



Full wwPDB EM Validation Report ⓘ

Nov 19, 2022 – 09:41 am GMT

PDB ID : 4V92
EMDB ID : EMD-2604
Title : Kluyveromyces lactis 80S ribosome in complex with CrPV-IRES
Authors : Fernandez, I.S.; Bai, X.; Scheres, S.H.W.; Ramakrishnan, V.
Deposited on : 2014-03-21
Resolution : 3.70 Å (reported)
Based on initial model : 3B31

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) : 2.31.2

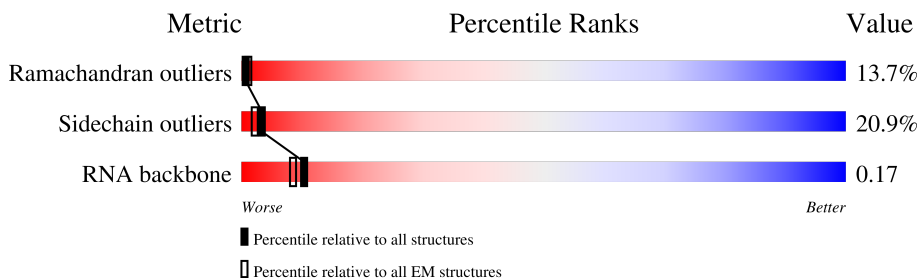
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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	A2	1767	6% (Upper red), 34% (Green), 43% (Yellow), 23% (Orange)
2	AZ	190	14% (Upper red), 18% (Green), 57% (Yellow), 25% (Orange)
3	BA	206	83% (Upper red), 63% (Green), 26% (Yellow), 8% (Orange), . (Grey)
4	BB	213	63% (Upper red), 70% (Green), 24% (Yellow), 6% (Orange)
5	BC	216	68% (Upper red), 81% (Green), 15% (Yellow), . (Grey)
6	BD	222	76% (Upper red), 76% (Green), 18% (Yellow), 5% (Orange), . (Grey)
7	BE	260	68% (Upper red), 72% (Green), 25% (Yellow), . (Grey)
8	BF	206	60% (Upper red), 73% (Green), 20% (Yellow), 6% (Orange)



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Mol	Chain	Length	Quality of chain
9	BG	226	70% 69% 25% 5%
10	BH	184	89% 72% 23% 5%
11	BI	187	73% 65% 29% 6%
12	BJ	179	73% 70% 26% .
13	BK	93	61% 68% 26% 6%
14	BL	142	87% 74% 18% 7% .
15	BM	120	88% 74% 22% .
16	BN	150	82% 72% 25% .
17	BO	127	68% 73% 21% 6%
18	BP	115	60% 77% 20% .
19	BQ	140	39% 62% 34% . .
20	BR	121	80% 73% 24% .
21	BS	140	54% 66% 26% 6% .
22	BT	142	53% 74% 21% . .
23	BU	104	68% 69% 26% 5%
24	BV	87	69% 82% 13% 5% .
25	BW	129	54% 82% 18%
26	BX	142	58% 77% 19% .
27	BY	134	60% 75% 24% .
28	BZ	64	64% 67% 27% 6%
29	Ba	97	55% 72% 19% 9%
30	Bb	81	78% 74% 23% .
31	Bc	63	75% 76% 19% 5%
32	Bd	52	65% 63% 33% .
33	Be	55	80% 67% 27% 5%

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Mol	Chain	Length	Quality of chain
34	Bf	64	
35	Bg	315	

2 Entry composition [i](#)

There are 35 unique types of molecules in this entry. The entry contains 79002 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A2	1764	37579	16801	6644	12370	1764	0	0

- Molecule 2 is a RNA chain called RNA OF CRICKET-PARALYSIS-VIRUS-IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	AZ	190	4018	1801	685	1342	190	0	0

- Molecule 3 is a protein called US2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	BA	206	1577	1014	278	283	2	0	0

- Molecule 4 is a protein called ES1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	BB	213	1686	1070	302	310	4	0	0

- Molecule 5 is a protein called US5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	BC	216	1626	1042	287	295	2	0	0

- Molecule 6 is a protein called US3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	BD	222	1729	1098	312	313	6	0	0

- Molecule 7 is a protein called ES4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	BE	260	2068	1316	389	360	3	0	0

- Molecule 8 is a protein called US7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	BF	206	1603	1004	297	299	3	0	0

- Molecule 9 is a protein called ES6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	BG	226	1790	1123	343	321	3	0	0

- Molecule 10 is a protein called ES7.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	BH	184	1481	951	265	265	0	0

- Molecule 11 is a protein called ES8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	BI	187	1480	919	296	263	2	0	0

- Molecule 12 is a protein called US4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	BJ	179	1452	919	282	250	1	0	0

- Molecule 13 is a protein called ES10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	BK	93	765	496	123	144	2	0	0

- Molecule 14 is a protein called US17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	BL	142	1146	735	217	191	3	0	0

- Molecule 15 is a protein called ES12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	BM	120	870	548	152	168	2	0	0

- Molecule 16 is a protein called US15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	BN	150	1192	759	224	207	2	0	0

- Molecule 17 is a protein called US11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	BO	127	905	555	183	165	2	0	0

- Molecule 18 is a protein called US19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	BP	115	914	585	165	157	7	0	0

- Molecule 19 is a protein called US9.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
19	BQ	140	1082	696	193	193	0	0

- Molecule 20 is a protein called ES17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	BR	121	934	583	179	170	2	0	0

- Molecule 21 is a protein called US13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BS	140	Total	C	N	O	S	0	0
			1150	720	223	205	2		

- Molecule 22 is a protein called ES19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BT	142	Total	C	N	O	S	0	0
			1105	689	207	207	2		

- Molecule 23 is a protein called US10.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	BU	104	Total	C	N	O	S	0	0
			829	525	150	153	1		

- Molecule 24 is a protein called ES21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BV	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 25 is a protein called US8.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 26 is a protein called US12.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BX	142	Total	C	N	O	S	0	0
			1101	698	215	186	2		

- Molecule 27 is a protein called ES24.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	BY	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 28 is a protein called ES25.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	BZ	64	Total	C	N	O	0	0
			518	331	95	92		

- Molecule 29 is a protein called ES26.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ba	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 30 is a protein called ES27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Bb	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 31 is a protein called ES28.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Bc	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 32 is a protein called US14.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Bd	52	Total	C	N	O	S	0	0
			433	269	91	69	4		

- Molecule 33 is a protein called ES30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Be	55	Total	C	N	O	S	0	0
			440	277	90	72	1		

- Molecule 34 is a protein called ES31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Bf	64	Total	C	N	O	S	0	0
			458	289	83	82	4		

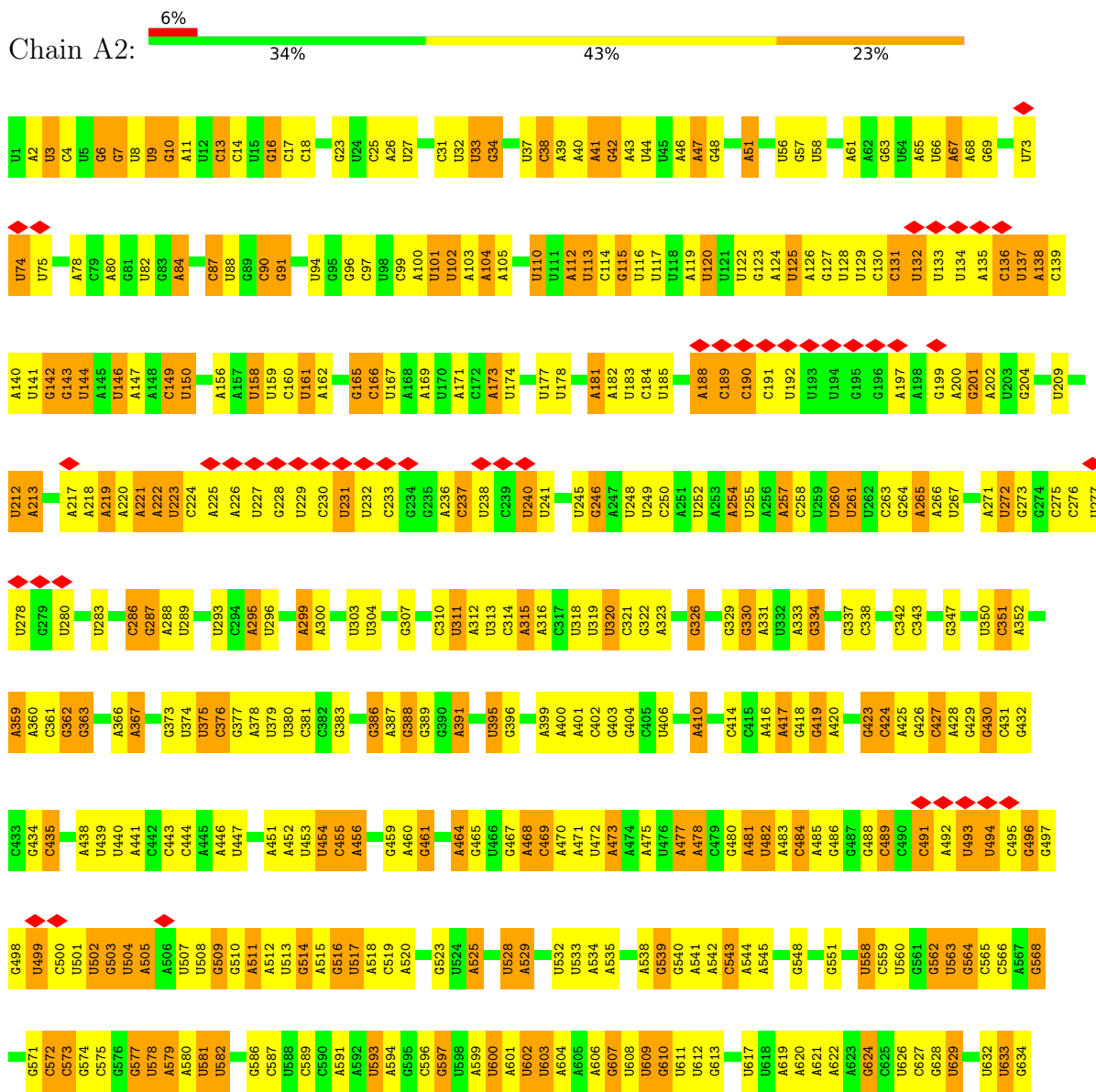
- Molecule 35 is a protein called RACK1.

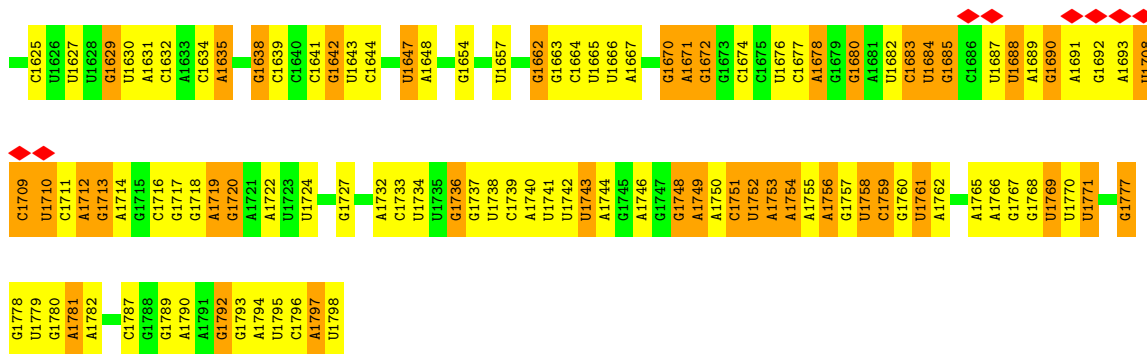
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	Bg	315	2417	1531	414	464	8	0	0

3 Residue-property plots

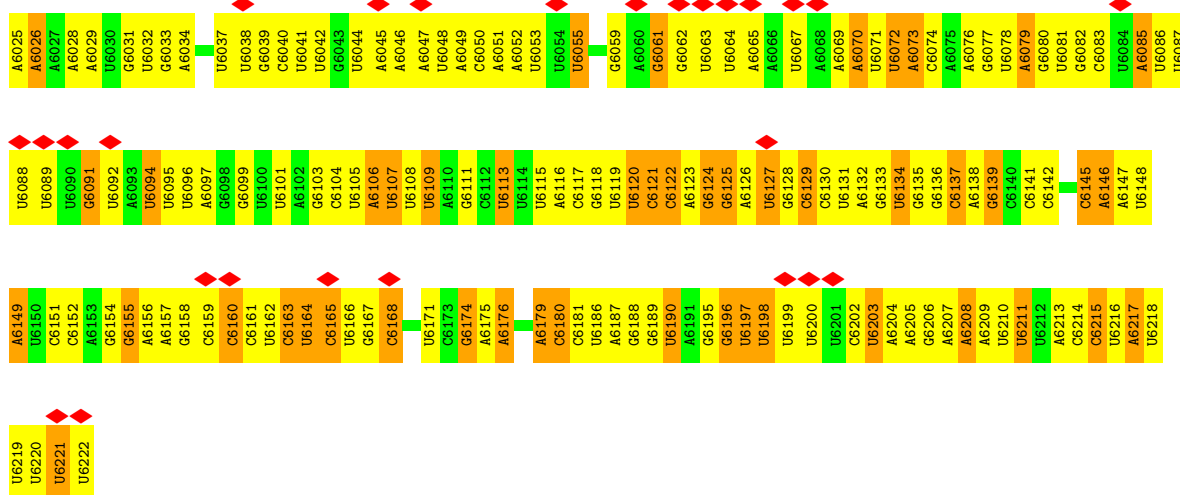
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 18S RRNA

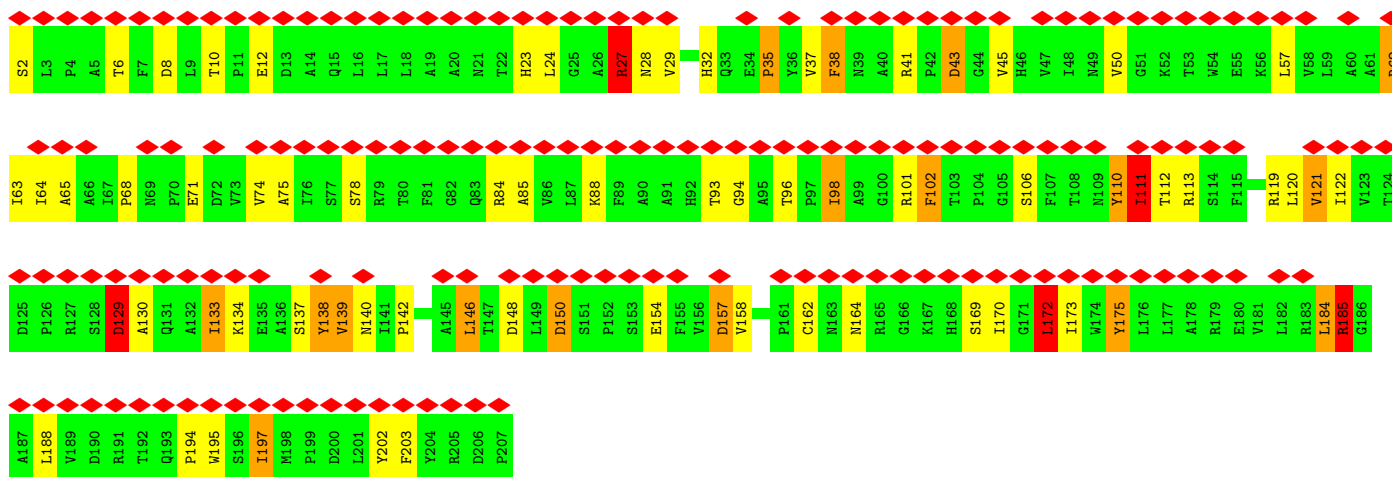
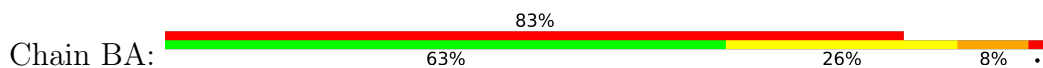




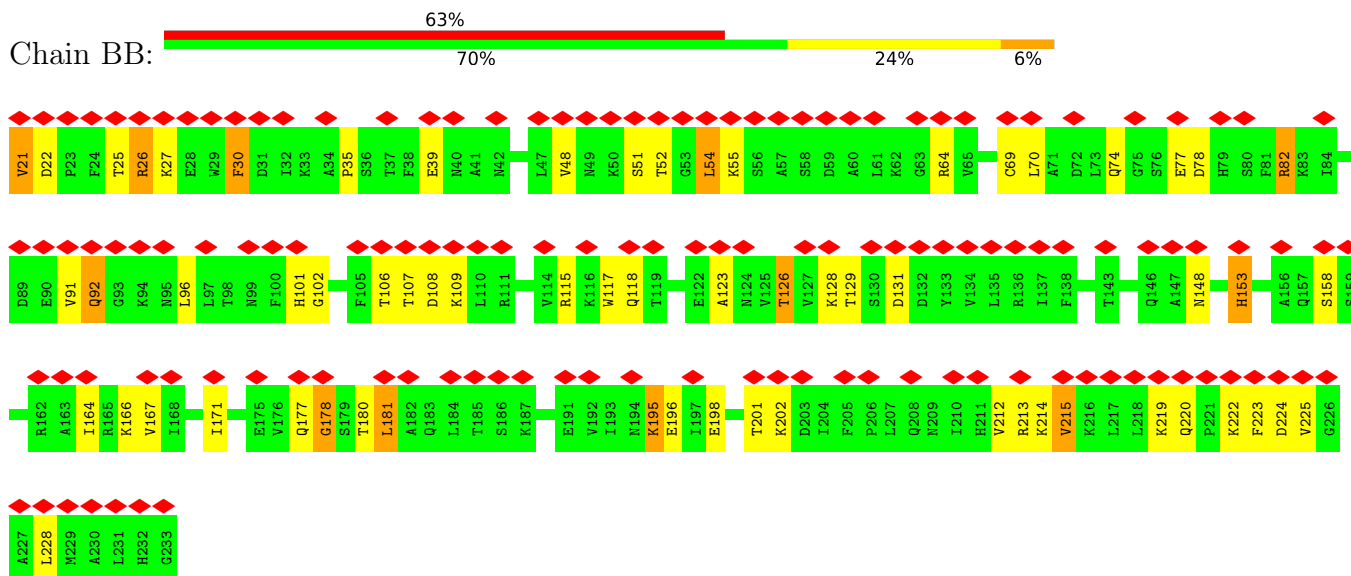
• Molecule 2: RNA OF CRICKET-PARALYSIS-VIRUS-IRES



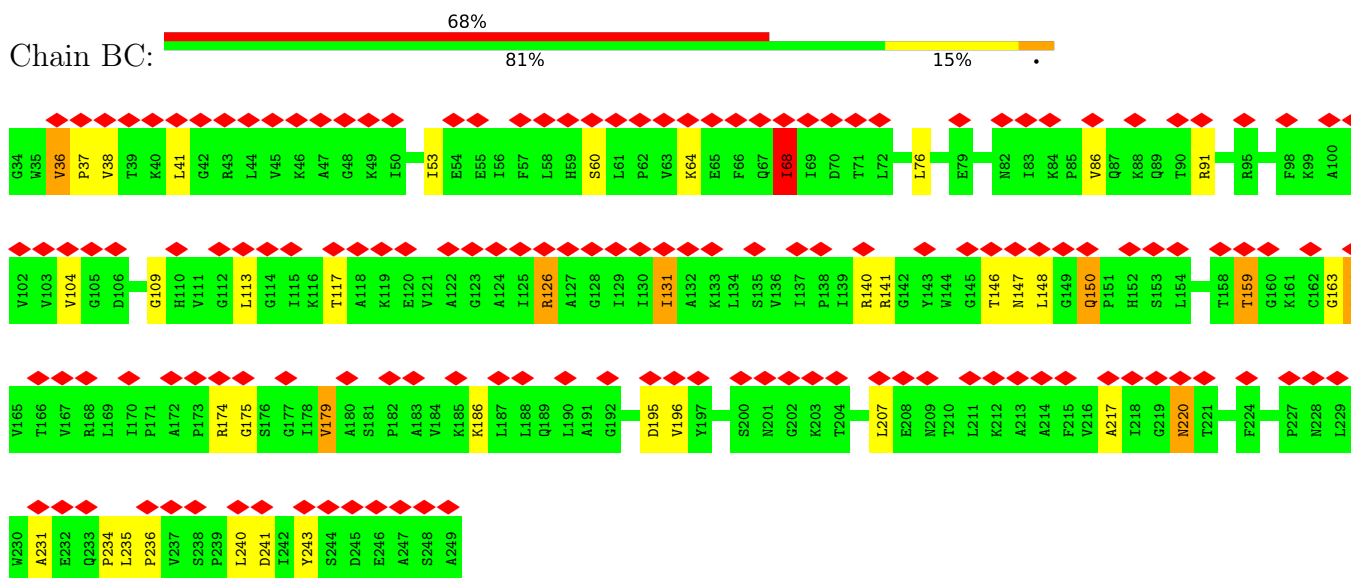
• Molecule 3: US2



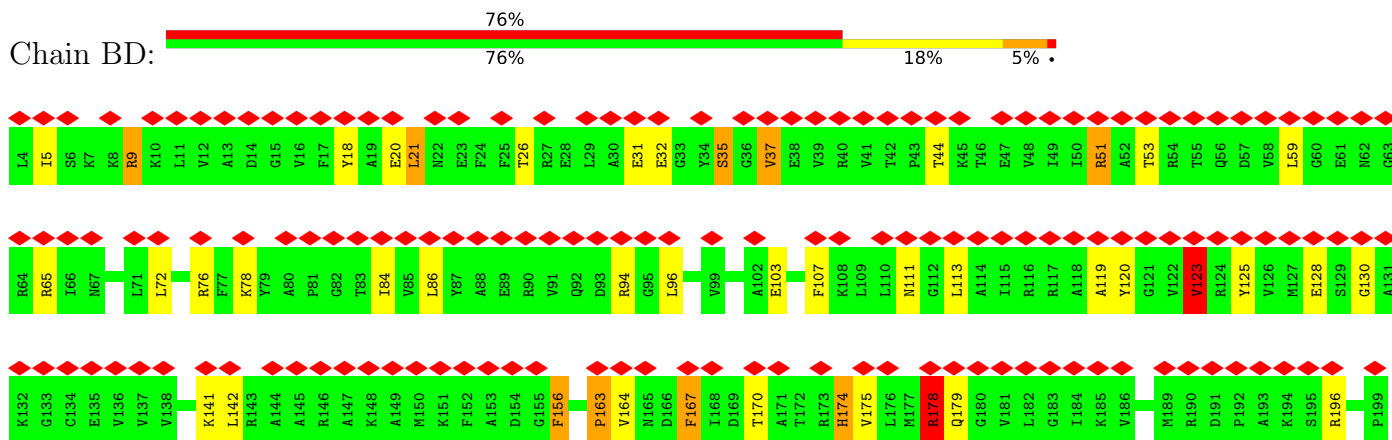
• Molecule 4: ES1

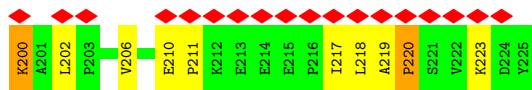


• Molecule 5: US5

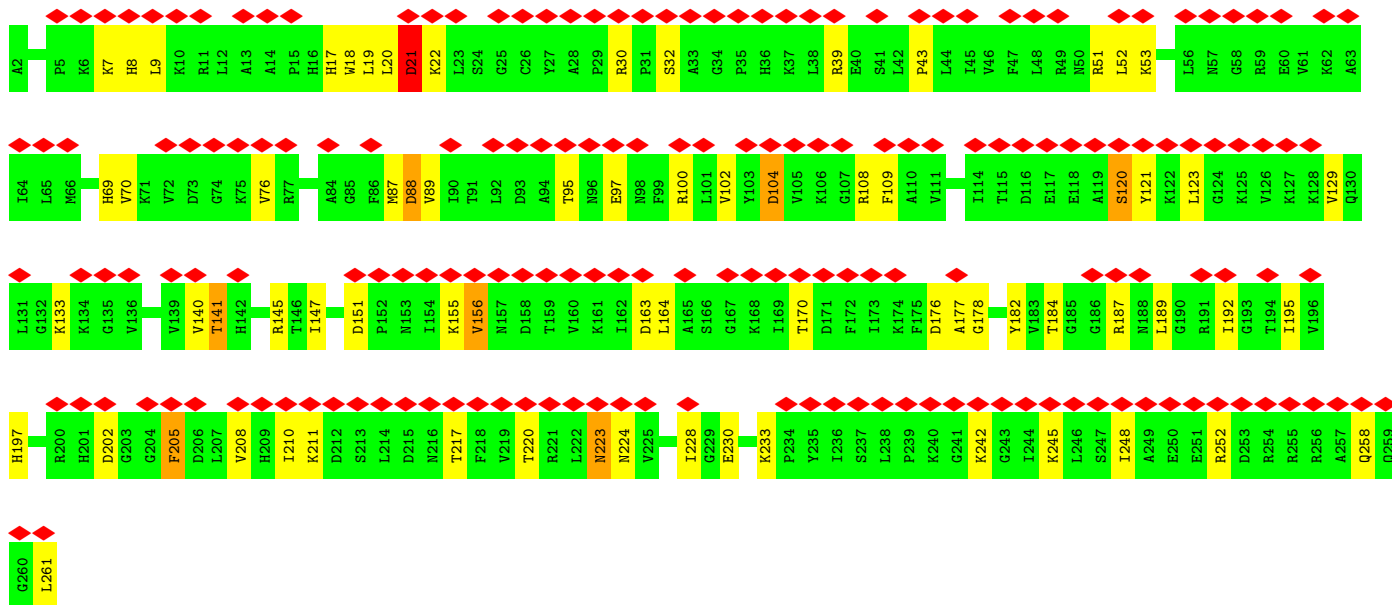
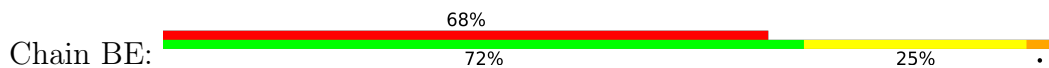


• Molecule 6: US3

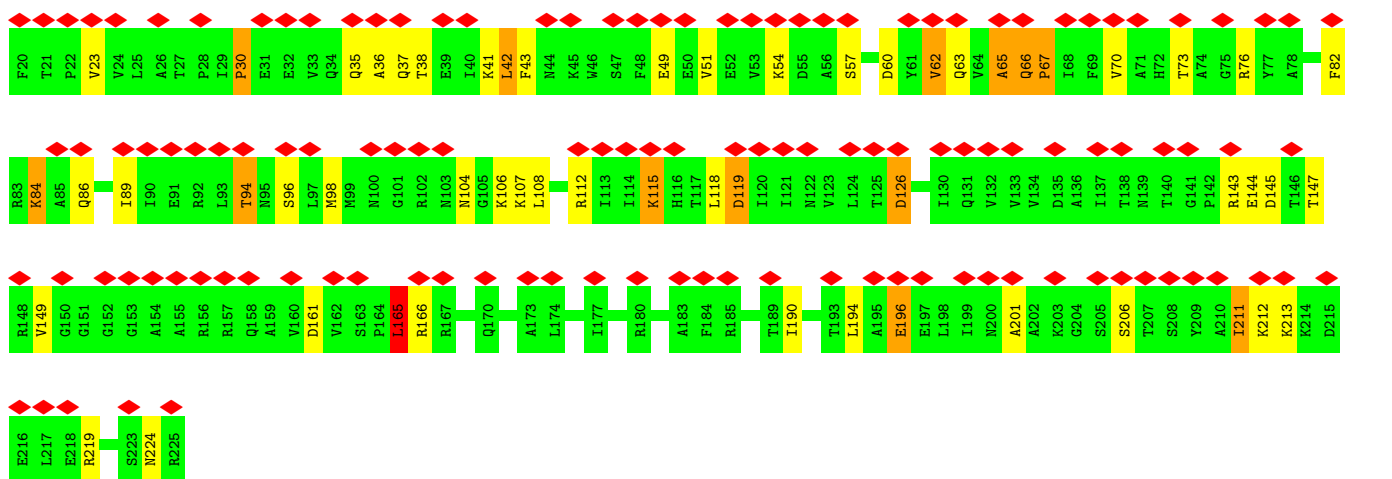
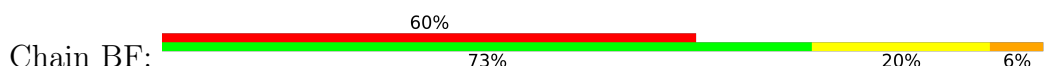




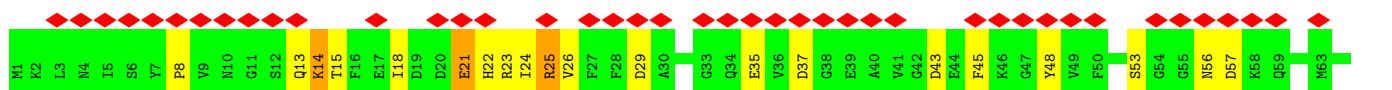
• Molecule 7: ES4

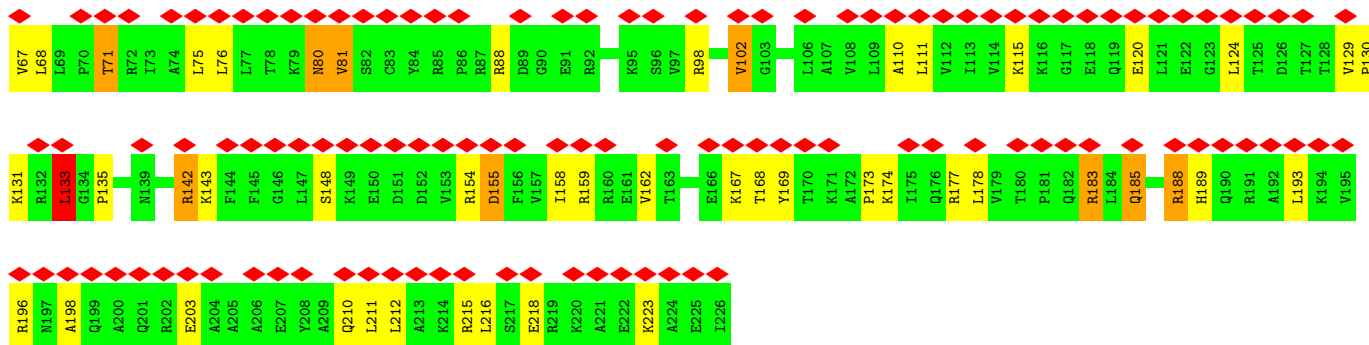


• Molecule 8: US7

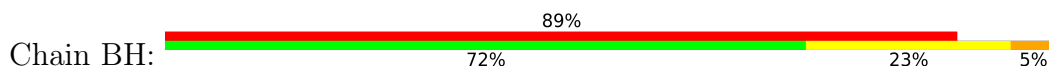


• Molecule 9: ES6

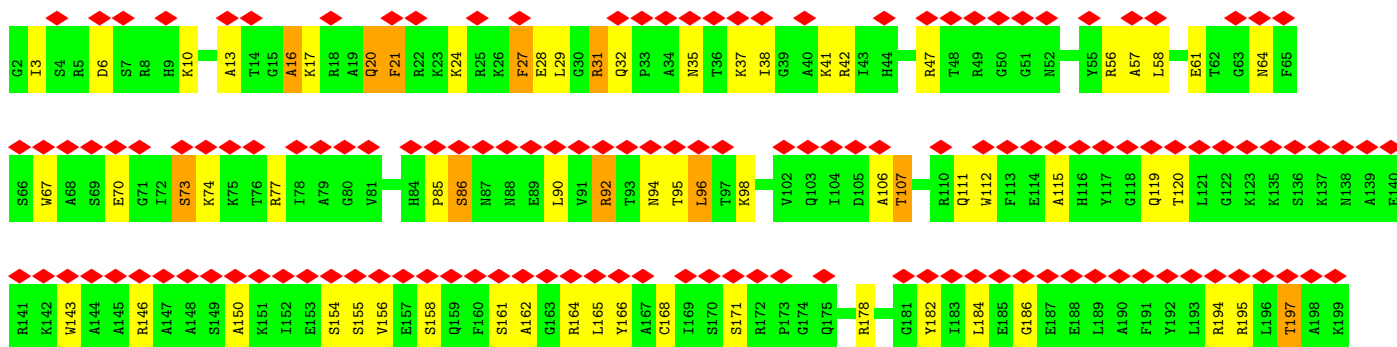
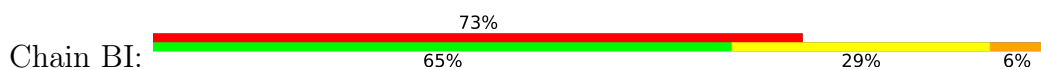




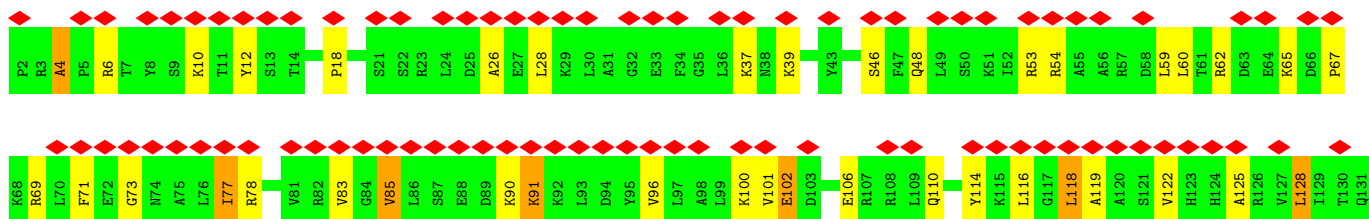
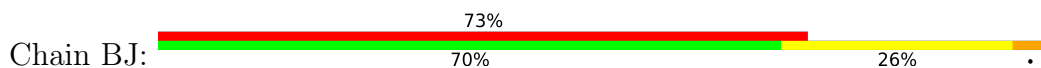
• Molecule 10: ES7



• Molecule 11: ES8

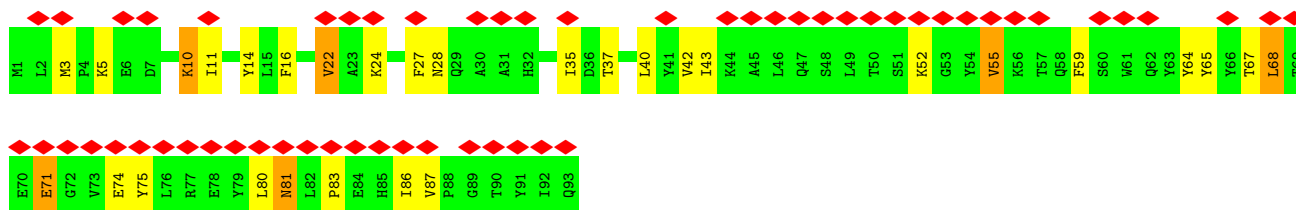


• Molecule 12: US4

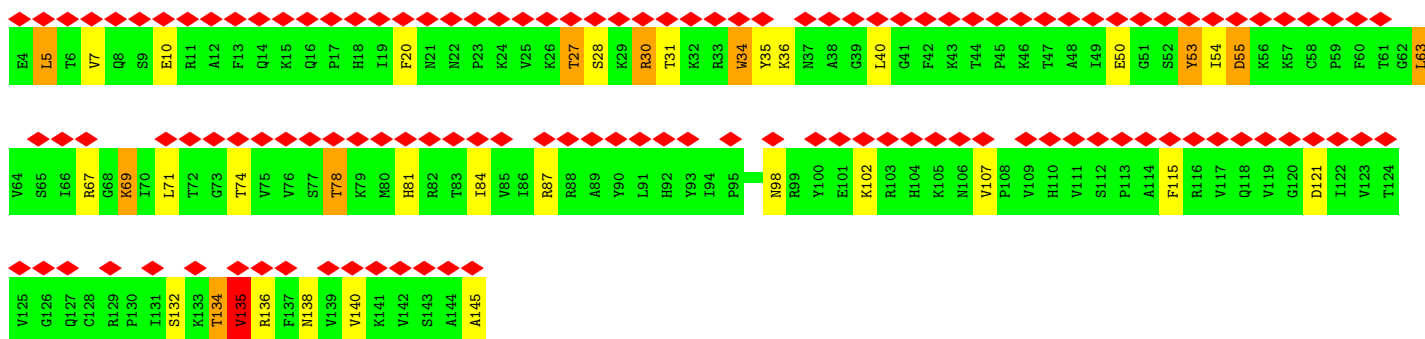
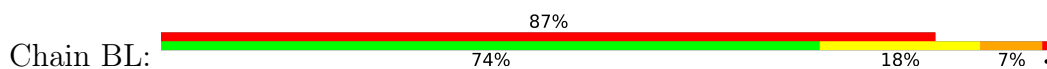




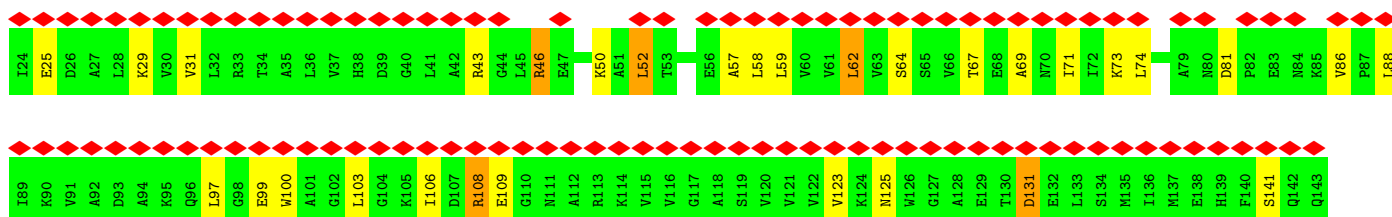
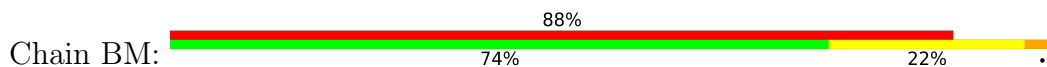
• Molecule 13: ES10



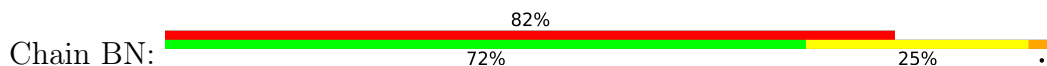
• Molecule 14: US17

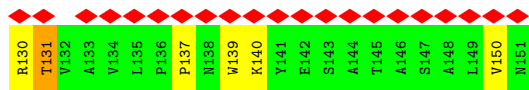


• Molecule 15: ES12

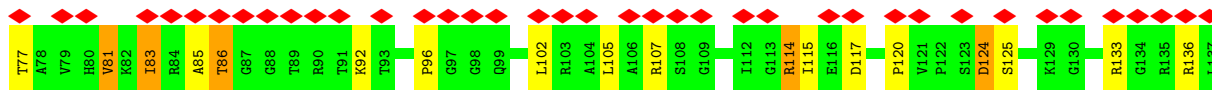
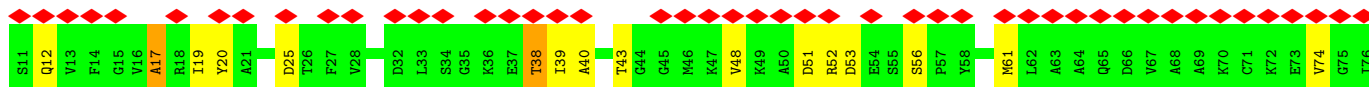
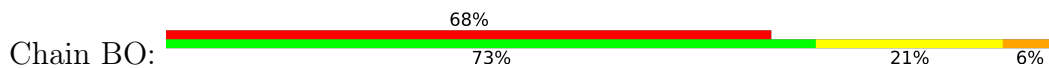


• Molecule 16: US15

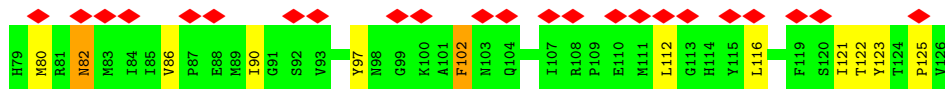
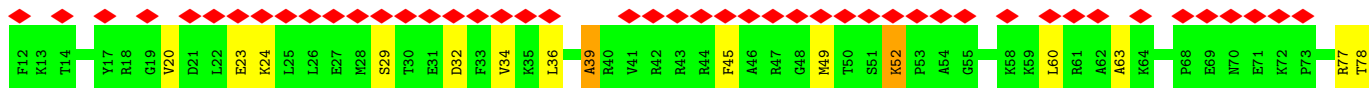
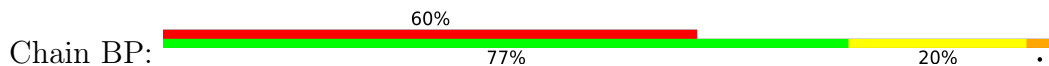




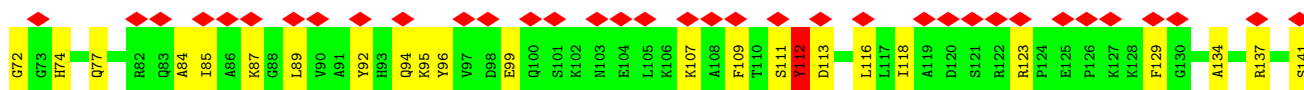
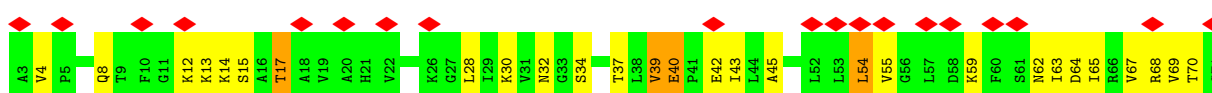
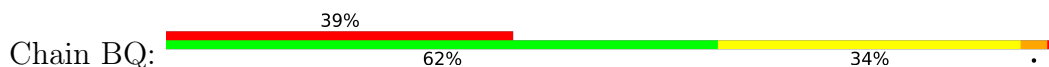
• Molecule 17: US11



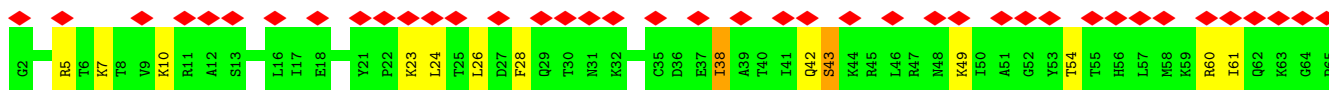
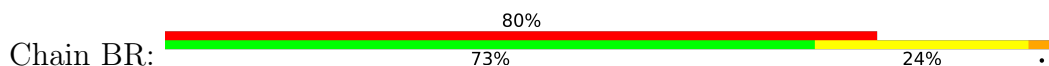
• Molecule 18: US19

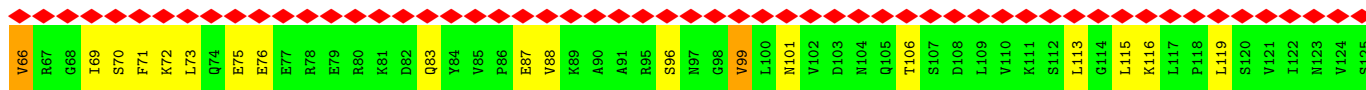


• Molecule 19: US9

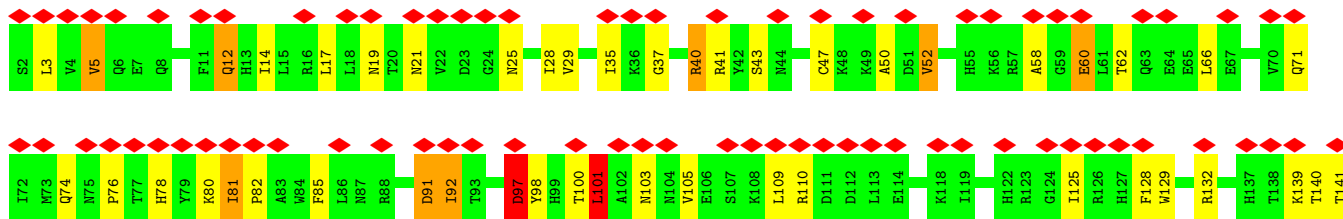


• Molecule 20: ES17

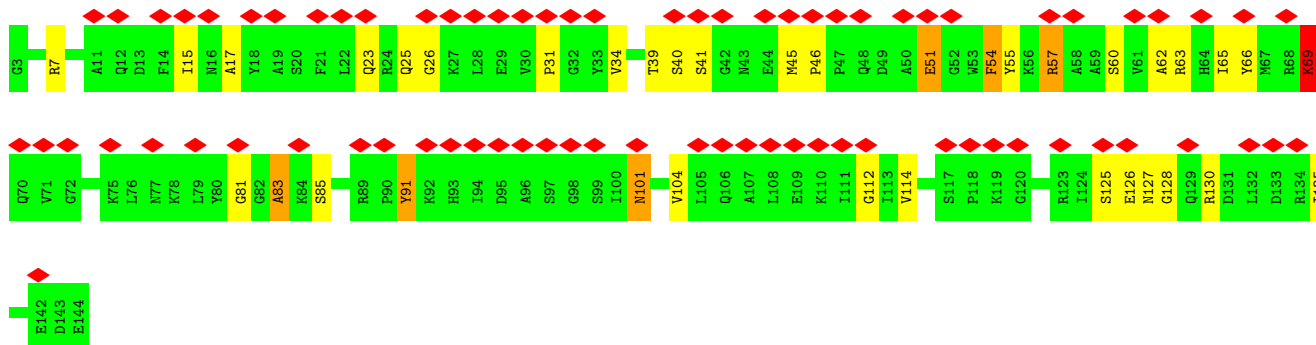
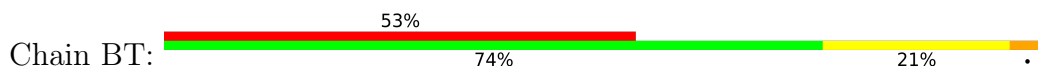




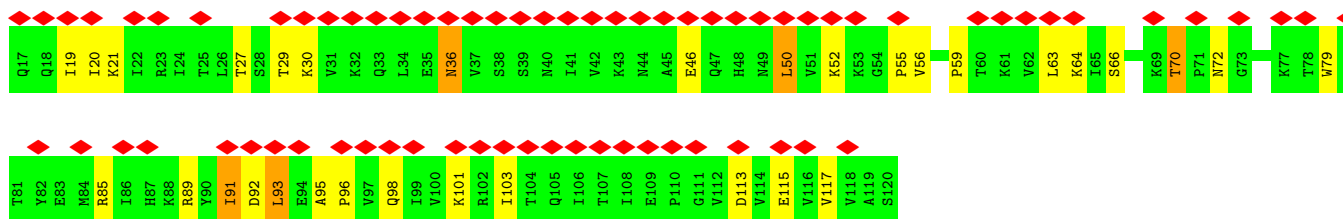
• Molecule 21: US13



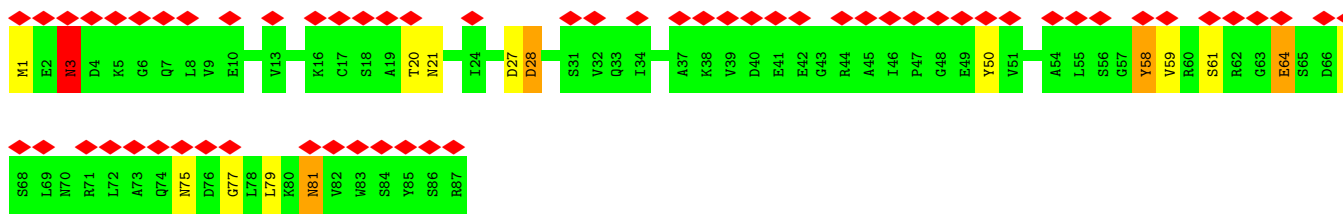
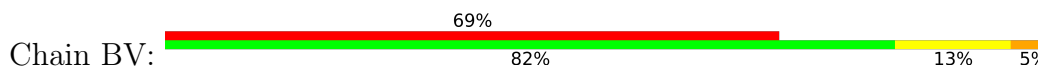
• Molecule 22: ES19



