



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 08:25 AM UTC

PDB ID : 6P5N / pdb_00006p5n
EMDB ID : EMD-20258
Title : Structure of a mammalian 80S ribosome in complex with a single translocated Israeli Acute Paralysis Virus IRES and eRF1
Authors : Acosta-Reyes, F.J.; Neupane, R.; Frank, J.; Fernandez, I.S.
Deposited on : 2019-05-30
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

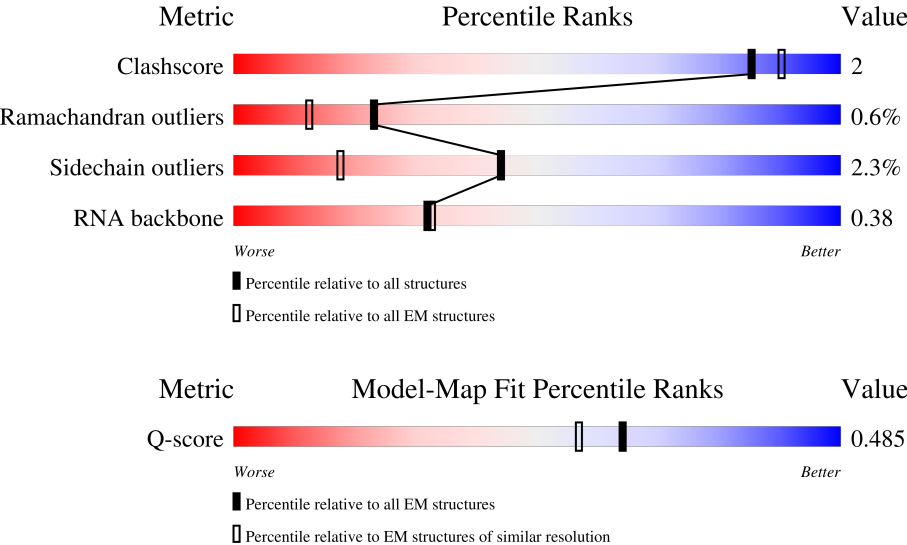
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.20 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.



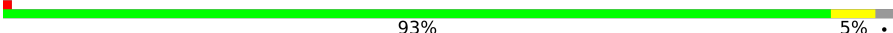
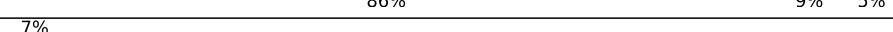
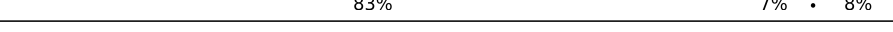
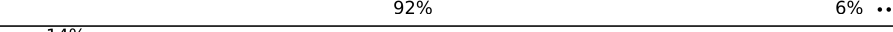
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	5	3594	7% 69% 27% .
2	7	119	82% 18% .
3	8	156	69% 26% ..

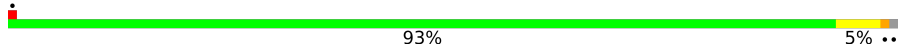
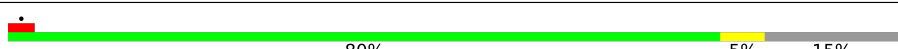
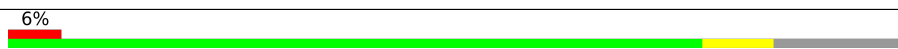
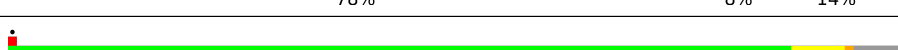
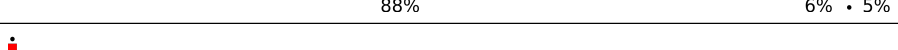
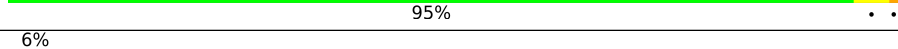
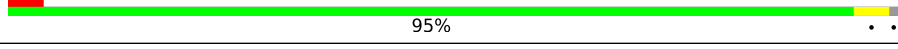
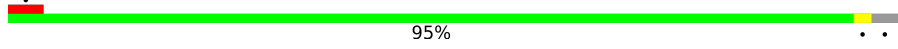
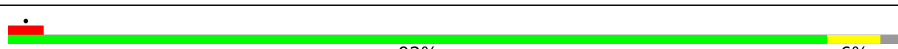
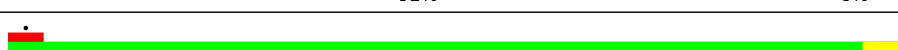
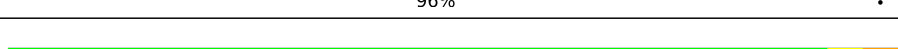
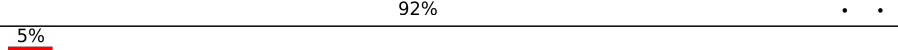
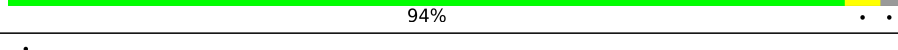
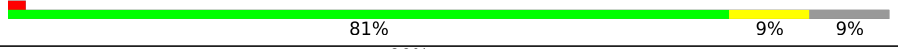
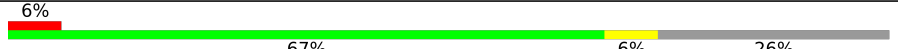
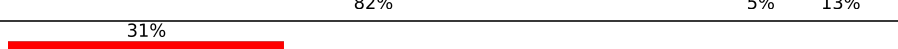
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Mol	Chain	Length	Quality of chain
4	AA	257	
5	AB	402	
6	AC	392	
7	AD	297	
8	AE	291	
9	AF	249	
10	AG	242	
11	AH	192	
12	AI	214	
13	AJ	178	
14	AL	211	
15	AM	198	
16	AN	204	
17	AO	203	
18	AP	184	
19	AQ	188	
20	AR	196	
21	AS	176	
22	AT	160	
23	AU	128	
24	AV	140	
25	AW	157	
26	AX	156	
27	AY	145	
28	AZ	136	

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Mol	Chain	Length	Quality of chain
29	Aa	148	
30	Ab	226	
31	Ac	115	
32	Ad	125	
33	Ae	135	
34	Af	110	
35	Ag	126	
36	Ah	123	
37	Ai	105	
38	Aj	97	
39	Ak	70	
40	Al	51	
41	Am	52	
42	An	25	
43	Ao	106	
44	Ap	92	
45	Ar	137	
46	AK	217	
47	2	1869	
48	B	295	
49	C	264	
50	D	255	
51	E	281	
52	F	263	
53	G	204	

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Mol	Chain	Length	Quality of chain
54	H	249	
55	I	194	
56	J	207	
57	K	194	
58	L	149	
59	M	158	
60	N	132	
61	O	151	
62	P	151	
63	Q	145	
64	R	172	
65	S	135	
66	T	152	
67	U	145	
68	V	119	
69	W	83	
70	X	130	
71	Y	143	
72	Z	134	
73	a	125	
74	b	115	
75	c	84	
76	d	69	
77	e	56	
78	f	133	

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Mol	Chain	Length	Quality of chain
79	g	156	42%36%8%56%
80	h	317	46%90%9%
81	Aq	437	76%84%10%5%
82	1	251	68%34%37%11%18%

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 219295 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3594	Total	C	N	O	P	0	0
			77074	34325	14116	25039	3594		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

- Molecule 3 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 4 is a protein called uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AA	248	Total	C	N	O	S	0	0
			1895	1186	389	314	6		

- Molecule 5 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AB	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 6 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AC	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 7 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AD	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 8 is a protein called eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AE	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 9 is a protein called L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AF	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 10 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AG	225	Total	C	N	O	S	0	0
			1819	1161	351	303	4		

- Molecule 11 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AH	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 12 is a protein called uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AI	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 13 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AJ	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 14 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AL	201	Total	C	N	O	S	0	0
			1627	1020	341	262	4		

- Molecule 15 is a protein called L14e.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AM	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 16 is a protein called eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 17 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AO	199	Total	C	N	O	S	0	0
			1631	1052	319	255	5		

- Molecule 18 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AP	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 19 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AQ	187	Total	C	N	O	S	0	0
			1526	964	306	252	4		

- Molecule 20 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AR	180	Total	C	N	O	S	0	0
			1503	931	324	238	10		

- Molecule 21 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AS	176	Total	C	N	O	S	0	0
			1457	928	283	235	11		

- Molecule 22 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 23 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AU	99	Total	C	N	O	S	0	0
			818	520	146	150	2		

- Molecule 24 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AV	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 25 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AW	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 26 is a protein called eL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AX	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 27 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 28 is a protein called eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 29 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Aa	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 30 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ab	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 31 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ac	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 32 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ad	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 33 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ae	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Af	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 35 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ag	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 36 is a protein called eL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Ah	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 37 is a protein called eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ai	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 38 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Aj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 39 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Ak	69	Total	C	N	O	S	0	0
			569	366	101	99	3		

- Molecule 40 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Al	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 41 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Am	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 42 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	An	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 43 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Ao	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 44 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ap	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 45 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Ar	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 46 is a protein called uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AK	212	Total	C	N	O	S	0	0
			1705	1091	306	300	8		

- Molecule 47 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2	1697	Total	C	N	O	P	0	0
			36229	16171	6507	11855	1696		

- Molecule 48 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	B	217	Total	C	N	O	S	0	0
			1706	1085	295	317	9		

- Molecule 49 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	C	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 50 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	D	221	Total	C	N	O	S	0	0
			1712	1107	296	299	10		

- Molecule 51 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	E	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 52 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	F	262	Total	C	N	O	S	0	0
			2073	1323	384	357	9		

- Molecule 53 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	G	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 54 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	H	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 55 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	I	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 56 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	J	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 57 is a protein called uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	K	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 58 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	L	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 59 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	M	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 60 is a protein called eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	N	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 61 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	O	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 62 is a protein called uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	P	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 63 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Q	119	Total	C	N	O	S	0	0
			990	630	186	167	7		

- Molecule 64 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	R	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 65 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	S	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 66 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	T	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 67 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	U	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

- Molecule 68 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	V	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 69 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	W	83	Total	C	N	O	S	0	0
			630	387	118	120	5		

- Molecule 70 is a protein called uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	X	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 71 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Y	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 72 is a protein called eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Z	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 73 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	a	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 74 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	b	98	Total	C	N	O	S	0	0
			778	485	158	129	6		

- Molecule 75 is a protein called eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	c	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 76 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	d	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 77 is a protein called eS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	e	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 78 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	f	56	Total	C	N	O	S	0	0
			447	276	98	72	1		

- Molecule 79 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	g	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 80 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	h	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 81 is a protein called Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Aq	416	Total	C	N	O	S	0	0
			3278	2085	559	623	11		

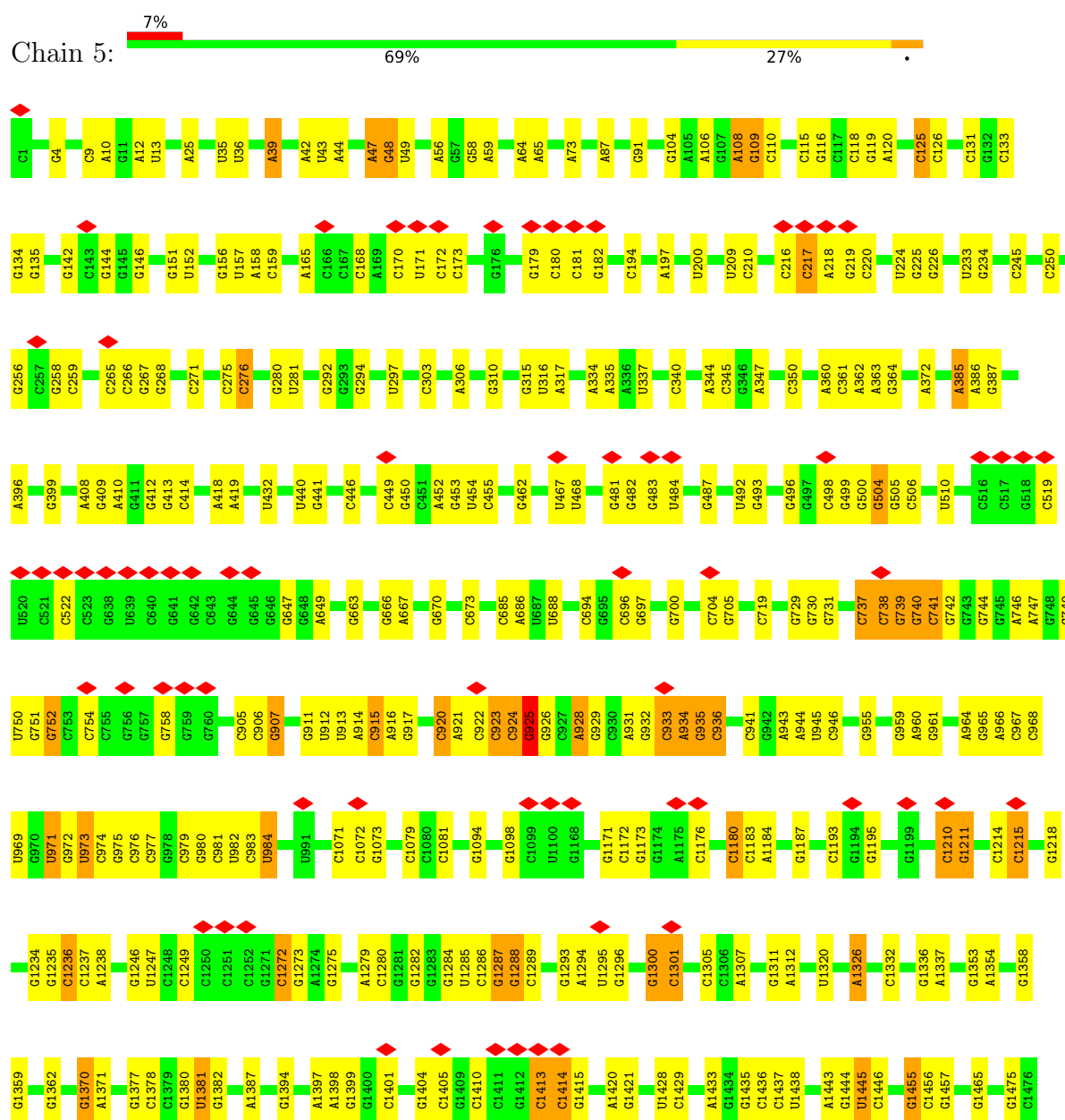
- Molecule 82 is a RNA chain called IAPV-IRES.

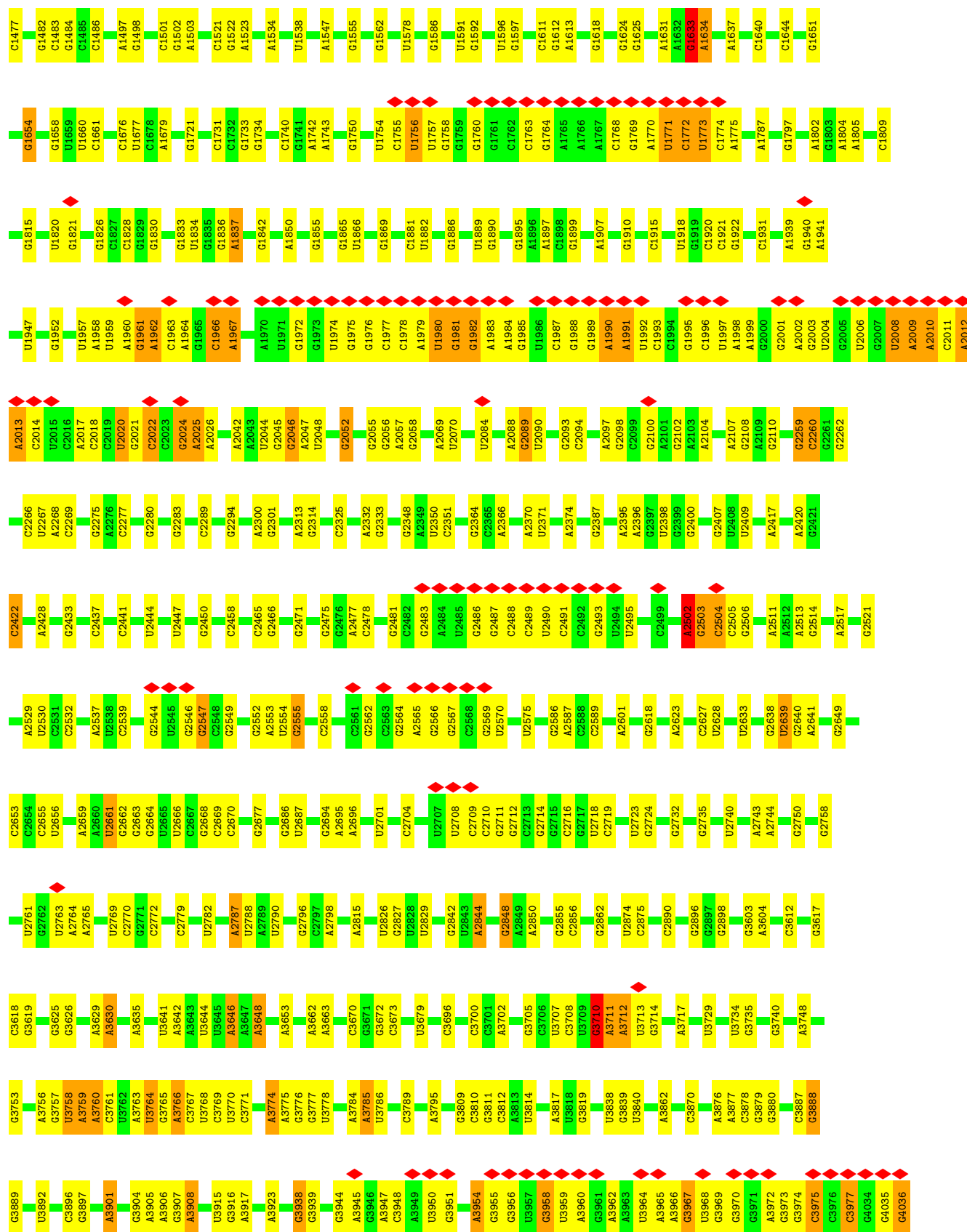
Mol	Chain	Residues	Atoms					AltConf	Trace
82	1	207	Total	C	N	O	P	0	0
			4407	1970	781	1449	207		

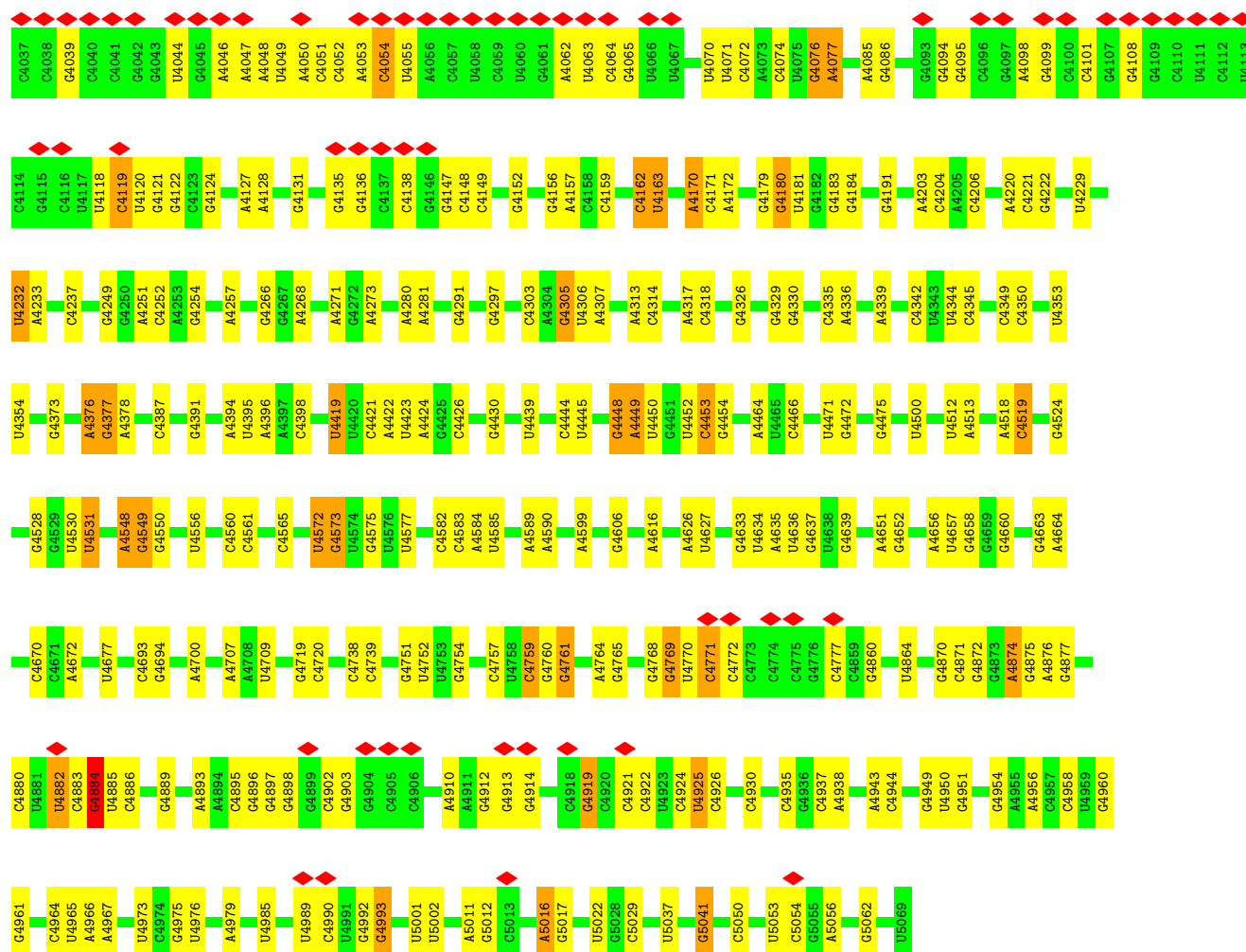
3 Residue-property plots

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

• Molecule 1: 28S rRNA





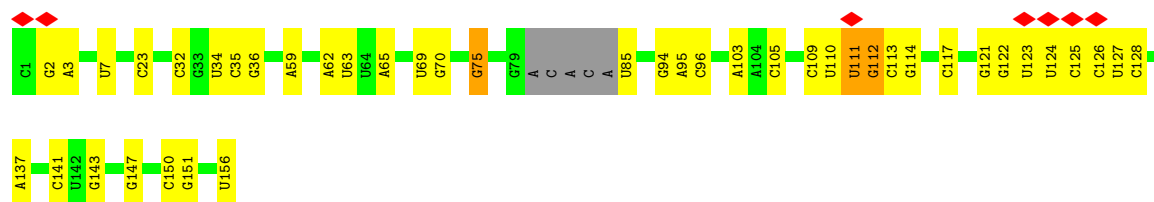


Chain 7: 82% 18%



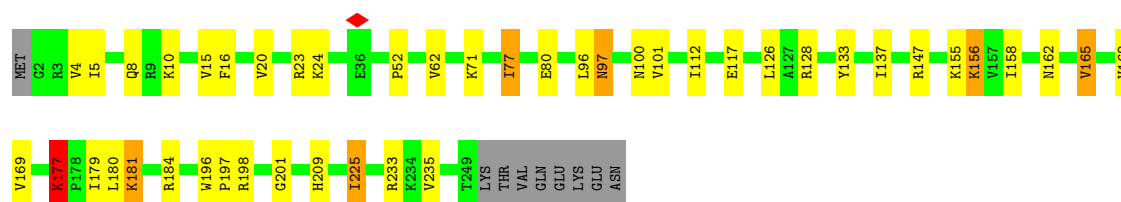
• Molecule 3: 5.8S rRNA

Chain 8: 69% 26%

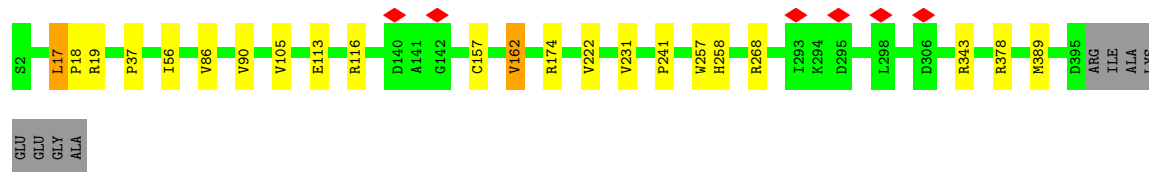


• Molecule 4: uL2

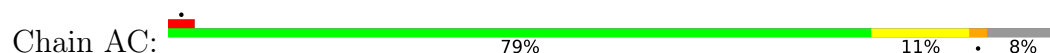
Chain AA: 79% 15%



• Molecule 5: uL3



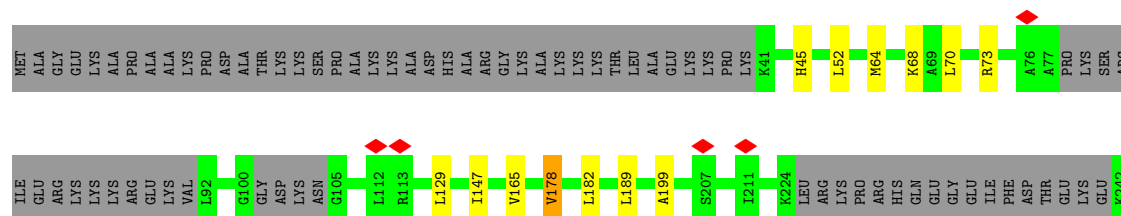
• Molecule 6: uL4



• Molecule 7: uL18



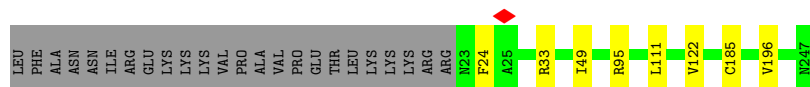
• Molecule 8: eL6





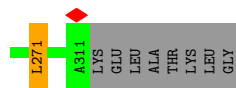
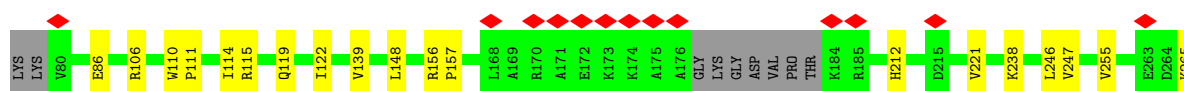
- Molecule 9: L30

Chain AF: 87% 10%



- Molecule 10: eL8

Chain AG: 6% 85% 8% 7%



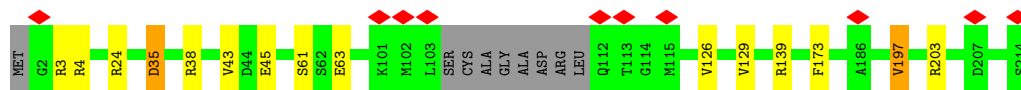
- Molecule 11: uL6

Chain AH: 92% 7%



- Molecule 12: uL16

Chain AI: 5% 89% 6% 6%



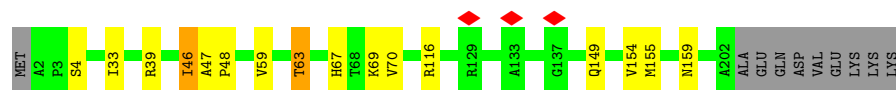
- Molecule 13: uL11

Chain AJ: 7% 89% 5% 5%

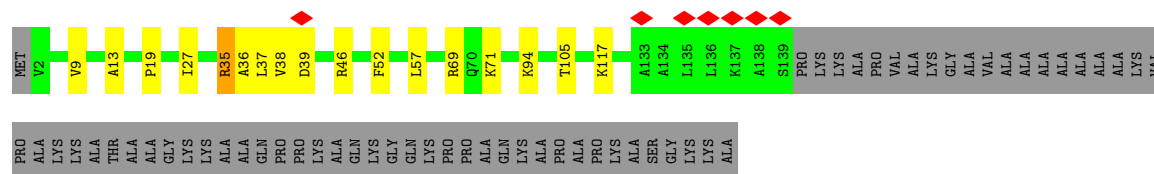


- Molecule 14: eL13

Chain AL: 88% 7% 5%



• Molecule 15: L14e



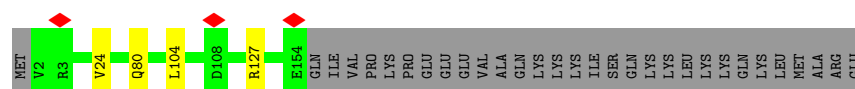
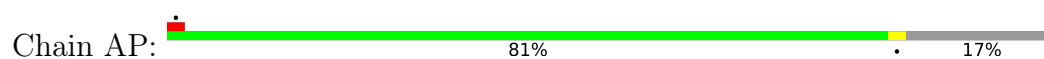
• Molecule 16: eL15



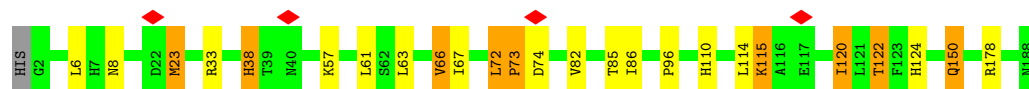
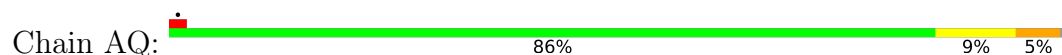
• Molecule 17: uL13



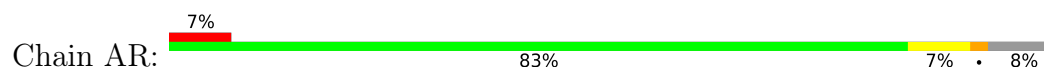
• Molecule 18: uL22



• Molecule 19: eL18

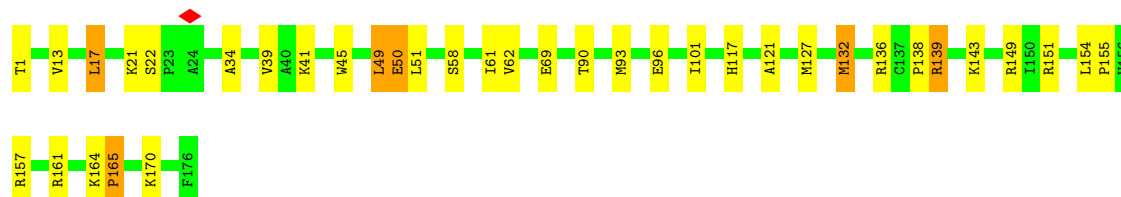


• Molecule 20: eL19

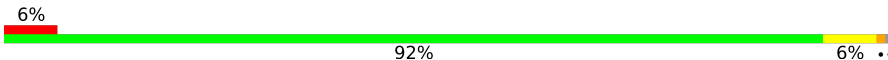


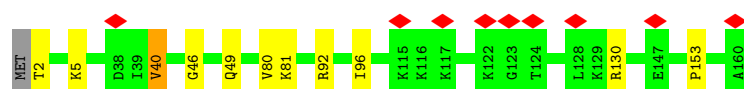
- Molecule 21: eL20

Chain AS:  79% 18%



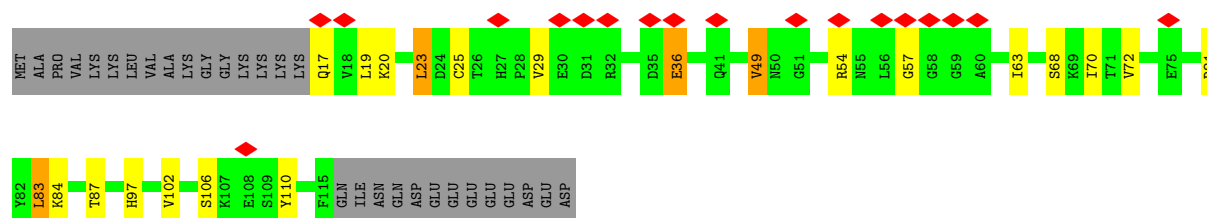
- Molecule 22: eL21

Chain AT:  92% 6% 6%



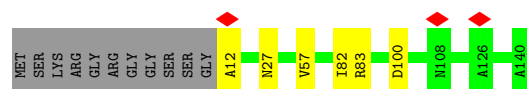
- Molecule 23: eL22

Chain AU:  14% 60% 14% 23%



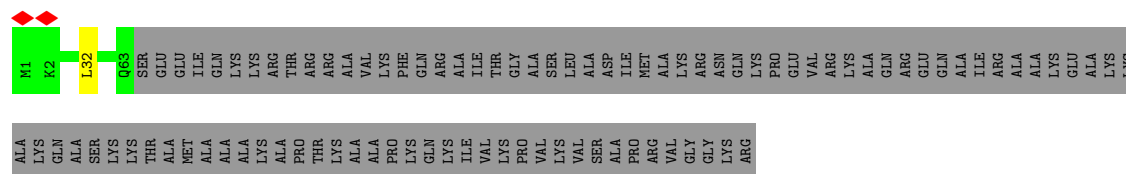
- Molecule 24: uL14

Chain AV:  88% 8%



- Molecule 25: eL24

Chain AW:  39% 60%

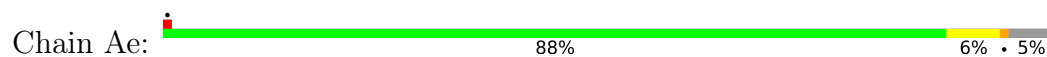


- Molecule 26: eL23

Chain AX:  72% 24%



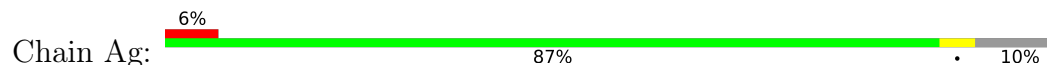
• Molecule 33: eL32



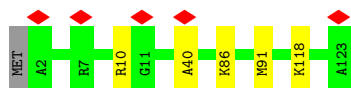
• Molecule 34: eL33



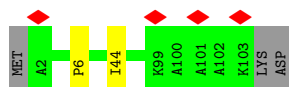
• Molecule 35: eL34



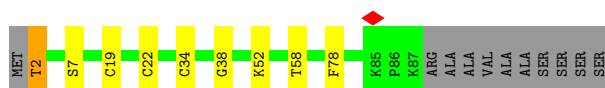
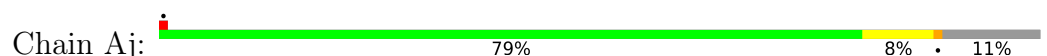
• Molecule 36: eL35



