



Full wwPDB EM Validation Report ⓘ

Dec 11, 2022 – 08:33 am GMT

PDB ID : 6RXY
EMDB ID : EMD-10055
Title : Cryo-EM structure of the 90S pre-ribosome (Kre33-Noc4) from *Chaetomium thermophilum*, state a
Authors : Cheng, J.; Kellner, N.; Griesel, S.; Berninghausen, O.; Beckmann, R.; Hurt, E.
Deposited on : 2019-06-10
Resolution : 4.70 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:

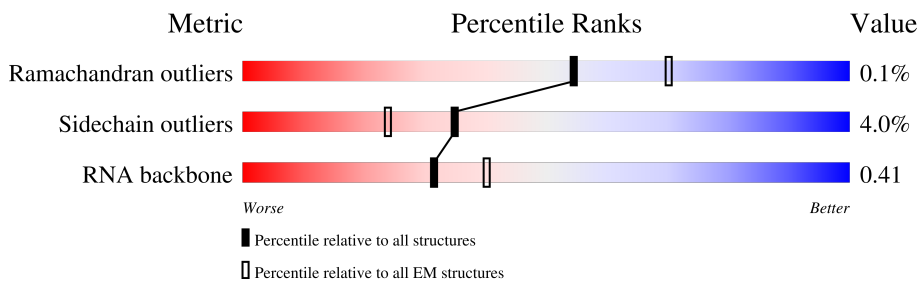
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

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 4.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	UA	904	
2	UB	907	
3	UC	648	
4	UD	884	
5	UF	414	
6	UG	558	
7	UJ	1802	
8	UK	270	





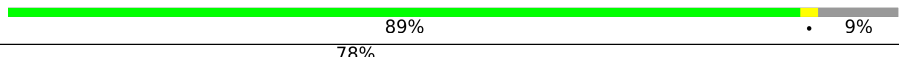

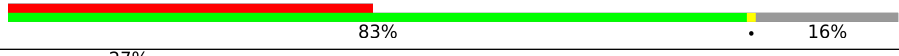
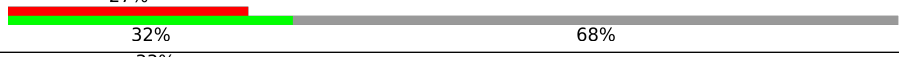


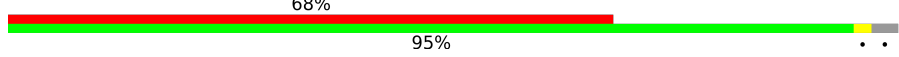


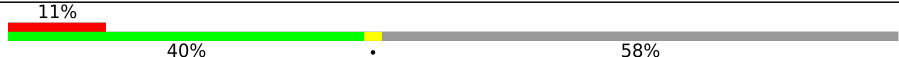
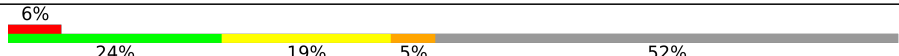

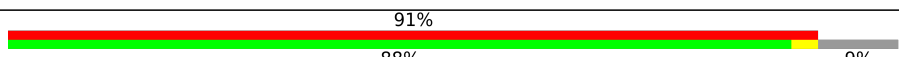
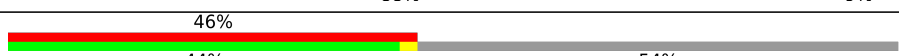

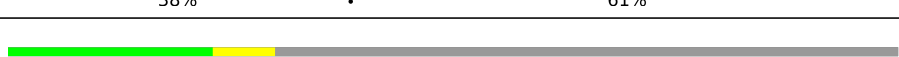



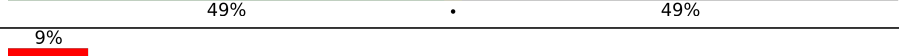
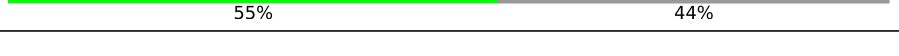
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Mol	Chain	Length	Quality of chain
9	UL	962	
10	UM	912	
11	UN	938	
12	UO	557	
13	UQ	960	
14	UR	618	
15	UU	1049	
16	UX	193	
17	UZ	391	
18	CA	313	
18	CB	313	
19	CC	523	
20	CD	582	
21	CE	127	
21	CF	127	
22	CG	630	
23	CH	411	
24	CI	1163	
25	CJ	183	
26	CK	297	
27	CL	785	
28	CM	446	
29	CN	252	
29	CO	252	
30	CP	322	

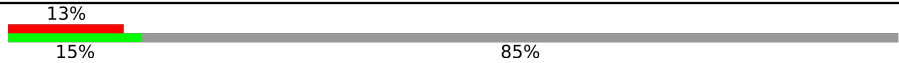
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Mol	Chain	Length	Quality of chain
31	CQ	259	
32	CR	1073	
32	CS	1073	
33	CT	203	
34	Cc	212	
35	Ce	203	
36	Cg	190	
37	Ch	151	
38	Ci	150	
39	Cj	143	
40	Cm	130	
41	Cn	145	
42	Cp	68	
43	CU	311	
44	C1	2323	
45	C2	230	
46	UV	1171	
47	CV	322	
48	UH	930	
49	UE	410	
49	UI	410	
50	US	549	
51	Cl	156	
52	CX	480	
53	UP	364	

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Mol	Chain	Length	Quality of chain
54	Cz	1796	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a red segment on the left labeled '13%', a green segment in the middle labeled '15%', and a grey segment on the right labeled '85%'. The total length of the bar represents 100%.</p>

2 Entry composition [i](#)

There are 55 unique types of molecules in this entry. The entry contains 180242 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 Periodic tryptophan protein 2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	UA	839	6366	4101	1136	1105	24	0	0

- Molecule 2 is a protein called Utp2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	UB	512	4079	2576	781	711	11	0	0

- Molecule 3 is a protein called Utp3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	UC	74	588	371	120	97	0	0

- Molecule 4 is a protein called Utp4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	UD	772	6071	3851	1093	1103	24	0	0

- Molecule 5 is a protein called Utp6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	UF	331	2591	1674	504	399	14	0	0

- Molecule 6 is a protein called Utp7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	UG	448	3444	2197	646	590	11	0	0

- Molecule 7 is a protein called Utp10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	UJ	808	6180	3965	1077	1115	23	0	0

- Molecule 8 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	UK	217	1687	1062	351	269	5	0	0

- Molecule 9 is a protein called Utp12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	UL	785	6175	3940	1088	1130	17	0	0

- Molecule 10 is a protein called Utp13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	UM	679	5273	3351	924	986	12	0	0

- Molecule 11 is a protein called Utp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	UN	154	1209	770	228	206	5	0	0

- Molecule 12 is a protein called Utp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	UO	504	3819	2422	699	684	14	0	0

- Molecule 13 is a protein called Utp17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	UQ	789	6008	3831	1037	1119	21	0	0

- Molecule 14 is a protein called Utp18.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	UR	447	Total	C	N	O	S	0	0
			3491	2209	656	616	10		

- Molecule 15 is a protein called Utp21.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	UU	902	Total	C	N	O	S	0	0
			6734	4336	1236	1136	26		

- Molecule 16 is a protein called Utp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	UX	190	Total	C	N	O	S	0	0
			1470	932	282	246	10		

- Molecule 17 is a protein called Utp30.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	UZ	235	Total	C	N	O	S	0	0
			1815	1184	330	298	3		

- Molecule 18 is a protein called Nop1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	CA	242	Total	C	N	O	S	0	0
			1778	1149	327	293	9		
18	CB	237	Total	C	N	O	S	0	0
			1816	1154	318	335	9		

- Molecule 19 is a protein called Nop56.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	CC	387	Total	C	N	O	S	0	0
			2866	1836	527	492	11		

- Molecule 20 is a protein called Nop58.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	CD	420	Total	C	N	O	S	0	0
			3150	2023	560	557	10		

- Molecule 21 is a protein called Snu13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CE	121	Total	C	N	O	S	0	0
			879	557	165	154	3		
21	CF	120	Total	C	N	O	S	0	0
			864	550	161	150	3		

- Molecule 22 is a protein called Rrp9.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	CG	378	Total	C	N	O	S	0	0
			2922	1865	527	517	13		

- Molecule 23 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	CH	389	Total	C	N	O	S	0	0
			2888	1827	526	525	10		

- Molecule 24 is a protein called Bms1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	CI	822	Total	C	N	O	S	0	0
			6486	4169	1213	1077	27		

- Molecule 25 is a protein called Imp3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	CJ	179	Total	C	N	O	S	0	0
			1434	918	283	226	7		

- Molecule 26 is a protein called Imp4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	CK	297	Total	C	N	O	S	0	0
			2329	1476	445	400	8		

- Molecule 27 is a protein called Mpp10.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	CL	231	Total	C	N	O	S	0	0
			1786	1114	339	327	6		

- Molecule 28 is a protein called Sof1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	CM	445	3501	2195	672	619	15	0	0

- Molecule 29 is a protein called Emg1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	CN	226	1762	1119	306	327	10	0	0
29	CO	215	1683	1067	293	313	10	0	0

- Molecule 30 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	CP	187	1504	961	269	265	9	0	0

- Molecule 31 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	CQ	175	1361	862	250	242	7	0	0

- Molecule 32 is a protein called Kre33.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	CR	760	5989	3851	1024	1087	27	0	0
32	CS	760	5989	3851	1024	1087	27	0	0

- Molecule 33 is a protein called Fcf2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	CT	131	1035	656	197	178	4	0	0

- Molecule 34 is a protein called 40S ribosomal protein s5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	Cc	192	1464	926	278	253	7	0	0

- Molecule 35 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
35	Ce	159	1279	810	237	232	0	0

- Molecule 36 is a protein called 40S ribosomal protein s9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	Cg	159	1242	801	255	184	2	0	0

- Molecule 37 is a protein called 40S ribosomal protein S13-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
37	Ch	49	416	270	82	64	0	0

- Molecule 38 is a protein called 40S ribosomal protein S14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	Ci	115	791	492	154	141	4	0	0

- Molecule 39 is a protein called 40S ribosomal protein S16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	Cj	126	943	613	177	151	2	0	0

- Molecule 40 is a protein called 40S ribosomal protein S22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	Cm	126	985	632	184	164	5	0	0

- Molecule 41 is a protein called 40S ribosomal protein s23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	Cn	96	702	456	134	110	2	0	0

- Molecule 42 is a protein called 40S ribosomal protein S28-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	Cp	61	Total	C	N	O	0	0
			455	284	97	74		

- Molecule 43 is a protein called Faf1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	CU	131	Total	C	N	O	S	0	0
			1009	623	205	175	6		

- Molecule 44 is a RNA chain called 35S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	C1	1106	Total	C	N	O	P	0	0
			23604	10525	4233	7740	1106		

- Molecule 45 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	C2	230	Total	C	N	O	P	0	0
			4891	2182	856	1623	230		

- Molecule 46 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	UV	1061	Total	C	N	O	S	0	0
			8424	5399	1480	1523	22		

- Molecule 47 is a protein called Rrp7.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	CV	148	Total	C	N	O	S	0	0
			1145	729	198	216	2		

- Molecule 48 is a protein called Utp8.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	UH	359	Total	C	N	O	S	0	0
			2809	1773	496	527	13		

- Molecule 49 is a protein called Utp5.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	UE	125	Total	C	N	O	S	0	0
			972	608	183	175	6		
49	UI	125	Total	C	N	O	S	0	0
			972	608	183	175	6		

- Molecule 50 is a protein called Noc4.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	US	451	Total	C	N	O	S	0	0
			3672	2389	608	660	15		

- Molecule 51 is a protein called Rps18.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Cl	80	Total	C	N	O	S	0	0
			633	400	115	117	1		

- Molecule 52 is a protein called Enp1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CX	267	Total	C	N	O	S	0	0
			2130	1384	374	362	10		

- Molecule 53 is a protein called Utp16.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	UP	54	Total	C	N	O	0	0
			422	264	88	70		

- Molecule 54 is a protein called Rrp5.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Cz	275	Total	C	N	O	S	0	0
			2259	1435	401	420	3		

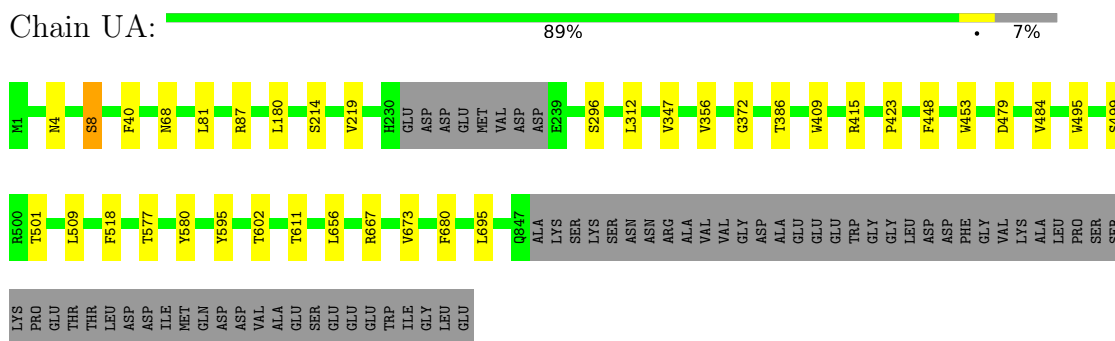
- Molecule 55 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
55	UX	1	Total	Zn	0
			1	1	

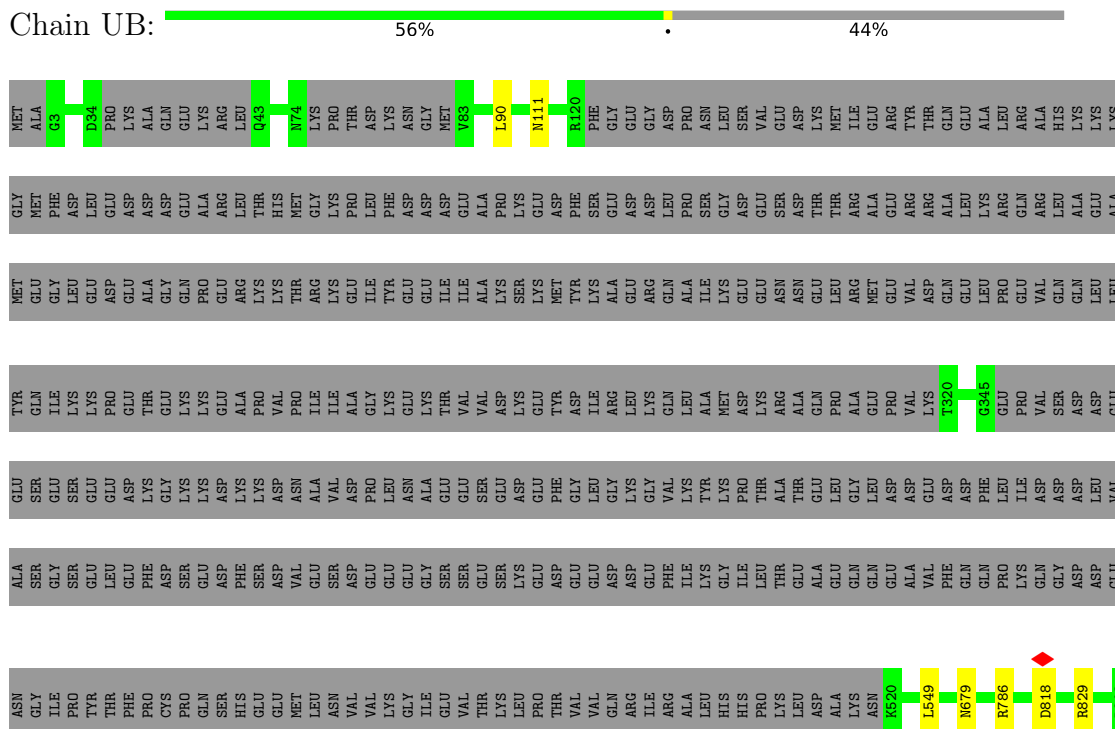
3 Residue-property plots [i](#)

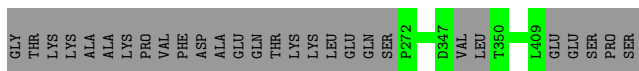
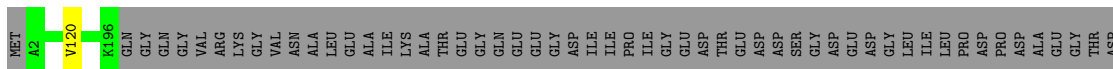
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Periodic tryptophan protein 2-like protein

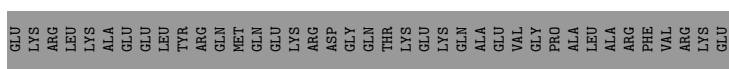
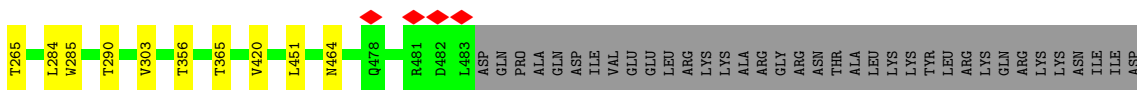
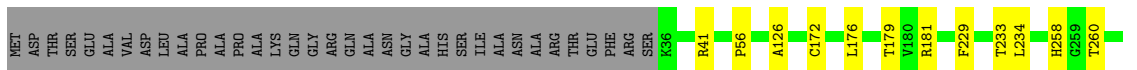
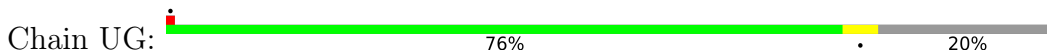


- Molecule 2: Utp2

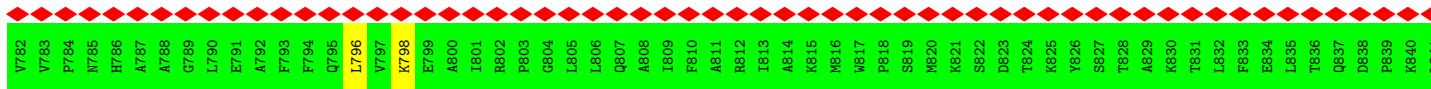
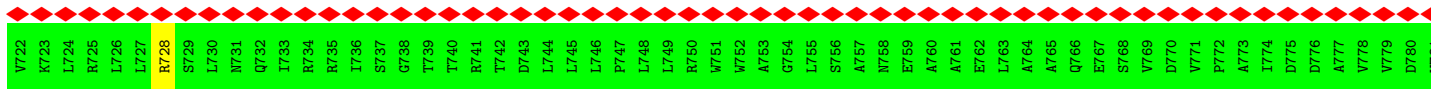
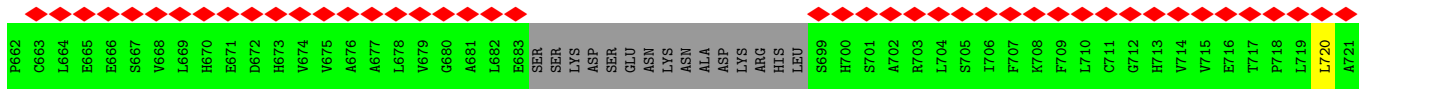
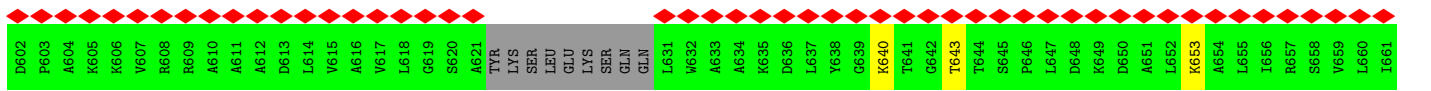
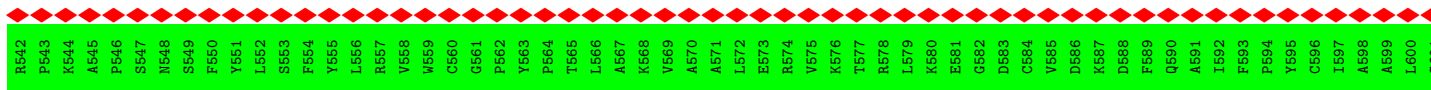
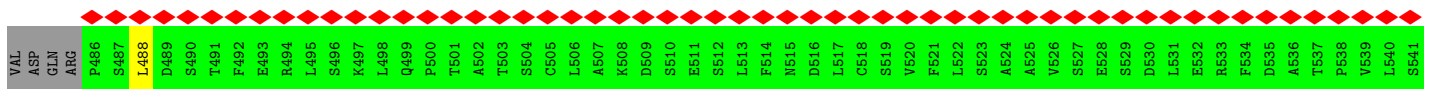
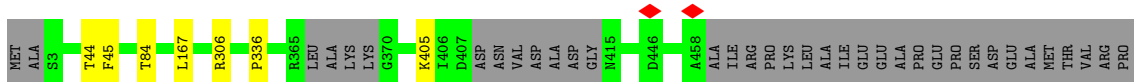
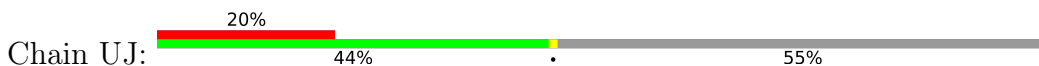


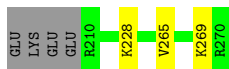


• Molecule 6: Utp7

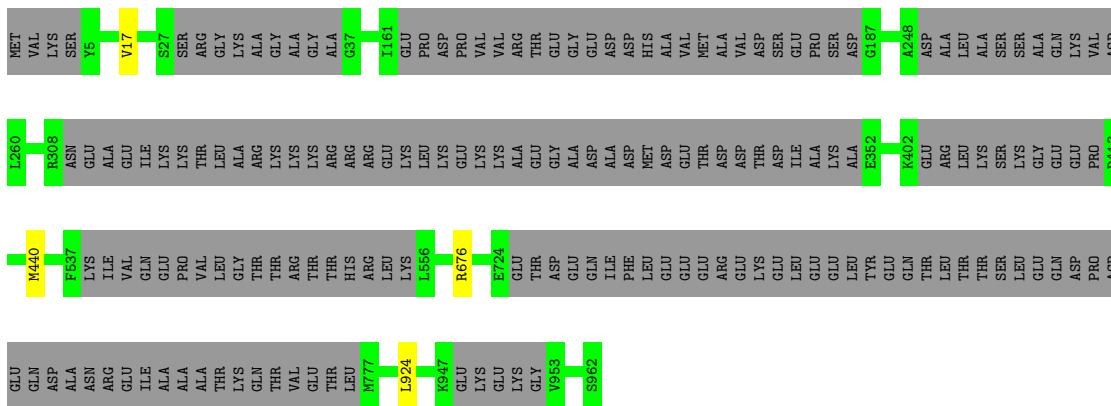
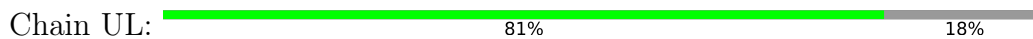


• Molecule 7: Utp10

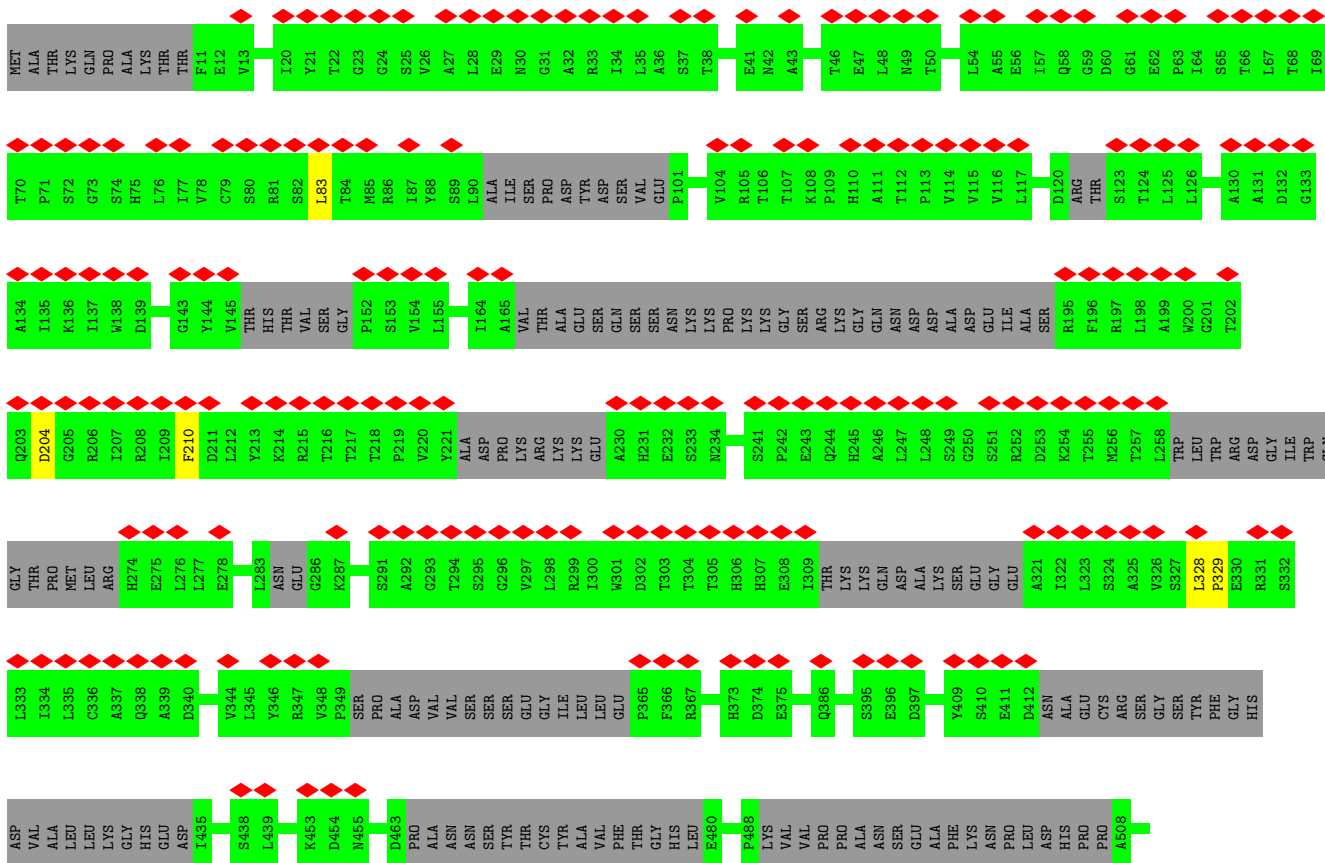
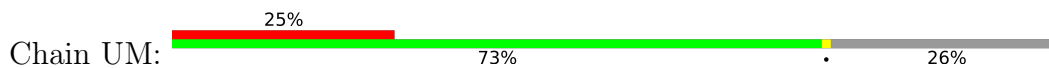