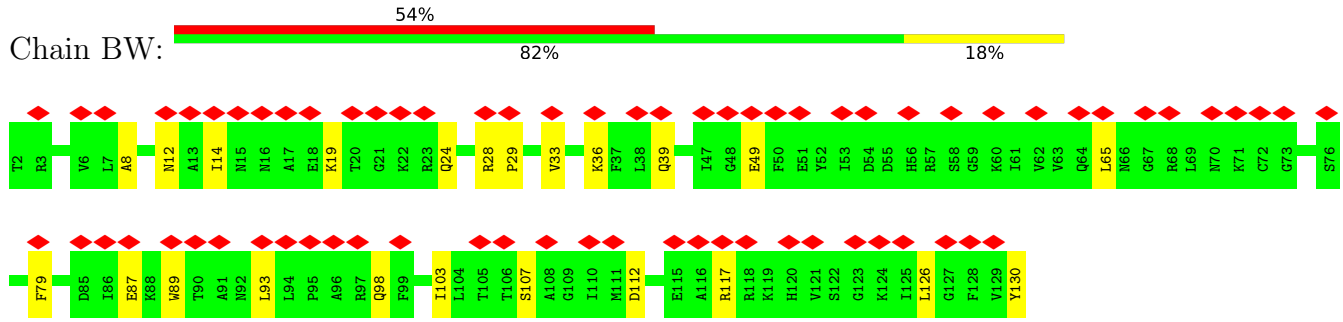
• Molecule 23: US10



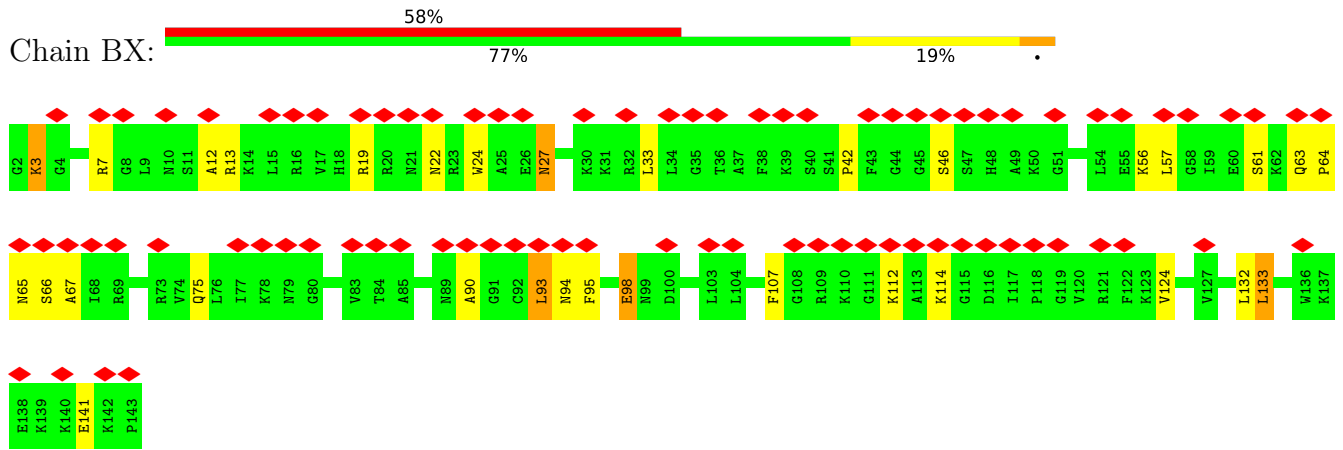
• Molecule 24: ES21



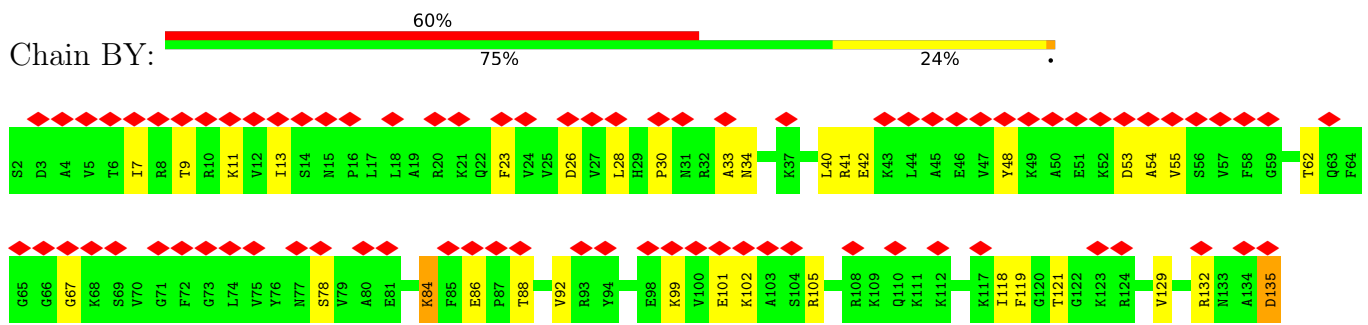
• Molecule 25: US8



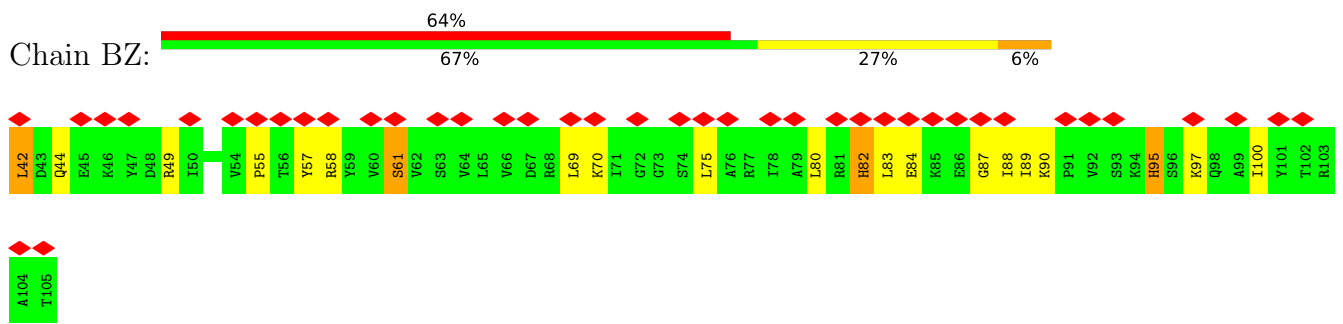
• Molecule 26: US12



• Molecule 27: ES24

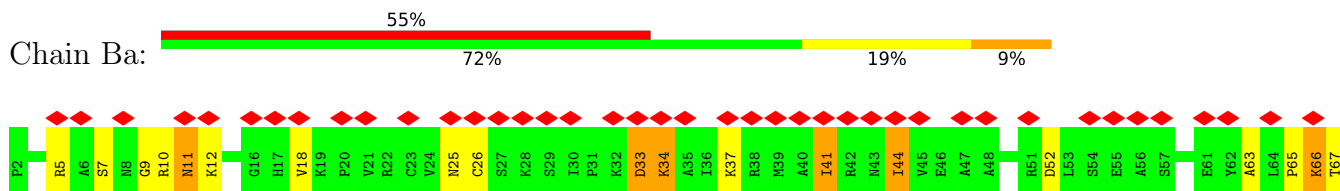


• Molecule 28: ES25

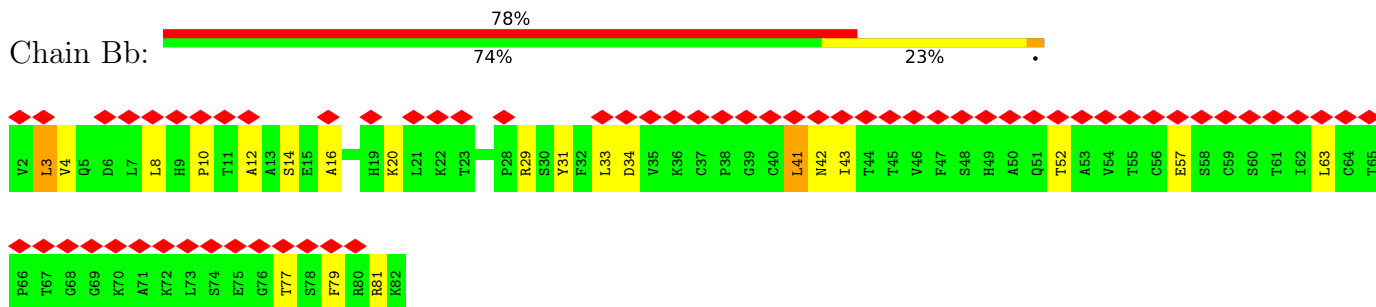


• Molecule 29: ES26

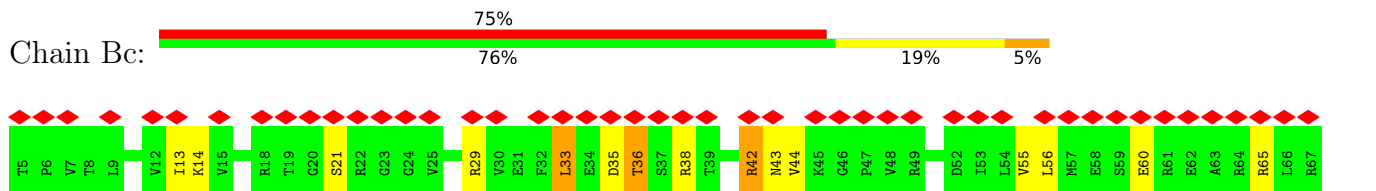




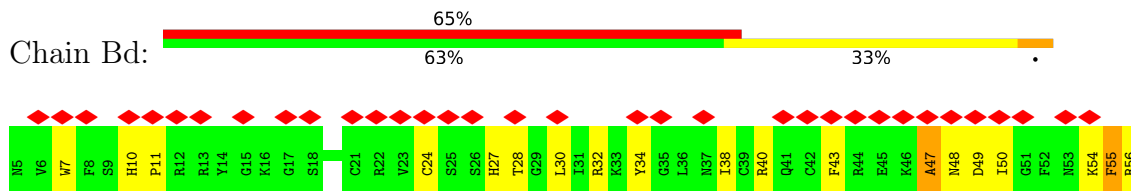
• Molecule 30: ES27



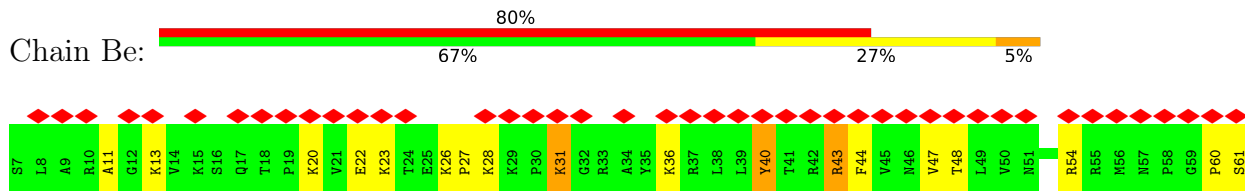
• Molecule 31: ES28



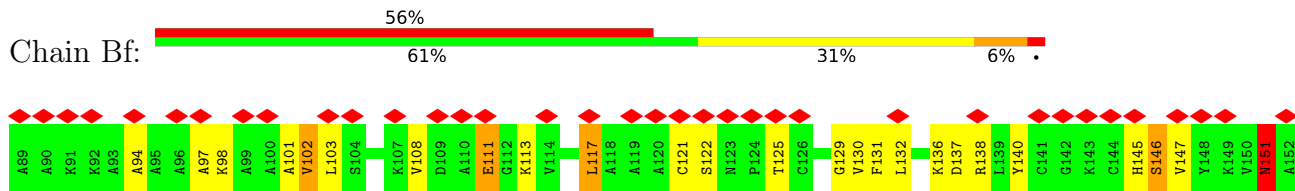
• Molecule 32: US14



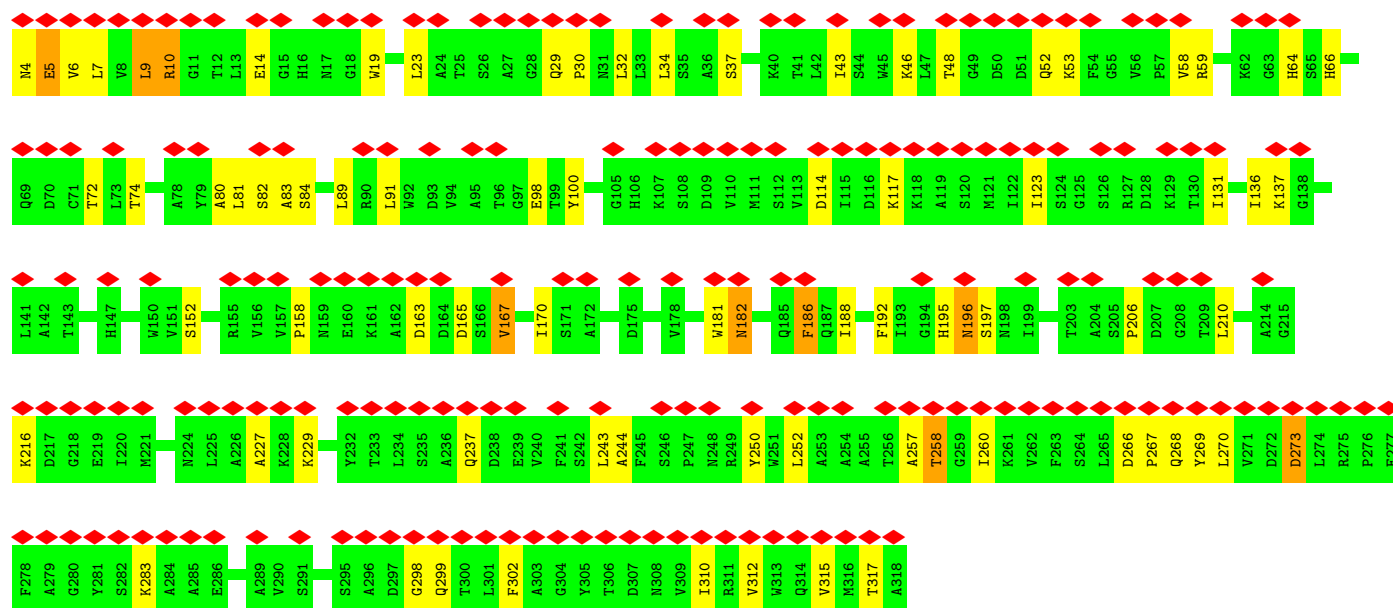
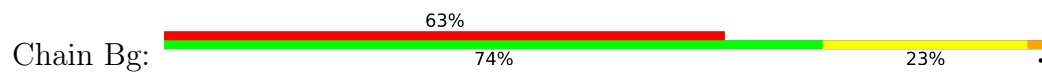
• Molecule 33: ES30



• Molecule 34: ES31



- Molecule 35: RACK1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	18132	Depositor
Resolution determination method	Not provided	
CTF correction method	EACH PARTICLE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1.8	Depositor
Maximum defocus (nm)	3	Depositor
Magnification	47000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.990	Depositor
Minimum map value	-0.618	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.07	Depositor
Map size (\AA)	428.80002, 428.80002, 428.80002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.34, 1.34, 1.34	Depositor

5 Model quality i

5.1 Standard geometry i

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	A2	1.00	25/41655 (0.1%)	1.31	1105/63991 (1.7%)
2	AZ	0.91	5/4449 (0.1%)	1.28	113/6827 (1.7%)
3	BA	0.95	2/1574 (0.1%)	1.25	26/2086 (1.2%)
4	BB	0.50	0/1661	1.06	16/2154 (0.7%)
5	BC	0.40	0/1610	0.99	14/2113 (0.7%)
6	BD	0.46	0/1692	1.06	19/2175 (0.9%)
7	BE	0.42	1/2045 (0.0%)	0.99	23/2647 (0.9%)
8	BF	0.53	0/1571	1.00	14/2039 (0.7%)
9	BG	0.49	1/1767 (0.1%)	1.06	13/2288 (0.6%)
10	BH	0.43	0/1455	1.04	17/1875 (0.9%)
11	BI	0.53	0/1448	1.18	19/1839 (1.0%)
12	BJ	0.40	0/1435	0.99	18/1854 (1.0%)
13	BK	0.56	0/759	1.07	8/988 (0.8%)
14	BL	0.52	1/1140 (0.1%)	1.12	15/1484 (1.0%)
15	BM	0.70	0/845	1.03	8/1093 (0.7%)
16	BN	0.45	0/1186	1.04	12/1551 (0.8%)
17	BO	0.39	0/893	0.96	9/1167 (0.8%)
18	BP	0.66	1/903 (0.1%)	1.09	8/1162 (0.7%)
19	BQ	0.63	1/1072 (0.1%)	1.15	13/1392 (0.9%)
20	BR	0.44	0/908	1.02	10/1159 (0.9%)
21	BS	0.69	0/1140	1.18	11/1487 (0.7%)
22	BT	0.92	3/1083 (0.3%)	1.16	15/1389 (1.1%)
23	BU	0.57	0/812	1.06	9/1053 (0.9%)
24	BV	0.47	0/675	0.89	4/881 (0.5%)
25	BW	0.42	0/999	0.91	4/1278 (0.3%)
26	BX	0.38	0/1079	0.97	11/1372 (0.8%)
27	BY	0.50	0/1056	1.15	14/1356 (1.0%)
28	BZ	0.73	0/511	1.11	5/663 (0.8%)
29	Ba	0.43	0/758	1.06	7/975 (0.7%)
30	Bb	0.41	0/596	1.05	6/766 (0.8%)
31	Bc	0.42	0/485	1.03	5/628 (0.8%)
32	Bd	0.51	0/427	1.04	5/540 (0.9%)
33	Be	0.47	0/436	1.16	6/562 (1.1%)
34	Bf	0.71	0/456	1.07	5/599 (0.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Bg	0.55	0/2390	1.01	23/3123 (0.7%)
All	All	0.83	40/82971 (0.0%)	1.21	1610/118556 (1.4%)

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	A2	98	0
2	AZ	8	0
3	BA	8	3
4	BB	11	2
5	BC	8	1
6	BD	6	1
7	BE	8	0
8	BF	6	1
9	BG	10	3
10	BH	7	2
11	BI	12	2
12	BJ	5	1
13	BK	2	0
14	BL	8	0
15	BM	2	0
16	BN	6	0
17	BO	4	1
18	BP	4	0
19	BQ	8	2
20	BR	5	0
21	BS	6	4
22	BT	6	0
23	BU	1	1
24	BV	2	1
25	BW	3	0
26	BX	5	2
27	BY	6	0
28	BZ	1	0
29	Ba	4	1
30	Bb	5	0
31	Bc	2	0
32	Bd	3	1
33	Be	3	0

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Mol	Chain	#Chirality outliers	#Planarity outliers
34	Bf	2	1
35	Bg	9	1
All	All	284	31

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A2	897	C	O3'-P	48.97	2.19	1.61
1	A2	633	U	O3'-P	48.70	2.19	1.61
1	A2	1797	A	O3'-P	47.72	2.18	1.61
1	A2	1388	A	O3'-P	46.19	2.16	1.61
1	A2	388	G	O3'-P	45.98	2.16	1.61
1	A2	56	U	O3'-P	45.37	2.15	1.61
1	A2	935	U	O3'-P	45.16	2.15	1.61
1	A2	419	G	O3'-P	44.76	2.14	1.61
1	A2	1377	U	O3'-P	44.75	2.14	1.61
2	AZ	6106	A	O3'-P	44.02	2.13	1.61
1	A2	47	A	O3'-P	42.43	2.12	1.61
1	A2	1732	A	O3'-P	39.87	2.08	1.61
1	A2	862	A	O3'-P	39.80	2.08	1.61
1	A2	464	A	O3'-P	38.50	2.07	1.61
1	A2	997	G	O3'-P	37.72	2.06	1.61
1	A2	399	A	O3'-P	37.54	2.06	1.61
1	A2	352	A	O3'-P	35.33	2.03	1.61
1	A2	1030	A	O3'-P	31.40	1.98	1.61
1	A2	960	U	O3'-P	29.89	1.97	1.61
1	A2	1417	A	O3'-P	24.57	1.90	1.61
1	A2	104	A	O3'-P	23.65	1.89	1.61
22	BT	54	PHE	C-O	14.82	1.51	1.23
1	A2	1298	U	P-O5'	14.38	1.74	1.59
22	BT	62	ALA	C-O	11.24	1.44	1.23
19	BQ	72	GLY	C-O	10.94	1.41	1.23
14	BL	78	THR	CB-OG1	9.34	1.61	1.43
2	AZ	6026	A	O3'-P	8.23	1.71	1.61
3	BA	138	TYR	CB-CG	7.75	1.63	1.51
22	BT	60	SER	C-O	7.72	1.38	1.23
1	A2	221	A	O3'-P	6.94	1.69	1.61
2	AZ	6028	A	P-OP2	6.81	1.60	1.49
3	BA	110	TYR	CB-CG	6.29	1.61	1.51
2	AZ	6123	A	O3'-P	5.74	1.68	1.61
1	A2	1298	U	P-OP1	5.64	1.58	1.49
7	BE	121	TYR	CE1-CZ	5.60	1.45	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	BP	77	ARG	C-O	5.42	1.33	1.23
9	BG	131	LYS	C-O	5.34	1.33	1.23
1	A2	1296	A	O3'-P	-5.26	1.54	1.61
2	AZ	6025	A	P-OP2	5.19	1.57	1.49
1	A2	1684	U	O3'-P	5.15	1.67	1.61