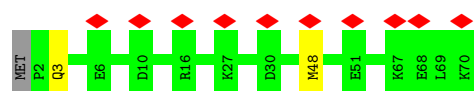
• Molecule 37: eL36



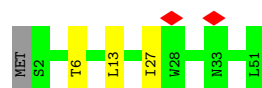
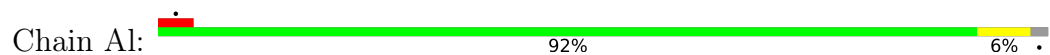
• Molecule 38: eL37



• Molecule 39: eL38



- Molecule 40: eL39



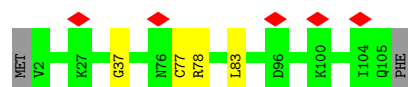
- Molecule 41: eL40



- Molecule 42: eL41



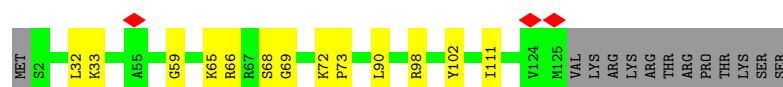
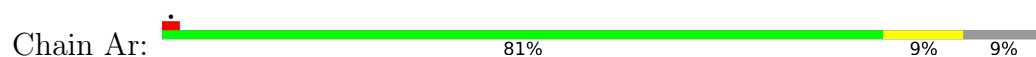
- Molecule 43: eL42



- Molecule 44: eL43

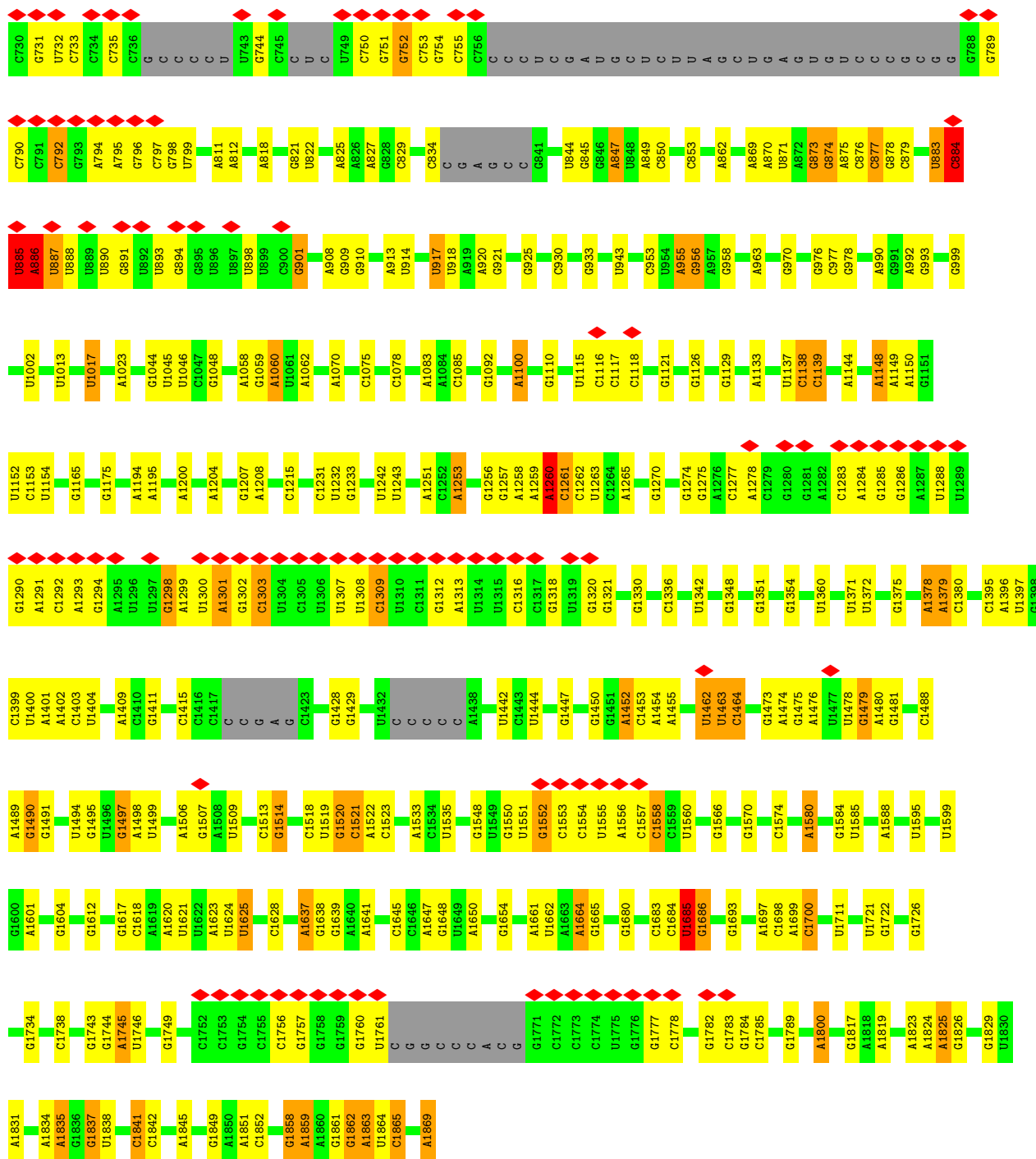


- Molecule 45: eL28

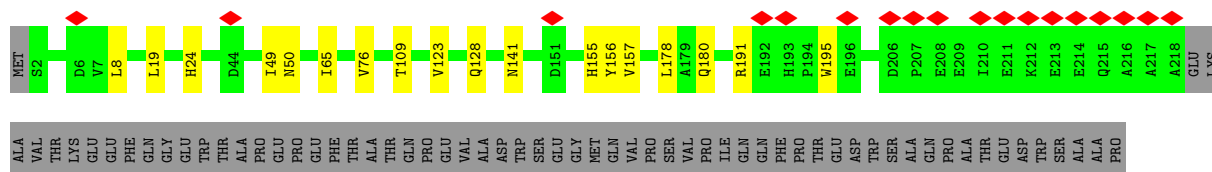


Chain AK: 90% 76% 17%





• Molecule 48: uS2



THR
ALA
GLN
ALA
THR
GLU
TRP
MET
GLY
THR
THR
THR
GLU
TRP
SER

• Molecule 49: eS1

Chain C: 7% 78% 19%

MET
VAL
GLY
LYS
ASN
LYS
ARG
LEU
THR
LYS
GLY
LYS
LYS
ALA
LYS
LYS
LYS
V21
V22
D23
P24
F25
K28
A37
R42
L43
T55
K56
E68
N76
D77
T98
V114
D126
D131
D180
L181
K182
E183
I189
F190
D191
K195

G233
GLU
SER
SER
SER
GLY
LYS
ALA
THR
GLY
ASP
THR
GLY
ALA
LYS
VAL
GLU
ARG
ALA
ASP
GLY
TYR
PRO
PRO
VAL
GLN
SER
VAL

• Molecule 50: uS5

Chain D: 82% 5% 13%

MET
ALA
ASP
GLN
THR
GLY
ALA
ALA
ALA
GLY
PRO
GLY
GLY
PRO
GLY
GLY
ASN
K58
E59
I75
D95
L141
N172
V191
I196
P199
R200
I204
L215
D220
Y223
L233
F236
V260
N271
M274
K275
T276
H277
T278
VAL

SER
VAL
GLN
THR
GLN
ALA
PRO
VAL
ALA
THR
THR

• Molecule 51: uS3

Chain E: 31% 78% 19%

MET
SER
ALA
ARG
ARG
ARG
ARG
ARG
ALA
ALA
PHE
ARG
ARG
ALA
ALA
PRO
PHE
ILE
PRO
ILE
SER
VAL
ARG
GLU
PRO
LEU
PRO
PHE
LEU
SER
ALA
ALA
ARG
GLY
LYS
M1
A2
V3
R9
G15
N22
E23
F24
L25
E28
L29
A30
E31
D32
E38
V39
R40

V41
T42
P43
T44
R45
T46
E47
I48
I49
I50
L51
A52
T53
T55
R54
Q56
N57
V58
L59
G60
E61
K62
G63
R64
R65
I66
R67
E68
L69
V73
Q74
K75
R76
F79
P80
E81
G82
S83
V84
E85
L86
Y87
A88
E89
K90
V91
A92
L96
L110
G111
G112
R117
V122
L123

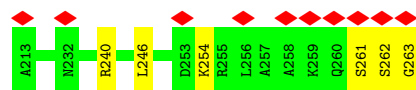
R124
E128
L142
R143
G144
Q145
R146
A147
M150
D162
P163
L176
L177
R178
Q179
P191
P194
S195
G196
K197
K202
D206
V211
K214
D215
E216
I217
L218
P219
T220
T221
P222
I223
S224
E225
Q226
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PRO
ALA
MET
PRO
GLN
PRO

VAL
PRO
THR
ALA

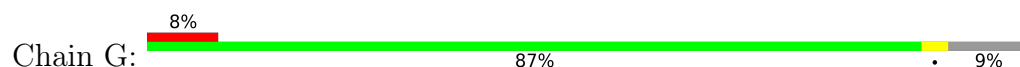
• Molecule 52: eS4

Chain F: 10% 90% 10%

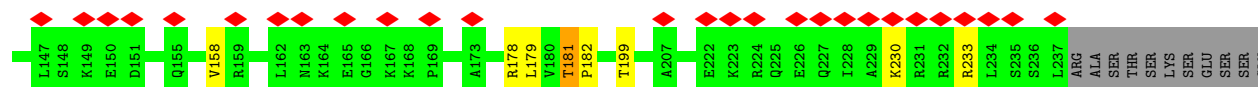
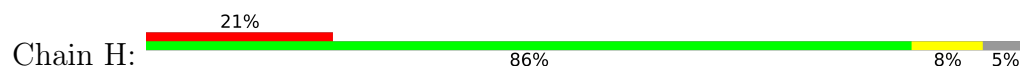
MET
A2
V12
P15
K16
H17
W18
M19
L20
D21
K22
L23
E40
I46
F47
L48
K51
L52
K53
Y54
A55
L56
I64
D79
I80
T81
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K134
M156
E165
T166
G167
K168
D176
C181
I195



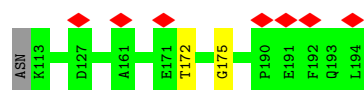
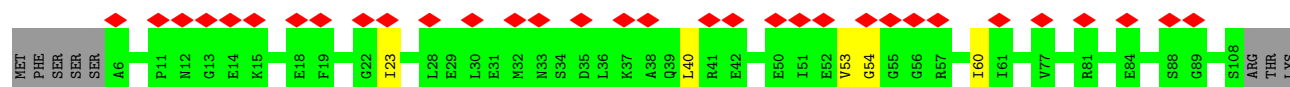
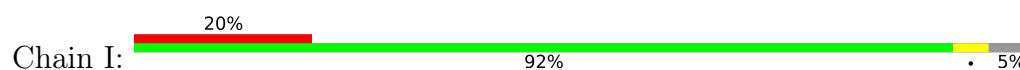
- Molecule 53: uS7



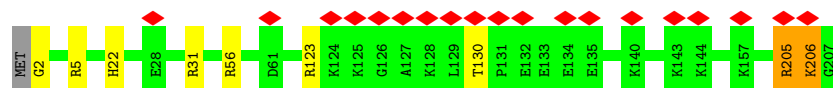
- Molecule 54: eS6



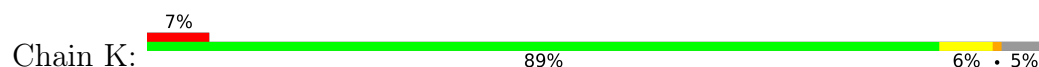
- Molecule 55: eS7



- Molecule 56: eS8

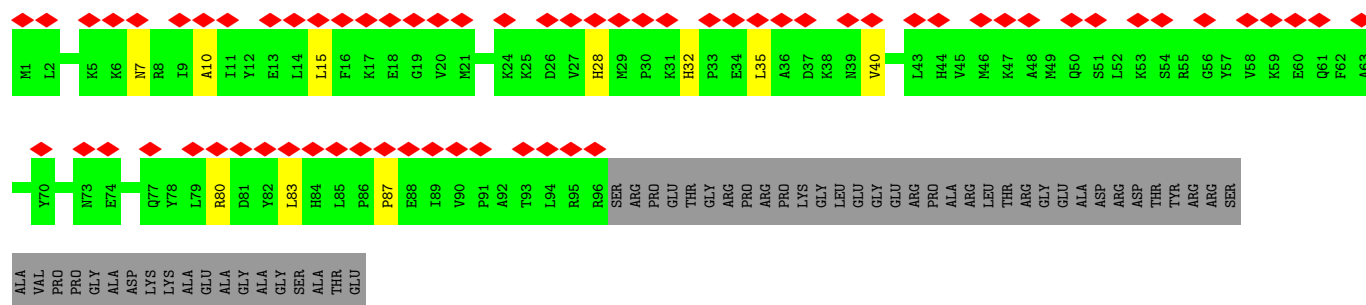
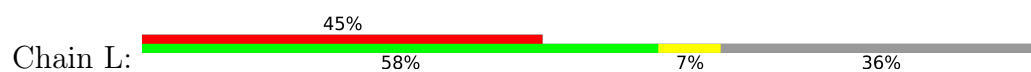


- Molecule 57: uS4

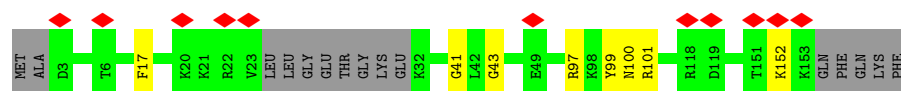
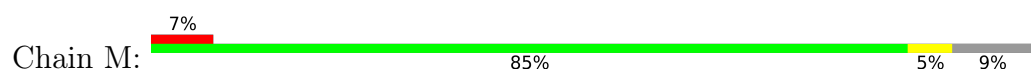




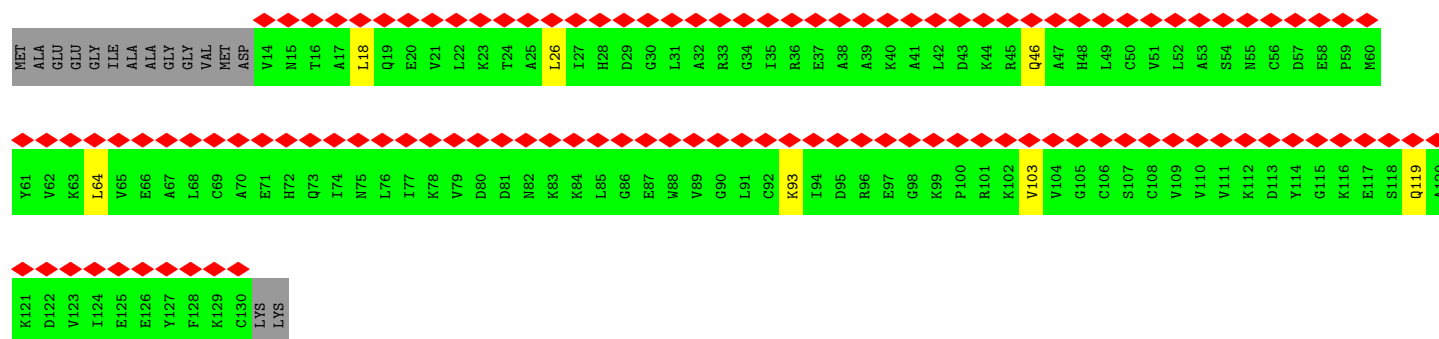
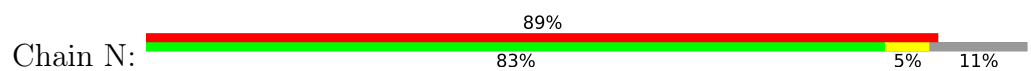
• Molecule 58: eS10



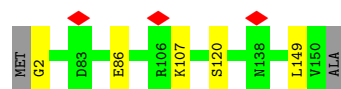
• Molecule 59: uS17



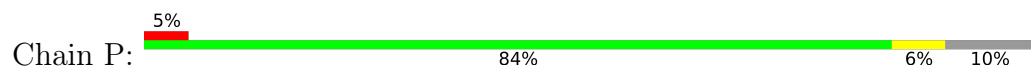
• Molecule 60: eS12

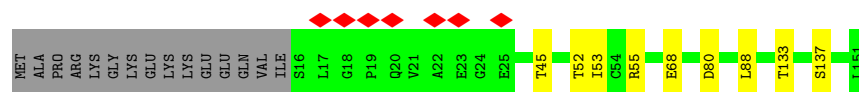


• Molecule 61: uS15

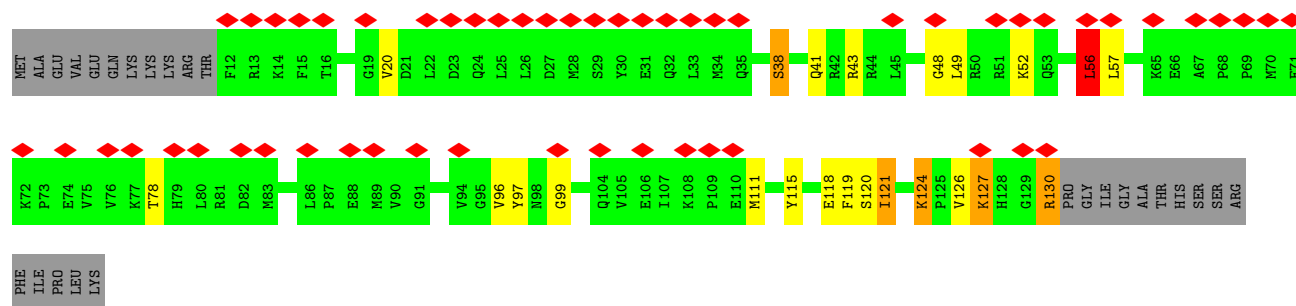
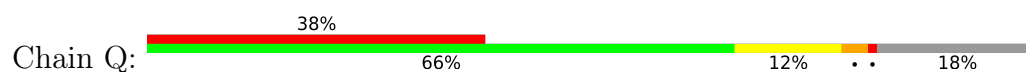


• Molecule 62: uS11

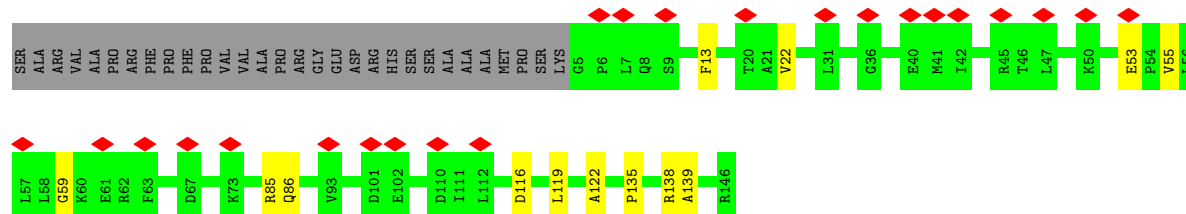
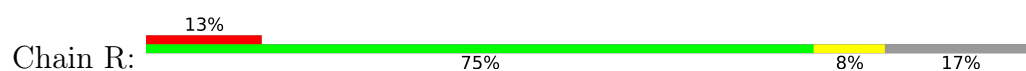




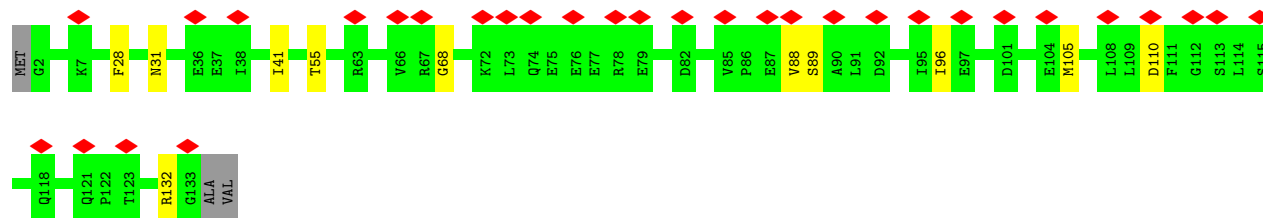
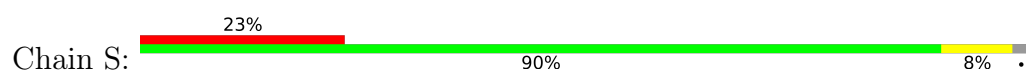
• Molecule 63: uS19



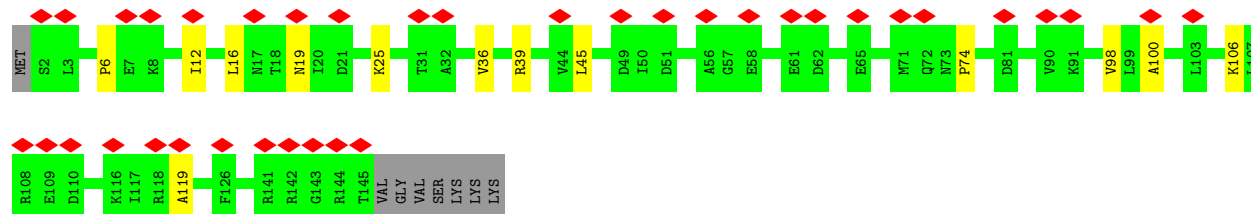
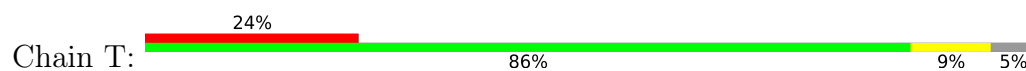
• Molecule 64: uS9



