



Full wwPDB EM Validation Report ⓘ

Mar 10, 2025 – 04:51 PM EDT

PDB ID : 9B0Q
EMDB ID : EMD-44050
Title : In situ human top-back di-ribosome structure (Composite map)
Authors : Wei, Z.; Yong, Z.
Deposited on : 2024-03-12
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.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

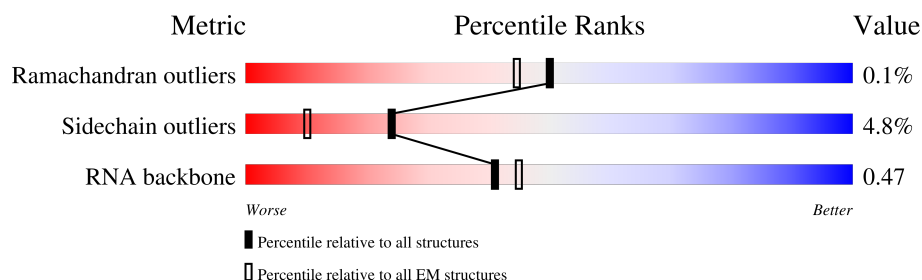
1 Overall quality at a glance

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.



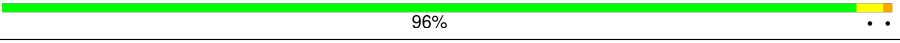
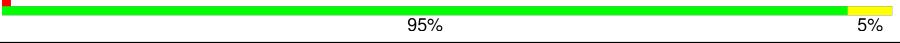
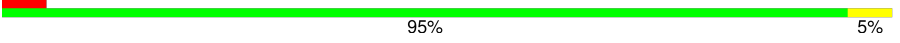

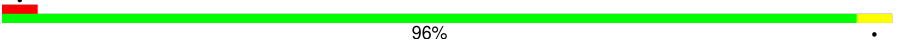
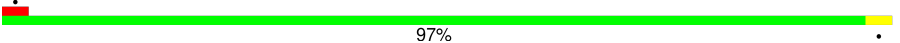



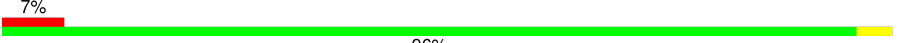
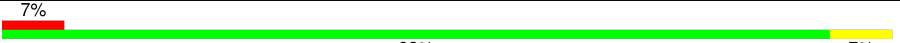
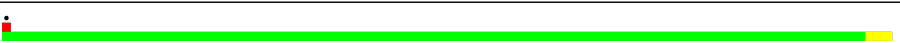



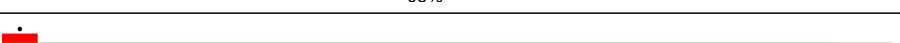
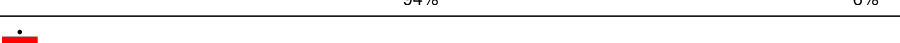
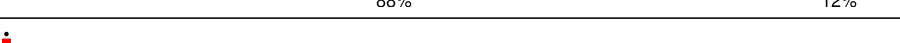
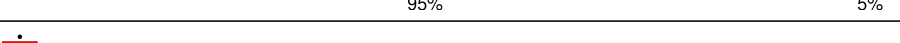
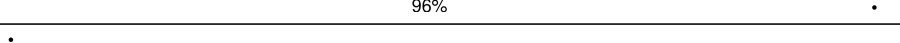
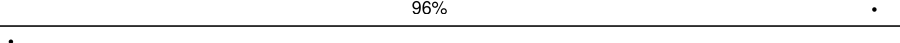
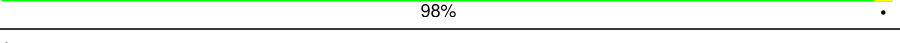
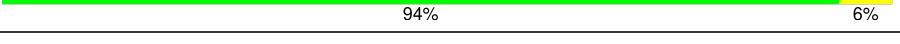
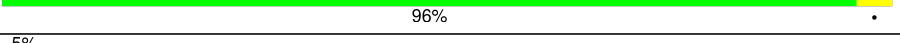
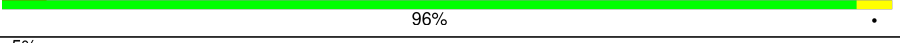
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	CH	125	
1	cH	125	
2	SE	262	
2	sE	262	
3	SI	206	
3	sI	206	
4	SL	153	
4	sL	153	

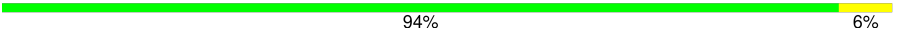
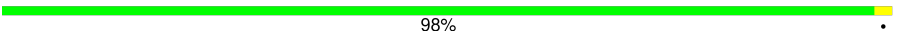
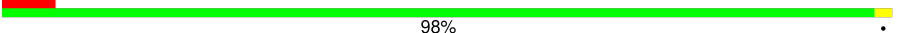












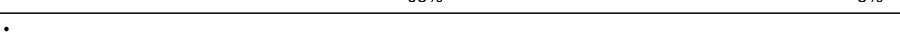
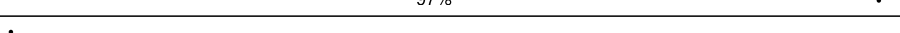

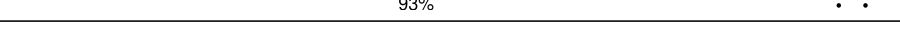
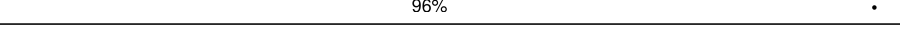
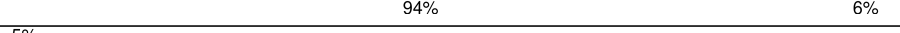
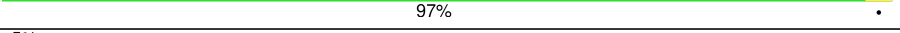
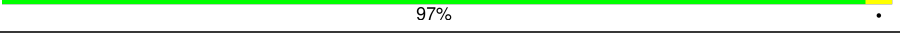
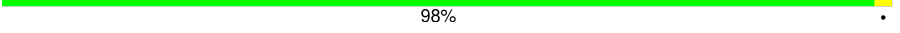
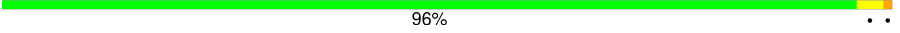
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Mol	Chain	Length	Quality of chain
5	SX	141	 96%
5	sX	141	 95%
6	SG	237	 95%
6	sG	237	 93%
7	SJ	185	 96%
7	sJ	185	 97%
8	SY	131	 91%
8	sY	131	 93%
9	se	58	 98%
10	SA	221	 96%
10	sA	221	 93%
11	SB	214	 97%
11	sB	214	 95%
12	SH	189	 92%
12	sH	189	 95%
13	SV	83	 94%
13	sV	83	 88%
14	Sa	102	 95%
14	sa	102	 96%
15	SC	222	 96%
15	sC	222	 98%
16	SN	150	 94%
16	sN	150	 96%
17	SO	140	 96%
17	sO	140	 96%


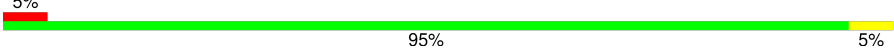
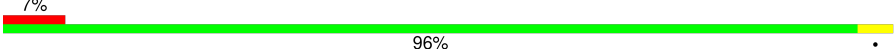
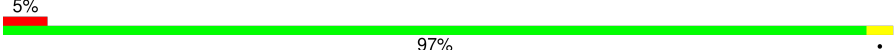
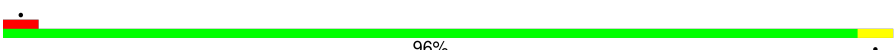

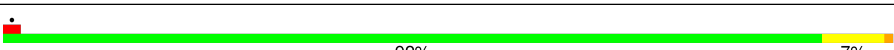
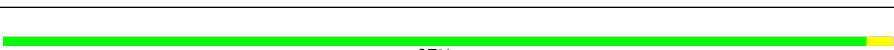
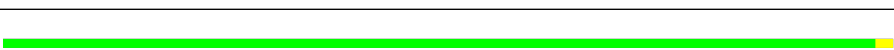
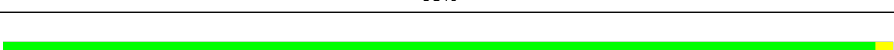
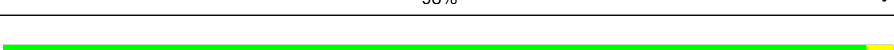
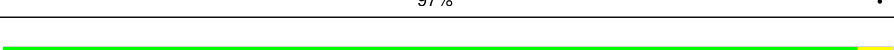
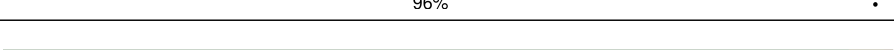
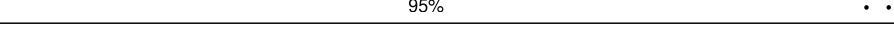
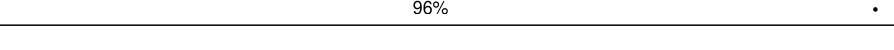
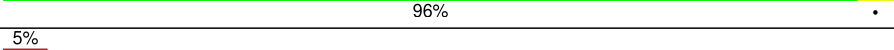
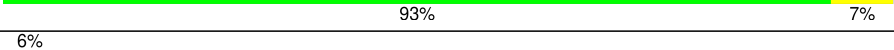
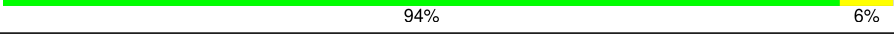
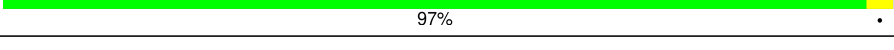
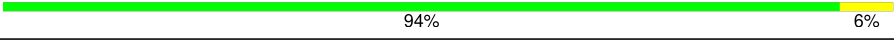
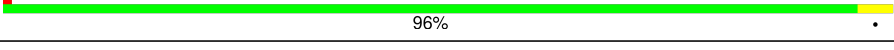
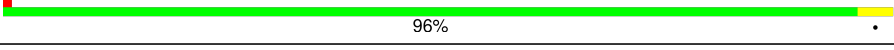
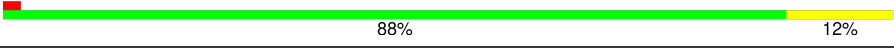

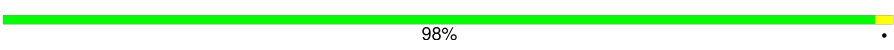
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Mol	Chain	Length	Quality of chain
18	SW	129	 94% 6%
18	sW	129	 98%
19	Sb	83	 6% 98%
19	sb	83	 93% 7%
20	L7	120	 88% 12%
20	l7	120	 87% 13%
21	L8	156	 82% 18%
21	l8	156	 77% 23%
22	LA	248	 97%
22	lA	248	 96%
23	LB	402	 98%
23	lB	402	 97%
24	LC	368	 96%
24	lC	368	 95% 5%
25	LD	293	 95% 5%
25	lD	293	 97%
26	LE	247	 92%
26	lE	247	 93%
27	LF	225	 96%
27	lF	225	 94% 6%
28	LG	241	 5% 97%
28	lG	241	 5% 97%
29	LH	190	 98%
29	lH	190	 96%
30	LI	213	 91% 5%

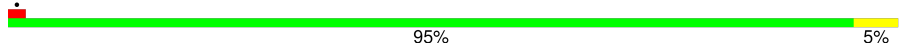
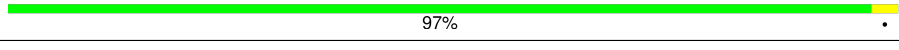
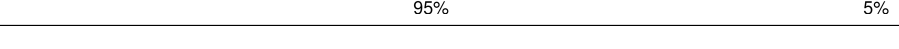
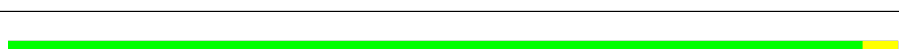
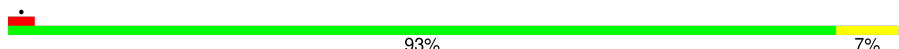
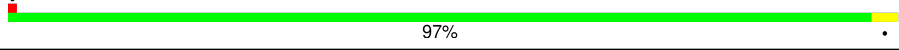
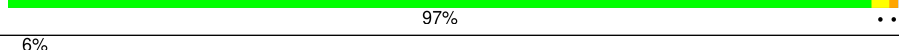
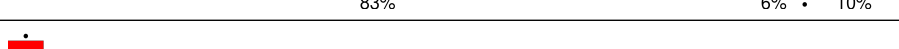

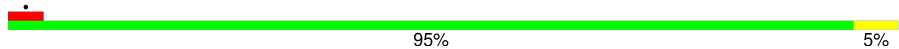
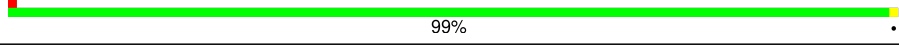
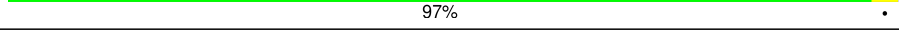
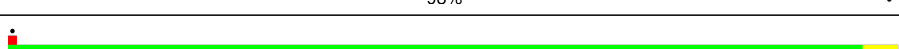
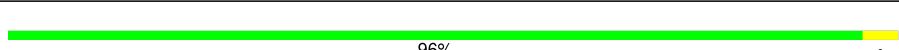
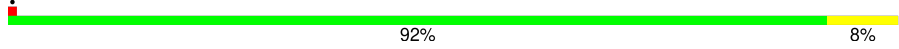
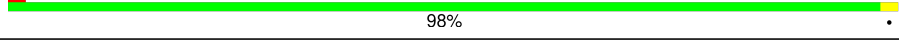
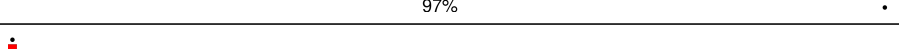


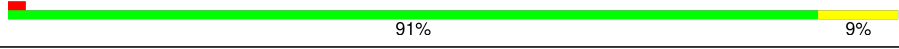
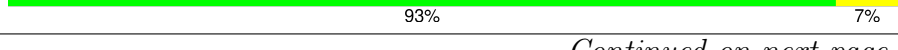



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Mol	Chain	Length	Quality of chain
30	II	213	
31	LJ	176	
31	IJ	176	
32	LL	210	
32	IL	210	
33	LM	139	
33	IM	139	
34	LN	203	
34	IN	203	
35	LO	201	
35	IO	201	
36	LP	153	
36	IP	153	
37	LQ	187	
37	IQ	187	
38	LR	187	
38	IR	187	
39	LS	175	
39	IS	175	
40	LT	159	
40	IT	159	
41	LU	101	
41	IU	101	
42	LV	131	
42	IV	131	

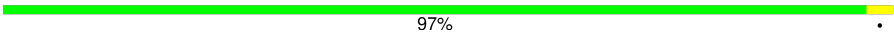
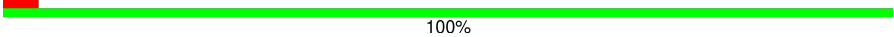
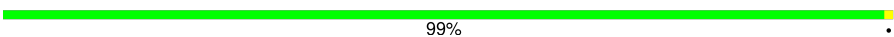
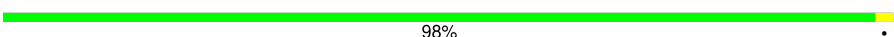

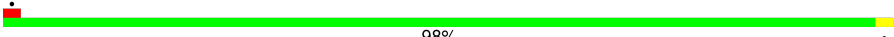
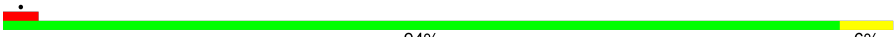



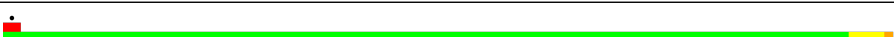


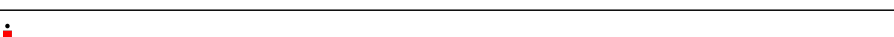
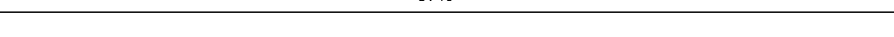
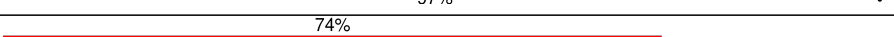
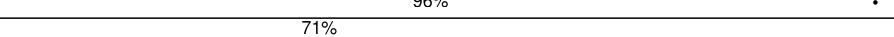

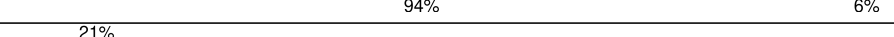
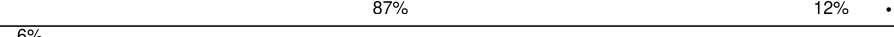
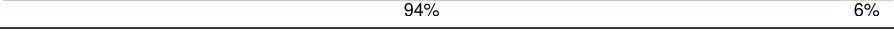
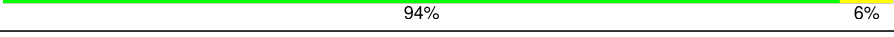
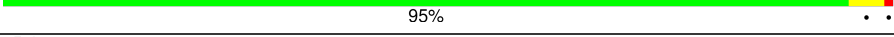
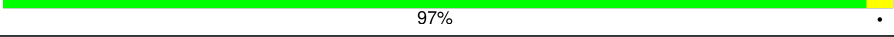

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Mol	Chain	Length	Quality of chain
43	LX	120	
43	IX	120	
44	LY	134	
44	IY	134	
45	LZ	135	
45	IZ	135	
46	La	147	
46	la	147	
47	Lb	121	
47	lb	121	
48	Lc	98	
48	lc	98	
49	Ld	107	
49	ld	107	
50	Le	128	
50	le	128	
51	Lf	109	
51	lf	109	
52	Lg	114	
52	lg	114	
53	Lh	122	
53	lh	122	
54	Li	102	
54	li	102	
55	Lj	86	

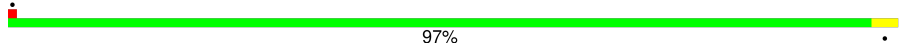
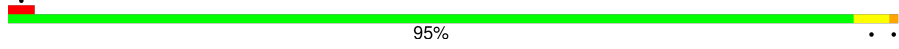
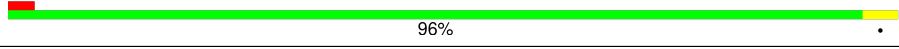
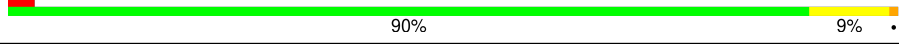
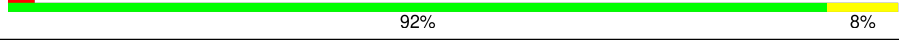
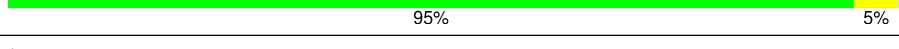
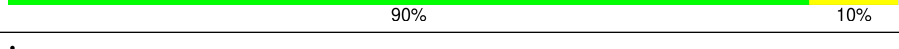
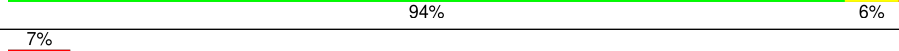
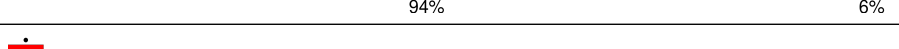
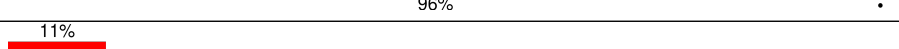
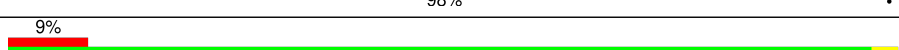
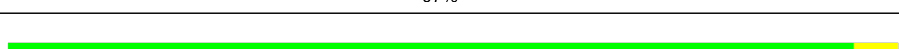
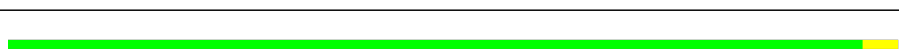
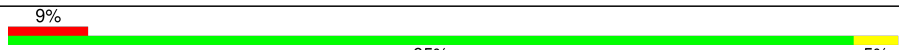
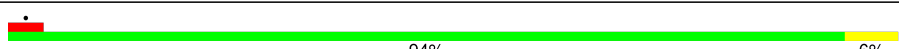
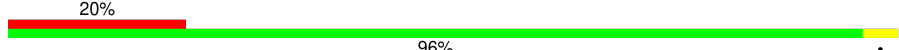
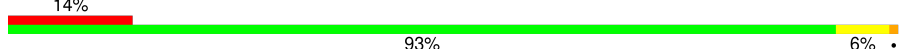

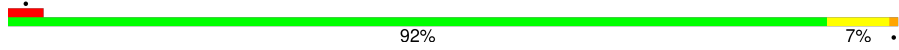
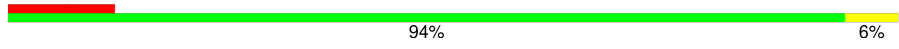
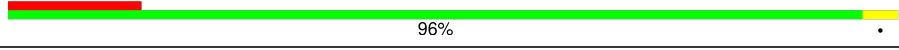
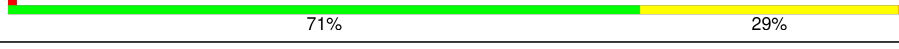

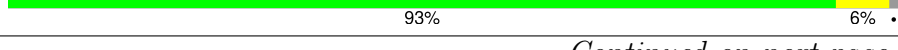

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Mol	Chain	Length	Quality of chain
55	lj	86	 97%
56	Lk	69	 100%
56	lk	69	 99%
57	Ll	50	 98%
57	ll	50	 90% 10%
58	Lm	52	 98%
58	lm	52	 94% 6%
59	Ln	24	 100%
59	ln	24	 92% 8%
60	Lo	105	 95% 5%
60	lo	105	 95% 5%
61	Lp	91	 98%
61	lp	91	 97%
62	Lr	125	 97%
62	lr	125	 97%
63	Lz	217	 74% 96%
63	lz	217	 71% 90% 10%
64	SR	135	 7% 94% 6%
64	sR	135	 21% 87% 12%
65	SD	227	 6% 94% 6%
65	sD	227	 94% 6%
66	SF	189	 95%
66	sF	189	 5% 97%
67	SK	98	 84% 16%
67	sK	98	 92% 8%

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Mol	Chain	Length	Quality of chain
68	SP	121	
68	sP	121	
69	SQ	144	
69	sQ	144	
70	SS	145	
70	sS	145	
71	ST	143	
71	sT	143	
72	SU	104	
72	sU	104	
73	Sc	64	
73	sc	64	
74	Sd	55	
74	sd	55	
75	Sg	313	
75	sg	313	
76	SM	122	
76	sM	122	
77	SZ	75	
77	sZ	75	
78	Sf	67	
78	sf	67	
79	S2	1740	
79	s2	1740	
80	CB	856	

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Mol	Chain	Length	Quality of chain
80	cB	856	
81	AP	73	
81	aP	73	
82	PE	76	
82	pE	76	
83	Ls	196	
83	ls	196	
84	Lt	141	
84	lt	141	
85	L5	3740	
85	l5	3740	
86	Se	47	
87	LW	124	
87	IW	124	

2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 459641 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Endothelial differentiation-related factor 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	CH	125	Total	C	N	O	0	0
			968	595	189	184		
1	cH	125	Total	C	N	O	0	0
			968	595	189	184		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CH	30	ARG	GLN	conflict	UNP O60869
CH	32	ALA	ARG	conflict	UNP O60869
CH	33	ALA	-	insertion	UNP O60869
CH	34	ALA	-	insertion	UNP O60869
cH	30	ARG	GLN	conflict	UNP O60869
cH	32	ALA	ARG	conflict	UNP O60869
cH	33	ALA	-	insertion	UNP O60869
cH	34	ALA	-	insertion	UNP O60869

- Molecule 2 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	sE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		
2	SE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 3 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	sI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		
3	SI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 4 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	sL	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		
4	SL	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 5 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	sX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		
5	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 6 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	sG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		
6	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 7 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	sJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		
7	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	sY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		
8	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 9 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	sA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		
10	SA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 11 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	sB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		
11	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 12 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	sH	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		
12	SH	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		

- Molecule 13 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	sV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		
13	SV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 14 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	sa	102	Total	C	N	O	S	0	0
			821	512	171	133	5		
14	Sa	102	Total	C	N	O	S	0	0
			821	512	171	133	5		

- Molecule 15 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	sC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		
15	SC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 16 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	sN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		
16	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 17 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	sO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		
17	SO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		

- Molecule 18 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	sW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		
18	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 19 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		
19	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 20 is a RNA chain called RNA (120-MER)5S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
20	17	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		
20	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 21 is a RNA chain called RNA (156-MER)5.8S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
21	18	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		
21	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 22 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	1A	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		
22	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 23 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	1B	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		
23	LB	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

- Molecule 24 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	1C	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		
24	LC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 25 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	1D	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

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Mol	Chain	Residues	Atoms					AltConf	Trace
25	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 26 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	lE	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		
26	LE	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		

- Molecule 27 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	lF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		
27	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 28 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	lG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		
28	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 29 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	lH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		
29	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 30 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	lI	202	Total	C	N	O	S	0	0
			1634	1037	314	269	14		
30	LI	202	Total	C	N	O	S	0	0
			1634	1037	314	269	14		

- Molecule 31 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	IJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		
31	LJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 32 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	IL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		
32	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 33 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	IM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		
33	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 34 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	IN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		
34	LN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 35 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	IO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		
35	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 36 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	IP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		
36	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 37 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	lQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		
37	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 38 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	lR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		
38	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 39 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	lS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		
39	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 40 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	lT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		
40	LT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 41 is a protein called Heparin-binding protein HBp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	lU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
41	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 42 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	IV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		
42	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 43 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	IX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		
43	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

- Molecule 44 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	IY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		
44	LY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 45 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	IZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		
45	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 46 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	la	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		
46	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 47 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		
47	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 48 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		
48	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 49 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		
49	Ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 50 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		
50	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 51 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		
51	Lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 52 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	lg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		
52	Lg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 53 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		
53	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 54 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		
54	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 55 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		
55	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 56 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		
56	Lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 57 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
57	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 58 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		
58	Lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 59 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		
59	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		
60	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 61 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		
61	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 62 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		
62	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 63 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	lz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		
63	Lz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 64 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	sR	135	Total	C	N	O	S	0	0
			1090	685	202	198	5		
64	SR	135	Total	C	N	O	S	0	0
			1090	685	202	198	5		

- Molecule 65 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	sD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		
65	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 66 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	sF	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		
66	SF	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 67 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	sK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		
67	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 68 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	sP	121	Total	C	N	O	S	0	0
			985	623	185	170	7		
68	SP	121	Total	C	N	O	S	0	0
			985	623	185	170	7		

- Molecule 69 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	sQ	144	Total	C	N	O	S	0	0
			1142	726	216	197	3		
69	SQ	144	Total	C	N	O	S	0	0
			1142	726	216	197	3		

- Molecule 70 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	sS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		
70	SS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		

- Molecule 71 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	sT	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		
71	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 72 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	sU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		
72	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 73 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
73	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 74 is a protein called 40S ribosomal protein S29.

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

- Molecule 75 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		
75	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 76 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	sM	122	Total	C	N	O	S	0	0
			940	590	164	177	9		
76	SM	122	Total	C	N	O	S	0	0
			940	590	164	177	9		

- Molecule 77 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	sZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		
77	SZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 78 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	sf	67	Total	C	N	O	S	0	0
			548	346	102	93	7		
78	Sf	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 79 is a RNA chain called 18S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
79	s2	1740	Total	C	N	O	P	0	0
			36898	16459	6599	12101	1739		
79	S2	1740	Total	C	N	O	P	0	0
			36898	16459	6599	12101	1739		

- Molecule 80 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	cB	846	Total	C	N	O	S	0	0
			6605	4193	1136	1232	44		
80	CB	846	Total	C	N	O	S	0	0
			6605	4193	1136	1232	44		

- Molecule 81 is a RNA chain called A/P site tRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
81	aP	71	Total	C	N	O	P	0	0
			1514	677	275	492	70		
81	AP	71	Total	C	N	O	P	0	0
			1514	677	275	492	70		

- Molecule 82 is a RNA chain called P/E site tRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
82	pE	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		
82	PE	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 83 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		
83	Ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		

- Molecule 84 is a protein called 60S ribosomal protein L12 [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
84	lt	141	Total	C	N	O	S	0	0
			1046	652	191	199	4		
84	Lt	141	Total	C	N	O	S	0	0
			1046	652	191	199	4		

- Molecule 85 is a RNA chain called 28S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
85	l5	3708	Total	C	N	O	P	0	0
			79496	35401	14553	25835	3707		
85	L5	3708	Total	C	N	O	P	0	0
			79496	35401	14553	25835	3707		

- Molecule 86 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	Se	47	Total	C	N	O	S	0	0
			378	234	84	59	1		

- Molecule 87 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	lW	118	Total	C	N	O	S	0	0
			965	604	199	158	4		
87	LW	118	Total	C	N	O	S	0	0
			965	604	199	158	4		

- Molecule 88 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
88	sa	1	Total	Zn	0
			1	1	
88	lg	1	Total	Zn	0
			1	1	
88	lj	1	Total	Zn	0
			1	1	
88	lm	1	Total	Zn	0
			1	1	
88	lo	1	Total	Zn	0
			1	1	
88	lp	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
88	Sa	1	Total 1	Zn 1	0
88	Lg	1	Total 1	Zn 1	0
88	Lj	1	Total 1	Zn 1	0
88	Lm	1	Total 1	Zn 1	0
88	Lo	1	Total 1	Zn 1	0
88	Lp	1	Total 1	Zn 1	0

- Molecule 89 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
89	l7	3	Total 3	Mg 3	0
89	l8	5	Total 5	Mg 5	0
89	lA	1	Total 1	Mg 1	0
89	lB	1	Total 1	Mg 1	0
89	le	2	Total 2	Mg 2	0
89	lg	1	Total 1	Mg 1	0
89	lj	1	Total 1	Mg 1	0
89	s2	29	Total 29	Mg 29	0
89	l5	212	Total 212	Mg 212	0
89	L5	213	Total 213	Mg 213	0
89	L7	3	Total 3	Mg 3	0
89	L8	5	Total 5	Mg 5	0
89	LA	1	Total 1	Mg 1	0

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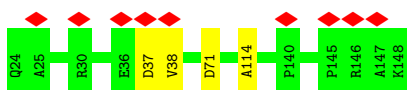
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Mol	Chain	Residues	Atoms		AltConf
89	LP	1	Total 1	Mg 1	0
89	LV	1	Total 1	Mg 1	0
89	Le	1	Total 1	Mg 1	0
89	Lj	1	Total 1	Mg 1	0
89	S2	29	Total 29	Mg 29	0

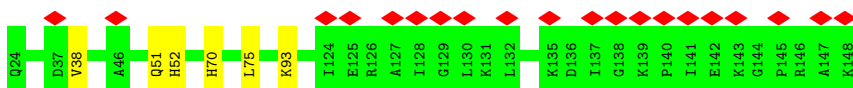
3 Residue-property plots

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: Endothelial differentiation-related factor 1



- Molecule 1: Endothelial differentiation-related factor 1



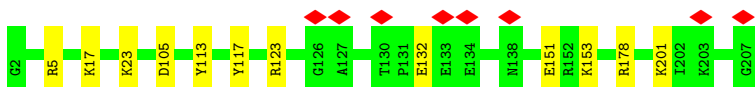
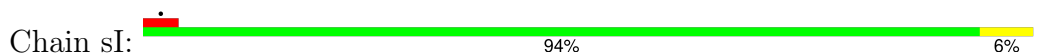
- Molecule 2: Small ribosomal subunit protein eS4, X isoform



- Molecule 2: Small ribosomal subunit protein eS4, X isoform



- Molecule 3: 40S ribosomal protein S8



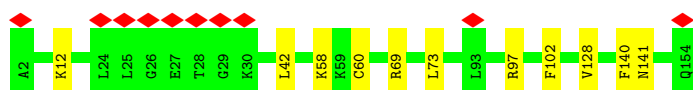
- Molecule 3: 40S ribosomal protein S8

Chain SI:  98%



- Molecule 4: 40S ribosomal protein S11

Chain sL:  7% 93% 7%



- Molecule 4: 40S ribosomal protein S11

Chain SL:  5% 96%



- Molecule 5: 40S ribosomal protein S23

Chain sX:  95% 5%



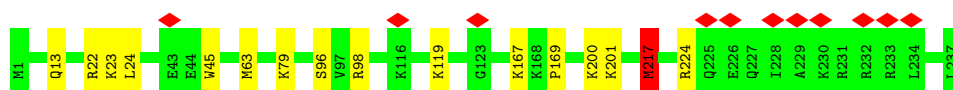
- Molecule 5: 40S ribosomal protein S23

Chain SX:  96%



- Molecule 6: 40S ribosomal protein S6

Chain sG:  5% 93% 6%

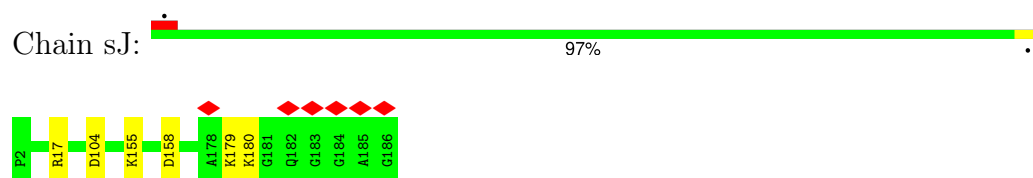


- Molecule 6: 40S ribosomal protein S6

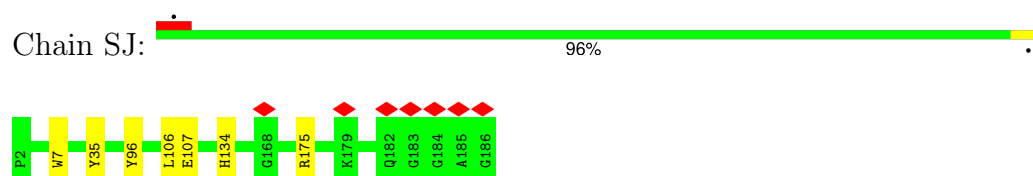
Chain SG:  5% 95% 5%



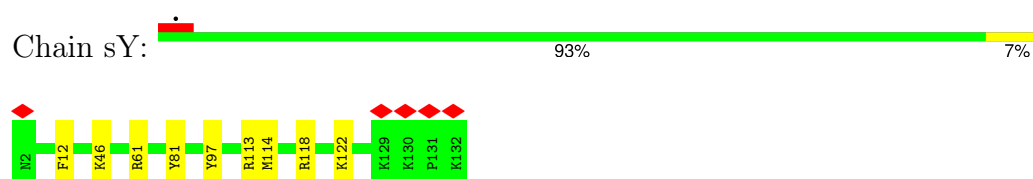
- Molecule 7: 40S ribosomal protein S9



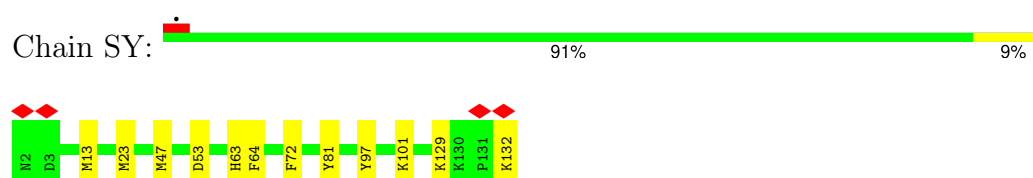
- Molecule 7: 40S ribosomal protein S9



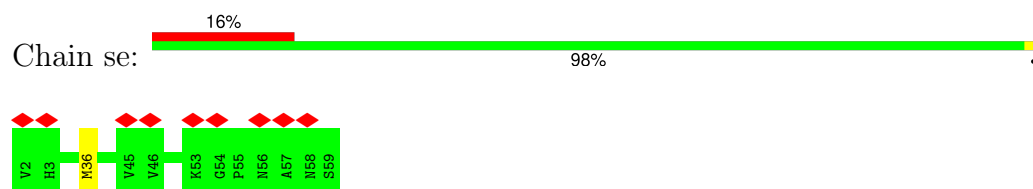
- Molecule 8: 40S ribosomal protein S24



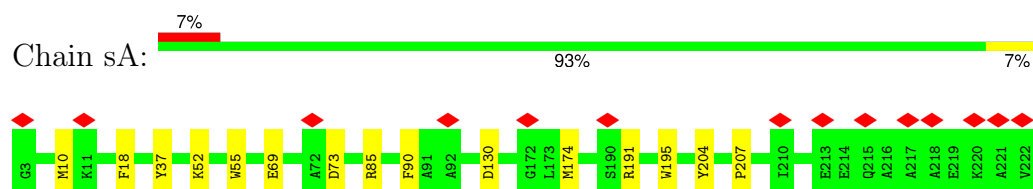
- Molecule 8: 40S ribosomal protein S24



- Molecule 9: Small ribosomal subunit protein eS30

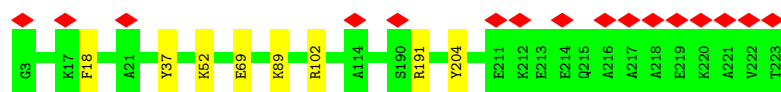


- Molecule 10: 40S ribosomal protein SA



- Molecule 10: 40S ribosomal protein SA

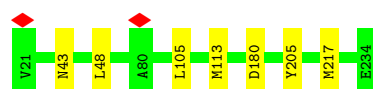




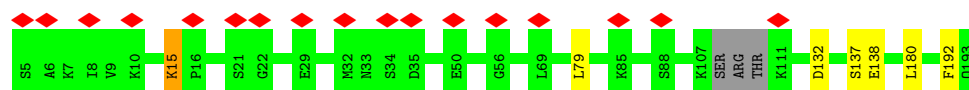
- Molecule 11: 40S ribosomal protein S3a



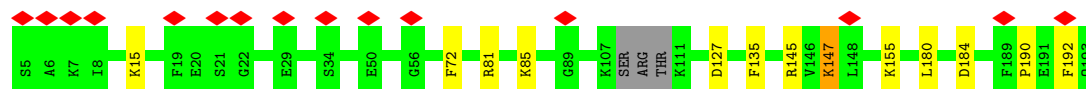
- Molecule 11: 40S ribosomal protein S3a



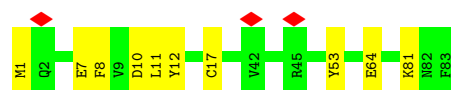
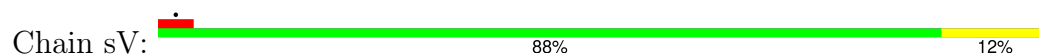
- Molecule 12: Small ribosomal subunit protein eS7



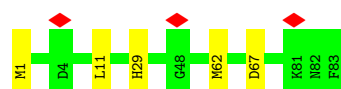
- Molecule 12: Small ribosomal subunit protein eS7



- Molecule 13: 40S ribosomal protein S21



- Molecule 13: 40S ribosomal protein S21



- Molecule 14: 40S ribosomal protein S26

Chain sa:  96%



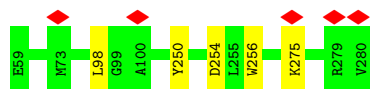
- Molecule 14: 40S ribosomal protein S26

Chain Sa:  95%



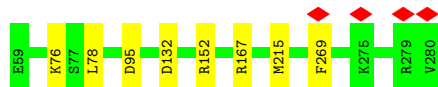
- Molecule 15: 40S ribosomal protein S2

Chain sC:  98%



- Molecule 15: 40S ribosomal protein S2

Chain SC:  96%



- Molecule 16: 40S ribosomal protein S13

Chain sN:  96%



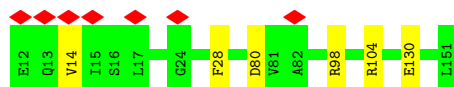
- Molecule 16: 40S ribosomal protein S13

Chain SN:  94%

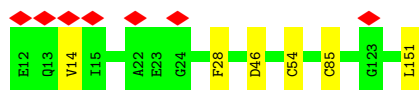


- Molecule 17: Small ribosomal subunit protein uS11

Chain sO:  96%



- Molecule 17: Small ribosomal subunit protein uS11



- Molecule 18: 40S ribosomal protein S15a



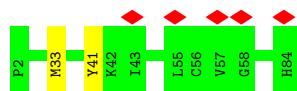
- Molecule 18: 40S ribosomal protein S15a



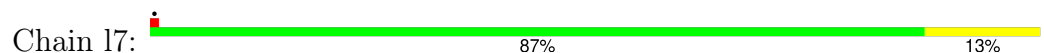
- Molecule 19: Small ribosomal subunit protein eS27



- Molecule 19: Small ribosomal subunit protein eS27



- Molecule 20: RNA (120-MER)5S rRNA [Homo sapiens]

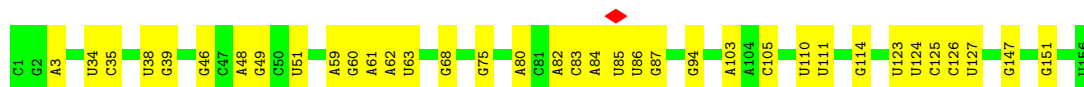
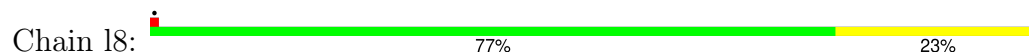


- Molecule 20: RNA (120-MER)5S rRNA [Homo sapiens]

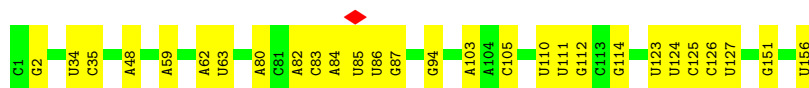
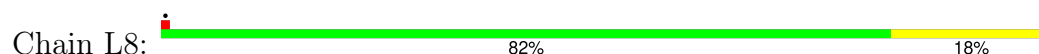




- Molecule 21: RNA (156-MER)5.8S rRNA [Homo sapiens]



- Molecule 21: RNA (156-MER)5.8S rRNA [Homo sapiens]



- Molecule 22: 60S ribosomal protein L8



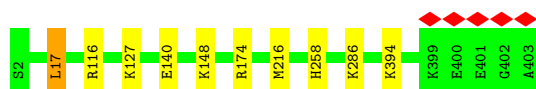
- Molecule 22: 60S ribosomal protein L8



- Molecule 23: Large ribosomal subunit protein uL3



- Molecule 23: Large ribosomal subunit protein uL3



- Molecule 24: 60S ribosomal protein L4

M1	A2	Q50	W67	R78	M95	M101	K157	K175	D179	R188	M189	R190	N223	H245	F257	R291	K325	L326	K348	K353	A359	A360	L361	Q362	A363	K364	S365	D366	E367	R369
----	----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

- | | | | | | | | | | | | | | | | | | | | | | | | |
|----|----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| M1 | A2 | V10 | K14 | N38 | Q50 | F102 | M196 | K234 | F249 | P257 | R258 | K259 | L273 | M325 | Y331 | M335 | A360 | A363 | K364 | S365 | D366 | E367 | K368 |
|----|----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|

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- A horizontal bar chart showing the distribution of 20 amino acids. The x-axis represents the count of each amino acid, ranging from 0 to 20. The y-axis lists the amino acids: G2, K5, K41, R68, N94, C100, N111, G127, D128, L146, M208, D217, A218, Y219, N229, M235, M236, M239, K258, Q291, and A294. The bars are colored in a repeating pattern of green, yellow, and orange. Red diamonds are placed above the bars for G127, D128, K258, and A294.