• Molecule 9: Utp12

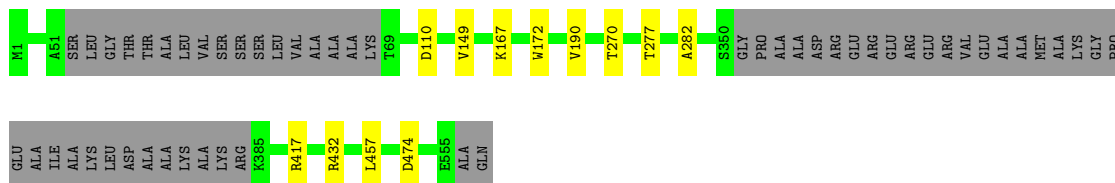


• Molecule 10: Utp13




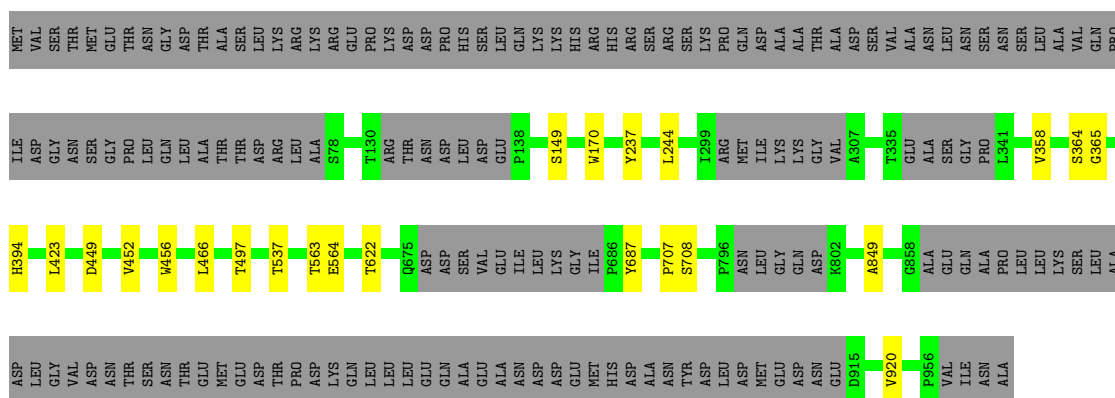
• Molecule 12: Utp15

Chain UO:  88% 10%



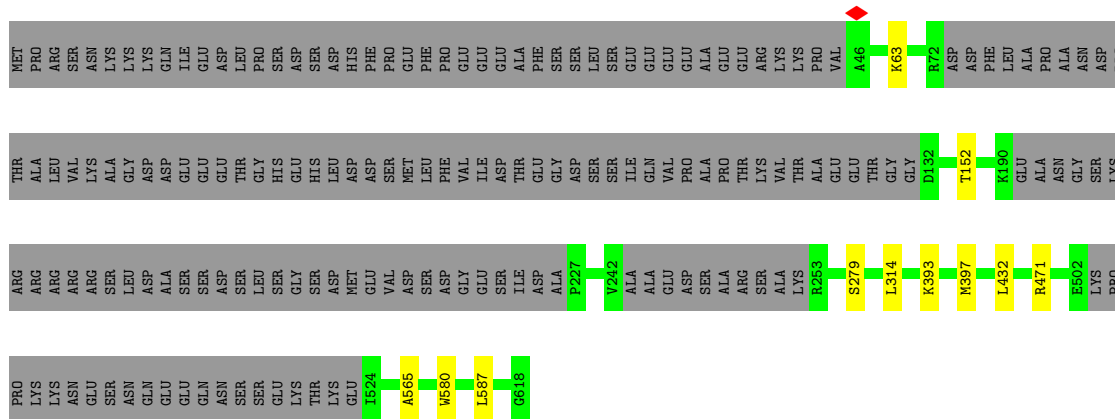
• Molecule 13: Utp17

Chain UQ:  80% 18%




• Molecule 14: Utp18

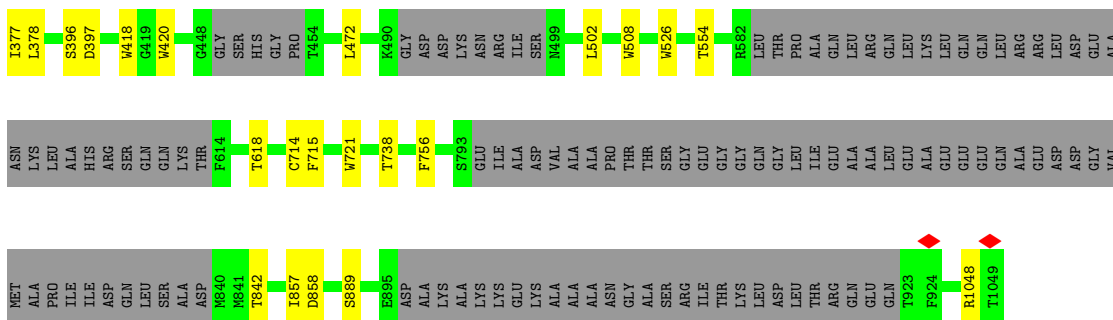
Chain UR:  71% 28%



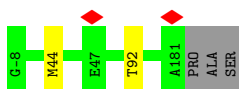
• Molecule 15: Utp21

Chain UU:  83% 14%

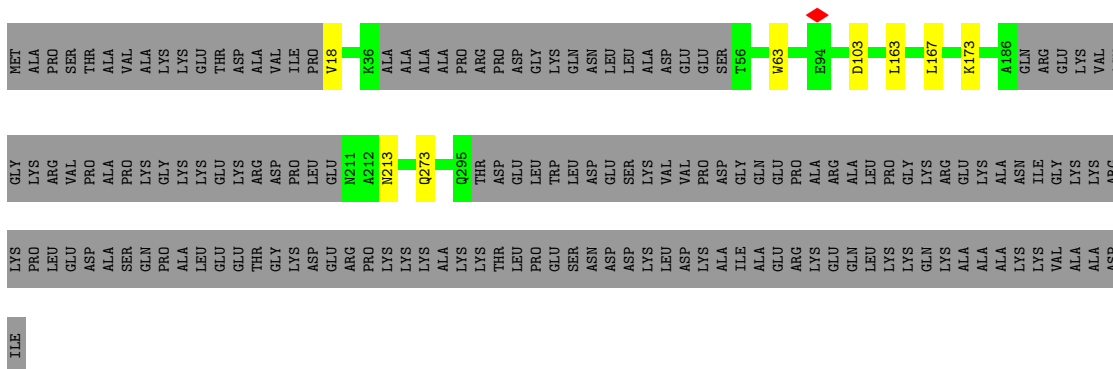




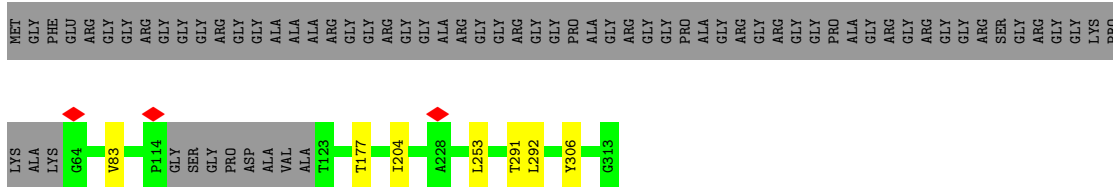
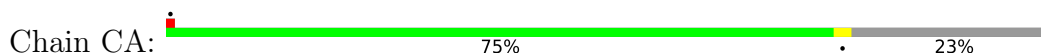
• Molecule 16: Utp24



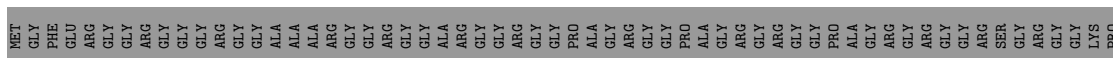
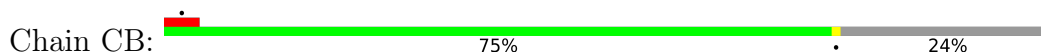
• Molecule 17: Utp30

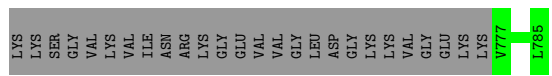


• Molecule 18: Nop1

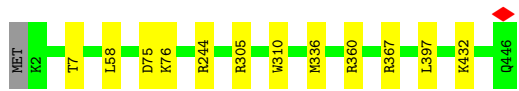


• Molecule 18: Nop1

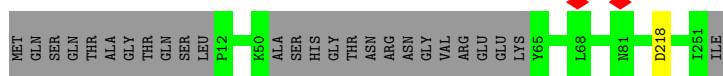




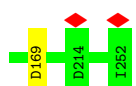
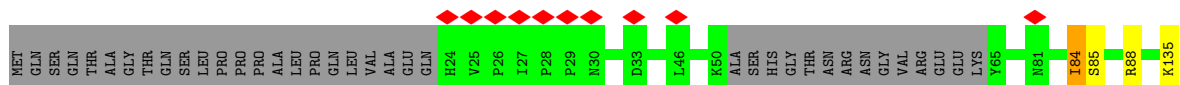
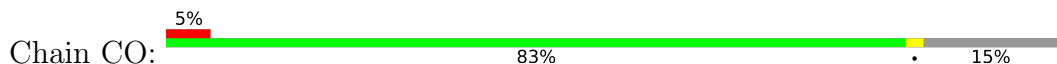
• Molecule 28: Sof1



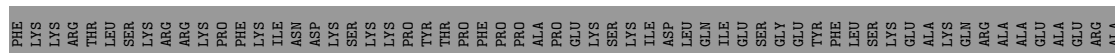
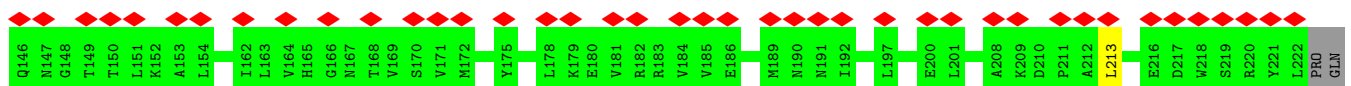
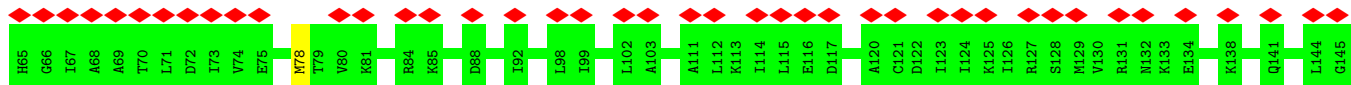
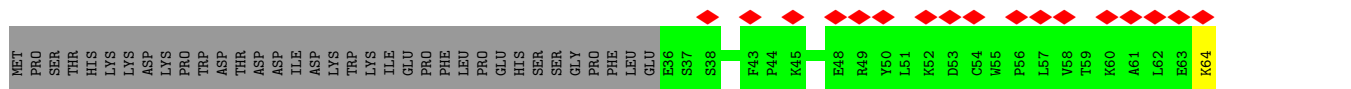
• Molecule 29: Emg1



• Molecule 29: Emg1



• Molecule 30: KRR1 small subunit processome component

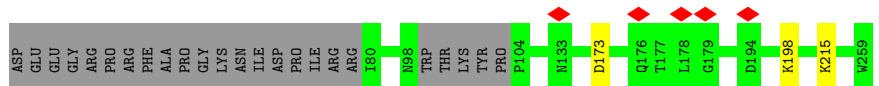


GLU
LYS
ALA
ARG
GLN
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LYS
ARG
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ARG
GLU
ARG
GLU
PHE
VAL
PRO
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GLY
GLY
LYS
LYS
LYS
LYS
GLY
GLY
GLU

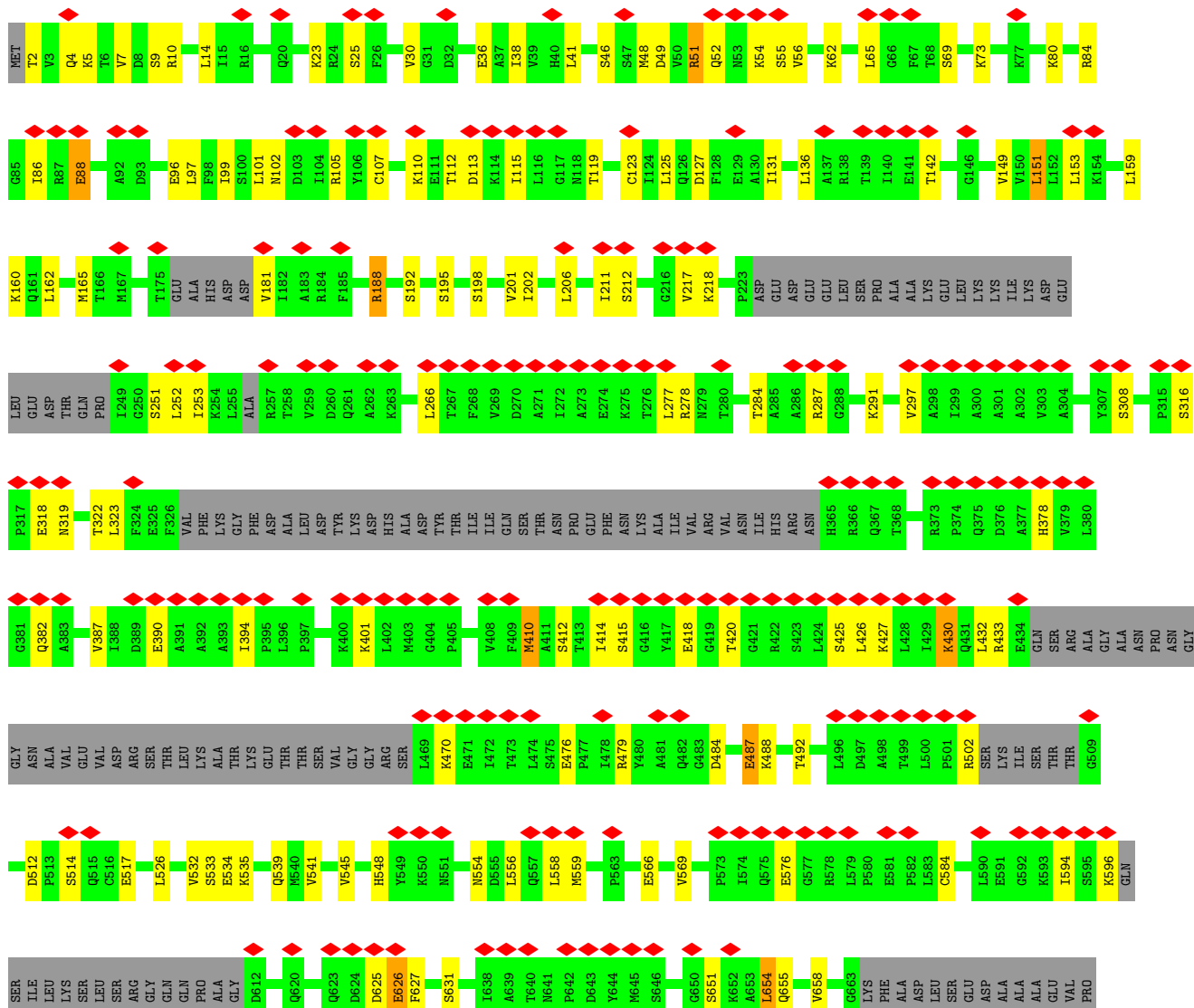
• Molecule 31: Pre-rRNA-processing protein PNO1



MET
PRO
ALA
PRO
THR
ALA
LEU
LEU
GLN
ALA
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PRO
PRO
PRO
PRO
PRO
GLY
GLY
GLY
PHE
VAL
PRO
PRO
ILE
THR
THR
ASN
GLY
ASN
GLY
ASP
GLY
LYS
LYS
LYS
LYS
LYS
LYS
GLN
GLY
GLY
GLY
VAL

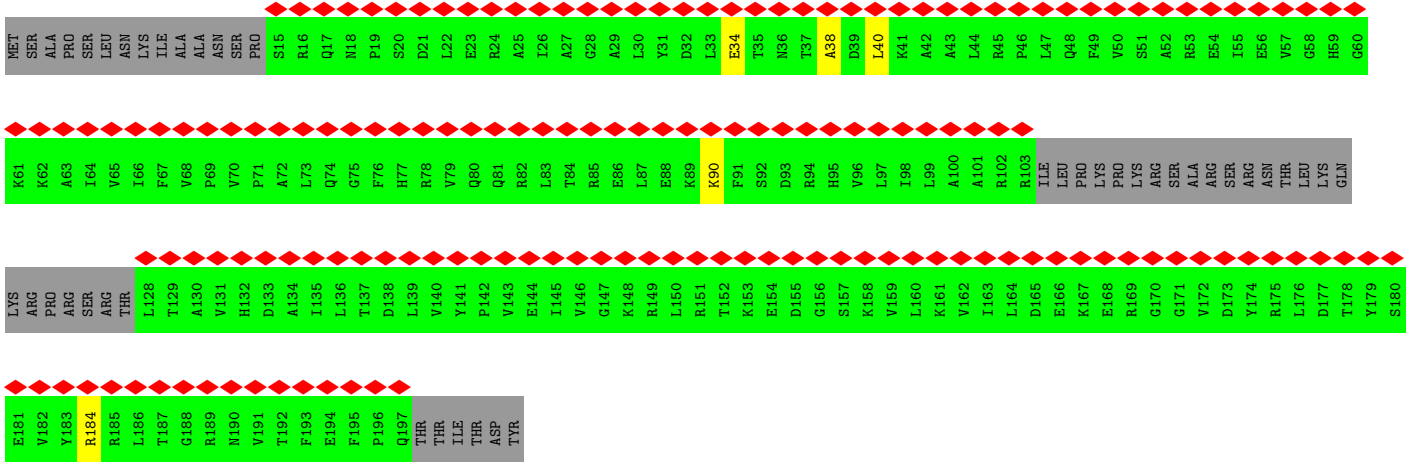
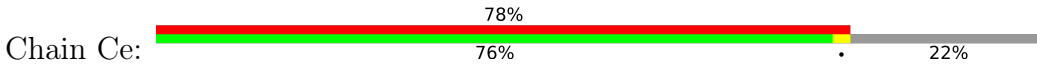


• Molecule 32: Kre33

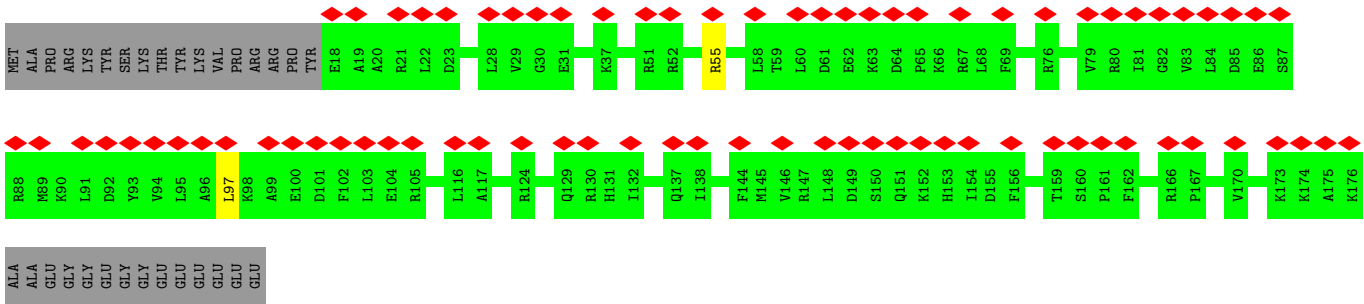
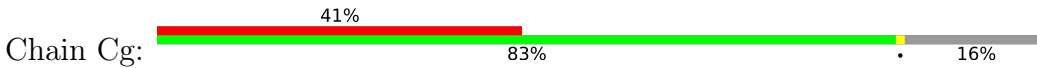




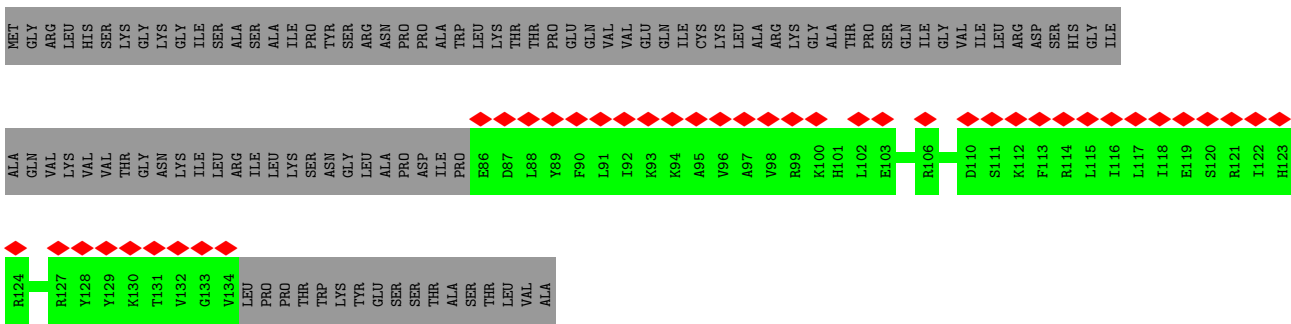
• Molecule 35: 40S ribosomal protein S7



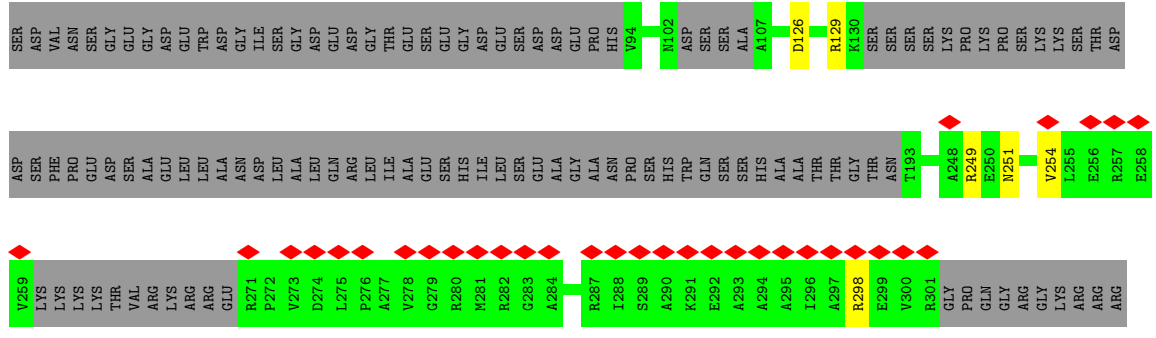
• Molecule 36: 40S ribosomal protein s9-like protein



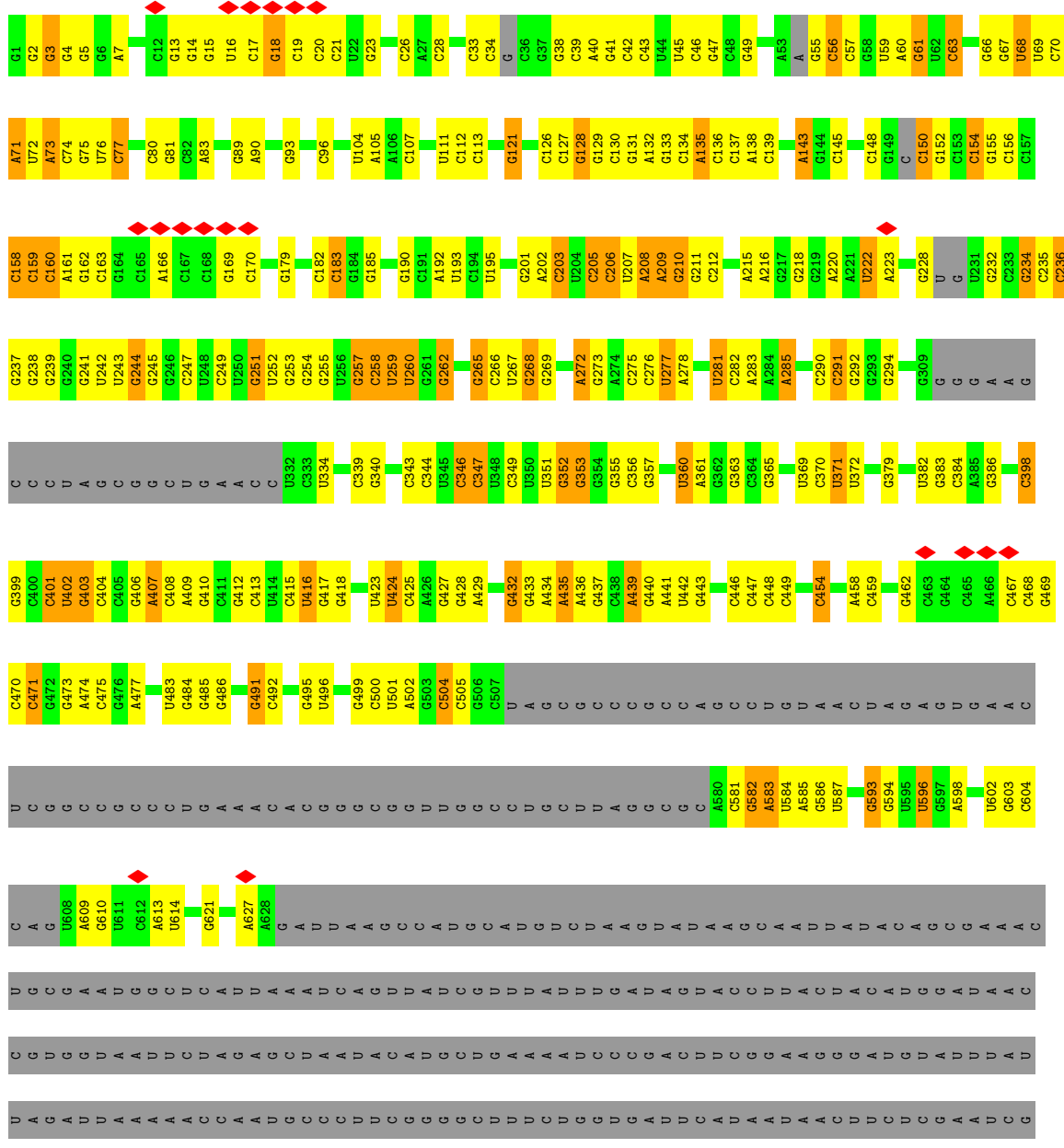
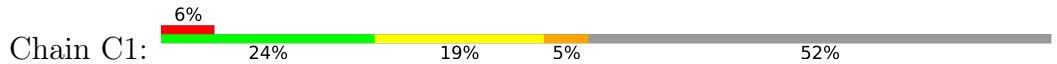
• Molecule 37: 40S ribosomal protein S13-like protein

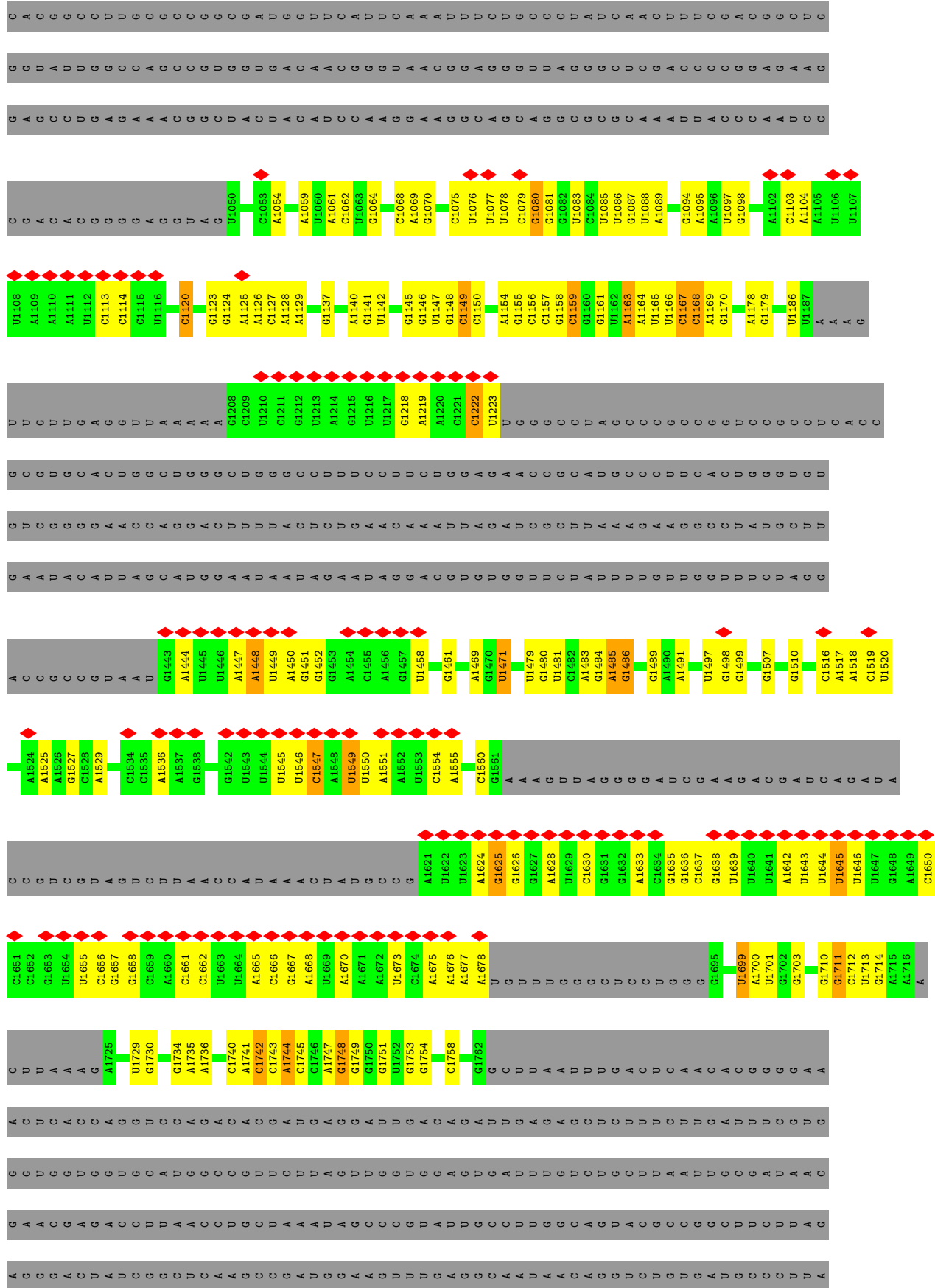


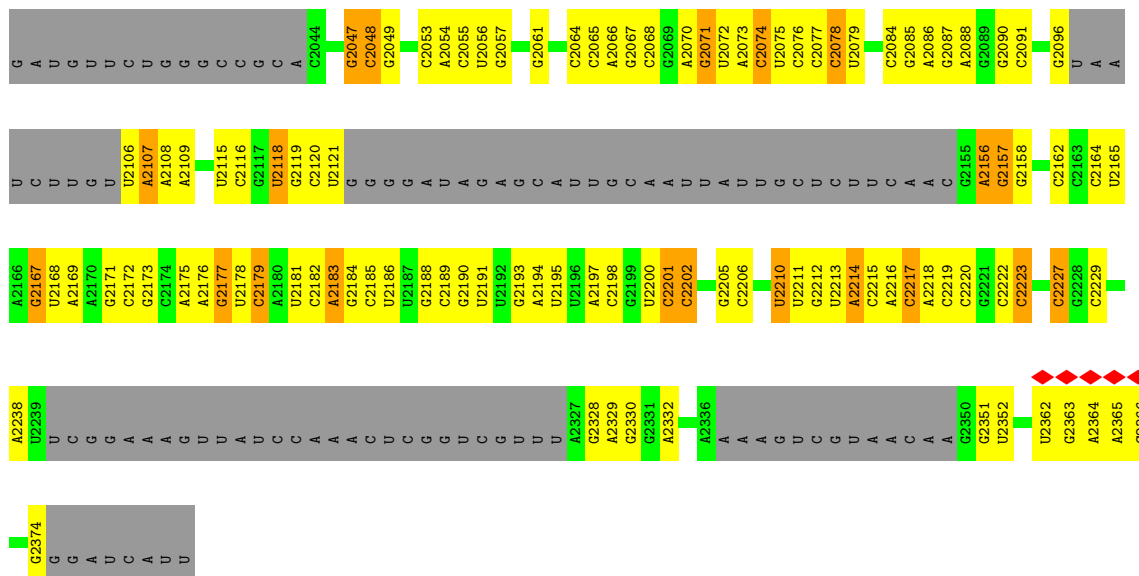
• Molecule 38: 40S ribosomal protein S14-like protein