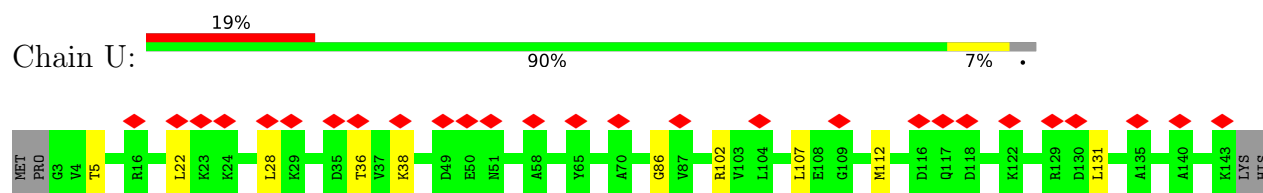
• Molecule 65: eS17



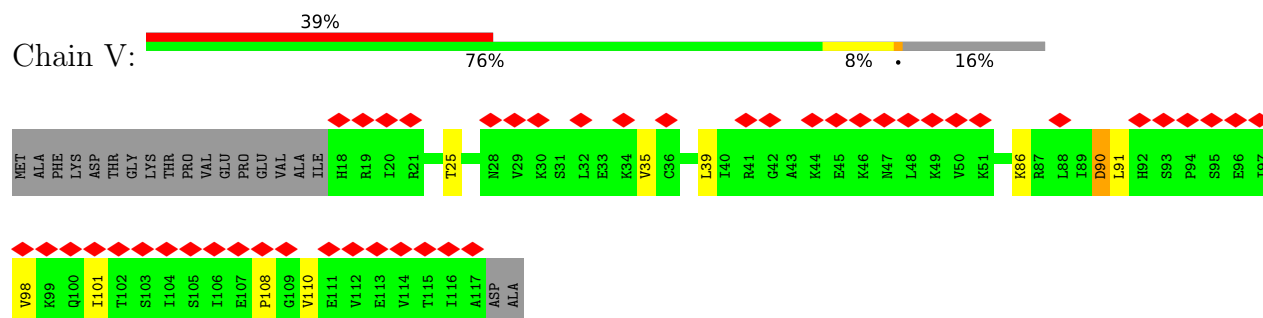
• Molecule 66: uS13



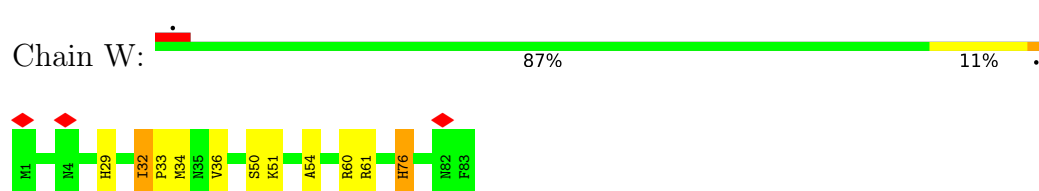
- Molecule 67: eS19



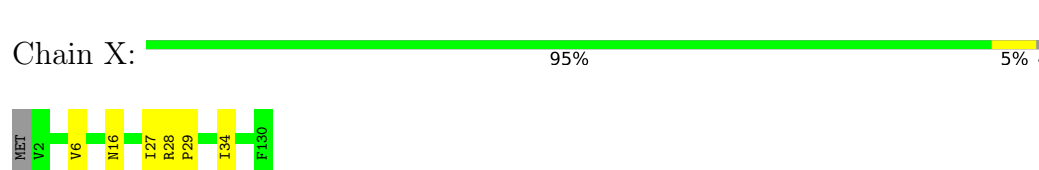
- Molecule 68: uS10



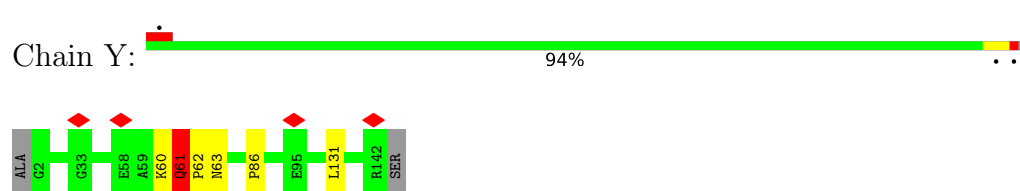
- Molecule 69: eS21



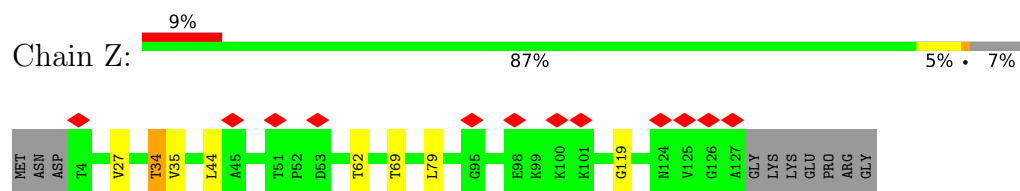
- Molecule 70: uS8



- Molecule 71: uS12

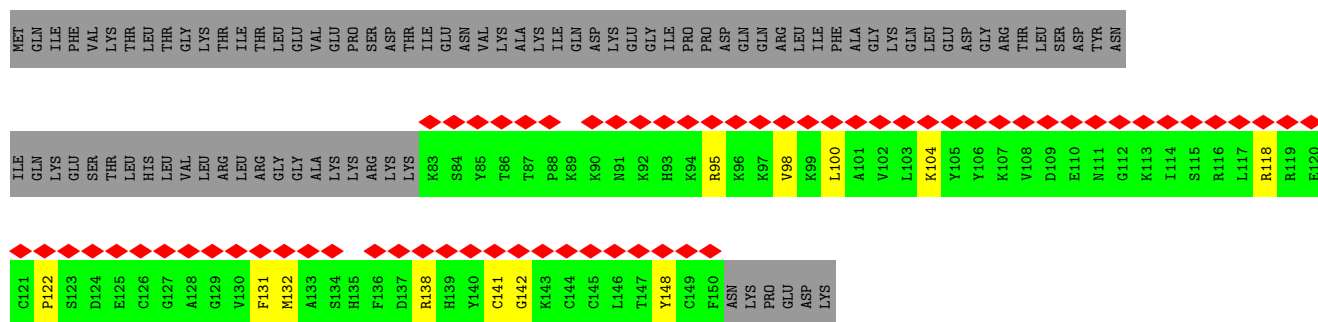


- Molecule 72: eS24



- Molecule 73: eS25

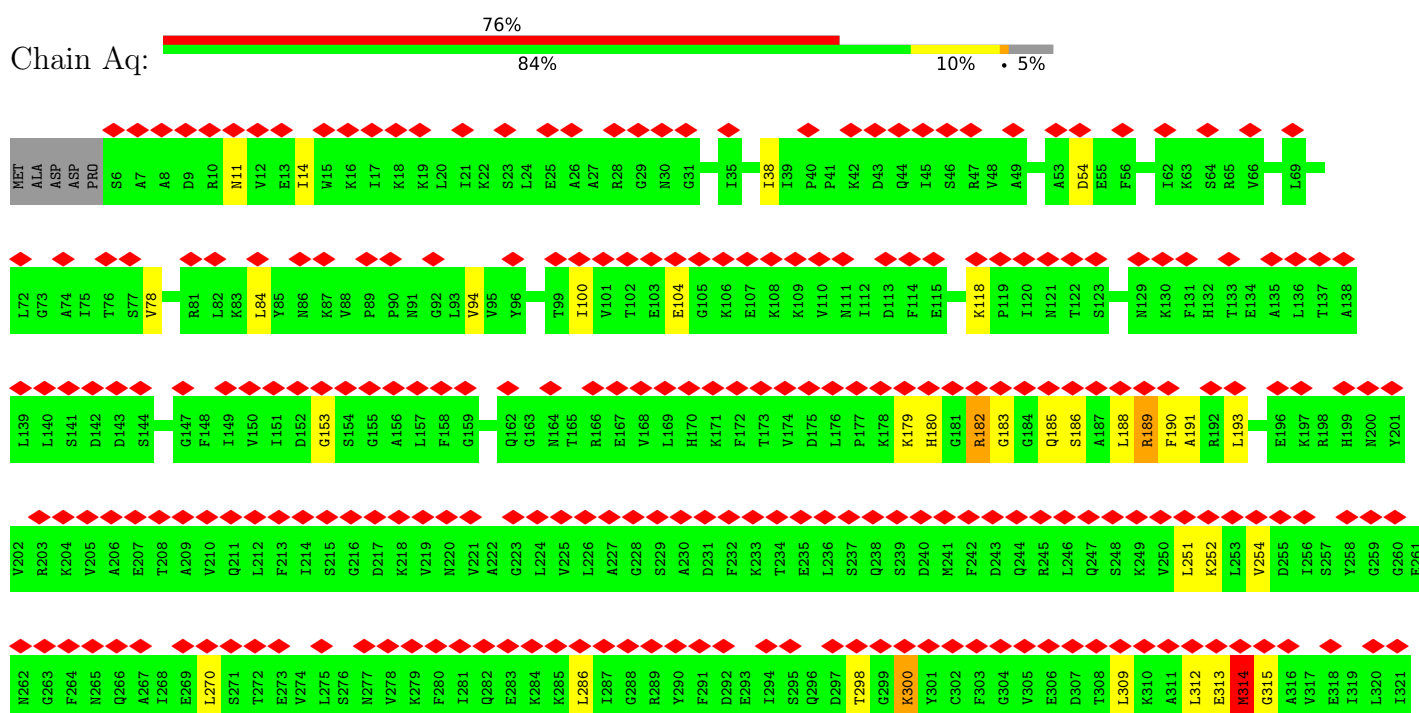


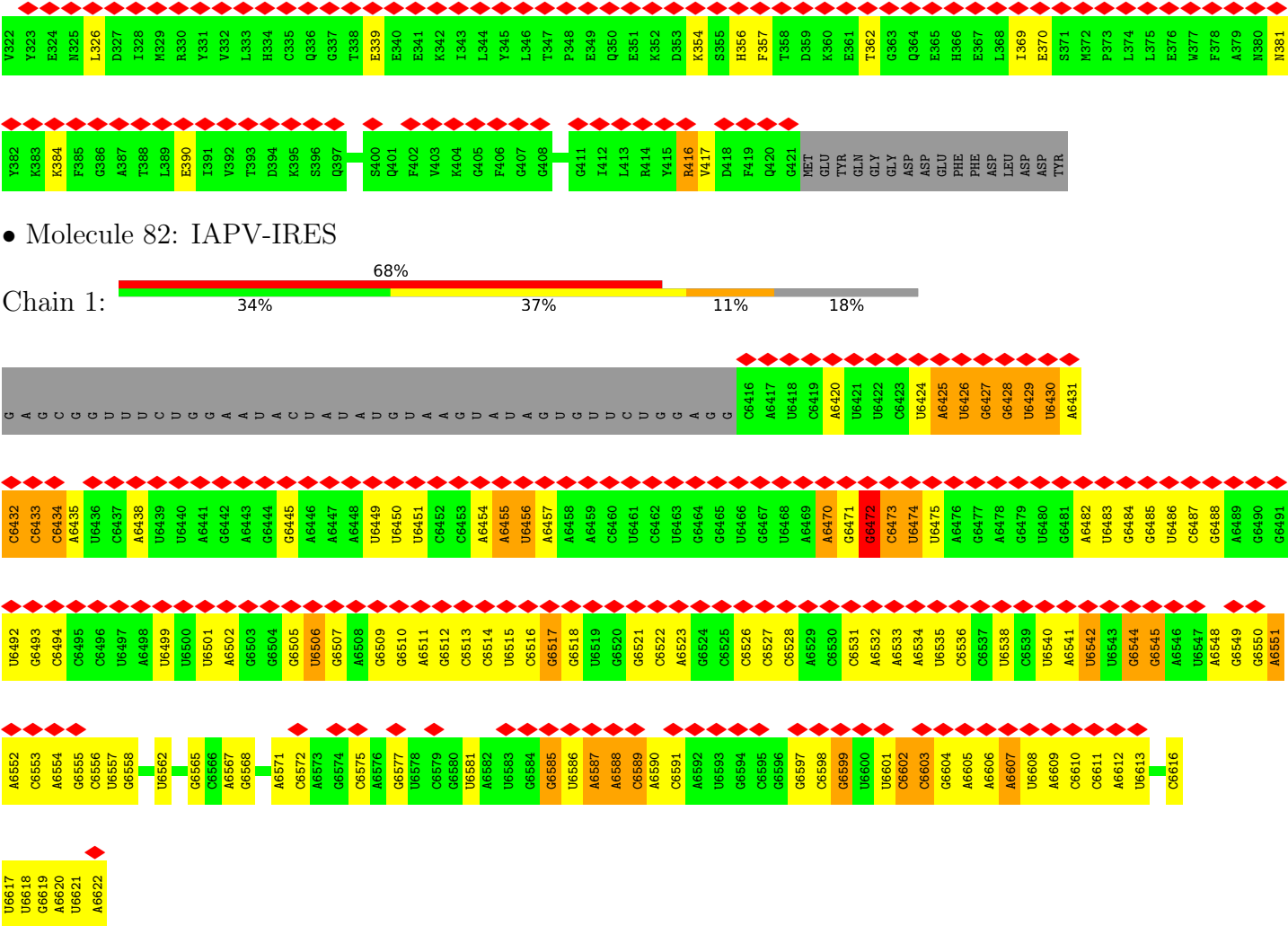


• Molecule 80: RACK1



• Molecule 81: Eukaryotic peptide chain release factor subunit 1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	27658	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	56.90	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4900	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.192	Depositor
Minimum map value	-0.108	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	441.168, 441.168, 441.168	wwPDB
Map dimensions	416, 416, 416	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0605, 1.0605, 1.0605	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	5	0.38	0/86214	0.71	43/134455 (0.0%)
2	7	0.37	0/2836	0.66	0/4421
3	8	0.38	0/3581	0.70	0/5577
4	AA	1.07	0/1933	1.41	4/2592 (0.2%)
5	AB	1.03	0/3240	1.39	0/4339
6	AC	1.01	0/2937	1.40	1/3946 (0.0%)
7	AD	1.03	0/2437	1.51	0/3264
8	AE	1.06	0/1762	1.40	0/2362
9	AF	1.02	0/1911	1.53	0/2549
10	AG	1.05	0/1850	1.47	2/2491 (0.1%)
11	AH	1.08	0/1535	1.40	0/2063
12	AI	1.03	0/1702	1.43	0/2272
13	AJ	1.05	0/1385	1.44	1/1852 (0.1%)
14	AL	1.05	0/1658	1.51	2/2219 (0.1%)
15	AM	1.03	0/1158	1.48	0/1547
16	AN	1.00	0/1746	1.42	2/2338 (0.1%)
17	AO	1.05	1/1663 (0.1%)	1.52	1/2223 (0.0%)
18	AP	1.02	0/1268	1.39	0/1700
19	AQ	1.01	0/1557	1.40	1/2086 (0.0%)
20	AR	1.02	0/1519	1.55	0/2006
21	AS	1.02	0/1498	1.36	3/2012 (0.1%)
22	AT	1.02	0/1326	1.35	0/1770
23	AU	1.02	0/832	1.34	0/1116
24	AV	1.11	0/983	1.40	0/1319
25	AW	0.97	0/541	1.42	0/720
26	AX	1.03	0/984	1.42	0/1323
27	AY	1.04	0/1132	1.44	0/1504
28	AZ	1.03	0/1130	1.42	0/1507
29	Aa	1.01	0/1191	1.42	0/1590
30	Ab	1.03	0/861	1.54	1/1138 (0.1%)
31	Ac	1.06	0/771	1.49	0/1034
32	Ad	1.04	0/903	1.38	0/1216
33	Ae	1.02	0/1071	1.40	0/1429
34	Af	1.05	0/895	1.31	0/1198

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Ag	1.05	0/916	1.45	0/1220
36	Ah	1.02	0/1021	1.52	0/1348
37	Ai	1.04	0/841	1.56	0/1112
38	Aj	0.98	0/720	1.40	0/952
39	Ak	1.02	0/575	1.37	0/759
40	Al	0.97	0/459	1.37	0/608
41	Am	1.05	0/435	1.40	0/575
42	An	0.91	0/240	1.50	0/305
43	Ao	1.02	0/864	1.38	0/1140
44	Ap	1.05	0/718	1.51	0/953
45	Ar	1.05	0/1010	1.45	3/1354 (0.2%)
46	AK	1.10	0/1733	1.39	1/2324 (0.0%)
47	2	0.38	0/40509	0.73	26/63128 (0.0%)
48	B	1.04	0/1744	1.45	0/2371
49	C	1.05	0/1756	1.39	0/2350
50	D	1.06	0/1748	1.42	0/2362
51	E	1.07	0/1796	1.44	0/2417
52	F	1.05	0/2115	1.39	0/2843
53	G	1.06	0/1492	1.53	0/2005
54	H	1.07	0/1946	1.45	0/2590
55	I	1.06	0/1510	1.43	0/2022
56	J	1.05	0/1715	1.39	0/2287
57	K	1.03	0/1550	1.49	0/2069
58	L	1.05	0/834	1.39	0/1125
59	M	1.03	0/1195	1.30	1/1597 (0.1%)
60	N	1.10	0/918	1.43	0/1233
61	O	1.03	0/1226	1.50	0/1649
62	P	1.07	0/1029	1.47	2/1380 (0.1%)
63	Q	1.05	0/1009	1.35	4/1346 (0.3%)
64	R	1.05	0/1146	1.45	0/1534
65	S	1.06	1/1082 (0.1%)	1.50	0/1452
66	T	1.05	0/1208	1.47	0/1618
67	U	1.06	0/1115	1.50	0/1493
68	V	1.07	0/805	1.43	2/1081 (0.2%)
69	W	1.07	0/638	1.43	0/855
70	X	1.04	0/1051	1.44	0/1406
71	Y	1.08	0/1116	1.39	0/1490
72	Z	1.05	0/1028	1.36	0/1366
73	a	1.10	0/604	1.44	0/810
74	b	1.06	0/791	1.42	0/1062
75	c	1.07	0/665	1.35	0/891
76	d	1.07	0/490	1.29	0/656
77	e	1.02	0/470	1.37	0/623

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	f	1.09	0/451	1.46	1/592 (0.2%)
79	g	1.07	0/567	1.44	0/753
80	h	1.08	0/2493	1.35	0/3394
81	Aq	1.08	0/3331	1.44	3/4479 (0.1%)
82	l	0.39	0/4927	0.78	7/7675 (0.1%)
All	All	0.73	2/235612 (0.0%)	1.04	111/345832 (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
5	AB	0	3
14	AL	0	1
30	Ab	0	1
34	Af	0	1
36	Ah	0	1
46	AK	0	4
49	C	0	1
53	G	0	1
60	N	0	1
63	Q	0	1
65	S	0	1
66	T	0	1
70	X	0	1
71	Y	0	1
79	g	0	1
All	All	0	20

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	AO	108	ILE	N-CA	5.33	1.50	1.45
65	S	41	ILE	N-CA	5.28	1.50	1.45

All (111) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	2	884	C	C4'-C3'-O3'	-10.06	97.91	113.00
47	2	1858	G	C2'-C3'-O3'	9.88	128.52	113.70
47	2	1664	A	C4'-C3'-O3'	9.48	123.62	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	48	G	C2'-C3'-O3'	9.04	123.07	109.50
82	1	6506	U	C2'-C3'-O3'	9.04	123.05	109.50
17	AO	110	PRO	N-CA-C	8.96	121.63	110.70
1	5	2046	G	C2'-C3'-O3'	8.96	122.94	109.50
47	2	73	C	C4'-C3'-O3'	7.97	121.36	109.40
47	2	1497	G	C4'-C3'-O3'	7.92	121.28	109.40
1	5	47	A	C4'-C3'-O3'	7.89	121.24	109.40
1	5	4170	A	C2'-C3'-O3'	7.80	121.20	109.50
1	5	385	A	C4'-C3'-O3'	7.47	120.60	109.40
30	Ab	101	HIS	CB-CA-C	7.30	118.29	109.31
1	5	4119	C	C4'-C3'-O3'	7.28	120.32	109.40
1	5	2661	U	C2'-C3'-O3'	7.26	120.39	109.50
46	AK	151	VAL	N-CA-C	-7.00	106.09	111.62
4	AA	177	LYS	CA-C-N	6.91	126.67	119.76
4	AA	177	LYS	C-N-CA	6.91	126.67	119.76
82	1	6472	G	C4'-C3'-O3'	-6.84	99.14	109.40
82	1	6607	A	C2'-C3'-O3'	6.76	119.65	109.50
1	5	3888	G	C4'-C3'-O3'	6.75	123.12	113.00
1	5	2089	G	C2'-C3'-O3'	6.55	119.32	109.50
47	2	465	A	C4'-C3'-O3'	6.53	119.20	109.40
47	2	886	A	C4'-C3'-O3'	6.45	119.08	109.40
1	5	928	A	C2'-C3'-O3'	6.38	123.27	113.70
63	Q	124	LYS	CA-C-N	6.37	126.39	119.90
63	Q	124	LYS	C-N-CA	6.37	126.39	119.90
1	5	3938	G	C2'-C3'-O3'	6.35	119.03	109.50
1	5	3758	U	C4'-C3'-O3'	6.31	118.87	109.40
1	5	2694	G	C2'-C3'-O3'	-6.30	100.04	109.50
1	5	4925	U	C4'-C3'-O3'	6.27	118.81	109.40
47	2	885	U	C2'-C3'-O3'	6.21	123.02	113.70
1	5	4180	G	C2'-C3'-O3'	6.18	122.97	113.70
47	2	874	G	C2'-C3'-O3'	6.17	122.96	113.70
47	2	24	C	C2'-C3'-O3'	6.17	122.96	113.70
21	AS	139	ARG	CA-C-N	6.05	125.67	119.56
21	AS	139	ARG	C-N-CA	6.05	125.67	119.56
1	5	217	C	C4'-C3'-O3'	6.05	118.47	109.40
1	5	3758	U	C3'-C2'-O2'	-6.03	105.56	114.60
21	AS	138	PRO	N-CA-C	6.00	121.85	114.35
47	2	1685	U	C2'-C3'-O3'	6.00	122.70	113.70
1	5	4582	C	C4'-C3'-O3'	-5.97	104.05	113.00
78	f	123	GLY	CA-C-O	-5.93	118.14	122.23
82	1	6585	G	C4'-C3'-O3'	-5.92	104.12	113.00
82	1	6589	C	C2'-C3'-O3'	5.90	118.35	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	1370	G	C2'-C3'-O3'	5.90	118.35	109.50
13	AJ	123	ILE	N-CA-C	-5.87	104.34	112.50
47	2	917	U	C2'-C3'-O3'	5.85	122.47	113.70
81	Aq	384	LYS	CB-CA-C	5.83	118.82	109.02
47	2	316	G	C2'-C3'-O3'	5.81	118.21	109.50
47	2	493	A	C4'-C3'-O3'	5.80	118.10	109.40
1	5	3710	G	C2'-C3'-O3'	5.77	118.15	109.50
6	AC	68	GLY	CA-C-O	-5.77	118.30	122.45
1	5	4884	G	C2'-C3'-O3'	5.69	122.23	113.70
1	5	973	U	C4'-C3'-O3'	-5.67	100.89	109.40
47	2	110	U	C2'-C3'-O3'	5.67	122.21	113.70
47	2	501	C	N1-C1'-C2'	5.67	120.50	112.00
1	5	2089	G	C4'-C3'-O3'	-5.67	100.90	109.40
47	2	1260	A	C3'-C2'-O2'	5.63	119.15	110.70
82	1	6456	U	C4'-C3'-O3'	5.61	117.81	109.40
1	5	1370	G	C4'-C3'-O3'	5.53	117.69	109.40
1	5	4448	G	C2'-C3'-O3'	5.52	121.97	113.70
1	5	925	G	C2'-C3'-O3'	5.49	117.73	109.50
1	5	1236	C	C4'-C3'-O3'	5.48	121.22	113.00
47	2	461	U	C2'-C3'-O3'	5.47	121.90	113.70
1	5	2844	A	C3'-C2'-O2'	5.45	118.88	110.70
19	AQ	73	PRO	N-CA-C	5.39	121.02	113.53
82	1	6551	A	C4'-C3'-O3'	5.38	117.46	109.40
1	5	1336	G	C3'-C2'-O2'	5.34	118.72	110.70
1	5	4335	C	C4'-C3'-O3'	-5.34	104.99	113.00
1	5	1445	U	C2'-C3'-O3'	5.32	121.67	113.70
68	V	108	PRO	CA-C-N	5.31	126.00	119.99
68	V	108	PRO	C-N-CA	5.31	126.00	119.99
1	5	3619	G	C4'-C3'-O3'	-5.29	105.06	113.00
1	5	1455	G	C2'-C3'-O3'	5.29	121.64	113.70
62	P	68	GLU	CA-C-N	5.29	127.31	120.44
62	P	68	GLU	C-N-CA	5.29	127.31	120.44
59	M	41	GLY	CA-C-O	-5.29	118.34	122.52
47	2	1452	A	C4'-C3'-O3'	5.27	117.31	109.40
47	2	1298	G	C4'-C3'-O3'	5.23	117.24	109.40
47	2	493	A	C2'-C3'-O3'	5.21	117.32	109.50
1	5	1522	G	C3'-C2'-O2'	5.21	118.52	110.70
1	5	125	C	C2'-C3'-O3'	5.21	121.51	113.70
1	5	1633	G	C2'-C3'-O3'	-5.19	105.92	113.70
47	2	1637	A	C2'-C3'-O3'	5.18	117.27	109.50
47	2	1637	A	C4'-C3'-O3'	5.16	117.14	109.40
47	2	1490	G	N9-C1'-C2'	5.16	119.73	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	48	G	C4'-C3'-O3'	5.15	117.12	109.40
45	Ar	59	GLY	CA-C-O	-5.15	118.45	122.52
4	AA	225	ILE	CA-C-N	5.14	128.14	120.90
4	AA	225	ILE	C-N-CA	5.14	128.14	120.90
14	AL	46	ILE	CA-C-N	5.13	125.53	119.83
14	AL	46	ILE	C-N-CA	5.13	125.53	119.83
47	2	1048	G	C4'-C3'-O3'	-5.13	105.31	113.00
1	5	2502	A	C2'-C3'-O3'	5.13	121.39	113.70
1	5	504	G	C2'-C3'-O3'	5.10	121.36	113.70
1	5	4232	U	C4'-C3'-O3'	5.10	117.06	109.40
45	Ar	66	ARG	CA-C-N	5.08	127.05	120.44
45	Ar	66	ARG	C-N-CA	5.08	127.05	120.44
1	5	3710	G	C4'-C3'-O3'	5.08	117.02	109.40
47	2	561	A	C2'-C3'-O3'	5.05	121.28	113.70
63	Q	38	SER	CA-C-N	5.04	127.04	120.28
63	Q	38	SER	C-N-CA	5.04	127.04	120.28
10	AG	265	LYS	CA-C-N	5.04	125.54	120.00
10	AG	265	LYS	C-N-CA	5.04	125.54	120.00
1	5	4448	G	C4'-C3'-O3'	5.04	120.55	113.00
81	Aq	313	GLU	CA-C-N	5.02	131.12	121.54
81	Aq	313	GLU	C-N-CA	5.02	131.12	121.54
16	AN	119	TYR	CA-C-N	5.01	127.97	120.95
16	AN	119	TYR	C-N-CA	5.01	127.97	120.95
1	5	1300	G	C4'-C3'-O3'	5.01	120.51	113.00

There are no chirality outliers.

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	AB	241	PRO	Peptide
5	AB	257	TRP	Peptide
5	AB	258	HIS	Peptide
46	AK	136	SER	Peptide
46	AK	139	THR	Peptide
46	AK	150	GLU	Peptide
46	AK	17	VAL	Peptide
14	AL	46	ILE	Peptide
30	Ab	101	HIS	Peptide
34	Af	106	TYR	Peptide
36	Ah	86	LYS	Peptide
49	C	189	ILE	Peptide
53	G	42	LYS	Peptide