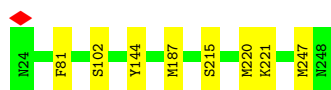
- P42
R59
A76
LYS
SER
LYS
VAL
GLU
LYS
LYS
LYS
LYS
LYS
GLU
V88
R114
K130
F164
K224
P225
R226
H227
Q228
E231
I232
F233
E238
N279
Y282
F288

-
- A horizontal bar chart showing the distribution of 28 amino acids across three categories: Amino acids in the protein (green), Amino acids in the protein and in the protein-protein interface (grey), and Amino acids in the protein-protein interface and in the protein-protein interface (yellow). The x-axis represents the count of amino acids, ranging from 0 to 28. The y-axis lists the amino acids: P42, R52, M68, A76, LYS, SER, LYS, VAL, GLU, LYS, LYS, LYS, LYS, GLU, LYS, V88, E119, K130, Q191, T205, P225, R226, H227, F233, D234, T236, K262, and F288. The bars are color-coded: green for 'Amino acids in the protein', grey for 'Amino acids in the protein and in the protein-protein interface', and yellow for 'Amino acids in the protein-protein interface and in the protein-protein interface'. The chart shows that LYS is the most common amino acid in all three categories, followed by GLU and VAL. The amino acids in the protein-protein interface (yellow) are P42, R52, M68, E119, K130, Q191, R226, H227, K262, and F288. The amino acids in the protein (green) are A76, LYS, SER, VAL, GLU, LYS, LYS, LYS, GLU, LYS, V88, and T205. The amino acids in the protein and in the protein-protein interface (grey) are LYS, SER, LYS, VAL, GLU, LYS, LYS, LYS, GLU, LYS, and F233, D234, T236.

-
- | Letter | Count |
|--------|-------|
| M | 24 |
| R | 34 |
| R | 43 |
| K | 44 |
| M | 64 |
| E | 68 |
| K | 88 |
| Y | 144 |
| C | 186 |
| D | 189 |
| M | 220 |
| D | 232 |
| D | 238 |
| M | 247 |
| N | 248 |

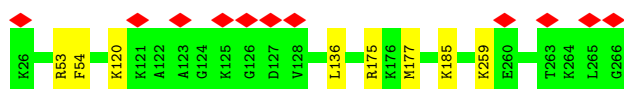
- Molecule 27: 60S ribosomal protein L7

Chain LF:  96%



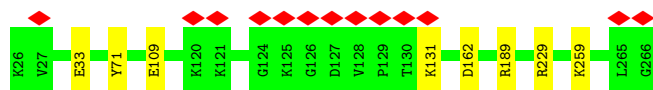
- Molecule 28: 60S ribosomal protein L7a

Chain IG:  97%



- Molecule 28: 60S ribosomal protein L7a

Chain LG:  97%



- Molecule 29: 60S ribosomal protein L9

Chain IH:  96%




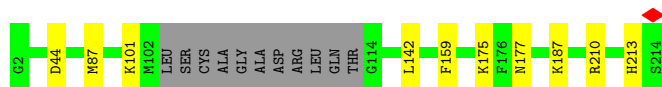
- Molecule 29: 60S ribosomal protein L9

Chain LH:  98%



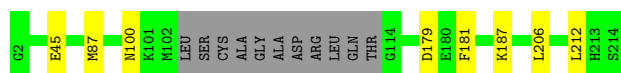
- Molecule 30: Ribosomal protein uL16-like

Chain II:  90% 5% 5%

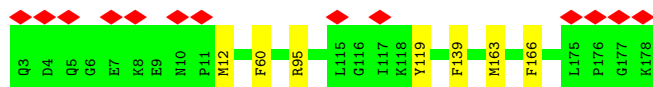


- Molecule 30: Ribosomal protein uL16-like

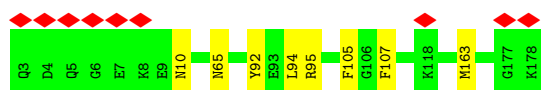
Chain LI:  91%



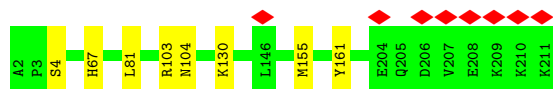
- Molecule 31: 60S ribosomal protein L11



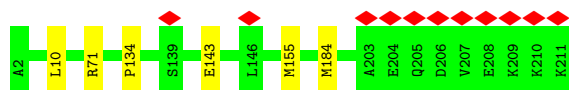
- Molecule 31: 60S ribosomal protein L11



- Molecule 32: Large ribosomal subunit protein eL13



- Molecule 32: Large ribosomal subunit protein eL13



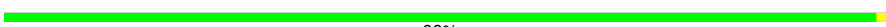
- Molecule 33: 60S ribosomal protein L14



- Molecule 33: 60S ribosomal protein L14



- Molecule 34: 60S ribosomal protein L15

Chain IN:  98% .



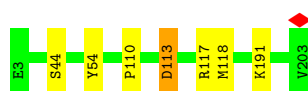
- Molecule 34: 60S ribosomal protein L15

Chain LN:  97% .



- Molecule 35: 60S ribosomal protein L13a

Chain LO:  97% .



- Molecule 35: 60S ribosomal protein L13a

Chain LO:  98% .



- Molecule 36: 60S ribosomal protein L17

Chain IP:  95% . .



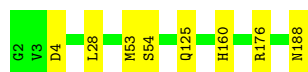
- Molecule 36: 60S ribosomal protein L17

Chain LP:  96% .



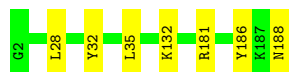
- Molecule 37: 60S ribosomal protein L18

Chain IQ:  96% .



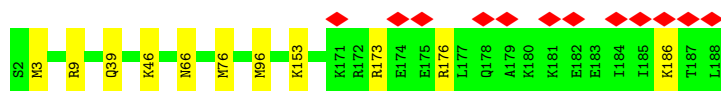
- Molecule 37: 60S ribosomal protein L18

Chain LQ:  96% .



- Molecule 38: 60S ribosomal protein L19

Chain LR:  94% 6% 6%



- Molecule 38: 60S ribosomal protein L19

Chain LR:  93% 5% 7%



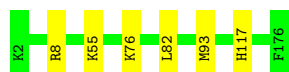
- Molecule 39: 60S ribosomal protein L18a

Chain LS:  94% 6%



- Molecule 39: 60S ribosomal protein L18a

Chain LS:  97% .



- Molecule 40: 60S ribosomal protein L21

Chain IT:  96% .



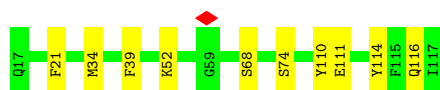
- Molecule 40: 60S ribosomal protein L21

Chain LT:  96% .




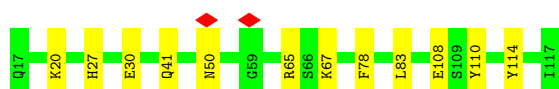
- Molecule 41: Heparin-binding protein HBp15

Chain IU:  90% 10%



- Molecule 41: Heparin-binding protein HBp15

Chain LU:  88% 12%



- Molecule 42: 60S ribosomal protein L23

Chain IV:  97%



- Molecule 42: 60S ribosomal protein L23

Chain LV:  98%



- Molecule 43: 60S ribosomal protein L23a

Chain IX:  97%



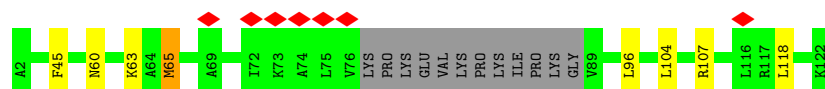
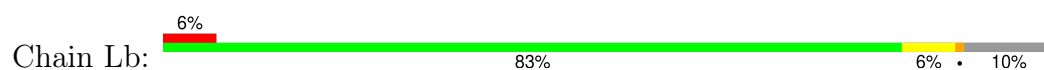
- Molecule 43: 60S ribosomal protein L23a

Chain LX:  95% 5%



- Molecule 44: 60S ribosomal protein L26

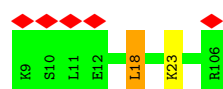
Chain IY:  96%



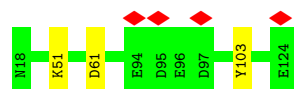
- Molecule 48: 60S ribosomal protein L30



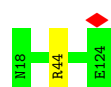
- Molecule 48: 60S ribosomal protein L30



- Molecule 49: 60S ribosomal protein L31



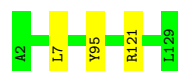
- Molecule 49: 60S ribosomal protein L31



- Molecule 50: 60S ribosomal protein L32



- Molecule 50: 60S ribosomal protein L32



- Molecule 51: 60S ribosomal protein L35a

Chain lf:  92% 8%



- Molecule 51: 60S ribosomal protein L35a

Chain Lf:  96% .



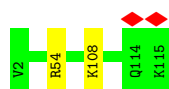
- Molecule 52: 60S ribosomal protein L34

Chain lg:  97% .



- Molecule 52: 60S ribosomal protein L34

Chain Lg:  98% .



- Molecule 53: 60S ribosomal protein L35

Chain lh:  97% .



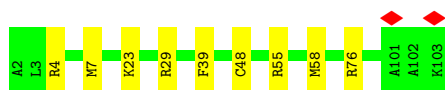
- Molecule 53: 60S ribosomal protein L35

Chain Lh:  94% 6%



- Molecule 54: 60S ribosomal protein L36

Chain li:  91% 9%



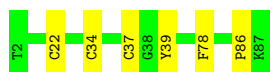
- Molecule 54: 60S ribosomal protein L36



- Molecule 55: 60S ribosomal protein L37



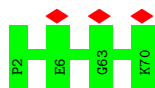
- Molecule 55: 60S ribosomal protein L37



- Molecule 56: 60S ribosomal protein L38



- Molecule 56: 60S ribosomal protein L38



- Molecule 57: 60S ribosomal protein L39



- Molecule 57: 60S ribosomal protein L39

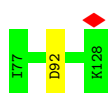




- Molecule 58: Large ribosomal subunit protein eL40



- Molecule 58: Large ribosomal subunit protein eL40



- Molecule 59: 60S ribosomal protein L41

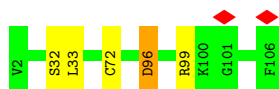


- Molecule 59: 60S ribosomal protein L41



There are no outlier residues recorded for this chain.

- Molecule 60: 60S ribosomal protein L36a



- Molecule 60: 60S ribosomal protein L36a



- Molecule 61: 60S ribosomal protein L37a





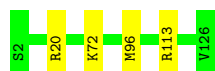
- Molecule 61: 60S ribosomal protein L37a

Chain Lp: 98%



- Molecule 62: 60S ribosomal protein L28

Chain lr: 97%



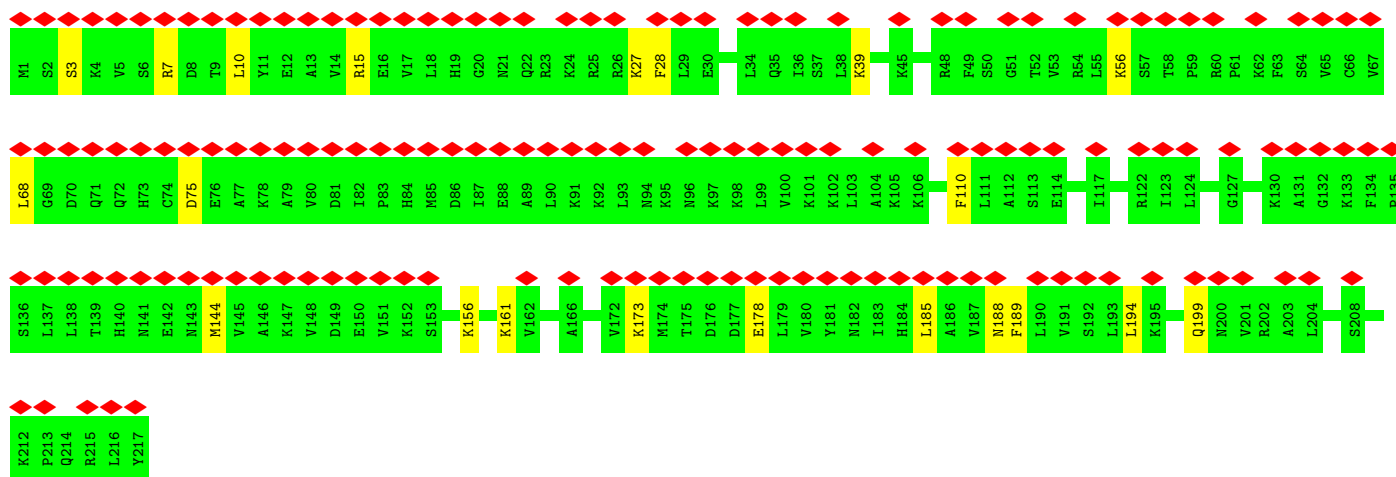
- Molecule 62: 60S ribosomal protein L28

Chain Lr: 97%



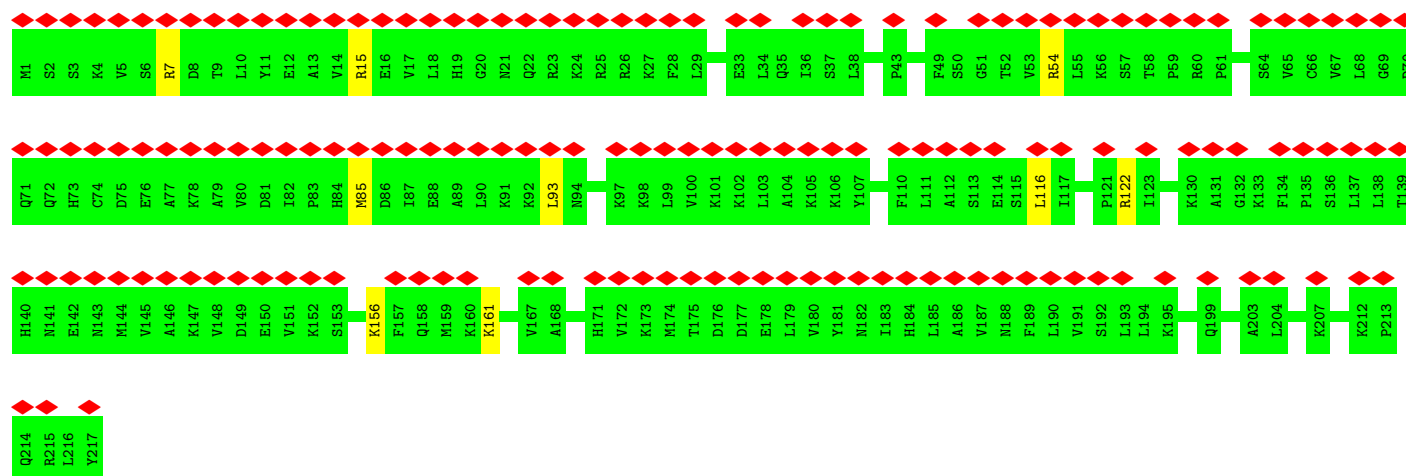
- Molecule 63: 60S ribosomal protein L10a

Chain lz: 71% 90% 10%

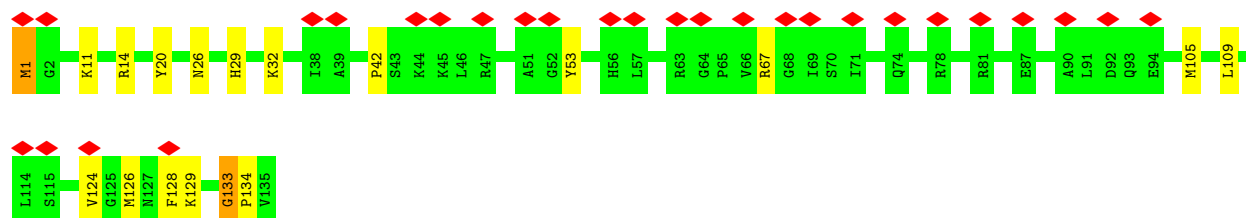
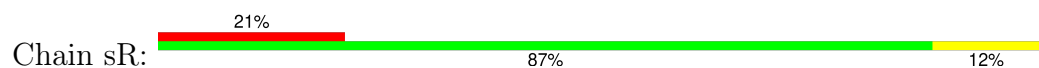


- Molecule 63: 60S ribosomal protein L10a

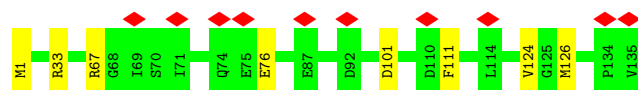
Chain Lz: 74% 96%



- Molecule 64: 40S ribosomal protein S17



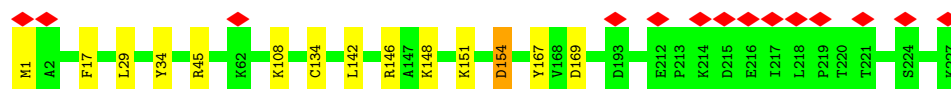
- Molecule 64: 40S ribosomal protein S17



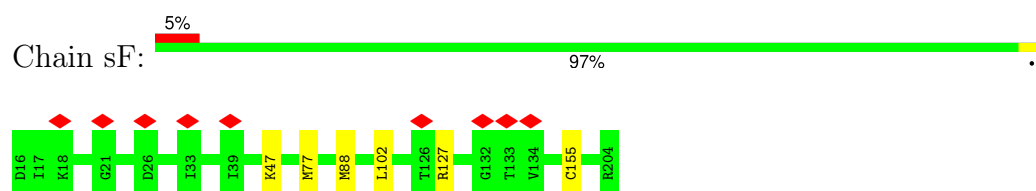
- Molecule 65: Small ribosomal subunit protein uS3



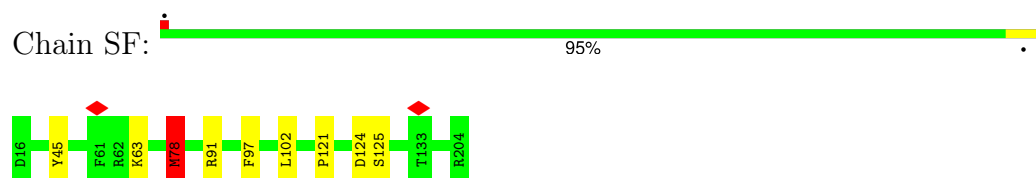
- Molecule 65: Small ribosomal subunit protein uS3



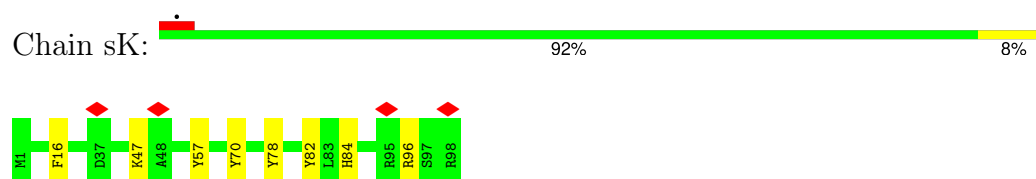
- Molecule 66: 40S ribosomal protein S5



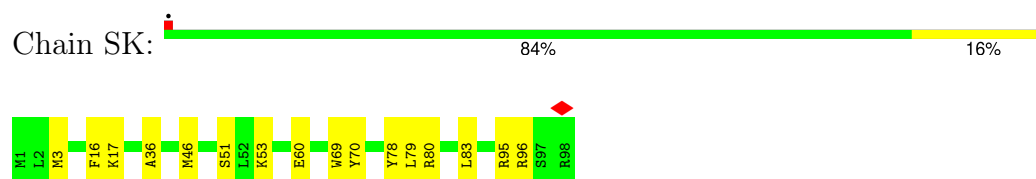
- Molecule 66: 40S ribosomal protein S5



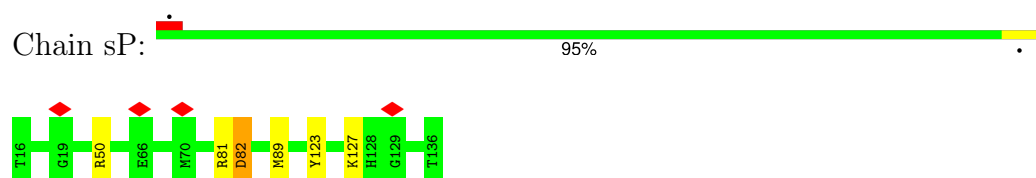
- Molecule 67: 40S ribosomal protein S10



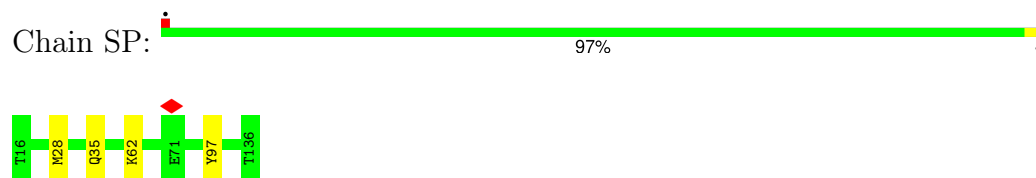
- Molecule 67: 40S ribosomal protein S10



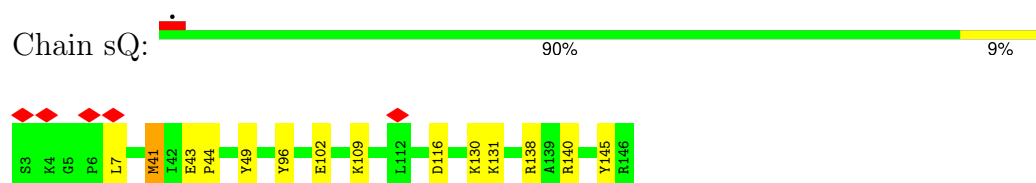
- Molecule 68: Small ribosomal subunit protein uS19



- Molecule 68: Small ribosomal subunit protein uS19

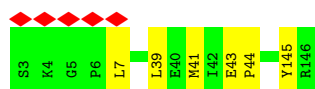


- Molecule 69: Small ribosomal subunit protein uS9



- Molecule 69: Small ribosomal subunit protein uS9

Chain SQ:  96%



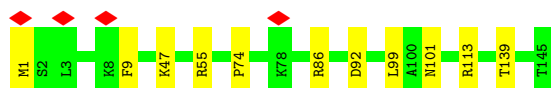
- Molecule 70: 40S ribosomal protein S18

Chain sS:  95%



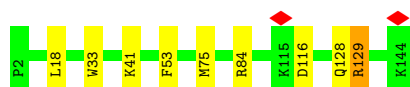
- Molecule 70: 40S ribosomal protein S18

Chain SS:  92%




- Molecule 71: 40S ribosomal protein S19

Chain sT:  94%



- Molecule 71: 40S ribosomal protein S19

Chain ST:  90%



- Molecule 72: 40S ribosomal protein S20

Chain sU:  96%

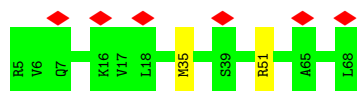


- Molecule 72: 40S ribosomal protein S20

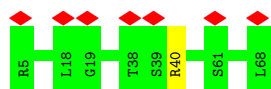
Chain SU:  94%



- Molecule 73: 40S ribosomal protein S28



- Molecule 73: 40S ribosomal protein S28



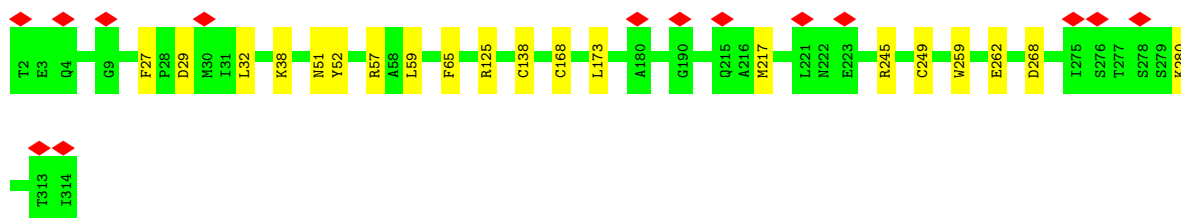
- Molecule 74: 40S ribosomal protein S29



- Molecule 74: 40S ribosomal protein S29

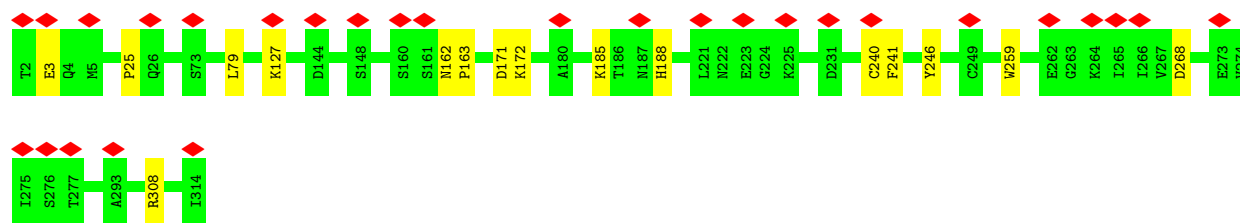


- Molecule 75: Receptor of activated protein C kinase 1

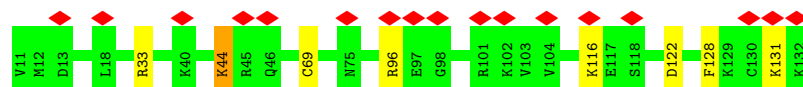


- Molecule 75: Receptor of activated protein C kinase 1

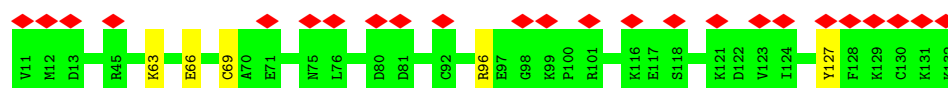




- Molecule 76: Small ribosomal subunit protein eS12



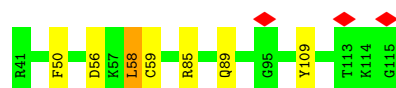
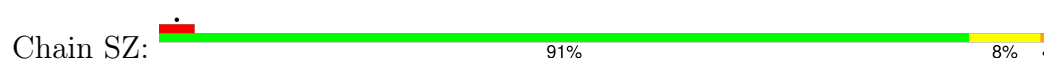
- Molecule 76: Small ribosomal subunit protein eS12



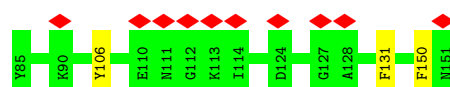
- Molecule 77: Small ribosomal subunit protein eS25



- Molecule 77: Small ribosomal subunit protein eS25

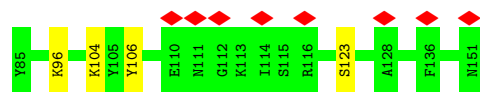


- Molecule 78: Ubiquitin-40S ribosomal protein S27a



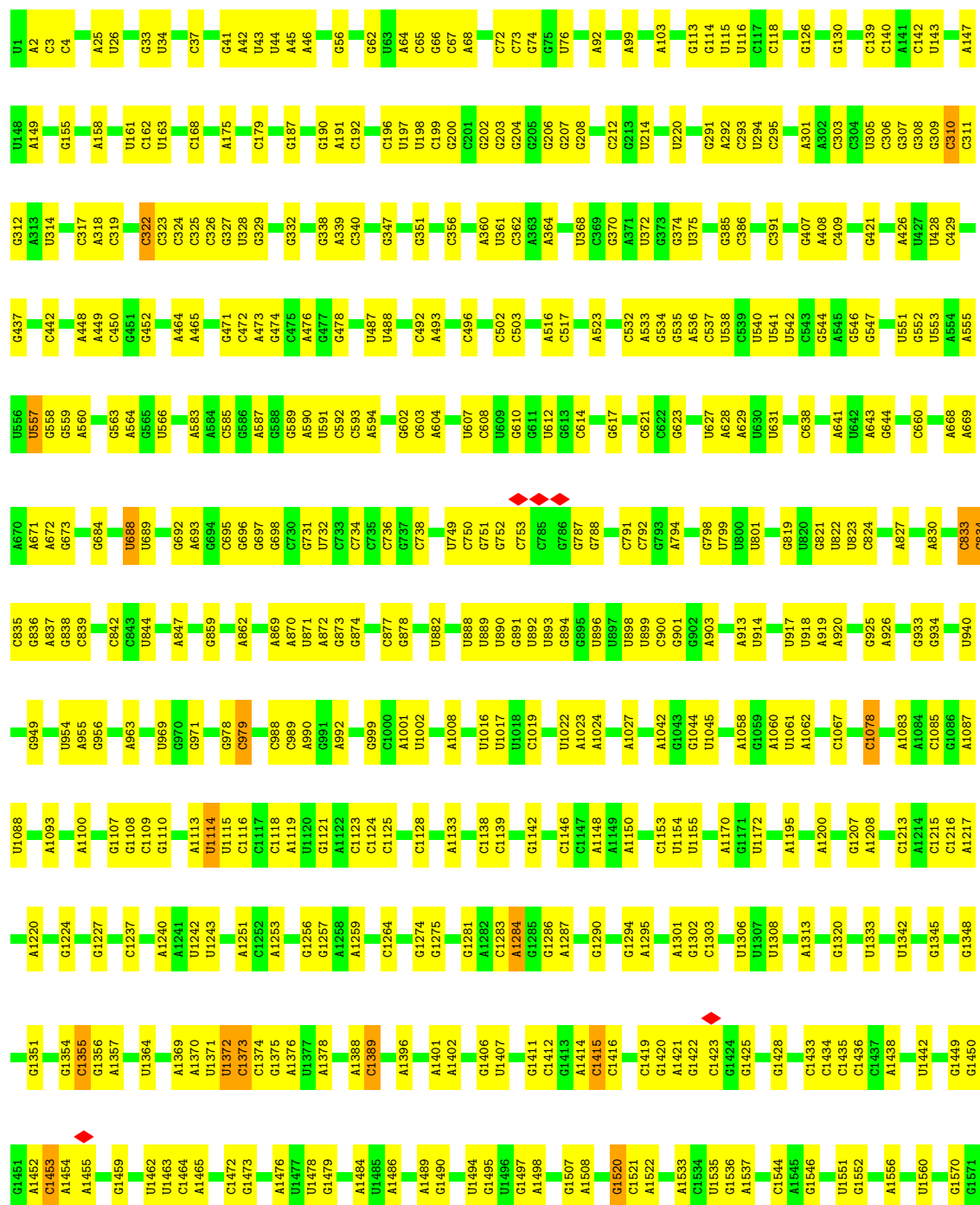
- Molecule 78: Ubiquitin-40S ribosomal protein S27a

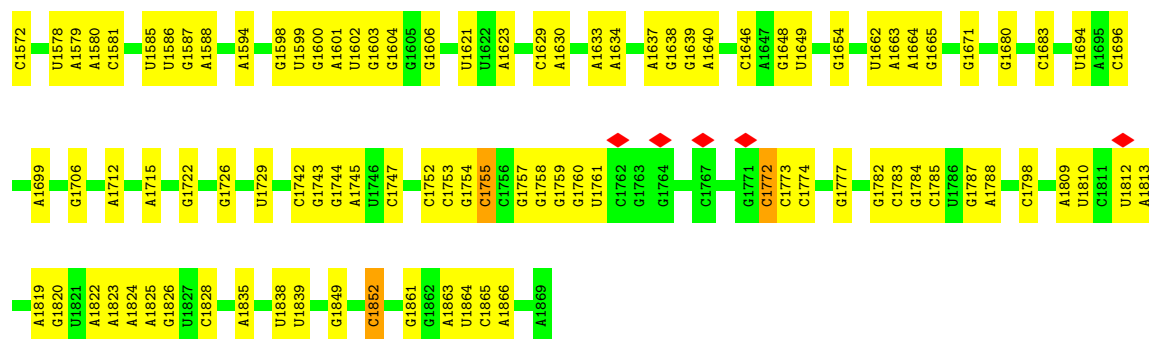




• Molecule 79: 18S rRNA [Homo sapiens]

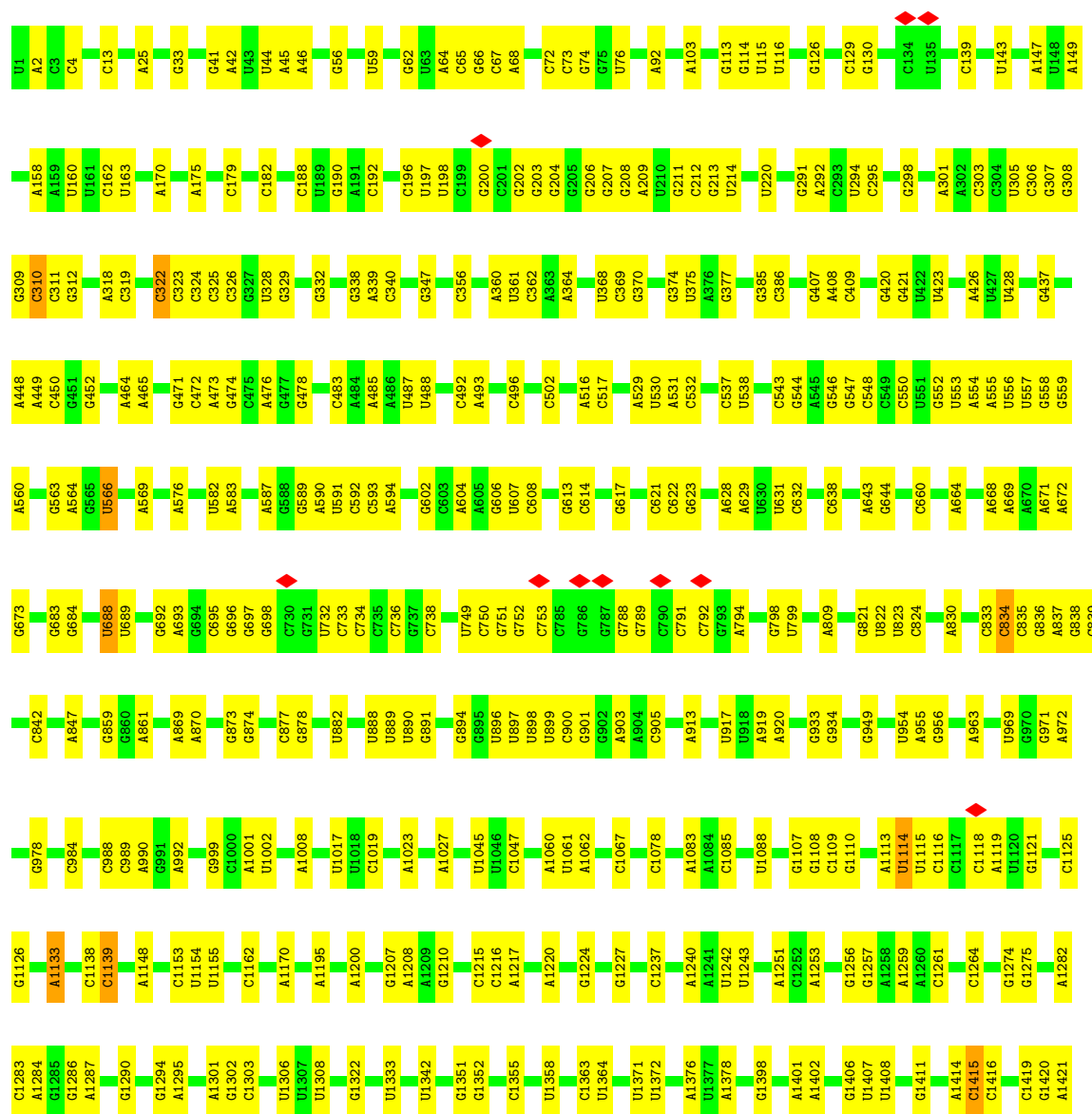
Chain s2: 68% 31%

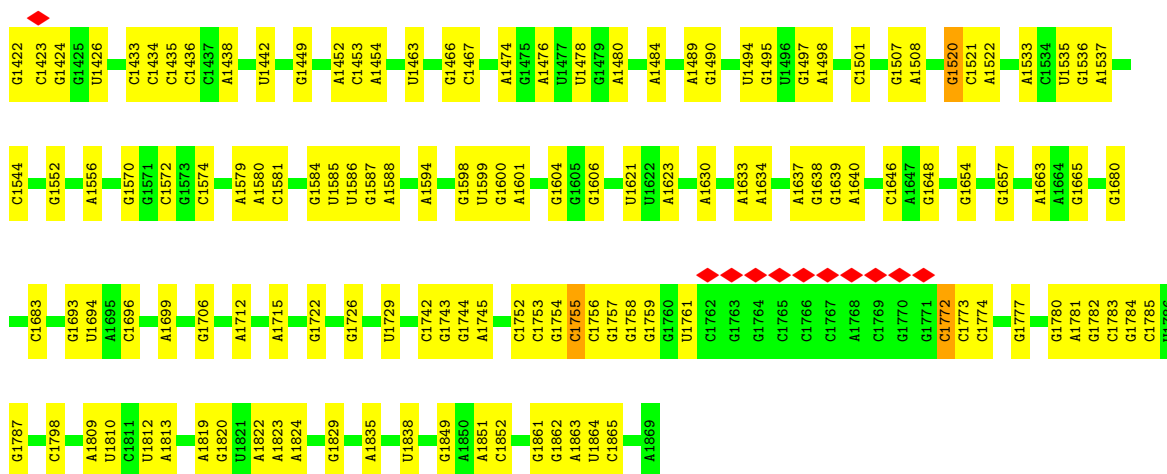




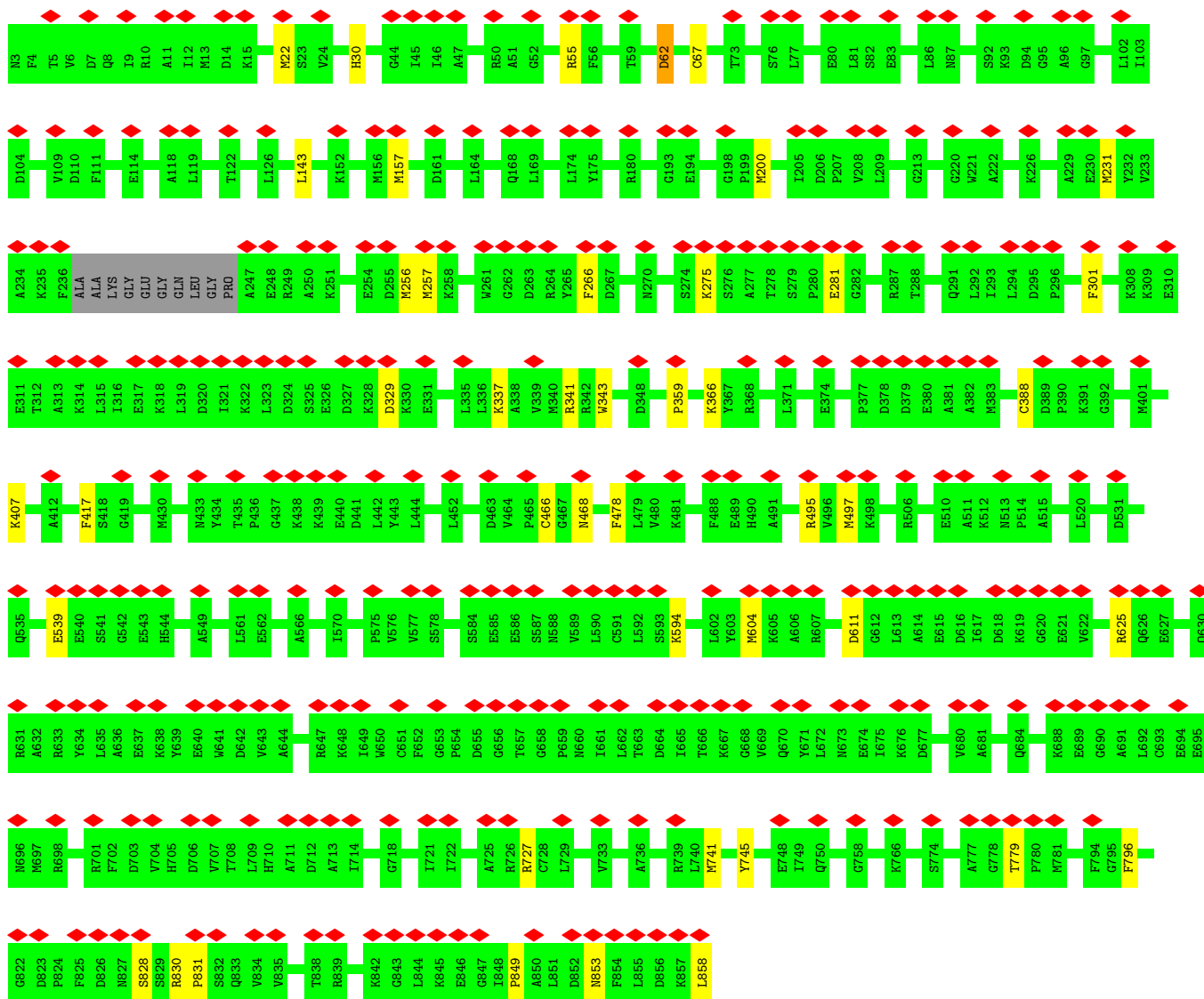
• Molecule 79: 18S rRNA [Homo sapiens]