All (1610) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	104	A	P-O3'-C3'	41.97	170.06	119.70
1	A2	56	U	P-O3'-C3'	36.36	163.33	119.70
1	A2	1797	A	O3'-P-O5'	29.86	160.74	104.00
1	A2	862	A	P-O3'-C3'	26.83	151.90	119.70
1	A2	960	U	P-O3'-C3'	-25.06	89.62	119.70
1	A2	897	C	P-O3'-C3'	-18.59	97.40	119.70
1	A2	104	A	O3'-P-O5'	-18.27	69.29	104.00
1	A2	997	G	P-O3'-C3'	18.07	141.38	119.70
1	A2	352	A	P-O3'-C3'	17.54	140.74	119.70
1	A2	1797	A	OP1-P-O3'	-17.24	67.27	105.20
1	A2	464	A	P-O3'-C3'	-16.32	100.11	119.70
1	A2	633	U	P-O3'-C3'	-16.18	100.28	119.70
1	A2	997	G	OP1-P-O3'	15.54	139.38	105.20
1	A2	352	A	OP2-P-O3'	14.41	136.89	105.20
1	A2	1377	U	P-O3'-C3'	14.12	136.65	119.70
1	A2	960	U	O3'-P-O5'	-13.88	77.63	104.00
1	A2	47	A	O3'-P-O5'	13.05	128.79	104.00
1	A2	1388	A	OP1-P-O3'	-12.22	78.32	105.20
1	A2	419	G	OP1-P-O3'	12.10	131.81	105.20
1	A2	835	U	N1-C1'-C2'	12.10	129.72	114.00
1	A2	1449	U	N1-C1'-C2'	11.91	129.49	114.00
1	A2	724	C	N1-C1'-C2'	11.88	129.45	114.00
1	A2	74	U	N1-C1'-C2'	11.32	128.71	114.00
1	A2	254	A	C2'-C3'-O3'	11.15	134.03	109.50
1	A2	545	A	N9-C1'-C2'	11.09	128.42	114.00
19	BQ	96	TYR	CD1-CE1-CZ	11.03	129.72	119.80
1	A2	1580	C	N1-C1'-C2'	10.98	128.28	114.00
1	A2	47	A	P-O3'-C3'	10.93	132.81	119.70
1	A2	1388	A	P-O3'-C3'	10.81	132.67	119.70
1	A2	452	A	N9-C1'-C2'	10.80	128.04	114.00
1	A2	1685	G	N9-C1'-C2'	10.79	128.02	114.00
1	A2	352	A	O3'-P-O5'	-10.77	83.53	104.00
1	A2	201	G	C2'-C3'-O3'	10.68	133.00	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	16	G	N9-C1'-C2'	10.62	127.81	114.00
7	BE	182	TYR	CZ-CE2-CD2	10.61	129.35	119.80
27	BY	48	TYR	CD1-CE1-CZ	10.58	129.32	119.80
1	A2	607	G	C2'-C3'-O3'	10.57	132.75	109.50
16	BN	128	TYR	CD1-CE1-CZ	10.50	129.25	119.80
5	BC	243	TYR	CD1-CE1-CZ	10.46	129.22	119.80
1	A2	1797	A	P-O3'-C3'	10.44	132.23	119.70
22	BT	55	TYR	CD1-CE1-CZ	10.44	129.20	119.80
2	AZ	6163	C	N1-C1'-C2'	10.42	127.55	114.00
9	BG	169	TYR	CZ-CE2-CD2	10.41	129.17	119.80
1	A2	7	G	C2'-C3'-O3'	10.39	132.37	109.50
1	A2	1732	A	OP1-P-O3'	10.37	128.02	105.20
1	A2	1092	A	N9-C1'-C2'	10.36	127.47	114.00
10	BH	173	TYR	CZ-CE2-CD2	10.36	129.13	119.80
1	A2	1170	G	C2'-C3'-O3'	10.33	132.22	109.50
1	A2	1058	U	N1-C1'-C2'	10.32	127.41	114.00
1	A2	419	G	O3'-P-O5'	-10.25	84.53	104.00
1	A2	1417	A	P-O3'-C3'	10.24	131.99	119.70
1	A2	803	A	C2'-C3'-O3'	10.24	132.02	109.50
1	A2	1582	U	C2'-C3'-O3'	10.07	131.65	109.50
1	A2	1493	A	N9-C1'-C2'	10.06	127.08	114.00
1	A2	933	A	N9-C1'-C2'	10.02	127.03	114.00
1	A2	1363	U	N1-C1'-C2'	10.01	127.01	114.00
1	A2	1710	U	C2'-C3'-O3'	10.01	131.52	109.50
2	AZ	6208	A	C4'-C3'-O3'	10.00	133.01	113.00
1	A2	1732	A	O3'-P-O5'	-9.96	85.08	104.00
1	A2	894	U	N1-C1'-C2'	9.95	126.93	114.00
1	A2	376	C	C2'-C3'-O3'	9.93	131.35	109.50
1	A2	424	C	C2'-C3'-O3'	9.91	131.30	109.50
1	A2	112	A	C2'-C3'-O3'	9.89	131.26	109.50
1	A2	1344	A	C2'-C3'-O3'	9.89	131.26	109.50
1	A2	1432	U	N1-C1'-C2'	9.88	126.84	114.00
1	A2	935	U	P-O3'-C3'	-9.81	107.93	119.70
22	BT	55	TYR	CG-CD2-CE2	9.75	129.10	121.30
1	A2	1154	G	C2'-C3'-O3'	9.71	130.87	109.50
2	AZ	6125	G	C5'-C4'-O4'	9.70	120.74	109.10
1	A2	1720	G	C2'-C3'-O3'	9.65	130.74	109.50
2	AZ	6168	C	N1-C1'-C2'	9.60	126.48	114.00
1	A2	454	U	C2'-C3'-O3'	9.59	130.59	109.50
1	A2	1106	U	C2'-C3'-O3'	9.58	130.58	109.50
1	A2	572	C	C2'-C3'-O3'	9.57	130.55	109.50
1	A2	928	U	N1-C1'-C2'	9.56	126.43	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	1781	A	C2'-C3'-O3'	9.54	130.48	109.50
1	A2	1293	U	C2'-C3'-O3'	9.53	130.46	109.50
1	A2	1447	C	C2'-C3'-O3'	9.49	130.39	109.50
1	A2	1171	A	C2'-C3'-O3'	9.46	130.31	109.50
1	A2	1769	U	N1-C1'-C2'	9.46	126.29	114.00
1	A2	1638	G	C5'-C4'-O4'	9.41	120.39	109.10
1	A2	1568	C	C2'-C3'-O3'	9.40	130.17	109.50
1	A2	609	U	C4'-C3'-O3'	9.39	131.78	113.00
1	A2	1294	G	N9-C1'-C2'	9.39	126.21	114.00
1	A2	516	G	N9-C1'-C2'	9.38	126.19	114.00
1	A2	430	G	C2'-C3'-O3'	9.36	130.09	109.50
2	AZ	6146	A	C2'-C3'-O3'	9.36	130.08	109.50
2	AZ	6091	G	C2'-C3'-O3'	9.32	130.01	109.50
1	A2	835	U	O4'-C1'-N1	9.32	115.66	108.20
22	BT	91	TYR	CG-CD2-CE2	9.29	128.73	121.30
1	A2	816	G	C2'-C3'-O3'	9.29	129.93	109.50
1	A2	1642	G	C2'-C3'-O3'	9.26	129.88	109.50
1	A2	1608	U	C2'-C3'-O3'	9.25	129.85	109.50
1	A2	1216	C	C4'-C3'-O3'	9.24	131.49	113.00
1	A2	158	U	C2'-C3'-O3'	9.22	129.78	109.50
1	A2	1712	A	C4'-C3'-O3'	9.22	131.44	113.00
2	AZ	6145	C	N1-C1'-C2'	9.21	125.97	114.00
1	A2	1629	G	C2'-C3'-O3'	9.20	129.75	109.50
1	A2	1364	G	C2'-C3'-O3'	9.18	129.70	109.50
1	A2	1442	U	C2'-C3'-O3'	9.18	129.69	109.50
1	A2	1377	U	OP1-P-O3'	9.18	125.39	105.20
1	A2	351	C	N1-C1'-C2'	9.17	125.92	114.00
1	A2	10	G	N9-C1'-C2'	9.17	125.92	114.00
1	A2	1752	U	C2'-C3'-O3'	9.16	129.65	109.50
1	A2	997	G	O3'-P-O5'	-9.15	86.62	104.00
1	A2	1415	U	C2'-C3'-O3'	9.13	129.59	109.50
2	AZ	6073	A	C2'-C3'-O3'	9.13	129.59	109.50
1	A2	1474	G	C2'-C3'-O3'	9.12	129.58	109.50
1	A2	1777	G	C2'-C3'-O3'	9.12	129.57	109.50
1	A2	1678	A	C4'-C3'-O3'	9.09	131.18	113.00
1	A2	1295	G	C2'-C3'-O3'	9.04	129.40	109.50
2	AZ	6109	U	N1-C1'-C2'	9.04	125.76	114.00
1	A2	558	U	C5'-C4'-O4'	9.01	119.92	109.10
1	A2	539	G	C2'-C3'-O3'	9.01	129.32	109.50
1	A2	794	U	C2'-C3'-O3'	9.01	129.31	109.50
1	A2	286	C	C2'-C3'-O3'	9.00	129.31	109.50
1	A2	1514	U	N1-C1'-C2'	9.00	125.70	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	BK	65	TYR	CG-CD1-CE1	9.00	128.50	121.30
1	A2	1789	G	C2'-C3'-O3'	8.98	129.26	109.50
1	A2	1369	U	N1-C1'-C2'	8.98	125.67	114.00
1	A2	1377	U	O3'-P-O5'	-8.98	86.94	104.00
1	A2	577	G	C2'-C3'-O3'	8.97	129.24	109.50
1	A2	1235	C	N1-C1'-C2'	8.97	125.66	114.00
1	A2	423	G	C2'-C3'-O3'	8.97	129.23	109.50
6	BD	125	TYR	CG-CD1-CE1	8.96	128.47	121.30
18	BP	123	TYR	CG-CD2-CE2	8.94	128.45	121.30
1	A2	104	A	OP2-P-O3'	8.90	124.78	105.20
1	A2	1787	C	N1-C1'-C2'	8.89	125.56	114.00
2	AZ	6215	C	C5'-C4'-O4'	8.89	119.77	109.10
1	A2	489	C	N1-C1'-C2'	8.88	125.54	114.00
14	BL	53	TYR	CG-CD2-CE2	8.88	128.40	121.30
1	A2	1573	A	C2'-C3'-O3'	8.87	129.02	109.50
14	BL	35	TYR	CG-CD1-CE1	8.86	128.39	121.30
14	BL	84	ILE	CG1-CB-CG2	8.85	130.88	111.40
1	A2	1647	U	C2'-C3'-O3'	8.85	128.97	109.50
1	A2	1237	G	C2'-C3'-O3'	8.85	128.97	109.50
1	A2	1471	A	C2'-C3'-O3'	8.83	128.92	109.50
1	A2	884	A	C2'-C3'-O3'	8.78	128.81	109.50
1	A2	1557	U	N1-C1'-C2'	8.77	125.41	114.00
1	A2	74	U	O4'-C1'-N1	8.76	115.21	108.20
1	A2	188	A	C2'-C3'-O3'	8.75	128.74	109.50
8	BF	67	PRO	N-CA-C	8.75	134.84	112.10
33	Be	40	TYR	CG-CD1-CE1	8.74	128.29	121.30
1	A2	74	U	C2'-C3'-O3'	8.74	128.73	109.50
1	A2	137	U	C2'-C3'-O3'	8.71	128.66	109.50
1	A2	504	U	C2'-C3'-O3'	8.71	128.66	109.50
1	A2	899	G	N9-C1'-C2'	8.70	125.31	114.00
1	A2	781	U	N1-C1'-C2'	8.70	125.31	114.00
1	A2	1065	A	C2'-C3'-O3'	8.70	128.63	109.50
1	A2	1020	A	C2'-C3'-O3'	8.68	128.60	109.50
1	A2	58	U	N1-C1'-C2'	8.67	125.27	114.00
2	AZ	6155	G	C2'-C3'-O3'	8.66	128.56	109.50
1	A2	142	G	C2'-C3'-O3'	8.65	128.54	109.50
1	A2	543	C	N1-C1'-C2'	8.64	125.24	114.00
1	A2	862	A	OP1-P-O3'	8.63	124.19	105.20
23	BU	79	TRP	CD1-NE1-CE2	8.63	116.76	109.00
16	BN	40	TYR	CG-CD1-CE1	8.62	128.20	121.30
1	A2	146	U	C2'-C3'-O3'	8.62	128.46	109.50
1	A2	921	U	C2'-C3'-O3'	8.62	128.46	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	733	A	C2'-C3'-O3'	8.61	128.44	109.50
1	A2	90	C	C2'-C3'-O3'	8.60	128.42	109.50
1	A2	1298	U	C4'-C3'-O3'	8.60	130.19	113.00
2	AZ	6113	U	N1-C1'-C2'	8.60	125.17	114.00
1	A2	792	U	N1-C1'-C2'	8.59	125.17	114.00
2	AZ	6139	G	C2'-C3'-O3'	8.58	128.38	109.50
1	A2	582	U	N1-C1'-C2'	8.57	125.14	114.00
1	A2	1756	A	C2'-C3'-O3'	8.56	128.34	109.50
1	A2	223	U	C2'-C3'-O3'	8.56	128.32	109.50
1	A2	514	G	C4'-C3'-O3'	8.56	130.11	113.00
1	A2	131	C	C2'-C3'-O3'	8.55	128.31	109.50
1	A2	1483	A	C2'-C3'-O3'	8.55	128.30	109.50
1	A2	1578	U	N1-C1'-C2'	8.54	125.10	114.00
1	A2	930	A	N9-C1'-C2'	8.53	125.09	114.00
1	A2	1236	A	N9-C1'-C2'	8.53	125.09	114.00
1	A2	1496	U	C2'-C3'-O3'	8.52	128.25	109.50
1	A2	1321	A	C2'-C3'-O3'	8.50	128.21	109.50
1	A2	597	G	N9-C1'-C2'	8.49	125.04	114.00
1	A2	1509	C	C2'-C3'-O3'	8.49	128.19	109.50
1	A2	744	U	C2'-C3'-O3'	8.48	128.16	109.50
1	A2	882	U	C2'-C3'-O3'	8.48	128.16	109.50
1	A2	1125	A	C2'-C3'-O3'	8.48	128.16	109.50
1	A2	990	C	C4'-C3'-O3'	8.48	129.96	113.00
1	A2	425	A	N9-C1'-C2'	8.47	125.01	114.00
1	A2	603	U	N1-C1'-C2'	8.47	125.01	114.00
1	A2	1638	G	C2'-C3'-O3'	8.46	128.12	109.50
1	A2	102	U	C2'-C3'-O3'	8.46	128.10	109.50
1	A2	237	C	N1-C1'-C2'	8.46	124.99	114.00
1	A2	939	A	C2'-C3'-O3'	8.45	128.10	109.50
1	A2	649	U	N1-C1'-C2'	8.44	124.97	114.00
1	A2	250	C	N1-C1'-C2'	8.43	124.97	114.00
1	A2	1176	G	C2'-C3'-O3'	8.42	128.03	109.50
29	Ba	41	ILE	CG1-CB-CG2	8.42	129.93	111.40
1	A2	261	U	N1-C1'-C2'	8.41	124.93	114.00
1	A2	473	A	N9-C1'-C2'	8.41	124.93	114.00
1	A2	1061	A	N9-C1'-C2'	8.40	124.92	114.00
1	A2	1325	A	C2'-C3'-O3'	8.40	127.99	109.50
1	A2	607	G	N9-C1'-C2'	8.40	124.92	114.00
1	A2	1420	C	C2'-C3'-O3'	8.39	127.96	109.50
1	A2	67	A	C2'-C3'-O3'	8.39	127.96	109.50
1	A2	1449	U	C5'-C4'-O4'	8.37	119.15	109.10
2	AZ	6129	C	C2'-C3'-O3'	8.37	127.90	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	762	A	N9-C1'-C2'	8.36	124.87	114.00
2	AZ	6107	U	N1-C1'-C2'	8.33	124.83	114.00
1	A2	1713	G	C2'-C3'-O3'	8.32	127.81	109.50
1	A2	761	G	C2'-C3'-O3'	8.31	127.78	109.50
1	A2	767	U	N1-C1'-C2'	8.30	124.79	114.00
1	A2	1259	U	C2'-C3'-O3'	8.30	127.76	109.50
1	A2	473	A	C2'-C3'-O3'	8.28	127.72	109.50
3	BA	111	ILE	CG1-CB-CG2	8.28	129.62	111.40
1	A2	1743	U	C2'-C3'-O3'	8.27	127.70	109.50
1	A2	1175	U	C2'-C3'-O3'	8.26	127.68	109.50
1	A2	1577	A	C2'-C3'-O3'	8.26	127.67	109.50
1	A2	1055	U	C2'-C3'-O3'	8.26	127.67	109.50
1	A2	852	C	C2'-C3'-O3'	8.26	127.67	109.50
1	A2	149	C	C2'-C3'-O3'	8.26	127.66	109.50
1	A2	759	U	C2'-C3'-O3'	8.25	127.66	109.50
1	A2	1196	A	N9-C1'-C2'	8.25	124.73	114.00
1	A2	603	U	C2'-C3'-O3'	8.25	127.65	109.50
2	AZ	6034	A	N9-C1'-C2'	8.25	124.73	114.00
1	A2	1603	U	C2'-C3'-O3'	8.25	127.65	109.50
1	A2	956	C	N1-C1'-C2'	8.25	124.72	114.00
1	A2	591	A	N9-C1'-C2'	8.24	124.71	114.00
1	A2	1100	G	N9-C1'-C2'	8.23	124.70	114.00
1	A2	82	U	C2'-C3'-O3'	8.23	127.60	109.50
1	A2	359	A	C4'-C3'-O3'	8.22	129.44	113.00
2	AZ	6121	C	C2'-C3'-O3'	8.22	127.59	109.50
1	A2	1472	C	C4'-C3'-O3'	8.22	129.44	113.00
1	A2	67	A	C4'-C3'-O3'	8.22	129.44	113.00
1	A2	1708	U	C2'-C3'-O3'	8.22	127.58	109.50
1	A2	502	U	C2'-C3'-O3'	8.21	127.56	109.50
1	A2	820	U	C2'-C3'-O3'	8.19	127.53	109.50
1	A2	1012	U	C2'-C3'-O3'	8.20	127.53	109.50
2	AZ	6197	U	C2'-C3'-O3'	8.18	127.48	109.50
1	A2	1561	U	C2'-C3'-O3'	8.16	127.46	109.50
1	A2	850	A	C5'-C4'-O4'	8.16	118.89	109.10
1	A2	505	A	N9-C1'-C2'	8.15	124.60	114.00
1	A2	528	U	C2'-C3'-O3'	8.15	127.43	109.50
1	A2	1287	A	C2'-C3'-O3'	8.15	127.43	109.50
1	A2	110	U	N1-C1'-C2'	8.13	124.58	114.00
1	A2	610	G	N9-C1'-C2'	8.14	124.58	114.00
1	A2	473	A	C5'-C4'-O4'	8.12	118.85	109.10
1	A2	362	G	C2'-C3'-O3'	8.11	127.34	109.50
1	A2	1570	A	C2'-C3'-O3'	8.09	127.30	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	644	C	C2'-C3'-O3'	8.08	127.28	109.50
1	A2	1372	U	C2'-C3'-O3'	8.07	127.26	109.50
1	A2	41	A	C2'-C3'-O3'	8.06	127.23	109.50
1	A2	143	G	C2'-C3'-O3'	8.06	127.23	109.50
1	A2	430	G	N9-C1'-C2'	8.06	124.47	114.00
1	A2	738	G	C2'-C3'-O3'	8.06	127.23	109.50
1	A2	1670	G	N9-C1'-C2'	8.06	124.47	114.00
1	A2	1317	C	C2'-C3'-O3'	8.05	127.22	109.50
2	AZ	6217	A	C2'-C3'-O3'	8.05	127.22	109.50
1	A2	246	G	N9-C1'-C2'	8.05	124.46	114.00
1	A2	1438	G	C2'-C3'-O3'	8.05	127.20	109.50
1	A2	1451	C	C2'-C3'-O3'	8.05	127.20	109.50
1	A2	33	U	C5'-C4'-O4'	8.04	118.75	109.10
1	A2	573	C	C2'-C3'-O3'	8.04	127.19	109.50
1	A2	599	A	C2'-C3'-O3'	8.04	127.18	109.50
1	A2	1266	U	N1-C1'-C2'	8.04	124.44	114.00
1	A2	1687	U	N1-C1'-C2'	8.03	124.44	114.00
1	A2	1340	U	N1-C1'-C2'	8.03	124.44	114.00
1	A2	514	G	C2'-C3'-O3'	8.03	127.15	109.50
2	AZ	6061	G	C2'-C3'-O3'	8.02	127.15	109.50
1	A2	1003	A	N9-C1'-C2'	8.01	124.41	114.00
1	A2	753	A	C2'-C3'-O3'	8.00	127.11	109.50
1	A2	564	G	N9-C1'-C2'	8.00	124.40	114.00
1	A2	295	A	C2'-C3'-O3'	8.00	127.09	109.50
1	A2	941	A	C2'-C3'-O3'	7.99	127.09	109.50
2	AZ	6124	G	C4'-C3'-O3'	7.99	128.98	113.00
1	A2	473	A	C5'-C4'-C3'	7.99	128.78	116.00
2	AZ	6055	U	C2'-C3'-O3'	7.98	127.06	109.50
1	A2	740	A	C2'-C3'-O3'	7.97	127.04	109.50
1	A2	265	A	N9-C1'-C2'	7.96	124.35	114.00
1	A2	1759	C	C2'-C3'-O3'	7.95	127.00	109.50
1	A2	38	C	C2'-C3'-O3'	7.95	126.98	109.50
2	AZ	6149	A	N9-C1'-C2'	7.94	124.32	114.00
1	A2	1414	U	N1-C1'-C2'	7.93	124.31	114.00
1	A2	1449	U	C5'-C4'-C3'	7.92	128.67	116.00
1	A2	120	U	C5'-C4'-O4'	7.92	118.60	109.10
2	AZ	6165	C	C5'-C4'-O4'	7.91	118.59	109.10
1	A2	138	A	C2'-C3'-O3'	7.91	126.89	109.50
3	BA	184	LEU	CB-CG-CD2	7.90	124.43	111.00
1	A2	562	G	C2'-C3'-O3'	7.89	126.86	109.50
2	AZ	6106	A	P-O3'-C3'	-7.89	110.23	119.70
33	Be	31	LYS	N-CA-C	7.88	132.28	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	334	G	C2'-C3'-O3'	7.87	126.82	109.50
1	A2	529	A	C2'-C3'-O3'	7.87	126.82	109.50
1	A2	743	U	C2'-C3'-O3'	7.87	126.81	109.50
6	BD	156	PHE	CG-CD2-CE2	7.87	129.46	120.80
1	A2	1418	G	C2'-C3'-O3'	7.86	126.79	109.50
4	BB	30	PHE	CZ-CE2-CD2	7.86	129.53	120.10
1	A2	87	C	C2'-C3'-O3'	7.86	126.79	109.50
1	A2	481	A	C2'-C3'-O3'	7.86	126.79	109.50
11	BI	27	PHE	CG-CD1-CE1	7.86	129.44	120.80
3	BA	110	TYR	CA-CB-CG	7.85	128.32	113.40
1	A2	257	A	C2'-C3'-O3'	7.85	126.77	109.50
1	A2	1662	G	C2'-C3'-O3'	7.84	126.75	109.50
1	A2	885	G	C2'-C3'-O3'	7.83	126.74	109.50
4	BB	102	GLY	C-N-CA	7.83	141.28	121.70
1	A2	1671	A	C2'-C3'-O3'	7.83	126.73	109.50
1	A2	1709	C	C2'-C3'-O3'	7.83	126.73	109.50
1	A2	1736	G	C2'-C3'-O3'	7.83	126.72	109.50
1	A2	816	G	C5'-C4'-O4'	7.82	118.48	109.10
1	A2	367	A	C5'-C4'-O4'	7.82	118.48	109.10
8	BF	30	PRO	N-CA-C	7.82	132.43	112.10
23	BU	19	ILE	CG1-CB-CG2	7.81	128.59	111.40
21	BS	128	PHE	CD1-CE1-CZ	7.81	129.47	120.10
1	A2	596	C	C2'-C3'-O3'	7.80	126.66	109.50
1	A2	1267	G	C2'-C3'-O3'	7.80	126.65	109.50
1	A2	427	C	C4'-C3'-O3'	7.79	128.59	113.00
1	A2	1797	A	OP2-P-O3'	-7.79	88.06	105.20
1	A2	220	A	C4'-C3'-O3'	7.79	128.57	113.00
1	A2	1295	G	C4'-C3'-O3'	7.78	128.57	113.00
1	A2	1482	C	C2'-C3'-O3'	7.78	126.62	109.50
3	BA	112	THR	N-CA-C	7.78	132.01	111.00
1	A2	1058	U	O4'-C1'-N1	7.78	114.43	108.20
13	BK	16	PHE	CD1-CE1-CZ	7.78	129.44	120.10
1	A2	1467	C	C2'-C3'-O3'	7.78	126.61	109.50
1	A2	1429	G	C5'-C4'-O4'	7.78	118.43	109.10
1	A2	702	G	C2'-C3'-O3'	7.77	126.59	109.50
1	A2	1771	U	C2'-C3'-O3'	7.76	126.58	109.50
1	A2	1638	G	C5'-C4'-O4'	7.75	128.40	116.00
2	AZ	6055	U	C5'-C4'-O4'	7.75	118.40	109.10
1	A2	1751	C	C5'-C4'-O4'	7.75	118.39	109.10
1	A2	1004	U	C4'-C3'-O3'	7.74	128.49	113.00
1	A2	1028	C	N1-C1'-C2'	7.74	124.06	114.00
1	A2	1571	C	N1-C1'-C2'	7.73	124.05	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	91	G	C2'-C3'-O3'	7.73	126.50	109.50
19	BQ	129	PHE	CG-CD1-CE1	7.73	129.30	120.80
1	A2	578	U	C4'-C3'-O3'	7.73	128.46	113.00
5	BC	131	ILE	N-CA-C	7.73	131.86	111.00
1	A2	1381	U	N1-C1'-C2'	7.72	124.03	114.00
1	A2	517	U	C2'-C3'-O3'	7.71	126.47	109.50
1	A2	212	U	N1-C1'-C2'	7.71	124.02	114.00
1	A2	113	U	N1-C1'-C2'	7.70	124.01	114.00
10	BH	183	PHE	CD1-CE1-CZ	7.69	129.32	120.10
1	A2	949	C	C2'-C3'-O3'	7.69	126.41	109.50
35	Bg	186	PHE	CG-CD2-CE2	7.68	129.25	120.80
1	A2	558	U	C5'-C4'-C3'	7.68	128.28	116.00
2	AZ	6195	G	C2'-C3'-O3'	7.67	126.37	109.50
14	BL	54	ILE	CG1-CB-CG2	7.67	128.27	111.40
1	A2	1002	G	C2'-C3'-O3'	7.66	126.35	109.50
1	A2	240	U	C5'-C4'-O4'	7.64	118.27	109.10
11	BI	21	PHE	CG-CD1-CE1	7.64	129.21	120.80
1	A2	563	U	N1-C1'-C2'	7.64	123.93	114.00
1	A2	1151	A	C2'-C3'-O3'	7.63	126.28	109.50
1	A2	1092	A	C2'-C3'-O3'	7.62	126.27	109.50
1	A2	767	U	C2'-C3'-O3'	7.61	126.25	109.50
1	A2	1397	U	C2'-C3'-O3'	7.61	126.24	109.50
1	A2	499	U	N1-C1'-C2'	7.61	123.89	114.00
1	A2	120	U	N1-C1'-C2'	7.61	123.89	114.00
1	A2	1452	U	N1-C1'-C2'	7.60	123.89	114.00
2	AZ	6174	G	C2'-C3'-O3'	7.60	126.23	109.50
1	A2	876	G	N9-C1'-C2'	7.59	123.87	114.00
1	A2	161	U	C2'-C3'-O3'	7.59	126.20	109.50
1	A2	711	U	C2'-C3'-O3'	7.59	126.20	109.50
1	A2	461	G	C2'-C3'-O3'	7.59	126.20	109.50
1	A2	1261	G	C2'-C3'-O3'	7.57	126.16	109.50
1	A2	1389	C	N1-C1'-C2'	7.57	123.84	114.00
1	A2	1495	C	C2'-C3'-O3'	7.57	126.14	109.50
1	A2	366	A	N9-C1'-C2'	7.56	123.83	114.00
1	A2	435	C	C2'-C3'-O3'	7.56	126.14	109.50
2	AZ	6070	A	C5'-C4'-O4'	7.56	118.17	109.10
1	A2	6	G	N9-C1'-C2'	7.56	123.83	114.00
1	A2	1197	C	C5'-C4'-O4'	7.56	118.17	109.10
1	A2	330	G	C2'-C3'-O3'	7.55	126.11	109.50
1	A2	1690	G	N9-C1'-C2'	7.55	123.81	114.00
1	A2	1688	U	C2'-C3'-O3'	7.55	126.10	109.50
1	A2	190	C	C2'-C3'-O3'	7.54	126.09	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	636	A	N9-C1'-C2'	7.54	123.80	114.00
1	A2	326	G	C5'-C4'-O4'	7.53	118.13	109.10
1	A2	1298	U	C2'-C3'-O3'	7.53	126.06	109.50
1	A2	1528	U	C2'-C3'-O3'	7.52	126.04	109.50
2	AZ	6106	A	N9-C1'-C2'	7.51	123.77	114.00
2	AZ	6091	G	C4'-C3'-O3'	7.50	128.01	113.00
22	BT	54	PHE	CG-CD1-CE1	7.50	129.06	120.80
1	A2	311	U	N1-C1'-C2'	7.49	123.74	114.00
1	A2	629	U	C2'-C3'-O3'	7.49	125.97	109.50
1	A2	383	G	N9-C1'-C2'	7.49	123.73	114.00
1	A2	188	A	N9-C1'-C2'	7.48	123.73	114.00
1	A2	1078	C	N1-C1'-C2'	7.48	123.73	114.00
1	A2	491	C	C2'-C3'-O3'	7.48	125.96	109.50
1	A2	960	U	OP2-P-O3'	7.48	121.65	105.20
2	AZ	6160	C	N1-C1'-C2'	7.47	123.71	114.00
10	BH	24	PHE	CG-CD1-CE1	7.47	129.01	120.80
1	A2	621	A	C2'-C3'-O3'	7.46	125.92	109.50
1	A2	150	U	N1-C1'-C2'	7.46	123.69	114.00
1	A2	453	U	C2'-C3'-O3'	7.44	125.86	109.50
1	A2	1067	C	C5'-C4'-O4'	7.43	118.02	109.10
1	A2	1252	C	C5'-C4'-O4'	7.42	118.01	109.10
1	A2	1357	A	C5'-C4'-O4'	7.42	118.00	109.10
2	AZ	6072	U	C2'-C3'-O3'	7.42	125.81	109.50
1	A2	223	U	C4'-C3'-O3'	7.42	127.83	113.00
1	A2	9	U	C2'-C3'-O3'	7.41	125.80	109.50
1	A2	724	C	O4'-C1'-N1	7.41	114.13	108.20
1	A2	511	A	C2'-C3'-O3'	7.41	125.80	109.50
1	A2	1432	U	O4'-C1'-N1	7.41	114.13	108.20
1	A2	1602	C	C5'-C4'-O4'	7.40	117.98	109.10
1	A2	836	U	C2'-C3'-O3'	7.39	125.77	109.50
1	A2	1240	U	C4'-C3'-O3'	7.39	127.77	113.00
1	A2	1290	U	C2'-C3'-O3'	7.38	125.74	109.50
1	A2	918	U	C4'-C3'-O3'	7.37	127.74	113.00
2	AZ	6179	A	C2'-C3'-O3'	7.37	125.71	109.50
1	A2	455	C	N1-C1'-C2'	7.37	123.58	114.00
1	A2	115	G	C2'-C3'-O3'	7.36	125.70	109.50
1	A2	787	G	C2'-C3'-O3'	7.36	125.70	109.50
1	A2	330	G	N9-C1'-C2'	7.36	123.57	114.00
1	A2	681	U	C5'-C4'-O4'	7.36	117.93	109.10
1	A2	221	A	C5'-C4'-O4'	7.35	117.92	109.10
1	A2	918	U	C2'-C3'-O3'	7.35	125.67	109.50
6	BD	119	ALA	N-CA-C	7.35	130.84	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	597	G	C2'-C3'-O3'	7.34	125.66	109.50
1	A2	853	G	N9-C1'-C2'	7.34	123.55	114.00
27	BY	92	VAL	CG1-CB-CG2	7.34	122.65	110.90
1	A2	1186	U	C2'-C3'-O3'	7.33	125.63	109.50
1	A2	1430	U	C2'-C3'-O3'	7.33	125.63	109.50
1	A2	1758	U	C2'-C3'-O3'	7.33	125.61	109.50
1	A2	1753	A	C4'-C3'-O3'	7.32	127.64	113.00
1	A2	9	U	C4'-C3'-O3'	7.32	127.64	113.00
1	A2	1406	A	N9-C1'-C2'	7.32	123.51	114.00
1	A2	1495	C	C4'-C3'-O3'	7.32	127.63	113.00
1	A2	263	C	N1-C1'-C2'	7.31	123.50	114.00
1	A2	493	U	C2'-C3'-O3'	7.31	125.59	109.50
1	A2	460	A	N9-C1'-C2'	7.31	123.50	114.00
1	A2	945	U	N1-C1'-C2'	7.31	123.50	114.00
1	A2	456	A	C2'-C3'-O3'	7.30	125.57	109.50
1	A2	1455	G	C5'-C4'-O4'	7.30	117.87	109.10
1	A2	600	U	C5'-C4'-O4'	7.30	117.86	109.10
1	A2	1471	A	C4'-C3'-O3'	7.30	127.60	113.00
1	A2	578	U	C2'-C3'-O3'	7.30	125.56	109.50
1	A2	1629	G	C4'-C3'-O3'	7.30	127.59	113.00
1	A2	213	A	N9-C1'-C2'	7.29	123.48	114.00
1	A2	320	U	C2'-C3'-O3'	7.29	125.54	109.50
1	A2	711	U	C4'-C3'-O3'	7.29	127.58	113.00
1	A2	939	A	C4'-C3'-O3'	7.29	127.58	113.00
1	A2	496	G	C2'-C3'-O3'	7.29	125.53	109.50
2	AZ	6039	G	C2'-C3'-O3'	7.28	125.52	109.50
5	BC	68	ILE	CG1-CB-CG2	7.28	127.42	111.40
1	A2	1450	U	C2'-C3'-O3'	7.27	125.50	109.50
17	BO	81	VAL	CG1-CB-CG2	7.27	122.53	110.90
1	A2	525	A	C5'-C4'-O4'	7.26	117.82	109.10
1	A2	1576	A	N9-C1'-C2'	7.26	123.44	114.00
2	AZ	6085	A	C5'-C4'-O4'	7.26	117.81	109.10
1	A2	1317	C	C4'-C3'-O3'	7.26	127.52	113.00
1	A2	1289	U	C2'-C3'-O3'	7.25	125.44	109.50
1	A2	161	U	C4'-C3'-O3'	7.24	127.47	113.00
29	Ba	10	ARG	N-CA-C	7.23	130.52	111.00
14	BL	63	LEU	CB-CG-CD1	7.23	123.28	111.00
19	BQ	54	LEU	CB-CG-CD1	7.23	123.28	111.00
1	A2	1580	C	C5'-C4'-O4'	7.22	117.77	109.10
1	A2	1012	U	C4'-C3'-O3'	7.22	127.44	113.00
1	A2	427	C	C2'-C3'-O3'	7.21	125.36	109.50
1	A2	452	A	O4'-C1'-N9	7.21	113.97	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	BH	91	ILE	CG1-CB-CG2	7.21	127.25	111.40
7	BE	121	TYR	CG-CD2-CE2	7.19	127.05	121.30
1	A2	990	C	C2'-C3'-O3'	7.19	125.32	109.50
8	BF	194	LEU	CB-CG-CD2	7.19	123.22	111.00
1	A2	1001	A	N9-C1'-C2'	7.18	123.34	114.00
4	BB	181	LEU	CB-CG-CD1	7.18	123.20	111.00
1	A2	9	U	C5'-C4'-O4'	7.18	117.71	109.10
1	A2	1388	A	O3'-P-O5'	7.17	117.63	104.00
1	A2	1188	G	C5'-C4'-O4'	7.17	117.70	109.10
2	AZ	6125	G	C5'-C4'-C3'	7.17	127.47	116.00
1	A2	1178	G	C2'-C3'-O3'	7.16	125.25	109.50
1	A2	1734	U	N1-C1'-C2'	7.16	123.31	114.00
3	BA	64	ILE	CG1-CB-CG2	7.15	127.13	111.40
1	A2	1232	U	C5'-C4'-O4'	7.15	117.67	109.10
1	A2	509	G	N9-C1'-C2'	7.14	123.29	114.00
1	A2	1677	C	N1-C1'-C2'	7.14	123.29	114.00
1	A2	51	A	C2'-C3'-O3'	7.14	125.21	109.50
1	A2	1226	A	N9-C1'-C2'	7.14	123.29	114.00
1	A2	997	G	OP2-P-O3'	-7.14	89.50	105.20
1	A2	1204	A	N9-C1'-C2'	7.14	123.28	114.00
1	A2	1247	U	C2'-C3'-O3'	7.14	125.20	109.50
1	A2	1748	G	N9-C1'-C2'	7.14	123.28	114.00
7	BE	70	VAL	CG1-CB-CG2	7.12	122.30	110.90
1	A2	930	A	C4'-C3'-O3'	7.12	127.24	113.00
1	A2	602	U	C2'-C3'-O3'	7.11	125.14	109.50
1	A2	1344	A	C5'-C4'-O4'	7.11	117.63	109.10
2	AZ	6179	A	C5'-C4'-O4'	7.11	117.63	109.10
2	AZ	6215	C	C5'-C4'-C3'	7.11	127.37	116.00
6	BD	163	PRO	N-CA-C	7.10	130.56	112.10
1	A2	713	A	C2'-C3'-O3'	7.10	125.12	109.50
1	A2	775	G	C2'-C3'-O3'	7.10	125.11	109.50
1	A2	395	U	C5'-C4'-O4'	7.09	117.61	109.10
1	A2	842	C	C3'-C2'-O2'	7.09	133.86	113.30
6	BD	37	VAL	CG1-CB-CG2	7.09	122.24	110.90
1	A2	1450	U	C5'-C4'-O4'	7.08	117.60	109.10
2	AZ	6120	U	O4'-C1'-N1	7.08	113.87	108.20
2	AZ	6176	A	N9-C1'-C2'	7.08	123.21	114.00
1	A2	581	U	C2'-C3'-O3'	7.08	125.08	109.50
1	A2	1683	C	C4'-C3'-O3'	7.08	127.16	113.00
1	A2	787	G	C5'-C4'-O4'	7.08	117.60	109.10
1	A2	1749	A	C2'-C3'-O3'	7.08	125.08	109.50
13	BK	59	PHE	N-CA-C	7.08	130.12	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	417	A	C2'-C3'-O3'	7.08	125.07	109.50
1	A2	478	A	N9-C1'-C2'	7.08	123.20	114.00
1	A2	1580	C	O4'-C1'-N1	7.07	113.86	108.20
1	A2	386	G	C5'-C4'-O4'	7.07	117.58	109.10
1	A2	947	U	N1-C1'-C2'	7.07	123.19	114.00
5	BC	126	ARG	N-CA-C	7.07	130.09	111.00
1	A2	456	A	N9-C1'-C2'	7.06	123.18	114.00
1	A2	1683	C	C2'-C3'-O3'	7.06	125.04	109.50
1	A2	755	A	N9-C1'-C2'	7.06	123.18	114.00
2	AZ	6198	U	C2'-C3'-O3'	7.03	124.97	109.50
7	BE	140	VAL	CG1-CB-CG2	7.03	122.14	110.90
1	A2	66	U	C5'-C4'-O4'	7.03	117.53	109.10
1	A2	165	G	N9-C1'-C2'	7.02	123.13	114.00
1	A2	716	C	C2'-C3'-O3'	7.02	124.95	109.50
1	A2	934	C	N1-C1'-C2'	7.02	123.12	114.00
1	A2	930	A	C2'-C3'-O3'	7.01	124.92	109.50
1	A2	756	A	N9-C1'-C2'	7.01	123.11	114.00
1	A2	821	U	C2'-C3'-O3'	7.01	124.92	109.50
1	A2	1422	A	C2'-C3'-O3'	7.01	124.91	109.50
1	A2	419	G	OP2-P-O3'	-7.00	89.80	105.20
1	A2	1178	G	C4'-C3'-O3'	7.00	126.99	113.00
1	A2	388	G	P-O3'-C3'	-6.99	111.31	119.70
1	A2	467	G	N9-C1'-C2'	6.98	123.08	114.00
1	A2	469	C	C2'-C3'-O3'	6.98	124.87	113.70
1	A2	1161	C	C5'-C4'-O4'	6.98	117.48	109.10
1	A2	753	A	C5'-C4'-O4'	6.97	117.46	109.10
1	A2	1240	U	C2'-C3'-O3'	6.97	124.85	113.70
1	A2	1525	A	C4'-C3'-O3'	6.97	126.93	113.00
1	A2	1779	U	N1-C1'-C2'	6.96	123.05	114.00
16	BN	56	ASP	N-CA-C	6.96	129.80	111.00
1	A2	257	A	C4'-C3'-O3'	6.96	126.92	113.00
1	A2	1089	U	N1-C1'-C2'	6.96	123.05	114.00
7	BE	121	TYR	CG-CD1-CE1	6.96	126.86	121.30
2	AZ	6165	C	C5'-C4'-C3'	6.95	127.12	116.00
1	A2	1118	G	C5'-C4'-O4'	6.95	117.44	109.10
1	A2	1041	G	C4'-C3'-O3'	6.94	126.88	113.00
1	A2	1738	U	N1-C1'-C2'	6.94	123.02	114.00
1	A2	1535	U	N1-C1'-C2'	6.94	123.02	114.00
1	A2	1291	G	C2'-C3'-O3'	6.93	124.79	113.70
1	A2	1506	G	C5'-C4'-C3'	6.93	127.08	116.00
1	A2	1294	G	C4'-C3'-O3'	6.91	126.82	113.00
1	A2	1445	G	C5'-C4'-O4'	6.90	117.39	109.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	481	A	C4'-C3'-O3'	6.89	126.77	113.00
1	A2	245	U	C5'-C4'-O4'	6.88	117.36	109.10
1	A2	88	U	C4'-C3'-O3'	6.87	126.74	113.00
1	A2	1102	G	C5'-C4'-O4'	6.87	117.34	109.10
1	A2	1627	U	N1-C1'-C2'	6.86	122.92	114.00
1	A2	735	C	C5'-C4'-O4'	6.86	117.33	109.10
7	BE	120	SER	N-CA-C	6.84	129.48	111.00
1	A2	938	G	C5'-C4'-O4'	6.84	117.31	109.10
1	A2	375	U	C5'-C4'-O4'	6.84	117.31	109.10
1	A2	299	A	C2'-C3'-O3'	6.83	124.63	113.70
20	BR	61	ILE	CG1-CB-CG2	6.83	126.42	111.40
1	A2	1672	G	C5'-C4'-O4'	6.83	117.29	109.10
11	BI	96	LEU	CB-CG-CD1	6.81	122.57	111.00
26	BX	90	ALA	N-CA-C	6.80	129.37	111.00
1	A2	820	U	C4'-C3'-O3'	6.80	126.60	113.00
1	A2	1234	A	N9-C1'-C2'	6.80	122.84	114.00
25	BW	14	ILE	CG1-CB-CG2	6.80	126.36	111.40
1	A2	1450	U	C4'-C3'-O3'	6.80	126.60	113.00
1	A2	1420	C	C5'-C4'-O4'	6.79	117.25	109.10
7	BE	20	LEU	CB-CG-CD2	6.79	122.55	111.00
1	A2	862	A	C5'-C4'-O4'	6.79	117.25	109.10
1	A2	504	U	C4'-C3'-O3'	6.78	126.56	113.00
1	A2	1222	C	N1-C1'-C2'	6.77	122.80	114.00
3	BA	138	TYR	CA-CB-CG	6.77	126.27	113.40
22	BT	57	ARG	N-CA-CB	6.77	122.79	110.60
1	A2	1293	U	C4'-C3'-O3'	6.77	126.54	113.00
1	A2	921	U	N1-C1'-C2'	6.76	122.79	114.00
3	BA	197	ILE	CG1-CB-CG2	6.75	126.26	111.40
12	BJ	77	ILE	CG1-CB-CG2	6.75	126.26	111.40
8	BF	115	LYS	CB-CA-C	6.75	123.90	110.40
1	A2	9	U	C5'-C4'-C3'	6.75	126.80	116.00
1	A2	738	G	C5'-C4'-O4'	6.75	117.20	109.10
1	A2	1266	U	O4'-C1'-N1	6.74	113.59	108.20
2	AZ	6197	U	C5'-C4'-O4'	6.74	117.18	109.10
1	A2	953	G	N9-C1'-C2'	6.73	122.75	114.00
4	BB	164	ILE	CG1-CB-CG2	6.73	126.21	111.40
2	AZ	6124	G	C5'-C4'-C3'	6.73	126.77	116.00
35	Bg	244	ALA	N-CA-C	6.73	129.18	111.00
1	A2	1038	U	N1-C1'-C2'	6.73	122.75	114.00
1	A2	423	G	C4'-C3'-O3'	6.73	126.45	113.00
1	A2	1448	G	C5'-C4'-O4'	6.72	117.17	109.10
1	A2	1354	G	N9-C1'-C2'	6.71	122.72	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	1291	G	C4'-C3'-O3'	6.70	126.41	113.00
26	BX	98	GLU	N-CA-C	6.70	129.09	111.00
1	A2	1777	G	C4'-C3'-O3'	6.70	126.39	113.00
6	BD	220	PRO	N-CA-C	6.68	129.47	112.10
1	A2	1125	A	C5'-C4'-O4'	6.68	117.12	109.10
1	A2	376	C	C4'-C3'-O3'	6.68	126.36	113.00
1	A2	568	G	C5'-C4'-O4'	6.68	117.11	109.10
1	A2	721	U	C2'-C3'-O3'	6.68	124.39	113.70
1	A2	315	A	C5'-C4'-O4'	6.67	117.11	109.10
1	A2	612	U	N1-C1'-C2'	6.67	122.67	114.00
21	BS	81	ILE	CG1-CB-CG2	6.67	126.07	111.40
1	A2	910	C	C5'-C4'-O4'	6.66	117.10	109.10
1	A2	295	A	C4'-C3'-O3'	6.66	126.32	113.00
7	BE	192	ILE	CG1-CB-CG2	6.65	126.03	111.40
1	A2	482	U	C5'-C4'-O4'	6.65	117.08	109.10
1	A2	473	A	C4'-C3'-O3'	6.64	126.28	113.00
2	AZ	6120	U	N1-C1'-C2'	6.64	122.63	114.00
24	BV	28	ASP	N-CA-C	6.64	128.92	111.00
1	A2	212	U	O4'-C1'-N1	6.64	113.51	108.20
3	BA	173	ILE	CG1-CB-CG2	6.64	126.00	111.40
1	A2	1467	C	C5'-C4'-O4'	6.63	117.06	109.10
1	A2	1095	U	N1-C1'-C2'	6.63	122.62	114.00
2	AZ	6070	A	C2'-C3'-O3'	6.63	124.30	113.70
30	Bb	12	ALA	N-CA-C	6.62	128.88	111.00
2	AZ	6163	C	O4'-C1'-N1	6.62	113.50	108.20
1	A2	821	U	C4'-C3'-O3'	6.62	126.23	113.00
1	A2	472	U	C5'-C4'-O4'	6.61	117.03	109.10
8	BF	211	ILE	CG1-CB-CG2	6.61	125.94	111.40
16	BN	98	VAL	CG1-CB-CG2	6.61	121.48	110.90
1	A2	240	U	C5'-C4'-C3'	6.61	126.57	116.00
2	AZ	6124	G	C2'-C3'-O3'	6.60	124.27	113.70
20	BR	54	THR	N-CA-C	6.60	128.82	111.00
1	A2	1092	A	O4'-C1'-N9	6.60	113.48	108.20
1	A2	1720	G	C4'-C3'-O3'	6.60	126.19	113.00
22	BT	17	ALA	N-CA-C	6.59	128.81	111.00
26	BX	124	VAL	CG1-CB-CG2	6.59	121.45	110.90
1	A2	1304	G	C5'-C4'-O4'	6.58	117.00	109.10
2	AZ	6025	A	C1'-C2'-O2'	6.58	130.35	110.60
32	Bd	11	PRO	N-CA-C	6.58	129.19	112.10
1	A2	787	G	C4'-C3'-O3'	6.57	126.15	113.00
9	BG	26	VAL	CG1-CB-CG2	6.57	121.42	110.90
4	BB	153	HIS	N-CA-C	6.57	128.74	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AZ	6085	A	C5'-C4'-C3'	6.57	126.51	116.00
1	A2	1340	U	O4'-C1'-N1	6.56	113.45	108.20
1	A2	1418	G	C4'-C3'-O3'	6.56	126.12	113.00
1	A2	1467	C	C4'-C3'-O3'	6.56	126.12	113.00
1	A2	1516	A	C5'-C4'-O4'	6.55	116.96	109.10
1	A2	944	A	C5'-C4'-O4'	6.55	116.96	109.10
1	A2	1054	U	N1-C1'-C2'	6.55	122.51	114.00
3	BA	185	ARG	N-CA-C	6.54	128.66	111.00
5	BC	179	VAL	N-CA-C	6.54	128.67	111.00
9	BG	198	ALA	N-CA-C	6.54	128.66	111.00
1	A2	1205	C	N1-C1'-C2'	6.54	122.50	114.00
15	BM	57	ALA	N-CA-C	6.54	128.64	111.00
1	A2	330	G	C4'-C3'-O3'	6.53	126.07	113.00
35	Bg	5	GLU	N-CA-C	6.53	128.64	111.00
1	A2	734	A	N9-C1'-C2'	6.51	122.46	114.00
1	A2	914	G	N9-C1'-C2'	6.51	122.46	114.00
1	A2	1502	G	N9-C1'-C2'	6.51	122.46	114.00
1	A2	1414	U	C3'-C2'-O2'	6.50	132.16	113.30
1	A2	1041	G	C5'-C4'-O4'	6.50	116.90	109.10
1	A2	1493	A	O4'-C1'-N9	6.50	113.40	108.20
1	A2	1226	A	C5'-C4'-O4'	6.50	116.90	109.10
11	BI	13	ALA	N-CA-C	6.50	128.55	111.00
1	A2	88	U	C2'-C3'-O3'	6.50	124.10	113.70
1	A2	501	U	C3'-C2'-O2'	6.50	132.14	113.30
1	A2	744	U	C5'-C4'-O4'	6.50	116.89	109.10
1	A2	511	A	C5'-C4'-O4'	6.49	116.89	109.10
1	A2	1347	U	C2'-C3'-O3'	6.48	124.07	113.70
1	A2	750	U	C5'-C4'-O4'	6.48	116.87	109.10
1	A2	188	A	C4'-C3'-O3'	6.47	125.94	113.00
1	A2	587	C	N1-C1'-C2'	6.47	122.41	114.00
27	BY	13	ILE	CG1-CB-CG2	6.47	125.64	111.40
5	BC	131	ILE	CG1-CB-CG2	6.47	125.62	111.40
1	A2	804	A	C1'-C2'-O2'	6.46	130.00	110.60
1	A2	310	C	C5'-C4'-O4'	6.46	116.85	109.10
2	AZ	6081	U	C4'-C3'-O3'	6.46	125.91	113.00
1	A2	629	U	C5'-C4'-O4'	6.46	116.85	109.10
1	A2	1752	U	C4'-C3'-O3'	6.46	125.91	113.00
13	BK	22	VAL	CG1-CB-CG2	6.46	121.23	110.90
1	A2	359	A	N9-C1'-C2'	6.45	122.38	114.00
20	BR	66	VAL	CG1-CB-CG2	6.45	121.21	110.90
5	BC	36	VAL	CB-CA-C	6.44	123.64	111.40
1	A2	1792	G	C5'-C4'-O4'	6.44	116.83	109.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	921	U	O4'-C1'-N1	6.43	113.35	108.20
1	A2	1568	C	C4'-C3'-O3'	6.42	125.85	113.00
21	BS	101	LEU	N-CA-C	6.42	128.35	111.00
1	A2	459	G	C5'-C4'-O4'	6.42	116.80	109.10
1	A2	1407	U	C5'-C4'-O4'	6.42	116.80	109.10
29	Ba	11	ASN	N-CA-C	6.42	128.32	111.00
17	BO	83	ILE	CG1-CB-CG2	6.41	125.51	111.40
1	A2	1749	A	C4'-C3'-O3'	6.41	125.82	113.00
8	BF	201	ALA	N-CA-C	6.39	128.27	111.00
1	A2	1528	U	C4'-C3'-O3'	6.39	125.78	113.00
1	A2	1252	C	C5'-C4'-C3'	6.39	126.22	116.00
1	A2	1638	G	O4'-C4'-C3'	6.39	111.21	106.10
1	A2	1146	G	C4'-C3'-O3'	6.39	125.78	113.00
6	BD	175	VAL	CB-CA-C	6.39	123.53	111.40
1	A2	146	U	C5'-C4'-O4'	6.38	116.76	109.10
1	A2	258	C	C5'-C4'-O4'	6.38	116.76	109.10
1	A2	1290	U	C4'-C3'-O3'	6.38	125.77	113.00
10	BH	59	ALA	N-CA-C	6.38	128.23	111.00
35	Bg	46	LYS	CB-CA-C	6.38	123.16	110.40
6	BD	21	LEU	CB-CG-CD1	6.38	121.84	111.00
35	Bg	48	THR	N-CA-C	6.37	128.21	111.00
1	A2	272	U	C5'-C4'-C3'	6.37	126.19	116.00
1	A2	451	A	C5'-C4'-C3'	6.37	126.19	116.00
32	Bd	47	ALA	N-CA-C	6.37	128.21	111.00
1	A2	1713	G	C4'-C3'-O3'	6.37	125.74	113.00
19	BQ	84	ALA	N-CA-C	6.37	128.20	111.00
1	A2	352	A	OP1-P-O3'	-6.37	91.19	105.20
1	A2	517	U	C4'-C3'-O3'	6.37	125.73	113.00
1	A2	231	U	C1'-C2'-O2'	6.36	129.67	110.60
1	A2	562	G	C5'-C4'-O4'	6.36	116.73	109.10
1	A2	41	A	C4'-C3'-O3'	6.36	125.71	113.00
1	A2	1525	A	C2'-C3'-O3'	6.34	123.85	113.70
1	A2	1680	G	C1'-C2'-O2'	6.34	129.62	110.60
3	BA	111	ILE	N-CA-C	6.33	128.10	111.00
9	BG	25	ARG	N-CA-C	6.33	128.08	111.00
1	A2	469	C	C4'-C3'-O3'	6.32	125.63	113.00
13	BK	11	ILE	CG1-CB-CG2	6.31	125.28	111.40
1	A2	1389	C	C5'-C4'-O4'	6.31	116.67	109.10
1	A2	289	U	C1'-C2'-O2'	6.30	129.51	110.60
31	Bc	44	VAL	CG1-CB-CG2	6.30	120.98	110.90
1	A2	1445	G	C5'-C4'-C3'	6.30	126.08	116.00
1	A2	1289	U	C4'-C3'-O3'	6.29	125.59	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	1455	G	C5'-C4'-C3'	6.29	126.07	116.00
1	A2	42	G	C5'-C4'-C3'	6.29	126.07	116.00
1	A2	143	G	N9-C1'-C2'	6.28	122.17	114.00
1	A2	1357	A	C5'-C4'-C3'	6.28	126.05	116.00
6	BD	51	ARG	N-CA-C	6.27	127.93	111.00
1	A2	769	A	C5'-C4'-O4'	6.27	116.62	109.10
1	A2	67	A	C3'-C2'-O2'	6.26	131.47	113.30
1	A2	1221	A	C5'-C4'-O4'	6.26	116.62	109.10
1	A2	960	U	N1-C1'-C2'	6.26	122.14	114.00
1	A2	1196	A	O4'-C1'-N9	6.26	113.21	108.20
8	BF	165	LEU	CB-CA-C	6.26	122.10	110.20
1	A2	1424	A	C5'-C4'-O4'	6.26	116.61	109.10
1	A2	303	U	N1-C1'-C2'	6.25	122.13	114.00
1	A2	1058	U	C5'-C4'-O4'	6.25	116.60	109.10
1	A2	1347	U	C4'-C3'-O3'	6.25	125.50	113.00
1	A2	131	C	C4'-C3'-O3'	6.25	125.49	113.00
1	A2	468	A	C5'-C4'-O4'	6.25	116.60	109.10
35	Bg	80	ALA	N-CA-C	6.25	127.86	111.00
1	A2	756	A	C5'-C4'-O4'	6.24	116.59	109.10
1	A2	1097	U	C5'-C4'-O4'	6.24	116.59	109.10
1	A2	51	A	C4'-C3'-O3'	6.24	125.48	113.00
1	A2	1415	U	C4'-C3'-O3'	6.24	125.48	113.00
1	A2	1442	U	C4'-C3'-O3'	6.24	125.48	113.00
18	BP	63	ALA	N-CA-C	6.24	127.84	111.00
1	A2	120	U	C5'-C4'-C3'	6.24	125.98	116.00
1	A2	461	G	C4'-C3'-O3'	6.23	125.45	113.00
1	A2	1337	A	N9-C1'-C2'	6.23	122.10	114.00
1	A2	539	G	C5'-C4'-O4'	6.22	116.57	109.10
1	A2	939	A	C5'-C4'-O4'	6.22	116.57	109.10
1	A2	1777	G	C5'-C4'-O4'	6.22	116.57	109.10
1	A2	738	G	C4'-C3'-O3'	6.22	125.43	113.00
2	AZ	6121	C	C4'-C3'-O3'	6.22	125.44	113.00
34	Bf	151	ASN	N-CA-C	6.21	127.78	111.00
1	A2	320	U	C4'-C3'-O3'	6.21	125.43	113.00
1	A2	1118	G	C5'-C4'-C3'	6.21	125.94	116.00
22	BT	7	ARG	N-CA-C	6.21	127.77	111.00
1	A2	885	G	C4'-C3'-O3'	6.21	125.41	113.00
1	A2	1475	A	N9-C1'-C2'	6.20	122.06	114.00
2	AZ	6160	C	O4'-C1'-N1	6.20	113.16	108.20
1	A2	1267	G	C4'-C3'-O3'	6.20	125.39	113.00
19	BQ	89	LEU	N-CA-C	6.20	127.73	111.00
1	A2	248	U	N1-C1'-C2'	6.19	122.05	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	1197	C	C5'-C4'-C3'	6.19	125.90	116.00
1	A2	1501	C	C3'-C2'-O2'	6.19	131.24	113.30
11	BI	162	ALA	N-CA-C	6.19	127.71	111.00
1	A2	1286	U	C3'-C2'-O2'	6.18	131.23	113.30
1	A2	753	A	C4'-C3'-O3'	6.18	125.36	113.00
1	A2	1003	A	O4'-C1'-N9	6.17	113.14	108.20
1	A2	1297	G	C1'-C2'-O2'	6.17	129.10	110.60
1	A2	1441	C	N1-C1'-C2'	6.17	122.02	114.00
16	BN	121	ARG	N-CA-C	6.17	127.66	111.00
1	A2	222	A	C3'-C2'-O2'	6.17	131.18	113.30
1	A2	792	U	O4'-C1'-N1	6.17	113.13	108.20
17	BO	61	MET	N-CA-C	6.17	127.65	111.00
1	A2	299	A	C4'-C3'-O3'	6.17	125.33	113.00
1	A2	367	A	C5'-C4'-C3'	6.15	125.84	116.00
17	BO	17	ALA	N-CA-C	6.15	127.61	111.00
1	A2	138	A	C5'-C4'-O4'	6.15	116.48	109.10
14	BL	78	THR	OG1-CB-CG2	6.15	124.15	110.00
1	A2	1771	U	C5'-C4'-O4'	6.15	116.48	109.10
12	BJ	26	ALA	N-CA-C	6.15	127.60	111.00
28	BZ	42	LEU	N-CA-C	6.15	127.59	111.00
2	AZ	6164	U	C5'-C4'-C3'	6.14	125.83	116.00
2	AZ	6164	U	C5'-C4'-O4'	6.14	116.47	109.10
1	A2	748	U	C5'-C4'-O4'	6.13	116.46	109.10
2	AZ	6221	U	C5'-C4'-O4'	6.13	116.46	109.10
1	A2	1570	A	C4'-C3'-O3'	6.13	125.26	113.00
9	BG	81	VAL	CB-CA-C	6.13	123.04	111.40
12	BJ	163	PRO	N-CA-C	6.13	128.04	112.10
35	Bg	10	ARG	N-CA-C	6.12	127.52	111.00
26	BX	22	ASN	N-CA-C	6.12	127.52	111.00
1	A2	173	A	C1'-C2'-O2'	6.12	128.95	110.60
1	A2	1320	U	C5'-C4'-O4'	6.11	116.44	109.10
10	BH	65	PRO	N-CA-C	6.11	127.99	112.10
35	Bg	227	ALA	N-CA-C	6.11	127.51	111.00
1	A2	1188	G	C5'-C4'-C3'	6.11	125.78	116.00
2	AZ	6115	U	C3'-C2'-O2'	6.11	131.02	113.30
1	A2	1603	U	C5'-C4'-O4'	6.10	116.42	109.10
1	A2	13	C	N1-C1'-C2'	6.10	121.93	114.00
14	BL	138	ASN	N-CA-C	6.10	127.47	111.00
6	BD	123	VAL	N-CA-C	6.09	127.45	111.00
1	A2	1514	U	C1'-C2'-O2'	6.09	128.87	110.60
1	A2	713	A	C4'-C3'-O3'	6.09	125.18	113.00
22	BT	55	TYR	CG-CD1-CE1	-6.09	116.43	121.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	1751	C	C5'-C4'-C3'	6.09	125.74	116.00
2	AZ	6164	U	N1-C1'-C2'	6.09	121.91	114.00
1	A2	1688	U	C4'-C3'-O3'	6.08	125.16	113.00
1	A2	1085	G	N9-C1'-C2'	6.08	121.90	114.00
5	BC	159	THR	OG1-CB-CG2	6.08	123.97	110.00
1	A2	545	A	O4'-C1'-N9	6.07	113.06	108.20
2	AZ	6079	A	C1'-C2'-O2'	6.07	128.82	110.60
1	A2	189	C	N1-C1'-C2'	6.07	121.88	114.00
2	AZ	6055	U	C4'-C3'-O3'	6.07	125.13	113.00
1	A2	805	U	C5'-C4'-O4'	6.06	116.38	109.10
35	Bg	257	ALA	N-CA-C	6.06	127.37	111.00
1	A2	1213	G	C3'-C2'-O2'	6.06	130.88	113.30
1	A2	1442	U	C5'-C4'-O4'	6.06	116.37	109.10
1	A2	58	U	O4'-C1'-N1	6.06	113.05	108.20
1	A2	1561	U	C4'-C3'-O3'	6.05	125.11	113.00
9	BG	142	ARG	N-CA-C	6.05	127.34	111.00
16	BN	11	ILE	CG1-CB-CG2	6.05	124.71	111.40
1	A2	161	U	C5'-C4'-C3'	6.05	125.67	116.00
1	A2	473	A	O4'-C4'-C3'	6.04	110.94	106.10
2	AZ	6188	G	C5'-C4'-O4'	6.04	116.35	109.10
1	A2	399	A	OP1-P-O3'	6.04	118.48	105.20
1	A2	472	U	C5'-C4'-C3'	6.03	125.65	116.00
1	A2	577	G	C4'-C3'-O3'	6.03	125.06	113.00
1	A2	417	A	C4'-C3'-O3'	6.03	125.06	113.00
1	A2	362	G	C4'-C3'-O3'	6.03	125.06	113.00
1	A2	1753	A	C2'-C3'-O3'	6.03	123.34	113.70
1	A2	600	U	N1-C1'-C2'	6.03	121.83	114.00
1	A2	945	U	C5'-C4'-O4'	6.03	116.33	109.10
19	BQ	134	ALA	N-CA-C	6.03	127.27	111.00
1	A2	351	C	O4'-C1'-N1	6.02	113.02	108.20
1	A2	1161	C	C5'-C4'-C3'	6.02	125.63	116.00
1	A2	1096	C	C5'-C4'-C3'	6.02	125.63	116.00
1	A2	88	U	C5'-C4'-C3'	6.01	125.62	116.00
18	BP	36	LEU	N-CA-C	6.01	127.24	111.00
14	BL	145	ALA	N-CA-C	6.01	127.23	111.00
1	A2	1097	U	C5'-C4'-C3'	6.01	125.61	116.00
1	A2	1176	G	C4'-C3'-O3'	6.01	125.01	113.00
1	A2	166	C	C1'-C2'-O2'	6.00	128.62	110.60
1	A2	703	G	C5'-C4'-O4'	6.00	116.31	109.10
2	AZ	6195	G	C4'-C3'-O3'	6.00	125.01	113.00
1	A2	1448	G	C5'-C4'-C3'	6.00	125.60	116.00
1	A2	781	U	C1'-C2'-O2'	6.00	128.60	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	1600	A	C5'-C4'-O4'	6.00	116.30	109.10
1	A2	1226	A	O4'-C1'-N9	5.99	112.99	108.20
1	A2	1754	A	C5'-C4'-O4'	5.99	116.29	109.10
1	A2	1130	G	N9-C1'-C2'	5.99	121.79	114.00
1	A2	1551	U	N1-C1'-C2'	5.99	121.79	114.00
1	A2	1247	U	C5'-C4'-O4'	5.99	116.29	109.10
4	BB	21	VAL	N-CA-C	5.99	127.18	111.00
1	A2	213	A	C3'-C2'-O2'	5.99	130.66	113.30
1	A2	260	U	C1'-C2'-O2'	5.99	128.56	110.60
1	A2	161	U	C5'-C4'-O4'	5.99	116.28	109.10
7	BE	89	VAL	CB-CA-C	5.98	122.77	111.40
1	A2	689	G	C5'-C4'-O4'	5.98	116.28	109.10
1	A2	499	U	C3'-C2'-O2'	5.98	130.65	113.30
1	A2	1151	A	C4'-C3'-O3'	5.98	124.95	113.00
1	A2	1771	U	C4'-C3'-O3'	5.98	124.95	113.00
1	A2	917	U	C3'-C2'-O2'	5.97	130.63	113.30
1	A2	928	U	O4'-C1'-N1	5.97	112.98	108.20
2	AZ	6129	C	C5'-C4'-C3'	5.97	125.55	116.00
18	BP	20	VAL	N-CA-C	5.97	127.12	111.00
12	BJ	85	VAL	CG1-CB-CG2	5.97	120.45	110.90
1	A2	143	G	C4'-C3'-O3'	5.97	124.93	113.00
11	BI	73	SER	N-CA-C	5.97	127.11	111.00
15	BM	141	SER	N-CA-C	5.96	127.10	111.00
1	A2	1170	G	C4'-C3'-O3'	5.96	124.93	113.00
26	BX	65	ASN	N-CA-C	5.96	127.10	111.00
2	AZ	6034	A	C3'-C2'-O2'	5.96	130.58	113.30
28	BZ	84	GLU	N-CA-C	5.96	127.08	111.00
33	Be	43	ARG	N-CA-C	5.96	127.09	111.00
27	BY	118	ILE	CG1-CB-CG2	5.96	124.50	111.40
1	A2	461	G	C5'-C4'-C3'	5.95	125.52	116.00
1	A2	465	G	C5'-C4'-O4'	5.95	116.24	109.10
1	A2	836	U	C4'-C3'-O3'	5.95	124.90	113.00
1	A2	877	G	C5'-C4'-C3'	5.95	125.52	116.00
1	A2	743	U	C5'-C4'-O4'	5.94	116.23	109.10
1	A2	395	U	N1-C1'-C2'	5.94	121.72	114.00
1	A2	1748	G	C1'-C2'-O2'	5.94	128.41	110.60
2	AZ	6174	G	C5'-C4'-O4'	5.94	116.22	109.10
1	A2	146	U	C4'-C3'-O3'	5.94	124.87	113.00
2	AZ	6124	G	C5'-C4'-O4'	5.94	116.22	109.10
1	A2	1407	U	C5'-C4'-C3'	5.93	125.49	116.00
18	BP	82	ASN	N-CA-C	5.93	127.02	111.00
28	BZ	82	HIS	CB-CA-C	5.92	122.24	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AZ	6113	U	C1'-C2'-O2'	5.92	128.35	110.60
9	BG	67	VAL	N-CA-C	5.92	126.98	111.00
18	BP	122	THR	N-CA-C	5.92	126.98	111.00
1	A2	272	U	C5'-C4'-O4'	5.91	116.19	109.10
2	AZ	6197	U	C5'-C4'-C3'	5.91	125.46	116.00
2	AZ	6039	G	C5'-C4'-C3'	5.91	125.45	116.00
1	A2	750	U	N1-C1'-C2'	5.90	121.67	114.00
1	A2	1449	U	O4'-C4'-C3'	5.90	110.82	106.10
1	A2	468	A	C5'-C4'-C3'	5.90	125.44	116.00
15	BM	62	LEU	CA-CB-CG	5.90	128.87	115.30
1	A2	525	A	C5'-C4'-C3'	5.90	125.44	116.00
1	A2	1032	G	N9-C1'-C2'	5.90	121.67	114.00
1	A2	1100	G	C1'-C2'-O2'	5.90	128.29	110.60
1	A2	921	U	C4'-C3'-O3'	5.89	124.78	113.00
30	Bb	57	GLU	N-CA-C	5.89	126.91	111.00
1	A2	1268	G	C1'-C2'-O2'	5.89	128.27	110.60
1	A2	740	A	C4'-C3'-O3'	5.89	124.78	113.00
1	A2	1430	U	C4'-C3'-O3'	5.89	124.78	113.00
1	A2	1064	G	C3'-C2'-O2'	5.89	130.37	113.30
1	A2	33	U	C5'-C4'-C3'	5.88	125.41	116.00
1	A2	1450	U	C5'-C4'-C3'	5.88	125.42	116.00
1	A2	882	U	C4'-C3'-O3'	5.88	124.76	113.00
3	BA	146	LEU	CA-CB-CG	5.88	128.83	115.30
9	BG	169	TYR	CG-CD2-CE2	-5.88	116.60	121.30
1	A2	1429	G	C5'-C4'-C3'	5.88	125.40	116.00
1	A2	1571	C	O4'-C1'-N1	5.88	112.90	108.20
17	BO	120	PRO	N-CA-C	5.87	127.37	112.10
1	A2	315	A	C5'-C4'-C3'	5.87	125.39	116.00
1	A2	941	A	C4'-C3'-O3'	5.87	124.74	113.00
1	A2	949	C	C5'-C4'-O4'	5.87	116.14	109.10
9	BG	110	ALA	N-CA-C	5.87	126.84	111.00
1	A2	427	C	C5'-C4'-O4'	5.87	116.14	109.10
1	A2	430	G	C4'-C3'-O3'	5.87	124.73	113.00
1	A2	1247	U	C4'-C3'-O3'	5.87	124.73	113.00
1	A2	138	A	C5'-C4'-C3'	5.87	125.39	116.00
1	A2	1535	U	C3'-C2'-O2'	5.86	130.30	113.30
18	BP	39	ALA	N-CA-C	5.86	126.83	111.00
3	BA	130	ALA	N-CA-C	5.86	126.82	111.00
27	BY	28	LEU	CB-CG-CD2	5.86	120.96	111.00
1	A2	10	G	C1'-C2'-O2'	5.86	128.17	110.60
21	BS	97	ASP	N-CA-C	5.86	126.81	111.00
23	BU	72	ASN	N-CA-C	5.86	126.81	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	813	U	C3'-C2'-O2'	5.85	130.27	113.30
31	Bc	33	LEU	CB-CG-CD1	5.85	120.95	111.00
3	BA	110	TYR	CB-CG-CD1	5.85	124.51	121.00
1	A2	943	C	C5'-C4'-O4'	5.85	116.12	109.10
12	BJ	102	GLU	N-CA-C	5.85	126.79	111.00
1	A2	681	U	C5'-C4'-C3'	5.84	125.35	116.00
1	A2	219	A	N9-C1'-C2'	5.84	121.59	114.00
26	BX	12	ALA	N-CA-C	5.84	126.76	111.00
1	A2	42	G	C5'-C4'-O4'	5.83	116.10	109.10
1	A2	482	U	C5'-C4'-C3'	5.83	125.33	116.00
3	BA	129	ASP	N-CA-C	5.83	126.74	111.00
1	A2	1248	C	N1-C1'-C2'	5.83	121.58	114.00
7	BE	233	LYS	N-CA-C	5.83	126.73	111.00
1	A2	1677	C	C1'-C2'-O2'	5.83	128.08	110.60
1	A2	1102	G	C5'-C4'-C3'	5.82	125.32	116.00
12	BJ	122	VAL	N-CA-C	5.82	126.73	111.00
1	A2	1759	C	C4'-C3'-O3'	5.82	124.64	113.00
1	A2	738	G	C5'-C4'-C3'	5.82	125.31	116.00
2	AZ	6127	U	C3'-C2'-O2'	5.82	130.18	113.30
2	AZ	6134	U	C5'-C4'-O4'	5.82	116.08	109.10
1	A2	1563	C	C5'-C4'-C3'	5.82	125.31	116.00
5	BC	113	LEU	CB-CG-CD1	5.82	120.89	111.00
2	AZ	6198	U	C4'-C3'-O3'	5.82	124.63	113.00
1	A2	752	A	C3'-C2'-O2'	5.81	130.16	113.30
1	A2	1542	G	C1'-C2'-O2'	5.81	128.04	110.60
2	AZ	6196	G	C5'-C4'-O4'	5.81	116.08	109.10
11	BI	16	ALA	N-CA-C	5.81	126.69	111.00
2	AZ	6217	A	C4'-C3'-O3'	5.81	124.61	113.00
1	A2	644	C	C5'-C4'-O4'	5.81	116.07	109.10
1	A2	363	G	O4'-C1'-N9	5.80	112.84	108.20
22	BT	66	TYR	N-CA-C	5.80	126.66	111.00
22	BT	101	ASN	N-CA-C	5.80	126.66	111.00
1	A2	391	A	C3'-C2'-O2'	5.80	130.12	113.30
1	A2	1096	C	C5'-C4'-O4'	5.80	116.06	109.10
1	A2	1259	U	C4'-C3'-O3'	5.80	124.59	113.00
2	AZ	6052	A	C3'-C2'-O2'	5.80	130.11	113.30
1	A2	248	U	O4'-C1'-N1	5.79	112.84	108.20
1	A2	733	A	C4'-C3'-O3'	5.79	124.59	113.00
1	A2	1092	A	C4'-C3'-O3'	5.79	124.59	113.00
1	A2	1125	A	C5'-C4'-C3'	5.79	125.27	116.00
1	A2	717	C	C3'-C2'-O2'	5.79	130.09	113.30
1	A2	1319	A	C5'-C4'-O4'	5.79	116.05	109.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	Bg	196	ASN	N-CA-C	5.79	126.64	111.00
1	A2	149	C	C4'-C3'-O3'	5.79	124.58	113.00
1	A2	1282	U	C1'-C2'-O2'	5.79	127.97	110.60
1	A2	1749	A	C5'-C4'-O4'	5.79	116.04	109.10
1	A2	461	G	C5'-C4'-O4'	5.78	116.04	109.10
1	A2	1674	C	C3'-C2'-O2'	5.78	130.07	113.30
9	BG	120	GLU	N-CA-C	5.78	126.61	111.00
1	A2	31	C	N1-C1'-C2'	5.78	121.51	114.00
1	A2	1363	U	O4'-C1'-N1	5.78	112.82	108.20
14	BL	27	THR	N-CA-C	5.78	126.59	111.00
1	A2	822	U	C1'-C2'-O2'	5.77	127.92	110.60
1	A2	1493	A	C1'-C2'-O2'	5.77	127.92	110.60
1	A2	528	U	C4'-C3'-O3'	5.77	124.55	113.00
1	A2	1743	U	C4'-C3'-O3'	5.76	124.53	113.00
1	A2	644	C	C4'-C3'-O3'	5.76	124.52	113.00
2	AZ	6137	C	C5'-C4'-C3'	5.76	125.21	116.00
19	BQ	85	ILE	CG1-CB-CG2	5.75	124.06	111.40
1	A2	1041	G	C5'-C4'-C3'	5.75	125.20	116.00
1	A2	852	C	C5'-C4'-C3'	5.75	125.20	116.00
1	A2	1053	G	C3'-C2'-O2'	5.75	129.97	113.30
2	AZ	6070	A	C5'-C4'-C3'	5.75	125.20	116.00
1	A2	131	C	C3'-C2'-O2'	5.75	129.96	113.30
1	A2	1032	G	C3'-C2'-O2'	5.75	129.97	113.30
2	AZ	6179	A	C5'-C4'-C3'	5.75	125.19	116.00
1	A2	753	A	C5'-C4'-C3'	5.75	125.19	116.00
1	A2	944	A	C5'-C4'-C3'	5.75	125.19	116.00
11	BI	92	ARG	N-CA-C	5.74	126.50	111.00
1	A2	363	G	N9-C1'-C2'	5.74	121.46	114.00
1	A2	136	C	N1-C1'-C2'	5.74	121.46	114.00
1	A2	716	C	C4'-C3'-O3'	5.74	124.47	113.00
28	BZ	61	SER	CB-CA-C	5.74	121.00	110.10
1	A2	629	U	C4'-C3'-O3'	5.73	124.47	113.00
1	A2	810	G	C5'-C4'-O4'	5.73	115.98	109.10
4	BB	26	ARG	N-CA-C	5.73	126.48	111.00
1	A2	1509	C	C4'-C3'-O3'	5.73	124.47	113.00
1	A2	65	A	C1'-C2'-O2'	5.73	127.79	110.60
1	A2	600	U	C5'-C4'-C3'	5.73	125.16	116.00
32	Bd	55	PHE	N-CA-C	5.73	126.46	111.00
6	BD	141	LYS	N-CA-C	5.72	126.46	111.00
1	A2	1374	C	C5'-C4'-C3'	5.72	125.16	116.00
1	A2	1557	U	C1'-C2'-O2'	5.72	127.77	110.60
7	BE	147	ILE	N-CA-C	5.72	126.45	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	1509	C	C5'-C4'-O4'	5.72	115.97	109.10
1	A2	846	G	C1'-C2'-O2'	5.72	127.76	110.60
1	A2	1367	G	C3'-C2'-O2'	5.72	129.88	113.30
1	A2	88	U	C5'-C4'-O4'	5.72	115.96	109.10
1	A2	1563	C	C5'-C4'-O4'	5.71	115.96	109.10
1	A2	1647	U	C5'-C4'-O4'	5.71	115.96	109.10
35	Bg	206	PRO	N-CA-C	5.71	126.95	112.10
1	A2	900	A	C3'-C2'-O2'	5.71	129.86	113.30
1	A2	37	U	C5'-C4'-O4'	5.71	115.95	109.10
1	A2	499	U	O4'-C1'-N1	5.71	112.77	108.20
1	A2	1444	A	C5'-C4'-O4'	5.71	115.95	109.10
6	BD	31	GLU	N-CA-C	5.71	126.40	111.00
1	A2	484	C	C5'-C4'-O4'	5.70	115.94	109.10
1	A2	504	U	C5'-C4'-C3'	5.70	125.13	116.00
1	A2	523	G	C3'-C2'-O2'	5.70	129.84	113.30
1	A2	1761	U	C2'-C3'-O3'	5.70	122.83	113.70
1	A2	603	U	O4'-C1'-N1	5.70	112.76	108.20
2	AZ	6061	G	C4'-C3'-O3'	5.70	124.40	113.00
1	A2	220	A	C3'-C2'-O2'	5.70	129.82	113.30
1	A2	1131	A	C5'-C4'-O4'	5.70	115.94	109.10
1	A2	1586	A	C3'-C2'-O2'	5.69	129.81	113.30
1	A2	894	U	O4'-C1'-N1	5.69	112.75	108.20
1	A2	1414	U	O4'-C1'-N1	5.69	112.75	108.20
9	BG	133	LEU	N-CA-C	5.69	126.36	111.00
1	A2	1113	A	C5'-C4'-O4'	5.69	115.92	109.10
2	AZ	6175	A	C3'-C2'-O2'	5.68	129.78	113.30
1	A2	1219	A	C1'-C2'-O2'	5.68	127.64	110.60
12	BJ	125	ALA	N-CA-C	5.68	126.34	111.00
1	A2	1242	A	C3'-C2'-O2'	5.68	129.77	113.30
1	A2	1611	A	C1'-C2'-O2'	5.67	127.62	110.60
1	A2	1374	C	C5'-C4'-O4'	5.67	115.91	109.10
1	A2	1500	C	C3'-C2'-O2'	5.67	129.75	113.30
1	A2	221	A	C5'-C4'-C3'	5.67	125.07	116.00
1	A2	938	G	C5'-C4'-C3'	5.67	125.07	116.00
11	BI	94	ASN	N-CA-C	5.67	126.31	111.00
1	A2	1448	G	C1'-C2'-O2'	5.67	127.60	110.60
1	A2	1580	C	C5'-C4'-C3'	5.67	125.07	116.00
2	AZ	6129	C	C5'-C4'-O4'	5.67	115.90	109.10
1	A2	902	G	C1'-C2'-O2'	5.66	127.59	110.60
12	BJ	67	PRO	N-CA-C	5.66	126.83	112.10
1	A2	3	U	C5'-C4'-O4'	5.66	115.89	109.10
1	A2	1118	G	C3'-C2'-O2'	5.66	129.72	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	144	U	C1'-C2'-O2'	5.66	127.58	110.60
1	A2	1687	U	C3'-C2'-O2'	5.66	129.71	113.30
15	BM	50	LYS	N-CA-C	5.66	126.28	111.00
1	A2	430	G	C5'-C4'-O4'	5.66	115.89	109.10
1	A2	1106	U	C4'-C3'-O3'	5.66	124.31	113.00
1	A2	488	G	C5'-C4'-O4'	5.66	115.89	109.10
1	A2	1343	U	C3'-C2'-O2'	5.66	129.70	113.30
4	BB	198	GLU	N-CA-C	5.65	126.27	111.00
1	A2	124	A	C1'-C2'-O2'	5.65	127.56	110.60
1	A2	649	U	O4'-C1'-N1	5.65	112.72	108.20
1	A2	1474	G	C4'-C3'-O3'	5.65	124.31	113.00
26	BX	61	SER	N-CA-C	5.65	126.26	111.00
1	A2	1738	U	O4'-C1'-N1	5.65	112.72	108.20
3	BA	2	SER	N-CA-C	5.65	126.25	111.00
1	A2	115	G	C4'-C3'-O3'	5.65	124.29	113.00
1	A2	943	C	C5'-C4'-C3'	5.65	125.03	116.00
1	A2	166	C	N1-C1'-C2'	5.65	121.34	114.00
1	A2	545	A	C1'-C2'-O2'	5.64	127.53	110.60
2	AZ	6197	U	C4'-C3'-O3'	5.64	124.29	113.00
4	BB	123	ALA	N-CA-C	5.64	126.24	111.00
21	BS	43	SER	N-CA-C	5.64	126.24	111.00
27	BY	101	GLU	N-CA-C	5.64	126.23	111.00
1	A2	1002	G	C5'-C4'-O4'	5.64	115.87	109.10
1	A2	914	G	C1'-C2'-O2'	5.64	127.52	110.60
11	BI	150	ALA	N-CA-C	5.64	126.23	111.00
11	BI	154	SER	N-CA-C	5.64	126.22	111.00
1	A2	511	A	C4'-C3'-O3'	5.64	124.27	113.00
1	A2	1676	U	C1'-C2'-O2'	5.64	127.51	110.60
1	A2	1641	C	C1'-C2'-O2'	5.63	127.50	110.60
16	BN	112	LYS	N-CA-C	5.63	126.21	111.00
13	BK	55	VAL	CB-CA-C	5.63	122.09	111.40
1	A2	87	C	C4'-C3'-O3'	5.63	124.25	113.00
1	A2	326	G	C5'-C4'-C3'	5.63	125.00	116.00
29	Ba	33	ASP	C-N-CA	5.62	135.76	121.70
1	A2	1346	A	C1'-C2'-O2'	5.62	127.47	110.60
1	A2	1600	A	C5'-C4'-C3'	5.62	124.99	116.00
11	BI	74	LYS	N-CA-C	5.62	126.18	111.00
1	A2	66	U	C5'-C4'-C3'	5.62	124.99	116.00
1	A2	379	U	C1'-C2'-O2'	5.62	127.45	110.60
1	A2	1611	A	C3'-C2'-O2'	5.62	129.59	113.30
1	A2	102	U	C4'-C3'-O3'	5.62	124.23	113.00
1	A2	919	A	C3'-C2'-O2'	5.61	129.57	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	BI	96	LEU	CB-CG-CD2	5.61	120.54	111.00
1	A2	1642	G	C4'-C3'-O3'	5.61	124.22	113.00
1	A2	579	A	C5'-C4'-C3'	5.61	124.97	116.00
19	BQ	67	VAL	N-CA-C	5.61	126.14	111.00
1	A2	644	C	C5'-C4'-C3'	5.60	124.96	116.00
1	A2	1319	A	C5'-C4'-C3'	5.60	124.96	116.00
2	AZ	6174	G	C4'-C3'-O3'	5.60	124.20	113.00
1	A2	1401	A	C3'-C2'-O2'	5.60	129.54	113.30
1	A2	562	G	C4'-C3'-O3'	5.60	124.19	113.00
1	A2	1647	U	C4'-C3'-O3'	5.60	124.19	113.00
1	A2	844	A	C3'-C2'-O2'	5.60	129.53	113.30
1	A2	503	G	C4'-C3'-O3'	5.59	124.19	113.00
22	BT	51	GLU	N-CA-C	5.59	126.10	111.00
33	Be	36	LYS	N-CA-C	5.59	126.09	111.00
1	A2	220	A	C1'-C2'-O2'	5.59	127.36	110.60
1	A2	1548	G	C1'-C2'-O2'	5.59	127.36	110.60
27	BY	28	LEU	CB-CG-CD1	5.59	120.50	111.00
1	A2	1152	A	C1'-C2'-O2'	5.58	127.36	110.60
1	A2	743	U	C4'-C3'-O3'	5.58	124.17	113.00
1	A2	351	C	C1'-C2'-O2'	5.58	127.32	110.60
1	A2	1619	C	C3'-C2'-O2'	5.58	129.47	113.30
24	BV	58	TYR	N-CA-C	5.58	126.06	111.00
35	Bg	182	ASN	N-CA-C	5.57	126.05	111.00
20	BR	42	GLN	N-CA-C	5.57	126.05	111.00
1	A2	1769	U	O4'-C1'-N1	5.57	112.66	108.20
1	A2	315	A	C1'-C2'-O2'	5.57	127.30	110.60
1	A2	451	A	C5'-C4'-O4'	5.57	115.78	109.10
1	A2	459	G	C5'-C4'-C3'	5.57	124.91	116.00
1	A2	564	G	C1'-C2'-O2'	5.57	127.30	110.60
1	A2	1619	C	C1'-C2'-O2'	5.57	127.30	110.60
2	AZ	6180	C	C3'-C2'-O2'	5.57	129.44	113.30
10	BH	55	LYS	N-CA-C	5.57	126.03	111.00
14	BL	69	LYS	N-CA-C	5.57	126.03	111.00
1	A2	775	G	C4'-C3'-O3'	5.56	124.12	113.00
2	AZ	6198	U	C5'-C4'-O4'	5.56	115.77	109.10
34	Bf	111	GLU	N-CA-C	5.56	126.00	111.00
1	A2	38	C	C5'-C4'-O4'	5.55	115.76	109.10
1	A2	972	G	C1'-C2'-O2'	5.55	127.25	110.60
35	Bg	258	THR	N-CA-C	5.55	125.99	111.00
1	A2	1230	A	C3'-C2'-O2'	5.55	129.39	113.30
1	A2	878	G	C1'-C2'-O2'	5.55	127.24	110.60
1	A2	810	G	C5'-C4'-C3'	5.54	124.87	116.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	82	U	C4'-C3'-O3'	5.54	124.09	113.00
12	BJ	128	LEU	N-CA-C	5.54	125.97	111.00
1	A2	188	A	O4'-C1'-N9	5.54	112.63	108.20
1	A2	1304	G	C5'-C4'-C3'	5.54	124.87	116.00
1	A2	502	U	C5'-C4'-O4'	5.54	115.75	109.10
21	BS	21	ASN	N-CA-C	5.54	125.96	111.00
1	A2	386	G	C5'-C4'-C3'	5.54	124.86	116.00
20	BR	43	SER	N-CA-C	5.53	125.94	111.00
1	A2	1671	A	C4'-C3'-O3'	5.53	124.06	113.00
1	A2	573	C	C5'-C4'-O4'	5.53	115.73	109.10
1	A2	735	C	C5'-C4'-C3'	5.52	124.84	116.00
1	A2	1226	A	C5'-C4'-C3'	5.52	124.83	116.00
1	A2	1714	A	N9-C1'-C2'	5.52	121.18	114.00
1	A2	1204	A	C5'-C4'-O4'	5.52	115.72	109.10
1	A2	1757	G	N9-C1'-C2'	5.52	121.18	114.00
1	A2	1410	A	C3'-C2'-O2'	5.52	129.30	113.30
1	A2	915	A	C5'-C4'-O4'	5.51	115.72	109.10
1	A2	1685	G	O4'-C1'-N9	5.51	112.61	108.20
1	A2	1719	A	C3'-C2'-O2'	5.51	129.29	113.30
3	BA	172	LEU	CA-CB-CG	5.51	127.98	115.30
19	BQ	142	TYR	N-CA-C	5.51	125.89	111.00
20	BR	24	LEU	N-CA-C	5.51	125.89	111.00
2	AZ	6129	C	C4'-C3'-O3'	5.51	124.02	113.00
1	A2	910	C	C5'-C4'-C3'	5.51	124.81	116.00
1	A2	245	U	C5'-C4'-C3'	5.51	124.81	116.00
1	A2	1120	U	C1'-C2'-O2'	5.51	127.12	110.60
1	A2	1221	A	C5'-C4'-C3'	5.51	124.81	116.00
26	BX	33	LEU	N-CA-C	5.50	125.86	111.00
1	A2	491	C	C4'-C3'-O3'	5.50	124.00	113.00
1	A2	744	U	C4'-C3'-O3'	5.50	124.00	113.00
35	Bg	299	GLN	N-CA-C	5.50	125.85	111.00
1	A2	1472	C	C2'-C3'-O3'	5.50	122.50	113.70
1	A2	34	G	C1'-C2'-O2'	5.50	127.09	110.60
1	A2	852	C	C4'-C3'-O3'	5.50	123.99	113.00
1	A2	342	C	C1'-C2'-O2'	5.50	127.09	110.60
1	A2	1137	A	C3'-C2'-O2'	5.49	129.22	113.30
1	A2	1389	C	C5'-C4'-C3'	5.49	124.78	116.00
2	AZ	6139	G	C4'-C3'-O3'	5.49	123.98	113.00
6	BD	167	PHE	N-CA-C	5.49	125.82	111.00
1	A2	1020	A	C4'-C3'-O3'	5.49	123.98	113.00
1	A2	1053	G	C1'-C2'-O2'	5.49	127.06	110.60
1	A2	137	U	C4'-C3'-O3'	5.49	123.97	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	183	U	C1'-C2'-O2'	5.49	127.06	110.60
7	BE	129	VAL	N-CA-C	5.49	125.81	111.00
21	BS	5	VAL	N-CA-C	5.48	125.81	111.00
1	A2	1236	A	C3'-C2'-O2'	5.48	129.20	113.30
1	A2	1286	U	C5'-C4'-O4'	5.48	115.68	109.10
8	BF	49	GLU	N-CA-C	5.48	125.80	111.00
1	A2	603	U	C4'-C3'-O3'	5.48	123.96	113.00
1	A2	881	A	C1'-C2'-O2'	5.48	127.04	110.60
1	A2	34	G	C3'-C2'-O2'	5.48	129.19	113.30
6	BD	32	GLU	N-CA-C	5.48	125.79	111.00
1	A2	787	G	C5'-C4'-C3'	5.48	124.76	116.00
1	A2	1342	C	C3'-C2'-O2'	5.47	129.17	113.30
1	A2	1635	A	C1'-C2'-O2'	5.47	127.02	110.60
1	A2	870	C	C3'-C2'-O2'	5.47	129.17	113.30
1	A2	1678	A	C2'-C3'-O3'	5.47	122.45	113.70
1	A2	632	U	C1'-C2'-O2'	5.47	127.01	110.60
14	BL	5	LEU	CB-CG-CD1	5.47	120.30	111.00
1	A2	824	G	C3'-C2'-O2'	5.47	129.16	113.30
5	BC	243	TYR	CG-CD1-CE1	-5.47	116.93	121.30
1	A2	756	A	C3'-C2'-O2'	5.46	129.15	113.30
26	BX	133	LEU	N-CA-C	5.46	125.76	111.00
27	BY	84	LYS	N-CA-C	5.46	125.75	111.00
1	A2	150	U	C3'-C2'-O2'	5.46	129.14	113.30
1	A2	859	A	C3'-C2'-O2'	5.46	129.13	113.30
1	A2	600	U	C1'-C2'-O2'	5.46	126.97	110.60
3	BA	27	ARG	N-CA-C	5.46	125.74	111.00
4	BB	178	GLY	N-CA-C	-5.46	99.45	113.10
14	BL	20	PHE	N-CA-C	5.46	125.74	111.00
21	BS	60	GLU	N-CA-C	5.46	125.74	111.00
1	A2	347	G	N9-C1'-C2'	5.46	121.09	114.00
1	A2	478	A	C1'-C2'-O2'	5.46	126.97	110.60
22	BT	54	PHE	N-CA-C	5.46	125.73	111.00
1	A2	1509	C	C5'-C4'-C3'	5.46	124.73	116.00
1	A2	1719	A	C1'-C2'-O2'	5.46	126.97	110.60
1	A2	1792	G	C5'-C4'-C3'	5.45	124.72	116.00
35	Bg	252	LEU	CB-CA-C	5.45	120.55	110.20
7	BE	88	ASP	N-CA-C	5.45	125.71	111.00
34	Bf	131	PHE	CE1-CZ-CE2	5.45	129.81	120.00
1	A2	38	C	C4'-C3'-O3'	5.45	123.89	113.00
1	A2	213	A	C1'-C2'-O2'	5.45	126.94	110.60
3	BA	133	ILE	CG1-CB-CG2	5.45	123.38	111.40
1	A2	764	U	C3'-C2'-O2'	5.44	129.08	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AZ	6190	U	N1-C1'-C2'	5.44	121.08	114.00
10	BH	176	LEU	N-CA-C	5.44	125.69	111.00
1	A2	125	U	C3'-C2'-O2'	5.44	129.08	113.30
16	BN	117	LEU	N-CA-C	5.44	125.69	111.00
1	A2	568	G	C5'-C4'-C3'	5.44	124.70	116.00
2	AZ	6106	A	C5'-C4'-O4'	5.44	115.62	109.10
7	BE	95	THR	N-CA-C	5.44	125.68	111.00
20	BR	99	VAL	N-CA-C	5.44	125.68	111.00
1	A2	478	A	O4'-C1'-N9	5.43	112.55	108.20
1	A2	579	A	C5'-C4'-O4'	5.43	115.62	109.10
1	A2	1635	A	C3'-C2'-O2'	5.43	129.05	113.30
21	BS	50	ALA	N-CA-C	5.43	125.67	111.00
1	A2	252	U	O4'-C4'-C3'	5.43	110.44	106.10
1	A2	859	A	C1'-C2'-O2'	5.43	126.89	110.60
1	A2	113	U	O4'-C1'-N1	5.43	112.54	108.20
1	A2	1573	A	C4'-C3'-O3'	5.43	123.86	113.00
6	BD	78	LYS	N-CA-C	5.43	125.66	111.00
22	BT	69	LYS	N-CA-CB	5.43	120.37	110.60
1	A2	894	U	C1'-C2'-O2'	5.43	126.88	110.60
1	A2	1344	A	C4'-C3'-O3'	5.42	123.85	113.00
12	BJ	12	TYR	N-CA-C	5.42	125.65	111.00
29	Ba	84	VAL	N-CA-C	5.42	125.65	111.00
1	A2	1342	C	C1'-C2'-O2'	5.42	126.86	110.60
1	A2	1468	U	C1'-C2'-O2'	5.42	126.86	110.60
1	A2	1603	U	C4'-C3'-O3'	5.42	123.84	113.00
3	BA	157	ASP	N-CA-C	5.42	125.63	111.00
7	BE	21	ASP	N-CA-C	5.42	125.63	111.00
1	A2	1066	C	C3'-C2'-O2'	5.42	129.01	113.30
1	A2	389	G	C1'-C2'-O2'	5.41	126.84	110.60
1	A2	395	U	C5'-C4'-C3'	5.41	124.66	116.00
4	BB	54	LEU	CA-CB-CG	5.41	127.75	115.30
31	Bc	33	LEU	CB-CG-CD2	5.41	120.20	111.00
1	A2	150	U	C1'-C2'-O2'	5.41	126.83	110.60
13	BK	10	LYS	N-CA-C	5.41	125.61	111.00
1	A2	265	A	C1'-C2'-O2'	5.41	126.83	110.60
1	A2	877	G	C5'-C4'-O4'	5.41	115.59	109.10
1	A2	1239	U	C3'-C2'-O2'	5.41	128.98	113.30
1	A2	1396	U	C3'-C2'-O2'	5.41	128.98	113.30
29	Ba	66	LYS	CB-CA-C	5.41	121.21	110.40
1	A2	689	G	C5'-C4'-C3'	5.40	124.65	116.00
1	A2	744	U	C5'-C4'-C3'	5.40	124.65	116.00
1	A2	287	G	C3'-C2'-O2'	5.40	128.97	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	478	A	C3'-C2'-O2'	5.40	128.96	113.30
1	A2	1106	U	C5'-C4'-O4'	5.40	115.58	109.10
10	BH	58	LEU	N-CA-C	5.40	125.58	111.00
1	A2	703	G	C5'-C4'-C3'	5.40	124.64	116.00
1	A2	1247	U	C5'-C4'-C3'	5.40	124.64	116.00
1	A2	1447	C	C4'-C3'-O3'	5.40	123.80	113.00
1	A2	1261	G	C4'-C3'-O3'	5.39	123.79	113.00
1	A2	1677	C	C3'-C2'-O2'	5.39	128.94	113.30
1	A2	142	G	C4'-C3'-O3'	5.39	123.78	113.00
1	A2	1138	A	C1'-C2'-O2'	5.38	126.75	110.60
12	BJ	4	ALA	N-CA-C	5.38	125.54	111.00
1	A2	122	U	C3'-C2'-O2'	5.38	128.91	113.30
1	A2	597	G	C4'-C3'-O3'	5.38	123.76	113.00
23	BU	50	LEU	N-CA-C	5.38	125.53	111.00
17	BO	85	ALA	CB-CA-C	5.38	118.17	110.10
19	BQ	96	TYR	CG-CD1-CE1	-5.38	117.00	121.30
2	AZ	6198	U	C5'-C4'-C3'	5.38	124.61	116.00
22	BT	83	ALA	N-CA-C	5.38	125.52	111.00
1	A2	1516	A	C5'-C4'-C3'	5.38	124.60	116.00
1	A2	273	G	O4'-C1'-N9	5.37	112.50	108.20
1	A2	573	C	C4'-C3'-O3'	5.37	123.75	113.00
1	A2	1433	G	C1'-C2'-O2'	5.37	126.72	110.60
19	BQ	116	LEU	N-CA-C	5.37	125.50	111.00
1	A2	1198	G	C5'-C4'-C3'	5.37	124.59	116.00
9	BG	111	LEU	N-CA-C	5.37	125.49	111.00
1	A2	122	U	C1'-C2'-O2'	5.37	126.70	110.60
1	A2	562	G	C5'-C4'-C3'	5.36	124.58	116.00
1	A2	1420	C	C5'-C4'-C3'	5.36	124.58	116.00
1	A2	181	A	C3'-C2'-O2'	5.36	128.85	113.30
1	A2	1451	C	C4'-C3'-O3'	5.36	123.72	113.00
1	A2	1232	U	C5'-C4'-C3'	5.36	124.58	116.00
1	A2	1371	A	C1'-C2'-O2'	5.36	126.68	110.60
1	A2	1272	U	N1-C1'-C2'	5.36	120.97	114.00
1	A2	593	U	C1'-C2'-O2'	5.36	126.67	110.60
1	A2	761	G	C4'-C3'-O3'	5.36	123.71	113.00
1	A2	1066	C	C1'-C2'-O2'	5.35	126.66	110.60
1	A2	1285	U	C1'-C2'-O2'	5.35	126.66	110.60
1	A2	1467	C	C5'-C4'-C3'	5.35	124.56	116.00
1	A2	1690	G	C3'-C2'-O2'	5.35	128.82	113.30
1	A2	334	G	C4'-C3'-O3'	5.35	123.70	113.00
1	A2	539	G	C5'-C4'-C3'	5.35	124.56	116.00
1	A2	1119	G	C3'-C2'-O2'	5.35	128.81	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	1452	U	O4'-C1'-N1	5.35	112.48	108.20
4	BB	64	ARG	N-CA-C	5.35	125.44	111.00
6	BD	35	SER	N-CA-C	5.35	125.44	111.00
31	Bc	55	VAL	N-CA-C	5.35	125.43	111.00
1	A2	101	U	C1'-C2'-O2'	5.34	126.63	110.60
1	A2	1137	A	C1'-C2'-O2'	5.34	126.64	110.60
16	BN	128	TYR	CG-CD1-CE1	-5.34	117.02	121.30
1	A2	173	A	C3'-C2'-O2'	5.34	128.79	113.30
1	A2	221	A	C2'-C3'-O3'	5.34	122.25	113.70
6	BD	9	ARG	N-CA-C	5.34	125.42	111.00
20	BR	76	GLU	N-CA-C	5.34	125.42	111.00
1	A2	424	C	C4'-C3'-O3'	5.34	123.67	113.00
1	A2	1406	A	C3'-C2'-O2'	5.34	128.78	113.30
7	BE	156	VAL	N-CA-C	5.34	125.41	111.00
31	Bc	60	GLU	N-CA-C	5.34	125.41	111.00
2	AZ	6107	U	O4'-C1'-N1	5.33	112.47	108.20
1	A2	1642	G	C5'-C4'-O4'	5.33	115.50	109.10
1	A2	852	C	C5'-C4'-O4'	5.33	115.50	109.10
1	A2	1325	A	C4'-C3'-O3'	5.33	123.66	113.00
2	AZ	6039	G	C5'-C4'-O4'	5.33	115.49	109.10
2	AZ	6133	G	C3'-C2'-O2'	5.33	128.75	113.30
1	A2	1013	A	C1'-C2'-O2'	5.33	126.58	110.60
1	A2	471	A	C1'-C2'-O2'	5.33	126.58	110.60
2	AZ	6164	U	O4'-C1'-N1	5.33	112.46	108.20
35	Bg	9	LEU	N-CA-C	5.33	125.38	111.00
1	A2	1061	A	O4'-C1'-N9	5.32	112.46	108.20
1	A2	1105	C	C5'-C4'-O4'	5.32	115.48	109.10
1	A2	1258	U	C1'-C2'-O2'	5.32	126.56	110.60
21	BS	47	CYS	N-CA-C	5.32	125.36	111.00
35	Bg	72	THR	N-CA-C	5.32	125.36	111.00
1	A2	1002	G	C4'-C3'-O3'	5.32	123.63	113.00
1	A2	870	C	C1'-C2'-O2'	5.31	126.53	110.60
1	A2	1119	G	C1'-C2'-O2'	5.31	126.53	110.60
10	BH	173	TYR	CG-CD2-CE2	-5.31	117.05	121.30
2	AZ	6106	A	O4'-C1'-C2'	5.31	112.38	107.60
12	BJ	114	TYR	N-CA-C	5.31	125.33	111.00
1	A2	287	G	C1'-C2'-O2'	5.30	126.52	110.60
8	BF	94	THR	CA-CB-CG2	5.30	119.83	112.40
1	A2	894	U	C3'-C2'-O2'	5.30	128.68	113.30
1	A2	1749	A	C5'-C4'-C3'	5.30	124.48	116.00
16	BN	139	TRP	N-CA-C	5.30	125.32	111.00
22	BT	39	THR	N-CA-C	5.30	125.32	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	102	U	C5'-C4'-O4'	5.30	115.46	109.10
1	A2	977	A	C3'-C2'-O2'	5.30	128.68	113.30
5	BC	164	SER	N-CA-C	5.30	125.31	111.00
1	A2	1032	G	C1'-C2'-O2'	5.30	126.50	110.60
1	A2	1343	U	C1'-C2'-O2'	5.30	126.50	110.60
2	AZ	6083	C	C3'-C2'-O2'	5.29	128.66	113.30
1	A2	578	U	C5'-C4'-O4'	5.29	115.45	109.10
2	AZ	6146	A	C4'-C3'-O3'	5.29	123.58	113.00
4	BB	215	VAL	N-CA-C	5.29	125.29	111.00
1	A2	1041	G	C2'-C3'-O3'	5.29	122.16	113.70
1	A2	621	A	C4'-C3'-O3'	5.29	123.58	113.00
1	A2	1198	G	C5'-C4'-O4'	5.29	115.45	109.10
1	A2	435	C	C4'-C3'-O3'	5.29	123.57	113.00
1	A2	1186	U	C4'-C3'-O3'	5.29	123.58	113.00
3	BA	85	ALA	N-CA-C	5.29	125.28	111.00
21	BS	58	ALA	N-CA-C	5.28	125.27	111.00
2	AZ	6188	G	C5'-C4'-C3'	5.28	124.45	116.00
1	A2	596	C	C4'-C3'-O3'	5.28	123.56	113.00
1	A2	523	G	C1'-C2'-O2'	5.28	126.44	110.60
1	A2	465	G	C3'-C2'-O2'	5.28	128.60	113.30
12	BJ	77	ILE	N-CA-C	5.28	125.24	111.00
1	A2	110	U	C1'-C2'-O2'	5.27	126.42	110.60
1	A2	1718	G	C2'-C3'-O3'	5.27	122.14	113.70
5	BC	113	LEU	CB-CG-CD2	5.27	119.96	111.00
27	BY	48	TYR	CG-CD1-CE1	-5.27	117.08	121.30
1	A2	465	G	C1'-C2'-O2'	5.27	126.41	110.60
1	A2	1535	U	O4'-C1'-N1	5.27	112.42	108.20
1	A2	1438	G	C4'-C3'-O3'	5.27	123.53	113.00
7	BE	182	TYR	CG-CD2-CE2	-5.27	117.09	121.30
2	AZ	6059	G	C1'-C2'-O2'	5.26	126.40	110.60
20	BR	61	ILE	N-CA-C	5.26	125.21	111.00
25	BW	49	GLU	N-CA-C	5.26	125.21	111.00
35	Bg	302	PHE	CE1-CZ-CE2	5.26	129.48	120.00
1	A2	1028	C	O4'-C1'-N1	5.26	112.41	108.20
1	A2	1710	U	C4'-C3'-O3'	5.26	123.52	113.00
32	Bd	32	ARG	CB-CA-C	5.26	120.92	110.40
1	A2	391	A	C1'-C2'-O2'	5.26	126.37	110.60
23	BU	101	LYS	N-CA-C	5.26	125.20	111.00
1	A2	1515	A	C5'-C4'-O4'	5.26	115.41	109.10
4	BB	101	HIS	N-CA-C	5.26	125.19	111.00
4	BB	195	LYS	N-CA-C	5.26	125.19	111.00
1	A2	386	G	O4'-C4'-C3'	5.25	110.30	106.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	769	A	C5'-C4'-C3'	5.25	124.40	116.00
34	Bf	136	LYS	N-CA-C	5.25	125.19	111.00
1	A2	750	U	C1'-C2'-O2'	5.25	126.36	110.60
3	BA	102	PHE	N-CA-C	5.25	125.17	111.00
19	BQ	64	ASP	N-CA-C	5.24	125.16	111.00
29	Ba	72	HIS	N-CA-C	5.24	125.16	111.00
3	BA	65	ALA	N-CA-C	5.24	125.15	111.00
10	BH	26	GLU	N-CA-C	5.24	125.15	111.00
32	Bd	43	PHE	N-CA-C	5.24	125.15	111.00
2	AZ	6221	U	C5'-C4'-C3'	5.24	124.38	116.00
1	A2	1002	G	C5'-C4'-C3'	5.24	124.38	116.00
2	AZ	6203	U	C3'-C2'-O2'	5.24	128.49	113.30
1	A2	1320	U	C5'-C4'-C3'	5.23	124.38	116.00
1	A2	1441	C	O4'-C1'-N1	5.23	112.39	108.20
3	BA	75	ALA	CB-CA-C	5.23	117.95	110.10
1	A2	470	A	C3'-C2'-O2'	5.23	128.48	113.30
1	A2	511	A	C5'-C4'-C3'	5.23	124.37	116.00
1	A2	1397	U	C4'-C3'-O3'	5.23	123.46	113.00
24	BV	81	ASN	N-CA-C	5.23	125.12	111.00
9	BG	14	LYS	CB-CA-C	5.23	120.86	110.40
1	A2	781	U	O4'-C1'-N1	5.23	112.38	108.20
1	A2	1401	A	C1'-C2'-O2'	5.22	126.27	110.60
10	BH	66	SER	N-CA-C	5.22	125.11	111.00
2	AZ	6168	C	O4'-C1'-N1	5.22	112.38	108.20
1	A2	1131	A	O4'-C4'-C3'	5.22	110.28	106.10
1	A2	1442	U	C5'-C4'-C3'	5.22	124.35	116.00
1	A2	1514	U	O4'-C1'-N1	5.22	112.38	108.20
2	AZ	6211	U	C1'-C2'-O2'	5.22	126.26	110.60
7	BE	104	ASP	N-CA-C	5.22	125.09	111.00
1	A2	1506	G	C5'-C4'-O4'	5.22	115.36	109.10
1	A2	1578	U	C3'-C2'-O2'	5.22	128.43	113.30
20	BR	38	ILE	CG1-CB-CG2	5.22	122.88	111.40
1	A2	430	G	C5'-C4'-C3'	5.21	124.34	116.00
5	BC	186	LYS	N-CA-C	5.21	125.07	111.00
1	A2	488	G	C5'-C4'-C3'	5.21	124.33	116.00
1	A2	581	U	C4'-C3'-O3'	5.21	123.42	113.00
1	A2	529	A	C4'-C3'-O3'	5.21	123.41	113.00
1	A2	477	A	C3'-C2'-O2'	5.20	128.39	113.30
2	AZ	6034	A	C1'-C2'-O2'	5.20	126.21	110.60
1	A2	84	A	C1'-C2'-O2'	5.20	126.21	110.60
1	A2	1204	A	O4'-C4'-C3'	5.20	110.26	106.10
1	A2	1343	U	N1-C1'-C2'	5.20	120.76	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	658	C	C1'-C2'-O2'	5.20	126.18	110.60
1	A2	1205	C	O4'-C1'-N1	5.20	112.36	108.20
1	A2	1360	A	C3'-C2'-O2'	5.20	128.37	113.30
1	A2	1416	G	C1'-C2'-O2'	5.20	126.18	110.60
27	BY	23	PHE	CE1-CZ-CE2	5.20	129.35	120.00
1	A2	65	A	C3'-C2'-O2'	5.19	128.36	113.30
1	A2	624	G	C3'-C2'-O2'	5.19	128.36	113.30
15	BM	108	ARG	N-CA-C	5.19	125.02	111.00
1	A2	543	C	O4'-C1'-N1	5.19	112.35	108.20
1	A2	612	U	O4'-C1'-N1	5.19	112.35	108.20
1	A2	1219	A	C3'-C2'-O2'	5.19	128.35	113.30
2	AZ	6196	G	C5'-C4'-C3'	5.19	124.30	116.00
24	BV	3	ASN	N-CA-C	5.19	125.01	111.00
11	BI	31	ARG	N-CA-C	5.18	125.00	111.00
1	A2	258	C	C5'-C4'-C3'	5.18	124.29	116.00
1	A2	1388	A	OP2-P-O3'	5.18	116.60	105.20
1	A2	600	U	C3'-C2'-O2'	5.18	128.32	113.30
1	A2	1152	A	C3'-C2'-O2'	5.17	128.31	113.30
1	A2	1175	U	C4'-C3'-O3'	5.17	123.35	113.00
30	Bb	41	LEU	CB-CA-C	5.17	120.03	110.20
1	A2	816	G	C5'-C4'-C3'	5.17	124.28	116.00
1	A2	166	C	O4'-C1'-N1	5.17	112.34	108.20
2	AZ	6175	A	C1'-C2'-O2'	5.17	126.12	110.60
14	BL	115	PHE	CE1-CZ-CE2	5.17	129.31	120.00
8	BF	82	PHE	CE1-CZ-CE2	5.17	129.31	120.00
3	BA	202	TYR	N-CA-C	5.17	124.95	111.00
11	BI	86	SER	N-CA-C	5.17	124.95	111.00
1	A2	1420	C	C4'-C3'-O3'	5.17	123.33	113.00
10	BH	14	THR	N-CA-C	5.17	124.95	111.00
23	BU	70	THR	OG1-CB-CG2	5.17	121.88	110.00
1	A2	410	A	C1'-C2'-O2'	5.16	126.09	110.60
1	A2	1736	G	C4'-C3'-O3'	5.16	123.33	113.00
30	Bb	42	ASN	N-CA-C	5.16	124.94	111.00
1	A2	1647	U	C5'-C4'-C3'	5.16	124.26	116.00
1	A2	1724	U	C1'-C2'-O2'	5.16	126.08	110.60
28	BZ	61	SER	N-CA-CB	5.16	118.24	110.50
1	A2	949	C	C5'-C4'-C3'	5.16	124.25	116.00
25	BW	89	TRP	CE3-CZ3-CH2	5.16	126.87	121.20
14	BL	34	TRP	N-CA-C	5.16	124.92	111.00
1	A2	545	A	C3'-C2'-O2'	5.15	128.25	113.30
27	BY	135	ASP	N-CA-C	5.15	124.91	111.00
1	A2	990	C	C5'-C4'-C3'	5.15	124.24	116.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	BH	147	ASN	N-CA-C	5.15	124.91	111.00
1	A2	578	U	C5'-C4'-C3'	5.15	124.24	116.00
1	A2	602	U	C4'-C3'-O3'	5.15	123.30	113.00
11	BI	90	LEU	CB-CA-C	5.15	119.98	110.20
1	A2	183	U	C3'-C2'-O2'	5.15	128.22	113.30
1	A2	1371	A	C3'-C2'-O2'	5.15	128.22	113.30
1	A2	1597	A	C3'-C2'-O2'	5.15	128.22	113.30
2	AZ	6083	C	C1'-C2'-O2'	5.15	126.04	110.60
1	A2	1367	G	C1'-C2'-O2'	5.14	126.04	110.60
2	AZ	6122	C	C1'-C2'-O2'	5.14	126.03	110.60
18	BP	102	PHE	N-CA-C	5.14	124.89	111.00
11	BI	20	GLN	N-CA-C	5.14	124.89	111.00
1	A2	124	A	C3'-C2'-O2'	5.14	128.21	113.30
17	BO	86	THR	N-CA-C	5.14	124.88	111.00
1	A2	794	U	C4'-C3'-O3'	5.14	123.28	113.00
1	A2	972	G	C3'-C2'-O2'	5.14	128.21	113.30
10	BH	151	LYS	N-CA-C	5.14	124.88	111.00
3	BA	38	PHE	CE1-CZ-CE2	5.14	129.25	120.00
1	A2	263	C	O4'-C1'-N1	5.14	112.31	108.20
1	A2	1239	U	C1'-C2'-O2'	5.14	126.01	110.60
1	A2	881	A	C3'-C2'-O2'	5.13	128.19	113.30
1	A2	1690	G	C1'-C2'-O2'	5.13	125.99	110.60
1	A2	131	C	C1'-C2'-O2'	5.13	125.99	110.60
1	A2	1213	G	C1'-C2'-O2'	5.13	125.98	110.60
15	BM	25	GLU	N-CA-C	5.12	124.84	111.00
34	Bf	117	LEU	CA-CB-CG	5.12	127.08	115.30
3	BA	184	LEU	CB-CG-CD1	5.12	119.71	111.00
10	BH	72	LYS	N-CA-C	5.12	124.83	111.00
30	Bb	3	LEU	N-CA-C	5.12	124.83	111.00
1	A2	862	A	C5'-C4'-C3'	5.12	124.19	116.00
33	Be	47	VAL	N-CA-C	5.12	124.82	111.00
1	A2	456	A	C4'-C3'-O3'	5.11	123.23	113.00
1	A2	1771	U	C5'-C4'-C3'	5.11	124.18	116.00
12	BJ	39	LYS	CB-CA-C	5.11	120.63	110.40
27	BY	41	ARG	N-CA-C	5.11	124.80	111.00
30	Bb	8	LEU	N-CA-C	5.11	124.80	111.00
33	Be	61	SER	N-CA-C	5.11	124.80	111.00
25	BW	79	PHE	CE1-CZ-CE2	5.11	129.20	120.00
1	A2	1216	C	C2'-C3'-O3'	5.11	121.87	113.70
16	BN	45	LEU	N-CA-C	5.10	124.78	111.00
1	A2	805	U	C3'-C2'-O2'	5.10	128.09	113.30
12	BJ	150	LEU	N-CA-C	5.10	124.78	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	BO	38	THR	CA-CB-CG2	5.10	119.54	112.40
1	A2	375	U	C5'-C4'-C3'	5.10	124.16	116.00
1	A2	1498	G	C5'-C4'-O4'	5.10	115.22	109.10
7	BE	39	ARG	N-CA-C	5.10	124.77	111.00
1	A2	1578	U	O4'-C1'-N1	5.10	112.28	108.20
1	A2	1004	U	C2'-C3'-O3'	5.09	121.85	113.70
8	BF	96	SER	N-CA-C	5.09	124.75	111.00
1	A2	1067	C	C5'-C4'-C3'	5.09	124.14	116.00
1	A2	1235	C	O4'-C1'-N1	5.09	112.27	108.20
1	A2	1724	U	C3'-C2'-O2'	5.09	128.06	113.30
1	A2	505	A	O4'-C1'-N9	5.09	112.27	108.20
2	AZ	6094	U	C5'-C4'-C3'	5.09	124.14	116.00
12	BJ	48	GLN	N-CA-C	5.09	124.74	111.00
1	A2	750	U	C3'-C2'-O2'	5.09	128.06	113.30
2	AZ	6109	U	O4'-C1'-N1	5.09	112.27	108.20
1	A2	690	G	C3'-C2'-O2'	5.09	128.05	113.30
1	A2	969	C	C1'-C2'-O2'	5.09	125.86	110.60
11	BI	150	ALA	N-CA-CB	5.09	117.22	110.10
1	A2	1677	C	O4'-C1'-N1	5.08	112.27	108.20
1	A2	1406	A	C1'-C2'-O2'	5.08	125.85	110.60
1	A2	944	A	C1'-C2'-O2'	5.08	125.84	110.60
6	BD	21	LEU	CB-CG-CD2	5.08	119.64	111.00
10	BH	67	LEU	N-CA-C	5.08	124.72	111.00
1	A2	805	U	C1'-C2'-O2'	5.08	125.84	110.60
27	BY	86	GLU	N-CA-C	5.08	124.71	111.00
27	BY	92	VAL	CA-CB-CG2	5.08	118.52	110.90
1	A2	1422	A	C4'-C3'-O3'	5.08	123.15	113.00
1	A2	930	A	O4'-C1'-N9	5.07	112.26	108.20
1	A2	494	U	C3'-C2'-O2'	5.07	128.00	113.30
1	A2	636	A	O4'-C1'-N9	5.07	112.26	108.20
7	BE	108	ARG	N-CA-C	5.07	124.68	111.00
1	A2	610	G	O4'-C1'-N9	5.07	112.25	108.20
2	AZ	6174	G	C5'-C4'-C3'	5.07	124.11	116.00
19	BQ	17	THR	CA-CB-CG2	5.07	119.49	112.40
35	Bg	273	ASP	N-CA-C	5.06	124.67	111.00
1	A2	1378	U	C3'-C2'-O2'	5.06	127.98	113.30
12	BJ	71	PHE	N-CA-C	5.06	124.67	111.00
23	BU	93	LEU	CB-CA-C	5.06	119.82	110.20
26	BX	66	SER	N-CA-C	5.06	124.67	111.00
1	A2	944	A	C3'-C2'-O2'	5.06	127.97	113.30
1	A2	1105	C	C5'-C4'-C3'	5.06	124.09	116.00
35	Bg	32	LEU	N-CA-C	5.06	124.65	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AZ	6055	U	C5'-C4'-C3'	5.05	124.09	116.00
35	Bg	91	LEU	CA-CB-CG	5.05	126.92	115.30
23	BU	20	ILE	N-CA-C	5.05	124.64	111.00
35	Bg	181	TRP	CE3-CZ3-CH2	5.05	126.76	121.20
1	A2	846	G	C3'-C2'-O2'	5.05	127.95	113.30
8	BF	66	GLN	CB-CA-C	5.05	120.50	110.40
14	BL	135	VAL	N-CA-C	5.05	124.64	111.00
15	BM	123	VAL	N-CA-C	5.05	124.64	111.00
7	BE	141	THR	CA-CB-CG2	5.05	119.47	112.40
8	BF	196	GLU	N-CA-C	5.05	124.63	111.00
23	BU	36	ASN	N-CA-C	5.05	124.63	111.00
1	A2	252	U	C5'-C4'-O4'	5.05	115.16	109.10
7	BE	87	MET	N-CA-C	5.05	124.63	111.00
8	BF	119	ASP	CB-CA-C	5.05	120.49	110.40
1	A2	684	A	C2'-C3'-O3'	5.04	121.77	113.70
1	A2	714	G	C1'-C2'-O2'	5.04	125.74	110.60
13	BK	71	GLU	N-CA-C	5.04	124.62	111.00
16	BN	130	ARG	N-CA-C	5.04	124.62	111.00
1	A2	1287	A	C4'-C3'-O3'	5.04	123.08	113.00
35	Bg	188	ILE	CB-CA-C	5.04	121.68	111.60
1	A2	1373	C	C1'-C2'-O2'	5.04	125.71	110.60
1	A2	1475	A	O4'-C1'-N9	5.04	112.23	108.20
1	A2	1548	G	C3'-C2'-O2'	5.04	127.91	113.30
26	BX	75	GLN	N-CA-C	5.04	124.61	111.00
1	A2	388	G	OP1-P-O3'	5.04	116.28	105.20
1	A2	1372	U	C4'-C3'-O3'	5.04	123.08	113.00
1	A2	47	A	OP1-P-O3'	-5.04	94.12	105.20
1	A2	132	U	C3'-C2'-O2'	5.04	127.90	113.30
1	A2	1052	U	C1'-C2'-O2'	5.04	125.71	110.60
1	A2	1777	G	C5'-C4'-C3'	5.04	124.06	116.00
4	BB	126	THR	CA-CB-CG2	5.04	119.45	112.40
1	A2	759	U	C4'-C3'-O3'	5.03	123.07	113.00
1	A2	470	A	C1'-C2'-O2'	5.03	125.69	110.60
1	A2	847	A	N9-C1'-C2'	5.03	120.54	114.00
1	A2	1171	A	C4'-C3'-O3'	5.03	123.06	113.00
5	BC	150	GLN	N-CA-C	5.03	124.58	111.00
1	A2	91	G	C4'-C3'-O3'	5.03	123.06	113.00
1	A2	824	G	C1'-C2'-O2'	5.03	125.69	110.60
1	A2	1574	G	C1'-C2'-O2'	5.03	125.69	110.60
1	A2	1344	A	C5'-C4'-C3'	5.03	124.05	116.00
11	BI	57	ALA	N-CA-C	5.03	124.57	111.00
1	A2	330	G	O4'-C1'-N9	5.03	112.22	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	1500	C	C1'-C2'-O2'	5.03	125.68	110.60
15	BM	52	LEU	N-CA-C	5.02	124.57	111.00
1	A2	878	G	C3'-C2'-O2'	5.02	127.86	113.30
1	A2	1542	G	C3'-C2'-O2'	5.02	127.85	113.30
6	BD	200	LYS	N-CA-C	5.02	124.55	111.00
1	A2	1687	U	O4'-C1'-N1	5.02	112.22	108.20
17	BO	85	ALA	N-CA-CB	5.02	117.13	110.10
1	A2	1286	U	C5'-C4'-C3'	5.01	124.02	116.00
1	A2	1369	U	O4'-C1'-N1	5.01	112.21	108.20
1	A2	1424	A	C5'-C4'-C3'	5.01	124.02	116.00
12	BJ	157	ASP	CB-CA-C	5.01	120.43	110.40
1	A2	990	C	C5'-C4'-O4'	5.01	115.12	109.10
7	BE	205	PHE	N-CA-C	5.01	124.53	111.00
1	A2	221	A	C3'-C2'-O2'	5.01	127.83	113.30
1	A2	767	U	O4'-C1'-C2'	5.01	112.11	107.60
1	A2	166	C	C3'-C2'-O2'	5.01	127.83	113.30
1	A2	399	A	OP2-P-O3'	-5.01	94.18	105.20
1	A2	566	C	C3'-C2'-O2'	5.01	127.83	113.30
1	A2	764	U	C1'-C2'-O2'	5.01	125.63	110.60
1	A2	1013	A	C3'-C2'-O2'	5.01	127.83	113.30
1	A2	1125	A	O4'-C4'-C3'	5.01	110.11	106.10
1	A2	265	A	O4'-C1'-N9	5.00	112.20	108.20
1	A2	1300	A	C3'-C2'-O2'	5.00	127.81	113.30