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Mol	Chain	Res	Type	Group
60	N	26	LEU	Peptide
63	Q	56	LEU	Peptide
65	S	89	SER	Peptide
66	T	25	LYS	Peptide
70	X	27	ILE	Peptide
71	Y	61	GLN	Peptide
79	g	131	PHE	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	5	77074	0	38937	219	0
2	7	2538	0	1286	4	0
3	8	3208	0	1629	9	0
4	AA	1895	0	1984	27	0
5	AB	3172	0	3310	9	0
6	AC	2883	0	3053	36	0
7	AD	2391	0	2424	7	0
8	AE	1729	0	1887	12	0
9	AF	1875	0	1995	4	0
10	AG	1819	0	1956	10	0
11	AH	1516	0	1597	5	0
12	AI	1664	0	1712	8	0
13	AJ	1362	0	1399	5	0
14	AL	1627	0	1743	6	0
15	AM	1137	0	1211	8	0
16	AN	1701	0	1749	13	0
17	AO	1631	0	1780	8	0
18	AP	1242	0	1274	3	0
19	AQ	1526	0	1623	25	0
20	AR	1503	0	1657	11	0
21	AS	1457	0	1490	19	0
22	AT	1298	0	1366	5	0
23	AU	818	0	838	13	0
24	AV	969	0	1031	3	0
25	AW	528	0	541	1	0
26	AX	967	0	1040	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	AY	1115	0	1205	8	0
28	AZ	1107	0	1182	3	0
29	Aa	1162	0	1209	6	0
30	Ab	848	0	920	2	0
31	Ac	761	0	794	2	0
32	Ad	888	0	930	4	0
33	Ae	1053	0	1147	4	0
34	Af	876	0	912	1	0
35	Ag	906	0	1002	4	0
36	Ah	1013	0	1147	3	0
37	Ai	830	0	916	2	0
38	Aj	705	0	741	6	0
39	Ak	569	0	634	0	0
40	Al	447	0	480	1	0
41	Am	429	0	469	1	0
42	An	239	0	289	2	0
43	Ao	851	0	924	2	0
44	Ap	708	0	760	6	0
45	Ar	994	0	1051	6	0
46	AK	1705	0	1810	23	0
47	2	36229	0	18300	125	0
48	B	1706	0	1697	11	0
49	C	1729	0	1803	3	0
50	D	1712	0	1808	6	0
51	E	1768	0	1866	5	0
52	F	2073	0	2173	12	0
53	G	1471	0	1522	4	0
54	H	1923	0	2089	12	0
55	I	1488	0	1582	3	0
56	J	1686	0	1772	6	0
57	K	1525	0	1640	10	0
58	L	810	0	836	6	0
59	M	1175	0	1249	4	0
60	N	908	0	939	1	0
61	O	1202	0	1289	3	0
62	P	1016	0	1039	4	0
63	Q	990	0	1038	16	0
64	R	1128	0	1195	8	0
65	S	1068	0	1121	5	0
66	T	1190	0	1249	5	0
67	U	1097	0	1130	5	0
68	V	795	0	862	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	W	630	0	631	10	0
70	X	1034	0	1080	3	0
71	Y	1098	0	1167	1	0
72	Z	1011	0	1083	3	0
73	a	598	0	656	4	0
74	b	778	0	828	6	0
75	c	651	0	672	1	0
76	d	488	0	514	3	0
77	e	459	0	452	5	0
78	f	447	0	495	2	0
79	g	555	0	567	6	0
80	h	2436	0	2393	13	0
81	Aq	3278	0	3322	26	0
82	1	4407	0	2224	30	0
All	All	219295	0	163317	778	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (778) 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)
23:AU:23:LEU:HD12	23:AU:110:TYR:HB2	1.55	0.88
4:AA:20:VAL:HA	4:AA:23:ARG:HG3	1.57	0.86
1:5:1991:A:H4'	1:5:1991:A:OP1	1.81	0.81
1:5:3768:U:H2'	1:5:3769:C:C6	2.18	0.79
19:AQ:82:VAL:HG21	19:AQ:86:ILE:HD11	1.65	0.79
1:5:920:C:H4'	1:5:920:C:OP1	1.81	0.79
47:2:887:U:H2'	47:2:887:U:O2	1.82	0.78
1:5:933:C:H4'	1:5:934:A:H3'	1.64	0.77
1:5:923:C:H5''	1:5:923:C:H6	1.50	0.76
47:2:590:A:N3	47:2:590:A:H2'	2.01	0.75
6:AC:358:LEU:HA	6:AC:361:LYS:HE3	1.72	0.72
17:AO:37:ARG:HD2	17:AO:108:ILE:HD11	1.72	0.72
19:AQ:61:LEU:HD23	19:AQ:86:ILE:HD11	1.71	0.71
47:2:1620:A:H5''	63:Q:115:TYR:HE2	1.55	0.70
47:2:1863:A:H1'	74:b:79:ILE:HD13	1.73	0.70
4:AA:5:ILE:HG12	4:AA:8:GLN:HG3	1.74	0.70
19:AQ:150:GLN:HE21	19:AQ:150:GLN:N	1.89	0.69
1:5:3768:U:H2'	1:5:3769:C:H6	1.57	0.69
1:5:741:C:H2'	1:5:742:G:C8	2.28	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:923:C:H5''	1:5:923:C:C6	2.29	0.67
1:5:924:C:H3'	1:5:925:G:H5'	1.75	0.67
1:5:738:C:H5'	1:5:739:G:H5''	1.75	0.67
21:AS:96:GLU:HG3	21:AS:139:ARG:HG3	1.77	0.66
1:5:1282:G:H3'	1:5:1282:G:N3	2.10	0.66
1:5:738:C:C5'	1:5:739:G:H5''	2.26	0.65
81:Aq:416:ARG:HG3	81:Aq:416:ARG:HH11	1.61	0.65
1:5:740:G:H2'	1:5:740:G:OP2	1.97	0.65
63:Q:38:SER:HB2	63:Q:41:GLN:HE22	1.60	0.65
1:5:3756:A:H2'	1:5:3757:G:C8	2.32	0.65
47:2:384:U:O4	56:J:5:ARG:NH2	2.29	0.64
1:5:739:G:O2'	1:5:740:G:H5'	1.98	0.64
63:Q:127:LYS:HD2	63:Q:127:LYS:O	1.97	0.64
1:5:3756:A:H2'	1:5:3757:G:H8	1.60	0.64
1:5:4549:G:H4'	1:5:4549:G:OP2	1.95	0.64
46:AK:150:GLU:HA	46:AK:153:SER:HB2	1.80	0.64
69:W:34:MET:HE2	69:W:36:VAL:HG22	1.80	0.63
10:AG:110:TRP:O	10:AG:115:ARG:NH2	2.31	0.63
4:AA:126:LEU:HD11	4:AA:156:LYS:HE3	1.80	0.62
63:Q:130:ARG:HD2	63:Q:130:ARG:N	2.15	0.62
4:AA:179:ILE:HG23	4:AA:184:ARG:HB2	1.81	0.62
19:AQ:122:THR:HB	19:AQ:124:HIS:CD2	2.35	0.62
47:2:884:C:H2'	47:2:885:U:C6	2.35	0.61
23:AU:36:GLU:HG2	23:AU:68:SER:HA	1.81	0.61
47:2:190:G:O2'	47:2:209:A:N6	2.33	0.61
65:S:28:PHE:HA	65:S:55:THR:HG21	1.82	0.61
82:1:6434:C:H2'	82:1:6434:C:O2	1.99	0.61
80:h:197:THR:HG21	80:h:238:ALA:HA	1.81	0.61
1:5:971:U:H2'	1:5:971:U:O2	2.02	0.60
1:5:1802:A:N3	22:AT:130:ARG:NH1	2.49	0.60
1:5:2532:C:O2'	26:AX:93:ASN:ND2	2.35	0.60
13:AJ:119:TYR:CE2	13:AJ:121:PRO:HA	2.36	0.60
79:g:141:CYS:SG	79:g:142:GLY:N	2.74	0.60
82:1:6428:G:H4'	82:1:6428:G:OP1	1.99	0.60
71:Y:61:GLN:O	71:Y:63:ASN:N	2.35	0.60
20:AR:164:SER:O	20:AR:168:GLU:N	2.35	0.60
1:5:1272:C:OP2	9:AF:33:ARG:NH1	2.34	0.60
47:2:1521:C:H5'	63:Q:126:VAL:HB	1.83	0.59
4:AA:180:LEU:HD22	44:Ap:18:TYR:HB3	1.84	0.59
24:AV:82:ILE:HG22	24:AV:83:ARG:HG3	1.85	0.59
19:AQ:33:ARG:HG2	19:AQ:33:ARG:HH21	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:687:C:O2	47:2:687:C:H2'	2.02	0.59
1:5:1247:U:O4	30:Ab:111:ARG:NH1	2.36	0.59
47:2:1208:A:O2'	47:2:1835:A:N1	2.30	0.59
21:AS:164:LYS:HB3	21:AS:165:PRO:HD3	1.86	0.58
1:5:1962:A:H62	1:5:2024:G:H21	1.51	0.58
55:I:53:VAL:HG21	55:I:172:THR:HA	1.84	0.58
1:5:3896:C:O2'	5:AB:268:ARG:NH1	2.37	0.58
19:AQ:114:LEU:HD21	19:AQ:120:ILE:HG13	1.86	0.58
48:B:19:LEU:HB3	65:S:96:ILE:HG21	1.86	0.58
80:h:165:ILE:HG12	80:h:177:TRP:HB2	1.84	0.58
19:AQ:72:LEU:HG	19:AQ:73:PRO:HD3	1.86	0.58
80:h:251:ALA:HB2	80:h:289:LEU:HD22	1.85	0.57
1:5:1966:C:N4	1:5:2022:C:N3	2.52	0.57
6:AC:348:LYS:HG2	6:AC:349:LEU:HD23	1.86	0.57
47:2:1738:C:OP1	54:H:92:ARG:NH1	2.35	0.57
4:AA:77:ILE:HD13	4:AA:128:ARG:HB2	1.87	0.57
15:AM:36:ALA:HB2	15:AM:52:PHE:CZ	2.39	0.57
1:5:4163:U:OP2	10:AG:106:ARG:NH2	2.37	0.57
1:5:1967:A:N6	1:5:2020:U:O2	2.37	0.57
6:AC:340:ILE:CG2	8:AE:52:LEU:HD21	2.35	0.57
23:AU:36:GLU:HG2	23:AU:68:SER:CA	2.35	0.57
1:5:4377:G:O6	29:Aa:42:ARG:NH2	2.37	0.57
2:7:11:A:N6	7:AD:16:TYR:O	2.37	0.57
81:Aq:416:ARG:HG3	81:Aq:416:ARG:NH1	2.20	0.57
1:5:1555:G:N7	44:Ap:4:ARG:NH2	2.53	0.56
1:5:3717:A:OP2	1:5:3735:G:N2	2.38	0.56
1:5:2422:C:OP1	18:AP:127:ARG:NH2	2.39	0.56
48:B:155:HIS:CD2	69:W:61:ARG:HA	2.40	0.56
1:5:2758:G:O2'	1:5:2765:A:N3	2.38	0.56
1:5:2890:C:O2'	1:5:5016:A:N6	2.38	0.56
48:B:141:ASN:ND2	69:W:29:HIS:O	2.37	0.56
1:5:4874:A:O2'	21:AS:170:LYS:NZ	2.39	0.56
1:5:3967:G:N2	1:5:4054:C:N3	2.53	0.56
47:2:588:G:H1'	47:2:590:A:OP2	2.06	0.56
20:AR:173:ARG:HB3	20:AR:173:ARG:CZ	2.36	0.56
1:5:1980:U:H6	1:5:1980:U:O5'	1.89	0.56
27:AY:48:PRO:O	27:AY:115:ARG:NH2	2.38	0.56
1:5:4616:A:HO2'	24:AV:12:ALA:N	2.04	0.56
23:AU:36:GLU:HG3	23:AU:70:ILE:HD11	1.88	0.55
64:R:53:GLU:OE2	64:R:85:ARG:NH2	2.40	0.55
47:2:883:U:H4'	47:2:883:U:OP1	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:3759:A:H2	1:5:3764:U:H3	1.54	0.55
48:B:180:GLN:HE21	48:B:195:TRP:HB2	1.71	0.55
47:2:885:U:H6	47:2:885:U:O5'	1.89	0.55
47:2:1628:C:OP1	67:U:38:LYS:NZ	2.39	0.55
1:5:2009:A:H5''	1:5:2009:A:N3	2.21	0.55
47:2:1734:G:O2'	47:2:1800:A:N6	2.40	0.55
6:AC:134:PRO:HB3	6:AC:150:LEU:HG	1.89	0.55
6:AC:340:ILE:HG21	8:AE:52:LEU:HD21	1.89	0.55
59:M:97:ARG:O	59:M:100:ASN:ND2	2.40	0.55
82:1:6425:A:H8	82:1:6425:A:H5'	1.71	0.55
23:AU:36:GLU:N	23:AU:36:GLU:CD	2.65	0.54
4:AA:77:ILE:HG23	4:AA:169:VAL:HG13	1.88	0.54
21:AS:1:THR:HG23	21:AS:121:ALA:HB1	1.89	0.54
34:Af:74:VAL:HG13	34:Af:84:VAL:HG13	1.89	0.54
47:2:570:C:O2	72:Z:34:THR:OG1	2.25	0.54
1:5:935:G:H21	15:AM:46:ARG:HB2	1.72	0.54
1:5:2638:G:H2'	1:5:2639:U:O4'	2.07	0.54
26:AX:104:ALA:O	26:AX:134:LYS:NZ	2.40	0.54
47:2:925:G:H1	47:2:1017:U:H3	1.56	0.54
47:2:1620:A:H5''	63:Q:115:TYR:CE2	2.39	0.54
6:AC:285:LEU:HB2	19:AQ:124:HIS:CE1	2.43	0.54
6:AC:350:ARG:HE	6:AC:353:ARG:HH21	1.56	0.54
47:2:114:G:N1	47:2:350:C:O2	2.39	0.54
1:5:4220:A:OP2	22:AT:2:THR:N	2.41	0.54
1:5:1521:C:OP1	6:AC:100:ARG:NH2	2.36	0.54
1:5:3975:C:N4	1:5:4036:G:O6	2.41	0.54
1:5:4453:C:H4'	81:Aq:188:LEU:HD22	1.90	0.54
63:Q:130:ARG:HD3	81:Aq:84:LEU:HB3	1.90	0.54
47:2:1360:U:O2'	47:2:1379:A:OP2	2.21	0.54
70:X:6:VAL:HG12	70:X:34:ILE:HD11	1.89	0.54
14:AL:69:LYS:HA	14:AL:159:ASN:HD21	1.73	0.53
6:AC:358:LEU:HA	6:AC:361:LYS:HG2	1.89	0.53
7:AD:37:VAL:HG13	7:AD:67:ALA:CB	2.38	0.53
47:2:1444:U:O2'	47:2:1580:A:N1	2.41	0.53
6:AC:134:PRO:HB3	6:AC:150:LEU:CD2	2.38	0.53
27:AY:49:ILE:HD13	27:AY:80:ILE:HD13	1.89	0.53
1:5:1180:C:O4'	1:5:1180:C:O2	2.26	0.53
1:5:4565:C:O2	5:AB:268:ARG:NH2	2.41	0.53
80:h:133:ASN:HD21	80:h:139:LYS:HD3	1.72	0.53
1:5:1990:A:N3	1:5:1990:A:H2'	2.23	0.53
1:5:1210:C:O2	1:5:1210:C:O4'	2.27	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:AQ:150:GLN:HE21	19:AQ:150:GLN:H	1.57	0.53
1:5:2503:G:H3'	1:5:2504:C:H4'	1.91	0.53
4:AA:4:VAL:HG13	4:AA:8:GLN:HB2	1.91	0.53
47:2:4:C:O2'	57:K:18:ARG:NH1	2.42	0.53
47:2:1650:A:H5''	64:R:139:ALA:HB2	1.90	0.52
1:5:977:C:O5'	1:5:977:C:H6	1.92	0.52
12:AI:3:ARG:NE	12:AI:63:GLU:OE1	2.41	0.52
19:AQ:6:LEU:HD22	19:AQ:8:ASN:HD21	1.74	0.52
46:AK:92:LYS:HE3	46:AK:96:ASN:HD21	1.75	0.52
54:H:134:GLY:HA3	54:H:158:VAL:HG11	1.91	0.52
67:U:22:LEU:HB2	67:U:28:LEU:HD21	1.90	0.52
47:2:1232:U:H2'	47:2:1233:G:H8	1.72	0.52
74:b:50:VAL:HG23	74:b:64:LEU:HD12	1.91	0.52
1:5:924:C:C3'	1:5:925:G:H5'	2.40	0.52
15:AM:27:ILE:HA	15:AM:38:VAL:HG12	1.90	0.52
47:2:1865:C:O4'	47:2:1865:C:O2	2.27	0.52
47:2:1863:A:H2'	47:2:1863:A:N3	2.25	0.52
69:W:32:ILE:HG12	69:W:60:ARG:HD2	1.92	0.52
1:5:4872:G:OP2	15:AM:94:LYS:NZ	2.40	0.52
1:5:106:A:O2'	1:5:335:A:N3	2.41	0.52
1:5:2465:C:H1'	1:5:3672:G:H1	1.76	0.51
47:2:1139:C:O4'	47:2:1139:C:O2	2.27	0.51
62:P:53:ILE:HG23	62:P:88:LEU:HD22	1.92	0.51
74:b:25:ASN:HD21	74:b:77:CYS:HB3	1.75	0.51
76:d:44:ARG:NH1	76:d:60:GLU:O	2.42	0.51
47:2:1550:G:O2'	47:2:1558:C:O2	2.23	0.51
57:K:136:ARG:HD2	57:K:139:LYS:HA	1.91	0.51
29:Aa:124:VAL:HG21	29:Aa:137:ILE:HD13	1.92	0.51
47:2:182:C:H5'	47:2:183:G:C5	2.45	0.51
47:2:1336:C:O2'	77:e:44:ARG:NH2	2.44	0.51
65:S:31:ASN:HD21	65:S:55:THR:HG22	1.75	0.51
1:5:419:A:N3	1:5:1332:C:O2'	2.39	0.51
1:5:3967:G:O2'	1:5:3968:U:O4'	2.28	0.51
6:AC:302:LEU:HD22	19:AQ:38:HIS:HB3	1.93	0.51
1:5:152:U:P	16:AN:49:ARG:HH12	2.34	0.51
3:8:75:G:OP2	27:AY:74:TYR:OH	2.27	0.51
3:8:85:U:O4	27:AY:50:ARG:NH2	2.40	0.51
66:T:12:ILE:HD12	66:T:19:ASN:HB2	1.91	0.51
82:1:6432:C:H1'	82:1:6433:C:C6	2.46	0.51
1:5:1981:G:H3'	1:5:1982:G:H5''	1.92	0.51
47:2:844:U:OP2	52:F:240:ARG:NH1	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:AO:79:ILE:HG21	17:AO:138:LEU:HD11	1.93	0.51
63:Q:115:TYR:HB2	63:Q:118:GLU:HG3	1.93	0.51
1:5:946:C:H5'	6:AC:336:ARG:HD3	1.93	0.51
1:5:4769:G:OP2	17:AO:172:LYS:HE3	2.10	0.51
47:2:1231:C:O2'	47:2:1253:A:N6	2.44	0.51
20:AR:155:LEU:N	20:AR:155:LEU:HD12	2.26	0.50
69:W:33:PRO:HA	69:W:54:ALA:HA	1.93	0.50
1:5:115:C:O2	1:5:115:C:O4'	2.28	0.50
4:AA:225:ILE:HD11	4:AA:233:ARG:HG3	1.94	0.50
19:AQ:63:LEU:O	19:AQ:66:VAL:HG12	2.11	0.50
52:F:48:LEU:HD21	52:F:64:ILE:HG21	1.94	0.50
1:5:2259:G:O2'	1:5:2260:C:OP1	2.18	0.50
38:Aj:19:CYS:SG	38:Aj:34:CYS:SG	3.10	0.50
1:5:4759:C:O4'	1:5:4759:C:O2	2.30	0.50
43:Ao:77:CYS:SG	43:Ao:78:ARG:N	2.84	0.50
47:2:55:U:C2'	47:2:55:U:O2	2.60	0.50
80:h:10:THR:HB	80:h:306:LEU:HD12	1.93	0.50
1:5:4770:U:H2'	1:5:4771:C:C2	2.47	0.50
47:2:677:G:OP1	61:O:120:SER:OG	2.29	0.50
52:F:166:THR:HB	52:F:168:LYS:HD3	1.94	0.50
64:R:86:GLN:HE22	64:R:122:ALA:HB2	1.75	0.50
1:5:151:G:OP2	16:AN:4:TYR:OH	2.24	0.50
1:5:1890:G:N3	1:5:1890:G:H2'	2.26	0.50
1:5:4303:C:H2'	1:5:4305:G:C8	2.46	0.50
1:5:4548:A:H5''	81:Aq:182:ARG:HB3	1.93	0.50
11:AH:41:ILE:HG21	11:AH:73:ILE:HD11	1.94	0.50
38:Aj:19:CYS:SG	38:Aj:22:CYS:SG	3.09	0.50
44:Ap:92:GLN:OE1	44:Ap:92:GLN:HA	2.12	0.50
47:2:1303:C:O2	47:2:1303:C:O4'	2.28	0.50
47:2:1535:U:H2'	47:2:1535:U:O2	2.11	0.50
82:1:6517:G:O6	82:1:6531:C:N4	2.45	0.50
82:1:6587:A:O3'	82:1:6588:A:H4'	2.11	0.50
1:5:974:C:O4'	1:5:974:C:O2	2.28	0.49
15:AM:35:ARG:HH11	15:AM:35:ARG:HB3	1.77	0.49
74:b:26:CYS:HG	74:b:77:CYS:HG	1.57	0.49
5:AB:222:VAL:O	5:AB:343:ARG:NH1	2.45	0.49
20:AR:91:GLU:HA	20:AR:94:LYS:HE2	1.94	0.49
68:V:39:LEU:HD22	68:V:101:ILE:HG22	1.94	0.49
21:AS:93:MET:HE1	21:AS:117:HIS:CE1	2.47	0.49
27:AY:11:ARG:O	27:AY:15:ARG:HG3	2.13	0.49
47:2:476:A:N3	47:2:488:U:O2'	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:886:A:H1'	47:2:887:U:O5'	2.11	0.49
81:Aq:179:LYS:HD2	81:Aq:179:LYS:C	2.36	0.49
63:Q:96:VAL:HG11	63:Q:120:SER:HB2	1.94	0.49
1:5:3958:G:H2'	1:5:3959:U:H6	1.77	0.49
6:AC:55:SER:HB3	6:AC:58:ALA:HB2	1.95	0.49
19:AQ:86:ILE:HG22	19:AQ:86:ILE:O	2.11	0.49
28:AZ:89:ILE:HD11	28:AZ:117:LYS:HB3	1.94	0.49
47:2:1693:G:H21	47:2:1834:A:H8	1.60	0.49
1:5:4903:G:C6	1:5:4919:G:N2	2.81	0.49
23:AU:25:CYS:O	23:AU:29:VAL:HG23	2.12	0.49
28:AZ:91:LEU:HD21	28:AZ:114:ALA:HA	1.95	0.49
32:Ad:60:PRO:HD2	32:Ad:100:ASN:HD21	1.76	0.49
47:2:94:G:O2'	47:2:508:A:O2'	2.26	0.49
47:2:1862:G:H4'	47:2:1863:A:OP1	2.11	0.49
1:5:1866:U:O4'	12:AI:4:ARG:NH2	2.46	0.49
1:5:2787:A:N3	1:5:2787:A:H2'	2.27	0.49
4:AA:147:ARG:HH21	4:AA:155:LYS:HD3	1.77	0.49
19:AQ:72:LEU:HG	19:AQ:73:PRO:CD	2.42	0.49
47:2:1013:U:OP1	47:2:1129:G:O2'	2.30	0.49
1:5:1768:C:O2	1:5:1768:C:O4'	2.29	0.49
6:AC:147:VAL:O	45:Ar:73:PRO:HD2	2.12	0.49
6:AC:289:LEU:HA	6:AC:292:ILE:HB	1.95	0.49
82:1:6553:C:N4	82:1:6599:G:O6	2.45	0.49
1:5:740:G:O2'	1:5:741:C:H5''	2.12	0.48
47:2:217:A:OP1	47:2:309:G:N2	2.46	0.48
52:F:20:LEU:HD21	52:F:46:ILE:HD12	1.95	0.48
1:5:115:C:O2'	1:5:276:C:OP1	2.31	0.48
1:5:971:U:H2'	1:5:972:G:H5'	1.94	0.48
1:5:4519:C:N4	81:Aq:188:LEU:HD23	2.28	0.48
1:5:4884:G:N7	8:AE:275:ARG:NH2	2.61	0.48
82:1:6429:U:H3'	82:1:6430:U:H2'	1.94	0.48
1:5:2012:A:C2	1:5:2013:A:H1'	2.48	0.48
8:AE:165:VAL:HG12	8:AE:178:VAL:HG22	1.94	0.48
80:h:174:VAL:HB	80:h:188:HIS:HB2	1.96	0.48
47:2:55:U:O2	47:2:55:U:H2'	2.14	0.48
50:D:191:VAL:HG11	50:D:236:PHE:HA	1.95	0.48
69:W:32:ILE:O	69:W:32:ILE:HD12	2.13	0.48
1:5:2420:A:OP2	18:AP:127:ARG:NH1	2.46	0.48
1:5:3612:C:H1'	1:5:5016:A:C8	2.48	0.48
1:5:4548:A:H5''	81:Aq:182:ARG:CB	2.44	0.48
1:5:5001:U:H2'	1:5:5002:U:O4'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AC:347:HIS:C	6:AC:347:HIS:CD2	2.91	0.48
42:An:2:ARG:CD	47:2:1841:C:H5''	2.42	0.48
47:2:1137:U:O4	47:2:1148:A:H2	1.96	0.48
47:2:1481:G:N2	51:E:162:ASP:OD2	2.46	0.48
70:X:28:ARG:HB2	70:X:29:PRO:HD3	1.95	0.48
1:5:946:C:C5'	6:AC:336:ARG:HD3	2.43	0.48
47:2:853:C:O4'	47:2:853:C:O2	2.31	0.48
47:2:887:U:O2	47:2:887:U:C2'	2.51	0.48
80:h:125:ARG:HA	80:h:150:TRP:HB3	1.96	0.48
1:5:2458:C:OP1	16:AN:67:ARG:NH1	2.47	0.48
2:7:105:C:OP2	12:AI:203:ARG:NH2	2.47	0.48
4:AA:101:VAL:HG22	4:AA:165:VAL:HG12	1.95	0.48
17:AO:54:TYR:CD1	17:AO:145:VAL:HG21	2.49	0.48
72:Z:27:VAL:HG11	72:Z:35:VAL:HG21	1.95	0.48
1:5:2779:C:O2'	3:8:112:G:OP1	2.26	0.48
1:5:4903:G:O6	1:5:4919:G:C2	2.67	0.48
21:AS:139:ARG:C	21:AS:143:LYS:HE3	2.38	0.48
46:AK:9:THR:CG2	46:AK:201:VAL:HG11	2.44	0.48
47:2:887:U:H1'	47:2:888:U:H5	1.78	0.48
82:1:6433:C:H5''	82:1:6433:C:H6	1.79	0.48
1:5:2045:G:O6	1:5:3870:C:O2'	2.30	0.47
1:5:3760:A:C2	47:2:1825:A:C8	3.02	0.47
1:5:4162:C:O4'	1:5:4162:C:O2	2.31	0.47
14:AL:48:PRO:HG3	36:Ah:118:LYS:HE3	1.96	0.47
21:AS:34:ALA:HB1	21:AS:39:VAL:HG13	1.96	0.47
21:AS:127:MET:HA	22:AT:153:PRO:HD2	1.95	0.47
1:5:739:G:H2'	1:5:740:G:C8	2.49	0.47
6:AC:60:HIS:NE2	6:AC:100:ARG:HD2	2.28	0.47
82:1:6472:G:C4'	82:1:6472:G:OP1	2.61	0.47
1:5:737:C:H2'	1:5:739:G:H4'	1.96	0.47
1:5:964:A:H2'	1:5:965:G:O4'	2.15	0.47
1:5:3702:A:C8	1:5:3774:A:H1'	2.49	0.47
1:5:3770:U:H2'	1:5:3771:C:C6	2.48	0.47
6:AC:284:MET:HA	19:AQ:122:THR:HG21	1.96	0.47
46:AK:137:LEU:HB2	46:AK:150:GLU:HG2	1.95	0.47
66:T:6:PRO:HD3	73:a:49:LEU:HD23	1.95	0.47
80:h:214:GLY:O	80:h:232:GLY:N	2.47	0.47
1:5:974:C:C2	8:AE:129:LEU:HD13	2.48	0.47
1:5:1326:A:OP2	1:5:4445:U:O2'	2.32	0.47
1:5:2666:U:O2'	1:5:2668:G:N7	2.42	0.47
8:AE:284:VAL:HG13	8:AE:289:LEU:HD11	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:B:24:HIS:O	48:B:49:ILE:N	2.45	0.47
1:5:1081:C:H42	1:5:1218:G:H1	1.62	0.47
1:5:1771:U:C4	1:5:1772:C:N4	2.83	0.47
4:AA:24:LYS:HE3	4:AA:52:PRO:HD3	1.95	0.47
20:AR:94:LYS:HE2	20:AR:94:LYS:HB2	1.79	0.47
21:AS:41:LYS:HD2	21:AS:61:ILE:HD13	1.95	0.47
32:Ad:90:ARG:HD3	32:Ad:102:LEU:HD23	1.97	0.47
47:2:1552:G:N3	51:E:9:ARG:NH2	2.60	0.47
49:C:28:LYS:HD2	49:C:48:LEU:HD13	1.96	0.47
81:Aq:38:ILE:HG12	81:Aq:94:VAL:HG13	1.97	0.47
81:Aq:417:VAL:HG12	81:Aq:417:VAL:O	2.15	0.47
82:1:6425:A:H2'	82:1:6427:G:O4'	2.14	0.47
10:AG:111:PRO:HD2	10:AG:114:ILE:HD12	1.95	0.47
11:AH:167:VAL:HG12	11:AH:170:LYS:HB2	1.97	0.47
21:AS:132:MET:HB3	21:AS:132:MET:HE2	1.74	0.47
31:Ac:38:ILE:HG21	31:Ac:63:TYR:HB3	1.96	0.47
47:2:433:A:H5''	56:J:22:HIS:HB3	1.97	0.47
64:R:13:PHE:HA	64:R:22:VAL:HA	1.96	0.47
1:5:1961:G:C2'	1:5:2025:A:H62	2.28	0.47
46:AK:111:LEU:HD12	46:AK:137:LEU:HD21	1.96	0.47
47:2:96:C:O2	47:2:473:A:O2'	2.31	0.47
47:2:501:C:O2	47:2:501:C:C2'	2.62	0.47
54:H:63:MET:SD	54:H:98:ARG:NH1	2.88	0.47
1:5:3908:A:N7	1:5:4449:A:N6	2.62	0.47
1:5:3977:C:O2	1:5:4035:G:N2	2.48	0.47
1:5:4768:G:OP1	17:AO:168:TYR:OH	2.31	0.47
9:AF:111:LEU:HD22	9:AF:122:VAL:HG11	1.97	0.47
44:Ap:38:THR:HA	44:Ap:45:THR:HA	1.96	0.47
47:2:183:G:N3	47:2:183:G:C2'	2.78	0.47
66:T:98:VAL:HG11	66:T:106:LYS:HG3	1.97	0.47
1:5:39:A:O2'	1:5:1654:G:O6	2.28	0.46
1:5:3892:U:H4'	18:AP:80:GLN:HE22	1.80	0.46
6:AC:358:LEU:HA	6:AC:361:LYS:CG	2.44	0.46
13:AJ:119:TYR:O	13:AJ:119:TYR:CD2	2.68	0.46
16:AN:104:GLU:HA	16:AN:160:GLU:HG3	1.97	0.46
47:2:222:U:OP1	59:M:17:PHE:HB3	2.15	0.46
1:5:3974:G:N7	1:5:3975:C:N4	2.63	0.46
7:AD:75:VAL:O	7:AD:112:ARG:NH1	2.48	0.46
33:Ae:89:LEU:HD13	33:Ae:118:LEU:HD22	1.97	0.46
47:2:1520:G:H2'	63:Q:126:VAL:HG21	1.97	0.46
77:e:39:CYS:SG	77:e:42:CYS:SG	3.11	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:1:6471:G:H2'	82:1:6472:G:H5''	1.98	0.46
17:AO:37:ARG:CG	17:AO:108:ILE:HG12	2.46	0.46
47:2:1309:C:OP1	79:g:118:ARG:NH2	2.48	0.46
53:G:45:TYR:HB3	53:G:67:PRO:HG3	1.98	0.46
4:AA:112:ILE:HG23	4:AA:133:TYR:HB2	1.97	0.46
79:g:100:LEU:O	79:g:104:LYS:NZ	2.49	0.46
80:h:254:PRO:HA	80:h:285:GLN:HA	1.98	0.46
82:1:6432:C:H4'	82:1:6433:C:OP1	2.14	0.46
47:2:1092:G:OP1	61:O:2:GLY:N	2.48	0.46
52:F:47:PHE:HA	52:F:51:LYS:HG3	1.97	0.46
68:V:35:VAL:HG11	68:V:110:VAL:HG11	1.97	0.46
1:5:3766:A:C8	1:5:3766:A:H5''	2.50	0.46
3:8:36:G:O2'	3:8:103:A:N1	2.38	0.46
4:AA:133:TYR:HB3	4:AA:168:VAL:HG12	1.98	0.46
63:Q:97:TYR:CZ	63:Q:99:GLY:HA2	2.51	0.46
81:Aq:190:PHE:HA	81:Aq:193:LEU:HB3	1.96	0.46
1:5:4880:C:O4'	1:5:4880:C:O2	2.32	0.46
4:AA:97:ASN:OD1	4:AA:100:ASN:ND2	2.48	0.46
12:AI:35:ASP:N	12:AI:35:ASP:OD1	2.49	0.46
19:AQ:23:MET:H	19:AQ:23:MET:HG3	1.48	0.46
47:2:590:A:N3	47:2:590:A:C2'	2.77	0.46
51:E:162:ASP:N	51:E:163:PRO:CD	2.78	0.46
6:AC:346:ASN:N	6:AC:346:ASN:HD22	2.13	0.46
77:e:21:CYS:SG	77:e:24:CYS:SG	3.12	0.46
82:1:6432:C:H1'	82:1:6433:C:H5''	1.98	0.46
82:1:6602:C:N4	82:1:6603:C:N3	2.63	0.46
1:5:4549:G:OP2	1:5:4549:G:C4'	2.63	0.46
4:AA:77:ILE:O	4:AA:77:ILE:HG22	2.15	0.46
6:AC:322:LEU:HD13	6:AC:336:ARG:NH1	2.31	0.46
82:1:6426:U:H3'	82:1:6427:G:H5''	1.97	0.46
2:7:43:U:H4'	13:AJ:143:ASP:O	2.16	0.46
17:AO:37:ARG:HG2	17:AO:108:ILE:HG12	1.98	0.46
19:AQ:33:ARG:HG2	19:AQ:33:ARG:NH2	2.29	0.46
44:Ap:7:LYS:O	44:Ap:27:LYS:NZ	2.44	0.46
47:2:155:G:H4'	54:H:15:LEU:HD13	1.98	0.46
81:Aq:179:LYS:HD2	81:Aq:179:LYS:O	2.15	0.46
82:1:6454:A:N1	82:1:6455:A:C8	2.84	0.46
1:5:980:G:H2'	1:5:981:C:C6	2.51	0.45
1:5:2010:A:H4'	1:5:2010:A:OP1	2.16	0.45
23:AU:49:VAL:HG11	23:AU:57:GLY:HA2	1.98	0.45
58:L:10:ALA:HB1	58:L:35:LEU:HD21	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:M:100:ASN:N	59:M:100:ASN:HD22	2.14	0.45
1:5:2517:A:O3'	35:Ag:66:ARG:NH2	2.50	0.45
1:5:4882:U:OP1	15:AM:117:LYS:NZ	2.49	0.45
1:5:4985:U:O2	5:AB:174:ARG:NH1	2.49	0.45
4:AA:117:GLU:HB2	4:AA:162:ASN:HB2	1.99	0.45
5:AB:17:LEU:O	5:AB:19:ARG:N	2.50	0.45
29:Aa:75:LEU:HB3	29:Aa:117:LEU:HD13	1.96	0.45
47:2:887:U:H1'	47:2:888:U:C5	2.52	0.45
53:G:91:ARG:HD2	73:a:103:HIS:CE1	2.51	0.45
59:M:99:TYR:O	59:M:101:ARG:N	2.49	0.45
47:2:564:A:N6	47:2:586:G:O2'	2.49	0.45
81:Aq:189:ARG:HA	81:Aq:189:ARG:HD2	1.74	0.45
82:1:6434:C:O2	82:1:6434:C:C2'	2.65	0.45
1:5:1895:G:OP1	9:AF:95:ARG:NH2	2.50	0.45
1:5:4035:G:H2'	1:5:4036:G:O4'	2.16	0.45
21:AS:69:GLU:HB2	21:AS:101:ILE:HG23	1.98	0.45
27:AY:55:VAL:CG2	27:AY:104:VAL:HG13	2.46	0.45
47:2:127:C:O2	52:F:134:LYS:NZ	2.48	0.45
54:H:54:GLY:HA2	54:H:63:MET:HE3	1.98	0.45
82:1:6470:A:N3	82:1:6470:A:H2'	2.31	0.45
1:5:1773:U:H2'	1:5:1774:C:C6	2.51	0.45
13:AJ:160:GLU:HA	13:AJ:163:MET:HG2	1.99	0.45
20:AR:155:LEU:HD12	20:AR:155:LEU:H	1.81	0.45
82:1:6542:U:O2	82:1:6542:U:O4'	2.35	0.45
1:5:1211:G:OP2	1:5:1215:C:N4	2.50	0.45
1:5:1826:G:H21	30:Ab:50:ASN:HD21	1.64	0.45
1:5:3958:G:H2'	1:5:3959:U:C6	2.52	0.45
4:AA:156:LYS:HD2	4:AA:158:ILE:HG23	1.98	0.45
45:Ar:65:LYS:O	45:Ar:102:TYR:OH	2.29	0.45
46:AK:67:VAL:HG13	46:AK:82:ILE:HG13	1.98	0.45
63:Q:121:ILE:O	63:Q:121:ILE:HG23	2.16	0.45
1:5:2640:G:H2'	1:5:2641:A:C8	2.52	0.45
1:5:3642:A:HO2'	38:Aj:2:THR:N	2.14	0.45
3:8:65:A:O2'	36:Ah:10:ARG:NH2	2.49	0.45
10:AG:156:ARG:NE	10:AG:246:LEU:O	2.43	0.45
14:AL:47:ALA:HB3	14:AL:48:PRO:HD3	1.99	0.45
47:2:847:A:O2'	52:F:106:LYS:NZ	2.41	0.45
47:2:1685:U:H2'	47:2:1686:G:O4'	2.17	0.45
72:Z:62:THR:HA	72:Z:69:THR:HA	1.98	0.45
81:Aq:190:PHE:O	81:Aq:191:ALA:C	2.58	0.45
82:1:6427:G:C2	82:1:6428:G:H1'	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:4572:U:O2'	1:5:4573:G:O4'	2.30	0.45
19:AQ:150:GLN:H	19:AQ:150:GLN:NE2	2.14	0.45
46:AK:10:LEU:HA	46:AK:10:LEU:HD23	1.78	0.45
47:2:659:G:N3	47:2:659:G:H2'	2.32	0.45
47:2:1060:A:O2'	47:2:1062:A:N7	2.43	0.45
6:AC:159:GLU:HA	6:AC:217:ILE:HB	1.98	0.44
17:AO:105:PHE:CG	17:AO:109:PRO:HG2	2.51	0.44
28:AZ:89:ILE:HD12	28:AZ:121:ARG:HD3	1.99	0.44
47:2:1479:G:OP1	64:R:138:ARG:NH2	2.50	0.44
1:5:364:G:O6	38:Aj:52:LYS:NZ	2.49	0.44
8:AE:147:ILE:HD13	8:AE:199:ALA:HB2	1.98	0.44
23:AU:87:THR:HG23	23:AU:102:VAL:HG21	1.99	0.44
47:2:641:A:O2'	47:2:645:C:OP1	2.34	0.44
48:B:155:HIS:HD2	69:W:61:ARG:HA	1.81	0.44
1:5:152:U:OP2	16:AN:49:ARG:NH2	2.45	0.44
1:5:3641:U:H5	1:5:3646:A:N7	2.16	0.44
1:5:4770:U:H3	1:5:4864:U:H3	1.65	0.44
4:AA:181:LYS:HB2	4:AA:181:LYS:HE3	1.77	0.44
20:AR:177:LEU:HA	20:AR:180:LYS:HB2	1.98	0.44
21:AS:50:GLU:HG2	21:AS:51:LEU:HD23	2.00	0.44
47:2:531:A:H2'	47:2:531:A:N3	2.31	0.44
48:B:8:LEU:HD21	48:B:191:ARG:NH1	2.32	0.44
56:J:205:ARG:H	56:J:205:ARG:HG3	1.55	0.44
57:K:127:ARG:HD2	78:f:104:ARG:NE	2.33	0.44
57:K:137:VAL:HG22	57:K:157:ILE:HG22	1.98	0.44
64:R:116:ASP:HB3	64:R:119:LEU:HD23	1.98	0.44
1:5:936:C:OP1	1:5:936:C:H2'	2.18	0.44
21:AS:161:ARG:HG2	21:AS:164:LYS:HB2	2.00	0.44
58:L:28:HIS:HB3	77:e:8:TRP:CD1	2.52	0.44
82:1:6433:C:H2'	82:1:6434:C:O4'	2.17	0.44
1:5:5041:G:N3	1:5:5041:G:H3'	2.33	0.44
4:AA:196:TRP:O	4:AA:198:ARG:N	2.51	0.44
6:AC:134:PRO:HB3	6:AC:150:LEU:CG	2.47	0.44
6:AC:284:MET:HE2	6:AC:287:THR:HA	2.00	0.44
21:AS:17:LEU:HD11	21:AS:58:SER:HA	2.00	0.44
22:AT:46:GLY:O	22:AT:49:GLN:NE2	2.50	0.44
35:Ag:102:ILE:HA	35:Ag:105:LYS:HG2	2.00	0.44
45:Ar:69:GLY:HA3	45:Ar:72:LYS:HD2	2.00	0.44
82:1:6434:C:H4'	82:1:6434:C:OP1	2.17	0.44
1:5:752:G:OP1	1:5:915:C:N4	2.50	0.44
5:AB:378:ARG:HG2	25:AW:32:LEU:HD21	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AM:13:ALA:HA	15:AM:57:LEU:HA	2.00	0.44
62:P:45:THR:HA	62:P:52:THR:HA	1.99	0.44
14:AL:116:ARG:NH1	14:AL:155:MET:O	2.51	0.44
16:AN:45:PRO:O	16:AN:49:ARG:HG2	2.17	0.44
50:D:141:LEU:O	50:D:141:LEU:HG	2.17	0.44
50:D:200:ARG:O	57:K:54:ARG:NH1	2.49	0.44
58:L:80:ARG:HD3	58:L:87:PRO:HB3	1.98	0.44
79:g:122:PRO:HD2	79:g:132:MET:HE1	2.00	0.44
1:5:982:U:H2'	1:5:983:C:C6	2.53	0.44
1:5:984:U:C5	8:AE:73:ARG:HD2	2.52	0.44
1:5:1633:G:H5'	1:5:1634:A:OP1	2.18	0.44
1:5:3770:U:H2'	1:5:3771:C:H6	1.82	0.44
1:5:4572:U:H2'	1:5:4573:G:C8	2.53	0.44
10:AG:212:HIS:ND1	10:AG:238:LYS:HA	2.33	0.44
47:2:64:A:N3	47:2:64:A:H2'	2.33	0.44
47:2:955:A:N3	47:2:956:G:H1'	2.33	0.44
47:2:1462:U:O2	47:2:1462:U:O4'	2.36	0.44
63:Q:56:LEU:HD22	63:Q:78:THR:HG23	2.00	0.44
68:V:91:LEU:HD22	68:V:98:VAL:HG11	1.99	0.44
1:5:935:G:OP2	1:5:935:G:H3'	2.18	0.43
1:5:1282:G:N3	1:5:1282:G:C3'	2.80	0.43
1:5:1413:C:H2'	1:5:1414:C:C6	2.53	0.43
1:5:2517:A:N3	1:5:2539:C:O2'	2.50	0.43
6:AC:204:ARG:NH1	6:AC:205:ARG:O	2.51	0.43
7:AD:65:ALA:HB2	7:AD:74:ILE:HD13	2.00	0.43
46:AK:29:LEU:O	46:AK:29:LEU:HG	2.18	0.43
46:AK:128:LEU:HG	46:AK:135:PRO:HD3	2.00	0.43
47:2:183:G:N3	47:2:183:G:O2'	2.51	0.43
47:2:953:C:O2	62:P:55:ARG:NH1	2.50	0.43
1:5:976:C:O2	6:AC:327:LYS:NZ	2.51	0.43
1:5:2633:U:O4	23:AU:81:ARG:NH2	2.51	0.43
8:AE:261:LEU:N	8:AE:262:PRO:HD2	2.33	0.43
15:AM:35:ARG:HH11	15:AM:35:ARG:CB	2.31	0.43
47:2:885:U:H3	47:2:901:G:H1	1.67	0.43
47:2:1624:U:O2	47:2:1624:U:O4'	2.35	0.43
76:d:14:VAL:HG13	76:d:30:VAL:HG13	2.00	0.43
81:Aq:11:ASN:HA	81:Aq:14:ILE:HB	2.00	0.43
1:5:2001:G:N2	1:5:2017:A:N7	2.66	0.43
1:5:2555:G:H8	1:5:2555:G:H5''	1.83	0.43
1:5:4530:U:O2'	81:Aq:183:GLY:HA2	2.18	0.43
4:AA:137:ILE:HD11	4:AA:155:LYS:HG2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AG:157:PRO:HG3	10:AG:247:VAL:HG12	2.00	0.43
32:Ad:22:THR:HG22	32:Ad:89:SER:HA	2.01	0.43
55:I:53:VAL:HG23	55:I:175:GLY:HA3	1.99	0.43
82:1:6472:G:N3	82:1:6472:G:C2'	2.81	0.43
1:5:1301:C:H2'	33:Ae:17:THR:HG21	2.00	0.43
1:5:4098:A:H2'	1:5:4098:A:N3	2.33	0.43
21:AS:13:VAL:HG23	21:AS:62:VAL:HB	2.00	0.43
46:AK:58:THR:N	46:AK:59:PRO:HD3	2.33	0.43
47:2:1152:U:O2'	70:X:16:ASN:ND2	2.51	0.43
48:B:65:ILE:HD12	48:B:178:LEU:HD21	2.01	0.43
48:B:76:VAL:HG12	48:B:123:VAL:HB	2.00	0.43
63:Q:111:MET:HG2	63:Q:119:PHE:CE1	2.54	0.43
76:d:14:VAL:HG22	76:d:30:VAL:HG11	1.99	0.43
81:Aq:252:LYS:HG3	81:Aq:254:VAL:HG22	2.00	0.43
82:1:6473:C:H2'	82:1:6474:U:H5''	2.01	0.43
1:5:924:C:O2	1:5:924:C:H2'	2.17	0.43
11:AH:48:LEU:HD11	11:AH:56:ARG:HD2	2.00	0.43
21:AS:45:TRP:O	21:AS:49:LEU:HB2	2.18	0.43
47:2:501:C:O2	47:2:501:C:H2'	2.17	0.43
54:H:230:LYS:HA	54:H:233:ARG:HB3	2.01	0.43
1:5:907:G:H5''	21:AS:149:ARG:HH21	1.82	0.43
7:AD:120:GLU:O	7:AD:248:ARG:NH2	2.52	0.43
69:W:32:ILE:CG1	69:W:60:ARG:HD2	2.49	0.43
6:AC:150:LEU:HD22	6:AC:150:LEU:HA	1.74	0.43
16:AN:116:LEU:HD22	16:AN:135:ILE:HD11	2.01	0.43
36:Ah:91:MET:HE1	38:Aj:78:PHE:CD2	2.54	0.43
57:K:100:LEU:HD12	57:K:100:LEU:HA	1.93	0.43
67:U:107:LEU:HD22	67:U:112:MET:HB2	2.01	0.43
82:1:6471:G:H3'	82:1:6472:G:H5''	2.00	0.43
1:5:194:C:O2	27:AY:121:ARG:NH1	2.52	0.43
1:5:1381:U:O2	1:5:1381:U:O4'	2.33	0.43
1:5:2008:U:H3'	1:5:2008:U:O2	2.18	0.43
1:5:2262:G:OP2	45:Ar:98:ARG:NH2	2.52	0.43
1:5:3760:A:C2	47:2:1825:A:O2'	2.69	0.43
1:5:3954:A:H3'	1:5:3955:G:H8	1.84	0.43
1:5:3968:U:H2'	1:5:3969:G:C8	2.54	0.43
3:8:141:C:H5'	16:AN:113:LEU:HD11	2.00	0.43
5:AB:113:GLU:HA	5:AB:116:ARG:HD2	1.99	0.43
47:2:993:G:O6	74:b:15:ARG:HG2	2.18	0.43
56:J:205:ARG:HD3	56:J:206:LYS:HG3	1.99	0.43
81:Aq:54:ASP:HA	82:1:6565:G:H4'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:1850:A:N3	1:5:2283:G:O2'	2.52	0.43
6:AC:151:PRO:O	6:AC:152:LEU:C	2.60	0.43
12:AI:61:SER:HA	12:AI:126:VAL:HG23	2.00	0.43
23:AU:83:LEU:HD13	23:AU:83:LEU:HA	1.77	0.43
47:2:1290:G:OP2	79:g:95:ARG:NH1	2.52	0.43
47:2:1566:G:OP2	67:U:102:ARG:NH1	2.52	0.43
1:5:1287:G:O2'	1:5:1288:G:OP1	2.30	0.43
1:5:1895:G:O2'	1:5:1907:A:N3	2.48	0.43
1:5:2547:G:N2	1:5:2772:C:O2	2.44	0.43
12:AI:38:ARG:NH2	12:AI:45:GLU:OE1	2.52	0.43
80:h:172:LYS:HA	80:h:195:LEU:HD13	2.01	0.43
1:5:303:C:OP2	16:AN:68:ARG:NH2	2.52	0.42
1:5:3612:C:H1'	1:5:5016:A:H8	1.84	0.42
1:5:4903:G:C6	1:5:4919:G:C2	3.07	0.42
12:AI:139:ARG:HD3	12:AI:173:PHE:CD2	2.54	0.42
47:2:64:A:N3	47:2:64:A:C2'	2.82	0.42
47:2:1270:G:O2'	47:2:1301:A:N7	2.51	0.42
58:L:7:ASN:HD21	58:L:40:VAL:HG23	1.83	0.42
75:c:40:CYS:SG	75:c:41:TYR:N	2.91	0.42
80:h:31:ILE:HD11	80:h:299:PHE:CE2	2.54	0.42
1:5:372:A:N1	1:5:1644:C:O2'	2.37	0.42
1:5:2465:C:H2'	1:5:2466:G:O4'	2.19	0.42
4:AA:177:LYS:HB3	44:Ap:69:TRP:CZ2	2.54	0.42
6:AC:123:ALA:HB1	6:AC:237:ILE:HD12	2.01	0.42
47:2:191:A:H2'	47:2:192:C:OP1	2.19	0.42
47:2:752:G:N2	47:2:792:C:O2	2.52	0.42
47:2:1260:A:HO2'	47:2:1261:C:C5'	2.31	0.42
50:D:199:PRO:HG3	57:K:58:ARG:HD3	2.01	0.42
58:L:80:ARG:HA	58:L:83:LEU:HB3	2.01	0.42
81:Aq:298:THR:HG22	81:Aq:300:LYS:HD3	2.01	0.42
1:5:981:C:O5'	1:5:981:C:H6	2.02	0.42
1:5:1755:C:O2	1:5:1756:U:C2	2.72	0.42
1:5:3901:A:H8	1:5:4518:A:N1	2.18	0.42
19:AQ:61:LEU:HB3	19:AQ:86:ILE:HD13	2.00	0.42
19:AQ:67:ILE:HD12	19:AQ:96:PRO:HD2	2.01	0.42
29:Aa:103:VAL:HG12	29:Aa:108:TYR:HB2	2.01	0.42
46:AK:34:LEU:HB2	46:AK:169:VAL:HG13	2.01	0.42
54:H:50:VAL:HA	54:H:113:ILE:HA	2.02	0.42
68:V:90:ASP:N	68:V:90:ASP:OD1	2.52	0.42
19:AQ:115:LYS:HA	19:AQ:115:LYS:HD3	1.66	0.42
23:AU:20:LYS:HA	23:AU:72:VAL:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Aa:148:ALA:HB2	37:Ai:6:PRO:HB2	2.01	0.42
45:Ar:32:LEU:O	45:Ar:33:LYS:HB2	2.20	0.42
46:AK:23:ARG:HB3	46:AK:211:GLY:HA3	2.01	0.42
46:AK:128:LEU:HD13	46:AK:128:LEU:HA	1.81	0.42
47:2:1463:U:H1'	47:2:1464:C:C6	2.55	0.42
47:2:1869:A:N6	49:C:114:VAL:O	2.53	0.42
56:J:31:ARG:HB2	56:J:56:ARG:HH22	1.85	0.42
79:g:138:ARG:HB2	79:g:148:TYR:HB2	2.01	0.42
80:h:29:ASP:OD1	80:h:47:ARG:NH2	2.52	0.42
1:5:2521:G:O2'	35:Ag:26:PRO:HG2	2.20	0.42
5:AB:86:VAL:HG13	5:AB:162:VAL:HG22	2.01	0.42
49:C:25:PHE:CD1	62:P:88:LEU:HD21	2.54	0.42
1:5:2502:A:H4'	1:5:2503:G:OP1	2.20	0.42
1:5:4376:A:O2'	29:Aa:42:ARG:NH1	2.53	0.42
11:AH:23:ARG:HA	11:AH:45:LEU:HD12	2.02	0.42
46:AK:54:ARG:HG3	46:AK:154:THR:HG22	2.02	0.42
47:2:1535:U:O2	47:2:1535:U:C2'	2.67	0.42
47:2:1645:C:H4'	64:R:138:ARG:O	2.19	0.42
47:2:1825:A:C8	82:1:6619:G:C6	3.08	0.42
48:B:156:TYR:CE1	69:W:61:ARG:HB3	2.54	0.42
52:F:246:LEU:HD11	52:F:254:LYS:HD2	2.01	0.42
63:Q:119:PHE:CE1	66:T:119:ALA:HB2	2.55	0.42
33:Ae:66:THR:HA	33:Ae:69:MET:HE3	2.00	0.42
38:Aj:2:THR:O	38:Aj:7:SER:OG	2.38	0.42
46:AK:170:GLY:HA3	46:AK:179:LEU:HD11	2.02	0.42
46:AK:192:SER:OG	46:AK:193:LEU:N	2.53	0.42
47:2:1700:C:C2	47:2:1834:A:N6	2.88	0.42
81:Aq:314:MET:HG2	81:Aq:315:GLY:H	1.85	0.42
1:5:934:A:O2'	1:5:935:G:H3'	2.20	0.42
1:5:2006:U:O2	1:5:2006:U:H2'	2.18	0.42
1:5:4770:U:H2'	1:5:4771:C:O2	2.19	0.42
3:8:69:U:C4	3:8:70:G:C6	3.07	0.42
6:AC:134:PRO:HB3	6:AC:150:LEU:HD21	2.00	0.42
10:AG:139:VAL:HG11	10:AG:238:LYS:HG3	2.00	0.42
46:AK:61:PRO:HD2	46:AK:151:VAL:O	2.20	0.42
52:F:15:PRO:HG2	52:F:18:TRP:CE2	2.55	0.42
52:F:80:ILE:HG13	52:F:81:THR:HG23	2.02	0.42
1:5:4549:G:H5'	81:Aq:180:HIS:NE2	2.35	0.42
1:5:4633:G:N2	1:5:4664:A:N7	2.68	0.42
26:AX:91:GLU:HG2	26:AX:147:LEU:HD13	2.00	0.42
47:2:217:A:C2'	47:2:218:U:OP1	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:1617:G:N1	47:2:1620:A:OP2	2.52	0.42
47:2:1745:A:N6	47:2:1789:G:O2'	2.53	0.42
1:5:441:G:C2	1:5:1307:A:C2	3.08	0.42
1:5:1381:U:H2'	1:5:1382:G:O4'	2.20	0.42
1:5:2407:G:H2'	40:Al:13:LEU:HD22	2.02	0.42
1:5:3648:A:H1'	1:5:3785:A:N6	2.35	0.42
1:5:3789:C:O3'	81:Aq:153:GLY:HA3	2.19	0.42
1:5:4076:G:H4'	1:5:4077:A:OP1	2.20	0.42
47:2:876:C:H2'	47:2:877:C:O4'	2.20	0.42
1:5:108:A:H4'	1:5:109:G:OP1	2.20	0.41
1:5:981:C:H4'	8:AE:45:HIS:O	2.20	0.41
1:5:1353:G:O6	19:AQ:85:THR:HG21	2.19	0.41
1:5:3973:G:H2'	1:5:3974:G:C4	2.55	0.41
1:5:4896:G:H2'	1:5:4897:G:H8	1.84	0.41
16:AN:110:CYS:HB3	16:AN:113:LEU:HD12	2.02	0.41
47:2:126:G:N2	47:2:180:G:O2'	2.52	0.41
47:2:1513:C:H2'	47:2:1514:G:C8	2.55	0.41
52:F:181:CYS:HB3	52:F:195:ILE:HD11	2.01	0.41
64:R:55:VAL:O	64:R:59:GLY:N	2.52	0.41
81:Aq:354:LYS:HE3	81:Aq:356:HIS:HB3	2.01	0.41
1:5:156:G:N2	1:5:157:U:O4	2.53	0.41
1:5:2848:G:O2'	1:5:3838:U:O4	2.33	0.41
1:5:3700:C:O2'	1:5:3774:A:N3	2.49	0.41
1:5:4760:G:H2'	1:5:4761:G:O4'	2.20	0.41
4:AA:156:LYS:HD2	4:AA:158:ILE:CG2	2.50	0.41
20:AR:154:LEU:HD23	20:AR:154:LEU:HA	1.95	0.41
45:Ar:90:LEU:HG	45:Ar:111:ILE:HG23	2.02	0.41
46:AK:67:VAL:HG22	46:AK:82:ILE:HD12	2.01	0.41
47:2:1075:C:OP1	61:O:107:LYS:NZ	2.53	0.41
53:G:39:ILE:HA	53:G:68:ILE:HD11	2.02	0.41
54:H:181:THR:HG22	54:H:182:PRO:HD2	2.01	0.41
81:Aq:309:LEU:HD13	81:Aq:312:LEU:HB3	2.02	0.41
82:1:6472:G:N3	82:1:6472:G:O2'	2.47	0.41
1:5:975:G:H2'	1:5:976:C:C6	2.55	0.41
1:5:3629:A:H2'	1:5:3630:A:O4'	2.20	0.41
6:AC:152:LEU:HD22	6:AC:152:LEU:HA	1.76	0.41
7:AD:118:ILE:HD13	7:AD:138:GLN:HE21	1.85	0.41
16:AN:145:ASN:HD22	16:AN:148:THR:HG22	1.86	0.41
19:AQ:86:ILE:HD13	19:AQ:86:ILE:HA	1.95	0.41
47:2:126:G:H2'	54:H:199:THR:HG21	2.02	0.41
47:2:420:G:O2'	47:2:660:C:N3	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:441:C:OP2	56:J:2:GLY:N	2.54	0.41
47:2:1834:A:H2	47:2:1837:G:H1	1.68	0.41
68:V:25:THR:HG22	68:V:86:LYS:HG3	2.01	0.41
81:Aq:286:LEU:HD11	81:Aq:390:GLU:OE1	2.20	0.41
1:5:3711:A:C5	1:5:3712:A:H2	2.38	0.41
1:5:4530:U:H2'	1:5:4531:U:H2'	2.02	0.41
4:AA:62:VAL:HG13	4:AA:71:LYS:HG2	2.02	0.41
6:AC:286:ASN:H	19:AQ:124:HIS:CE1	2.39	0.41
14:AL:47:ALA:O	14:AL:149:GLN:NE2	2.54	0.41
51:E:62:LYS:O	51:E:67:ARG:NH1	2.54	0.41
1:5:2639:U:O2	35:Ag:26:PRO:HB3	2.20	0.41
1:5:2664:G:H4'	1:5:2677:G:H4'	2.01	0.41
1:5:2896:G:C5'	20:AR:134:ASN:HD22	2.33	0.41
1:5:4419:U:OP1	1:5:4421:C:N4	2.53	0.41
11:AH:20:LEU:HD12	11:AH:47:LEU:HB2	2.02	0.41
23:AU:36:GLU:HB3	23:AU:70:ILE:HD11	2.02	0.41
24:AV:27:ASN:HD21	24:AV:100:ASP:HB2	1.85	0.41
47:2:1617:G:O6	63:Q:43:ARG:NH1	2.54	0.41
53:G:99:ILE:HG23	73:a:67:LEU:HD11	2.02	0.41
1:5:1311:G:H2'	1:5:1312:A:O4'	2.21	0.41
1:5:4423:U:O2	1:5:4423:U:O4'	2.38	0.41
10:AG:119:GLN:HA	10:AG:122:ILE:HB	2.02	0.41
13:AJ:112:HIS:HB3	13:AJ:126:TYR:O	2.21	0.41
19:AQ:61:LEU:HD23	19:AQ:86:ILE:CD1	2.43	0.41
20:AR:44:LEU:HD23	20:AR:44:LEU:HA	1.90	0.41
46:AK:73:HIS:HB2	46:AK:82:ILE:HD13	2.02	0.41
52:F:261:SER:C	52:F:263:GLY:H	2.27	0.41
57:K:125:HIS:NE2	57:K:129:LEU:HD13	2.35	0.41
60:N:93:LYS:HG3	60:N:103:VAL:HG21	2.01	0.41
73:a:58:LEU:HA	73:a:62:VAL:HG23	2.02	0.41
1:5:2566:G:H2'	1:5:2567:G:H8	1.85	0.41
1:5:4128:A:O2'	10:AG:86:GLU:O	2.34	0.41
1:5:5041:G:N1	5:AB:389:MET:O	2.53	0.41
31:Ac:29:LEU:HD22	31:Ac:91:VAL:HG11	2.02	0.41
46:AK:82:ILE:HG12	46:AK:84:HIS:HB2	2.02	0.41
47:2:508:A:H3'	47:2:509:G:H8	1.86	0.41
47:2:538:U:O4	47:2:546:G:N2	2.54	0.41
48:B:50:ASN:HA	65:S:105:MET:HE1	2.03	0.41
54:H:1:MET:HE3	54:H:106:LEU:HB2	2.03	0.41
78:f:112:ASN:HA	78:f:116:VAL:HG22	2.01	0.41
1:5:226:G:N7	6:AC:184:TYR:OH	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:1362:G:OP1	14:AL:39:ARG:NH2	2.47	0.41
6:AC:358:LEU:HA	6:AC:361:LYS:CE	2.46	0.41
9:AF:49:ILE:HD12	9:AF:185:CYS:HB3	2.02	0.41
21:AS:136:ARG:HD2	21:AS:136:ARG:HA	1.88	0.41
66:T:39:ARG:NH1	67:U:36:THR:O	2.53	0.41
1:5:1305:C:OP1	3:8:7:U:O2'	2.39	0.41
1:5:4342:C:O3'	43:Ao:37:GLY:HA3	2.21	0.41
20:AR:166:THR:HB	47:2:873:G:OP2	2.21	0.41
21:AS:154:LEU:HD13	21:AS:157:ARG:HH22	1.85	0.41
27:AY:55:VAL:HG21	27:AY:104:VAL:HG13	2.03	0.41
32:Ad:36:VAL:HG23	32:Ad:41:ARG:HG2	2.03	0.41
46:AK:111:LEU:HA	46:AK:137:LEU:CD2	2.51	0.41
50:D:196:ILE:HB	50:D:223:TYR:HB2	2.01	0.41
82:1:6544:G:C2	82:1:6545:G:C6	3.09	0.41
1:5:1802:A:O2'	1:5:1837:A:OP1	2.38	0.41
1:5:2052:G:O2'	1:5:2057:A:N1	2.46	0.41
1:5:3707:U:H2'	1:5:3708:C:C6	2.56	0.41
1:5:3710:G:N2	1:5:3711:A:C6	2.89	0.41
1:5:3759:A:N3	1:5:3759:A:H2'	2.36	0.41
2:7:6:C:O2'	7:AD:72:ASP:OD2	2.32	0.41
4:AA:10:LYS:HG2	4:AA:16:PHE:CD1	2.56	0.41
6:AC:11:TYR:CZ	6:AC:148:PRO:HB2	2.56	0.41
47:2:146:G:OP1	54:H:143:LYS:NZ	2.53	0.41
47:2:526:A:O2'	57:K:125:HIS:ND1	2.54	0.41
47:2:1351:G:O2'	47:2:1378:A:N1	2.44	0.41
47:2:1859:A:OP2	74:b:10:ARG:NH2	2.52	0.41
12:AI:43:VAL:HG11	12:AI:197:VAL:HG23	2.03	0.40
16:AN:155:VAL:O	16:AN:162:ARG:NH2	2.51	0.40
42:An:2:ARG:HD3	47:2:1841:C:H5''	2.03	0.40
46:AK:111:LEU:HA	46:AK:137:LEU:HD21	2.03	0.40
47:2:293:C:O2	47:2:293:C:H2'	2.21	0.40
47:2:687:C:O2	47:2:687:C:C2'	2.67	0.40
47:2:1138:C:H5'	47:2:1138:C:C6	2.56	0.40
69:W:51:LYS:HD2	69:W:76:HIS:CE1	2.56	0.40
1:5:4770:U:H6	1:5:4770:U:H5''	1.86	0.40
10:AG:148:LEU:HA	10:AG:271:LEU:HD21	2.04	0.40
16:AN:6:TYR:HA	37:AI:44:ILE:HD11	2.03	0.40
46:AK:33:GLU:HA	46:AK:168:ALA:HA	2.03	0.40
47:2:3:C:O2	57:K:18:ARG:NH2	2.55	0.40
50:D:204:ILE:HD13	50:D:215:LEU:HG	2.03	0.40
58:L:32:HIS:HB3	58:L:35:LEU:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2638:G:N2	1:5:2718:U:H2'	2.36	0.40
3:8:111:U:O2	3:8:111:U:O4'	2.37	0.40
4:AA:196:TRP:HB3	4:AA:197:PRO:HD3	2.03	0.40
33:Ae:35:TRP:CZ2	33:Ae:56:PRO:HD2	2.57	0.40
47:2:958:G:H8	47:2:958:G:O5'	2.04	0.40
51:E:96:LEU:HD21	51:E:191:PRO:HD2	2.02	0.40
77:e:17:GLY:O	77:e:27:ARG:NH2	2.54	0.40
80:h:87:LEU:HB2	80:h:101:PHE:HB2	2.02	0.40
81:Aq:188:LEU:HD12	81:Aq:188:LEU:HA	1.76	0.40
1:5:738:C:H2'	1:5:738:C:O2	2.21	0.40
4:AA:201:GLY:HA3	4:AA:209:HIS:CE1	2.56	0.40
8:AE:70:LEU:HA	8:AE:73:ARG:HB2	2.02	0.40
23:Au:84:LYS:HB2	23:Au:110:TYR:CZ	2.57	0.40
41:Am:83:ASN:ND2	41:Am:91:HIS:O	2.54	0.40
47:2:1100:A:O5'	65:S:132:ARG:NH2	2.54	0.40
1:5:4992:G:H2'	1:5:4993:G:C8	2.56	0.40
8:AE:64:MET:HG3	8:AE:68:LYS:HE2	2.03	0.40
22:AT:40:VAL:CG1	22:AT:96:ILE:HD12	2.51	0.40
47:2:168:C:O2'	54:H:133:LEU:O	2.38	0.40
47:2:1624:U:H2'	47:2:1625:U:O4'	2.21	0.40
55:I:23:ILE:HG12	55:I:60:ILE:HD11	2.03	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	
4	AA	246/257 (96%)	222 (90%)	24 (10%)	0	100	100
5	AB	392/402 (98%)	372 (95%)	18 (5%)	2 (0%)	24	59
6	AC	360/392 (92%)	329 (91%)	28 (8%)	3 (1%)	16	50
7	AD	291/297 (98%)	272 (94%)	18 (6%)	1 (0%)	36	68