Chain S2: 71% 29%

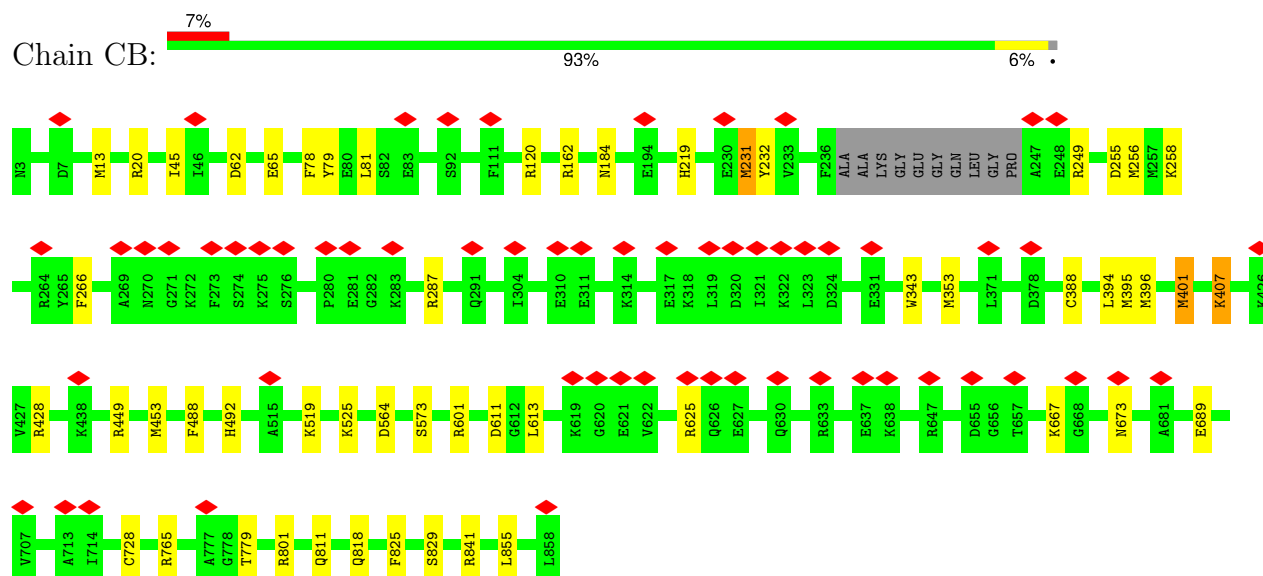




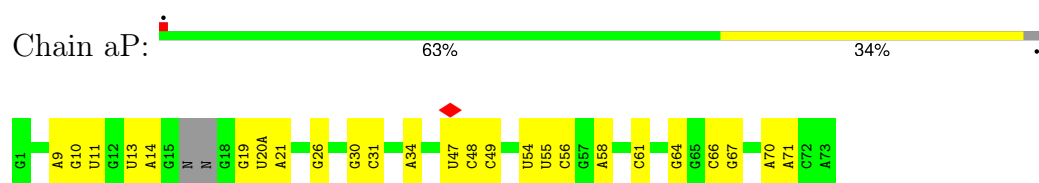
• Molecule 80: Elongation factor 2



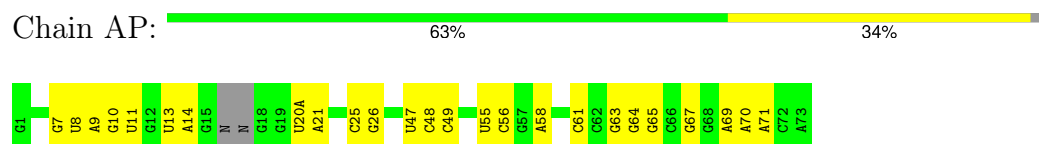
- Molecule 80: Elongation factor 2



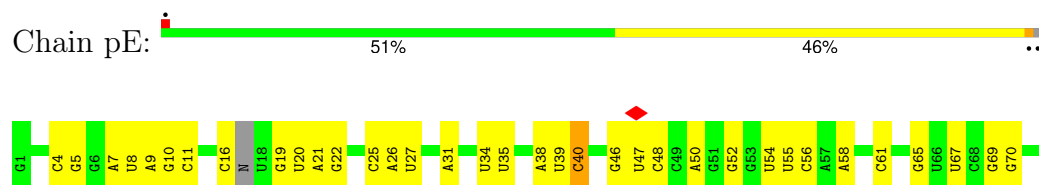
- Molecule 81: A/P site tRNA [Homo sapiens]



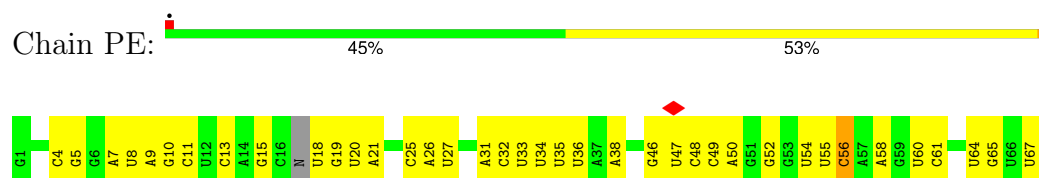
- Molecule 81: A/P site tRNA [Homo sapiens]



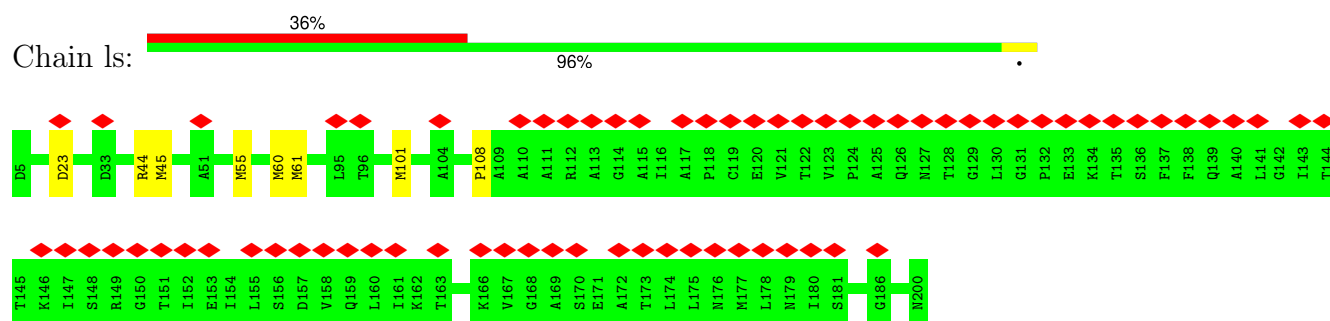
- Molecule 82: P/E site tRNA [Homo sapiens]



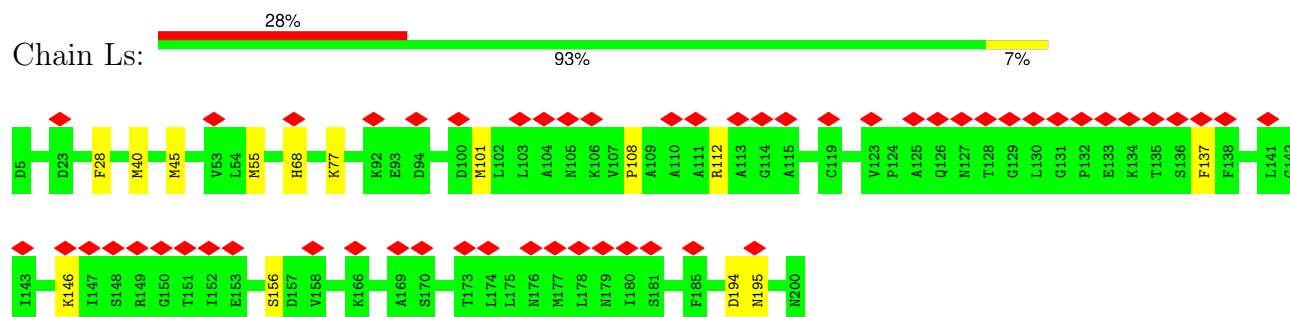
- Molecule 82: P/E site tRNA [Homo sapiens]



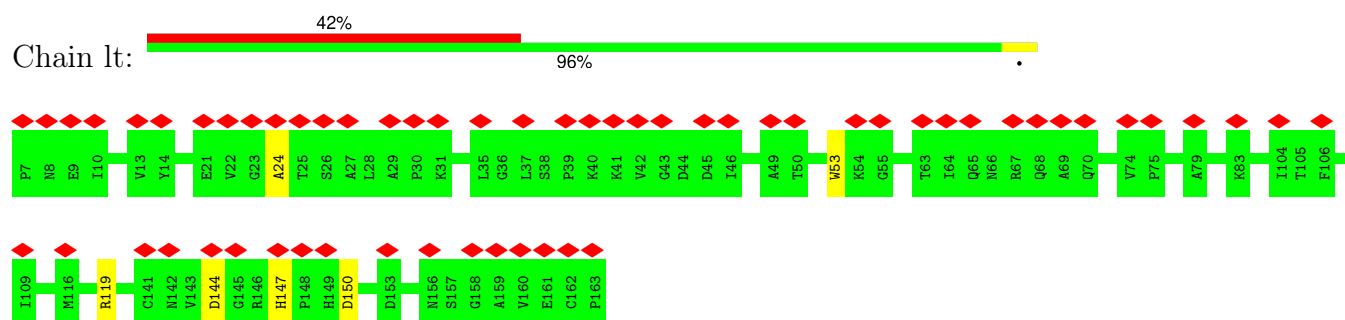
- Molecule 83: 60S acidic ribosomal protein P0



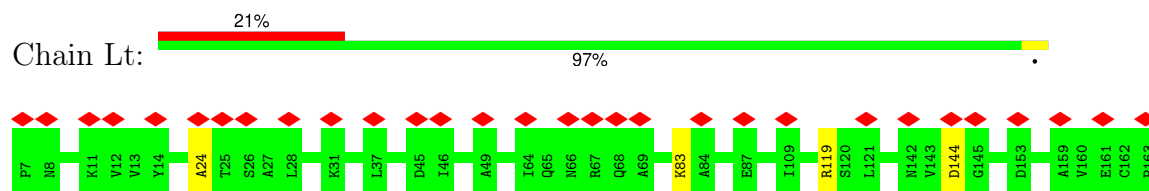
- Molecule 83: 60S acidic ribosomal protein P0



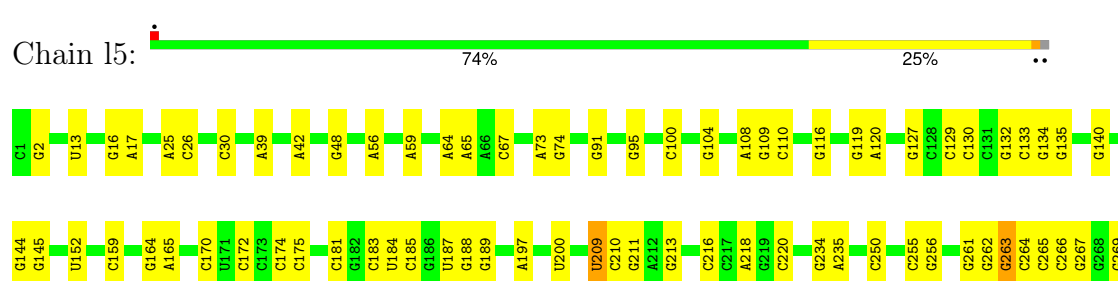
- Molecule 84: 60S ribosomal protein L12 [Homo sapiens]



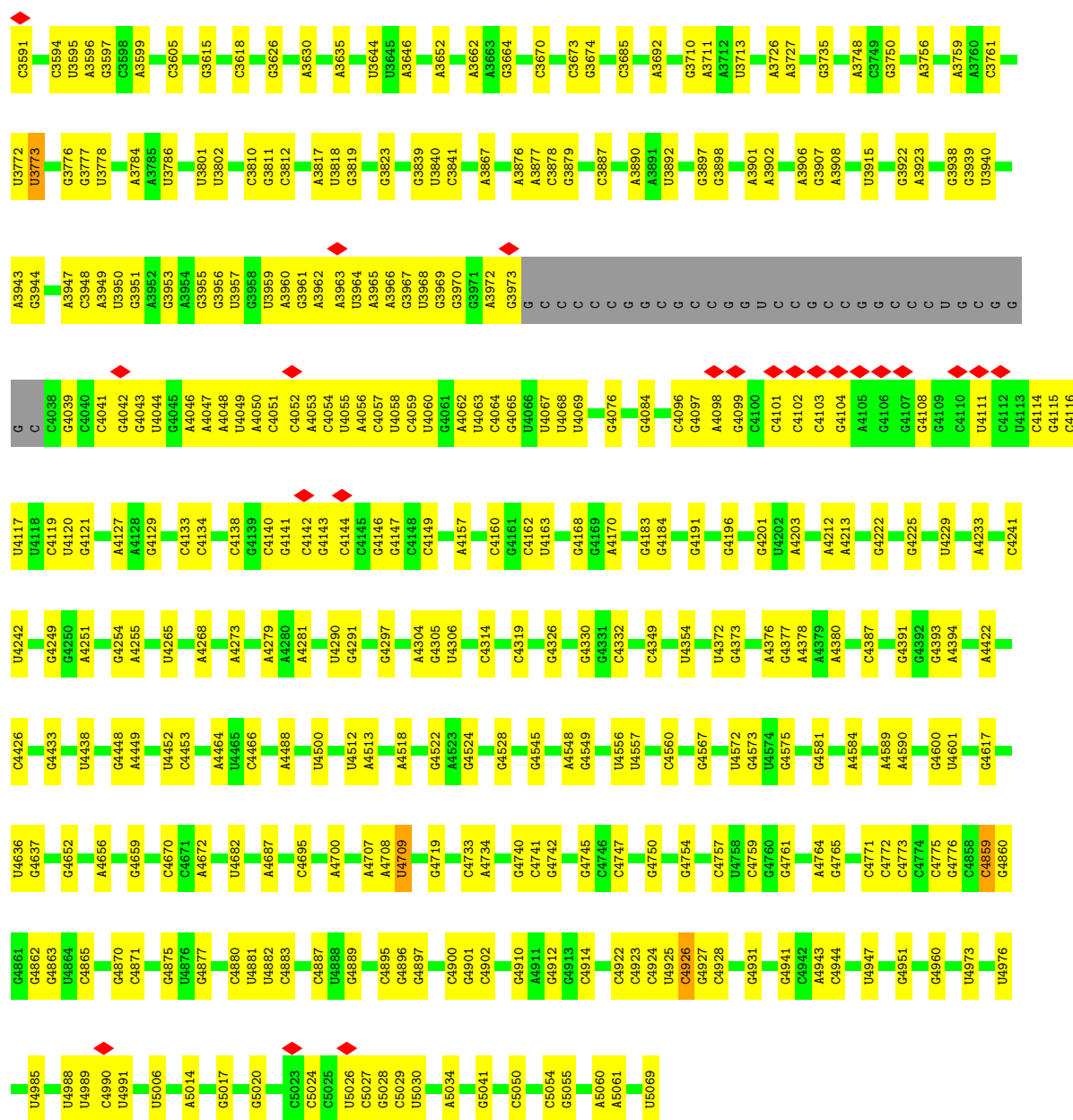
- Molecule 84: 60S ribosomal protein L12 [Homo sapiens]



- Molecule 85: 28S rRNA [Homo sapiens]

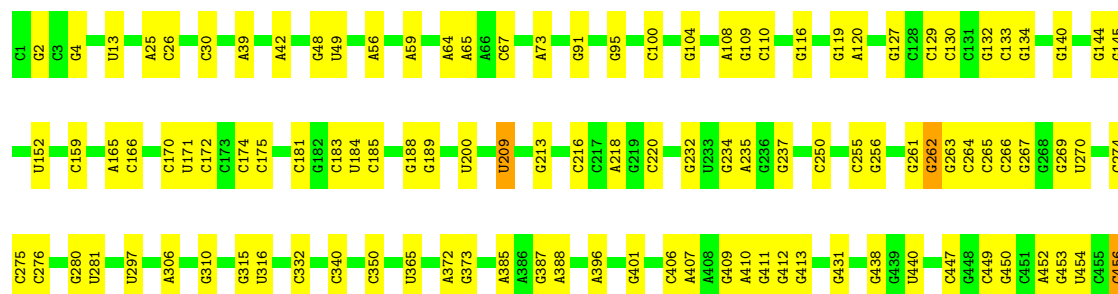


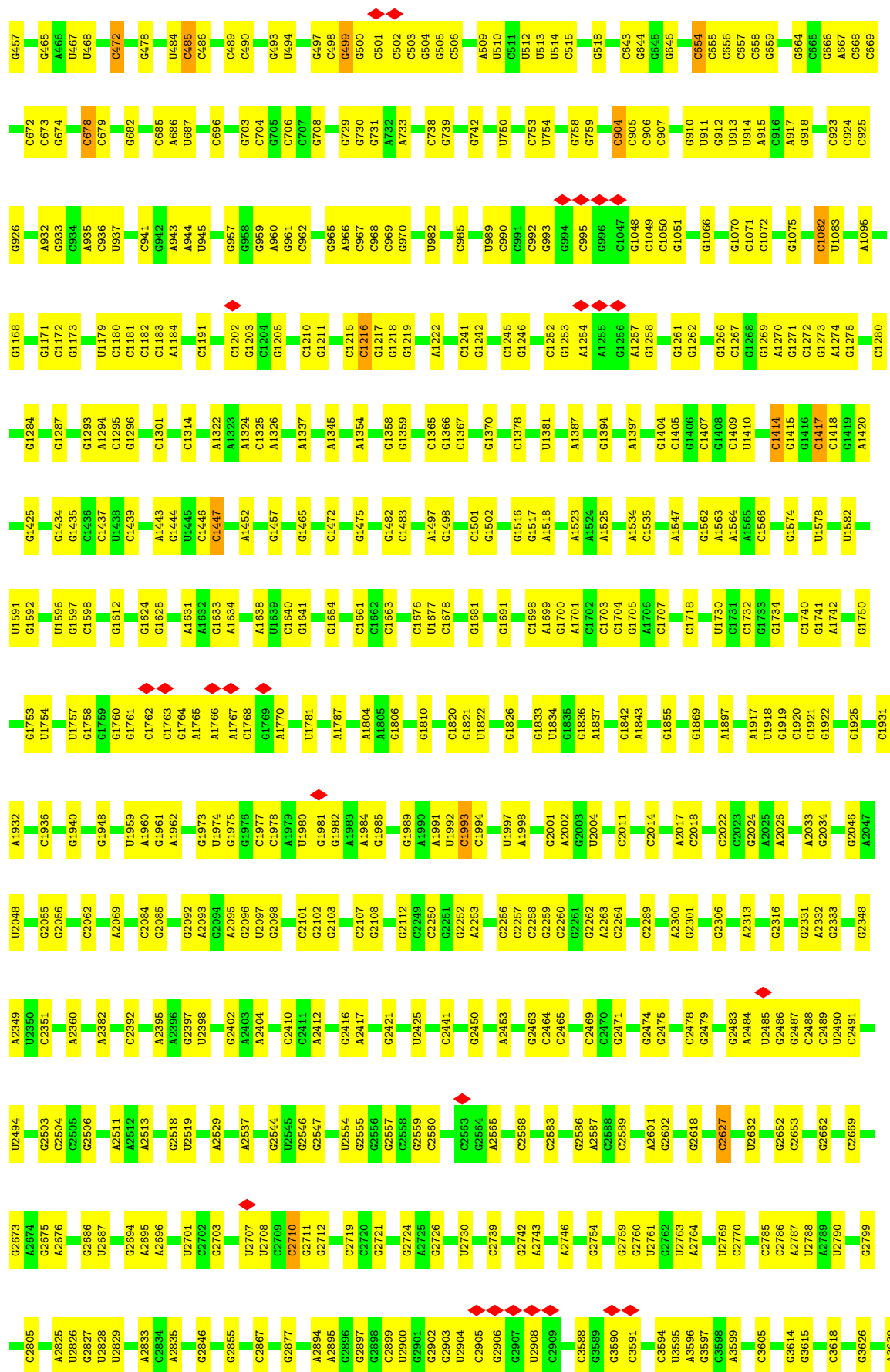


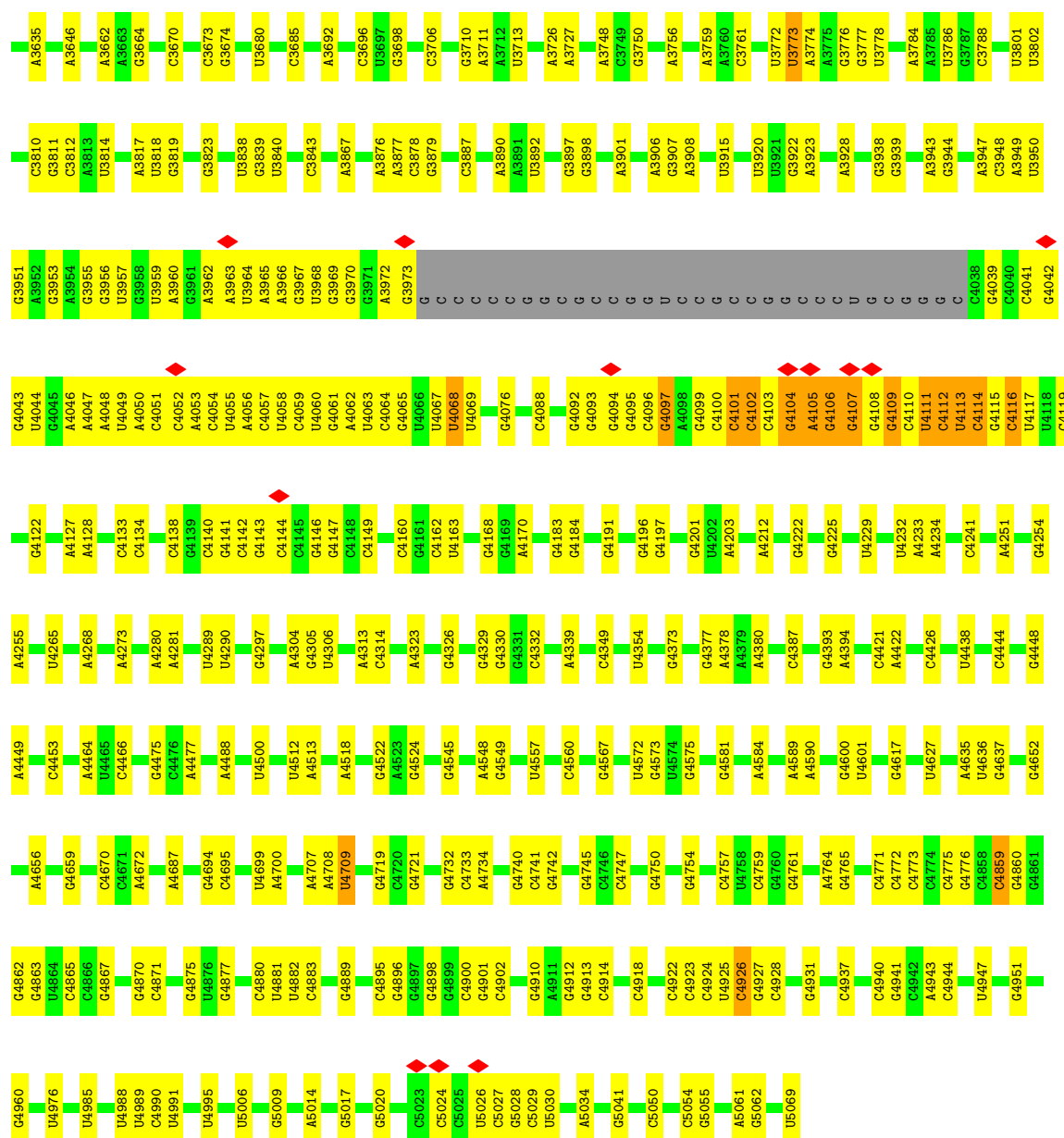


• Molecule 85: 28S rRNA [Homo sapiens]

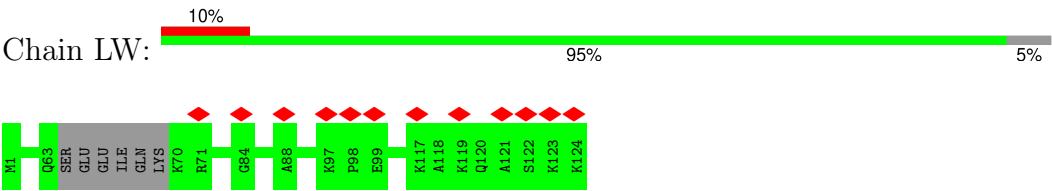
Chain L5: 72% 26%







● Molecule 87: Ribosomal protein L24



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45867	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.580	Depositor
Minimum map value	-0.081	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.032	Depositor
Recommended contour level	0.096	Depositor
Map size (\AA)	640.8, 640.8, 640.8	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.068, 1.068, 1.068	Depositor

5 Model quality

5.1 Standard geometry

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

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	CH	0.34	0/977	0.67	1/1306 (0.1%)
1	cH	0.32	0/977	0.66	0/1306
2	SE	0.33	1/2118 (0.0%)	0.62	4/2849 (0.1%)
2	sE	0.39	0/2118	0.68	5/2849 (0.2%)
3	SI	0.30	0/1715	0.60	0/2287
3	sI	0.32	0/1715	0.59	0/2287
4	SL	0.31	0/1268	0.59	1/1696 (0.1%)
4	sL	0.44	0/1268	0.69	3/1696 (0.2%)
5	SX	0.32	0/1116	0.59	0/1490
5	sX	0.40	0/1116	0.66	1/1490 (0.1%)
6	SG	0.30	0/1946	0.63	1/2590 (0.0%)
6	sG	0.32	0/1946	0.66	3/2590 (0.1%)
7	SJ	0.29	0/1550	0.65	0/2069
7	sJ	0.31	0/1550	0.62	0/2069
8	SY	0.29	0/1083	0.60	0/1438
8	sY	0.33	0/1083	0.64	0/1438
9	se	0.30	0/465	0.67	0/612
10	SA	0.33	0/1778	0.63	0/2416
10	sA	0.56	3/1778 (0.2%)	0.85	5/2416 (0.2%)
11	SB	0.30	0/1765	0.58	0/2362
11	sB	0.47	2/1765 (0.1%)	0.65	1/2362 (0.0%)
12	SH	0.32	0/1519	0.62	1/2033 (0.0%)
12	sH	0.31	0/1519	0.62	0/2033
13	SV	0.31	0/643	0.59	0/860
13	sV	0.43	0/643	0.77	1/860 (0.1%)
14	Sa	0.39	1/836 (0.1%)	0.76	2/1121 (0.2%)
14	sa	0.37	0/836	0.66	0/1121
15	SC	0.36	0/1762	0.65	1/2381 (0.0%)
15	sC	0.38	0/1762	0.64	1/2381 (0.0%)
16	SN	0.30	0/1232	0.62	1/1656 (0.1%)
16	sN	0.37	0/1232	0.66	0/1656
17	SO	0.33	0/1062	0.67	1/1425 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	sO	0.33	0/1062	0.69	2/1425 (0.1%)
18	SW	0.35	0/1051	0.68	1/1406 (0.1%)
18	sW	0.38	0/1051	0.65	0/1406
19	Sb	0.30	0/665	0.60	0/891
19	sb	0.56	3/665 (0.5%)	0.95	3/891 (0.3%)
20	L7	0.38	0/2861	0.78	0/4459
20	l7	0.53	0/2861	0.81	0/4459
21	L8	0.39	0/3701	0.80	0/5766
21	l8	0.51	0/3701	0.81	1/5766 (0.0%)
22	LA	0.37	0/1936	0.69	3/2596 (0.1%)
22	lA	0.41	0/1936	0.67	2/2596 (0.1%)
23	LB	0.31	0/3306	0.58	1/4424 (0.0%)
23	lB	0.36	0/3306	0.61	1/4424 (0.0%)
24	LC	0.50	6/2981 (0.2%)	0.76	6/4002 (0.1%)
24	lC	0.35	0/2981	0.63	3/4002 (0.1%)
25	LD	0.33	0/2428	0.64	2/3252 (0.1%)
25	lD	0.35	0/2428	0.59	0/3252
26	LE	0.29	0/1942	0.57	0/2606
26	lE	0.38	0/1942	0.61	0/2606
27	LF	0.33	0/1905	0.60	0/2539
27	lF	0.37	0/1905	0.63	1/2539 (0.0%)
28	LG	0.29	0/1960	0.57	1/2637 (0.0%)
28	lG	0.34	0/1960	0.61	0/2637
29	LH	0.28	0/1537	0.58	0/2066
29	lH	0.41	1/1537 (0.1%)	0.63	0/2066
30	LI	0.32	0/1673	0.61	0/2233
30	lI	0.36	0/1673	0.61	0/2233
31	LJ	0.33	0/1433	0.65	0/1915
31	lJ	0.36	0/1433	0.67	1/1915 (0.1%)
32	LL	0.30	0/1732	0.60	0/2315
32	lL	0.33	0/1732	0.62	0/2315
33	LM	0.36	1/1161 (0.1%)	0.62	0/1554
33	lM	0.46	1/1161 (0.1%)	0.79	2/1554 (0.1%)
34	LN	0.31	0/1746	0.60	0/2338
34	lN	0.40	0/1746	0.63	0/2338
35	LO	0.31	0/1682	0.60	1/2250 (0.0%)
35	lO	0.41	0/1682	0.65	1/2250 (0.0%)
36	LP	0.31	0/1268	0.57	0/1701
36	lP	0.38	0/1268	0.66	2/1701 (0.1%)
37	LQ	0.33	0/1537	0.68	1/2052 (0.0%)
37	lQ	0.36	0/1537	0.66	2/2052 (0.1%)
38	LR	0.27	0/1582	0.61	0/2091
38	lR	0.33	0/1582	0.66	1/2091 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
39	LS	0.31	0/1493	0.59	0/2003
39	IS	0.37	0/1493	0.64	0/2003
40	LT	0.33	0/1326	0.63	0/1770
40	IT	0.37	0/1326	0.64	1/1770 (0.1%)
41	LU	0.31	0/839	0.64	0/1126
41	IU	0.41	0/839	0.66	0/1126
42	LV	0.30	0/993	0.53	0/1332
42	IV	0.37	0/993	0.63	1/1332 (0.1%)
43	LX	0.31	0/1002	0.63	0/1345
43	IX	0.37	0/1002	0.62	0/1345
44	LY	0.30	0/1132	0.59	0/1504
44	IY	0.32	0/1132	0.59	0/1504
45	LZ	0.33	0/1130	0.59	0/1507
45	IZ	0.45	0/1130	0.72	1/1507 (0.1%)
46	La	0.32	0/1191	0.60	0/1591
46	la	0.38	0/1191	0.62	1/1591 (0.1%)
47	Lb	0.30	0/889	0.68	1/1175 (0.1%)
47	lb	0.33	0/889	0.66	0/1175
48	Lc	0.32	0/774	0.68	1/1038 (0.1%)
48	lc	0.37	0/774	0.63	0/1038
49	Ld	0.30	0/903	0.63	0/1216
49	ld	0.35	0/903	0.62	0/1216
50	Le	0.32	0/1071	0.68	1/1429 (0.1%)
50	le	0.38	0/1071	0.62	0/1429
51	Lf	0.29	0/895	0.60	0/1198
51	lf	0.38	0/895	0.67	1/1198 (0.1%)
52	Lg	0.30	0/916	0.60	0/1220
52	lg	0.37	0/916	0.71	0/1220
53	Lh	0.34	0/1023	0.66	0/1351
53	lh	0.42	1/1023 (0.1%)	0.61	0/1351
54	Li	0.43	0/843	0.84	5/1115 (0.4%)
54	li	0.33	0/843	0.67	0/1115
55	Lj	0.34	0/720	0.74	2/952 (0.2%)
55	lj	0.46	0/720	0.69	0/952
56	Lk	0.32	0/575	0.60	0/761
56	lk	0.36	0/575	0.63	0/761
57	Ll	0.27	0/454	0.58	0/599
57	ll	0.36	0/454	0.84	2/599 (0.3%)
58	Lm	0.29	0/435	0.61	0/575
58	lm	0.33	0/435	0.63	0/575
59	Ln	0.29	0/231	0.83	0/294
59	ln	0.31	0/231	0.84	0/294
60	Lo	0.29	0/876	0.62	0/1156

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
60	lo	0.39	0/876	0.68	2/1156 (0.2%)
61	Lp	0.31	0/718	0.62	1/953 (0.1%)
61	lp	0.40	0/718	0.63	0/953
62	Lr	0.31	0/1017	0.68	2/1364 (0.1%)
62	lr	0.44	0/1017	0.67	1/1364 (0.1%)
63	Lz	0.26	0/1769	0.60	1/2371 (0.0%)
63	lz	0.26	0/1769	0.57	1/2371 (0.0%)
64	SR	0.37	0/1105	0.78	2/1484 (0.1%)
64	sR	0.73	2/1105 (0.2%)	1.14	7/1484 (0.5%)
65	SD	0.33	0/1793	0.63	2/2414 (0.1%)
65	sD	0.86	6/1793 (0.3%)	0.97	7/2414 (0.3%)
66	SF	0.33	0/1516	0.64	1/2037 (0.0%)
66	sF	0.41	1/1516 (0.1%)	0.70	2/2037 (0.1%)
67	SK	0.35	0/851	0.72	1/1147 (0.1%)
67	sK	0.41	0/851	0.70	0/1147
68	SP	0.30	0/1003	0.66	0/1342
68	sP	0.37	0/1003	0.72	2/1342 (0.1%)
69	SQ	0.35	0/1160	0.78	2/1553 (0.1%)
69	sQ	0.38	0/1160	0.75	1/1553 (0.1%)
70	SS	0.30	0/1216	0.67	1/1628 (0.1%)
70	sS	0.34	0/1216	0.71	1/1628 (0.1%)
71	ST	0.33	0/1131	0.67	1/1515 (0.1%)
71	sT	0.38	0/1131	0.66	1/1515 (0.1%)
72	SU	0.30	0/831	0.64	0/1115
72	sU	0.34	0/831	0.69	1/1115 (0.1%)
73	Sc	0.28	0/508	0.66	0/680
73	sc	0.39	0/508	0.77	0/680
74	Sd	0.31	0/470	0.66	0/623
74	sd	0.37	0/470	0.60	0/623
75	Sg	0.46	2/2493 (0.1%)	0.84	5/3394 (0.1%)
75	sg	0.33	0/2493	0.61	1/3394 (0.0%)
76	SM	0.35	0/950	0.61	0/1275
76	sM	0.38	0/950	0.67	1/1275 (0.1%)
77	SZ	0.39	0/604	0.79	2/810 (0.2%)
77	sZ	0.37	0/604	0.76	1/810 (0.1%)
78	Sf	0.29	0/560	0.59	0/745
78	sf	0.31	0/560	0.63	0/745
79	S2	0.38	0/41243	0.85	44/64259 (0.1%)
79	s2	0.49	2/41241 (0.0%)	0.90	68/64251 (0.1%)
80	CB	0.32	0/6734	0.59	4/9094 (0.0%)
80	cB	0.63	4/6734 (0.1%)	0.78	15/9094 (0.2%)
81	AP	0.29	0/1692	0.82	0/2634
81	aP	0.33	0/1692	0.83	0/2634

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
82	PE	0.34	0/1778	0.94	1/2767 (0.0%)
82	pE	0.41	0/1778	0.95	2/2767 (0.1%)
83	Ls	0.29	0/1519	0.59	1/2052 (0.0%)
83	ls	0.33	0/1519	0.70	2/2052 (0.1%)
84	Lt	0.28	0/1058	0.58	0/1430
84	lt	0.27	0/1058	0.60	0/1430
85	L5	0.68	29/88929 (0.0%)	1.08	184/138727 (0.1%)
85	l5	0.52	0/88929	0.88	74/138727 (0.1%)
86	Se	0.30	0/382	0.62	0/504
87	LW	0.29	0/979	0.58	0/1295
87	IW	0.39	0/979	0.62	0/1295
All	All	0.48	66/492435 (0.0%)	0.84	533/721182 (0.1%)

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
1	cH	0	1
5	SX	0	1
5	sX	0	1
12	SH	0	1
12	sH	0	1
22	lA	0	1
23	LB	0	2
23	lB	0	2
31	LJ	0	1
33	LM	0	2
33	lM	0	2
35	LO	0	1
35	lO	0	1
46	la	0	1
51	Lf	0	1
51	lf	0	1
55	Lj	0	1
55	lj	0	1
64	sR	0	4
66	SF	0	1
68	sP	0	1
69	SQ	0	1
69	sQ	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
71	ST	0	1
71	sT	0	1
All	All	0	32

All (66) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	L5	4102	C	N1-C6	69.44	1.78	1.37
85	L5	4102	C	N3-C4	65.95	1.80	1.33
85	L5	4105	A	N9-C4	59.75	1.73	1.37
85	L5	4102	C	C2-N3	57.78	1.81	1.35
85	L5	4102	C	C4-C5	50.94	1.83	1.43
85	L5	4102	C	C5-C6	48.84	1.73	1.34
85	L5	4102	C	N1-C2	47.51	1.87	1.40
85	L5	4105	A	C1'-N9	32.97	1.98	1.48
80	cB	849	PRO	CG-CD	-32.75	0.42	1.50
85	L5	4105	A	N9-C8	24.07	1.57	1.37
65	sD	213	PRO	CG-CD	-21.13	0.81	1.50
80	cB	831	PRO	CB-CG	20.96	2.54	1.50
65	sD	213	PRO	CB-CG	18.89	2.44	1.50
64	sR	134	PRO	CG-CD	-17.43	0.93	1.50
80	cB	831	PRO	CG-CD	-14.59	1.02	1.50
85	L5	4106	G	N9-C4	12.74	1.48	1.38
75	Sg	163	PRO	CG-CD	-12.57	1.09	1.50
85	L5	4105	A	C5-C4	11.55	1.46	1.38
80	cB	849	PRO	CB-CG	11.29	2.06	1.50
24	LC	335	MET	CB-CG	-10.54	1.17	1.51
85	L5	4105	A	P-O5'	10.33	1.70	1.59
10	sA	207	PRO	CG-CD	-10.08	1.17	1.50
85	L5	4104	G	O3'-P	9.39	1.72	1.61
24	LC	331	TYR	CE1-CZ	-8.82	1.27	1.38
85	L5	4104	G	C3'-O3'	8.20	1.53	1.42
65	sD	47	GLU	CG-CD	-7.93	1.40	1.51
85	L5	4105	A	C5'-C4'	7.72	1.60	1.51
24	LC	331	TYR	CG-CD1	-7.68	1.29	1.39
24	LC	331	TYR	CE2-CZ	-7.68	1.28	1.38
10	sA	55	TRP	CE3-CZ3	-7.65	1.25	1.38
65	sD	212	GLU	C-N	7.39	1.48	1.34
24	LC	331	TYR	CG-CD2	-7.34	1.29	1.39
10	sA	55	TRP	CB-CG	-7.32	1.37	1.50
79	s2	1284	A	N7-C5	-7.25	1.34	1.39
85	L5	4101	C	O3'-P	7.24	1.69	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	sB	198	GLU	CB-CG	-7.20	1.38	1.52
85	L5	4111	U	C2-O2	-7.19	1.15	1.22
85	L5	4105	A	N7-C5	-7.19	1.34	1.39
85	L5	4105	A	N3-C4	6.99	1.39	1.34
11	sB	198	GLU	CG-CD	-6.96	1.41	1.51
85	L5	4116	C	C4-N4	-6.66	1.27	1.33
65	sD	213	PRO	N-CD	6.63	1.57	1.47
85	L5	4101	C	C2-O2	-6.62	1.18	1.24
85	L5	4102	C	C5'-C4'	6.56	1.59	1.51
79	s2	1284	A	N9-C8	-6.40	1.32	1.37
85	L5	4102	C	P-O5'	6.31	1.66	1.59
64	sR	133	GLY	C-N	6.29	1.46	1.34
85	L5	4097	G	C6-N1	-6.13	1.35	1.39
85	L5	4101	C	C1'-N1	5.95	1.57	1.48
75	Sg	163	PRO	CB-CG	-5.92	1.20	1.50
14	Sa	13	LYS	CB-CG	-5.80	1.36	1.52
53	lh	78	TYR	CD1-CE1	-5.66	1.30	1.39
85	L5	4104	G	P-O5'	5.65	1.65	1.59
66	sF	155	CYS	CB-SG	-5.61	1.72	1.81
29	lH	96	TYR	CD2-CE2	-5.58	1.30	1.39
24	LC	335	MET	CG-SD	-5.49	1.66	1.81
85	L5	4101	C	C4-C5	-5.48	1.38	1.43
2	SE	140	VAL	CB-CG1	-5.34	1.41	1.52
85	L5	4105	A	C4'-O4'	5.30	1.52	1.45
85	L5	4097	G	C6-O6	-5.25	1.19	1.24
65	sD	47	GLU	CB-CG	-5.24	1.42	1.52
19	sb	12	PRO	CG-CD	-5.20	1.33	1.50
19	sb	70	LYS	CD-CE	-5.17	1.38	1.51
19	sb	70	LYS	CB-CG	-5.17	1.38	1.52
33	LM	38	VAL	CB-CG1	-5.13	1.42	1.52
33	lM	118	MET	CB-CG	-5.00	1.35	1.51