All (284) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A2	7	G	C3'
1	A2	41	A	C3'
1	A2	67	A	C3'
1	A2	102	U	C3'
1	A2	124	A	C2'
1	A2	131	C	C3'
1	A2	146	U	C3'
1	A2	158	U	C3'
1	A2	173	A	C2'
1	A2	213	A	C2'
1	A2	220	A	C2'
1	A2	222	A	C2'
1	A2	231	U	C2'
1	A2	286	C	C3'
1	A2	295	A	C3'

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Mol	Chain	Res	Type	Atom
1	A2	376	C	C3'
1	A2	389	G	C2'
1	A2	391	A	C2'
1	A2	423	G	C3'
1	A2	427	C	C3'
1	A2	430	G	C3'
1	A2	454	U	C3'
1	A2	473	A	C4'
1	A2	478	A	C2'
1	A2	481	A	C3'
1	A2	499	U	C2'
1	A2	501	U	C2'
1	A2	504	U	C3'
1	A2	514	G	C3'
1	A2	523	G	C2'
1	A2	525	A	C4'
1	A2	578	U	C3'
1	A2	607	G	C3'
1	A2	740	A	C3'
1	A2	764	U	C2'
1	A2	794	U	C3'
1	A2	803	A	C3'
1	A2	820	U	C3'
1	A2	842	C	C2'
1	A2	894	U	C2'
1	A2	918	U	C3'
1	A2	921	U	C3'
1	A2	930	A	C3'
1	A2	939	A	C3'
1	A2	977	A	C2'
1	A2	990	C	C3'
1	A2	1012	U	C3'
1	A2	1032	G	C2'
1	A2	1053	G	C2'
1	A2	1066	C	C2'
1	A2	1097	U	C4'
1	A2	1106	U	C3'
1	A2	1131	A	C4'
1	A2	1152	A	C2'
1	A2	1170	G	C3'
1	A2	1171	A	C3'
1	A2	1216	C	C3'

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Mol	Chain	Res	Type	Atom
1	A2	1219	A	C2'
1	A2	1240	U	C3'
1	A2	1242	A	C2'
1	A2	1259	U	C3'
1	A2	1268	G	C2'
1	A2	1286	U	C2'
1	A2	1289	U	C3'
1	A2	1293	U	C3'
1	A2	1295	G	C3'
1	A2	1297	G	C2'
1	A2	1298	U	C3'
1	A2	1317	C	C3'
1	A2	1343	U	C2'
1	A2	1344	A	C3'
1	A2	1371	A	C2'
1	A2	1396	U	C2'
1	A2	1401	A	C2'
1	A2	1415	U	C3'
1	A2	1418	G	C3'
1	A2	1442	U	C3'
1	A2	1447	C	C3'
1	A2	1449	U	C4'
1	A2	1471	A	C3'
1	A2	1500	C	C2'
1	A2	1501	C	C2'
1	A2	1514	U	C2'
1	A2	1568	C	C3'
1	A2	1570	A	C3'
1	A2	1573	A	C3'
1	A2	1582	U	C3'
1	A2	1608	U	C3'
1	A2	1611	A	C2'
1	A2	1629	G	C3'
1	A2	1635	A	C2'
1	A2	1638	G	C4'
1	A2	1678	A	C3'
1	A2	1719	A	C2'
1	A2	1720	G	C3'
1	A2	1748	G	C2'
1	A2	1752	U	C3'
1	A2	1777	G	C3'
2	AZ	6025	A	C2'

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Mol	Chain	Res	Type	Atom
2	AZ	6034	A	C2'
2	AZ	6079	A	C2'
2	AZ	6091	G	C3'
2	AZ	6115	U	C2'
2	AZ	6124	G	C4'
2	AZ	6175	A	C2'
2	AZ	6195	G	C3'
3	BA	50	VAL	CA
3	BA	102	PHE	CA
3	BA	111	ILE	CB
3	BA	112	THR	CA
3	BA	129	ASP	CA
3	BA	150	ASP	CA
3	BA	173	ILE	CB
3	BA	204	TYR	CA
4	BB	21	VAL	CA
4	BB	26	ARG	CA
4	BB	91	VAL	CA
4	BB	98	THR	CA
4	BB	101	HIS	CA
4	BB	108	ASP	CA
4	BB	123	ALA	CA
4	BB	153	HIS	CA
4	BB	211	HIS	CA
4	BB	215	VAL	CA
4	BB	224	ASP	CA
5	BC	77	GLN	CA
5	BC	86	VAL	CA
5	BC	126	ARG	CA
5	BC	131	ILE	CA
5	BC	150	GLN	CA
5	BC	174	ARG	CA
5	BC	186	LYS	CA
5	BC	220	ASN	CA
6	BD	9	ARG	CA
6	BD	31	GLU	CA
6	BD	51	ARG	CA
6	BD	78	LYS	CA
6	BD	123	VAL	CA
6	BD	175	VAL	CA
7	BE	21	ASP	CA
7	BE	39	ARG	CA

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Mol	Chain	Res	Type	Atom
7	BE	95	THR	CA
7	BE	104	ASP	CA
7	BE	108	ARG	CA
7	BE	147	ILE	CA
7	BE	156	VAL	CA
7	BE	194	THR	CA
8	BF	23	VAL	CA
8	BF	66	GLN	CA
8	BF	115	LYS	CA
8	BF	119	ASP	CA
8	BF	162	VAL	CA
8	BF	165	LEU	CA
9	BG	14	LYS	CA
9	BG	25	ARG	CA
9	BG	67	VAL	CA
9	BG	81	VAL	CA
9	BG	120	GLU	CA
9	BG	133	LEU	CA
9	BG	142	ARG	CA
9	BG	149	LYS	CA
9	BG	198	ALA	CA
9	BG	206	ALA	CA
10	BH	14	THR	CA
10	BH	39	ARG	CA
10	BH	59	ALA	CA
10	BH	72	LYS	CA
10	BH	147	ASN	CA
10	BH	151	LYS	CA
10	BH	152	VAL	CA
11	BI	13	ALA	CA
11	BI	17	LYS	CA
11	BI	18	ARG	CA
11	BI	74	LYS	CA
11	BI	90	LEU	CA
11	BI	92	ARG	CA
11	BI	94	ASN	CA
11	BI	120	THR	CA
11	BI	150	ALA	CA
11	BI	154	SER	CA
11	BI	162	ALA	CA
11	BI	197	THR	CA
12	BJ	48	GLN	CA