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	AE	208/291 (72%)	187 (90%)	20 (10%)	1 (0%)	24	59
9	AF	223/249 (90%)	210 (94%)	11 (5%)	2 (1%)	14	47
10	AG	221/242 (91%)	208 (94%)	13 (6%)	0	100	100
11	AH	188/192 (98%)	176 (94%)	12 (6%)	0	100	100
12	AI	201/214 (94%)	181 (90%)	20 (10%)	0	100	100
13	AJ	168/178 (94%)	160 (95%)	7 (4%)	1 (1%)	21	56
14	AL	199/211 (94%)	191 (96%)	7 (4%)	1 (0%)	24	59
15	AM	136/198 (69%)	122 (90%)	13 (10%)	1 (1%)	18	52
16	AN	201/204 (98%)	194 (96%)	6 (3%)	1 (0%)	24	59
17	AO	197/203 (97%)	191 (97%)	5 (2%)	1 (0%)	24	59
18	AP	151/184 (82%)	140 (93%)	11 (7%)	0	100	100
19	AQ	185/188 (98%)	170 (92%)	14 (8%)	1 (0%)	24	59
20	AR	178/196 (91%)	171 (96%)	6 (3%)	1 (1%)	21	56
21	AS	174/176 (99%)	159 (91%)	13 (8%)	2 (1%)	11	43
22	AT	157/160 (98%)	145 (92%)	9 (6%)	3 (2%)	6	33
23	AU	97/128 (76%)	90 (93%)	7 (7%)	0	100	100
24	AV	127/140 (91%)	122 (96%)	5 (4%)	0	100	100
25	AW	61/157 (39%)	57 (93%)	4 (7%)	0	100	100
26	AX	116/156 (74%)	111 (96%)	5 (4%)	0	100	100
27	AY	132/145 (91%)	125 (95%)	7 (5%)	0	100	100
28	AZ	133/136 (98%)	125 (94%)	8 (6%)	0	100	100
29	Aa	145/148 (98%)	135 (93%)	10 (7%)	0	100	100
30	Ab	100/226 (44%)	92 (92%)	6 (6%)	2 (2%)	6	31
31	Ac	96/115 (84%)	91 (95%)	5 (5%)	0	100	100
32	Ad	105/125 (84%)	96 (91%)	7 (7%)	2 (2%)	6	33
33	Ae	126/135 (93%)	118 (94%)	8 (6%)	0	100	100
34	Af	107/110 (97%)	95 (89%)	11 (10%)	1 (1%)	14	47
35	Ag	112/126 (89%)	108 (96%)	4 (4%)	0	100	100
36	Ah	120/123 (98%)	119 (99%)	0	1 (1%)	16	50
37	Ai	100/105 (95%)	94 (94%)	6 (6%)	0	100	100
38	Aj	84/97 (87%)	77 (92%)	6 (7%)	1 (1%)	10	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	Ak	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
40	Al	48/51 (94%)	43 (90%)	5 (10%)	0	100	100
41	Am	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
42	An	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
43	Ao	102/106 (96%)	95 (93%)	7 (7%)	0	100	100
44	Ap	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
45	Ar	122/137 (89%)	112 (92%)	9 (7%)	1 (1%)	16	50
46	AK	210/217 (97%)	149 (71%)	53 (25%)	8 (4%)	2	18
48	B	215/295 (73%)	194 (90%)	21 (10%)	0	100	100
49	C	211/264 (80%)	192 (91%)	19 (9%)	0	100	100
50	D	219/255 (86%)	208 (95%)	11 (5%)	0	100	100
51	E	226/281 (80%)	204 (90%)	22 (10%)	0	100	100
52	F	260/263 (99%)	237 (91%)	23 (9%)	0	100	100
53	G	181/204 (89%)	167 (92%)	14 (8%)	0	100	100
54	H	235/249 (94%)	213 (91%)	20 (8%)	2 (1%)	14	47
55	I	181/194 (93%)	167 (92%)	13 (7%)	1 (1%)	21	56
56	J	204/207 (99%)	184 (90%)	18 (9%)	2 (1%)	12	45
57	K	183/194 (94%)	169 (92%)	14 (8%)	0	100	100
58	L	94/149 (63%)	83 (88%)	11 (12%)	0	100	100
59	M	139/158 (88%)	126 (91%)	12 (9%)	1 (1%)	18	52
60	N	115/132 (87%)	91 (79%)	24 (21%)	0	100	100
61	O	147/151 (97%)	138 (94%)	9 (6%)	0	100	100
62	P	134/151 (89%)	117 (87%)	16 (12%)	1 (1%)	18	52
63	Q	117/145 (81%)	100 (86%)	12 (10%)	5 (4%)	2	16
64	R	140/172 (81%)	128 (91%)	11 (8%)	1 (1%)	18	52
65	S	130/135 (96%)	112 (86%)	16 (12%)	2 (2%)	8	37
66	T	142/152 (93%)	124 (87%)	16 (11%)	2 (1%)	9	39
67	U	139/145 (96%)	127 (91%)	11 (8%)	1 (1%)	18	52
68	V	98/119 (82%)	91 (93%)	7 (7%)	0	100	100
69	W	81/83 (98%)	75 (93%)	6 (7%)	0	100	100
70	X	127/130 (98%)	118 (93%)	9 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
71	Y	139/143 (97%)	127 (91%)	8 (6%)	4 (3%)	3	24
72	Z	122/134 (91%)	112 (92%)	9 (7%)	1 (1%)	16	50
73	a	73/125 (58%)	69 (94%)	4 (6%)	0	100	100
74	b	96/115 (84%)	86 (90%)	10 (10%)	0	100	100
75	c	81/84 (96%)	74 (91%)	7 (9%)	0	100	100
76	d	60/69 (87%)	55 (92%)	5 (8%)	0	100	100
77	e	53/56 (95%)	47 (89%)	6 (11%)	0	100	100
78	f	54/133 (41%)	47 (87%)	7 (13%)	0	100	100
79	g	66/156 (42%)	56 (85%)	10 (15%)	0	100	100
80	h	311/317 (98%)	263 (85%)	46 (15%)	2 (1%)	21	56
81	Aq	414/437 (95%)	359 (87%)	50 (12%)	5 (1%)	10	42
All	All	11735/13353 (88%)	10732 (92%)	936 (8%)	67 (1%)	23	56

All (67) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
45	Ar	68	SER
46	AK	152	LYS
56	J	206	LYS
6	AC	126	SER
13	AJ	147	ARG
19	AQ	178	ARG
20	AR	153	LYS
22	AT	5	LYS
46	AK	19	HIS
46	AK	140	HIS
54	H	178	ARG
54	H	179	LEU
63	Q	48	GLY
63	Q	57	LEU
65	S	68	GLY
81	Aq	104	GLU
81	Aq	357	PHE
6	AC	187	GLN
7	AD	44	TYR
8	AE	189	LEU
9	AF	196	VAL
32	Ad	58	GLY

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Mol	Chain	Res	Type
46	AK	127	GLY
56	J	123	ARG
62	P	137	SER
63	Q	52	LYS
67	U	86	GLY
71	Y	61	GLN
80	h	13	GLY
9	AF	24	PHE
17	AO	16	LEU
21	AS	155	PRO
22	AT	80	VAL
38	Aj	38	GLY
46	AK	84	HIS
46	AK	115	SER
46	AK	173	LYS
63	Q	49	LEU
65	S	88	VAL
71	Y	86	PRO
80	h	216	ALA
6	AC	99	GLY
22	AT	81	LYS
30	Ab	25	ARG
32	Ad	56	GLU
36	Ah	40	ALA
63	Q	56	LEU
71	Y	60	LYS
81	Aq	314	MET
81	Aq	370	GLU
14	AL	63	THR
34	Af	107	PRO
66	T	100	ALA
71	Y	62	PRO
21	AS	165	PRO
30	Ab	102	PRO
55	I	54	GLY
59	M	43	GLY
66	T	74	PRO
72	Z	119	GLY
5	AB	37	PRO
16	AN	84	PRO
5	AB	18	PRO
15	AM	19	PRO

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Mol	Chain	Res	Type
46	AK	213	PRO
64	R	135	PRO
81	Aq	118	LYS

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	
4	AA	189/199 (95%)	179 (95%)	10 (5%)	20	53
5	AB	342/347 (99%)	335 (98%)	7 (2%)	48	72
6	AC	302/323 (94%)	282 (93%)	20 (7%)	15	47
7	AD	247/250 (99%)	245 (99%)	2 (1%)	73	82
8	AE	190/251 (76%)	187 (98%)	3 (2%)	55	75
9	AF	196/218 (90%)	196 (100%)	0	100	100
10	AG	194/208 (93%)	191 (98%)	3 (2%)	57	76
11	AH	169/171 (99%)	165 (98%)	4 (2%)	43	70
12	AI	175/181 (97%)	171 (98%)	4 (2%)	44	70
13	AJ	143/149 (96%)	139 (97%)	4 (3%)	38	68
14	AL	167/176 (95%)	160 (96%)	7 (4%)	26	60
15	AM	117/151 (78%)	110 (94%)	7 (6%)	17	50
16	AN	171/172 (99%)	168 (98%)	3 (2%)	51	74
17	AO	171/173 (99%)	164 (96%)	7 (4%)	27	60
18	AP	134/163 (82%)	132 (98%)	2 (2%)	57	76
19	AQ	166/167 (99%)	155 (93%)	11 (7%)	15	47
20	AR	159/175 (91%)	152 (96%)	7 (4%)	25	59
21	AS	155/155 (100%)	147 (95%)	8 (5%)	21	54
22	AT	139/140 (99%)	137 (99%)	2 (1%)	59	77
23	AU	91/116 (78%)	81 (89%)	10 (11%)	6	26
24	AV	100/107 (94%)	99 (99%)	1 (1%)	68	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	AW	55/126 (44%)	55 (100%)	0	100	100
26	AX	106/134 (79%)	105 (99%)	1 (1%)	70	81
27	AY	124/135 (92%)	121 (98%)	3 (2%)	43	70
28	AZ	117/118 (99%)	117 (100%)	0	100	100
29	Aa	119/120 (99%)	117 (98%)	2 (2%)	53	75
30	Ab	84/172 (49%)	83 (99%)	1 (1%)	63	79
31	Ac	84/98 (86%)	82 (98%)	2 (2%)	43	70
32	Ad	98/110 (89%)	98 (100%)	0	100	100
33	Ae	114/121 (94%)	111 (97%)	3 (3%)	40	69
34	Af	88/89 (99%)	86 (98%)	2 (2%)	44	70
35	Ag	98/106 (92%)	97 (99%)	1 (1%)	68	80
36	Ah	109/110 (99%)	109 (100%)	0	100	100
37	Ai	86/89 (97%)	86 (100%)	0	100	100
38	Aj	73/80 (91%)	71 (97%)	2 (3%)	39	68
39	Ak	64/65 (98%)	62 (97%)	2 (3%)	35	66
40	Al	47/48 (98%)	45 (96%)	2 (4%)	26	59
41	Am	48/48 (100%)	48 (100%)	0	100	100
42	An	24/24 (100%)	22 (92%)	2 (8%)	10	38
43	Ao	92/94 (98%)	91 (99%)	1 (1%)	65	79
44	Ap	74/75 (99%)	73 (99%)	1 (1%)	59	77
45	Ar	108/121 (89%)	108 (100%)	0	100	100
46	AK	190/196 (97%)	180 (95%)	10 (5%)	20	53
48	B	180/245 (74%)	177 (98%)	3 (2%)	53	75
49	C	194/231 (84%)	193 (100%)	1 (0%)	81	85
50	D	186/205 (91%)	182 (98%)	4 (2%)	45	71
51	E	190/232 (82%)	189 (100%)	1 (0%)	81	85
52	F	223/225 (99%)	219 (98%)	4 (2%)	51	74
53	G	158/170 (93%)	158 (100%)	0	100	100
54	H	207/218 (95%)	204 (99%)	3 (1%)	59	77
55	I	165/174 (95%)	164 (99%)	1 (1%)	78	84
56	J	178/179 (99%)	176 (99%)	2 (1%)	65	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	K	161/168 (96%)	159 (99%)	2 (1%)	63	79
58	L	87/125 (70%)	86 (99%)	1 (1%)	65	79
59	M	130/142 (92%)	129 (99%)	1 (1%)	73	82
60	N	99/108 (92%)	95 (96%)	4 (4%)	28	61
61	O	130/131 (99%)	128 (98%)	2 (2%)	57	76
62	P	106/119 (89%)	104 (98%)	2 (2%)	50	73
63	Q	108/130 (83%)	103 (95%)	5 (5%)	24	58
64	R	117/140 (84%)	117 (100%)	0	100	100
65	S	119/121 (98%)	118 (99%)	1 (1%)	73	82
66	T	125/132 (95%)	122 (98%)	3 (2%)	43	70
67	U	111/116 (96%)	109 (98%)	2 (2%)	51	74
68	V	92/107 (86%)	91 (99%)	1 (1%)	65	79
69	W	68/68 (100%)	65 (96%)	3 (4%)	25	59
70	X	112/113 (99%)	112 (100%)	0	100	100
71	Y	113/114 (99%)	112 (99%)	1 (1%)	70	81
72	Z	107/115 (93%)	104 (97%)	3 (3%)	38	68
73	a	66/103 (64%)	64 (97%)	2 (3%)	36	66
74	b	86/99 (87%)	83 (96%)	3 (4%)	32	64
75	c	75/76 (99%)	75 (100%)	0	100	100
76	d	55/62 (89%)	54 (98%)	1 (2%)	51	74
77	e	48/49 (98%)	47 (98%)	1 (2%)	47	71
78	f	46/106 (43%)	45 (98%)	1 (2%)	45	71
79	g	61/140 (44%)	60 (98%)	1 (2%)	55	75
80	h	272/275 (99%)	270 (99%)	2 (1%)	76	83
81	Aq	358/376 (95%)	342 (96%)	16 (4%)	24	58
All	All	10252/11385 (90%)	10018 (98%)	234 (2%)	44	70