All (533) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	L5	4105	A	C8-N9-C4	-169.83	37.87	105.80
85	L5	4105	A	C5-N7-C8	-93.32	57.24	103.90
85	L5	4101	C	C6-N1-C2	-59.99	96.30	120.30
85	L5	4105	A	N7-C8-N9	51.78	139.69	113.80
85	L5	4101	C	C5-C6-N1	37.79	139.90	121.00
85	L5	4105	A	N9-C4-C5	34.76	119.70	105.80
80	cB	831	PRO	CB-CG-CD	-27.30	0.03	106.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	L5	4106	G	C8-N9-C4	-26.84	95.67	106.40
85	L5	4116	C	N3-C4-N4	-25.26	100.32	118.00
85	L5	4101	C	N3-C4-C5	-24.14	112.24	121.90
85	L5	4097	G	N1-C6-O6	-23.74	105.66	119.90
75	Sg	163	PRO	N-CD-CG	-22.52	69.42	103.20
24	LC	335	MET	CG-SD-CE	-22.49	64.21	100.20
85	L5	4105	A	N3-C4-C5	-21.59	111.69	126.80
85	L5	4106	G	N3-C4-C5	-21.30	117.95	128.60
64	sR	134	PRO	N-CD-CG	-20.29	72.76	103.20
85	L5	4105	A	C2-N3-C4	20.23	120.72	110.60
85	L5	4105	A	C8-N9-C1'	20.00	163.70	127.70
85	L5	4106	G	N7-C8-N9	19.53	122.86	113.10
85	L5	4097	G	C5-C6-O6	18.29	139.57	128.60
85	L5	4106	G	C4-N9-C1'	18.25	150.22	126.50
85	L5	4105	A	C4-N9-C1'	17.84	158.42	126.30
65	sD	213	PRO	CA-CB-CG	-17.16	71.39	104.00
75	Sg	163	PRO	CA-CB-CG	-17.01	71.68	104.00
85	L5	4105	A	O4'-C1'-N9	16.96	121.77	108.20
69	SQ	41	MET	CG-SD-CE	-16.63	73.59	100.20
85	L5	4111	U	N1-C2-N3	16.23	124.64	114.90
65	sD	213	PRO	CB-CG-CD	-16.05	43.92	106.50
85	L5	4101	C	C2-N1-C1'	15.91	136.31	118.80
85	L5	4116	C	C5-C4-N4	15.86	131.30	120.20
65	sD	213	PRO	N-CA-CB	-15.80	84.34	103.30
65	sD	213	PRO	N-CD-CG	-15.77	79.55	103.20
85	L5	4106	G	C2-N3-C4	15.66	119.73	111.90
80	cB	849	PRO	N-CD-CG	-15.58	79.83	103.20
75	Sg	163	PRO	CB-CG-CD	15.19	165.74	106.50
85	L5	4101	C	N1-C2-N3	15.19	129.83	119.20
33	lM	118	MET	CG-SD-CE	-14.86	76.43	100.20
80	cB	849	PRO	CA-CB-CG	-14.84	75.80	104.00
85	L5	4100	C	C6-N1-C2	-14.60	114.46	120.30
64	sR	134	PRO	CA-CB-CG	-14.24	76.94	104.00
85	L5	4106	G	O4'-C1'-N9	13.55	119.04	108.20
85	L5	4116	C	N3-C4-C5	13.50	127.30	121.90
19	sb	12	PRO	CA-N-CD	-12.99	93.32	111.50
83	ls	108	PRO	CA-N-CD	-12.84	93.52	111.50
85	L5	4101	C	N3-C2-O2	-12.72	112.99	121.90
19	sb	70	LYS	CD-CE-NZ	-12.64	82.62	111.70
85	L5	4105	A	C4-C5-C6	12.37	123.19	117.00
57	ll	29	MET	CG-SD-CE	-12.18	80.72	100.20
69	sQ	41	MET	CG-SD-CE	-11.90	81.16	100.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
80	cB	831	PRO	CA-N-CD	-11.82	94.94	111.50
10	sA	207	PRO	N-CD-CG	-11.81	85.48	103.20
85	L5	4106	G	N3-C4-N9	11.72	133.03	126.00
64	SR	126	MET	CG-SD-CE	-11.69	81.49	100.20
10	sA	207	PRO	CA-N-CD	-11.59	95.27	111.50
85	L5	4111	U	C6-N1-C2	-11.54	114.07	121.00
79	s2	940	U	O5'-P-OP2	-11.49	95.36	105.70
85	L5	4105	A	C4-C5-N7	-11.23	105.08	110.70
80	cB	831	PRO	N-CA-CB	-11.06	90.02	103.30
85	L5	4101	C	O4'-C1'-N1	11.02	117.01	108.20
18	SW	4	MET	CG-SD-CE	-10.95	82.67	100.20
66	sF	77	MET	CG-SD-CE	-10.78	82.95	100.20
45	lZ	90	PRO	CA-N-CD	-10.73	96.48	111.50
85	L5	4111	U	N1-C2-O2	-10.61	115.37	122.80
85	L5	4112	C	C2-N1-C1'	-10.45	107.30	118.80
80	cB	849	PRO	N-CA-CB	-10.43	90.78	103.30
85	L5	4116	C	C4-C5-C6	-10.34	112.23	117.40
85	L5	4106	G	N9-C1'-C2'	10.31	127.40	114.00
79	s2	1284	A	C4-C5-C6	10.21	122.10	117.00
85	l5	174	C	N3-C2-O2	-10.15	114.80	121.90
85	L5	4106	G	C8-N9-C1'	-10.10	113.87	127.00
85	L5	174	C	N3-C2-O2	-9.99	114.91	121.90
85	L5	4107	G	O5'-P-OP1	-9.89	96.80	105.70
79	s2	1416	C	C6-N1-C2	-9.79	116.39	120.30
66	sF	88	MET	CG-SD-CE	-9.72	84.64	100.20
85	L5	2710	C	N1-C2-O2	9.64	124.68	118.90
85	l5	2710	C	N1-C2-O2	9.62	124.67	118.90
72	sU	82	MET	CG-SD-CE	-9.58	84.88	100.20
85	L5	4105	A	N9-C1'-C2'	9.54	126.40	114.00
85	L5	4104	G	O4'-C1'-N9	-9.53	100.58	108.20
54	Li	6	PRO	CA-N-CD	-9.31	98.47	111.50
85	L5	485	C	C2-N1-C1'	9.29	129.02	118.80
80	cB	830	ARG	C-N-CD	9.24	147.81	128.40
14	Sa	13	LYS	CD-CE-NZ	9.22	132.91	111.70
85	L5	129	C	N3-C2-O2	-9.17	115.48	121.90
85	l5	485	C	C2-N1-C1'	9.11	128.82	118.80
2	sE	19	MET	CG-SD-CE	-9.10	85.64	100.20
85	L5	4112	C	C6-N1-C1'	8.95	131.54	120.80
85	L5	4101	C	C2-N3-C4	8.77	124.28	119.90
85	L5	4114	C	O4'-C1'-N1	8.75	115.20	108.20
75	Sg	25	PRO	CA-N-CD	-8.75	99.25	111.50
79	s2	1284	A	N1-C2-N3	8.72	133.66	129.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	L5	4105	A	C5'-C4'-O4'	8.72	119.57	109.10
79	S2	1772	C	N1-C2-O2	8.71	124.12	118.90
10	sA	10	MET	CB-CG-SD	8.67	138.42	112.40
79	s2	1416	C	C5-C6-N1	8.66	125.33	121.00
85	l5	129	C	N3-C2-O2	-8.64	115.86	121.90
40	lT	155	PRO	CA-N-CD	-8.59	99.47	111.50
85	L5	4104	G	P-O3'-C3'	8.59	130.00	119.70
85	L5	4101	C	N3-C4-N4	8.56	123.99	118.00
85	L5	4111	U	C5-C4-O4	8.55	131.03	125.90
85	L5	2710	C	C2-N1-C1'	8.53	128.18	118.80
85	L5	4323	A	N1-C2-N3	8.51	133.56	129.30
85	L5	4106	G	N9-C4-C5	8.51	108.80	105.40
79	S2	1772	C	N3-C2-O2	-8.45	115.99	121.90
85	l5	2710	C	C2-N1-C1'	8.44	128.09	118.80
85	L5	4111	U	C6-N1-C1'	8.42	132.98	121.20
79	s2	1772	C	N1-C2-O2	8.41	123.95	118.90
77	sZ	98	LYS	CD-CE-NZ	-8.40	92.39	111.70
83	ls	108	PRO	N-CD-CG	-8.38	90.62	103.20
79	s2	1374	C	C2-N1-C1'	8.37	128.01	118.80
79	s2	1772	C	N3-C2-O2	-8.31	116.08	121.90
85	L5	4100	C	C2-N1-C1'	8.22	127.84	118.80
13	sV	10	ASP	CB-CG-OD2	-8.13	110.98	118.30
79	S2	1453	C	N1-C2-O2	8.12	123.77	118.90
79	S2	1453	C	C2-N1-C1'	8.10	127.71	118.80
80	cB	849	PRO	CB-CG-CD	-8.07	75.01	106.50
85	l5	1378	C	C2-N3-C4	8.02	123.91	119.90
85	l5	1994	C	N3-C2-O2	-8.02	116.28	121.90
2	sE	234	PRO	CA-N-CD	-7.96	100.36	111.50
10	sA	207	PRO	CA-CB-CG	-7.95	88.90	104.00
64	SR	1	MET	CB-CG-SD	-7.94	88.58	112.40
64	sR	126	MET	CA-CB-CG	7.82	126.60	113.30
79	S2	356	C	C2-N1-C1'	7.81	127.39	118.80
23	lB	148	LYS	CD-CE-NZ	-7.79	93.80	111.70
83	Ls	108	PRO	CA-N-CD	-7.78	100.61	111.50
85	L5	2710	C	N3-C2-O2	-7.77	116.46	121.90
85	l5	209	U	C2-N1-C1'	7.76	127.02	117.70
85	L5	1994	C	N3-C2-O2	-7.75	116.47	121.90
85	L5	1252	C	N3-C2-O2	-7.74	116.49	121.90
85	L5	4111	U	O5'-P-OP2	-7.72	98.75	105.70
65	sD	212	GLU	CA-CB-CG	7.70	130.34	113.40
85	L5	209	U	C2-N1-C1'	7.70	126.94	117.70
79	s2	1852	C	O5'-P-OP2	-7.59	98.87	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	s2	1755	C	N1-C2-O2	7.55	123.43	118.90
79	S2	356	C	N1-C2-O2	7.55	123.43	118.90
85	L5	4107	G	O5'-P-OP2	7.54	119.75	110.70
85	l5	4372	U	O5'-P-OP2	-7.53	98.92	105.70
85	L5	456	C	N3-C2-O2	-7.51	116.64	121.90
85	l5	456	C	O4'-C1'-N1	7.50	114.20	108.20
15	sC	98	LEU	CA-CB-CG	7.50	132.55	115.30
70	sS	71	MET	CG-SD-CE	7.43	112.09	100.20
85	L5	4106	G	C4-C5-C6	7.39	123.24	118.80
19	sb	12	PRO	N-CD-CG	-7.37	92.14	103.20
85	L5	4100	C	N3-C4-C5	-7.37	118.95	121.90
85	L5	4138	C	N3-C2-O2	-7.34	116.76	121.90
85	l5	2710	C	N3-C2-O2	-7.32	116.78	121.90
2	SE	19	MET	CG-SD-CE	-7.31	88.50	100.20
76	sM	44	LYS	CA-CB-CG	7.31	129.48	113.40
85	l5	16	G	C8-N9-C4	7.28	109.31	106.40
85	l5	1082	C	O4'-C1'-N1	7.27	114.02	108.20
79	S2	1125	C	C6-N1-C2	7.26	123.21	120.30
85	L5	4113	U	O5'-P-OP1	-7.26	99.17	105.70
6	sG	217	MET	CA-CB-CG	7.26	125.64	113.30
37	LQ	28	LEU	CA-CB-CG	7.25	131.98	115.30
85	L5	1447	C	N3-C2-O2	-7.21	116.86	121.90
55	Lj	86	PRO	CA-N-CD	-7.20	101.42	111.50
85	L5	456	C	O4'-C1'-N1	7.20	113.96	108.20
79	s2	557	U	N3-C2-O2	-7.18	117.17	122.20
85	l5	490	C	N3-C2-O2	-7.17	116.88	121.90
65	SD	154	ASP	CB-CG-OD2	7.14	124.72	118.30
79	s2	592	C	N1-C2-O2	7.13	123.18	118.90
69	SQ	41	MET	CA-CB-CG	-7.13	101.18	113.30
85	L5	4147	G	C5-C6-O6	7.12	132.88	128.60
85	L5	175	C	N3-C2-O2	-7.11	116.92	121.90
79	s2	1284	A	N1-C6-N6	7.09	122.85	118.60
80	cB	62	ASP	CB-CG-OD1	7.08	124.68	118.30
85	l5	130	C	C6-N1-C2	-7.08	117.47	120.30
80	cB	497	MET	CG-SD-CE	-7.04	88.94	100.20
79	S2	1416	C	N3-C2-O2	-7.04	116.97	121.90
85	l5	209	U	N1-C2-O2	7.03	127.72	122.80
85	L5	485	C	C6-N1-C1'	-7.02	112.37	120.80
85	l5	1082	C	N3-C2-O2	-7.01	116.99	121.90
85	L5	4114	C	N3-C4-C5	6.96	124.68	121.90
79	S2	1453	C	N3-C2-O2	-6.91	117.06	121.90
37	lQ	4	ASP	CB-CG-OD1	6.91	124.52	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
70	SS	99	LEU	CB-CG-CD1	-6.91	99.25	111.00
85	l5	130	C	N3-C2-O2	-6.89	117.08	121.90
5	sX	101	LEU	CB-CG-CD2	6.89	122.71	111.00
85	l5	485	C	C6-N1-C1'	-6.87	112.56	120.80
85	L5	130	C	N3-C2-O2	-6.86	117.09	121.90
85	l5	456	C	N3-C2-O2	-6.83	117.12	121.90
85	L5	4102	C	N1-C2-N3	-6.83	114.42	119.20
79	s2	1284	A	C6-N1-C2	-6.83	114.50	118.60
80	CB	394	LEU	CB-CG-CD1	-6.82	99.40	111.00
85	L5	4101	C	C2'-C3'-O3'	6.82	124.61	113.70
85	L5	129	C	C6-N1-C2	-6.80	117.58	120.30
79	s2	1415	C	N1-C2-O2	6.77	122.96	118.90
22	LA	80	GLU	OE1-CD-OE2	-6.76	115.19	123.30
64	sR	134	PRO	N-CA-CB	-6.75	95.18	102.60
85	L5	1082	C	O4'-C1'-N1	6.75	113.60	108.20
85	L5	209	U	N1-C2-O2	6.74	127.52	122.80
36	lP	7	ASP	CB-CG-OD1	6.73	124.36	118.30
79	s2	1284	A	C6-C5-N7	-6.72	127.60	132.30
22	LA	96	LEU	CA-CB-CG	6.71	130.74	115.30
79	S2	1019	C	N3-C2-O2	-6.71	117.21	121.90
80	cB	831	PRO	CA-CB-CG	-6.70	91.28	104.00
85	L5	4097	G	O4'-C1'-N9	6.69	113.55	108.20
17	sO	14	VAL	C-N-CA	6.68	138.41	121.70
4	sL	128	VAL	CB-CA-C	6.68	124.08	111.40
85	L5	4113	U	C6-N1-C2	-6.67	117.00	121.00
85	L5	678	C	C2-N1-C1'	6.67	126.14	118.80
79	s2	1355	C	N1-C2-O2	-6.65	114.91	118.90
22	lA	47	ASP	CB-CG-OD2	6.65	124.28	118.30
17	SO	14	VAL	C-N-CA	6.65	138.32	121.70
2	SE	140	VAL	CA-CB-CG1	-6.65	100.93	110.90
66	SF	78	MET	CA-CB-CG	6.65	124.60	113.30
24	LC	2	ALA	C-N-CA	6.63	138.28	121.70
85	l5	1447	C	N3-C2-O2	-6.62	117.26	121.90
85	l5	4138	C	N3-C2-O2	-6.62	117.26	121.90
85	l5	1252	C	N3-C2-O2	-6.62	117.27	121.90
85	L5	4147	G	N1-C6-O6	-6.62	115.93	119.90
85	L5	4102	C	C2-N3-C4	6.60	123.20	119.90
79	s2	1372	U	C2-N1-C1'	6.58	125.60	117.70
79	s2	1284	A	N3-C4-N9	6.58	132.66	127.40
85	L5	654	C	N1-C2-O2	6.57	122.84	118.90
14	Sa	13	LYS	CB-CG-CD	-6.54	94.59	111.60
85	L5	4106	G	C6-C5-N7	-6.51	126.49	130.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	s2	356	C	C2-N1-C1'	6.49	125.94	118.80
85	L5	174	C	C6-N1-C2	-6.49	117.70	120.30
85	l5	175	C	N3-C2-O2	-6.47	117.37	121.90
79	s2	979	C	C2-N1-C1'	6.45	125.90	118.80
85	l5	209	U	N3-C2-O2	-6.45	117.69	122.20
55	Lj	86	PRO	N-CD-CG	-6.45	93.53	103.20
85	L5	925	C	N1-C2-O2	6.45	122.77	118.90
85	L5	4106	G	OP1-P-O3'	6.44	119.37	105.20
85	L5	4102	C	P-O5'-C5'	6.44	131.20	120.90
79	s2	1772	C	C2-N1-C1'	6.43	125.88	118.80
79	s2	557	U	N1-C2-O2	6.42	127.29	122.80
79	s2	607	U	C2-N1-C1'	6.41	125.39	117.70
79	s2	356	C	N1-C2-O2	6.39	122.73	118.90
85	L5	4097	G	C5-C6-N1	6.38	114.69	111.50
79	S2	592	C	N1-C2-O2	6.38	122.73	118.90
85	L5	4100	C	N3-C2-O2	-6.37	117.44	121.90
57	ll	29	MET	CA-CB-CG	6.36	124.11	113.30
35	LO	174	LEU	CA-CB-CG	6.35	129.91	115.30
85	l5	1308	C	C6-N1-C2	6.34	122.84	120.30
79	S2	1755	C	N1-C2-O2	6.34	122.70	118.90
2	sE	15	PRO	CA-N-CD	-6.33	102.64	111.50
85	l5	4147	G	C5-C6-O6	6.33	132.40	128.60
85	L5	489	C	N1-C2-O2	6.32	122.69	118.90
85	l5	1414	C	N3-C2-O2	-6.31	117.48	121.90
79	s2	834	C	N3-C2-O2	-6.30	117.49	121.90
85	L5	2710	C	C6-N1-C2	-6.30	117.78	120.30
85	L5	4859	C	N3-C2-O2	-6.30	117.49	121.90
79	S2	1019	C	N1-C2-O2	6.30	122.68	118.90
63	Lz	116	LEU	CB-CG-CD1	6.29	121.69	111.00
79	S2	356	C	N3-C2-O2	-6.26	117.52	121.90
85	L5	4100	C	C5-C6-N1	6.26	124.13	121.00
75	Sg	163	PRO	CA-N-CD	-6.24	102.77	111.50
85	L5	2785	C	N3-C2-O2	-6.23	117.54	121.90
38	lR	96	MET	CA-CB-CG	6.21	123.86	113.30
6	sG	63	MET	CG-SD-CE	-6.20	90.28	100.20
62	Lr	5	LEU	CB-CG-CD2	-6.19	100.47	111.00
79	S2	1133	A	C8-N9-C4	6.19	108.28	105.80
85	L5	485	C	N1-C2-O2	6.18	122.61	118.90
85	l5	1994	C	C6-N1-C2	-6.18	117.83	120.30
85	L5	174	C	N1-C2-O2	6.17	122.60	118.90
79	s2	607	U	N1-C2-O2	6.15	127.11	122.80
85	L5	4111	U	C2-N3-C4	-6.15	123.31	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	lJ	12	MET	CA-CB-CG	6.14	123.74	113.30
79	S2	1078	C	N1-C2-O2	6.14	122.58	118.90
79	s2	1416	C	N3-C2-O2	-6.14	117.60	121.90
25	LD	146	LEU	CB-CG-CD1	-6.13	100.58	111.00
85	L5	1414	C	N3-C2-O2	-6.12	117.62	121.90
85	l5	4859	C	N3-C2-O2	-6.12	117.62	121.90
85	L5	100	C	C2-N1-C1'	6.12	125.53	118.80
67	SK	79	LEU	CB-CG-CD2	-6.12	100.60	111.00
64	sR	1	MET	CA-CB-CG	6.12	123.70	113.30
68	sP	82	ASP	CB-CG-OD1	6.11	123.80	118.30
85	L5	4709	U	C2-N1-C1'	6.10	125.02	117.70
79	s2	1374	C	C5-C6-N1	6.10	124.05	121.00
1	CH	37	ASP	CB-CG-OD1	-6.09	112.81	118.30
80	cB	257	MET	CG-SD-CE	-6.09	90.45	100.20
85	l5	174	C	N1-C2-O2	6.07	122.54	118.90
79	s2	1520	G	C4-N9-C1'	6.07	134.39	126.50
85	l5	654	C	N1-C2-O2	6.07	122.54	118.90
85	L5	4113	U	N1-C2-N3	6.03	118.52	114.90
85	l5	4859	C	N1-C2-O2	6.02	122.51	118.90
79	s2	1772	C	C6-N1-C2	-6.01	117.89	120.30
85	l5	904	C	C2-N1-C1'	6.01	125.41	118.80
85	L5	2785	C	N1-C2-O2	6.01	122.50	118.90
79	S2	688	U	P-O3'-C3'	6.00	126.89	119.70
79	S2	1772	C	C2-N1-C1'	6.00	125.39	118.80
85	L5	4107	G	C4-N9-C1'	5.99	134.29	126.50
80	CB	45	ILE	CG1-CB-CG2	-5.98	98.24	111.40
12	SH	147	LYS	CA-CB-CG	5.98	126.56	113.40
46	la	87	ARG	CG-CD-NE	-5.98	99.24	111.80
85	L5	4114	C	C5-C4-N4	-5.97	116.02	120.20
85	L5	490	C	N3-C2-O2	-5.96	117.72	121.90
10	sA	73	ASP	CB-CG-OD2	5.96	123.66	118.30
85	l5	100	C	C2-N1-C1'	5.96	125.35	118.80
85	l5	2710	C	C6-N1-C1'	-5.94	113.68	120.80
79	S2	1114	U	O4'-C1'-N1	5.93	112.95	108.20
79	s2	602	G	N3-C4-N9	-5.93	122.44	126.00
85	l5	263	G	C5-C6-O6	5.93	132.16	128.60
79	s2	607	U	N3-C2-O2	-5.93	118.05	122.20
24	LC	196	MET	CG-SD-CE	-5.92	90.73	100.20
24	LC	331	TYR	CD1-CE1-CZ	5.91	125.12	119.80
79	s2	1142	G	N3-C4-N9	-5.91	122.45	126.00
85	L5	4102	C	C5-C6-N1	5.90	123.95	121.00
79	S2	834	C	N3-C2-O2	-5.88	117.78	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	L5	4112	C	C5-C6-N1	-5.87	118.07	121.00
17	sO	80	ASP	CB-CG-OD2	5.86	123.57	118.30
65	sD	150	MET	CG-SD-CE	-5.85	90.84	100.20
85	l5	4924	C	N3-C2-O2	-5.85	117.81	121.90
2	SE	87	MET	CA-CB-CG	5.84	123.23	113.30
79	s2	1355	C	N3-C2-O2	5.82	125.98	121.90
85	l5	489	C	N1-C2-O2	5.82	122.39	118.90
85	L5	4102	C	OP1-P-OP2	-5.82	110.87	119.60
71	ST	130	ASP	CB-CG-OD2	5.82	123.53	118.30
85	L5	4068	U	C2-N1-C1'	5.80	124.66	117.70
79	S2	1424	G	N3-C4-N9	5.79	129.48	126.00
85	L5	4112	C	N3-C4-N4	-5.79	113.95	118.00
85	L5	4113	U	C5-C4-O4	5.79	129.37	125.90
6	sG	169	PRO	CA-N-CD	-5.78	103.40	111.50
85	L5	4113	U	C4-C5-C6	5.78	123.17	119.70
79	s2	1374	C	C6-N1-C2	-5.78	117.99	120.30
85	L5	1082	C	C2-N1-C1'	-5.77	112.46	118.80
85	L5	140	G	N3-C4-N9	-5.76	122.54	126.00
79	s2	1453	C	N3-C2-O2	-5.76	117.87	121.90
82	PE	56	C	N3-C2-O2	-5.76	117.87	121.90
85	L5	4147	G	N3-C4-N9	-5.75	122.55	126.00
85	L5	1414	C	N1-C2-O2	5.75	122.35	118.90
79	S2	1453	C	C6-N1-C2	-5.75	118.00	120.30
79	s2	1453	C	C6-N1-C2	-5.73	118.01	120.30
79	s2	1755	C	C2-N1-C1'	5.73	125.11	118.80
79	S2	621	C	O5'-P-OP1	-5.73	100.55	105.70
85	L5	209	U	N3-C2-O2	-5.72	118.19	122.20
85	L5	472	C	C2-N1-C1'	5.72	125.09	118.80
79	S2	322	C	N1-C2-O2	5.71	122.33	118.90
64	sR	1	MET	CB-CG-SD	5.71	129.52	112.40
80	cB	22	MET	CG-SD-CE	-5.71	91.07	100.20
79	s2	1374	C	C6-N1-C1'	-5.70	113.96	120.80
85	L5	4107	G	O4'-C1'-N9	5.70	112.76	108.20
54	Li	61	LEU	CB-CG-CD2	5.70	120.68	111.00
79	s2	1078	C	N3-C2-O2	-5.69	117.92	121.90
85	l5	2847	G	N1-C6-O6	-5.69	116.49	119.90
63	lz	194	LEU	CA-CB-CG	5.68	128.37	115.30
79	S2	1078	C	N3-C2-O2	-5.68	117.92	121.90
79	s2	1389	C	N1-C2-O2	5.68	122.31	118.90
24	lC	101	MET	CG-SD-CE	-5.68	91.11	100.20
33	lM	39	ASP	CB-CG-OD2	-5.68	113.19	118.30
79	s2	1078	C	N1-C2-O2	5.68	122.31	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	l5	490	C	C6-N1-C2	-5.67	118.03	120.30
79	s2	1455	A	O4'-C1'-N9	5.64	112.71	108.20
85	l5	1414	C	N1-C2-O2	5.64	122.28	118.90
85	L5	1082	C	N3-C2-O2	-5.64	117.95	121.90
85	L5	4105	A	P-O5'-C5'	5.64	129.92	120.90
85	l5	4129	G	C8-N9-C4	5.63	108.65	106.40
85	L5	2710	C	C6-N1-C1'	-5.63	114.04	120.80
79	s2	310	C	N3-C2-O2	-5.63	117.96	121.90
85	L5	1082	C	C6-N1-C1'	5.63	127.56	120.80
28	LG	162	ASP	CB-CG-OD2	5.63	123.36	118.30
85	L5	4109	G	C4-N9-C1'	5.62	133.81	126.50
79	s2	1520	G	C8-N9-C1'	-5.61	119.71	127.00
85	l5	925	C	N3-C2-O2	-5.61	117.97	121.90
85	L5	140	G	C5-C6-O6	5.60	131.96	128.60
85	l5	925	C	N1-C2-O2	5.60	122.26	118.90
65	SD	154	ASP	CB-CG-OD1	-5.60	113.26	118.30
79	s2	1453	C	C2-N1-C1'	5.58	124.94	118.80
85	L5	3761	C	N1-C2-O2	5.58	122.25	118.90
82	pE	40	C	C2-N1-C1'	5.57	124.92	118.80
50	Le	7	LEU	CD1-CG-CD2	-5.57	93.80	110.50
2	sE	87	MET	CA-CB-CG	5.56	122.76	113.30
85	L5	1994	C	N1-C2-O2	5.56	122.23	118.90
85	L5	664	G	C5-C6-O6	5.55	131.93	128.60
22	LA	106	THR	C-N-CA	-5.54	107.84	121.70
85	l5	1241	C	C2-N1-C1'	5.54	124.89	118.80
65	sD	150	MET	CB-CA-C	5.53	121.47	110.40
68	sP	123	TYR	C-N-CA	-5.53	107.86	121.70
85	L5	4323	A	C2-N3-C4	-5.53	107.83	110.60
24	LC	10	VAL	CG1-CB-CG2	-5.53	102.05	110.90
79	S2	1467	C	C6-N1-C2	-5.52	118.09	120.30
85	l5	3761	C	C2-N1-C1'	5.51	124.86	118.80
85	l5	174	C	C6-N1-C2	-5.51	118.10	120.30
85	l5	4709	U	C2-N1-C1'	5.49	124.29	117.70
85	L5	3761	C	C2-N1-C1'	5.49	124.84	118.80
85	L5	4101	C	P-O3'-C3'	5.49	126.29	119.70
85	L5	4107	G	C8-N9-C4	-5.48	104.21	106.40
37	lQ	28	LEU	CA-CB-CG	5.48	127.91	115.30
85	L5	4109	G	N3-C4-C5	-5.48	125.86	128.60
85	L5	456	C	C6-N1-C2	-5.48	118.11	120.30
11	sB	207	LEU	CA-CB-CG	5.47	127.89	115.30
85	L5	3773	U	C2-N1-C1'	5.47	124.27	117.70
85	l5	2785	C	N1-C2-O2	5.47	122.18	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	lF	44	LYS	CD-CE-NZ	-5.46	99.14	111.70
79	s2	621	C	N3-C2-O2	-5.46	118.08	121.90
85	l5	654	C	C5-C6-N1	5.45	123.72	121.00
85	L5	209	U	C6-N1-C1'	-5.45	113.58	121.20
85	L5	678	C	C6-N1-C1'	-5.45	114.26	120.80
85	L5	4709	U	C5-C4-O4	-5.45	122.63	125.90
79	S2	1453	C	C6-N1-C1'	-5.43	114.28	120.80
62	Lr	56	ASP	CB-CG-OD1	5.43	123.19	118.30
79	S2	1261	C	N1-C2-O2	5.43	122.16	118.90
36	lP	148	MET	CG-SD-CE	-5.43	91.52	100.20
79	S2	834	C	C6-N1-C2	-5.42	118.13	120.30
64	sR	1	MET	CB-CA-C	5.42	121.23	110.40
85	l5	4129	G	N9-C4-C5	-5.41	103.23	105.40
60	lo	96	ASP	CB-CG-OD2	5.41	123.17	118.30
85	L5	1417	C	C2-N1-C1'	5.40	124.74	118.80
85	l5	485	C	N1-C2-O2	5.40	122.14	118.90
85	l5	1417	C	C2-N1-C1'	5.39	124.73	118.80
79	S2	356	C	C6-N1-C1'	-5.39	114.33	120.80
85	L5	4924	C	N3-C2-O2	-5.39	118.13	121.90
85	L5	1216	C	C2-N1-C1'	5.38	124.72	118.80
85	L5	4112	C	C5-C4-N4	5.38	123.96	120.20
79	S2	592	C	C2-N1-C1'	5.38	124.72	118.80
16	SN	110	ASP	CB-CG-OD2	5.37	123.13	118.30
85	L5	4107	G	N7-C8-N9	5.37	115.78	113.10
85	l5	209	U	C6-N1-C1'	-5.36	113.70	121.20
85	L5	2627	C	N1-C2-O2	5.36	122.11	118.90
85	L5	3773	U	N3-C2-O2	-5.35	118.45	122.20
80	CB	401	MET	CB-CG-SD	5.34	128.42	112.40
85	L5	4859	C	N1-C2-O2	5.34	122.10	118.90
85	L5	1191	C	N3-C2-O2	-5.34	118.16	121.90
2	SE	123	LEU	CA-CB-CG	5.34	127.57	115.30
24	lC	2	ALA	C-N-CA	5.33	135.03	121.70
85	L5	925	C	N3-C2-O2	-5.33	118.17	121.90
85	L5	1993	C	N1-C2-O2	5.33	122.10	118.90
25	LD	235	MET	CA-CB-CG	5.33	122.36	113.30
71	sT	129	ARG	CG-CD-NE	-5.33	100.61	111.80
85	L5	4101	C	O5'-P-OP1	-5.32	100.91	105.70
85	L5	4104	G	C8-N9-C4	-5.32	104.27	106.40
54	Li	94	LEU	CB-CG-CD2	-5.32	101.96	111.00
79	s2	1123	C	N3-C2-O2	-5.31	118.18	121.90
4	SL	136	LYS	CD-CE-NZ	-5.31	99.49	111.70
85	l5	1191	C	N3-C2-O2	-5.31	118.18	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	L5	263	G	C5-C6-O6	5.31	131.78	128.60
2	sE	66	MET	CG-SD-CE	-5.31	91.71	100.20
79	s2	322	C	N1-C2-O2	5.31	122.08	118.90
85	l5	262	G	N1-C2-N2	-5.30	111.42	116.20
85	L5	1501	C	C5-C6-N1	5.30	123.65	121.00
79	S2	566	U	N3-C2-O2	-5.29	118.49	122.20
85	l5	140	G	C5-C6-O6	5.29	131.78	128.60
79	s2	1114	U	O4'-C1'-N1	5.29	112.43	108.20
85	L5	130	C	C6-N1-C2	-5.29	118.19	120.30
48	Lc	18	LEU	CA-CB-CG	5.28	127.44	115.30
77	SZ	58	LEU	CA-CB-CG	5.28	127.44	115.30
85	l5	472	C	C2-N1-C1'	5.27	124.60	118.80
85	L5	262	G	N1-C6-O6	-5.27	116.74	119.90
85	L5	4104	G	N9-C4-C5	5.26	107.50	105.40
85	L5	904	C	C2-N1-C1'	5.26	124.58	118.80
79	s2	1284	A	C8-N9-C1'	-5.25	118.24	127.70
23	LB	216	MET	CG-SD-CE	-5.25	91.79	100.20
42	IV	96	LEU	CB-CG-CD2	-5.25	102.07	111.00
79	S2	1424	G	C4-N9-C1'	5.25	133.33	126.50
85	l5	3761	C	N1-C2-O2	5.25	122.05	118.90
85	l5	963	G	C4-N9-C1'	5.24	133.32	126.50
85	L5	4106	G	P-O3'-C3'	5.24	125.99	119.70
79	s2	1373	C	N3-C2-O2	-5.24	118.23	121.90
85	L5	1973	G	N1-C2-N2	-5.24	111.48	116.20
85	L5	664	G	N1-C6-O6	-5.23	116.76	119.90
75	sg	59	LEU	CB-CG-CD1	-5.23	102.11	111.00
79	s2	1016	U	N3-C2-O2	-5.23	118.54	122.20
77	SZ	89	GLN	CA-CB-CG	5.23	124.91	113.40
79	s2	1755	C	N3-C2-O2	-5.23	118.24	121.90
85	L5	1082	C	P-O3'-C3'	5.22	125.97	119.70
85	L5	4898	G	C5-C6-O6	5.22	131.74	128.60
79	s2	1146	C	N3-C2-O2	-5.22	118.25	121.90
85	L5	2805	C	N1-C2-O2	5.22	122.03	118.90
80	cB	337	LYS	CD-CE-NZ	-5.21	99.70	111.70
85	L5	2257	C	C2-N1-C1'	5.21	124.53	118.80
85	L5	1447	C	N1-C2-O2	5.20	122.02	118.90
15	SC	95	ASP	CB-CG-OD2	5.20	122.98	118.30
85	L5	4107	G	OP1-P-OP2	-5.20	111.81	119.60
85	l5	1439	C	O5'-P-OP1	-5.20	101.03	105.70
80	CB	231	MET	CA-CB-CG	5.20	122.13	113.30
79	S2	621	C	N3-C2-O2	-5.19	118.26	121.90
85	L5	262	G	N1-C2-N2	-5.19	111.53	116.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	Li	61	LEU	CB-CG-CD1	-5.18	102.19	111.00
85	L5	4101	C	N1-C1'-C2'	5.17	120.72	114.00
85	L5	2262	G	C4-N9-C1'	5.17	133.22	126.50
85	l5	2710	C	C6-N1-C2	-5.16	118.23	120.30
85	L5	4926	C	C2-N1-C1'	5.16	124.48	118.80
85	l5	262	G	N1-C6-O6	-5.16	116.80	119.90
62	lr	96	MET	CA-CB-CG	5.16	122.07	113.30
6	SG	126	ASP	CB-CG-OD1	5.16	122.94	118.30
24	LC	331	TYR	CZ-CE2-CD2	5.16	124.44	119.80
85	L5	1973	G	N3-C2-N2	5.15	123.50	119.90
85	l5	4147	G	N1-C6-O6	-5.15	116.81	119.90
85	l5	3773	U	C2-N1-C1'	5.14	123.87	117.70
79	s2	1453	C	N1-C2-O2	5.14	121.98	118.90
24	lC	326	LEU	CA-CB-CG	5.14	127.12	115.30
85	l5	3773	U	O5'-P-OP1	5.14	116.87	110.70
85	L5	4926	C	N1-C2-O2	5.14	121.98	118.90
79	S2	356	C	C6-N1-C2	-5.14	118.25	120.30
85	l5	1241	C	N1-C2-O2	5.13	121.98	118.90
85	l5	3773	U	N1-C2-O2	5.13	126.39	122.80
79	s2	1372	U	C6-N1-C1'	-5.13	114.01	121.20
54	Li	90	LEU	CA-CB-CG	5.13	127.11	115.30
79	s2	834	C	C6-N1-C2	-5.13	118.25	120.30
85	L5	1501	C	C6-N1-C2	-5.13	118.25	120.30
85	L5	4101	C	C6-N1-C1'	5.11	126.94	120.80
79	s2	1389	C	C2-N1-C1'	5.11	124.42	118.80
47	Lb	65	MET	CA-CB-CG	5.11	121.98	113.30
79	S2	834	C	N1-C2-O2	5.11	121.96	118.90
4	sL	128	VAL	CA-CB-CG1	5.10	118.55	110.90
22	lA	228	ASP	CB-CG-OD2	5.10	122.89	118.30
79	S2	1415	C	N1-C2-O2	5.10	121.96	118.90
79	s2	1139	C	C2-N1-C1'	5.09	124.40	118.80
85	L5	499	G	O4'-C1'-N9	5.09	112.28	108.20
79	s2	979	C	C6-N1-C1'	-5.09	114.69	120.80
79	S2	1772	C	C6-N1-C2	-5.09	118.26	120.30
85	L5	4709	U	C6-N1-C1'	-5.09	114.08	121.20
51	lf	83	MET	CG-SD-CE	-5.07	92.09	100.20
85	l5	4926	C	C2-N1-C1'	5.07	124.38	118.80
79	S2	1139	C	C2-N1-C1'	5.07	124.38	118.80
79	S2	1424	G	C8-N9-C1'	-5.07	120.41	127.00
80	cB	266	PHE	C-N-CA	-5.07	109.03	121.70
85	l5	129	C	C6-N1-C2	-5.07	118.27	120.30
85	l5	1275	G	N3-C4-N9	-5.07	122.96	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	s2	1022	U	C2-N1-C1'	5.06	123.78	117.70
85	L5	1216	C	N1-C2-O2	5.06	121.94	118.90
79	S2	602	G	N3-C4-N9	-5.06	122.97	126.00
85	l5	673	C	C2-N1-C1'	5.06	124.36	118.80
79	S2	310	C	N3-C2-O2	-5.06	118.36	121.90
35	lO	113	ASP	CB-CG-OD1	5.05	122.85	118.30
79	S2	1520	G	C4-N9-C1'	5.05	133.06	126.50
85	l5	2257	C	N1-C2-O2	5.05	121.93	118.90
85	L5	129	C	N1-C2-N3	5.04	122.73	119.20
21	l8	75	G	C8-N9-C4	5.04	108.42	106.40
61	Lp	25	MET	CG-SD-CE	-5.04	92.14	100.20
79	s2	1016	U	N1-C2-O2	5.04	126.33	122.80
82	pE	4	C	C2-N1-C1'	5.03	124.34	118.80
79	s2	688	U	P-O3'-C3'	5.03	125.73	119.70
85	L5	4116	C	N1-C2-N3	-5.03	115.68	119.20
79	S2	1139	C	N1-C2-O2	5.03	121.92	118.90
79	s2	118	C	C2-N1-C1'	5.02	124.33	118.80
79	s2	1828	C	N1-C2-O2	5.01	121.91	118.90
85	L5	4109	G	N3-C4-N9	5.01	129.01	126.00
4	sL	73	LEU	CA-CB-CG	5.01	126.82	115.30
60	lo	33	LEU	CA-CB-CG	5.01	126.81	115.30
79	s2	833	C	N1-C2-O2	5.00	121.90	118.90

There are no chirality outliers.