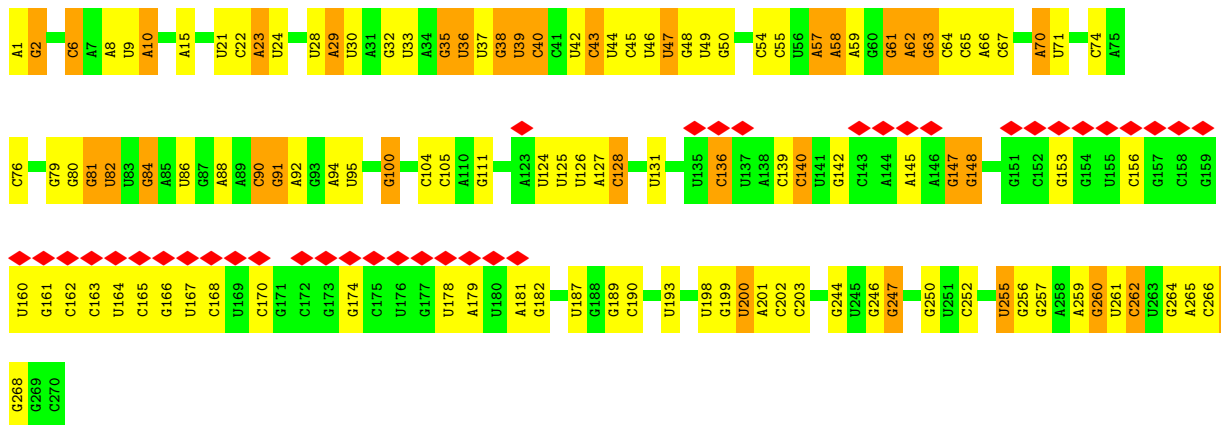
• Molecule 44: 35S rRNA



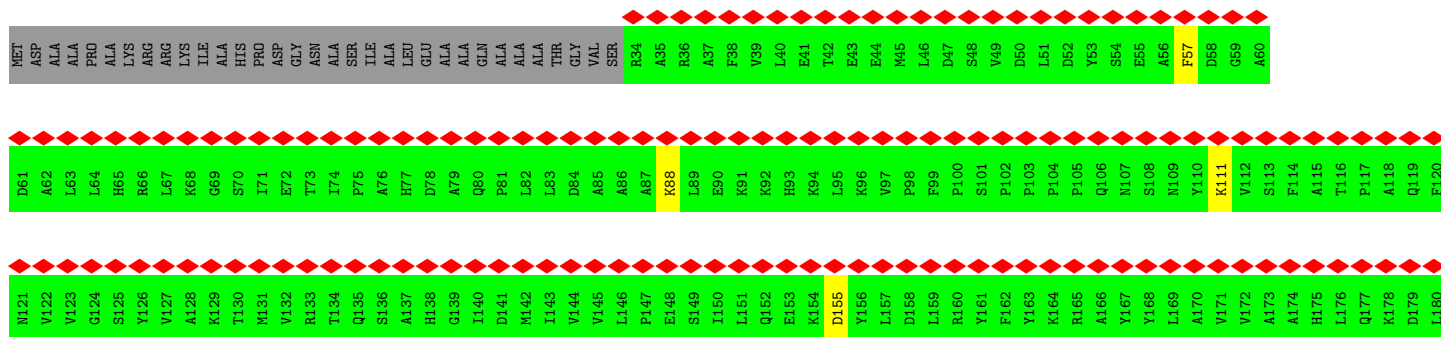
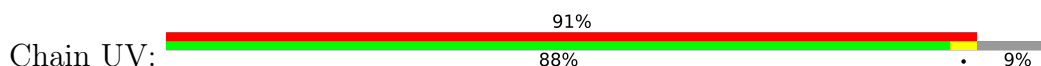




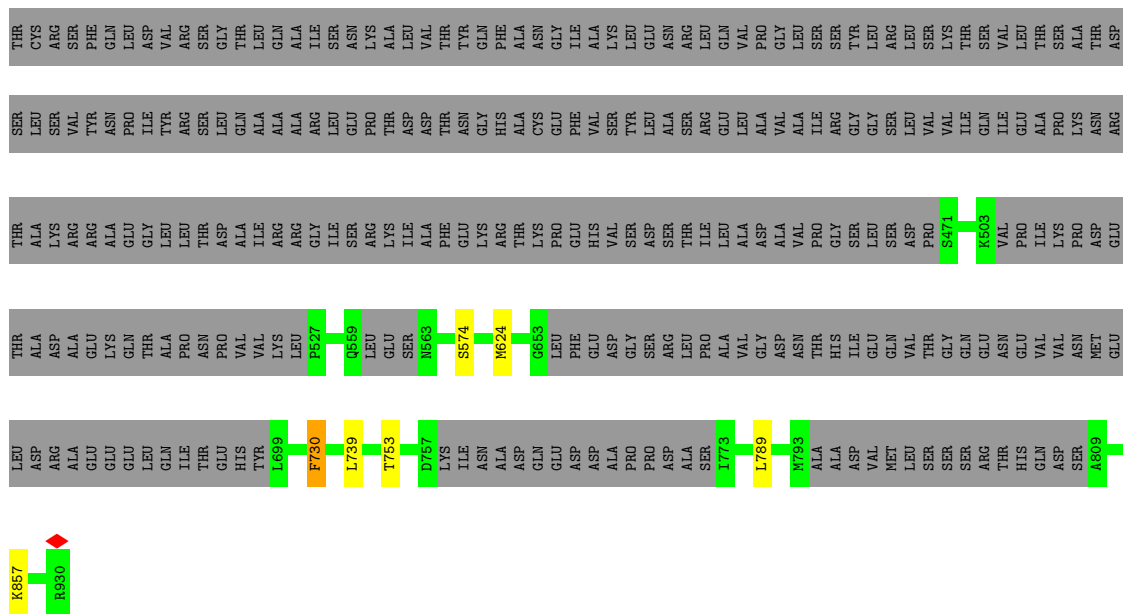
• Molecule 45: U3 snoRNA



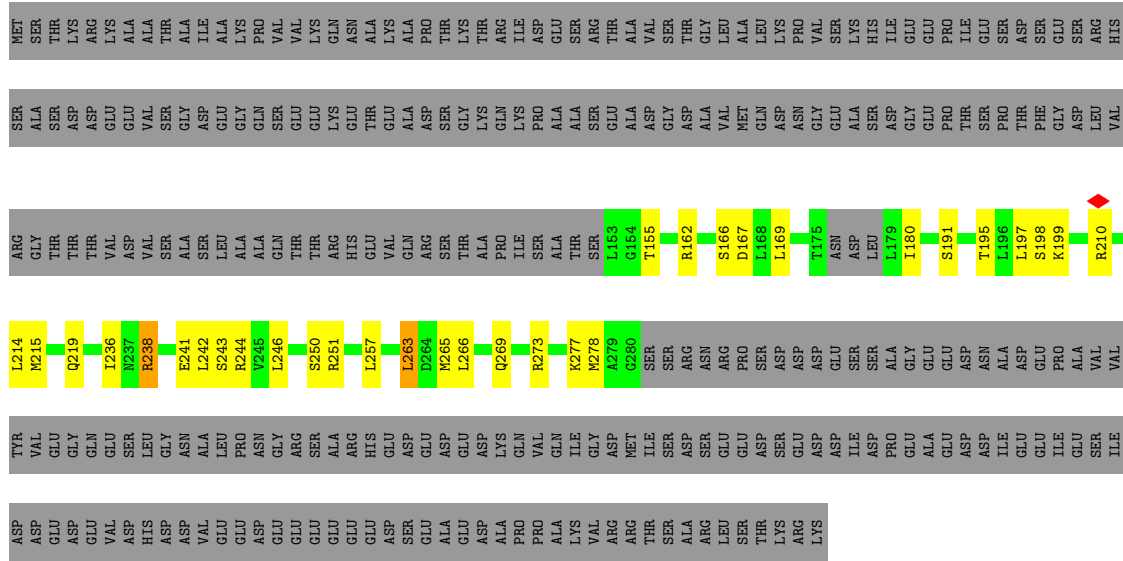
• Molecule 46: U3 small nucleolar RNA-associated protein 22



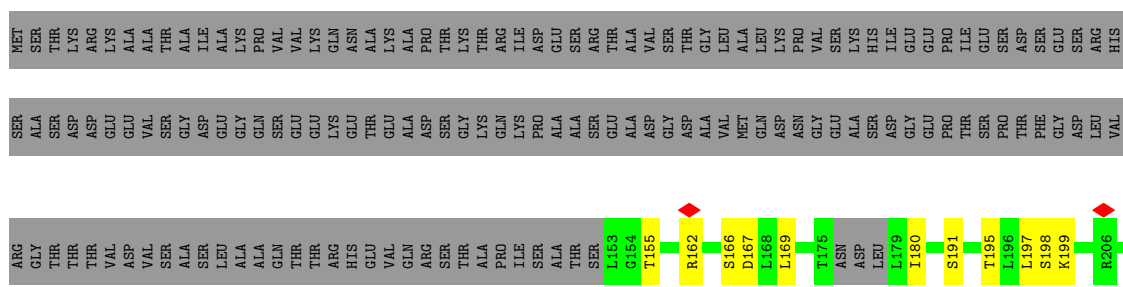
T961	K181	I301	T421	K481	L541	E601	L661	F721	R781	H841	G1Y
A962	G182	L302	R422	V482	N542	L602	P662	L722	Q782	K842	GLU
L963	E183	G303	K423	Y483	M543	M603	L663	L723	T783	L843	LEU
A964	A184	R304	L424	R484	A544	R604	R664	W724	K784	S844	ALA
K965	T185	I305	L425	I485	R545	Y605	L665	L725	D785	H845	GLN
S966	L186	W306	A426	L486	R546	L606	R666	G726	K786	H846	GLU
A967	S187	V307	D427	R487	T547	L607	H667	R727	T787	F847	ARG
A968	Y188	Q308	G428	R488	D548	G608	V668	L728	T788	P848	ALA
R969	E189	Q309	A429	A489	R549	L609	N669	L729	E789	P849	ALA
V970	Y190	R310	V430	L490	G550	H610	P670	E730	Q790	E850	ALA
I971	H191	G311	D431	L491	P551	L611	L671	R731	Y791	L851	THR
R972	N192	F312	Q432	D492	S552	R612	C672	F732	L792	L852	ARG
E973	G193	P313	F433	K493	A553	Y613	P673	K733	R793	E853	L915
Q974	N194	G314	Q434	N494	G554	G614	E674	P734	Q794	L854	D916
G975	S195	D315	P435	N495	P555	Q615	L675	G735	R795	F855	A917
V976	L196	V316	T436	E496	S556	L616	R676	E736	A796	W856	W918
D977	L197	G317	F437	G497	A557	Q617	H677	I737	S797	L857	K920
L978	P198	K318	I438	G498	E558	D618	S678	R738	T798	H858	L921
D979	V199	G319	L439	E499	E559	D619	S679	T739	Q799	T859	D922
V980	L200	G320	K440	R500	K560	I620	L680	H740	L800	F860	P923
R981	S201	F321	A441	A501	E561	V621	K681	W741	A801	L861	G924
R982	V202	G322	D442	R502	F622	F623	T682	G742	S802	A862	N925
L983	K203	Y323	L443	L503	C563	Y623	P683	L743	F803	P863	Q926
F984	P204	F324	P444	I504	E564	G624	S684	D744	R804	D864	H927
V985	N205	E325	T445	H505	K565	R625	F685	D745	R805	P865	T928
P986	G206	W326	H446	L506	F566	S626	G686	A746	T806	W866	V929
S987	G207	A327	T447	K507	R567	L627	P687	R747	F807	D867	L930
L988	K208	V328	Y448	V508	R568	P628	S688	Y748	W808	H868	F931
K989	D209	L329	D449	S509	F569	A629	K689	E749	H809	P869	V932
Y990	E210	L330	L450	P510	W570	L630	S690	T750	L810	S870	A933
D992	D211	A331	V451	G511	G571	L631	G691	E751	P811	S871	T934
V993	E212	L332	A452	F512	E572	S632	P692	W752	L812	R872	A935
L994	K213	L333	R453	S513	K573	I633	R693	L753	H813	T873	H936
L995	K214	L334	M454	S514	S574	K634	P694	A754	T814	T874	E937
Y996	K215	Q335	D455	S515	E575	P635	M695	F755	Q815	G875	Q938
L997	K216	G336	P456	S516	L576	S636	E696	L756	W816	F876	S939
N998	K217	P337	E457	W517	R577	D637	V697	D757	L817	L877	G940
T999	G218	G338	R458	S518	R578	T638	V698	W758	T818	R878	T941
K1000	V219	A339	V459	L519	F579	A639	L699	L759	T819	T879	M942
V1001	L220	D340	S460	N520	G580	L640	S700	Y760	A820	L880	W943
L1002	D221	T341	E461	E521	G581	F641	F701	A761	T821	L881	T944
K1003	Y222	K342	A462	K522	D582	N642	E702	S762	E702	F882	S945
S1004	R223	G343	A463	P523	T583	V643	A703	G763	A703	L883	V946
A1005	I224	A344	P464	Q524	I584	A644	S704	A764	S704	F884	D947
L1006	R225	A345	D465	P525	R585	R645	G705	C765	P825	R885	G948
R1007	I226	P346	K466	Q526	E586	K646	K706	F766	A826	W886	H949
Y1008	P228	L347	V467	K527	T587	T647	W707	R767	L827	D887	P950
Y1009	C229	S348	A468	A528	L588	F648	P708	V768	S828	W888	R951
I1010	C229	P349	H469	G529	V589	T649	E709	R769	P829	R889	F952
T1011	A230	S350	E470	T530	W590	S650	S710	I770	T830	T890	S953
V1012	P231	L351	A471	P531	S591	F651	L711	Q771	L831	D891	K954
P1013	E232	S352	R472	I532	A592	G652	I712	A772	R832	P892	V955
A1015	F233	S353	G473	E533	Q593	R653	A713	D773	L833	L893	W956
T1016	F235	Q355	R474	I534	Q594	D654	I714	L774	V834	A957	A957
E1017	P236	Q356	H475	G535	P595	L655	Q715	E775	K835	I895	A958
M1018	R237	L356	V476	V536	F596	R656	R716	E776	H836	D896	R959
N1019	Q238	F357	Q477	L537	D597	D657	T717	S777	W837	T897	H960
G1020	K239	A299	G479	D539	C599	E660	I719	L779	F838	S839	SER
	L240	L360	H480	P540	E600	D660	A720	E780	W840	LEU	ASN



• Molecule 49: Utp5



• Molecule 49: Utp5



A1752	K1753	S1754	R1755	E1756	S1759	A1762	Q1763	E1764	W1765	A1766	R1767	A1768	LYS	ALA	ALA	ALA	THR	GLY	LYS	ALA	LEU	GLU	ASP	GLN	GLY	GLN	GLU	GLY	GLU	SER	SER	GLY	ALA	GLU	GLU	GLU	GLY	GLU	GLU
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	20250	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.437	Depositor
Minimum map value	-0.319	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	520.32, 520.32, 520.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section:
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	UA	0.99	12/6521 (0.2%)	0.86	6/8867 (0.1%)
2	UB	0.48	1/4154 (0.0%)	0.60	1/5583 (0.0%)
3	UC	0.49	0/595	0.59	0/786
4	UD	0.68	4/6211 (0.1%)	0.70	3/8408 (0.0%)
5	UF	0.54	0/2657	0.60	0/3596
6	UG	0.88	4/3516 (0.1%)	0.79	3/4761 (0.1%)
7	UJ	0.52	0/6291	0.69	3/8543 (0.0%)
8	UK	0.80	0/1701	0.79	1/2251 (0.0%)
9	UL	0.47	0/6299	0.65	1/8531 (0.0%)
10	UM	0.38	0/5366	0.62	4/7282 (0.1%)
11	UN	0.60	0/1232	0.62	0/1662
12	UO	0.72	3/3903 (0.1%)	0.74	3/5312 (0.1%)
13	UQ	0.70	1/6136 (0.0%)	0.72	3/8348 (0.0%)
14	UR	0.94	2/3564 (0.1%)	0.80	2/4816 (0.0%)
15	UU	0.81	8/6903 (0.1%)	0.77	5/9392 (0.1%)
16	UX	0.63	0/1493	0.67	0/2011
17	UZ	0.48	1/1857 (0.1%)	0.66	3/2526 (0.1%)
18	CA	0.75	1/1814 (0.1%)	0.72	0/2456
18	CB	0.48	0/1853	0.61	0/2511
19	CC	0.53	0/2911	0.65	1/3937 (0.0%)
20	CD	0.53	1/3205 (0.0%)	0.68	2/4338 (0.0%)
21	CE	0.84	0/891	0.80	0/1214
21	CF	0.40	0/876	0.64	0/1195
22	CG	0.33	0/2983	0.58	0/4032
23	CH	0.51	0/2939	0.67	0/3988
24	CI	0.63	1/6631 (0.0%)	0.67	3/8943 (0.0%)
25	CJ	1.09	3/1462 (0.2%)	0.86	0/1967
26	CK	0.95	2/2376 (0.1%)	0.86	4/3214 (0.1%)
27	CL	0.70	0/1812	0.66	0/2437
28	CM	0.70	1/3573 (0.0%)	0.71	2/4829 (0.0%)
29	CN	0.52	0/1797	0.64	0/2443
29	CO	0.41	0/1714	0.62	0/2325

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	CP	0.31	0/1528	0.67	1/2057 (0.0%)
31	CQ	0.37	0/1379	0.58	0/1850
32	CR	0.42	1/6108 (0.0%)	0.84	20/8266 (0.2%)
32	CS	0.42	1/6108 (0.0%)	0.84	20/8266 (0.2%)
33	CT	0.67	0/1053	0.70	0/1413
34	Cc	0.78	0/1485	0.74	0/2008
35	Ce	0.36	0/1298	0.75	1/1750 (0.1%)
36	Cg	0.37	0/1259	0.63	0/1687
37	Ch	0.28	0/422	0.50	0/561
38	Ci	0.31	0/801	0.60	0/1087
39	Cj	1.02	0/958	0.88	0/1293
40	Cm	0.35	0/1001	0.65	1/1345 (0.1%)
41	Cn	0.62	0/712	0.67	0/954
42	Cp	0.58	0/458	0.68	0/617
43	CU	0.37	0/1015	0.60	0/1351
44	C1	1.32	203/26369 (0.8%)	1.49	504/41071 (1.2%)
45	C2	1.37	62/5459 (1.1%)	1.61	134/8498 (1.6%)
46	UV	0.35	1/8638 (0.0%)	0.72	9/11725 (0.1%)
47	CV	0.33	0/1172	0.69	0/1592
48	UH	0.50	1/2852 (0.0%)	0.68	2/3846 (0.1%)
49	UE	0.47	0/980	0.91	5/1316 (0.4%)
49	UI	0.47	0/980	0.91	5/1316 (0.4%)
50	US	0.52	0/3765	0.62	0/5100
51	Cl	0.42	0/638	0.66	0/857
52	CX	0.31	0/2180	0.57	1/2956 (0.0%)
53	UP	0.55	0/428	0.62	0/570
54	Cz	0.33	0/2310	0.58	0/3120
All	All	0.78	314/186592 (0.2%)	0.92	753/258976 (0.3%)

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	UA	0	4
4	UD	0	2
5	UF	0	1
6	UG	0	2
9	UL	0	1
10	UM	0	3
12	UO	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
13	UQ	0	6
15	UU	0	8
17	UZ	0	3
18	CA	0	1
18	CB	0	1
21	CF	0	1
23	CH	0	1
24	CI	0	2
26	CK	0	1
29	CO	0	2
31	CQ	0	1
32	CR	0	2
32	CS	0	2
34	Cc	0	2
35	Ce	0	1
38	Ci	0	1
39	Cj	0	2
46	UV	0	5
47	CV	0	2
48	UH	0	2
50	US	0	1
51	CI	0	1
54	Cz	0	1
All	All	0	64

