



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 10:00 PM EDT

PDB ID : 4V9H / pdb_00004v9h
Title : Crystal structure of the ribosome bound to elongation factor G in the guanosine triphosphatase state
Authors : Tourigny, D.S.; Fernandez, I.S.; Kelley, A.C.; Ramakrishnan, V.
Deposited on : 2013-03-25
Resolution : 2.86 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

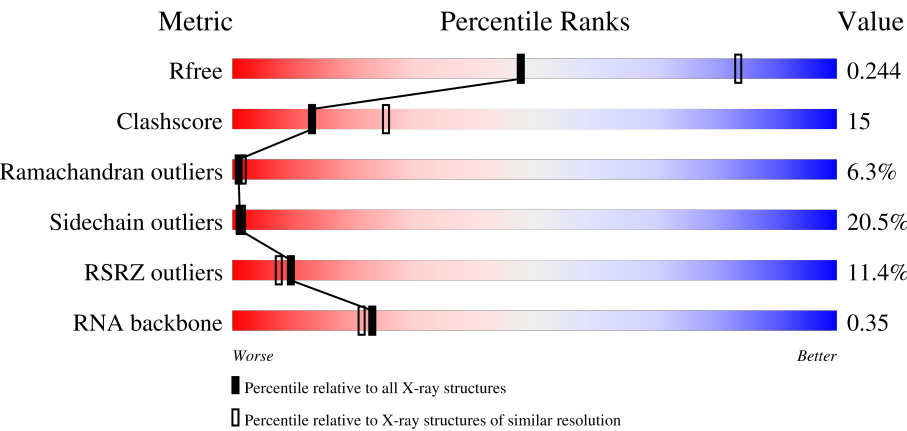
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.86 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)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)
RNA backbone	3983	1009 (3.06-2.66)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	1516	3% 46%38%13%
2	AV	76	4% 36%29%22%11%
3	AX	25	4% 12%8% 76%
4	AJ	98	24% 56%31%12%

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Mol	Chain	Length	Quality of chain
5	AK	119	
6	AL	124	
7	AM	124	
8	AN	60	
9	AO	88	
10	AP	83	
11	AQ	99	
12	AR	70	
13	AS	78	
14	AT	99	
15	AB	234	
16	AC	206	
17	AD	208	
18	AE	150	
19	AF	101	
20	AG	155	
21	AH	138	
22	AI	127	
23	AY	680	
24	AU	24	
25	BA	2915	
26	BB	122	
27	BN	140	
28	BO	122	
29	BP	150	

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Mol	Chain	Length	Quality of chain
30	BQ	141	
31	BR	118	
32	BS	112	
33	BT	146	
34	BU	118	
35	BV	101	
36	BW	113	
37	BX	96	
38	BY	110	
39	BZ	206	
40	B0	85	
41	B1	98	
42	B2	72	
43	BD	276	
44	B3	60	
45	B4	71	
46	B5	60	
47	B6	54	
48	B7	49	
49	B8	65	
50	B9	37	
51	BC	229	
52	BE	206	
53	BF	210	
54	BG	182	

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Mol	Chain	Length	Quality of chain
55	BH	180	15% 46% 38% 9%
56	BK	147	81% 38% 40% 7% 14%
57	BJ	130	81% 69% 26% 5%
58	BL	125	46% 11% 42%

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 151831 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	1514	Total	C	N	O	P	0	0	0
			32529	14480	6018	10518	1513			

- Molecule 2 is a RNA chain called PE hybrid state tRNA Phe.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AV	74	Total	C	N	O	P	0	0	0
			1579	705	285	516	73			

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AX	6	Total	C	N	O	P	0	0	0
			125	56	19	44	6			

- Molecule 4 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AJ	98	Total	C	N	O	S	0	0	0
			795	499	156	139	1			

- Molecule 5 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AK	119	Total	C	N	O	S	0	0	0
			885	549	168	165	3			

- Molecule 6 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AL	124	Total	C	N	O	S	0	0	0
			971	611	195	164	1			

- Molecule 7 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AM	124	Total	C	N	O	S	0	0	0
			988	611	205	170	2			

- Molecule 8 is a protein called 30S ribosomal protein S14 TYPE Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

- Molecule 9 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	AO	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			

- Molecule 10 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	AP	83	Total	C	N	O	S	0	0	0
			701	443	139	118	1			

- Molecule 11 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	AQ	99	Total	C	N	O	S	0	0	0
			824	528	151	143	2			

- Molecule 12 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
12	AR	70	Total	C	N	O	0	0	0
			574	367	112	95			

- Molecule 13 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	AS	78	Total	C	N	O	S	0	0	0
			630	403	114	111	2			

- Molecule 14 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	AT	99	Total	C	N	O	S	0	0	0
			763	470	162	129	2			

- Molecule 15 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	AB	234	Total	C	N	O	S	0	0	0
			1901	1213	341	342	5			

- Molecule 16 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	AC	206	Total	C	N	O	S	0	0	0
			1613	1016	314	282	1			

- Molecule 17 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AD	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			

- Molecule 18 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	AE	150	Total	C	N	O	S	0	0	0
			1147	724	217	202	4			

- Molecule 19 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AF	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			

- Molecule 20 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AG	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			

- Molecule 21 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	AH	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			

- Molecule 22 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AI	127	Total	C	N	O		0	0	0
			1011	639	198	174				

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AI	58	ARG	HIS	conflict	UNP P80374

- Molecule 23 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	AY	622	Total	C	N	O	S	0	0	0
			4877	3097	837	924	19			

- Molecule 24 is a protein called 30S ribosomal protein THX.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	AU	24	Total	C	N	O		0	0	0
			209	128	50	31				

- Molecule 25 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	BA	2859	Total	C	N	O	P	0	0	0
			61580	27407	11519	19796	2858			

- Molecule 26 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	BB	119	Total	C	N	O	P	0	0	0
			2551	1136	471	826	118			

- Molecule 27 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	BN	138	Total	C	N	O	S	0	0	0
			1104	712	206	182	4			

- Molecule 28 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	BO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

- Molecule 29 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	BP	146	Total	C	N	O	S	0	0	0
			1114	692	227	193	2			

- Molecule 30 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	BQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

- Molecule 31 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
31	BR	117	Total	C	N	O	0	0	0
			960	599	202	159			

- Molecule 32 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
32	BS	98	Total	C	N	O	0	0	0
			770	486	154	130			

- Molecule 33 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	BT	137	Total	C	N	O	S	0	0	0
			1141	710	234	196	1			

- Molecule 34 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	BU	117	Total	C	N	O	S	0	0	0
			958	604	202	151	1			

- Molecule 35 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	BV	101	Total	C	N	O	S	0	0	0
			779	501	142	135	1			

- Molecule 36 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	BW	113	Total	C	N	O	S	0	0	0
			896	563	176	155	2			

- Molecule 37 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	BX	92	Total	C	N	O	S	0	0	0
			725	471	131	123				

- Molecule 38 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	BY	100	Total	C	N	O	S	0	0	0
			775	500	148	123	4			

- Molecule 39 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	BZ	198	Total	C	N	O	S	0	0	0
			1508	960	274	272	2			

- Molecule 40 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	B0	84	Total	C	N	O	S	0	0	0
			662	410	140	111	1			

- Molecule 41 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	B1	93	Total	C	N	O	S	0	0	0
			731	460	145	125	1			

- Molecule 42 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	B2	71	Total	C	N	O	S	0	0	0
			598	370	121	106	1			

- Molecule 43 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	BD	271	Total	C	N	O	S	0	0	0
			2104	1329	416	356	3			

- Molecule 44 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	B3	59	Total	C	N	O	S	0	0	0
			467	298	90	78	1			

- Molecule 45 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	B4	30	Total	C	N	O	S	0	0	0
			225	142	36	43	4			

- Molecule 46 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	B5	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			

- Molecule 47 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	B6	44	Total	C	N	O	S	0	0	0
			380	235	77	64	4			

- Molecule 48 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	B7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 49 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	B8	63	Total	C	N	O	S	0	0	0
			507	326	101	78	2			

- Molecule 50 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	B9	36	Total	C	N	O	S	0	0	0
			299	183	67	46	3			

- Molecule 51 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	BC	225	Total	C	N	O	S	0	0	0
			1718	1085	315	316	2			

- Molecule 52 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	BE	204	Total	C	N	O	S	0	0	0
			1563	988	299	270	6			

- Molecule 53 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	BF	207	Total	C	N	O	S	0	0	0
			1623	1035	303	282	3			

- Molecule 54 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	BG	181	Total	C	N	O	S	0	0	0
			1474	942	268	260	4			

- Molecule 55 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	BH	173	Total	C	N	O	S	0	0	0
			1303	824	244	234	1			

- Molecule 56 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	BK	127	Total	C	N	O	S	0	0	0
			936	598	161	172	5			

- Molecule 57 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
57	BJ	130	Total	C	N	O		0	0	0
			651	390	130	131				

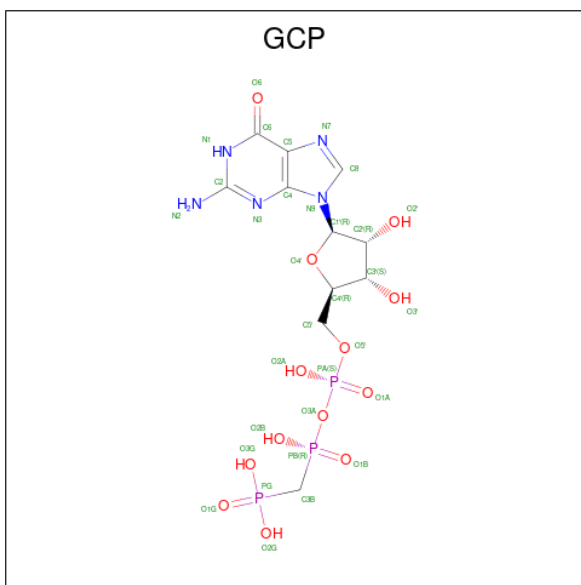
- Molecule 58 is a protein called 50S ribosomal protein L12 CTD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
58	BL	72	Total	C	N	O		0	0	1
			356	213	72	71				

- Molecule 59 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	AA	45	Total	Mg	0	0
			45	45		
59	AY	1	Total	Mg	0	0
			1	1		
59	BA	88	Total	Mg	0	0
			88	88		
59	BD	1	Total	Mg	0	0
			1	1		
59	B8	1	Total	Mg	0	0
			1	1		
59	BE	1	Total	Mg	0	0
			1	1		
59	BF	1	Total	Mg	0	0
			1	1		

- Molecule 60 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
60	AY	1	Total	C	N	O	P	0	0
			32	11	5	13	3		

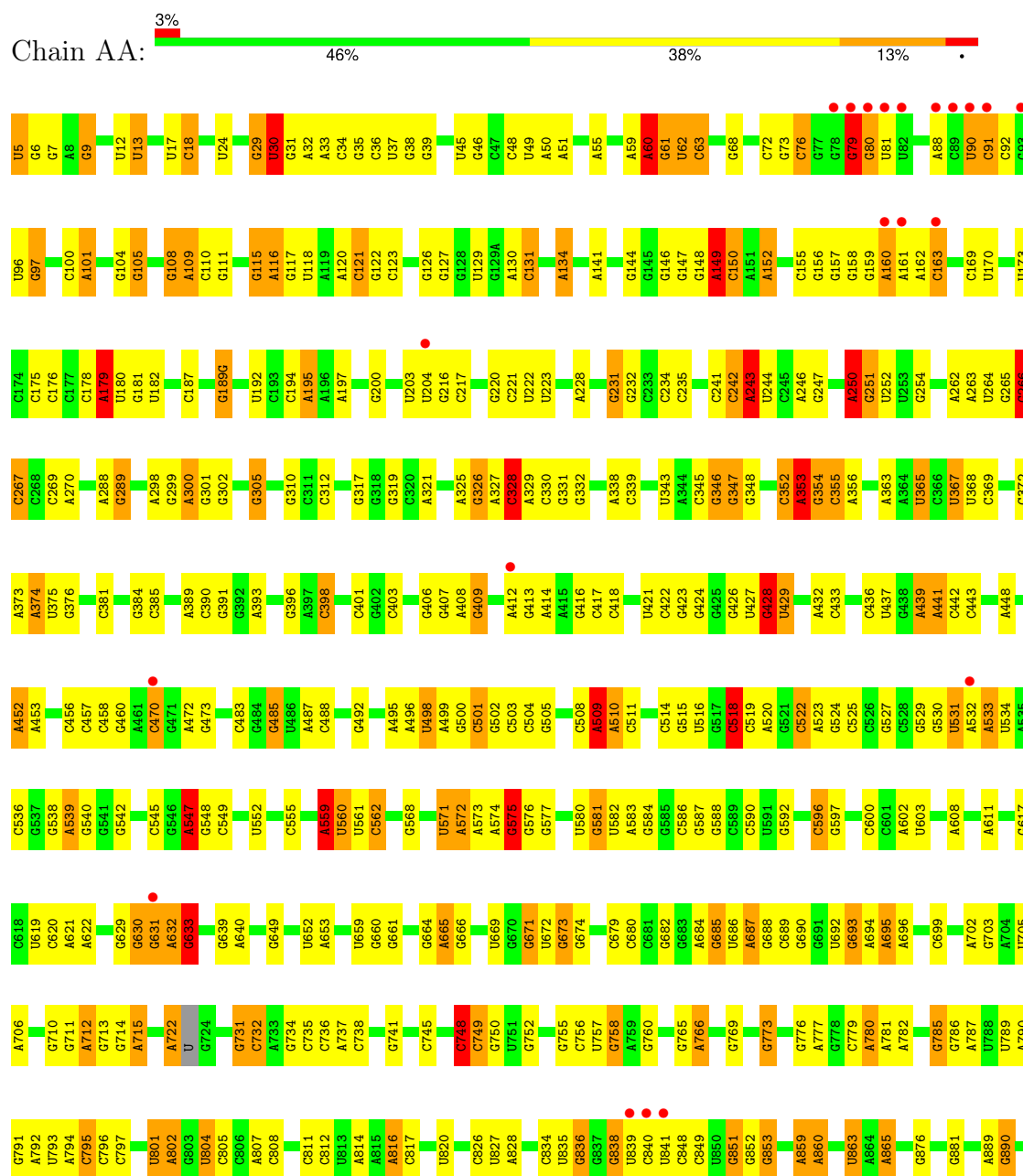
- Molecule 61 is water.

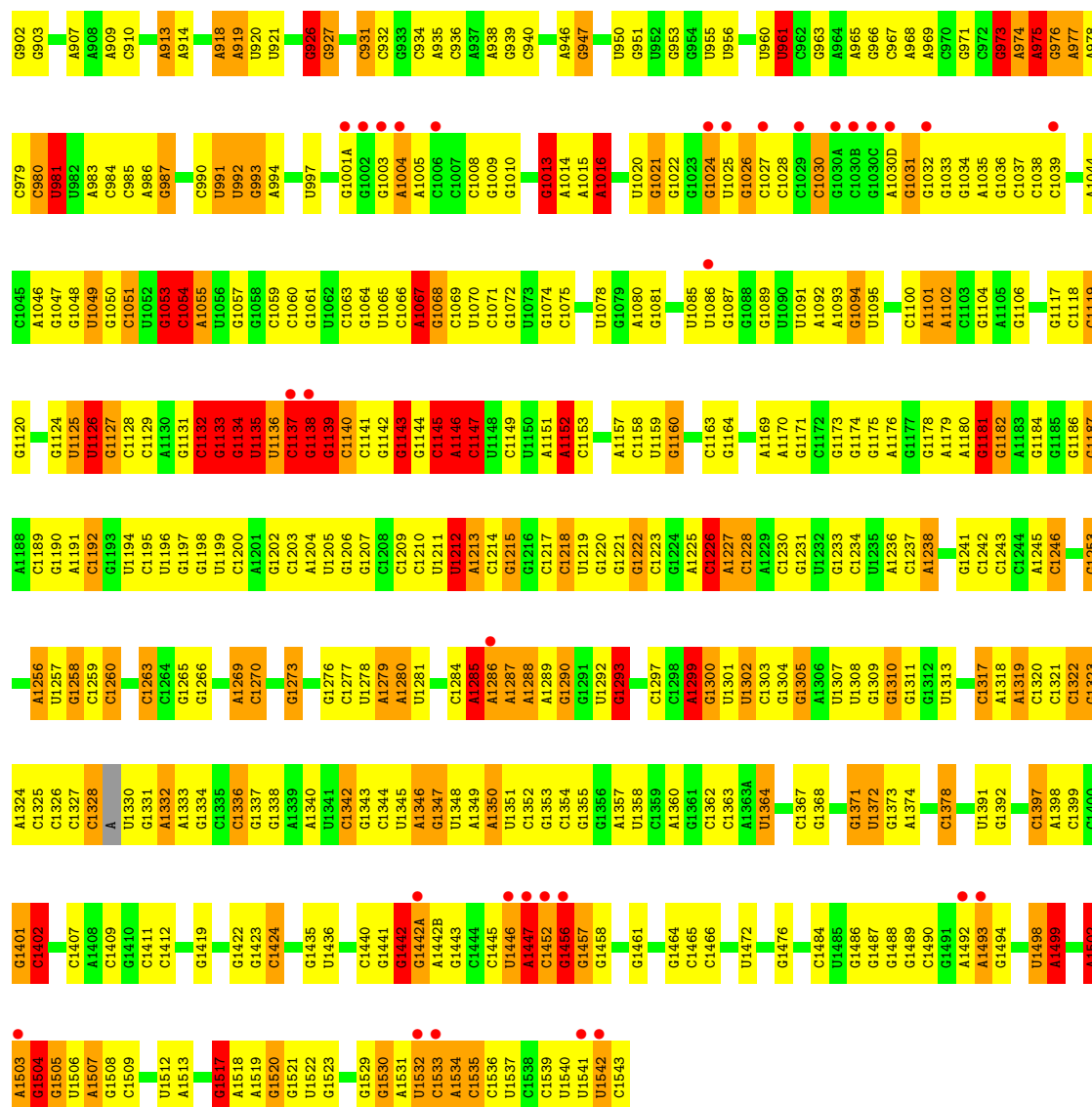
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	AY	4	Total O 4 4	0	0