All (32) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
23	LB	17	LEU	Peptide
23	LB	258	HIS	Peptide
31	LJ	94	LEU	Peptide
33	LM	87	ALA	Peptide
33	LM	88	ALA	Peptide
35	LO	110	PRO	Peptide
51	Lf	106	TYR	Peptide
55	Lj	39	TYR	Peptide
66	SF	78	MET	Peptide
12	SH	15	LYS	Peptide
69	SQ	43	GLU	Peptide
71	ST	46	ALA	Peptide
5	SX	126	ALA	Peptide
1	cH	51	GLN	Peptide
22	lA	13	GLY	Peptide

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Mol	Chain	Res	Type	Group
23	lB	17	LEU	Peptide
23	lB	258	HIS	Peptide
33	lM	87	ALA	Peptide
33	lM	88	ALA	Peptide
35	lO	110	PRO	Peptide
46	la	87	ARG	Sidechain
51	lf	106	TYR	Peptide
55	lj	39	TYR	Peptide
12	sH	15	LYS	Peptide
68	sP	127	LYS	Peptide
69	sQ	43	GLU	Peptide
64	sR	133	GLY	Mainchain,Peptide
64	sR	26	ASN	Peptide
64	sR	42	PRO	Peptide
71	sT	129	ARG	Sidechain
5	sX	126	ALA	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CH	123/125 (98%)	109 (89%)	12 (10%)	2 (2%)	8	37
1	cH	123/125 (98%)	106 (86%)	16 (13%)	1 (1%)	16	51
2	SE	260/262 (99%)	246 (95%)	14 (5%)	0	100	100
2	sE	260/262 (99%)	243 (94%)	16 (6%)	1 (0%)	30	64
3	SI	204/206 (99%)	191 (94%)	13 (6%)	0	100	100
3	sI	204/206 (99%)	191 (94%)	13 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	SL	151/153 (99%)	137 (91%)	14 (9%)	0	100	100
4	sL	151/153 (99%)	136 (90%)	15 (10%)	0	100	100
5	SX	139/141 (99%)	124 (89%)	14 (10%)	1 (1%)	19	54
5	sX	139/141 (99%)	121 (87%)	17 (12%)	1 (1%)	19	54
6	SG	235/237 (99%)	219 (93%)	16 (7%)	0	100	100
6	sG	235/237 (99%)	220 (94%)	14 (6%)	1 (0%)	30	64
7	SJ	183/185 (99%)	168 (92%)	15 (8%)	0	100	100
7	sJ	183/185 (99%)	171 (93%)	12 (7%)	0	100	100
8	SY	129/131 (98%)	116 (90%)	13 (10%)	0	100	100
8	sY	129/131 (98%)	117 (91%)	12 (9%)	0	100	100
9	se	56/58 (97%)	47 (84%)	9 (16%)	0	100	100
10	SA	219/221 (99%)	201 (92%)	18 (8%)	0	100	100
10	sA	219/221 (99%)	196 (90%)	23 (10%)	0	100	100
11	SB	212/214 (99%)	204 (96%)	8 (4%)	0	100	100
11	sB	212/214 (99%)	199 (94%)	13 (6%)	0	100	100
12	SH	182/189 (96%)	159 (87%)	23 (13%)	0	100	100
12	sH	182/189 (96%)	156 (86%)	26 (14%)	0	100	100
13	SV	81/83 (98%)	74 (91%)	7 (9%)	0	100	100
13	sV	81/83 (98%)	70 (86%)	11 (14%)	0	100	100
14	Sa	100/102 (98%)	81 (81%)	18 (18%)	1 (1%)	13	47
14	sa	100/102 (98%)	90 (90%)	10 (10%)	0	100	100
15	SC	220/222 (99%)	202 (92%)	18 (8%)	0	100	100
15	sC	220/222 (99%)	203 (92%)	17 (8%)	0	100	100
16	SN	148/150 (99%)	142 (96%)	6 (4%)	0	100	100
16	sN	148/150 (99%)	143 (97%)	5 (3%)	0	100	100
17	SO	138/140 (99%)	125 (91%)	13 (9%)	0	100	100
17	sO	138/140 (99%)	124 (90%)	14 (10%)	0	100	100
18	SW	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
18	sW	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
19	Sb	81/83 (98%)	70 (86%)	11 (14%)	0	100	100
19	sb	81/83 (98%)	69 (85%)	12 (15%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	LA	246/248 (99%)	219 (89%)	27 (11%)	0	100	100
22	lA	246/248 (99%)	225 (92%)	21 (8%)	0	100	100
23	LB	400/402 (100%)	364 (91%)	36 (9%)	0	100	100
23	lB	400/402 (100%)	371 (93%)	29 (7%)	0	100	100
24	LC	366/368 (100%)	347 (95%)	19 (5%)	0	100	100
24	lC	366/368 (100%)	340 (93%)	26 (7%)	0	100	100
25	LD	291/293 (99%)	279 (96%)	12 (4%)	0	100	100
25	lD	291/293 (99%)	271 (93%)	20 (7%)	0	100	100
26	LE	232/247 (94%)	212 (91%)	20 (9%)	0	100	100
26	lE	232/247 (94%)	210 (90%)	22 (10%)	0	100	100
27	LF	223/225 (99%)	211 (95%)	12 (5%)	0	100	100
27	lF	223/225 (99%)	211 (95%)	12 (5%)	0	100	100
28	LG	239/241 (99%)	224 (94%)	15 (6%)	0	100	100
28	lG	239/241 (99%)	224 (94%)	15 (6%)	0	100	100
29	LH	188/190 (99%)	174 (93%)	14 (7%)	0	100	100
29	lH	188/190 (99%)	173 (92%)	15 (8%)	0	100	100
30	LI	198/213 (93%)	183 (92%)	15 (8%)	0	100	100
30	lI	198/213 (93%)	188 (95%)	10 (5%)	0	100	100
31	LJ	174/176 (99%)	158 (91%)	16 (9%)	0	100	100
31	lJ	174/176 (99%)	155 (89%)	19 (11%)	0	100	100
32	LL	208/210 (99%)	190 (91%)	18 (9%)	0	100	100
32	lL	208/210 (99%)	191 (92%)	17 (8%)	0	100	100
33	LM	137/139 (99%)	127 (93%)	9 (7%)	1 (1%)	19	54
33	lM	137/139 (99%)	126 (92%)	10 (7%)	1 (1%)	19	54
34	LN	201/203 (99%)	184 (92%)	16 (8%)	1 (0%)	25	60
34	lN	201/203 (99%)	190 (94%)	10 (5%)	1 (0%)	25	60
35	LO	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
35	lO	199/201 (99%)	190 (96%)	9 (4%)	0	100	100
36	LP	151/153 (99%)	140 (93%)	11 (7%)	0	100	100
36	lP	151/153 (99%)	138 (91%)	13 (9%)	0	100	100
37	LQ	185/187 (99%)	175 (95%)	10 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	lQ	185/187 (99%)	175 (95%)	10 (5%)	0	100	100
38	LR	185/187 (99%)	179 (97%)	6 (3%)	0	100	100
38	lR	185/187 (99%)	175 (95%)	10 (5%)	0	100	100
39	LS	173/175 (99%)	160 (92%)	13 (8%)	0	100	100
39	lS	173/175 (99%)	159 (92%)	14 (8%)	0	100	100
40	LT	157/159 (99%)	149 (95%)	8 (5%)	0	100	100
40	lT	157/159 (99%)	143 (91%)	14 (9%)	0	100	100
41	LU	99/101 (98%)	84 (85%)	15 (15%)	0	100	100
41	lU	99/101 (98%)	81 (82%)	18 (18%)	0	100	100
42	LV	129/131 (98%)	121 (94%)	8 (6%)	0	100	100
42	lV	129/131 (98%)	119 (92%)	10 (8%)	0	100	100
43	LX	118/120 (98%)	114 (97%)	4 (3%)	0	100	100
43	lX	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
44	LY	132/134 (98%)	130 (98%)	2 (2%)	0	100	100
44	lY	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
45	LZ	133/135 (98%)	123 (92%)	10 (8%)	0	100	100
45	lZ	133/135 (98%)	120 (90%)	13 (10%)	0	100	100
46	La	145/147 (99%)	137 (94%)	8 (6%)	0	100	100
46	la	145/147 (99%)	137 (94%)	8 (6%)	0	100	100
47	Lb	105/121 (87%)	95 (90%)	10 (10%)	0	100	100
47	lb	105/121 (87%)	94 (90%)	11 (10%)	0	100	100
48	Lc	96/98 (98%)	89 (93%)	7 (7%)	0	100	100
48	lc	96/98 (98%)	90 (94%)	6 (6%)	0	100	100
49	Ld	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
49	ld	105/107 (98%)	101 (96%)	4 (4%)	0	100	100
50	Le	126/128 (98%)	119 (94%)	7 (6%)	0	100	100
50	le	126/128 (98%)	116 (92%)	10 (8%)	0	100	100
51	Lf	107/109 (98%)	97 (91%)	10 (9%)	0	100	100
51	lf	107/109 (98%)	97 (91%)	10 (9%)	0	100	100
52	Lg	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
52	lg	112/114 (98%)	100 (89%)	12 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	Lh	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
53	lh	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
54	Li	100/102 (98%)	96 (96%)	4 (4%)	0	100	100
54	li	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
55	Lj	84/86 (98%)	76 (90%)	8 (10%)	0	100	100
55	lj	84/86 (98%)	73 (87%)	11 (13%)	0	100	100
56	Lk	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
56	lk	67/69 (97%)	64 (96%)	3 (4%)	0	100	100
57	Ll	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
57	ll	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
58	Lm	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
58	lm	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
59	Ln	22/24 (92%)	22 (100%)	0	0	100	100
59	ln	22/24 (92%)	22 (100%)	0	0	100	100
60	Lo	103/105 (98%)	94 (91%)	9 (9%)	0	100	100
60	lo	103/105 (98%)	99 (96%)	4 (4%)	0	100	100
61	Lp	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
61	lp	89/91 (98%)	82 (92%)	7 (8%)	0	100	100
62	Lr	123/125 (98%)	116 (94%)	7 (6%)	0	100	100
62	lr	123/125 (98%)	110 (89%)	13 (11%)	0	100	100
63	Lz	215/217 (99%)	166 (77%)	49 (23%)	0	100	100
63	lz	215/217 (99%)	172 (80%)	43 (20%)	0	100	100
64	SR	133/135 (98%)	114 (86%)	18 (14%)	1 (1%)	16	51
64	sR	133/135 (98%)	106 (80%)	25 (19%)	2 (2%)	8	38
65	SD	225/227 (99%)	208 (92%)	17 (8%)	0	100	100
65	sD	225/227 (99%)	205 (91%)	19 (8%)	1 (0%)	30	64
66	SF	187/189 (99%)	159 (85%)	28 (15%)	0	100	100
66	sF	187/189 (99%)	165 (88%)	22 (12%)	0	100	100
67	SK	96/98 (98%)	85 (88%)	9 (9%)	2 (2%)	5	31
67	sK	96/98 (98%)	85 (88%)	10 (10%)	1 (1%)	13	47
68	SP	119/121 (98%)	112 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	sP	119/121 (98%)	109 (92%)	10 (8%)	0	100	100
69	SQ	142/144 (99%)	121 (85%)	20 (14%)	1 (1%)	19	54
69	sQ	142/144 (99%)	122 (86%)	19 (13%)	1 (1%)	19	54
70	SS	143/145 (99%)	132 (92%)	11 (8%)	0	100	100
70	sS	143/145 (99%)	131 (92%)	12 (8%)	0	100	100
71	ST	141/143 (99%)	127 (90%)	13 (9%)	1 (1%)	19	54
71	sT	141/143 (99%)	128 (91%)	12 (8%)	1 (1%)	19	54
72	SU	102/104 (98%)	91 (89%)	11 (11%)	0	100	100
72	sU	102/104 (98%)	93 (91%)	9 (9%)	0	100	100
73	Sc	62/64 (97%)	51 (82%)	11 (18%)	0	100	100
73	sc	62/64 (97%)	50 (81%)	12 (19%)	0	100	100
74	Sd	53/55 (96%)	49 (92%)	4 (8%)	0	100	100
74	sd	53/55 (96%)	48 (91%)	5 (9%)	0	100	100
75	Sg	311/313 (99%)	275 (88%)	36 (12%)	0	100	100
75	sg	311/313 (99%)	274 (88%)	37 (12%)	0	100	100
76	SM	120/122 (98%)	101 (84%)	18 (15%)	1 (1%)	16	51
76	sM	120/122 (98%)	109 (91%)	10 (8%)	1 (1%)	16	51
77	SZ	73/75 (97%)	58 (80%)	15 (20%)	0	100	100
77	sZ	73/75 (97%)	62 (85%)	11 (15%)	0	100	100
78	Sf	65/67 (97%)	55 (85%)	10 (15%)	0	100	100
78	sf	65/67 (97%)	55 (85%)	10 (15%)	0	100	100
80	CB	842/856 (98%)	782 (93%)	57 (7%)	3 (0%)	30	64
80	cB	842/856 (98%)	782 (93%)	57 (7%)	3 (0%)	30	64
83	Ls	194/196 (99%)	184 (95%)	10 (5%)	0	100	100
83	ls	194/196 (99%)	176 (91%)	18 (9%)	0	100	100
84	Lt	137/141 (97%)	103 (75%)	32 (23%)	2 (2%)	8	38
84	lt	137/141 (97%)	104 (76%)	31 (23%)	2 (2%)	8	38
86	Se	45/47 (96%)	43 (96%)	2 (4%)	0	100	100
87	LW	114/124 (92%)	109 (96%)	5 (4%)	0	100	100
87	IW	114/124 (92%)	112 (98%)	2 (2%)	0	100	100
All	All	25645/26099 (98%)	23469 (92%)	2141 (8%)	35 (0%)	50	80

All (35) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	sG	217	MET
67	sK	96	ARG
80	cB	779	THR
80	CB	407	LYS
80	CB	779	THR
67	SK	96	ARG
84	Lt	144	ASP
1	CH	38	VAL
1	cH	38	VAL
2	sE	87	MET
5	sX	127	ASN
71	sT	41	LYS
80	cB	62	ASP
80	cB	407	LYS
5	SX	127	ASN
64	SR	124	VAL
67	SK	36	ALA
69	SQ	44	PRO
71	ST	39	LEU
76	sM	96	ARG
84	lt	24	ALA
80	CB	611	ASP
76	SM	96	ARG
84	Lt	24	ALA
1	CH	114	ALA
69	sQ	44	PRO
34	LN	124	ASP
33	LM	88	ALA
34	LN	124	ASP
64	sR	124	VAL
64	sR	128	PHE
84	lt	144	ASP
33	LM	88	ALA
14	Sa	46	GLU
65	sD	213	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CH	100/100 (100%)	99 (99%)	1 (1%)	73	87
1	cH	100/100 (100%)	96 (96%)	4 (4%)	27	59
2	SE	224/224 (100%)	215 (96%)	9 (4%)	27	59
2	sE	224/224 (100%)	214 (96%)	10 (4%)	23	56
3	SI	178/178 (100%)	173 (97%)	5 (3%)	38	68
3	sI	178/178 (100%)	166 (93%)	12 (7%)	13	44
4	SL	137/137 (100%)	132 (96%)	5 (4%)	30	62
4	sL	137/137 (100%)	128 (93%)	9 (7%)	14	45
5	SX	113/113 (100%)	109 (96%)	4 (4%)	31	63
5	sX	113/113 (100%)	109 (96%)	4 (4%)	31	63
6	SG	207/207 (100%)	195 (94%)	12 (6%)	17	49
6	sG	207/207 (100%)	193 (93%)	14 (7%)	13	43
7	SJ	161/161 (100%)	154 (96%)	7 (4%)	25	57
7	sJ	161/161 (100%)	155 (96%)	6 (4%)	29	62
8	SY	113/113 (100%)	101 (89%)	12 (11%)	5	24
8	sY	113/113 (100%)	104 (92%)	9 (8%)	10	37
9	se	47/47 (100%)	46 (98%)	1 (2%)	48	74
10	SA	183/183 (100%)	175 (96%)	8 (4%)	24	57
10	sA	183/183 (100%)	172 (94%)	11 (6%)	16	48
11	SB	195/195 (100%)	188 (96%)	7 (4%)	30	62
11	sB	195/195 (100%)	187 (96%)	8 (4%)	26	59
12	SH	166/169 (98%)	154 (93%)	12 (7%)	12	41
12	sH	166/169 (98%)	159 (96%)	7 (4%)	25	58
13	SV	67/67 (100%)	62 (92%)	5 (8%)	11	40
13	sV	67/67 (100%)	58 (87%)	9 (13%)	3	15
14	Sa	89/89 (100%)	86 (97%)	3 (3%)	32	63
14	sa	89/89 (100%)	85 (96%)	4 (4%)	23	56
15	SC	188/188 (100%)	181 (96%)	7 (4%)	29	62
15	sC	188/188 (100%)	184 (98%)	4 (2%)	48	74
16	SN	130/130 (100%)	122 (94%)	8 (6%)	15	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	sN	130/130 (100%)	124 (95%)	6 (5%)	23	56
17	SO	110/110 (100%)	105 (96%)	5 (4%)	23	56
17	sO	110/110 (100%)	106 (96%)	4 (4%)	30	62
18	SW	112/112 (100%)	105 (94%)	7 (6%)	15	46
18	sW	112/112 (100%)	109 (97%)	3 (3%)	40	69
19	Sb	75/75 (100%)	73 (97%)	2 (3%)	40	69
19	sb	75/75 (100%)	71 (95%)	4 (5%)	19	52
22	LA	190/190 (100%)	185 (97%)	5 (3%)	41	70
22	lA	190/190 (100%)	181 (95%)	9 (5%)	22	55
23	LB	348/348 (100%)	340 (98%)	8 (2%)	45	72
23	lB	348/348 (100%)	335 (96%)	13 (4%)	29	62
24	LC	306/306 (100%)	295 (96%)	11 (4%)	30	62
24	lC	306/306 (100%)	289 (94%)	17 (6%)	17	50
25	LD	246/247 (100%)	232 (94%)	14 (6%)	17	50
25	lD	246/247 (100%)	237 (96%)	9 (4%)	29	62
26	LE	209/220 (95%)	201 (96%)	8 (4%)	28	60
26	lE	209/220 (95%)	203 (97%)	6 (3%)	37	67
27	LF	194/194 (100%)	186 (96%)	8 (4%)	26	59
27	lF	194/194 (100%)	182 (94%)	12 (6%)	15	47
28	LG	203/205 (99%)	196 (97%)	7 (3%)	32	63
28	lG	203/205 (99%)	195 (96%)	8 (4%)	27	60
29	LH	169/169 (100%)	165 (98%)	4 (2%)	44	71
29	lH	169/169 (100%)	162 (96%)	7 (4%)	26	59
30	LI	172/180 (96%)	164 (95%)	8 (5%)	22	55
30	lI	172/180 (96%)	162 (94%)	10 (6%)	17	49
31	LJ	148/148 (100%)	141 (95%)	7 (5%)	22	55
31	lJ	148/148 (100%)	142 (96%)	6 (4%)	26	59
32	LL	176/176 (100%)	170 (97%)	6 (3%)	32	63
32	lL	176/176 (100%)	168 (96%)	8 (4%)	23	56
33	LM	118/118 (100%)	112 (95%)	6 (5%)	20	53
33	lM	118/118 (100%)	111 (94%)	7 (6%)	16	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	LN	171/171 (100%)	165 (96%)	6 (4%)	31	63
34	IN	171/171 (100%)	167 (98%)	4 (2%)	45	72
35	LO	173/173 (100%)	170 (98%)	3 (2%)	56	78
35	IO	173/173 (100%)	167 (96%)	6 (4%)	31	63
36	LP	134/134 (100%)	128 (96%)	6 (4%)	23	56
36	IP	134/134 (100%)	126 (94%)	8 (6%)	16	48
37	LQ	164/164 (100%)	158 (96%)	6 (4%)	29	62
37	IQ	164/164 (100%)	158 (96%)	6 (4%)	29	62
38	LR	166/166 (100%)	152 (92%)	14 (8%)	9	34
38	IR	166/166 (100%)	156 (94%)	10 (6%)	16	48
39	LS	156/156 (100%)	150 (96%)	6 (4%)	28	60
39	IS	156/156 (100%)	146 (94%)	10 (6%)	14	46
40	LT	139/139 (100%)	133 (96%)	6 (4%)	25	57
40	IT	139/139 (100%)	134 (96%)	5 (4%)	30	62
41	LU	91/91 (100%)	79 (87%)	12 (13%)	3	16
41	IU	91/91 (100%)	81 (89%)	10 (11%)	5	23
42	LV	101/101 (100%)	99 (98%)	2 (2%)	50	75
42	IV	101/101 (100%)	98 (97%)	3 (3%)	36	66
43	LX	108/108 (100%)	102 (94%)	6 (6%)	17	50
43	IX	108/108 (100%)	104 (96%)	4 (4%)	29	62
44	LY	124/124 (100%)	117 (94%)	7 (6%)	17	50
44	IY	124/124 (100%)	119 (96%)	5 (4%)	27	59
45	LZ	117/117 (100%)	112 (96%)	5 (4%)	25	57
45	IZ	117/117 (100%)	109 (93%)	8 (7%)	13	43
46	La	120/120 (100%)	116 (97%)	4 (3%)	33	64
46	la	120/120 (100%)	117 (98%)	3 (2%)	42	71
47	Lb	88/101 (87%)	80 (91%)	8 (9%)	7	29
47	lb	88/101 (87%)	85 (97%)	3 (3%)	32	63
48	Lc	83/83 (100%)	81 (98%)	2 (2%)	44	71
48	lc	83/83 (100%)	78 (94%)	5 (6%)	16	48
49	Ld	98/98 (100%)	97 (99%)	1 (1%)	73	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	ld	98/98 (100%)	95 (97%)	3 (3%)	35	66
50	Le	114/114 (100%)	112 (98%)	2 (2%)	54	77
50	le	114/114 (100%)	109 (96%)	5 (4%)	24	57
51	Lf	88/88 (100%)	85 (97%)	3 (3%)	32	63
51	lf	88/88 (100%)	81 (92%)	7 (8%)	10	37
52	Lg	98/98 (100%)	96 (98%)	2 (2%)	50	75
52	lg	98/98 (100%)	95 (97%)	3 (3%)	35	66
53	Lh	109/109 (100%)	102 (94%)	7 (6%)	14	46
53	lh	109/109 (100%)	106 (97%)	3 (3%)	38	68
54	Li	86/86 (100%)	80 (93%)	6 (7%)	12	42
54	li	86/86 (100%)	77 (90%)	9 (10%)	5	24
55	Lj	73/73 (100%)	69 (94%)	4 (6%)	18	51
55	lj	73/73 (100%)	71 (97%)	2 (3%)	40	69
56	Lk	64/64 (100%)	64 (100%)	0	100	100
56	lk	64/64 (100%)	63 (98%)	1 (2%)	58	79
57	Ll	47/47 (100%)	46 (98%)	1 (2%)	48	74
57	ll	47/47 (100%)	43 (92%)	4 (8%)	8	34
58	Lm	48/48 (100%)	47 (98%)	1 (2%)	48	74
58	lm	48/48 (100%)	45 (94%)	3 (6%)	15	46
59	Ln	23/23 (100%)	23 (100%)	0	100	100
59	ln	23/23 (100%)	21 (91%)	2 (9%)	8	32
60	Lo	93/93 (100%)	88 (95%)	5 (5%)	18	51
60	lo	93/93 (100%)	89 (96%)	4 (4%)	25	57
61	Lp	74/74 (100%)	73 (99%)	1 (1%)	62	82
61	lp	74/74 (100%)	71 (96%)	3 (4%)	26	59
62	Lr	109/109 (100%)	106 (97%)	3 (3%)	38	68
62	lr	109/109 (100%)	106 (97%)	3 (3%)	38	68
63	Lz	195/196 (100%)	187 (96%)	8 (4%)	26	59
63	lz	195/196 (100%)	175 (90%)	20 (10%)	6	25
64	SR	122/122 (100%)	117 (96%)	5 (4%)	26	59
64	sR	122/122 (100%)	111 (91%)	11 (9%)	8	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
65	SD	190/190 (100%)	176 (93%)	14 (7%)	11	40
65	sD	190/190 (100%)	179 (94%)	11 (6%)	17	49
66	SF	159/159 (100%)	150 (94%)	9 (6%)	17	50
66	sF	159/159 (100%)	156 (98%)	3 (2%)	52	76
67	SK	89/89 (100%)	76 (85%)	13 (15%)	2	13
67	sK	89/89 (100%)	82 (92%)	7 (8%)	10	38
68	SP	107/107 (100%)	103 (96%)	4 (4%)	29	62
68	sP	107/107 (100%)	103 (96%)	4 (4%)	29	62
69	SQ	119/119 (100%)	116 (98%)	3 (2%)	42	71
69	sQ	119/119 (100%)	107 (90%)	12 (10%)	6	26
70	SS	126/126 (100%)	116 (92%)	10 (8%)	10	38
70	sS	126/126 (100%)	120 (95%)	6 (5%)	21	55
71	ST	113/113 (100%)	102 (90%)	11 (10%)	6	27
71	sT	113/113 (100%)	106 (94%)	7 (6%)	15	47
72	SU	94/94 (100%)	88 (94%)	6 (6%)	14	46
72	sU	94/94 (100%)	91 (97%)	3 (3%)	34	65
73	Sc	57/57 (100%)	56 (98%)	1 (2%)	54	77
73	sc	57/57 (100%)	55 (96%)	2 (4%)	31	63
74	Sd	48/48 (100%)	45 (94%)	3 (6%)	15	46
74	sd	48/48 (100%)	46 (96%)	2 (4%)	25	58
75	Sg	272/272 (100%)	258 (95%)	14 (5%)	20	53
75	sg	272/272 (100%)	253 (93%)	19 (7%)	12	42
76	SM	102/104 (98%)	98 (96%)	4 (4%)	27	60
76	sM	102/104 (98%)	95 (93%)	7 (7%)	13	43
77	SZ	66/66 (100%)	60 (91%)	6 (9%)	7	29
77	sZ	66/66 (100%)	60 (91%)	6 (9%)	7	29
78	Sf	60/60 (100%)	56 (93%)	4 (7%)	13	44
78	sf	60/60 (100%)	57 (95%)	3 (5%)	20	54
80	CB	722/728 (99%)	672 (93%)	50 (7%)	13	43
80	cB	722/728 (99%)	688 (95%)	34 (5%)	22	55
83	Ls	162/164 (99%)	149 (92%)	13 (8%)	10	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
83	ls	162/164 (99%)	155 (96%)	7 (4%)	25	57
84	Lt	112/115 (97%)	110 (98%)	2 (2%)	54	77
84	lt	112/115 (97%)	108 (96%)	4 (4%)	30	62
86	Se	39/39 (100%)	36 (92%)	3 (8%)	10	39
87	LW	97/103 (94%)	97 (100%)	0	100	100
87	lW	97/103 (94%)	95 (98%)	2 (2%)	48	74
All	All	22282/22398 (100%)	21206 (95%)	1076 (5%)	24	55

All (1076) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	CH	71	ASP
1	cH	52	HIS
1	cH	70	HIS
1	cH	75	LEU
1	cH	93	LYS
2	sE	51	ARG
2	sE	62	LYS
2	sE	69	PHE
2	sE	87	MET
2	sE	91	SER
2	sE	94	LYS
2	sE	164	LEU
2	sE	181	CYS
2	sE	198	ARG
2	sE	233	LYS
3	sI	5	ARG
3	sI	17	LYS
3	sI	23	LYS
3	sI	105	ASP
3	sI	113	TYR
3	sI	117	TYR
3	sI	123	ARG
3	sI	132	GLU
3	sI	151	GLU
3	sI	153	LYS
3	sI	178	ARG
3	sI	201	LYS
4	sL	12	LYS
4	sL	42	LEU

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Mol	Chain	Res	Type
4	sL	58	LYS
4	sL	60	CYS
4	sL	69	ARG
4	sL	97	ARG
4	sL	102	PHE
4	sL	140	PHE
4	sL	141	ASN
5	sX	71	ARG
5	sX	98	ASP
5	sX	105	PHE
5	sX	142	ARG
6	sG	13	GLN
6	sG	22	ARG
6	sG	23	LYS
6	sG	24	LEU
6	sG	45	TRP
6	sG	79	LYS
6	sG	96	SER
6	sG	98	ARG
6	sG	119	LYS
6	sG	167	LYS
6	sG	200	LYS
6	sG	201	LYS
6	sG	217	MET
6	sG	224	ARG
7	sJ	17	ARG
7	sJ	104	ASP
7	sJ	155	LYS
7	sJ	158	ASP
7	sJ	179	LYS
7	sJ	180	LYS
8	sY	12	PHE
8	sY	46	LYS
8	sY	61	ARG
8	sY	81	TYR
8	sY	97	TYR
8	sY	113	ARG
8	sY	114	MET
8	sY	118	ARG
8	sY	122	LYS
9	se	36	MET
10	sA	18	PHE

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Mol	Chain	Res	Type
10	sA	37	TYR
10	sA	52	LYS
10	sA	69	GLU
10	sA	85	ARG
10	sA	90	PHE
10	sA	130	ASP
10	sA	174	MET
10	sA	191	ARG
10	sA	195	TRP
10	sA	204	TYR
11	sB	60	ASP
11	sB	63	LYS
11	sB	71	LEU
11	sB	159	GLN
11	sB	199	LYS
11	sB	211	PHE
11	sB	220	LYS
11	sB	229	MET
12	sH	15	LYS
12	sH	79	LEU
12	sH	132	ASP
12	sH	137	SER
12	sH	138	GLU
12	sH	180	LEU
12	sH	192	PHE
13	sV	1	MET
13	sV	7	GLU
13	sV	8	PHE
13	sV	11	LEU
13	sV	12	TYR
13	sV	17	CYS
13	sV	53	TYR
13	sV	64	GLU
13	sV	81	LYS
14	sa	34	LYS
14	sa	52	ASP
14	sa	68	TYR
14	sa	74	CYS
15	sC	250	TYR
15	sC	254	ASP
15	sC	256	TRP
15	sC	275	LYS

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Mol	Chain	Res	Type
16	sN	31	ASP
16	sN	73	ARG
16	sN	83	ASP
16	sN	114	ARG
16	sN	138	ASN
16	sN	140	LYS
17	sO	28	PHE
17	sO	98	ARG
17	sO	104	ARG
17	sO	130	GLU
18	sW	9	ASP
18	sW	32	LYS
18	sW	97	ARG
19	sb	7	LEU
19	sb	9	HIS
19	sb	56	CYS
19	sb	63	LEU
22	lA	6	ARG
22	lA	30	ARG
22	lA	40	TYR
22	lA	47	ASP
22	lA	96	LEU
22	lA	123	ARG
22	lA	159	SER
22	lA	176	ASP
22	lA	204	MET
23	lB	5	LYS
23	lB	17	LEU
23	lB	61	ASP
23	lB	126	LYS
23	lB	134	CYS
23	lB	148	LYS
23	lB	174	ARG
23	lB	216	MET
23	lB	294	LYS
23	lB	298	LEU
23	lB	305	THR
23	lB	373	LYS
23	lB	374	PHE
24	lC	50	GLN
24	lC	67	TRP
24	lC	78	ARG

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Mol	Chain	Res	Type
24	1C	95	MET
24	1C	157	LYS
24	1C	175	LYS
24	1C	179	ASP
24	1C	188	ARG
24	1C	190	ARG
24	1C	223	ASN
24	1C	245	HIS
24	1C	257	PHE
24	1C	291	ARG
24	1C	325	MET
24	1C	348	LYS
24	1C	353	LYS
24	1C	366	ASP
25	1D	5	LYS
25	1D	44	TYR
25	1D	180	PHE
25	1D	196	ARG
25	1D	213	GLU
25	1D	217	ASP
25	1D	221	LYS
25	1D	224	SER
25	1D	239	MET
26	1E	59	ARG
26	1E	114	ARG
26	1E	130	LYS
26	1E	164	PHE
26	1E	279	ASN
26	1E	282	TYR
27	1F	34	ARG
27	1F	43	ARG
27	1F	64	MET
27	1F	68	GLU
27	1F	88	LYS
27	1F	144	TYR
27	1F	186	CYS
27	1F	189	ASP
27	1F	220	MET
27	1F	232	ASP
27	1F	238	ASP
27	1F	247	MET
28	1G	53	ARG

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Mol	Chain	Res	Type
28	IG	54	PHE
28	IG	120	LYS
28	IG	136	LEU
28	IG	175	ARG
28	IG	177	MET
28	IG	185	LYS
28	IG	259	LYS
29	IH	40	HIS
29	IH	50	LYS
29	IH	51	LYS
29	IH	96	TYR
29	IH	110	SER
29	IH	128	MET
29	IH	134	CYS
30	II	44	ASP
30	II	87	MET
30	II	101	LYS
30	II	142	LEU
30	II	159	PHE
30	II	175	LYS
30	II	177	ASN
30	II	187	LYS
30	II	210	ARG
30	II	213	HIS
31	IJ	60	PHE
31	IJ	95	ARG
31	IJ	119	TYR
31	IJ	139	PHE
31	IJ	163	MET
31	IJ	166	PHE
32	IL	4	SER
32	IL	67	HIS
32	IL	81	LEU
32	IL	103	ARG
32	IL	104	ASN
32	IL	130	LYS
32	IL	155	MET
32	IL	161	TYR
33	IM	4	ARG
33	IM	6	PHE
33	IM	35	ARG
33	IM	50	MET

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Mol	Chain	Res	Type
33	IM	62	LEU
33	IM	96	GLU
33	IM	121	ARG
34	IN	34	SER
34	IN	41	ARG
34	IN	87	HIS
34	IN	150	TRP
35	IO	44	SER
35	IO	54	TYR
35	IO	113	ASP
35	IO	117	ARG
35	IO	118	MET
35	IO	191	LYS
36	IP	7	ASP
36	IP	9	GLU
36	IP	18	ARG
36	IP	39	MET
36	IP	85	LYS
36	IP	116	HIS
36	IP	148	MET
36	IP	150	LEU
37	IQ	53	MET
37	IQ	54	SER
37	IQ	125	GLN
37	IQ	160	HIS
37	IQ	176	ARG
37	IQ	188	ASN
38	IR	3	MET
38	IR	9	ARG
38	IR	39	GLN
38	IR	46	LYS
38	IR	66	ASN
38	IR	76	MET
38	IR	153	LYS
38	IR	173	ARG
38	IR	176	ARG
38	IR	186	LYS
39	IS	46	TYR
39	IS	50	GLN
39	IS	52	LYS
39	IS	54	MET
39	IS	68	PHE

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Mol	Chain	Res	Type
39	IS	76	LYS
39	IS	77	ASN
39	IS	85	ASP
39	IS	111	ARG
39	IS	152	PHE
40	IT	63	ARG
40	IT	83	LYS
40	IT	104	SER
40	IT	157	GLU
40	IT	159	MET
41	IU	21	PHE
41	IU	34	MET
41	IU	39	PHE
41	IU	52	LYS
41	IU	68	SER
41	IU	74	SER
41	IU	110	TYR
41	IU	111	GLU
41	IU	114	TYR
41	IU	116	GLN
42	IV	36	ASN
42	IV	48	ARG
42	IV	62	MET
43	IX	88	LYS
43	IX	118	ASP
43	IX	127	LEU
43	IX	144	TYR
44	IY	12	SER
44	IY	20	ASN
44	IY	41	LYS
44	IY	74	TYR
44	IY	125	SER
45	IZ	57	MET
45	IZ	84	ARG
45	IZ	85	TYR
45	IZ	86	SER
45	IZ	97	ASN
45	IZ	119	GLU
45	IZ	128	LYS
45	IZ	131	PHE
46	la	75	LEU
46	la	85	GLN

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Mol	Chain	Res	Type
46	la	125	LYS
47	lb	33	LYS
47	lb	44	ARG
47	lb	65	MET
48	lc	50	ASN
48	lc	56	ARG
48	lc	68	LYS
48	lc	103	ASP
48	lc	106	ARG
49	ld	51	LYS
49	ld	61	ASP
49	ld	103	TYR
50	le	32	LYS
50	le	37	LYS
50	le	42	ASP
50	le	92	ASN
50	le	129	LEU
51	lf	37	ASP
51	lf	43	LEU
51	lf	47	CYS
51	lf	51	TYR
51	lf	73	LYS
51	lf	90	SER
51	lf	104	MET
52	lg	54	ARG
52	lg	64	LEU
52	lg	81	SER
53	lh	14	LYS
53	lh	45	SER
53	lh	71	LYS
54	li	4	ARG
54	li	7	MET
54	li	23	LYS
54	li	29	ARG
54	li	39	PHE
54	li	48	CYS
54	li	55	ARG
54	li	58	MET
54	li	76	ARG
55	lj	11	ARG
55	lj	36	LYS
56	lk	18	LYS

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Mol	Chain	Res	Type
57	ll	28	ARG
57	ll	37	TYR
57	ll	42	ARG
57	ll	51	LEU
58	lm	92	ASP
58	lm	110	CYS
58	lm	128	LYS
59	ln	20	MET
59	ln	23	ARG
60	lo	32	SER
60	lo	72	CYS
60	lo	96	ASP
60	lo	99	ARG
61	lp	32	SER
61	lp	46	LYS
61	lp	61	MET
62	lr	20	ARG
62	lr	72	LYS
62	lr	113	ARG
63	lz	3	SER
63	lz	7	ARG
63	lz	10	LEU
63	lz	15	ARG
63	lz	27	LYS
63	lz	28	PHE
63	lz	39	LYS
63	lz	56	LYS
63	lz	68	LEU
63	lz	75	ASP
63	lz	110	PHE
63	lz	144	MET
63	lz	156	LYS
63	lz	161	LYS
63	lz	173	LYS
63	lz	178	GLU
63	lz	185	LEU
63	lz	188	ASN
63	lz	189	PHE
63	lz	199	GLN
64	sR	1	MET
64	sR	11	LYS
64	sR	14	ARG

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Mol	Chain	Res	Type
64	sR	20	TYR
64	sR	29	HIS
64	sR	32	LYS
64	sR	53	TYR
64	sR	67	ARG
64	sR	105	MET
64	sR	109	LEU
64	sR	129	LYS
65	sD	14	ASP
65	sD	76	ARG
65	sD	79	PHE
65	sD	97	CYS
65	sD	124	ARG
65	sD	134	CYS
65	sD	148	LYS
65	sD	151	LYS
65	sD	166	TYR
65	sD	178	ARG
65	sD	213	PRO
66	sF	47	LYS
66	sF	102	LEU
66	sF	127	ARG
67	sK	16	PHE
67	sK	47	LYS
67	sK	57	TYR
67	sK	70	TYR
67	sK	78	TYR
67	sK	82	TYR
67	sK	84	HIS
68	sP	50	ARG
68	sP	81	ARG
68	sP	82	ASP
68	sP	89	MET
69	sQ	7	LEU
69	sQ	41	MET
69	sQ	49	TYR
69	sQ	96	TYR
69	sQ	102	GLU
69	sQ	109	LYS
69	sQ	116	ASP
69	sQ	130	LYS
69	sQ	131	LYS

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Mol	Chain	Res	Type
69	sQ	138	ARG
69	sQ	140	ARG
69	sQ	145	TYR
70	sS	25	LYS
70	sS	40	TYR
70	sS	49	ASP
70	sS	62	ASP
70	sS	104	ASP
70	sS	126	PHE
71	sT	18	LEU
71	sT	33	TRP
71	sT	53	PHE
71	sT	75	MET
71	sT	84	ARG
71	sT	116	ASP
71	sT	128	GLN
72	sU	18	HIS
72	sU	30	LYS
72	sU	79	ARG
73	sc	35	MET
73	sc	51	ARG
74	sd	18	SER
74	sd	20	SER
75	sg	27	PHE
75	sg	29	ASP
75	sg	32	LEU
75	sg	38	LYS
75	sg	51	ASN
75	sg	52	TYR
75	sg	57	ARG
75	sg	65	PHE
75	sg	125	ARG
75	sg	138	CYS
75	sg	168	CYS
75	sg	173	LEU
75	sg	217	MET
75	sg	245	ARG
75	sg	249	CYS
75	sg	259	TRP
75	sg	262	GLU
75	sg	268	ASP
75	sg	280	LYS

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Mol	Chain	Res	Type
76	sM	33	ARG
76	sM	44	LYS
76	sM	69	CYS
76	sM	116	LYS
76	sM	122	ASP
76	sM	128	PHE
76	sM	131	LYS
77	sZ	66	LYS
77	sZ	77	LEU
77	sZ	92	LEU
77	sZ	98	LYS
77	sZ	101	SER
77	sZ	114	LYS
78	sf	106	TYR
78	sf	131	PHE
78	sf	150	PHE
80	cB	30	HIS
80	cB	55	ARG
80	cB	67	CYS
80	cB	143	LEU
80	cB	157	MET
80	cB	200	MET
80	cB	231	MET
80	cB	256	MET
80	cB	275	LYS
80	cB	281	GLU
80	cB	301	PHE
80	cB	329	ASP
80	cB	341	ARG
80	cB	343	TRP
80	cB	359	PRO
80	cB	366	LYS
80	cB	388	CYS
80	cB	417	PHE
80	cB	466	CYS
80	cB	468	ASN
80	cB	478	PHE
80	cB	495	ARG
80	cB	539	GLU
80	cB	594	LYS
80	cB	604	MET
80	cB	611	ASP

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Mol	Chain	Res	Type
80	cB	625	ARG
80	cB	727	ARG
80	cB	741	MET
80	cB	745	TYR
80	cB	796	PHE
80	cB	828	SER
80	cB	853	ASN
80	cB	858	LEU
83	ls	23	ASP
83	ls	44	ARG
83	ls	45	MET
83	ls	55	MET
83	ls	60	MET
83	ls	61	MET
83	ls	101	MET
84	lt	53	TRP
84	lt	119	ARG
84	lt	147	HIS
84	lt	150	ASP
80	CB	13	MET
80	CB	20	ARG
80	CB	62	ASP
80	CB	65	GLU
80	CB	78	PHE
80	CB	79	TYR
80	CB	81	LEU
80	CB	120	ARG
80	CB	162	ARG
80	CB	184	ASN
80	CB	219	HIS
80	CB	231	MET
80	CB	232	TYR
80	CB	249	ARG
80	CB	255	ASP
80	CB	256	MET
80	CB	258	LYS
80	CB	266	PHE
80	CB	287	ARG
80	CB	343	TRP
80	CB	353	MET
80	CB	388	CYS
80	CB	395	MET

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Mol	Chain	Res	Type
80	CB	396	MET
80	CB	401	MET
80	CB	407	LYS
80	CB	428	ARG
80	CB	449	ARG
80	CB	453	MET
80	CB	488	PHE
80	CB	492	HIS
80	CB	519	LYS
80	CB	525	LYS
80	CB	564	ASP
80	CB	573	SER
80	CB	601	ARG
80	CB	613	LEU
80	CB	625	ARG
80	CB	667	LYS
80	CB	673	ASN
80	CB	689	GLU
80	CB	728	CYS
80	CB	765	ARG
80	CB	801	ARG
80	CB	811	GLN
80	CB	818	GLN
80	CB	825	PHE
80	CB	829	SER
80	CB	841	ARG
80	CB	855	LEU
2	SE	44	LEU
2	SE	50	ASN
2	SE	62	LYS
2	SE	69	PHE
2	SE	71	LYS
2	SE	179	ASN
2	SE	198	ARG
2	SE	226	PHE
2	SE	254	LYS
3	SI	22	HIS
3	SI	35	ASN
3	SI	124	LYS
3	SI	140	LYS
3	SI	166	PHE
4	SL	58	LYS

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Mol	Chain	Res	Type
4	SL	69	ARG
4	SL	74	SER
4	SL	83	GLN
4	SL	109	MET
5	SX	67	ARG
5	SX	84	PHE
5	SX	105	PHE
5	SX	127	ASN
6	SG	1	MET
6	SG	19	ASP
6	SG	22	ARG
6	SG	30	LYS
6	SG	32	MET
6	SG	87	ARG
6	SG	98	ARG
6	SG	126	ASP
6	SG	155	GLN
6	SG	200	LYS
6	SG	201	LYS
6	SG	224	ARG
7	SJ	7	TRP
7	SJ	35	TYR
7	SJ	96	TYR
7	SJ	106	LEU
7	SJ	107	GLU
7	SJ	134	HIS
7	SJ	175	ARG
8	SY	13	MET
8	SY	23	MET
8	SY	47	MET
8	SY	53	ASP
8	SY	63	HIS
8	SY	64	PHE
8	SY	72	PHE
8	SY	81	TYR
8	SY	97	TYR
8	SY	101	LYS
8	SY	129	LYS
8	SY	132	LYS
86	Se	6	LEU
86	Se	31	ARG
86	Se	34	ARG

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Mol	Chain	Res	Type
10	SA	18	PHE
10	SA	37	TYR
10	SA	52	LYS
10	SA	69	GLU
10	SA	89	LYS
10	SA	102	ARG
10	SA	191	ARG
10	SA	204	TYR
11	SB	43	ASN
11	SB	48	LEU
11	SB	105	LEU
11	SB	113	MET
11	SB	180	ASP
11	SB	205	TYR
11	SB	217	MET
12	SH	72	PHE
12	SH	81	ARG
12	SH	85	LYS
12	SH	127	ASP
12	SH	135	PHE
12	SH	145	ARG
12	SH	147	LYS
12	SH	155	LYS
12	SH	180	LEU
12	SH	184	ASP
12	SH	190	PRO
12	SH	192	PHE
13	SV	1	MET
13	SV	11	LEU
13	SV	29	HIS
13	SV	62	MET
13	SV	67	ASP
14	Sa	15	ARG
14	Sa	64	LEU
14	Sa	74	CYS
15	SC	76	LYS
15	SC	78	LEU
15	SC	132	ASP
15	SC	152	ARG
15	SC	167	ARG
15	SC	215	MET
15	SC	269	PHE

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Mol	Chain	Res	Type
16	SN	32	ASP
16	SN	65	PHE
16	SN	70	LYS
16	SN	73	ARG
16	SN	76	LYS
16	SN	121	ARG
16	SN	129	TYR
16	SN	140	LYS
17	SO	28	PHE
17	SO	46	ASP
17	SO	54	CYS
17	SO	85	CYS
17	SO	151	LEU
18	SW	3	ARG
18	SW	23	ARG
18	SW	28	ARG
18	SW	57	ARG
18	SW	78	ARG
18	SW	97	ARG
18	SW	111	MET
19	Sb	33	MET
19	Sb	41	TYR
22	LA	47	ASP
22	LA	63	PHE
22	LA	139	HIS
22	LA	176	ASP
22	LA	217	GLN
23	LB	17	LEU
23	LB	116	ARG
23	LB	127	LYS
23	LB	140	GLU
23	LB	148	LYS
23	LB	174	ARG
23	LB	286	LYS
23	LB	394	LYS
24	LC	14	LYS
24	LC	38	ASN
24	LC	50	GLN
24	LC	102	PHE
24	LC	234	LYS
24	LC	249	PHE
24	LC	257	PHE

