:ALA:HB2	2.00	0.44
65:Cg:15:THR:HG22	79:A5:1543:G:O2'	2.16	0.44
77:CE:215:ALA:HA	77:CE:218:LYS:HE3	2.00	0.44
12:Ab:55:LEU:HD13	12:Ab:56:CYS:N	2.32	0.44
12:Ab:55:LEU:HD11	12:Ab:60:SER:HA	2.00	0.44
25:AK:32:HIS:O	25:AK:36:ALA:HB2	2.18	0.44
70:CC:331:TYR:O	70:CC:335:MET:HG2	2.17	0.44
77:CE:168:LEU:HD21	77:CE:214:ASP:CG	2.42	0.44
79:A5:2090:U:C1'	82:A6:2259:G:H5''	2.44	0.44
83:CR:106:LEU:HD23	83:CR:120:TYR:CE1	2.53	0.44
8:AA:68:ILE:HG21	8:AA:74:VAL:CG2	2.48	0.44
42:CM:20:HIS:CD2	42:CM:45:VAL:HG13	2.53	0.44
45:CI:102:MET:HE2	45:CI:102:MET:HA	2.00	0.44
83:CR:102:LEU:HD11	83:CR:134:ASN:C	2.43	0.44
83:CR:113:LYS:HE2	83:CR:113:LYS:H	1.82	0.44
83:CR:137:ILE:HA	83:CR:140:GLU:OE1	2.17	0.44
7:AB:97:LEU:HD21	7:AB:232:HIS:CG	2.53	0.44
14:AJ:47:LYS:HE3	14:AJ:102:ILE:HD11	2.00	0.44
14:AJ:78:LEU:O	14:AJ:82:VAL:HG23	2.18	0.44
40:CL:9:VAL:HG23	40:CL:9:VAL:O	2.18	0.44
49:CS:82:LEU:HD23	49:CS:95:ARG:CD	2.47	0.44
70:CC:95:MET:N	70:CC:95:MET:HE3	2.33	0.44
77:CE:45:SER:O	77:CE:54:ILE:HD12	2.18	0.44
79:A5:950:G:H2'	79:A5:951:G:O4'	2.17	0.44
33:Ac:31:ARG:HD2	33:Ac:41:SER:HB3	1.99	0.43
34:AD:116:ARG:H	34:AD:116:ARG:CD	2.31	0.43
39:CO:126:VAL:HG23	82:A6:4762:A:H2'	2.00	0.43
83:CR:107:ARG:HH11	83:CR:107:ARG:HG3	1.83	0.43
2:Ct:331:GLU:HA	2:Ct:335:LEU:HD12	1.99	0.43
2:Ct:577:VAL:HG13	2:Ct:579:TYR:CE1	2.53	0.43
2:Ct:664:ASP:OD1	2:Ct:666:THR:HG22	2.18	0.43
4:AX:135:LYS:HB2	4:AX:135:LYS:HZ3	1.83	0.43
7:AB:35:ALA:HB2	7:AB:44:ILE:HD11	1.98	0.43
8:AA:146:ALA:CB	8:AA:157:VAL:HG21	2.48	0.43
22:CW:20:ARG:HG2	41:CV:96:LEU:HB3	2.00	0.43
23:Ag:10:THR:HB	23:Ag:306:LEU:HD21	1.99	0.43
23:Ag:205:SER:C	23:Ag:206:LEU:HD23	2.44	0.43
34:AD:158:ILE:HG21	34:AD:163:PRO:HB2	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AF:72:LEU:HD22	36:AF:155:CYS:SG	2.58	0.43
44:CN:21:PHE:HD1	44:CN:22:LEU:HD22	1.83	0.43
47:CQ:34:PHE:CG	70:CC:293:LEU:HD11	2.53	0.43
66:CI:37:THR:HA	66:CI:40:VAL:HG12	1.99	0.43
69:CI:9:ILE:O	69:CI:13:LEU:HD23	2.17	0.43
76:CH:20:LEU:HD23	76:CH:25:VAL:HG12	2.00	0.43
77:CE:186:LEU:HD12	77:CE:212:LEU:HD21	2.00	0.43
83:CR:64:ARG:HA	83:CR:67:THR:CG2	2.48	0.43
83:CR:146:LYS:HB3	83:CR:146:LYS:HE3	1.52	0.43
1:tR:19:G:H22	1:tR:59:A:H5'	1.83	0.43
10:AY:121:ALA:HB3	21:B2:84:A:H4'	1.99	0.43
21:B2:1231:C:OP2	27:AS:139:THR:HG21	2.18	0.43
23:Ag:249:CYS:HA	23:Ag:258:ILE:HG22	2.00	0.43
24:AU:63:ILE:HD11	28:Ad:43:PHE:CE2	2.53	0.43
43:Ca:100:ILE:HD12	43:Ca:100:ILE:O	2.19	0.43
56:Cr:61:VAL:CG2	56:Cr:86:ALA:HB3	2.48	0.43
79:A5:516:G:H1	79:A5:645:G:H1	1.66	0.43
83:CR:133:LYS:HZ2	83:CR:134:ASN:HB3	1.83	0.43
83:CR:151:ARG:NH1	83:CR:151:ARG:HB2	2.33	0.43
2:Ct:174:LEU:HD12	2:Ct:178:PHE:CZ	2.52	0.43
2:Ct:583:VAL:HG22	2:Ct:700:VAL:HG12	2.00	0.43
8:AA:185:MET:HE2	9:AV:39:VAL:HG12	2.00	0.43
10:AY:89:HIS:HB2	10:AY:93:ARG:HH22	1.83	0.43
21:B2:1523:C:H5''	27:AS:141:ARG:HE	1.84	0.43
23:Ag:205:SER:O	23:Ag:206:LEU:HD23	2.17	0.43
23:Ag:260:ASP:H	23:Ag:267:VAL:HG23	1.83	0.43
26:AM:74:ILE:O	26:AM:74:ILE:HD12	2.18	0.43
46:CD:104:LEU:HD13	46:CD:104:LEU:O	2.18	0.43
53:CX:116:LEU:HD13	53:CX:117:TYR:CZ	2.53	0.43
59:CB:77:THR:HG21	59:CB:337:VAL:CG1	2.48	0.43
3:AO:119:LEU:HD12	3:AO:120:ALA:N	2.34	0.43
21:B2:421:G:H4'	21:B2:660:C:H42	1.83	0.43
21:B2:1284:A:N1	26:AM:91:LEU:HD21	2.33	0.43
38:Cz:29:LEU:HD22	38:Cz:172:VAL:HG22	2.00	0.43
44:CN:188:ARG:HD3	44:CN:189:ARG:H	1.83	0.43
48:CA:48:ILE:HD11	48:CA:57:PRO:HB2	2.00	0.43
48:CA:238:ILE:HD12	48:CA:238:ILE:O	2.19	0.43
59:CB:232:THR:HG21	59:CB:249:ARG:HA	2.01	0.43
64:Cf:53:ALA:HB1	79:A5:442:G:H4'	2.01	0.43
70:CC:294:LYS:HZ1	79:A5:2089:G:P	2.41	0.43
70:CC:333:LYS:HD2	77:CE:46:ARG:CZ	2.49	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:Co:81:ARG:CZ	82:A6:4294:C:H5''	2.49	0.43
74:Co:85:ILE:HG21	82:A6:4292:A:H2	1.84	0.43
77:CE:94:LYS:N	77:CE:95:PRO:HD2	2.34	0.43
77:CE:113:PRO:CB	79:A5:458:C:H4'	2.48	0.43
83:CR:162:ARG:O	83:CR:165:LYS:HB3	2.18	0.43
83:CR:170:ARG:O	83:CR:174:GLU:HB3	2.19	0.43
2:Ct:469:ILE:O	2:Ct:469:ILE:HD12	2.19	0.43
5:AN:63:VAL:HG11	5:AN:71:ILE:HG22	1.99	0.43
7:AB:85:LYS:HB2	7:AB:101:HIS:O	2.19	0.43
8:AA:42:LYS:HZ1	29:AR:102:THR:HG23	1.82	0.43
83:CR:89:MET:HA	83:CR:89:MET:CE	2.34	0.43
83:CR:109:TYR:HD1	83:CR:114:LYS:HB3	1.84	0.43
83:CR:164:SER:HA	83:CR:167:LYS:HE3	1.99	0.43
8:AA:38:ILE:HD11	8:AA:47:TYR:HB3	2.01	0.43
16:AC:106:VAL:CG2	16:AC:109:ILE:HD11	2.49	0.43
16:AC:174:ILE:HD12	16:AC:174:ILE:O	2.18	0.43
25:AK:22:VAL:HG13	34:AD:75:LYS:HE2	2.00	0.43
37:AQ:57:LEU:HD13	37:AQ:112:LEU:HD23	2.01	0.43
50:CT:64:VAL:HG13	50:CT:73:GLY:O	2.19	0.43
59:CB:99:LEU:HD12	82:A6:4582:C:H4'	2.00	0.43
61:Cc:48:LEU:CD2	61:Cc:60:ILE:HD13	2.49	0.43
70:CC:222:ARG:HD2	70:CC:223:ASN:N	2.34	0.43
2:Ct:249:ARG:O	2:Ct:253:VAL:HG23	2.19	0.43
21:B2:1259:A:H62	21:B2:1518:C:H2'	1.82	0.43
37:AQ:56:LEU:H	37:AQ:56:LEU:HD23	1.84	0.43
39:CO:8:VAL:HG21	39:CO:115:LYS:HG2	2.01	0.43
53:CX:76:ILE:O	53:CX:100:VAL:HG13	2.19	0.43
75:CJ:124:GLY:O	75:CJ:125:ILE:HD13	2.19	0.43
77:CE:180:VAL:HB	77:CE:258:LEU:HD21	2.00	0.43
83:CR:45:ILE:HD13	83:CR:50:ILE:HD12	2.01	0.43
83:CR:134:ASN:OD1	83:CR:136:ARG:HB2	2.19	0.43
8:AA:28:THR:HG22	8:AA:45:GLY:O	2.18	0.43
10:AY:16:ARG:HG2	15:AE:95:THR:HG23	1.99	0.43
14:AJ:72:PHE:CD2	15:AE:248:ILE:HD12	2.54	0.43
38:Cz:55:LEU:HD12	38:Cz:153:SER:O	2.18	0.43
51:CP:49:LYS:HE2	51:CP:49:LYS:HA	2.00	0.43
60:CF:156:LYS:HD2	70:CC:317:ASN:OD1	2.19	0.43
63:Ce:53:ILE:HD12	63:Ce:53:ILE:O	2.19	0.43
76:CH:111:LEU:HD12	76:CH:125:ARG:HB2	2.01	0.43
79:A5:1979:A:H3'	79:A5:1980:G:C5'	2.48	0.43
82:A6:4646:U:H5	83:CR:62:ARG:HH22	1.67	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:CR:14:VAL:HG11	83:CR:41:ILE:HG22	1.99	0.43
83:CR:75:HIS:HB3	83:CR:80:LYS:HE2	2.00	0.43
83:CR:106:LEU:HB3	83:CR:120:TYR:CE1	2.53	0.43
83:CR:119:MET:HG3	83:CR:119:MET:H	1.66	0.43
83:CR:177:LEU:HD22	83:CR:180:LYS:NZ	2.34	0.43
8:AA:118:GLU:OE1	16:AC:64:THR:HG22	2.19	0.43
37:AQ:32:ILE:HG12	37:AQ:68:ILE:HD12	2.01	0.43
56:Cr:126:VAL:HA	56:Cr:129:LYS:HG3	2.01	0.43
75:CJ:139:PHE:HA	75:CJ:151:ILE:HD11	2.01	0.43
82:A6:2387:G:H1'	83:CR:26:PRO:HG3	2.01	0.43
2:Ct:12:ILE:HD12	2:Ct:99:LEU:HD23	2.00	0.42
36:AF:100:ILE:CD1	36:AF:177:LEU:HD12	2.49	0.42
38:Cz:65:VAL:O	38:Cz:82:ILE:HD11	2.19	0.42
51:CP:32:THR:O	51:CP:36:ILE:HG22	2.19	0.42
57:Ch:28:LEU:CD2	57:Ch:31:LEU:HD22	2.47	0.42
65:Cg:11:LEU:HD13	65:Cg:12:SER:N	2.34	0.42
65:Cg:96:LEU:HD12	65:Cg:97:ILE:N	2.34	0.42
75:CJ:159:LYS:CG	75:CJ:163:MET:HE3	2.48	0.42
82:A6:4749:C:N4	82:A6:4951:G:H22	2.17	0.42
83:CR:23:TRP:HB2	83:CR:53:LYS:HE3	2.01	0.42
2:Ct:143:LEU:HD23	2:Ct:143:LEU:O	2.19	0.42
7:AB:141:GLY:CA	7:AB:210:VAL:HG22	2.49	0.42
8:AA:7:VAL:HG11	9:AV:43:THR:OG1	2.19	0.42
15:AE:153:LEU:HD21	15:AE:172:PHE:CZ	2.55	0.42
16:AC:210:PRO:O	16:AC:214:LEU:HD22	2.19	0.42
39:CO:120:VAL:HG12	39:CO:122:ALA:H	1.83	0.42
40:CL:111:GLN:HA	40:CL:114:VAL:HG22	2.01	0.42
45:CI:91:LEU:HG	45:CI:135:ILE:HD13	2.01	0.42
46:CD:53:VAL:HG22	46:CD:62:CYS:HB3	2.01	0.42
56:Cr:6:GLN:HB3	56:Cr:43:LEU:HD13	2.00	0.42
56:Cr:51:VAL:CB	56:Cr:113:ARG:HB2	2.49	0.42
56:Cr:112:ARG:HH12	77:CE:118:THR:HG23	1.84	0.42
64:Cf:46:ARG:N	64:Cf:107:PRO:HD2	2.34	0.42
66:Ci:7:MET:HE3	66:Ci:8:ALA:H	1.84	0.42
78:CG:157:ILE:HG23	78:CG:167:VAL:CG1	2.49	0.42
79:A5:65:A:H61	79:A5:75:G:H1'	1.83	0.42
82:A6:3596:A:H4'	83:CR:146:LYS:NZ	2.33	0.42
83:CR:180:LYS:HA	83:CR:183:GLU:OE1	2.19	0.42
4:AX:51:VAL:HG22	4:AX:70:VAL:CG1	2.46	0.42
17:AG:68:LEU:HG	17:AG:69:THR:HG23	2.01	0.42
26:AM:57:ASP:C	26:AM:58:GLU:OE1	2.62	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:CO:170:LYS:HD2	39:CO:171:LYS:N	2.34	0.42
48:CA:104:VAL:HG11	48:CA:146:THR:HG21	2.01	0.42
70:CC:152:LEU:HD23	70:CC:249:PHE:HZ	1.82	0.42
76:CH:141:LYS:HD3	76:CH:142:ASP:HB3	1.99	0.42
77:CE:254:ASP:O	77:CE:258:LEU:HG	2.20	0.42
82:A6:2664:G:OP1	83:CR:117:ARG:HG2	2.20	0.42
83:CR:8:LYS:HG3	83:CR:22:VAL:CG2	2.48	0.42
54:CY:47:MET:HE1	54:CY:119:LEU:HD22	2.01	0.42
70:CC:227:ILE:HG22	70:CC:229:LEU:HD12	2.01	0.42
77:CE:96:VAL:H	77:CE:104:THR:HG22	1.85	0.42
83:CR:28:GLU:HB3	83:CR:31:GLU:CD	2.44	0.42
3:AO:53:ILE:HG21	7:AB:48:LEU:HD21	2.00	0.42
7:AB:223:PHE:CE1	7:AB:225:LEU:HD23	2.55	0.42
8:AA:53:ARG:HH22	9:AV:70:LEU:HD13	1.83	0.42
14:AJ:65:GLU:O	14:AJ:66:LYS:HB3	2.19	0.42
23:Ag:260:ASP:N	23:Ag:267:VAL:HG23	2.34	0.42
45:CI:135:ILE:HG22	45:CI:136:MET:SD	2.59	0.42
47:CQ:87:THR:HB	79:A5:1503:A:H62	1.84	0.42
59:CB:333:LEU:HD22	59:CB:334:LYS:H	1.84	0.42
64:Cf:10:ILE:HD12	64:Cf:99:HIS:O	2.20	0.42
64:Cf:28:LEU:CD2	64:Cf:86:ALA:HB3	2.49	0.42
77:CE:91:THR:CB	77:CE:106:VAL:HG13	2.50	0.42
79:A5:1100:U:H3	79:A5:1195:G:H22	1.68	0.42
82:A6:2667:C:O4'	83:CR:96:MET:HE1	2.19	0.42
2:Ct:652:PHE:HE1	2:Ct:661:ILE:HD13	1.83	0.42
2:Ct:781:MET:HE3	2:Ct:781:MET:HA	2.01	0.42
6:AL:145:VAL:HG22	6:AL:147:LYS:H	1.85	0.42
19:AW:52:ILE:O	19:AW:52:ILE:HD12	2.20	0.42
42:CM:103:LYS:HE3	42:CM:103:LYS:HA	2.01	0.42
54:CY:118:ILE:HD11	81:A8:70:G:OP1	2.19	0.42
76:CH:16:VAL:HG21	76:CH:85:THR:HG23	2.00	0.42
82:A6:3956:G:H1	82:A6:4056:A:H61	1.66	0.42
83:CR:3:MET:O	83:CR:4:LEU:HD23	2.19	0.42
83:CR:170:ARG:HA	83:CR:173:ARG:NE	2.34	0.42
3:AO:76:LEU:HD12	3:AO:77:ALA:N	2.35	0.42
15:AE:102:ILE:HD11	15:AE:112:HIS:HB2	2.00	0.42
18:AH:122:LEU:HD12	18:AH:123:THR:N	2.35	0.42
19:AW:65:LEU:HD12	19:AW:66:THR:O	2.19	0.42
23:Ag:217:MET:HA	23:Ag:217:MET:HE2	2.02	0.42
24:AU:111:GLU:N	24:AU:111:GLU:OE1	2.53	0.42
48:CA:57:PRO:HD2	48:CA:170:ALA:HB3	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:Cr:51:VAL:HG13	56:Cr:63:VAL:HG22	2.02	0.42
56:Cr:120:SER:HA	56:Cr:123:PRO:HG2	2.01	0.42
57:Ch:43:LYS:O	57:Ch:47:ILE:HG23	2.19	0.42
63:Ce:70:LEU:HD21	63:Ce:76:LYS:HB3	2.01	0.42
64:Cf:95:LYS:HA	64:Cf:95:LYS:HD3	1.81	0.42
77:CE:264:ILE:CG2	77:CE:267:LEU:HD22	2.49	0.42
2:Ct:22:MET:O	2:Ct:122:THR:HG21	2.20	0.42
2:Ct:580:ARG:O	2:Ct:740:LEU:HD23	2.18	0.42
10:AY:74:MET:HE3	10:AY:74:MET:HA	2.02	0.42
21:B2:1219:C:H42	21:B2:1646:C:H41	1.67	0.42
36:AF:26:ASP:O	36:AF:27:ASP:HB3	2.20	0.42
42:CM:29:ASP:OD2	49:CS:75:VAL:HG21	2.19	0.42
59:CB:82:PRO:HG3	59:CB:171:LEU:HD21	2.02	0.42
64:Cf:7:SER:HB3	64:Cf:103:VAL:O	2.20	0.42
67:Cj:5:THR:HG22	82:A6:2793:G:O2'	2.19	0.42
70:CC:305:PRO:C	70:CC:306:ARG:HD3	2.45	0.42
77:CE:61:ALA:HB1	79:A5:1239:C:H41	1.85	0.42
77:CE:233:PHE:C	77:CE:235:THR:H	2.28	0.42
3:AO:44:VAL:HG23	3:AO:53:ILE:O	2.19	0.42
6:AL:137:THR:HG22	20:AI:13:LYS:HB2	2.01	0.42
21:B2:1288:U:H3	21:B2:1311:C:H42	1.67	0.42
32:AZ:62:VAL:HG11	32:AZ:91:LEU:CD1	2.49	0.42
38:Cz:68:LEU:HD23	38:Cz:90:LEU:HD12	2.01	0.42
47:CQ:27:LEU:CD1	70:CC:287:THR:HG23	2.49	0.42
51:CP:16:LYS:HB3	51:CP:149:ILE:HG22	2.00	0.42
55:CZ:95:VAL:O	55:CZ:100:VAL:HG21	2.20	0.42
64:Cf:30:ILE:O	64:Cf:33:VAL:HG12	2.19	0.42
70:CC:242:PRO:HB2	82:A6:2297:G:H4'	2.01	0.42
77:CE:76:ALA:HB2	79:A5:1274:A:H4'	2.00	0.42
77:CE:181:LEU:HD22	77:CE:271:LEU:HD13	2.01	0.42
83:CR:102:LEU:HB2	83:CR:127:VAL:HG21	2.01	0.42
2:Ct:671:TYR:C	2:Ct:672:LEU:HD22	2.45	0.42
3:AO:135:ILE:HD12	3:AO:136:PRO:HD2	2.02	0.42
14:AJ:58:ARG:O	14:AJ:62:THR:HG22	2.20	0.42
17:AG:123:GLY:O	17:AG:124:LEU:HD12	2.20	0.42
18:AH:61:ILE:HD11	18:AH:95:ILE:HG13	2.02	0.42
21:B2:1284:A:C6	26:AM:91:LEU:HD21	2.55	0.42
21:B2:1520:G:H21	30:AP:126:VAL:HG13	1.84	0.42
23:Ag:32:LEU:HB2	23:Ag:71:ILE:HD11	2.01	0.42
33:Ac:9:ILE:HD11	33:Ac:57:THR:HG22	2.01	0.42
41:CV:105:ILE:C	41:CV:105:ILE:HD12	2.45	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:CQ:67:ILE:HG13	47:CQ:92:VAL:HG21	2.02	0.42
82:A6:4937:C:H4'	82:A6:4938:A:OP2	2.20	0.42
5:AN:61:ALA:HB1	21:B2:1016:U:H6	1.84	0.41
18:AH:109:ARG:CG	21:B2:744:G:H21	2.33	0.41
22:CW:70:LYS:C	22:CW:70:LYS:HD2	2.45	0.41
23:Ag:150:TRP:CH2	29:AR:34:VAL:HG22	2.52	0.41
28:Ad:46:TYR:O	28:Ad:50:ILE:HG22	2.20	0.41
36:AF:69:VAL:O	36:AF:73:THR:HG23	2.20	0.41
39:CO:128:ARG:HE	49:CS:161:ARG:NH2	2.18	0.41
44:CN:22:LEU:HD11	78:CG:164:ILE:CD1	2.44	0.41
50:CT:52:MET:HE2	50:CT:52:MET:HA	2.02	0.41
54:CY:111:LEU:HD11	54:CY:116:LYS:HG3	2.02	0.41
55:CZ:2:GLY:N	61:Cc:67:ALA:HB1	2.35	0.41
83:CR:90:PRO:CB	83:CR:93:VAL:HG12	2.34	0.41
2:Ct:609:PHE:CE1	2:Ct:661:ILE:HG22	2.55	0.41
15:AE:87:MET:HE1	15:AE:100:ARG:NE	2.35	0.41
16:AC:137:VAL:HG23	16:AC:216:MET:HG3	2.02	0.41
27:AS:123:LEU:HD11	27:AS:127:TRP:CZ3	2.54	0.41
39:CO:93:LYS:HG3	79:A5:1308:C:H5''	2.02	0.41
77:CE:205:ASN:O	77:CE:206:VAL:HG23	2.20	0.41
79:A5:113:A:H61	79:A5:158:A:H62	1.68	0.41
79:A5:2090:U:H1'	82:A6:2258:C:O2'	2.20	0.41
2:Ct:652:PHE:CE1	2:Ct:661:ILE:HD13	2.56	0.41
21:B2:191:A:H3'	21:B2:192:C:H5''	2.02	0.41
26:AM:60:MET:HE3	26:AM:61:TYR:HB3	2.03	0.41
31:AT:107:LEU:CB	31:AT:113:VAL:HG22	2.50	0.41
38:Cz:163:LEU:HD12	38:Cz:163:LEU:O	2.20	0.41
46:CD:207:TYR:CE1	46:CD:211:LEU:HD21	2.56	0.41
50:CT:110:LYS:O	50:CT:114:GLN:NE2	2.51	0.41
59:CB:325:GLU:O	59:CB:326:VAL:HG22	2.20	0.41
60:CF:171:ASP:OD2	60:CF:173:ALA:HB3	2.19	0.41
63:Ce:8:VAL:HG13	79:A5:702:U:H5'	2.01	0.41
74:Co:22:LYS:HE2	74:Co:22:LYS:H	1.85	0.41
79:A5:1241:C:H3'	79:A5:1242:G:H5''	2.02	0.41
83:CR:71:ARG:HE	83:CR:71:ARG:CA	2.24	0.41
2:Ct:743:PRO:O	2:Ct:790:VAL:HG23	2.19	0.41
6:AL:93:LEU:HD12	6:AL:102:PHE:CB	2.50	0.41
10:AY:48:TYR:O	10:AY:50:THR:HG23	2.20	0.41
21:B2:1556:A:H1'	21:B2:1557:C:OP1	2.20	0.41
23:Ag:5:MET:HE3	23:Ag:258:ILE:HD12	2.03	0.41
28:Ad:50:ILE:HG23	28:Ad:52:PHE:HB2	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:Ac:7:GLN:OE1	33:Ac:59:LEU:HD12	2.20	0.41
39:CO:192:TYR:HD1	42:CM:122:ILE:HD13	1.86	0.41
40:CL:141:ALA:O	40:CL:147:ALA:HB3	2.19	0.41
42:CM:27:ILE:HD11	42:CM:29:ASP:O	2.19	0.41
60:CF:50:ILE:HD11	60:CF:185:ILE:HD13	2.03	0.41
70:CC:101:MET:HE1	82:A6:2343:G:C5	2.56	0.41
78:CG:170:LEU:H	78:CG:171:PRO:HD2	1.84	0.41
82:A6:2694:G:H5'	82:A6:2696:A:H62	1.85	0.41
2:Ct:590:LEU:HD11	2:Ct:705:HIS:HB2	2.03	0.41
2:Ct:604:MET:HE2	2:Ct:728:CYS:HB3	2.02	0.41
8:AA:176:TRP:HZ3	8:AA:177:MET:HE3	1.85	0.41
15:AE:45:ILE:HG13	15:AE:61:VAL:HG21	2.03	0.41
20:AI:194:GLU:HA	20:AI:194:GLU:OE2	2.21	0.41
23:Ag:44:LYS:HZ1	23:Ag:54:ILE:HD12	1.85	0.41
23:Ag:165:ILE:HG23	23:Ag:179:LEU:HD11	2.02	0.41
36:AF:68:ILE:HD12	36:AF:68:ILE:N	2.36	0.41
54:CY:47:MET:CE	54:CY:119:LEU:HD22	2.50	0.41
64:Cf:93:PRO:O	64:Cf:94:ALA:HB3	2.21	0.41
82:A6:2376:A:C2'	83:CR:1:MET:HE1	2.50	0.41
82:A6:3751:G:H21	82:A6:3775:A:H8	1.68	0.41
83:CR:120:TYR:CD1	83:CR:124:TYR:HB2	2.54	0.41
2:Ct:519:LYS:HZ1	2:Ct:567:CYS:N	2.18	0.41
15:AE:206:ASP:H	15:AE:222:LEU:HD22	1.86	0.41
16:AC:88:ILE:C	16:AC:88:ILE:HD12	2.45	0.41
25:AK:11:ILE:O	25:AK:15:LEU:HD23	2.20	0.41
29:AR:122:PRO:HB3	29:AR:123:THR:HG23	2.01	0.41
32:AZ:102:LYS:HE2	32:AZ:107:VAL:HG12	2.02	0.41
38:Cz:85:MET:HB2	38:Cz:89:ALA:HB2	2.02	0.41
59:CB:382:MET:HA	59:CB:382:MET:HE3	2.01	0.41
70:CC:217:ILE:HG13	70:CC:221:PHE:CZ	2.55	0.41
79:A5:2090:U:C5'	82:A6:2259:G:H5'	2.50	0.41
82:A6:2809:G:H4'	83:CR:63:CYS:HB2	2.02	0.41
83:CR:96:MET:HE2	83:CR:96:MET:CA	2.46	0.41
15:AE:20:LEU:HD12	15:AE:20:LEU:O	2.20	0.41
16:AC:108:LYS:C	16:AC:109:ILE:HD13	2.45	0.41
18:AH:28:LEU:O	18:AH:32:MET:HE3	2.20	0.41
24:AU:24:LEU:HD21	24:AU:110:VAL:HB	2.03	0.41
37:AQ:44:PRO:C	37:AQ:45:ARG:HD3	2.45	0.41
46:CD:167:VAL:HG21	46:CD:175:HIS:CD2	2.55	0.41
50:CT:61:THR:O	50:CT:76:VAL:HG23	2.21	0.41
56:Cr:90:LEU:HB2	56:Cr:118:LEU:CD1	2.50	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:Ci:70:LEU:HD23	66:Ci:70:LEU:O	2.21	0.41
74:Co:85:ILE:HG21	82:A6:4292:A:C2	2.55	0.41
77:CE:109:LEU:HD12	77:CE:109:LEU:H	1.85	0.41
77:CE:160:LYS:HE3	77:CE:184:VAL:HG23	2.03	0.41
82:A6:2812:A:C8	83:CR:83:GLY:HA3	2.56	0.41
10:AY:20:ARG:HD3	10:AY:74:MET:HE2	2.02	0.41
15:AE:11:ARG:HG3	15:AE:20:LEU:HD13	2.02	0.41
17:AG:52:ILE:HA	17:AG:111:LEU:HD13	2.03	0.41
18:AH:71:SER:O	18:AH:75:ILE:HG22	2.21	0.41
21:B2:1605:G:H21	21:B2:1634:C:H5	1.69	0.41
23:Ag:5:MET:HE3	23:Ag:258:ILE:CD1	2.51	0.41
39:CO:47:PHE:HA	39:CO:136:ALA:HB2	2.03	0.41
48:CA:126:LEU:HD12	48:CA:150:LEU:HD21	2.03	0.41
55:CZ:42:LEU:HD12	55:CZ:73:LYS:O	2.21	0.41
70:CC:266:THR:HG23	70:CC:269:LYS:H	1.84	0.41
79:A5:708:G:N2	82:A6:4942:C:H41	2.19	0.41
2:Ct:357:HIS:O	2:Ct:358:LEU:HD22	2.20	0.41
2:Ct:731:ALA:O	2:Ct:735:THR:HG22	2.21	0.41
8:AA:40:LYS:O	8:AA:48:ILE:HD12	2.21	0.41
15:AE:55:ALA:C	15:AE:56:LEU:HD22	2.45	0.41
17:AG:153:VAL:HG11	17:AG:176:ILE:HG12	2.03	0.41
21:B2:752:G:H21	21:B2:753:C:H41	1.69	0.41
27:AS:42:HIS:HB2	31:AT:45:LEU:HD11	2.03	0.41
27:AS:114:LEU:HA	27:AS:117:ILE:HG22	2.03	0.41
34:AD:54:ARG:O	34:AD:58:VAL:HG13	2.20	0.41
39:CO:108:ILE:HD12	39:CO:117:ARG:HD3	2.02	0.41
45:CI:175:LYS:HE2	45:CI:175:LYS:N	2.36	0.41
46:CD:73:MET:HE3	46:CD:73:MET:HA	2.03	0.41
47:CQ:9:LYS:HA	47:CQ:9:LYS:HE2	2.02	0.41
48:CA:204:MET:SD	48:CA:208:GLU:OE2	2.79	0.41
53:CX:127:LEU:HD13	53:CX:128:ILE:N	2.36	0.41
54:CY:80:ILE:CD1	54:CY:82:ILE:HD11	2.50	0.41
56:Cr:49:VAL:HG23	56:Cr:106:LEU:HD23	2.03	0.41
56:Cr:126:VAL:HG13	56:Cr:129:LYS:HE3	2.02	0.41
60:CF:101:VAL:HG22	60:CF:105:VAL:HG13	2.03	0.41
61:Cc:58:SER:CB	65:Cg:96:LEU:HD22	2.51	0.41
68:Ck:11:PHE:HD2	68:Ck:45:LEU:HD22	1.85	0.41
68:Ck:13:LEU:HD12	68:Ck:14:THR:N	2.36	0.41
70:CC:190:ARG:CD	70:CC:202:ILE:HD11	2.50	0.41
70:CC:321:ASN:CB	70:CC:324:ILE:HD12	2.51	0.41
70:CC:338:ASN:O	70:CC:339:THR:HG23	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:CE:92:VAL:HG11	82:A6:2254:G:O6	2.21	0.41
79:A5:1101:C:N4	79:A5:1195:G:H21	2.15	0.41
82:A6:2386:U:O3'	83:CR:24:LEU:HD23	2.20	0.41
83:CR:23:TRP:CZ3	83:CR:51:ILE:HG12	2.55	0.41
83:CR:62:ARG:O	83:CR:65:LYS:HG2	2.21	0.41
83:CR:168:GLU:HA	83:CR:171:LYS:CD	2.51	0.41
2:Ct:43:ALA:HB1	2:Ct:77:LEU:CD2	2.50	0.41
2:Ct:592:LEU:HD22	2:Ct:593:SER:N	2.35	0.41
24:AU:26:SER:CB	24:AU:32:LEU:HD13	2.51	0.41
27:AS:10:GLN:HB3	27:AS:13:LEU:HD21	2.02	0.41
33:Ac:14:VAL:HG13	33:Ac:30:VAL:HG13	2.02	0.41
47:CQ:24:TYR:CE1	56:Cr:5:LEU:HD13	2.56	0.41
56:Cr:10:VAL:O	56:Cr:10:VAL:HG12	2.20	0.41
60:CF:192:HIS:CE1	60:CF:196:THR:HG21	2.56	0.41
76:CH:80:MET:O	76:CH:84:VAL:HG23	2.20	0.41
2:Ct:398:ILE:HG12	2:Ct:485:ILE:HD11	2.01	0.40
3:AO:78:ALA:HB3	3:AO:118:ALA:HB3	2.02	0.40
5:AN:22:VAL:HB	5:AN:23:PRO:HA	2.03	0.40
5:AN:113:PHE:CZ	5:AN:117:LEU:HD21	2.57	0.40
8:AA:176:TRP:CZ3	8:AA:177:MET:HE3	2.56	0.40
21:B2:872:A:H4'	83:CR:163:ARG:NH1	2.36	0.40
24:AU:29:VAL:HG22	24:AU:85:HIS:NE2	2.36	0.40
34:AD:190:LEU:H	34:AD:190:LEU:HD23	1.86	0.40
40:CL:155:MET:H	40:CL:155:MET:HE3	1.87	0.40
65:Cg:11:LEU:HD12	65:Cg:18:ASN:ND2	2.35	0.40
76:CH:66:GLU:O	76:CH:70:VAL:HG13	2.21	0.40
77:CE:46:ARG:HH21	77:CE:50:LEU:HD22	1.86	0.40
77:CE:213:THR:HG23	77:CE:215:ALA:N	2.35	0.40
79:A5:516:G:H22	79:A5:645:G:N2	2.15	0.40
83:CR:134:ASN:CG	83:CR:137:ILE:HG22	2.46	0.40
2:Ct:304:ILE:HG21	2:Ct:336:LEU:HB2	2.03	0.40
2:Ct:519:LYS:HD3	2:Ct:519:LYS:C	2.46	0.40
16:AC:127:PHE:CD1	16:AC:141:VAL:HG22	2.56	0.40
17:AG:109:LEU:N	17:AG:109:LEU:HD22	2.36	0.40
23:Ag:87:LEU:HG	23:Ag:108:VAL:HG11	2.02	0.40
39:CO:138:LEU:CD1	39:CO:141:LEU:HD12	2.51	0.40
39:CO:196:LEU:HD22	42:CM:119:ARG:CZ	2.52	0.40
42:CM:8:GLU:O	42:CM:27:ILE:HG23	2.21	0.40
43:Ca:133:ALA:O	43:Ca:137:ILE:HD13	2.21	0.40
48:CA:83:HIS:HB3	73:Cp:64:VAL:HG22	2.02	0.40
56:Cr:5:LEU:O	56:Cr:9:VAL:HG12	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:Ce:118:LEU:HD13	63:Ce:120:ILE:HD13	2.03	0.40
75:CJ:43:LEU:HD23	75:CJ:117:ILE:HD11	2.03	0.40
77:CE:164:PHE:CE1	77:CE:173:LEU:HD22	2.56	0.40
83:CR:28:GLU:HG3	83:CR:49:LEU:HD22	2.02	0.40
83:CR:106:LEU:HD12	83:CR:138:LEU:HD11	2.03	0.40
4:AX:46:HIS:CD2	4:AX:103:ALA:HB2	2.57	0.40
15:AE:125:LYS:HA	15:AE:159:THR:HG22	2.03	0.40
21:B2:798:G:H4'	21:B2:799:U:OP2	2.22	0.40
23:Ag:44:LYS:NZ	23:Ag:54:ILE:HD12	2.36	0.40
25:AK:85:LEU:HD22	25:AK:89:ILE:HD11	2.03	0.40
36:AF:143:PRO:O	36:AF:147:VAL:HG23	2.21	0.40
38:Cz:57:SER:O	38:Cz:58:THR:HG22	2.21	0.40
43:Ca:86:THR:HG22	79:A5:510:U:C4'	2.51	0.40
45:CI:174:THR:HA	45:CI:175:LYS:HE2	2.03	0.40
70:CC:38:ASN:O	70:CC:42:THR:HG23	2.22	0.40
70:CC:162:LYS:HA	70:CC:220:ALA:HB2	2.03	0.40
70:CC:349:LEU:HD13	70:CC:349:LEU:O	2.21	0.40
2:Ct:745:TYR:CZ	2:Ct:788:LEU:HD21	2.56	0.40
3:AO:147:ARG:HE	3:AO:150:ARG:HG2	1.86	0.40
4:AX:131:LEU:HD13	4:AX:135:LYS:NZ	2.36	0.40
10:AY:20:ARG:HD2	10:AY:74:MET:HE2	2.03	0.40
19:AW:34:ILE:HG22	19:AW:38:LEU:CD2	2.51	0.40
23:Ag:217:MET:HE1	23:Ag:229:THR:HG23	2.02	0.40
35:Af:90:LYS:HD2	35:Af:91:ASN:N	2.36	0.40
39:CO:192:TYR:CE1	42:CM:122:ILE:HG21	2.56	0.40
40:CL:173:GLU:HG3	43:Ca:143:ALA:HB1	2.03	0.40
56:Cr:126:VAL:HG12	56:Cr:130:ARG:HB2	2.02	0.40
76:CH:17:ASP:C	76:CH:18:ILE:HD12	2.47	0.40
77:CE:56:ARG:HG2	77:CE:57:TYR:HB3	2.03	0.40
79:A5:2090:U:C1'	82:A6:2259:G:P	3.10	0.40
83:CR:15:LEU:HD12	83:CR:52:ARG:HH11	1.86	0.40
83:CR:152:LYS:HG2	83:CR:152:LYS:H	1.64	0.40
2:Ct:157:MET:HE1	2:Ct:181:ILE:HD13	2.03	0.40
5:AN:21:SER:O	5:AN:22:VAL:HG22	2.22	0.40
11:Aa:45:VAL:O	11:Aa:49:ALA:HB3	2.21	0.40
32:AZ:92:LEU:HD11	32:AZ:109:TYR:CZ	2.56	0.40
42:CM:17:PHE:CE2	79:A5:1921:C:H2'	2.57	0.40
43:Ca:72:THR:HB	43:Ca:112:LEU:HD13	2.04	0.40
59:CB:47:LEU:HD12	59:CB:345:LEU:O	2.21	0.40
61:Cc:49:ALA:HB2	61:Cc:81:LEU:HD11	2.03	0.40
64:Cf:55:ASN:C	64:Cf:57:THR:H	2.30	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:CC:138:MET:HA	70:CC:138:MET:HE3	2.04	0.40
82:A6:2596:G:H1	82:A6:2749:G:H22	1.69	0.40
82:A6:4881:U:H3'	82:A6:4882:U:H5''	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	Ct	842/847 (99%)	730 (87%)	98 (12%)	14 (2%)	7	28
3	AO	134/136 (98%)	109 (81%)	23 (17%)	2 (2%)	8	30
4	AX	137/139 (99%)	119 (87%)	16 (12%)	2 (2%)	8	30
5	AN	147/149 (99%)	127 (86%)	18 (12%)	2 (1%)	9	31
6	AL	155/157 (99%)	126 (81%)	28 (18%)	1 (1%)	21	50
7	AB	208/212 (98%)	181 (87%)	23 (11%)	4 (2%)	6	26
8	AA	206/208 (99%)	162 (79%)	40 (19%)	4 (2%)	6	26
9	AV	80/82 (98%)	61 (76%)	16 (20%)	3 (4%)	2	15
10	AY	124/126 (98%)	104 (84%)	18 (14%)	2 (2%)	7	29
11	Aa	100/102 (98%)	79 (79%)	19 (19%)	2 (2%)	6	25
12	Ab	82/84 (98%)	64 (78%)	16 (20%)	2 (2%)	4	22
13	Ae	55/57 (96%)	43 (78%)	8 (14%)	4 (7%)	1	5
14	AJ	176/178 (99%)	161 (92%)	11 (6%)	4 (2%)	5	23
15	AE	260/262 (99%)	220 (85%)	33 (13%)	7 (3%)	4	20
16	AC	218/220 (99%)	195 (89%)	21 (10%)	2 (1%)	14	42
17	AG	235/237 (99%)	209 (89%)	21 (9%)	5 (2%)	5	24
18	AH	187/189 (99%)	151 (81%)	24 (13%)	12 (6%)	1	7