3 Residue-property plots

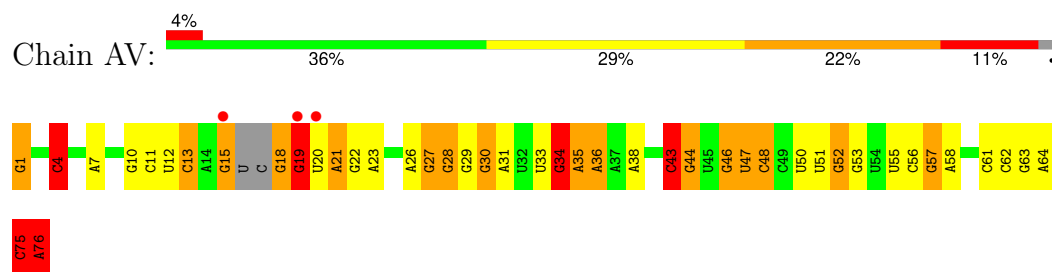
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: 16S ribosomal RNA





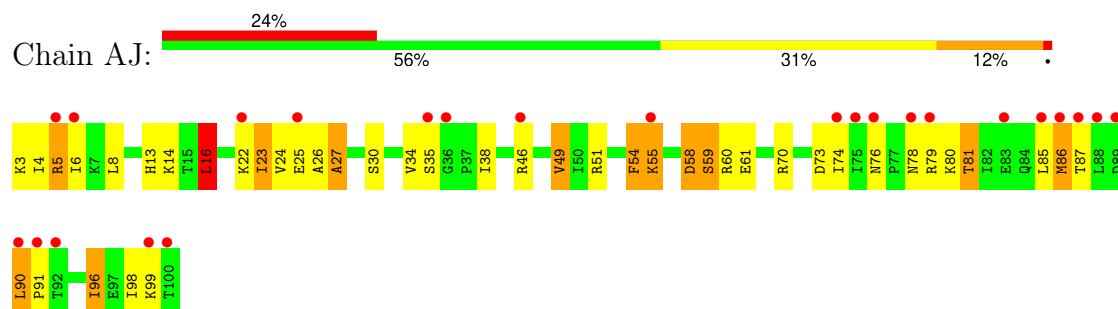
• Molecule 2: PE hybrid state tRNA Phe



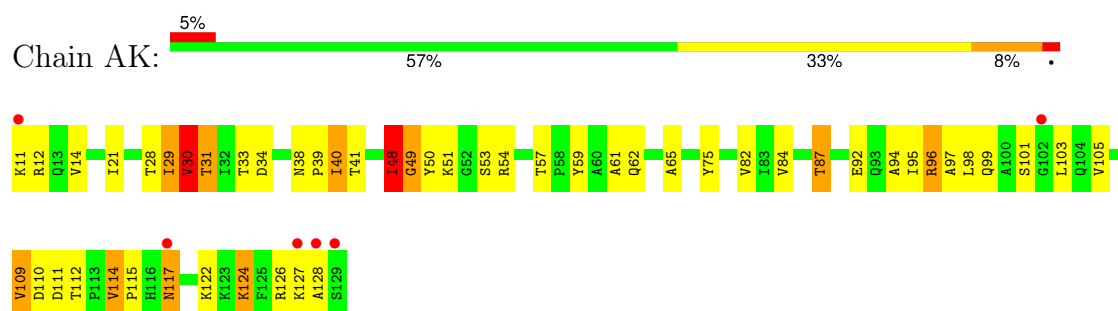
• Molecule 3: mRNA



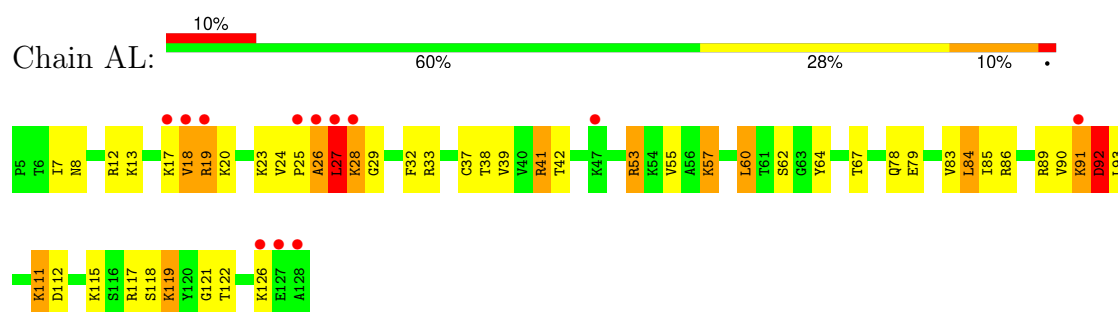
- Molecule 4: 30S ribosomal protein S10



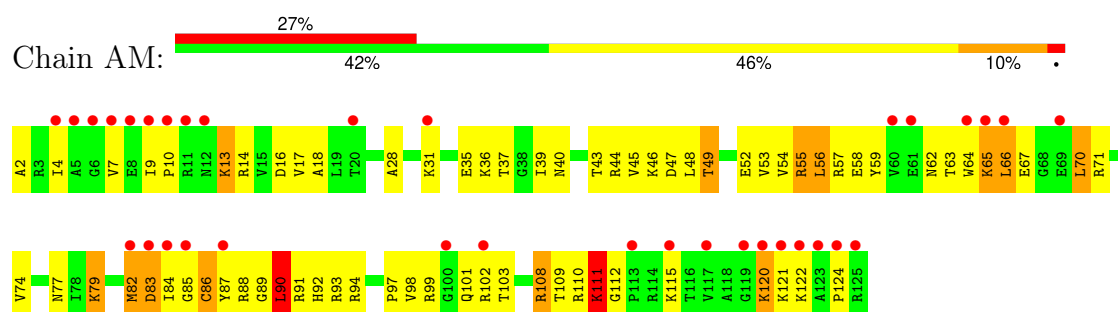
- Molecule 5: 30S ribosomal protein S11



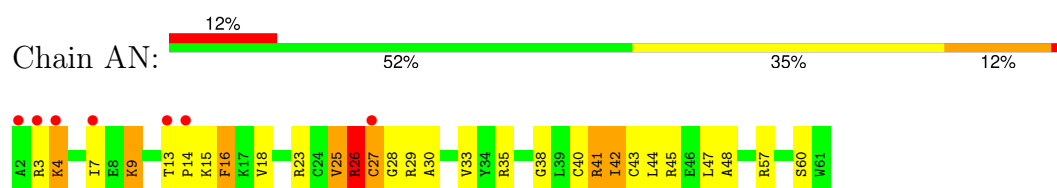
- Molecule 6: 30S ribosomal protein S12



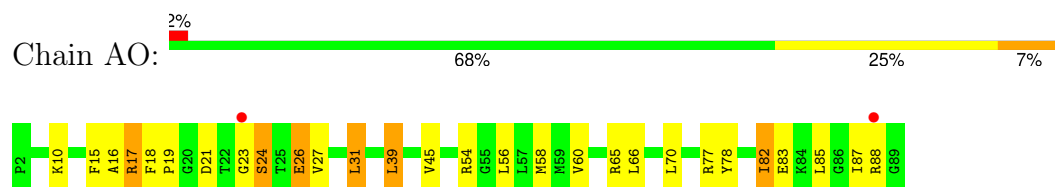
- Molecule 7: 30S ribosomal protein S13



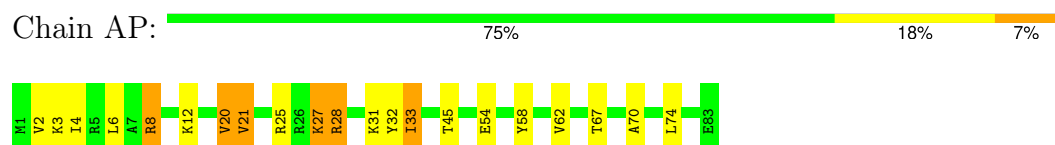
- Molecule 8: 30S ribosomal protein S14 TYPE Z



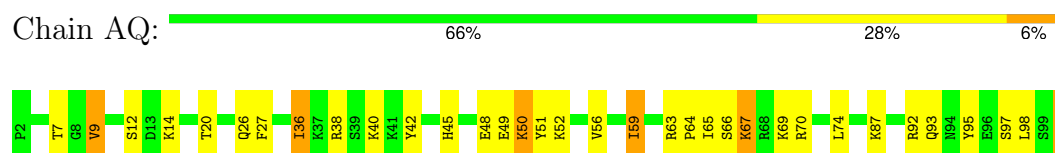
- Molecule 9: 30S ribosomal protein S15



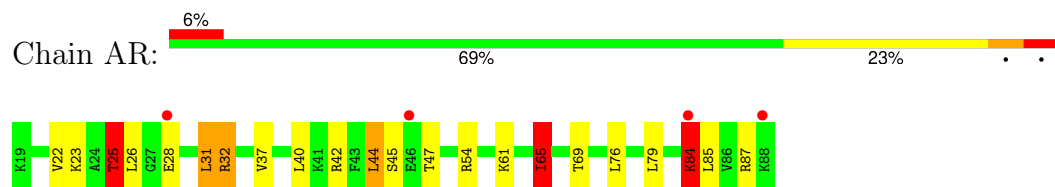
- Molecule 10: 30S ribosomal protein S16



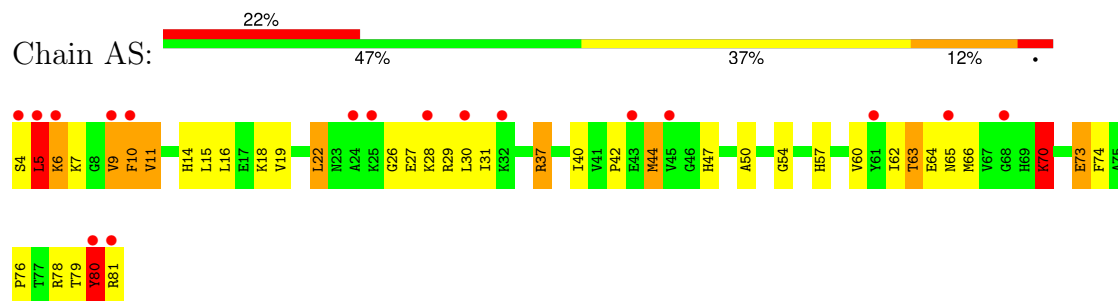
- Molecule 11: 30S ribosomal protein S17



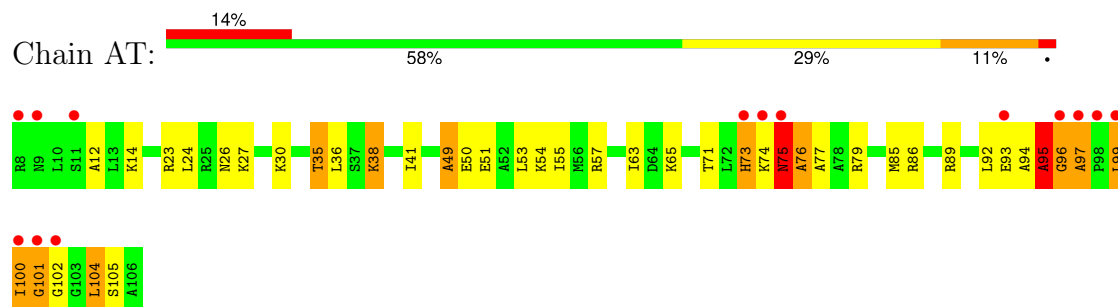
- Molecule 12: 30S ribosomal protein S18



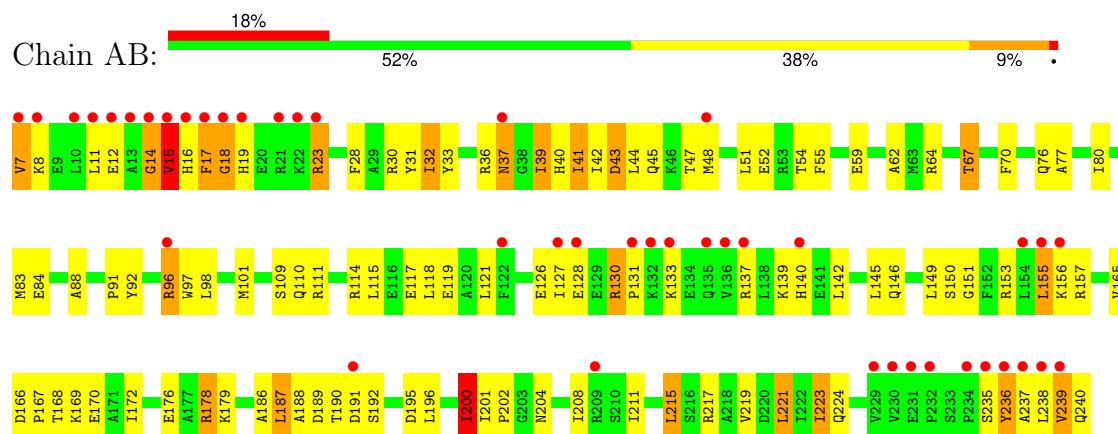
- Molecule 13: 30S ribosomal protein S19



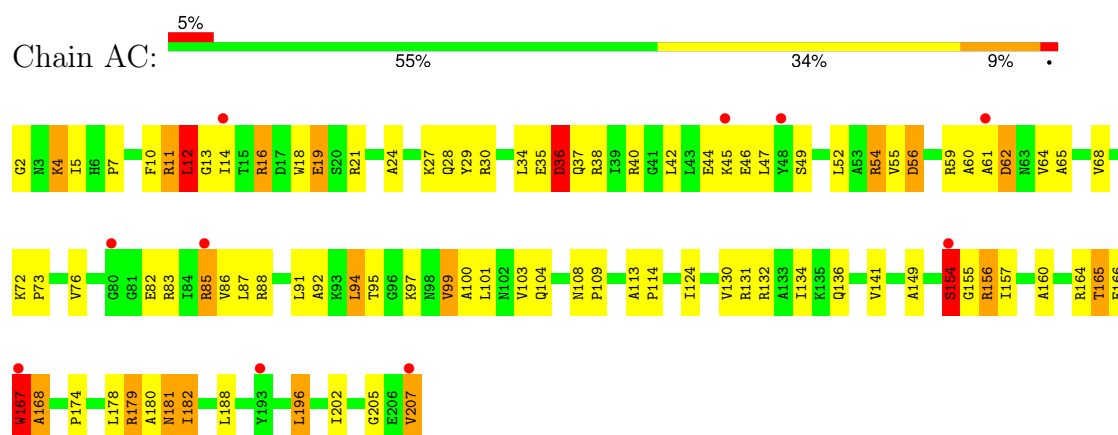
- Molecule 14: 30S ribosomal protein S20