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Mol	Chain	Res	Type
24	LC	259	LYS
24	LC	273	LEU
24	LC	325	MET
24	LC	366	ASP
25	LD	5	LYS
25	LD	41	LYS
25	LD	68	ARG
25	LD	94	ASN
25	LD	100	CYS
25	LD	111	ASN
25	LD	208	MET
25	LD	217	ASP
25	LD	219	TYR
25	LD	229	ASN
25	LD	235	MET
25	LD	236	MET
25	LD	239	MET
25	LD	291	GLN
26	LE	52	ARG
26	LE	68	MET
26	LE	119	GLU
26	LE	130	LYS
26	LE	191	GLN
26	LE	226	ARG
26	LE	227	HIS
26	LE	262	LYS
27	LF	81	PHE
27	LF	102	SER
27	LF	144	TYR
27	LF	187	MET
27	LF	215	SER
27	LF	220	MET
27	LF	221	LYS
27	LF	247	MET
28	LG	33	GLU
28	LG	71	TYR
28	LG	109	GLU
28	LG	131	LYS
28	LG	189	ARG
28	LG	229	ARG
28	LG	259	LYS
29	LH	35	ARG

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Mol	Chain	Res	Type
29	LH	50	LYS
29	LH	56	ARG
29	LH	134	CYS
30	LI	45	GLU
30	LI	87	MET
30	LI	100	ASN
30	LI	179	ASP
30	LI	181	PHE
30	LI	187	LYS
30	LI	206	LEU
30	LI	212	LEU
31	LJ	10	ASN
31	LJ	65	ASN
31	LJ	92	TYR
31	LJ	95	ARG
31	LJ	105	PHE
31	LJ	107	PHE
31	LJ	163	MET
32	LL	10	LEU
32	LL	71	ARG
32	LL	134	PRO
32	LL	143	GLU
32	LL	155	MET
32	LL	184	MET
33	LM	35	ARG
33	LM	50	MET
33	LM	55	MET
33	LM	66	HIS
33	LM	103	LYS
33	LM	113	MET
34	LN	19	MET
34	LN	50	ARG
34	LN	53	TYR
34	LN	123	GLU
34	LN	150	TRP
34	LN	161	MET
35	LO	49	ARG
35	LO	178	ARG
35	LO	190	ASP
36	LP	69	ARG
36	LP	100	SER
36	LP	105	LYS

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Mol	Chain	Res	Type
36	LP	110	ASP
36	LP	128	ARG
36	LP	148	MET
37	LQ	32	TYR
37	LQ	35	LEU
37	LQ	132	LYS
37	LQ	181	ARG
37	LQ	186	TYR
37	LQ	188	ASN
38	LR	17	CYS
38	LR	65	LYS
38	LR	89	MET
38	LR	111	GLU
38	LR	122	SER
38	LR	139	MET
38	LR	165	LYS
38	LR	170	ARG
38	LR	171	LYS
38	LR	173	ARG
38	LR	176	ARG
38	LR	178	GLN
38	LR	186	LYS
38	LR	188	LEU
39	LS	8	ARG
39	LS	55	LYS
39	LS	76	LYS
39	LS	82	LEU
39	LS	93	MET
39	LS	117	HIS
40	LT	38	ASP
40	LT	45	MET
40	LT	83	LYS
40	LT	102	ARG
40	LT	146	LYS
40	LT	158	PHE
41	LU	20	LYS
41	LU	27	HIS
41	LU	30	GLU
41	LU	41	GLN
41	LU	50	ASN
41	LU	65	ARG
41	LU	67	LYS

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Mol	Chain	Res	Type
41	LU	78	PHE
41	LU	83	LEU
41	LU	108	GLU
41	LU	110	TYR
41	LU	114	TYR
42	LV	90	ARG
42	LV	112	MET
43	LX	54	LEU
43	LX	87	MET
43	LX	93	ASN
43	LX	114	LYS
43	LX	144	TYR
43	LX	145	ASP
44	LY	42	TYR
44	LY	47	MET
44	LY	69	LYS
44	LY	74	TYR
44	LY	110	LYS
44	LY	115	ARG
44	LY	119	LEU
45	LZ	59	LYS
45	LZ	60	LYS
45	LZ	64	LYS
45	LZ	80	LEU
45	LZ	134	LEU
46	La	24	LYS
46	La	66	ASN
46	La	78	LEU
46	La	106	SER
47	Lb	45	PHE
47	Lb	60	ASN
47	Lb	63	LYS
47	Lb	65	MET
47	Lb	96	LEU
47	Lb	104	LEU
47	Lb	107	ARG
47	Lb	118	LEU
48	Lc	18	LEU
48	Lc	23	LYS
49	Ld	44	ARG
50	Le	95	TYR
50	Le	121	ARG

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Mol	Chain	Res	Type
51	Lf	11	PHE
51	Lf	41	PHE
51	Lf	104	MET
52	Lg	54	ARG
52	Lg	108	LYS
53	Lh	8	ASP
53	Lh	35	LYS
53	Lh	58	LEU
53	Lh	66	LYS
53	Lh	70	ARG
53	Lh	79	LYS
53	Lh	99	GLU
54	Li	4	ARG
54	Li	23	LYS
54	Li	29	ARG
54	Li	35	LYS
54	Li	46	GLU
54	Li	61	LEU
55	Lj	22	CYS
55	Lj	34	CYS
55	Lj	37	CYS
55	Lj	78	PHE
57	Ll	8	ARG
58	Lm	92	ASP
60	Lo	6	LYS
60	Lo	11	PHE
60	Lo	43	ARG
60	Lo	88	CYS
60	Lo	99	ARG
61	Lp	6	LYS
62	Lr	56	ASP
62	Lr	77	TYR
62	Lr	105	ASP
63	Lz	7	ARG
63	Lz	15	ARG
63	Lz	54	ARG
63	Lz	85	MET
63	Lz	93	LEU
63	Lz	122	ARG
63	Lz	156	LYS
63	Lz	161	LYS
64	SR	33	ARG

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Mol	Chain	Res	Type
64	SR	67	ARG
64	SR	76	GLU
64	SR	101	ASP
64	SR	111	PHE
65	SD	1	MET
65	SD	17	PHE
65	SD	29	LEU
65	SD	34	TYR
65	SD	45	ARG
65	SD	108	LYS
65	SD	134	CYS
65	SD	142	LEU
65	SD	146	ARG
65	SD	148	LYS
65	SD	151	LYS
65	SD	154	ASP
65	SD	167	TYR
65	SD	169	ASP
66	SF	45	TYR
66	SF	63	LYS
66	SF	78	MET
66	SF	91	ARG
66	SF	97	PHE
66	SF	102	LEU
66	SF	121	PRO
66	SF	124	ASP
66	SF	125	SER
67	SK	3	MET
67	SK	16	PHE
67	SK	17	LYS
67	SK	46	MET
67	SK	51	SER
67	SK	53	LYS
67	SK	60	GLU
67	SK	69	TRP
67	SK	70	TYR
67	SK	78	TYR
67	SK	80	ARG
67	SK	83	LEU
67	SK	95	ARG
68	SP	28	MET
68	SP	35	GLN

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Mol	Chain	Res	Type
68	SP	62	LYS
68	SP	97	TYR
69	SQ	7	LEU
69	SQ	39	LEU
69	SQ	145	TYR
70	SS	1	MET
70	SS	9	PHE
70	SS	47	LYS
70	SS	55	ARG
70	SS	74	PRO
70	SS	86	ARG
70	SS	92	ASP
70	SS	101	ASN
70	SS	113	ARG
70	SS	139	THR
71	ST	14	PHE
71	ST	21	PHE
71	ST	28	LEU
71	ST	35	ASP
71	ST	65	TYR
71	ST	75	MET
71	ST	82	ARG
71	ST	90	SER
71	ST	122	LYS
71	ST	123	LEU
71	ST	142	ASN
72	SU	18	HIS
72	SU	34	LYS
72	SU	48	LEU
72	SU	79	ARG
72	SU	92	HIS
72	SU	93	SER
73	Sc	40	ARG
74	Sd	12	ARG
74	Sd	25	SER
74	Sd	37	ASN
75	Sg	3	GLU
75	Sg	79	LEU
75	Sg	127	LYS
75	Sg	162	ASN
75	Sg	171	ASP
75	Sg	172	LYS

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Mol	Chain	Res	Type
75	Sg	185	LYS
75	Sg	188	HIS
75	Sg	240	CYS
75	Sg	241	PHE
75	Sg	246	TYR
75	Sg	259	TRP
75	Sg	268	ASP
75	Sg	308	ARG
76	SM	63	LYS
76	SM	66	GLU
76	SM	69	CYS
76	SM	127	TYR
77	SZ	50	PHE
77	SZ	56	ASP
77	SZ	58	LEU
77	SZ	59	CYS
77	SZ	85	ARG
77	SZ	109	TYR
78	Sf	96	LYS
78	Sf	104	LYS
78	Sf	106	TYR
78	Sf	123	SER
83	Ls	28	PHE
83	Ls	40	MET
83	Ls	45	MET
83	Ls	55	MET
83	Ls	68	HIS
83	Ls	77	LYS
83	Ls	101	MET
83	Ls	112	ARG
83	Ls	137	PHE
83	Ls	146	LYS
83	Ls	156	SER
83	Ls	194	ASP
83	Ls	195	ASN
84	Lt	83	LYS
84	Lt	119	ARG
87	IW	12	LYS
87	IW	80	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (141) such sidechains are listed below:

Mol	Chain	Res	Type
1	cH	51	GLN
1	cH	82	GLN
2	sE	17	HIS
6	sG	65	GLN
7	sJ	132	GLN
8	sY	19	GLN
8	sY	85	ASN
9	se	15	GLN
9	se	56	ASN
10	sA	132	GLN
10	sA	141	ASN
11	sB	101	HIS
12	sH	76	GLN
13	sV	21	ASN
13	sV	29	HIS
17	sO	103	ASN
18	sW	24	GLN
18	sW	90	GLN
18	sW	92	ASN
19	sb	19	HIS
19	sb	51	GLN
19	sb	83	GLN
23	lB	145	GLN
23	lB	302	ASN
25	lD	291	GLN
26	lE	128	HIS
27	lF	151	ASN
28	lG	64	GLN
28	lG	90	GLN
28	lG	94	GLN
30	lI	144	ASN
31	lJ	10	ASN
31	lJ	46	GLN
31	lJ	98	ASN
32	lL	188	ASN
33	lM	56	GLN
34	lN	37	HIS
34	lN	57	GLN
34	lN	99	GLN
36	lP	34	GLN
36	lP	101	ASN
37	lQ	188	ASN
38	lR	134	ASN

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Mol	Chain	Res	Type
39	lS	92	ASN
39	lS	144	GLN
40	lT	90	ASN
41	lU	44	GLN
42	lV	135	ASN
43	lX	93	ASN
43	lX	125	ASN
48	lc	40	GLN
50	le	102	ASN
50	le	124	ASN
53	lh	98	HIS
54	li	80	HIS
54	li	92	ASN
58	lm	90	ASN
61	lp	33	GLN
62	lr	121	GLN
63	lz	143	ASN
63	lz	182	ASN
69	sQ	114	GLN
71	sT	42	HIS
74	sd	5	GLN
75	sg	15	ASN
75	sg	64	HIS
75	sg	143	GLN
75	sg	162	ASN
75	sg	285	GLN
80	cB	21	ASN
80	cB	227	GLN
80	cB	306	ASN
80	cB	468	ASN
80	cB	553	HIS
80	cB	684	GLN
80	cB	750	GLN
80	CB	18	ASN
80	CB	21	ASN
80	CB	176	GLN
4	SL	11	GLN
5	SX	97	ASN
6	SG	197	GLN
7	SJ	140	GLN
8	SY	19	GLN
10	SA	111	GLN

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Mol	Chain	Res	Type
10	SA	141	ASN
10	SA	165	ASN
12	SH	163	GLN
12	SH	193	GLN
14	Sa	7	ASN
15	SC	113	GLN
16	SN	62	GLN
17	SO	32	HIS
18	SW	98	GLN
19	Sb	51	GLN
19	Sb	83	GLN
22	LA	19	HIS
23	LB	354	GLN
24	LC	142	HIS
24	LC	212	ASN
25	LD	195	HIS
25	LD	225	GLN
26	LE	266	GLN
27	LF	226	HIS
28	LG	82	GLN
28	LG	108	GLN
28	LG	112	GLN
28	LG	159	HIS
30	LI	100	ASN
30	LI	147	HIS
31	LJ	42	GLN
32	LL	67	HIS
33	LM	34	ASN
34	LN	37	HIS
34	LN	86	HIS
35	LO	63	ASN
36	LP	118	GLN
37	LQ	93	GLN
37	LQ	188	ASN
39	LS	117	HIS
41	LU	41	GLN
42	LV	101	ASN
43	LX	111	GLN
44	LY	14	ASN
44	LY	100	HIS
49	Ld	69	ASN
51	Lf	91	ASN

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Mol	Chain	Res	Type
53	Lh	107	GLN
61	Lp	56	HIS
63	Lz	96	ASN
66	SF	149	GLN
67	SK	32	HIS
69	SQ	97	GLN
70	SS	85	ASN
73	Sc	29	GLN
75	Sg	64	HIS
75	Sg	162	ASN
75	Sg	215	GLN
76	SM	28	HIS
77	SZ	64	ASN
87	IW	79	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
20	L7	119/120 (99%)	15 (12%)	0
20	l7	119/120 (99%)	16 (13%)	0
21	L8	155/156 (99%)	28 (18%)	0
21	l8	155/156 (99%)	35 (22%)	0
79	S2	1716/1740 (98%)	496 (28%)	12 (0%)
79	s2	1714/1740 (98%)	547 (31%)	0
81	AP	69/73 (94%)	25 (36%)	1 (1%)
81	aP	69/73 (94%)	25 (36%)	0
82	PE	74/76 (97%)	40 (54%)	3 (4%)
82	pE	73/76 (96%)	35 (47%)	0
85	L5	3696/3740 (98%)	969 (26%)	34 (0%)
85	l5	3696/3740 (98%)	929 (25%)	0
All	All	11655/11810 (98%)	3160 (27%)	50 (0%)

All (3160) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
20	l7	2	U
20	l7	7	G
20	l7	22	A
20	l7	24	C
20	l7	33	U
20	l7	37	G

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Mol	Chain	Res	Type
20	17	38	U
20	17	39	C
20	17	54	A
20	17	63	C
20	17	64	G
20	17	66	G
20	17	89	G
20	17	97	G
20	17	100	A
20	17	111	C
21	18	3	A
21	18	34	U
21	18	35	C
21	18	38	U
21	18	39	G
21	18	46	G
21	18	48	A
21	18	49	G
21	18	51	U
21	18	59	A
21	18	60	G
21	18	61	A
21	18	62	A
21	18	63	U
21	18	68	G
21	18	80	A
21	18	82	A
21	18	83	C
21	18	84	A
21	18	85	U
21	18	86	U
21	18	87	G
21	18	94	G
21	18	103	A
21	18	105	C
21	18	110	U
21	18	111	U
21	18	114	G
21	18	123	U
21	18	124	U
21	18	125	C
21	18	126	C

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Mol	Chain	Res	Type
21	l8	127	U
21	l8	147	G
21	l8	151	G
79	s2	2	A
79	s2	3	C
79	s2	4	C
79	s2	25	A
79	s2	26	U
79	s2	33	G
79	s2	34	U
79	s2	37	C
79	s2	41	G
79	s2	42	A
79	s2	43	U
79	s2	44	U
79	s2	45	A
79	s2	46	A
79	s2	56	G
79	s2	62	G
79	s2	64	A
79	s2	65	C
79	s2	66	G
79	s2	67	C
79	s2	68	A
79	s2	72	C
79	s2	73	C
79	s2	74	G
79	s2	76	U
79	s2	92	A
79	s2	99	A
79	s2	103	A
79	s2	113	G
79	s2	114	G
79	s2	115	U
79	s2	116	U
79	s2	126	G
79	s2	130	G
79	s2	139	C
79	s2	140	C
79	s2	142	C
79	s2	143	U
79	s2	147	A

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Mol	Chain	Res	Type
79	s2	149	A
79	s2	155	G
79	s2	158	A
79	s2	161	U
79	s2	162	C
79	s2	163	U
79	s2	168	C
79	s2	175	A
79	s2	179	C
79	s2	187	G
79	s2	190	G
79	s2	191	A
79	s2	192	C
79	s2	196	C
79	s2	197	U
79	s2	198	U
79	s2	199	C
79	s2	200	G
79	s2	202	G
79	s2	203	G
79	s2	204	G
79	s2	206	G
79	s2	207	G
79	s2	208	G
79	s2	212	C
79	s2	214	U
79	s2	220	U
79	s2	291	G
79	s2	292	A
79	s2	293	C
79	s2	294	U
79	s2	295	C
79	s2	301	A
79	s2	303	C
79	s2	305	U
79	s2	306	C
79	s2	307	G
79	s2	308	G
79	s2	309	G
79	s2	310	C
79	s2	311	C
79	s2	312	G

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Mol	Chain	Res	Type
79	s2	314	U
79	s2	317	C
79	s2	318	A
79	s2	319	C
79	s2	322	C
79	s2	323	C
79	s2	324	C
79	s2	325	C
79	s2	326	C
79	s2	327	G
79	s2	328	U
79	s2	329	G
79	s2	332	G
79	s2	338	G
79	s2	339	A
79	s2	340	C
79	s2	347	G
79	s2	351	G
79	s2	360	A
79	s2	361	U
79	s2	362	C
79	s2	364	A
79	s2	368	U
79	s2	370	G
79	s2	372	U
79	s2	374	G
79	s2	375	U
79	s2	385	G
79	s2	386	C
79	s2	391	C
79	s2	407	G
79	s2	408	A
79	s2	409	C
79	s2	421	G
79	s2	426	A
79	s2	428	U
79	s2	429	C
79	s2	437	G
79	s2	442	C
79	s2	448	A
79	s2	449	A
79	s2	450	C

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Mol	Chain	Res	Type
79	s2	452	G
79	s2	464	A
79	s2	465	A
79	s2	471	G
79	s2	472	C
79	s2	473	A
79	s2	474	G
79	s2	476	A
79	s2	478	G
79	s2	487	U
79	s2	488	U
79	s2	492	C
79	s2	493	A
79	s2	496	C
79	s2	502	C
79	s2	503	C
79	s2	516	A
79	s2	517	C
79	s2	523	A
79	s2	532	C
79	s2	533	A
79	s2	534	G
79	s2	535	G
79	s2	536	A
79	s2	537	C
79	s2	538	U
79	s2	540	U
79	s2	541	U
79	s2	542	U
79	s2	544	G
79	s2	546	G
79	s2	547	G
79	s2	551	U
79	s2	552	G
79	s2	553	U
79	s2	555	A
79	s2	557	U
79	s2	558	G
79	s2	559	G
79	s2	560	A
79	s2	563	G
79	s2	564	A

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Mol	Chain	Res	Type
79	s2	566	U
79	s2	583	A
79	s2	585	C
79	s2	587	A
79	s2	589	G
79	s2	590	A
79	s2	591	U
79	s2	593	C
79	s2	594	A
79	s2	603	C
79	s2	604	A
79	s2	608	C
79	s2	610	G
79	s2	612	U
79	s2	614	C
79	s2	617	G
79	s2	623	G
79	s2	627	U
79	s2	628	A
79	s2	629	A
79	s2	631	U
79	s2	638	C
79	s2	641	A
79	s2	643	A
79	s2	644	G
79	s2	660	C
79	s2	668	A
79	s2	669	A
79	s2	671	A
79	s2	672	A
79	s2	673	G
79	s2	684	G
79	s2	688	U
79	s2	689	U
79	s2	692	G
79	s2	693	A
79	s2	695	C
79	s2	696	G
79	s2	697	G
79	s2	698	G
79	s2	731	G
79	s2	732	U

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Mol	Chain	Res	Type
79	s2	734	C
79	s2	736	C
79	s2	738	C
79	s2	749	U
79	s2	750	C
79	s2	751	G
79	s2	752	G
79	s2	753	C
79	s2	787	G
79	s2	788	G
79	s2	791	C
79	s2	792	C
79	s2	794	A
79	s2	798	G
79	s2	799	U
79	s2	801	U
79	s2	819	G
79	s2	821	G
79	s2	822	U
79	s2	823	U
79	s2	824	C
79	s2	827	A
79	s2	830	A
79	s2	833	C
79	s2	834	C
79	s2	835	C
79	s2	836	G
79	s2	837	A
79	s2	838	G
79	s2	839	C
79	s2	842	C
79	s2	844	U
79	s2	847	A
79	s2	859	G
79	s2	862	A
79	s2	869	A
79	s2	870	A
79	s2	871	U
79	s2	872	A
79	s2	873	G
79	s2	874	G
79	s2	877	C

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Mol	Chain	Res	Type
79	s2	878	G
79	s2	882	U
79	s2	888	U
79	s2	889	U
79	s2	890	U
79	s2	891	G
79	s2	892	U
79	s2	893	U
79	s2	894	G
79	s2	896	U
79	s2	898	U
79	s2	899	U
79	s2	900	C
79	s2	901	G
79	s2	903	A
79	s2	913	A
79	s2	914	U
79	s2	917	U
79	s2	918	U
79	s2	919	A
79	s2	920	A
79	s2	925	G
79	s2	926	A
79	s2	933	G
79	s2	934	G
79	s2	949	G
79	s2	954	U
79	s2	955	A
79	s2	956	G
79	s2	963	A
79	s2	969	U
79	s2	971	G
79	s2	978	G
79	s2	979	C
79	s2	988	C
79	s2	989	C
79	s2	990	A
79	s2	992	A
79	s2	999	G
79	s2	1001	A
79	s2	1002	U
79	s2	1008	A

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Mol	Chain	Res	Type
79	s2	1017	U
79	s2	1019	C
79	s2	1023	A
79	s2	1024	A
79	s2	1027	A
79	s2	1042	A
79	s2	1044	G
79	s2	1045	U
79	s2	1058	A
79	s2	1060	A
79	s2	1061	U
79	s2	1062	A
79	s2	1067	C
79	s2	1078	C
79	s2	1083	A
79	s2	1085	C
79	s2	1087	A
79	s2	1088	U
79	s2	1093	A
79	s2	1100	A
79	s2	1107	G
79	s2	1108	G
79	s2	1109	C
79	s2	1110	G
79	s2	1113	A
79	s2	1114	U
79	s2	1115	U
79	s2	1116	C
79	s2	1118	C
79	s2	1119	A
79	s2	1121	G
79	s2	1124	C
79	s2	1125	C
79	s2	1128	C
79	s2	1133	A
79	s2	1138	C
79	s2	1148	A
79	s2	1150	A
79	s2	1153	C
79	s2	1154	U
79	s2	1155	U
79	s2	1170	A

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Mol	Chain	Res	Type
79	s2	1172	U
79	s2	1195	A
79	s2	1200	A
79	s2	1207	G
79	s2	1208	A
79	s2	1213	C
79	s2	1215	C
79	s2	1216	C
79	s2	1217	A
79	s2	1220	A
79	s2	1224	G
79	s2	1227	G
79	s2	1237	C
79	s2	1240	A
79	s2	1242	U
79	s2	1243	U
79	s2	1251	A
79	s2	1253	A
79	s2	1256	G
79	s2	1257	G
79	s2	1259	A
79	s2	1264	C
79	s2	1274	G
79	s2	1275	G
79	s2	1281	G
79	s2	1283	C
79	s2	1284	A
79	s2	1286	G
79	s2	1287	A
79	s2	1290	G
79	s2	1294	G
79	s2	1295	A
79	s2	1301	A
79	s2	1302	G
79	s2	1303	C
79	s2	1306	U
79	s2	1308	U
79	s2	1313	A
79	s2	1320	G
79	s2	1333	U
79	s2	1342	U
79	s2	1345	G

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Mol	Chain	Res	Type
79	s2	1348	G
79	s2	1351	G
79	s2	1354	G
79	s2	1355	C
79	s2	1356	G
79	s2	1357	A
79	s2	1364	U
79	s2	1369	A
79	s2	1370	A
79	s2	1371	U
79	s2	1372	U
79	s2	1373	C
79	s2	1375	G
79	s2	1376	A
79	s2	1378	A
79	s2	1388	A
79	s2	1389	C
79	s2	1396	A
79	s2	1401	A
79	s2	1402	A
79	s2	1406	G
79	s2	1407	U
79	s2	1411	G
79	s2	1412	C
79	s2	1414	A
79	s2	1415	C
79	s2	1419	C
79	s2	1420	G
79	s2	1421	A
79	s2	1422	G
79	s2	1423	C
79	s2	1425	G
79	s2	1428	G
79	s2	1433	C
79	s2	1434	C
79	s2	1435	C
79	s2	1436	C
79	s2	1438	A
79	s2	1442	U
79	s2	1449	G
79	s2	1450	G
79	s2	1452	A

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Mol	Chain	Res	Type
79	s2	1453	C
79	s2	1454	A
79	s2	1459	G
79	s2	1462	U
79	s2	1463	U
79	s2	1464	C
79	s2	1465	A
79	s2	1472	C
79	s2	1473	G
79	s2	1476	A
79	s2	1478	U
79	s2	1479	G
79	s2	1484	A
79	s2	1486	A
79	s2	1489	A
79	s2	1490	G
79	s2	1494	U
79	s2	1495	G
79	s2	1497	G
79	s2	1498	A
79	s2	1507	G
79	s2	1508	A
79	s2	1520	G
79	s2	1521	C
79	s2	1522	A
79	s2	1533	A
79	s2	1535	U
79	s2	1536	G
79	s2	1537	A
79	s2	1544	C
79	s2	1546	G
79	s2	1551	U
79	s2	1552	G
79	s2	1556	A
79	s2	1560	U
79	s2	1570	G
79	s2	1572	C
79	s2	1578	U
79	s2	1579	A
79	s2	1580	A
79	s2	1581	C
79	s2	1585	U

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Mol	Chain	Res	Type
79	s2	1586	U
79	s2	1587	G
79	s2	1588	A
79	s2	1594	A
79	s2	1598	G
79	s2	1599	U
79	s2	1600	G
79	s2	1601	A
79	s2	1602	U
79	s2	1603	G
79	s2	1604	G
79	s2	1606	G
79	s2	1621	U
79	s2	1623	A
79	s2	1629	C
79	s2	1630	A
79	s2	1633	A
79	s2	1634	A
79	s2	1637	A
79	s2	1638	G
79	s2	1639	G
79	s2	1640	A
79	s2	1646	C
79	s2	1648	G
79	s2	1649	U
79	s2	1654	G
79	s2	1662	U
79	s2	1663	A
79	s2	1664	A
79	s2	1665	G
79	s2	1671	G
79	s2	1680	G
79	s2	1683	C
79	s2	1694	U
79	s2	1696	C
79	s2	1699	A
79	s2	1706	G
79	s2	1712	A
79	s2	1715	A
79	s2	1722	G
79	s2	1726	G
79	s2	1729	U

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Mol	Chain	Res	Type
79	s2	1742	C
79	s2	1743	G
79	s2	1744	G
79	s2	1745	A
79	s2	1747	C
79	s2	1752	C
79	s2	1753	C
79	s2	1754	G
79	s2	1755	C
79	s2	1757	G
79	s2	1758	G
79	s2	1759	G
79	s2	1760	G
79	s2	1761	U
79	s2	1772	C
79	s2	1773	C
79	s2	1774	C
79	s2	1777	G
79	s2	1782	G
79	s2	1783	C
79	s2	1784	G
79	s2	1785	C
79	s2	1787	G
79	s2	1788	A
79	s2	1798	C
79	s2	1809	A
79	s2	1810	U
79	s2	1812	U
79	s2	1813	A
79	s2	1819	A
79	s2	1820	G
79	s2	1822	A
79	s2	1823	A
79	s2	1824	A
79	s2	1825	A
79	s2	1826	G
79	s2	1835	A
79	s2	1838	U
79	s2	1839	U
79	s2	1849	G
79	s2	1852	C
79	s2	1861	G

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Mol	Chain	Res	Type
79	s2	1863	A
79	s2	1864	U
79	s2	1865	C
79	s2	1866	A
81	aP	9	A
81	aP	10	G
81	aP	11	U
81	aP	13	U
81	aP	14	A
81	aP	19	G
81	aP	20(A)	U
81	aP	21	A
81	aP	26	G
81	aP	30	G
81	aP	31	C
81	aP	34	A
81	aP	47	U
81	aP	48	C
81	aP	49	C
81	aP	54	U
81	aP	55	U
81	aP	56	C
81	aP	58	A
81	aP	61	C
81	aP	64	G
81	aP	66	C
81	aP	67	G
81	aP	70	A
81	aP	71	A
82	pE	5	G
82	pE	7	A
82	pE	8	U
82	pE	9	A
82	pE	10	G
82	pE	11	C
82	pE	16	C
82	pE	19	G
82	pE	20	U
82	pE	21	A
82	pE	22	G
82	pE	25	C
82	pE	26	A

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Mol	Chain	Res	Type
82	pE	27	U
82	pE	31	A
82	pE	34	U
82	pE	35	U
82	pE	38	A
82	pE	39	U
82	pE	40	C
82	pE	46	G
82	pE	47	U
82	pE	48	C
82	pE	50	A
82	pE	52	G
82	pE	54	U
82	pE	55	U
82	pE	56	C
82	pE	58	A
82	pE	61	C
82	pE	65	G
82	pE	67	U
82	pE	69	G
82	pE	70	G
82	pE	76	A
85	l5	2	G
85	l5	13	U
85	l5	17	A
85	l5	25	A
85	l5	26	C
85	l5	30	C
85	l5	39	A
85	l5	42	A
85	l5	48	G
85	l5	56	A
85	l5	59	A
85	l5	64	A
85	l5	65	A
85	l5	67	C
85	l5	73	A
85	l5	74	G
85	l5	91	G
85	l5	95	G
85	l5	104	G
85	l5	108	A

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Mol	Chain	Res	Type
85	l5	109	G
85	l5	110	C
85	l5	116	G
85	l5	119	G
85	l5	120	A
85	l5	127	G
85	l5	132	G
85	l5	133	C
85	l5	134	G
85	l5	135	G
85	l5	144	G
85	l5	145	G
85	l5	152	U
85	l5	159	C
85	l5	164	G
85	l5	165	A
85	l5	170	C
85	l5	172	C
85	l5	181	C
85	l5	183	C
85	l5	184	U
85	l5	185	C
85	l5	187	U
85	l5	188	G
85	l5	189	G
85	l5	197	A
85	l5	200	U
85	l5	209	U
85	l5	210	C
85	l5	211	G
85	l5	213	G
85	l5	216	C
85	l5	218	A
85	l5	220	C
85	l5	234	G
85	l5	235	A
85	l5	250	C
85	l5	255	C
85	l5	256	G
85	l5	261	G
85	l5	263	G
85	l5	264	C

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Mol	Chain	Res	Type
85	l5	265	C
85	l5	266	C
85	l5	267	G
85	l5	269	G
85	l5	274	C
85	l5	275	C
85	l5	276	C
85	l5	280	G
85	l5	281	U
85	l5	297	U
85	l5	306	A
85	l5	310	G
85	l5	315	G
85	l5	316	U
85	l5	340	C
85	l5	350	C
85	l5	373	G
85	l5	385	A
85	l5	387	G
85	l5	388	A
85	l5	396	A
85	l5	401	G
85	l5	407	A
85	l5	409	G
85	l5	410	A
85	l5	411	G
85	l5	412	G
85	l5	413	G
85	l5	414	C
85	l5	431	G
85	l5	432	U
85	l5	436	C
85	l5	440	U
85	l5	449	C
85	l5	450	G
85	l5	452	A
85	l5	453	G
85	l5	454	U
85	l5	456	C
85	l5	457	G
85	l5	462	G
85	l5	464	G

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Mol	Chain	Res	Type
85	l5	467	U
85	l5	468	U
85	l5	469	C
85	l5	472	C
85	l5	485	C
85	l5	486	C
85	l5	489	C
85	l5	493	G
85	l5	494	U
85	l5	497	G
85	l5	498	C
85	l5	499	G
85	l5	500	G
85	l5	501	C
85	l5	502	C
85	l5	503	C
85	l5	504	G
85	l5	505	G
85	l5	506	C
85	l5	509	A
85	l5	510	U
85	l5	511	C
85	l5	512	U
85	l5	513	U
85	l5	514	U
85	l5	518	G
85	l5	519	C
85	l5	643	C
85	l5	644	G
85	l5	646	G
85	l5	654	C
85	l5	656	C
85	l5	657	C
85	l5	659	G
85	l5	666	G
85	l5	667	A
85	l5	668	C
85	l5	669	C
85	l5	672	C
85	l5	673	C
85	l5	685	C
85	l5	686	A

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Mol	Chain	Res	Type
85	15	687	U
85	15	696	C
85	15	700	G
85	15	703	G
85	15	704	C
85	15	706	C
85	15	708	G
85	15	731	G
85	15	738	C
85	15	739	G
85	15	741	C
85	15	742	G
85	15	750	U
85	15	753	C
85	15	754	U
85	15	758	G
85	15	759	G
85	15	760	G
85	15	904	C
85	15	906	C
85	15	907	C
85	15	910	G
85	15	911	U
85	15	912	G
85	15	913	U
85	15	914	U
85	15	915	A
85	15	917	A
85	15	918	G
85	15	923	C
85	15	924	C
85	15	926	G
85	15	932	A
85	15	933	G
85	15	935	A
85	15	936	C
85	15	937	U
85	15	941	C
85	15	944	A
85	15	945	U
85	15	946	C
85	15	957	G

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Mol	Chain	Res	Type
85	l5	959	G
85	l5	960	A
85	l5	961	G
85	l5	962	C
85	l5	965	G
85	l5	967	C
85	l5	969	C
85	l5	970	G
85	l5	977	C
85	l5	982	U
85	l5	985	C
85	l5	989	U
85	l5	990	C
85	l5	992	C
85	l5	993	G
85	l5	995	C
85	l5	1048	G
85	l5	1049	C
85	l5	1050	C
85	l5	1051	G
85	l5	1066	G
85	l5	1070	G
85	l5	1071	C
85	l5	1072	C
85	l5	1075	G
85	l5	1076	C
85	l5	1082	C
85	l5	1083	U
85	l5	1094	G
85	l5	1095	A
85	l5	1168	G
85	l5	1171	G
85	l5	1172	C
85	l5	1173	G
85	l5	1178	G
85	l5	1179	U
85	l5	1180	C
85	l5	1182	C
85	l5	1183	C
85	l5	1200	G
85	l5	1202	C
85	l5	1203	G

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Mol	Chain	Res	Type
85	l5	1204	C
85	l5	1205	G
85	l5	1210	C
85	l5	1211	G
85	l5	1214	C
85	l5	1215	C
85	l5	1216	C
85	l5	1217	G
85	l5	1218	G
85	l5	1219	G
85	l5	1221	G
85	l5	1222	A
85	l5	1235	G
85	l5	1241	C
85	l5	1242	G
85	l5	1245	C
85	l5	1246	G
85	l5	1247	U
85	l5	1253	G
85	l5	1254	A
85	l5	1257	A
85	l5	1258	G
85	l5	1261	G
85	l5	1262	G
85	l5	1266	G
85	l5	1267	C
85	l5	1269	G
85	l5	1270	A
85	l5	1271	G
85	l5	1272	C
85	l5	1273	G
85	l5	1274	A
85	l5	1275	G
85	l5	1277	G
85	l5	1280	C
85	l5	1284	G
85	l5	1285	U
85	l5	1287	G
85	l5	1293	G
85	l5	1294	A
85	l5	1295	C
85	l5	1296	G

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Mol	Chain	Res	Type
85	l5	1301	C
85	l5	1324	A
85	l5	1326	A
85	l5	1337	A
85	l5	1344	C
85	l5	1345	A
85	l5	1354	A
85	l5	1358	G
85	l5	1359	G
85	l5	1365	C
85	l5	1367	C
85	l5	1370	G
85	l5	1378	C
85	l5	1381	U
85	l5	1387	A
85	l5	1394	G
85	l5	1397	A
85	l5	1404	G
85	l5	1405	C
85	l5	1407	C
85	l5	1408	G
85	l5	1409	C
85	l5	1410	U
85	l5	1411	C
85	l5	1414	C
85	l5	1415	G
85	l5	1417	C
85	l5	1418	C
85	l5	1420	A
85	l5	1425	G
85	l5	1437	C
85	l5	1439	C
85	l5	1443	A
85	l5	1444	G
85	l5	1446	C
85	l5	1447	C
85	l5	1452	A
85	l5	1457	G
85	l5	1465	G
85	l5	1482	G
85	l5	1483	C
85	l5	1493	G

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Mol	Chain	Res	Type
85	l5	1497	A
85	l5	1498	G
85	l5	1501	C
85	l5	1502	G
85	l5	1517	G
85	l5	1518	A
85	l5	1523	A
85	l5	1534	A
85	l5	1547	A
85	l5	1549	G
85	l5	1564	A
85	l5	1566	C
85	l5	1574	G
85	l5	1578	U
85	l5	1582	U
85	l5	1591	U
85	l5	1596	U
85	l5	1624	G
85	l5	1625	G
85	l5	1626	G
85	l5	1631	A
85	l5	1633	G
85	l5	1634	A
85	l5	1641	G
85	l5	1654	G
85	l5	1661	C
85	l5	1676	C
85	l5	1677	U
85	l5	1678	C
85	l5	1681	G
85	l5	1691	G
85	l5	1698	C
85	l5	1699	A
85	l5	1700	G
85	l5	1703	C
85	l5	1704	C
85	l5	1705	G
85	l5	1707	C
85	l5	1715	C
85	l5	1718	C
85	l5	1730	U
85	l5	1740	C

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Mol	Chain	Res	Type
85	l5	1741	G
85	l5	1742	A
85	l5	1750	G
85	l5	1753	G
85	l5	1754	U
85	l5	1757	U
85	l5	1758	G
85	l5	1760	G
85	l5	1761	G
85	l5	1762	C
85	l5	1763	C
85	l5	1764	G
85	l5	1765	A
85	l5	1766	A
85	l5	1767	A
85	l5	1768	C
85	l5	1769	G
85	l5	1770	A
85	l5	1775	A
85	l5	1787	A
85	l5	1803	G
85	l5	1804	A
85	l5	1806	G
85	l5	1810	G
85	l5	1820	C
85	l5	1821	G
85	l5	1822	U
85	l5	1833	G
85	l5	1836	G
85	l5	1837	A
85	l5	1842	G
85	l5	1843	A
85	l5	1855	G
85	l5	1869	G
85	l5	1882	U
85	l5	1897	A
85	l5	1917	A
85	l5	1918	U
85	l5	1919	G
85	l5	1920	C
85	l5	1921	C
85	l5	1922	G

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Mol	Chain	Res	Type
85	l5	1925	G
85	l5	1931	C
85	l5	1932	A
85	l5	1936	C
85	l5	1940	G
85	l5	1948	G
85	l5	1959	U
85	l5	1960	A
85	l5	1961	G
85	l5	1962	A
85	l5	1974	U
85	l5	1975	G
85	l5	1976	G
85	l5	1978	C
85	l5	1980	U
85	l5	1981	G
85	l5	1982	G
85	l5	1983	A
85	l5	1984	A
85	l5	1985	G
85	l5	1989	G
85	l5	1991	A
85	l5	1992	U
85	l5	1993	C
85	l5	1997	U
85	l5	1998	A
85	l5	2001	G
85	l5	2002	A
85	l5	2004	U
85	l5	2011	C
85	l5	2014	C
85	l5	2017	A
85	l5	2018	C
85	l5	2022	C
85	l5	2024	G
85	l5	2026	A
85	l5	2033	A
85	l5	2034	G
85	l5	2046	G
85	l5	2048	U
85	l5	2052	G
85	l5	2055	G

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Mol	Chain	Res	Type
85	15	2056	G
85	15	2069	A
85	15	2084	C
85	15	2085	G
85	15	2092	G
85	15	2093	A
85	15	2095	A
85	15	2096	G
85	15	2097	U
85	15	2098	G
85	15	2101	C
85	15	2102	G
85	15	2103	G
85	15	2106	G
85	15	2107	C
85	15	2108	G
85	15	2112	G
85	15	2250	C
85	15	2252	G
85	15	2253	A
85	15	2255	C
85	15	2256	C
85	15	2257	C
85	15	2258	C
85	15	2259	G
85	15	2260	C
85	15	2289	C
85	15	2300	A
85	15	2301	G
85	15	2306	G
85	15	2313	A
85	15	2331	G
85	15	2332	A
85	15	2333	G
85	15	2348	G
85	15	2349	A
85	15	2351	C
85	15	2360	A
85	15	2364	G
85	15	2389	A
85	15	2395	A
85	15	2397	G

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Mol	Chain	Res	Type
85	15	2398	U
85	15	2402	G
85	15	2404	A
85	15	2410	C
85	15	2417	A
85	15	2421	G
85	15	2425	U
85	15	2441	C
85	15	2450	G
85	15	2453	A
85	15	2463	G
85	15	2464	C
85	15	2465	C
85	15	2471	G
85	15	2474	G
85	15	2475	G
85	15	2478	C
85	15	2479	G
85	15	2483	G
85	15	2484	A
85	15	2485	U
85	15	2487	G
85	15	2488	C
85	15	2489	C
85	15	2490	U
85	15	2491	C
85	15	2494	U
85	15	2503	G
85	15	2504	C
85	15	2505	C
85	15	2506	G
85	15	2511	A
85	15	2513	A
85	15	2518	G
85	15	2519	U
85	15	2520	C
85	15	2529	A
85	15	2537	A
85	15	2544	G
85	15	2546	G
85	15	2547	G
85	15	2554	U

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Mol	Chain	Res	Type
85	15	2555	G
85	15	2557	G
85	15	2560	C
85	15	2565	A
85	15	2568	C
85	15	2583	C
85	15	2586	G
85	15	2587	A
85	15	2588	C
85	15	2589	C
85	15	2601	A
85	15	2618	G
85	15	2627	C
85	15	2638	G
85	15	2643	G
85	15	2652	G
85	15	2653	C
85	15	2662	G
85	15	2669	C
85	15	2673	G
85	15	2676	A
85	15	2687	U
85	15	2694	G
85	15	2695	A
85	15	2696	A
85	15	2703	G
85	15	2707	U
85	15	2708	U
85	15	2710	C
85	15	2711	G
85	15	2719	C
85	15	2721	G
85	15	2724	G
85	15	2726	G
85	15	2730	U
85	15	2739	C
85	15	2742	G
85	15	2743	A
85	15	2746	A
85	15	2761	U
85	15	2763	U
85	15	2764	A