All (234) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	AA	15	VAL
4	AA	77	ILE
4	AA	80	GLU

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Mol	Chain	Res	Type
4	AA	96	LEU
4	AA	97	ASN
4	AA	156	LYS
4	AA	165	VAL
4	AA	177	LYS
4	AA	181	LYS
4	AA	235	VAL
5	AB	17	LEU
5	AB	56	ILE
5	AB	90	VAL
5	AB	105	VAL
5	AB	157	CYS
5	AB	162	VAL
5	AB	231	VAL
6	AC	69	THR
6	AC	100	ARG
6	AC	149	GLU
6	AC	150	LEU
6	AC	152	LEU
6	AC	154	VAL
6	AC	227	ILE
6	AC	232	VAL
6	AC	334	THR
6	AC	335	MET
6	AC	336	ARG
6	AC	342	ARG
6	AC	343	GLN
6	AC	346	ASN
6	AC	347	HIS
6	AC	348	LYS
6	AC	349	LEU
6	AC	351	VAL
6	AC	352	GLU
6	AC	358	LEU
7	AD	37	VAL
7	AD	90	VAL
8	AE	178	VAL
8	AE	182	LEU
8	AE	281	THR
10	AG	221	VAL
10	AG	255	VAL
10	AG	271	LEU

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Mol	Chain	Res	Type
11	AH	84	VAL
11	AH	111	LEU
11	AH	112	VAL
11	AH	177	ASP
12	AI	24	ARG
12	AI	35	ASP
12	AI	129	VAL
12	AI	197	VAL
13	AJ	117	ILE
13	AJ	123	ILE
13	AJ	128	LEU
13	AJ	147	ARG
14	AL	4	SER
14	AL	33	ILE
14	AL	59	VAL
14	AL	63	THR
14	AL	67	HIS
14	AL	70	VAL
14	AL	154	VAL
15	AM	9	VAL
15	AM	35	ARG
15	AM	37	LEU
15	AM	39	ASP
15	AM	69	ARG
15	AM	71	LYS
15	AM	105	THR
16	AN	125	SER
16	AN	142	ILE
16	AN	151	ILE
17	AO	7	LEU
17	AO	43	ILE
17	AO	108	ILE
17	AO	113	ASP
17	AO	145	VAL
17	AO	174	ILE
17	AO	194	GLU
18	AP	24	VAL
18	AP	104	LEU
19	AQ	23	MET
19	AQ	38	HIS
19	AQ	57	LYS
19	AQ	66	VAL

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Mol	Chain	Res	Type
19	AQ	72	LEU
19	AQ	74	ASP
19	AQ	110	HIS
19	AQ	115	LYS
19	AQ	120	ILE
19	AQ	122	THR
19	AQ	150	GLN
20	AR	15	LEU
20	AR	94	LYS
20	AR	105	LEU
20	AR	137	ILE
20	AR	153	LYS
20	AR	163	ARG
20	AR	173	ARG
21	AS	17	LEU
21	AS	21	LYS
21	AS	22	SER
21	AS	49	LEU
21	AS	50	GLU
21	AS	90	THR
21	AS	132	MET
21	AS	151	ARG
22	AT	40	VAL
22	AT	92	ARG
23	AU	17	GLN
23	AU	19	LEU
23	AU	23	LEU
23	AU	36	GLU
23	AU	49	VAL
23	AU	54	ARG
23	AU	63	ILE
23	AU	83	LEU
23	AU	97	HIS
23	AU	106	SER
24	AV	57	VAL
26	AX	95	THR
27	AY	50	ARG
27	AY	97	VAL
27	AY	104	VAL
29	Aa	82	VAL
29	Aa	124	VAL
30	Ab	101	HIS

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Mol	Chain	Res	Type
31	Ac	81	LEU
31	Ac	94	LEU
33	Ae	17	THR
33	Ae	26	ASP
33	Ae	78	LEU
34	Af	33	VAL
34	Af	84	VAL
35	Ag	38	VAL
38	Aj	2	THR
38	Aj	58	THR
39	Ak	3	GLN
39	Ak	48	MET
40	Al	6	THR
40	Al	27	ILE
42	An	2	ARG
42	An	13	LEU
43	Ao	83	LEU
44	Ap	16	THR
46	AK	10	LEU
46	AK	67	VAL
46	AK	80	VAL
46	AK	100	VAL
46	AK	111	LEU
46	AK	128	LEU
46	AK	148	VAL
46	AK	169	VAL
46	AK	179	LEU
46	AK	216	LEU
48	B	109	THR
48	B	128	GLN
48	B	157	VAL
49	C	98	THR
50	D	75	ILE
50	D	233	LEU
50	D	260	VAL
50	D	274	MET
51	E	69	LEU
52	F	12	VAL
52	F	23	LEU
52	F	156	MET
52	F	262	SER
54	H	114	VAL

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Mol	Chain	Res	Type
54	H	125	THR
54	H	181	THR
55	I	40	LEU
56	J	130	THR
56	J	205	ARG
57	K	21	GLU
57	K	58	ARG
58	L	15	LEU
59	M	152	LYS
60	N	18	LEU
60	N	46	GLN
60	N	64	LEU
60	N	119	GLN
61	O	86	GLU
61	O	149	LEU
62	P	80	ASP
62	P	133	THR
63	Q	20	VAL
63	Q	121	ILE
63	Q	124	LYS
63	Q	127	LYS
63	Q	130	ARG
65	S	110	ASP
66	T	16	LEU
66	T	36	VAL
66	T	45	LEU
67	U	5	THR
67	U	131	LEU
68	V	90	ASP
69	W	32	ILE
69	W	50	SER
69	W	76	HIS
71	Y	131	LEU
72	Z	34	THR
72	Z	44	LEU
72	Z	79	LEU
73	a	58	LEU
73	a	110	THR
74	b	45	VAL
74	b	56	VAL
74	b	95	ARG
76	d	38	THR

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Mol	Chain	Res	Type
77	e	24	CYS
78	f	118	VAL
79	g	98	VAL
80	h	165	ILE
80	h	198	VAL
81	Aq	78	VAL
81	Aq	100	ILE
81	Aq	182	ARG
81	Aq	185	GLN
81	Aq	186	SER
81	Aq	189	ARG
81	Aq	251	LEU
81	Aq	270	LEU
81	Aq	300	LYS
81	Aq	314	MET
81	Aq	326	LEU
81	Aq	339	GLU
81	Aq	362	THR
81	Aq	369	ILE
81	Aq	381	ASN
81	Aq	416	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (185) such sidechains are listed below:

Mol	Chain	Res	Type
4	AA	83	HIS
4	AA	132	ASN
4	AA	140	ASN
4	AA	215	ASN
5	AB	121	ASN
5	AB	145	GLN
5	AB	167	GLN
5	AB	175	GLN
5	AB	184	GLN
5	AB	203	GLN
5	AB	271	GLN
6	AC	50	GLN
6	AC	61	GLN
6	AC	119	GLN
6	AC	212	ASN
6	AC	245	HIS
6	AC	286	ASN

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Mol	Chain	Res	Type
6	AC	346	ASN
6	AC	347	HIS
7	AD	138	GLN
7	AD	175	HIS
7	AD	202	GLN
7	AD	282	GLN
8	AE	253	GLN
8	AE	287	HIS
9	AF	98	ASN
9	AF	118	ASN
9	AF	204	ASN
10	AG	82	ASN
10	AG	91	ASN
10	AG	96	GLN
10	AG	212	HIS
10	AG	259	GLN
11	AH	39	ASN
11	AH	98	HIS
11	AH	106	GLN
11	AH	188	GLN
12	AI	14	ASN
12	AI	59	GLN
12	AI	95	HIS
12	AI	100	ASN
12	AI	163	GLN
12	AI	166	HIS
13	AJ	104	ASN
14	AL	104	ASN
14	AL	149	GLN
14	AL	159	ASN
15	AM	33	GLN
15	AM	56	GLN
15	AM	70	GLN
16	AN	99	GLN
16	AN	117	ASN
16	AN	145	ASN
17	AO	26	GLN
17	AO	42	ASN
17	AO	63	ASN
18	AP	21	ASN
18	AP	80	GLN
18	AP	120	ASN

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Mol	Chain	Res	Type
19	AQ	8	ASN
19	AQ	38	HIS
19	AQ	93	GLN
19	AQ	125	GLN
19	AQ	150	GLN
19	AQ	188	ASN
20	AR	86	ASN
21	AS	77	ASN
21	AS	95	HIS
21	AS	146	HIS
22	AT	127	GLN
22	AT	131	GLN
23	AU	41	GLN
24	AV	27	ASN
26	AX	93	ASN
26	AX	105	ASN
26	AX	111	GLN
26	AX	125	ASN
26	AX	151	ASN
27	AY	14	ASN
27	AY	65	GLN
28	AZ	40	HIS
28	AZ	76	ASN
28	AZ	79	HIS
28	AZ	127	ASN
30	Ab	17	HIS
30	Ab	50	ASN
30	Ab	60	ASN
32	Ad	34	HIS
32	Ad	79	ASN
32	Ad	100	ASN
33	Ae	23	HIS
33	Ae	52	GLN
33	Ae	57	ASN
33	Ae	92	ASN
34	Af	56	ASN
34	Af	65	ASN
36	Ah	20	GLN
36	Ah	62	ASN
36	Ah	68	ASN
37	Ai	80	HIS
38	Aj	13	ASN

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Mol	Chain	Res	Type
41	Am	61	GLN
45	Ar	4	HIS
45	Ar	6	GLN
45	Ar	23	GLN
46	AK	96	ASN
46	AK	129	ASN
46	AK	199	GLN
48	B	128	GLN
48	B	141	ASN
48	B	180	GLN
49	C	124	HIS
49	C	208	HIS
50	D	115	GLN
50	D	235	ASN
50	D	267	GLN
51	E	22	ASN
51	E	74	GLN
52	F	67	GLN
52	F	138	HIS
53	G	65	GLN
53	G	74	ASN
53	G	83	ASN
53	G	107	ASN
53	G	118	ASN
53	G	137	GLN
53	G	165	ASN
53	G	203	ASN
54	H	202	ASN
55	I	68	GLN
55	I	76	GLN
55	I	114	GLN
55	I	165	ASN
55	I	168	HIS
55	I	186	ASN
55	I	193	GLN
56	J	138	ASN
57	K	177	ASN
58	L	7	ASN
58	L	50	GLN
59	M	11	GLN
59	M	19	ASN
59	M	100	ASN

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Mol	Chain	Res	Type
59	M	121	GLN
60	N	46	GLN
62	P	20	GLN
62	P	32	HIS
63	Q	53	GLN
64	R	29	ASN
64	R	80	GLN
64	R	86	GLN
65	S	26	ASN
65	S	48	ASN
65	S	62	GLN
65	S	83	ASN
65	S	127	ASN
66	T	72	GLN
66	T	105	ASN
67	U	85	ASN
68	V	100	GLN
69	W	35	ASN
70	X	16	ASN
70	X	56	HIS
70	X	82	GLN
70	X	113	HIS
71	Y	16	HIS
71	Y	46	HIS
71	Y	63	ASN
71	Y	127	ASN
72	Z	89	HIS
73	a	46	ASN
73	a	112	ASN
75	c	84	HIS
77	e	4	GLN
78	f	117	ASN
80	h	76	GLN
80	h	133	ASN
80	h	178	ASN
80	h	187	ASN
80	h	191	HIS
81	Aq	91	ASN
81	Aq	129	ASN
81	Aq	185	GLN
81	Aq	247	GLN
81	Aq	266	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3570/3594 (99%)	952 (26%)	77 (2%)
2	7	118/119 (99%)	18 (15%)	1 (0%)
3	8	149/156 (95%)	34 (22%)	1 (0%)
47	2	1685/1869 (90%)	505 (29%)	50 (2%)
82	1	206/251 (82%)	115 (55%)	14 (6%)
All	All	5728/5989 (95%)	1624 (28%)	143 (2%)

All (1624) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	4	G
1	5	9	C
1	5	10	A
1	5	12	A
1	5	13	U
1	5	25	A
1	5	35	U
1	5	36	U
1	5	39	A
1	5	42	A
1	5	43	U
1	5	44	A
1	5	48	G
1	5	49	U
1	5	56	A
1	5	58	G
1	5	59	A
1	5	64	A
1	5	65	A
1	5	73	A
1	5	87	A
1	5	91	G
1	5	104	G
1	5	108	A
1	5	109	G
1	5	110	C
1	5	116	G
1	5	118	C
1	5	119	G
1	5	120	A
1	5	126	C

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Mol	Chain	Res	Type
1	5	131	C
1	5	133	C
1	5	134	G
1	5	135	G
1	5	142	G
1	5	144	G
1	5	146	G
1	5	158	A
1	5	159	C
1	5	165	A
1	5	168	C
1	5	171	U
1	5	172	C
1	5	173	C
1	5	179	G
1	5	180	C
1	5	181	C
1	5	182	G
1	5	197	A
1	5	200	U
1	5	209	U
1	5	210	C
1	5	216	C
1	5	217	C
1	5	218	A
1	5	219	G
1	5	220	C
1	5	224	U
1	5	225	G
1	5	233	U
1	5	234	G
1	5	245	C
1	5	250	C
1	5	256	G
1	5	258	G
1	5	259	C
1	5	265	C
1	5	266	C
1	5	267	G
1	5	268	G
1	5	271	C
1	5	276	C

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Mol	Chain	Res	Type
1	5	280	G
1	5	281	U
1	5	292	G
1	5	294	G
1	5	297	U
1	5	306	A
1	5	310	G
1	5	315	G
1	5	316	U
1	5	317	A
1	5	334	A
1	5	337	U
1	5	340	C
1	5	344	A
1	5	345	C
1	5	347	A
1	5	350	C
1	5	360	A
1	5	361	C
1	5	362	A
1	5	363	A
1	5	386	A
1	5	387	G
1	5	396	A
1	5	399	G
1	5	408	A
1	5	409	G
1	5	410	A
1	5	412	G
1	5	413	G
1	5	414	C
1	5	418	A
1	5	432	U
1	5	440	U
1	5	446	C
1	5	449	C
1	5	450	G
1	5	452	A
1	5	453	G
1	5	454	U
1	5	455	C
1	5	462	G

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Mol	Chain	Res	Type
1	5	467	U
1	5	468	U
1	5	481	G
1	5	482	G
1	5	483	G
1	5	484	U
1	5	487	G
1	5	492	U
1	5	493	G
1	5	496	G
1	5	498	C
1	5	499	G
1	5	500	G
1	5	505	G
1	5	506	C
1	5	510	U
1	5	519	C
1	5	522	C
1	5	647	G
1	5	649	A
1	5	663	G
1	5	666	G
1	5	667	A
1	5	670	G
1	5	673	C
1	5	685	C
1	5	686	A
1	5	688	U
1	5	694	C
1	5	696	C
1	5	697	G
1	5	700	G
1	5	704	C
1	5	705	G
1	5	719	C
1	5	729	G
1	5	730	G
1	5	731	G
1	5	737	C
1	5	738	C
1	5	739	G
1	5	740	G

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Mol	Chain	Res	Type
1	5	741	C
1	5	744	G
1	5	746	A
1	5	747	A
1	5	749	G
1	5	750	U
1	5	751	G
1	5	752	G
1	5	754	C
1	5	758	G
1	5	905	C
1	5	906	C
1	5	907	G
1	5	911	G
1	5	912	U
1	5	913	U
1	5	914	A
1	5	915	C
1	5	916	A
1	5	917	G
1	5	920	C
1	5	921	A
1	5	922	C
1	5	923	C
1	5	924	C
1	5	925	G
1	5	926	G
1	5	928	A
1	5	929	G
1	5	931	A
1	5	932	G
1	5	933	C
1	5	934	A
1	5	935	G
1	5	936	C
1	5	941	C
1	5	943	A
1	5	944	A
1	5	945	U
1	5	959	G
1	5	960	A
1	5	961	G

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Mol	Chain	Res	Type
1	5	966	A
1	5	967	C
1	5	968	C
1	5	969	U
1	5	971	U
1	5	973	U
1	5	979	C
1	5	984	U
1	5	1071	C
1	5	1072	C
1	5	1073	G
1	5	1079	C
1	5	1094	G
1	5	1098	G
1	5	1171	G
1	5	1172	C
1	5	1173	G
1	5	1176	C
1	5	1180	C
1	5	1184	A
1	5	1187	G
1	5	1193	C
1	5	1195	G
1	5	1210	C
1	5	1211	G
1	5	1214	C
1	5	1215	C
1	5	1234	G
1	5	1235	G
1	5	1236	C
1	5	1237	C
1	5	1238	A
1	5	1246	G
1	5	1249	C
1	5	1272	C
1	5	1273	G
1	5	1275	G
1	5	1279	A
1	5	1280	C
1	5	1284	G
1	5	1285	U
1	5	1286	C

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Mol	Chain	Res	Type
1	5	1287	G
1	5	1288	G
1	5	1289	C
1	5	1293	G
1	5	1294	A
1	5	1295	U
1	5	1296	G
1	5	1301	C
1	5	1320	U
1	5	1326	A
1	5	1337	A
1	5	1354	A
1	5	1358	G
1	5	1359	G
1	5	1370	G
1	5	1371	A
1	5	1377	G
1	5	1378	C
1	5	1380	G
1	5	1381	U
1	5	1387	A
1	5	1394	G
1	5	1397	A
1	5	1398	A
1	5	1399	G
1	5	1401	C
1	5	1404	G
1	5	1405	C
1	5	1410	C
1	5	1413	C
1	5	1414	C
1	5	1415	G
1	5	1420	A
1	5	1421	G
1	5	1428	U
1	5	1429	C
1	5	1433	A
1	5	1435	G
1	5	1436	C
1	5	1437	C
1	5	1438	U
1	5	1443	A

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Mol	Chain	Res	Type
1	5	1444	G
1	5	1445	U
1	5	1446	C
1	5	1456	C
1	5	1457	G
1	5	1465	G
1	5	1475	G
1	5	1477	C
1	5	1482	G
1	5	1483	C
1	5	1484	G
1	5	1486	C
1	5	1497	A
1	5	1498	G
1	5	1501	C
1	5	1502	G
1	5	1503	A
1	5	1523	A
1	5	1534	A
1	5	1538	U
1	5	1547	A
1	5	1562	G
1	5	1578	U
1	5	1586	G
1	5	1591	U
1	5	1592	G
1	5	1596	U
1	5	1597	G
1	5	1611	C
1	5	1612	G
1	5	1613	A
1	5	1618	G
1	5	1624	G
1	5	1625	G
1	5	1631	A
1	5	1633	G
1	5	1634	A
1	5	1637	A
1	5	1640	C
1	5	1651	G
1	5	1654	G
1	5	1658	G

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Mol	Chain	Res	Type
1	5	1660	U
1	5	1661	C
1	5	1676	C
1	5	1677	U
1	5	1679	A
1	5	1721	G
1	5	1731	C
1	5	1733	G
1	5	1734	G
1	5	1742	A
1	5	1743	A
1	5	1750	G
1	5	1754	U
1	5	1756	U
1	5	1757	U
1	5	1758	G
1	5	1760	G
1	5	1763	C
1	5	1764	G
1	5	1769	G
1	5	1770	A
1	5	1771	U
1	5	1772	C
1	5	1773	U
1	5	1775	A
1	5	1787	A
1	5	1797	G
1	5	1804	A
1	5	1805	A
1	5	1809	C
1	5	1815	G
1	5	1820	U
1	5	1821	G
1	5	1828	C
1	5	1830	G
1	5	1833	G
1	5	1834	U
1	5	1836	G
1	5	1837	A
1	5	1842	G
1	5	1855	G
1	5	1865	G

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Mol	Chain	Res	Type
1	5	1869	G
1	5	1881	C
1	5	1882	U
1	5	1886	G
1	5	1889	U
1	5	1897	A
1	5	1899	G
1	5	1910	G
1	5	1915	C
1	5	1918	U
1	5	1920	C
1	5	1921	C
1	5	1922	G
1	5	1931	C
1	5	1939	A
1	5	1940	G
1	5	1941	A
1	5	1947	U
1	5	1952	G
1	5	1957	U
1	5	1958	A
1	5	1959	U
1	5	1960	A
1	5	1961	G
1	5	1962	A
1	5	1963	C
1	5	1964	A
1	5	1966	C
1	5	1967	A
1	5	1972	G
1	5	1974	U
1	5	1975	G
1	5	1976	G
1	5	1977	C
1	5	1978	C
1	5	1979	A
1	5	1980	U
1	5	1981	G
1	5	1982	G
1	5	1983	A
1	5	1984	A
1	5	1985	G

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Mol	Chain	Res	Type
1	5	1987	C
1	5	1988	G
1	5	1989	G
1	5	1990	A
1	5	1991	A
1	5	1992	U
1	5	1993	C
1	5	1995	G
1	5	1996	C
1	5	1997	U
1	5	1998	A
1	5	1999	A
1	5	2002	A
1	5	2003	G
1	5	2004	U
1	5	2008	U
1	5	2009	A
1	5	2010	A
1	5	2011	C
1	5	2012	A
1	5	2013	A
1	5	2014	C
1	5	2018	C
1	5	2020	U
1	5	2021	G
1	5	2022	C
1	5	2024	G
1	5	2025	A
1	5	2026	A
1	5	2042	A
1	5	2044	U
1	5	2046	G
1	5	2047	A
1	5	2048	U
1	5	2052	G
1	5	2055	G
1	5	2056	G
1	5	2058	G
1	5	2069	A
1	5	2070	U
1	5	2084	U
1	5	2088	A

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Mol	Chain	Res	Type
1	5	2089	G
1	5	2090	U
1	5	2093	G
1	5	2094	C
1	5	2097	A
1	5	2098	G
1	5	2100	G
1	5	2102	G
1	5	2104	A
1	5	2107	A
1	5	2108	G
1	5	2110	G
1	5	2259	G
1	5	2260	C
1	5	2266	C
1	5	2267	U
1	5	2268	A
1	5	2269	C
1	5	2275	G
1	5	2277	C
1	5	2280	G
1	5	2289	C
1	5	2294	G
1	5	2300	A
1	5	2301	G
1	5	2313	A
1	5	2314	G
1	5	2325	C
1	5	2332	A
1	5	2333	G
1	5	2348	G
1	5	2350	U
1	5	2351	C
1	5	2364	G
1	5	2366	A
1	5	2370	A
1	5	2371	U
1	5	2374	A
1	5	2387	G
1	5	2395	A
1	5	2396	A
1	5	2398	U

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Mol	Chain	Res	Type
1	5	2400	G
1	5	2409	U
1	5	2417	A
1	5	2422	C
1	5	2428	A
1	5	2433	G
1	5	2437	C
1	5	2441	C
1	5	2444	U
1	5	2447	U
1	5	2450	G
1	5	2471	G
1	5	2475	G
1	5	2477	A
1	5	2478	C
1	5	2481	G
1	5	2483	G
1	5	2486	G
1	5	2487	G
1	5	2488	C
1	5	2489	C
1	5	2490	U
1	5	2491	C
1	5	2493	G
1	5	2495	U
1	5	2503	G
1	5	2504	C
1	5	2505	C
1	5	2506	G
1	5	2511	A
1	5	2513	A
1	5	2514	G
1	5	2529	A
1	5	2530	U
1	5	2537	A
1	5	2544	G
1	5	2546	G
1	5	2547	G
1	5	2549	G
1	5	2552	G
1	5	2553	A
1	5	2554	U

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Mol	Chain	Res	Type
1	5	2555	G
1	5	2558	C
1	5	2562	G
1	5	2564	G
1	5	2565	A
1	5	2569	G
1	5	2570	U
1	5	2575	U
1	5	2586	G
1	5	2587	A
1	5	2589	C
1	5	2601	A
1	5	2618	G
1	5	2623	A
1	5	2627	C
1	5	2628	U
1	5	2639	U
1	5	2649	G
1	5	2653	C
1	5	2655	C
1	5	2656	U
1	5	2659	A
1	5	2661	U
1	5	2662	G
1	5	2663	G
1	5	2669	C
1	5	2670	C
1	5	2686	G
1	5	2687	U
1	5	2695	A
1	5	2696	A
1	5	2701	U
1	5	2704	C
1	5	2708	U
1	5	2709	C
1	5	2710	C
1	5	2711	G
1	5	2712	G
1	5	2714	G
1	5	2716	C
1	5	2719	C
1	5	2723	U

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Mol	Chain	Res	Type
1	5	2724	G
1	5	2732	G
1	5	2735	G
1	5	2740	U
1	5	2743	A
1	5	2744	A
1	5	2750	G
1	5	2761	U
1	5	2763	U
1	5	2764	A
1	5	2769	U
1	5	2770	C
1	5	2787	A
1	5	2788	U
1	5	2790	U
1	5	2796	G
1	5	2798	A
1	5	2815	A
1	5	2826	U
1	5	2827	G
1	5	2829	U
1	5	2842	G
1	5	2844	A
1	5	2848	G
1	5	2850	A
1	5	2855	G
1	5	2856	C
1	5	2862	G
1	5	2874	U
1	5	2875	C
1	5	2898	G
1	5	3604	A
1	5	3617	G
1	5	3618	C
1	5	3625	G
1	5	3626	G
1	5	3630	A
1	5	3635	A
1	5	3644	U
1	5	3646	A
1	5	3648	A
1	5	3653	A

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Mol	Chain	Res	Type
1	5	3662	A
1	5	3663	A
1	5	3670	C
1	5	3673	C
1	5	3679	U
1	5	3696	C
1	5	3705	G
1	5	3710	G
1	5	3711	A
1	5	3712	A
1	5	3713	U
1	5	3714	G
1	5	3729	U
1	5	3734	U
1	5	3740	G
1	5	3748	A
1	5	3753	G
1	5	3759	A
1	5	3760	A
1	5	3761	C
1	5	3763	A
1	5	3764	U
1	5	3765	G
1	5	3766	A
1	5	3767	C
1	5	3774	A
1	5	3775	A
1	5	3776	G
1	5	3777	G
1	5	3778	U
1	5	3784	A
1	5	3786	U
1	5	3795	A
1	5	3809	G
1	5	3810	C
1	5	3811	G
1	5	3812	C
1	5	3814	U
1	5	3817	A
1	5	3819	G
1	5	3839	G
1	5	3840	U

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Mol	Chain	Res	Type
1	5	3862	A
1	5	3876	A
1	5	3877	A
1	5	3878	C
1	5	3879	G
1	5	3880	G
1	5	3887	C
1	5	3888	G
1	5	3889	G
1	5	3897	G
1	5	3901	A
1	5	3905	A
1	5	3906	A
1	5	3907	G
1	5	3908	A
1	5	3915	U
1	5	3916	G
1	5	3917	A
1	5	3923	A
1	5	3938	G
1	5	3939	G
1	5	3944	G
1	5	3945	A
1	5	3947	A
1	5	3948	C
1	5	3950	U
1	5	3951	G
1	5	3954	A
1	5	3956	G
1	5	3958	G
1	5	3960	A
1	5	3962	A
1	5	3964	U
1	5	3965	A
1	5	3966	A
1	5	3967	G
1	5	3970	G
1	5	3972	A
1	5	3975	C
1	5	3977	C
1	5	4036	G
1	5	4039	G

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Mol	Chain	Res	Type
1	5	4044	U
1	5	4046	A
1	5	4047	A
1	5	4048	A
1	5	4049	U
1	5	4050	A
1	5	4051	C
1	5	4052	C
1	5	4053	A
1	5	4054	C
1	5	4055	U
1	5	4062	A
1	5	4063	U
1	5	4064	C
1	5	4065	G
1	5	4070	U
1	5	4071	U
1	5	4072	C
1	5	4074	C
1	5	4076	G
1	5	4077	A
1	5	4085	A
1	5	4086	G
1	5	4094	G
1	5	4095	G
1	5	4099	G
1	5	4101	C
1	5	4108	G
1	5	4118	U
1	5	4119	C
1	5	4120	U
1	5	4121	G
1	5	4122	G
1	5	4124	G
1	5	4127	A
1	5	4131	G
1	5	4135	G
1	5	4136	G
1	5	4138	C
1	5	4147	G
1	5	4148	C
1	5	4149	C

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Mol	Chain	Res	Type
1	5	4152	G
1	5	4156	G
1	5	4157	A
1	5	4159	C
1	5	4162	C
1	5	4163	U
1	5	4170	A
1	5	4171	C
1	5	4172	A
1	5	4179	G
1	5	4181	U
1	5	4183	G
1	5	4184	G
1	5	4191	G
1	5	4203	A
1	5	4204	C
1	5	4206	C
1	5	4221	C
1	5	4222	G
1	5	4229	U
1	5	4232	U
1	5	4233	A
1	5	4237	C
1	5	4249	G
1	5	4251	A
1	5	4252	C
1	5	4254	G
1	5	4257	A
1	5	4266	G
1	5	4268	A
1	5	4271	A
1	5	4273	A
1	5	4280	A
1	5	4281	A
1	5	4291	G
1	5	4297	G
1	5	4305	G
1	5	4306	U
1	5	4307	A
1	5	4313	A
1	5	4314	C
1	5	4317	A

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Mol	Chain	Res	Type
1	5	4318	C
1	5	4326	G
1	5	4329	G
1	5	4330	G
1	5	4336	A
1	5	4339	A
1	5	4344	U
1	5	4345	C
1	5	4349	C
1	5	4350	C
1	5	4353	U
1	5	4354	U
1	5	4373	G
1	5	4376	A
1	5	4377	G
1	5	4378	A
1	5	4387	C
1	5	4391	G
1	5	4394	A
1	5	4395	U
1	5	4396	A
1	5	4398	C
1	5	4419	U
1	5	4422	A
1	5	4424	A
1	5	4426	C
1	5	4430	G
1	5	4439	U
1	5	4444	C
1	5	4448	G
1	5	4449	A
1	5	4450	U
1	5	4452	U
1	5	4453	C
1	5	4454	G
1	5	4464	A
1	5	4466	C
1	5	4471	U
1	5	4472	G
1	5	4475	G
1	5	4500	U
1	5	4512	U

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Mol	Chain	Res	Type
1	5	4513	A
1	5	4519	C
1	5	4524	G
1	5	4528	G
1	5	4531	U
1	5	4548	A
1	5	4549	G
1	5	4550	G
1	5	4556	U
1	5	4560	C
1	5	4561	C
1	5	4572	U
1	5	4573	G
1	5	4575	G
1	5	4577	U
1	5	4583	C
1	5	4584	A
1	5	4585	U
1	5	4589	A
1	5	4590	A
1	5	4599	A
1	5	4606	G
1	5	4627	U
1	5	4634	U
1	5	4635	A
1	5	4636	U
1	5	4637	G
1	5	4639	G
1	5	4651	A
1	5	4652	G
1	5	4656	A
1	5	4657	U
1	5	4658	G
1	5	4660	G
1	5	4663	G
1	5	4670	C
1	5	4672	A
1	5	4677	U
1	5	4693	C
1	5	4694	G
1	5	4700	A
1	5	4707	A

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Mol	Chain	Res	Type
1	5	4709	U
1	5	4719	G
1	5	4720	C
1	5	4738	C
1	5	4739	C
1	5	4751	G
1	5	4752	U
1	5	4754	G
1	5	4757	C
1	5	4759	C
1	5	4761	G
1	5	4764	A
1	5	4765	G
1	5	4769	G
1	5	4771	C
1	5	4772	C
1	5	4777	C
1	5	4860	G
1	5	4870	G
1	5	4871	C
1	5	4874	A
1	5	4875	G
1	5	4876	A
1	5	4877	G
1	5	4882	U
1	5	4883	C
1	5	4885	U
1	5	4886	C
1	5	4889	G
1	5	4893	A
1	5	4895	C
1	5	4898	G
1	5	4902	C
1	5	4910	A
1	5	4912	G
1	5	4913	G
1	5	4914	G
1	5	4919	G
1	5	4921	C
1	5	4922	C
1	5	4924	C
1	5	4925	U

Continued on next page...