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Mol	Chain	Res	Type	Atom
12	BJ	71	PHE	CA
12	BJ	77	ILE	CA
12	BJ	102	GLU	CA
12	BJ	157	ASP	CA
13	BK	59	PHE	CA
13	BK	71	GLU	CA
14	BL	27	THR	CA
14	BL	29	LYS	CA
14	BL	31	THR	CA
14	BL	63	LEU	CA
14	BL	78	THR	CB
14	BL	107	VAL	CA
14	BL	138	ASN	CA
14	BL	145	ALA	CA
15	BM	50	LYS	CA
15	BM	141	SER	CA
16	BN	45	LEU	CA
16	BN	76	LYS	CA
16	BN	112	LYS	CA
16	BN	117	LEU	CA
16	BN	121	ARG	CA
16	BN	139	TRP	CA
17	BO	17	ALA	CA
17	BO	61	MET	CA
17	BO	85	ALA	CA
17	BO	86	THR	CA
18	BP	20	VAL	CA
18	BP	36	LEU	CA
18	BP	80	MET	CA
18	BP	122	THR	CA
19	BQ	64	ASP	CA
19	BQ	89	LEU	CA
19	BQ	94	GLN	CA
19	BQ	116	LEU	CA
19	BQ	123	ARG	CA
19	BQ	136	SER	CA
19	BQ	141	SER	CA
19	BQ	142	TYR	CA
20	BR	18	GLU	CA
20	BR	24	LEU	CA
20	BR	42	GLN	CA
20	BR	54	THR	CA

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Mol	Chain	Res	Type	Atom
20	BR	99	VAL	CA
21	BS	5	VAL	CA
21	BS	21	ASN	CA
21	BS	43	SER	CA
21	BS	47	CYS	CA
21	BS	77	THR	CA
21	BS	97	ASP	CA
22	BT	7	ARG	CA
22	BT	54	PHE	CA
22	BT	65	ILE	CA
22	BT	66	TYR	CA
22	BT	69	LYS	CA
22	BT	101	ASN	CA
23	BU	41	ILE	CA
24	BV	58	TYR	CA
24	BV	81	ASN	CA
25	BW	65	LEU	CA
25	BW	83	ILE	CA
25	BW	126	LEU	CA
26	BX	22	ASN	CA
26	BX	33	LEU	CA
26	BX	61	SER	CA
26	BX	75	GLN	CA
26	BX	90	ALA	CA
27	BY	11	LYS	CA
27	BY	41	ARG	CA
27	BY	47	VAL	CA
27	BY	62	THR	CB
27	BY	84	LYS	CA
27	BY	129	VAL	CA
28	BZ	82	HIS	CA
29	Ba	11	ASN	CA
29	Ba	45	VAL	CA
29	Ba	66	LYS	CA
29	Ba	84	VAL	CA
30	Bb	8	LEU	CA
30	Bb	12	ALA	CA
30	Bb	19	HIS	CA
30	Bb	41	LEU	CA
30	Bb	57	GLU	CA
31	Bc	51	ASN	CA
31	Bc	55	VAL	CA

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Mol	Chain	Res	Type	Atom
32	Bd	43	PHE	CA
32	Bd	47	ALA	CA
32	Bd	55	PHE	CA
33	Be	31	LYS	CA
33	Be	36	LYS	CA
33	Be	43	ARG	CA
34	Bf	111	GLU	CA
34	Bf	151	ASN	CA
35	Bg	5	GLU	CA
35	Bg	10	ARG	CA
35	Bg	131	ILE	CA
35	Bg	153	GLN	CA
35	Bg	182	ASN	CA
35	Bg	188	ILE	CA
35	Bg	211	ILE	CB
35	Bg	273	ASP	CA
35	Bg	299	GLN	CA

All (31) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	BA	138	TYR	Peptide
3	BA	35	PRO	Peptide
3	BA	62	ARG	Peptide
4	BB	177	GLN	Peptide
4	BB	178	GLY	Peptide
5	BC	220	ASN	Peptide
6	BD	178	ARG	Peptide
8	BF	65	ALA	Peptide
9	BG	129	VAL	Peptide
9	BG	162	VAL	Peptide
9	BG	43	ASP	Peptide
10	BH	14	THR	Peptide
10	BH	161	GLN	Peptide
11	BI	16	ALA	Peptide
11	BI	31	ARG	Peptide
12	BJ	156	ILE	Peptide
17	BO	124	ASP	Peptide
19	BQ	112	TYR	Peptide
19	BQ	8	GLN	Peptide
21	BS	12	GLN	Peptide
21	BS	35	ILE	Peptide

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Mol	Chain	Res	Type	Group
21	BS	52	VAL	Peptide
21	BS	97	ASP	Peptide
23	BU	56	VAL	Peptide
24	BV	61	SER	Peptide
26	BX	63	GLN	Peptide
26	BX	93	LEU	Peptide
29	Ba	9	GLY	Peptide
32	Bd	47	ALA	Peptide
34	Bf	97	ALA	Peptide
35	Bg	266	ASP	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	BA	129/206 (63%)	60 (46%)	39 (30%)	30 (23%)	0	0
4	BB	118/213 (55%)	88 (75%)	17 (14%)	13 (11%)	0	6
5	BC	136/216 (63%)	84 (62%)	31 (23%)	21 (15%)	0	3
6	BD	116/222 (52%)	83 (72%)	17 (15%)	16 (14%)	0	3
7	BE	143/260 (55%)	100 (70%)	26 (18%)	17 (12%)	0	5
8	BF	116/206 (56%)	81 (70%)	20 (17%)	15 (13%)	0	4
9	BG	141/226 (62%)	88 (62%)	32 (23%)	21 (15%)	0	3
10	BH	100/184 (54%)	61 (61%)	22 (22%)	17 (17%)	0	2
11	BI	87/187 (46%)	51 (59%)	22 (25%)	14 (16%)	0	3
12	BJ	101/179 (56%)	58 (57%)	27 (27%)	16 (16%)	0	3
13	BK	48/93 (52%)	29 (60%)	9 (19%)	10 (21%)	0	1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	BL	85/142 (60%)	53 (62%)	25 (29%)	7 (8%)	1	11
15	BM	63/120 (52%)	36 (57%)	20 (32%)	7 (11%)	0	5
16	BN	97/150 (65%)	62 (64%)	22 (23%)	13 (13%)	0	4
17	BO	84/127 (66%)	58 (69%)	16 (19%)	10 (12%)	0	5
18	BP	60/115 (52%)	40 (67%)	14 (23%)	6 (10%)	0	8
19	BQ	85/140 (61%)	56 (66%)	19 (22%)	10 (12%)	0	5
20	BR	59/121 (49%)	45 (76%)	9 (15%)	5 (8%)	1	10
21	BS	89/140 (64%)	61 (68%)	13 (15%)	15 (17%)	0	2
22	BT	72/142 (51%)	47 (65%)	14 (19%)	11 (15%)	0	3
23	BU	57/104 (55%)	38 (67%)	12 (21%)	7 (12%)	0	4
24	BV	53/87 (61%)	38 (72%)	10 (19%)	5 (9%)	0	9
25	BW	58/129 (45%)	41 (71%)	11 (19%)	6 (10%)	0	7
26	BX	70/142 (49%)	49 (70%)	12 (17%)	9 (13%)	0	4
27	BY	77/134 (58%)	55 (71%)	15 (20%)	7 (9%)	1	9
28	BZ	37/64 (58%)	22 (60%)	9 (24%)	6 (16%)	0	3
29	Ba	51/97 (53%)	29 (57%)	12 (24%)	10 (20%)	0	1
30	Bb	38/81 (47%)	24 (63%)	11 (29%)	3 (8%)	1	12
31	Bc	38/63 (60%)	29 (76%)	7 (18%)	2 (5%)	2	21
32	Bd	25/52 (48%)	15 (60%)	8 (32%)	2 (8%)	1	12
33	Be	33/55 (60%)	16 (48%)	12 (36%)	5 (15%)	0	3
34	Bf	45/64 (70%)	18 (40%)	14 (31%)	13 (29%)	0	0
35	Bg	170/315 (54%)	115 (68%)	38 (22%)	17 (10%)	0	8
All	All	2681/4776 (56%)	1730 (64%)	585 (22%)	366 (14%)	1	3

All (366) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	BA	27	ARG
3	BA	43	ASP
3	BA	50	VAL
3	BA	121	VAL
3	BA	122	ILE
3	BA	129	ASP
3	BA	140	ASN

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Mol	Chain	Res	Type
3	BA	150	ASP
3	BA	175	TYR
3	BA	194	PRO
3	BA	195	TRP
4	BB	30	PHE
4	BB	91	VAL
4	BB	92	GLN
4	BB	158	SER
4	BB	225	VAL
5	BC	37	PRO
5	BC	91	ARG
5	BC	109	GLY
5	BC	126	ARG
5	BC	150	GLN
5	BC	174	ARG
5	BC	179	VAL
5	BC	196	VAL
5	BC	220	ASN
5	BC	236	PRO
6	BD	123	VAL
6	BD	163	PRO
6	BD	178	ARG
6	BD	179	GLN
6	BD	211	PRO
6	BD	217	ILE
6	BD	220	PRO
7	BE	22	LYS
7	BE	76	VAL
7	BE	120	SER
7	BE	177	ALA
7	BE	205	PHE
8	BF	62	VAL
8	BF	67	PRO
8	BF	144	GLU
8	BF	206	SER
9	BG	8	PRO
9	BG	80	ASN
9	BG	88	ARG
9	BG	102	VAL
9	BG	133	LEU
9	BG	135	PRO
9	BG	177	ARG

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Mol	Chain	Res	Type
9	BG	189	HIS
10	BH	12	ALA
10	BH	58	LEU
10	BH	64	VAL
10	BH	114	ARG
10	BH	131	PHE
10	BH	152	VAL
11	BI	10	LYS
11	BI	32	GLN
11	BI	61	GLU
11	BI	86	SER
11	BI	186	GLY
11	BI	197	THR
12	BJ	18	PRO
12	BJ	37	LYS
12	BJ	91	LYS
12	BJ	118	LEU
12	BJ	150	LEU
13	BK	68	LEU
13	BK	81	ASN
13	BK	83	PRO
14	BL	30	ARG
14	BL	53	TYR
14	BL	55	ASP
14	BL	135	VAL
15	BM	106	ILE
16	BN	3	ARG
16	BN	22	ALA
16	BN	43	LYS
16	BN	71	ILE
16	BN	131	THR
17	BO	114	ARG
17	BO	125	SER
18	BP	39	ALA
19	BQ	45	ALA
19	BQ	113	ASP
20	BR	88	VAL
20	BR	99	VAL
21	BS	29	VAL
21	BS	40	ARG
21	BS	60	GLU
21	BS	76	PRO

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Mol	Chain	Res	Type
21	BS	80	LYS
21	BS	139	LYS
22	BT	69	LYS
22	BT	83	ALA
23	BU	95	ALA
23	BU	96	PRO
24	BV	58	TYR
24	BV	64	GLU
25	BW	8	ALA
25	BW	28	ARG
25	BW	33	VAL
26	BX	3	LYS
26	BX	27	ASN
26	BX	98	GLU
28	BZ	75	LEU
29	Ba	11	ASN
29	Ba	34	LYS
29	Ba	44	ILE
29	Ba	63	ALA
29	Ba	65	PRO
29	Ba	66	LYS
30	Bb	63	LEU
32	Bd	34	TYR
33	Be	13	LYS
33	Be	48	THR
34	Bf	94	ALA
34	Bf	101	ALA
34	Bf	121	CYS
34	Bf	130	VAL
34	Bf	137	ASP
34	Bf	145	HIS
34	Bf	147	VAL
34	Bf	151	ASN
35	Bg	5	GLU
35	Bg	84	SER
35	Bg	165	ASP
35	Bg	186	PHE
35	Bg	195	HIS
35	Bg	197	SER
35	Bg	267	PRO
35	Bg	283	LYS
3	BA	62	ARG

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Mol	Chain	Res	Type
3	BA	63	ILE
3	BA	94	GLY
3	BA	113	ARG
3	BA	157	ASP
3	BA	169	SER
3	BA	185	ARG
5	BC	68	ILE
5	BC	76	LEU
5	BC	146	THR
5	BC	147	ASN
5	BC	175	GLY
5	BC	234	PRO
6	BD	9	ARG
6	BD	26	THR
6	BD	44	THR
6	BD	130	GLY
6	BD	167	PHE
7	BE	21	ASP
7	BE	32	SER
7	BE	53	LYS
7	BE	102	VAL
7	BE	248	ILE
8	BF	30	PRO
8	BF	60	ASP
8	BF	98	MET
8	BF	104	ASN
8	BF	196	GLU
9	BG	71	THR
9	BG	158	ILE
9	BG	167	LYS
9	BG	178	LEU
9	BG	183	ARG
9	BG	185	GLN
9	BG	215	ARG
10	BH	126	LEU
11	BI	41	LYS
11	BI	106	ALA
11	BI	115	ALA
12	BJ	59	LEU
12	BJ	128	LEU
12	BJ	171	ARG
13	BK	3	MET

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Mol	Chain	Res	Type
13	BK	42	VAL
13	BK	43	ILE
13	BK	64	TYR
15	BM	69	ALA
15	BM	131	ASP
16	BN	12	SER
16	BN	32	SER
16	BN	44	GLY
16	BN	59	GLY
16	BN	93	LYS
17	BO	40	ALA
17	BO	48	VAL
17	BO	124	ASP
19	BQ	99	GLU
19	BQ	109	PHE
19	BQ	111	SER
21	BS	28	ILE
21	BS	37	GLY
21	BS	78	HIS
21	BS	101	LEU
22	BT	26	GLY
22	BT	125	SER
22	BT	128	GLY
24	BV	3	ASN
24	BV	28	ASP
25	BW	19	LYS
25	BW	107	SER
26	BX	24	TRP
26	BX	67	ALA
27	BY	53	ASP
31	Bc	42	ARG
33	Be	11	ALA
35	Bg	6	VAL
3	BA	139	VAL
3	BA	142	PRO
3	BA	148	ASP
4	BB	51	SER
4	BB	201	THR
5	BC	217	ALA
5	BC	231	ALA
6	BD	218	LEU
7	BE	43	PRO

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Mol	Chain	Res	Type
7	BE	170	THR
7	BE	223	ASN
7	BE	245	LYS
8	BF	84	LYS
9	BG	21	GLU
9	BG	35	GLU
9	BG	188	ARG
10	BH	44	LYS
10	BH	115	SER
10	BH	169	PHE
11	BI	67	TRP
12	BJ	110	GLN
12	BJ	165	GLY
13	BK	40	LEU
13	BK	67	THR
15	BM	31	VAL
15	BM	46	ARG
15	BM	108	ARG
16	BN	137	PRO
17	BO	52	ARG
18	BP	29	SER
18	BP	32	ASP
19	BQ	40	GLU
19	BQ	112	TYR
21	BS	91	ASP
21	BS	140	THR
22	BT	31	PRO
23	BU	55	PRO
24	BV	77	GLY
27	BY	33	ALA
28	BZ	55	PRO
28	BZ	95	HIS
29	Ba	7	SER
29	Ba	33	ASP
29	Ba	93	LYS
30	Bb	10	PRO
35	Bg	298	GLY
3	BA	134	LYS
4	BB	55	LYS
5	BC	235	LEU
6	BD	174	HIS
7	BE	164	LEU

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Mol	Chain	Res	Type
8	BF	65	ALA
8	BF	126	ASP
8	BF	165	LEU
10	BH	134	GLU
10	BH	158	ASP
10	BH	174	ASN
11	BI	24	LYS
12	BJ	85	VAL
14	BL	132	SER
14	BL	134	THR
16	BN	123	HIS
17	BO	17	ALA
17	BO	74	VAL
18	BP	80	MET
19	BQ	15	SER
20	BR	10	LYS
20	BR	96	SER
20	BR	116	LYS
23	BU	92	ASP
26	BX	94	ASN
27	BY	54	ALA
28	BZ	61	SER
28	BZ	87	GLY
28	BZ	88	ILE
34	Bf	111	GLU
34	Bf	122	SER
35	Bg	82	SER
35	Bg	83	ALA
35	Bg	158	PRO
35	Bg	163	ASP
35	Bg	317	THR
3	BA	10	THR
3	BA	35	PRO
3	BA	68	PRO
3	BA	78	SER
3	BA	162	CYS
3	BA	172	LEU
4	BB	35	PRO
4	BB	54	LEU
4	BB	82	ARG
5	BC	36	VAL
5	BC	163	GLY

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Mol	Chain	Res	Type
6	BD	219	ALA
7	BE	178	GLY
8	BF	36	ALA
9	BG	155	ASP
10	BH	127	GLU
11	BI	156	VAL
12	BJ	119	ALA
13	BK	28	ASN
15	BM	109	GLU
16	BN	40	TYR
17	BO	20	TYR
17	BO	96	PRO
18	BP	125	PRO
19	BQ	34	SER
19	BQ	39	VAL
21	BS	97	ASP
22	BT	46	PRO
22	BT	65	ILE
26	BX	95	PHE
27	BY	105	ARG
30	Bb	16	ALA
31	Bc	36	THR
4	BB	22	ASP
8	BF	42	LEU
12	BJ	4	ALA
12	BJ	65	LYS
14	BL	81	HIS
21	BS	82	PRO
22	BT	81	GLY
22	BT	91	TYR
27	BY	67	GLY
27	BY	78	SER
29	Ba	69	ASN
32	Bd	49	ASP
33	Be	60	PRO
34	Bf	102	VAL
34	Bf	146	SER
3	BA	98	ILE
7	BE	195	ILE
9	BG	130	PRO
11	BI	107	THR
21	BS	92	ILE

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Mol	Chain	Res	Type
23	BU	91	ILE
23	BU	117	VAL
35	Bg	30	PRO
3	BA	111	ILE
6	BD	210	GLU
12	BJ	101	VAL
18	BP	52	LYS
23	BU	59	PRO
25	BW	29	PRO
27	BY	30	PRO
33	Be	27	PRO
10	BH	73	VAL
26	BX	42	PRO
10	BH	54	GLY
10	BH	130	VAL
11	BI	85	PRO
12	BJ	73	GLY
22	BT	112	GLY
34	Bf	129	GLY
35	Bg	167	VAL
4	BB	48	VAL
9	BG	173	PRO
26	BX	64	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
3	BA	164/173 (95%)	117 (71%)	47 (29%)	0 2
4	BB	187/187 (100%)	142 (76%)	45 (24%)	0 5
5	BC	175/175 (100%)	156 (89%)	19 (11%)	6 29
6	BD	182/182 (100%)	148 (81%)	34 (19%)	1 10
7	BE	221/221 (100%)	178 (80%)	43 (20%)	1 9
8	BF	172/172 (100%)	131 (76%)	41 (24%)	0 5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	BG	185/191 (97%)	138 (75%)	47 (25%)	0	4
10	BH	165/165 (100%)	138 (84%)	27 (16%)	2	15
11	BI	149/149 (100%)	105 (70%)	44 (30%)	0	2
12	BJ	154/154 (100%)	126 (82%)	28 (18%)	1	11
13	BK	80/84 (95%)	62 (78%)	18 (22%)	1	6
14	BL	127/127 (100%)	100 (79%)	27 (21%)	1	7
15	BM	88/97 (91%)	67 (76%)	21 (24%)	0	5
16	BN	127/127 (100%)	104 (82%)	23 (18%)	1	11
17	BO	84/96 (88%)	62 (74%)	22 (26%)	0	4
18	BP	97/97 (100%)	81 (84%)	16 (16%)	2	14
19	BQ	114/114 (100%)	80 (70%)	34 (30%)	0	2
20	BR	94/109 (86%)	71 (76%)	23 (24%)	0	5
21	BS	125/125 (100%)	96 (77%)	29 (23%)	1	6
22	BT	114/114 (100%)	94 (82%)	20 (18%)	2	12
23	BU	97/97 (100%)	77 (79%)	20 (21%)	1	7
24	BV	74/74 (100%)	62 (84%)	12 (16%)	2	15
25	BW	110/110 (100%)	97 (88%)	13 (12%)	5	26
26	BX	116/116 (100%)	101 (87%)	15 (13%)	4	22
27	BY	112/112 (100%)	94 (84%)	18 (16%)	2	15
28	BZ	57/57 (100%)	42 (74%)	15 (26%)	0	3
29	Ba	83/83 (100%)	65 (78%)	18 (22%)	1	7
30	Bb	70/70 (100%)	56 (80%)	14 (20%)	1	8
31	Bc	56/56 (100%)	44 (79%)	12 (21%)	1	7
32	Bd	46/46 (100%)	33 (72%)	13 (28%)	0	2
33	Be	48/48 (100%)	38 (79%)	10 (21%)	1	7
34	Bf	43/43 (100%)	31 (72%)	12 (28%)	0	2
35	Bg	257/259 (99%)	208 (81%)	49 (19%)	1	9
All	All	3973/4030 (99%)	3144 (79%)	829 (21%)	3	7

All (829) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	BA	6	THR

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Mol	Chain	Res	Type
3	BA	8	ASP
3	BA	12	GLU
3	BA	23	HIS
3	BA	24	LEU
3	BA	27	ARG
3	BA	28	ASN
3	BA	29	VAL
3	BA	32	HIS
3	BA	37	VAL
3	BA	38	PHE
3	BA	41	ARG
3	BA	43	ASP
3	BA	45	VAL
3	BA	57	LEU
3	BA	71	GLU
3	BA	74	VAL
3	BA	84	ARG
3	BA	88	LYS
3	BA	93	THR
3	BA	96	THR
3	BA	98	ILE
3	BA	101	ARG
3	BA	102	PHE
3	BA	106	SER
3	BA	110	TYR
3	BA	111	ILE
3	BA	119	ARG
3	BA	120	LEU
3	BA	121	VAL
3	BA	129	ASP
3	BA	133	ILE
3	BA	137	SER
3	BA	139	VAL
3	BA	146	LEU
3	BA	150	ASP
3	BA	154	GLU
3	BA	158	VAL
3	BA	164	ASN
3	BA	170	ILE
3	BA	172	LEU
3	BA	175	TYR
3	BA	184	LEU

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Mol	Chain	Res	Type
3	BA	185	ARG
3	BA	188	LEU
3	BA	197	ILE
3	BA	203	PHE
4	BB	21	VAL
4	BB	25	THR
4	BB	26	ARG
4	BB	27	LYS
4	BB	39	GLU
4	BB	52	THR
4	BB	69	CYS
4	BB	70	LEU
4	BB	74	GLN
4	BB	77	GLU
4	BB	78	ASP
4	BB	82	ARG
4	BB	92	GLN
4	BB	96	LEU
4	BB	106	THR
4	BB	107	THR
4	BB	108	ASP
4	BB	109	LYS
4	BB	115	ARG
4	BB	117	TRP
4	BB	118	GLN
4	BB	126	THR
4	BB	128	LYS
4	BB	129	THR
4	BB	131	ASP
4	BB	148	ASN
4	BB	153	HIS
4	BB	166	LYS
4	BB	167	VAL
4	BB	171	ILE
4	BB	180	THR
4	BB	181	LEU
4	BB	195	LYS
4	BB	196	GLU
4	BB	202	LYS
4	BB	212	VAL
4	BB	213	ARG
4	BB	214	LYS

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Mol	Chain	Res	Type
4	BB	215	VAL
4	BB	219	LYS
4	BB	220	GLN
4	BB	222	LYS
4	BB	223	PHE
4	BB	224	ASP
4	BB	228	LEU
5	BC	38	VAL
5	BC	41	LEU
5	BC	53	ILE
5	BC	60	SER
5	BC	64	LYS
5	BC	68	ILE
5	BC	86	VAL
5	BC	104	VAL
5	BC	117	THR
5	BC	131	ILE
5	BC	140	ARG
5	BC	141	ARG
5	BC	148	LEU
5	BC	159	THR
5	BC	164	SER
5	BC	195	ASP
5	BC	207	LEU
5	BC	240	LEU
5	BC	241	ASP
6	BD	5	ILE
6	BD	18	TYR
6	BD	20	GLU
6	BD	21	LEU
6	BD	35	SER
6	BD	37	VAL
6	BD	51	ARG
6	BD	53	THR
6	BD	59	LEU
6	BD	65	ARG
6	BD	72	LEU
6	BD	76	ARG
6	BD	84	ILE
6	BD	86	LEU
6	BD	94	ARG
6	BD	96	LEU

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Mol	Chain	Res	Type
6	BD	103	GLU
6	BD	107	PHE
6	BD	111	ASN
6	BD	113	LEU
6	BD	120	TYR
6	BD	123	VAL
6	BD	128	GLU
6	BD	142	LEU
6	BD	156	PHE
6	BD	164	VAL
6	BD	170	THR
6	BD	174	HIS
6	BD	178	ARG
6	BD	196	ARG
6	BD	200	LYS
6	BD	202	LEU
6	BD	206	VAL
6	BD	223	LYS
7	BE	7	LYS
7	BE	8	HIS
7	BE	9	LEU
7	BE	17	HIS
7	BE	18	TRP
7	BE	19	LEU
7	BE	21	ASP
7	BE	30	ARG
7	BE	51	ARG
7	BE	52	LEU
7	BE	69	HIS
7	BE	88	ASP
7	BE	97	GLU
7	BE	100	ARG
7	BE	104	ASP
7	BE	109	PHE
7	BE	123	LEU
7	BE	133	LYS
7	BE	141	THR
7	BE	145	ARG
7	BE	151	ASP
7	BE	155	LYS
7	BE	156	VAL
7	BE	163	ASP

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Mol	Chain	Res	Type
7	BE	176	ASP
7	BE	184	THR
7	BE	187	ARG
7	BE	189	LEU
7	BE	197	HIS
7	BE	202	ASP
7	BE	208	VAL
7	BE	210	ILE
7	BE	211	LYS
7	BE	217	THR
7	BE	220	THR
7	BE	223	ASN
7	BE	224	ASN
7	BE	228	ILE
7	BE	230	GLU
7	BE	242	LYS
7	BE	252	ARG
7	BE	258	GLN
7	BE	261	LEU
8	BF	23	VAL
8	BF	35	GLN
8	BF	37	GLN
8	BF	38	THR
8	BF	41	LYS
8	BF	42	LEU
8	BF	43	PHE
8	BF	51	VAL
8	BF	54	LYS
8	BF	57	SER
8	BF	62	VAL
8	BF	63	GLN
8	BF	66	GLN
8	BF	70	VAL
8	BF	73	THR
8	BF	76	ARG
8	BF	84	LYS
8	BF	86	GLN
8	BF	89	ILE
8	BF	94	THR
8	BF	106	LYS
8	BF	107	LYS
8	BF	108	LEU

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Mol	Chain	Res	Type
8	BF	112	ARG
8	BF	115	LYS
8	BF	118	LEU
8	BF	119	ASP
8	BF	126	ASP
8	BF	143	ARG
8	BF	145	ASP
8	BF	147	THR
8	BF	149	VAL
8	BF	161	ASP
8	BF	165	LEU
8	BF	166	ARG
8	BF	190	ILE
8	BF	211	ILE
8	BF	212	LYS
8	BF	213	LYS
8	BF	219	ARG
8	BF	224	ASN
9	BG	13	GLN
9	BG	14	LYS
9	BG	15	THR
9	BG	18	ILE
9	BG	21	GLU
9	BG	22	HIS
9	BG	23	ARG
9	BG	24	ILE
9	BG	25	ARG
9	BG	29	ASP
9	BG	37	ASP
9	BG	45	PHE
9	BG	48	TYR
9	BG	53	SER
9	BG	56	ASN
9	BG	57	ASP
9	BG	68	LEU
9	BG	71	THR
9	BG	75	LEU
9	BG	76	LEU
9	BG	80	ASN
9	BG	81	VAL
9	BG	98	ARG
9	BG	102	VAL

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Mol	Chain	Res	Type
9	BG	115	LYS
9	BG	124	LEU
9	BG	133	LEU
9	BG	142	ARG
9	BG	143	LYS
9	BG	148	SER
9	BG	154	ARG
9	BG	155	ASP
9	BG	159	ARG
9	BG	168	THR
9	BG	174	LYS
9	BG	183	ARG
9	BG	185	GLN
9	BG	188	ARG
9	BG	193	LEU
9	BG	196	ARG
9	BG	203	GLU
9	BG	210	GLN
9	BG	211	LEU
9	BG	212	LEU
9	BG	216	LEU
9	BG	218	GLU
9	BG	223	LYS
10	BH	7	LYS
10	BH	22	GLN
10	BH	38	LEU
10	BH	39	ARG
10	BH	51	VAL
10	BH	56	LYS
10	BH	60	ILE
10	BH	66	SER
10	BH	67	LEU
10	BH	71	HIS
10	BH	72	LYS
10	BH	75	THR
10	BH	78	THR
10	BH	91	ILE
10	BH	93	LEU
10	BH	95	GLU
10	BH	111	LYS
10	BH	129	LEU
10	BH	131	PHE

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Mol	Chain	Res	Type
10	BH	136	VAL
10	BH	147	ASN
10	BH	154	LEU
10	BH	158	ASP
10	BH	162	ILE
10	BH	175	LYS
10	BH	176	LEU
10	BH	180	GLN
11	BI	3	ILE
11	BI	6	ASP
11	BI	17	LYS
11	BI	20	GLN
11	BI	21	PHE
11	BI	27	PHE
11	BI	28	GLU
11	BI	29	LEU
11	BI	35	ASN
11	BI	37	LYS
11	BI	38	ILE
11	BI	42	ARG
11	BI	47	ARG
11	BI	56	ARG
11	BI	58	LEU
11	BI	64	ASN
11	BI	70	GLU
11	BI	73	SER
11	BI	77	ARG
11	BI	92	ARG
11	BI	95	THR
11	BI	96	LEU
11	BI	98	LYS
11	BI	107	THR
11	BI	111	GLN
11	BI	112	TRP
11	BI	119	GLN
11	BI	120	THR
11	BI	143	TRP
11	BI	146	ARG
11	BI	155	SER
11	BI	158	SER
11	BI	161	SER
11	BI	164	ARG

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Mol	Chain	Res	Type
11	BI	165	LEU
11	BI	166	TYR
11	BI	168	CYS
11	BI	171	SER
11	BI	178	ARG
11	BI	182	TYR
11	BI	184	LEU
11	BI	194	ARG
11	BI	195	ARG
11	BI	197	THR
12	BJ	6	ARG
12	BJ	10	LYS
12	BJ	28	LEU
12	BJ	46	SER
12	BJ	53	ARG
12	BJ	54	ARG
12	BJ	60	LEU
12	BJ	62	ARG
12	BJ	69	ARG
12	BJ	77	ILE
12	BJ	78	ARG
12	BJ	83	VAL
12	BJ	90	LYS
12	BJ	91	LYS
12	BJ	96	VAL
12	BJ	100	LYS
12	BJ	102	GLU
12	BJ	106	GLU
12	BJ	116	LEU
12	BJ	118	LEU
12	BJ	134	ILE
12	BJ	138	LYS
12	BJ	139	GLN
12	BJ	149	ARG
12	BJ	151	ASP
12	BJ	161	THR
12	BJ	172	VAL
12	BJ	179	ARG
13	BK	5	LYS
13	BK	10	LYS
13	BK	14	TYR
13	BK	22	VAL

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Mol	Chain	Res	Type
13	BK	24	LYS
13	BK	27	PHE
13	BK	35	ILE
13	BK	37	THR
13	BK	52	LYS
13	BK	55	VAL
13	BK	68	LEU
13	BK	71	GLU
13	BK	74	GLU
13	BK	75	TYR
13	BK	80	LEU
13	BK	81	ASN
13	BK	86	ILE
13	BK	87	VAL
14	BL	5	LEU
14	BL	7	VAL
14	BL	10	GLU
14	BL	27	THR
14	BL	28	SER
14	BL	30	ARG
14	BL	31	THR
14	BL	34	TRP
14	BL	36	LYS
14	BL	40	LEU
14	BL	50	GLU
14	BL	55	ASP
14	BL	63	LEU
14	BL	67	ARG
14	BL	69	LYS
14	BL	71	LEU
14	BL	74	THR
14	BL	78	THR
14	BL	87	ARG
14	BL	98	ASN
14	BL	102	LYS
14	BL	107	VAL
14	BL	121	ASP
14	BL	134	THR
14	BL	135	VAL
14	BL	136	ARG
14	BL	140	VAL
15	BM	29	LYS

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Mol	Chain	Res	Type
15	BM	43	ARG
15	BM	46	ARG
15	BM	52	LEU
15	BM	58	LEU
15	BM	59	LEU
15	BM	62	LEU
15	BM	64	SER
15	BM	67	THR
15	BM	71	ILE
15	BM	73	LYS
15	BM	74	LEU
15	BM	81	ASP
15	BM	86	VAL
15	BM	88	LEU
15	BM	97	LEU
15	BM	99	GLU
15	BM	100	TRP
15	BM	103	LEU
15	BM	125	ASN
15	BM	131	ASP
16	BN	3	ARG
16	BN	4	MET
16	BN	11	ILE
16	BN	27	LYS
16	BN	29	SER
16	BN	39	LYS
16	BN	42	ARG
16	BN	46	THR
16	BN	50	ILE
16	BN	56	ASP
16	BN	64	ARG
16	BN	66	ILE
16	BN	76	LYS
16	BN	77	SER
16	BN	92	ILE
16	BN	97	SER
16	BN	105	ASN
16	BN	109	LYS
16	BN	118	ILE
16	BN	125	LEU
16	BN	131	THR
16	BN	140	LYS

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Mol	Chain	Res	Type
16	BN	150	VAL
17	BO	12	GLN
17	BO	19	ILE
17	BO	25	ASP
17	BO	38	THR
17	BO	39	ILE
17	BO	43	THR
17	BO	51	ASP
17	BO	53	ASP
17	BO	56	SER
17	BO	77	THR
17	BO	81	VAL
17	BO	83	ILE
17	BO	86	THR
17	BO	92	LYS
17	BO	102	LEU
17	BO	105	LEU
17	BO	107	ARG
17	BO	114	ARG
17	BO	115	ILE
17	BO	117	ASP
17	BO	133	ARG
17	BO	136	ARG
18	BP	23	GLU
18	BP	24	LYS
18	BP	34	VAL
18	BP	45	PHE
18	BP	49	MET
18	BP	52	LYS
18	BP	60	LEU
18	BP	78	THR
18	BP	82	ASN
18	BP	86	VAL
18	BP	90	ILE
18	BP	97	TYR
18	BP	102	PHE
18	BP	112	LEU
18	BP	116	LEU
18	BP	121	ILE
19	BQ	4	VAL
19	BQ	12	LYS
19	BQ	13	LYS

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Mol	Chain	Res	Type
19	BQ	14	LYS
19	BQ	17	THR
19	BQ	28	LEU
19	BQ	30	LYS
19	BQ	32	ASN
19	BQ	37	THR
19	BQ	39	VAL
19	BQ	40	GLU
19	BQ	42	GLU
19	BQ	43	ILE
19	BQ	54	LEU
19	BQ	55	VAL
19	BQ	59	LYS
19	BQ	62	ASN
19	BQ	63	ILE
19	BQ	65	ILE
19	BQ	68	ARG
19	BQ	69	VAL
19	BQ	70	THR
19	BQ	74	HIS
19	BQ	77	GLN
19	BQ	87	LYS
19	BQ	92	TYR
19	BQ	94	GLN
19	BQ	95	LYS
19	BQ	107	LYS
19	BQ	112	TYR
19	BQ	118	ILE
19	BQ	123	ARG
19	BQ	137	ARG
19	BQ	141	SER
20	BR	5	ARG
20	BR	7	LYS
20	BR	23	LYS
20	BR	26	LEU
20	BR	28	PHE
20	BR	38	ILE
20	BR	43	SER
20	BR	49	LYS
20	BR	60	ARG
20	BR	66	VAL
20	BR	69	ILE

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Mol	Chain	Res	Type
20	BR	70	SER
20	BR	71	PHE
20	BR	72	LYS
20	BR	73	LEU
20	BR	75	GLU
20	BR	83	GLN
20	BR	87	GLU
20	BR	101	ASN
20	BR	106	THR
20	BR	113	LEU
20	BR	115	LEU
20	BR	119	LEU
21	BS	3	LEU
21	BS	5	VAL
21	BS	12	GLN
21	BS	14	ILE
21	BS	17	LEU
21	BS	19	ASN
21	BS	25	ASN
21	BS	40	ARG
21	BS	41	ARG
21	BS	52	VAL
21	BS	62	THR
21	BS	66	LEU
21	BS	71	GLN
21	BS	74	GLN
21	BS	81	ILE
21	BS	85	PHE
21	BS	91	ASP
21	BS	92	ILE
21	BS	98	TYR
21	BS	100	THR
21	BS	101	LEU
21	BS	103	ASN
21	BS	105	VAL
21	BS	109	LEU
21	BS	110	ARG
21	BS	125	ILE
21	BS	129	TRP
21	BS	132	ARG
21	BS	141	THR
22	BT	15	ILE

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Mol	Chain	Res	Type
22	BT	23	GLN
22	BT	25	GLN
22	BT	34	VAL
22	BT	40	SER
22	BT	41	SER
22	BT	45	MET
22	BT	51	GLU
22	BT	54	PHE
22	BT	57	ARG
22	BT	63	ARG
22	BT	69	LYS
22	BT	85	SER
22	BT	101	ASN
22	BT	104	VAL
22	BT	114	VAL
22	BT	126	GLU
22	BT	127	ASN
22	BT	130	ARG
22	BT	135	ILE
23	BU	21	LYS
23	BU	27	THR
23	BU	29	THR
23	BU	30	LYS
23	BU	36	ASN
23	BU	46	GLU
23	BU	50	LEU
23	BU	52	LYS
23	BU	63	LEU
23	BU	64	LYS
23	BU	66	SER
23	BU	70	THR
23	BU	85	ARG
23	BU	89	ARG
23	BU	91	ILE
23	BU	93	LEU
23	BU	98	GLN
23	BU	103	ILE
23	BU	113	ASP
23	BU	115	GLU
24	BV	1	MET
24	BV	3	ASN
24	BV	20	THR

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Mol	Chain	Res	Type
24	BV	21	ASN
24	BV	27	ASP
24	BV	50	TYR
24	BV	59	VAL
24	BV	64	GLU
24	BV	67	ASP
24	BV	75	ASN
24	BV	79	LEU
24	BV	81	ASN
25	BW	12	ASN
25	BW	24	GLN
25	BW	36	LYS
25	BW	39	GLN
25	BW	65	LEU
25	BW	87	GLU
25	BW	93	LEU
25	BW	98	GLN
25	BW	103	ILE
25	BW	112	ASP
25	BW	117	ARG
25	BW	126	LEU
25	BW	130	TYR
26	BX	3	LYS
26	BX	7	ARG
26	BX	13	ARG
26	BX	19	ARG
26	BX	27	ASN
26	BX	46	SER
26	BX	56	LYS
26	BX	57	LEU
26	BX	93	LEU
26	BX	107	PHE
26	BX	112	LYS
26	BX	114	LYS
26	BX	132	LEU
26	BX	133	LEU
26	BX	141	GLU
27	BY	7	ILE
27	BY	9	THR
27	BY	11	LYS
27	BY	26	ASP
27	BY	34	ASN

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Mol	Chain	Res	Type
27	BY	40	LEU
27	BY	42	GLU
27	BY	55	VAL
27	BY	62	THR
27	BY	84	LYS
27	BY	88	THR
27	BY	99	LYS
27	BY	102	LYS
27	BY	119	PHE
27	BY	121	THR
27	BY	129	VAL
27	BY	132	ARG
27	BY	135	ASP
28	BZ	42	LEU
28	BZ	44	GLN
28	BZ	49	ARG
28	BZ	57	TYR
28	BZ	58	ARG
28	BZ	69	LEU
28	BZ	70	LYS
28	BZ	80	LEU
28	BZ	82	HIS
28	BZ	83	LEU
28	BZ	89	ILE
28	BZ	90	LYS
28	BZ	95	HIS
28	BZ	97	LYS
28	BZ	100	ILE
29	Ba	5	ARG
29	Ba	12	LYS
29	Ba	18	VAL
29	Ba	25	ASN
29	Ba	26	CYS
29	Ba	34	LYS
29	Ba	37	LYS
29	Ba	41	ILE
29	Ba	44	ILE
29	Ba	52	ASP
29	Ba	67	THR
29	Ba	69	ASN
29	Ba	71	LEU
29	Ba	72	HIS

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Mol	Chain	Res	Type
29	Ba	76	SER
29	Ba	82	ARG
29	Ba	84	VAL
29	Ba	85	ARG
30	Bb	3	LEU
30	Bb	4	VAL
30	Bb	14	SER
30	Bb	20	LYS
30	Bb	29	ARG
30	Bb	31	TYR
30	Bb	33	LEU
30	Bb	34	ASP
30	Bb	41	LEU
30	Bb	43	ILE
30	Bb	52	THR
30	Bb	77	THR
30	Bb	79	PHE
30	Bb	81	ARG
31	Bc	13	ILE
31	Bc	14	LYS
31	Bc	21	SER
31	Bc	29	ARG
31	Bc	33	LEU
31	Bc	35	ASP
31	Bc	36	THR
31	Bc	38	ARG
31	Bc	42	ARG
31	Bc	43	ASN
31	Bc	56	LEU
31	Bc	65	ARG
32	Bd	7	TRP
32	Bd	10	HIS
32	Bd	24	CYS
32	Bd	27	HIS
32	Bd	28	THR
32	Bd	30	LEU
32	Bd	38	ILE
32	Bd	40	ARG
32	Bd	48	ASN
32	Bd	50	ILE
32	Bd	54	LYS
32	Bd	55	PHE

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Mol	Chain	Res	Type
32	Bd	56	ARG
33	Be	20	LYS
33	Be	22	GLU
33	Be	23	LYS
33	Be	26	LYS
33	Be	28	LYS
33	Be	31	LYS
33	Be	40	TYR
33	Be	43	ARG
33	Be	44	PHE
33	Be	54	ARG
34	Bf	98	LYS
34	Bf	102	VAL
34	Bf	103	LEU
34	Bf	108	VAL
34	Bf	113	LYS
34	Bf	117	LEU
34	Bf	125	THR
34	Bf	132	LEU
34	Bf	138	ARG
34	Bf	140	TYR
34	Bf	146	SER
34	Bf	151	ASN
35	Bg	4	ASN
35	Bg	7	LEU
35	Bg	9	LEU
35	Bg	10	ARG
35	Bg	14	GLU
35	Bg	19	TRP
35	Bg	23	LEU
35	Bg	29	GLN
35	Bg	34	LEU
35	Bg	37	SER
35	Bg	43	ILE
35	Bg	52	GLN
35	Bg	53	LYS
35	Bg	58	VAL
35	Bg	59	ARG
35	Bg	64	HIS
35	Bg	66	HIS
35	Bg	74	THR
35	Bg	81	LEU

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Mol	Chain	Res	Type
35	Bg	89	LEU
35	Bg	98	GLU
35	Bg	100	TYR
35	Bg	114	ASP
35	Bg	117	LYS
35	Bg	123	ILE
35	Bg	131	ILE
35	Bg	136	ILE
35	Bg	137	LYS
35	Bg	152	SER
35	Bg	167	VAL
35	Bg	170	ILE
35	Bg	182	ASN
35	Bg	192	PHE
35	Bg	196	ASN
35	Bg	210	LEU
35	Bg	216	LYS
35	Bg	229	LYS
35	Bg	237	GLN
35	Bg	243	LEU
35	Bg	250	TYR
35	Bg	258	THR
35	Bg	260	ILE
35	Bg	268	GLN
35	Bg	269	TYR
35	Bg	270	LEU
35	Bg	273	ASP
35	Bg	310	ILE
35	Bg	312	VAL
35	Bg	315	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (96) such sidechains are listed below:

Mol	Chain	Res	Type
3	BA	21	ASN
3	BA	28	ASN
3	BA	33	GLN
3	BA	131	GLN
3	BA	163	ASN
4	BB	95	ASN
4	BB	124	ASN
4	BB	148	ASN

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Mol	Chain	Res	Type
5	BC	89	GLN
5	BC	147	ASN
5	BC	228	ASN
6	BD	67	ASN
6	BD	74	GLN
6	BD	165	ASN
7	BE	17	HIS
7	BE	67	GLN
7	BE	223	ASN
8	BF	44	ASN
8	BF	63	GLN
8	BF	66	GLN
8	BF	95	ASN
8	BF	100	ASN
8	BF	131	GLN
8	BF	170	GLN
8	BF	186	ASN
9	BG	4	ASN
9	BG	13	GLN
9	BG	34	GLN
9	BG	56	ASN
9	BG	59	GLN
9	BG	80	ASN
9	BG	182	GLN
9	BG	185	GLN
10	BH	19	GLN
10	BH	147	ASN
10	BH	180	GLN
11	BI	35	ASN
11	BI	52	ASN
11	BI	64	ASN
11	BI	88	ASN
11	BI	111	GLN
11	BI	175	GLN
12	BJ	38	ASN
12	BJ	131	GLN
13	BK	28	ASN
13	BK	47	GLN
13	BK	62	GLN
14	BL	92	HIS
14	BL	98	ASN
14	BL	104	HIS

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Mol	Chain	Res	Type
14	BL	127	GLN
15	BM	139	HIS
16	BN	105	ASN
18	BP	79	HIS
18	BP	114	HIS
19	BQ	32	ASN
19	BQ	74	HIS
20	BR	31	ASN
20	BR	74	GLN
20	BR	83	GLN
21	BS	74	GLN
21	BS	137	HIS
22	BT	16	ASN
22	BT	23	GLN
22	BT	48	GLN
22	BT	70	GLN
22	BT	77	ASN
23	BU	48	HIS
24	BV	21	ASN
24	BV	35	ASN
24	BV	70	ASN
24	BV	75	ASN
25	BW	24	GLN
25	BW	39	GLN
25	BW	42	GLN
25	BW	56	HIS
25	BW	64	GLN
25	BW	70	ASN
26	BX	27	ASN
26	BX	75	GLN
27	BY	34	ASN
27	BY	107	GLN
27	BY	133	ASN
29	Ba	25	ASN
29	Ba	69	ASN
31	Bc	27	GLN
32	Bd	27	HIS
32	Bd	48	ASN
34	Bf	145	HIS
35	Bg	29	GLN
35	Bg	64	HIS
35	Bg	66	HIS

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Mol	Chain	Res	Type
35	Bg	159	ASN
35	Bg	185	GLN
35	Bg	196	ASN
35	Bg	288	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A2	1459/1767 (82%)	899 (61%)	316 (21%)
2	AZ	160/190 (84%)	128 (80%)	43 (26%)
All	All	1619/1957 (82%)	1027 (63%)	359 (22%)

All (1027) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A2	2	A
1	A2	3	U
1	A2	4	C
1	A2	6	G
1	A2	7	G
1	A2	8	U
1	A2	9	U
1	A2	10	G
1	A2	11	A
1	A2	13	C
1	A2	14	C
1	A2	16	G
1	A2	17	C
1	A2	18	C
1	A2	23	G
1	A2	25	C
1	A2	26	A
1	A2	27	U
1	A2	32	U
1	A2	34	G
1	A2	38	C
1	A2	39	A
1	A2	40	A
1	A2	42	G
1	A2	43	A
1	A2	44	U

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Mol	Chain	Res	Type
1	A2	46	A
1	A2	47	A
1	A2	48	G
1	A2	57	G
1	A2	61	A
1	A2	63	G
1	A2	68	A
1	A2	69	G
1	A2	73	U
1	A2	74	U
1	A2	75	U
1	A2	78	A
1	A2	80	A
1	A2	84	A
1	A2	87	C
1	A2	91	G
1	A2	94	U
1	A2	96	G
1	A2	97	C
1	A2	99	C
1	A2	100	A
1	A2	101	U
1	A2	103	A
1	A2	104	A
1	A2	105	A
1	A2	110	U
1	A2	114	C
1	A2	115	G
1	A2	116	U
1	A2	117	U
1	A2	119	A
1	A2	123	G
1	A2	125	U
1	A2	126	A
1	A2	127	G
1	A2	128	U
1	A2	129	U
1	A2	130	C
1	A2	131	C
1	A2	133	U
1	A2	134	U
1	A2	136	C

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Mol	Chain	Res	Type
1	A2	137	U
1	A2	139	C
1	A2	140	A
1	A2	141	U
1	A2	142	G
1	A2	143	G
1	A2	144	U
1	A2	147	A
1	A2	149	C
1	A2	150	U
1	A2	156	A
1	A2	158	U
1	A2	159	U
1	A2	160	C
1	A2	161	U
1	A2	162	A
1	A2	165	G
1	A2	166	C
1	A2	167	U
1	A2	169	A
1	A2	171	A
1	A2	173	A
1	A2	174	U
1	A2	177	U
1	A2	178	U
1	A2	181	A
1	A2	182	A
1	A2	184	C
1	A2	185	U
1	A2	188	A
1	A2	189	C
1	A2	190	C
1	A2	191	C
1	A2	192	U
1	A2	197	A
1	A2	199	G
1	A2	200	A
1	A2	201	G
1	A2	202	A
1	A2	204	G
1	A2	209	U
1	A2	212	U

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Mol	Chain	Res	Type
1	A2	213	A
1	A2	217	A
1	A2	218	A
1	A2	219	A
1	A2	221	A
1	A2	222	A
1	A2	223	U
1	A2	224	C
1	A2	225	A
1	A2	226	A
1	A2	227	U
1	A2	228	G
1	A2	229	U
1	A2	230	C
1	A2	231	U
1	A2	232	U
1	A2	233	C
1	A2	236	A
1	A2	237	C
1	A2	238	U
1	A2	240	U
1	A2	241	U
1	A2	246	G
1	A2	249	U
1	A2	254	A
1	A2	255	U
1	A2	257	A
1	A2	260	U
1	A2	264	G
1	A2	265	A
1	A2	266	A
1	A2	267	U
1	A2	271	A
1	A2	272	U
1	A2	275	C
1	A2	276	C
1	A2	277	U
1	A2	278	U
1	A2	280	U
1	A2	283	U
1	A2	286	C
1	A2	287	G

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Mol	Chain	Res	Type
1	A2	288	A
1	A2	293	U
1	A2	295	A
1	A2	296	U
1	A2	299	A
1	A2	300	A
1	A2	304	U
1	A2	307	G
1	A2	311	U
1	A2	312	A
1	A2	313	U
1	A2	314	C
1	A2	315	A
1	A2	316	A
1	A2	318	U
1	A2	319	U
1	A2	321	C
1	A2	323	A
1	A2	329	G
1	A2	330	G
1	A2	331	A
1	A2	333	A
1	A2	334	G
1	A2	337	G
1	A2	338	C
1	A2	343	C
1	A2	350	U
1	A2	351	C
1	A2	359	A
1	A2	360	A
1	A2	361	C
1	A2	362	G
1	A2	363	G
1	A2	367	A
1	A2	373	G
1	A2	374	U
1	A2	375	U
1	A2	376	C
1	A2	377	G
1	A2	378	A
1	A2	380	U
1	A2	381	C