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Mol	Chain	Res	Type
85	15	2769	U
85	15	2770	C
85	15	2787	A
85	15	2788	U
85	15	2790	U
85	15	2794	C
85	15	2802	C
85	15	2826	U
85	15	2827	G
85	15	2829	U
85	15	2833	A
85	15	2835	A
85	15	2847	G
85	15	2855	G
85	15	2867	C
85	15	2877	G
85	15	2894	A
85	15	2895	A
85	15	2897	G
85	15	2900	U
85	15	2901	G
85	15	2902	G
85	15	2903	G
85	15	2904	U
85	15	2905	C
85	15	2906	G
85	15	2908	U
85	15	3590	G
85	15	3591	C
85	15	3594	C
85	15	3595	U
85	15	3596	A
85	15	3597	G
85	15	3599	A
85	15	3605	C
85	15	3615	G
85	15	3618	C
85	15	3626	G
85	15	3630	A
85	15	3635	A
85	15	3644	U
85	15	3646	A

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Mol	Chain	Res	Type
85	15	3652	A
85	15	3662	A
85	15	3664	G
85	15	3670	C
85	15	3673	C
85	15	3674	G
85	15	3685	C
85	15	3692	A
85	15	3710	G
85	15	3711	A
85	15	3713	U
85	15	3726	A
85	15	3727	A
85	15	3735	G
85	15	3748	A
85	15	3750	G
85	15	3756	A
85	15	3759	A
85	15	3772	U
85	15	3773	U
85	15	3776	G
85	15	3777	G
85	15	3778	U
85	15	3784	A
85	15	3786	U
85	15	3801	U
85	15	3802	U
85	15	3810	C
85	15	3811	G
85	15	3812	C
85	15	3817	A
85	15	3818	U
85	15	3819	G
85	15	3823	G
85	15	3839	G
85	15	3840	U
85	15	3841	C
85	15	3867	A
85	15	3876	A
85	15	3877	A
85	15	3878	C
85	15	3879	G

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Mol	Chain	Res	Type
85	15	3887	C
85	15	3890	A
85	15	3892	U
85	15	3897	G
85	15	3898	G
85	15	3901	A
85	15	3902	A
85	15	3906	A
85	15	3907	G
85	15	3908	A
85	15	3915	U
85	15	3922	G
85	15	3923	A
85	15	3938	G
85	15	3939	G
85	15	3940	U
85	15	3943	A
85	15	3944	G
85	15	3947	A
85	15	3948	C
85	15	3949	A
85	15	3950	U
85	15	3951	G
85	15	3953	G
85	15	3955	G
85	15	3956	G
85	15	3957	U
85	15	3959	U
85	15	3960	A
85	15	3961	G
85	15	3962	A
85	15	3963	A
85	15	3964	U
85	15	3965	A
85	15	3966	A
85	15	3967	G
85	15	3968	U
85	15	3969	G
85	15	3970	G
85	15	3972	A
85	15	3973	G
85	15	4039	G

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Mol	Chain	Res	Type
85	l5	4041	C
85	l5	4042	G
85	l5	4043	G
85	l5	4044	U
85	l5	4046	A
85	l5	4047	A
85	l5	4048	A
85	l5	4049	U
85	l5	4050	A
85	l5	4051	C
85	l5	4052	C
85	l5	4053	A
85	l5	4054	C
85	l5	4055	U
85	l5	4056	A
85	l5	4057	C
85	l5	4058	U
85	l5	4059	C
85	l5	4060	U
85	l5	4062	A
85	l5	4063	U
85	l5	4064	C
85	l5	4065	G
85	l5	4067	U
85	l5	4068	U
85	l5	4069	U
85	l5	4076	G
85	l5	4084	G
85	l5	4096	C
85	l5	4097	G
85	l5	4098	A
85	l5	4099	G
85	l5	4101	C
85	l5	4102	C
85	l5	4103	C
85	l5	4104	G
85	l5	4108	G
85	l5	4111	U
85	l5	4114	C
85	l5	4115	G
85	l5	4116	C
85	l5	4117	U

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Mol	Chain	Res	Type
85	l5	4119	C
85	l5	4120	U
85	l5	4121	G
85	l5	4127	A
85	l5	4133	C
85	l5	4134	C
85	l5	4140	C
85	l5	4141	G
85	l5	4142	C
85	l5	4143	G
85	l5	4144	C
85	l5	4146	G
85	l5	4149	C
85	l5	4157	A
85	l5	4160	C
85	l5	4162	C
85	l5	4163	U
85	l5	4168	G
85	l5	4170	A
85	l5	4183	G
85	l5	4184	G
85	l5	4191	G
85	l5	4196	G
85	l5	4201	G
85	l5	4203	A
85	l5	4212	A
85	l5	4213	A
85	l5	4222	G
85	l5	4225	G
85	l5	4229	U
85	l5	4233	A
85	l5	4241	C
85	l5	4242	U
85	l5	4249	G
85	l5	4251	A
85	l5	4254	G
85	l5	4255	A
85	l5	4265	U
85	l5	4268	A
85	l5	4273	A
85	l5	4279	A
85	l5	4281	A

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Mol	Chain	Res	Type
85	l5	4290	U
85	l5	4291	G
85	l5	4297	G
85	l5	4304	A
85	l5	4305	G
85	l5	4306	U
85	l5	4314	C
85	l5	4319	C
85	l5	4326	G
85	l5	4330	G
85	l5	4332	C
85	l5	4349	C
85	l5	4354	U
85	l5	4373	G
85	l5	4376	A
85	l5	4377	G
85	l5	4378	A
85	l5	4380	A
85	l5	4387	C
85	l5	4391	G
85	l5	4393	G
85	l5	4394	A
85	l5	4422	A
85	l5	4426	C
85	l5	4433	G
85	l5	4438	U
85	l5	4448	G
85	l5	4449	A
85	l5	4452	U
85	l5	4453	C
85	l5	4464	A
85	l5	4466	C
85	l5	4488	A
85	l5	4500	U
85	l5	4512	U
85	l5	4513	A
85	l5	4518	A
85	l5	4522	G
85	l5	4524	G
85	l5	4528	G
85	l5	4545	G
85	l5	4548	A

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Mol	Chain	Res	Type
85	l5	4549	G
85	l5	4556	U
85	l5	4557	U
85	l5	4560	C
85	l5	4567	G
85	l5	4572	U
85	l5	4573	G
85	l5	4575	G
85	l5	4581	G
85	l5	4584	A
85	l5	4589	A
85	l5	4590	A
85	l5	4600	G
85	l5	4601	U
85	l5	4617	G
85	l5	4636	U
85	l5	4637	G
85	l5	4652	G
85	l5	4656	A
85	l5	4659	G
85	l5	4670	C
85	l5	4672	A
85	l5	4682	U
85	l5	4687	A
85	l5	4695	C
85	l5	4700	A
85	l5	4707	A
85	l5	4708	A
85	l5	4709	U
85	l5	4719	G
85	l5	4733	C
85	l5	4734	A
85	l5	4740	G
85	l5	4741	C
85	l5	4742	G
85	l5	4745	G
85	l5	4747	C
85	l5	4750	G
85	l5	4754	G
85	l5	4757	C
85	l5	4759	C
85	l5	4761	G

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Mol	Chain	Res	Type
85	15	4764	A
85	15	4765	G
85	15	4771	C
85	15	4772	C
85	15	4773	C
85	15	4775	C
85	15	4776	G
85	15	4859	C
85	15	4860	G
85	15	4862	G
85	15	4863	G
85	15	4865	C
85	15	4870	G
85	15	4871	C
85	15	4875	G
85	15	4877	G
85	15	4880	C
85	15	4881	U
85	15	4882	U
85	15	4883	C
85	15	4887	C
85	15	4889	G
85	15	4895	C
85	15	4896	G
85	15	4897	G
85	15	4900	C
85	15	4901	G
85	15	4902	C
85	15	4910	G
85	15	4912	G
85	15	4914	C
85	15	4922	C
85	15	4923	C
85	15	4925	U
85	15	4926	C
85	15	4927	G
85	15	4928	C
85	15	4931	G
85	15	4941	G
85	15	4943	A
85	15	4944	C
85	15	4947	U

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Mol	Chain	Res	Type
85	l5	4951	G
85	l5	4960	G
85	l5	4973	U
85	l5	4976	U
85	l5	4985	U
85	l5	4988	U
85	l5	4989	U
85	l5	4990	C
85	l5	4991	U
85	l5	5006	U
85	l5	5014	A
85	l5	5017	G
85	l5	5020	G
85	l5	5024	C
85	l5	5026	U
85	l5	5027	C
85	l5	5028	G
85	l5	5029	C
85	l5	5030	U
85	l5	5034	A
85	l5	5041	G
85	l5	5050	C
85	l5	5054	C
85	l5	5055	G
85	l5	5060	A
85	l5	5061	A
85	l5	5069	U
85	L5	2	G
85	L5	4	G
85	L5	13	U
85	L5	25	A
85	L5	26	C
85	L5	30	C
85	L5	39	A
85	L5	42	A
85	L5	48	G
85	L5	49	U
85	L5	56	A
85	L5	59	A
85	L5	64	A
85	L5	65	A
85	L5	67	C

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Mol	Chain	Res	Type
85	L5	73	A
85	L5	91	G
85	L5	95	G
85	L5	104	G
85	L5	108	A
85	L5	109	G
85	L5	110	C
85	L5	116	G
85	L5	119	G
85	L5	120	A
85	L5	127	G
85	L5	132	G
85	L5	133	C
85	L5	134	G
85	L5	144	G
85	L5	145	G
85	L5	152	U
85	L5	159	C
85	L5	165	A
85	L5	166	C
85	L5	170	C
85	L5	171	U
85	L5	172	C
85	L5	181	C
85	L5	183	C
85	L5	184	U
85	L5	185	C
85	L5	188	G
85	L5	189	G
85	L5	200	U
85	L5	209	U
85	L5	213	G
85	L5	216	C
85	L5	218	A
85	L5	220	C
85	L5	232	G
85	L5	234	G
85	L5	235	A
85	L5	237	G
85	L5	250	C
85	L5	255	C
85	L5	256	G

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Mol	Chain	Res	Type
85	L5	261	G
85	L5	262	G
85	L5	264	C
85	L5	265	C
85	L5	266	C
85	L5	267	G
85	L5	269	G
85	L5	270	U
85	L5	274	C
85	L5	275	C
85	L5	276	C
85	L5	280	G
85	L5	281	U
85	L5	297	U
85	L5	306	A
85	L5	310	G
85	L5	315	G
85	L5	316	U
85	L5	332	C
85	L5	340	C
85	L5	350	C
85	L5	365	U
85	L5	372	A
85	L5	373	G
85	L5	385	A
85	L5	387	G
85	L5	388	A
85	L5	396	A
85	L5	401	G
85	L5	407	A
85	L5	409	G
85	L5	410	A
85	L5	411	G
85	L5	412	G
85	L5	413	G
85	L5	431	G
85	L5	438	G
85	L5	440	U
85	L5	447	C
85	L5	449	C
85	L5	450	G
85	L5	452	A

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Mol	Chain	Res	Type
85	L5	453	G
85	L5	454	U
85	L5	456	C
85	L5	457	G
85	L5	465	G
85	L5	467	U
85	L5	468	U
85	L5	472	C
85	L5	478	G
85	L5	484	U
85	L5	485	C
85	L5	486	C
85	L5	493	G
85	L5	494	U
85	L5	497	G
85	L5	498	C
85	L5	499	G
85	L5	500	G
85	L5	501	C
85	L5	502	C
85	L5	503	C
85	L5	504	G
85	L5	505	G
85	L5	506	C
85	L5	509	A
85	L5	510	U
85	L5	512	U
85	L5	513	U
85	L5	514	U
85	L5	515	C
85	L5	518	G
85	L5	643	C
85	L5	644	G
85	L5	646	G
85	L5	654	C
85	L5	655	C
85	L5	656	C
85	L5	657	C
85	L5	658	C
85	L5	659	G
85	L5	666	G
85	L5	667	A

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Mol	Chain	Res	Type
85	L5	668	C
85	L5	669	C
85	L5	672	C
85	L5	673	C
85	L5	674	G
85	L5	678	C
85	L5	679	C
85	L5	682	G
85	L5	685	C
85	L5	686	A
85	L5	687	U
85	L5	696	C
85	L5	703	G
85	L5	704	C
85	L5	706	C
85	L5	708	G
85	L5	729	G
85	L5	730	G
85	L5	731	G
85	L5	733	A
85	L5	738	C
85	L5	739	G
85	L5	742	G
85	L5	750	U
85	L5	753	C
85	L5	754	U
85	L5	758	G
85	L5	759	G
85	L5	904	C
85	L5	905	C
85	L5	906	C
85	L5	907	C
85	L5	910	G
85	L5	911	U
85	L5	912	G
85	L5	913	U
85	L5	914	U
85	L5	915	A
85	L5	917	A
85	L5	918	G
85	L5	923	C
85	L5	924	C

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Mol	Chain	Res	Type
85	L5	926	G
85	L5	932	A
85	L5	933	G
85	L5	935	A
85	L5	936	C
85	L5	937	U
85	L5	941	C
85	L5	943	A
85	L5	944	A
85	L5	945	U
85	L5	957	G
85	L5	959	G
85	L5	960	A
85	L5	961	G
85	L5	962	C
85	L5	965	G
85	L5	966	A
85	L5	967	C
85	L5	968	C
85	L5	969	C
85	L5	970	G
85	L5	982	U
85	L5	985	C
85	L5	989	U
85	L5	990	C
85	L5	992	C
85	L5	993	G
85	L5	995	C
85	L5	1048	G
85	L5	1049	C
85	L5	1050	C
85	L5	1051	G
85	L5	1066	G
85	L5	1070	G
85	L5	1071	C
85	L5	1072	C
85	L5	1075	G
85	L5	1082	C
85	L5	1083	U
85	L5	1095	A
85	L5	1168	G
85	L5	1171	G

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Mol	Chain	Res	Type
85	L5	1172	C
85	L5	1173	G
85	L5	1179	U
85	L5	1180	C
85	L5	1181	C
85	L5	1182	C
85	L5	1183	C
85	L5	1184	A
85	L5	1202	C
85	L5	1203	G
85	L5	1205	G
85	L5	1210	C
85	L5	1211	G
85	L5	1215	C
85	L5	1216	C
85	L5	1217	G
85	L5	1218	G
85	L5	1219	G
85	L5	1222	A
85	L5	1241	C
85	L5	1242	G
85	L5	1245	C
85	L5	1246	G
85	L5	1253	G
85	L5	1254	A
85	L5	1257	A
85	L5	1258	G
85	L5	1261	G
85	L5	1262	G
85	L5	1266	G
85	L5	1267	C
85	L5	1269	G
85	L5	1270	A
85	L5	1271	G
85	L5	1272	C
85	L5	1273	G
85	L5	1274	A
85	L5	1275	G
85	L5	1280	C
85	L5	1284	G
85	L5	1287	G
85	L5	1293	G

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Mol	Chain	Res	Type
85	L5	1294	A
85	L5	1295	C
85	L5	1296	G
85	L5	1301	C
85	L5	1314	C
85	L5	1322	A
85	L5	1325	C
85	L5	1326	A
85	L5	1337	A
85	L5	1345	A
85	L5	1354	A
85	L5	1358	G
85	L5	1359	G
85	L5	1365	C
85	L5	1366	G
85	L5	1367	C
85	L5	1370	G
85	L5	1378	C
85	L5	1381	U
85	L5	1387	A
85	L5	1394	G
85	L5	1397	A
85	L5	1404	G
85	L5	1405	C
85	L5	1407	C
85	L5	1409	C
85	L5	1410	U
85	L5	1414	C
85	L5	1415	G
85	L5	1417	C
85	L5	1418	C
85	L5	1420	A
85	L5	1425	G
85	L5	1434	G
85	L5	1435	G
85	L5	1437	C
85	L5	1439	C
85	L5	1443	A
85	L5	1444	G
85	L5	1446	C
85	L5	1447	C
85	L5	1452	A

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Mol	Chain	Res	Type
85	L5	1457	G
85	L5	1465	G
85	L5	1472	C
85	L5	1475	G
85	L5	1482	G
85	L5	1483	C
85	L5	1497	A
85	L5	1498	G
85	L5	1502	G
85	L5	1516	G
85	L5	1517	G
85	L5	1518	A
85	L5	1523	A
85	L5	1525	A
85	L5	1534	A
85	L5	1535	C
85	L5	1547	A
85	L5	1562	G
85	L5	1563	A
85	L5	1564	A
85	L5	1566	C
85	L5	1574	G
85	L5	1578	U
85	L5	1582	U
85	L5	1591	U
85	L5	1592	G
85	L5	1596	U
85	L5	1597	G
85	L5	1598	C
85	L5	1612	G
85	L5	1624	G
85	L5	1625	G
85	L5	1631	A
85	L5	1633	G
85	L5	1634	A
85	L5	1638	A
85	L5	1640	C
85	L5	1641	G
85	L5	1654	G
85	L5	1661	C
85	L5	1663	C
85	L5	1676	C

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Mol	Chain	Res	Type
85	L5	1677	U
85	L5	1678	C
85	L5	1681	G
85	L5	1691	G
85	L5	1698	C
85	L5	1699	A
85	L5	1700	G
85	L5	1701	A
85	L5	1703	C
85	L5	1704	C
85	L5	1705	G
85	L5	1707	C
85	L5	1718	C
85	L5	1730	U
85	L5	1732	C
85	L5	1734	G
85	L5	1740	C
85	L5	1741	G
85	L5	1742	A
85	L5	1750	G
85	L5	1753	G
85	L5	1754	U
85	L5	1757	U
85	L5	1758	G
85	L5	1760	G
85	L5	1761	G
85	L5	1762	C
85	L5	1763	C
85	L5	1764	G
85	L5	1765	A
85	L5	1766	A
85	L5	1767	A
85	L5	1768	C
85	L5	1770	A
85	L5	1781	U
85	L5	1787	A
85	L5	1804	A
85	L5	1806	G
85	L5	1810	G
85	L5	1820	C
85	L5	1821	G
85	L5	1822	U

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Mol	Chain	Res	Type
85	L5	1826	G
85	L5	1833	G
85	L5	1834	U
85	L5	1836	G
85	L5	1837	A
85	L5	1842	G
85	L5	1843	A
85	L5	1855	G
85	L5	1869	G
85	L5	1897	A
85	L5	1917	A
85	L5	1918	U
85	L5	1919	G
85	L5	1920	C
85	L5	1921	C
85	L5	1922	G
85	L5	1925	G
85	L5	1931	C
85	L5	1932	A
85	L5	1936	C
85	L5	1940	G
85	L5	1948	G
85	L5	1959	U
85	L5	1960	A
85	L5	1961	G
85	L5	1962	A
85	L5	1974	U
85	L5	1975	G
85	L5	1978	C
85	L5	1980	U
85	L5	1981	G
85	L5	1982	G
85	L5	1984	A
85	L5	1985	G
85	L5	1989	G
85	L5	1991	A
85	L5	1992	U
85	L5	1993	C
85	L5	1997	U
85	L5	1998	A
85	L5	2001	G
85	L5	2002	A

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Mol	Chain	Res	Type
85	L5	2004	U
85	L5	2011	C
85	L5	2014	C
85	L5	2017	A
85	L5	2018	C
85	L5	2022	C
85	L5	2024	G
85	L5	2026	A
85	L5	2033	A
85	L5	2034	G
85	L5	2046	G
85	L5	2048	U
85	L5	2055	G
85	L5	2056	G
85	L5	2062	C
85	L5	2069	A
85	L5	2084	C
85	L5	2085	G
85	L5	2092	G
85	L5	2093	A
85	L5	2095	A
85	L5	2096	G
85	L5	2097	U
85	L5	2098	G
85	L5	2101	C
85	L5	2102	G
85	L5	2103	G
85	L5	2107	C
85	L5	2108	G
85	L5	2112	G
85	L5	2250	C
85	L5	2252	G
85	L5	2253	A
85	L5	2256	C
85	L5	2258	C
85	L5	2259	G
85	L5	2260	C
85	L5	2263	A
85	L5	2264	C
85	L5	2289	C
85	L5	2300	A
85	L5	2301	G

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Mol	Chain	Res	Type
85	L5	2306	G
85	L5	2313	A
85	L5	2316	G
85	L5	2331	G
85	L5	2332	A
85	L5	2333	G
85	L5	2348	G
85	L5	2349	A
85	L5	2351	C
85	L5	2360	A
85	L5	2382	A
85	L5	2392	C
85	L5	2395	A
85	L5	2397	G
85	L5	2398	U
85	L5	2402	G
85	L5	2404	A
85	L5	2410	C
85	L5	2412	A
85	L5	2417	A
85	L5	2421	G
85	L5	2425	U
85	L5	2441	C
85	L5	2450	G
85	L5	2453	A
85	L5	2463	G
85	L5	2464	C
85	L5	2465	C
85	L5	2469	C
85	L5	2471	G
85	L5	2474	G
85	L5	2475	G
85	L5	2478	C
85	L5	2479	G
85	L5	2483	G
85	L5	2484	A
85	L5	2485	U
85	L5	2486	G
85	L5	2487	G
85	L5	2488	C
85	L5	2489	C
85	L5	2490	U

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Mol	Chain	Res	Type
85	L5	2491	C
85	L5	2494	U
85	L5	2503	G
85	L5	2504	C
85	L5	2506	G
85	L5	2511	A
85	L5	2513	A
85	L5	2518	G
85	L5	2519	U
85	L5	2529	A
85	L5	2537	A
85	L5	2544	G
85	L5	2546	G
85	L5	2547	G
85	L5	2554	U
85	L5	2555	G
85	L5	2557	G
85	L5	2559	G
85	L5	2560	C
85	L5	2565	A
85	L5	2568	C
85	L5	2583	C
85	L5	2586	G
85	L5	2587	A
85	L5	2589	C
85	L5	2601	A
85	L5	2602	G
85	L5	2618	G
85	L5	2627	C
85	L5	2632	U
85	L5	2652	G
85	L5	2653	C
85	L5	2662	G
85	L5	2669	C
85	L5	2673	G
85	L5	2676	A
85	L5	2686	G
85	L5	2687	U
85	L5	2694	G
85	L5	2695	A
85	L5	2696	A
85	L5	2701	U

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Mol	Chain	Res	Type
85	L5	2703	G
85	L5	2707	U
85	L5	2708	U
85	L5	2710	C
85	L5	2711	G
85	L5	2712	G
85	L5	2719	C
85	L5	2721	G
85	L5	2724	G
85	L5	2726	G
85	L5	2730	U
85	L5	2739	C
85	L5	2742	G
85	L5	2743	A
85	L5	2746	A
85	L5	2754	G
85	L5	2759	G
85	L5	2761	U
85	L5	2763	U
85	L5	2764	A
85	L5	2769	U
85	L5	2770	C
85	L5	2786	C
85	L5	2787	A
85	L5	2788	U
85	L5	2790	U
85	L5	2799	G
85	L5	2825	A
85	L5	2826	U
85	L5	2827	G
85	L5	2828	U
85	L5	2829	U
85	L5	2833	A
85	L5	2835	A
85	L5	2846	G
85	L5	2855	G
85	L5	2867	C
85	L5	2877	G
85	L5	2894	A
85	L5	2895	A
85	L5	2897	G
85	L5	2899	C

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Mol	Chain	Res	Type
85	L5	2900	U
85	L5	2902	G
85	L5	2903	G
85	L5	2904	U
85	L5	2905	C
85	L5	2906	G
85	L5	2908	U
85	L5	3588	C
85	L5	3590	G
85	L5	3591	C
85	L5	3594	C
85	L5	3595	U
85	L5	3596	A
85	L5	3597	G
85	L5	3599	A
85	L5	3605	C
85	L5	3615	G
85	L5	3618	C
85	L5	3626	G
85	L5	3630	A
85	L5	3635	A
85	L5	3646	A
85	L5	3662	A
85	L5	3664	G
85	L5	3670	C
85	L5	3673	C
85	L5	3674	G
85	L5	3680	U
85	L5	3685	C
85	L5	3692	A
85	L5	3696	C
85	L5	3698	G
85	L5	3706	C
85	L5	3710	G
85	L5	3711	A
85	L5	3713	U
85	L5	3726	A
85	L5	3727	A
85	L5	3748	A
85	L5	3750	G
85	L5	3756	A
85	L5	3759	A

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Mol	Chain	Res	Type
85	L5	3772	U
85	L5	3773	U
85	L5	3774	A
85	L5	3776	G
85	L5	3777	G
85	L5	3778	U
85	L5	3784	A
85	L5	3786	U
85	L5	3788	C
85	L5	3801	U
85	L5	3802	U
85	L5	3810	C
85	L5	3811	G
85	L5	3812	C
85	L5	3814	U
85	L5	3817	A
85	L5	3818	U
85	L5	3819	G
85	L5	3823	G
85	L5	3838	U
85	L5	3839	G
85	L5	3840	U
85	L5	3843	C
85	L5	3867	A
85	L5	3876	A
85	L5	3877	A
85	L5	3878	C
85	L5	3879	G
85	L5	3887	C
85	L5	3890	A
85	L5	3892	U
85	L5	3897	G
85	L5	3898	G
85	L5	3901	A
85	L5	3906	A
85	L5	3907	G
85	L5	3908	A
85	L5	3915	U
85	L5	3920	U
85	L5	3922	G
85	L5	3923	A
85	L5	3928	A

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Mol	Chain	Res	Type
85	L5	3938	G
85	L5	3939	G
85	L5	3943	A
85	L5	3944	G
85	L5	3947	A
85	L5	3948	C
85	L5	3949	A
85	L5	3950	U
85	L5	3951	G
85	L5	3953	G
85	L5	3955	G
85	L5	3956	G
85	L5	3957	U
85	L5	3959	U
85	L5	3960	A
85	L5	3962	A
85	L5	3963	A
85	L5	3964	U
85	L5	3965	A
85	L5	3966	A
85	L5	3967	G
85	L5	3968	U
85	L5	3969	G
85	L5	3970	G
85	L5	3972	A
85	L5	3973	G
85	L5	4039	G
85	L5	4041	C
85	L5	4042	G
85	L5	4043	G
85	L5	4044	U
85	L5	4046	A
85	L5	4047	A
85	L5	4048	A
85	L5	4049	U
85	L5	4050	A
85	L5	4051	C
85	L5	4052	C
85	L5	4053	A
85	L5	4054	C
85	L5	4055	U
85	L5	4056	A

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Mol	Chain	Res	Type
85	L5	4057	C
85	L5	4058	U
85	L5	4059	C
85	L5	4060	U
85	L5	4061	G
85	L5	4062	A
85	L5	4063	U
85	L5	4064	C
85	L5	4065	G
85	L5	4067	U
85	L5	4068	U
85	L5	4069	U
85	L5	4076	G
85	L5	4088	C
85	L5	4092	G
85	L5	4093	G
85	L5	4094	G
85	L5	4095	G
85	L5	4096	C
85	L5	4097	G
85	L5	4099	G
85	L5	4101	C
85	L5	4102	C
85	L5	4103	C
85	L5	4104	G
85	L5	4105	A
85	L5	4106	G
85	L5	4107	G
85	L5	4108	G
85	L5	4109	G
85	L5	4110	C
85	L5	4111	U
85	L5	4112	C
85	L5	4113	U
85	L5	4114	C
85	L5	4115	G
85	L5	4116	C
85	L5	4117	U
85	L5	4119	C
85	L5	4122	G
85	L5	4127	A
85	L5	4128	A

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Mol	Chain	Res	Type
85	L5	4133	C
85	L5	4134	C
85	L5	4140	C
85	L5	4141	G
85	L5	4142	C
85	L5	4143	G
85	L5	4144	C
85	L5	4146	G
85	L5	4149	C
85	L5	4160	C
85	L5	4162	C
85	L5	4163	U
85	L5	4168	G
85	L5	4170	A
85	L5	4183	G
85	L5	4184	G
85	L5	4191	G
85	L5	4196	G
85	L5	4197	G
85	L5	4201	G
85	L5	4203	A
85	L5	4212	A
85	L5	4222	G
85	L5	4225	G
85	L5	4229	U
85	L5	4232	U
85	L5	4233	A
85	L5	4234	A
85	L5	4241	C
85	L5	4251	A
85	L5	4254	G
85	L5	4255	A
85	L5	4265	U
85	L5	4268	A
85	L5	4273	A
85	L5	4280	A
85	L5	4281	A
85	L5	4289	U
85	L5	4290	U
85	L5	4297	G
85	L5	4304	A
85	L5	4305	G

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Mol	Chain	Res	Type
85	L5	4306	U
85	L5	4313	A
85	L5	4314	C
85	L5	4326	G
85	L5	4329	G
85	L5	4330	G
85	L5	4332	C
85	L5	4339	A
85	L5	4349	C
85	L5	4354	U
85	L5	4373	G
85	L5	4377	G
85	L5	4378	A
85	L5	4380	A
85	L5	4387	C
85	L5	4393	G
85	L5	4394	A
85	L5	4421	C
85	L5	4422	A
85	L5	4426	C
85	L5	4438	U
85	L5	4444	C
85	L5	4448	G
85	L5	4449	A
85	L5	4453	C
85	L5	4464	A
85	L5	4466	C
85	L5	4475	G
85	L5	4477	A
85	L5	4488	A
85	L5	4500	U
85	L5	4512	U
85	L5	4513	A
85	L5	4518	A
85	L5	4522	G
85	L5	4524	G
85	L5	4545	G
85	L5	4548	A
85	L5	4549	G
85	L5	4557	U
85	L5	4560	C
85	L5	4567	G

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Mol	Chain	Res	Type
85	L5	4572	U
85	L5	4573	G
85	L5	4575	G
85	L5	4581	G
85	L5	4584	A
85	L5	4589	A
85	L5	4590	A
85	L5	4600	G
85	L5	4601	U
85	L5	4617	G
85	L5	4627	U
85	L5	4635	A
85	L5	4636	U
85	L5	4637	G
85	L5	4652	G
85	L5	4656	A
85	L5	4659	G
85	L5	4670	C
85	L5	4672	A
85	L5	4687	A
85	L5	4694	G
85	L5	4695	C
85	L5	4700	A
85	L5	4707	A
85	L5	4708	A
85	L5	4709	U
85	L5	4719	G
85	L5	4721	G
85	L5	4732	G
85	L5	4733	C
85	L5	4734	A
85	L5	4740	G
85	L5	4741	C
85	L5	4742	G
85	L5	4745	G
85	L5	4747	C
85	L5	4750	G
85	L5	4754	G
85	L5	4757	C
85	L5	4759	C
85	L5	4761	G
85	L5	4764	A

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Mol	Chain	Res	Type
85	L5	4765	G
85	L5	4771	C
85	L5	4772	C
85	L5	4773	C
85	L5	4775	C
85	L5	4776	G
85	L5	4859	C
85	L5	4860	G
85	L5	4862	G
85	L5	4863	G
85	L5	4865	C
85	L5	4867	G
85	L5	4870	G
85	L5	4871	C
85	L5	4875	G
85	L5	4877	G
85	L5	4880	C
85	L5	4881	U
85	L5	4882	U
85	L5	4883	C
85	L5	4889	G
85	L5	4895	C
85	L5	4896	G
85	L5	4900	C
85	L5	4901	G
85	L5	4902	C
85	L5	4910	G
85	L5	4912	G
85	L5	4913	G
85	L5	4914	C
85	L5	4918	C
85	L5	4922	C
85	L5	4923	C
85	L5	4925	U
85	L5	4926	C
85	L5	4927	G
85	L5	4928	C
85	L5	4931	G
85	L5	4937	C
85	L5	4940	C
85	L5	4941	G
85	L5	4943	A

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Mol	Chain	Res	Type
85	L5	4944	C
85	L5	4947	U
85	L5	4951	G
85	L5	4960	G
85	L5	4976	U
85	L5	4985	U
85	L5	4988	U
85	L5	4989	U
85	L5	4990	C
85	L5	4991	U
85	L5	4995	U
85	L5	5006	U
85	L5	5009	G
85	L5	5014	A
85	L5	5017	G
85	L5	5020	G
85	L5	5024	C
85	L5	5026	U
85	L5	5027	C
85	L5	5028	G
85	L5	5029	C
85	L5	5030	U
85	L5	5034	A
85	L5	5041	G
85	L5	5050	C
85	L5	5054	C
85	L5	5055	G
85	L5	5061	A
85	L5	5062	G
85	L5	5069	U
20	L7	2	U
20	L7	4	U
20	L7	5	A
20	L7	22	A
20	L7	24	C
20	L7	33	U
20	L7	38	U
20	L7	53	U
20	L7	54	A
20	L7	63	C
20	L7	64	G
20	L7	91	C

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Mol	Chain	Res	Type
20	L7	97	G
20	L7	100	A
20	L7	111	C
21	L8	2	G
21	L8	34	U
21	L8	35	C
21	L8	48	A
21	L8	59	A
21	L8	62	A
21	L8	63	U
21	L8	80	A
21	L8	82	A
21	L8	83	C
21	L8	84	A
21	L8	85	U
21	L8	86	U
21	L8	87	G
21	L8	94	G
21	L8	103	A
21	L8	105	C
21	L8	110	U
21	L8	111	U
21	L8	112	G
21	L8	114	G
21	L8	123	U
21	L8	124	U
21	L8	125	C
21	L8	126	C
21	L8	127	U
21	L8	151	G
21	L8	156	U
79	S2	2	A
79	S2	4	C
79	S2	13	C
79	S2	25	A
79	S2	33	G
79	S2	41	G
79	S2	42	A
79	S2	44	U
79	S2	45	A
79	S2	46	A
79	S2	56	G

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Mol	Chain	Res	Type
79	S2	59	U
79	S2	62	G
79	S2	64	A
79	S2	65	C
79	S2	66	G
79	S2	67	C
79	S2	68	A
79	S2	72	C
79	S2	73	C
79	S2	74	G
79	S2	76	U
79	S2	92	A
79	S2	103	A
79	S2	113	G
79	S2	114	G
79	S2	115	U
79	S2	116	U
79	S2	126	G
79	S2	129	C
79	S2	130	G
79	S2	139	C
79	S2	143	U
79	S2	147	A
79	S2	149	A
79	S2	158	A
79	S2	160	U
79	S2	162	C
79	S2	163	U
79	S2	170	A
79	S2	175	A
79	S2	179	C
79	S2	182	C
79	S2	188	C
79	S2	190	G
79	S2	192	C
79	S2	196	C
79	S2	197	U
79	S2	198	U
79	S2	200	G
79	S2	202	G
79	S2	203	G
79	S2	204	G

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Mol	Chain	Res	Type
79	S2	206	G
79	S2	207	G
79	S2	208	G
79	S2	209	A
79	S2	211	G
79	S2	212	C
79	S2	213	G
79	S2	214	U
79	S2	220	U
79	S2	291	G
79	S2	292	A
79	S2	294	U
79	S2	295	C
79	S2	298	G
79	S2	301	A
79	S2	303	C
79	S2	305	U
79	S2	306	C
79	S2	307	G
79	S2	308	G
79	S2	309	G
79	S2	310	C
79	S2	311	C
79	S2	312	G
79	S2	318	A
79	S2	319	C
79	S2	322	C
79	S2	323	C
79	S2	324	C
79	S2	325	C
79	S2	326	C
79	S2	328	U
79	S2	329	G
79	S2	332	G
79	S2	338	G
79	S2	339	A
79	S2	340	C
79	S2	347	G
79	S2	360	A
79	S2	361	U
79	S2	362	C
79	S2	364	A

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Mol	Chain	Res	Type
79	S2	368	U
79	S2	369	C
79	S2	370	G
79	S2	374	G
79	S2	375	U
79	S2	377	G
79	S2	385	G
79	S2	386	C
79	S2	407	G
79	S2	408	A
79	S2	409	C
79	S2	421	G
79	S2	423	U
79	S2	426	A
79	S2	428	U
79	S2	437	G
79	S2	448	A
79	S2	449	A
79	S2	450	C
79	S2	452	G
79	S2	464	A
79	S2	465	A
79	S2	471	G
79	S2	472	C
79	S2	473	A
79	S2	474	G
79	S2	476	A
79	S2	478	G
79	S2	483	C
79	S2	485	A
79	S2	487	U
79	S2	488	U
79	S2	492	C
79	S2	493	A
79	S2	496	C
79	S2	502	C
79	S2	516	A
79	S2	517	C
79	S2	529	A
79	S2	530	U
79	S2	532	C
79	S2	537	C

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Mol	Chain	Res	Type
79	S2	538	U
79	S2	543	C
79	S2	544	G
79	S2	546	G
79	S2	547	G
79	S2	548	C
79	S2	550	C
79	S2	552	G
79	S2	553	U
79	S2	554	A
79	S2	555	A
79	S2	556	U
79	S2	557	U
79	S2	558	G
79	S2	559	G
79	S2	560	A
79	S2	563	G
79	S2	564	A
79	S2	566	U
79	S2	569	A
79	S2	576	A
79	S2	582	U
79	S2	583	A
79	S2	587	A
79	S2	589	G
79	S2	590	A
79	S2	591	U
79	S2	593	C
79	S2	594	A
79	S2	604	A
79	S2	606	G
79	S2	607	U
79	S2	608	C
79	S2	613	G
79	S2	614	C
79	S2	617	G
79	S2	622	C
79	S2	623	G
79	S2	628	A
79	S2	629	A
79	S2	631	U
79	S2	632	C

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Mol	Chain	Res	Type
79	S2	638	C
79	S2	643	A
79	S2	644	G
79	S2	660	C
79	S2	664	A
79	S2	668	A
79	S2	669	A
79	S2	671	A
79	S2	672	A
79	S2	673	G
79	S2	683	G
79	S2	684	G
79	S2	688	U
79	S2	689	U
79	S2	692	G
79	S2	693	A
79	S2	695	C
79	S2	696	G
79	S2	697	G
79	S2	698	G
79	S2	732	U
79	S2	733	C
79	S2	734	C
79	S2	736	C
79	S2	738	C
79	S2	749	U
79	S2	750	C
79	S2	751	G
79	S2	752	G
79	S2	753	C
79	S2	788	G
79	S2	789	G
79	S2	791	C
79	S2	792	C
79	S2	794	A
79	S2	798	G
79	S2	799	U
79	S2	809	A
79	S2	821	G
79	S2	822	U
79	S2	823	U
79	S2	824	C

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Mol	Chain	Res	Type
79	S2	830	A
79	S2	833	C
79	S2	834	C
79	S2	835	C
79	S2	836	G
79	S2	837	A
79	S2	838	G
79	S2	839	C
79	S2	842	C
79	S2	847	A
79	S2	859	G
79	S2	861	A
79	S2	869	A
79	S2	870	A
79	S2	873	G
79	S2	874	G
79	S2	877	C
79	S2	878	G
79	S2	882	U
79	S2	888	U
79	S2	889	U
79	S2	890	U
79	S2	891	G
79	S2	894	G
79	S2	896	U
79	S2	897	U
79	S2	898	U
79	S2	899	U
79	S2	900	C
79	S2	901	G
79	S2	903	A
79	S2	905	C
79	S2	913	A
79	S2	917	U
79	S2	919	A
79	S2	920	A
79	S2	933	G
79	S2	934	G
79	S2	949	G
79	S2	954	U
79	S2	955	A
79	S2	956	G

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Mol	Chain	Res	Type
79	S2	963	A
79	S2	969	U
79	S2	971	G
79	S2	972	A
79	S2	978	G
79	S2	984	C
79	S2	988	C
79	S2	989	C
79	S2	990	A
79	S2	992	A
79	S2	999	G
79	S2	1001	A
79	S2	1002	U
79	S2	1008	A
79	S2	1017	U
79	S2	1023	A
79	S2	1027	A
79	S2	1045	U
79	S2	1047	C
79	S2	1060	A
79	S2	1061	U
79	S2	1062	A
79	S2	1067	C
79	S2	1083	A
79	S2	1085	C
79	S2	1088	U
79	S2	1107	G
79	S2	1108	G
79	S2	1109	C
79	S2	1110	G
79	S2	1113	A
79	S2	1114	U
79	S2	1115	U
79	S2	1116	C
79	S2	1118	C
79	S2	1119	A
79	S2	1121	G
79	S2	1126	G
79	S2	1133	A
79	S2	1138	C
79	S2	1139	C
79	S2	1148	A

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Mol	Chain	Res	Type
79	S2	1153	C
79	S2	1154	U
79	S2	1155	U
79	S2	1162	C
79	S2	1170	A
79	S2	1195	A
79	S2	1200	A
79	S2	1207	G
79	S2	1208	A
79	S2	1210	G
79	S2	1215	C
79	S2	1216	C
79	S2	1217	A
79	S2	1220	A
79	S2	1224	G
79	S2	1227	G
79	S2	1237	C
79	S2	1240	A
79	S2	1242	U
79	S2	1243	U
79	S2	1251	A
79	S2	1253	A
79	S2	1256	G
79	S2	1257	G
79	S2	1259	A
79	S2	1264	C
79	S2	1274	G
79	S2	1275	G
79	S2	1282	A
79	S2	1283	C
79	S2	1284	A
79	S2	1286	G
79	S2	1287	A
79	S2	1290	G
79	S2	1294	G
79	S2	1295	A
79	S2	1301	A
79	S2	1302	G
79	S2	1303	C
79	S2	1306	U
79	S2	1308	U
79	S2	1322	G

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Mol	Chain	Res	Type
79	S2	1333	U
79	S2	1342	U
79	S2	1351	G
79	S2	1352	G
79	S2	1358	U
79	S2	1363	C
79	S2	1364	U
79	S2	1371	U
79	S2	1372	U
79	S2	1376	A
79	S2	1378	A
79	S2	1398	G
79	S2	1401	A
79	S2	1402	A
79	S2	1406	G
79	S2	1407	U
79	S2	1408	U
79	S2	1411	G
79	S2	1414	A
79	S2	1415	C
79	S2	1419	C
79	S2	1420	G
79	S2	1421	A
79	S2	1422	G
79	S2	1423	C
79	S2	1426	U
79	S2	1433	C
79	S2	1434	C
79	S2	1435	C
79	S2	1436	C
79	S2	1438	A
79	S2	1442	U
79	S2	1449	G
79	S2	1452	A
79	S2	1454	A
79	S2	1463	U
79	S2	1466	G
79	S2	1474	A
79	S2	1476	A
79	S2	1478	U
79	S2	1480	A
79	S2	1484	A