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	AW	127/129 (98%)	108 (85%)	19 (15%)	0	100	100
20	AI	204/206 (99%)	165 (81%)	34 (17%)	5 (2%)	4	21
22	CW	122/124 (98%)	105 (86%)	14 (12%)	3 (2%)	4	21
23	Ag	311/313 (99%)	268 (86%)	39 (12%)	4 (1%)	9	33
24	AU	102/104 (98%)	84 (82%)	11 (11%)	7 (7%)	1	6
25	AK	96/98 (98%)	61 (64%)	24 (25%)	11 (12%)	0	2
26	AM	120/122 (98%)	87 (72%)	28 (23%)	5 (4%)	2	14
27	AS	135/137 (98%)	114 (84%)	19 (14%)	2 (2%)	8	30
28	Ad	51/53 (96%)	43 (84%)	8 (16%)	0	100	100
29	AR	124/126 (98%)	103 (83%)	15 (12%)	6 (5%)	2	11
30	AP	122/124 (98%)	98 (80%)	18 (15%)	6 (5%)	1	11
31	AT	139/141 (99%)	131 (94%)	7 (5%)	1 (1%)	18	47
32	AZ	73/75 (97%)	58 (80%)	14 (19%)	1 (1%)	9	31
33	Ac	62/64 (97%)	51 (82%)	11 (18%)	0	100	100
34	AD	225/227 (99%)	190 (84%)	28 (12%)	7 (3%)	3	18
35	Af	69/71 (97%)	44 (64%)	20 (29%)	5 (7%)	1	5
36	AF	184/188 (98%)	162 (88%)	20 (11%)	2 (1%)	11	38
37	AQ	139/141 (99%)	114 (82%)	21 (15%)	4 (3%)	3	19
38	Cz	205/207 (99%)	165 (80%)	35 (17%)	5 (2%)	4	22
39	CO	197/199 (99%)	183 (93%)	12 (6%)	2 (1%)	12	40
40	CL	206/208 (99%)	171 (83%)	30 (15%)	5 (2%)	4	22
41	CV	130/132 (98%)	118 (91%)	12 (9%)	0	100	100
42	CM	137/139 (99%)	118 (86%)	17 (12%)	2 (2%)	8	30
43	Ca	145/147 (99%)	117 (81%)	24 (17%)	4 (3%)	4	19
44	CN	201/203 (99%)	175 (87%)	24 (12%)	2 (1%)	12	40
45	CI	203/207 (98%)	171 (84%)	30 (15%)	2 (1%)	12	40
46	CD	287/289 (99%)	244 (85%)	37 (13%)	6 (2%)	5	24
47	CQ	186/188 (99%)	158 (85%)	26 (14%)	2 (1%)	11	38
48	CA	253/255 (99%)	215 (85%)	37 (15%)	1 (0%)	30	59
49	CS	173/175 (99%)	142 (82%)	27 (16%)	4 (2%)	5	23
50	CT	157/159 (99%)	138 (88%)	16 (10%)	3 (2%)	6	26