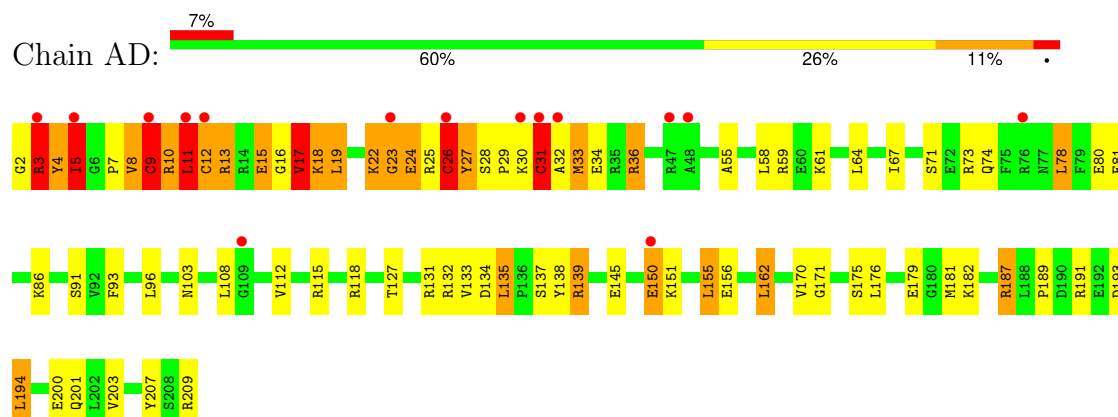
- Molecule 15: 30S ribosomal protein S2



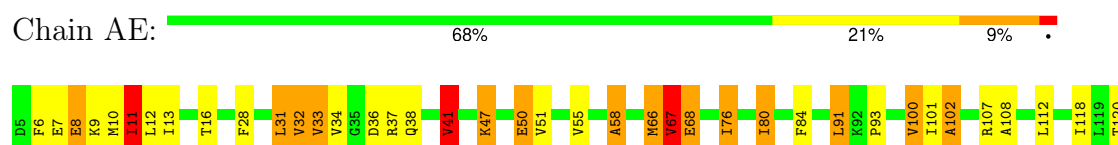
- Molecule 16: 30S ribosomal protein S3



- Molecule 17: 30S ribosomal protein S4



- Molecule 18: 30S ribosomal protein S5

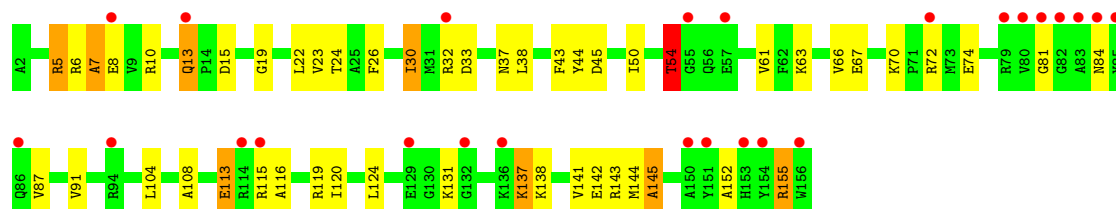




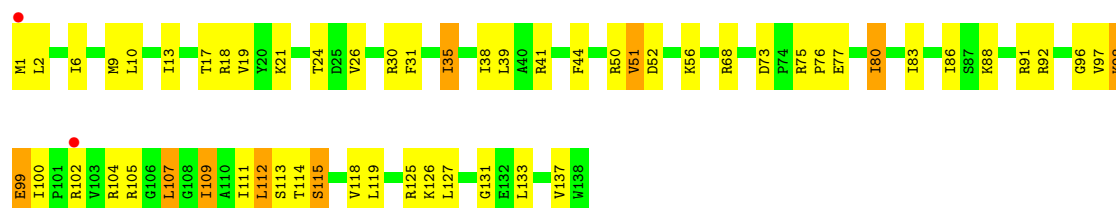
- Molecule 19: 30S ribosomal protein S6



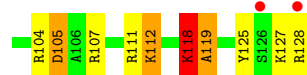
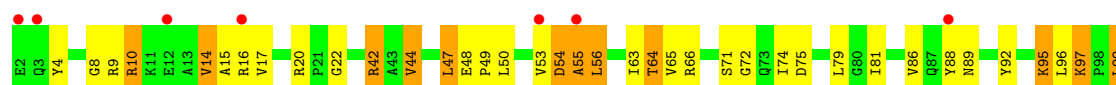
- Molecule 20: 30S ribosomal protein S7



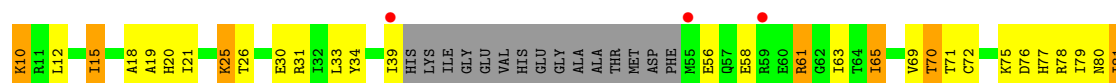
- Molecule 21: 30S ribosomal protein S8

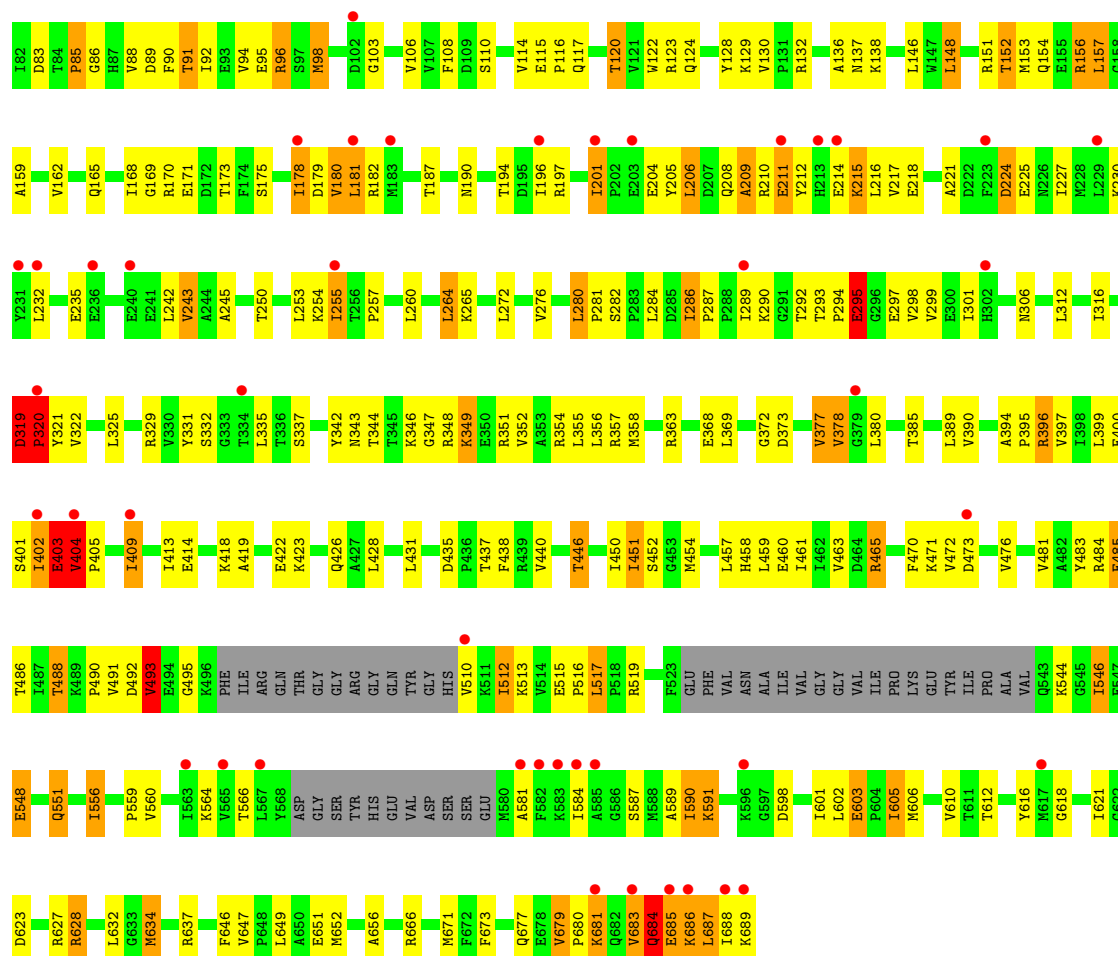


- Molecule 22: 30S ribosomal protein S9

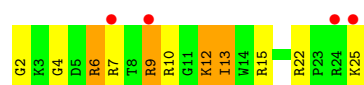


- Molecule 23: Elongation factor G

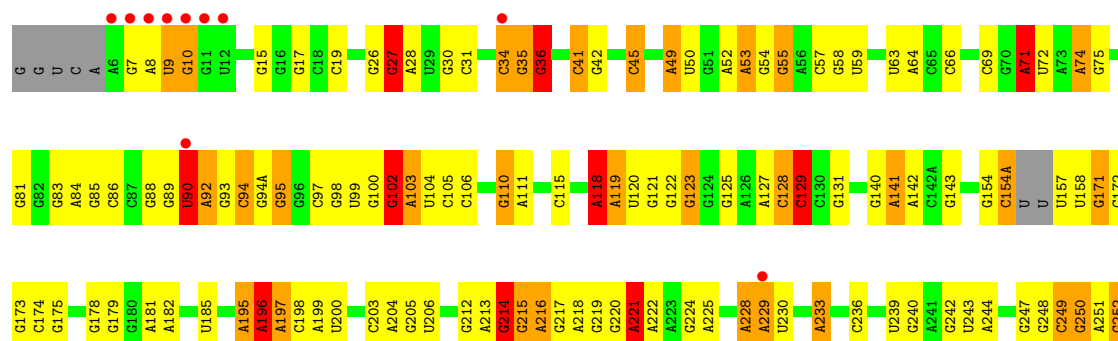
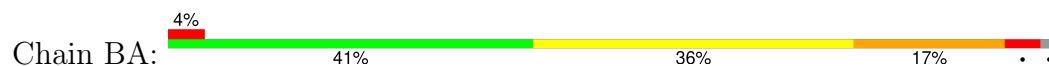