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Mol	Chain	Res	Type
1	5	4926	C
1	5	4930	C
1	5	4935	C
1	5	4937	C
1	5	4938	A
1	5	4943	A
1	5	4944	C
1	5	4949	G
1	5	4950	U
1	5	4951	G
1	5	4954	G
1	5	4956	A
1	5	4958	C
1	5	4960	G
1	5	4961	G
1	5	4964	C
1	5	4965	U
1	5	4966	A
1	5	4967	A
1	5	4973	U
1	5	4975	G
1	5	4976	U
1	5	4979	A
1	5	4989	U
1	5	4990	C
1	5	4993	G
1	5	5011	A
1	5	5012	G
1	5	5016	A
1	5	5017	G
1	5	5022	U
1	5	5029	C
1	5	5037	U
1	5	5041	G
1	5	5050	C
1	5	5053	U
1	5	5054	C
1	5	5056	A
1	5	5062	G
2	7	5	A
2	7	7	G
2	7	10	C

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Mol	Chain	Res	Type
2	7	11	A
2	7	13	A
2	7	21	G
2	7	25	G
2	7	42	A
2	7	49	A
2	7	51	G
2	7	53	U
2	7	54	A
2	7	64	G
2	7	97	G
2	7	99	G
2	7	100	A
2	7	110	G
2	7	111	C
3	8	2	G
3	8	3	A
3	8	23	C
3	8	32	C
3	8	34	U
3	8	35	C
3	8	59	A
3	8	62	A
3	8	63	U
3	8	75	G
3	8	95	A
3	8	96	C
3	8	105	C
3	8	109	C
3	8	110	U
3	8	111	U
3	8	112	G
3	8	113	C
3	8	114	G
3	8	117	C
3	8	121	G
3	8	122	G
3	8	123	U
3	8	124	U
3	8	125	C
3	8	126	C
3	8	127	U

Continued on next page...

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Mol	Chain	Res	Type
3	8	128	C
3	8	137	A
3	8	143	G
3	8	147	G
3	8	150	C
3	8	151	G
3	8	156	U
47	2	3	C
47	2	4	C
47	2	5	U
47	2	17	C
47	2	25	A
47	2	33	G
47	2	42	A
47	2	46	A
47	2	56	G
47	2	59	U
47	2	62	G
47	2	64	A
47	2	65	C
47	2	66	G
47	2	67	C
47	2	68	A
47	2	69	C
47	2	72	C
47	2	73	C
47	2	74	G
47	2	76	U
47	2	77	A
47	2	79	A
47	2	81	U
47	2	84	A
47	2	88	G
47	2	91	A
47	2	92	A
47	2	99	A
47	2	100	U
47	2	103	A
47	2	111	A
47	2	113	G
47	2	115	U
47	2	123	G

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Mol	Chain	Res	Type
47	2	125	C
47	2	126	G
47	2	128	U
47	2	129	C
47	2	142	C
47	2	143	U
47	2	145	G
47	2	146	G
47	2	147	A
47	2	155	G
47	2	158	A
47	2	160	U
47	2	162	C
47	2	163	U
47	2	164	A
47	2	170	A
47	2	172	U
47	2	173	A
47	2	175	A
47	2	182	C
47	2	183	G
47	2	184	G
47	2	187	G
47	2	189	U
47	2	190	G
47	2	191	A
47	2	192	C
47	2	196	C
47	2	200	G
47	2	201	C
47	2	203	G
47	2	210	U
47	2	212	C
47	2	213	G
47	2	214	U
47	2	215	G
47	2	216	C
47	2	217	A
47	2	218	U
47	2	219	U
47	2	221	A
47	2	224	A

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Mol	Chain	Res	Type
47	2	292	A
47	2	294	U
47	2	297	A
47	2	304	C
47	2	305	U
47	2	308	G
47	2	309	G
47	2	310	C
47	2	312	G
47	2	317	C
47	2	319	C
47	2	320	G
47	2	321	C
47	2	322	C
47	2	323	C
47	2	335	G
47	2	336	A
47	2	347	G
47	2	360	A
47	2	361	U
47	2	362	C
47	2	364	A
47	2	368	U
47	2	370	G
47	2	373	G
47	2	381	C
47	2	382	C
47	2	385	G
47	2	386	C
47	2	389	A
47	2	391	C
47	2	400	C
47	2	407	G
47	2	409	C
47	2	418	A
47	2	420	G
47	2	429	C
47	2	441	C
47	2	447	A
47	2	448	A
47	2	450	C
47	2	462	C

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Mol	Chain	Res	Type
47	2	464	A
47	2	465	A
47	2	466	G
47	2	467	G
47	2	468	A
47	2	472	C
47	2	473	A
47	2	474	G
47	2	482	G
47	2	487	U
47	2	488	U
47	2	489	A
47	2	492	C
47	2	493	A
47	2	494	C
47	2	496	C
47	2	497	C
47	2	498	C
47	2	500	A
47	2	501	C
47	2	507	G
47	2	517	C
47	2	525	A
47	2	526	A
47	2	528	A
47	2	530	U
47	2	531	A
47	2	532	C
47	2	533	A
47	2	537	C
47	2	541	U
47	2	542	U
47	2	543	C
47	2	544	G
47	2	547	G
47	2	548	C
47	2	549	C
47	2	550	C
47	2	551	U
47	2	553	U
47	2	554	A
47	2	556	U

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Mol	Chain	Res	Type
47	2	559	G
47	2	561	A
47	2	562	U
47	2	564	A
47	2	568	C
47	2	575	A
47	2	576	A
47	2	577	U
47	2	579	C
47	2	587	A
47	2	588	G
47	2	590	A
47	2	591	U
47	2	592	C
47	2	594	A
47	2	600	G
47	2	604	A
47	2	606	G
47	2	607	U
47	2	608	C
47	2	609	U
47	2	614	C
47	2	615	C
47	2	617	G
47	2	627	U
47	2	629	A
47	2	643	A
47	2	644	G
47	2	655	A
47	2	657	U
47	2	659	G
47	2	660	C
47	2	664	A
47	2	668	A
47	2	669	A
47	2	671	A
47	2	672	A
47	2	673	G
47	2	674	C
47	2	684	G
47	2	687	C
47	2	692	G

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Mol	Chain	Res	Type
47	2	694	G
47	2	697	G
47	2	731	G
47	2	732	U
47	2	733	C
47	2	735	C
47	2	744	G
47	2	750	C
47	2	751	G
47	2	752	G
47	2	753	C
47	2	754	G
47	2	755	C
47	2	789	G
47	2	790	C
47	2	792	C
47	2	794	A
47	2	795	A
47	2	796	G
47	2	797	C
47	2	798	G
47	2	799	U
47	2	811	A
47	2	812	A
47	2	818	A
47	2	821	G
47	2	822	U
47	2	825	A
47	2	827	A
47	2	829	C
47	2	834	C
47	2	845	G
47	2	847	A
47	2	849	A
47	2	850	C
47	2	862	A
47	2	869	A
47	2	870	A
47	2	871	U
47	2	873	G
47	2	874	G
47	2	875	A

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Mol	Chain	Res	Type
47	2	877	C
47	2	878	G
47	2	879	C
47	2	883	U
47	2	884	C
47	2	885	U
47	2	886	A
47	2	887	U
47	2	890	U
47	2	891	G
47	2	893	U
47	2	894	G
47	2	898	U
47	2	901	G
47	2	908	A
47	2	909	G
47	2	910	G
47	2	913	A
47	2	914	U
47	2	918	U
47	2	920	A
47	2	921	G
47	2	930	C
47	2	933	G
47	2	943	U
47	2	955	A
47	2	956	G
47	2	963	A
47	2	970	G
47	2	976	G
47	2	977	C
47	2	978	G
47	2	990	A
47	2	992	A
47	2	999	G
47	2	1002	U
47	2	1017	U
47	2	1023	A
47	2	1044	G
47	2	1045	U
47	2	1046	U
47	2	1058	A

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Mol	Chain	Res	Type
47	2	1059	G
47	2	1060	A
47	2	1070	A
47	2	1078	C
47	2	1083	A
47	2	1085	C
47	2	1100	A
47	2	1110	G
47	2	1115	U
47	2	1116	C
47	2	1117	C
47	2	1118	C
47	2	1121	G
47	2	1126	G
47	2	1133	A
47	2	1138	C
47	2	1139	C
47	2	1144	A
47	2	1148	A
47	2	1149	A
47	2	1150	A
47	2	1153	C
47	2	1154	U
47	2	1175	G
47	2	1194	A
47	2	1195	A
47	2	1200	A
47	2	1204	A
47	2	1207	G
47	2	1215	C
47	2	1242	U
47	2	1243	U
47	2	1251	A
47	2	1253	A
47	2	1256	G
47	2	1257	G
47	2	1258	A
47	2	1259	A
47	2	1260	A
47	2	1261	C
47	2	1263	U
47	2	1265	A

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Mol	Chain	Res	Type
47	2	1274	G
47	2	1275	G
47	2	1277	C
47	2	1278	A
47	2	1283	C
47	2	1284	A
47	2	1285	G
47	2	1286	G
47	2	1288	U
47	2	1291	A
47	2	1292	C
47	2	1293	A
47	2	1294	G
47	2	1298	G
47	2	1299	A
47	2	1300	U
47	2	1301	A
47	2	1302	G
47	2	1303	C
47	2	1307	U
47	2	1308	U
47	2	1309	C
47	2	1312	G
47	2	1313	A
47	2	1316	C
47	2	1318	G
47	2	1320	G
47	2	1321	G
47	2	1330	G
47	2	1342	U
47	2	1348	G
47	2	1354	G
47	2	1371	U
47	2	1372	U
47	2	1375	G
47	2	1378	A
47	2	1379	A
47	2	1380	C
47	2	1395	C
47	2	1396	A
47	2	1397	U
47	2	1399	C

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Mol	Chain	Res	Type
47	2	1400	U
47	2	1401	A
47	2	1402	A
47	2	1403	C
47	2	1404	U
47	2	1409	A
47	2	1411	G
47	2	1415	C
47	2	1428	G
47	2	1429	G
47	2	1442	U
47	2	1447	G
47	2	1450	G
47	2	1452	A
47	2	1453	C
47	2	1454	A
47	2	1455	A
47	2	1462	U
47	2	1463	U
47	2	1464	C
47	2	1473	G
47	2	1475	G
47	2	1476	A
47	2	1478	U
47	2	1479	G
47	2	1480	A
47	2	1488	C
47	2	1489	A
47	2	1490	G
47	2	1491	G
47	2	1494	U
47	2	1495	G
47	2	1498	A
47	2	1499	U
47	2	1506	A
47	2	1507	G
47	2	1509	U
47	2	1514	G
47	2	1518	C
47	2	1519	U
47	2	1520	G
47	2	1521	C

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Mol	Chain	Res	Type
47	2	1522	A
47	2	1523	C
47	2	1533	A
47	2	1548	G
47	2	1551	U
47	2	1552	G
47	2	1553	C
47	2	1554	C
47	2	1555	U
47	2	1556	A
47	2	1557	C
47	2	1558	C
47	2	1560	U
47	2	1570	G
47	2	1574	C
47	2	1580	A
47	2	1584	G
47	2	1585	U
47	2	1588	A
47	2	1595	U
47	2	1599	U
47	2	1601	A
47	2	1604	G
47	2	1612	G
47	2	1618	C
47	2	1621	U
47	2	1623	A
47	2	1625	U
47	2	1637	A
47	2	1638	G
47	2	1639	G
47	2	1641	A
47	2	1647	A
47	2	1648	G
47	2	1654	G
47	2	1661	A
47	2	1662	U
47	2	1664	A
47	2	1665	G
47	2	1680	G
47	2	1683	C
47	2	1684	C

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Mol	Chain	Res	Type
47	2	1685	U
47	2	1686	G
47	2	1697	A
47	2	1698	C
47	2	1699	A
47	2	1700	C
47	2	1711	U
47	2	1721	U
47	2	1722	G
47	2	1726	G
47	2	1744	G
47	2	1745	A
47	2	1746	U
47	2	1749	G
47	2	1756	C
47	2	1757	G
47	2	1760	G
47	2	1761	U
47	2	1777	G
47	2	1778	C
47	2	1782	G
47	2	1783	C
47	2	1784	G
47	2	1785	C
47	2	1800	A
47	2	1817	G
47	2	1819	A
47	2	1823	A
47	2	1824	A
47	2	1825	A
47	2	1826	G
47	2	1829	G
47	2	1831	A
47	2	1835	A
47	2	1837	G
47	2	1838	U
47	2	1841	C
47	2	1842	C
47	2	1845	A
47	2	1849	G
47	2	1851	A
47	2	1852	C

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Mol	Chain	Res	Type
47	2	1858	G
47	2	1859	A
47	2	1861	G
47	2	1862	G
47	2	1863	A
47	2	1864	U
47	2	1865	C
47	2	1869	A
82	1	6420	A
82	1	6424	U
82	1	6425	A
82	1	6426	U
82	1	6427	G
82	1	6428	G
82	1	6429	U
82	1	6430	U
82	1	6431	A
82	1	6432	C
82	1	6433	C
82	1	6434	C
82	1	6435	A
82	1	6438	A
82	1	6445	G
82	1	6449	U
82	1	6450	U
82	1	6451	U
82	1	6455	A
82	1	6457	A
82	1	6470	A
82	1	6472	G
82	1	6473	C
82	1	6474	U
82	1	6475	U
82	1	6482	A
82	1	6483	U
82	1	6484	G
82	1	6485	G
82	1	6486	U
82	1	6487	C
82	1	6488	G
82	1	6492	U
82	1	6493	G

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Mol	Chain	Res	Type
82	1	6494	C
82	1	6499	U
82	1	6501	U
82	1	6502	A
82	1	6505	G
82	1	6506	U
82	1	6507	G
82	1	6509	G
82	1	6510	G
82	1	6511	A
82	1	6512	G
82	1	6513	C
82	1	6514	C
82	1	6515	U
82	1	6516	C
82	1	6517	G
82	1	6518	G
82	1	6521	G
82	1	6522	C
82	1	6523	A
82	1	6526	C
82	1	6527	C
82	1	6528	C
82	1	6532	A
82	1	6533	A
82	1	6534	A
82	1	6535	U
82	1	6536	C
82	1	6538	U
82	1	6540	U
82	1	6541	A
82	1	6542	U
82	1	6544	G
82	1	6545	G
82	1	6548	A
82	1	6549	G
82	1	6550	G
82	1	6551	A
82	1	6552	A
82	1	6554	A
82	1	6555	G
82	1	6556	C

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Mol	Chain	Res	Type
82	1	6557	U
82	1	6558	G
82	1	6562	U
82	1	6567	A
82	1	6568	G
82	1	6571	A
82	1	6572	C
82	1	6575	C
82	1	6577	G
82	1	6581	U
82	1	6585	G
82	1	6586	U
82	1	6587	A
82	1	6588	A
82	1	6589	C
82	1	6590	A
82	1	6591	C
82	1	6597	G
82	1	6598	C
82	1	6599	G
82	1	6601	U
82	1	6602	C
82	1	6603	C
82	1	6604	G
82	1	6605	A
82	1	6606	A
82	1	6607	A
82	1	6608	U
82	1	6609	A
82	1	6610	C
82	1	6611	C
82	1	6612	A
82	1	6613	U
82	1	6616	C
82	1	6617	U
82	1	6618	U
82	1	6620	A
82	1	6621	U
82	1	6622	A

All (143) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	47	A
1	5	48	G
1	5	125	C
1	5	170	C
1	5	209	U
1	5	217	C
1	5	275	C
1	5	385	A
1	5	408	A
1	5	449	C
1	5	504	G
1	5	920	C
1	5	922	C
1	5	923	C
1	5	925	G
1	5	928	A
1	5	935	G
1	5	936	C
1	5	955	G
1	5	1183	C
1	5	1236	C
1	5	1237	C
1	5	1287	G
1	5	1300	G
1	5	1370	G
1	5	1445	U
1	5	1455	G
1	5	1633	G
1	5	1654	G
1	5	1676	C
1	5	1733	G
1	5	1740	C
1	5	1881	C
1	5	1960	A
1	5	1974	U
1	5	2046	G
1	5	2259	G
1	5	2313	A
1	5	2370	A
1	5	2428	A
1	5	2490	U
1	5	2502	A
1	5	2529	A

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Mol	Chain	Res	Type
1	5	2554	U
1	5	2587	A
1	5	2661	U
1	5	2782	U
1	5	2848	G
1	5	3603	G
1	5	3710	G
1	5	3758	U
1	5	3759	A
1	5	3765	G
1	5	3774	A
1	5	3784	A
1	5	3785	A
1	5	3876	A
1	5	3888	G
1	5	3904	G
1	5	3938	G
1	5	4054	C
1	5	4076	G
1	5	4119	C
1	5	4170	A
1	5	4180	G
1	5	4221	C
1	5	4232	U
1	5	4448	G
1	5	4560	C
1	5	4572	U
1	5	4583	C
1	5	4626	A
1	5	4719	G
1	5	4882	U
1	5	4884	G
1	5	4925	U
1	5	5016	A
2	7	109	U
3	8	94	G
47	2	24	C
47	2	73	C
47	2	80	G
47	2	98	C
47	2	110	U
47	2	172	U

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Mol	Chain	Res	Type
47	2	293	C
47	2	316	G
47	2	407	G
47	2	449	A
47	2	461	U
47	2	465	A
47	2	493	A
47	2	500	A
47	2	532	C
47	2	553	U
47	2	561	A
47	2	587	A
47	2	659	G
47	2	752	G
47	2	874	G
47	2	885	U
47	2	886	A
47	2	908	A
47	2	917	U
47	2	1165	G
47	2	1258	A
47	2	1260	A
47	2	1262	C
47	2	1277	C
47	2	1298	G
47	2	1300	U
47	2	1312	G
47	2	1452	A
47	2	1462	U
47	2	1474	A
47	2	1488	C
47	2	1490	G
47	2	1497	G
47	2	1519	U
47	2	1554	C
47	2	1556	A
47	2	1637	A
47	2	1664	A
47	2	1685	U
47	2	1743	G
47	2	1744	G
47	2	1824	A

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Mol	Chain	Res	Type
47	2	1858	G
47	2	1862	G
82	1	6432	C
82	1	6450	U
82	1	6456	U
82	1	6472	G
82	1	6493	G
82	1	6506	U
82	1	6514	C
82	1	6538	U
82	1	6551	A
82	1	6589	C
82	1	6604	G
82	1	6607	A
82	1	6608	U
82	1	6617	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	5	26

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	41.75
1	5	1252:C	O3'	1271:G	P	37.28
1	5	1405:C	O3'	1409:G	P	20.58
1	5	1219:G	O3'	1233:G	P	19.67
1	5	1696:C	O3'	1720:C	P	18.85
1	5	4138:C	O3'	4146:G	P	18.54
1	5	991:U	O3'	1064:G	P	17.85
1	5	4101:C	O3'	4107:G	P	17.31
1	5	3977:C	O3'	4034:G	P	16.55
1	5	523:C	O3'	638:G	P	16.52
1	5	5022:U	O3'	5028:G	P	15.62
1	5	760:G	O3'	903:C	P	14.99
1	5	1364:U	O3'	1368:A	P	14.85
1	5	4777:C	O3'	4859:C	P	14.39
1	5	2901:G	O3'	3597:G	P	12.73
1	5	4729:A	O3'	4735:G	P	9.82
1	5	1180:C	O3'	1183:C	P	9.58
1	5	182:G	O3'	189:G	P	8.45
1	5	4740:G	O3'	4743:G	P	8.00
1	5	512:U	O3'	515:C	P	7.78
1	5	500:G	O3'	504:G	P	7.67
1	5	1438:U	O3'	1440:U	P	4.58
1	5	1411:C	O3'	1412:G	P	4.41
1	5	1100:U	O3'	1168:G	P	4.02
1	5	1239:C	O3'	1244:G	P	3.64
1	5	4899:G	O3'	4902:C	P	3.30

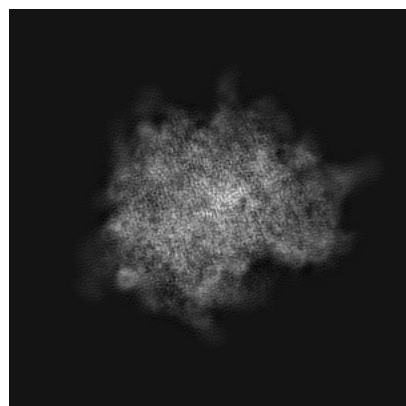
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20258. These allow visual inspection of the internal detail of the map and identification of artifacts.

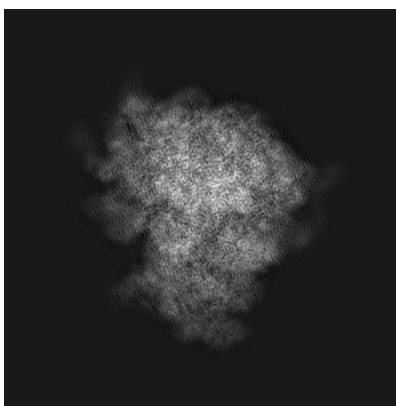
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

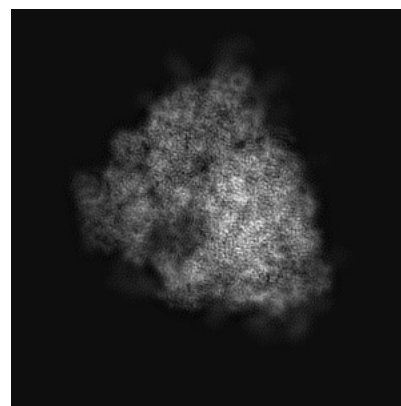
6.1.1 Primary map



X

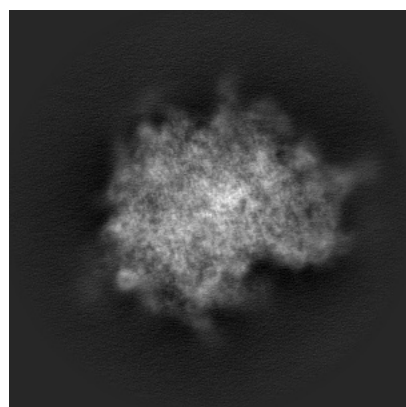


Y

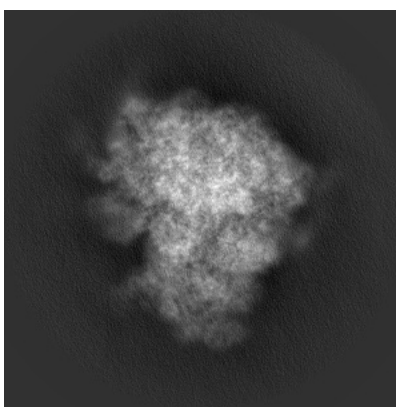


Z

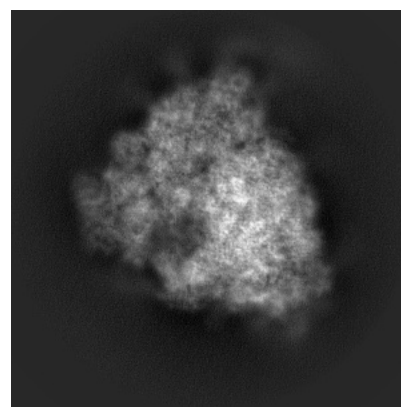
6.1.2 Raw map



X



Y

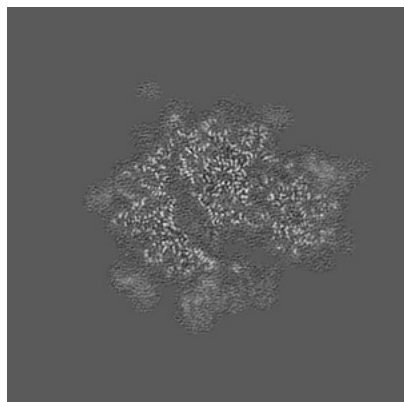


Z

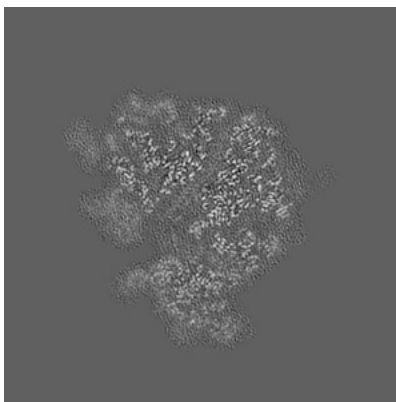
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

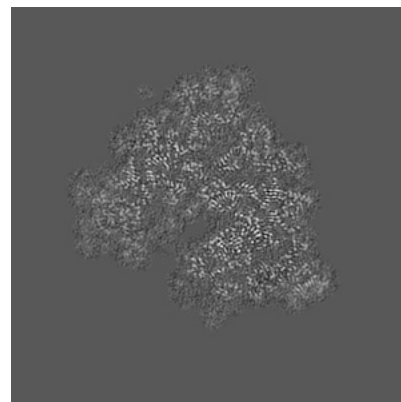
6.2.1 Primary map



X Index: 208

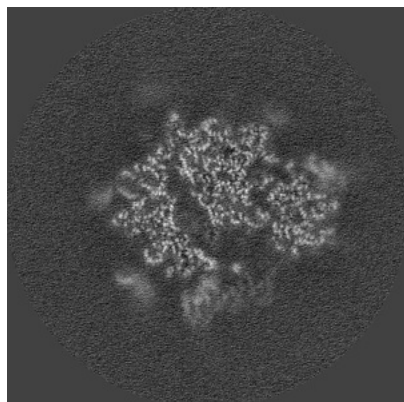


Y Index: 208

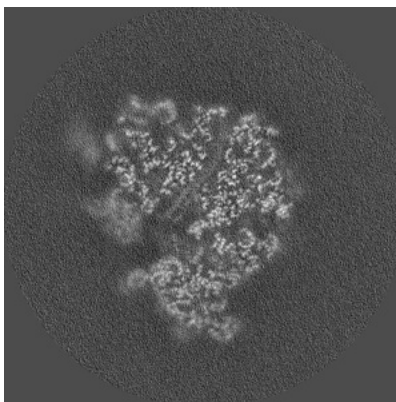


Z Index: 208

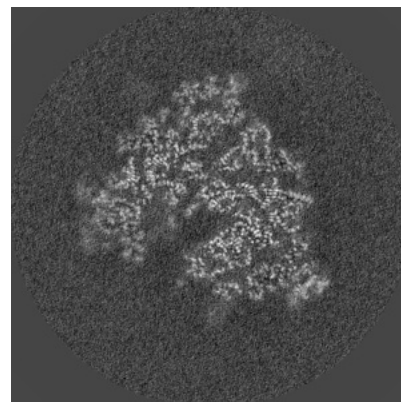
6.2.2 Raw map



X Index: 208



Y Index: 208

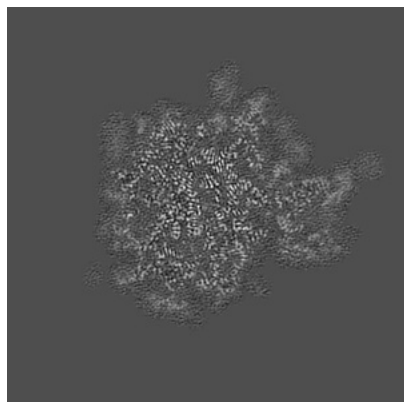


Z Index: 208

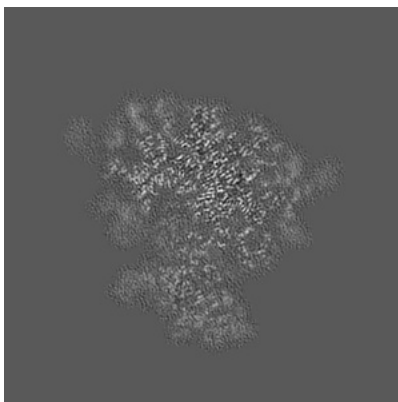
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

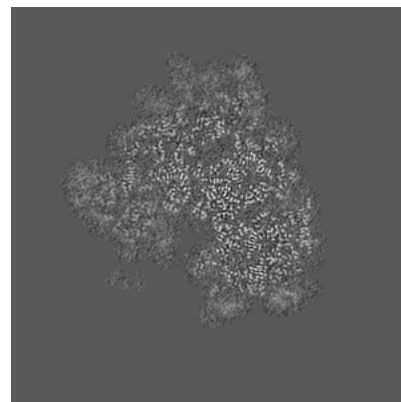
6.3.1 Primary map



X Index: 239

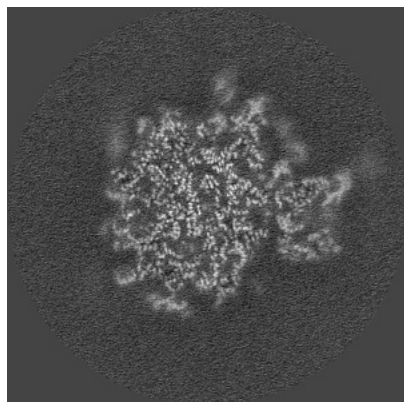


Y Index: 217

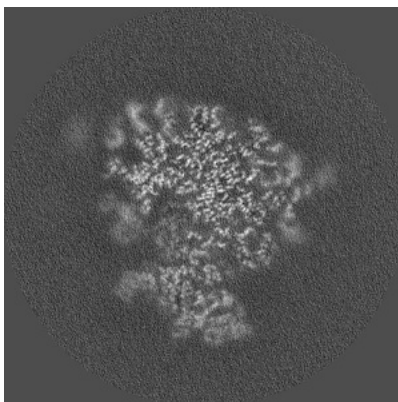


Z Index: 225

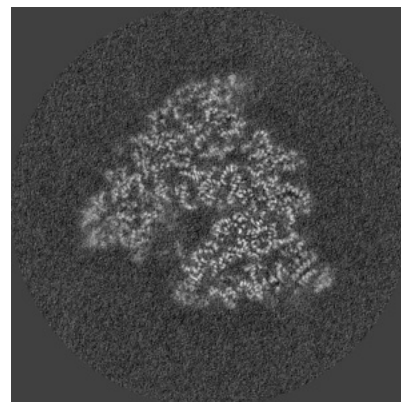
6.3.2 Raw map



X Index: 239



Y Index: 217

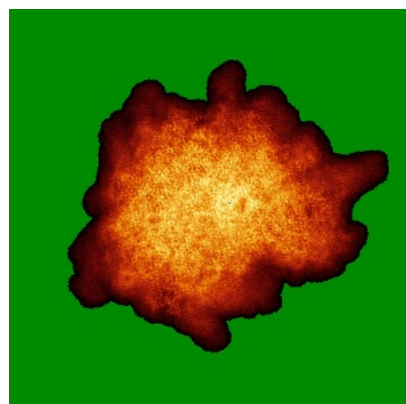


Z Index: 199

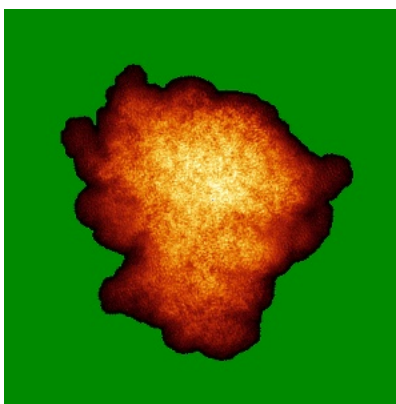
The images above show the largest variance slices of the map in three orthogonal directions.