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Mol	Chain	Res	Type
79	S2	1489	A
79	S2	1490	G
79	S2	1494	U
79	S2	1495	G
79	S2	1497	G
79	S2	1498	A
79	S2	1501	C
79	S2	1507	G
79	S2	1508	A
79	S2	1520	G
79	S2	1521	C
79	S2	1522	A
79	S2	1533	A
79	S2	1535	U
79	S2	1536	G
79	S2	1537	A
79	S2	1544	C
79	S2	1552	G
79	S2	1556	A
79	S2	1570	G
79	S2	1572	C
79	S2	1574	C
79	S2	1579	A
79	S2	1580	A
79	S2	1581	C
79	S2	1584	G
79	S2	1585	U
79	S2	1586	U
79	S2	1587	G
79	S2	1588	A
79	S2	1594	A
79	S2	1598	G
79	S2	1599	U
79	S2	1600	G
79	S2	1601	A
79	S2	1604	G
79	S2	1606	G
79	S2	1621	U
79	S2	1623	A
79	S2	1630	A
79	S2	1633	A
79	S2	1634	A

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Mol	Chain	Res	Type
79	S2	1637	A
79	S2	1638	G
79	S2	1639	G
79	S2	1640	A
79	S2	1646	C
79	S2	1648	G
79	S2	1654	G
79	S2	1657	G
79	S2	1663	A
79	S2	1665	G
79	S2	1680	G
79	S2	1683	C
79	S2	1694	U
79	S2	1696	C
79	S2	1699	A
79	S2	1706	G
79	S2	1712	A
79	S2	1715	A
79	S2	1722	G
79	S2	1726	G
79	S2	1729	U
79	S2	1742	C
79	S2	1743	G
79	S2	1744	G
79	S2	1745	A
79	S2	1752	C
79	S2	1753	C
79	S2	1754	G
79	S2	1755	C
79	S2	1756	C
79	S2	1757	G
79	S2	1758	G
79	S2	1759	G
79	S2	1761	U
79	S2	1772	C
79	S2	1773	C
79	S2	1774	C
79	S2	1777	G
79	S2	1780	G
79	S2	1782	G
79	S2	1783	C
79	S2	1784	G

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Mol	Chain	Res	Type
79	S2	1785	C
79	S2	1787	G
79	S2	1798	C
79	S2	1809	A
79	S2	1810	U
79	S2	1812	U
79	S2	1813	A
79	S2	1819	A
79	S2	1820	G
79	S2	1822	A
79	S2	1823	A
79	S2	1824	A
79	S2	1829	G
79	S2	1835	A
79	S2	1838	U
79	S2	1849	G
79	S2	1851	A
79	S2	1852	C
79	S2	1861	G
79	S2	1862	G
79	S2	1863	A
79	S2	1864	U
79	S2	1865	C
81	AP	7	G
81	AP	8	U
81	AP	9	A
81	AP	10	G
81	AP	11	U
81	AP	13	U
81	AP	14	A
81	AP	20(A)	U
81	AP	21	A
81	AP	25	C
81	AP	26	G
81	AP	47	U
81	AP	48	C
81	AP	49	C
81	AP	55	U
81	AP	56	C
81	AP	58	A
81	AP	61	C
81	AP	63	G

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Mol	Chain	Res	Type
81	AP	64	G
81	AP	65	G
81	AP	67	G
81	AP	69	A
81	AP	70	A
81	AP	71	A
82	PE	4	C
82	PE	5	G
82	PE	7	A
82	PE	8	U
82	PE	9	A
82	PE	10	G
82	PE	11	C
82	PE	13	C
82	PE	15	G
82	PE	19	G
82	PE	20	U
82	PE	21	A
82	PE	25	C
82	PE	26	A
82	PE	27	U
82	PE	31	A
82	PE	32	C
82	PE	33	U
82	PE	34	U
82	PE	35	U
82	PE	36	U
82	PE	38	A
82	PE	46	G
82	PE	47	U
82	PE	48	C
82	PE	49	C
82	PE	50	A
82	PE	52	G
82	PE	54	U
82	PE	55	U
82	PE	56	C
82	PE	58	A
82	PE	60	U
82	PE	61	C
82	PE	64	U
82	PE	65	G

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Mol	Chain	Res	Type
82	PE	67	U
82	PE	69	G
82	PE	70	G
82	PE	76	A

All (50) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
85	L5	265	C
85	L5	406	C
85	L5	493	G
85	L5	509	A
85	L5	912	G
85	L5	914	U
85	L5	935	A
85	L5	1082	C
85	L5	1324	A
85	L5	1633	G
85	L5	1977	C
85	L5	2033	A
85	L5	2416	G
85	L5	2485	U
85	L5	2675	G
85	L5	2760	G
85	L5	2786	C
85	L5	3614	G
85	L5	3673	C
85	L5	3948	C
85	L5	4055	U
85	L5	4061	G
85	L5	4101	C
85	L5	4102	C
85	L5	4106	G
85	L5	4107	G
85	L5	4108	G
85	L5	4110	C
85	L5	4111	U
85	L5	4112	C
85	L5	4114	C
85	L5	4600	G
85	L5	4699	U
85	L5	4913	G

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Mol	Chain	Res	Type
79	S2	291	G
79	S2	307	G
79	S2	420	G
79	S2	531	A
79	S2	557	U
79	S2	563	G
79	S2	688	U
79	S2	1355	C
79	S2	1434	C
79	S2	1521	C
79	S2	1693	G
79	S2	1781	A
81	AP	9	A
82	PE	18	U
82	PE	33	U
82	PE	34	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](#)

Of 522 ligands modelled in this entry, 522 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
85	L5	10
85	l5	10
79	s2	7
79	S2	5
84	Lt	1
84	lt	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	S2	753:C	O3'	785:C	P	27.80
1	s2	753:C	O3'	785:C	P	27.36
1	L5	2910:G	O3'	3584:C	P	20.89
1	l5	2910:G	O3'	3584:C	P	20.75
1	l5	760:G	O3'	903:C	P	17.11
1	L5	760:G	O3'	903:C	P	16.89
1	l5	519:C	O3'	642:G	P	16.44
1	L5	519:C	O3'	642:G	P	16.09
1	l5	4776:G	O3'	4858:C	P	16.06
1	S2	698:G	O3'	730:C	P	16.04
1	L5	4776:G	O3'	4858:C	P	15.73
1	s2	698:G	O3'	730:C	P	15.29
1	l5	996:G	O3'	1047:C	P	14.03
1	L5	996:G	O3'	1047:C	P	13.71
1	S2	739:C	O3'	746:C	P	13.70
1	l5	2112:G	O3'	2249:C	P	13.56
1	L5	2112:G	O3'	2249:C	P	13.45
1	s2	739:C	O3'	746:C	P	13.16
1	l5	1222:A	O3'	1234:G	P	11.54
1	L5	1222:A	O3'	1234:G	P	11.34
1	Lt	87:GLU	C	104:ILE	N	11.05
1	lt	87:GLU	C	104:ILE	N	9.67
1	s2	553:U	O3'	554:A	P	9.47
1	l5	1051:G	O3'	1064:G	P	8.75
1	s2	530:U	O3'	531:A	P	8.59

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	L5	1051:G	O3'	1064:G	P	8.51
1	s2	225:G	O3'	287:U	P	7.98
1	S2	225:G	O3'	287:U	P	6.68
1	L5	1100:U	O3'	1167:C	P	6.64
1	l5	1100:U	O3'	1167:C	P	6.41
1	L5	1709:C	O3'	1714:C	P	5.51
1	l5	1709:C	O3'	1714:C	P	5.38
1	s2	1210:G	O3'	1211:G	P	3.70
1	S2	1210:G	O3'	1211:G	P	3.50

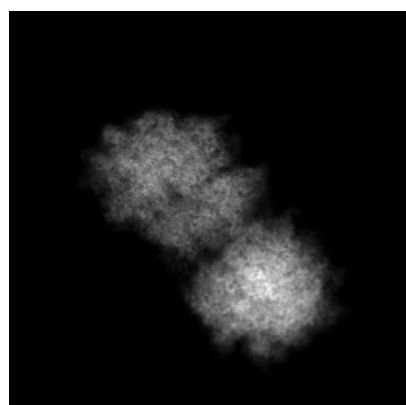
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44050. These allow visual inspection of the internal detail of the map and identification of artifacts.

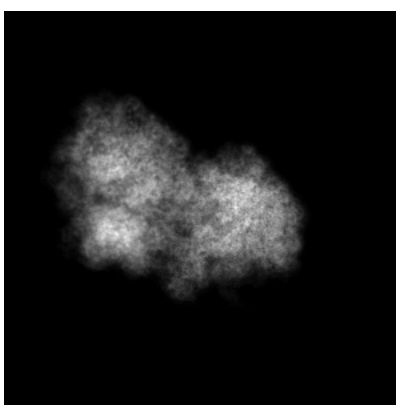
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

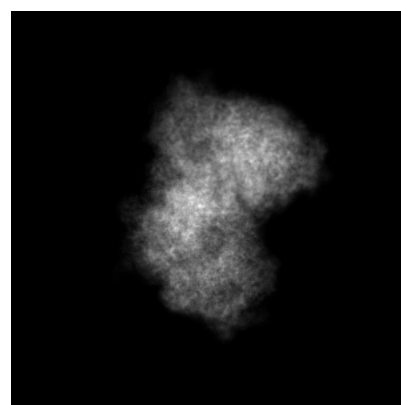
6.1.1 Primary map



X



Y

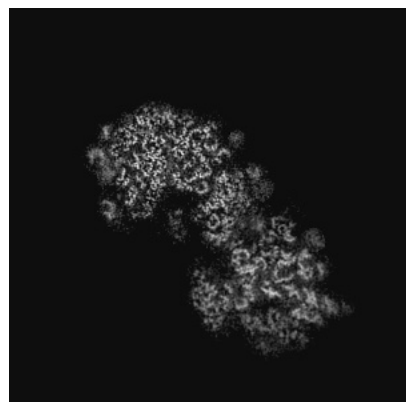


Z

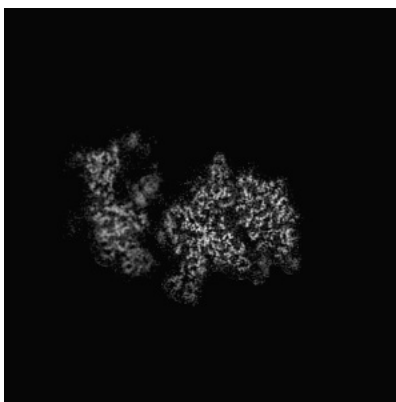
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

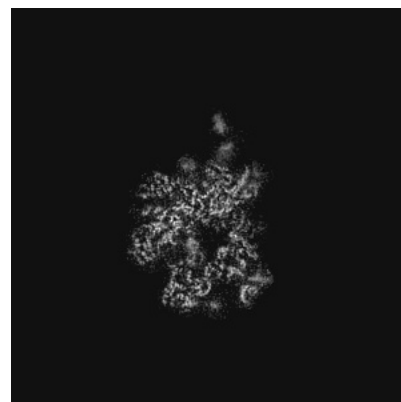
6.2.1 Primary map



X Index: 300



Y Index: 300

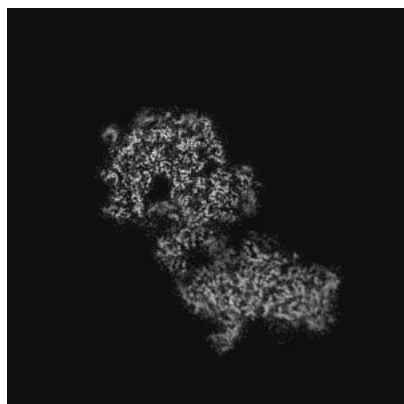


Z Index: 300

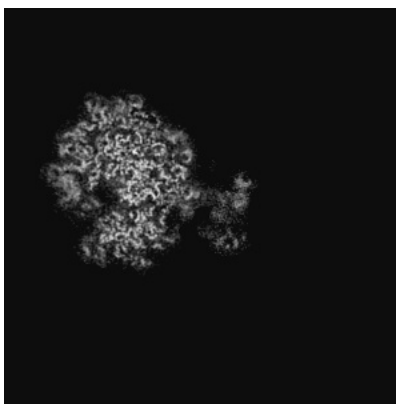
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

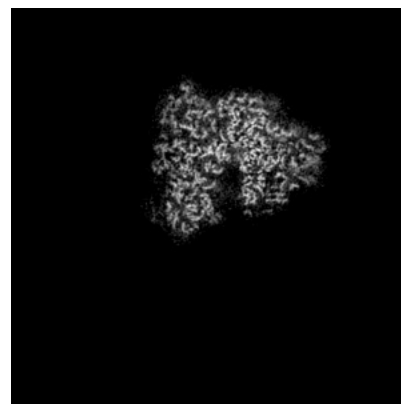
6.3.1 Primary map



X Index: 266



Y Index: 375

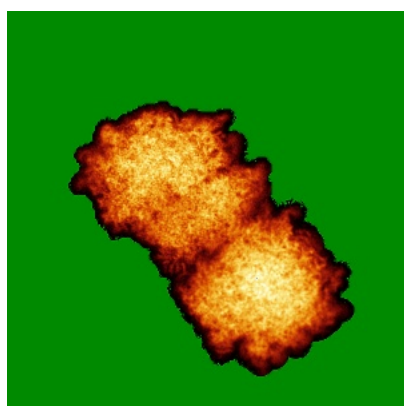


Z Index: 176

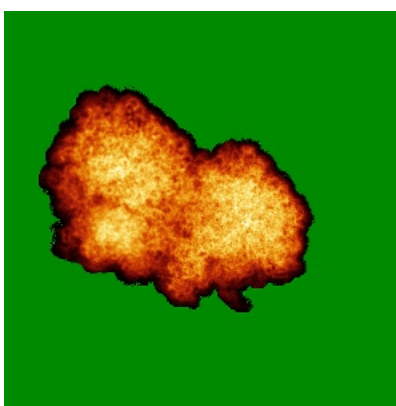
The images above show the largest variance slices of the map in three orthogonal directions.

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

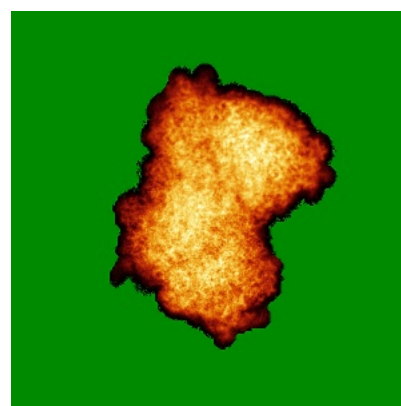
6.4.1 Primary map



X



Y

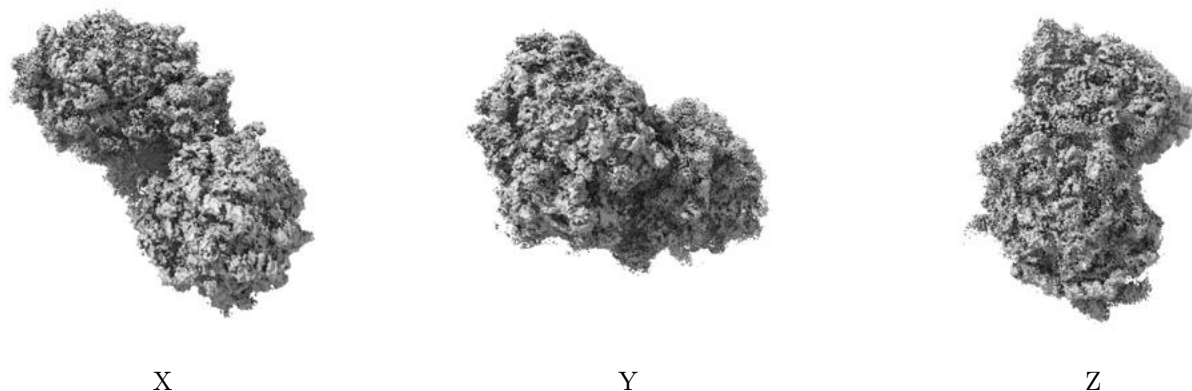


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.096. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

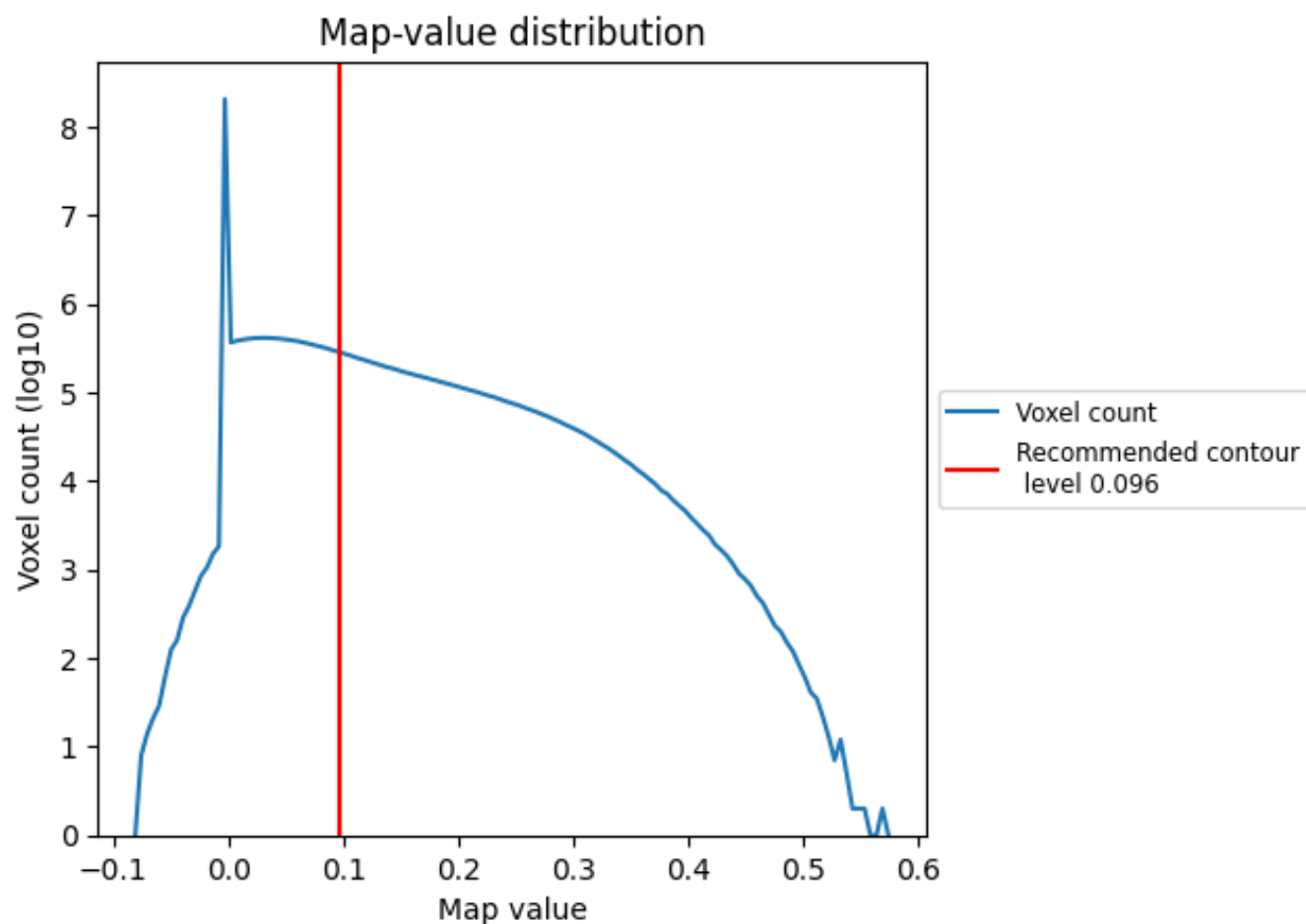
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

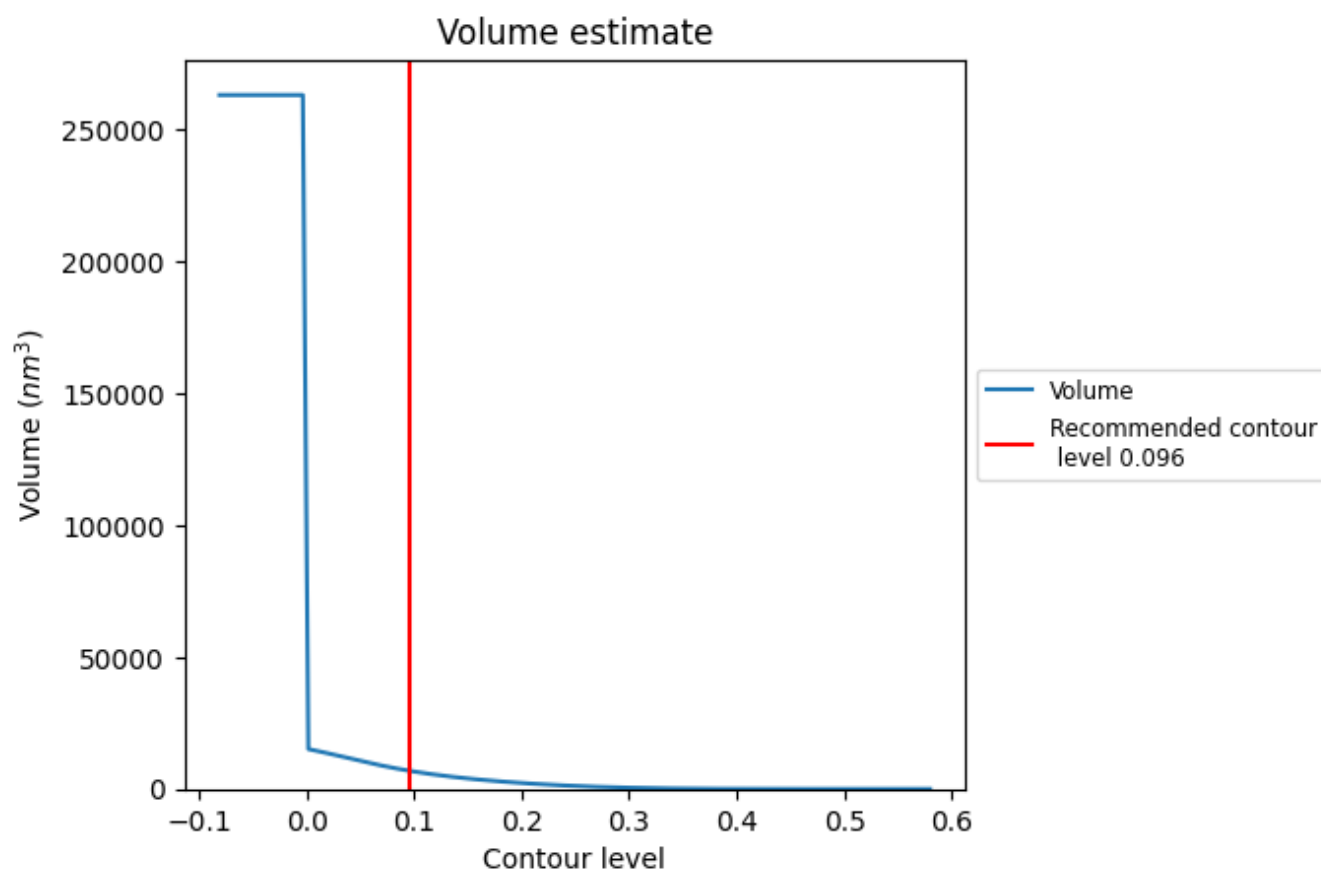
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

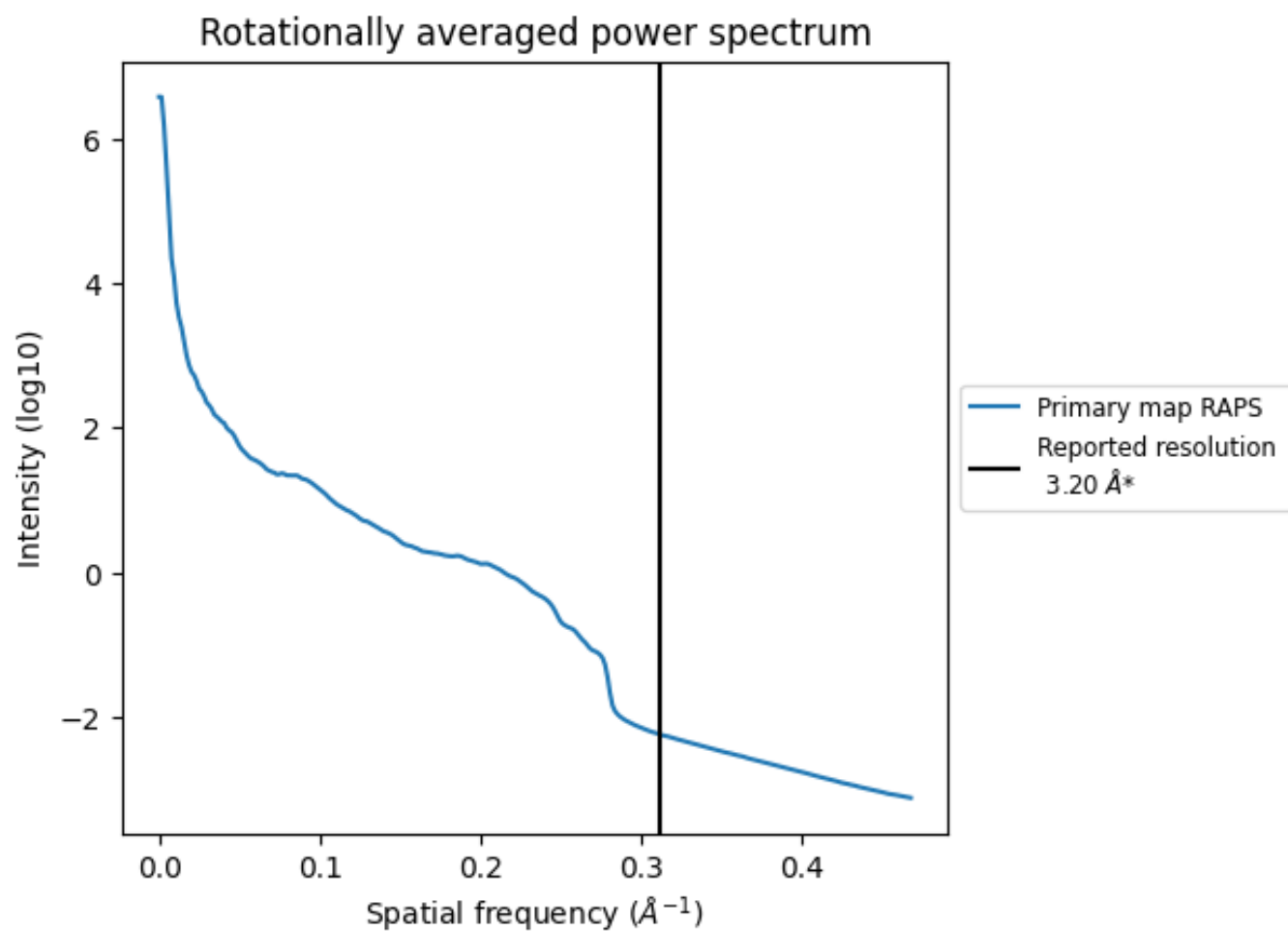
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6868 nm^3 ; this corresponds to an approximate mass of 6204 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

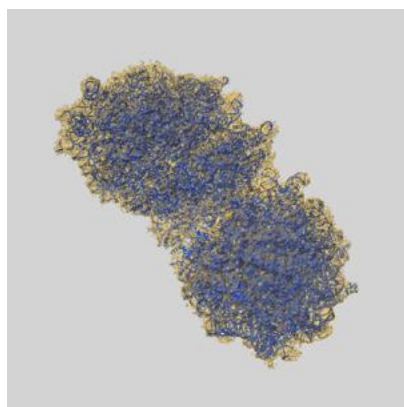
8 Fourier-Shell correlation

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

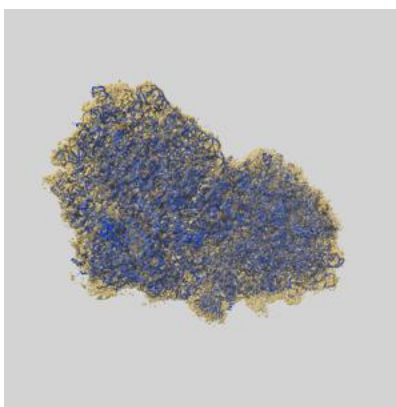
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-44050 and PDB model 9B0Q. Per-residue inclusion information can be found in section [3](#) on page [29](#).

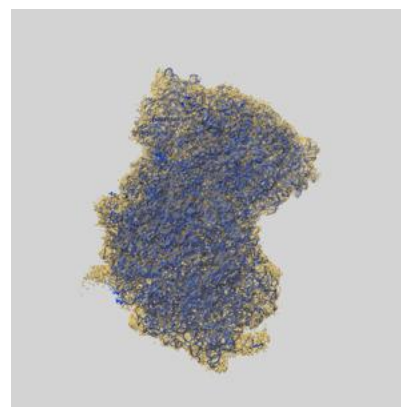
9.1 Map-model overlay [i](#)



X



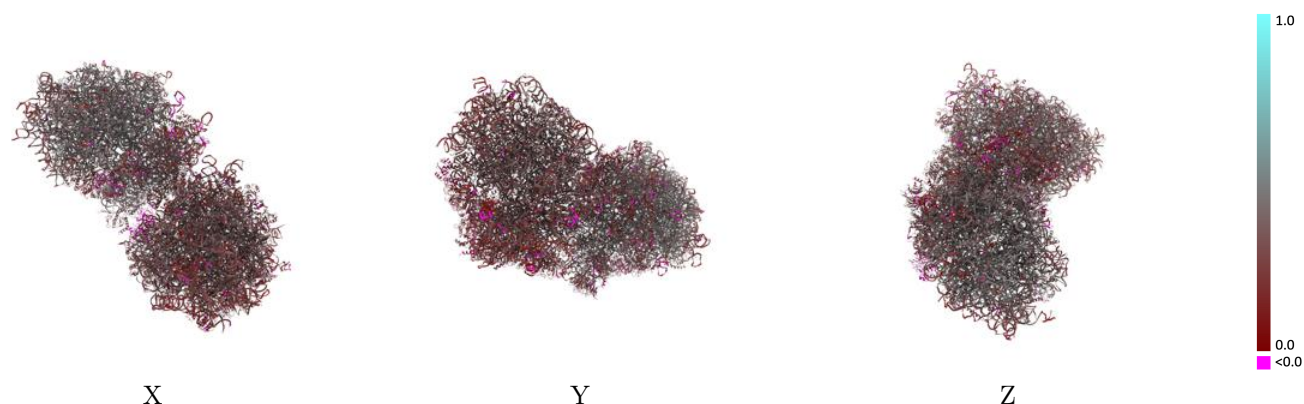
Y



Z

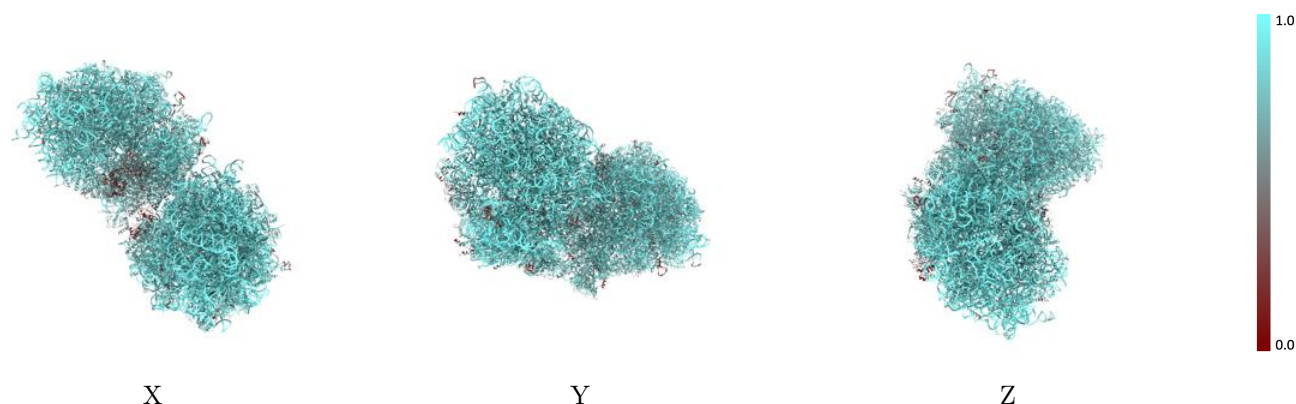
The images above show the 3D surface view of the map at the recommended contour level 0.096 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



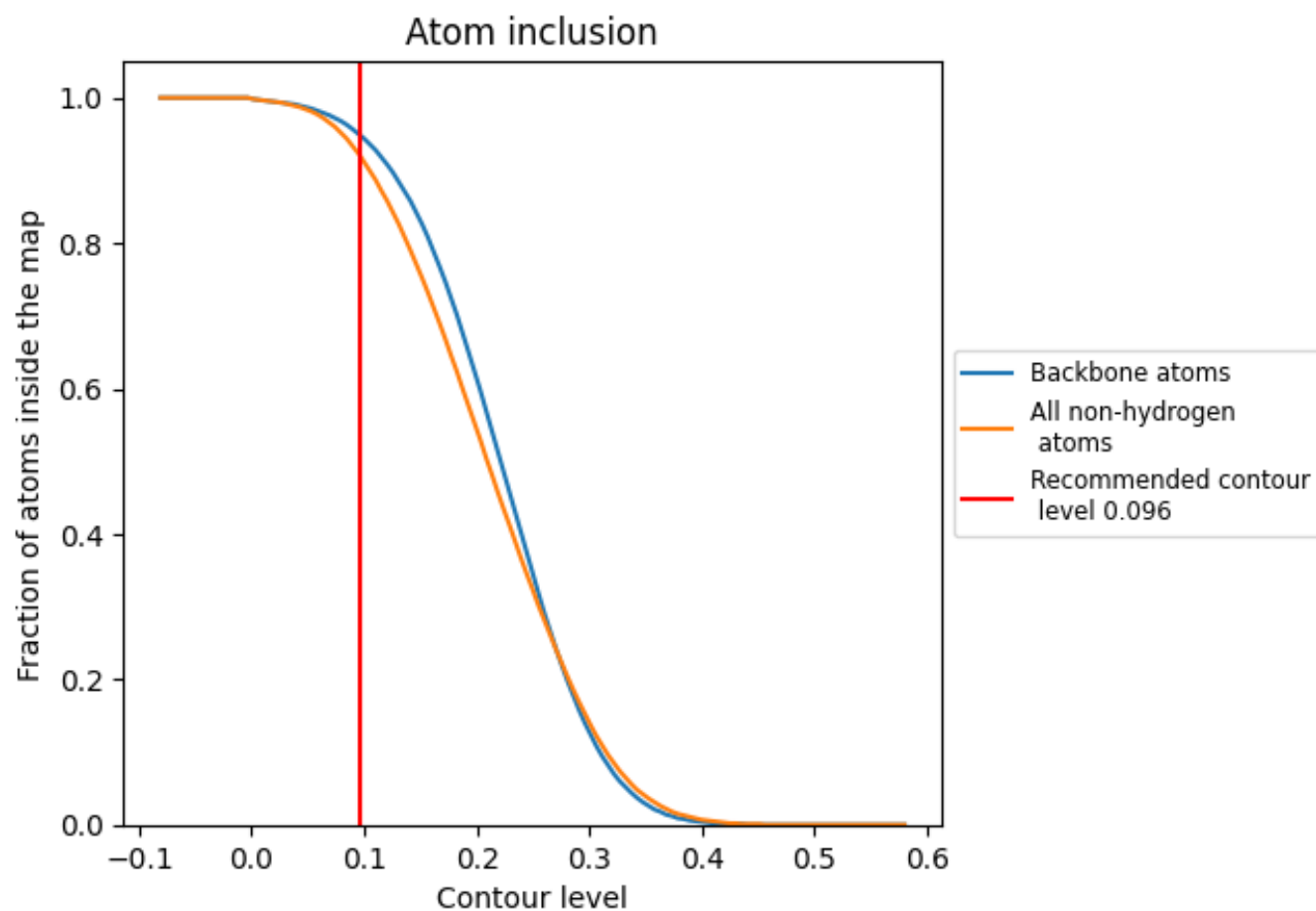
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.096).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 92% 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 (0.096) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9210	 0.3380
AP	 0.9890	 0.2490
CB	 0.7800	 0.2340
CH	 0.8100	 0.2630
L5	 0.9770	 0.3260
L7	 0.9940	 0.3480
L8	 0.9890	 0.3380
LA	 0.9430	 0.3620
LB	 0.9500	 0.3260
LC	 0.9170	 0.3350
LD	 0.8620	 0.3050
LE	 0.8910	 0.2770
LF	 0.9420	 0.3060
LG	 0.8550	 0.3020
LH	 0.9460	 0.2980
LI	 0.9600	 0.3440
LJ	 0.8400	 0.2860
LL	 0.8590	 0.3240
LM	 0.9390	 0.2950
LN	 0.9520	 0.3440
LO	 0.9490	 0.3060
LP	 0.9710	 0.3410
LQ	 0.9360	 0.3500
LR	 0.8780	 0.2920
LS	 0.9630	 0.3360
LT	 0.9420	 0.3450
LU	 0.8790	 0.2710
LV	 0.9800	 0.3660
LW	 0.8630	 0.2550
LX	 0.9060	 0.3360
LY	 0.9390	 0.3400
LZ	 0.8370	 0.3300
La	 0.9270	 0.3560
Lb	 0.8700	 0.3000
Lc	 0.8180	 0.3150























































































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Chain	Atom inclusion	Q-score
Ld	 0.9580	 0.3460
Le	 0.9750	 0.3560
Lf	 0.9830	 0.3420
Lg	 0.9210	 0.3380
Lh	 0.8980	 0.3140
Li	 0.8760	 0.3220
Lj	 0.9760	 0.3360
Lk	 0.8350	 0.3020
Ll	 0.9860	 0.3620
Lm	 0.9660	 0.3330
Ln	 1.0000	 0.3110
Lo	 0.9250	 0.3720
Lp	 0.9450	 0.3520
Lr	 0.9200	 0.3330
Ls	 0.6150	 0.1490
Lt	 0.6780	 0.1520
Lz	 0.2280	 0.0230
PE	 0.9750	 0.2490
S2	 0.9770	 0.3130
SA	 0.7830	 0.2940
SB	 0.8680	 0.3190
SC	 0.8790	 0.3120
SD	 0.8310	 0.2850
SE	 0.9030	 0.2810
SF	 0.8540	 0.2690
SG	 0.8750	 0.2410
SH	 0.7460	 0.2620
SI	 0.8770	 0.2800
SJ	 0.8770	 0.2650
SK	 0.8680	 0.2670
SL	 0.8780	 0.3170
SM	 0.6840	 0.2260
SN	 0.8540	 0.3050
SO	 0.8680	 0.3130
SP	 0.9020	 0.2970
SQ	 0.8740	 0.2650
SR	 0.7730	 0.2640
SS	 0.8410	 0.2900
ST	 0.8760	 0.2640
SU	 0.8450	 0.2660
SV	 0.8390	 0.2970
SW	 0.9210	 0.3140





















































































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Chain	Atom inclusion	Q-score
SX	 0.9570	 0.3270
SY	 0.8950	 0.2280
SZ	 0.7920	 0.2820
Sa	 0.9240	 0.3510
Sb	 0.7920	 0.3030
Sc	 0.7690	 0.2130
Sd	 0.9910	 0.2900
Se	 0.9280	 0.2890
Sf	 0.7800	 0.2520
Sg	 0.7610	 0.2190
aP	 0.9410	 0.2670
cB	 0.4910	 0.2650
cH	 0.7590	 0.2850
l5	 0.9720	 0.3850
l7	 0.9900	 0.4140
l8	 0.9840	 0.3920
lA	 0.9490	 0.4410
lB	 0.9010	 0.4250
lC	 0.9370	 0.4300
lD	 0.9060	 0.3910
lE	 0.8760	 0.3780
lF	 0.9490	 0.4230
lG	 0.8750	 0.3660
lH	 0.8760	 0.4080
lI	 0.9190	 0.4380
lJ	 0.8060	 0.3410
lL	 0.9140	 0.4000
lM	 0.9010	 0.4050
lN	 0.9620	 0.4360
lO	 0.9270	 0.4220
lP	 0.9510	 0.4590
lQ	 0.9600	 0.4480
lR	 0.8850	 0.3770
lS	 0.9360	 0.4390
lT	 0.9530	 0.4330
lU	 0.8650	 0.3410
lV	 0.9000	 0.4350
lW	 0.8700	 0.3470
lX	 0.9200	 0.4110
lY	 0.9520	 0.4120
lZ	 0.8750	 0.3880
la	 0.9630	 0.4400

























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Chain	Atom inclusion	Q-score
lb	 0.9070	 0.3700
lc	 0.8720	 0.3740
ld	 0.9290	 0.4230
le	 0.9600	 0.4530
lf	 0.9570	 0.4440
lg	 0.9400	 0.4310
lh	 0.9380	 0.3960
li	 0.9010	 0.3950
lj	 0.9910	 0.4490
lk	 0.8740	 0.3870
ll	 0.9740	 0.4330
lm	 0.9210	 0.4170
ln	 0.9670	 0.4230
lo	 0.9200	 0.4420
lp	 0.9300	 0.4150
lr	 0.9490	 0.4310
ls	 0.5370	 0.1750
lt	 0.4830	 0.1610
lz	 0.2500	 0.0520
pE	 0.9460	 0.2340
s2	 0.9720	 0.3540
sA	 0.8050	 0.3430
sB	 0.8870	 0.3690
sC	 0.8850	 0.3830
sD	 0.8530	 0.3680
sE	 0.9170	 0.3530
sF	 0.8590	 0.3310
sG	 0.8450	 0.2910
sH	 0.7730	 0.3100
sI	 0.8830	 0.3390
sJ	 0.8870	 0.3260
sK	 0.8550	 0.3460
sL	 0.8900	 0.3770
sM	 0.6750	 0.2310
sN	 0.9180	 0.3770
sO	 0.8750	 0.3800
sP	 0.8440	 0.3730
sQ	 0.8870	 0.3290
sR	 0.6810	 0.1450
sS	 0.8760	 0.3500
sT	 0.8650	 0.3330
sU	 0.8590	 0.3370

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Chain	Atom inclusion	Q-score
sV	 0.8180	 0.3410
sW	 0.9360	 0.4060
sX	 0.8980	 0.3890
sY	 0.8750	 0.2830
sZ	 0.8340	 0.3240
sa	 0.9020	 0.3880
sb	 0.8700	 0.3570
sc	 0.7570	 0.2720
sd	 0.9410	 0.3860
se	 0.7370	 0.2490
sf	 0.7320	 0.2540
sg	 0.7940	 0.2850