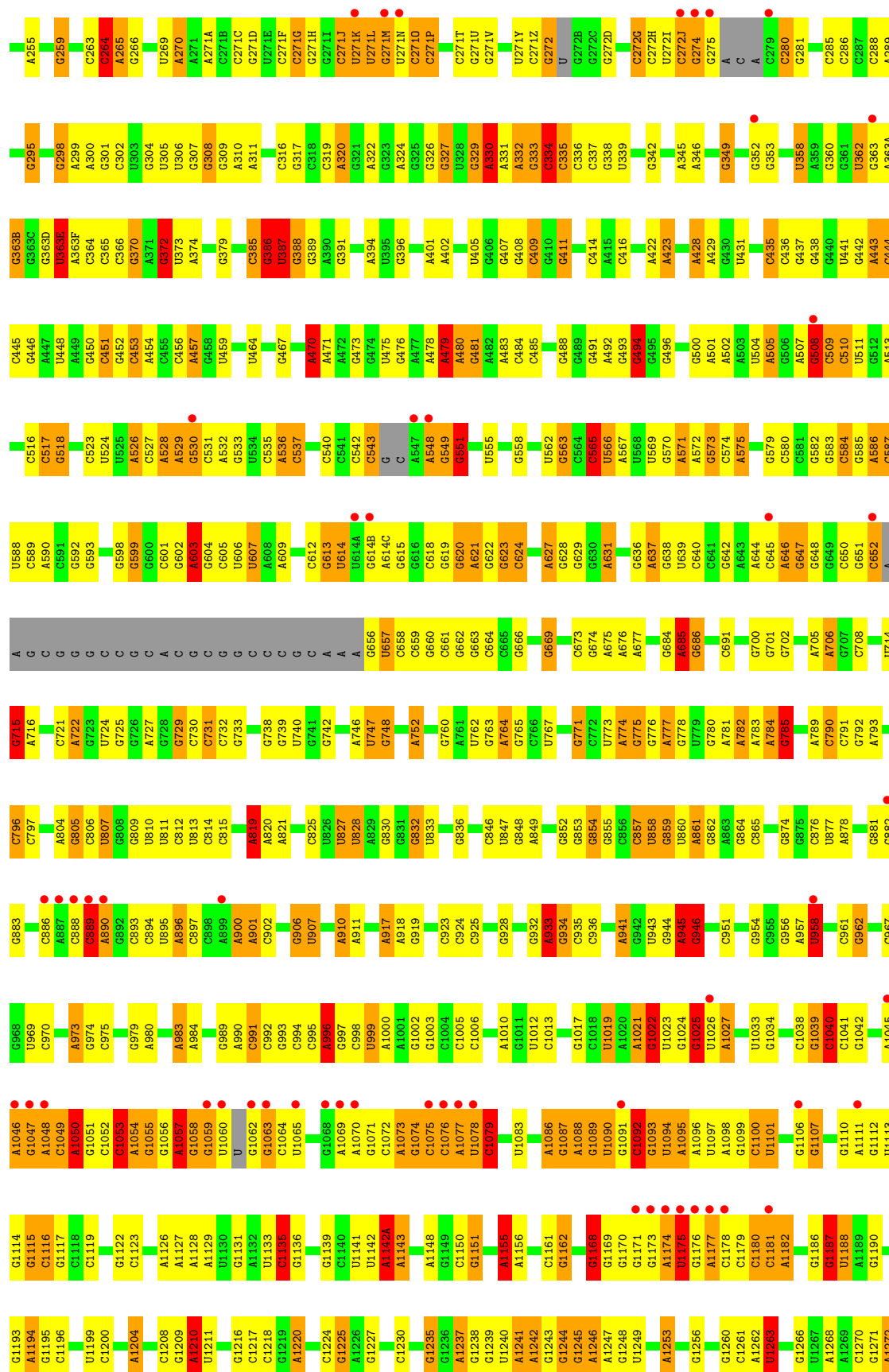


• Molecule 24: 30S ribosomal protein THX

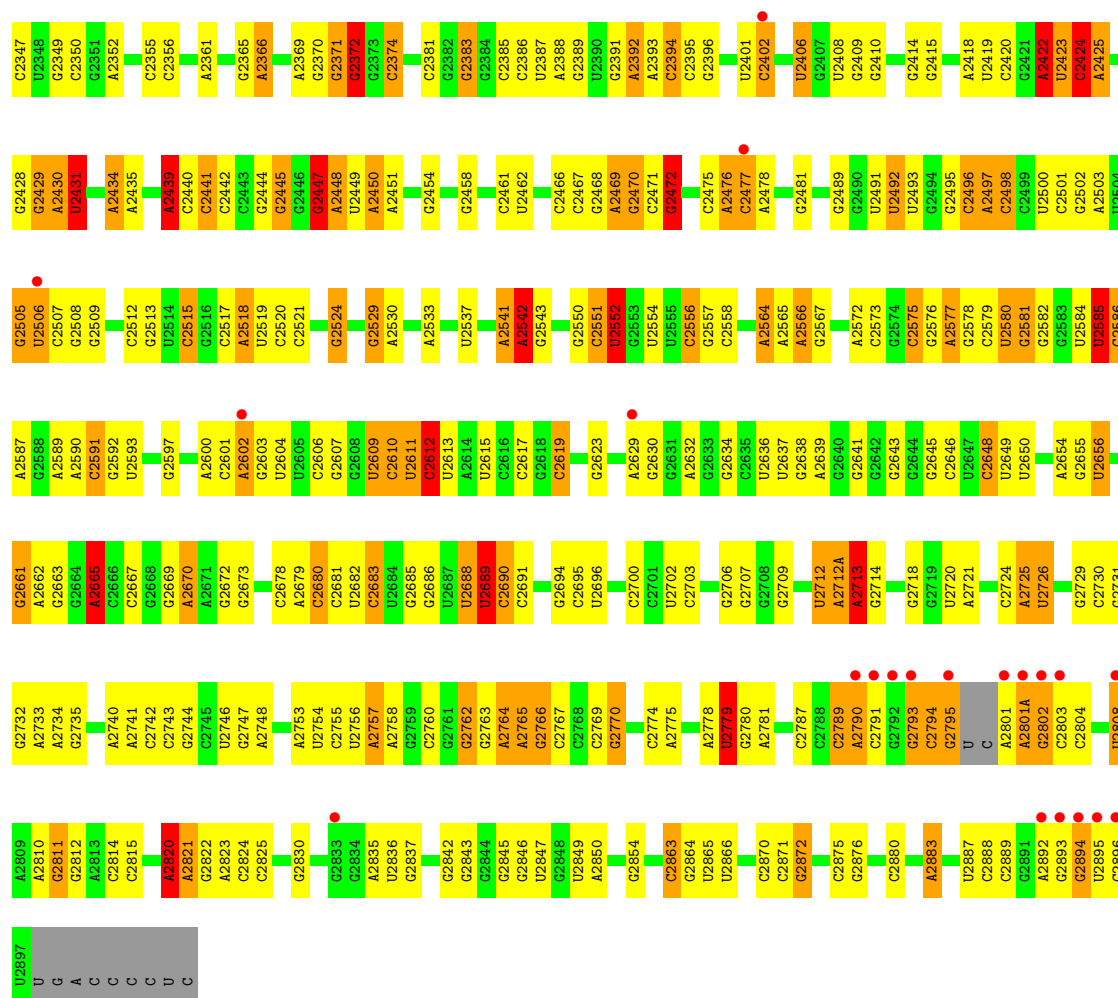


• Molecule 25: 23S ribosomal RNA

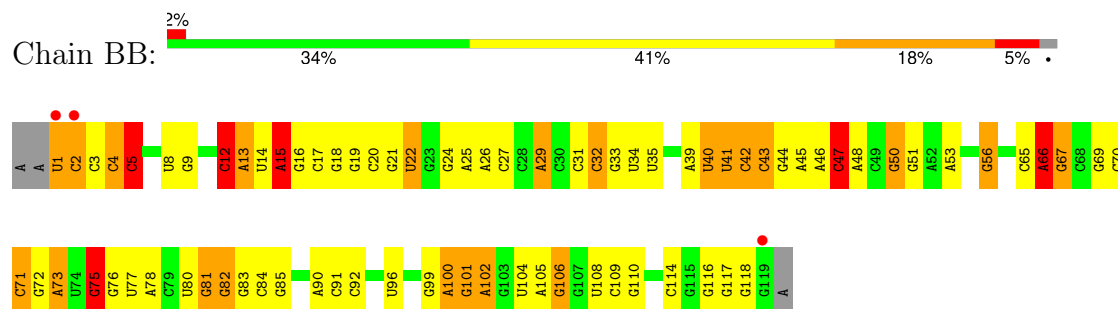




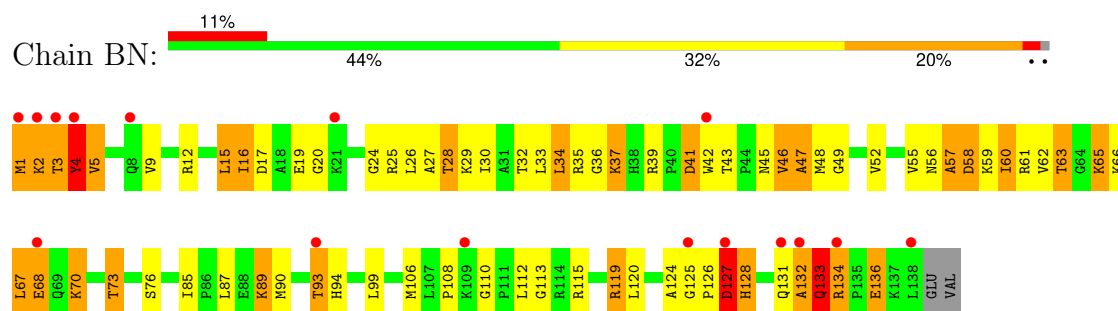
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G2285	G2191	G2126	C2055	U1976	C1904	G1814	C1743	A1652	U1576	C1505	G1358	A1275
A2286	G2192	G2127	G2056	A1977	G1905	G1815	G1744	G1653	U1577	C1506	A1359	
A2287	G2194	G2131	C2056	A1978	G1906	G1816	G1745A	A1654	U1578	A1507	G1364	A1278
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G2290	A2198	A2134	A2061	G1980	G1909	U1818	G1747	C1656	A1580	C1509	A1366	G1280
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	C2201	C2137	C2064	C1983	A1913	A1821	A1749	U1659	A1583	C1512	G1368	A1284
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C2297		C2139		G1987	U1915	G1823		C1663	A1586	U1514	G1371	A1286
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G2302	G2219	U2144	G2072	U1992	A1939	G1763	G1764	C1675		G1524	A1379	G1295
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A2311		G2153	U2086	G2009	A1947	U1772	G1772	U1681	G1606	C1532	U1390	U1307
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G2318	A2247	G2161	U2096	A2019	G1860	C1686	U1779	U1688	A1616	G1539	U1395	U1313
C2319	G2248	C2162	C2097	A2020	G1860	C1687	U1779	U1689	C1617	G1540	U1397	C1314
A2320	U2249	C2163	U2098	C2021	G1863	U1688	G1781	A1689	A1618	U1541		C1315
G2321	G2250	G2164	U2099	U2022	U1943	U1689	G1782	A1690	G1619	A1542	C1403	A1322
A2322	G2251	G2165	G2100	G2023	G1945	U1691	C1783	C1691	G1620	C1543	C1404	U1323
G2323	G2252	G2166	G2101	G2024	G1946	C1692	A1783	U1692	U1621	A1544	U1405	
C2324	G2253	U2167	G2102	C2025	C1947	U1693	A1784	C1693	G1622	A1545	U1406	U1326
G2325	G2259	G2168	C2103	C2026	A1876	C1694	A1785	C1694	G1623	C1546	C1407	G1327
C2326	C2260	A2169	G2104	G2027	A1877	C1695	A1786	C1695	G1624	C1547	C1408	
A2327	C2261	C2170	C2105	A1952	G1878	C1696	A1787	G1696		G1548	U1329	U1328
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	C2263	U2172	C2107	U1956	C1880	A1789	A1789	G1697			G1416	C1331
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G2334	A2267	C2176	C2110	U2034	G1884	C1795	U1796	G1710	G1635	G1559	U1420	
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		C2178	G2112	C2036	C1886	U1798	U1798	G1715	U1637	A1563	G1422	C1345
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G2337	A2273	U2180	G2115	C2040	A1888	C1800	C1800	U1720	U1639	C1565	A1427	G1347
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C2342	G2276	G2183		C2043	C1966	A1802	A1802	G1721	C1644	A1569	C1430	
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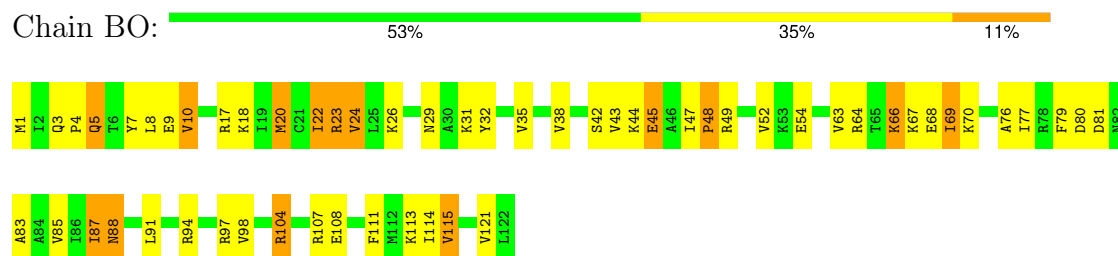
- Molecule 26: 5S ribosomal RNA



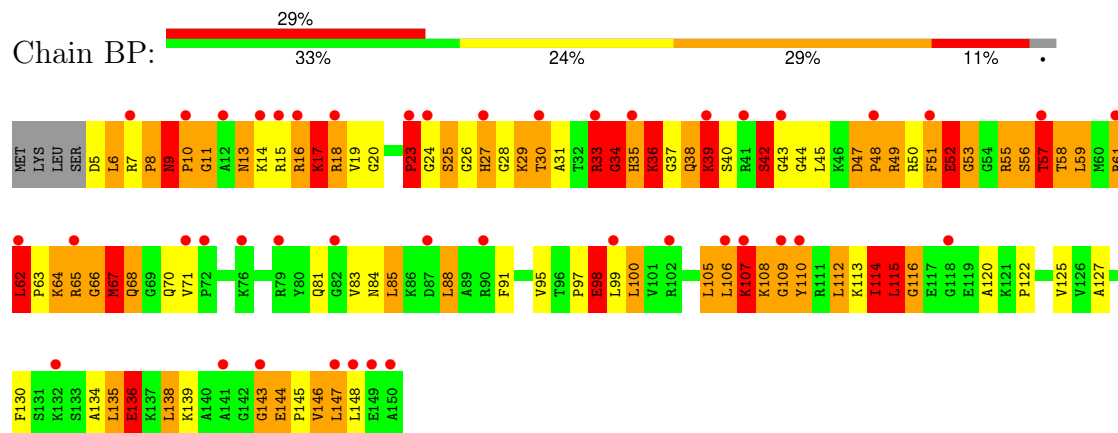
- Molecule 27: 50S ribosomal protein L13



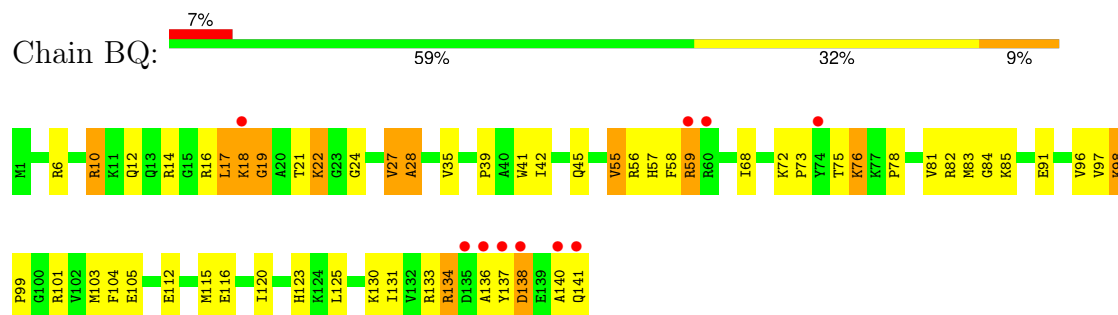
- Molecule 28: 50S ribosomal protein L14



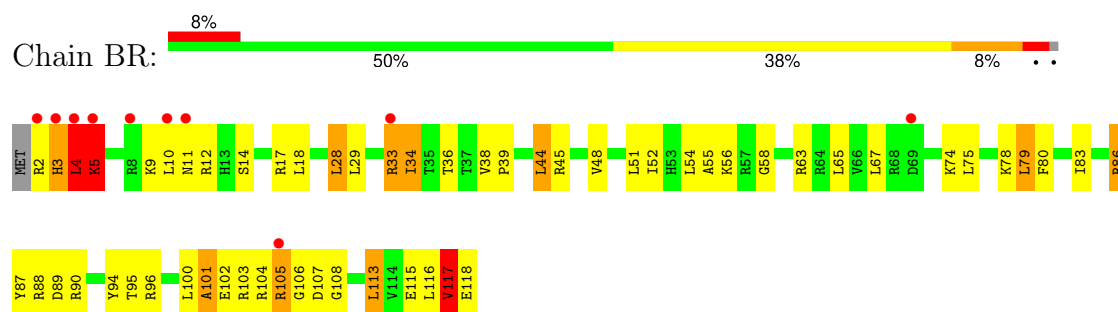
- Molecule 29: 50S ribosomal protein L15



- Molecule 30: 50S ribosomal protein L16

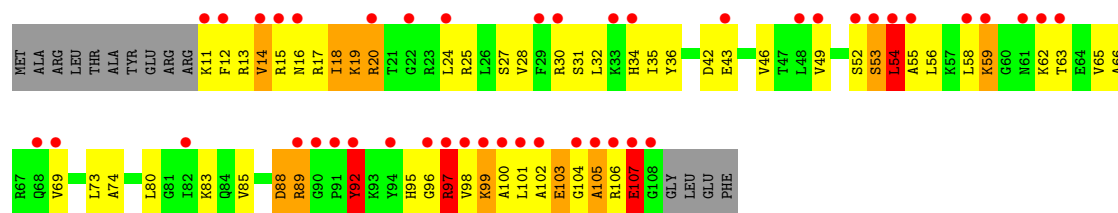


- Molecule 31: 50S ribosomal protein L17

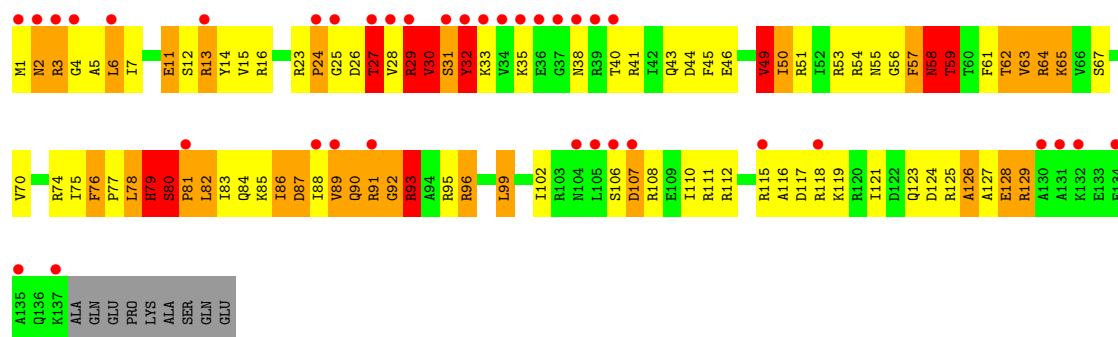


- Molecule 32: 50S ribosomal protein L18

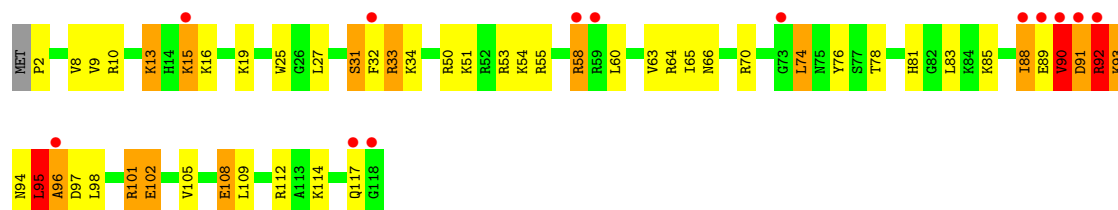




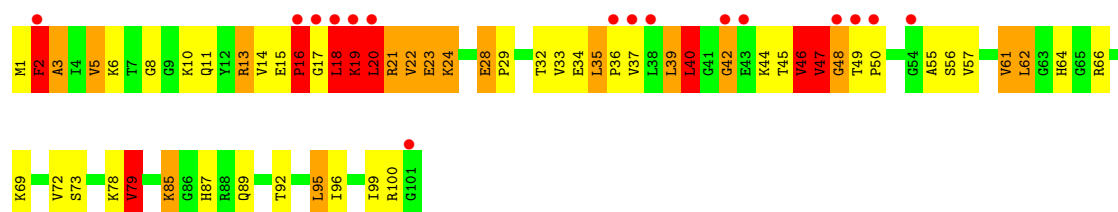
• Molecule 33: 50S ribosomal protein L19



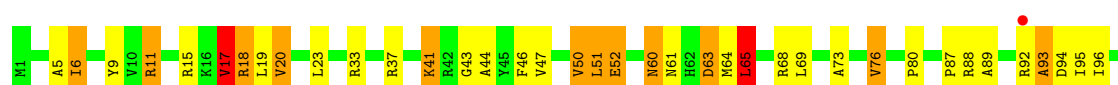
• Molecule 34: 50S ribosomal protein L20



• Molecule 35: 50S ribosomal protein L21

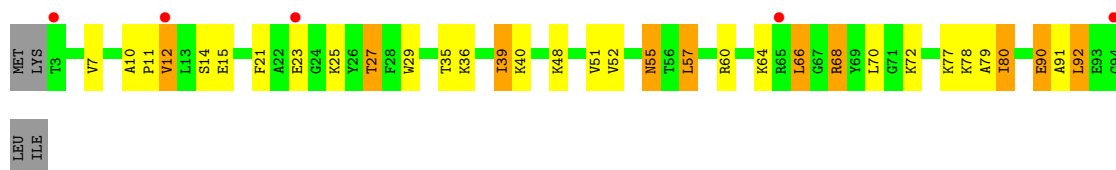


• Molecule 36: 50S ribosomal protein L22

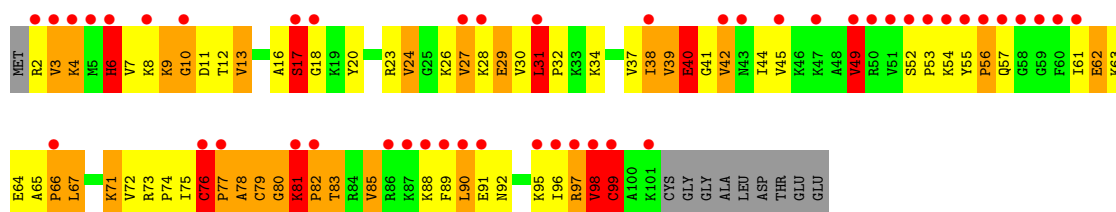
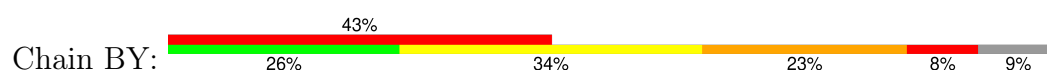




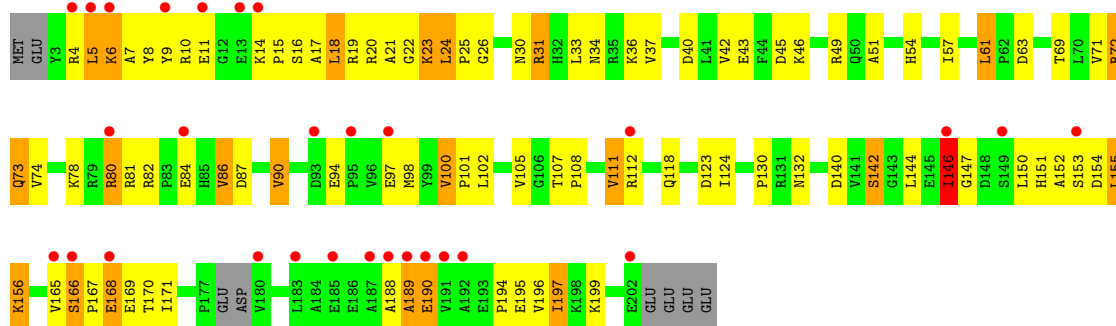
- Molecule 37: 50S ribosomal protein L23



- Molecule 38: 50S ribosomal protein L24



- Molecule 39: 50S ribosomal protein L25

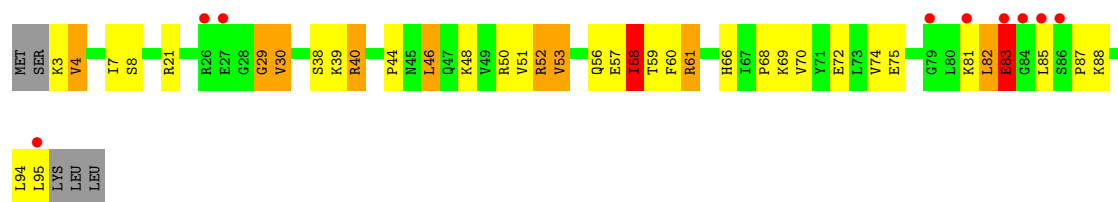


- Molecule 40: 50S ribosomal protein L27



- Molecule 41: 50S ribosomal protein L28

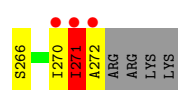
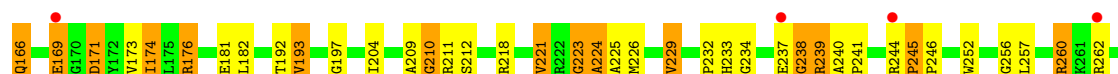
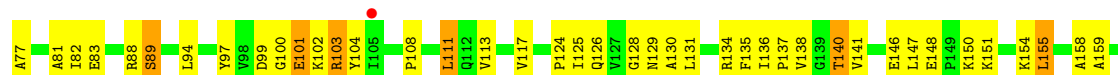
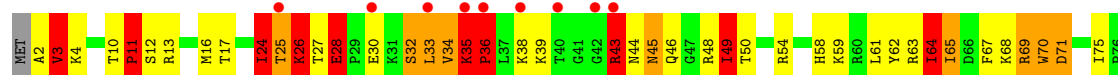