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Mol	Chain	Res	Type
1	A2	386	G
1	A2	388	G
1	A2	391	A
1	A2	395	U
1	A2	396	G
1	A2	400	A
1	A2	401	A
1	A2	402	C
1	A2	403	G
1	A2	404	G
1	A2	406	U
1	A2	410	A
1	A2	414	C
1	A2	416	A
1	A2	417	A
1	A2	418	G
1	A2	419	G
1	A2	420	A
1	A2	423	G
1	A2	424	C
1	A2	427	C
1	A2	428	A
1	A2	429	G
1	A2	430	G
1	A2	431	C
1	A2	432	G
1	A2	434	G
1	A2	435	C
1	A2	438	A
1	A2	439	U
1	A2	441	A
1	A2	443	C
1	A2	444	C
1	A2	447	U
1	A2	454	U
1	A2	455	C
1	A2	456	A
1	A2	461	G
1	A2	464	A
1	A2	468	A
1	A2	473	A
1	A2	475	A

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Mol	Chain	Res	Type
1	A2	477	A
1	A2	478	A
1	A2	481	A
1	A2	482	U
1	A2	483	A
1	A2	484	C
1	A2	485	A
1	A2	486	G
1	A2	489	C
1	A2	492	A
1	A2	494	U
1	A2	495	C
1	A2	496	G
1	A2	497	G
1	A2	498	G
1	A2	499	U
1	A2	500	C
1	A2	503	G
1	A2	504	U
1	A2	505	A
1	A2	507	U
1	A2	508	U
1	A2	509	G
1	A2	510	G
1	A2	511	A
1	A2	512	A
1	A2	513	U
1	A2	515	A
1	A2	516	G
1	A2	518	A
1	A2	519	C
1	A2	520	A
1	A2	525	A
1	A2	528	U
1	A2	529	A
1	A2	532	U
1	A2	533	U
1	A2	534	A
1	A2	535	A
1	A2	538	A
1	A2	540	G
1	A2	541	A

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Mol	Chain	Res	Type
1	A2	542	A
1	A2	543	C
1	A2	544	A
1	A2	548	G
1	A2	551	G
1	A2	559	C
1	A2	560	U
1	A2	563	U
1	A2	564	G
1	A2	565	C
1	A2	568	G
1	A2	571	G
1	A2	572	C
1	A2	573	C
1	A2	574	G
1	A2	575	C
1	A2	577	G
1	A2	579	A
1	A2	580	A
1	A2	582	U
1	A2	586	G
1	A2	589	C
1	A2	593	U
1	A2	594	A
1	A2	597	G
1	A2	601	A
1	A2	603	U
1	A2	604	A
1	A2	606	A
1	A2	607	G
1	A2	608	U
1	A2	609	U
1	A2	610	G
1	A2	611	U
1	A2	613	G
1	A2	617	U
1	A2	619	A
1	A2	620	A
1	A2	622	A
1	A2	624	G
1	A2	626	U
1	A2	628	G

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Mol	Chain	Res	Type
1	A2	629	U
1	A2	634	G
1	A2	635	A
1	A2	638	U
1	A2	640	U
1	A2	641	G
1	A2	646	C
1	A2	647	G
1	A2	648	G
1	A2	650	U
1	A2	652	G
1	A2	653	C
1	A2	656	G
1	A2	657	U
1	A2	658	C
1	A2	681	U
1	A2	682	C
1	A2	684	A
1	A2	687	G
1	A2	688	G
1	A2	689	G
1	A2	690	G
1	A2	691	C
1	A2	694	U
1	A2	695	U
1	A2	696	C
1	A2	698	U
1	A2	703	G
1	A2	704	C
1	A2	706	A
1	A2	707	A
1	A2	708	C
1	A2	709	C
1	A2	710	U
1	A2	712	G
1	A2	714	G
1	A2	715	U
1	A2	716	C
1	A2	717	C
1	A2	718	U
1	A2	719	U
1	A2	721	U

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Mol	Chain	Res	Type
1	A2	722	G
1	A2	723	G
1	A2	725	U
1	A2	726	C
1	A2	727	U
1	A2	729	G
1	A2	730	G
1	A2	731	C
1	A2	732	G
1	A2	733	A
1	A2	734	A
1	A2	737	A
1	A2	738	G
1	A2	739	G
1	A2	741	C
1	A2	742	U
1	A2	743	U
1	A2	745	U
1	A2	749	U
1	A2	753	A
1	A2	754	A
1	A2	755	A
1	A2	759	U
1	A2	760	A
1	A2	761	G
1	A2	762	A
1	A2	764	U
1	A2	765	G
1	A2	766	U
1	A2	767	U
1	A2	773	C
1	A2	774	A
1	A2	775	G
1	A2	776	G
1	A2	777	C
1	A2	778	G
1	A2	779	U
1	A2	780	A
1	A2	781	U
1	A2	785	U
1	A2	788	A
1	A2	789	A

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Mol	Chain	Res	Type
1	A2	792	U
1	A2	794	U
1	A2	798	C
1	A2	802	G
1	A2	804	A
1	A2	807	A
1	A2	810	G
1	A2	811	A
1	A2	814	A
1	A2	817	A
1	A2	818	C
1	A2	820	U
1	A2	821	U
1	A2	822	U
1	A2	823	G
1	A2	824	G
1	A2	828	U
1	A2	831	U
1	A2	836	U
1	A2	841	U
1	A2	843	U
1	A2	845	G
1	A2	848	C
1	A2	850	A
1	A2	852	C
1	A2	853	G
1	A2	855	A
1	A2	856	A
1	A2	857	U
1	A2	860	U
1	A2	863	A
1	A2	864	U
1	A2	865	A
1	A2	866	G
1	A2	867	G
1	A2	870	C
1	A2	874	C
1	A2	876	G
1	A2	880	C
1	A2	882	U
1	A2	884	A
1	A2	885	G

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Mol	Chain	Res	Type
1	A2	887	A
1	A2	892	A
1	A2	896	U
1	A2	898	A
1	A2	903	U
1	A2	909	U
1	A2	913	G
1	A2	916	U
1	A2	917	U
1	A2	918	U
1	A2	919	A
1	A2	921	U
1	A2	922	G
1	A2	927	C
1	A2	928	U
1	A2	929	A
1	A2	930	A
1	A2	931	C
1	A2	933	A
1	A2	935	U
1	A2	938	G
1	A2	939	A
1	A2	940	A
1	A2	941	A
1	A2	942	G
1	A2	944	A
1	A2	945	U
1	A2	946	U
1	A2	949	C
1	A2	950	C
1	A2	956	C
1	A2	959	U
1	A2	960	U
1	A2	961	U
1	A2	969	C
1	A2	970	A
1	A2	971	A
1	A2	972	G
1	A2	981	U
1	A2	982	U
1	A2	987	G
1	A2	990	C

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Mol	Chain	Res	Type
1	A2	991	G
1	A2	992	A
1	A2	993	A
1	A2	996	U
1	A2	998	A
1	A2	1003	A
1	A2	1005	A
1	A2	1006	C
1	A2	1007	C
1	A2	1011	G
1	A2	1012	U
1	A2	1013	A
1	A2	1015	U
1	A2	1020	A
1	A2	1021	C
1	A2	1022	C
1	A2	1023	A
1	A2	1026	A
1	A2	1027	A
1	A2	1028	C
1	A2	1029	U
1	A2	1031	U
1	A2	1032	G
1	A2	1033	C
1	A2	1034	C
1	A2	1039	A
1	A2	1040	G
1	A2	1041	G
1	A2	1042	G
1	A2	1045	C
1	A2	1047	G
1	A2	1048	G
1	A2	1052	U
1	A2	1054	U
1	A2	1057	U
1	A2	1058	U
1	A2	1059	U
1	A2	1060	U
1	A2	1061	A
1	A2	1063	U
1	A2	1066	C
1	A2	1071	U

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Mol	Chain	Res	Type
1	A2	1074	G
1	A2	1075	C
1	A2	1078	C
1	A2	1079	U
1	A2	1082	C
1	A2	1087	A
1	A2	1089	U
1	A2	1091	A
1	A2	1092	A
1	A2	1095	U
1	A2	1096	C
1	A2	1097	U
1	A2	1098	U
1	A2	1100	G
1	A2	1101	G
1	A2	1103	U
1	A2	1104	U
1	A2	1105	C
1	A2	1106	U
1	A2	1107	G
1	A2	1108	G
1	A2	1109	G
1	A2	1111	G
1	A2	1113	A
1	A2	1120	U
1	A2	1121	C
1	A2	1122	G
1	A2	1124	A
1	A2	1126	G
1	A2	1131	A
1	A2	1132	A
1	A2	1138	A
1	A2	1140	G
1	A2	1142	A
1	A2	1145	U
1	A2	1146	G
1	A2	1147	A
1	A2	1148	C
1	A2	1150	G
1	A2	1151	A
1	A2	1152	A
1	A2	1154	G

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Mol	Chain	Res	Type
1	A2	1155	G
1	A2	1158	C
1	A2	1159	C
1	A2	1160	A
1	A2	1162	C
1	A2	1167	G
1	A2	1168	U
1	A2	1170	G
1	A2	1171	A
1	A2	1172	G
1	A2	1175	U
1	A2	1176	G
1	A2	1180	C
1	A2	1182	U
1	A2	1183	A
1	A2	1184	A
1	A2	1185	U
1	A2	1189	A
1	A2	1191	U
1	A2	1194	A
1	A2	1195	C
1	A2	1196	A
1	A2	1197	C
1	A2	1198	G
1	A2	1200	G
1	A2	1201	G
1	A2	1205	C
1	A2	1207	C
1	A2	1208	A
1	A2	1209	C
1	A2	1210	C
1	A2	1213	G
1	A2	1214	U
1	A2	1217	A
1	A2	1218	G
1	A2	1219	A
1	A2	1220	C
1	A2	1226	A
1	A2	1227	A
1	A2	1228	G
1	A2	1229	G
1	A2	1230	A

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Mol	Chain	Res	Type
1	A2	1232	U
1	A2	1233	G
1	A2	1234	A
1	A2	1236	A
1	A2	1237	G
1	A2	1240	U
1	A2	1241	G
1	A2	1243	G
1	A2	1244	A
1	A2	1245	G
1	A2	1246	C
1	A2	1248	C
1	A2	1250	U
1	A2	1251	U
1	A2	1252	C
1	A2	1256	A
1	A2	1257	U
1	A2	1258	U
1	A2	1259	U
1	A2	1260	U
1	A2	1261	G
1	A2	1262	U
1	A2	1266	U
1	A2	1271	G
1	A2	1273	G
1	A2	1276	U
1	A2	1279	C
1	A2	1284	C
1	A2	1286	U
1	A2	1287	A
1	A2	1288	G
1	A2	1291	G
1	A2	1292	G
1	A2	1294	G
1	A2	1296	A
1	A2	1300	A
1	A2	1301	U
1	A2	1304	G
1	A2	1305	U
1	A2	1307	U
1	A2	1312	A
1	A2	1314	U

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Mol	Chain	Res	Type
1	A2	1315	U
1	A2	1318	G
1	A2	1319	A
1	A2	1320	U
1	A2	1321	A
1	A2	1332	C
1	A2	1334	U
1	A2	1337	A
1	A2	1338	C
1	A2	1339	C
1	A2	1340	U
1	A2	1341	A
1	A2	1343	U
1	A2	1344	A
1	A2	1346	A
1	A2	1348	A
1	A2	1349	G
1	A2	1353	U
1	A2	1356	U
1	A2	1357	A
1	A2	1358	G
1	A2	1361	U
1	A2	1362	U
1	A2	1364	G
1	A2	1365	C
1	A2	1370	U
1	A2	1372	U
1	A2	1373	C
1	A2	1375	A
1	A2	1376	C
1	A2	1377	U
1	A2	1379	C
1	A2	1381	U
1	A2	1383	G
1	A2	1384	A
1	A2	1385	G
1	A2	1388	A
1	A2	1389	C
1	A2	1390	U
1	A2	1391	A
1	A2	1393	C
1	A2	1395	G

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Mol	Chain	Res	Type
1	A2	1397	U
1	A2	1398	U
1	A2	1399	C
1	A2	1400	A
1	A2	1401	A
1	A2	1404	C
1	A2	1409	G
1	A2	1415	U
1	A2	1416	G
1	A2	1417	A
1	A2	1418	G
1	A2	1420	C
1	A2	1421	A
1	A2	1422	A
1	A2	1427	A
1	A2	1428	G
1	A2	1431	C
1	A2	1432	U
1	A2	1433	G
1	A2	1440	C
1	A2	1441	C
1	A2	1442	U
1	A2	1443	U
1	A2	1444	A
1	A2	1445	G
1	A2	1446	A
1	A2	1448	G
1	A2	1449	U
1	A2	1451	C
1	A2	1453	G
1	A2	1456	C
1	A2	1458	G
1	A2	1460	A
1	A2	1464	G
1	A2	1467	C
1	A2	1468	U
1	A2	1470	C
1	A2	1471	A
1	A2	1472	C
1	A2	1473	U
1	A2	1478	G
1	A2	1479	A

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Mol	Chain	Res	Type
1	A2	1480	G
1	A2	1481	C
1	A2	1482	C
1	A2	1483	A
1	A2	1485	C
1	A2	1486	G
1	A2	1488	G
1	A2	1490	C
1	A2	1491	U
1	A2	1492	A
1	A2	1494	C
1	A2	1496	U
1	A2	1499	G
1	A2	1505	A
1	A2	1507	G
1	A2	1509	C
1	A2	1511	U
1	A2	1512	G
1	A2	1514	U
1	A2	1517	U
1	A2	1521	G
1	A2	1524	A
1	A2	1525	A
1	A2	1526	A
1	A2	1527	C
1	A2	1528	U
1	A2	1529	C
1	A2	1530	C
1	A2	1533	C
1	A2	1535	U
1	A2	1538	U
1	A2	1539	G
1	A2	1540	G
1	A2	1545	A
1	A2	1547	A
1	A2	1548	G
1	A2	1551	U
1	A2	1553	G
1	A2	1555	A
1	A2	1557	U
1	A2	1558	U
1	A2	1560	U

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Mol	Chain	Res	Type
1	A2	1562	G
1	A2	1563	C
1	A2	1569	A
1	A2	1571	C
1	A2	1573	A
1	A2	1574	G
1	A2	1575	G
1	A2	1582	U
1	A2	1583	A
1	A2	1585	U
1	A2	1586	A
1	A2	1587	A
1	A2	1588	G
1	A2	1590	G
1	A2	1591	C
1	A2	1592	A
1	A2	1594	G
1	A2	1595	U
1	A2	1596	C
1	A2	1597	A
1	A2	1598	U
1	A2	1600	A
1	A2	1601	G
1	A2	1602	C
1	A2	1604	U
1	A2	1606	C
1	A2	1607	G
1	A2	1608	U
1	A2	1609	U
1	A2	1612	U
1	A2	1614	A
1	A2	1615	C
1	A2	1616	G
1	A2	1618	C
1	A2	1621	U
1	A2	1625	C
1	A2	1629	G
1	A2	1630	U
1	A2	1631	A
1	A2	1632	C
1	A2	1634	C
1	A2	1635	A

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Mol	Chain	Res	Type
1	A2	1639	C
1	A2	1642	G
1	A2	1643	U
1	A2	1644	C
1	A2	1647	U
1	A2	1648	A
1	A2	1654	G
1	A2	1657	U
1	A2	1662	G
1	A2	1663	G
1	A2	1664	C
1	A2	1665	U
1	A2	1666	U
1	A2	1667	A
1	A2	1670	G
1	A2	1671	A
1	A2	1672	G
1	A2	1678	A
1	A2	1680	G
1	A2	1682	U
1	A2	1683	C
1	A2	1684	U
1	A2	1685	G
1	A2	1688	U
1	A2	1689	A
1	A2	1690	G
1	A2	1691	A
1	A2	1692	G
1	A2	1693	A
1	A2	1709	C
1	A2	1710	U
1	A2	1711	C
1	A2	1713	G
1	A2	1716	C
1	A2	1717	G
1	A2	1719	A
1	A2	1720	G
1	A2	1722	A
1	A2	1727	G
1	A2	1733	C
1	A2	1737	G
1	A2	1739	C

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Mol	Chain	Res	Type
1	A2	1740	A
1	A2	1741	U
1	A2	1743	U
1	A2	1744	A
1	A2	1746	A
1	A2	1748	G
1	A2	1750	A
1	A2	1752	U
1	A2	1753	A
1	A2	1754	A
1	A2	1755	A
1	A2	1756	A
1	A2	1758	U
1	A2	1760	G
1	A2	1761	U
1	A2	1762	A
1	A2	1766	A
1	A2	1767	G
1	A2	1768	G
1	A2	1769	U
1	A2	1770	U
1	A2	1771	U
1	A2	1777	G
1	A2	1778	G
1	A2	1780	G
1	A2	1781	A
1	A2	1782	A
1	A2	1790	A
1	A2	1793	G
1	A2	1794	A
1	A2	1795	U
1	A2	1797	A
1	A2	1798	U
2	AZ	6026	A
2	AZ	6029	A
2	AZ	6031	G
2	AZ	6033	G
2	AZ	6037	U
2	AZ	6038	U
2	AZ	6040	C
2	AZ	6041	U
2	AZ	6042	U

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Mol	Chain	Res	Type
2	AZ	6044	U
2	AZ	6045	A
2	AZ	6046	A
2	AZ	6048	U
2	AZ	6049	A
2	AZ	6050	C
2	AZ	6051	A
2	AZ	6053	U
2	AZ	6055	U
2	AZ	6061	G
2	AZ	6063	U
2	AZ	6064	U
2	AZ	6065	A
2	AZ	6067	U
2	AZ	6070	A
2	AZ	6071	U
2	AZ	6072	U
2	AZ	6073	A
2	AZ	6074	C
2	AZ	6077	G
2	AZ	6078	U
2	AZ	6079	A
2	AZ	6080	G
2	AZ	6082	G
2	AZ	6086	U
2	AZ	6087	U
2	AZ	6088	U
2	AZ	6089	U
2	AZ	6091	G
2	AZ	6092	U
2	AZ	6094	U
2	AZ	6095	U
2	AZ	6096	U
2	AZ	6097	A
2	AZ	6099	G
2	AZ	6101	U
2	AZ	6103	G
2	AZ	6104	C
2	AZ	6105	U
2	AZ	6106	A
2	AZ	6107	U
2	AZ	6109	U

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Mol	Chain	Res	Type
2	AZ	6111	G
2	AZ	6113	U
2	AZ	6116	A
2	AZ	6117	C
2	AZ	6118	G
2	AZ	6119	U
2	AZ	6120	U
2	AZ	6121	C
2	AZ	6122	C
2	AZ	6124	G
2	AZ	6125	G
2	AZ	6126	A
2	AZ	6127	U
2	AZ	6128	G
2	AZ	6129	C
2	AZ	6130	C
2	AZ	6131	U
2	AZ	6132	A
2	AZ	6134	U
2	AZ	6135	G
2	AZ	6136	G
2	AZ	6137	C
2	AZ	6138	A
2	AZ	6139	G
2	AZ	6141	C
2	AZ	6142	C
2	AZ	6145	C
2	AZ	6146	A
2	AZ	6147	A
2	AZ	6148	U
2	AZ	6149	A
2	AZ	6151	C
2	AZ	6152	C
2	AZ	6154	G
2	AZ	6156	A
2	AZ	6157	A
2	AZ	6158	G
2	AZ	6159	C
2	AZ	6160	C
2	AZ	6161	C
2	AZ	6162	U
2	AZ	6163	C

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Mol	Chain	Res	Type
2	AZ	6165	C
2	AZ	6166	U
2	AZ	6167	G
2	AZ	6168	C
2	AZ	6171	U
2	AZ	6174	G
2	AZ	6176	A
2	AZ	6180	C
2	AZ	6181	C
2	AZ	6187	A
2	AZ	6189	G
2	AZ	6190	U
2	AZ	6196	G
2	AZ	6197	U
2	AZ	6198	U
2	AZ	6199	U
2	AZ	6200	U
2	AZ	6202	C
2	AZ	6203	U
2	AZ	6204	A
2	AZ	6205	A
2	AZ	6206	G
2	AZ	6207	A
2	AZ	6208	A
2	AZ	6209	A
2	AZ	6210	U
2	AZ	6211	U
2	AZ	6213	A
2	AZ	6214	C
2	AZ	6215	C
2	AZ	6216	U
2	AZ	6218	U
2	AZ	6219	U
2	AZ	6220	U
2	AZ	6222	U

All (359) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A2	2	A
1	A2	3	U
1	A2	9	U

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Mol	Chain	Res	Type
1	A2	25	C
1	A2	33	U
1	A2	38	C
1	A2	41	A
1	A2	42	G
1	A2	51	A
1	A2	67	A
1	A2	68	A
1	A2	73	U
1	A2	74	U
1	A2	90	C
1	A2	91	G
1	A2	99	C
1	A2	102	U
1	A2	103	A
1	A2	104	A
1	A2	112	A
1	A2	113	U
1	A2	114	C
1	A2	115	G
1	A2	120	U
1	A2	126	A
1	A2	128	U
1	A2	129	U
1	A2	132	U
1	A2	133	U
1	A2	135	A
1	A2	138	A
1	A2	139	C
1	A2	141	U
1	A2	142	G
1	A2	143	G
1	A2	146	U
1	A2	149	C
1	A2	158	U
1	A2	161	U
1	A2	177	U
1	A2	188	A
1	A2	190	C
1	A2	201	G
1	A2	217	A
1	A2	218	A

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Mol	Chain	Res	Type
1	A2	221	A
1	A2	223	U
1	A2	227	U
1	A2	232	U
1	A2	240	U
1	A2	254	A
1	A2	261	U
1	A2	266	A
1	A2	286	C
1	A2	295	A
1	A2	299	A
1	A2	312	A
1	A2	315	A
1	A2	320	U
1	A2	322	G
1	A2	326	G
1	A2	330	G
1	A2	362	G
1	A2	367	A
1	A2	376	C
1	A2	387	A
1	A2	395	U
1	A2	400	A
1	A2	417	A
1	A2	420	A
1	A2	423	G
1	A2	426	G
1	A2	427	C
1	A2	430	G
1	A2	435	C
1	A2	438	A
1	A2	440	U
1	A2	444	C
1	A2	446	A
1	A2	454	U
1	A2	469	C
1	A2	480	G
1	A2	481	A
1	A2	482	U
1	A2	485	A
1	A2	491	C
1	A2	493	U

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Mol	Chain	Res	Type
1	A2	494	U
1	A2	498	G
1	A2	499	U
1	A2	502	U
1	A2	503	G
1	A2	504	U
1	A2	508	U
1	A2	511	A
1	A2	512	A
1	A2	514	G
1	A2	517	U
1	A2	528	U
1	A2	529	A
1	A2	539	G
1	A2	558	U
1	A2	562	G
1	A2	571	G
1	A2	572	C
1	A2	573	C
1	A2	578	U
1	A2	581	U
1	A2	600	U
1	A2	602	U
1	A2	603	U
1	A2	606	A
1	A2	607	G
1	A2	609	U
1	A2	627	C
1	A2	628	G
1	A2	633	U
1	A2	639	U
1	A2	645	C
1	A2	656	G
1	A2	681	U
1	A2	686	C
1	A2	690	G
1	A2	697	C
1	A2	705	U
1	A2	708	C
1	A2	711	U
1	A2	713	A
1	A2	716	C

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Mol	Chain	Res	Type
1	A2	720	G
1	A2	721	U
1	A2	728	U
1	A2	729	G
1	A2	733	A
1	A2	738	G
1	A2	744	U
1	A2	753	A
1	A2	759	U
1	A2	761	G
1	A2	765	G
1	A2	766	U
1	A2	769	A
1	A2	772	G
1	A2	773	C
1	A2	779	U
1	A2	787	G
1	A2	803	A
1	A2	816	G
1	A2	820	U
1	A2	821	U
1	A2	822	U
1	A2	823	G
1	A2	835	U
1	A2	836	U
1	A2	852	C
1	A2	855	A
1	A2	856	A
1	A2	884	A
1	A2	897	C
1	A2	910	C
1	A2	918	U
1	A2	921	U
1	A2	930	A
1	A2	939	A
1	A2	941	A
1	A2	944	A
1	A2	945	U
1	A2	949	C
1	A2	960	U
1	A2	990	C
1	A2	1002	G

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Mol	Chain	Res	Type
1	A2	1004	U
1	A2	1020	A
1	A2	1021	C
1	A2	1026	A
1	A2	1030	A
1	A2	1031	U
1	A2	1041	G
1	A2	1055	U
1	A2	1057	U
1	A2	1058	U
1	A2	1059	U
1	A2	1065	A
1	A2	1067	C
1	A2	1074	G
1	A2	1077	C
1	A2	1081	A
1	A2	1092	A
1	A2	1096	C
1	A2	1097	U
1	A2	1102	G
1	A2	1106	U
1	A2	1108	G
1	A2	1118	G
1	A2	1125	A
1	A2	1131	A
1	A2	1137	A
1	A2	1145	U
1	A2	1151	A
1	A2	1154	G
1	A2	1158	C
1	A2	1159	C
1	A2	1161	C
1	A2	1170	G
1	A2	1175	U
1	A2	1183	A
1	A2	1186	U
1	A2	1188	G
1	A2	1196	A
1	A2	1197	C
1	A2	1207	C
1	A2	1216	C
1	A2	1221	A

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Mol	Chain	Res	Type
1	A2	1226	A
1	A2	1229	G
1	A2	1232	U
1	A2	1235	C
1	A2	1240	U
1	A2	1247	U
1	A2	1250	U
1	A2	1258	U
1	A2	1259	U
1	A2	1261	G
1	A2	1273	G
1	A2	1285	U
1	A2	1287	A
1	A2	1293	U
1	A2	1295	G
1	A2	1306	C
1	A2	1314	U
1	A2	1325	A
1	A2	1340	U
1	A2	1357	A
1	A2	1364	G
1	A2	1372	U
1	A2	1382	A
1	A2	1397	U
1	A2	1398	U
1	A2	1399	C
1	A2	1407	U
1	A2	1415	U
1	A2	1420	C
1	A2	1424	A
1	A2	1426	C
1	A2	1427	A
1	A2	1430	U
1	A2	1442	U
1	A2	1444	A
1	A2	1445	G
1	A2	1447	C
1	A2	1448	G
1	A2	1450	U
1	A2	1455	G
1	A2	1457	C
1	A2	1463	C

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Mol	Chain	Res	Type
1	A2	1467	C
1	A2	1471	A
1	A2	1472	C
1	A2	1478	G
1	A2	1483	A
1	A2	1491	U
1	A2	1493	A
1	A2	1495	C
1	A2	1516	A
1	A2	1525	A
1	A2	1528	U
1	A2	1529	C
1	A2	1532	U
1	A2	1537	C
1	A2	1538	U
1	A2	1539	G
1	A2	1561	U
1	A2	1568	C
1	A2	1570	A
1	A2	1572	G
1	A2	1573	A
1	A2	1582	U
1	A2	1590	G
1	A2	1591	C
1	A2	1600	A
1	A2	1601	G
1	A2	1603	U
1	A2	1608	U
1	A2	1629	G
1	A2	1638	G
1	A2	1642	G
1	A2	1647	U
1	A2	1662	G
1	A2	1671	A
1	A2	1678	A
1	A2	1682	U
1	A2	1683	C
1	A2	1685	G
1	A2	1688	U
1	A2	1708	U
1	A2	1710	U
1	A2	1712	A

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Mol	Chain	Res	Type
1	A2	1716	C
1	A2	1736	G
1	A2	1742	U
1	A2	1743	U
1	A2	1749	A
1	A2	1751	C
1	A2	1752	U
1	A2	1753	A
1	A2	1754	A
1	A2	1759	C
1	A2	1761	U
1	A2	1765	A
1	A2	1769	U
1	A2	1771	U
1	A2	1777	G
1	A2	1781	A
1	A2	1792	G
1	A2	1793	G
1	A2	1796	C
2	AZ	6032	U
2	AZ	6047	A
2	AZ	6050	C
2	AZ	6062	G
2	AZ	6063	U
2	AZ	6069	A
2	AZ	6070	A
2	AZ	6073	A
2	AZ	6076	A
2	AZ	6085	A
2	AZ	6087	U
2	AZ	6091	G
2	AZ	6096	U
2	AZ	6108	U
2	AZ	6109	U
2	AZ	6117	C
2	AZ	6118	G
2	AZ	6121	C
2	AZ	6124	G
2	AZ	6125	G
2	AZ	6129	C
2	AZ	6130	C
2	AZ	6137	C

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Mol	Chain	Res	Type
2	AZ	6141	C
2	AZ	6146	A
2	AZ	6155	G
2	AZ	6156	A
2	AZ	6164	U
2	AZ	6165	C
2	AZ	6166	U
2	AZ	6168	C
2	AZ	6179	A
2	AZ	6186	U
2	AZ	6197	U
2	AZ	6198	U
2	AZ	6203	U
2	AZ	6206	G
2	AZ	6208	A
2	AZ	6209	A
2	AZ	6210	U
2	AZ	6215	C
2	AZ	6217	A
2	AZ	6221	U

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A2	393
35	Bg	80
7	BE	64
6	BD	62
11	BI	58
8	BF	52
10	BH	51
4	BB	51
9	BG	47
5	BC	46
3	BA	43
12	BJ	42
2	AZ	40
26	BX	40
22	BT	39
25	BW	39
20	BR	36
15	BM	33
14	BL	32
18	BP	31
27	BY	31
19	BQ	30
21	BS	29
16	BN	29
23	BU	27
13	BK	25
30	Bb	24
29	Ba	24
17	BO	23
24	BV	18
32	Bd	16
28	BZ	14
31	Bc	14
33	Be	11
34	Bf	9

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	1693:A	O3'	1708:U	P	22.38

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	658:C	O3'	676:G	P	18.27
1	BI	123:LYS	C	135:LYS	N	16.74
1	BA	190:ASP	C	191:ARG	N	10.15
1	BR	124:VAL	C	125:SER	N	8.71
1	BR	91:ALA	C	95:ARG	N	8.21
1	BZ	84:GLU	C	85:LYS	N	7.70
1	BT	66:TYR	C	67:MET	N	7.45
1	BP	19:GLY	C	20:VAL	N	7.22
1	AZ	6089:U	O3'	6090:U	P	6.99
1	A2	712:G	O3'	713:A	P	6.85
1	BM	141:SER	C	142:GLN	N	6.82
1	A2	1564:U	O3'	1565:C	P	6.79
1	BA	66:ALA	C	67:ILE	N	6.70
1	BF	25:LEU	C	26:ALA	N	6.70
1	BA	58:VAL	C	59:LEU	N	6.64
1	A2	719:U	O3'	720:G	P	6.52
1	A2	492:A	O3'	493:U	P	6.40
1	A2	833:U	O3'	834:G	P	6.33
1	BP	18:ARG	C	19:GLY	N	6.32
1	BA	37:VAL	C	38:PHE	N	6.29
1	BQ	72:GLY	C	73:GLY	N	6.22
1	BM	80:ASN	C	81:ASP	N	6.21
1	A2	1267:G	O3'	1268:G	P	6.06
1	AZ	6061:G	O3'	6062:G	P	6.03
1	BF	34:GLN	C	35:GLN	N	6.00
1	BA	127:ARG	C	128:SER	N	5.96
1	BS	6:GLN	C	7:GLU	N	5.95
1	BA	200:ASP	C	201:LEU	N	5.91
1	BU	107:THR	C	108:ILE	N	5.88
1	AZ	6056:U	O3'	6057:G	P	5.84
1	BG	142:ARG	C	143:LYS	N	5.82
1	Bf	106:TYR	C	107:LYS	N	5.82
1	BM	111:ASN	C	112:ALA	N	5.81
1	BA	106:SER	C	107:PHE	N	5.80
1	BA	36:TYR	C	37:VAL	N	5.79
1	A2	234:G	O3'	235:G	P	5.76
1	BF	68:ILE	C	69:PHE	N	5.76
1	A2	194:U	O3'	195:G	P	5.73
1	BM	25:GLU	C	26:ASP	N	5.72
1	BP	20:VAL	C	21:ASP	N	5.70
1	A2	1563:C	O3'	1564:U	P	5.69
1	A2	489:C	O3'	490:C	P	5.67

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BM	82:PRO	C	83:GLU	N	5.65
1	AZ	6067:U	O3'	6068:A	P	5.62
1	BA	65:ALA	C	66:ALA	N	5.61
1	BA	47:VAL	C	48:ILE	N	5.60
1	A2	682:C	O3'	683:C	P	5.59
1	BA	126:PRO	C	127:ARG	N	5.53
1	BA	32:HIS	C	33:GLN	N	5.52
1	BG	146:GLY	C	147:LEU	N	5.49
1	BQ	53:LEU	C	54:LEU	N	5.49
1	A2	1234:A	O3'	1235:C	P	5.48
1	AZ	6171:U	O3'	6173:C	P	5.48
1	A2	1054:U	O3'	1055:U	P	5.45
1	A2	1571:C	O3'	1572:G	P	5.41
1	BA	170:ILE	C	171:GLY	N	5.41
1	BZ	96:SER	C	97:LYS	N	5.41
1	Bg	156:VAL	C	157:VAL	N	5.40
1	BZ	82:HIS	C	83:LEU	N	5.39
1	BM	26:ASP	C	27:ALA	N	5.38
1	A2	654:C	O3'	655:G	P	5.37
1	BZ	69:LEU	C	70:LYS	N	5.37
1	BG	165:GLY	C	166:GLU	N	5.35
1	Bg	48:THR	C	49:GLY	N	5.34
1	Bf	107:LYS	C	108:VAL	N	5.30
1	Bg	160:GLU	C	161:LYS	N	5.29
1	A2	841:U	O3'	842:C	P	5.26
1	A2	696:C	O3'	697:C	P	5.25
1	BS	74:GLN	C	75:ASN	N	5.25
1	BA	4:PRO	C	5:ALA	N	5.22
1	BM	137:MET	C	138:GLU	N	5.21
1	BU	49:ASN	C	50:LEU	N	5.16
1	BA	6:THR	C	7:PHE	N	5.15
1	BT	54:PHE	C	55:TYR	N	5.15
1	Bd	5:ASN	C	6:VAL	N	5.14
1	BR	76:GLU	C	77:GLU	N	5.12
1	Bg	284:ALA	C	285:ALA	N	5.12
1	AZ	6152:C	O3'	6153:A	P	5.11
1	BM	142:GLN	C	143:GLN	N	5.10
1	BP	21:ASP	C	22:LEU	N	5.10
1	Bb	58:SER	C	59:CYS	N	5.09
1	BT	40:SER	C	41:SER	N	5.06
1	A2	698:U	O3'	699:U	P	5.01
1	BA	46:HIS	C	47:VAL	N	5.01

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BH	6:ALA	C	7:LYS	N	5.01
1	BH	13:PRO	C	14:THR	N	5.01
1	BM	72:ILE	C	73:LYS	N	4.99
1	AZ	6082:G	O3'	6083:C	P	4.96
1	BD	59:LEU	C	60:GLY	N	4.96
1	A2	1449:U	O3'	1450:U	P	4.91
1	A2	1713:G	O3'	1714:A	P	4.90
1	BA	81:PHE	C	82:GLY	N	4.90
1	AZ	6139:G	O3'	6140:C	P	4.89
1	BG	131:LYS	C	132:ARG	N	4.88
1	BK	70:GLU	C	71:GLU	N	4.86
1	BP	77:ARG	C	78:THR	N	4.81
1	BS	31:ALA	C	32:LEU	N	4.81
1	A2	386:G	O3'	387:A	P	4.80
1	A2	1555:A	O3'	1556:A	P	4.80
1	BG	147:LEU	C	148:SER	N	4.80
1	A2	838:G	O3'	839:U	P	4.79
1	BF	100:ASN	C	101:GLY	N	4.78
1	BU	77:LYS	C	78:THR	N	4.78
1	BC	122:ALA	C	123:GLY	N	4.77
1	A2	1540:G	O3'	1541:G	P	4.75
1	Bg	172:ALA	C	173:GLY	N	4.75
1	BA	189:VAL	C	190:ASP	N	4.73
1	A2	1496:U	O3'	1497:U	P	4.71
1	BF	71:ALA	C	72:HIS	N	4.71
1	BI	150:ALA	C	151:LYS	N	4.71
1	BM	136:ILE	C	137:MET	N	4.71
1	BG	198:ALA	C	199:GLN	N	4.70
1	BT	62:ALA	C	63:ARG	N	4.70
1	AZ	6027:A	O3'	6028:A	P	4.69
1	BM	39:ASP	C	40:GLY	N	4.68
1	BM	76:GLU	C	77:GLY	N	4.68
1	BS	7:GLU	C	8:GLN	N	4.68
1	BB	36:SER	C	37:THR	N	4.67
1	BD	121:GLY	C	122:VAL	N	4.67
1	BS	16:ARG	C	17:LEU	N	4.67
1	A2	76:A	O3'	77:U	P	4.66
1	A2	1201:G	O3'	1202:A	P	4.66
1	AZ	6084:U	O3'	6085:A	P	4.66
1	BF	194:LEU	C	195:ALA	N	4.66
1	A2	894:U	O3'	895:G	P	4.65
1	Bg	296:ALA	C	297:ASP	N	4.64

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BR	22:PRO	C	23:LYS	N	4.63
1	Bc	34:GLU	C	35:ASP	N	4.63
1	BR	97:ASN	C	98:GLY	N	4.62
1	Bg	31:ASN	C	32:LEU	N	4.62
1	BM	117:GLY	C	118:ALA	N	4.61
1	Bg	276:PRO	C	277:GLU	N	4.61
1	BH	32:PRO	C	33:GLU	N	4.60
1	BA	115:PHE	C	116:LYS	N	4.59
1	Bg	301:LEU	C	302:PHE	N	4.57
1	A2	648:G	O3'	649:U	P	4.55
1	BR	23:LYS	C	24:LEU	N	4.55
1	BT	27:LYS	C	28:LEU	N	4.55
1	A2	278:U	O3'	279:G	P	4.54
1	BA	56:LYS	C	57:LEU	N	4.52
1	BK	60:SER	C	61:TRP	N	4.52
1	BQ	57:LEU	C	58:ASP	N	4.52
1	A2	1305:U	O3'	1306:C	P	4.51
1	BT	52:GLY	C	53:TRP	N	4.51
1	BH	108:GLN	C	109:VAL	N	4.50
1	BB	93:GLY	C	94:LYS	N	4.49
1	BQ	5:PRO	C	6:SER	N	4.49
1	BP	92:SER	C	93:VAL	N	4.48
1	BV	19:ALA	C	20:THR	N	4.48
1	BM	50:LYS	C	51:ALA	N	4.46
1	Bg	159:ASN	C	160:GLU	N	4.46
1	A2	1230:A	O3'	1231:U	P	4.44
1	BT	72:GLY	C	73:VAL	N	4.44
1	Bg	26:SER	C	27:ALA	N	4.43
1	BG	225:GLU	C	226:ILE	N	4.42
1	BK	30:ALA	C	31:ALA	N	4.42
1	BJ	71:PHE	C	72:GLU	N	4.41
1	BR	106:THR	C	107:SER	N	4.41
1	A2	834:G	O3'	835:U	P	4.40
1	A2	1535:U	O3'	1536:G	P	4.36
1	BL	5:LEU	C	6:THR	N	4.35
1	Bf	90:ALA	C	91:LYS	N	4.35
1	A2	238:U	O3'	239:C	P	4.34
1	A2	516:G	O3'	517:U	P	4.34
1	Bg	63:GLY	C	64:HIS	N	4.34
1	BG	138:ALA	C	139:ASN	N	4.33
1	BT	5:SER	C	6:VAL	N	4.32
1	Bg	148:ASN	C	149:ASP	N	4.32

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	145:A	O3'	146:U	P	4.31
1	AZ	6033:G	O3'	6034:A	P	4.31
1	BV	29:HIS	C	30:ALA	N	4.30
1	BF	199:ILE	C	200:ASN	N	4.29
1	BG	148:SER	C	149:LYS	N	4.29
1	BG	161:GLU	C	162:VAL	N	4.29
1	Bd	6:VAL	C	7:TRP	N	4.28
1	Bg	285:ALA	C	286:GLU	N	4.28
1	BD	35:SER	C	36:GLY	N	4.27
1	BF	203:LYS	C	204:GLY	N	4.27
1	BK	5:LYS	C	6:GLU	N	4.27
1	BU	74:GLU	C	75:GLY	N	4.27
1	BZ	103:ARG	C	104:ALA	N	4.27
1	BD	34:TYR	C	35:SER	N	4.26
1	Bd	11:PRO	C	12:ARG	N	4.26
1	Bg	136:ILE	C	137:LYS	N	4.26
1	BH	153:LEU	C	154:LEU	N	4.25
1	BA	33:GLN	C	34:GLU	N	4.24
1	BP	23:GLU	C	24:LYS	N	4.24
1	Bg	95:ALA	C	96:THR	N	4.24
1	A2	233:C	O3'	234:G	P	4.23
1	A2	1198:G	O3'	1199:G	P	4.23
1	BI	118:GLY	C	119:GLN	N	4.23
1	Ba	2:PRO	C	3:LYS	N	4.23
1	BI	181:GLY	C	182:TYR	N	4.22
1	BM	28:LEU	C	29:LYS	N	4.22
1	BN	60:VAL	C	61:THR	N	4.22
1	Bg	248:ASN	C	249:ARG	N	4.22
1	A2	71:A	O3'	72:A	P	4.21
1	BE	236:ILE	C	237:SER	N	4.20
1	A2	501:U	O3'	502:U	P	4.19
1	BI	162:ALA	C	163:GLY	N	4.19
1	Bd	9:SER	C	10:HIS	N	4.19
1	A2	913:G	O3'	914:G	P	4.18
1	A2	1178:G	O3'	1179:G	P	4.18
1	Bg	223:TRP	C	224:ASN	N	4.18
1	A2	487:G	O3'	488:G	P	4.17
1	BF	94:THR	C	95:ASN	N	4.17
1	BH	160:GLN	C	161:GLN	N	4.17
1	BA	72:ASP	C	73:VAL	N	4.16
1	Bb	2:VAL	C	3:LEU	N	4.16
1	A2	1353:U	O3'	1354:G	P	4.15

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BP	115:TYR	C	116:LEU	N	4.15
1	A2	1284:C	O3'	1285:U	P	4.14
1	BK	17:GLN	C	18:GLU	N	4.14
1	AZ	6055:U	O3'	6056:U	P	4.13
1	Bc	61:ARG	C	62:GLU	N	4.13
1	A2	839:U	O3'	840:U	P	4.12
1	A2	1609:U	O3'	1610:G	P	4.12
1	BF	191:ALA	C	192:GLU	N	4.12
1	Bg	262:VAL	C	263:PHE	N	4.12
1	Bg	258:THR	C	259:GLY	N	4.11
1	A2	1298:U	O3'	1299:G	P	4.10
1	BG	37:ASP	C	38:GLY	N	4.10
1	A2	1350:U	O3'	1351:G	P	4.09
1	BS	126:ARG	C	127:HIS	N	4.09
1	Bf	114:VAL	C	115:THR	N	4.09
1	Bg	7:LEU	C	8:VAL	N	4.09
1	BQ	132:LYS	C	133:GLY	N	4.08
1	BY	41:ARG	C	42:GLU	N	4.07
1	A2	57:G	O3'	58:U	P	4.06
1	A2	710:U	O3'	711:U	P	4.06
1	A2	1569:A	O3'	1570:A	P	4.06
1	BA	31:VAL	C	32:HIS	N	4.06
1	BH	86:GLN	C	87:ASP	N	4.06
1	AZ	6178:A	O3'	6179:A	P	4.04
1	BI	92:ARG	C	93:THR	N	4.04
1	BM	93:ASP	C	94:ALA	N	4.04
1	A2	280:U	O3'	281:G	P	4.03
1	BT	122:ARG	C	123:ARG	N	4.03
1	BW	24:GLN	C	25:VAL	N	4.03
1	Bg	289:ALA	C	290:VAL	N	4.02
1	BF	202:ALA	C	203:LYS	N	4.01
1	BM	100:TRP	C	101:ALA	N	4.01
1	A2	473:A	O3'	474:A	P	4.00
1	A2	861:U	O3'	862:A	P	4.00
1	A2	831:U	O3'	832:U	P	3.99
1	Bd	50:ILE	C	51:GLY	N	3.99
1	A2	1644:C	O3'	1645:G	P	3.98
1	BR	54:THR	C	55:THR	N	3.98
1	A2	1580:C	O3'	1581:C	P	3.97
1	BB	227:ALA	C	228:LEU	N	3.97
1	BK	29:GLN	C	30:ALA	N	3.96
1	BR	27:ASP	C	28:PHE	N	3.96

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	182:A	O3'	183:U	P	3.95
1	BI	120:THR	C	121:LEU	N	3.95
1	A2	828:U	O3'	829:A	P	3.94
1	BB	96:LEU	C	97:LEU	N	3.94
1	BO	97:GLY	C	98:GLY	N	3.94
1	Bg	99:THR	C	100:TYR	N	3.94
1	BA	100:GLY	C	101:ARG	N	3.93
1	BR	102:VAL	C	103:ASP	N	3.93
1	BS	71:GLN	C	72:ILE	N	3.93
1	Be	43:ARG	C	44:PHE	N	3.93
1	BB	73:LEU	C	74:GLN	N	3.92
1	Bb	42:ASN	C	43:ILE	N	3.92
1	Bg	206:PRO	C	207:ASP	N	3.92
1	A2	131:C	O3'	132:U	P	3.91
1	A2	478:A	O3'	479:C	P	3.91
1	A2	885:G	O3'	886:U	P	3.91
1	BQ	71:GLY	C	72:GLY	N	3.91
1	BX	36:THR	C	37:ALA	N	3.91
1	A2	471:A	O3'	472:U	P	3.90
1	BC	89:GLN	C	90:THR	N	3.90
1	BT	104:VAL	C	105:LEU	N	3.90
1	BH	146:GLY	C	147:ASN	N	3.89
1	BS	120:ARG	C	121:ALA	N	3.89
1	A2	1560:U	O3'	1561:U	P	3.88
1	BA	179:ARG	C	180:GLU	N	3.88
1	BF	212:LYS	C	213:LYS	N	3.88
1	BI	144:ALA	C	145:ALA	N	3.88
1	A2	644:C	O3'	645:C	P	3.87
1	BQ	36:ILE	C	37:THR	N	3.86
1	BQ	51:PRO	C	52:LEU	N	3.86
1	BZ	49:ARG	C	50:ILE	N	3.86
1	Bf	148:TYR	C	149:LYS	N	3.86
1	BA	48:ILE	C	49:ASN	N	3.85
1	BB	151:LYS	C	152:ALA	N	3.85
1	Bc	65:ARG	C	66:LEU	N	3.85
1	Bd	55:PHE	C	56:ARG	N	3.85
1	BB	71:ALA	C	72:ASP	N	3.83
1	BE	126:VAL	C	127:LYS	N	3.83
1	BG	112:VAL	C	113:ILE	N	3.82
1	BR	2:GLY	C	3:ARG	N	3.82
1	BS	26:ILE	C	27:LYS	N	3.82
1	A2	704:C	O3'	705:U	P	3.81

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	1294:G	O3'	1295:G	P	3.81
1	AZ	6200:U	O3'	6201:U	P	3.81
1	BA	45:VAL	C	46:HIS	N	3.81
1	BK	91:TYR	C	92:ILE	N	3.81
1	Bd	7:TRP	C	8:PHE	N	3.81
1	Bg	227:ALA	C	228:LYS	N	3.81
1	BU	102:ARG	C	103:ILE	N	3.80
1	A2	195:G	O3'	196:G	P	3.79
1	A2	1042:G	O3'	1043:A	P	3.79
1	A2	82:U	O3'	83:G	P	3.78
1	BD	55:THR	C	56:GLN	N	3.78
1	BP	59:LYS	C	60:LEU	N	3.78
1	A2	1069:A	O3'	1070:C	P	3.77
1	A2	1180:C	O3'	1181:U	P	3.77
1	BA	123:VAL	C	124:THR	N	3.77
1	BB	204:ILE	C	205:PHE	N	3.77
1	BH	5:GLN	C	6:ALA	N	3.77
1	BM	103:LEU	C	104:GLY	N	3.77
1	BT	28:LEU	C	29:GLU	N	3.77
1	BF	47:SER	C	48:PHE	N	3.76
1	BH	106:SER	C	107:ARG	N	3.76
1	Bg	97:GLY	C	98:GLU	N	3.76
1	BF	38:THR	C	39:GLU	N	3.75
1	BO	82:LYS	C	83:ILE	N	3.75
1	BW	98:GLN	C	99:PHE	N	3.75
1	Bg	151:VAL	C	152:SER	N	3.75
1	BA	146:LEU	C	147:THR	N	3.74
1	BI	111:GLN	C	112:TRP	N	3.74
1	BV	51:VAL	C	52:THR	N	3.74
1	A2	1409:G	O3'	1410:A	P	3.73
1	BT	22:LEU	C	23:GLN	N	3.73
1	A2	1373:C	O3'	1374:C	P	3.72
1	AZ	6038:U	O3'	6039:G	P	3.72
1	BE	78:THR	C	79:ASP	N	3.72
1	BU	101:LYS	C	102:ARG	N	3.72
1	A2	414:C	O3'	415:C	P	3.71
1	A2	734:A	O3'	735:C	P	3.71
1	BU	87:HIS	C	88:LYS	N	3.71
1	A2	1297:G	O3'	1298:U	P	3.70
1	BF	69:PHE	C	70:VAL	N	3.69
1	BF	112:ARG	C	113:ILE	N	3.69
1	BQ	70:THR	C	71:GLY	N	3.69