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	CP	150/152 (99%)	133 (89%)	15 (10%)	2 (1%)	9	33
52	CU	108/110 (98%)	96 (89%)	12 (11%)	0	100	100
53	CX	119/121 (98%)	101 (85%)	15 (13%)	3 (2%)	4	21
54	CY	131/133 (98%)	120 (92%)	11 (8%)	0	100	100
55	CZ	133/135 (98%)	116 (87%)	16 (12%)	1 (1%)	16	44
56	Cr	135/137 (98%)	92 (68%)	28 (21%)	15 (11%)	0	2
57	Ch	121/123 (98%)	104 (86%)	14 (12%)	3 (2%)	4	21
58	Cb	71/73 (97%)	62 (87%)	8 (11%)	1 (1%)	9	31
59	CB	393/395 (100%)	349 (89%)	37 (9%)	7 (2%)	6	26
60	CF	227/229 (99%)	200 (88%)	22 (10%)	5 (2%)	5	24
61	Cc	98/100 (98%)	89 (91%)	8 (8%)	1 (1%)	12	40
62	Cd	111/113 (98%)	92 (83%)	17 (15%)	2 (2%)	6	26
63	Ce	128/130 (98%)	108 (84%)	16 (12%)	4 (3%)	3	18
64	Cf	107/109 (98%)	85 (79%)	18 (17%)	4 (4%)	2	16
65	Cg	112/114 (98%)	95 (85%)	17 (15%)	0	100	100
66	Ci	101/103 (98%)	88 (87%)	9 (9%)	4 (4%)	2	15
67	Cj	87/89 (98%)	76 (87%)	10 (12%)	1 (1%)	11	38
68	Ck	66/68 (97%)	61 (92%)	4 (6%)	1 (2%)	8	30
69	Cl	47/49 (96%)	42 (89%)	4 (8%)	1 (2%)	5	24
70	CC	363/365 (100%)	276 (76%)	62 (17%)	25 (7%)	1	6
71	Cm	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
72	Cn	22/24 (92%)	22 (100%)	0	0	100	100
73	Cp	87/89 (98%)	75 (86%)	11 (13%)	1 (1%)	11	38
74	Co	102/104 (98%)	79 (78%)	19 (19%)	4 (4%)	2	15
75	CJ	166/168 (99%)	150 (90%)	15 (9%)	1 (1%)	21	50
76	CH	189/191 (99%)	167 (88%)	21 (11%)	1 (0%)	24	54
77	CE	250/254 (98%)	156 (62%)	67 (27%)	27 (11%)	0	2
78	CG	244/246 (99%)	198 (81%)	41 (17%)	5 (2%)	6	25
83	CR	187/189 (99%)	164 (88%)	19 (10%)	4 (2%)	5	24
All	All	12334/12499 (99%)	10384 (84%)	1648 (13%)	302 (2%)	7	22

All (302) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	Ct	333	LYS
2	Ct	345	PRO
2	Ct	443	TYR
2	Ct	716	ARG
3	AO	56	VAL
5	AN	138	ASN
6	AL	23	VAL
8	AA	206	ASP
11	Aa	98	PRO
13	Ae	3	HIS
14	AJ	120	ALA
15	AE	118	GLU
15	AE	171	ASP
15	AE	194	VAL
17	AG	153	VAL
18	AH	66	VAL
18	AH	190	PRO
20	AI	22	HIS
20	AI	105	ASP
22	CW	71	ARG
23	Ag	96	THR
23	Ag	282	GLU
24	AU	50	VAL
24	AU	51	LYS
24	AU	107	GLU
25	AK	30	PRO
25	AK	34	GLU
25	AK	36	ALA
25	AK	39	ASN
25	AK	84	HIS
26	AM	73	GLN
26	AM	79	VAL
26	AM	114	TYR
29	AR	86	PRO
29	AR	100	PRO
29	AR	101	ASP
30	AP	71	GLU
30	AP	73	PRO
30	AP	126	VAL
31	AT	34	VAL
34	AD	202	LYS
34	AD	222	PRO
34	AD	223	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	AF	42	LYS
36	AF	106	GLU
37	AQ	100	VAL
38	Cz	60	ARG
38	Cz	81	ASP
38	Cz	163	LEU
39	CO	111	PRO
40	CL	47	ALA
40	CL	49	ARG
40	CL	50	PRO
40	CL	151	THR
44	CN	77	LYS
45	CI	113	THR
46	CD	253	TYR
46	CD	261	VAL
46	CD	271	MET
47	CQ	20	SER
47	CQ	98	LEU
48	CA	219	ILE
49	CS	75	VAL
49	CS	76	LYS
49	CS	155	PRO
50	CT	139	HIS
51	CP	8	PRO
53	CX	54	LEU
53	CX	58	PRO
56	Cr	53	PRO
56	Cr	60	VAL
56	Cr	62	VAL
56	Cr	73	PRO
56	Cr	76	SER
56	Cr	77	TYR
56	Cr	126	VAL
56	Cr	127	LYS
59	CB	40	PRO
59	CB	189	THR
59	CB	326	VAL
60	CF	21	LYS
60	CF	23	ARG
62	Cd	57	MET
64	Cf	5	LEU
64	Cf	55	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
64	Cf	65	ASN
66	Ci	5	TYR
66	Ci	63	VAL
66	Ci	65	LYS
69	Cl	4	HIS
70	CC	87	SER
70	CC	91	ALA
70	CC	184	TYR
70	CC	214	ASP
70	CC	294	LYS
70	CC	306	ARG
70	CC	313	VAL
70	CC	319	LEU
70	CC	337	ARG
70	CC	339	THR
74	Co	65	LYS
77	CE	31	ASN
77	CE	42	PRO
77	CE	84	LYS
77	CE	94	LYS
77	CE	95	PRO
77	CE	99	ASP
77	CE	101	ASN
77	CE	108	LYS
77	CE	117	PRO
77	CE	208	ILE
77	CE	244	GLU
83	CR	131	VAL
2	Ct	264	ARG
2	Ct	564	ASP
2	Ct	713	ALA
7	AB	209	ASP
7	AB	224	GLU
8	AA	159	ILE
8	AA	163	CYS
9	AV	42	VAL
13	Ae	45	VAL
15	AE	245	ARG
15	AE	261	SER
17	AG	150	GLU
17	AG	174	PRO
18	AH	11	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
18	AH	135	PHE
20	AI	131	PRO
20	AI	142	SER
20	AI	158	ILE
24	AU	116	ILE
26	AM	94	ILE
30	AP	17	TYR
30	AP	75	VAL
34	AD	93	THR
35	Af	98	VAL
35	Af	102	VAL
37	AQ	19	ALA
37	AQ	141	TYR
38	Cz	153	SER
40	CL	149	GLN
42	CM	31	ILE
43	Ca	89	ASN
46	CD	20	PHE
46	CD	257	PRO
50	CT	134	PRO
50	CT	135	PRO
53	CX	40	ILE
56	Cr	56	ASP
56	Cr	78	VAL
56	Cr	105	ASP
59	CB	281	ASN
59	CB	293	ILE
63	Ce	6	PRO
64	Cf	7	SER
66	Ci	34	THR
70	CC	17	SER
70	CC	24	LEU
70	CC	25	PRO
70	CC	90	GLY
70	CC	264	TYR
74	Co	67	VAL
75	CJ	117	ILE
76	CH	53	LYS
77	CE	45	SER
77	CE	51	VAL
77	CE	72	LYS
77	CE	85	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
77	CE	118	THR
77	CE	119	GLU
77	CE	265	PRO
78	CG	87	LEU
78	CG	161	VAL
78	CG	207	VAL
83	CR	3	MET
2	Ct	20	ARG
7	AB	27	LYS
7	AB	210	VAL
10	AY	5	VAL
14	AJ	19	PRO
14	AJ	148	ILE
18	AH	160	LYS
35	Af	91	ASN
56	Cr	82	ILE
57	Ch	115	PRO
58	Cb	21	ILE
63	Ce	3	ALA
68	Ck	32	VAL
70	CC	216	GLY
70	CC	296	PRO
70	CC	309	ILE
74	Co	77	CYS
77	CE	96	VAL
77	CE	120	ASP
77	CE	224	LYS
77	CE	233	PHE
83	CR	187	THR
2	Ct	26	ALA
2	Ct	462	GLU
2	Ct	567	CYS
11	Aa	58	VAL
12	Ab	37	CYS
15	AE	30	ARG
15	AE	90	ILE
17	AG	154	ARG
18	AH	16	PRO
25	AK	3	MET
25	AK	63	ALA
25	AK	90	VAL
37	AQ	32	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
43	Ca	98	ALA
44	CN	188	ARG
46	CD	187	SER
51	CP	7	ASP
59	CB	323	TYR
61	Cc	11	LEU
63	Ce	9	LYS
70	CC	16	GLU
70	CC	133	LEU
70	CC	318	PRO
77	CE	56	ARG
77	CE	185	PRO
83	CR	53	LYS
2	Ct	812	CYS
8	AA	104	THR
13	Ae	51	LYS
18	AH	116	ARG
26	AM	58	GLU
27	AS	12	ILE
29	AR	95	ILE
32	AZ	108	ILE
60	CF	184	ILE
70	CC	18	SER
77	CE	209	PRO
2	Ct	781	MET
4	AX	68	LYS
4	AX	99	GLU
5	AN	22	VAL
9	AV	45	ARG
10	AY	120	THR
12	Ab	62	VAL
14	AJ	138	ARG
17	AG	20	ASP
18	AH	109	ARG
18	AH	159	ASP
22	CW	72	THR
22	CW	83	THR
23	Ag	159	ASN
24	AU	70	CYS
24	AU	118	ASP
25	AK	95	ARG
27	AS	11	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
29	AR	83	ASN
29	AR	88	VAL
30	AP	70	MET
34	AD	201	LYS
34	AD	215	ASP
43	Ca	91	ALA
43	Ca	116	LYS
45	CI	175	LYS
49	CS	16	CYS
56	Cr	45	HIS
56	Cr	75	THR
59	CB	157	CYS
60	CF	233	ALA
62	Cd	19	GLU
63	Ce	4	LEU
70	CC	295	SER
70	CC	310	HIS
70	CC	311	ARG
74	Co	32	SER
77	CE	80	VAL
78	CG	44	ASP
3	AO	58	GLY
9	AV	9	VAL
35	Af	112	GLY
42	CM	2	VAL
78	CG	184	ILE
13	Ae	46	VAL
18	AH	100	ILE
57	Ch	121	VAL
60	CF	230	GLY
73	Cp	11	VAL
2	Ct	408	GLY
16	AC	176	LYS
18	AH	170	VAL
23	Ag	274	VAL
24	AU	109	GLY
25	AK	91	PRO
34	AD	115	VAL
35	Af	129	GLY
38	Cz	58	THR
39	CO	110	PRO
55	CZ	90	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
56	Cr	50	GLY
67	Cj	83	THR
77	CE	116	TYR
16	AC	171	GLY
18	AH	15	LYS
25	AK	41	PRO
57	Ch	4	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Ct	722/722 (100%)	698 (97%)	24 (3%)	33	57
3	AO	105/106 (99%)	100 (95%)	5 (5%)	23	50
4	AX	112/112 (100%)	109 (97%)	3 (3%)	39	60
5	AN	130/130 (100%)	127 (98%)	3 (2%)	44	63
6	AL	141/141 (100%)	134 (95%)	7 (5%)	22	49
7	AB	194/194 (100%)	189 (97%)	5 (3%)	40	61
8	AA	174/174 (100%)	168 (97%)	6 (3%)	32	57
9	AV	66/66 (100%)	64 (97%)	2 (3%)	36	59
10	AY	108/108 (100%)	100 (93%)	8 (7%)	13	38
11	Aa	89/89 (100%)	87 (98%)	2 (2%)	45	63
12	Ab	76/76 (100%)	76 (100%)	0	100	100
13	Ae	46/46 (100%)	45 (98%)	1 (2%)	45	63
14	AJ	157/157 (100%)	153 (98%)	4 (2%)	42	62
15	AE	225/225 (100%)	219 (97%)	6 (3%)	39	60
16	AC	186/186 (100%)	178 (96%)	8 (4%)	26	51
17	AG	207/207 (100%)	194 (94%)	13 (6%)	16	42
18	AH	169/169 (100%)	164 (97%)	5 (3%)	36	59
19	AW	112/112 (100%)	108 (96%)	4 (4%)	31	56

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	AI	178/178 (100%)	172 (97%)	6 (3%)	32	57
22	CW	103/103 (100%)	97 (94%)	6 (6%)	18	45
23	Ag	272/272 (100%)	266 (98%)	6 (2%)	45	63
24	AU	94/94 (100%)	91 (97%)	3 (3%)	34	58
25	AK	89/89 (100%)	88 (99%)	1 (1%)	65	74
26	AM	102/102 (100%)	90 (88%)	12 (12%)	5	20
27	AS	119/119 (100%)	114 (96%)	5 (4%)	26	52
28	Ad	47/47 (100%)	47 (100%)	0	100	100
29	AR	114/114 (100%)	107 (94%)	7 (6%)	17	43
30	AP	114/114 (100%)	106 (93%)	8 (7%)	14	40
31	AT	112/112 (100%)	110 (98%)	2 (2%)	51	67
32	AZ	66/66 (100%)	64 (97%)	2 (3%)	36	59
33	Ac	57/57 (100%)	56 (98%)	1 (2%)	51	67
34	AD	190/190 (100%)	183 (96%)	7 (4%)	30	55
35	Af	64/64 (100%)	63 (98%)	1 (2%)	55	68
36	AF	160/160 (100%)	150 (94%)	10 (6%)	16	42
37	AQ	117/117 (100%)	116 (99%)	1 (1%)	70	76
38	Cz	185/186 (100%)	177 (96%)	8 (4%)	26	51
39	CO	171/171 (100%)	159 (93%)	12 (7%)	14	40
40	CL	174/174 (100%)	169 (97%)	5 (3%)	37	60
41	CV	102/102 (100%)	100 (98%)	2 (2%)	48	65
42	CM	118/118 (100%)	112 (95%)	6 (5%)	21	48
43	Ca	120/120 (100%)	116 (97%)	4 (3%)	33	57
44	CN	171/171 (100%)	164 (96%)	7 (4%)	27	52
45	CI	177/177 (100%)	174 (98%)	3 (2%)	53	67
46	CD	243/243 (100%)	234 (96%)	9 (4%)	30	55
47	CQ	165/165 (100%)	161 (98%)	4 (2%)	43	62
48	CA	197/197 (100%)	193 (98%)	4 (2%)	48	65
49	CS	156/156 (100%)	148 (95%)	8 (5%)	21	48
50	CT	139/139 (100%)	136 (98%)	3 (2%)	45	63
51	CP	133/133 (100%)	131 (98%)	2 (2%)	57	69

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	CU	99/100 (99%)	97 (98%)	2 (2%)	48	65
53	CX	109/109 (100%)	101 (93%)	8 (7%)	13	39
54	CY	123/123 (100%)	117 (95%)	6 (5%)	22	49
55	CZ	117/117 (100%)	113 (97%)	4 (3%)	32	57
56	Cr	121/121 (100%)	106 (88%)	15 (12%)	4	18
57	Ch	110/110 (100%)	105 (96%)	5 (4%)	24	51
58	Cb	61/61 (100%)	59 (97%)	2 (3%)	33	57
59	CB	344/344 (100%)	333 (97%)	11 (3%)	34	58
60	CF	198/198 (100%)	190 (96%)	8 (4%)	28	53
61	Cc	85/85 (100%)	82 (96%)	3 (4%)	32	56
62	Cd	102/102 (100%)	101 (99%)	1 (1%)	68	75
63	Ce	116/116 (100%)	113 (97%)	3 (3%)	40	61
64	Cf	88/88 (100%)	77 (88%)	11 (12%)	4	18
65	Cg	98/98 (100%)	95 (97%)	3 (3%)	35	59
66	Ci	87/87 (100%)	84 (97%)	3 (3%)	32	57
67	Cj	74/74 (100%)	72 (97%)	2 (3%)	39	60
68	Ck	63/63 (100%)	63 (100%)	0	100	100
69	Cl	46/46 (100%)	46 (100%)	0	100	100
70	CC	304/304 (100%)	286 (94%)	18 (6%)	18	44
71	Cm	46/46 (100%)	42 (91%)	4 (9%)	9	32
72	Cn	23/23 (100%)	23 (100%)	0	100	100
73	Cp	73/73 (100%)	73 (100%)	0	100	100
74	Co	92/92 (100%)	90 (98%)	2 (2%)	45	63
75	CJ	142/142 (100%)	135 (95%)	7 (5%)	22	49
76	CH	170/170 (100%)	161 (95%)	9 (5%)	20	47
77	CE	225/225 (100%)	195 (87%)	30 (13%)	4	15
78	CG	209/209 (100%)	199 (95%)	10 (5%)	23	50
83	CR	168/168 (100%)	158 (94%)	10 (6%)	17	43
All	All	10761/10764 (100%)	10323 (96%)	438 (4%)	28	52