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

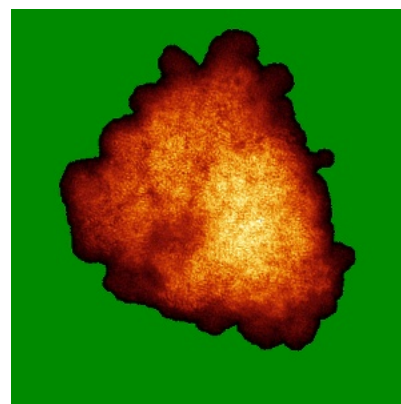
6.4.1 Primary map



X

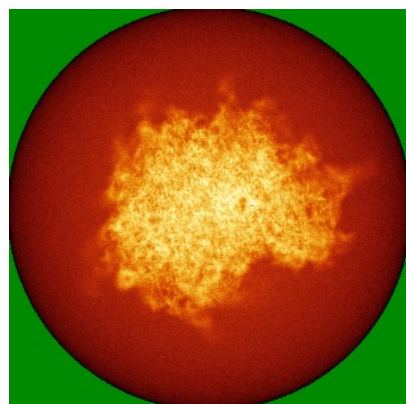


Y

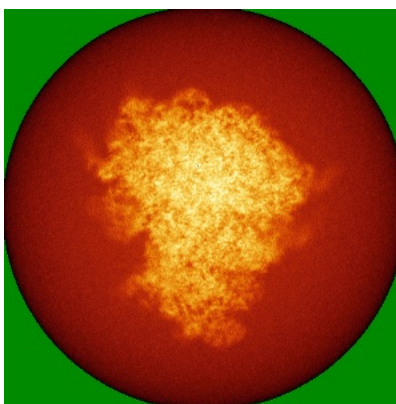


Z

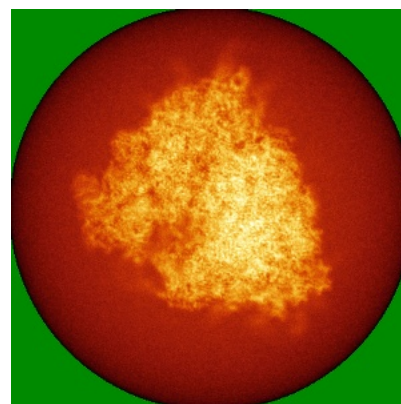
6.4.2 Raw map



X



Y

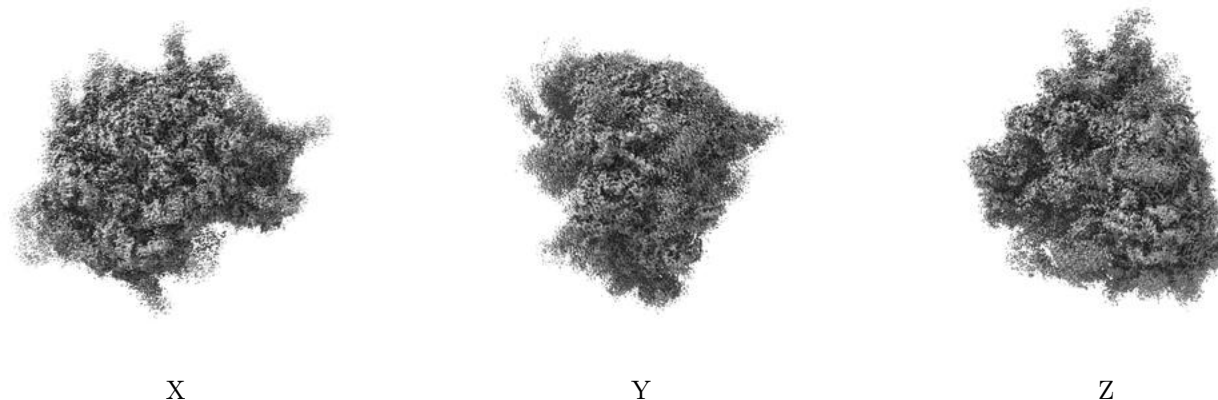


Z

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.

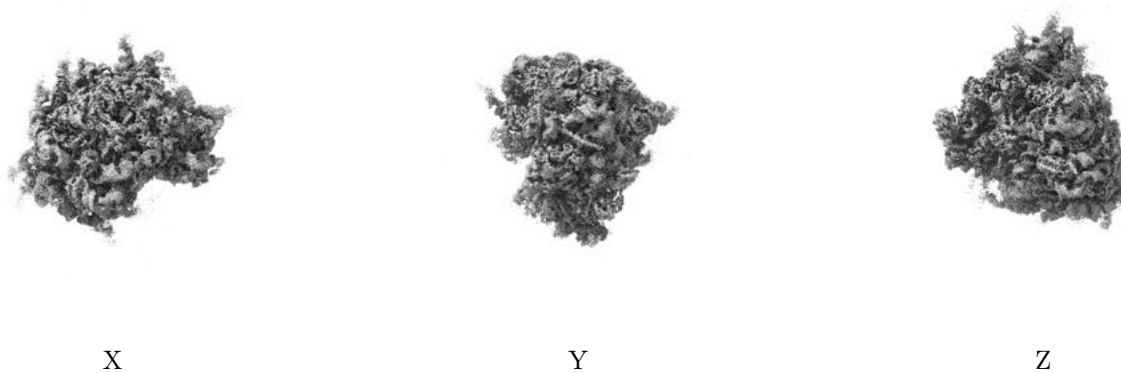
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. 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.

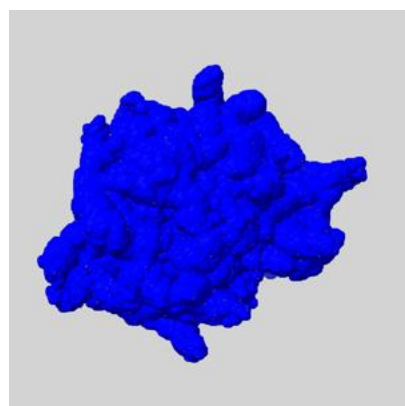
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

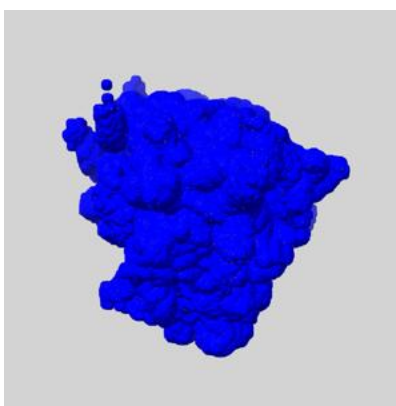
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

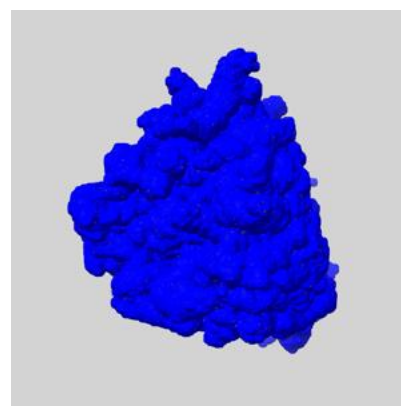
6.6.1 emd_20258_msk_1.map [i](#)



X



Y

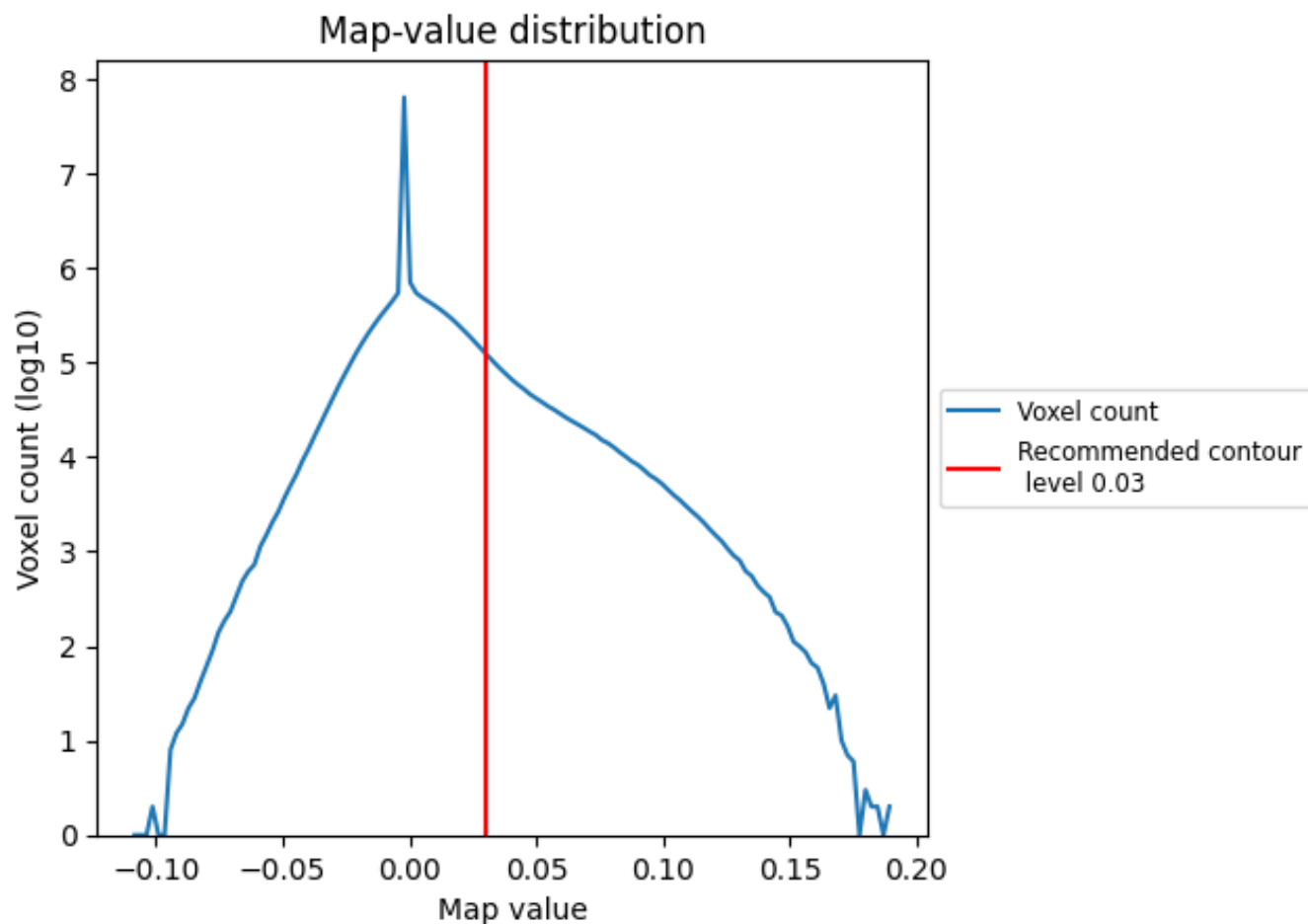


Z

7 Map analysis [i](#)

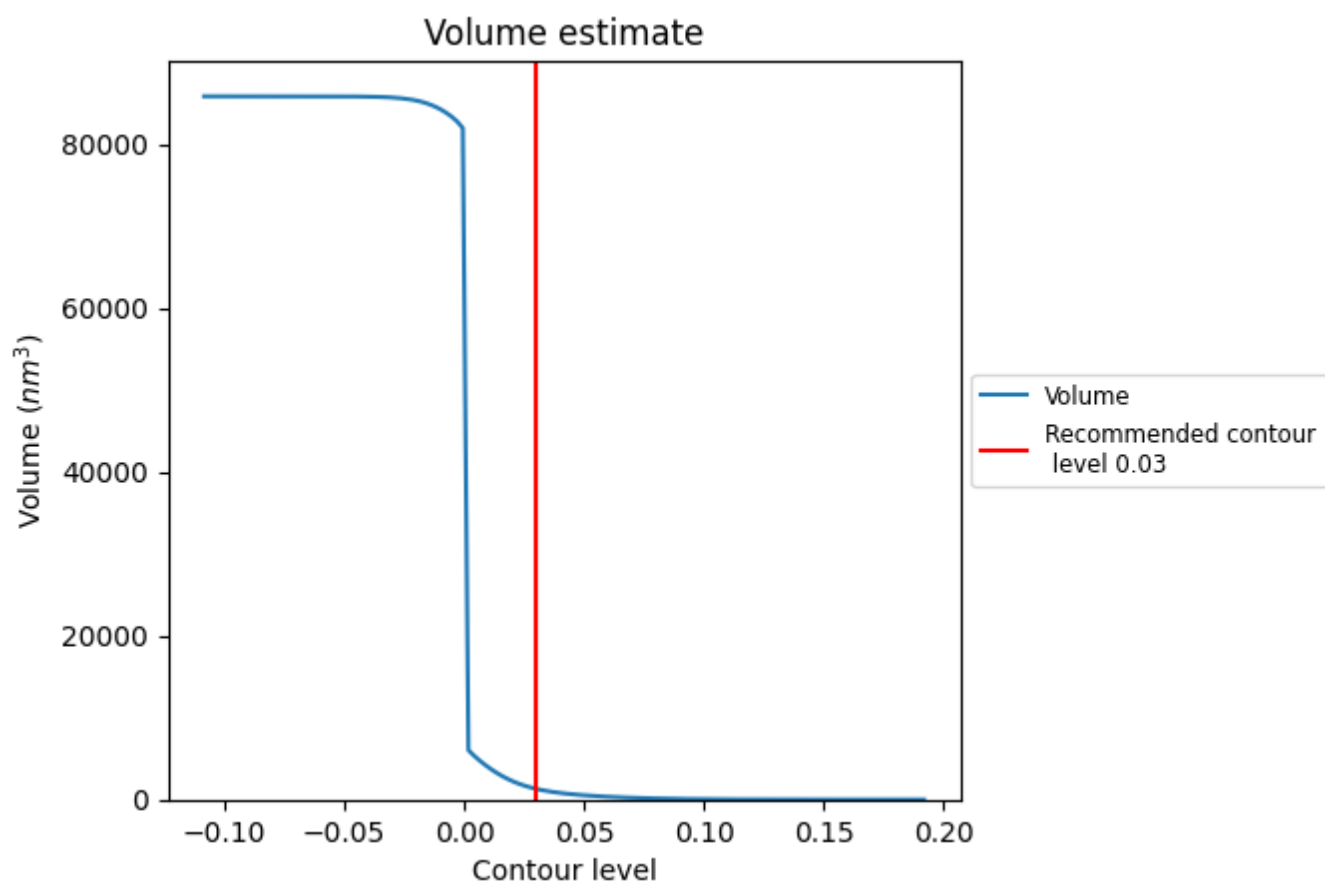
This section contains the results of statistical analysis of the map.

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.

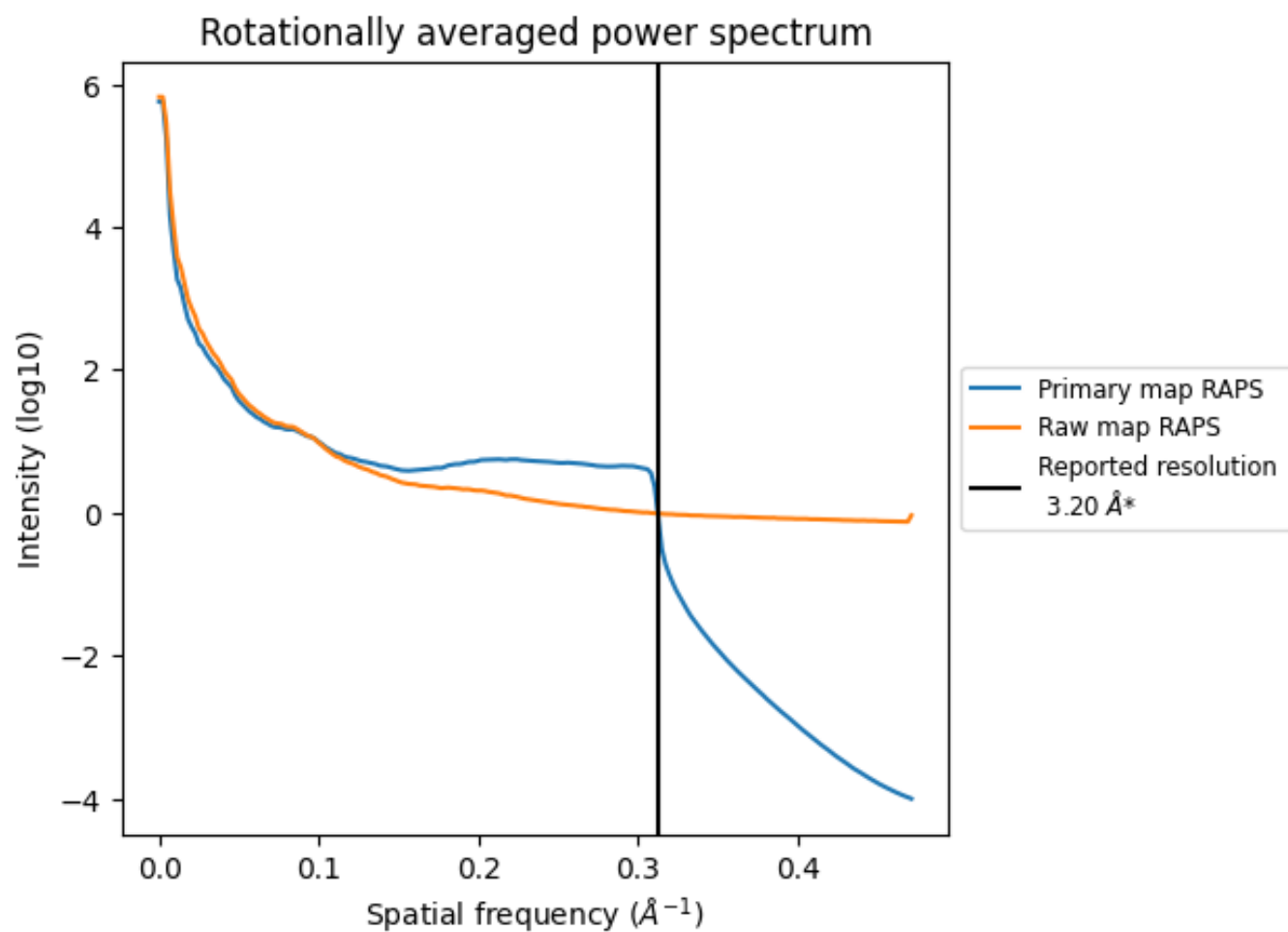
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1309 nm³; this corresponds to an approximate mass of 1182 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 ⓘ

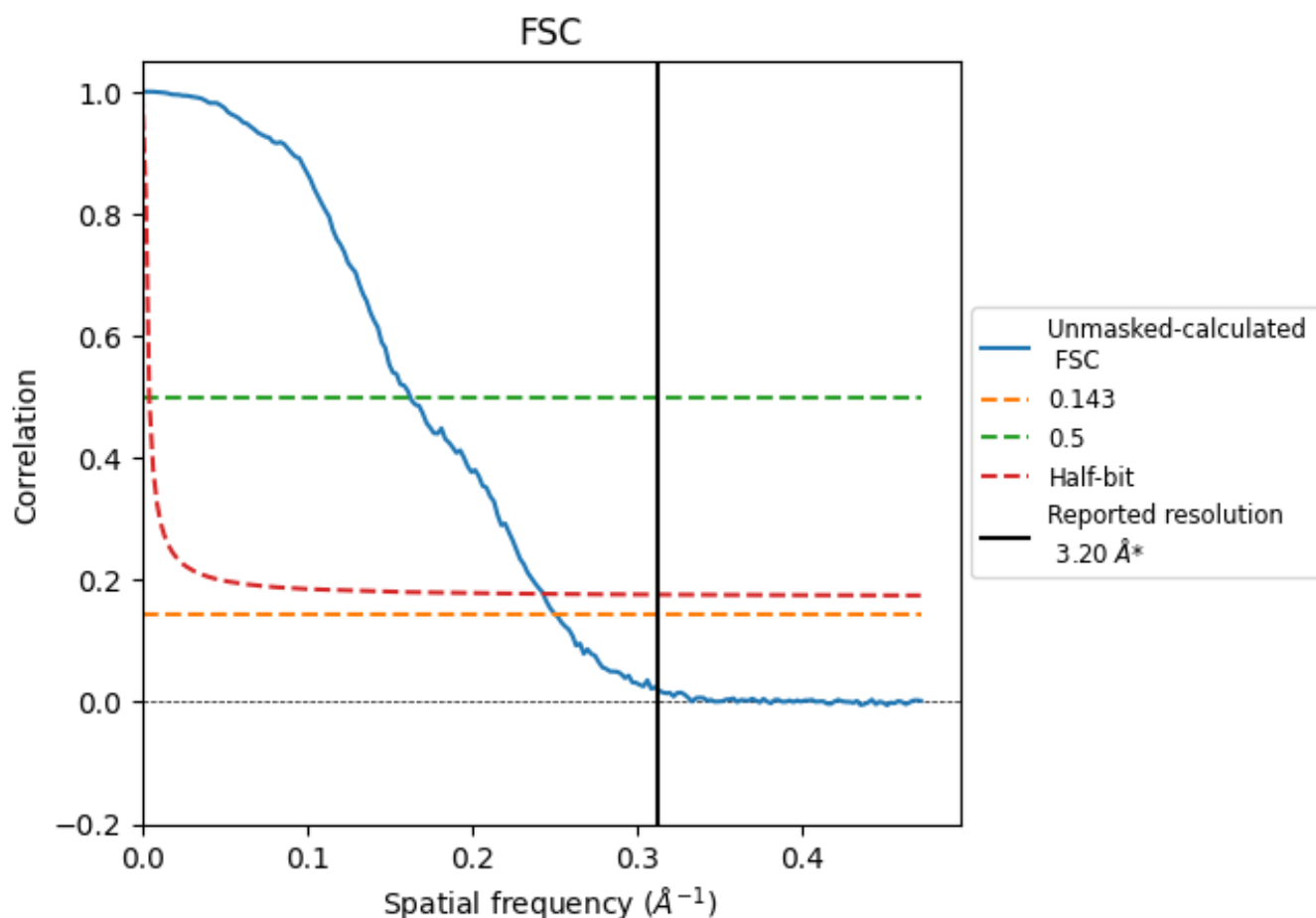


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.99	6.16	4.12

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.99 differs from the reported value 3.2 by more than 10 %

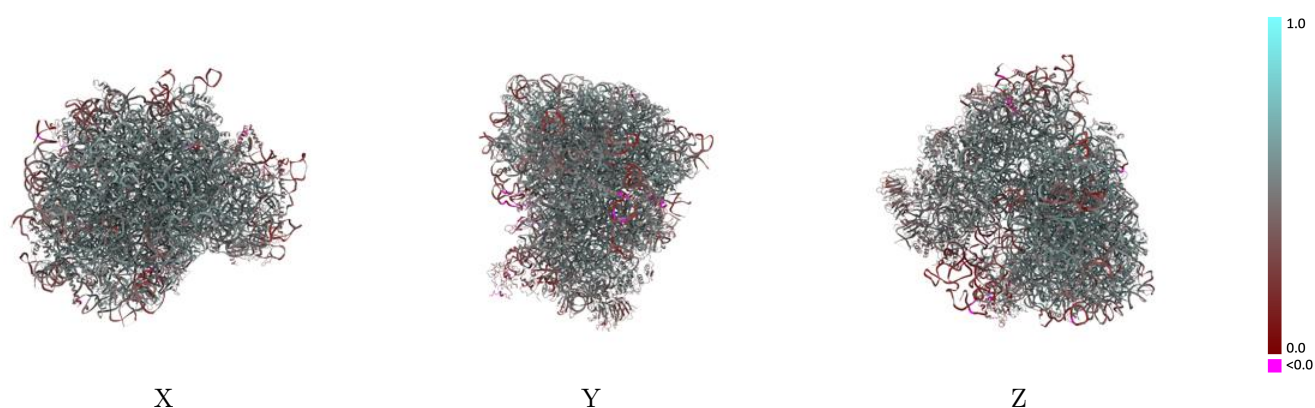
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20258 and PDB model 6P5N. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)

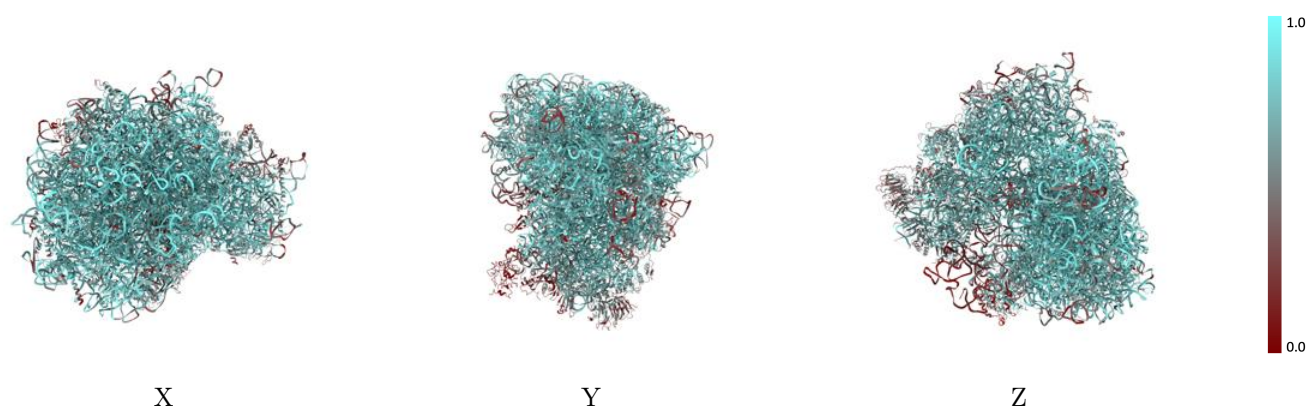
This section was not generated.

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



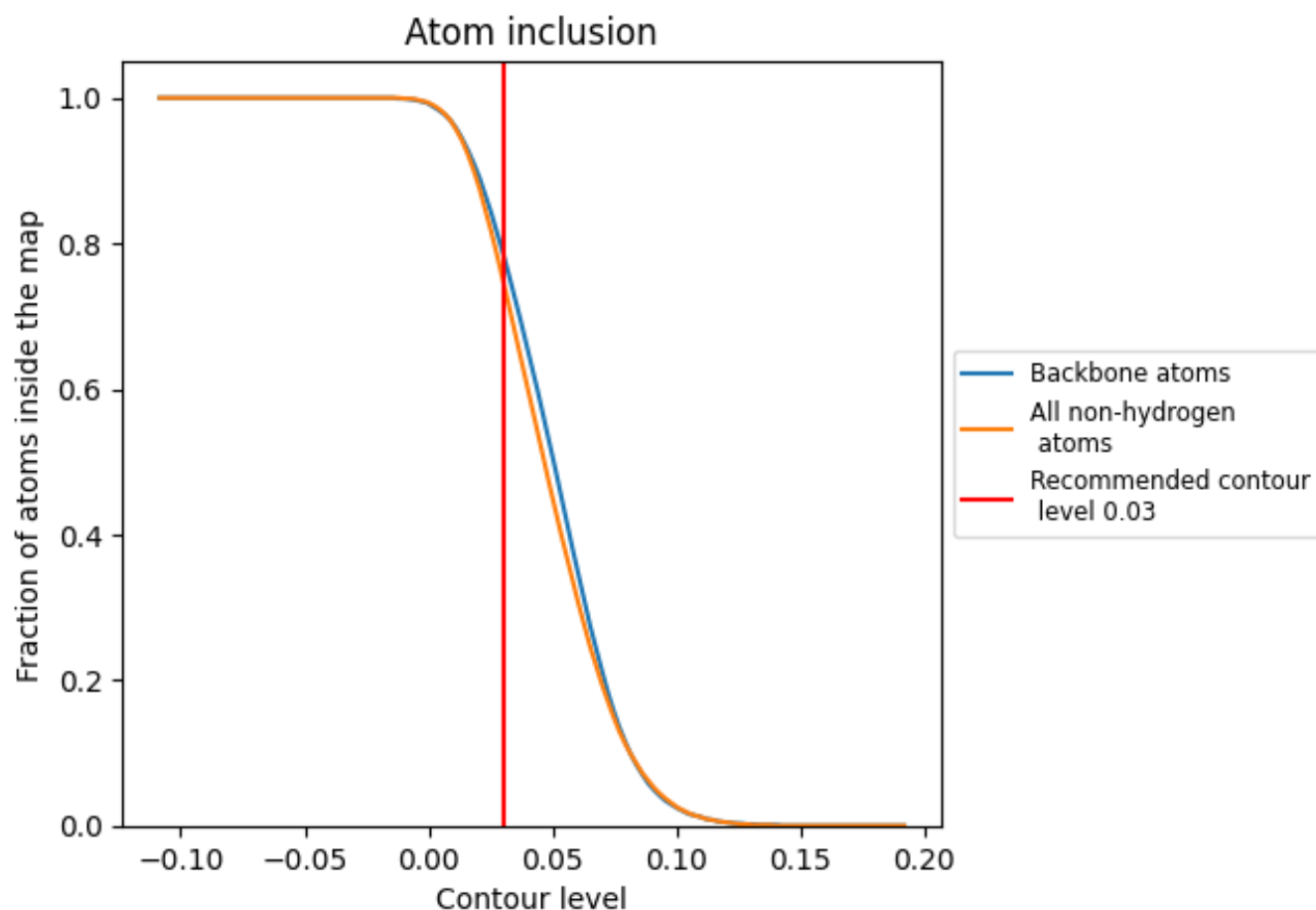
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 75% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7500	 0.4850
1	 0.2500	 0.2150
2	 0.8020	 0.4770
5	 0.8370	 0.4960
7	 0.9270	 0.5430
8	 0.8660	 0.5170
AA	 0.8280	 0.5530
AB	 0.8060	 0.5410
AC	 0.7950	 0.5350
AD	 0.7600	 0.5180
AE	 0.7440	 0.5010
AF	 0.8030	 0.5440
AG	 0.7180	 0.5010
AH	 0.7190	 0.5150
AI	 0.7530	 0.5300
AJ	 0.7010	 0.4970
AK	 0.1630	 0.2730
AL	 0.7700	 0.5280
AM	 0.7580	 0.5210
AN	 0.8590	 0.5640
AO	 0.7950	 0.5310
AP	 0.8040	 0.5460
AQ	 0.7950	 0.5490
AR	 0.7290	 0.4860
AS	 0.8020	 0.5340
AT	 0.7610	 0.5360
AU	 0.6580	 0.4710
AV	 0.7830	 0.5410
AW	 0.7840	 0.5430
AX	 0.7480	 0.5300
AY	 0.7680	 0.5330
AZ	 0.7640	 0.5230
Aa	 0.8380	 0.5550
Ab	 0.6810	 0.4740
Ac	 0.7900	 0.5340



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Chain	Atom inclusion	Q-score
Ad	 0.7360	 0.5270
Ae	 0.7950	 0.5480
Af	 0.8210	 0.5500
Ag	 0.7710	 0.5320
Ah	 0.7340	 0.5040
Ai	 0.7240	 0.5050
Aj	 0.8500	 0.5560
Ak	 0.6460	 0.4770
Al	 0.7890	 0.5420
Am	 0.7590	 0.5380
An	 0.7890	 0.5430
Ao	 0.7830	 0.5460
Ap	 0.7640	 0.5340
Aq	 0.2120	 0.3460
Ar	 0.7940	 0.5400
B	 0.6870	 0.4970
C	 0.6960	 0.5030
D	 0.7290	 0.5150
E	 0.4890	 0.4330
F	 0.7010	 0.5030
G	 0.6380	 0.4810
H	 0.5800	 0.4290
I	 0.5890	 0.4480
J	 0.7190	 0.5110
K	 0.6970	 0.4950
L	 0.3140	 0.3490
M	 0.7260	 0.5250
N	 0.0270	 0.2410
O	 0.7570	 0.5240
P	 0.7220	 0.5180
Q	 0.4420	 0.3940
R	 0.6160	 0.4630
S	 0.5710	 0.4440
T	 0.5390	 0.4260
U	 0.5600	 0.4150
V	 0.4630	 0.4270
W	 0.6900	 0.4890
X	 0.7720	 0.5240
Y	 0.7300	 0.5240
Z	 0.6630	 0.4740
a	 0.5160	 0.4170
b	 0.7460	 0.5230

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Chain	Atom inclusion	Q-score
c	 0.6530	 0.4970
d	 0.6470	 0.5090
e	 0.6120	 0.4390
f	 0.5650	 0.4630
g	 0.0820	 0.2690
h	 0.4220	 0.3740