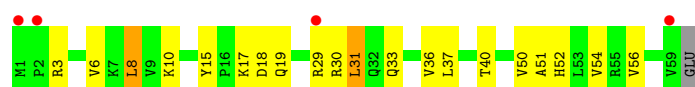
- Molecule 42: 50S ribosomal protein L29



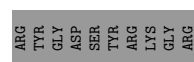
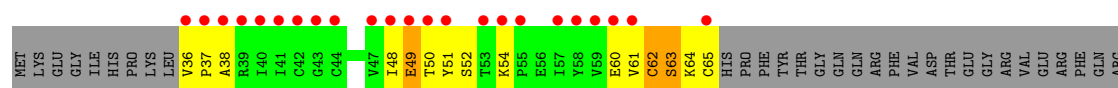
- Molecule 43: 50S ribosomal protein L2



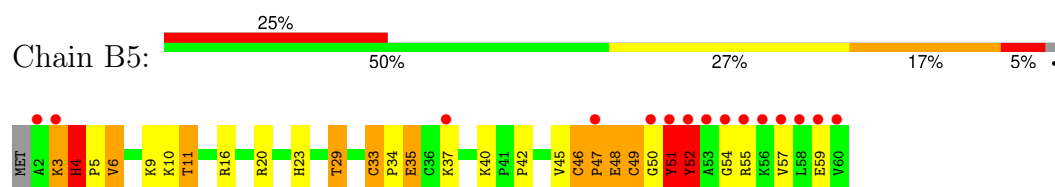
- Molecule 44: 50S ribosomal protein L30



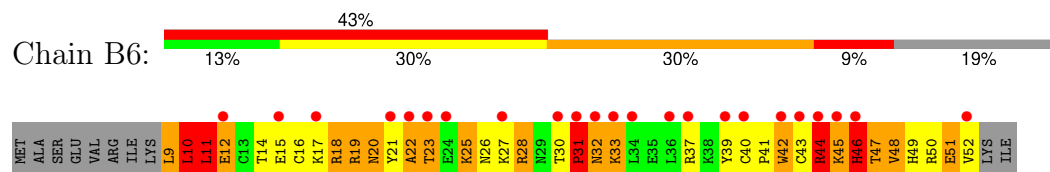
- Molecule 45: 50S ribosomal protein L31



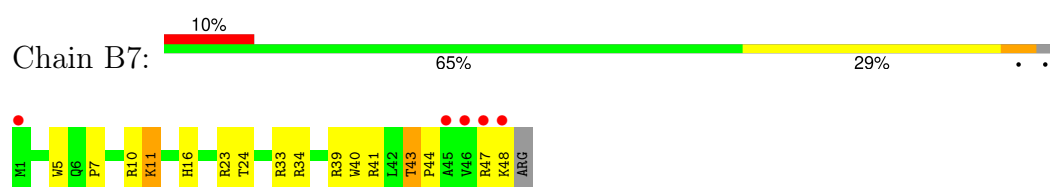
- Molecule 46: 50S ribosomal protein L32



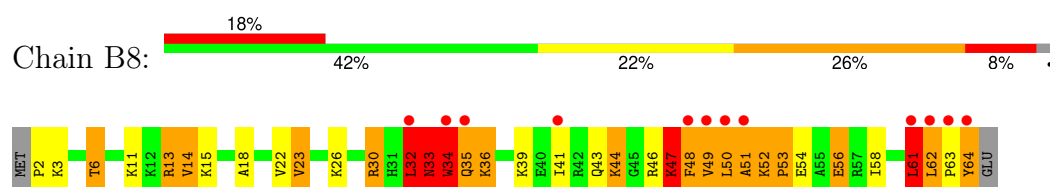
- Molecule 47: 50S ribosomal protein L33



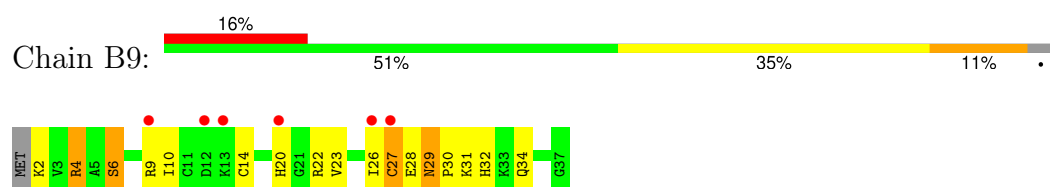
- Molecule 48: 50S ribosomal protein L34



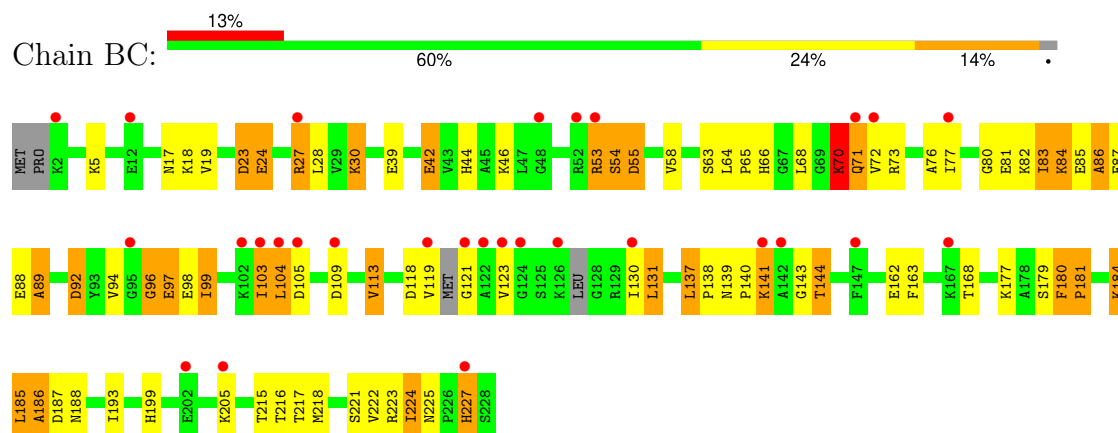
- Molecule 49: 50S ribosomal protein L35



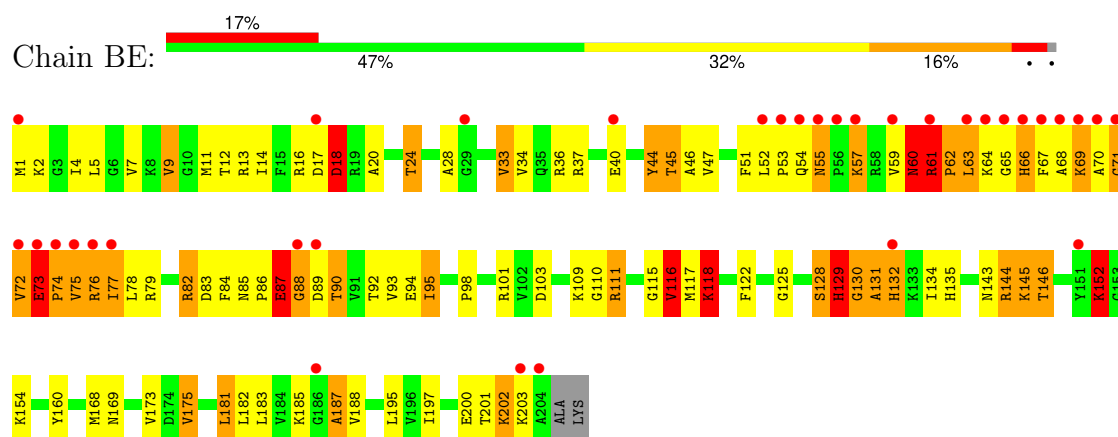
- Molecule 50: 50S ribosomal protein L36



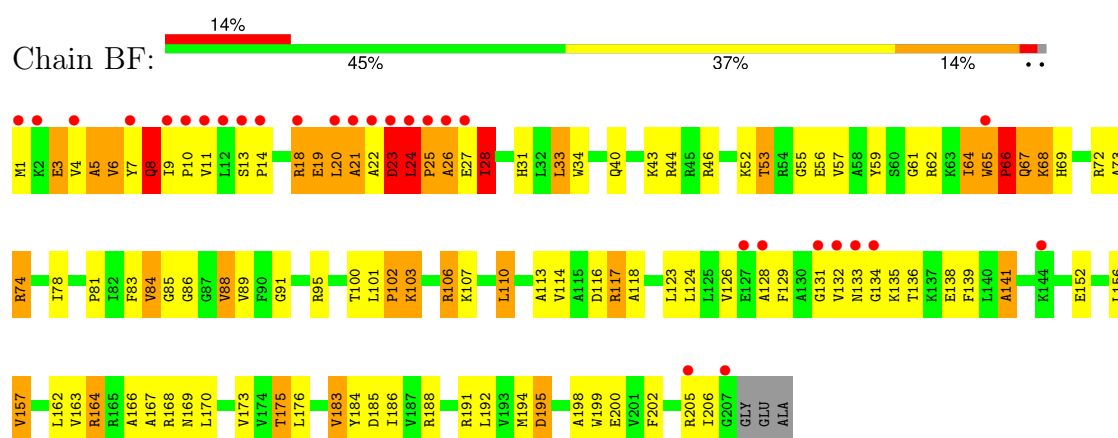
- Molecule 51: 50S ribosomal protein L1



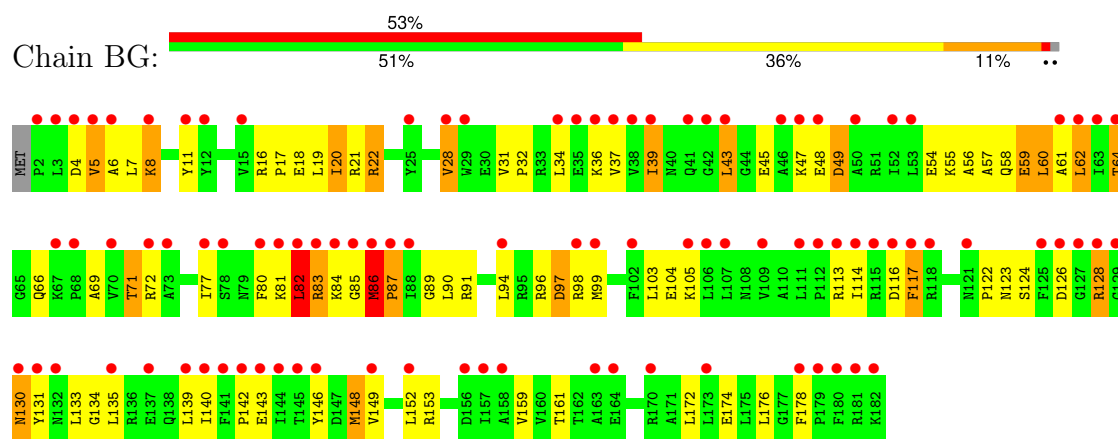
- Molecule 52: 50S ribosomal protein L3



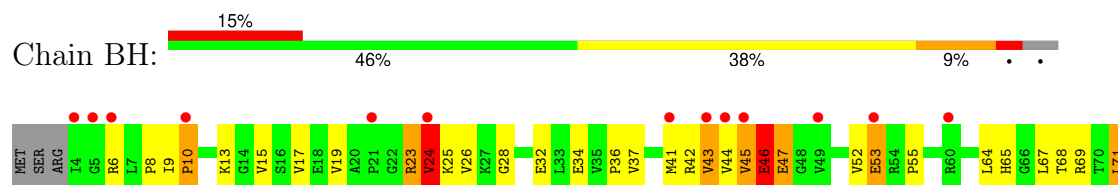
• Molecule 53: 50S ribosomal protein L4

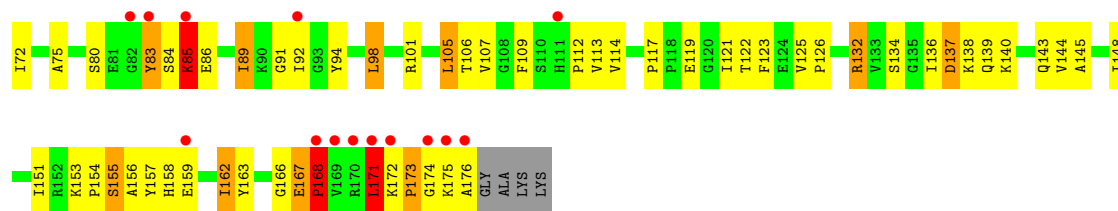


• Molecule 54: 50S ribosomal protein L5

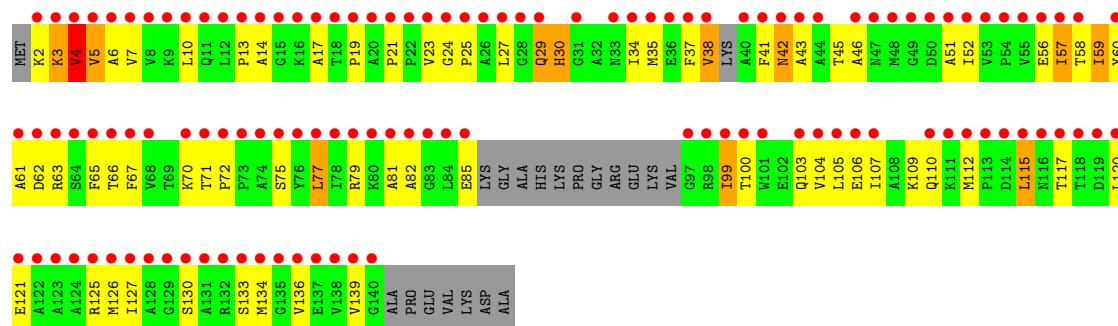
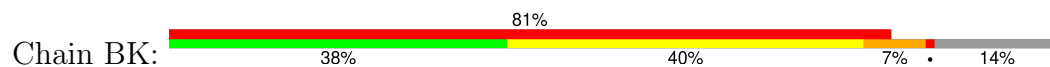


• Molecule 55: 50S ribosomal protein L6

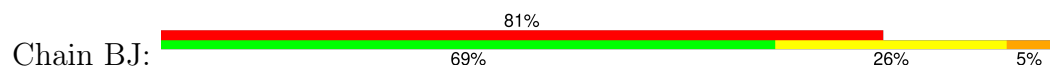




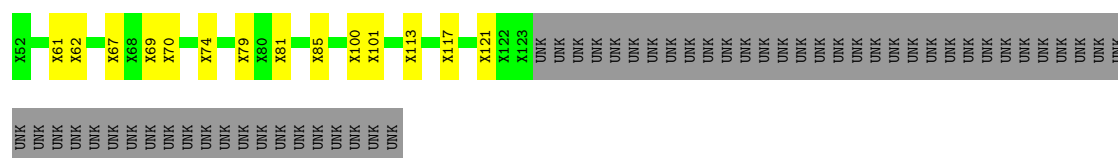
• Molecule 56: 50S ribosomal protein L11