All (438) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	Ct	23	SER
2	Ct	29	ASP
2	Ct	35	LEU
2	Ct	102	LEU
2	Ct	115	VAL
2	Ct	119	LEU
2	Ct	169	LEU
2	Ct	272	LYS
2	Ct	289	PHE
2	Ct	314	LYS
2	Ct	335	LEU
2	Ct	340	MET
2	Ct	350	LEU
2	Ct	388	CYS
2	Ct	391	LYS
2	Ct	469	ILE
2	Ct	551	GLU
2	Ct	585	GLU
2	Ct	590	LEU
2	Ct	635	LEU
2	Ct	649	ILE
2	Ct	728	CYS
2	Ct	771	PHE
2	Ct	837	GLU
3	AO	40	THR
3	AO	80	ASP
3	AO	93	LEU
3	AO	95	ILE
3	AO	135	ILE
4	AX	55	VAL
4	AX	58	GLU
4	AX	100	VAL
5	AN	27	LYS
5	AN	73	ARG
5	AN	104	ARG
6	AL	6	THR
6	AL	20	LYS
6	AL	28	THR
6	AL	56	ILE
6	AL	74	SER
6	AL	85	THR
6	AL	156	GLN
7	AB	48	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	AB	137	LEU
7	AB	182	LYS
7	AB	199	LYS
7	AB	225	LEU
8	AA	44	ASP
8	AA	58	LEU
8	AA	60	LEU
8	AA	132	GLN
8	AA	174	MET
8	AA	201	LEU
9	AV	31	SER
9	AV	78	ILE
10	AY	25	ILE
10	AY	29	HIS
10	AY	46	LYS
10	AY	75	ILE
10	AY	79	LEU
10	AY	96	LEU
10	AY	99	LYS
10	AY	102	THR
11	Aa	66	LYS
11	Aa	79	ILE
13	Ae	43	VAL
14	AJ	61	LEU
14	AJ	66	LYS
14	AJ	165	TYR
14	AJ	180	LYS
15	AE	51	ARG
15	AE	102	ILE
15	AE	242	LYS
15	AE	250	GLU
15	AE	259	LYS
15	AE	261	SER
16	AC	108	LYS
16	AC	160	LEU
16	AC	167	ARG
16	AC	174	ILE
16	AC	211	LYS
16	AC	233	LEU
16	AC	250	TYR
16	AC	262	THR
17	AG	3	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
17	AG	41	LEU
17	AG	50	VAL
17	AG	59	GLN
17	AG	63	MET
17	AG	98	ARG
17	AG	109	LEU
17	AG	149	LYS
17	AG	172	LYS
17	AG	181	THR
17	AG	191	ARG
17	AG	201	LYS
17	AG	212	LEU
18	AH	27	LEU
18	AH	98	ARG
18	AH	125	VAL
18	AH	160	LYS
18	AH	168	HIS
19	AW	30	CYS
19	AW	52	ILE
19	AW	91	ASN
19	AW	126	LEU
20	AI	18	ARG
20	AI	61	ASP
20	AI	77	ARG
20	AI	78	ILE
20	AI	174	CYS
20	AI	202	ILE
22	CW	32	LEU
22	CW	59	HIS
22	CW	73	ARG
22	CW	89	ASP
22	CW	96	GLN
22	CW	113	LYS
23	Ag	24	THR
23	Ag	43	TRP
23	Ag	64	HIS
23	Ag	131	LEU
23	Ag	184	LEU
23	Ag	305	ASN
24	AU	46	LYS
24	AU	91	LEU
24	AU	107	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
25	AK	16	PHE
26	AM	12	MET
26	AM	42	LEU
26	AM	58	GLU
26	AM	61	TYR
26	AM	71	GLU
26	AM	74	ILE
26	AM	83	LYS
26	AM	94	ILE
26	AM	101	ARG
26	AM	112	LYS
26	AM	121	LYS
26	AM	128	PHE
27	AS	60	THR
27	AS	67	VAL
27	AS	103	LEU
27	AS	118	ARG
27	AS	123	LEU
29	AR	17	ILE
29	AR	57	LEU
29	AR	69	ILE
29	AR	83	ASN
29	AR	100	PRO
29	AR	104	GLU
29	AR	123	THR
30	AP	10	ARG
30	AP	36	LEU
30	AP	65	LYS
30	AP	71	GLU
30	AP	83	MET
30	AP	111	MET
30	AP	116	LEU
30	AP	127	LYS
31	AT	23	LYS
31	AT	83	GLN
32	AZ	52	LYS
32	AZ	114	LYS
33	Ac	58	LEU
34	AD	1	MET
34	AD	7	LYS
34	AD	58	VAL
34	AD	62	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	AD	79	PHE
34	AD	182	LEU
34	AD	185	LYS
35	Af	98	VAL
36	AF	51	HIS
36	AF	59	LYS
36	AF	72	LEU
36	AF	82	ASN
36	AF	94	LYS
36	AF	97	PHE
36	AF	112	LEU
36	AF	136	ARG
36	AF	191	LYS
36	AF	196	LEU
37	AQ	47	LEU
38	Cz	32	VAL
38	Cz	55	LEU
38	Cz	66	CYS
38	Cz	102	LYS
38	Cz	147	LYS
38	Cz	152	LYS
38	Cz	159	MET
38	Cz	184	HIS
39	CO	18	ARG
39	CO	51	LYS
39	CO	55	LEU
39	CO	85	ARG
39	CO	105	PHE
39	CO	111	PRO
39	CO	173	GLN
39	CO	186	GLU
39	CO	187	LYS
39	CO	191	LYS
39	CO	196	LEU
39	CO	201	LEU
40	CL	110	LEU
40	CL	124	LEU
40	CL	144	LEU
40	CL	165	LYS
40	CL	191	LEU
41	CV	98	PHE
41	CV	109	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
42	CM	14	TYR
42	CM	54	CYS
42	CM	77	TRP
42	CM	85	LYS
42	CM	103	LYS
42	CM	108	ASP
43	Ca	65	ARG
43	Ca	69	PHE
43	Ca	100	ILE
43	Ca	137	ILE
44	CN	10	LEU
44	CN	59	TYR
44	CN	64	ILE
44	CN	96	ARG
44	CN	135	ILE
44	CN	184	ILE
44	CN	201	HIS
45	CI	35	ASP
45	CI	45	GLU
45	CI	51	HIS
46	CD	27	LYS
46	CD	85	LYS
46	CD	158	LYS
46	CD	197	LYS
46	CD	253	TYR
46	CD	255	LYS
46	CD	256	LYS
46	CD	258	LYS
46	CD	259	LYS
47	CQ	71	LYS
47	CQ	140	SER
47	CQ	161	SER
47	CQ	162	HIS
48	CA	102	LEU
48	CA	144	LYS
48	CA	149	LYS
48	CA	237	LEU
49	CS	17	LEU
49	CS	19	THR
49	CS	54	MET
49	CS	73	LEU
49	CS	84	TYR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	CS	158	VAL
49	CS	162	GLN
49	CS	167	PHE
50	CT	41	ASP
50	CT	74	ILE
50	CT	139	HIS
51	CP	2	VAL
51	CP	95	LEU
52	CU	80	LYS
52	CU	115	PHE
53	CX	41	ARG
53	CX	43	SER
53	CX	52	LEU
53	CX	53	ARG
53	CX	91	GLU
53	CX	98	PHE
53	CX	105	ASN
53	CX	147	LEU
54	CY	32	SER
54	CY	42	TYR
54	CY	82	ILE
54	CY	91	ASN
54	CY	99	ILE
54	CY	116	LYS
55	CZ	19	SER
55	CZ	28	ASN
55	CZ	40	HIS
55	CZ	79	HIS
56	Cr	18	ILE
56	Cr	26	SER
56	Cr	32	LEU
56	Cr	33	LYS
56	Cr	37	SER
56	Cr	41	ASN
56	Cr	66	ARG
56	Cr	87	ARG
56	Cr	89	THR
56	Cr	90	LEU
56	Cr	91	SER
56	Cr	94	ARG
56	Cr	106	LEU
56	Cr	108	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
56	Cr	127	LYS
57	Ch	31	LEU
57	Ch	43	LYS
57	Ch	58	LEU
57	Ch	95	LEU
57	Ch	118	LYS
58	Cb	8	THR
58	Cb	73	LYS
59	CB	31	SER
59	CB	32	PHE
59	CB	46	PHE
59	CB	95	THR
59	CB	99	LEU
59	CB	248	LEU
59	CB	286	LYS
59	CB	297	LYS
59	CB	326	VAL
59	CB	362	LYS
59	CB	365	LEU
60	CF	107	LYS
60	CF	116	GLN
60	CF	123	VAL
60	CF	133	LEU
60	CF	157	ARG
60	CF	181	LYS
60	CF	194	ILE
60	CF	244	ILE
61	Cc	88	TYR
61	Cc	91	VAL
61	Cc	94	LEU
62	Cd	100	ASN
63	Ce	9	LYS
63	Ce	86	GLU
63	Ce	89	LEU
64	Cf	21	GLN
64	Cf	31	GLU
64	Cf	37	ASP
64	Cf	45	LYS
64	Cf	52	LYS
64	Cf	63	LYS
64	Cf	80	ASN
64	Cf	95	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
64	Cf	102	ARG
64	Cf	105	LEU
64	Cf	107	PRO
65	Cg	66	ARG
65	Cg	82	MET
65	Cg	102	ILE
66	Ci	11	LEU
66	Ci	43	MET
66	Ci	64	SER
67	Cj	66	HIS
67	Cj	74	PHE
70	CC	18	SER
70	CC	29	LYS
70	CC	115	VAL
70	CC	119	GLN
70	CC	128	LEU
70	CC	205	ARG
70	CC	209	ILE
70	CC	214	ASP
70	CC	218	ILE
70	CC	221	PHE
70	CC	238	LEU
70	CC	254	GLU
70	CC	269	LYS
70	CC	289	LEU
70	CC	303	ARG
70	CC	308	LYS
70	CC	313	VAL
70	CC	351	VAL
71	Cm	79	GLU
71	Cm	97	ARG
71	Cm	98	LYS
71	Cm	125	LYS
74	Co	24	THR
74	Co	66	ILE
75	CJ	22	LEU
75	CJ	25	CYS
75	CJ	52	LYS
75	CJ	55	TYR
75	CJ	72	CYS
75	CJ	118	LYS
75	CJ	169	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
76	CH	19	THR
76	CH	26	ILE
76	CH	45	LEU
76	CH	113	GLU
76	CH	118	LEU
76	CH	121	LYS
76	CH	134	CYS
76	CH	179	ILE
76	CH	182	SER
77	CE	38	LYS
77	CE	46	ARG
77	CE	52	ARG
77	CE	62	MET
77	CE	65	ARG
77	CE	84	LYS
77	CE	93	THR
77	CE	108	LYS
77	CE	114	ARG
77	CE	116	TYR
77	CE	141	ARG
77	CE	145	THR
77	CE	179	LEU
77	CE	186	LEU
77	CE	191	GLN
77	CE	199	THR
77	CE	207	LYS
77	CE	210	LYS
77	CE	219	LYS
77	CE	223	ARG
77	CE	227	HIS
77	CE	228	GLN
77	CE	237	LYS
77	CE	247	LYS
77	CE	250	GLN
77	CE	251	LYS
77	CE	260	LYS
77	CE	271	LEU
77	CE	277	LEU
77	CE	281	ILE
78	CG	63	LEU
78	CG	101	LYS
78	CG	156	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
78	CG	160	ASP
78	CG	167	VAL
78	CG	173	LEU
78	CG	193	LEU
78	CG	197	LYS
78	CG	218	LEU
78	CG	259	LYS
83	CR	6	LEU
83	CR	30	ASN
83	CR	32	ILE
83	CR	42	ARG
83	CR	63	CYS
83	CR	99	MET
83	CR	146	LYS
83	CR	152	LYS
83	CR	166	THR
83	CR	181	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (50) such sidechains are listed below:

Mol	Chain	Res	Type
2	Ct	84	ASN
2	Ct	108	HIS
2	Ct	158	ASN
2	Ct	186	ASN
5	AN	101	HIS
6	AL	5	GLN
7	AB	75	GLN
8	AA	9	GLN
8	AA	29	ASN
15	AE	209	HIS
16	AC	136	HIS
16	AC	272	HIS
17	AG	227	GLN
18	AH	193	GLN
19	AW	92	ASN
20	AI	52	ASN
23	Ag	56	GLN
26	AM	46	GLN
27	AS	87	GLN
29	AR	26	ASN
29	AR	62	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
29	AR	121	GLN
37	AQ	35	ASN
39	CO	90	HIS
39	CO	167	HIS
43	Ca	67	GLN
46	CD	138	GLN
46	CD	175	HIS
46	CD	202	GLN
47	CQ	160	HIS
48	CA	205	ASN
48	CA	218	HIS
49	CS	162	GLN
50	CT	112	ASN
51	CP	34	GLN
52	CU	27	HIS
55	CZ	79	HIS
56	Cr	70	GLN
64	Cf	24	HIS
64	Cf	56	ASN
69	Cl	20	ASN
70	CC	212	ASN
70	CC	278	ASN
70	CC	310	HIS
76	CH	15	ASN
76	CH	76	HIS
77	CE	250	GLN
77	CE	284	HIS
83	CR	66	ASN
83	CR	178	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	tR	76/77 (98%)	34 (44%)	0
21	B2	1747/1786 (97%)	431 (24%)	52 (2%)
79	A5	1657/1722 (96%)	527 (31%)	84 (5%)
80	A7	120/121 (99%)	25 (20%)	1 (0%)
81	A8	156/157 (99%)	39 (25%)	6 (3%)
82	A6	2003/2069 (96%)	450 (22%)	61 (3%)
All	All	5759/5932 (97%)	1506 (26%)	204 (3%)