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BY	64:PHE	C	65:GLY	N	3.69
1	A2	88:U	O3'	89:G	P	3.68
1	A2	1788:G	O3'	1789:G	P	3.68
1	BJ	28:LEU	C	29:LYS	N	3.68
1	Bd	35:GLY	C	36:LEU	N	3.68
1	A2	743:U	O3'	744:U	P	3.67
1	BE	260:GLY	C	261:LEU	N	3.67
1	BQ	128:LYS	C	129:PHE	N	3.67
1	A2	197:A	O3'	198:A	P	3.66
1	A2	1327:C	O3'	1328:G	P	3.66
1	AZ	6177:A	O3'	6178:A	P	3.66
1	BI	55:TYR	C	56:ARG	N	3.66
1	A2	783:G	O3'	784:C	P	3.65
1	A2	889:U	O3'	890:C	P	3.65
1	BE	201:HIS	C	202:ASP	N	3.65
1	BT	75:LYS	C	76:LEU	N	3.65
1	A2	629:U	O3'	630:A	P	3.64
1	A2	1509:C	O3'	1510:U	P	3.64
1	BE	130:GLN	C	131:LEU	N	3.64
1	BF	58:LEU	C	59:VAL	N	3.64
1	BZ	93:SER	C	94:LYS	N	3.64
1	A2	544:A	O3'	545:A	P	3.63
1	A2	843:U	O3'	844:A	P	3.63
1	BD	196:ARG	C	197:THR	N	3.63
1	BI	39:GLY	C	40:ALA	N	3.63
1	BS	17:LEU	C	18:LEU	N	3.63
1	BT	39:THR	C	40:SER	N	3.63
1	BV	72:LEU	C	73:ALA	N	3.63
1	BT	14:PHE	C	15:ILE	N	3.62
1	BM	118:ALA	C	119:SER	N	3.61
1	Be	19:PRO	C	20:LYS	N	3.61
1	A2	369:A	O3'	370:A	P	3.60
1	AZ	6111:G	O3'	6112:C	P	3.60
1	AZ	6191:A	O3'	6195:G	P	3.60
1	BA	8:ASP	C	9:LEU	N	3.60
1	BC	98:PHE	C	99:LYS	N	3.60
1	BI	93:THR	C	94:ASN	N	3.60
1	BK	37:THR	C	38:LYS	N	3.60
1	Bg	254:ALA	C	255:ALA	N	3.60
1	A2	370:A	O3'	371:G	P	3.59
1	A2	829:A	O3'	830:U	P	3.59
1	BA	144:ILE	C	145:ALA	N	3.59

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BD	39:VAL	C	40:ARG	N	3.59
1	BZ	102:THR	C	103:ARG	N	3.59
1	Bb	54:VAL	C	55:THR	N	3.59
1	A2	1370:U	O3'	1371:A	P	3.58
1	BA	70:PRO	C	71:GLU	N	3.58
1	BH	56:LYS	C	57:ALA	N	3.58
1	BI	80:GLY	C	81:VAL	N	3.58
1	BF	40:ILE	C	41:LYS	N	3.57
1	BS	69:ILE	C	70:VAL	N	3.57
1	Be	36:LYS	C	37:ARG	N	3.57
1	BL	26:LYS	C	27:THR	N	3.56
1	BY	114:ARG	C	115:ASP	N	3.56
1	Bd	37:ASN	C	38:ILE	N	3.56
1	Bg	103:PHE	C	104:VAL	N	3.56
1	A2	396:G	O3'	397:A	P	3.55
1	A2	1224:A	O3'	1225:U	P	3.55
1	BU	31:VAL	C	32:LYS	N	3.55
1	BW	17:ALA	C	18:GLU	N	3.55
1	Bc	66:LEU	C	67:ARG	N	3.55
1	A2	241:U	O3'	242:U	P	3.54
1	A2	1578:U	O3'	1579:U	P	3.54
1	AZ	6058:A	O3'	6059:G	P	3.54
1	BH	111:LYS	C	112:ARG	N	3.54
1	BI	89:GLU	C	90:LEU	N	3.54
1	BM	121:VAL	C	122:VAL	N	3.54
1	BP	30:THR	C	31:GLU	N	3.54
1	BT	19:ALA	C	20:SER	N	3.54
1	A2	1667:A	O3'	1668:G	P	3.53
1	AZ	6211:U	O3'	6212:U	P	3.53
1	BF	149:VAL	C	150:GLY	N	3.53
1	BI	43:ILE	C	44:HIS	N	3.53
1	BU	65:ILE	C	66:SER	N	3.53
1	BU	108:ILE	C	109:GLU	N	3.53
1	BY	65:GLY	C	66:GLY	N	3.53
1	Bg	57:PRO	C	58:VAL	N	3.53
1	Bg	183:LEU	C	184:ASN	N	3.53
1	BA	13:ASP	C	14:ALA	N	3.52
1	BB	129:THR	C	130:SER	N	3.52
1	BF	73:THR	C	74:ALA	N	3.52
1	BH	107:ARG	C	108:GLN	N	3.52
1	BM	41:LEU	C	42:ALA	N	3.52
1	BS	64:GLU	C	65:GLU	N	3.52

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	1202:A	O3'	1203:A	P	3.51
1	BN	72:MET	C	73:ARG	N	3.51
1	A2	525:A	O3'	526:A	P	3.50
1	A2	1536:G	O3'	1537:C	P	3.50
1	BA	86:VAL	C	87:LEU	N	3.50
1	BF	148:ARG	C	149:VAL	N	3.50
1	A2	1451:C	O3'	1452:U	P	3.49
1	A2	1680:G	O3'	1681:A	P	3.49
1	BT	133:ASP	C	134:ARG	N	3.49
1	A2	676:G	O3'	677:G	P	3.48
1	AZ	6149:A	O3'	6150:U	P	3.48
1	BG	220:LYS	C	221:ALA	N	3.48
1	BJ	77:ILE	C	78:ARG	N	3.48
1	BM	104:GLY	C	105:LYS	N	3.48
1	BM	119:SER	C	120:VAL	N	3.48
1	BW	51:GLU	C	52:TYR	N	3.48
1	BW	83:ILE	C	84:GLY	N	3.48
1	Bb	61:THR	C	62:ILE	N	3.48
1	A2	1645:G	O3'	1646:C	P	3.47
1	BA	202:TYR	C	203:PHE	N	3.47
1	BB	153:HIS	C	154:SER	N	3.47
1	BI	110:ARG	C	111:GLN	N	3.47
1	BP	58:LYS	C	59:LYS	N	3.47
1	BW	3:ARG	C	4:SER	N	3.47
1	Bg	278:PHE	C	279:ALA	N	3.47
1	A2	66:U	O3'	67:A	P	3.46
1	BA	40:ALA	C	41:ARG	N	3.46
1	BB	199:ASN	C	200:ALA	N	3.46
1	BE	217:THR	C	218:PHE	N	3.46
1	BG	12:SER	C	13:GLN	N	3.46
1	BQ	12:LYS	C	13:LYS	N	3.46
1	BR	78:ARG	C	79:GLU	N	3.46
1	Bg	101:GLN	C	102:ARG	N	3.46
1	BI	15:GLY	C	16:ALA	N	3.45
1	Bg	32:LEU	C	33:LEU	N	3.45
1	A2	867:G	O3'	868:G	P	3.44
1	BJ	161:THR	C	162:SER	N	3.44
1	BZ	53:GLU	C	54:VAL	N	3.44
1	Bg	55:GLY	C	56:VAL	N	3.44
1	Bg	108:SER	C	109:ASP	N	3.44
1	Bg	215:GLY	C	216:LYS	N	3.44
1	BE	241:GLY	C	242:LYS	N	3.43

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BG	160:ARG	C	161:GLU	N	3.43
1	BP	78:THR	C	79:HIS	N	3.43
1	BP	123:TYR	C	124:THR	N	3.43
1	Ba	61:GLU	C	62:TYR	N	3.43
1	A2	397:A	O3'	398:G	P	3.42
1	BC	86:VAL	C	87:GLN	N	3.42
1	BM	29:LYS	C	30:VAL	N	3.42
1	A2	792:U	O3'	793:A	P	3.41
1	A2	1246:C	O3'	1247:U	P	3.41
1	BF	39:GLU	C	40:ILE	N	3.41
1	BF	48:PHE	C	49:GLU	N	3.41
1	BG	153:VAL	C	154:ARG	N	3.41
1	A2	257:A	O3'	258:C	P	3.40
1	A2	371:G	O3'	372:G	P	3.40
1	A2	781:U	O3'	782:U	P	3.40
1	A2	1787:C	O3'	1788:G	P	3.40
1	AZ	6174:G	O3'	6175:A	P	3.40
1	BF	211:ILE	C	212:LYS	N	3.40
1	BG	141:ILE	C	142:ARG	N	3.40
1	BQ	68:ARG	C	69:VAL	N	3.40
1	BU	40:ASN	C	41:ILE	N	3.40
1	A2	1492:A	O3'	1493:A	P	3.39
1	BB	72:ASP	C	73:LEU	N	3.39
1	BB	123:ALA	C	124:ASN	N	3.39
1	BB	130:SER	C	131:ASP	N	3.39
1	BD	119:ALA	C	120:TYR	N	3.39
1	BE	131:LEU	C	132:GLY	N	3.39
1	BS	30:TYR	C	31:ALA	N	3.39
1	A2	461:G	O3'	462:G	P	3.38
1	A2	1061:A	O3'	1062:A	P	3.38
1	A2	1362:U	O3'	1363:U	P	3.38
1	A2	1406:A	O3'	1407:U	P	3.38
1	BL	75:VAL	C	76:VAL	N	3.38
1	BO	85:ALA	C	86:THR	N	3.38
1	Bb	6:ASP	C	7:LEU	N	3.38
1	A2	1672:G	O3'	1673:G	P	3.37
1	AZ	6132:A	O3'	6133:G	P	3.37
1	BJ	81:VAL	C	82:ARG	N	3.37
1	BL	42:PHE	C	43:LYS	N	3.37
1	BR	26:LEU	C	27:ASP	N	3.37
1	Bb	34:ASP	C	35:VAL	N	3.37
1	Bd	36:LEU	C	37:ASN	N	3.37

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BG	181:PRO	C	182:GLN	N	3.36
1	BH	155:ASP	C	156:SER	N	3.36
1	Bg	300:THR	C	301:LEU	N	3.36
1	A2	1266:U	O3'	1267:G	P	3.35
1	A2	1308:G	O3'	1309:C	P	3.35
1	BJ	20:GLU	C	21:SER	N	3.35
1	A2	1434:U	O3'	1435:G	P	3.34
1	A2	1474:G	O3'	1475:A	P	3.34
1	A2	1499:G	O3'	1500:C	P	3.34
1	A2	1576:A	O3'	1577:A	P	3.34
1	AZ	6181:C	O3'	6186:U	P	3.34
1	BP	71:GLU	C	72:LYS	N	3.34
1	A2	850:A	O3'	851:U	P	3.33
1	A2	1321:A	O3'	1322:A	P	3.33
1	BD	61:GLU	C	62:ASN	N	3.33
1	BG	27:PHE	C	28:PHE	N	3.33
1	BT	21:PHE	C	22:LEU	N	3.33
1	A2	500:C	O3'	501:U	P	3.32
1	A2	1001:A	O3'	1002:G	P	3.32
1	A2	1366:U	O3'	1367:G	P	3.32
1	A2	1711:C	O3'	1712:A	P	3.32
1	AZ	6101:U	O3'	6102:A	P	3.32
1	BA	95:ALA	C	96:THR	N	3.32
1	BB	229:MET	C	230:ALA	N	3.32
1	BF	22:PRO	C	23:VAL	N	3.32
1	BI	83:TYR	C	84:HIS	N	3.32
1	Bg	294:TRP	C	295:SER	N	3.32
1	A2	505:A	O3'	506:A	P	3.31
1	A2	538:A	O3'	539:G	P	3.31
1	A2	555:A	O3'	556:A	P	3.31
1	A2	745:U	O3'	746:A	P	3.31
1	A2	762:A	O3'	763:G	P	3.31
1	A2	1163:A	O3'	1164:G	P	3.31
1	A2	1346:A	O3'	1347:U	P	3.31
1	BG	139:ASN	C	140:ASN	N	3.31
1	BJ	83:VAL	C	84:GLY	N	3.31
1	BK	19:GLY	C	20:VAL	N	3.31
1	BX	22:ASN	C	23:ARG	N	3.31
1	Bg	222:LEU	C	223:TRP	N	3.31
1	A2	479:C	O3'	480:G	P	3.30
1	AZ	6122:C	O3'	6123:A	P	3.30
1	BD	91:VAL	C	92:GLN	N	3.30

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BG	24:ILE	C	25:ARG	N	3.30
1	BG	36:VAL	C	37:ASP	N	3.30
1	BI	8:ARG	C	9:HIS	N	3.30
1	BI	64:ASN	C	65:PHE	N	3.30
1	BP	41:VAL	C	42:ARG	N	3.30
1	BS	87:ASN	C	88:ARG	N	3.30
1	Bb	52:THR	C	53:ALA	N	3.30
1	Bg	231:MET	C	232:TYR	N	3.30
1	A2	638:U	O3'	639:U	P	3.29
1	A2	882:U	O3'	883:C	P	3.29
1	A2	1456:C	O3'	1457:C	P	3.29
1	A2	1494:C	O3'	1495:C	P	3.29
1	BB	40:ASN	C	41:ALA	N	3.29
1	BD	117:ARG	C	118:ALA	N	3.29
1	BF	138:THR	C	139:ASN	N	3.29
1	BF	182:ALA	C	183:ALA	N	3.29
1	BS	61:LEU	C	62:THR	N	3.29
1	BS	93:THR	C	94:ASP	N	3.29
1	BS	114:GLU	C	115:ARG	N	3.29
1	BX	82:LYS	C	83:VAL	N	3.29
1	Ba	51:ARG	C	52:ASP	N	3.29
1	Bg	141:LEU	C	142:ALA	N	3.29
1	Bg	226:ALA	C	227:ALA	N	3.29
1	Bg	242:SER	C	243:LEU	N	3.29
1	A2	914:G	O3'	915:A	P	3.28
1	A2	1365:C	O3'	1366:U	P	3.28
1	AZ	6059:G	O3'	6060:A	P	3.28
1	AZ	6107:U	O3'	6108:U	P	3.28
1	BE	189:LEU	C	190:GLY	N	3.28
1	BI	38:ILE	C	39:GLY	N	3.28
1	BI	97:THR	C	98:LYS	N	3.28
1	BP	47:ARG	C	48:GLY	N	3.28
1	BS	10:SER	C	11:PHE	N	3.28
1	BS	94:ASP	C	95:GLY	N	3.28
1	BX	75:GLN	C	76:LEU	N	3.28
1	BZ	68:ARG	C	69:LEU	N	3.28
1	A2	110:U	O3'	111:U	P	3.27
1	A2	252:U	O3'	253:A	P	3.27
1	A2	1302:U	O3'	1303:U	P	3.27
1	BD	224:ASP	C	225:TYR	N	3.27
1	BE	95:THR	C	96:ASN	N	3.27
1	BG	104:PRO	C	105:ASP	N	3.27

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BH	175:LYS	C	176:LEU	N	3.27
1	BQ	56:GLY	C	57:LEU	N	3.27
1	BS	72:ILE	C	73:MET	N	3.27
1	BS	109:LEU	C	110:ARG	N	3.27
1	BT	126:GLU	C	127:ASN	N	3.27
1	Ba	12:LYS	C	13:LYS	N	3.27
1	Bc	29:ARG	C	30:VAL	N	3.27
1	Bg	15:GLY	C	16:HIS	N	3.27
1	A2	1117:U	O3'	1118:G	P	3.26
1	BB	195:LYS	C	196:GLU	N	3.26
1	BE	110:ALA	C	111:VAL	N	3.26
1	BE	175:PHE	C	176:ASP	N	3.26
1	BH	89:HIS	C	90:VAL	N	3.26
1	BI	91:VAL	C	92:ARG	N	3.26
1	BI	99:ALA	C	100:ALA	N	3.26
1	BQ	80:ALA	C	81:ILE	N	3.26
1	BW	48:GLY	C	49:GLU	N	3.26
1	Bd	54:LYS	C	55:PHE	N	3.26
1	A2	389:G	O3'	390:G	P	3.25
1	A2	1254:U	O3'	1255:G	P	3.25
1	A2	1332:C	O3'	1333:C	P	3.25
1	AZ	6163:C	O3'	6164:U	P	3.25
1	BA	197:ILE	C	198:MET	N	3.25
1	BB	202:LYS	C	203:ASP	N	3.25
1	BE	40:GLU	C	41:SER	N	3.25
1	BF	215:ASP	C	216:GLU	N	3.25
1	BG	32:ILE	C	33:GLY	N	3.25
1	BH	8:ILE	C	9:LEU	N	3.25
1	BI	119:GLN	C	120:THR	N	3.25
1	BI	158:SER	C	159:GLN	N	3.25
1	BK	88:PRO	C	89:GLY	N	3.25
1	BU	104:THR	C	105:GLN	N	3.25
1	Bg	245:PHE	C	246:SER	N	3.25
1	Bg	271:VAL	C	272:ASP	N	3.25
1	A2	750:U	O3'	751:G	P	3.24
1	BD	51:ARG	C	52:ALA	N	3.24
1	BD	172:THR	C	173:ARG	N	3.24
1	BD	176:LEU	C	177:MET	N	3.24
1	BF	95:ASN	C	96:SER	N	3.24
1	BF	189:THR	C	190:ILE	N	3.24
1	BL	143:SER	C	144:ALA	N	3.24
1	BQ	83:GLN	C	84:ALA	N	3.24

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BR	7:LYS	C	8:THR	N	3.24
1	BU	61:LYS	C	62:VAL	N	3.24
1	Bb	12:ALA	C	13:ALA	N	3.24
1	Be	9:ALA	C	10:ARG	N	3.24
1	Be	35:TYR	C	36:LYS	N	3.24
1	A2	643:G	O3'	644:C	P	3.23
1	A2	987:G	O3'	988:A	P	3.23
1	A2	1735:U	O3'	1736:G	P	3.23
1	AZ	6053:U	O3'	6054:U	P	3.23
1	BD	56:GLN	C	57:ASP	N	3.23
1	BD	120:TYR	C	121:GLY	N	3.23
1	BF	99:MET	C	100:ASN	N	3.23
1	BQ	3:ALA	C	4:VAL	N	3.23
1	BU	37:VAL	C	38:SER	N	3.23
1	BX	34:LEU	C	35:GLY	N	3.23
1	BY	130:ALA	C	131:ARG	N	3.23
1	Bb	36:LYS	C	37:CYS	N	3.23
1	Bg	111:MET	C	112:SER	N	3.23
1	A2	1156:C	O3'	1157:A	P	3.22
1	AZ	6031:G	O3'	6032:U	P	3.22
1	BB	212:VAL	C	213:ARG	N	3.22
1	BC	119:LYS	C	120:GLU	N	3.22
1	BD	38:GLU	C	39:VAL	N	3.22
1	BD	111:ASN	C	112:GLY	N	3.22
1	BG	57:ASP	C	58:LYS	N	3.22
1	BK	15:LEU	C	16:PHE	N	3.22
1	BM	36:LEU	C	37:VAL	N	3.22
1	BQ	106:LYS	C	107:LYS	N	3.22
1	BY	97:ALA	C	98:GLU	N	3.22
1	Bb	13:ALA	C	14:SER	N	3.22
1	Bg	147:HIS	C	148:ASN	N	3.22
1	A2	1189:A	O3'	1190:C	P	3.21
1	A2	1579:U	O3'	1580:C	P	3.21
1	BC	246:GLU	C	247:ALA	N	3.21
1	BD	84:ILE	C	85:VAL	N	3.21
1	BD	85:VAL	C	86:LEU	N	3.21
1	BD	142:LEU	C	143:ARG	N	3.21
1	BE	197:HIS	C	198:LYS	N	3.21
1	BE	256:ARG	C	257:ALA	N	3.21
1	BI	154:SER	C	155:SER	N	3.21
1	BP	17:TYR	C	18:ARG	N	3.21
1	Bg	59:ARG	C	60:SER	N	3.21

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Bg	212:ALA	C	213:SER	N	3.21
1	A2	97:C	O3'	98:U	P	3.20
1	A2	186:C	O3'	187:G	P	3.20
1	BC	123:GLY	C	124:ALA	N	3.20
1	BG	84:TYR	C	85:ARG	N	3.20
1	BI	4:SER	C	5:ARG	N	3.20
1	BT	3:GLY	C	4:VAL	N	3.20
1	BU	51:VAL	C	52:LYS	N	3.20
1	BX	118:PRO	C	119:GLY	N	3.20
1	BY	19:ALA	C	20:ARG	N	3.20
1	A2	204:G	O3'	205:U	P	3.19
1	A2	451:A	O3'	452:A	P	3.19
1	A2	906:A	O3'	907:A	P	3.19
1	BH	4:PRO	C	5:GLN	N	3.19
1	BO	110:LEU	C	111:ARG	N	3.19
1	BP	68:PRO	C	69:GLU	N	3.19
1	BY	103:ALA	C	104:SER	N	3.19
1	Bb	75:GLU	C	76:GLY	N	3.19
1	Bc	62:GLU	C	63:ALA	N	3.19
1	Be	46:ASN	C	47:VAL	N	3.19
1	A2	84:A	O3'	85:A	P	3.18
1	BC	70:ASP	C	71:THR	N	3.18
1	BC	124:ALA	C	125:ILE	N	3.18
1	BE	203:GLY	C	204:GLY	N	3.18
1	BI	161:SER	C	162:ALA	N	3.18
1	BL	98:ASN	C	99:ARG	N	3.18
1	BO	79:VAL	C	80:HIS	N	3.18
1	BR	90:ALA	C	91:ALA	N	3.18
1	BT	92:LYS	C	93:HIS	N	3.18
1	BX	46:SER	C	47:SER	N	3.18
1	Bb	71:ALA	C	72:LYS	N	3.18
1	A2	178:U	O3'	179:A	P	3.17
1	A2	272:U	O3'	273:G	P	3.17
1	A2	812:A	O3'	813:U	P	3.17
1	A2	1610:G	O3'	1611:A	P	3.17
1	BB	174:LYS	C	175:GLU	N	3.17
1	BE	56:LEU	C	57:ASN	N	3.17
1	BM	57:ALA	C	58:LEU	N	3.17
1	BQ	28:LEU	C	29:ILE	N	3.17
1	BU	62:VAL	C	63:LEU	N	3.17
1	Bg	170:ILE	C	171:SER	N	3.17
1	Bg	241:PHE	C	242:SER	N	3.17

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	169:A	O3'	170:U	P	3.16
1	A2	319:U	O3'	320:U	P	3.16
1	BF	157:ARG	C	158:GLN	N	3.16
1	BH	150:GLN	C	151:LYS	N	3.16
1	BK	6:GLU	C	7:ASP	N	3.16
1	BN	143:SER	C	144:ALA	N	3.16
1	BP	13:LYS	C	14:THR	N	3.16
1	BT	108:LEU	C	109:GLU	N	3.16
1	BW	45:GLY	C	46:TYR	N	3.16
1	BX	61:SER	C	62:LYS	N	3.16
1	Bg	14:GLU	C	15:GLY	N	3.16
1	Bg	237:GLN	C	238:ASP	N	3.16
1	A2	137:U	O3'	138:A	P	3.15
1	A2	845:G	O3'	846:G	P	3.15
1	AZ	6092:U	O3'	6093:A	P	3.15
1	BD	194:LYS	C	195:SER	N	3.15
1	BE	36:HIS	C	37:LYS	N	3.15
1	BG	55:GLY	C	56:ASN	N	3.15
1	BL	25:VAL	C	26:LYS	N	3.15
1	BO	61:MET	C	62:LEU	N	3.15
1	BT	36:ILE	C	37:VAL	N	3.15
1	BW	99:PHE	C	100:GLY	N	3.15
1	BY	61:ARG	C	62:THR	N	3.15
1	AZ	6035:U	O3'	6036:C	P	3.14
1	BC	121:VAL	C	122:ALA	N	3.14
1	BC	168:ARG	C	169:LEU	N	3.14
1	BD	7:LYS	C	8:LYS	N	3.14
1	BD	147:ALA	C	148:LYS	N	3.14
1	BF	79:ASN	C	80:LYS	N	3.14
1	BH	140:VAL	C	141:ARG	N	3.14
1	BI	194:ARG	C	195:ARG	N	3.14
1	BJ	19:TYR	C	20:GLU	N	3.14
1	BJ	115:LYS	C	116:LEU	N	3.14
1	BJ	166:GLY	C	167:ALA	N	3.14
1	BL	18:HIS	C	19:ILE	N	3.14
1	BM	67:THR	C	68:GLU	N	3.14
1	BN	121:ARG	C	122:ILE	N	3.14
1	BV	60:ARG	C	61:SER	N	3.14
1	BX	91:GLY	C	92:CYS	N	3.14
1	Bg	256:THR	C	257:ALA	N	3.14
1	A2	404:G	O3'	405:C	P	3.13
1	AZ	6080:G	O3'	6081:U	P	3.13

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BB	49:ASN	C	50:LYS	N	3.13
1	BB	218:LEU	C	219:LYS	N	3.13
1	BJ	114:TYR	C	115:LYS	N	3.13
1	BS	20:THR	C	21:ASN	N	3.13
1	BU	103:ILE	C	104:THR	N	3.13
1	Bg	259:GLY	C	260:ILE	N	3.13
1	A2	61:A	O3'	62:A	P	3.12
1	A2	163:G	O3'	164:A	P	3.12
1	A2	269:G	O3'	270:C	P	3.12
1	A2	561:G	O3'	562:G	P	3.12
1	A2	613:G	O3'	614:C	P	3.12
1	A2	1458:G	O3'	1459:C	P	3.12
1	A2	1533:C	O3'	1534:G	P	3.12
1	AZ	6220:U	O3'	6221:U	P	3.12
1	BF	223:SER	C	224:ASN	N	3.12
1	BI	47:ARG	C	48:THR	N	3.12
1	BM	92:ALA	C	93:ASP	N	3.12
1	BQ	104:GLU	C	105:LEU	N	3.12
1	BV	42:GLU	C	43:GLY	N	3.12
1	A2	64:U	O3'	65:A	P	3.11
1	A2	1116:A	O3'	1117:U	P	3.11
1	BB	211:HIS	C	212:VAL	N	3.11
1	BD	92:GLN	C	93:ASP	N	3.11
1	BD	102:ALA	C	103:GLU	N	3.11
1	BG	9:VAL	C	10:ASN	N	3.11
1	BI	163:GLY	C	164:ARG	N	3.11
1	BP	63:ALA	C	64:LYS	N	3.11
1	BS	32:LEU	C	33:THR	N	3.11
1	BY	71:GLY	C	72:PHE	N	3.11
1	Bc	25:VAL	C	26:THR	N	3.11
1	A2	78:A	O3'	79:C	P	3.10
1	A2	892:A	O3'	893:U	P	3.10
1	BB	171:ILE	C	172:LEU	N	3.10
1	BD	63:GLY	C	64:ARG	N	3.10
1	BD	83:THR	C	84:ILE	N	3.10
1	BH	74:GLN	C	75:THR	N	3.10
1	BU	80:GLU	C	81:THR	N	3.10
1	BW	31:SER	C	32:LYS	N	3.10
1	Bf	99:ALA	C	100:ALA	N	3.10
1	A2	1238:A	O3'	1239:U	P	3.09
1	BB	121:ILE	C	122:GLU	N	3.09
1	BC	43:ARG	C	44:LEU	N	3.09

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BG	179:VAL	C	180:THR	N	3.09
1	BH	55:LYS	C	56:LYS	N	3.09
1	BK	69:THR	C	70:GLU	N	3.09
1	BN	80:LEU	C	81:ALA	N	3.09
1	BR	38:ILE	C	39:ALA	N	3.09
1	BY	26:ASP	C	27:VAL	N	3.09
1	Ba	53:LEU	C	54:SER	N	3.09
1	Bb	33:LEU	C	34:ASP	N	3.09
1	Bg	130:THR	C	131:ILE	N	3.09
1	A2	48:G	O3'	49:C	P	3.08
1	A2	119:A	O3'	120:U	P	3.08
1	A2	1423:U	O3'	1424:A	P	3.08
1	BA	101:ARG	C	102:PHE	N	3.08
1	BE	57:ASN	C	58:GLY	N	3.08
1	BO	80:HIS	C	81:VAL	N	3.08
1	BQ	7:VAL	C	8:GLN	N	3.08
1	BQ	115:THR	C	116:LEU	N	3.08
1	BX	128:SER	C	129:GLY	N	3.08
1	Bg	181:TRP	C	182:ASN	N	3.08
1	A2	1052:U	O3'	1053:G	P	3.07
1	BB	23:PRO	C	24:PHE	N	3.07
1	BD	182:LEU	C	183:GLY	N	3.07
1	BF	85:ALA	C	86:GLN	N	3.07
1	BF	91:GLU	C	92:ARG	N	3.07
1	BI	136:SER	C	137:LYS	N	3.07
1	BK	44:LYS	C	45:ALA	N	3.07
1	BL	45:PRO	C	46:LYS	N	3.07
1	BN	105:ASN	C	106:ARG	N	3.07
1	BN	110:ASP	C	111:ALA	N	3.07
1	BN	118:ILE	C	119:GLU	N	3.07
1	BO	89:THR	C	90:ARG	N	3.07
1	BO	135:ARG	C	136:ARG	N	3.07
1	BP	122:THR	C	123:TYR	N	3.07
1	BQ	88:GLY	C	89:LEU	N	3.07
1	A2	1281:G	O3'	1282:U	P	3.06
1	A2	1659:A	O3'	1660:A	P	3.06
1	A2	1744:A	O3'	1745:G	P	3.06
1	BB	80:SER	C	81:PHE	N	3.06
1	BD	106:LYS	C	107:PHE	N	3.06
1	BE	18:TRP	C	19:LEU	N	3.06
1	BE	67:GLN	C	68:ARG	N	3.06
1	BE	93:ASP	C	94:ALA	N	3.06

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BJ	42:ILE	C	43:TYR	N	3.06
1	BK	75:TYR	C	76:LEU	N	3.06
1	BS	95:GLY	C	96:LYS	N	3.06
1	BT	74:GLY	C	75:LYS	N	3.06
1	BU	60:THR	C	61:LYS	N	3.06
1	BY	102:LYS	C	103:ALA	N	3.06
1	Bg	96:THR	C	97:GLY	N	3.06
1	A2	794:U	O3'	795:U	P	3.05
1	BB	62:LYS	C	63:GLY	N	3.05
1	BB	198:GLU	C	199:ASN	N	3.05
1	BC	140:ARG	C	141:ARG	N	3.05
1	BD	161:GLY	C	162:GLN	N	3.05
1	BE	193:GLY	C	194:THR	N	3.05
1	BF	63:GLN	C	64:VAL	N	3.05
1	BG	30:ALA	C	31:ARG	N	3.05
1	BJ	15:PRO	C	16:LYS	N	3.05
1	BL	33:ARG	C	34:TRP	N	3.05
1	BN	63:ALA	C	64:ARG	N	3.05
1	BO	136:ARG	C	137:LEU	N	3.05
1	BR	62:GLN	C	63:LYS	N	3.05
1	BS	131:LEU	C	132:ARG	N	3.05
1	BU	72:ASN	C	73:GLY	N	3.05
1	BY	75:VAL	C	76:TYR	N	3.05
1	BZ	77:ARG	C	78:ILE	N	3.05
1	A2	767:U	O3'	768:C	P	3.04
1	A2	786:C	O3'	787:G	P	3.04
1	A2	1756:A	O3'	1757:G	P	3.04
1	BD	31:GLU	C	32:GLU	N	3.04
1	BR	43:SER	C	44:LYS	N	3.04
1	BR	66:VAL	C	67:ARG	N	3.04
1	BR	101:ASN	C	102:VAL	N	3.04
1	BW	108:ALA	C	109:GLY	N	3.04
1	BX	65:ASN	C	66:SER	N	3.04
1	Ba	45:VAL	C	46:GLU	N	3.04
1	Bb	60:SER	C	61:THR	N	3.04
1	Bc	28:VAL	C	29:ARG	N	3.04
1	Bf	141:CYS	C	142:GLY	N	3.04
1	A2	853:G	O3'	854:U	P	3.03
1	A2	893:U	O3'	894:U	P	3.03
1	BD	79:TYR	C	80:ALA	N	3.03
1	BH	93:LEU	C	94:ALA	N	3.03
1	BJ	139:GLN	C	140:ILE	N	3.03

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BP	112:LEU	C	113:GLY	N	3.03
1	BT	42:GLY	C	43:ASN	N	3.03
1	BT	60:SER	C	61:VAL	N	3.03
1	Bb	56:CYS	C	57:GLU	N	3.03
1	Bg	88:THR	C	89:LEU	N	3.03
1	Bg	306:THR	C	307:ASP	N	3.03
1	A2	521:A	O3'	522:U	P	3.02
1	A2	597:G	O3'	598:U	P	3.02
1	A2	735:C	O3'	736:C	P	3.02
1	A2	808:U	O3'	809:A	P	3.02
1	A2	1322:A	O3'	1323:C	P	3.02
1	A2	1741:U	O3'	1742:U	P	3.02
1	BB	147:ALA	C	148:ASN	N	3.02
1	BB	214:LYS	C	215:VAL	N	3.02
1	BE	123:LEU	C	124:GLY	N	3.02
1	BH	7:LYS	C	8:ILE	N	3.02
1	BH	103:SER	C	104:ARG	N	3.02
1	BJ	31:ALA	C	32:GLY	N	3.02
1	BL	32:LYS	C	33:ARG	N	3.02
1	BR	24:LEU	C	25:THR	N	3.02
1	BW	30:SER	C	31:SER	N	3.02
1	A2	406:U	O3'	407:A	P	3.01
1	BF	124:LEU	C	125:THR	N	3.01
1	BF	156:ARG	C	157:ARG	N	3.01
1	BL	9:SER	C	10:GLU	N	3.01
1	BM	40:GLY	C	41:LEU	N	3.01
1	BO	22:SER	C	23:PHE	N	3.01
1	BO	49:LYS	C	50:ALA	N	3.01
1	BY	89:TYR	C	90:ARG	N	3.01
1	Bb	32:PHE	C	33:LEU	N	3.01
1	Bg	104:VAL	C	105:GLY	N	3.01
1	Bg	127:ARG	C	128:ASP	N	3.01
1	A2	23:G	O3'	24:U	P	3.00
1	A2	782:U	O3'	783:G	P	3.00
1	A2	1003:A	O3'	1004:U	P	3.00
1	A2	1519:U	O3'	1520:U	P	3.00
1	BF	80:LYS	C	81:ARG	N	3.00
1	BG	73:ILE	C	74:ALA	N	3.00
1	BI	45:SER	C	46:VAL	N	3.00
1	BJ	21:SER	C	22:SER	N	3.00
1	BK	71:GLU	C	72:GLY	N	3.00
1	BL	10:GLU	C	11:ARG	N	3.00

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BM	63:VAL	C	64:SER	N	3.00
1	BP	117:GLY	C	118:GLU	N	3.00
1	BU	50:LEU	C	51:VAL	N	3.00
1	A2	526:A	O3'	527:A	P	2.99
1	BD	37:VAL	C	38:GLU	N	2.99
1	BJ	152:SER	C	153:GLU	N	2.99
1	BN	91:LEU	C	92:ILE	N	2.99
1	BO	44:GLY	C	45:GLY	N	2.99
1	BQ	54:LEU	C	55:VAL	N	2.99
1	BQ	91:ALA	C	92:TYR	N	2.99
1	BR	41:ILE	C	42:GLN	N	2.99
1	BS	108:LYS	C	109:LEU	N	2.99
1	BT	129:GLN	C	130:ARG	N	2.99
1	A2	117:U	O3'	118:U	P	2.98
1	A2	535:A	O3'	536:C	P	2.98
1	A2	1309:C	O3'	1310:U	P	2.98
1	A2	1746:A	O3'	1747:G	P	2.98
1	BD	32:GLU	C	33:GLY	N	2.98
1	BD	96:LEU	C	97:SER	N	2.98
1	BE	77:ARG	C	78:THR	N	2.98
1	BF	216:GLU	C	217:LEU	N	2.98
1	BG	186:ARG	C	187:LYS	N	2.98
1	BM	32:LEU	C	33:ARG	N	2.98
1	BN	34:ILE	C	35:GLU	N	2.98
1	BV	83:TRP	C	84:SER	N	2.98
1	BW	55:ASP	C	56:HIS	N	2.98
1	Bg	24:ALA	C	25:THR	N	2.98
1	A2	393:C	O3'	394:C	P	2.97
1	BA	135:GLU	C	136:ALA	N	2.97
1	BC	62:PRO	C	63:VAL	N	2.97
1	BD	40:ARG	C	41:VAL	N	2.97
1	BD	114:ALA	C	115:ILE	N	2.97
1	BG	59:GLN	C	60:GLY	N	2.97
1	BK	11:ILE	C	12:HIS	N	2.97
1	BV	70:ASN	C	71:ARG	N	2.97
1	BY	2:SER	C	3:ASP	N	2.97
1	Be	32:GLY	C	33:ARG	N	2.97
1	A2	81:G	O3'	82:U	P	2.96
1	A2	87:C	O3'	88:U	P	2.96
1	A2	456:A	O3'	457:G	P	2.96
1	A2	470:A	O3'	471:A	P	2.96
1	A2	1185:U	O3'	1186:U	P	2.96

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BB	137:ILE	C	138:PHE	N	2.96
1	BC	34:GLY	C	35:TRP	N	2.96
1	BC	247:ALA	C	248:SER	N	2.96
1	BH	42:GLN	C	43:PHE	N	2.96
1	BI	12:SER	C	13:ALA	N	2.96
1	BP	62:ALA	C	63:ALA	N	2.96
1	BV	36:VAL	C	37:ALA	N	2.96
1	BX	49:ALA	C	50:LYS	N	2.96
1	A2	339:C	O3'	340:U	P	2.95
1	BA	20:ALA	C	21:ASN	N	2.95
1	BA	196:SER	C	197:ILE	N	2.95
1	BC	131:ILE	C	132:ALA	N	2.95
1	BC	186:LYS	C	187:LEU	N	2.95
1	BF	160:VAL	C	161:ASP	N	2.95
1	BH	120:ALA	C	121:VAL	N	2.95
1	BH	166:LEU	C	167:GLU	N	2.95
1	BJ	61:THR	C	62:ARG	N	2.95
1	BK	4:PRO	C	5:LYS	N	2.95
1	BN	76:LYS	C	77:SER	N	2.95
1	BN	104:ARG	C	105:ASN	N	2.95
1	BN	139:TRP	C	140:LYS	N	2.95
1	BT	95:ASP	C	96:ALA	N	2.95
1	BU	89:ARG	C	90:TYR	N	2.95
1	BX	29:TYR	C	30:LYS	N	2.95
1	Bc	40:ILE	C	41:VAL	N	2.95
1	Bc	52:ASP	C	53:ILE	N	2.95
1	A2	249:U	O3'	250:C	P	2.94
1	A2	262:U	O3'	263:C	P	2.94
1	A2	1625:C	O3'	1626:U	P	2.94
1	BC	53:ILE	C	54:GLU	N	2.94
1	BC	63:VAL	C	64:LYS	N	2.94
1	BC	193:VAL	C	194:GLU	N	2.94
1	BE	61:VAL	C	62:LYS	N	2.94
1	BE	124:GLY	C	125:LYS	N	2.94
1	BF	121:ILE	C	122:ASN	N	2.94
1	BG	81:VAL	C	82:SER	N	2.94
1	BH	167:GLU	C	168:SER	N	2.94
1	BR	83:GLN	C	84:TYR	N	2.94
1	BY	70:VAL	C	71:GLY	N	2.94
1	BY	83:LYS	C	84:LYS	N	2.94
1	Bc	21:SER	C	22:ARG	N	2.94
1	A2	260:U	O3'	261:U	P	2.93

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	321:C	O3'	322:G	P	2.93
1	A2	458:G	O3'	459:G	P	2.93
1	A2	903:U	O3'	904:G	P	2.93
1	BC	207:LEU	C	208:GLU	N	2.93
1	BD	195:SER	C	196:ARG	N	2.93
1	BH	9:LEU	C	10:SER	N	2.93
1	BJ	178:ALA	C	179:ARG	N	2.93
1	BP	107:ILE	C	108:ARG	N	2.93
1	BR	3:ARG	C	4:VAL	N	2.93
1	Bg	232:TYR	C	233:THR	N	2.93
1	A2	994:G	O3'	995:A	P	2.92
1	A2	1326:A	O3'	1327:C	P	2.92
1	A2	1413:U	O3'	1414:U	P	2.92
1	A2	1791:A	O3'	1792:G	P	2.92
1	BD	66:ILE	C	67:ASN	N	2.92
1	BD	89:GLU	C	90:ARG	N	2.92
1	BD	221:SER	C	222:VAL	N	2.92
1	BE	133:LYS	C	134:LYS	N	2.92
1	BI	195:ARG	C	196:LEU	N	2.92
1	BJ	93:LEU	C	94:ASP	N	2.92
1	BJ	95:TYR	C	96:VAL	N	2.92
1	BL	92:HIS	C	93:TYR	N	2.92
1	BL	142:VAL	C	143:SER	N	2.92
1	BO	18:ARG	C	19:ILE	N	2.92
1	BR	52:GLY	C	53:TYR	N	2.92
1	BR	121:VAL	C	122:ILE	N	2.92
1	BT	88:VAL	C	89:ARG	N	2.92
1	BT	119:LYS	C	120:GLY	N	2.92
1	BX	81:LYS	C	82:LYS	N	2.92
1	Ba	60:PRO	C	61:GLU	N	2.92
1	Be	22:GLU	C	23:LYS	N	2.92
1	Be	42:ARG	C	43:ARG	N	2.92
1	A2	757:A	O3'	758:U	P	2.91
1	A2	1214:U	O3'	1215:C	P	2.91
1	BC	182:PRO	C	183:ALA	N	2.91
1	BY	34:ASN	C	35:VAL	N	2.91
1	BY	88:THR	C	89:TYR	N	2.91
1	Ba	73:TYR	C	74:CYS	N	2.91
1	Bc	59:SER	C	60:GLU	N	2.91
1	A2	911:U	O3'	912:U	P	2.90
1	A2	985:G	O3'	986:G	P	2.90
1	AZ	6114:U	O3'	6115:U	P	2.90

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BD	24:PHE	C	25:PHE	N	2.90
1	BE	97:GLU	C	98:ASN	N	2.90
1	BG	50:PHE	C	51:LYS	N	2.90
1	BH	95:GLU	C	96:ARG	N	2.90
1	BH	118:LEU	C	119:THR	N	2.90
1	BI	167:ALA	C	168:CYS	N	2.90
1	BJ	175:ARG	C	176:ASN	N	2.90
1	BT	17:ALA	C	18:TYR	N	2.90
1	BV	15:ARG	C	16:LYS	N	2.90
1	BX	31:LYS	C	32:ARG	N	2.90
1	BY	7:ILE	C	8:ARG	N	2.90
1	BB	105:PHE	C	106:THR	N	2.89
1	BF	217:LEU	C	218:GLU	N	2.89
1	BL	38:ALA	C	39:GLY	N	2.89
1	BN	41:ALA	C	42:ARG	N	2.89
1	BO	31:THR	C	32:ASP	N	2.89
1	A2	749:U	O3'	750:U	P	2.88
1	A2	898:A	O3'	899:G	P	2.88
1	A2	1292:G	O3'	1293:U	P	2.88
1	A2	1657:U	O3'	1658:G	P	2.88
1	BE	185:GLY	C	186:GLY	N	2.88
1	Bg	180:ALA	C	181:TRP	N	2.88
1	A2	1655:A	O3'	1656:U	P	2.87
1	BB	138:PHE	C	139:ALA	N	2.87
1	BD	71:LEU	C	72:LEU	N	2.87
1	BD	160:SER	C	161:GLY	N	2.87
1	BE	103:TYR	C	104:ASP	N	2.87
1	BG	1:MET	C	2:LYS	N	2.87
1	BP	49:MET	C	50:THR	N	2.87
1	BW	5:SER	C	6:VAL	N	2.87
1	BW	44:HIS	C	45:GLY	N	2.87
1	BW	50:PHE	C	51:GLU	N	2.87
1	Bb	51:GLN	C	52:THR	N	2.87
1	A2	334:G	O3'	335:U	P	2.86
1	A2	432:G	O3'	433:C	P	2.86
1	A2	993:A	O3'	994:G	P	2.86
1	A2	998:A	O3'	999:U	P	2.86
1	A2	1035:G	O3'	1036:A	P	2.86
1	A2	1438:G	O3'	1439:C	P	2.86
1	BC	223:GLY	C	224:PHE	N	2.86
1	BE	5:PRO	C	6:LYS	N	2.86
1	BG	192:ALA	C	193:LEU	N	2.86

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BI	58:LEU	C	59:ARG	N	2.86
1	BR	79:GLU	C	80:ARG	N	2.86
1	BT	102:ARG	C	103:LYS	N	2.86
1	BU	57:ARG	C	58:LEU	N	2.86
1	BW	9:ASP	C	10:ALA	N	2.86
1	A2	1282:U	O3'	1283:U	P	2.85
1	A2	1778:G	O3'	1779:U	P	2.85
1	BB	43:VAL	C	44:GLY	N	2.85
1	BC	64:LYS	C	65:GLU	N	2.85
1	BD	12:VAL	C	13:ALA	N	2.85
1	BE	26:CYS	C	27:TYR	N	2.85
1	BE	114:ILE	C	115:THR	N	2.85
1	BE	143:ASP	C	144:GLY	N	2.85
1	BE	192:ILE	C	193:GLY	N	2.85
1	BG	213:ALA	C	214:LYS	N	2.85
1	BH	20:VAL	C	21:ALA	N	2.85
1	BH	79:ARG	C	80:GLU	N	2.85
1	BH	186:PRO	C	187:SER	N	2.85
1	BK	13:GLN	C	14:TYR	N	2.85
1	BL	21:ASN	C	22:ASN	N	2.85
1	BN	120:SER	C	121:ARG	N	2.85
1	BX	131:SER	C	132:LEU	N	2.85
1	Bf	125:THR	C	126:CYS	N	2.85
1	Bg	199:ILE	C	200:ASN	N	2.85
1	A2	636:A	O3'	637:C	P	2.84
1	A2	789:A	O3'	790:U	P	2.84
1	A2	1191:U	O3'	1192:C	P	2.84
1	A2	1334:U	O3'	1335:U	P	2.84
1	A2	1379:C	O3'	1380:U	P	2.84
1	BH	164:TYR	C	165:LYS	N	2.84
1	BJ	35:GLY	C	36:LEU	N	2.84
1	BQ	17:THR	C	18:ALA	N	2.84
1	BS	66:LEU	C	67:GLU	N	2.84
1	BT	101:ASN	C	102:ARG	N	2.84
1	BU	67:THR	C	68:ARG	N	2.84
1	Ba	29:SER	C	30:ILE	N	2.84
1	A2	1429:G	O3'	1430:U	P	2.83
1	A2	1473:U	O3'	1474:G	P	2.83
1	A2	1727:G	O3'	1728:A	P	2.83
1	BH	109:VAL	C	110:GLN	N	2.83
1	BH	135:ILE	C	136:VAL	N	2.83
1	BJ	96:VAL	C	97:LEU	N	2.83

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BJ	122:VAL	C	123:HIS	N	2.83
1	BR	8:THR	C	9:VAL	N	2.83
1	BV	18:SER	C	19:ALA	N	2.83
1	BV	21:ASN	C	22:ARG	N	2.83
1	BX	25:ALA	C	26:GLU	N	2.83
1	BX	133:LEU	C	134:ALA	N	2.83
1	Bg	312:VAL	C	313:TRP	N	2.83
1	A2	106:U	O3'	107:C	P	2.82
1	A2	977:A	O3'	978:A	P	2.82
1	A2	1024:U	O3'	1025:A	P	2.82
1	BE	160:VAL	C	161:LYS	N	2.82
1	BH	68:ALA	C	69:GLY	N	2.82
1	BN	116:ILE	C	117:LEU	N	2.82
1	BQ	129:PHE	C	130:GLY	N	2.82
1	BY	101:GLU	C	102:LYS	N	2.82
1	BZ	80:LEU	C	81:ARG	N	2.82
1	Ba	4:LYS	C	5:ARG	N	2.82
1	Ba	87:ARG	C	88:SER	N	2.82
1	A2	304:U	O3'	305:C	P	2.81
1	A2	598:U	O3'	599:A	P	2.81
1	A2	1276:U	O3'	1277:G	P	2.81
1	BF	88:PRO	C	89:ILE	N	2.81
1	BH	67:LEU	C	68:ALA	N	2.81
1	BI	176:SER	C	177:GLY	N	2.81
1	BO	77:THR	C	78:ALA	N	2.81
1	BY	14:SER	C	15:ASN	N	2.81
1	Ba	39:MET	C	40:ALA	N	2.81
1	Ba	94:ASN	C	95:ARG	N	2.81
1	A2	351:C	O3'	352:A	P	2.80
1	A2	811:A	O3'	812:A	P	2.80
1	A2	1782:A	O3'	1783:C	P	2.80
1	BB	112:SER	C	113:MET	N	2.80
1	BG	193:LEU	C	194:LYS	N	2.80
1	BH	137:GLY	C	138:LYS	N	2.80
1	BI	11:ARG	C	12:SER	N	2.80
1	BI	101:ILE	C	102:VAL	N	2.80
1	Bb	23:THR	C	24:LEU	N	2.80
1	Bg	153:GLN	C	154:VAL	N	2.80
1	A2	18:C	O3'	19:A	P	2.79
1	A2	617:U	O3'	618:U	P	2.79
1	A2	880:C	O3'	881:A	P	2.79
1	A2	1220:C	O3'	1221:A	P	2.79

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	1558:U	O3'	1559:A	P	2.79
1	AZ	6216:U	O3'	6217:A	P	2.79
1	BC	203:LYS	C	204:THR	N	2.79
1	BD	87:TYR	C	88:ALA	N	2.79
1	BD	175:VAL	C	176:LEU	N	2.79
1	BE	54:TYR	C	55:ALA	N	2.79
1	BF	162:VAL	C	163:SER	N	2.79
1	BH	34:LEU	C	35:LYS	N	2.79
1	BL	111:VAL	C	112:SER	N	2.79
1	BO	102:LEU	C	103:ARG	N	2.79
1	A2	27:U	O3'	28:A	P	2.78
1	A2	30:G	O3'	31:C	P	2.78
1	A2	398:G	O3'	399:A	P	2.78
1	A2	1034:C	O3'	1035:G	P	2.78
1	BC	54:GLU	C	55:GLU	N	2.78
1	BE	3:ARG	C	4:GLY	N	2.78
1	BL	68:GLY	C	69:LYS	N	2.78
1	BL	137:PHE	C	138:ASN	N	2.78
1	BP	95:GLY	C	96:ILE	N	2.78
1	BS	33:THR	C	34:THR	N	2.78
1	BW	60:LYS	C	61:ILE	N	2.78
1	BY	76:TYR	C	77:ASN	N	2.78
1	Ba	31:PRO	C	32:LYS	N	2.78
1	BI	180:ASP	C	181:GLY	N	2.77
1	BK	23:ALA	C	24:LYS	N	2.77
1	BK	61:TRP	C	62:GLN	N	2.77
1	BT	6:VAL	C	7:ARG	N	2.77
1	BV	20:THR	C	21:ASN	N	2.77
1	BW	35:ILE	C	36:LYS	N	2.77
1	Ba	85:ARG	C	86:VAL	N	2.77
1	A2	1795:U	O3'	1796:C	P	2.76
1	BC	169:LEU	C	170:ILE	N	2.76
1	BE	234:PRO	C	235:TYR	N	2.76
1	BH	36:ALA	C	37:GLU	N	2.76
1	BI	34:ALA	C	35:ASN	N	2.76
1	BO	90:ARG	C	91:THR	N	2.76
1	BO	120:PRO	C	121:VAL	N	2.76
1	BT	123:ARG	C	124:ILE	N	2.76
1	Bg	40:LYS	C	41:THR	N	2.76
1	A2	80:A	O3'	81:G	P	2.75
1	A2	1279:C	O3'	1280:C	P	2.75
1	A2	1518:C	O3'	1519:U	P	2.75