• Molecule 57: 50S ribosomal protein L10



• Molecule 58: 50S ribosomal protein L12 CTD



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	201.58Å 241.65Å 305.80Å 90.00° 99.48° 90.00°	Depositor
Resolution (Å)	39.60 – 2.86 39.60 – 2.86	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.60-2.86) 98.5 (39.60-2.86)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.22	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 2.86Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.200 , 0.250 0.201 , 0.244	Depositor DCC
R_{free} test set	32790 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	33.5	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 36.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	151831	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.69% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	AA	0.53	2/36408 (0.0%)	1.06	278/56818 (0.5%)
2	AV	0.50	1/1764 (0.1%)	1.18	23/2747 (0.8%)
3	AX	0.49	0/138	1.23	2/212 (0.9%)
4	AJ	0.95	0/808	1.17	4/1085 (0.4%)
5	AK	0.84	0/900	1.13	7/1213 (0.6%)
6	AL	0.95	1/987 (0.1%)	1.22	3/1320 (0.2%)
7	AM	0.78	0/999	1.14	6/1336 (0.4%)
8	AN	0.88	1/501 (0.2%)	1.29	6/664 (0.9%)
9	AO	0.88	0/745	1.08	0/992
10	AP	0.85	0/717	1.05	0/963
11	AQ	0.91	0/837	1.14	1/1117 (0.1%)
12	AR	0.81	0/579	1.08	2/768 (0.3%)
13	AS	0.81	0/643	1.10	2/865 (0.2%)
14	AT	0.90	1/765 (0.1%)	1.21	4/1007 (0.4%)
15	AB	0.76	0/1936	1.05	3/2609 (0.1%)
16	AC	0.90	2/1637 (0.1%)	1.12	2/2205 (0.1%)
17	AD	0.89	7/1733 (0.4%)	1.13	13/2318 (0.6%)
18	AE	0.94	0/1163	1.23	10/1564 (0.6%)
19	AF	0.79	0/856	1.00	1/1154 (0.1%)
20	AG	0.75	0/1276	1.04	2/1709 (0.1%)
21	AH	0.90	0/1136	1.13	3/1527 (0.2%)
22	AI	0.76	0/1029	1.09	3/1378 (0.2%)
23	AY	0.73	1/4961 (0.0%)	1.06	16/6710 (0.2%)
24	AU	0.77	0/213	0.98	0/277
25	BA	0.57	8/68964 (0.0%)	1.11	627/107644 (0.6%)
26	BB	0.46	0/2853	1.02	19/4451 (0.4%)
27	BN	0.99	3/1131 (0.3%)	1.31	9/1525 (0.6%)
28	BO	0.91	0/943	1.24	3/1269 (0.2%)
29	BP	1.21	8/1131 (0.7%)	1.53	13/1504 (0.9%)
30	BQ	0.87	0/1143	1.18	9/1527 (0.6%)
31	BR	1.03	3/974 (0.3%)	1.21	6/1302 (0.5%)
32	BS	0.76	0/778	1.05	1/1036 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BT	0.99	1/1155 (0.1%)	1.43	17/1542 (1.1%)
34	BU	1.02	1/975 (0.1%)	1.28	6/1297 (0.5%)
35	BV	0.97	0/790	1.23	6/1057 (0.6%)
36	BW	0.96	0/907	1.19	2/1216 (0.2%)
37	BX	0.93	0/739	1.20	2/993 (0.2%)
38	BY	1.23	3/788 (0.4%)	1.51	12/1051 (1.1%)
39	BZ	0.80	0/1539	1.09	5/2093 (0.2%)
40	B0	0.78	0/671	0.99	0/892
41	B1	0.97	0/738	1.24	5/981 (0.5%)
42	B2	0.81	0/600	1.12	0/793
43	BD	1.16	3/2154 (0.1%)	1.33	19/2905 (0.7%)
44	B3	0.81	0/472	1.02	0/634
45	B4	0.81	0/228	0.92	0/309
46	B5	1.22	3/473 (0.6%)	1.69	15/639 (2.3%)
47	B6	1.31	2/387 (0.5%)	1.61	6/518 (1.2%)
48	B7	1.03	0/426	1.02	0/561
49	B8	1.08	2/515 (0.4%)	1.44	8/679 (1.2%)
50	B9	0.98	0/302	1.30	5/397 (1.3%)
51	BC	0.75	2/1747 (0.1%)	1.17	12/2351 (0.5%)
52	BE	1.06	4/1596 (0.3%)	1.32	15/2153 (0.7%)
53	BF	0.91	0/1658	1.21	10/2244 (0.4%)
54	BG	0.71	1/1499 (0.1%)	0.95	3/2016 (0.1%)
55	BH	0.83	0/1327	1.24	10/1794 (0.6%)
56	BK	0.65	0/951	0.88	0/1290
57	BJ	0.91	1/650 (0.2%)	1.07	4/907 (0.4%)
All	All	0.69	61/163935 (0.0%)	1.12	1240/244128 (0.5%)

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
4	AJ	0	1
6	AL	0	1
8	AN	0	1
14	AT	0	2
17	AD	0	2
23	AY	0	4
27	BN	0	2
29	BP	0	15
30	BQ	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
31	BR	0	2
32	BS	0	1
33	BT	0	6
34	BU	0	3
35	BV	0	3
38	BY	0	6
41	B1	0	2
43	BD	0	4
46	B5	0	2
47	B6	0	3
51	BC	0	2
52	BE	0	5
53	BF	0	1
55	BH	0	1
58	BL	0	1
All	All	0	72

All (61) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	BA	2506	U	O3'-P	10.11	1.76	1.61
17	AD	26	CYS	CA-C	9.30	1.65	1.52
31	BR	5	LYS	CA-C	8.74	1.60	1.52
17	AD	26	CYS	CA-CB	7.62	1.66	1.53
29	BP	27	HIS	CA-C	7.58	1.62	1.52
54	BG	47	LYS	CA-C	7.27	1.55	1.52
17	AD	13	ARG	N-CA	7.25	1.53	1.46
25	BA	1695	G	O3'-P	-7.23	1.50	1.61
27	BN	127	ASP	CB-CG	7.10	1.69	1.52
34	BU	32	PHE	CA-C	-6.62	1.44	1.52
27	BN	127	ASP	CA-C	6.59	1.61	1.52
17	AD	12	CYS	CA-CB	6.55	1.64	1.53
49	B8	50	LEU	N-CA	6.35	1.53	1.46
29	BP	42	SER	CA-C	6.30	1.61	1.52
52	BE	116	VAL	CA-C	-6.26	1.44	1.52
17	AD	12	CYS	CA-C	6.26	1.61	1.52
47	B6	45	LYS	CA-C	6.26	1.60	1.52
52	BE	129	HIS	CA-C	-5.99	1.44	1.52
27	BN	128	HIS	N-CA	5.91	1.51	1.46
47	B6	46	HIS	N-CA	5.90	1.53	1.46
25	BA	1299	G	O3'-P	-5.86	1.52	1.61
46	B5	6	VAL	C-O	-5.84	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	BE	132	HIS	CA-CB	5.73	1.63	1.53
29	BP	27	HIS	N-CA	5.66	1.53	1.46
38	BY	76	CYS	N-CA	5.66	1.51	1.46
29	BP	36	LYS	CA-C	5.62	1.60	1.52
17	AD	27	TYR	N-CA	5.61	1.53	1.46
14	AT	76	ALA	N-CA	5.61	1.52	1.46
43	BD	36	PRO	N-CA	-5.58	1.40	1.47
38	BY	99	CYS	CA-C	5.56	1.60	1.52
31	BR	5	LYS	N-CA	5.56	1.51	1.47
51	BC	27	ARG	CD-NE	-5.56	1.38	1.46
25	BA	1300	U	O3'-P	-5.54	1.52	1.61
46	B5	4	HIS	N-CA	5.47	1.53	1.46
51	BC	27	ARG	CG-CD	-5.43	1.36	1.52
2	AV	72	C	O3'-P	-5.43	1.53	1.61
57	BJ	8	ALA	N-CA	5.41	1.49	1.46
1	AA	1363	C	O3'-P	-5.39	1.54	1.61
25	BA	1779	U	O3'-P	-5.39	1.53	1.61
23	AY	85	PRO	N-CA	-5.38	1.40	1.46
29	BP	39	LYS	CA-C	5.37	1.59	1.52
49	B8	35	GLN	CA-C	-5.36	1.47	1.53
33	BT	79	HIS	CA-C	5.36	1.59	1.52
1	AA	1145	C	O3'-P	-5.35	1.53	1.61
29	BP	62	LEU	CB-CG	5.35	1.64	1.53
16	AC	182	ILE	N-CA	-5.34	1.39	1.46
43	BD	43	ARG	N-CA	5.28	1.53	1.46
25	BA	2591	C	O3'-P	-5.27	1.53	1.61
16	AC	11	ARG	CA-C	5.21	1.57	1.53
29	BP	30	THR	CA-CB	5.20	1.60	1.54
17	AD	9	CYS	CA-C	5.18	1.59	1.52
25	BA	330	A	O3'-P	-5.18	1.53	1.61
31	BR	105	ARG	CA-C	-5.14	1.48	1.53
6	AL	92	ASP	CA-C	-5.13	1.45	1.52
52	BE	131	ALA	N-CA	-5.13	1.39	1.46
38	BY	12	THR	N-CA	5.11	1.52	1.46
25	BA	1370	C	O3'-P	-5.10	1.53	1.61
29	BP	64	LYS	CA-C	-5.09	1.47	1.52
43	BD	64	ILE	CA-CB	5.07	1.59	1.54
8	AN	26	ARG	N-CA	5.04	1.52	1.46
46	B5	54	GLY	N-CA	5.01	1.50	1.45