All (1506) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	tR	3	C
1	tR	5	G
1	tR	6	G
1	tR	7	G
1	tR	8	U
1	tR	9	G
1	tR	16	C
1	tR	17	C
1	tR	18	C
1	tR	19	G
1	tR	20	G
1	tR	21	U
1	tR	22	A
1	tR	23	G
1	tR	27	G
1	tR	28	U
1	tR	31	G
1	tR	32	G
1	tR	34	U
1	tR	35	C
1	tR	36	A
1	tR	41	C
1	tR	47	G
1	tR	48	U
1	tR	49	C
1	tR	50	G
1	tR	51	U
1	tR	60	A
1	tR	62	C
1	tR	63	C
1	tR	67	C
1	tR	71	G
1	tR	76	C
1	tR	77	A
21	B2	3	C
21	B2	4	C
21	B2	25	A
21	B2	26	U
21	B2	33	G
21	B2	42	A
21	B2	44	U
21	B2	46	A
21	B2	56	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
21	B2	65	C
21	B2	67	C
21	B2	68	A
21	B2	72	C
21	B2	73	C
21	B2	74	G
21	B2	75	G
21	B2	76	U
21	B2	77	A
21	B2	78	C
21	B2	79	A
21	B2	80	G
21	B2	103	A
21	B2	113	G
21	B2	115	U
21	B2	122	G
21	B2	123	G
21	B2	125	C
21	B2	126	G
21	B2	127	C
21	B2	140	C
21	B2	141	A
21	B2	142	C
21	B2	143	U
21	B2	147	A
21	B2	148	U
21	B2	155	G
21	B2	158	A
21	B2	162	C
21	B2	168	C
21	B2	170	A
21	B2	183	G
21	B2	188	C
21	B2	189	U
21	B2	190	G
21	B2	191	A
21	B2	192	C
21	B2	206	G
21	B2	226	A
21	B2	227	U
21	B2	228	C
21	B2	229	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
21	B2	231	A
21	B2	235	A
21	B2	237	C
21	B2	238	C
21	B2	284	C
21	B2	285	C
21	B2	286	U
21	B2	287	U
21	B2	288	G
21	B2	294	U
21	B2	295	C
21	B2	304	C
21	B2	307	G
21	B2	308	G
21	B2	309	G
21	B2	312	G
21	B2	318	A
21	B2	319	C
21	B2	324	C
21	B2	325	C
21	B2	326	C
21	B2	328	U
21	B2	332	G
21	B2	340	C
21	B2	346	C
21	B2	347	G
21	B2	350	C
21	B2	351	G
21	B2	353	C
21	B2	362	C
21	B2	364	A
21	B2	367	U
21	B2	368	U
21	B2	378	U
21	B2	382	C
21	B2	385	G
21	B2	386	C
21	B2	394	G
21	B2	395	G
21	B2	396	U
21	B2	398	A
21	B2	399	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
21	B2	400	C
21	B2	408	A
21	B2	409	C
21	B2	426	A
21	B2	447	A
21	B2	448	A
21	B2	450	C
21	B2	452	G
21	B2	464	A
21	B2	466	G
21	B2	472	C
21	B2	473	A
21	B2	474	G
21	B2	482	G
21	B2	483	C
21	B2	487	C
21	B2	492	C
21	B2	516	A
21	B2	523	A
21	B2	524	U
21	B2	525	A
21	B2	527	C
21	B2	528	A
21	B2	532	C
21	B2	533	A
21	B2	535	G
21	B2	550	C
21	B2	551	U
21	B2	552	G
21	B2	553	U
21	B2	556	U
21	B2	559	G
21	B2	560	A
21	B2	564	A
21	B2	581	U
21	B2	583	A
21	B2	587	A
21	B2	588	G
21	B2	590	A
21	B2	591	U
21	B2	593	C
21	B2	604	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
21	B2	605	A
21	B2	606	G
21	B2	607	U
21	B2	608	C
21	B2	614	C
21	B2	617	G
21	B2	627	U
21	B2	628	A
21	B2	629	A
21	B2	634	A
21	B2	642	U
21	B2	643	A
21	B2	644	G
21	B2	655	A
21	B2	659	G
21	B2	660	C
21	B2	666	U
21	B2	668	A
21	B2	669	A
21	B2	671	A
21	B2	672	A
21	B2	673	G
21	B2	682	U
21	B2	683	G
21	B2	688	U
21	B2	689	U
21	B2	690	G
21	B2	693	A
21	B2	694	G
21	B2	695	C
21	B2	733	C
21	B2	735	C
21	B2	737	G
21	B2	738	C
21	B2	739	C
21	B2	740	C
21	B2	741	C
21	B2	743	U
21	B2	744	G
21	B2	747	U
21	B2	748	C
21	B2	749	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
21	B2	752	G
21	B2	753	C
21	B2	788	G
21	B2	797	C
21	B2	798	G
21	B2	799	U
21	B2	801	U
21	B2	809	A
21	B2	811	A
21	B2	812	A
21	B2	821	G
21	B2	822	U
21	B2	823	U
21	B2	830	A
21	B2	831	G
21	B2	834	C
21	B2	835	C
21	B2	836	G
21	B2	837	A
21	B2	838	G
21	B2	839	C
21	B2	840	C
21	B2	841	G
21	B2	845	G
21	B2	847	A
21	B2	853	C
21	B2	868	G
21	B2	870	A
21	B2	871	U
21	B2	873	G
21	B2	876	C
21	B2	877	C
21	B2	881	G
21	B2	887	U
21	B2	888	U
21	B2	890	U
21	B2	891	G
21	B2	895	G
21	B2	897	U
21	B2	903	A
21	B2	909	G
21	B2	911	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
21	B2	913	A
21	B2	914	U
21	B2	920	A
21	B2	921	G
21	B2	933	G
21	B2	940	U
21	B2	966	U
21	B2	969	U
21	B2	970	G
21	B2	971	G
21	B2	990	A
21	B2	1001	A
21	B2	1002	U
21	B2	1023	A
21	B2	1039	C
21	B2	1045	U
21	B2	1048	G
21	B2	1049	A
21	B2	1050	A
21	B2	1060	A
21	B2	1061	U
21	B2	1062	A
21	B2	1069	U
21	B2	1071	G
21	B2	1078	C
21	B2	1083	A
21	B2	1084	A
21	B2	1085	C
21	B2	1086	G
21	B2	1096	G
21	B2	1097	G
21	B2	1109	C
21	B2	1110	G
21	B2	1111	U
21	B2	1114	U
21	B2	1115	U
21	B2	1116	C
21	B2	1117	C
21	B2	1118	C
21	B2	1120	U
21	B2	1131	G
21	B2	1133	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
21	B2	1137	U
21	B2	1138	C
21	B2	1143	A
21	B2	1148	A
21	B2	1149	A
21	B2	1153	C
21	B2	1154	U
21	B2	1155	U
21	B2	1157	G
21	B2	1166	G
21	B2	1168	G
21	B2	1183	A
21	B2	1192	U
21	B2	1195	A
21	B2	1206	G
21	B2	1210	G
21	B2	1211	G
21	B2	1212	G
21	B2	1214	A
21	B2	1215	C
21	B2	1217	A
21	B2	1221	G
21	B2	1224	G
21	B2	1240	A
21	B2	1242	U
21	B2	1243	U
21	B2	1251	A
21	B2	1253	A
21	B2	1254	C
21	B2	1256	G
21	B2	1257	G
21	B2	1259	A
21	B2	1264	C
21	B2	1265	A
21	B2	1271	C
21	B2	1274	G
21	B2	1275	G
21	B2	1284	A
21	B2	1285	G
21	B2	1286	G
21	B2	1287	A
21	B2	1301	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
21	B2	1302	G
21	B2	1303	C
21	B2	1304	U
21	B2	1305	C
21	B2	1307	U
21	B2	1308	U
21	B2	1313	A
21	B2	1315	U
21	B2	1331	C
21	B2	1332	A
21	B2	1341	C
21	B2	1343	U
21	B2	1348	G
21	B2	1352	G
21	B2	1358	U
21	B2	1371	U
21	B2	1372	U
21	B2	1378	A
21	B2	1394	G
21	B2	1395	C
21	B2	1396	A
21	B2	1397	U
21	B2	1398	G
21	B2	1401	A
21	B2	1402	A
21	B2	1404	U
21	B2	1406	G
21	B2	1410	C
21	B2	1411	G
21	B2	1412	C
21	B2	1417	C
21	B2	1418	C
21	B2	1419	C
21	B2	1426	U
21	B2	1430	C
21	B2	1435	C
21	B2	1437	C
21	B2	1449	G
21	B2	1452	A
21	B2	1453	C
21	B2	1454	A
21	B2	1455	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
21	B2	1456	G
21	B2	1459	G
21	B2	1462	U
21	B2	1463	U
21	B2	1466	G
21	B2	1474	A
21	B2	1475	G
21	B2	1476	A
21	B2	1477	U
21	B2	1478	U
21	B2	1489	A
21	B2	1490	G
21	B2	1495	G
21	B2	1506	A
21	B2	1507	G
21	B2	1508	A
21	B2	1520	G
21	B2	1521	C
21	B2	1533	A
21	B2	1535	U
21	B2	1540	G
21	B2	1544	C
21	B2	1552	G
21	B2	1553	C
21	B2	1556	A
21	B2	1557	C
21	B2	1560	U
21	B2	1563	G
21	B2	1567	G
21	B2	1570	G
21	B2	1578	U
21	B2	1580	A
21	B2	1587	G
21	B2	1588	A
21	B2	1593	C
21	B2	1599	U
21	B2	1600	G
21	B2	1601	A
21	B2	1602	U
21	B2	1604	G
21	B2	1606	G
21	B2	1612	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
21	B2	1613	G
21	B2	1621	U
21	B2	1622	U
21	B2	1623	A
21	B2	1637	A
21	B2	1638	G
21	B2	1641	A
21	B2	1646	C
21	B2	1648	G
21	B2	1665	G
21	B2	1671	G
21	B2	1680	G
21	B2	1690	U
21	B2	1695	A
21	B2	1698	C
21	B2	1701	C
21	B2	1706	G
21	B2	1721	U
21	B2	1722	G
21	B2	1729	U
21	B2	1744	G
21	B2	1746	U
21	B2	1751	C
21	B2	1757	G
21	B2	1782	G
21	B2	1783	U
21	B2	1786	U
21	B2	1823	A
21	B2	1824	A
21	B2	1825	A
21	B2	1826	G
21	B2	1831	A
21	B2	1838	U
21	B2	1839	U
21	B2	1849	G
21	B2	1851	A
21	B2	1852	C
21	B2	1861	G
21	B2	1862	G
21	B2	1863	A
21	B2	1864	U
21	B2	1865	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
21	B2	1868	U
21	B2	1869	A
79	A5	5	A
79	A5	6	C
79	A5	12	A
79	A5	13	U
79	A5	15	A
79	A5	16	G
79	A5	21	G
79	A5	25	A
79	A5	29	G
79	A5	39	A
79	A5	48	G
79	A5	49	U
79	A5	59	A
79	A5	64	A
79	A5	65	A
79	A5	70	A
79	A5	72	C
79	A5	73	A
79	A5	76	A
79	A5	82	U
79	A5	84	A
79	A5	91	G
79	A5	107	G
79	A5	108	A
79	A5	109	G
79	A5	112	C
79	A5	115	C
79	A5	116	G
79	A5	117	C
79	A5	119	G
79	A5	120	A
79	A5	125	C
79	A5	126	C
79	A5	134	G
79	A5	136	C
79	A5	142	G
79	A5	143	C
79	A5	144	G
79	A5	149	A
79	A5	150	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
79	A5	151	G
79	A5	155	C
79	A5	159	C
79	A5	160	G
79	A5	164	G
79	A5	172	C
79	A5	173	C
79	A5	174	C
79	A5	184	U
79	A5	185	C
79	A5	186	G
79	A5	187	U
79	A5	188	G
79	A5	189	G
79	A5	195	C
79	A5	200	U
79	A5	201	C
79	A5	207	G
79	A5	210	C
79	A5	216	C
79	A5	217	C
79	A5	218	A
79	A5	219	G
79	A5	220	C
79	A5	221	C
79	A5	223	G
79	A5	224	U
79	A5	225	G
79	A5	226	G
79	A5	228	C
79	A5	233	U
79	A5	245	C
79	A5	246	G
79	A5	265	C
79	A5	274	C
79	A5	275	C
79	A5	276	C
79	A5	277	G
79	A5	280	G
79	A5	294	G
79	A5	297	U
79	A5	306	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
79	A5	308	G
79	A5	309	C
79	A5	310	G
79	A5	315	G
79	A5	316	U
79	A5	334	A
79	A5	336	A
79	A5	338	A
79	A5	340	C
79	A5	347	A
79	A5	350	C
79	A5	357	U
79	A5	360	A
79	A5	361	C
79	A5	362	A
79	A5	373	G
79	A5	379	G
79	A5	385	A
79	A5	387	G
79	A5	406	C
79	A5	407	A
79	A5	408	A
79	A5	409	G
79	A5	410	A
79	A5	412	G
79	A5	413	G
79	A5	414	C
79	A5	432	U
79	A5	433	A
79	A5	440	U
79	A5	449	C
79	A5	451	C
79	A5	452	A
79	A5	453	G
79	A5	454	U
79	A5	455	C
79	A5	456	C
79	A5	468	U
79	A5	469	C
79	A5	485	C
79	A5	486	C
79	A5	487	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
79	A5	490	C
79	A5	491	G
79	A5	498	C
79	A5	500	G
79	A5	502	C
79	A5	504	G
79	A5	506	C
79	A5	509	A
79	A5	510	U
79	A5	514	U
79	A5	639	U
79	A5	640	C
79	A5	641	G
79	A5	645	G
79	A5	649	A
79	A5	656	C
79	A5	664	G
79	A5	665	C
79	A5	666	G
79	A5	667	A
79	A5	668	C
79	A5	669	C
79	A5	670	G
79	A5	676	C
79	A5	681	G
79	A5	686	A
79	A5	687	U
79	A5	688	U
79	A5	690	C
79	A5	696	A
79	A5	704	C
79	A5	712	C
79	A5	720	G
79	A5	721	G
79	A5	727	C
79	A5	728	U
79	A5	729	G
79	A5	730	G
79	A5	731	G
79	A5	732	A
79	A5	734	G
79	A5	737	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
79	A5	746	A
79	A5	747	A
79	A5	748	G
79	A5	749	G
79	A5	912	G
79	A5	918	G
79	A5	926	G
79	A5	927	G
79	A5	928	C
79	A5	929	A
79	A5	931	C
79	A5	932	A
79	A5	933	G
79	A5	935	G
79	A5	936	C
79	A5	937	U
79	A5	938	C
79	A5	939	G
79	A5	944	A
79	A5	945	U
79	A5	946	C
79	A5	951	G
79	A5	952	G
79	A5	956	A
79	A5	957	G
79	A5	958	G
79	A5	959	G
79	A5	960	A
79	A5	961	G
79	A5	962	C
79	A5	963	C
79	A5	964	A
79	A5	965	G
79	A5	966	A
79	A5	967	C
79	A5	969	C
79	A5	970	G
79	A5	971	U
79	A5	972	C
79	A5	973	G
79	A5	974	C
79	A5	975	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
79	A5	976	G
79	A5	982	U
79	A5	1051	G
79	A5	1070	G
79	A5	1076	C
79	A5	1101	C
79	A5	1102	U
79	A5	1164	G
79	A5	1166	G
79	A5	1167	C
79	A5	1170	G
79	A5	1173	G
79	A5	1175	A
79	A5	1177	U
79	A5	1179	U
79	A5	1180	C
79	A5	1184	A
79	A5	1186	U
79	A5	1187	G
79	A5	1188	C
79	A5	1189	G
79	A5	1190	C
79	A5	1210	C
79	A5	1211	G
79	A5	1212	G
79	A5	1214	U
79	A5	1215	C
79	A5	1219	G
79	A5	1238	A
79	A5	1239	C
79	A5	1240	G
79	A5	1242	G
79	A5	1264	C
79	A5	1267	C
79	A5	1268	G
79	A5	1269	A
79	A5	1270	A
79	A5	1272	C
79	A5	1273	G
79	A5	1274	A
79	A5	1275	G
79	A5	1280	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
79	A5	1281	G
79	A5	1282	G
79	A5	1283	G
79	A5	1284	G
79	A5	1285	U
79	A5	1286	C
79	A5	1288	G
79	A5	1289	C
79	A5	1292	C
79	A5	1293	G
79	A5	1294	A
79	A5	1295	U
79	A5	1296	G
79	A5	1297	U
79	A5	1301	C
79	A5	1302	U
79	A5	1303	A
79	A5	1308	C
79	A5	1313	C
79	A5	1320	U
79	A5	1326	A
79	A5	1330	A
79	A5	1342	A
79	A5	1344	C
79	A5	1348	U
79	A5	1354	A
79	A5	1357	C
79	A5	1358	G
79	A5	1359	G
79	A5	1365	C
79	A5	1366	G
79	A5	1367	C
79	A5	1368	U
79	A5	1369	C
79	A5	1370	G
79	A5	1371	A
79	A5	1372	A
79	A5	1374	G
79	A5	1377	G
79	A5	1378	C
79	A5	1379	C
79	A5	1380	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
79	A5	1383	G
79	A5	1384	C
79	A5	1387	A
79	A5	1388	A
79	A5	1392	A
79	A5	1394	G
79	A5	1397	A
79	A5	1399	G
79	A5	1402	C
79	A5	1407	C
79	A5	1408	G
79	A5	1409	C
79	A5	1410	U
79	A5	1411	C
79	A5	1415	G
79	A5	1416	G
79	A5	1417	C
79	A5	1420	A
79	A5	1421	G
79	A5	1422	G
79	A5	1423	U
79	A5	1425	G
79	A5	1427	U
79	A5	1428	U
79	A5	1429	C
79	A5	1431	C
79	A5	1437	C
79	A5	1439	C
79	A5	1454	G
79	A5	1455	G
79	A5	1456	C
79	A5	1457	G
79	A5	1458	C
79	A5	1475	G
79	A5	1478	C
79	A5	1481	C
79	A5	1482	G
79	A5	1483	C
79	A5	1484	G
79	A5	1485	C
79	A5	1486	C
79	A5	1489	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
79	A5	1492	G
79	A5	1498	G
79	A5	1501	G
79	A5	1502	G
79	A5	1503	A
79	A5	1504	G
79	A5	1515	A
79	A5	1517	G
79	A5	1518	A
79	A5	1523	A
79	A5	1525	A
79	A5	1534	A
79	A5	1547	A
79	A5	1554	A
79	A5	1566	C
79	A5	1574	G
79	A5	1575	A
79	A5	1578	U
79	A5	1591	U
79	A5	1592	G
79	A5	1596	U
79	A5	1597	G
79	A5	1598	C
79	A5	1605	G
79	A5	1612	G
79	A5	1614	C
79	A5	1617	G
79	A5	1624	G
79	A5	1625	G
79	A5	1626	G
79	A5	1629	G
79	A5	1630	A
79	A5	1631	A
79	A5	1632	A
79	A5	1633	G
79	A5	1634	A
79	A5	1637	A
79	A5	1639	U
79	A5	1640	C
79	A5	1642	A
79	A5	1649	U
79	A5	1651	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
79	A5	1654	G
79	A5	1655	C
79	A5	1656	U
79	A5	1661	C
79	A5	1670	G
79	A5	1671	U
79	A5	1676	C
79	A5	1677	U
79	A5	1681	G
79	A5	1691	G
79	A5	1694	C
79	A5	1697	G
79	A5	1698	C
79	A5	1699	A
79	A5	1700	G
79	A5	1720	C
79	A5	1725	U
79	A5	1726	U
79	A5	1731	C
79	A5	1739	G
79	A5	1741	G
79	A5	1742	A
79	A5	1746	A
79	A5	1747	U
79	A5	1750	G
79	A5	1753	G
79	A5	1754	U
79	A5	1755	C
79	A5	1756	U
79	A5	1757	U
79	A5	1758	G
79	A5	1761	G
79	A5	1762	C
79	A5	1764	G
79	A5	1769	G
79	A5	1772	C
79	A5	1773	U
79	A5	1774	C
79	A5	1776	A
79	A5	1781	U
79	A5	1783	C
79	A5	1785	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
79	A5	1787	A
79	A5	1789	C
79	A5	1790	U
79	A5	1799	G
79	A5	1803	G
79	A5	1804	A
79	A5	1805	A
79	A5	1806	G
79	A5	1812	C
79	A5	1815	G
79	A5	1816	C
79	A5	1818	G
79	A5	1820	C
79	A5	1821	G
79	A5	1822	U
79	A5	1823	G
79	A5	1824	G
79	A5	1825	A
79	A5	1828	C
79	A5	1829	G
79	A5	1831	G
79	A5	1833	G
79	A5	1836	G
79	A5	1841	C
79	A5	1842	G
79	A5	1845	U
79	A5	1849	U
79	A5	1854	G
79	A5	1855	G
79	A5	1859	C
79	A5	1869	G
79	A5	1870	C
79	A5	1888	A
79	A5	1893	C
79	A5	1897	A
79	A5	1901	C
79	A5	1902	G
79	A5	1906	U
79	A5	1908	A
79	A5	1912	G
79	A5	1913	C
79	A5	1915	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
79	A5	1918	U
79	A5	1920	C
79	A5	1921	C
79	A5	1922	A
79	A5	1924	C
79	A5	1929	A
79	A5	1930	U
79	A5	1931	C
79	A5	1940	G
79	A5	1948	G
79	A5	1950	U
79	A5	1952	G
79	A5	1961	G
79	A5	1962	A
79	A5	1963	C
79	A5	1964	A
79	A5	1969	G
79	A5	1971	C
79	A5	1972	G
79	A5	1974	U
79	A5	1975	G
79	A5	1976	G
79	A5	1977	C
79	A5	1980	G
79	A5	1981	G
79	A5	1983	A
79	A5	1984	A
79	A5	1985	G
79	A5	1987	C
79	A5	1988	G
79	A5	1991	A
79	A5	1992	U
79	A5	1993	C
79	A5	1997	U
79	A5	2001	G
79	A5	2002	A
79	A5	2003	G
79	A5	2004	U
79	A5	2008	U
79	A5	2009	A
79	A5	2010	A
79	A5	2015	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
79	A5	2021	G
79	A5	2024	G
79	A5	2025	A
79	A5	2026	A
79	A5	2040	A
79	A5	2042	A
79	A5	2044	U
79	A5	2045	G
79	A5	2046	G
79	A5	2047	A
79	A5	2048	U
79	A5	2049	G
79	A5	2052	G
79	A5	2060	G
79	A5	2063	G
79	A5	2069	A
79	A5	2071	A
79	A5	2072	C
79	A5	2074	C
79	A5	2084	C
79	A5	2085	G
79	A5	2087	C
79	A5	2088	A
79	A5	2089	G
79	A5	2090	U
80	A7	7	G
80	A7	11	A
80	A7	13	A
80	A7	14	C
80	A7	22	A
80	A7	33	U
80	A7	39	C
80	A7	41	G
80	A7	49	A
80	A7	51	G
80	A7	61	G
80	A7	63	C
80	A7	64	G
80	A7	66	G
80	A7	73	U
80	A7	90	A
80	A7	91	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
80	A7	97	G
80	A7	100	A
80	A7	106	G
80	A7	108	G
80	A7	110	G
80	A7	115	A
80	A7	116	G
80	A7	121	U
81	A8	23	C
81	A8	24	G
81	A8	34	U
81	A8	35	C
81	A8	38	U
81	A8	39	G
81	A8	40	A
81	A8	41	A
81	A8	42	G
81	A8	46	G
81	A8	59	A
81	A8	62	A
81	A8	63	U
81	A8	72	A
81	A8	75	G
81	A8	81	C
81	A8	82	A
81	A8	83	C
81	A8	85	U
81	A8	86	U
81	A8	87	G
81	A8	94	G
81	A8	95	A
81	A8	96	C
81	A8	97	A
81	A8	99	U
81	A8	103	A
81	A8	105	C
81	A8	109	C
81	A8	110	U
81	A8	111	U
81	A8	112	G
81	A8	114	G
81	A8	125	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
81	A8	126	C
81	A8	127	U
81	A8	134	G
81	A8	150	C
81	A8	156	U
82	A6	2254	G
82	A6	2256	C
82	A6	2257	C
82	A6	2258	C
82	A6	2259	G
82	A6	2260	C
82	A6	2261	G
82	A6	2263	A
82	A6	2264	C
82	A6	2265	G
82	A6	2266	C
82	A6	2267	U
82	A6	2269	C
82	A6	2289	C
82	A6	2290	C
82	A6	2299	G
82	A6	2301	G
82	A6	2306	G
82	A6	2313	A
82	A6	2314	G
82	A6	2322	G
82	A6	2332	A
82	A6	2333	G
82	A6	2345	G
82	A6	2348	G
82	A6	2351	C
82	A6	2360	A
82	A6	2366	A
82	A6	2391	G
82	A6	2395	A
82	A6	2396	A
82	A6	2399	G
82	A6	2410	C
82	A6	2421	G
82	A6	2422	C
82	A6	2429	A
82	A6	2437	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
82	A6	2441	C
82	A6	2450	G
82	A6	2456	G
82	A6	2459	G
82	A6	2463	G
82	A6	2469	C
82	A6	2470	C
82	A6	2473	A
82	A6	2475	G
82	A6	2487	G
82	A6	2488	C
82	A6	2489	C
82	A6	2490	U
82	A6	2491	C
82	A6	2503	G
82	A6	2504	C
82	A6	2505	C
82	A6	2507	A
82	A6	2513	A
82	A6	2517	A
82	A6	2518	G
82	A6	2522	G
82	A6	2529	A
82	A6	2531	C
82	A6	2532	C
82	A6	2533	C
82	A6	2544	G
82	A6	2546	G
82	A6	2547	G
82	A6	2552	G
82	A6	2554	U
82	A6	2575	U
82	A6	2581	A
82	A6	2583	C
82	A6	2586	G
82	A6	2587	A
82	A6	2588	C
82	A6	2589	C
82	A6	2596	G
82	A6	2601	A
82	A6	2621	A
82	A6	2627	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
82	A6	2631	U
82	A6	2638	G
82	A6	2639	U
82	A6	2647	A
82	A6	2648	G
82	A6	2649	G
82	A6	2650	G
82	A6	2651	C
82	A6	2652	G
82	A6	2658	G
82	A6	2661	U
82	A6	2662	G
82	A6	2669	C
82	A6	2670	C
82	A6	2671	C
82	A6	2673	G
82	A6	2675	G
82	A6	2681	G
82	A6	2686	G
82	A6	2687	U
82	A6	2688	G
82	A6	2694	G
82	A6	2695	A
82	A6	2696	A
82	A6	2711	G
82	A6	2712	G
82	A6	2713	C
82	A6	2716	C
82	A6	2721	G
82	A6	2726	G
82	A6	2734	U
82	A6	2739	C
82	A6	2740	U
82	A6	2742	G
82	A6	2743	A
82	A6	2752	G
82	A6	2754	G
82	A6	2759	G
82	A6	2760	G
82	A6	2762	G
82	A6	2765	A
82	A6	2766	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
82	A6	2767	U
82	A6	2768	C
82	A6	2769	U
82	A6	2770	C
82	A6	2781	G
82	A6	2787	A
82	A6	2788	U
82	A6	2789	A
82	A6	2790	U
82	A6	2794	C
82	A6	2798	A
82	A6	2806	A
82	A6	2814	C
82	A6	2826	U
82	A6	2827	G
82	A6	2828	U
82	A6	2829	U
82	A6	2830	G
82	A6	2833	A
82	A6	2842	G
82	A6	2855	G
82	A6	2884	G
82	A6	2897	G
82	A6	2905	C
82	A6	3594	C
82	A6	3596	A
82	A6	3597	G
82	A6	3605	C
82	A6	3606	U
82	A6	3615	G
82	A6	3617	G
82	A6	3618	C
82	A6	3625	G
82	A6	3626	G
82	A6	3630	A
82	A6	3635	A
82	A6	3653	A
82	A6	3662	A
82	A6	3664	G
82	A6	3673	C
82	A6	3674	G
82	A6	3678	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
82	A6	3682	A
82	A6	3692	A
82	A6	3698	G
82	A6	3709	U
82	A6	3712	A
82	A6	3714	G
82	A6	3727	A
82	A6	3732	A
82	A6	3748	A
82	A6	3750	G
82	A6	3753	G
82	A6	3756	A
82	A6	3759	A
82	A6	3760	A
82	A6	3761	C
82	A6	3774	A
82	A6	3776	G
82	A6	3777	G
82	A6	3785	A
82	A6	3786	U
82	A6	3789	C
82	A6	3792	G
82	A6	3811	G
82	A6	3813	A
82	A6	3814	U
82	A6	3817	A
82	A6	3818	U
82	A6	3819	G
82	A6	3833	C
82	A6	3839	G
82	A6	3840	U
82	A6	3843	C
82	A6	3844	U
82	A6	3877	A
82	A6	3878	C
82	A6	3879	G
82	A6	3886	G
82	A6	3888	G
82	A6	3889	G
82	A6	3897	G
82	A6	3901	A
82	A6	3906	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
82	A6	3907	G
82	A6	3908	A
82	A6	3915	U
82	A6	3923	A
82	A6	3960	A
82	A6	3962	A
82	A6	3963	A
82	A6	3964	U
82	A6	3965	A
82	A6	3966	A
82	A6	3969	G
82	A6	3973	G
82	A6	3974	G
82	A6	4037	C
82	A6	4038	C
82	A6	4043	G
82	A6	4044	U
82	A6	4048	A
82	A6	4049	U
82	A6	4051	C
82	A6	4052	C
82	A6	4053	A
82	A6	4056	A
82	A6	4073	A
82	A6	4076	G
82	A6	4077	A
82	A6	4083	U
82	A6	4084	G
82	A6	4085	A
82	A6	4086	G
82	A6	4087	G
82	A6	4088	C
82	A6	4093	G
82	A6	4094	G
82	A6	4107	G
82	A6	4114	C
82	A6	4115	G
82	A6	4116	C
82	A6	4117	U
82	A6	4120	U
82	A6	4121	G
82	A6	4122	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
82	A6	4123	C
82	A6	4124	G
82	A6	4125	C
82	A6	4126	C
82	A6	4127	A
82	A6	4128	A
82	A6	4143	G
82	A6	4144	U
82	A6	4157	A
82	A6	4161	G
82	A6	4163	U
82	A6	4164	C
82	A6	4165	C
82	A6	4170	A
82	A6	4171	C
82	A6	4183	G
82	A6	4184	G
82	A6	4191	G
82	A6	4206	C
82	A6	4207	C
82	A6	4212	A
82	A6	4213	A
82	A6	4222	G
82	A6	4225	G
82	A6	4229	U
82	A6	4232	U
82	A6	4233	A
82	A6	4249	G
82	A6	4251	A
82	A6	4254	G
82	A6	4255	A
82	A6	4266	G
82	A6	4268	A
82	A6	4271	A
82	A6	4272	G
82	A6	4273	A
82	A6	4291	G
82	A6	4293	U
82	A6	4294	C
82	A6	4296	U
82	A6	4304	A
82	A6	4305	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
82	A6	4306	U
82	A6	4319	C
82	A6	4326	G
82	A6	4329	G
82	A6	4330	G
82	A6	4331	G
82	A6	4332	C
82	A6	4335	C
82	A6	4349	C
82	A6	4350	C
82	A6	4354	U
82	A6	4355	G
82	A6	4356	G
82	A6	4364	G
82	A6	4373	G
82	A6	4376	A
82	A6	4377	G
82	A6	4378	A
82	A6	4387	C
82	A6	4393	G
82	A6	4394	A
82	A6	4395	U
82	A6	4396	A
82	A6	4419	U
82	A6	4422	A
82	A6	4424	A
82	A6	4426	C
82	A6	4436	U
82	A6	4444	C
82	A6	4449	A
82	A6	4463	U
82	A6	4464	A
82	A6	4466	C
82	A6	4473	A
82	A6	4476	C
82	A6	4488	A
82	A6	4491	G
82	A6	4500	U
82	A6	4512	U
82	A6	4513	A
82	A6	4519	C
82	A6	4524	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
82	A6	4528	G
82	A6	4534	G
82	A6	4548	A
82	A6	4567	G
82	A6	4573	G
82	A6	4574	U
82	A6	4575	G
82	A6	4583	C
82	A6	4590	A
82	A6	4599	A
82	A6	4620	U
82	A6	4636	U
82	A6	4637	G
82	A6	4652	G
82	A6	4653	C
82	A6	4656	A
82	A6	4657	U
82	A6	4664	A
82	A6	4670	C
82	A6	4672	A
82	A6	4677	U
82	A6	4694	G
82	A6	4695	C
82	A6	4697	U
82	A6	4706	G
82	A6	4708	A
82	A6	4709	U
82	A6	4714	C
82	A6	4717	A
82	A6	4720	C
82	A6	4726	G
82	A6	4727	A
82	A6	4730	C
82	A6	4731	G
82	A6	4732	G
82	A6	4734	A
82	A6	4739	C
82	A6	4748	U
82	A6	4749	C
82	A6	4750	G
82	A6	4751	G
82	A6	4753	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
82	A6	4754	G
82	A6	4756	C
82	A6	4757	C
82	A6	4758	U
82	A6	4762	A
82	A6	4764	A
82	A6	4869	U
82	A6	4870	G
82	A6	4871	C
82	A6	4872	G
82	A6	4873	G
82	A6	4874	A
82	A6	4875	G
82	A6	4876	A
82	A6	4877	G
82	A6	4878	C
82	A6	4882	U
82	A6	4883	C
82	A6	4884	G
82	A6	4885	U
82	A6	4886	C
82	A6	4888	U
82	A6	4889	G
82	A6	4890	G
82	A6	4895	C
82	A6	4896	G
82	A6	4901	G
82	A6	4906	C
82	A6	4910	A
82	A6	4914	G
82	A6	4925	U
82	A6	4933	C
82	A6	4935	C
82	A6	4936	G
82	A6	4937	C
82	A6	4938	A
82	A6	4939	A
82	A6	4940	C
82	A6	4942	C
82	A6	4943	A
82	A6	4944	C
82	A6	4945	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
82	A6	4947	U
82	A6	4948	C
82	A6	4950	U
82	A6	4951	G
82	A6	4952	G
82	A6	4966	A
82	A6	4976	U
82	A6	4981	G
82	A6	4985	U
82	A6	4988	U
82	A6	4989	U
82	A6	4991	U
82	A6	4992	G
82	A6	4996	C
82	A6	4998	G
82	A6	5002	U
82	A6	5005	G
82	A6	5006	U
82	A6	5007	A
82	A6	5013	C
82	A6	5014	A
82	A6	5017	G
82	A6	5021	C
82	A6	5022	U
82	A6	5023	C
82	A6	5027	C
82	A6	5028	G
82	A6	5041	G
82	A6	5047	C
82	A6	5050	C
82	A6	5054	C
82	A6	5055	G
82	A6	5060	A
82	A6	5061	A
82	A6	5062	G