All (314) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	UQ	394	HIS	CA-CB	-13.98	1.23	1.53
45	C2	57	A	N7-C5	-10.06	1.33	1.39
15	UU	418	TRP	CB-CG	-9.97	1.32	1.50
44	C1	2107	A	N9-C4	-9.80	1.31	1.37
44	C1	254	G	N7-C5	-9.57	1.33	1.39
44	C1	2194	A	N9-C4	-9.33	1.32	1.37
15	UU	420	TRP	CB-CG	-8.64	1.34	1.50
44	C1	2107	A	N3-C4	-8.63	1.29	1.34
1	UA	495	TRP	CB-CG	-8.41	1.35	1.50
44	C1	254	G	C5-C6	-8.28	1.34	1.42
45	C2	62	A	N3-C4	-8.25	1.29	1.34
45	C2	88	A	C5-C6	-8.16	1.33	1.41
44	C1	2169	A	N7-C5	-8.15	1.34	1.39
44	C1	2107	A	C5-C4	-8.13	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	C2	265	A	N9-C4	-8.11	1.32	1.37
44	C1	2194	A	N3-C4	-8.05	1.30	1.34
44	C1	1744	A	N9-C4	-7.98	1.33	1.37
45	C2	63	G	N7-C5	-7.89	1.34	1.39
44	C1	2194	A	N7-C5	-7.85	1.34	1.39
45	C2	88	A	N7-C5	-7.50	1.34	1.39
45	C2	84	G	N3-C4	-7.32	1.30	1.35
1	UA	595	TYR	CD1-CE1	-7.27	1.28	1.39
44	C1	1146	G	N7-C5	-7.19	1.34	1.39
44	C1	2176	A	N7-C5	-7.14	1.34	1.39
44	C1	2172	C	N1-C6	-7.11	1.32	1.37
28	CM	310	TRP	CB-CG	-7.10	1.37	1.50
44	C1	262	G	C6-N1	-7.04	1.34	1.39
44	C1	413	C	N1-C6	-7.03	1.32	1.37
45	C2	62	A	C5-C4	-7.02	1.33	1.38
1	UA	409	TRP	CB-CG	-6.99	1.37	1.50
44	C1	2176	A	N9-C4	-6.95	1.33	1.37
44	C1	417	G	N7-C5	-6.94	1.35	1.39
45	C2	265	A	C5-C6	-6.92	1.34	1.41
44	C1	355	G	N7-C5	-6.91	1.35	1.39
44	C1	2214	A	C5-C6	-6.89	1.34	1.41
44	C1	2168	U	C2-N3	-6.88	1.32	1.37
45	C2	62	A	C6-N1	-6.83	1.30	1.35
44	C1	407	A	N3-C4	-6.78	1.30	1.34
48	UH	730	PHE	C-N	-6.77	1.18	1.34
44	C1	352	G	N7-C5	-6.74	1.35	1.39
44	C1	210	G	N3-C4	-6.73	1.30	1.35
44	C1	2066	A	N7-C5	-6.73	1.35	1.39
44	C1	257	G	C5-C4	-6.72	1.33	1.38
44	C1	407	A	N7-C5	-6.68	1.35	1.39
44	C1	2066	A	C5-C4	-6.67	1.34	1.38
45	C2	63	G	C5-C4	-6.66	1.33	1.38
45	C2	84	G	C5-C4	-6.66	1.33	1.38
44	C1	73	A	N9-C4	-6.62	1.33	1.37
45	C2	63	G	C5-C6	-6.59	1.35	1.42
15	UU	1048	ARG	CA-CB	-6.59	1.39	1.53
44	C1	2107	A	C5-C6	-6.54	1.35	1.41
44	C1	2193	G	N7-C5	-6.51	1.35	1.39
44	C1	135	A	N7-C5	-6.50	1.35	1.39
45	C2	84	G	C6-N1	-6.48	1.35	1.39
44	C1	257	G	N9-C4	-6.45	1.32	1.38
25	CJ	173	TYR	CD2-CE2	-6.44	1.29	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	C2	79	G	N7-C5	-6.44	1.35	1.39
44	C1	2176	A	C5-C6	-6.38	1.35	1.41
45	C2	62	A	N9-C4	-6.38	1.34	1.37
44	C1	254	G	N9-C8	-6.36	1.33	1.37
44	C1	407	A	N9-C4	-6.35	1.34	1.37
44	C1	272	A	N9-C4	-6.32	1.34	1.37
45	C2	265	A	C5-C4	-6.32	1.34	1.38
44	C1	355	G	N3-C4	-6.30	1.31	1.35
44	C1	294	G	N7-C5	-6.30	1.35	1.39
45	C2	63	G	C6-N1	-6.29	1.35	1.39
44	C1	2169	A	C5-C6	-6.29	1.35	1.41
44	C1	232	G	N3-C4	-6.26	1.31	1.35
45	C2	57	A	C6-N1	-6.25	1.31	1.35
44	C1	238	G	N7-C5	-6.23	1.35	1.39
44	C1	2177	G	N3-C4	-6.21	1.31	1.35
44	C1	135	A	N3-C4	-6.20	1.31	1.34
44	C1	2169	A	N3-C4	-6.20	1.31	1.34
44	C1	208	A	C5-C4	-6.19	1.34	1.38
44	C1	71	A	N9-C4	-6.17	1.34	1.37
1	UA	673	VAL	CB-CG2	-6.17	1.39	1.52
44	C1	2332	A	N9-C4	-6.16	1.34	1.37
44	C1	361	A	C5-C4	-6.14	1.34	1.38
44	C1	2067	G	C5-C4	-6.11	1.34	1.38
45	C2	54	C	N1-C6	-6.09	1.33	1.37
44	C1	2064	C	N3-C4	-6.09	1.29	1.33
44	C1	407	A	C5-C4	-6.05	1.34	1.38
44	C1	2218	A	N9-C4	-6.05	1.34	1.37
15	UU	721	TRP	CB-CG	-6.04	1.39	1.50
44	C1	2049	G	N7-C5	-6.04	1.35	1.39
45	C2	29	A	N9-C4	-6.04	1.34	1.37
45	C2	88	A	N3-C4	-6.02	1.31	1.34
45	C2	84	G	N7-C5	-6.01	1.35	1.39
44	C1	1146	G	C6-N1	-6.00	1.35	1.39
44	C1	409	A	N7-C5	-5.96	1.35	1.39
44	C1	262	G	N7-C5	-5.95	1.35	1.39
1	UA	4	ASN	CA-CB	-5.95	1.37	1.53
44	C1	257	G	N3-C4	-5.94	1.31	1.35
32	CS	626	GLU	CB-CG	5.93	1.63	1.52
44	C1	2072	U	C2-N3	-5.93	1.33	1.37
45	C2	50	G	N7-C5	-5.93	1.35	1.39
2	UB	679	ASN	C-N	-5.92	1.20	1.34
32	CR	626	GLU	CB-CG	5.91	1.63	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	C2	59	A	N9-C4	-5.90	1.34	1.37
44	C1	361	A	C5-C6	-5.89	1.35	1.41
44	C1	435	A	N9-C4	-5.88	1.34	1.37
44	C1	1744	A	N7-C5	-5.88	1.35	1.39
44	C1	2177	G	C5-C4	-5.88	1.34	1.38
6	UG	285	TRP	CB-CG	-5.88	1.39	1.50
12	UO	417	ARG	C-N	-5.88	1.20	1.34
44	C1	352	G	C5-C6	-5.88	1.36	1.42
44	C1	2183	A	C5-C6	-5.88	1.35	1.41
44	C1	2066	A	N3-C4	-5.88	1.31	1.34
44	C1	245	G	N7-C5	-5.88	1.35	1.39
44	C1	406	G	C5-C6	-5.87	1.36	1.42
45	C2	267	C	C2-O2	-5.87	1.19	1.24
44	C1	1145	G	C6-N1	-5.84	1.35	1.39
44	C1	417	G	C5-C4	-5.83	1.34	1.38
44	C1	404	C	N1-C6	-5.83	1.33	1.37
14	UR	565	ALA	CA-CB	-5.82	1.40	1.52
44	C1	2186	U	C4-C5	-5.81	1.38	1.43
44	C1	361	A	N7-C5	-5.80	1.35	1.39
44	C1	2179	C	N1-C6	-5.79	1.33	1.37
44	C1	241	G	C5-C4	-5.79	1.34	1.38
44	C1	294	G	N3-C4	-5.79	1.31	1.35
44	C1	1741	A	C5-C4	-5.78	1.34	1.38
45	C2	35	G	N9-C4	-5.78	1.33	1.38
45	C2	66	A	N9-C4	-5.78	1.34	1.37
24	CI	851	TRP	CB-CG	-5.77	1.39	1.50
45	C2	267	C	N1-C6	-5.76	1.33	1.37
45	C2	62	A	C5-C6	-5.75	1.35	1.41
44	C1	83	A	N9-C4	-5.75	1.34	1.37
44	C1	1146	G	C5-C4	-5.74	1.34	1.38
44	C1	2176	A	N3-C4	-5.73	1.31	1.34
44	C1	2167	G	C6-N1	-5.73	1.35	1.39
44	C1	215	A	N3-C4	-5.73	1.31	1.34
44	C1	2177	G	N9-C4	-5.72	1.33	1.38
44	C1	254	G	N3-C4	-5.72	1.31	1.35
44	C1	412	G	N7-C5	-5.72	1.35	1.39
45	C2	80	G	N3-C4	-5.72	1.31	1.35
4	UD	114	TRP	CB-CG	-5.70	1.40	1.50
44	C1	2194	A	C6-N6	-5.70	1.29	1.33
44	C1	254	G	C8-N7	-5.70	1.27	1.30
44	C1	1146	G	N1-C2	-5.67	1.33	1.37
44	C1	418	G	N7-C5	-5.66	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	C2	84	G	N9-C4	-5.66	1.33	1.38
44	C1	417	G	N3-C4	-5.66	1.31	1.35
44	C1	2066	A	C5-C6	-5.66	1.35	1.41
44	C1	1753	G	C5-C6	-5.65	1.36	1.42
44	C1	2072	U	N1-C2	-5.65	1.33	1.38
44	C1	254	G	C5-C4	-5.65	1.34	1.38
45	C2	57	A	C8-N7	-5.64	1.27	1.31
12	UO	432	ARG	CA-CB	-5.63	1.41	1.53
44	C1	2190	G	C5-C4	-5.63	1.34	1.38
44	C1	254	G	C6-N1	-5.63	1.35	1.39
44	C1	291	C	N1-C6	-5.63	1.33	1.37
45	C2	76	C	C4-C5	-5.63	1.38	1.43
15	UU	508	TRP	CB-CG	-5.62	1.40	1.50
44	C1	1744	A	C5-C4	-5.62	1.34	1.38
45	C2	66	A	N7-C5	-5.61	1.35	1.39
45	C2	40	C	N1-C6	-5.61	1.33	1.37
44	C1	255	G	N7-C5	-5.61	1.35	1.39
45	C2	63	G	N3-C4	-5.61	1.31	1.35
45	C2	88	A	N9-C4	-5.60	1.34	1.37
44	C1	399	G	C6-N1	-5.60	1.35	1.39
44	C1	133	G	N7-C5	-5.59	1.35	1.39
44	C1	239	G	N7-C5	-5.59	1.35	1.39
44	C1	138	A	N7-C5	-5.58	1.35	1.39
44	C1	2107	A	N7-C5	-5.58	1.35	1.39
44	C1	262	G	C5-C4	-5.58	1.34	1.38
44	C1	416	U	N1-C2	-5.58	1.33	1.38
45	C2	66	A	N3-C4	-5.55	1.31	1.34
44	C1	2067	G	N7-C5	-5.55	1.35	1.39
26	CK	186	GLU	CA-CB	-5.55	1.41	1.53
44	C1	1741	A	N7-C5	-5.54	1.35	1.39
45	C2	264	G	N3-C4	-5.54	1.31	1.35
44	C1	2214	A	N7-C5	-5.52	1.35	1.39
44	C1	2191	U	C2-N3	-5.52	1.33	1.37
45	C2	264	G	C6-N1	-5.52	1.35	1.39
44	C1	1753	G	N7-C5	-5.51	1.35	1.39
44	C1	2175	A	N3-C4	-5.51	1.31	1.34
44	C1	2156	A	N7-C5	-5.50	1.35	1.39
1	UA	40	PHE	CB-CG	-5.50	1.42	1.51
45	C2	57	A	N3-C4	-5.49	1.31	1.34
44	C1	218	G	N3-C4	-5.49	1.31	1.35
44	C1	435	A	N3-C4	-5.48	1.31	1.34
44	C1	2066	A	C6-N1	-5.48	1.31	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	C1	2107	A	C6-N1	-5.46	1.31	1.35
45	C2	49	U	C2-N3	-5.46	1.33	1.37
1	UA	453	TRP	CB-CG	-5.45	1.40	1.50
44	C1	272	A	N3-C4	-5.45	1.31	1.34
44	C1	435	A	C5-C4	-5.45	1.34	1.38
25	CJ	173	TYR	CD1-CE1	-5.45	1.31	1.39
4	UD	238	VAL	CB-CG1	-5.44	1.41	1.52
44	C1	412	G	N3-C4	-5.44	1.31	1.35
45	C2	84	G	N9-C8	-5.44	1.34	1.37
45	C2	65	C	N1-C6	-5.43	1.33	1.37
44	C1	365	G	N7-C5	-5.43	1.35	1.39
44	C1	1753	G	C5-C4	-5.43	1.34	1.38
45	C2	268	G	C5-C4	-5.43	1.34	1.38
44	C1	2064	C	N1-C6	-5.42	1.33	1.37
44	C1	73	A	C5-C6	-5.42	1.36	1.41
1	UA	518	PHE	CB-CG	-5.42	1.42	1.51
45	C2	62	A	N7-C5	-5.41	1.36	1.39
44	C1	355	G	C5-C4	-5.41	1.34	1.38
44	C1	2071	G	C5-C4	-5.41	1.34	1.38
45	C2	262	C	N1-C6	-5.41	1.33	1.37
44	C1	408	C	N3-C4	-5.40	1.30	1.33
45	C2	50	G	C5-C6	-5.40	1.36	1.42
44	C1	1749	G	C6-N1	-5.40	1.35	1.39
44	C1	76	U	C2-N3	-5.39	1.33	1.37
44	C1	148	C	C2-O2	-5.39	1.19	1.24
45	C2	35	G	C5-C6	-5.39	1.36	1.42
15	UU	86	THR	CB-CG2	-5.39	1.34	1.52
44	C1	210	G	C5-C4	-5.37	1.34	1.38
44	C1	2188	G	N3-C4	-5.37	1.31	1.35
44	C1	121	G	C6-N1	-5.35	1.35	1.39
44	C1	2198	C	N1-C6	-5.35	1.33	1.37
45	C2	265	A	N3-C4	-5.34	1.31	1.34
44	C1	2067	G	N9-C8	-5.34	1.34	1.37
18	CA	204	ILE	C-N	-5.34	1.24	1.34
44	C1	361	A	N3-C4	-5.34	1.31	1.34
44	C1	429	A	N9-C4	-5.33	1.34	1.37
44	C1	77	C	N1-C6	-5.32	1.33	1.37
44	C1	352	G	C8-N7	-5.31	1.27	1.30
44	C1	417	G	C6-N1	-5.30	1.35	1.39
44	C1	399	G	N7-C5	-5.30	1.36	1.39
44	C1	1146	G	C5-C6	-5.30	1.37	1.42
4	UD	63	TRP	CB-CG	-5.30	1.40	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	C1	417	G	C5-C6	-5.30	1.37	1.42
44	C1	401	C	N1-C6	-5.29	1.33	1.37
44	C1	1742	C	N1-C6	-5.29	1.33	1.37
44	C1	2169	A	N9-C4	-5.29	1.34	1.37
44	C1	294	G	N9-C4	-5.29	1.33	1.38
44	C1	2200	U	N1-C6	-5.29	1.33	1.38
44	C1	403	G	N3-C4	-5.28	1.31	1.35
44	C1	1748	G	C5-C4	-5.28	1.34	1.38
44	C1	2108	A	N9-C8	-5.27	1.33	1.37
45	C2	59	A	N3-C4	-5.27	1.31	1.34
44	C1	1145	G	N7-C5	-5.26	1.36	1.39
44	C1	2108	A	N3-C4	-5.26	1.31	1.34
44	C1	2167	G	N1-C2	-5.26	1.33	1.37
44	C1	73	A	N7-C5	-5.25	1.36	1.39
45	C2	265	A	N7-C5	-5.25	1.36	1.39
44	C1	1146	G	N9-C8	-5.25	1.34	1.37
44	C1	363	G	N7-C5	-5.24	1.36	1.39
44	C1	2090	G	N3-C4	-5.24	1.31	1.35
45	C2	50	G	C6-N1	-5.23	1.35	1.39
44	C1	81	G	C5-C4	-5.22	1.34	1.38
12	UO	172	TRP	CB-CG	-5.22	1.40	1.50
44	C1	2188	G	N7-C5	-5.22	1.36	1.39
4	UD	303	TYR	CD1-CE1	-5.21	1.31	1.39
44	C1	416	U	C2-N3	-5.21	1.34	1.37
44	C1	262	G	C5-C6	-5.21	1.37	1.42
44	C1	360	U	N1-C2	-5.20	1.33	1.38
44	C1	212	C	N1-C6	-5.19	1.34	1.37
44	C1	2194	A	C5-C6	-5.19	1.36	1.41
44	C1	598	A	N7-C5	-5.19	1.36	1.39
46	UV	1057	VAL	CB-CG1	-5.19	1.42	1.52
44	C1	2186	U	N1-C6	-5.19	1.33	1.38
6	UG	420	VAL	CB-CG2	-5.18	1.42	1.52
44	C1	2202	C	N3-C4	-5.18	1.30	1.33
44	C1	255	G	N9-C8	-5.18	1.34	1.37
44	C1	361	A	N9-C4	-5.18	1.34	1.37
44	C1	234	G	C6-N1	-5.17	1.35	1.39
44	C1	1155	G	N9-C4	-5.17	1.33	1.38
45	C2	82	U	C2-N3	-5.17	1.34	1.37
6	UG	229	PHE	CB-CG	-5.16	1.42	1.51
15	UU	526	TRP	CB-CG	-5.16	1.41	1.50
26	CK	282	TRP	CB-CG	-5.16	1.41	1.50
44	C1	1747	A	N7-C5	-5.16	1.36	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	C1	73	A	N3-C4	-5.15	1.31	1.34
44	C1	285	A	C5-C4	-5.15	1.35	1.38
44	C1	1155	G	C5-C6	-5.15	1.37	1.42
45	C2	46	U	N3-C4	-5.15	1.33	1.38
25	CJ	132	GLU	CB-CG	-5.15	1.42	1.52
44	C1	232	G	C6-N1	-5.15	1.35	1.39
44	C1	363	G	C6-N1	-5.15	1.35	1.39
44	C1	2065	C	N1-C6	-5.15	1.34	1.37
44	C1	1744	A	C5-C6	-5.14	1.36	1.41
44	C1	135	A	C6-N1	-5.14	1.31	1.35
44	C1	1747	A	N3-C4	-5.13	1.31	1.34
44	C1	2175	A	N7-C5	-5.13	1.36	1.39
44	C1	2071	G	C6-N1	-5.12	1.35	1.39
44	C1	2194	A	C5-C4	-5.12	1.35	1.38
1	UA	595	TYR	CD2-CE2	-5.12	1.31	1.39
1	UA	595	TYR	CE1-CZ	-5.12	1.31	1.38
17	UZ	63	TRP	CB-CG	-5.10	1.41	1.50
44	C1	404	C	C4-C5	-5.10	1.38	1.43
45	C2	55	C	N1-C6	-5.09	1.34	1.37
44	C1	1145	G	C5-C6	-5.09	1.37	1.42
44	C1	130	C	N1-C6	-5.09	1.34	1.37
44	C1	2198	C	C4-C5	-5.09	1.38	1.43
44	C1	403	G	N7-C5	-5.09	1.36	1.39
44	C1	1758	C	N1-C6	-5.08	1.34	1.37
44	C1	249	C	N3-C4	-5.07	1.30	1.33
1	UA	448	PHE	CB-CG	-5.07	1.42	1.51
44	C1	2090	G	N9-C4	-5.07	1.33	1.38
44	C1	2108	A	N7-C5	-5.06	1.36	1.39
44	C1	75	G	N7-C5	-5.06	1.36	1.39
44	C1	2214	A	N9-C4	-5.06	1.34	1.37
20	CD	432	TRP	CB-CG	-5.05	1.41	1.50
44	C1	234	G	C5-C4	-5.05	1.34	1.38
45	C2	71	U	N1-C6	-5.05	1.33	1.38
14	UR	580	TRP	CB-CG	-5.05	1.41	1.50
44	C1	406	G	N7-C5	-5.04	1.36	1.39
45	C2	267	C	N3-C4	-5.04	1.30	1.33
44	C1	2191	U	N3-C4	-5.04	1.33	1.38
1	UA	484	VAL	CB-CG2	-5.04	1.42	1.52
44	C1	2182	C	N1-C6	-5.04	1.34	1.37
45	C2	43	C	N3-C4	-5.04	1.30	1.33
45	C2	38	G	N9-C4	-5.03	1.33	1.38
6	UG	464	ASN	CA-CB	-5.03	1.40	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	C1	2107	A	N9-C8	-5.03	1.33	1.37
15	UU	74	TYR	CD2-CE2	-5.03	1.31	1.39
44	C1	253	G	C5-C6	-5.02	1.37	1.42
44	C1	241	G	N7-C5	-5.02	1.36	1.39
44	C1	262	G	C8-N7	-5.01	1.27	1.30
45	C2	63	G	N1-C2	-5.00	1.33	1.37