All (1240) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1498	U	C2'-C3'-O3'	18.14	136.71	109.50
1	AA	1067	A	C2'-C3'-O3'	16.92	134.88	109.50
1	AA	328	C	C2'-C3'-O3'	15.30	132.44	109.50
25	BA	1799	G	C2'-C3'-O3'	15.14	132.21	109.50
25	BA	2506	U	C2'-C3'-O3'	14.89	131.84	109.50
1	AA	1145	C	C2'-C3'-O3'	-14.17	88.25	109.50
25	BA	1992	G	C2'-C3'-O3'	13.67	130.00	109.50
47	B6	45	LYS	N-CA-C	13.38	131.24	108.23
1	AA	1139	G	C3'-C2'-O2'	-13.18	94.83	114.60
1	AA	30	U	C2'-C3'-O3'	13.15	129.22	109.50
25	BA	2225	A	C2'-C3'-O3'	13.09	129.13	109.50
25	BA	1962	C	C1'-C2'-O2'	-12.71	92.74	111.80
25	BA	1541	G	C4'-C3'-O3'	-12.50	94.25	113.00
51	BC	27	ARG	NE-CZ-NH2	-12.33	108.10	119.20
25	BA	387	U	C2'-C3'-O3'	12.04	127.56	109.50
25	BA	990	A	C4'-C3'-O3'	-11.97	95.04	113.00
25	BA	752	A	C2'-C3'-O3'	11.70	127.05	109.50
25	BA	752	A	C4'-C3'-O3'	-11.67	91.89	109.40
1	AA	115	G	C2'-C3'-O3'	11.43	126.65	109.50
25	BA	1653	G	C2'-C3'-O3'	11.37	126.55	109.50
1	AA	687	A	C2'-C3'-O3'	11.13	126.19	109.50
1	AA	1181	G	C4'-C3'-O3'	-10.98	96.53	113.00
25	BA	1819	A	C2'-C3'-O3'	10.93	125.89	109.50
1	AA	1145	C	C3'-C2'-O2'	-10.91	98.24	114.60
51	BC	27	ARG	CD-NE-CZ	-10.88	109.17	124.40
25	BA	508	G	C2'-C3'-O3'	-10.66	97.72	113.70
25	BA	2141	G	C2'-C3'-O3'	10.63	129.65	113.70
25	BA	272	G	C2'-C3'-O3'	10.61	125.42	109.50
25	BA	1300	U	P-O3'-C3'	10.56	136.04	120.20
2	AV	72	C	C4'-C3'-O3'	10.55	128.82	113.00
25	BA	1022	G	C2'-C3'-O3'	10.49	125.23	109.50
25	BA	603	A	C2'-C3'-O3'	10.44	125.15	109.50
1	AA	1145	C	C4'-C3'-O3'	-10.35	93.87	109.40
23	AY	320	PRO	N-CA-C	-10.26	95.08	111.19
25	BA	2447	G	C4'-C3'-O3'	-10.17	94.15	109.40
1	AA	243	A	C2'-C3'-O3'	10.14	124.70	109.50
25	BA	2585	U	C2'-C3'-O3'	10.11	124.67	109.50
1	AA	79	G	C2'-C3'-O3'	10.07	124.60	109.50
29	BP	27	HIS	N-CA-C	9.99	126.05	109.46
15	AB	23	ARG	N-CA-C	-9.94	98.79	112.30
1	AA	913	A	C2'-C3'-O3'	9.84	124.26	109.50
1	AA	533	A	C2'-C3'-O3'	9.82	124.23	109.50
25	BA	945	A	C2'-C3'-O3'	-9.78	94.83	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	666	G	C3'-C2'-O2'	9.70	125.25	110.70
25	BA	74	A	C2'-C3'-O3'	9.67	124.00	109.50
2	AV	34	G	C2'-C3'-O3'	9.59	128.08	113.70
25	BA	509	C	C2'-C3'-O3'	-9.55	99.37	113.70
30	BQ	136	ALA	N-CA-C	-9.46	101.88	112.57
29	BP	59	LEU	N-CA-C	-9.42	99.83	112.26
6	AL	119	LYS	N-CA-C	-9.37	98.57	110.19
51	BC	27	ARG	CB-CG-CD	9.32	132.73	111.30
1	AA	1504	G	C4'-C3'-O3'	9.23	123.24	109.40
25	BA	1835	G	C4'-C3'-O3'	-9.22	99.16	113.00
25	BA	1262	A	C3'-C2'-O2'	9.21	124.52	110.70
25	BA	2200	C	C4'-C3'-O3'	-9.18	99.24	113.00
25	BA	827	U	C2'-C3'-O3'	-9.15	95.78	109.50
25	BA	2450	A	C3'-C2'-O2'	9.15	124.42	110.70
25	BA	1633	G	C4'-C3'-O3'	-9.05	99.42	113.00
25	BA	195	A	C2'-C3'-O3'	-9.00	100.20	113.70
52	BE	132	HIS	CA-C-N	-8.99	108.14	122.79
52	BE	132	HIS	C-N-CA	-8.99	108.14	122.79
23	AY	88	VAL	CB-CA-C	-8.95	100.05	112.14
25	BA	1970	A	C4'-C3'-O3'	-8.94	95.99	109.40
1	AA	1143	G	C4'-C3'-O3'	-8.91	99.64	113.00
25	BA	1790	C	C2'-C3'-O3'	-8.89	100.36	113.70
25	BA	1545	A	C4'-C3'-O3'	-8.85	99.72	113.00
25	BA	1834	U	C2'-C3'-O3'	-8.83	100.46	113.70
1	AA	1143	G	C2'-C3'-O3'	8.81	126.92	113.70
1	AA	932	C	C4'-C3'-O3'	-8.78	99.83	113.00
29	BP	31	ALA	N-CA-C	-8.76	99.61	111.96
25	BA	2765	A	C4'-C3'-O3'	-8.74	99.89	113.00
1	AA	338	A	C3'-C2'-O2'	8.71	123.77	110.70
25	BA	110	G	C3'-C2'-O2'	8.68	123.72	110.70
25	BA	2321	G	C2'-C3'-O3'	-8.67	100.69	113.70
17	AD	12	CYS	N-CA-C	-8.64	92.39	110.80
25	BA	2031	A	C2'-C3'-O3'	8.64	122.47	109.50
1	AA	1457	G	C3'-C2'-O2'	8.61	123.61	110.70
17	AD	9	CYS	CA-CB-SG	8.60	134.19	114.40
25	BA	2429	G	C4'-C3'-O3'	-8.56	100.16	113.00
1	AA	1357	A	C2'-C3'-O3'	-8.55	100.87	113.70
1	AA	1143	G	C3'-C2'-O2'	8.52	123.48	110.70
17	AD	26	CYS	CA-CB-SG	8.48	133.91	114.40
25	BA	1558	A	C2'-C3'-O3'	8.48	122.23	109.50
25	BA	1326	U	C4'-C3'-O3'	-8.47	100.29	113.00
25	BA	1263	U	C4'-C3'-O3'	-8.45	100.32	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	2318	G	C2'-C3'-O3'	8.44	126.37	113.70
25	BA	2259	G	C2'-C3'-O3'	-8.42	101.07	113.70
25	BA	1920	C	C3'-C2'-O2'	8.41	123.32	110.70
2	AV	76	A	C2'-C3'-O3'	-8.38	101.12	113.70
53	BF	8	GLN	N-CA-C	8.37	122.10	108.55
25	BA	2541	A	C4'-C3'-O3'	-8.36	100.46	113.00
46	B5	6	VAL	CA-C-N	-8.35	111.42	119.85
46	B5	6	VAL	C-N-CA	-8.35	111.42	119.85
25	BA	739	G	C2'-C3'-O3'	-8.34	96.98	109.50
26	BB	15	A	C2'-C3'-O3'	8.30	121.95	109.50
1	AA	60	A	C2'-C3'-O3'	8.28	121.91	109.50
25	BA	1541	G	C2'-C3'-O3'	8.28	126.11	113.70
25	BA	221	A	C2'-C3'-O3'	8.21	121.82	109.50
25	BA	2700	C	C3'-C2'-O2'	8.19	122.98	110.70
33	BT	30	VAL	N-CA-C	8.19	126.36	109.34
25	BA	2036	C	C3'-C2'-O2'	8.18	122.97	110.70
25	BA	1899	G	C1'-C2'-O2'	-8.14	99.58	111.80
31	BR	105	ARG	N-CA-C	-8.14	98.24	109.71
25	BA	1692	U	C4'-C3'-O3'	-8.12	100.83	113.00
25	BA	945	A	C4'-C3'-O3'	8.11	121.56	109.40
25	BA	2506	U	C4'-C3'-O3'	-8.09	97.26	109.40
25	BA	1025	G	C1'-C2'-O2'	8.09	123.93	111.80
25	BA	2050	C	C4'-C3'-O3'	-8.09	100.87	113.00
25	BA	2198	A	C2'-C3'-O3'	-8.07	97.40	109.50
25	BA	2721	A	C3'-C2'-O2'	8.01	122.71	110.70
25	BA	54	G	C4'-C3'-O3'	-7.99	101.02	113.00
25	BA	2200	C	C2'-C3'-O3'	7.97	125.65	113.70
1	AA	785	G	C2'-C3'-O3'	7.95	125.63	113.70
25	BA	1838	C	C4'-C3'-O3'	-7.95	97.47	109.40
1	AA	1285	A	C4'-C3'-O3'	7.95	121.32	109.40
25	BA	1652	A	C4'-C3'-O3'	-7.94	101.08	113.00
25	BA	2139	C	C4'-C3'-O3'	7.91	121.26	109.40
25	BA	944	G	C2'-C3'-O3'	-7.89	101.86	113.70
25	BA	2689	U	C4'-C3'-O3'	7.89	121.24	109.40
1	AA	1054	C	C4'-C3'-O3'	-7.89	101.17	113.00
25	BA	49	A	C2'-C3'-O3'	7.88	121.32	109.50
25	BA	2191	G	C2'-C3'-O3'	7.88	125.51	113.70
25	BA	2820	A	C2'-C3'-O3'	-7.87	97.69	109.50
25	BA	1502	C	C3'-C2'-O2'	7.86	122.49	110.70
1	AA	1222	G	C3'-C2'-O2'	7.85	122.47	110.70
25	BA	2506	U	C3'-C2'-O2'	7.83	126.35	114.60
25	BA	1786	A	N9-C1'-C2'	7.83	125.74	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1133	G	C2'-C3'-O3'	7.82	125.43	113.70
25	BA	1155	A	C3'-C2'-O2'	7.82	122.43	110.70
25	BA	1142(A)	A	C4'-C3'-O3'	7.81	121.11	109.40
25	BA	1300	U	O3'-P-O5'	7.81	115.71	104.00
25	BA	846	C	C4'-C3'-O3'	7.80	121.11	109.40
25	BA	2575	C	C2'-C3'-O3'	-7.75	102.07	113.70
1	AA	1504	G	C2'-C3'-O3'	7.75	121.12	109.50
25	BA	2175	C	C3'-C2'-O2'	7.75	122.32	110.70
22	AI	22	GLY	N-CA-C	7.72	120.49	110.45
25	BA	1542	A	C3'-C2'-O2'	-7.71	103.03	114.60
25	BA	71	A	C4'-C3'-O3'	7.71	120.96	109.40
25	BA	2648	C	C3'-C2'-O2'	7.71	122.26	110.70
51	BC	225	ASN	CA-C-N	-7.70	112.82	120.21
51	BC	225	ASN	C-N-CA	-7.70	112.82	120.21
4	AJ	55	LYS	CA-C-N	-7.67	112.75	123.03
4	AJ	55	LYS	C-N-CA	-7.67	112.75	123.03
27	BN	132	ALA	N-CA-C	-7.67	104.84	112.97
25	BA	1956	U	C3'-C2'-O2'	7.67	122.21	110.70
25	BA	1502	C	C2'-C3'-O3'	7.65	125.18	113.70
46	B5	51	TYR	CA-CB-CG	7.64	127.65	113.90
25	BA	2714	G	C4'-C3'-O3'	-7.63	101.55	113.00
49	B8	50	LEU	N-CA-C	7.60	120.87	108.55
15	AB	200	ILE	CB-CA-C	-7.59	100.81	111.21
17	AD	12	CYS	CA-CB-SG	7.59	131.86	114.40
8	AN	43	CYS	N-CA-C	-7.59	102.95	111.07
25	BA	1504	C	C4'-C3'-O3'	7.59	120.78	109.40
1	AA	1195	C	C2'-C3'-O3'	-7.58	102.33	113.70
25	BA	1905	C	C4'-C3'-O3'	-7.57	101.65	113.00
25	BA	2199	A	C2'-C3'-O3'	7.56	125.04	113.70
38	BY	76	CYS	CA-C-N	7.54	129.27	119.84
38	BY	76	CYS	C-N-CA	7.54	129.27	119.84
46	B5	52	TYR	N-CA-C	-7.54	94.74	110.80
1	AA	428	G	C4'-C3'-O3'	7.54	120.70	109.40
25	BA	2612	C	C2'-C3'-O3'	-7.54	102.40	113.70
1	AA	987	G	C3'-C2'-O2'	7.51	121.97	110.70
25	BA	1779	U	C2'-C3'-O3'	-7.50	102.45	113.70
25	BA	1539	G	C4'-C3'-O3'	-7.50	101.75	113.00
25	BA	2282	G	C4'-C3'-O3'	7.50	120.65	109.40
25	BA	308	G	C2'-C3'-O3'	-7.49	102.47	113.70
1	AA	559	A	C1'-C2'-O2'	-7.48	100.57	111.80
25	BA	2497	A	C4'-C3'-O3'	-7.48	98.18	109.40
25	BA	2122	U	C4'-C3'-O3'	-7.46	101.80	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	AQ	67	LYS	N-CA-C	-7.46	99.98	110.50
25	BA	1287	A	C4'-C3'-O3'	-7.45	101.82	113.00
1	AA	7	G	C2'-C3'-O3'	-7.45	98.33	109.50
2	AV	28	G	C2'-C3'-O3'	7.45	124.87	113.70
55	BH	28	GLY	CA-C-N	7.42	128.08	119.47
55	BH	28	GLY	C-N-CA	7.42	128.08	119.47
25	BA	1471	A	C4'-C3'-O3'	-7.40	101.90	113.00
1	AA	1164	G	C3'-C2'-O2'	7.39	121.79	110.70
46	B5	33	CYS	CA-C-N	-7.39	112.71	120.03
46	B5	33	CYS	C-N-CA	-7.39	112.71	120.03
25	BA	1235	G	C4'-C3'-O3'	-7.38	101.92	113.00
25	BA	2171	A	C4'-C3'-O3'	-7.38	98.33	109.40
1	AA	572	A	C4'-C3'-O3'	-7.38	101.94	113.00
25	BA	1270	C	C2'-C3'-O3'	-7.34	102.69	113.70
52	BE	125	GLY	CA-C-N	7.34	127.10	119.76
52	BE	125	GLY	C-N-CA	7.34	127.10	119.76
25	BA	2060	A	C3'-C2'-O2'	7.32	125.58	114.60
25	BA	790	C	C2'-C3'-O3'	7.31	120.47	109.50
25	BA	121	G	C4'-C3'-O3'	-7.29	102.06	113.00
25	BA	27	G	C3'-C2'-O2'	-7.29	103.66	114.60
1	AA	926	G	C2'-C3'-O3'	-7.28	102.78	113.70
25	BA	1393	A	C3'-C2'-O2'	7.28	121.61	110.70
32	BS	20	ARG	N-CA-C	7.26	120.25	108.41
55	BH	8	PRO	N-CA-CB	7.26	109.39	103.36
25	BA	2282	G	C2'-C3'-O3'	7.25	120.38	109.50
1	AA	1194	U	C2'-C3'-O3'	-7.25	102.83	113.70
1	AA	1523	G	C4'-C3'-O3'	-7.23	102.16	113.00
25	BA	2156	G	C4'-C3'-O3'	-7.22	102.17	113.00
1	AA	575	G	C4'-C3'-O3'	7.22	120.23	109.40
25	BA	2541	A	C2'-C3'-O3'	7.21	124.51	113.70
3	AX	20	C	C2'-C3'-O3'	7.20	120.31	109.50
2	AV	74	C	C4'-C3'-O3'	7.19	120.19	109.40
25	BA	825	C	C3'-C2'-O2'	7.19	121.48	110.70
1	AA	149	A	C4'-C3'-O3'	7.19	123.78	113.00
25	BA	2199	A	C4'-C3'-O3'	-7.18	102.22	113.00
25	BA	1388	G	C3'-C2'-O2'	7.16	121.44	110.70
1	AA	1299	A	C2'-C3'-O3'	-7.16	102.96	113.70
25	BA	685	A	C1'-C2'-O2'	-7.16	101.06	111.80
1	AA	907	A	C3'-C2'-O2'	7.14	121.42	110.70
29	BP	15	ARG	N-CA-C	7.14	120.52	108.02
1	AA	860	A	C3'-C2'-O2'	7.14	121.41	110.70
1	AA	795	C	C3'-C2'-O2'	7.13	121.40	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	1540	U	C2'-C3'-O3'	-7.13	103.00	113.70
25	BA	1645	G	C4'-C3'-O3'	-7.12	102.32	113.00
18	AE	41	VAL	CB-CA-C	-7.12	99.30	110.69
25	BA	1802	A	C4'-C3'-O3'	-7.12	102.33	113.00
25	BA	2073	C	C3'-C2'-O2'	7.11	121.36	110.70
47	B6	47	THR	N-CA-C	7.10	118.54	108.74
25	BA	1620	G	C3'-C2'-O2'	7.10	121.35	110.70
34	BU	89	GLU	N-CA-C	-7.10	103.92	112.59
25	BA	470	A	C3'-C2'-O2'	7.10	121.35	110.70
25	BA	1679	U	C4'-C3'-O3'	-7.08	102.38	113.00
25	BA	1367	A	C3'-C2'-O2'	7.08	121.31	110.70
1	AA	514	C	C3'-C2'-O2'	7.06	121.29	110.70
25	BA	2025	C	C4'-C3'-O3'	-7.06	102.41	113.00
46	B5	48	GLU	N-CA-C	-7.05	95.77	110.80
25	BA	102	G	C4'-C3'-O3'	-7.04	102.44	113.00
25	BA	771	G	C4'-C3'-O3'	-7.03	102.45	113.00
25	BA	874	G	C3'-C2'-O2'	7.01	121.21	110.70
25	BA	2274	A	C4'-C3'-O3'	-7.00	102.50	113.00
25	BA	2763	G	C3'-C2'-O2'	-6.99	100.21	110.70
25	BA	102	G	O4'-C1'-C2'	-6.99	100.61	107.60
25	BA	1384	A	C4'-C3'-O3'	-6.98	102.53	113.00
25	BA	2779	U	C4'-C3'-O3'	-6.97	98.94	109.40
17	AD	31	CYS	CA-CB-SG	-6.97	98.36	114.40
7	AM	112	GLY	CA-C-N	-6.97	111.13	119.84
7	AM	112	GLY	C-N-CA	-6.97	111.13	119.84
23	AY	319	ASP	CA-C-N	-6.97	112.79	119.76
23	AY	319	ASP	C-N-CA	-6.97	112.79	119.76
43	BD	99	ASP	CB-CA-C	-6.97	96.55	110.42
25	BA	1598	C	C4'-C3'-O3'	-6.96	102.57	113.00
33	BT	80	SER	CA-C-N	-6.96	111.15	119.84
33	BT	80	SER	C-N-CA	-6.96	111.15	119.84
46	B5	46	CYS	N-CA-C	6.94	120.89	109.58
1	AA	129	U	C4'-C3'-O3'	-6.94	102.60	113.00
25	BA	1575	C	C3'-C2'-O2'	6.92	121.08	110.70
1	AA	758	G	C4'-C3'-O3'	-6.90	102.64	113.00
1	AA	1209	C	C3'-C2'-O2'	6.90	121.05	110.70
1	AA	267	C	P-O5'-C5'	-6.89	110.57	120.90
25	BA	2424	C	C3'-C2'-O2'	6.89	121.03	110.70
25	BA	203	C	C4'-C3'-O3'	-6.89	102.67	113.00
1	AA	1336	C	C2'-C3'-O3'	-6.88	99.18	109.50
25	BA	1597	A	C2'-C3'-O3'	-6.88	103.38	113.70
1	AA	581	G	C3'-C2'-O2'	6.87	121.00	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	BY	79	CYS	CB-CA-C	-6.87	107.18	117.07
8	AN	40	CYS	CA-CB-SG	6.87	130.20	114.40
25	BA	1432	C	C3'-C2'-O2'	6.86	120.99	110.70
25	BA	1786	A	C1'-C2'-O2'	6.83	122.05	111.80
25	BA	2163	C	C4'-C3'-O3'	-6.83	102.75	113.00
34	BU	97	ASP	N-CA-C	-6.83	104.98	113.38
25	BA	327	G	C4'-C3'-O3'	-6.82	102.76	113.00
1	AA	1211	U	C4'-C3'-O3'	6.82	119.63	109.40
47	B6	46	HIS	N-CA-C	6.82	125.32	110.80
1	AA	1330	U	C4'-C3'-O3'	-6.81	102.78	113.00
1	AA	24	U	C3'-C2'-O2'	6.79	120.89	110.70
8	AN	42	ILE	CB-CA-C	-6.79	103.15	112.04
25	BA	394	A	C3'-C2'-O2'	6.79	120.88	110.70
18	AE	68	GLU	CA-C-N	-6.78	115.97	123.02
18	AE	68	GLU	C-N-CA	-6.78	115.97	123.02
53	BF	65	TRP	N-CA-C	6.78	115.94	108.14
25	BA	2587	A	C4'-C3'-O3'	-6.77	102.85	113.00
25	BA	1480	G	C4'-C3'-O3'	-6.76	102.85	113.00
25	BA	657	U	C1'-C2'-O2'	6.76	118.54	108.40
1	AA	1205	U	C3'-C2'-O2'	6.76	120.84	110.70
1	AA	695	A	C3'-C2'-O2'	6.75	120.83	110.70
1	AA	1191	A	C2'-C3'-O3'	-6.75	103.57	113.70
25	BA	1021	A	C3'-C2'-O2'	6.75	120.83	110.70
29	BP	116	GLY	N-CA-C	6.75	129.17	113.18
25	BA	479	A	C4'-C3'-O3'	6.75	119.52	109.40