All (204) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
21	B2	24	C
21	B2	66	G
21	B2	72	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
21	B2	102	A
21	B2	127	C
21	B2	139	C
21	B2	140	C
21	B2	141	A
21	B2	190	G
21	B2	225	G
21	B2	228	C
21	B2	285	C
21	B2	327	G
21	B2	465	A
21	B2	532	C
21	B2	534	G
21	B2	552	G
21	B2	604	A
21	B2	641	A
21	B2	688	U
21	B2	732	U
21	B2	734	C
21	B2	746	C
21	B2	797	C
21	B2	798	G
21	B2	821	G
21	B2	833	C
21	B2	839	C
21	B2	869	A
21	B2	880	G
21	B2	939	U
21	B2	970	G
21	B2	1108	G
21	B2	1115	U
21	B2	1214	A
21	B2	1253	A
21	B2	1307	U
21	B2	1394	G
21	B2	1395	C
21	B2	1396	A
21	B2	1401	A
21	B2	1429	G
21	B2	1474	A
21	B2	1543	G
21	B2	1556	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
21	B2	1637	A
21	B2	1664	A
21	B2	1679	A
21	B2	1756	C
21	B2	1825	A
21	B2	1830	U
21	B2	1868	U
79	A5	12	A
79	A5	48	G
79	A5	64	A
79	A5	125	C
79	A5	142	G
79	A5	184	U
79	A5	186	G
79	A5	187	U
79	A5	215	C
79	A5	218	A
79	A5	220	C
79	A5	245	C
79	A5	293	G
79	A5	309	C
79	A5	333	U
79	A5	406	C
79	A5	431	G
79	A5	451	C
79	A5	452	A
79	A5	486	C
79	A5	489	C
79	A5	497	G
79	A5	505	G
79	A5	648	G
79	A5	655	C
79	A5	668	C
79	A5	685	C
79	A5	703	G
79	A5	746	A
79	A5	911	U
79	A5	917	A
79	A5	926	G
79	A5	931	C
79	A5	936	C
79	A5	945	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
79	A5	955	G
79	A5	957	G
79	A5	958	G
79	A5	959	G
79	A5	964	A
79	A5	966	A
79	A5	968	C
79	A5	969	C
79	A5	971	U
79	A5	974	C
79	A5	1163	G
79	A5	1210	C
79	A5	1211	G
79	A5	1237	C
79	A5	1238	A
79	A5	1239	C
79	A5	1269	A
79	A5	1274	A
79	A5	1281	G
79	A5	1284	G
79	A5	1287	G
79	A5	1288	G
79	A5	1293	G
79	A5	1296	G
79	A5	1356	U
79	A5	1365	C
79	A5	1370	G
79	A5	1379	C
79	A5	1398	A
79	A5	1407	C
79	A5	1410	U
79	A5	1426	G
79	A5	1455	G
79	A5	1481	C
79	A5	1484	G
79	A5	1574	G
79	A5	1633	G
79	A5	1696	G
79	A5	1804	A
79	A5	1835	G
79	A5	1841	C
79	A5	1853	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
79	A5	1920	C
79	A5	1921	C
79	A5	1974	U
79	A5	2009	A
79	A5	2046	G
79	A5	2083	C
79	A5	2089	G
80	A7	72	U
81	A8	85	U
81	A8	94	G
81	A8	96	C
81	A8	111	U
81	A8	124	U
81	A8	126	C
82	A6	2256	C
82	A6	2257	C
82	A6	2260	C
82	A6	2263	A
82	A6	2264	C
82	A6	2266	C
82	A6	2268	A
82	A6	2313	A
82	A6	2398	U
82	A6	2487	G
82	A6	2490	U
82	A6	2531	C
82	A6	2546	G
82	A6	2649	G
82	A6	2661	U
82	A6	2670	C
82	A6	2695	A
82	A6	2761	U
82	A6	2766	A
82	A6	2769	U
82	A6	2825	A
82	A6	3616	U
82	A6	3672	G
82	A6	3697	U
82	A6	3876	A
82	A6	3887	C
82	A6	3888	G
82	A6	3959	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
82	A6	3965	A
82	A6	3968	U
82	A6	4036	G
82	A6	4072	C
82	A6	4075	U
82	A6	4082	G
82	A6	4085	A
82	A6	4087	G
82	A6	4093	G
82	A6	4119	C
82	A6	4121	G
82	A6	4124	G
82	A6	4127	A
82	A6	4164	C
82	A6	4170	A
82	A6	4232	U
82	A6	4448	G
82	A6	4656	A
82	A6	4719	G
82	A6	4738	C
82	A6	4749	C
82	A6	4871	C
82	A6	4874	A
82	A6	4876	A
82	A6	4882	U
82	A6	4885	U
82	A6	4887	C
82	A6	4889	G
82	A6	4937	C
82	A6	4991	U
82	A6	4997	G
82	A6	5022	U
82	A6	5027	C

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	DDE	Ct	715	2	18,20,21	1.12	2 (11%)	17,28,30	0.92	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DDE	Ct	715	2	-	6/20/21/23	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Ct	715	DDE	CD2-CG	2.58	1.41	1.36
2	Ct	715	DDE	CBW-CBI	2.12	1.57	1.53

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Ct	715	DDE	CAU-CBW-CBI	-2.37	106.58	111.22

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	Ct	715	DDE	CA-CB-CG-ND1
2	Ct	715	DDE	NAD-CBI-CBW-NCB
2	Ct	715	DDE	OAG-CBI-CBW-CAU
2	Ct	715	DDE	CAT-CAU-CBW-NCB
2	Ct	715	DDE	CAT-CAU-CBW-CBI
2	Ct	715	DDE	CA-CB-CG-CD2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
21	B2	9
79	A5	9
82	A6	4
7	AB	1
45	CI	1
77	CE	1
2	Ct	1
36	AF	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B2	757:C	O3'	783:C	P	20.08
1	A5	1112:C	O3'	1157:G	P	20.00
1	A5	1439:C	O3'	1447:C	P	19.55
1	A6	3987:C	O3'	4011:G	P	18.44
1	B2	250:U	O3'	267:G	P	18.43
1	A5	1002:C	O3'	1042:G	P	18.07
1	A5	1051:G	O3'	1060:U	P	17.84
1	B2	697:G	O3'	732:U	P	17.34
1	A6	4793:G	O3'	4840:C	P	17.15
1	A6	4018:G	O3'	4029:C	P	16.99
1	A5	1242:G	O3'	1263:A	P	16.81
1	A5	759:G	O3'	888:G	P	16.37
1	A5	521:C	O3'	633:G	P	15.55

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B2	1762:C	O3'	1771:G	P	15.24
1	A6	2909:C	O3'	3581:C	P	12.02
1	AB	51:ARG	C	55:THR	N	9.10
1	CI	104:SER	C	111:LEU	N	8.97
1	CE	126:LEU	C	132:PRO	N	8.16
1	Ct	46:ILE	C	52:GLY	N	7.76
1	A5	1221:G	O3'	1233:G	P	7.56
1	B2	272:G	O3'	273:G	P	6.85
1	A5	990:C	O3'	991:C	P	6.42
1	AF	130:ARG	C	134:VAL	N	5.92
1	B2	1784:G	O3'	1785:C	P	4.59
1	B2	1747:C	O3'	1748:G	P	4.16
1	B2	1202:U	O3'	1203:G	P	3.11
1	B2	1690:U	O3'	1691:U	P	3.07

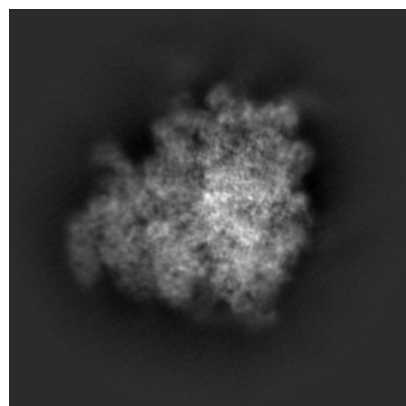
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72475. These allow visual inspection of the internal detail of the map and identification of artifacts.

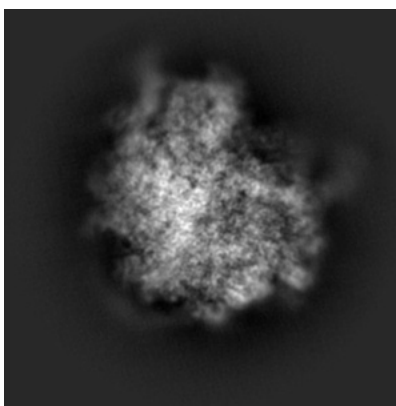
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

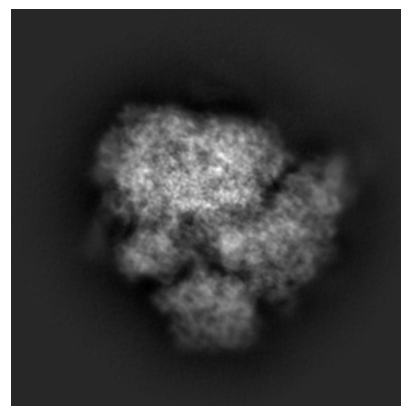
6.1.1 Primary map



X

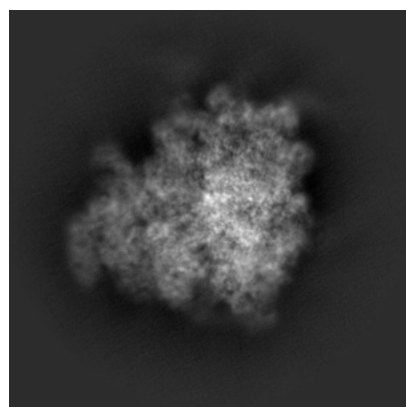


Y

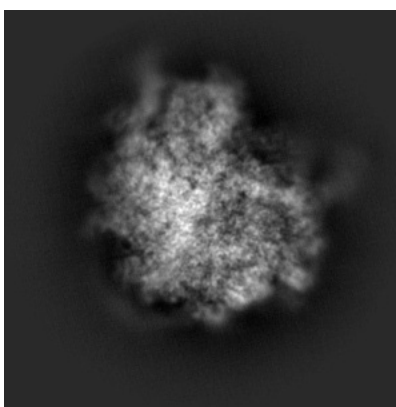


Z

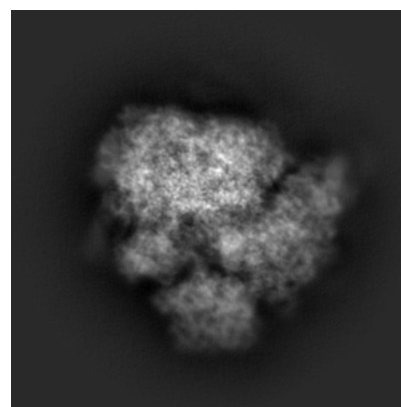
6.1.2 Raw map



X



Y

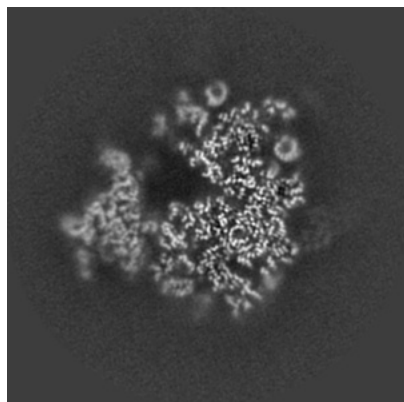


Z

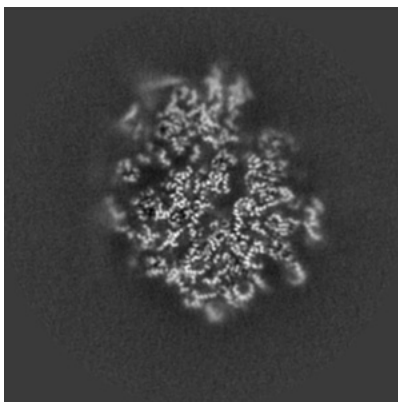
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