All (753) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	C2	2	G	O5'-P-OP1	-32.44	71.78	110.70
45	C2	2	G	OP1-P-OP2	-26.35	80.07	119.60
45	C2	2	G	O5'-P-OP2	19.04	133.54	110.70
44	C1	258	C	N1-C2-O2	13.22	126.83	118.90
45	C2	1	A	OP1-P-O3'	13.10	134.03	105.20
45	C2	1	A	OP2-P-O3'	-12.64	77.40	105.20
44	C1	258	C	C2-N1-C1'	12.50	132.55	118.80
44	C1	2168	U	N3-C2-O2	-12.41	113.51	122.20
44	C1	55	G	OP1-P-O3'	-12.05	78.68	105.20
24	CI	995	VAL	C-N-CA	12.03	151.76	121.70
45	C2	39	U	N3-C2-O2	-11.84	113.91	122.20
44	C1	2168	U	N1-C2-O2	11.17	130.62	122.80
44	C1	45	U	OP1-P-O3'	-11.01	80.98	105.20
44	C1	254	G	C6-C5-N7	-10.99	123.80	130.40
44	C1	254	G	C4-C5-N7	10.68	115.07	110.80
44	C1	258	C	N3-C2-O2	-10.49	114.56	121.90
44	C1	1146	G	N3-C4-N9	10.41	132.25	126.00
44	C1	160	C	N3-C2-O2	-10.39	114.63	121.90
44	C1	160	C	C6-N1-C2	-10.38	116.15	120.30
44	C1	265	G	C6-C5-N7	-10.20	124.28	130.40
44	C1	139	C	C6-N1-C2	-10.12	116.25	120.30
44	C1	434	A	N1-C6-N6	-9.98	112.61	118.60
45	C2	57	A	N1-C2-N3	9.92	134.26	129.30
44	C1	45	U	OP2-P-O3'	-9.73	83.80	105.20
44	C1	265	G	N9-C4-C5	-9.66	101.54	105.40
44	C1	1547	C	N1-C2-O2	9.49	124.59	118.90
44	C1	2214	A	N1-C6-N6	9.46	124.27	118.60
45	C2	267	C	N3-C2-O2	-9.42	115.31	121.90
44	C1	254	G	C5-N7-C8	-9.32	99.64	104.30
44	C1	2214	A	N9-C4-C5	-9.31	102.07	105.80
44	C1	505	C	N3-C2-O2	-9.24	115.43	121.90
44	C1	352	G	C4-C5-N7	9.18	114.47	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C1	258	C	C6-N1-C1'	-9.17	109.80	120.80
44	C1	1662	C	N3-C2-O2	-9.15	115.49	121.90
26	CK	289	ARG	NE-CZ-NH1	-9.12	115.74	120.30
44	C1	262	G	C6-C5-N7	-9.08	124.95	130.40
45	C2	140	C	N3-C2-O2	-9.01	115.59	121.90
44	C1	235	C	N3-C4-C5	8.99	125.50	121.90
44	C1	2214	A	C4-C5-N7	8.99	115.19	110.70
32	CS	188	ARG	NE-CZ-NH1	8.93	124.77	120.30
32	CR	188	ARG	NE-CZ-NH1	8.91	124.75	120.30
49	UE	238	ARG	NE-CZ-NH2	8.87	124.73	120.30
44	C1	265	G	C4-C5-N7	8.87	114.35	110.80
49	UI	238	ARG	NE-CZ-NH2	8.86	124.73	120.30
44	C1	1146	G	C6-C5-N7	-8.85	125.09	130.40
44	C1	1747	A	C6-N1-C2	-8.83	113.30	118.60
44	C1	1550	U	C2-N1-C1'	8.80	128.27	117.70
45	C2	88	A	N1-C6-N6	8.74	123.84	118.60
44	C1	262	G	N3-C4-N9	8.69	131.21	126.00
44	C1	2090	G	C2-N3-C4	-8.52	107.64	111.90
44	C1	404	C	C2-N1-C1'	8.45	128.09	118.80
44	C1	206	C	N1-C2-O2	8.43	123.96	118.90
44	C1	2090	G	N3-C4-N9	-8.42	120.95	126.00
45	C2	264	G	C8-N9-C4	-8.42	103.03	106.40
44	C1	159	C	C6-N1-C2	-8.38	116.95	120.30
44	C1	2238	A	N1-C6-N6	-8.35	113.59	118.60
30	CP	213	LEU	CA-CB-CG	8.23	134.22	115.30
45	C2	79	G	C6-C5-N7	-8.21	125.47	130.40
45	C2	35	G	C4-C5-N7	8.20	114.08	110.80
44	C1	2202	C	N3-C2-O2	-8.18	116.17	121.90
44	C1	2084	C	N3-C2-O2	-8.09	116.24	121.90
44	C1	1146	G	N3-C4-C5	-8.07	124.57	128.60
44	C1	2195	U	N3-C2-O2	-8.07	116.55	122.20
44	C1	2186	U	C5-C4-O4	-8.03	121.08	125.90
8	UK	51	LEU	CA-CB-CG	-8.02	96.86	115.30
44	C1	1486	G	C8-N9-C4	-7.99	103.20	106.40
44	C1	1486	G	N7-C8-N9	7.98	117.09	113.10
45	C2	266	C	N3-C4-C5	7.96	125.08	121.90
44	C1	1547	C	C2-N1-C1'	7.95	127.54	118.80
44	C1	148	C	N3-C2-O2	-7.93	116.34	121.90
44	C1	2214	A	C5-C6-N6	-7.92	117.36	123.70
4	UD	357	LEU	CB-CG-CD2	-7.91	97.55	111.00
45	C2	82	U	N1-C2-O2	7.88	128.32	122.80
44	C1	2186	U	C5-C6-N1	7.88	126.64	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C1	56	C	C2-N1-C1'	7.86	127.45	118.80
44	C1	2194	A	C8-N9-C4	-7.83	102.67	105.80
44	C1	265	G	N3-C4-N9	7.80	130.68	126.00
45	C2	46	U	N3-C2-O2	-7.79	116.75	122.20
44	C1	470	C	N1-C2-O2	7.78	123.57	118.90
44	C1	2165	U	C2-N1-C1'	7.77	127.02	117.70
44	C1	471	C	C6-N1-C2	-7.77	117.19	120.30
44	C1	2074	C	C2-N1-C1'	7.76	127.34	118.80
32	CR	188	ARG	NE-CZ-NH2	-7.76	116.42	120.30
32	CS	188	ARG	NE-CZ-NH2	-7.74	116.43	120.30
44	C1	254	G	N7-C8-N9	7.73	116.97	113.10
45	C2	57	A	C6-N1-C2	-7.72	113.97	118.60
44	C1	56	C	OP1-P-OP2	7.70	131.15	119.60
44	C1	1662	C	N1-C2-O2	7.67	123.50	118.90
44	C1	2164	C	C6-N1-C2	-7.67	117.23	120.30
44	C1	159	C	N3-C2-O2	-7.66	116.54	121.90
44	C1	2217	C	C2-N1-C1'	7.65	127.22	118.80
44	C1	2074	C	N1-C2-O2	7.63	123.48	118.90
45	C2	260	G	C4-N9-C1'	7.59	136.37	126.50
44	C1	46	C	OP1-P-OP2	7.59	130.99	119.60
44	C1	1655	U	N3-C2-O2	-7.56	116.91	122.20
44	C1	2177	G	N3-C4-N9	-7.56	121.47	126.00
44	C1	70	C	N1-C2-O2	7.54	123.43	118.90
44	C1	1146	G	C4-N9-C1'	7.54	136.31	126.50
44	C1	80	C	N3-C2-O2	-7.53	116.63	121.90
44	C1	505	C	N1-C2-O2	7.53	123.42	118.90
44	C1	2048	C	N3-C2-O2	-7.53	116.63	121.90
44	C1	2179	C	N1-C2-O2	7.52	123.41	118.90
45	C2	39	U	N1-C2-N3	7.52	119.41	114.90
44	C1	211	G	C8-N9-C1'	-7.50	117.25	127.00
44	C1	68	U	N3-C2-O2	-7.50	116.95	122.20
32	CS	913	MET	CB-CG-SD	7.50	134.90	112.40
32	CR	913	MET	CB-CG-SD	7.50	134.89	112.40
45	C2	76	C	N3-C4-C5	7.48	124.89	121.90
44	C1	2074	C	C6-N1-C1'	-7.45	111.86	120.80
44	C1	2176	A	C5-N7-C8	-7.45	100.17	103.90
44	C1	265	G	N1-C6-O6	7.45	124.37	119.90
44	C1	371	U	N3-C2-O2	-7.44	116.99	122.20
45	C2	35	G	N9-C4-C5	-7.44	102.42	105.40
44	C1	2107	A	C8-N9-C4	7.43	108.77	105.80
44	C1	2079	U	N3-C2-O2	-7.43	117.00	122.20
45	C2	90	C	C6-N1-C2	7.42	123.27	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	C2	260	G	C8-N9-C1'	-7.39	117.39	127.00
45	C2	88	A	C6-C5-N7	-7.37	127.14	132.30
44	C1	262	G	C4-C5-N7	7.36	113.75	110.80
44	C1	3	G	N3-C4-N9	-7.36	121.59	126.00
44	C1	1222	C	N1-C2-O2	7.35	123.31	118.90
44	C1	55	G	OP2-P-O3'	-7.34	89.05	105.20
44	C1	203	C	C6-N1-C2	-7.33	117.37	120.30
44	C1	1486	G	C4-N9-C1'	7.32	136.02	126.50
44	C1	238	G	C6-C5-N7	-7.32	126.01	130.40
45	C2	44	U	C5-C6-N1	7.32	126.36	122.70
45	C2	88	A	C4-C5-N7	7.31	114.36	110.70
44	C1	407	A	O5'-P-OP1	-7.30	99.12	105.70
44	C1	2214	A	C6-C5-N7	-7.30	127.19	132.30
32	CS	626	GLU	CA-CB-CG	7.29	129.44	113.40
45	C2	21	U	N3-C2-O2	-7.29	117.09	122.20
14	UR	587	LEU	CA-CB-CG	-7.29	98.53	115.30
32	CR	626	GLU	CA-CB-CG	7.29	129.44	113.40
44	C1	160	C	N1-C2-O2	7.28	123.27	118.90
44	C1	2195	U	N1-C2-O2	7.27	127.89	122.80
44	C1	1146	G	C8-N9-C1'	-7.27	117.55	127.00
44	C1	454	C	C2-N1-C1'	7.26	126.79	118.80
45	C2	140	C	N1-C2-O2	7.25	123.25	118.90
44	C1	352	G	C5-N7-C8	-7.23	100.68	104.30
44	C1	471	C	N3-C2-O2	-7.22	116.84	121.90
45	C2	200	U	N1-C2-O2	7.22	127.85	122.80
1	UA	695	LEU	CB-CG-CD2	-7.21	98.74	111.00
44	C1	1159	C	C6-N1-C2	7.17	123.17	120.30
44	C1	262	G	N9-C4-C5	-7.15	102.54	105.40
45	C2	203	C	N3-C2-O2	-7.14	116.90	121.90
44	C1	2194	A	N9-C4-C5	7.12	108.65	105.80
44	C1	356	C	N3-C4-C5	7.11	124.74	121.90
44	C1	446	C	N1-C2-O2	7.10	123.16	118.90
45	C2	200	U	C2-N1-C1'	7.09	126.21	117.70
44	C1	406	G	C4-C5-N7	7.09	113.64	110.80
46	UV	356	LEU	CA-CB-CG	7.09	131.61	115.30
45	C2	57	A	C4-C5-C6	7.06	120.53	117.00
46	UV	424	LEU	CA-CB-CG	7.05	131.51	115.30
44	C1	352	G	C5-C6-O6	-7.04	124.37	128.60
44	C1	34	C	N3-C2-O2	-7.00	117.00	121.90
44	C1	1165	U	N3-C2-O2	-7.00	117.30	122.20
45	C2	90	C	N3-C4-C5	7.00	124.70	121.90
44	C1	68	U	N1-C2-O2	6.99	127.69	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	UM	83	LEU	CA-CB-CG	6.97	131.33	115.30
44	C1	260	U	C2-N1-C1'	-6.95	109.36	117.70
44	C1	112	C	N1-C2-O2	6.94	123.07	118.90
44	C1	2169	A	C5-N7-C8	-6.94	100.43	103.90
44	C1	34	C	N1-C2-O2	6.93	123.06	118.90
44	C1	2210	U	C5-C4-O4	6.93	130.06	125.90
44	C1	2169	A	C6-C5-N7	-6.93	127.45	132.30
44	C1	346	C	N3-C2-O2	-6.92	117.05	121.90
32	CS	88	GLU	CA-CB-CG	6.90	128.59	113.40
44	C1	2090	G	C5-C6-O6	6.90	132.74	128.60
44	C1	2169	A	N7-C8-N9	6.90	117.25	113.80
32	CR	88	GLU	CA-CB-CG	6.89	128.56	113.40
44	C1	211	G	C4-N9-C1'	6.89	135.46	126.50
44	C1	294	G	C2-N3-C4	-6.89	108.46	111.90
44	C1	449	C	N3-C2-O2	-6.88	117.08	121.90
44	C1	1550	U	N1-C2-O2	6.88	127.62	122.80
45	C2	147	G	N3-C4-N9	6.88	130.12	126.00
44	C1	2168	U	C2-N1-C1'	6.87	125.95	117.70
44	C1	404	C	C6-N1-C2	-6.87	117.55	120.30
4	UD	253	ASP	CB-CG-OD1	6.86	124.48	118.30
44	C1	2091	C	C2-N1-C1'	6.85	126.34	118.80
44	C1	434	A	C6-N1-C2	-6.84	114.49	118.60
44	C1	504	C	N1-C2-O2	6.84	123.00	118.90
44	C1	1645	U	C2-N1-C1'	6.84	125.90	117.70
44	C1	2071	G	O4'-C1'-N9	-6.84	102.73	108.20
44	C1	2049	G	N7-C8-N9	6.83	116.52	113.10
45	C2	202	C	N1-C2-O2	6.82	122.99	118.90
44	C1	1167	C	N1-C2-O2	6.82	122.99	118.90
44	C1	2079	U	N1-C2-O2	6.82	127.57	122.80
32	CS	410	MET	CA-CB-CG	6.80	124.85	113.30
45	C2	79	G	N3-C4-N9	6.79	130.07	126.00
32	CR	410	MET	CA-CB-CG	6.79	124.84	113.30
44	C1	158	C	N1-C2-O2	6.78	122.97	118.90
45	C2	57	A	O4'-C1'-N9	6.77	113.62	108.20
45	C2	61	G	C6-C5-N7	-6.74	126.35	130.40
44	C1	404	C	C5-C6-N1	6.74	124.37	121.00
45	C2	246	G	C4-N9-C1'	6.74	135.26	126.50
46	UV	1051	LEU	CA-CB-CG	6.74	130.81	115.30
44	C1	1146	G	C4-C5-N7	6.74	113.49	110.80
44	C1	1222	C	C2-N1-C1'	6.74	126.21	118.80
45	C2	23	A	P-O3'-C3'	6.70	127.74	119.70
44	C1	346	C	C6-N1-C2	-6.70	117.62	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C1	2202	C	N1-C2-O2	6.70	122.92	118.90
45	C2	50	G	C6-C5-N7	-6.70	126.38	130.40
32	CR	654	LEU	CB-CG-CD1	-6.69	99.62	111.00
32	CS	654	LEU	CB-CG-CD1	-6.68	99.64	111.00
44	C1	239	G	N1-C6-O6	6.67	123.90	119.90
32	CR	526	LEU	CA-CB-CG	6.67	130.64	115.30
44	C1	1486	G	N3-C4-C5	-6.66	125.27	128.60
45	C2	50	G	C4-C5-N7	6.65	113.46	110.80
32	CS	526	LEU	CA-CB-CG	6.65	130.59	115.30
44	C1	1666	C	N1-C2-O2	6.63	122.88	118.90
44	C1	251	G	C4-N9-C1'	6.63	135.12	126.50
44	C1	417	G	C6-C5-N7	-6.63	126.42	130.40
44	C1	2068	C	C5-C6-N1	6.62	124.31	121.00
44	C1	258	C	C6-N1-C2	-6.62	117.65	120.30
44	C1	1630	C	N3-C2-O2	-6.62	117.27	121.90
44	C1	2176	A	N7-C8-N9	6.61	117.10	113.80
44	C1	2229	C	N1-C2-O2	6.60	122.86	118.90
44	C1	265	G	C5-C6-O6	-6.59	124.65	128.60
44	C1	56	C	N1-C2-O2	6.58	122.85	118.90
44	C1	2186	U	N3-C4-O4	6.58	124.00	119.40
32	CR	410	MET	CB-CG-SD	6.58	132.13	112.40
32	CS	410	MET	CB-CG-SD	6.57	132.12	112.40
45	C2	136	C	N1-C2-O2	6.56	122.84	118.90
44	C1	76	U	C5-C6-N1	-6.55	119.42	122.70
44	C1	2049	G	C8-N9-C4	-6.55	103.78	106.40
45	C2	79	G	C4-C5-N7	6.53	113.41	110.80
44	C1	160	C	C5-C6-N1	6.53	124.27	121.00
32	CS	487	GLU	CA-CB-CG	6.53	127.76	113.40
44	C1	485	G	N3-C4-N9	-6.52	122.09	126.00
32	CR	487	GLU	CA-CB-CG	6.52	127.75	113.40
44	C1	255	G	N3-C4-N9	6.52	129.91	126.00
44	C1	1758	C	C2-N1-C1'	-6.51	111.64	118.80
44	C1	238	G	C4-C5-N7	6.50	113.40	110.80
44	C1	1120	C	C2-N1-C1'	6.50	125.95	118.80
44	C1	1165	U	N1-C2-O2	6.50	127.35	122.80
44	C1	139	C	C5-C6-N1	6.49	124.25	121.00
44	C1	129	G	C2-N3-C4	-6.49	108.66	111.90
44	C1	2169	A	C2-N3-C4	-6.49	107.36	110.60
49	UI	238	ARG	CG-CD-NE	6.48	125.40	111.80
44	C1	2217	C	N1-C2-O2	6.47	122.78	118.90
6	UG	284	LEU	CB-CG-CD2	-6.46	100.02	111.00
49	UE	238	ARG	CG-CD-NE	6.46	125.36	111.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C1	2068	C	C4-C5-C6	-6.45	114.17	117.40
45	C2	39	U	C2-N3-C4	-6.44	123.14	127.00
44	C1	1747	A	N1-C2-N3	6.44	132.52	129.30
44	C1	222	U	O4'-C1'-N1	6.42	113.34	108.20
45	C2	88	A	C5-N7-C8	-6.41	100.70	103.90
44	C1	447	C	N3-C2-O2	-6.40	117.42	121.90
44	C1	1156	C	C5-C6-N1	-6.40	117.80	121.00
45	C2	45	C	N3-C4-C5	6.40	124.46	121.90
44	C1	265	G	C8-N9-C1'	-6.40	118.68	127.00
15	UU	472	LEU	CA-CB-CG	6.39	129.99	115.30
44	C1	402	U	N1-C2-O2	6.39	127.27	122.80
44	C1	2090	G	N1-C2-N3	6.38	127.73	123.90
44	C1	290	C	C5-C6-N1	-6.38	117.81	121.00
44	C1	602	U	N3-C2-O2	-6.37	117.74	122.20
7	UJ	488	LEU	CA-CB-CG	6.37	129.95	115.30
45	C2	202	C	N3-C2-O2	-6.36	117.45	121.90
44	C1	210	G	O5'-P-OP1	-6.36	99.97	105.70
44	C1	434	A	N9-C4-C5	6.36	108.34	105.80
44	C1	179	G	N3-C4-C5	6.36	131.78	128.60
45	C2	268	G	C4-C5-N7	6.35	113.34	110.80
45	C2	82	U	N3-C2-O2	-6.33	117.77	122.20
45	C2	39	U	O5'-P-OP2	-6.33	100.00	105.70
44	C1	70	C	C6-N1-C1'	-6.33	113.20	120.80
32	CS	855	LEU	CA-CB-CG	6.33	129.86	115.30
44	C1	236	C	C5-C6-N1	6.33	124.16	121.00
32	CR	855	LEU	CA-CB-CG	6.32	129.83	115.30
44	C1	1645	U	N1-C2-O2	6.32	127.22	122.80
44	C1	2191	U	N3-C2-O2	-6.31	117.78	122.20
44	C1	56	C	C6-N1-C1'	-6.31	113.23	120.80
44	C1	334	U	N1-C2-O2	6.31	127.22	122.80
44	C1	369	U	N3-C2-O2	-6.31	117.78	122.20
44	C1	258	C	C5-C6-N1	6.31	124.15	121.00
45	C2	49	U	N3-C2-O2	-6.30	117.79	122.20
44	C1	1645	U	N3-C2-O2	-6.29	117.79	122.20
44	C1	203	C	N3-C2-O2	-6.29	117.50	121.90
32	CS	51	ARG	CA-CB-CG	6.28	127.22	113.40
44	C1	415	C	C6-N1-C2	-6.28	117.79	120.30
32	CR	51	ARG	CA-CB-CG	6.28	127.21	113.40
44	C1	486	G	N3-C4-N9	-6.28	122.23	126.00
45	C2	42	U	N3-C2-O2	-6.26	117.81	122.20
44	C1	143	A	C5-C6-N1	6.26	120.83	117.70
49	UE	263	LEU	CA-CB-CG	-6.25	100.91	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C1	2214	A	C5-N7-C8	-6.25	100.77	103.90
48	UH	789	LEU	CB-CG-CD2	-6.25	100.38	111.00
49	UI	263	LEU	CA-CB-CG	-6.25	100.93	115.30
45	C2	23	A	C5-C6-N1	6.24	120.82	117.70
44	C1	2223	C	C2-N1-C1'	6.23	125.65	118.80
44	C1	432	G	C4-C5-N7	6.21	113.29	110.80
44	C1	70	C	C2-N1-C1'	6.21	125.63	118.80
44	C1	275	C	C5-C6-N1	6.21	124.10	121.00
24	CI	240	THR	C-N-CA	-6.20	106.20	121.70
44	C1	260	U	O5'-P-OP2	-6.19	100.13	105.70
44	C1	1080	G	N3-C4-N9	6.18	129.71	126.00
44	C1	2183	A	C4-C5-N7	6.18	113.79	110.70
44	C1	205	C	P-O3'-C3'	6.18	127.12	119.70
44	C1	1758	C	C2-N3-C4	-6.18	116.81	119.90
44	C1	63	C	N1-C2-O2	6.17	122.60	118.90
44	C1	471	C	C6-N1-C1'	6.17	128.20	120.80
15	UU	502	LEU	CB-CG-CD2	-6.16	100.52	111.00
44	C1	1753	G	C4-C5-N7	6.16	113.27	110.80
44	C1	3	G	N9-C4-C5	6.15	107.86	105.40
44	C1	1155	G	C4-C5-N7	6.14	113.26	110.80
44	C1	1711	G	N3-C4-C5	-6.14	125.53	128.60
45	C2	200	U	N3-C2-O2	-6.14	117.90	122.20
44	C1	398	C	N3-C4-C5	6.14	124.35	121.90
12	UO	474	ASP	CB-CG-OD1	6.13	123.82	118.30
44	C1	208	A	C5-C6-N1	6.13	120.77	117.70
44	C1	583	A	O5'-P-OP1	-6.13	100.19	105.70
44	C1	236	C	C2-N1-C1'	6.12	125.53	118.80
44	C1	2195	U	C2-N1-C1'	6.12	125.04	117.70
44	C1	1471	U	C2-N1-C1'	6.11	125.04	117.70
46	UV	1054	LEU	CA-CB-CG	6.11	129.36	115.30
44	C1	148	C	C6-N1-C2	-6.11	117.86	120.30
44	C1	179	G	N3-C4-N9	-6.11	122.33	126.00
44	C1	437	G	C8-N9-C4	6.11	108.84	106.40
32	CR	426	LEU	CA-CB-CG	6.10	129.32	115.30
44	C1	2177	G	N9-C4-C5	6.09	107.84	105.40
44	C1	281	U	P-O3'-C3'	6.09	127.01	119.70
44	C1	1658	G	C5-C6-O6	6.09	132.25	128.60
44	C1	446	C	N3-C2-O2	-6.09	117.64	121.90
44	C1	410	G	N3-C4-C5	-6.08	125.56	128.60
45	C2	42	U	C2-N1-C1'	6.08	125.00	117.70
32	CS	426	LEU	CA-CB-CG	6.08	129.28	115.30
44	C1	1549	U	N3-C4-C5	6.08	118.25	114.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C1	1146	G	N3-C2-N2	6.08	124.15	119.90
44	C1	253	G	C5-C6-N1	6.07	114.54	111.50
44	C1	352	G	C6-C5-N7	-6.07	126.76	130.40
44	C1	133	G	C5-N7-C8	-6.06	101.27	104.30
45	C2	265	A	C8-N9-C4	6.06	108.22	105.80
45	C2	88	A	C5-C6-N6	-6.06	118.85	123.70
44	C1	21	C	N3-C2-O2	-6.06	117.66	121.90
45	C2	61	G	N1-C6-O6	6.05	123.53	119.90
44	C1	1626	G	C8-N9-C4	-6.05	103.98	106.40
44	C1	1550	U	N3-C2-O2	-6.05	117.97	122.20
45	C2	246	G	N3-C4-N9	6.05	129.63	126.00
45	C2	38	G	O4'-C1'-N9	-6.04	103.36	108.20
44	C1	2176	A	C5-C6-N6	-6.04	118.87	123.70
44	C1	33	C	N3-C2-O2	-6.04	117.67	121.90
44	C1	262	G	C8-N9-C1'	-6.04	119.15	127.00
44	C1	1149	C	C6-N1-C2	6.04	122.72	120.30
32	CR	188	ARG	CG-CD-NE	6.03	124.46	111.80
44	C1	139	C	C2-N1-C1'	6.02	125.42	118.80
44	C1	236	C	C6-N1-C2	-6.02	117.89	120.30
44	C1	244	G	N1-C6-O6	-6.02	116.29	119.90
44	C1	470	C	C2-N1-C1'	6.01	125.41	118.80
44	C1	1736	A	N7-C8-N9	6.01	116.81	113.80
32	CS	188	ARG	CG-CD-NE	6.01	124.42	111.80
44	C1	1711	G	N3-C4-N9	6.00	129.60	126.00
45	C2	246	G	C8-N9-C1'	-5.99	119.21	127.00
44	C1	1646	U	O4'-C1'-N1	5.99	112.99	108.20
44	C1	428	G	C8-N9-C4	-5.99	104.00	106.40
44	C1	251	G	C8-N9-C1'	-5.99	119.22	127.00
44	C1	1075	C	C2-N1-C1'	-5.99	112.22	118.80
44	C1	154	C	C2-N1-C1'	5.98	125.38	118.80
44	C1	268	G	C4-C5-N7	5.98	113.19	110.80
44	C1	413	C	C2-N1-C1'	5.98	125.38	118.80
44	C1	1137	G	C6-C5-N7	-5.97	126.82	130.40
45	C2	35	G	C8-N9-C4	5.97	108.79	106.40
44	C1	1625	G	N3-C4-N9	5.96	129.58	126.00
44	C1	1163	A	P-O3'-C3'	5.96	126.85	119.70
44	C1	1550	U	C6-N1-C1'	-5.96	112.85	121.20
44	C1	434	A	C5-C6-N1	5.96	120.68	117.70
44	C1	2096	G	C5-C6-O6	5.95	132.17	128.60
45	C2	136	C	C2-N1-C1'	5.95	125.34	118.80
44	C1	206	C	C2-N1-C1'	5.93	125.32	118.80
44	C1	1146	G	N1-C2-N2	-5.93	110.86	116.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C1	2107	A	N7-C8-N9	-5.93	110.83	113.80
12	UO	110	ASP	CB-CG-OD2	5.93	123.63	118.30
45	C2	22	C	N1-C2-O2	5.92	122.45	118.90
12	UO	457	LEU	CA-CB-CG	-5.91	101.70	115.30
4	UD	253	ASP	CB-CG-OD2	-5.91	112.98	118.30
44	C1	75	G	C6-C5-N7	-5.90	126.86	130.40
44	C1	491	G	C4-N9-C1'	5.90	134.17	126.50
45	C2	47	U	C2-N1-C1'	5.90	124.78	117.70
44	C1	145	C	N1-C2-O2	5.89	122.44	118.90
44	C1	255	G	C6-C5-N7	-5.89	126.86	130.40
44	C1	2090	G	N3-C4-C5	5.89	131.55	128.60
44	C1	253	G	C4-C5-N7	5.89	113.16	110.80
44	C1	424	U	C5-C6-N1	5.88	125.64	122.70
44	C1	1547	C	N3-C2-O2	-5.88	117.78	121.90
45	C2	260	G	N3-C4-N9	5.88	129.53	126.00
1	UA	656	LEU	CA-CB-CG	-5.87	101.80	115.30
45	C2	255	U	P-O3'-C3'	5.87	126.75	119.70
44	C1	209	A	P-O3'-C3'	5.87	126.74	119.70
49	UI	238	ARG	NE-CZ-NH1	-5.87	117.37	120.30
44	C1	1758	C	C5-C6-N1	-5.85	118.07	121.00
26	CK	89	LEU	CB-CG-CD2	-5.85	101.06	111.00
32	CS	151	LEU	CA-CB-CG	5.85	128.75	115.30
44	C1	277	U	P-O3'-C3'	5.85	126.72	119.70
44	C1	1167	C	C6-N1-C2	-5.85	117.96	120.30
44	C1	2177	G	P-O3'-C3'	5.85	126.72	119.70
44	C1	1560	C	N3-C2-O2	-5.84	117.81	121.90
45	C2	79	G	C4-N9-C1'	5.84	134.09	126.50
45	C2	35	G	C6-C5-N7	-5.84	126.90	130.40
45	C2	61	G	C4-C5-N7	5.84	113.14	110.80
26	CK	116	ARG	NE-CZ-NH2	-5.83	117.38	120.30
45	C2	65	C	C6-N1-C2	-5.83	117.97	120.30
44	C1	1736	A	C5-N7-C8	-5.83	100.98	103.90
44	C1	2156	A	N1-C6-N6	5.83	122.10	118.60
44	C1	2157	G	C4-N9-C1'	-5.83	118.92	126.50
45	C2	35	G	N1-C6-O6	5.83	123.40	119.90
32	CR	151	LEU	CA-CB-CG	5.83	128.71	115.30
44	C1	239	G	C6-C5-N7	-5.83	126.90	130.40
28	CM	397	LEU	CA-CB-CG	-5.81	101.93	115.30
45	C2	90	C	C2-N3-C4	-5.81	116.99	119.90
44	C1	209	A	C5-C6-N1	5.81	120.60	117.70
44	C1	347	C	N1-C2-O2	5.80	122.38	118.90
44	C1	252	U	C2-N1-C1'	5.80	124.66	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C1	1711	G	C4-N9-C1'	5.80	134.04	126.50
15	UU	502	LEU	CA-CB-CG	5.80	128.63	115.30
46	UV	364	LEU	CA-CB-CG	5.80	128.63	115.30
44	C1	260	U	C6-N1-C1'	5.79	129.31	121.20
44	C1	238	G	C5-N7-C8	-5.79	101.40	104.30
44	C1	1745	C	C6-N1-C2	-5.79	117.98	120.30
44	C1	1157	C	C6-N1-C2	5.79	122.61	120.30
44	C1	334	U	C2-N1-C1'	5.79	124.64	117.70
44	C1	203	C	C2-N1-C1'	5.79	125.17	118.80
44	C1	1137	G	C4-C5-N7	5.78	113.11	110.80
32	CS	14	LEU	CA-CB-CG	5.78	128.58	115.30
44	C1	1753	G	N9-C4-C5	-5.77	103.09	105.40
44	C1	2183	A	C5-C6-N6	-5.77	119.08	123.70
45	C2	57	A	N3-C4-N9	5.77	132.02	127.40
44	C1	2186	U	N3-C2-O2	5.77	126.24	122.20
32	CR	14	LEU	CA-CB-CG	5.77	128.57	115.30
44	C1	133	G	C4-C5-N7	5.77	113.11	110.80
44	C1	433	G	N1-C6-O6	-5.77	116.44	119.90
44	C1	255	G	N9-C4-C5	-5.77	103.09	105.40
45	C2	128	C	O4'-C1'-N1	5.76	112.81	108.20
44	C1	241	G	C4-C5-N7	5.76	113.11	110.80
44	C1	275	C	N1-C2-O2	5.76	122.36	118.90
44	C1	1222	C	N3-C2-O2	-5.76	117.87	121.90
44	C1	433	G	N9-C4-C5	5.75	107.70	105.40
44	C1	1666	C	C2-N1-C1'	5.75	125.12	118.80
44	C1	404	C	N1-C2-O2	5.74	122.35	118.90
44	C1	1145	G	C4-C5-N7	5.74	113.10	110.80
15	UU	715	PHE	CB-CA-C	-5.74	98.92	110.40
32	CS	430	LYS	CA-CB-CG	5.74	126.03	113.40
44	C1	370	C	N1-C2-O2	5.74	122.34	118.90
44	C1	1155	G	C2-N3-C4	-5.74	109.03	111.90
44	C1	131	G	C8-N9-C4	5.74	108.69	106.40
44	C1	143	A	N9-C4-C5	-5.74	103.51	105.80
44	C1	208	A	C4-C5-C6	-5.74	114.13	117.00
45	C2	90	C	C5-C6-N1	-5.73	118.13	121.00
44	C1	2227	C	C2-N1-C1'	5.73	125.10	118.80
32	CR	430	LYS	CA-CB-CG	5.73	126.00	113.40
44	C1	254	G	C4-N9-C1'	5.72	133.94	126.50
49	UE	238	ARG	NE-CZ-NH1	-5.72	117.44	120.30
44	C1	183	C	C2-N1-C1'	5.72	125.09	118.80
44	C1	454	C	C6-N1-C1'	-5.72	113.94	120.80
44	C1	1714	G	N3-C4-N9	5.71	129.43	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	UQ	466	LEU	CA-CB-CG	-5.71	102.16	115.30
45	C2	66	A	C5-N7-C8	-5.71	101.05	103.90
28	CM	75	ASP	CB-CG-OD1	5.70	123.43	118.30
1	UA	81	LEU	CA-CB-CG	5.70	128.42	115.30
13	UQ	423	LEU	CB-CG-CD2	-5.70	101.31	111.00
44	C1	1145	G	C6-C5-N7	-5.70	126.98	130.40
44	C1	1167	C	N3-C2-O2	-5.70	117.91	121.90
45	C2	6	C	C5-C6-N1	5.70	123.85	121.00
44	C1	1113	C	N1-C2-O2	5.70	122.32	118.90
46	UV	1031	LEU	CA-CB-CG	5.69	128.39	115.30
44	C1	582	G	C8-N9-C4	5.69	108.67	106.40
45	C2	252	C	N3-C2-O2	-5.68	117.92	121.90
44	C1	491	G	C8-N9-C1'	-5.67	119.62	127.00
32	CS	913	MET	CA-CB-CG	5.67	122.94	113.30
44	C1	2084	C	C6-N1-C2	-5.67	118.03	120.30
45	C2	57	A	C6-C5-N7	-5.67	128.33	132.30
44	C1	1137	G	N9-C4-C5	-5.67	103.13	105.40
32	CR	913	MET	CA-CB-CG	5.66	122.93	113.30
44	C1	1560	C	N1-C2-O2	5.66	122.29	118.90
44	C1	247	C	N3-C2-O2	-5.65	117.95	121.90
44	C1	2177	G	OP2-P-O3'	5.65	117.62	105.20
45	C2	74	C	N3-C2-O2	-5.65	117.95	121.90
45	C2	35	G	C2-N3-C4	-5.64	109.08	111.90
44	C1	255	G	C8-N9-C1'	-5.64	119.67	127.00
44	C1	2179	C	N3-C4-N4	-5.63	114.06	118.00
45	C2	246	G	N3-C4-C5	-5.63	125.78	128.60
44	C1	434	A	C4-C5-N7	-5.62	107.89	110.70
44	C1	206	C	N3-C2-O2	-5.62	117.96	121.90
44	C1	371	U	N1-C2-O2	5.62	126.73	122.80
40	Cm	86	LEU	CA-CB-CG	5.62	128.22	115.30
45	C2	63	G	C6-C5-N7	-5.62	127.03	130.40
48	UH	739	LEU	CA-CB-CG	5.62	128.22	115.30
44	C1	2169	A	N1-C6-N6	5.61	121.97	118.60
44	C1	195	U	C5-C4-O4	-5.61	122.53	125.90
9	UL	924	LEU	CB-CG-CD2	-5.61	101.47	111.00
44	C1	3	G	C5-C6-O6	5.61	131.96	128.60
45	C2	100	G	N9-C4-C5	-5.61	103.16	105.40
44	C1	143	A	C5-C6-N6	-5.60	119.22	123.70
44	C1	222	U	C5-C6-N1	-5.59	119.91	122.70
44	C1	2165	U	C5-C6-N1	5.58	125.49	122.70
44	C1	73	A	C5-N7-C8	-5.58	101.11	103.90
44	C1	183	C	N1-C2-O2	5.58	122.25	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	UG	234	LEU	CA-CB-CG	-5.58	102.48	115.30
45	C2	35	G	C5-C6-O6	-5.58	125.25	128.60
45	C2	49	U	C5-C4-O4	5.58	129.25	125.90
44	C1	262	G	C5-C6-O6	-5.57	125.26	128.60
44	C1	428	G	N3-C4-C5	-5.57	125.81	128.60
44	C1	281	U	C2-N1-C1'	5.57	124.39	117.70
44	C1	113	C	C2-N1-C1'	5.57	124.93	118.80
44	C1	1625	G	N3-C4-C5	-5.57	125.82	128.60
44	C1	2183	A	C5-N7-C8	-5.57	101.12	103.90
44	C1	1745	C	C2-N1-C1'	5.57	124.92	118.80
44	C1	2074	C	C5-C4-N4	-5.57	116.30	120.20
44	C1	2216	A	C5-C6-N1	5.56	120.48	117.70
45	C2	81	G	C6-C5-N7	-5.56	127.07	130.40
45	C2	36	U	C2-N1-C1'	-5.56	111.03	117.70
44	C1	252	U	N3-C2-O2	-5.55	118.31	122.20
44	C1	1165	U	C2-N1-C1'	5.55	124.37	117.70
45	C2	63	G	C4-C5-N7	5.55	113.02	110.80
44	C1	1157	C	N3-C4-C5	5.54	124.12	121.90
44	C1	1658	G	N3-C4-N9	-5.54	122.68	126.00
44	C1	1168	C	C6-N1-C2	5.54	122.52	120.30
44	C1	281	U	OP1-P-O3'	5.54	117.38	105.20
44	C1	1146	G	N9-C4-C5	-5.53	103.19	105.40
44	C1	2049	G	C6-C5-N7	-5.53	127.08	130.40
45	C2	264	G	N9-C4-C5	5.53	107.61	105.40
44	C1	1547	C	C6-N1-C1'	-5.53	114.17	120.80
45	C2	39	U	N1-C2-O2	5.53	126.67	122.80
1	UA	312	LEU	CA-CB-CG	-5.53	102.59	115.30
44	C1	434	A	C2-N3-C4	5.53	113.36	110.60
44	C1	2189	C	N1-C2-O2	5.53	122.22	118.90
44	C1	1547	C	C5-C6-N1	5.51	123.76	121.00
26	CK	136	LEU	CB-CG-CD1	-5.50	101.65	111.00
44	C1	18	G	N3-C4-C5	-5.50	125.85	128.60
44	C1	1142	U	O5'-P-OP1	-5.50	100.75	105.70
45	C2	23	A	C6-N1-C2	-5.50	115.30	118.60
15	UU	130	GLU	C-N-CA	-5.50	107.95	121.70
45	C2	57	A	N3-C4-C5	-5.50	122.95	126.80
44	C1	2106	U	N3-C2-O2	-5.50	118.35	122.20
44	C1	404	C	C6-N1-C1'	-5.49	114.21	120.80
1	UA	680	PHE	C-N-CA	-5.48	107.99	121.70
17	UZ	163	LEU	CA-CB-CG	-5.48	102.69	115.30
7	UJ	167	LEU	CA-CB-CG	-5.48	102.70	115.30
44	C1	209	A	C8-N9-C4	-5.48	103.61	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C1	406	G	N1-C6-O6	5.48	123.19	119.90
44	C1	1167	C	C5-C6-N1	5.48	123.74	121.00
44	C1	1753	G	C6-C5-N7	-5.48	127.11	130.40
44	C1	39	C	C2-N1-C1'	5.47	124.82	118.80
44	C1	428	G	C6-N1-C2	-5.47	121.82	125.10
44	C1	2156	A	C5-C6-N6	-5.46	119.33	123.70
44	C1	398	C	C2-N3-C4	-5.46	117.17	119.90
44	C1	1626	G	N7-C8-N9	5.46	115.83	113.10
44	C1	2053	C	N3-C4-C5	5.46	124.08	121.90
44	C1	112	C	C5-C6-N1	5.45	123.73	121.00
44	C1	260	U	C5-C6-N1	-5.45	119.97	122.70
45	C2	67	C	C6-N1-C2	-5.45	118.12	120.30
44	C1	334	U	N3-C2-O2	-5.45	118.38	122.20
44	C1	2217	C	N3-C2-O2	-5.45	118.08	121.90
44	C1	1458	U	N1-C2-O2	5.44	126.61	122.80
44	C1	18	G	C4-N9-C1'	5.44	133.57	126.50
44	C1	1711	G	C2-N3-C4	5.43	114.61	111.90
44	C1	1753	G	C2-N3-C4	-5.42	109.19	111.90
7	UJ	796	LEU	CA-CB-CG	5.41	127.74	115.30
44	C1	247	C	C6-N1-C2	-5.41	118.14	120.30
44	C1	418	G	C6-C5-N7	-5.41	127.16	130.40
46	UV	329	LEU	CA-CB-CG	5.41	127.74	115.30
44	C1	259	U	P-O3'-C3'	5.41	126.19	119.70
44	C1	406	G	C5-C6-O6	-5.40	125.36	128.60
45	C2	131	U	N1-C2-O2	5.40	126.58	122.80
32	CR	188	ARG	CD-NE-CZ	5.40	131.16	123.60
32	CS	188	ARG	CD-NE-CZ	5.40	131.16	123.60
44	C1	593	G	OP2-P-O3'	5.39	117.06	105.20
17	UZ	167	LEU	CA-CB-CG	-5.39	102.90	115.30
44	C1	2118	U	C6-N1-C2	5.39	124.23	121.00
44	C1	2156	A	P-O3'-C3'	5.39	126.17	119.70
45	C2	10	A	N9-C4-C5	-5.38	103.65	105.80
44	C1	112	C	C2-N1-C1'	5.38	124.72	118.80
44	C1	1485	A	P-O3'-C3'	5.38	126.16	119.70
44	C1	148	C	N1-C2-N3	5.38	122.97	119.20
46	UV	640	LEU	CA-CB-CG	5.37	127.66	115.30
44	C1	63	C	C2-N1-C1'	5.37	124.71	118.80
44	C1	2176	A	C8-N9-C4	-5.37	103.65	105.80
45	C2	36	U	O4'-C1'-N1	5.37	112.50	108.20
44	C1	133	G	C8-N9-C4	-5.37	104.25	106.40
44	C1	346	C	C5-C6-N1	5.37	123.68	121.00
45	C2	63	G	C8-N9-C4	-5.36	104.25	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	C2	100	G	C4-C5-N7	5.36	112.94	110.80
45	C2	147	G	C4-N9-C1'	5.36	133.47	126.50
44	C1	121	G	C4-N9-C1'	5.36	133.46	126.50
45	C2	86	U	N3-C2-O2	-5.36	118.45	122.20
44	C1	215	A	C6-N1-C2	-5.35	115.39	118.60
44	C1	462	G	C5-C6-O6	5.35	131.81	128.60
45	C2	131	U	C2-N1-C1'	5.35	124.12	117.70
45	C2	61	G	C2-N3-C4	-5.35	109.23	111.90
44	C1	61	G	C4-N9-C1'	-5.34	119.55	126.50
14	UR	432	LEU	CA-CB-CG	5.34	127.59	115.30
44	C1	1658	G	N1-C6-O6	-5.34	116.70	119.90
44	C1	121	G	C6-C5-N7	-5.34	127.20	130.40
44	C1	448	C	N3-C2-O2	-5.33	118.17	121.90
44	C1	262	G	C4-N9-C1'	5.33	133.43	126.50
44	C1	268	G	N9-C4-C5	-5.33	103.27	105.40
10	UM	696	LEU	CA-CB-CG	5.33	127.55	115.30
44	C1	133	G	N7-C8-N9	5.33	115.76	113.10
44	C1	203	C	N1-C2-O2	5.33	122.10	118.90
44	C1	2206	C	N3-C4-C5	5.33	124.03	121.90
44	C1	158	C	C2-N1-C1'	5.32	124.66	118.80
45	C2	91	G	C4-C5-N7	5.32	112.93	110.80
44	C1	1754	G	N3-C4-C5	-5.32	125.94	128.60
44	C1	2078	C	C6-N1-C1'	5.32	127.18	120.80
44	C1	154	C	N1-C2-O2	5.32	122.09	118.90
44	C1	369	U	C2-N1-C1'	5.32	124.08	117.70
45	C2	63	G	C4-N9-C1'	5.31	133.41	126.50
44	C1	156	C	C5-C6-N1	5.31	123.66	121.00
44	C1	1666	C	C5-C6-N1	5.31	123.66	121.00
44	C1	2200	U	C5-C6-N1	-5.31	120.05	122.70
44	C1	2119	G	C4-N9-C1'	5.31	133.40	126.50
45	C2	44	U	C2-N1-C1'	5.31	124.07	117.70
44	C1	1661	C	C2-N3-C4	-5.30	117.25	119.90
44	C1	2078	C	C2-N1-C1'	-5.30	112.97	118.80
45	C2	22	C	N3-C2-O2	-5.30	118.19	121.90
45	C2	23	A	C5-C6-N6	-5.29	119.47	123.70
44	C1	135	A	OP2-P-O3'	5.29	116.84	105.20
44	C1	137	C	C6-N1-C2	-5.29	118.18	120.30
44	C1	2201	C	C6-N1-C2	5.29	122.42	120.30
44	C1	1156	C	C6-N1-C2	5.28	122.41	120.30
44	C1	2217	C	C6-N1-C1'	-5.28	114.46	120.80
46	UV	609	LEU	CA-CB-CG	5.28	127.45	115.30
44	C1	2156	A	C4-C5-N7	5.28	113.34	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	C2	264	G	N7-C8-N9	5.28	115.74	113.10
44	C1	255	G	C4-C5-N7	5.27	112.91	110.80
44	C1	18	G	N3-C4-N9	5.27	129.16	126.00
44	C1	1448	A	C5-C6-N1	5.27	120.34	117.70
44	C1	1658	G	N9-C4-C5	5.27	107.51	105.40
44	C1	129	G	N1-C2-N3	5.27	127.06	123.90
44	C1	208	A	N1-C6-N6	-5.27	115.44	118.60
44	C1	2090	G	N9-C4-C5	5.26	107.50	105.40
44	C1	344	C	N3-C4-C5	5.26	124.00	121.90
44	C1	2074	C	C5-C6-N1	5.26	123.63	121.00
45	C2	147	G	C8-N9-C1'	-5.26	120.16	127.00
45	C2	44	U	C6-N1-C2	-5.25	117.85	121.00
44	C1	1655	U	N1-C2-N3	5.25	118.05	114.90
45	C2	58	A	O5'-P-OP1	-5.25	100.97	105.70
44	C1	1161	G	C6-C5-N7	-5.24	127.25	130.40
45	C2	46	U	C6-N1-C2	-5.24	117.86	121.00
44	C1	135	A	N1-C6-N6	-5.24	115.46	118.60
44	C1	2169	A	C8-N9-C4	-5.24	103.71	105.80
52	CX	296	LEU	CA-CB-CG	5.23	127.33	115.30
45	C2	79	G	C8-N9-C1'	-5.23	120.20	127.00
44	C1	1633	A	N1-C6-N6	-5.23	115.46	118.60
44	C1	406	G	C5-N7-C8	-5.22	101.69	104.30
45	C2	66	A	C6-N1-C2	-5.22	115.47	118.60
44	C1	470	C	N3-C2-O2	-5.22	118.25	121.90
44	C1	343	C	N3-C2-O2	-5.21	118.25	121.90
44	C1	439	A	C4-C5-N7	5.21	113.31	110.70
44	C1	208	A	C6-C5-N7	5.21	135.95	132.30
45	C2	200	U	C5-C6-N1	5.21	125.31	122.70
1	UA	509	LEU	CB-CG-CD1	-5.21	102.15	111.00
44	C1	491	G	N3-C4-N9	5.21	129.12	126.00
44	C1	496	U	N1-C2-O2	5.21	126.44	122.80
44	C1	596	U	C2-N3-C4	-5.21	123.88	127.00
44	C1	28	C	N1-C2-O2	5.20	122.02	118.90
44	C1	133	G	N1-C6-O6	5.20	123.02	119.90
44	C1	2179	C	N3-C2-O2	-5.20	118.26	121.90
44	C1	1754	G	N1-C6-O6	-5.19	116.78	119.90
44	C1	290	C	C6-N1-C2	5.19	122.38	120.30
44	C1	69	U	O5'-P-OP1	-5.18	101.03	105.70
2	UB	818	ASP	CB-CG-OD2	5.18	122.96	118.30
44	C1	1114	C	N1-C2-O2	5.18	122.01	118.90
44	C1	190	G	N3-C4-N9	-5.17	122.90	126.00
44	C1	2084	C	N1-C2-N3	5.17	122.82	119.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C1	486	G	N3-C4-C5	5.16	131.18	128.60
44	C1	135	A	O4'-C1'-N9	-5.16	104.07	108.20
44	C1	447	C	C6-N1-C2	-5.16	118.24	120.30
44	C1	347	C	N3-C2-O2	-5.16	118.29	121.90
44	C1	1080	G	N3-C4-C5	-5.16	126.02	128.60
44	C1	247	C	C2-N1-C1'	5.15	124.46	118.80
44	C1	1075	C	N3-C2-O2	-5.15	118.30	121.90
45	C2	23	A	N3-C4-N9	5.15	131.52	127.40
44	C1	2047	G	P-O3'-C3'	5.15	125.88	119.70
44	C1	2091	C	C6-N1-C1'	-5.15	114.62	120.80
45	C2	139	C	N1-C2-O2	5.15	121.99	118.90
20	CD	107	ILE	C-N-CA	-5.14	108.84	121.70
44	C1	462	G	N1-C6-O6	-5.14	116.82	119.90
13	UQ	456	TRP	CA-CB-CG	-5.13	103.95	113.70
45	C2	70	A	N1-C6-N6	-5.13	115.52	118.60
45	C2	28	U	C5-C6-N1	-5.13	120.13	122.70
45	C2	161	G	C4-N9-C1'	5.13	133.17	126.50
45	C2	260	G	C6-C5-N7	-5.13	127.32	130.40
44	C1	239	G	C4-C5-N7	5.13	112.85	110.80
44	C1	111	U	N3-C2-O2	-5.13	118.61	122.20
44	C1	353	G	C4-C5-N7	5.13	112.85	110.80
44	C1	2169	A	C4-C5-N7	5.13	113.26	110.70
44	C1	2171	G	C4-C5-N7	5.13	112.85	110.80
44	C1	417	G	C4-C5-N7	5.12	112.85	110.80
44	C1	2176	A	N1-C6-N6	5.12	121.67	118.60
44	C1	244	G	C6-N1-C2	-5.12	122.03	125.10
20	CD	371	LEU	CB-CG-CD1	-5.11	102.31	111.00
44	C1	150	C	P-O3'-C3'	5.11	125.84	119.70
45	C2	36	U	C5-C6-N1	-5.11	120.14	122.70
44	C1	81	G	C5-C6-N1	5.11	114.06	111.50
44	C1	1547	C	C6-N1-C2	-5.11	118.26	120.30
44	C1	1149	C	C5-C6-N1	-5.11	118.45	121.00
45	C2	148	G	C5-C6-O6	5.11	131.66	128.60
45	C2	268	G	N9-C4-C5	-5.11	103.36	105.40
24	CI	263	LEU	CA-CB-CG	5.10	127.04	115.30
44	C1	2049	G	C5-N7-C8	-5.10	101.75	104.30
10	UM	861	ASP	CB-CG-OD2	5.10	122.89	118.30
32	CR	848	LEU	CA-CB-CG	5.10	127.03	115.30
44	C1	193	U	N1-C2-O2	5.10	126.37	122.80
44	C1	2157	G	C8-N9-C1'	5.10	133.63	127.00
44	C1	281	U	N1-C2-O2	5.09	126.37	122.80
35	Ce	40	LEU	CA-CB-CG	5.09	127.02	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C1	365	G	C4-C5-N7	5.09	112.84	110.80
44	C1	2217	C	C6-N1-C2	-5.09	118.26	120.30
44	C1	39	C	N1-C2-O2	5.09	121.95	118.90
44	C1	265	G	N3-C2-N2	5.08	123.46	119.90
44	C1	454	C	N1-C2-O2	5.08	121.95	118.90
44	C1	2078	C	N3-C4-N4	-5.08	114.44	118.00
45	C2	246	G	OP1-P-O3'	5.08	116.37	105.20
32	CS	848	LEU	CA-CB-CG	5.08	126.97	115.30
44	C1	370	C	N3-C2-O2	-5.08	118.35	121.90
44	C1	61	G	O4'-C1'-N9	5.07	112.26	108.20
44	C1	1626	G	C6-N1-C2	-5.07	122.06	125.10
44	C1	495	G	N3-C4-N9	5.07	129.04	126.00
44	C1	212	C	C6-N1-C2	5.07	122.33	120.30
44	C1	2116	C	N3-C4-C5	5.07	123.93	121.90
45	C2	35	G	N3-C4-C5	5.07	131.13	128.60
45	C2	57	A	C4-N9-C1'	5.07	135.42	126.30
44	C1	1155	G	N9-C4-C5	-5.06	103.38	105.40
45	C2	247	G	N3-C4-C5	5.06	131.13	128.60
45	C2	139	C	N3-C2-O2	-5.06	118.36	121.90
44	C1	1458	U	C2-N1-C1'	5.05	123.76	117.70
17	UZ	18	VAL	C-N-CA	-5.05	109.08	121.70
44	C1	602	U	C2-N1-C1'	5.05	123.76	117.70
44	C1	255	G	C4-N9-C1'	5.05	133.06	126.50
6	UG	451	LEU	CA-CB-CG	5.04	126.90	115.30
44	C1	281	U	N3-C2-O2	-5.04	118.67	122.20
44	C1	1699	U	N1-C2-O2	5.04	126.33	122.80
49	UE	265	MET	CB-CG-SD	5.04	127.51	112.40
19	CC	30	GLU	C-N-CA	-5.03	109.11	121.70
44	C1	2084	C	C6-N1-C1'	5.03	126.84	120.80
44	C1	2169	A	O5'-P-OP1	-5.03	101.17	105.70
44	C1	1650	C	N1-C2-O2	5.03	121.92	118.90
44	C1	356	C	C2-N3-C4	-5.03	117.39	119.90
49	UI	265	MET	CB-CG-SD	5.03	127.48	112.40
44	C1	2217	C	O4'-C1'-N1	5.02	112.22	108.20
44	C1	505	C	C6-N1-C2	-5.02	118.29	120.30
44	C1	128	G	C4-C5-N7	5.02	112.81	110.80
44	C1	202	A	C8-N9-C4	5.02	107.81	105.80
44	C1	2181	U	N1-C2-O2	5.02	126.31	122.80
44	C1	2210	U	N3-C2-O2	-5.02	118.69	122.20
44	C1	133	G	C6-C5-N7	-5.02	127.39	130.40
44	C1	2068	C	O5'-P-OP1	-5.02	101.19	105.70
10	UM	524	ILE	C-N-CD	5.01	138.93	128.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C1	56	C	O5'-P-OP1	5.01	116.71	110.70
44	C1	1758	C	C6-N1-C2	5.01	122.30	120.30
44	C1	402	U	N3-C2-O2	-5.01	118.69	122.20
45	C2	128	C	C5-C6-N1	5.01	123.50	121.00
44	C1	1510	G	N7-C8-N9	5.01	115.60	113.10
44	C1	257	G	C6-N1-C2	-5.00	122.10	125.10
45	C2	100	G	N3-C4-N9	5.00	129.00	126.00