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BB	94:LYS	C	95:ASN	N	2.75
1	BB	107:THR	C	108:ASP	N	2.75
1	BB	118:GLN	C	119:THR	N	2.75
1	BJ	25:ASP	C	26:ALA	N	2.75
1	BL	59:PRO	C	60:PHE	N	2.75
1	BN	56:ASP	C	57:ALA	N	2.75
1	BN	129:TYR	C	130:ARG	N	2.75
1	BR	12:ALA	C	13:SER	N	2.75
1	BR	70:SER	C	71:PHE	N	2.75
1	BW	92:ASN	C	93:LEU	N	2.75
1	BW	129:VAL	C	130:TYR	N	2.75
1	BX	80:GLY	C	81:LYS	N	2.75
1	Bg	150:TRP	C	151:VAL	N	2.75
1	A2	557:G	O3'	558:U	P	2.74
1	AZ	6042:U	O3'	6043:G	P	2.74
1	BB	64:ARG	C	65:VAL	N	2.74
1	BE	48:LEU	C	49:ARG	N	2.74
1	BE	208:VAL	C	209:HIS	N	2.74
1	BI	116:HIS	C	117:TYR	N	2.74
1	BJ	111:THR	C	112:GLN	N	2.74
1	BJ	141:VAL	C	142:ASN	N	2.74
1	BP	70:ASN	C	71:GLU	N	2.74
1	BU	24:ILE	C	25:THR	N	2.74
1	BX	11:SER	C	12:ALA	N	2.74
1	BX	111:GLY	C	112:LYS	N	2.74
1	A2	449:C	O3'	450:U	P	2.73
1	A2	631:G	O3'	632:U	P	2.73
1	BB	132:ASP	C	133:TYR	N	2.73
1	BE	232:GLY	C	233:LYS	N	2.73
1	BJ	2:PRO	C	3:ARG	N	2.73
1	BN	15:ALA	C	16:ILE	N	2.73
1	BN	119:GLU	C	120:SER	N	2.73
1	BO	91:THR	C	92:LYS	N	2.73
1	BR	75:GLU	C	76:GLU	N	2.73
1	BV	26:ALA	C	27:ASP	N	2.73
1	BX	77:ILE	C	78:LYS	N	2.73
1	BX	88:PRO	C	89:ASN	N	2.73
1	BX	90:ALA	C	91:GLY	N	2.73
1	Ba	90:GLU	C	91:ASP	N	2.73
1	Bg	21:THR	C	22:SER	N	2.73
1	A2	560:U	O3'	561:G	P	2.72
1	A2	1126:G	O3'	1127:G	P	2.72

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	1176:G	O3'	1177:C	P	2.72
1	A2	1758:U	O3'	1759:C	P	2.72
1	AZ	6075:A	O3'	6076:A	P	2.72
1	BH	136:VAL	C	137:GLY	N	2.72
1	BJ	75:ALA	C	76:LEU	N	2.72
1	BR	58:MET	C	59:LYS	N	2.72
1	BV	38:LYS	C	39:VAL	N	2.72
1	BW	75:ILE	C	76:SER	N	2.72
1	BZ	76:ALA	C	77:ARG	N	2.72
1	A2	21:U	O3'	22:A	P	2.71
1	BG	113:ILE	C	114:VAL	N	2.71
1	BI	142:LYS	C	143:TRP	N	2.71
1	BJ	33:GLU	C	34:PHE	N	2.71
1	BJ	173:ALA	C	174:ARG	N	2.71
1	BL	72:THR	C	73:GLY	N	2.71
1	BX	30:LYS	C	31:LYS	N	2.71
1	BX	122:PHE	C	123:LYS	N	2.71
1	Bc	26:THR	C	27:GLN	N	2.71
1	Bd	52:PHE	C	53:ASN	N	2.71
1	A2	1488:G	O3'	1489:U	P	2.70
1	A2	1729:C	O3'	1730:A	P	2.70
1	BC	72:LEU	C	73:LEU	N	2.70
1	BC	191:ALA	C	192:GLY	N	2.70
1	BD	23:GLU	C	24:PHE	N	2.70
1	BD	170:THR	C	171:ALA	N	2.70
1	BE	84:ALA	C	85:GLY	N	2.70
1	BE	221:ARG	C	222:LEU	N	2.70
1	BE	251:GLU	C	252:ARG	N	2.70
1	BI	49:ARG	C	50:GLY	N	2.70
1	BQ	13:LYS	C	14:LYS	N	2.70
1	BT	70:GLN	C	71:VAL	N	2.70
1	Be	25:GLU	C	26:LYS	N	2.70
1	A2	425:A	O3'	426:G	P	2.69
1	A2	594:A	O3'	595:G	P	2.69
1	A2	1140:G	O3'	1141:G	P	2.69
1	BH	90:VAL	C	91:ILE	N	2.69
1	BI	170:SER	C	171:SER	N	2.69
1	BO	58:TYR	C	59:ALA	N	2.69
1	BQ	140:LYS	C	141:SER	N	2.69
1	BT	138:GLN	C	139:THR	N	2.69
1	BX	107:PHE	C	108:GLY	N	2.69
1	Bd	46:LYS	C	47:ALA	N	2.69

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Bg	52:GLN	C	53:LYS	N	2.69
1	BC	157:LYS	C	158:THR	N	2.68
1	BD	109:LEU	C	110:LEU	N	2.68
1	BE	243:GLY	C	244:ILE	N	2.68
1	BP	85:ILE	C	86:VAL	N	2.68
1	Bb	70:LYS	C	71:ALA	N	2.68
1	BC	201:ASN	C	202:GLY	N	2.67
1	BC	204:THR	C	205:ARG	N	2.67
1	BL	110:HIS	C	111:VAL	N	2.67
1	BT	43:ASN	C	44:GLU	N	2.67
1	BY	59:GLY	C	60:PHE	N	2.67
1	BY	68:LYS	C	69:SER	N	2.67
1	A2	952:A	O3'	953:G	P	2.66
1	BC	139:ILE	C	140:ARG	N	2.66
1	BD	197:THR	C	198:GLY	N	2.66
1	BE	27:TYR	C	28:ALA	N	2.66
1	BE	29:PRO	C	30:ARG	N	2.66
1	BF	57:SER	C	58:LEU	N	2.66
1	BN	128:TYR	C	129:TYR	N	2.66
1	Bf	95:ALA	C	96:ALA	N	2.66
1	Bg	287:PRO	C	288:HIS	N	2.66
1	A2	848:C	O3'	849:C	P	2.65
1	A2	876:G	O3'	877:G	P	2.65
1	A2	1113:A	O3'	1114:G	P	2.65
1	A2	1237:G	O3'	1238:A	P	2.65
1	A2	1517:U	O3'	1518:C	P	2.65
1	BC	138:PRO	C	139:ILE	N	2.65
1	BM	34:THR	C	35:ALA	N	2.65
1	BN	96:VAL	C	97:SER	N	2.65
1	BS	83:ALA	C	84:TRP	N	2.65
1	Bd	43:PHE	C	44:ARG	N	2.65
1	A2	353:A	O3'	354:C	P	2.64
1	BC	161:LYS	C	162:CYS	N	2.64
1	BE	235:TYR	C	236:ILE	N	2.64
1	BH	21:ALA	C	22:GLN	N	2.64
1	BJ	62:ARG	C	63:ASP	N	2.64
1	BL	96:LYS	C	97:TYR	N	2.64
1	BN	18:TYR	C	19:SER	N	2.64
1	BQ	20:ALA	C	21:HIS	N	2.64
1	BQ	86:ALA	C	87:LYS	N	2.64
1	BX	37:ALA	C	38:PHE	N	2.64
1	A2	156:A	O3'	157:A	P	2.63

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	755:A	O3'	756:A	P	2.63
1	A2	1621:U	O3'	1622:G	P	2.63
1	BA	108:THR	C	109:ASN	N	2.63
1	BC	47:ALA	C	48:GLY	N	2.63
1	BI	7:SER	C	8:ARG	N	2.63
1	BI	96:LEU	C	97:THR	N	2.63
1	BJ	89:ASP	C	90:LYS	N	2.63
1	BL	128:CYS	C	129:ARG	N	2.63
1	BR	56:HIS	C	57:LEU	N	2.63
1	BW	6:VAL	C	7:LEU	N	2.63
1	BW	14:ILE	C	15:ASN	N	2.63
1	A2	1720:G	O3'	1721:A	P	2.62
1	BB	222:LYS	C	223:PHE	N	2.62
1	BC	133:LYS	C	134:LEU	N	2.62
1	BI	112:TRP	C	113:PHE	N	2.62
1	BJ	97:LEU	C	98:ALA	N	2.62
1	BK	50:THR	C	51:SER	N	2.62
1	BN	61:THR	C	62:GLN	N	2.62
1	Bg	65:SER	C	66:HIS	N	2.62
1	A2	89:G	O3'	90:C	P	2.61
1	BD	148:LYS	C	149:ALA	N	2.61
1	BG	75:LEU	C	76:LEU	N	2.61
1	BI	169:ILE	C	170:SER	N	2.61
1	BR	113:LEU	C	114:GLY	N	2.61
1	BX	120:VAL	C	121:ARG	N	2.61
1	BY	9:THR	C	10:ARG	N	2.61
1	Bd	23:VAL	C	24:CYS	N	2.61
1	Bg	70:ASP	C	71:CYS	N	2.61
1	A2	566:C	O3'	567:A	P	2.60
1	A2	1748:G	O3'	1749:A	P	2.60
1	BB	167:VAL	C	168:ILE	N	2.60
1	BC	199:GLN	C	200:SER	N	2.60
1	BE	140:VAL	C	141:THR	N	2.60
1	BG	19:ASP	C	20:ASP	N	2.60
1	BH	97:ARG	C	98:ILE	N	2.60
1	BN	64:ARG	C	65:VAL	N	2.60
1	BU	78:THR	C	79:TRP	N	2.60
1	BW	79:PHE	C	80:ASN	N	2.60
1	Ba	23:CYS	C	24:VAL	N	2.60
1	A2	341:A	O3'	342:C	P	2.59
1	A2	1036:A	O3'	1037:C	P	2.59
1	A2	1673:G	O3'	1674:C	P	2.59

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BC	211:LEU	C	212:LYS	N	2.59
1	BD	68:GLU	C	69:LEU	N	2.59
1	BD	152:PHE	C	153:ALA	N	2.59
1	BG	125:THR	C	126:ASP	N	2.59
1	BL	97:TYR	C	98:ASN	N	2.59
1	BX	83:VAL	C	84:THR	N	2.59
1	BB	126:THR	C	127:VAL	N	2.58
1	BD	101:GLN	C	102:ALA	N	2.58
1	BW	58:SER	C	59:GLY	N	2.58
1	BX	7:ARG	C	8:GLY	N	2.58
1	Ba	27:SER	C	28:LYS	N	2.58
1	A2	554:C	O3'	555:A	P	2.57
1	A2	1160:A	O3'	1161:C	P	2.57
1	BM	44:GLY	C	45:LEU	N	2.57
1	BV	35:ASN	C	36:VAL	N	2.57
1	BX	113:ALA	C	114:LYS	N	2.57
1	Bb	19:HIS	C	20:LYS	N	2.57
1	A2	936:G	O3'	937:C	P	2.56
1	BE	11:ARG	C	12:LEU	N	2.56
1	BU	93:LEU	C	94:GLU	N	2.56
1	BW	124:LYS	C	125:ILE	N	2.56
1	A2	410:A	O3'	411:C	P	2.55
1	A2	887:A	O3'	888:U	P	2.55
1	BE	200:ARG	C	201:HIS	N	2.55
1	BL	56:LYS	C	57:LYS	N	2.55
1	BW	112:ASP	C	113:HIS	N	2.55
1	Ba	35:ALA	C	36:ILE	N	2.55
1	Bd	40:ARG	C	41:GLN	N	2.55
1	A2	44:U	O3'	45:U	P	2.54
1	A2	365:G	O3'	366:A	P	2.54
1	A2	1023:A	O3'	1024:U	P	2.54
1	A2	1637:C	O3'	1638:G	P	2.54
1	BC	99:LYS	C	100:ALA	N	2.54
1	BE	108:ARG	C	109:PHE	N	2.54
1	BK	26:ASP	C	27:PHE	N	2.54
1	Bg	309:VAL	C	310:ILE	N	2.54
1	A2	1205:C	O3'	1206:U	P	2.53
1	A2	1269:U	O3'	1270:G	P	2.53
1	BC	116:LYS	C	117:THR	N	2.53
1	BE	159:THR	C	160:VAL	N	2.53
1	BG	175:ILE	C	176:GLN	N	2.53
1	BH	16:LEU	C	17:GLU	N	2.53

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BI	81:VAL	C	82:VAL	N	2.53
1	BJ	60:LEU	C	61:THR	N	2.53
1	BV	53:TYR	C	54:ALA	N	2.53
1	Ba	3:LYS	C	4:LYS	N	2.53
1	A2	49:C	O3'	50:C	P	2.52
1	A2	1315:U	O3'	1316:G	P	2.52
1	A2	1425:A	O3'	1426:C	P	2.52
1	A2	1316:G	O3'	1317:C	P	2.51
1	A2	1636:C	O3'	1637:C	P	2.51
1	BF	96:SER	C	97:LEU	N	2.51
1	BF	120:ILE	C	121:ILE	N	2.51
1	BX	74:VAL	C	75:GLN	N	2.51
1	Ba	8:ASN	C	9:GLY	N	2.51
1	A2	802:G	O3'	803:A	P	2.50
1	BE	150:PRO	C	151:ASP	N	2.50
1	BL	43:LYS	C	44:THR	N	2.50
1	Bb	8:LEU	C	9:HIS	N	2.50
1	Bg	299:GLN	C	300:THR	N	2.50
1	A2	599:A	O3'	600:U	P	2.49
1	A2	1136:U	O3'	1137:A	P	2.49
1	BB	142:PHE	C	143:THR	N	2.49
1	BB	149:GLN	C	150:VAL	N	2.49
1	BC	127:ALA	C	128:GLY	N	2.49
1	BE	158:ASP	C	159:THR	N	2.49
1	BY	109:LYS	C	110:GLN	N	2.49
1	A2	942:G	O3'	943:C	P	2.48
1	BB	228:LEU	C	229:MET	N	2.48
1	BC	184:VAL	C	185:LYS	N	2.48
1	BD	19:ALA	C	20:GLU	N	2.48
1	BJ	134:ILE	C	135:ALA	N	2.48
1	BL	17:PRO	C	18:HIS	N	2.48
1	A2	1068:C	O3'	1069:A	P	2.47
1	A2	1453:G	O3'	1454:G	P	2.47
1	BB	155:TYR	C	156:ALA	N	2.47
1	BH	163:ASP	C	164:TYR	N	2.47
1	BI	30:GLY	C	31:ARG	N	2.47
1	BJ	45:ILE	C	46:SER	N	2.47
1	BJ	157:ASP	C	158:PHE	N	2.47
1	BK	51:SER	C	52:LYS	N	2.47
1	BK	84:GLU	C	85:HIS	N	2.47
1	BZ	100:ILE	C	101:TYR	N	2.47
1	Bb	73:LEU	C	74:SER	N	2.47

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	611:U	O3'	612:U	P	2.46
1	BG	28:PHE	C	29:ASP	N	2.46
1	BR	118:PRO	C	119:LEU	N	2.46
1	A2	565:C	O3'	566:C	P	2.45
1	A2	965:U	O3'	966:A	P	2.45
1	A2	1344:A	O3'	1345:A	P	2.45
1	BI	42:ARG	C	43:ILE	N	2.45
1	BL	123:VAL	C	124:THR	N	2.45
1	BT	96:ALA	C	97:SER	N	2.45
1	BY	37:LYS	C	38:ASP	N	2.45
1	A2	590:C	O3'	591:A	P	2.44
1	A2	1588:G	O3'	1589:C	P	2.44
1	BD	164:VAL	C	165:ASN	N	2.44
1	BJ	87:SER	C	88:GLU	N	2.44
1	BW	77:PRO	C	78:ARG	N	2.44
1	BX	68:ILE	C	69:ARG	N	2.44
1	BY	4:ALA	C	5:VAL	N	2.44
1	A2	452:A	O3'	453:U	P	2.43
1	BC	96:THR	C	97:ARG	N	2.43
1	BF	166:ARG	C	167:ARG	N	2.43
1	BH	181:ILE	C	182:VAL	N	2.43
1	BJ	9:SER	C	10:LYS	N	2.43
1	BR	11:ARG	C	12:ALA	N	2.43
1	A2	20:G	O3'	21:U	P	2.42
1	A2	552:G	O3'	553:G	P	2.42
1	A2	622:A	O3'	623:A	P	2.42
1	Ba	17:HIS	C	18:VAL	N	2.42
1	Ba	78:ALA	C	79:ILE	N	2.42
1	Be	15:LYS	C	16:SER	N	2.42
1	A2	1731:A	O3'	1732:A	P	2.41
1	BF	173:ALA	C	174:LEU	N	2.41
1	BN	38:VAL	C	39:LYS	N	2.41
1	BW	89:TRP	C	90:THR	N	2.41
1	BX	73:ARG	C	74:VAL	N	2.41
1	A2	1084:A	O3'	1085:G	P	2.40
1	A2	1124:A	O3'	1125:A	P	2.40
1	BI	152:ILE	C	153:GLU	N	2.40
1	BW	68:ARG	C	69:LEU	N	2.40
1	BW	104:LEU	C	105:THR	N	2.40
1	Ba	25:ASN	C	26:CYS	N	2.40
1	A2	577:G	O3'	578:U	P	2.39
1	A2	800:U	O3'	801:G	P	2.39

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	872:G	O3'	873:U	P	2.39
1	BE	145:ARG	C	146:THR	N	2.39
1	BL	65:SER	C	66:ILE	N	2.39
1	BO	122:PRO	C	123:SER	N	2.39
1	Bb	21:LEU	C	22:LYS	N	2.39
1	Bc	47:PRO	C	48:VAL	N	2.39
1	A2	1785:U	O3'	1786:G	P	2.38
1	A2	1433:G	O3'	1434:U	P	2.37
1	A2	1790:A	O3'	1791:A	P	2.37
1	BB	67:GLU	C	68:VAL	N	2.37
1	BL	7:VAL	C	8:GLN	N	2.37
1	BX	135:LEU	C	136:TRP	N	2.37
1	A2	19:A	O3'	20:G	P	2.36
1	A2	522:U	O3'	523:G	P	2.36
1	BI	3:ILE	C	4:SER	N	2.36
1	BI	104:ILE	C	105:ASP	N	2.36
1	BJ	126:ARG	C	127:VAL	N	2.36
1	BD	135:GLU	C	136:VAL	N	2.35
1	BW	110:ILE	C	111:MET	N	2.35
1	BY	56:SER	C	57:VAL	N	2.35
1	Bg	61:PHE	C	62:LYS	N	2.35
1	A2	65:A	O3'	66:U	P	2.34
1	A2	468:A	O3'	469:C	P	2.34
1	BV	56:SER	C	57:GLY	N	2.34
1	BW	102:VAL	C	103:ILE	N	2.34
1	A2	424:C	O3'	425:A	P	2.33
1	A2	439:U	O3'	440:U	P	2.33
1	BC	44:LEU	C	45:VAL	N	2.33
1	BD	201:ALA	C	202:LEU	N	2.33
1	BW	25:VAL	C	26:LEU	N	2.33
1	BY	39:GLU	C	40:LEU	N	2.33
1	A2	4:C	O3'	5:U	P	2.32
1	BD	208:ILE	C	209:ILE	N	2.32
1	BG	123:GLY	C	124:LEU	N	2.31
1	BI	87:ASN	C	88:ASN	N	2.31
1	BP	103:ASN	C	104:GLN	N	2.31
1	BW	23:ARG	C	24:GLN	N	2.31
1	A2	624:G	O3'	625:C	P	2.30
1	BB	209:ASN	C	210:ILE	N	2.30
1	A2	459:G	O3'	460:A	P	2.29
1	A2	818:C	O3'	819:G	P	2.29
1	A2	988:A	O3'	989:U	P	2.29

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	1437:U	O3'	1438:G	P	2.29
1	BX	125:VAL	C	126:LYS	N	2.28
1	A2	40:A	O3'	41:A	P	2.27
1	BX	18:HIS	C	19:ARG	N	2.27
1	BX	130:VAL	C	131:SER	N	2.27
1	A2	1583:A	O3'	1584:G	P	2.26
1	BW	34:ILE	C	35:ILE	N	2.26
1	A2	975:C	O3'	976:G	P	2.25
1	BE	16:HIS	C	17:HIS	N	2.25
1	BG	96:SER	C	97:VAL	N	2.25
1	BW	71:LYS	C	72:CYS	N	2.25
1	A2	354:C	O3'	355:G	P	2.24
1	A2	1037:C	O3'	1038:U	P	2.24
1	BE	65:LEU	C	66:MET	N	2.24
1	BO	54:GLU	C	55:SER	N	2.23
1	A2	101:U	O3'	102:U	P	2.22
1	BN	5:HIS	C	6:SER	N	2.22
1	BN	112:LYS	C	113:PHE	N	2.21
1	BX	54:LEU	C	55:GLU	N	2.21
1	A2	633:U	O3'	634:G	P	2.19
1	A2	897:C	O3'	898:A	P	2.19
1	BE	137:PRO	C	138:TYR	N	2.19
1	BH	110:GLN	C	111:LYS	N	2.19
1	A2	1797:A	O3'	1798:U	P	2.18
1	BF	110:ALA	C	111:VAL	N	2.18
1	BB	100:PHE	C	101:HIS	N	2.17
1	BW	65:LEU	C	66:ASN	N	2.17
1	A2	388:G	O3'	389:G	P	2.16
1	A2	1388:A	O3'	1389:C	P	2.16
1	A2	56:U	O3'	57:G	P	2.15
1	A2	935:U	O3'	936:G	P	2.15
1	A2	419:G	O3'	420:A	P	2.14
1	A2	1377:U	O3'	1378:U	P	2.14
1	AZ	6106:A	O3'	6107:U	P	2.14
1	BE	106:LYS	C	107:GLY	N	2.14
1	BP	105:VAL	C	106:GLU	N	2.14
1	A2	47:A	O3'	48:G	P	2.12
1	BE	60:GLU	C	61:VAL	N	2.12
1	A2	1732:A	O3'	1733:C	P	2.09
1	A2	862:A	O3'	863:A	P	2.08
1	A2	464:A	O3'	465:G	P	2.07
1	A2	399:A	O3'	400:A	P	2.06

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	997:G	O3'	998:A	P	2.06
1	A2	352:A	O3'	353:A	P	2.03
1	A2	1030:A	O3'	1031:U	P	1.98
1	A2	960:U	O3'	961:U	P	1.97
1	A2	1417:A	O3'	1418:G	P	1.90
1	A2	104:A	O3'	105:A	P	1.89

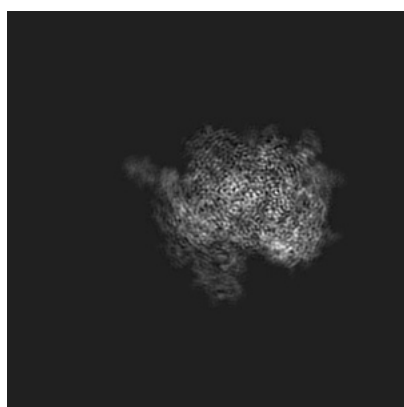
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2604. These allow visual inspection of the internal detail of the map and identification of artifacts.

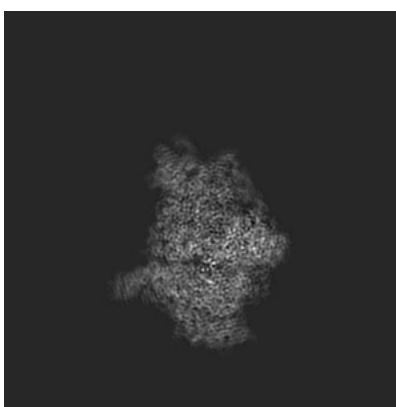
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

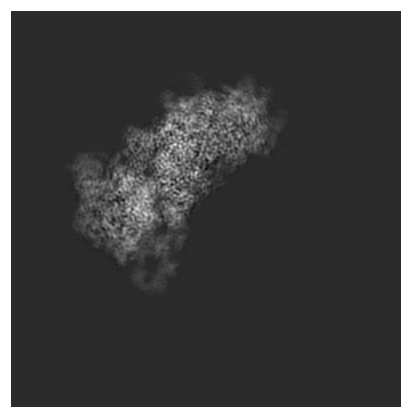
6.1.1 Primary map



X



Y

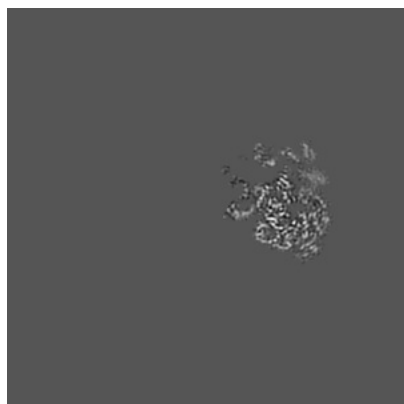


Z

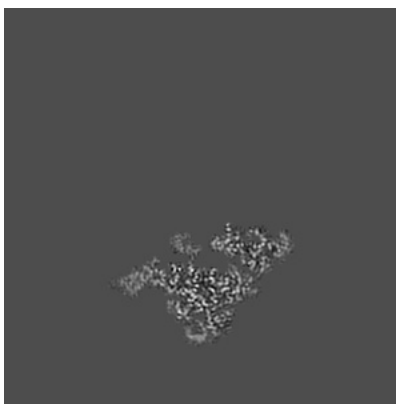
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

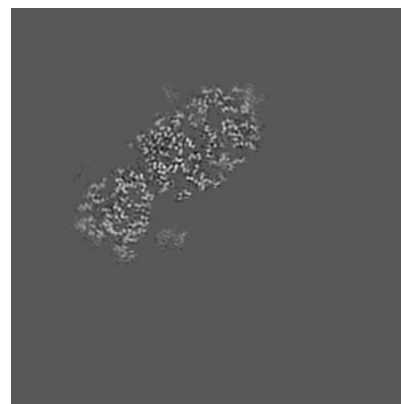
6.2.1 Primary map



X Index: 160



Y Index: 160

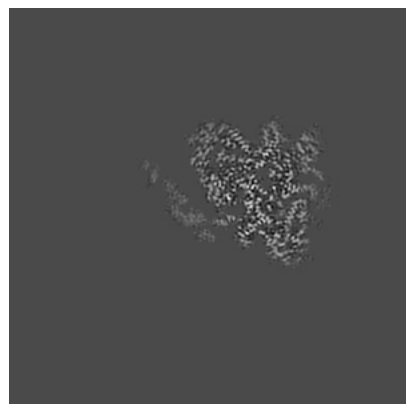


Z Index: 160

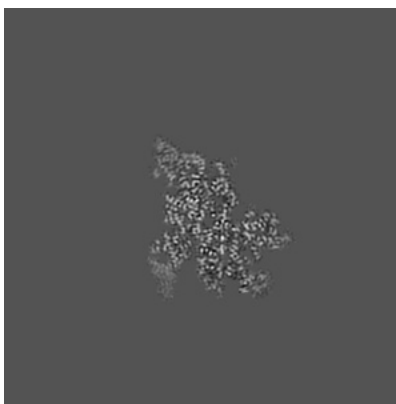
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

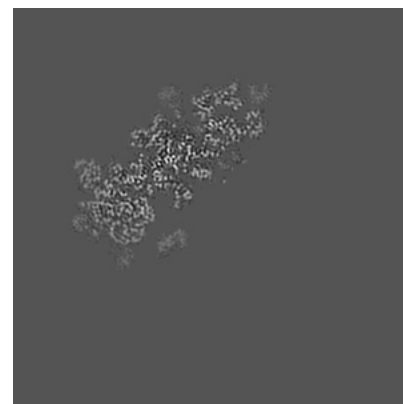
6.3.1 Primary map



X Index: 132



Y Index: 215

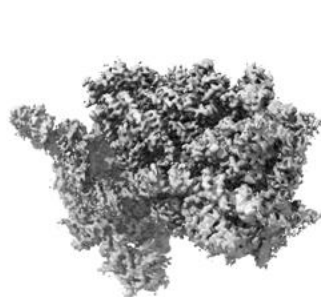


Z Index: 166

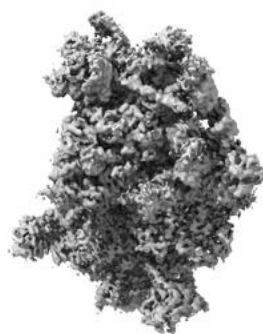
The images above show the largest variance slices of the map in three orthogonal directions.

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 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

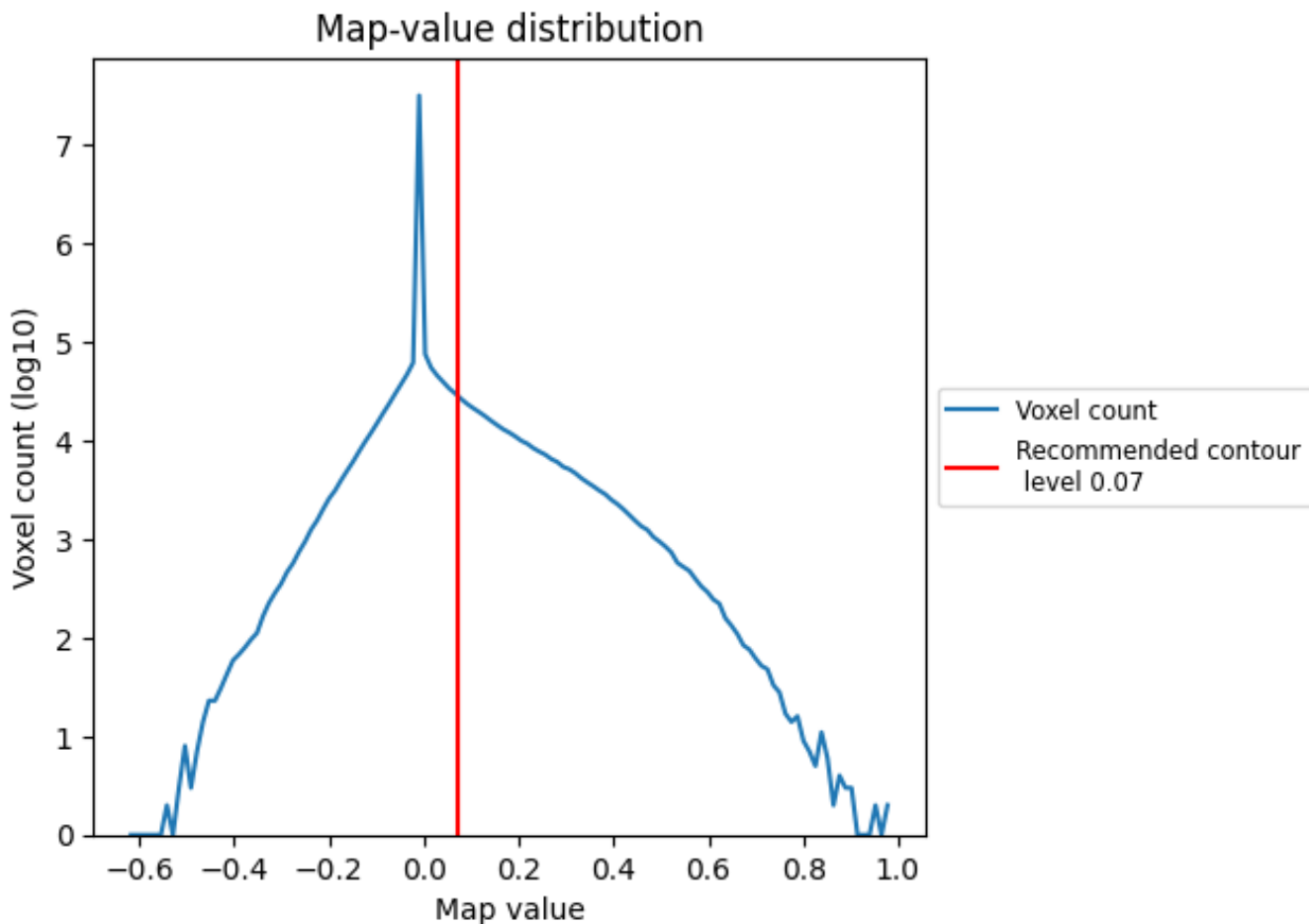
6.5 Mask visualisation

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

7 Map analysis [i](#)

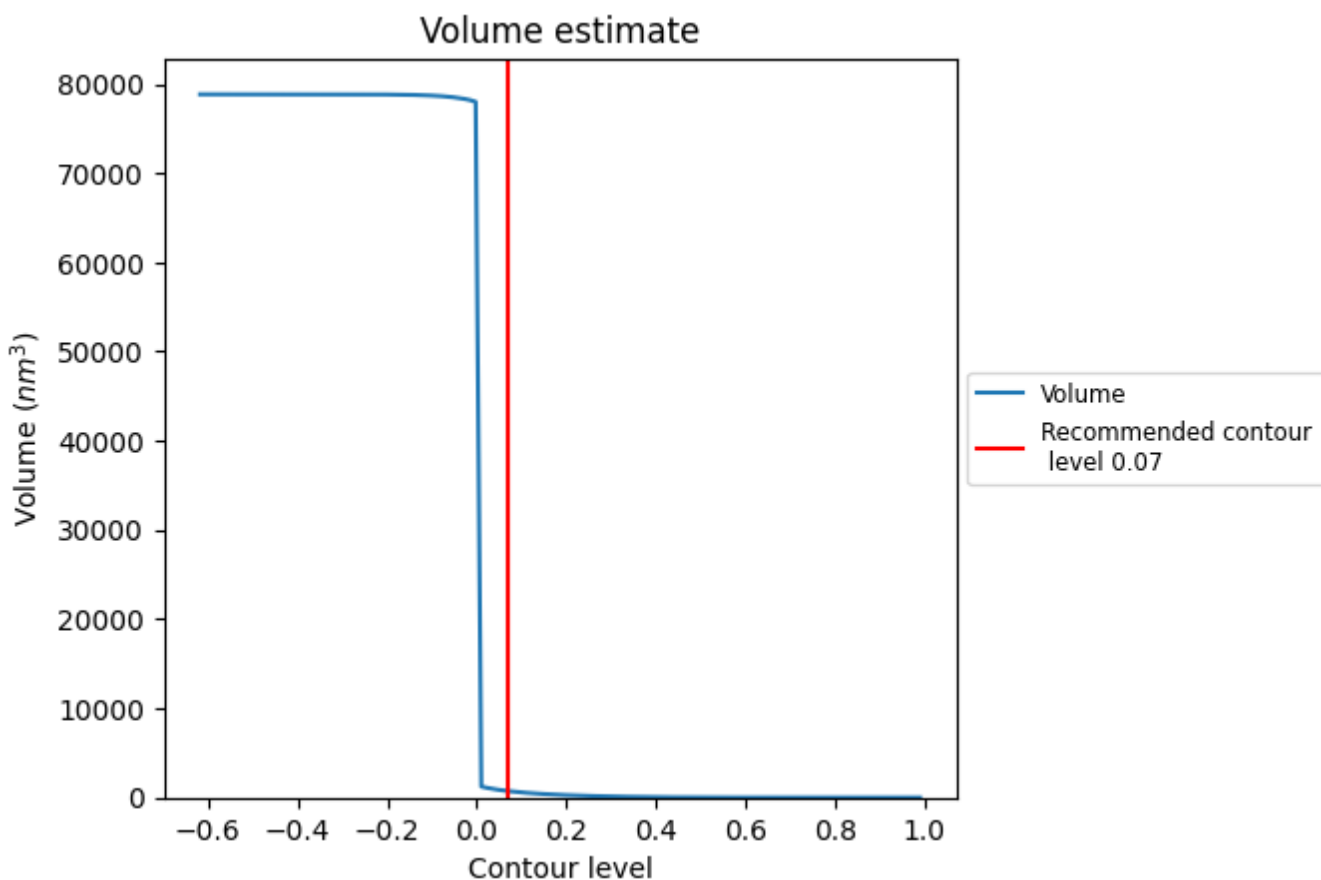
This section contains the results of statistical analysis of the map.

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.

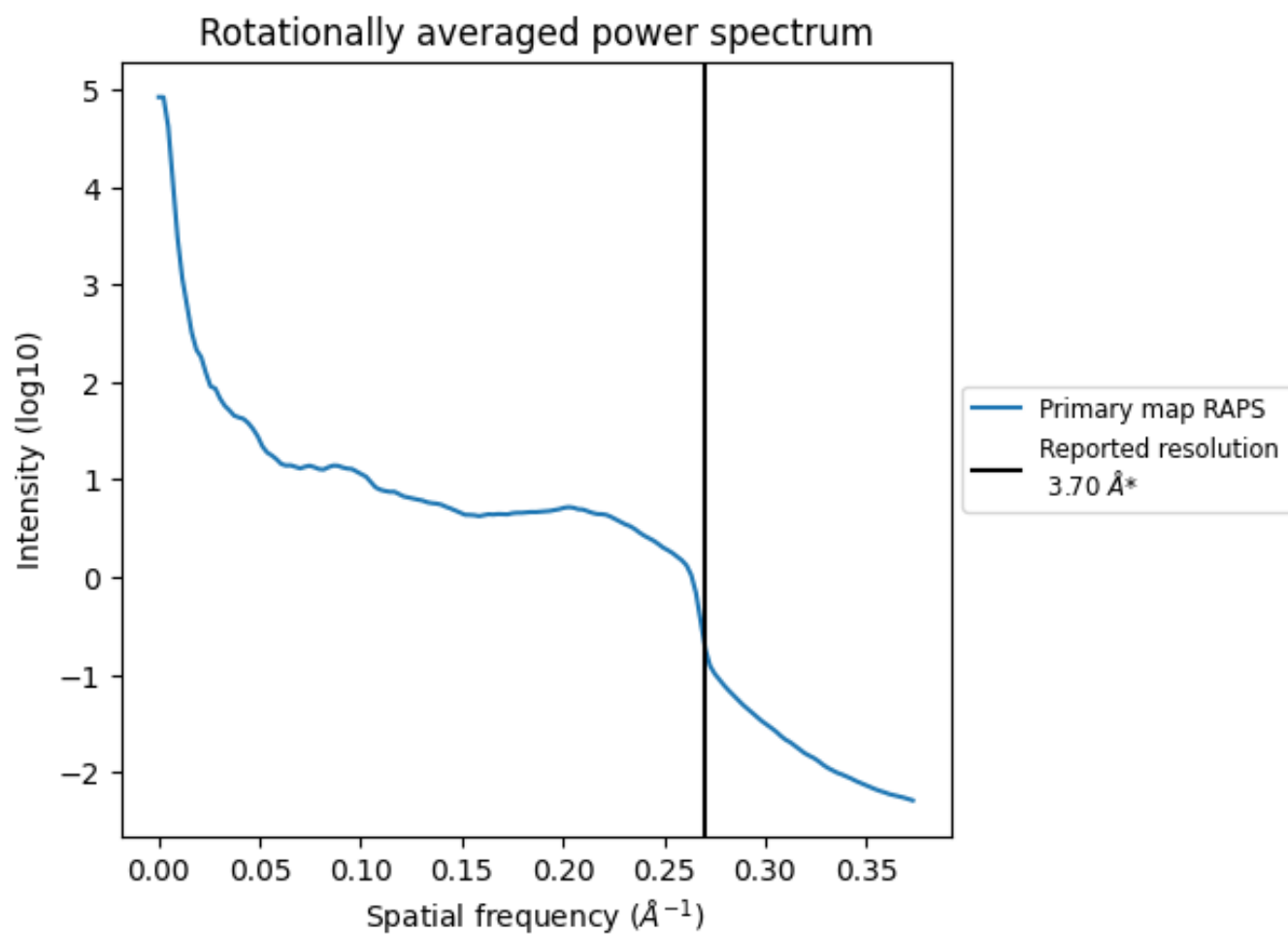
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 732 nm³; this corresponds to an approximate mass of 661 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 0.270 Å⁻¹

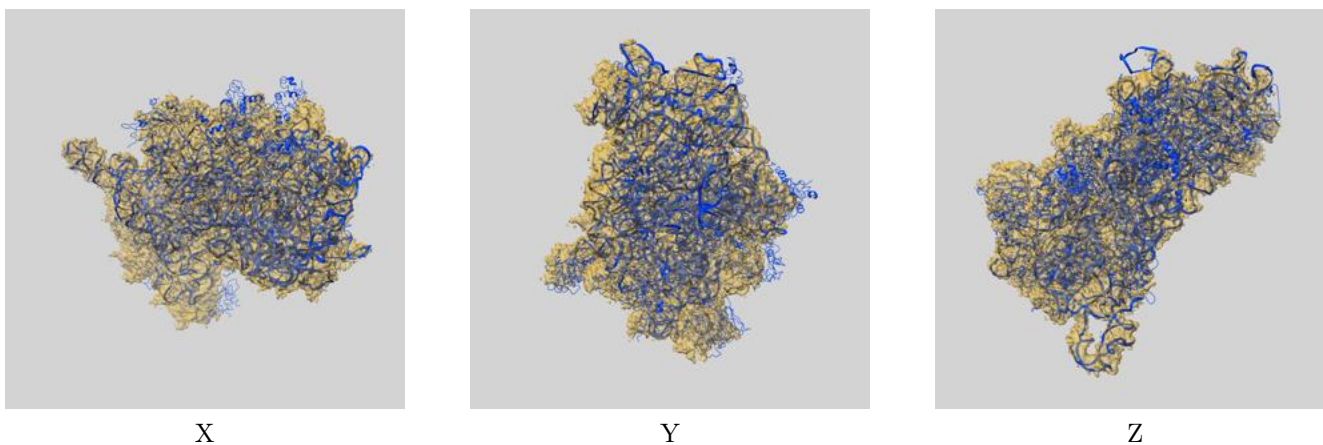
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

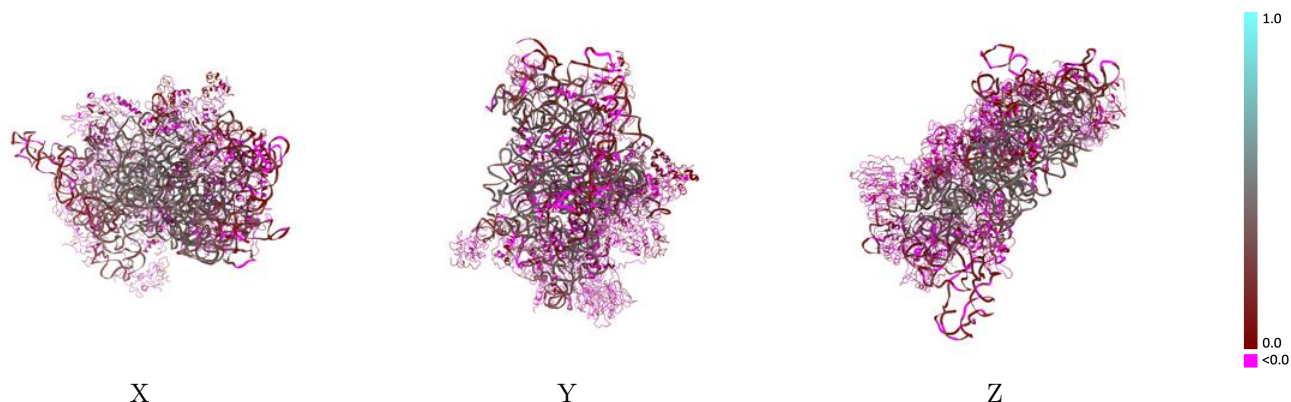
This section contains information regarding the fit between EMDB map EMD-2604 and PDB model 4V92. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



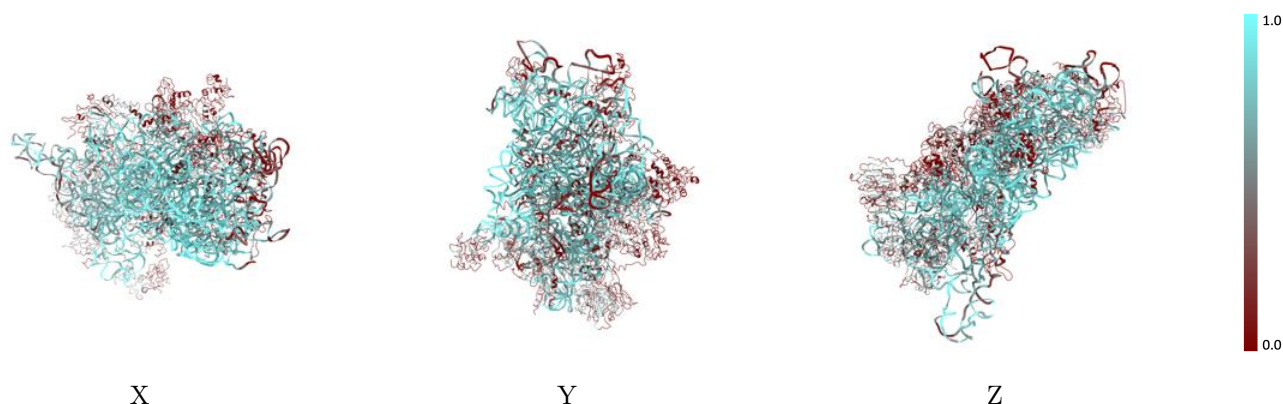
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



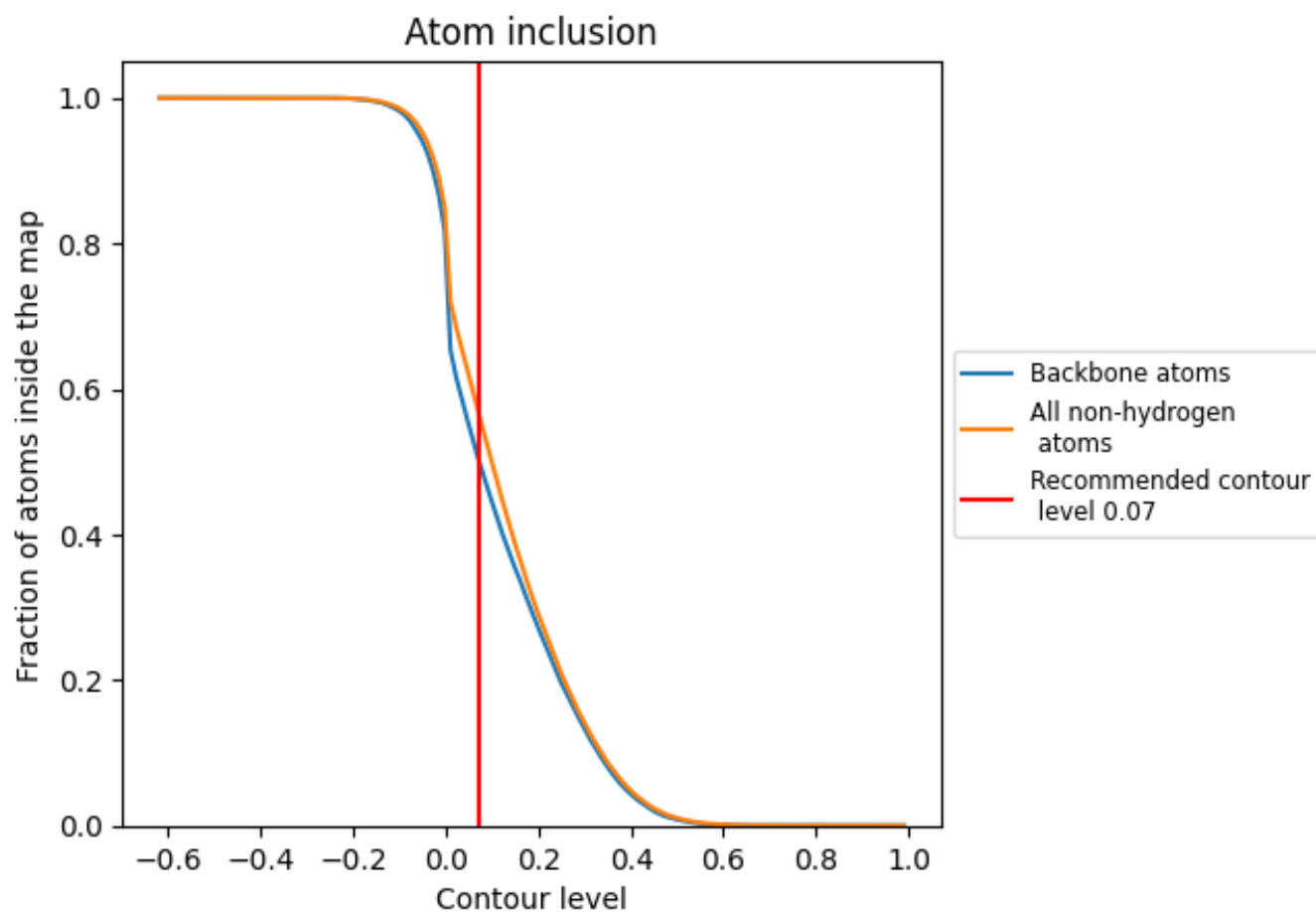
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).









































































9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 57% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5685	 0.1590
A2	 0.8413	 0.3170
AZ	 0.6807	 0.1240
BA	 0.1471	 -0.0090
BB	 0.3000	 0.0170
BC	 0.2877	 0.0070
BD	 0.2120	 -0.0100
BE	 0.2781	 0.0090
BF	 0.3504	 -0.0310
BG	 0.2786	 0.0230
BH	 0.1178	 0.0020
BI	 0.2242	 -0.0060
BJ	 0.2529	 0.0090
BK	 0.3049	 -0.0070
BL	 0.1121	 0.0110
BM	 0.1186	 -0.0300
BN	 0.1844	 0.0090
BO	 0.3120	 0.0220
BP	 0.3539	 0.0130
BQ	 0.4812	 0.0470
BR	 0.1718	 -0.0160
BS	 0.3775	 0.0120
BT	 0.4069	 -0.0030
BU	 0.2494	 0.0000
BV	 0.2349	 0.0060
BW	 0.3908	 0.0410
BX	 0.3364	 0.0340
BY	 0.3314	 0.0280
BZ	 0.3327	 -0.0250
Ba	 0.3708	 0.0150
Bb	 0.1847	 0.0230
Bc	 0.2327	 -0.0630
Bd	 0.2995	 -0.0060
Be	 0.1887	 0.0050
Bf	 0.3938	 -0.0050
Bg	 0.3249	 -0.0060