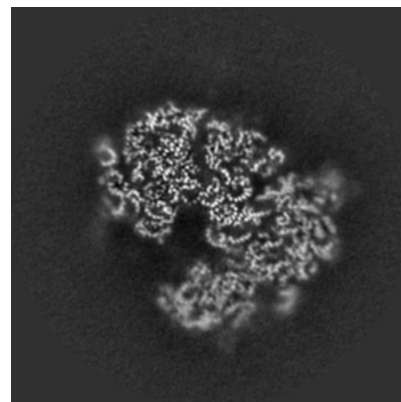
6.2.1 Primary map



X Index: 200

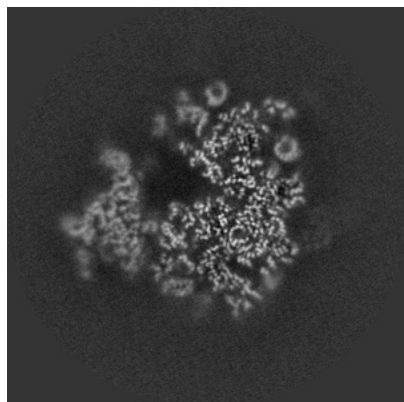


Y Index: 200

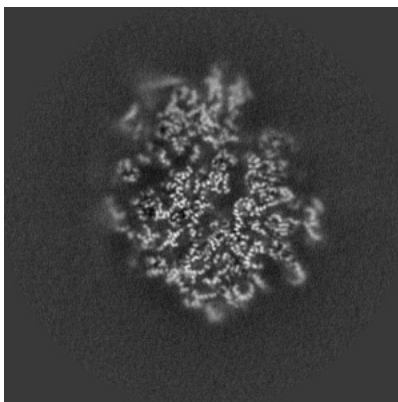


Z Index: 200

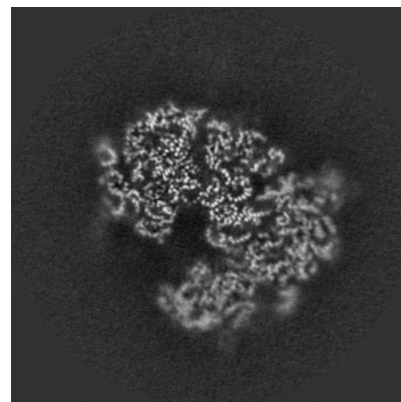
6.2.2 Raw map



X Index: 200



Y Index: 200

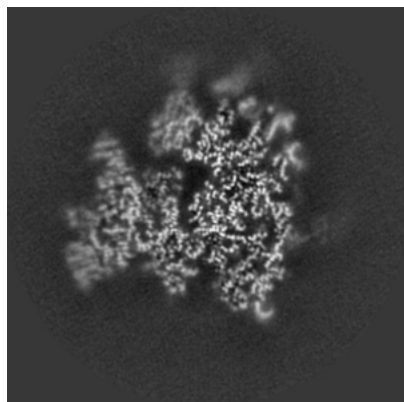


Z Index: 200

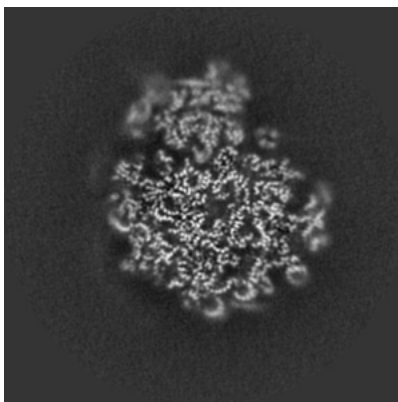
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

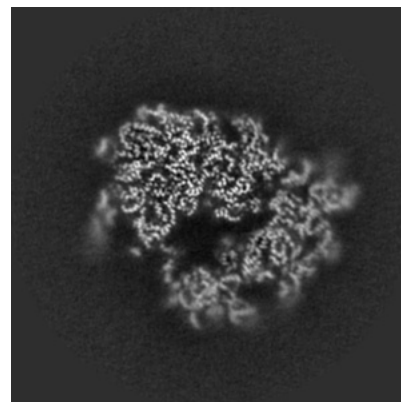
6.3.1 Primary map



X Index: 217

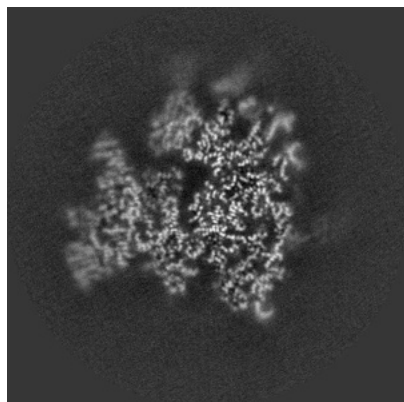


Y Index: 207

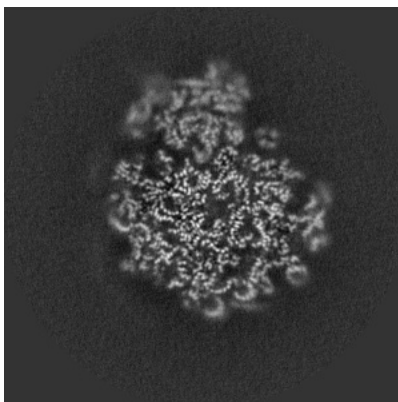


Z Index: 210

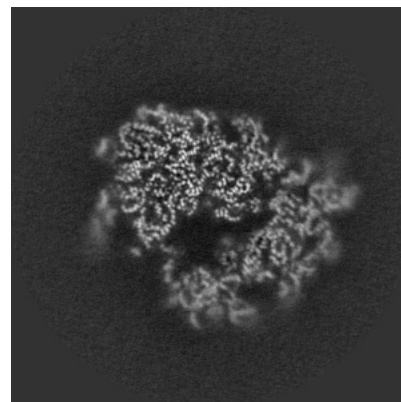
6.3.2 Raw map



X Index: 217



Y Index: 207

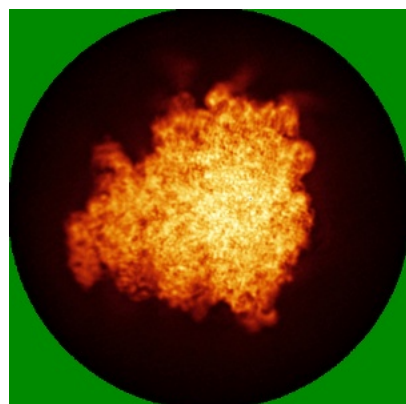


Z Index: 210

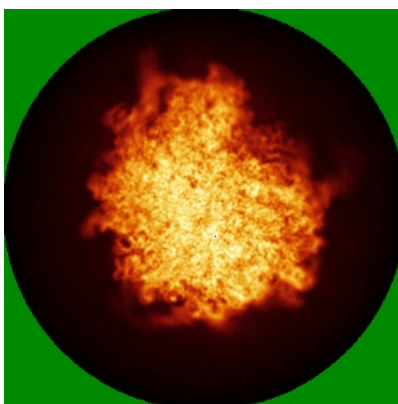
The images above show the largest variance slices of the map in three orthogonal directions.

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

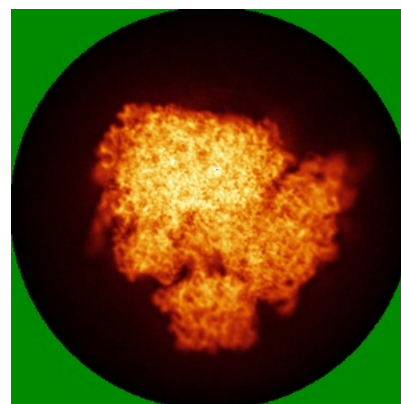
6.4.1 Primary map



X

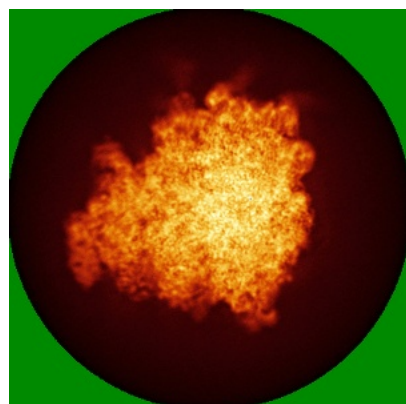


Y

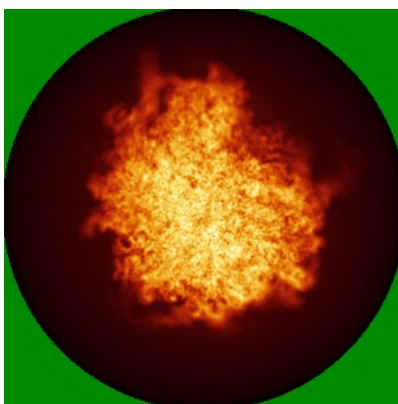


Z

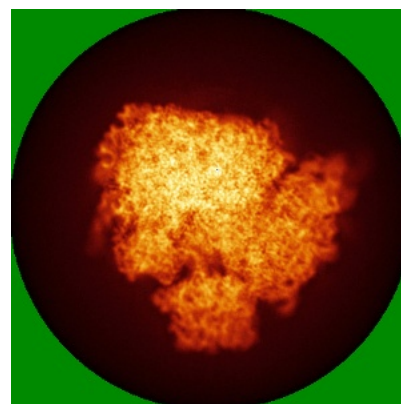
6.4.2 Raw map



X



Y

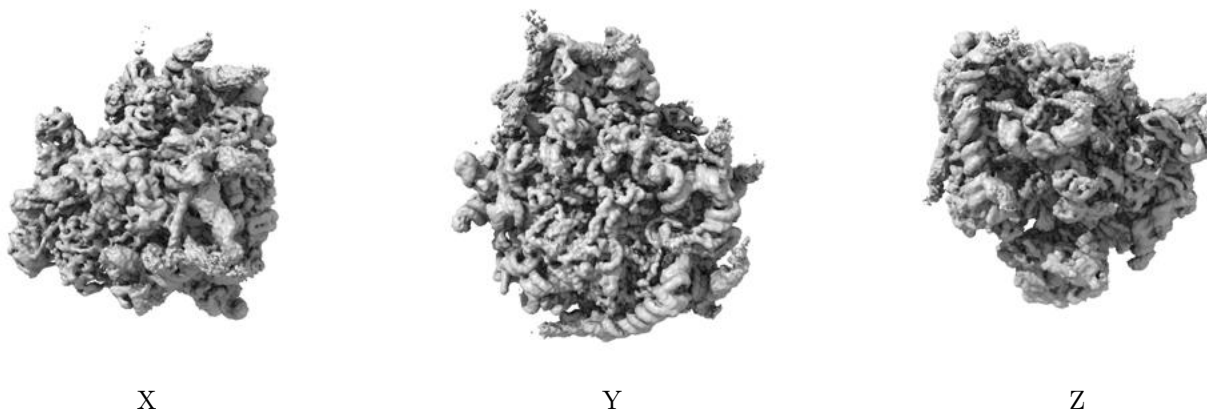


Z

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.

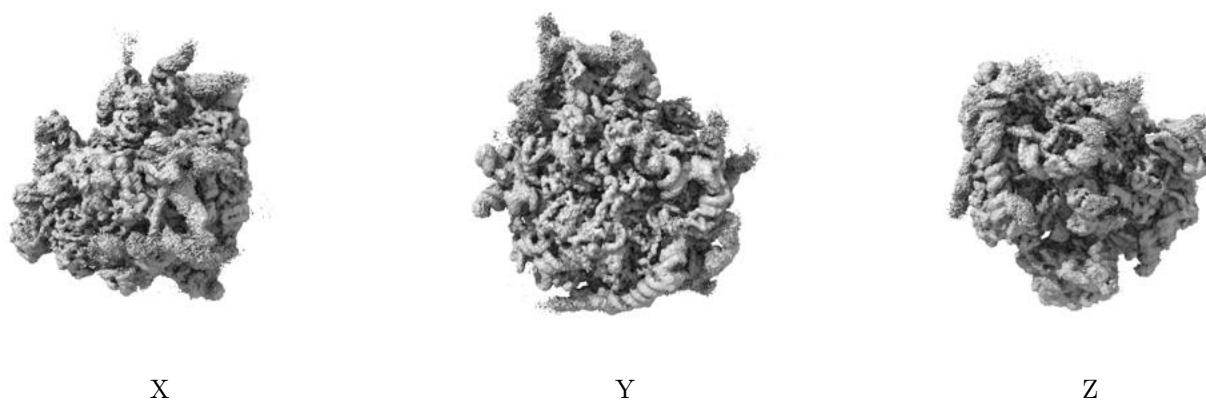
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.006. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

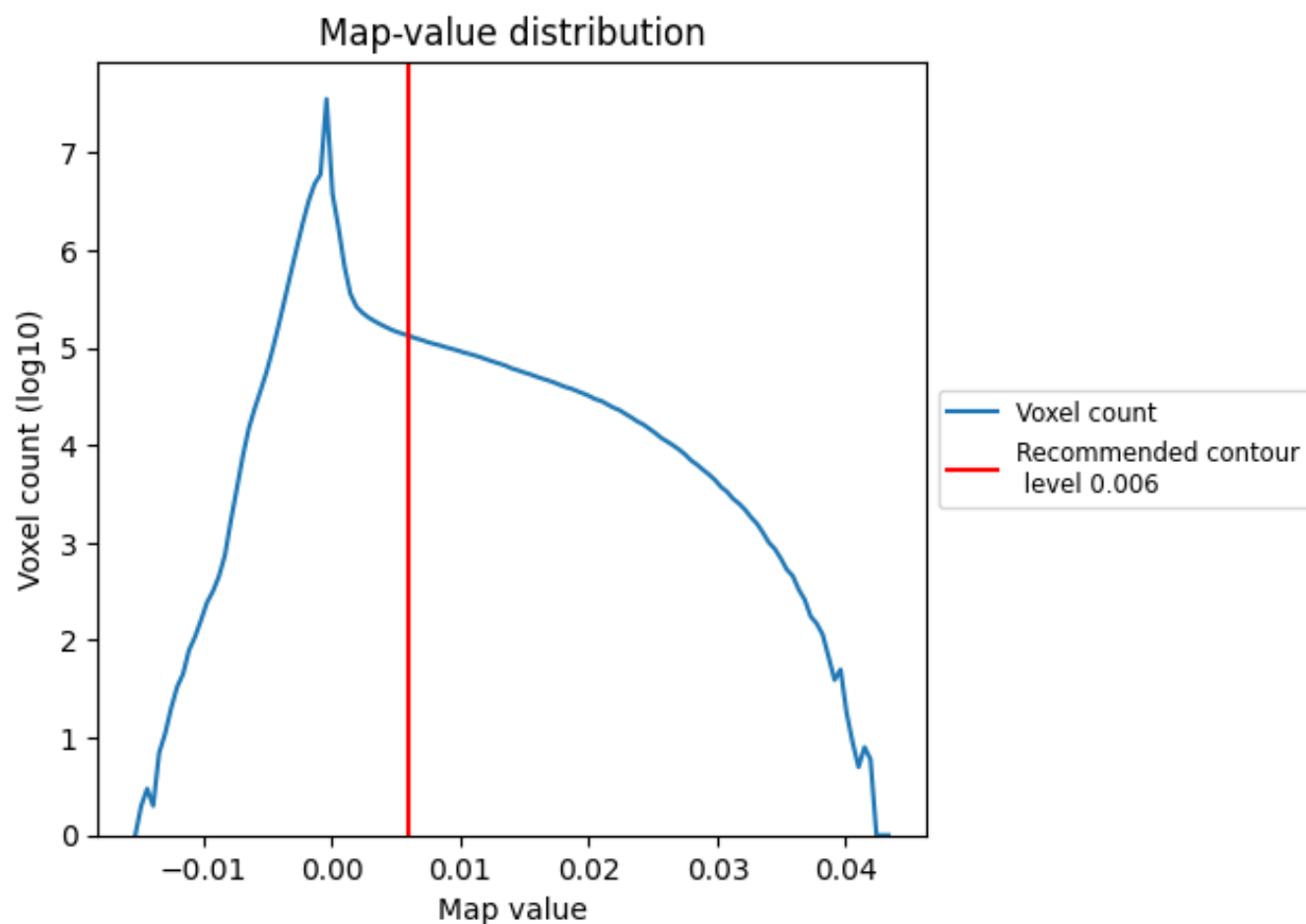
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

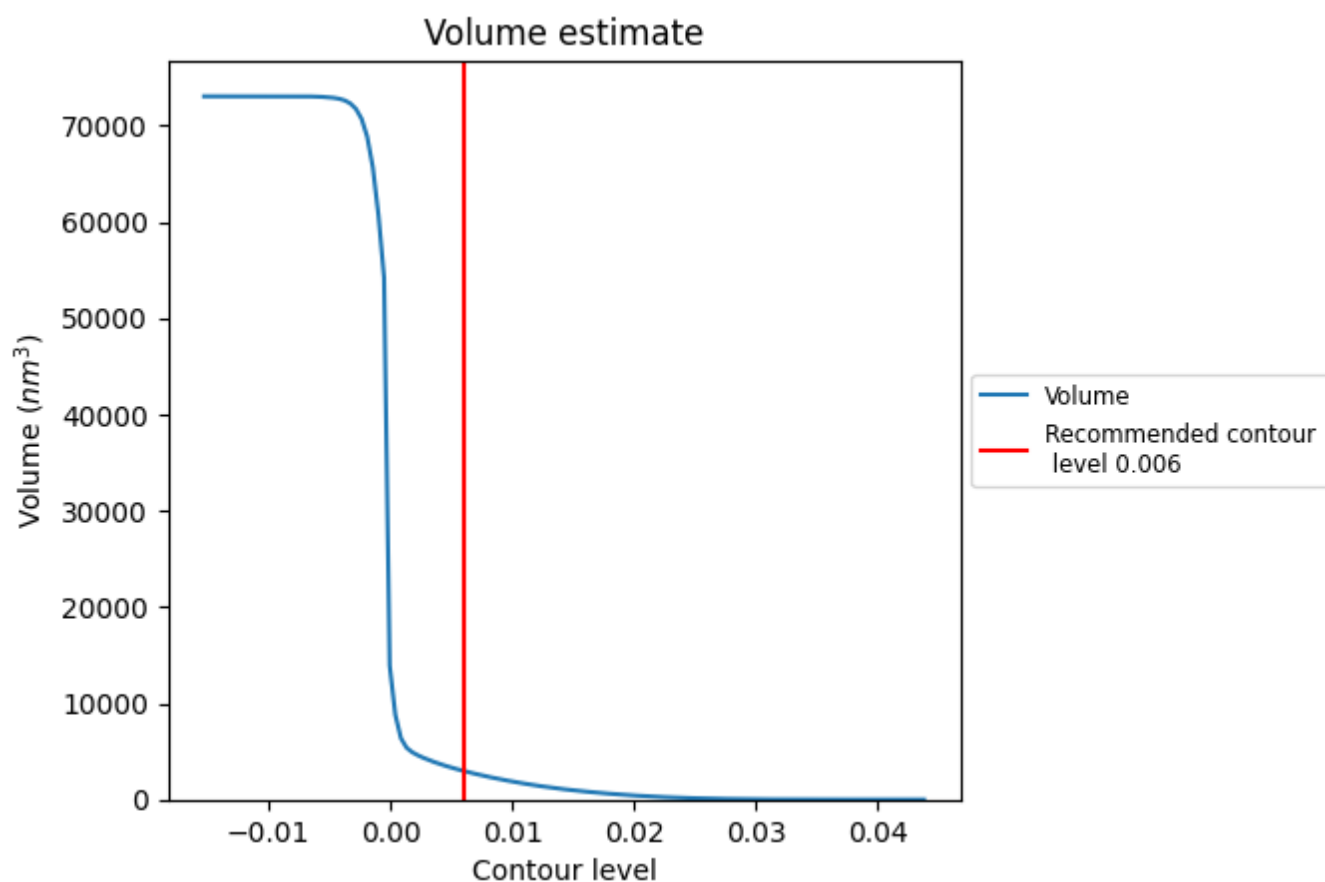
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