There are no chirality outliers.

All (64) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
18	CA	306	TYR	Peptide
18	CB	293	GLU	Peptide
21	CF	60	GLN	Peptide
23	CH	143	HIS	Peptide
24	CI	132	VAL	Peptide
24	CI	851	TRP	Peptide
26	CK	261	PHE	Peptide
29	CO	84	ILE	Peptide
29	CO	88	ARG	Peptide
31	CQ	173	ASP	Peptide
32	CR	48	MET	Peptide
32	CR	866	PHE	Peptide
32	CS	48	MET	Peptide
32	CS	866	PHE	Peptide
47	CV	88	LYS	Peptide
47	CV	91	HIS	Peptide
34	Cc	13	TYR	Peptide
34	Cc	86	MET	Peptide
35	Ce	38	ALA	Peptide
38	Ci	137	ASP	Peptide
39	Cj	126	PRO	Peptide
39	Cj	40	ALA	Peptide
51	Cl	79	TYR	Peptide
54	Cz	1628	THR	Peptide
1	UA	214	SER	Peptide
1	UA	386	THR	Peptide
1	UA	667	ARG	Peptide
1	UA	8	SER	Peptide
4	UD	309	GLN	Peptide
4	UD	387	TRP	Peptide

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Mol	Chain	Res	Type	Group
5	UF	120	VAL	Peptide
6	UG	126	ALA	Peptide
6	UG	258	HIS	Peptide
48	UH	753	THR	Peptide
48	UH	857	LYS	Peptide
9	UL	17	VAL	Peptide
10	UM	204	ASP	Peptide
10	UM	328	LEU	Peptide
10	UM	693	GLU	Peptide
12	UO	167	LYS	Peptide
12	UO	282	ALA	Peptide
13	UQ	170	TRP	Peptide
13	UQ	237	TYR	Peptide
13	UQ	364	SER	Peptide
13	UQ	563	THR	Peptide
13	UQ	707	PRO	Peptide
13	UQ	849	ALA	Peptide
50	US	510	LYS	Peptide
15	UU	100	TRP	Peptide
15	UU	252	PRO	Peptide
15	UU	313	LEU	Peptide
15	UU	369	SER	Peptide
15	UU	378	LEU	Peptide
15	UU	396	SER	Peptide
15	UU	397	ASP	Peptide
15	UU	857	ILE	Peptide
46	UV	1058	TYR	Peptide
46	UV	1104	LEU	Peptide
46	UV	57	PHE	Peptide
46	UV	611	LEU	Peptide
46	UV	951	ARG	Peptide
17	UZ	103	ASP	Peptide
17	UZ	173	LYS	Peptide
17	UZ	273	GLN	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

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	UA	835/904 (92%)	730 (87%)	103 (12%)	2 (0%)	47	81
2	UB	502/907 (55%)	466 (93%)	36 (7%)	0	100	100
3	UC	72/648 (11%)	67 (93%)	5 (7%)	0	100	100
4	UD	754/884 (85%)	689 (91%)	65 (9%)	0	100	100
5	UF	325/414 (78%)	304 (94%)	21 (6%)	0	100	100
6	UG	446/558 (80%)	384 (86%)	60 (14%)	2 (0%)	34	72
7	UJ	796/1802 (44%)	750 (94%)	45 (6%)	1 (0%)	51	85
8	UK	211/270 (78%)	201 (95%)	10 (5%)	0	100	100
9	UL	767/962 (80%)	685 (89%)	82 (11%)	0	100	100
10	UM	645/912 (71%)	605 (94%)	39 (6%)	1 (0%)	47	81
11	UN	150/938 (16%)	143 (95%)	6 (4%)	1 (1%)	22	62
12	UO	498/557 (89%)	450 (90%)	48 (10%)	0	100	100
13	UQ	775/960 (81%)	691 (89%)	81 (10%)	3 (0%)	34	72
14	UR	437/618 (71%)	399 (91%)	38 (9%)	0	100	100
15	UU	890/1049 (85%)	786 (88%)	103 (12%)	1 (0%)	51	85
16	UX	188/193 (97%)	174 (93%)	14 (7%)	0	100	100
17	UZ	229/391 (59%)	211 (92%)	18 (8%)	0	100	100
18	CA	238/313 (76%)	213 (90%)	25 (10%)	0	100	100
18	CB	235/313 (75%)	211 (90%)	24 (10%)	0	100	100
19	CC	383/523 (73%)	353 (92%)	30 (8%)	0	100	100
20	CD	416/582 (72%)	382 (92%)	34 (8%)	0	100	100
21	CE	119/127 (94%)	107 (90%)	12 (10%)	0	100	100
21	CF	118/127 (93%)	110 (93%)	8 (7%)	0	100	100
22	CG	368/630 (58%)	342 (93%)	26 (7%)	0	100	100
23	CH	383/411 (93%)	348 (91%)	35 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	CI	812/1163 (70%)	737 (91%)	73 (9%)	2 (0%)	47	81
25	CJ	177/183 (97%)	151 (85%)	26 (15%)	0	100	100
26	CK	295/297 (99%)	271 (92%)	24 (8%)	0	100	100
27	CL	225/785 (29%)	200 (89%)	24 (11%)	1 (0%)	34	72
28	CM	443/446 (99%)	398 (90%)	44 (10%)	1 (0%)	47	81
29	CN	222/252 (88%)	207 (93%)	15 (7%)	0	100	100
29	CO	211/252 (84%)	193 (92%)	16 (8%)	2 (1%)	17	56
30	CP	185/322 (58%)	179 (97%)	6 (3%)	0	100	100
31	CQ	171/259 (66%)	165 (96%)	6 (4%)	0	100	100
32	CR	746/1073 (70%)	699 (94%)	47 (6%)	0	100	100
32	CS	746/1073 (70%)	699 (94%)	47 (6%)	0	100	100
33	CT	127/203 (63%)	111 (87%)	16 (13%)	0	100	100
34	Cc	188/212 (89%)	170 (90%)	18 (10%)	0	100	100
35	Ce	155/203 (76%)	140 (90%)	15 (10%)	0	100	100
36	Cg	157/190 (83%)	153 (98%)	4 (2%)	0	100	100
37	Ch	47/151 (31%)	46 (98%)	1 (2%)	0	100	100
38	Ci	113/150 (75%)	103 (91%)	10 (9%)	0	100	100
39	Cj	124/143 (87%)	104 (84%)	20 (16%)	0	100	100
40	Cm	122/130 (94%)	116 (95%)	6 (5%)	0	100	100
41	Cn	92/145 (63%)	86 (94%)	6 (6%)	0	100	100
42	Cp	59/68 (87%)	53 (90%)	6 (10%)	0	100	100
43	CU	123/311 (40%)	108 (88%)	15 (12%)	0	100	100
46	UV	1057/1171 (90%)	946 (90%)	108 (10%)	3 (0%)	41	76
47	CV	144/322 (45%)	130 (90%)	13 (9%)	1 (1%)	22	62
48	UH	349/930 (38%)	327 (94%)	22 (6%)	0	100	100
49	UE	121/410 (30%)	109 (90%)	12 (10%)	0	100	100
49	UI	121/410 (30%)	109 (90%)	12 (10%)	0	100	100
50	US	443/549 (81%)	414 (94%)	28 (6%)	1 (0%)	47	81
51	CI	78/156 (50%)	72 (92%)	6 (8%)	0	100	100
52	CX	265/480 (55%)	252 (95%)	13 (5%)	0	100	100
53	UP	52/364 (14%)	42 (81%)	9 (17%)	1 (2%)	8	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	Cz	273/1796 (15%)	257 (94%)	15 (6%)	1 (0%)	34	72
All	All	19223/30592 (63%)	17548 (91%)	1651 (9%)	24 (0%)	54	85

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	UG	176	LEU
29	CO	85	SER
46	UV	1059	ASP
13	UQ	708	SER
11	UN	902	ARG
47	CV	92	SER
50	US	241	GLU
54	Cz	1673	ARG
1	UA	372	GLY
6	UG	56	PRO
27	CL	640	PRO
29	CO	84	ILE
13	UQ	365	GLY
13	UQ	564	GLU
24	CI	308	THR
24	CI	396	PHE
28	CM	336	MET
46	UV	567	ARG
46	UV	735	GLY
1	UA	423	PRO
7	UJ	336	PRO
10	UM	329	PRO
15	UU	190	ILE
53	UP	329	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	UA	651/775 (84%)	635 (98%)	16 (2%)	47	68
2	UB	425/788 (54%)	420 (99%)	5 (1%)	71	84
3	UC	61/536 (11%)	59 (97%)	2 (3%)	38	61
4	UD	653/738 (88%)	650 (100%)	3 (0%)	88	93
5	UF	248/341 (73%)	248 (100%)	0	100	100
6	UG	344/474 (73%)	333 (97%)	11 (3%)	39	62
7	UJ	658/1526 (43%)	647 (98%)	11 (2%)	60	78
8	UK	159/227 (70%)	155 (98%)	4 (2%)	47	68
9	UL	667/821 (81%)	665 (100%)	2 (0%)	92	95
10	UM	569/770 (74%)	565 (99%)	4 (1%)	84	90
11	UN	123/765 (16%)	123 (100%)	0	100	100
12	UO	404/456 (89%)	400 (99%)	4 (1%)	76	86
13	UQ	650/817 (80%)	640 (98%)	10 (2%)	65	80
14	UR	360/524 (69%)	353 (98%)	7 (2%)	57	75
15	UU	672/863 (78%)	657 (98%)	15 (2%)	52	71
16	UX	150/167 (90%)	148 (99%)	2 (1%)	69	82
17	UZ	186/329 (56%)	185 (100%)	1 (0%)	88	93
18	CA	175/228 (77%)	170 (97%)	5 (3%)	42	64
18	CB	195/228 (86%)	194 (100%)	1 (0%)	88	93
19	CC	287/435 (66%)	286 (100%)	1 (0%)	92	95
20	CD	319/489 (65%)	314 (98%)	5 (2%)	62	79
21	CE	91/108 (84%)	89 (98%)	2 (2%)	52	71
21	CF	88/108 (82%)	88 (100%)	0	100	100
22	CG	299/525 (57%)	299 (100%)	0	100	100
23	CH	303/320 (95%)	298 (98%)	5 (2%)	60	78
24	CI	661/1009 (66%)	644 (97%)	17 (3%)	46	67
25	CJ	147/169 (87%)	142 (97%)	5 (3%)	37	61
26	CK	245/266 (92%)	236 (96%)	9 (4%)	34	59
27	CL	181/642 (28%)	179 (99%)	2 (1%)	73	85
28	CM	364/383 (95%)	356 (98%)	8 (2%)	52	71
29	CN	202/223 (91%)	201 (100%)	1 (0%)	88	93
29	CO	193/223 (86%)	191 (99%)	2 (1%)	76	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	CP	164/287 (57%)	162 (99%)	2 (1%)	71	84
31	CQ	145/215 (67%)	143 (99%)	2 (1%)	67	81
32	CR	654/916 (71%)	474 (72%)	180 (28%)	0	3
32	CS	654/916 (71%)	474 (72%)	180 (28%)	0	3
33	CT	108/167 (65%)	106 (98%)	2 (2%)	57	75
34	Cc	149/178 (84%)	147 (99%)	2 (1%)	69	82
35	Ce	137/177 (77%)	134 (98%)	3 (2%)	52	71
36	Cg	122/162 (75%)	120 (98%)	2 (2%)	62	79
37	Ch	43/130 (33%)	43 (100%)	0	100	100
38	Ci	74/117 (63%)	74 (100%)	0	100	100
39	Cj	92/115 (80%)	90 (98%)	2 (2%)	52	71
40	Cm	103/113 (91%)	102 (99%)	1 (1%)	76	86
41	Cn	70/116 (60%)	70 (100%)	0	100	100
42	Cp	46/61 (75%)	46 (100%)	0	100	100
43	CU	103/260 (40%)	97 (94%)	6 (6%)	20	47
46	UV	908/989 (92%)	891 (98%)	17 (2%)	57	75
47	CV	129/276 (47%)	127 (98%)	2 (2%)	62	79
48	UH	301/788 (38%)	298 (99%)	3 (1%)	76	86
49	UE	105/346 (30%)	74 (70%)	31 (30%)	0	2
49	UI	105/346 (30%)	74 (70%)	31 (30%)	0	2
50	US	404/493 (82%)	401 (99%)	3 (1%)	84	90
51	Cl	71/135 (53%)	69 (97%)	2 (3%)	43	65
52	CX	227/411 (55%)	226 (100%)	1 (0%)	91	94
53	UP	44/314 (14%)	44 (100%)	0	100	100
54	Cz	235/1533 (15%)	234 (100%)	1 (0%)	91	94
All	All	15923/25834 (62%)	15290 (96%)	633 (4%)	35	56

All (633) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	UA	8	SER
1	UA	68	ASN
1	UA	87	ARG

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Mol	Chain	Res	Type
1	UA	180	LEU
1	UA	219	VAL
1	UA	296	SER
1	UA	347	VAL
1	UA	356	VAL
1	UA	415	ARG
1	UA	479	ASP
1	UA	499	SER
1	UA	501	THR
1	UA	577	THR
1	UA	580	TYR
1	UA	602	THR
1	UA	611	THR
2	UB	90	LEU
2	UB	111	ASN
2	UB	549	LEU
2	UB	786	ARG
2	UB	829	ARG
3	UC	607	LYS
3	UC	643	VAL
4	UD	152	ARG
4	UD	224	THR
4	UD	267	THR
6	UG	41	ARG
6	UG	172	CYS
6	UG	179	THR
6	UG	181	ARG
6	UG	233	THR
6	UG	260	THR
6	UG	265	THR
6	UG	290	THR
6	UG	303	VAL
6	UG	356	THR
6	UG	365	THR
7	UJ	44	THR
7	UJ	45	PHE
7	UJ	84	THR
7	UJ	306	ARG
7	UJ	405	LYS
7	UJ	640	LYS
7	UJ	643	THR
7	UJ	653	LYS

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Mol	Chain	Res	Type
7	UJ	720	LEU
7	UJ	728	ARG
7	UJ	798	LYS
8	UK	93	ASN
8	UK	228	LYS
8	UK	265	VAL
8	UK	269	LYS
9	UL	440	MET
9	UL	676	ARG
10	UM	210	PHE
10	UM	593	ARG
10	UM	755	ARG
10	UM	889	ARG
12	UO	149	VAL
12	UO	190	VAL
12	UO	270	THR
12	UO	277	THR
13	UQ	149	SER
13	UQ	244	LEU
13	UQ	358	VAL
13	UQ	449	ASP
13	UQ	452	VAL
13	UQ	497	THR
13	UQ	537	THR
13	UQ	622	THR
13	UQ	687	TYR
13	UQ	920	VAL
14	UR	63	LYS
14	UR	152	THR
14	UR	279	SER
14	UR	314	LEU
14	UR	393	LYS
14	UR	397	MET
14	UR	471	ARG
15	UU	40	THR
15	UU	58	LYS
15	UU	81	ASN
15	UU	192	MET
15	UU	222	LEU
15	UU	354	THR
15	UU	377	ILE
15	UU	554	THR

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Mol	Chain	Res	Type
15	UU	618	THR
15	UU	714	CYS
15	UU	738	THR
15	UU	756	PHE
15	UU	842	THR
15	UU	858	ASP
15	UU	889	SER
16	UX	44	MET
16	UX	92	THR
17	UZ	213	ASN
18	CA	83	VAL
18	CA	177	THR
18	CA	253	LEU
18	CA	291	THR
18	CA	292	LEU
18	CB	85	ARG
19	CC	38	MET
20	CD	94	LYS
20	CD	338	THR
20	CD	371	LEU
20	CD	372	SER
20	CD	442	ILE
21	CE	53	VAL
21	CE	94	VAL
23	CH	73	THR
23	CH	83	THR
23	CH	196	PHE
23	CH	208	LEU
23	CH	210	ARG
24	CI	91	ARG
24	CI	197	LEU
24	CI	214	TYR
24	CI	256	THR
24	CI	357	LYS
24	CI	367	VAL
24	CI	393	VAL
24	CI	754	LYS
24	CI	788	PHE
24	CI	840	ARG
24	CI	841	ARG
24	CI	854	ARG
24	CI	863	THR

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Mol	Chain	Res	Type
24	CI	872	THR
24	CI	986	ILE
24	CI	1034	THR
24	CI	1058	LEU
25	CJ	5	LEU
25	CJ	50	LEU
25	CJ	123	THR
25	CJ	140	VAL
25	CJ	159	THR
26	CK	18	LEU
26	CK	81	SER
26	CK	87	ARG
26	CK	90	VAL
26	CK	92	THR
26	CK	123	ILE
26	CK	229	THR
26	CK	235	ASP
26	CK	269	THR
27	CL	534	THR
27	CL	619	ILE
28	CM	7	THR
28	CM	58	LEU
28	CM	76	LYS
28	CM	244	ARG
28	CM	305	ARG
28	CM	360	ARG
28	CM	367	ARG
28	CM	432	LYS
29	CN	218	ASP
29	CO	135	LYS
29	CO	169	ASP
30	CP	64	LYS
30	CP	78	MET
31	CQ	198	LYS
31	CQ	215	LYS
32	CR	2	THR
32	CR	4	GLN
32	CR	5	LYS
32	CR	7	VAL
32	CR	9	SER
32	CR	10	ARG
32	CR	23	LYS

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Mol	Chain	Res	Type
32	CR	25	SER
32	CR	30	VAL
32	CR	36	GLU
32	CR	38	ILE
32	CR	41	LEU
32	CR	46	SER
32	CR	49	ASP
32	CR	51	ARG
32	CR	52	GLN
32	CR	54	LYS
32	CR	55	SER
32	CR	56	VAL
32	CR	62	LYS
32	CR	65	LEU
32	CR	69	SER
32	CR	73	LYS
32	CR	80	LYS
32	CR	84	ARG
32	CR	86	ILE
32	CR	88	GLU
32	CR	96	GLU
32	CR	97	LEU
32	CR	99	ILE
32	CR	101	LEU
32	CR	102	ASN
32	CR	105	ARG
32	CR	107	CYS
32	CR	110	LYS
32	CR	112	THR
32	CR	113	ASP
32	CR	115	ILE
32	CR	119	THR
32	CR	123	CYS
32	CR	125	LEU
32	CR	127	ASP
32	CR	131	ILE
32	CR	136	LEU
32	CR	142	THR
32	CR	149	VAL
32	CR	151	LEU
32	CR	153	LEU
32	CR	159	LEU

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Mol	Chain	Res	Type
32	CR	160	LYS
32	CR	162	LEU
32	CR	165	MET
32	CR	181	VAL
32	CR	188	ARG
32	CR	192	SER
32	CR	195	SER
32	CR	198	SER
32	CR	201	VAL
32	CR	202	ILE
32	CR	206	LEU
32	CR	211	ILE
32	CR	212	SER
32	CR	217	VAL
32	CR	218	LYS
32	CR	251	SER
32	CR	252	LEU
32	CR	253	ILE
32	CR	266	LEU
32	CR	277	LEU
32	CR	278	ARG
32	CR	284	THR
32	CR	287	ARG
32	CR	291	LYS
32	CR	297	VAL
32	CR	308	SER
32	CR	316	SER
32	CR	318	GLU
32	CR	319	ASN
32	CR	322	THR
32	CR	323	LEU
32	CR	378	HIS
32	CR	382	GLN
32	CR	387	VAL
32	CR	390	GLU
32	CR	394	ILE
32	CR	401	LYS
32	CR	410	MET
32	CR	412	SER
32	CR	414	ILE
32	CR	415	SER
32	CR	418	GLU

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Mol	Chain	Res	Type
32	CR	420	THR
32	CR	425	SER
32	CR	427	LYS
32	CR	430	LYS
32	CR	432	LEU
32	CR	433	ARG
32	CR	470	LYS
32	CR	476	GLU
32	CR	479	ARG
32	CR	484	ASP
32	CR	487	GLU
32	CR	488	LYS
32	CR	492	THR
32	CR	502	ARG
32	CR	512	ASP
32	CR	514	SER
32	CR	517	GLU
32	CR	532	VAL
32	CR	533	SER
32	CR	534	GLU
32	CR	535	LYS
32	CR	539	GLN
32	CR	541	VAL
32	CR	545	VAL
32	CR	548	HIS
32	CR	554	ASN
32	CR	556	LEU
32	CR	558	LEU
32	CR	559	MET
32	CR	566	GLU
32	CR	569	VAL
32	CR	576	GLU
32	CR	584	CYS
32	CR	594	ILE
32	CR	596	LYS
32	CR	625	ASP
32	CR	626	GLU
32	CR	627	PHE
32	CR	631	SER
32	CR	651	SER
32	CR	654	LEU
32	CR	655	GLN

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Mol	Chain	Res	Type
32	CR	658	VAL
32	CR	704	GLU
32	CR	711	LYS
32	CR	712	LEU
32	CR	713	SER
32	CR	716	ARG
32	CR	718	GLU
32	CR	719	LYS
32	CR	723	VAL
32	CR	725	VAL
32	CR	732	GLN
32	CR	745	VAL
32	CR	747	LEU
32	CR	750	THR
32	CR	753	ASP
32	CR	759	THR
32	CR	760	CYS
32	CR	768	ASP
32	CR	773	SER
32	CR	784	LYS
32	CR	788	SER
32	CR	789	LEU
32	CR	791	SER
32	CR	793	LYS
32	CR	800	ILE
32	CR	801	LEU
32	CR	806	GLU
32	CR	808	SER
32	CR	824	LEU
32	CR	830	ASP
32	CR	832	LEU
32	CR	834	THR
32	CR	848	LEU
32	CR	858	MET
32	CR	860	THR
32	CR	861	ILE
32	CR	867	THR
32	CR	870	LEU
32	CR	876	LEU
32	CR	887	LEU
32	CR	893	ASP
32	CR	902	ASN

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Mol	Chain	Res	Type
32	CR	907	GLN
32	CR	908	VAL
32	CR	909	LEU
32	CR	913	MET
32	CR	914	LYS
32	CS	2	THR
32	CS	4	GLN
32	CS	5	LYS
32	CS	7	VAL
32	CS	9	SER
32	CS	10	ARG
32	CS	23	LYS
32	CS	25	SER
32	CS	30	VAL
32	CS	36	GLU
32	CS	38	ILE
32	CS	41	LEU
32	CS	46	SER
32	CS	49	ASP
32	CS	51	ARG
32	CS	52	GLN
32	CS	54	LYS
32	CS	55	SER
32	CS	56	VAL
32	CS	62	LYS
32	CS	65	LEU
32	CS	69	SER
32	CS	73	LYS
32	CS	80	LYS
32	CS	84	ARG
32	CS	86	ILE
32	CS	88	GLU
32	CS	96	GLU
32	CS	97	LEU
32	CS	99	ILE
32	CS	101	LEU
32	CS	102	ASN
32	CS	105	ARG
32	CS	107	CYS
32	CS	110	LYS
32	CS	112	THR
32	CS	113	ASP

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Mol	Chain	Res	Type
32	CS	115	ILE
32	CS	119	THR
32	CS	123	CYS
32	CS	125	LEU
32	CS	127	ASP
32	CS	131	ILE
32	CS	136	LEU
32	CS	142	THR
32	CS	149	VAL
32	CS	151	LEU
32	CS	153	LEU
32	CS	159	LEU
32	CS	160	LYS
32	CS	162	LEU
32	CS	165	MET
32	CS	181	VAL
32	CS	188	ARG
32	CS	192	SER
32	CS	195	SER
32	CS	198	SER
32	CS	201	VAL
32	CS	202	ILE
32	CS	206	LEU
32	CS	211	ILE
32	CS	212	SER
32	CS	217	VAL
32	CS	218	LYS
32	CS	251	SER
32	CS	252	LEU
32	CS	253	ILE
32	CS	266	LEU
32	CS	277	LEU
32	CS	278	ARG
32	CS	284	THR
32	CS	287	ARG
32	CS	291	LYS
32	CS	297	VAL
32	CS	308	SER
32	CS	316	SER
32	CS	318	GLU
32	CS	319	ASN
32	CS	322	THR

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Mol	Chain	Res	Type
32	CS	323	LEU
32	CS	378	HIS
32	CS	382	GLN
32	CS	387	VAL
32	CS	390	GLU
32	CS	394	ILE
32	CS	401	LYS
32	CS	410	MET
32	CS	412	SER
32	CS	414	ILE
32	CS	415	SER
32	CS	418	GLU
32	CS	420	THR
32	CS	425	SER
32	CS	427	LYS
32	CS	430	LYS
32	CS	432	LEU
32	CS	433	ARG
32	CS	470	LYS
32	CS	476	GLU
32	CS	479	ARG
32	CS	484	ASP
32	CS	487	GLU
32	CS	488	LYS
32	CS	492	THR
32	CS	502	ARG
32	CS	512	ASP
32	CS	514	SER
32	CS	517	GLU
32	CS	532	VAL
32	CS	533	SER
32	CS	534	GLU
32	CS	535	LYS
32	CS	539	GLN
32	CS	541	VAL
32	CS	545	VAL
32	CS	548	HIS
32	CS	554	ASN
32	CS	556	LEU
32	CS	558	LEU
32	CS	559	MET
32	CS	566	GLU

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Mol	Chain	Res	Type
32	CS	569	VAL
32	CS	576	GLU
32	CS	584	CYS
32	CS	594	ILE
32	CS	596	LYS
32	CS	625	ASP
32	CS	626	GLU
32	CS	627	PHE
32	CS	631	SER
32	CS	651	SER
32	CS	654	LEU
32	CS	655	GLN
32	CS	658	VAL
32	CS	704	GLU
32	CS	711	LYS
32	CS	712	LEU
32	CS	713	SER
32	CS	716	ARG
32	CS	718	GLU
32	CS	719	LYS
32	CS	723	VAL
32	CS	725	VAL
32	CS	732	GLN
32	CS	745	VAL
32	CS	747	LEU
32	CS	750	THR
32	CS	753	ASP
32	CS	759	THR
32	CS	760	CYS
32	CS	768	ASP
32	CS	773	SER
32	CS	784	LYS
32	CS	788	SER
32	CS	789	LEU
32	CS	791	SER
32	CS	793	LYS
32	CS	800	ILE
32	CS	801	LEU
32	CS	806	GLU
32	CS	808	SER
32	CS	824	LEU
32	CS	830	ASP

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Mol	Chain	Res	Type
32	CS	832	LEU
32	CS	834	THR
32	CS	848	LEU
32	CS	858	MET
32	CS	860	THR
32	CS	861	ILE
32	CS	867	THR
32	CS	870	LEU
32	CS	876	LEU
32	CS	887	LEU
32	CS	893	ASP
32	CS	902	ASN
32	CS	907	GLN
32	CS	908	VAL
32	CS	909	LEU
32	CS	913	MET
32	CS	914	LYS
33	CT	86	THR
33	CT	151	ARG
34	Cc	134	THR
34	Cc	144	ARG
35	Ce	34	GLU
35	Ce	90	LYS
35	Ce	184	ARG
36	Cg	55	ARG
36	Cg	97	LEU
39	Cj	10	PHE
39	Cj	69	VAL
40	Cm	25	VAL
43	CU	126	ASP
43	CU	129	ARG
43	CU	249	ARG
43	CU	251	ASN
43	CU	254	VAL
43	CU	298	ARG
46	UV	88	LYS
46	UV	111	LYS
46	UV	155	ASP
46	UV	216	LYS
46	UV	287	ARG
46	UV	549	ARG
46	UV	612	ARG

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Mol	Chain	Res	Type
46	UV	634	LYS
46	UV	706	LYS
46	UV	733	LYS
46	UV	810	LEU
46	UV	823	ARG
46	UV	920	LYS
46	UV	941	THR
46	UV	989	LYS
46	UV	1003	LYS
46	UV	1080	THR
47	CV	156	LYS
47	CV	167	LYS
48	UH	574	SER
48	UH	624	MET
48	UH	730	PHE
49	UE	155	THR
49	UE	162	ARG
49	UE	166	SER
49	UE	167	ASP
49	UE	169	LEU
49	UE	180	ILE
49	UE	191	SER
49	UE	195	THR
49	UE	197	LEU
49	UE	198	SER
49	UE	199	LYS
49	UE	210	ARG
49	UE	214	LEU
49	UE	215	MET
49	UE	219	GLN
49	UE	236	ILE
49	UE	238	ARG
49	UE	241	GLU
49	UE	242	LEU
49	UE	243	SER
49	UE	244	ARG
49	UE	246	LEU
49	UE	250	SER
49	UE	251	ARG
49	UE	257	LEU
49	UE	263	LEU
49	UE	266	LEU

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Mol	Chain	Res	Type
49	UE	269	GLN
49	UE	273	ARG
49	UE	277	LYS
49	UE	278	MET
50	US	252	LYS
50	US	346	LEU
50	US	506	THR
51	Cl	16	ARG
51	Cl	48	LYS
52	CX	204	LYS
49	UI	155	THR
49	UI	162	ARG
49	UI	166	SER
49	UI	167	ASP
49	UI	169	LEU
49	UI	180	ILE
49	UI	191	SER
49	UI	195	THR
49	UI	197	LEU
49	UI	198	SER
49	UI	199	LYS
49	UI	210	ARG
49	UI	214	LEU
49	UI	215	MET
49	UI	219	GLN
49	UI	236	ILE
49	UI	238	ARG
49	UI	241	GLU
49	UI	242	LEU
49	UI	243	SER
49	UI	244	ARG
49	UI	246	LEU
49	UI	250	SER
49	UI	251	ARG
49	UI	257	LEU
49	UI	263	LEU
49	UI	266	LEU
49	UI	269	GLN
49	UI	273	ARG
49	UI	277	LYS
49	UI	278	MET
54	Cz	1571	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (265) such sidechains are listed below:

Mol	Chain	Res	Type
1	UA	9	ASN
1	UA	54	HIS
1	UA	78	GLN
1	UA	207	GLN
1	UA	253	GLN
1	UA	321	GLN
1	UA	336	GLN
1	UA	381	HIS
1	UA	467	HIS
1	UA	543	GLN
1	UA	576	ASN
1	UA	712	ASN
1	UA	801	HIS
2	UB	16	GLN
2	UB	22	GLN
2	UB	551	GLN
2	UB	645	GLN
2	UB	701	GLN
2	UB	741	HIS
2	UB	765	ASN
2	UB	803	HIS
4	UD	235	ASN
4	UD	322	HIS
4	UD	324	HIS
4	UD	370	GLN
4	UD	660	ASN
4	UD	673	ASN
4	UD	697	GLN
5	UF	45	HIS
5	UF	89	GLN
5	UF	289	GLN
5	UF	313	HIS
6	UG	127	GLN
6	UG	205	HIS
6	UG	206	ASN
6	UG	221	HIS
6	UG	277	GLN
6	UG	322	ASN
6	UG	378	GLN
6	UG	427	ASN
6	UG	476	GLN

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Mol	Chain	Res	Type
7	UJ	15	ASN
7	UJ	85	GLN
7	UJ	103	HIS
7	UJ	158	GLN
7	UJ	184	GLN
7	UJ	268	GLN
7	UJ	295	GLN
7	UJ	318	HIS
7	UJ	379	ASN
7	UJ	515	ASN
7	UJ	670	HIS
8	UK	13	HIS
9	UL	23	ASN
9	UL	107	ASN
9	UL	207	HIS
9	UL	296	HIS
9	UL	398	ASN
9	UL	453	ASN
9	UL	457	GLN
9	UL	594	ASN
10	UM	58	GLN
10	UM	203	GLN
10	UM	236	GLN
10	UM	520	GLN
10	UM	644	ASN
10	UM	652	HIS
10	UM	691	ASN
10	UM	741	GLN
10	UM	743	GLN
10	UM	747	ASN
10	UM	750	HIS
10	UM	772	ASN
10	UM	776	ASN
11	UN	348	HIS
11	UN	362	GLN
11	UN	916	GLN
12	UO	143	HIS
12	UO	306	ASN
12	UO	333	HIS
12	UO	522	GLN
13	UQ	112	GLN
13	UQ	262	HIS

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Mol	Chain	Res	Type
13	UQ	310	GLN
13	UQ	352	HIS
13	UQ	394	HIS
13	UQ	438	GLN
13	UQ	487	GLN
13	UQ	509	GLN
13	UQ	783	ASN
13	UQ	917	HIS
13	UQ	924	GLN
14	UR	312	ASN
14	UR	364	GLN
14	UR	370	GLN
14	UR	498	ASN
15	UU	197	ASN
15	UU	236	GLN
15	UU	379	HIS
15	UU	427	GLN
15	UU	571	GLN
15	UU	621	HIS
15	UU	711	ASN
15	UU	963	ASN
15	UU	1002	HIS
16	UX	141	HIS
17	UZ	105	GLN
18	CA	78	HIS
18	CA	277	GLN
18	CB	235	GLN
18	CB	299	HIS
19	CC	139	ASN
19	CC	154	GLN
19	CC	171	HIS
19	CC	173	ASN
19	CC	175	ASN
19	CC	179	GLN
19	CC	192	ASN
19	CC	272	GLN
19	CC	321	HIS
19	CC	394	ASN
20	CD	124	GLN
20	CD	128	ASN
20	CD	280	ASN
20	CD	314	ASN

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Mol	Chain	Res	Type
20	CD	404	ASN
21	CE	67	HIS
21	CE	76	ASN
21	CF	67	HIS
22	CG	198	GLN
22	CG	243	GLN
22	CG	274	ASN
22	CG	430	HIS
22	CG	462	GLN
23	CH	199	GLN
23	CH	232	ASN
23	CH	251	HIS
23	CH	323	GLN
24	CI	221	ASN
24	CI	239	ASN
24	CI	248	ASN
24	CI	287	HIS
24	CI	366	ASN
24	CI	374	GLN
24	CI	380	GLN
24	CI	753	ASN
24	CI	930	ASN
24	CI	1006	ASN
25	CJ	27	HIS
26	CK	8	GLN
26	CK	48	ASN
26	CK	121	ASN
26	CK	159	HIS
26	CK	190	HIS
27	CL	569	HIS
28	CM	41	GLN
28	CM	45	ASN
28	CM	120	ASN
28	CM	262	HIS
28	CM	277	ASN
28	CM	370	GLN
29	CN	111	GLN
29	CN	199	ASN
29	CO	24	HIS
29	CO	93	HIS
29	CO	111	GLN
30	CP	147	ASN

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Mol	Chain	Res	Type
30	CP	159	GLN
30	CP	190	ASN
31	CQ	203	ASN
31	CQ	224	ASN
32	CR	4	GLN
32	CR	20	GLN
32	CR	53	ASN
32	CR	102	ASN
32	CR	126	GLN
32	CR	161	GLN
32	CR	170	HIS
32	CR	207	ASN
32	CR	365	HIS
32	CR	485	ASN
32	CR	491	ASN
32	CR	565	HIS
32	CR	641	ASN
32	CR	731	GLN
32	CR	838	HIS
32	CR	846	ASN
32	CR	902	ASN
32	CR	921	GLN
32	CS	4	GLN
32	CS	20	GLN
32	CS	53	ASN
32	CS	102	ASN
32	CS	126	GLN
32	CS	161	GLN
32	CS	170	HIS
32	CS	365	HIS
32	CS	485	ASN
32	CS	491	ASN
32	CS	565	HIS
32	CS	641	ASN
32	CS	731	GLN
32	CS	838	HIS
32	CS	846	ASN
32	CS	902	ASN
32	CS	921	GLN
33	CT	120	GLN
33	CT	126	ASN
33	CT	179	HIS

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Mol	Chain	Res	Type
34	Cc	91	ASN
34	Cc	126	ASN
34	Cc	145	GLN
34	Cc	157	GLN
34	Cc	187	ASN
34	Cc	211	ASN
35	Ce	36	ASN
36	Cg	108	GLN
39	Cj	74	HIS
39	Cj	77	GLN
39	Cj	83	GLN
40	Cm	42	GLN
40	Cm	64	GLN
40	Cm	80	ASN
46	UV	77	HIS
46	UV	119	GLN
46	UV	205	ASN
46	UV	260	GLN
46	UV	270	ASN
46	UV	415	HIS
46	UV	417	HIS
46	UV	494	ASN
46	UV	520	ASN
46	UV	542	ASN
46	UV	615	GLN
46	UV	782	GLN
46	UV	813	HIS
46	UV	938	GLN
46	UV	949	HIS
46	UV	998	ASN
47	CV	55	ASN
47	CV	89	GLN
47	CV	199	ASN
48	UH	590	ASN
48	UH	862	HIS
49	UE	183	ASN
49	UE	237	ASN
49	UE	269	GLN
50	US	151	GLN
50	US	152	HIS
50	US	206	HIS
50	US	225	ASN

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Mol	Chain	Res	Type
50	US	261	HIS
50	US	372	HIS
50	US	419	HIS
50	US	464	GLN
51	CI	21	ASN
52	CX	290	ASN
52	CX	322	GLN
52	CX	364	ASN
52	CX	423	ASN
49	UI	183	ASN
49	UI	237	ASN
49	UI	269	GLN
54	Cz	1549	ASN
54	Cz	1631	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
44	C1	1088/2323 (46%)	373 (34%)	31 (2%)
45	C2	226/230 (98%)	83 (36%)	8 (3%)
All	All	1314/2553 (51%)	456 (34%)	39 (2%)

All (456) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
44	C1	2	G
44	C1	3	G
44	C1	4	G
44	C1	5	G
44	C1	7	A
44	C1	13	G
44	C1	14	G
44	C1	15	G
44	C1	16	U
44	C1	17	C
44	C1	18	G
44	C1	19	C
44	C1	20	C
44	C1	23	G
44	C1	26	C
44	C1	38	G

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Mol	Chain	Res	Type
44	C1	40	A
44	C1	41	G
44	C1	42	C
44	C1	43	C
44	C1	47	G
44	C1	49	G
44	C1	56	C
44	C1	57	C
44	C1	59	U
44	C1	60	A
44	C1	61	G
44	C1	63	C
44	C1	66	G
44	C1	68	U
44	C1	71	A
44	C1	72	U
44	C1	73	A
44	C1	74	C
44	C1	77	C
44	C1	89	G
44	C1	90	A
44	C1	93	G
44	C1	96	C
44	C1	104	U
44	C1	105	A
44	C1	107	C
44	C1	121	G
44	C1	126	C
44	C1	127	C
44	C1	128	G
44	C1	132	A
44	C1	134	C
44	C1	135	A
44	C1	136	C
44	C1	143	A
44	C1	152	G
44	C1	154	C
44	C1	155	G
44	C1	158	C
44	C1	159	C
44	C1	160	C
44	C1	161	A

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Mol	Chain	Res	Type
44	C1	162	G
44	C1	163	C
44	C1	166	A
44	C1	169	G
44	C1	170	C
44	C1	182	C
44	C1	183	C
44	C1	185	G
44	C1	192	A
44	C1	201	G
44	C1	203	C
44	C1	205	C
44	C1	206	C
44	C1	207	U
44	C1	208	A
44	C1	210	G
44	C1	216	A
44	C1	220	A
44	C1	222	U
44	C1	223	A
44	C1	228	G
44	C1	234	G
44	C1	236	C
44	C1	237	G
44	C1	242	U
44	C1	243	U
44	C1	244	G
44	C1	251	G
44	C1	257	G
44	C1	258	C
44	C1	259	U
44	C1	260	U
44	C1	262	G
44	C1	265	G
44	C1	266	C
44	C1	267	U
44	C1	268	G
44	C1	269	G
44	C1	272	A
44	C1	273	G
44	C1	276	C
44	C1	277	U

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Mol	Chain	Res	Type
44	C1	278	A
44	C1	281	U
44	C1	282	C
44	C1	283	A
44	C1	285	A
44	C1	291	C
44	C1	292	G
44	C1	339	C
44	C1	340	G
44	C1	346	C
44	C1	347	C
44	C1	349	C
44	C1	351	U
44	C1	352	G
44	C1	353	G
44	C1	357	G
44	C1	360	U
44	C1	371	U
44	C1	372	U
44	C1	379	G
44	C1	382	U
44	C1	383	G
44	C1	384	C
44	C1	386	G
44	C1	398	C
44	C1	401	C
44	C1	402	U
44	C1	403	G
44	C1	407	A
44	C1	416	U
44	C1	423	U
44	C1	425	C
44	C1	427	G
44	C1	432	G
44	C1	435	A
44	C1	436	A
44	C1	439	A
44	C1	440	G
44	C1	441	A
44	C1	442	U
44	C1	443	G
44	C1	454	C

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Mol	Chain	Res	Type
44	C1	458	A
44	C1	459	C
44	C1	467	C
44	C1	468	C
44	C1	469	G
44	C1	471	C
44	C1	473	G
44	C1	474	A
44	C1	475	C
44	C1	477	A
44	C1	483	U
44	C1	484	G
44	C1	491	G
44	C1	492	C
44	C1	499	G
44	C1	500	C
44	C1	501	U
44	C1	502	A
44	C1	504	C
44	C1	581	C
44	C1	582	G
44	C1	583	A
44	C1	584	U
44	C1	585	A
44	C1	586	G
44	C1	587	U
44	C1	594	G
44	C1	596	U
44	C1	603	G
44	C1	604	C
44	C1	609	A
44	C1	610	G
44	C1	613	A
44	C1	614	U
44	C1	621	G
44	C1	627	A
44	C1	1054	A
44	C1	1059	A
44	C1	1061	A
44	C1	1062	C
44	C1	1064	G
44	C1	1069	A

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Mol	Chain	Res	Type
44	C1	1070	G
44	C1	1076	U
44	C1	1077	U
44	C1	1078	U
44	C1	1079	C
44	C1	1080	G
44	C1	1081	G
44	C1	1083	U
44	C1	1085	U
44	C1	1086	U
44	C1	1088	U
44	C1	1089	A
44	C1	1094	G
44	C1	1095	A
44	C1	1097	U
44	C1	1098	G
44	C1	1103	C
44	C1	1104	A
44	C1	1120	C
44	C1	1123	G
44	C1	1124	G
44	C1	1125	A
44	C1	1126	A
44	C1	1127	C
44	C1	1128	A
44	C1	1129	A
44	C1	1140	A
44	C1	1141	G
44	C1	1147	U
44	C1	1148	G
44	C1	1149	C
44	C1	1150	C
44	C1	1154	A
44	C1	1158	G
44	C1	1159	C
44	C1	1163	A
44	C1	1164	A
44	C1	1166	U
44	C1	1167	C
44	C1	1168	C
44	C1	1169	A
44	C1	1170	G

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Mol	Chain	Res	Type
44	C1	1178	A
44	C1	1179	G
44	C1	1186	U
44	C1	1218	G
44	C1	1219	A
44	C1	1222	C
44	C1	1223	U
44	C1	1444	A
44	C1	1447	A
44	C1	1448	A
44	C1	1449	U
44	C1	1450	A
44	C1	1451	G
44	C1	1452	G
44	C1	1461	G
44	C1	1469	A
44	C1	1471	U
44	C1	1479	U
44	C1	1480	G
44	C1	1481	U
44	C1	1483	A
44	C1	1484	G
44	C1	1486	G
44	C1	1489	G
44	C1	1491	A
44	C1	1497	U
44	C1	1498	G
44	C1	1499	G
44	C1	1507	G
44	C1	1516	C
44	C1	1517	A
44	C1	1518	A
44	C1	1519	C
44	C1	1520	U
44	C1	1525	A
44	C1	1527	G
44	C1	1529	A
44	C1	1536	A
44	C1	1545	U
44	C1	1546	U
44	C1	1547	C
44	C1	1549	U

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Mol	Chain	Res	Type
44	C1	1551	A
44	C1	1554	C
44	C1	1555	A
44	C1	1624	A
44	C1	1625	G
44	C1	1628	A
44	C1	1635	G
44	C1	1636	G
44	C1	1637	C
44	C1	1638	G
44	C1	1639	U
44	C1	1642	A
44	C1	1643	U
44	C1	1644	U
44	C1	1645	U
44	C1	1656	C
44	C1	1657	G
44	C1	1665	A
44	C1	1667	G
44	C1	1668	A
44	C1	1670	A
44	C1	1673	U
44	C1	1675	A
44	C1	1676	A
44	C1	1677	A
44	C1	1678	A
44	C1	1699	U
44	C1	1700	A
44	C1	1701	U
44	C1	1703	G
44	C1	1710	G
44	C1	1711	G
44	C1	1712	C
44	C1	1713	U
44	C1	1729	U
44	C1	1730	G
44	C1	1735	A
44	C1	1740	C
44	C1	1742	C
44	C1	1743	C
44	C1	1744	A
44	C1	1748	G

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Mol	Chain	Res	Type
44	C1	1751	G
44	C1	2047	G
44	C1	2048	C
44	C1	2054	A
44	C1	2055	C
44	C1	2056	U
44	C1	2057	G
44	C1	2061	G
44	C1	2070	A
44	C1	2071	G
44	C1	2073	A
44	C1	2074	C
44	C1	2075	U
44	C1	2076	C
44	C1	2077	C
44	C1	2078	C
44	C1	2085	G
44	C1	2086	A
44	C1	2087	G
44	C1	2088	A
44	C1	2107	A
44	C1	2109	A
44	C1	2115	U
44	C1	2118	U
44	C1	2120	C
44	C1	2121	U
44	C1	2156	A
44	C1	2157	G
44	C1	2158	G
44	C1	2162	C
44	C1	2167	G
44	C1	2173	G
44	C1	2178	U
44	C1	2179	C
44	C1	2183	A
44	C1	2184	G
44	C1	2185	C
44	C1	2197	A
44	C1	2201	C
44	C1	2202	C
44	C1	2205	G
44	C1	2210	U

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Mol	Chain	Res	Type
44	C1	2211	U
44	C1	2212	G
44	C1	2213	U
44	C1	2214	A
44	C1	2215	C
44	C1	2217	C
44	C1	2220	C
44	C1	2222	C
44	C1	2223	C
44	C1	2227	C
44	C1	2328	G
44	C1	2329	A
44	C1	2330	G
44	C1	2351	G
44	C1	2352	U
44	C1	2362	U
44	C1	2363	G
44	C1	2364	A
44	C1	2365	A
44	C1	2366	C
44	C1	2374	G
45	C2	2	G
45	C2	6	C
45	C2	8	A
45	C2	9	U
45	C2	10	A
45	C2	15	A
45	C2	23	A
45	C2	24	U
45	C2	29	A
45	C2	30	U
45	C2	32	G
45	C2	33	U
45	C2	36	U
45	C2	37	U
45	C2	39	U
45	C2	40	C
45	C2	43	C
45	C2	47	U
45	C2	48	G
45	C2	57	A
45	C2	58	A

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Mol	Chain	Res	Type
45	C2	62	A
45	C2	63	G
45	C2	64	C
45	C2	70	A
45	C2	81	G
45	C2	82	U
45	C2	84	G
45	C2	90	C
45	C2	91	G
45	C2	92	A
45	C2	94	A
45	C2	95	U
45	C2	100	G
45	C2	104	C
45	C2	105	C
45	C2	111	G
45	C2	124	U
45	C2	125	U
45	C2	126	U
45	C2	127	A
45	C2	128	C
45	C2	136	C
45	C2	140	C
45	C2	142	G
45	C2	145	A
45	C2	147	G
45	C2	148	G
45	C2	153	G
45	C2	156	C
45	C2	160	U
45	C2	162	C
45	C2	163	C
45	C2	164	U
45	C2	165	C
45	C2	166	G
45	C2	167	U
45	C2	168	C
45	C2	170	C
45	C2	174	G
45	C2	178	U
45	C2	179	A
45	C2	181	A

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Mol	Chain	Res	Type
45	C2	182	G
45	C2	187	U
45	C2	189	G
45	C2	190	C
45	C2	193	U
45	C2	198	U
45	C2	199	G
45	C2	200	U
45	C2	201	A
45	C2	244	G
45	C2	247	G
45	C2	250	G
45	C2	255	U
45	C2	256	G
45	C2	257	G
45	C2	259	A
45	C2	260	G
45	C2	261	U
45	C2	262	C
45	C2	267	C

All (39) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
44	C1	67	G
44	C1	89	G
44	C1	135	A
44	C1	150	C
44	C1	205	C
44	C1	207	U
44	C1	209	A
44	C1	259	U
44	C1	260	U
44	C1	277	U
44	C1	281	U
44	C1	401	C
44	C1	424	U
44	C1	582	G
44	C1	593	G
44	C1	1068	C
44	C1	1077	U
44	C1	1085	U

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Mol	Chain	Res	Type
44	C1	1087	G
44	C1	1163	A
44	C1	1485	A
44	C1	1638	G
44	C1	1712	C
44	C1	1734	G
44	C1	2054	A
44	C1	2070	A
44	C1	2077	C
44	C1	2156	A
44	C1	2177	G
44	C1	2214	A
44	C1	2219	C
45	C2	23	A
45	C2	35	G
45	C2	38	G
45	C2	61	G
45	C2	91	G
45	C2	94	A
45	C2	255	U
45	C2	259	A

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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
45	C2	3
2	UB	1
48	UH	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C2	206:G	O3'	240:C	P	18.53
1	C2	105:C	O3'	110:A	P	15.27
1	C2	119:C	O3'	123:A	P	11.89
1	UB	679:ASN	C	680:PHE	N	1.20
1	UH	730:PHE	C	731:LYS	N	1.18

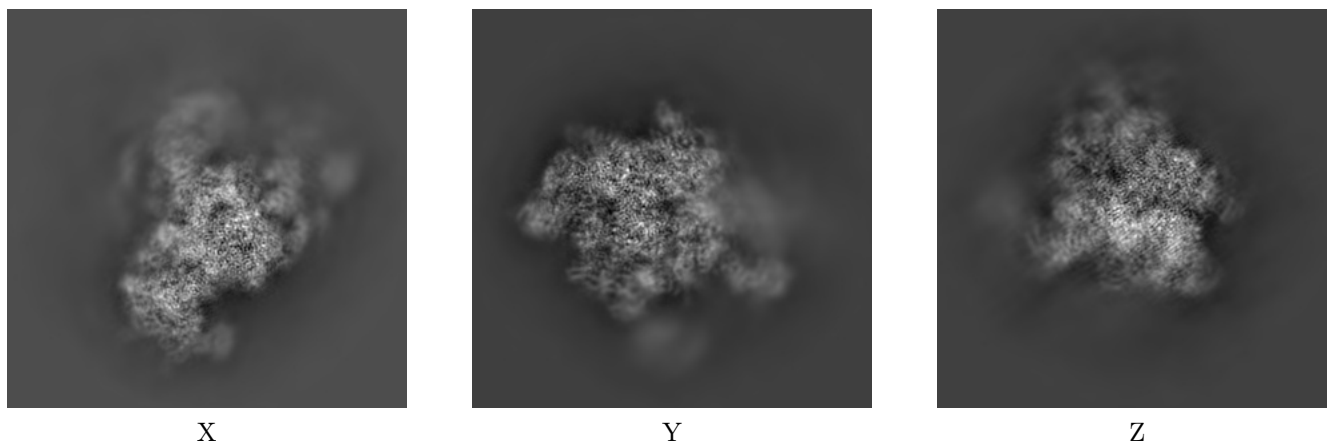
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10055. 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](#)