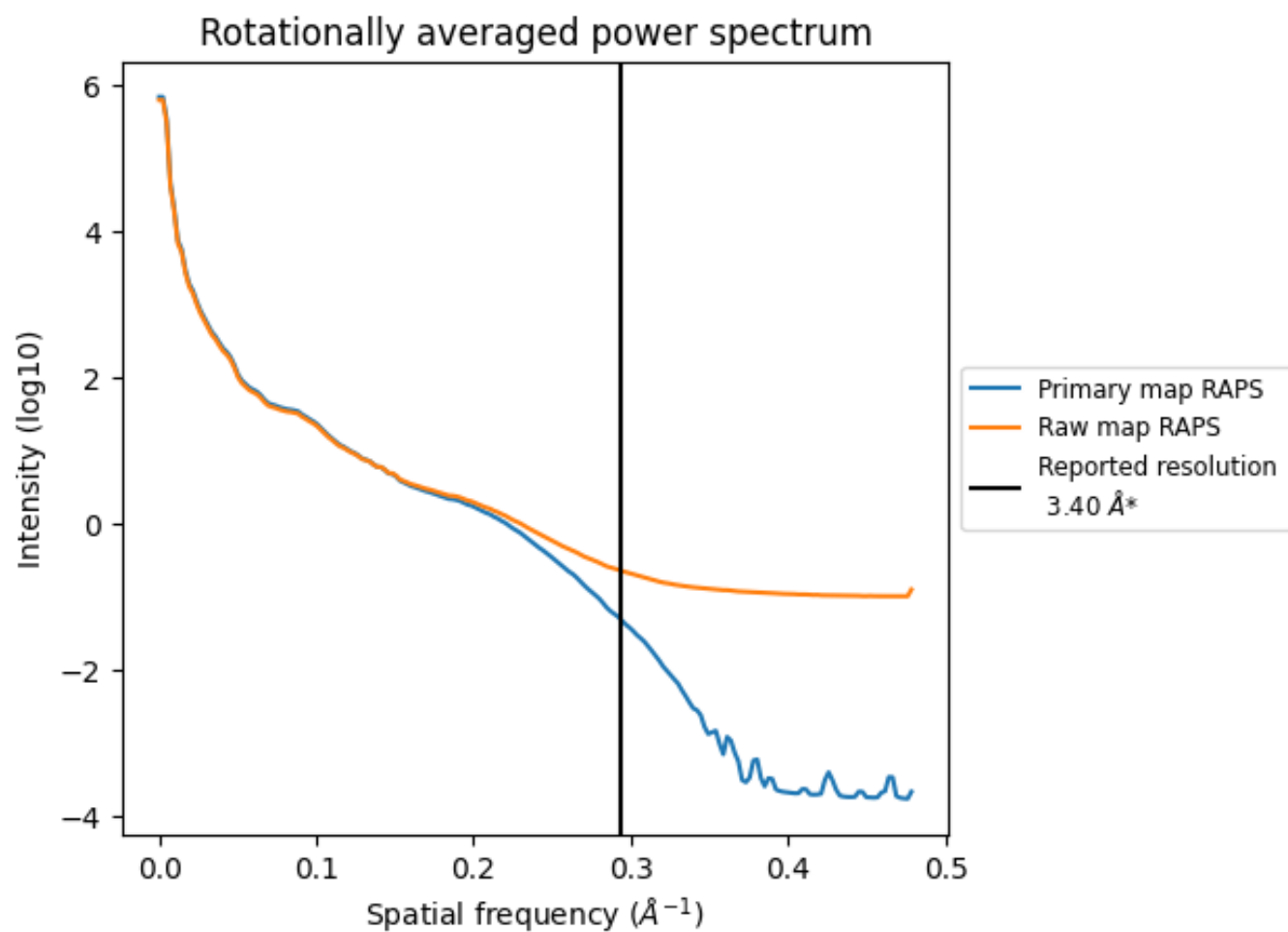
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2972 nm^3 ; this corresponds to an approximate mass of 2685 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 ⓘ

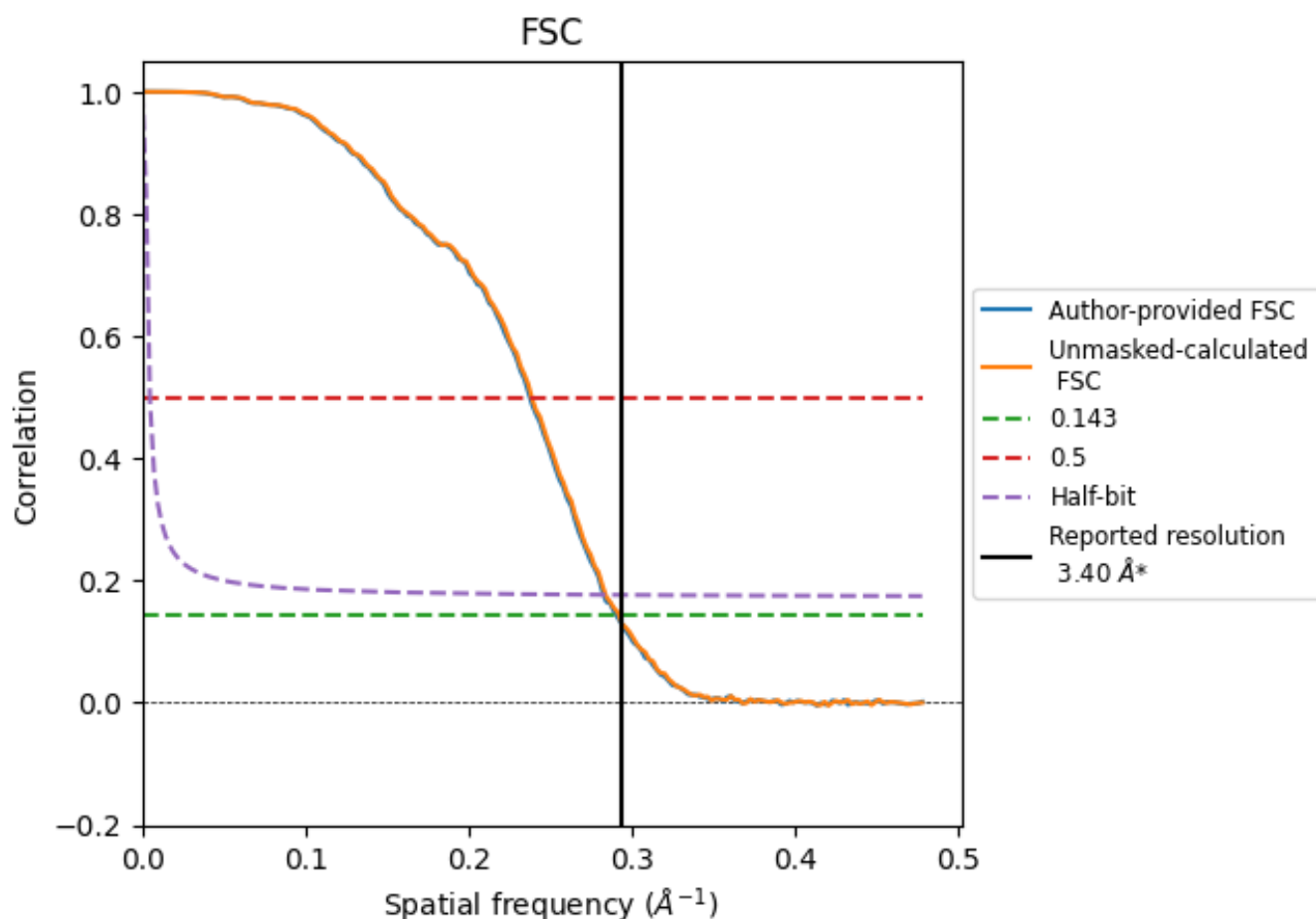


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

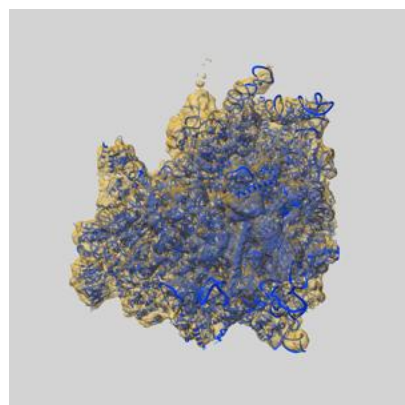
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.44	4.20	3.53
Unmasked-calculated*	3.42	4.18	3.52

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

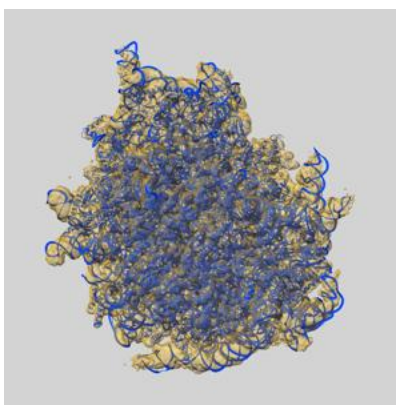
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-72475 and PDB model 9Y49. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

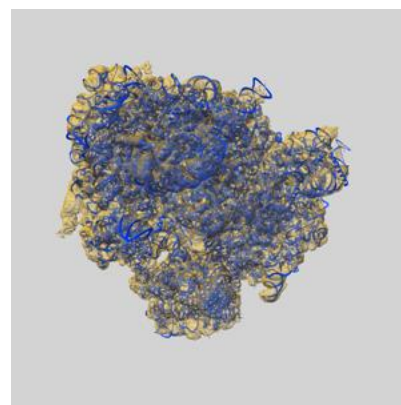
9.1 Map-model overlay [i](#)



X



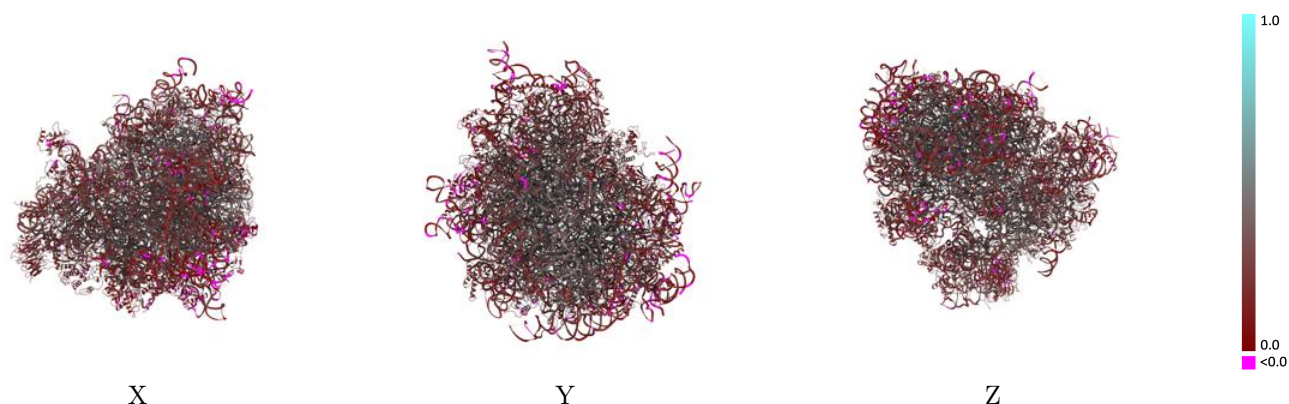
Y



Z

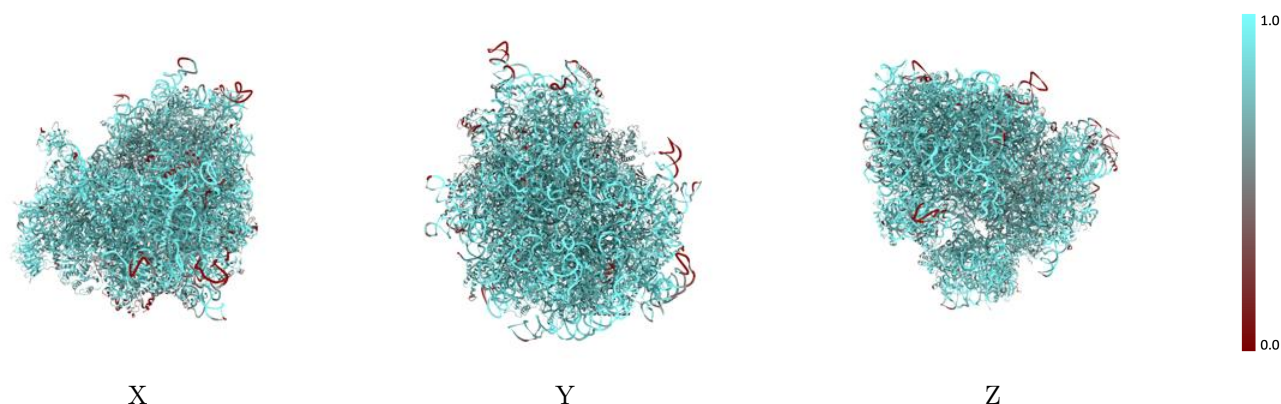
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



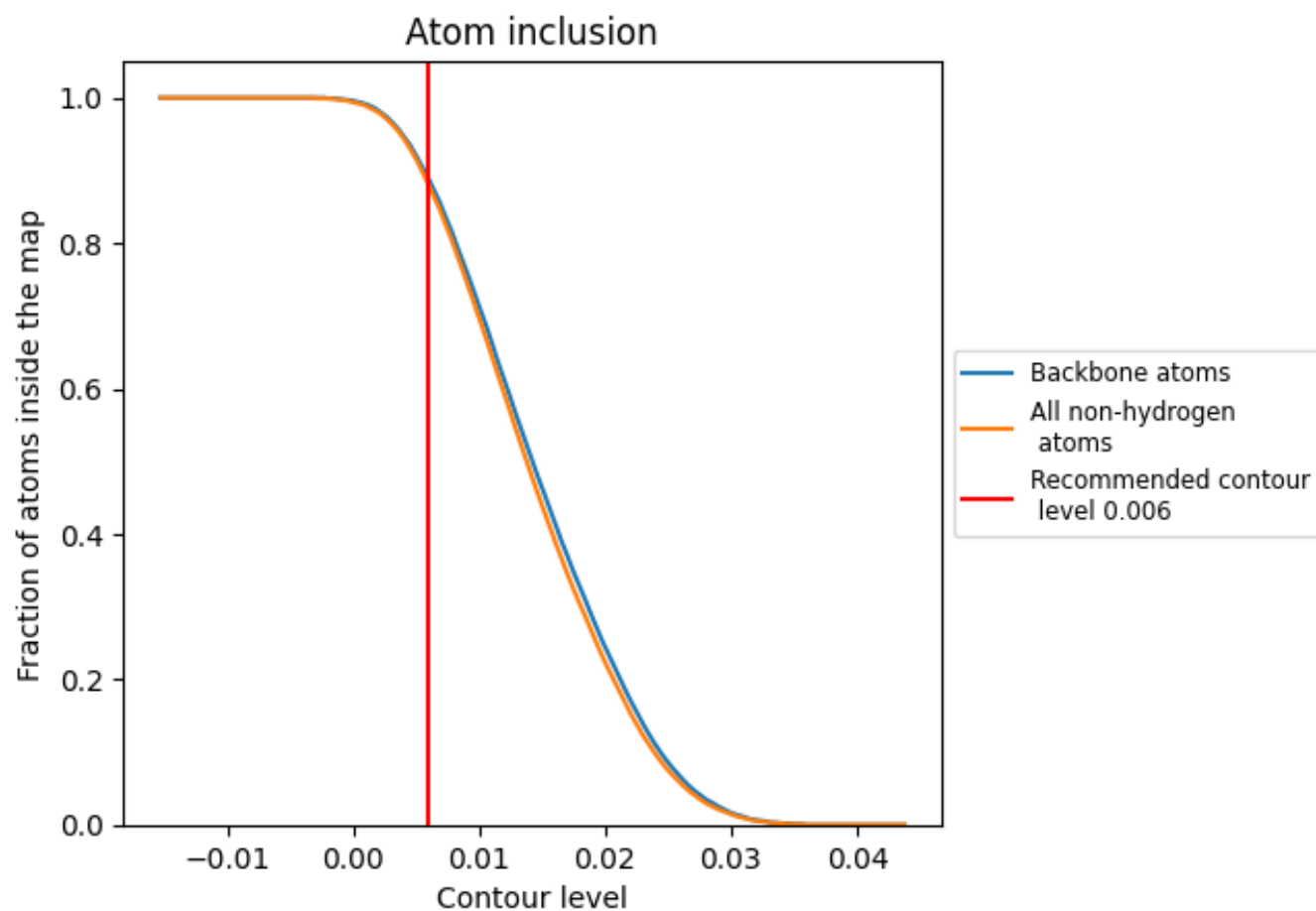
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.006).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 89% of all backbone atoms, 88% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8800	 0.2980
A5	 0.9360	 0.3060
A6	 0.9440	 0.3430
A7	 0.9510	 0.2870
A8	 0.9510	 0.3380
AA	 0.8300	 0.2880
AB	 0.8230	 0.2030
AC	 0.8150	 0.3080
AD	 0.8320	 0.2790
AE	 0.8490	 0.2770
AF	 0.8530	 0.2080
AG	 0.8770	 0.2110
AH	 0.6980	 0.2020
AI	 0.8450	 0.2510
AJ	 0.8800	 0.2660
AK	 0.8880	 0.1970
AL	 0.7550	 0.3160
AM	 0.7870	 0.1510
AN	 0.7800	 0.2780
AO	 0.8110	 0.2190
AP	 0.7650	 0.1830
AQ	 0.8670	 0.2100
AR	 0.7980	 0.2520
AS	 0.8440	 0.1880
AT	 0.8810	 0.1910
AU	 0.8750	 0.2500
AV	 0.7610	 0.2290
AW	 0.8280	 0.3250
AX	 0.8350	 0.3620
AY	 0.8480	 0.2020
AZ	 0.7860	 0.1630
Aa	 0.8270	 0.2880
Ab	 0.7420	 0.2300
Ac	 0.7280	 0.2250
Ad	 0.9090	 0.2480

















Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Ae	 0.7760	 0.2530
Af	 0.7100	 0.1480
Ag	 0.8900	 0.2150
B2	 0.9450	 0.3000
CA	 0.8280	 0.3510
CB	 0.8250	 0.2970
CC	 0.8810	 0.3870
CD	 0.9050	 0.2790
CE	 0.8340	 0.2500
CF	 0.8820	 0.3650
CG	 0.8090	 0.2910
CH	 0.8070	 0.2560
CI	 0.8110	 0.3120
CJ	 0.8690	 0.2970
CL	 0.8540	 0.3170
CM	 0.8510	 0.2260
CN	 0.8820	 0.3630
CO	 0.8050	 0.2970
CP	 0.8870	 0.3730
CQ	 0.7940	 0.2930
CR	 0.8430	 0.3470
CS	 0.8550	 0.2580
CT	 0.7900	 0.2760
CU	 0.6860	 0.1350
CV	 0.7960	 0.3590
CW	 0.6650	 0.2500
CX	 0.8210	 0.2610
CY	 0.8770	 0.2890
CZ	 0.7340	 0.1130
Ca	 0.8880	 0.3650
Cb	 0.7890	 0.2810
Cc	 0.7190	 0.1710
Cd	 0.8350	 0.3040
Ce	 0.8640	 0.3980
Cf	 0.8880	 0.3960
Cg	 0.8390	 0.2680
Ch	 0.8610	 0.2700
Ci	 0.7800	 0.2090
Cj	 0.8750	 0.3600
Ck	 0.7600	 0.2030
Cl	 0.9130	 0.3590
Cm	 0.8560	 0.3290

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Cn	 0.7990	 0.3220
Co	 0.8380	 0.3180
Cp	 0.8230	 0.3310
Cr	 0.8040	 0.3060
Ct	 0.6630	 0.2910
Cz	 0.7690	 0.1080
tR	 0.9510	 0.3030