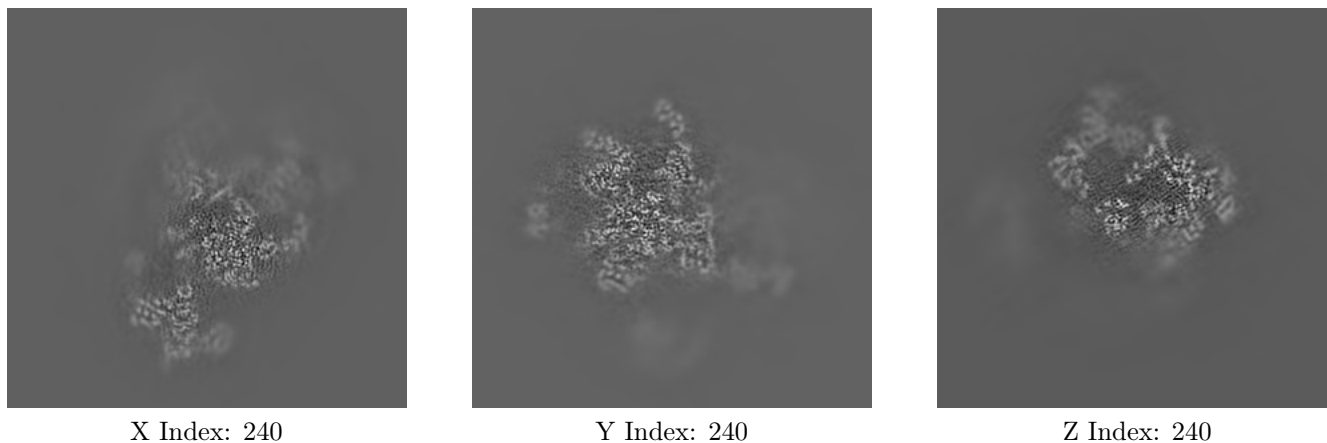
6.1.1 Primary map



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

6.2 Central slices [i](#)

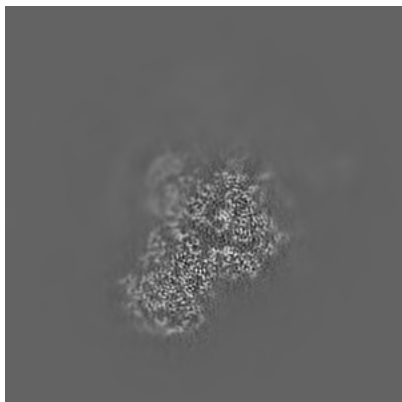
6.2.1 Primary map



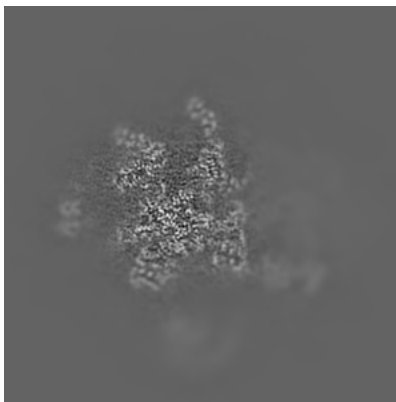
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

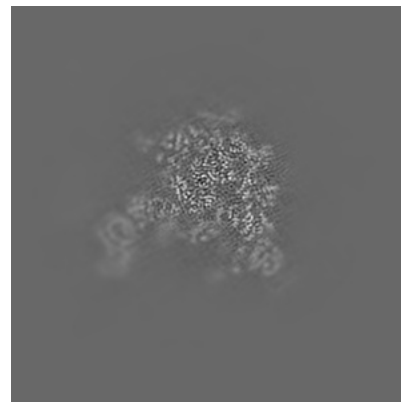
6.3.1 Primary map



X Index: 279



Y Index: 241



Z Index: 187

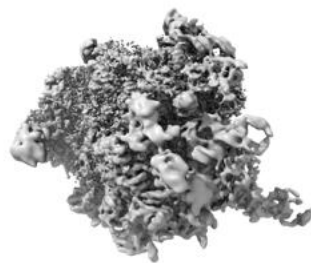
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

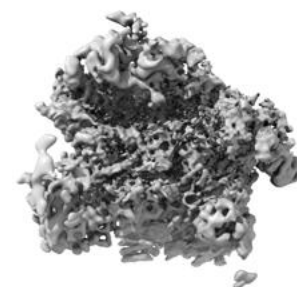
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

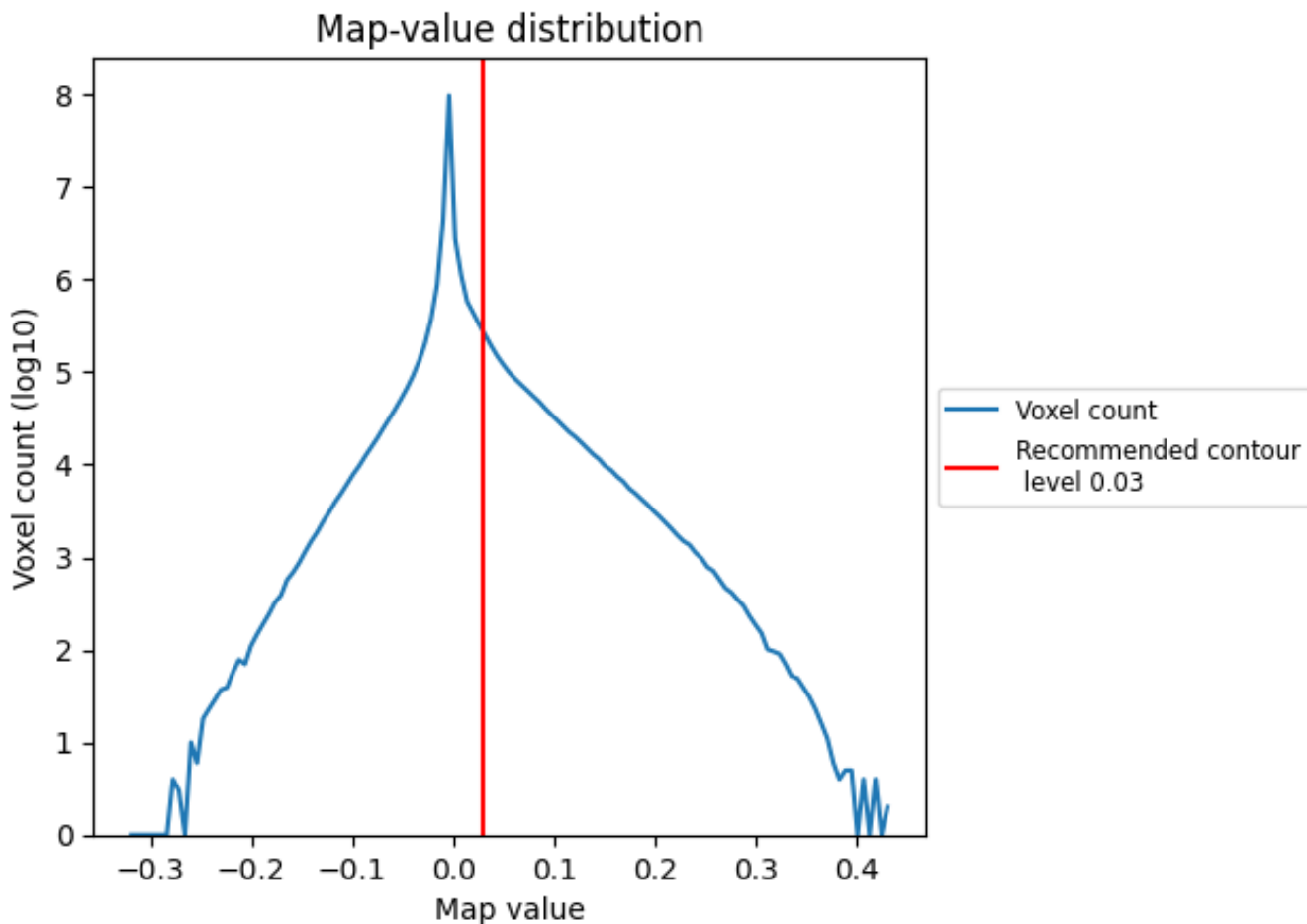
6.5 Mask visualisation

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

7 Map analysis [i](#)

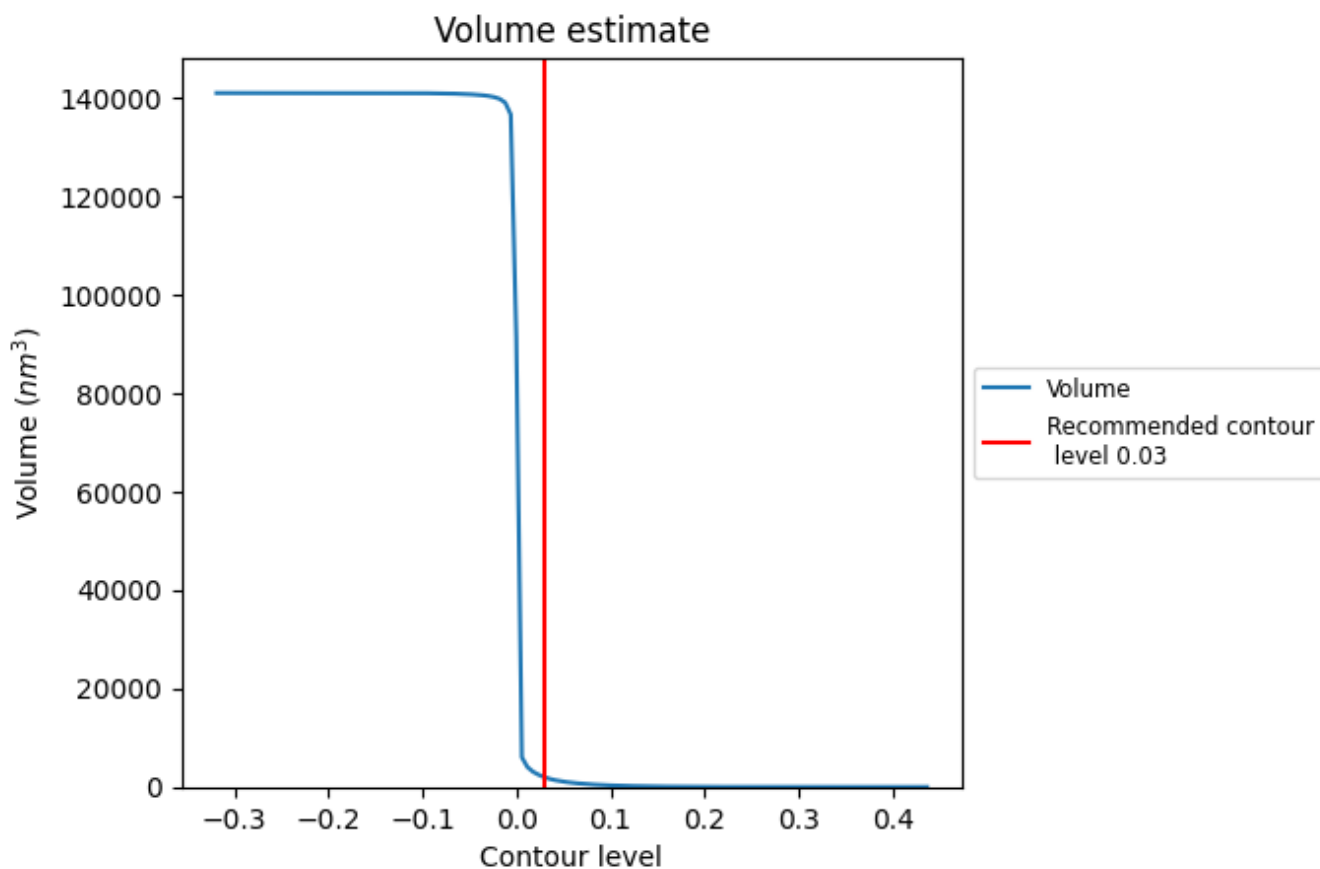
This section contains the results of statistical analysis of the map.

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.

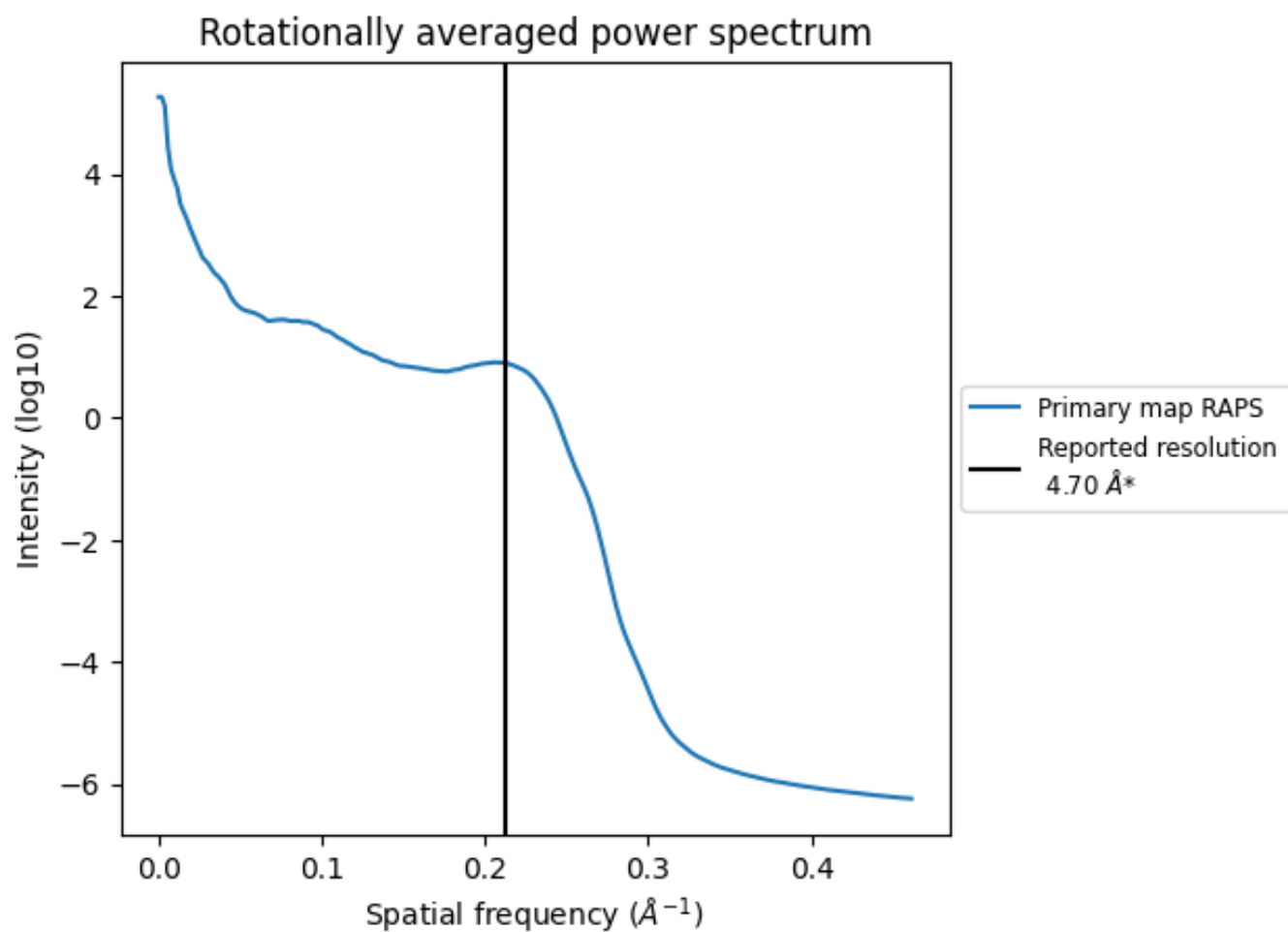
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1965 nm^3 ; this corresponds to an approximate mass of 1775 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 [i](#)

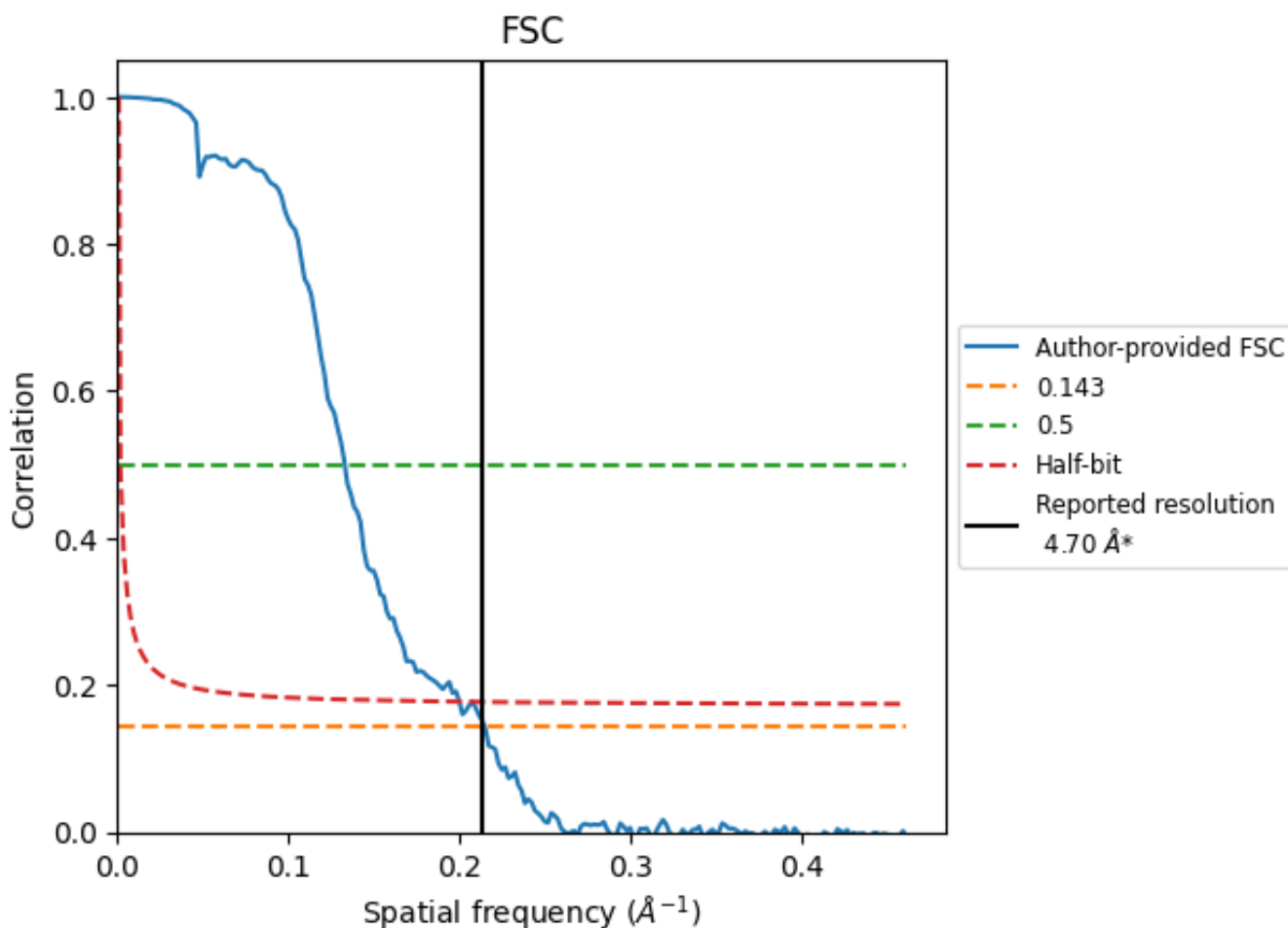


*Reported resolution corresponds to spatial frequency of 0.213\AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

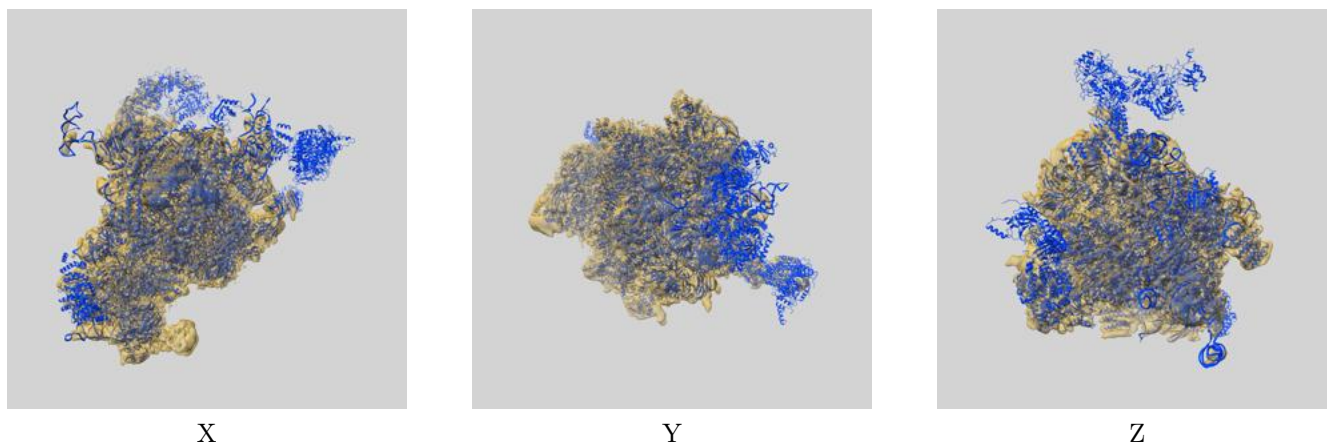
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.70	-	-
Author-provided FSC curve	4.66	7.52	5.00
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

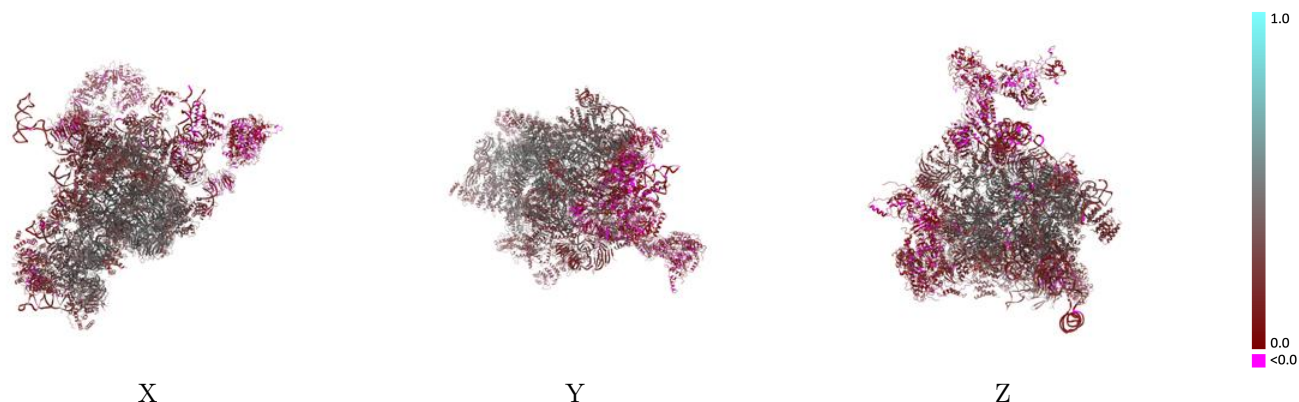
This section contains information regarding the fit between EMDB map EMD-10055 and PDB model 6RXY. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



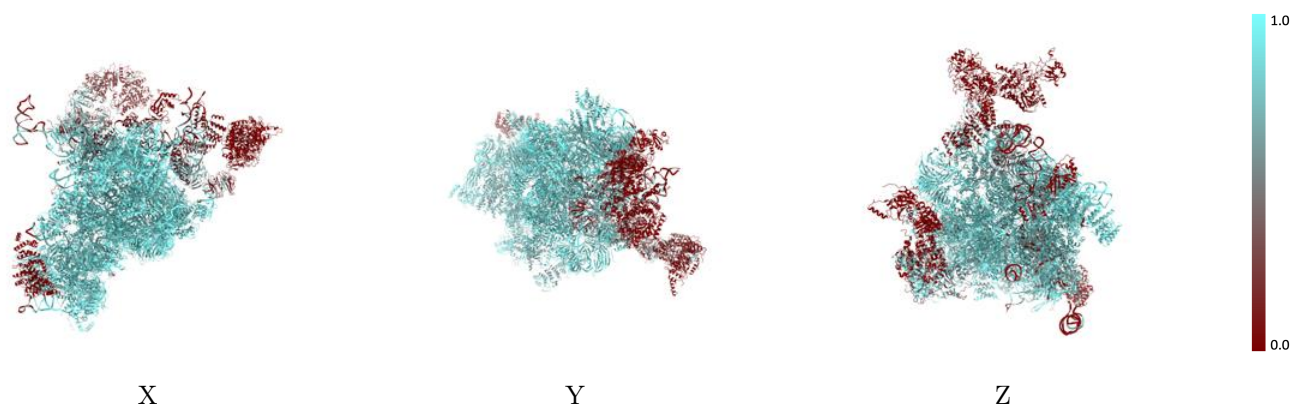
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



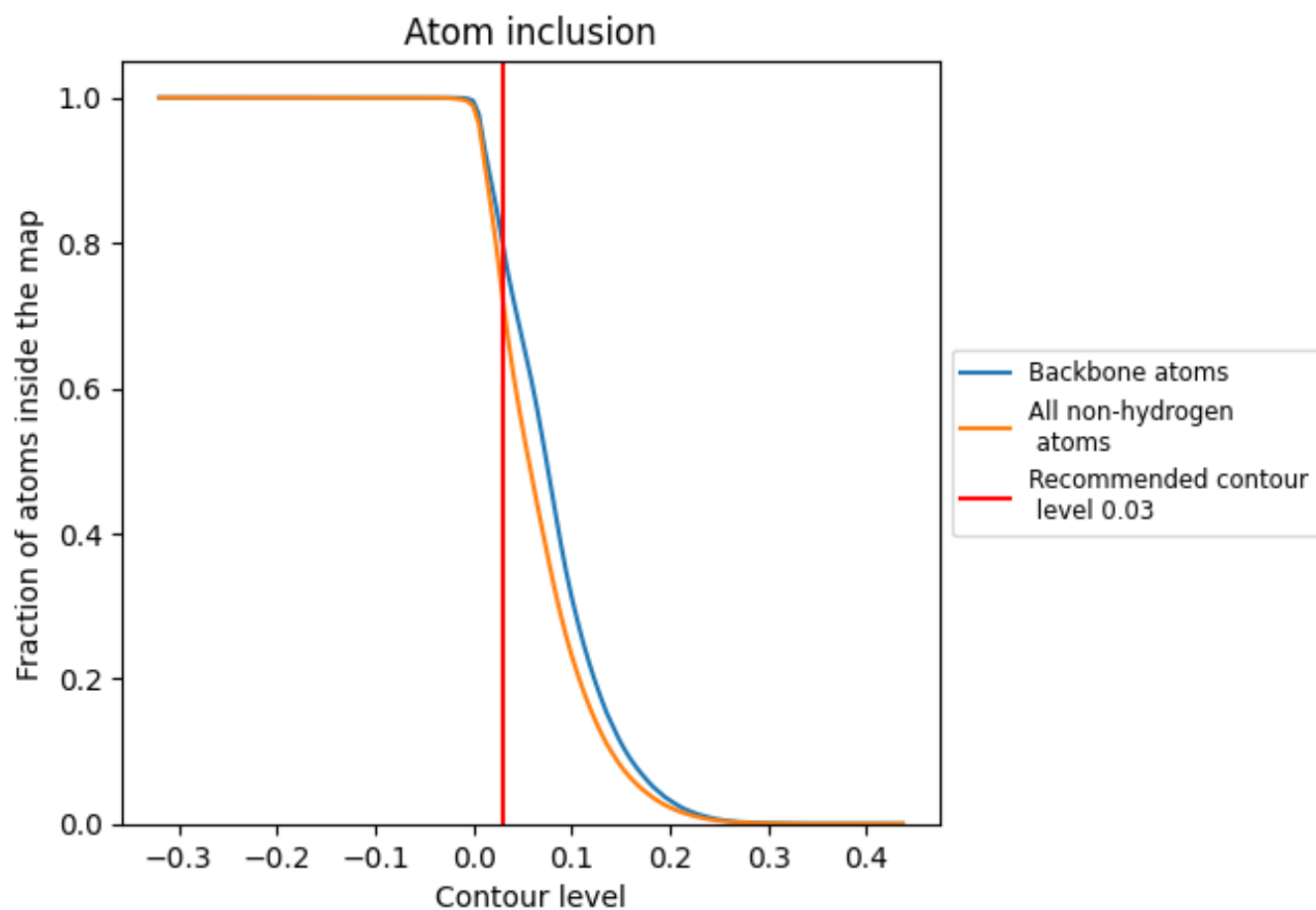
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary



















































The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7221	 0.2860
C1	 0.8230	 0.2910
C2	 0.7843	 0.2890
CA	 0.8907	 0.4010
CB	 0.7884	 0.2650
CC	 0.8329	 0.2940
CD	 0.8597	 0.3010
CE	 0.9210	 0.4520
CF	 0.6875	 0.2260
CG	 0.6172	 0.1410
CH	 0.8493	 0.3060
CI	 0.8292	 0.3190
CJ	 0.9338	 0.4690
CK	 0.9167	 0.4410
CL	 0.9008	 0.3840
CM	 0.9086	 0.3920
CN	 0.8396	 0.3450
CO	 0.7811	 0.2220
CP	 0.4007	 0.1470
CQ	 0.8352	 0.2360
CR	 0.4632	 0.1440
CS	 0.0677	 0.0790
CT	 0.8932	 0.4100
CU	 0.6205	 0.2920
CV	 0.0000	 0.0470
CX	 0.6833	 0.1390
Cc	 0.9179	 0.4140
Ce	 0.0048	 0.1440
Cg	 0.4204	 0.1990
Ch	 0.1504	 0.0740
Ci	 0.4974	 0.1250
Cj	 0.9349	 0.4730
Cl	 0.6355	 0.2730
Cm	 0.2661	 0.2370
Cn	 0.8596	 0.3770



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Chain	Atom inclusion	Q-score
Cp	 0.9149	 0.4200
Cz	 0.1529	 0.1050
UA	 0.9296	 0.4450
UB	 0.8646	 0.2900
UC	 0.7850	 0.3260
UD	 0.8939	 0.3560
UE	 0.8466	 0.3050
UF	 0.8891	 0.2880
UG	 0.9087	 0.4320
UH	 0.8533	 0.2590
UI	 0.7397	 0.1610
UJ	 0.4902	 0.2670
UK	 0.9126	 0.4090
UL	 0.8615	 0.2650
UM	 0.5662	 0.1270
UN	 0.8975	 0.3630
UO	 0.9161	 0.4160
UP	 0.8968	 0.3780
UQ	 0.9147	 0.3900
UR	 0.9332	 0.4440
US	 0.8449	 0.2750
UU	 0.9307	 0.4210
UV	 0.0000	 0.0550
UX	 0.8752	 0.3830
UZ	 0.8517	 0.3060