1	AA	699	C	C3'-C2'-O2'	6.74	120.81	110.70
25	BA	1326	U	C3'-C2'-O2'	6.74	120.81	110.70
1	AA	748	C	C4'-C3'-O3'	6.73	119.50	109.40
1	AA	1119	C	C3'-C2'-O2'	6.73	120.79	110.70
1	AA	1135	U	C4'-C3'-O3'	6.73	123.09	113.00
1	AA	1133	G	C1'-C2'-O2'	6.72	118.47	108.40
25	BA	1448	G	C1'-C2'-O2'	6.71	118.46	108.40
1	AA	1106	G	C3'-C2'-O2'	6.71	120.76	110.70
38	BY	17	SER	N-CA-C	6.70	121.42	111.04
25	BA	2753	A	C2'-C3'-O3'	-6.68	103.68	113.70
55	BH	10	PRO	N-CA-CB	6.68	110.27	103.25
1	AA	1132	C	C4'-C3'-O3'	-6.68	102.99	113.00
25	BA	585	G	C4'-C3'-O3'	6.68	123.02	113.00
25	BA	1838	C	C2'-C3'-O3'	6.67	119.51	109.50
2	AV	29	G	C4'-C3'-O3'	-6.67	102.99	113.00
1	AA	127	G	C3'-C2'-O2'	6.67	120.70	110.70
8	AN	27	CYS	N-CA-C	-6.66	101.58	110.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	BZ	100	VAL	N-CA-C	6.66	115.91	108.05
1	AA	195	A	C4'-C3'-O3'	-6.64	103.03	113.00
1	AA	1228	C	C4'-C3'-O3'	-6.64	103.04	113.00
25	BA	722	A	C2'-C3'-O3'	6.64	123.66	113.70
25	BA	906	G	C2'-C3'-O3'	6.64	123.66	113.70
25	BA	2830	G	C2'-C3'-O3'	6.64	123.66	113.70
1	AA	353	A	C2'-C3'-O3'	-6.64	103.75	113.70
25	BA	701	G	C2'-C3'-O3'	6.63	123.65	113.70
25	BA	1280	G	C1'-C2'-O2'	6.63	118.34	108.40
25	BA	962	G	C3'-C2'-O2'	6.62	120.64	110.70
25	BA	2366	A	C3'-C2'-O2'	6.62	120.63	110.70
25	BA	1987	G	C4'-C3'-O3'	-6.61	103.08	113.00
25	BA	2542	A	C4'-C3'-O3'	-6.61	99.48	109.40
26	BB	114	C	C3'-C2'-O2'	6.61	120.62	110.70
1	AA	1181	G	C3'-C2'-O2'	6.61	120.62	110.70
1	AA	586	C	C3'-C2'-O2'	6.60	120.61	110.70
25	BA	778	G	C4'-C3'-O3'	-6.60	103.09	113.00
25	BA	2428	G	C3'-C2'-O2'	6.60	120.59	110.70
52	BE	60	ASN	N-CA-C	6.59	124.85	110.80
33	BT	59	THR	N-CA-C	-6.59	101.39	110.35
5	AK	49	GLY	N-CA-C	6.58	122.03	113.27
25	BA	1693	U	O3'-P-O5'	6.57	113.85	104.00
1	AA	1051	C	C3'-C2'-O2'	6.56	120.54	110.70
38	BY	63	LYS	N-CA-C	6.55	118.36	108.46
12	AR	84	LYS	N-CA-C	6.55	120.72	110.17
41	B1	4	VAL	N-CA-C	6.54	117.54	108.12
1	AA	509	A	C2'-C3'-O3'	6.54	123.51	113.70
25	BA	1646	C	C2'-C3'-O3'	-6.54	103.89	113.70
25	BA	1783	A	C4'-C3'-O3'	-6.54	103.19	113.00
25	BA	774	A	C4'-C3'-O3'	6.53	119.20	109.40
25	BA	1017	G	C2'-C3'-O3'	6.53	123.50	113.70
3	AX	19	U	C3'-C2'-O2'	6.53	120.49	110.70
1	AA	228	A	C3'-C2'-O2'	6.52	120.48	110.70
25	BA	129	C	C4'-C3'-O3'	-6.52	103.22	113.00
25	BA	1330	C	C3'-C2'-O2'	6.51	120.47	110.70
1	AA	1067	A	C1'-C2'-O2'	-6.51	102.03	111.80
1	AA	1102	A	C4'-C3'-O3'	-6.51	103.24	113.00
25	BA	566	U	C4'-C3'-O3'	-6.50	103.25	113.00
25	BA	1963	U	C2'-C3'-O3'	6.49	119.24	109.50
25	BA	623	G	C4'-C3'-O3'	-6.49	103.27	113.00
25	BA	1899	G	C3'-C2'-O2'	6.48	124.32	114.60
26	BB	75	G	C2'-C3'-O3'	6.48	123.42	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	693	G	C3'-C2'-O2'	6.48	120.42	110.70
25	BA	386	G	C4'-C3'-O3'	6.48	119.12	109.40
25	BA	1929	G	C4'-C3'-O3'	-6.48	99.68	109.40
1	AA	509	A	C4'-C3'-O3'	6.48	122.71	113.00
25	BA	1757	U	C4'-C3'-O3'	-6.47	103.29	113.00
25	BA	1630	G	C3'-C2'-O2'	6.47	120.41	110.70
1	AA	773	G	C1'-C2'-O2'	6.47	118.10	108.40
25	BA	1370	C	C4'-C3'-O3'	-6.47	103.30	113.00
25	BA	1059	G	C3'-C2'-O2'	6.46	120.39	110.70
25	BA	2500	U	C2'-C3'-O3'	-6.46	104.02	113.70
25	BA	1253	A	C1'-C2'-O2'	-6.45	102.12	111.80
1	AA	834	C	C3'-C2'-O2'	6.45	120.38	110.70
49	B8	48	PHE	CB-CA-C	-6.45	99.11	109.75
25	BA	2263	C	C1'-C2'-O2'	6.45	118.07	108.40
25	BA	725	G	C4'-C3'-O3'	-6.44	103.34	113.00
5	AK	40	ILE	N-CA-C	-6.43	106.28	111.81
25	BA	1498	C	C4'-C3'-O3'	-6.43	103.36	113.00
2	AV	19	G	C4'-C3'-O3'	-6.42	99.78	109.40
25	BA	619	G	C2'-C3'-O3'	-6.41	104.09	113.70
27	BN	61	ARG	N-CA-C	-6.41	99.77	109.95
43	BD	244	ARG	CA-C-N	-6.40	113.79	120.38
43	BD	244	ARG	C-N-CA	-6.40	113.79	120.38
25	BA	2163	C	C2'-C3'-O3'	6.40	123.30	113.70
25	BA	1663	C	C3'-C2'-O2'	6.40	120.30	110.70
25	BA	1644	C	C3'-C2'-O2'	6.40	120.29	110.70
1	AA	571	U	C4'-C3'-O3'	-6.39	103.41	113.00
1	AA	105	G	C4'-C3'-O3'	-6.39	103.42	113.00
38	BY	31	LEU	CA-C-N	6.39	142.33	127.00
38	BY	31	LEU	C-N-CA	6.39	142.33	127.00
26	BB	66	A	C2'-C3'-O3'	6.38	119.08	109.50
37	BX	7	VAL	CB-CA-C	-6.38	105.44	111.06
25	BA	828	U	C4'-C3'-O3'	-6.38	103.43	113.00
25	BA	2498	C	C3'-C2'-O2'	6.38	120.27	110.70
17	AD	24	GLU	N-CA-C	6.38	117.90	111.07
1	AA	1233	G	C3'-C2'-O2'	6.38	120.27	110.70
25	BA	1349	A	O4'-C4'-C3'	-6.38	97.62	104.00
39	BZ	154	ASP	N-CA-C	-6.37	103.85	112.26
1	AA	12	U	C1'-C2'-O2'	6.37	117.95	108.40
25	BA	599	G	C3'-C2'-O2'	6.36	120.24	110.70
53	BF	7	TYR	CA-CB-CG	6.36	125.35	113.90
1	AA	328	C	C4'-C3'-O3'	-6.35	99.87	109.40
1	AA	852	G	C1'-C2'-O2'	6.35	117.93	108.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AV	12	U	C1'-C2'-O2'	6.35	117.93	108.40
25	BA	1693	U	C3'-C2'-O2'	-6.35	105.07	114.60
46	B5	59	GLU	N-CA-C	6.35	117.87	108.60
25	BA	575	A	C2'-C3'-O3'	-6.34	104.18	113.70
25	BA	2116	G	C2'-C3'-O3'	6.34	119.01	109.50
1	AA	1503	A	C4'-C3'-O3'	-6.34	99.89	109.40
17	AD	12	CYS	CB-CA-C	6.34	123.03	110.42
25	BA	1748	G	C3'-C2'-O2'	6.34	120.21	110.70
25	BA	1921	G	C4'-C3'-O3'	-6.33	103.50	113.00
25	BA	1846	G	C3'-C2'-O2'	6.33	120.20	110.70
25	BA	2489	G	C4'-C3'-O3'	-6.33	103.50	113.00
25	BA	54	G	C2'-C3'-O3'	6.33	123.19	113.70
25	BA	2296	U	C4'-C3'-O3'	6.32	118.89	109.40
5	AK	127	LYS	N-CA-C	-6.32	104.44	111.71
25	BA	2153	G	C3'-C2'-O2'	6.32	120.18	110.70
1	AA	631	G	C3'-C2'-O2'	6.32	120.17	110.70
25	BA	1833	U	C1'-C2'-O2'	-6.30	98.95	108.40
1	AA	368	U	C4'-C3'-O3'	-6.30	103.55	113.00
26	BB	82	G	C3'-C2'-O2'	6.30	120.15	110.70
25	BA	2003	G	C1'-C2'-O2'	6.29	117.84	108.40
25	BA	727	A	C4'-C3'-O3'	-6.29	103.56	113.00
1	AA	1489	G	C3'-C2'-O2'	6.29	120.13	110.70
13	AS	5	LEU	CA-CB-CG	6.29	138.30	116.30
1	AA	369	C	C3'-C2'-O2'	6.29	120.13	110.70
25	BA	1698	A	O4'-C1'-C2'	-6.28	99.52	105.80
1	AA	1147	C	C4'-C3'-O3'	-6.28	103.58	113.00
25	BA	1426	G	C4'-C3'-O3'	-6.28	103.58	113.00
1	AA	1147	C	C2'-C3'-O3'	6.27	123.11	113.70
49	B8	56	GLU	CB-CA-C	-6.27	100.95	110.92
1	AA	1127	G	C3'-C2'-O2'	6.27	120.10	110.70
25	BA	2565	A	C1'-C2'-O2'	6.27	117.80	108.40
25	BA	270	A	C3'-C2'-O2'	6.25	120.08	110.70
33	BT	3	ARG	N-CA-C	6.25	119.76	108.69
1	AA	169	C	C3'-C2'-O2'	6.25	120.08	110.70
25	BA	739	G	C4'-C3'-O3'	6.25	118.77	109.40
25	BA	102	G	N9-C1'-C2'	6.25	121.37	112.00
25	BA	1540	U	P-O5'-C5'	-6.24	111.54	120.90
31	BR	5	LYS	N-CA-C	-6.24	104.47	113.21
1	AA	562	C	C4'-C3'-O3'	6.24	118.76	109.40
52	BE	88	GLY	N-CA-C	6.24	127.96	113.18
25	BA	2020	A	C4'-C3'-O3'	-6.24	103.65	113.00
25	BA	2505	G	C3'-C2'-O2'	-6.23	101.35	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	443	A	C3'-C2'-O2'	6.23	120.05	110.70
25	BA	2287	A	C3'-C2'-O2'	6.23	123.94	114.60
1	AA	1049	U	C4'-C3'-O3'	6.22	118.74	109.40
52	BE	73	GLU	CA-C-N	6.22	127.62	119.84
52	BE	73	GLU	C-N-CA	6.22	127.62	119.84
25	BA	1882	C	C2'-C3'-O3'	6.22	123.03	113.70
25	BA	1057	A	C2'-C3'-O3'	6.21	123.02	113.70
7	AM	65	LYS	CA-C-N	6.21	132.88	121.70
7	AM	65	LYS	C-N-CA	6.21	132.88	121.70
25	BA	2872	G	C4'-C3'-O3'	-6.21	103.69	113.00
25	BA	2551	C	C4'-C3'-O3'	-6.21	103.69	113.00
33	BT	76	PHE	CA-C-N	6.20	125.82	119.56
33	BT	76	PHE	C-N-CA	6.20	125.82	119.56
25	BA	2729	G	C4'-C3'-O3'	-6.20	103.70	113.00
25	BA	1970	A	C5'-C4'-C3'	6.20	124.49	115.20
25	BA	1216	G	C3'-C2'-O2'	6.19	119.98	110.70
1	AA	932	C	C1'-C2'-O2'	6.18	117.67	108.40
25	BA	85	G	C3'-C2'-O2'	6.18	119.97	110.70
25	BA	363(D)	G	C3'-C2'-O2'	6.18	119.97	110.70
25	BA	739	G	C3'-C2'-O2'	-6.18	105.33	114.60
1	AA	1461	G	C3'-C2'-O2'	6.18	119.97	110.70
25	BA	453	C	C4'-C3'-O3'	-6.18	103.73	113.00
1	AA	1013	G	C2'-C3'-O3'	6.17	122.96	113.70
1	AA	669	U	C1'-C2'-O2'	6.17	117.66	108.40
25	BA	1187	G	C4'-C3'-O3'	-6.17	103.74	113.00
17	AD	31	CYS	N-CA-CB	6.17	120.92	110.49
25	BA	491	G	C3'-C2'-O2'	6.17	119.95	110.70
27	BN	5	VAL	N-CA-C	6.17	122.20	108.88
28	BO	115	VAL	N-CA-C	6.17	116.95	110.72
54	BG	89	GLY	N-CA-C	-6.17	98.57	113.18
25	BA	996	A	O5'-P-OP1	-6.16	89.51	108.00
38	BY	17	SER	CB-CA-C	-6.16	101.59	111.39
25	BA	271(G)	C	C3'-C2'-O2'	6.16	119.94	110.70
25	BA	2280	G	C4'-C3'-O3'	-6.16	103.76	113.00
52	BE	152	LYS	N-CA-C	-6.16	101.30	110.23
51	BC	224	ILE	N-CA-C	6.16	117.79	108.80
55	BH	159	GLU	N-CA-C	-6.16	103.12	111.55
1	AA	1163	C	C3'-C2'-O2'	6.15	119.92	110.70
25	BA	618	C	C2'-C3'-O3'	-6.15	104.47	113.70
25	BA	1547	C	C3'-C2'-O2'	6.15	119.92	110.70
33	BT	29	ARG	N-CA-C	6.15	123.90	110.80
25	BA	1025	G	C2'-C3'-O3'	6.15	118.72	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1402	C	C3'-C2'-O2'	6.14	119.91	110.70
18	AE	67	VAL	N-CA-C	6.14	116.68	108.27
2	AV	4	C	C2'-C3'-O3'	6.14	122.91	113.70
2	AV	76	A	C3'-C2'-O2'	-6.13	101.50	110.70
25	BA	1682	G	C1'-C2'-O2'	6.13	117.60	108.40
25	BA	1947	C	C4'-C3'-O3'	-6.13	103.81	113.00
1	AA	1253	G	C3'-C2'-O2'	6.12	119.89	110.70
5	AK	87	THR	N-CA-C	-6.12	100.59	110.32
25	BA	69	C	C4'-C3'-O3'	-6.12	103.82	113.00
43	BD	237	GLU	CB-CA-C	6.12	119.63	109.53
25	BA	1606	G	C2'-C3'-O3'	-6.12	104.53	113.70
25	BA	1959	G	C2'-C3'-O3'	6.12	122.87	113.70
25	BA	2509	G	C3'-C2'-O2'	6.12	119.87	110.70
25	BA	349	G	C1'-C2'-O2'	6.11	117.57	108.40
51	BC	27	ARG	N-CA-CB	6.11	118.83	109.91
25	BA	34	C	C4'-C3'-O3'	-6.11	103.84	113.00
43	BD	49	ILE	N-CA-CB	6.11	118.31	110.13
33	BT	30	VAL	CB-CA-C	-6.10	101.28	111.29
27	BN	85	ILE	N-CA-C	6.10	114.68	107.73
25	BA	1907	G	C3'-C2'-O2'	6.10	119.85	110.70
25	BA	2847	U	C4'-C3'-O3'	-6.10	103.85	113.00
1	AA	1010	G	C3'-C2'-O2'	6.09	119.84	110.70
25	BA	2636	U	C3'-C2'-O2'	6.09	119.84	110.70
50	B9	27	CYS	CA-CB-SG	6.09	128.41	114.40
25	BA	423	A	C1'-C2'-O2'	6.09	117.53	108.40
25	BA	1819	A	C4'-C3'-O3'	6.08	118.52	109.40
26	BB	19	G	C2'-C3'-O3'	6.08	122.83	113.70
25	BA	1494	A	C3'-C2'-O2'	6.08	119.82	110.70
25	BA	1475	G	C4'-C3'-O3'	-6.08	103.88	113.00
25	BA	337	C	C1'-C2'-O2'	6.08	117.52	108.40
38	BY	49	VAL	N-CA-C	-6.08	103.29	111.44
1	AA	1409	C	C3'-C2'-O2'	6.08	119.81	110.70
25	BA	2247	A	C3'-C2'-O2'	6.07	119.80	110.70
25	BA	332	A	C4'-C3'-O3'	6.07	118.50	109.40
25	BA	2764	A	C3'-C2'-O2'	6.07	119.80	110.70
25	BA	1786	A	C3'-C2'-O2'	-6.06	105.50	114.60
25	BA	2566	A	C4'-C3'-O3'	-6.06	100.30	109.40
51	BC	180	PHE	N-CA-C	-6.06	102.24	110.36
1	AA	961	U	C1'-C2'-O2'	6.05	117.48	108.40
1	AA	1537	U	C3'-C2'-O2'	6.05	119.78	110.70
26	BB	4	C	C3'-C2'-O2'	6.05	119.78	110.70
25	BA	1783	A	C2'-C3'-O3'	-6.05	104.62	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	2095	C	C2'-C3'-O3'	6.05	122.78	113.70
1	AA	1442	G	C3'-C2'-O2'	6.04	119.77	110.70
25	BA	1241	A	C3'-C2'-O2'	6.04	119.77	110.70
25	BA	2770	G	C3'-C2'-O2'	6.04	119.76	110.70
1	AA	1246	C	C3'-C2'-O2'	6.04	119.76	110.70
25	BA	804	A	C3'-C2'-O2'	6.04	119.76	110.70
1	AA	1440	C	C3'-C2'-O2'	6.04	119.75	110.70
25	BA	715	G	C3'-C2'-O2'	6.03	119.75	110.70
25	BA	1672	C	C4'-C3'-O3'	-6.03	103.96	113.00
25	BA	2098	U	C4'-C3'-O3'	6.03	118.45	109.40
1	AA	1226	C	C4'-C3'-O3'	6.03	118.44	109.40
25	BA	2537	U	C4'-C3'-O3'	-6.03	103.96	113.00
25	BA	1783	A	C3'-C2'-O2'	-6.02	101.66	110.70
25	BA	2064	C	C3'-C2'-O2'	6.02	119.73	110.70
1	AA	1212	U	C4'-C3'-O3'	-6.02	103.97	113.00
1	AA	1332	A	C2'-C3'-O3'	-6.02	104.67	113.70
25	BA	2552	U	C4'-C3'-O3'	-6.02	103.97	113.00
1	AA	1345	U	C1'-C2'-O2'	-6.02	102.78	111.80
27	BN	70	LYS	N-CA-C	-6.02	99.39	108.96
43	BD	260	ARG	N-CA-CB	6.02	118.92	109.83
1	AA	129	U	C3'-C2'-O2'	6.01	119.72	110.70
22	AI	55	ALA	N-CA-C	6.01	123.61	110.80
25	BA	2449	U	C2'-C3'-O3'	6.01	118.52	109.50
38	BY	62	GLU	N-CA-C	6.01	123.60	110.80
1	AA	317	G	C3'-C2'-O2'	6.01	119.71	110.70
25	BA	451	C	C2'-C3'-O3'	-6.00	104.69	113.70
25	BA	1915	U	C2'-C3'-O3'	6.00	122.70	113.70
1	AA	1285	A	C2'-C3'-O3'	6.00	118.50	109.50
25	BA	2065	C	C4'-C3'-O3'	-6.00	104.00	113.00
33	BT	29	ARG	CA-C-N	6.00	132.76	121.97
33	BT	29	ARG	C-N-CA	6.00	132.76	121.97
25	BA	1225	G	C4'-C3'-O3'	-6.00	104.01	113.00
25	BA	1050	A	C3'-C2'-O2'	5.99	119.69	110.70
1	AA	5	U	C2'-C3'-O3'	-5.99	100.51	109.50
25	BA	2724	C	C4'-C3'-O3'	-5.99	104.01	113.00
1	AA	1424	C	C3'-C2'-O2'	5.99	119.69	110.70
1	AA	1047	G	C1'-C2'-O2'	5.99	117.38	108.40
25	BA	724	U	C3'-C2'-O2'	5.98	119.67	110.70
25	BA	861	A	C4'-C3'-O3'	-5.98	104.03	113.00
25	BA	2061	G	C2'-C3'-O3'	-5.98	100.53	109.50
35	BV	18	LEU	N-CA-C	5.98	123.54	110.80
25	BA	1204	A	C4'-C3'-O3'	-5.98	100.43	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	428	G	C2'-C3'-O3'	5.98	118.47	109.50
25	BA	656	G	C3'-C2'-O2'	5.98	119.67	110.70
25	BA	781	A	C4'-C3'-O3'	-5.98	104.03	113.00
25	BA	1485	G	C2'-C3'-O3'	5.97	122.66	113.70
25	BA	685	A	C4'-C3'-O3'	5.97	118.36	109.40
25	BA	2109	U	C3'-C2'-O2'	5.97	119.65	110.70
25	BA	2580	U	C4'-C3'-O3'	-5.96	104.05	113.00
1	AA	1503	A	C2'-C3'-O3'	5.96	118.44	109.50
25	BA	1230	C	C3'-C2'-O2'	5.96	119.63	110.70
14	AT	76	ALA	N-CA-C	5.95	117.46	110.97
25	BA	2191	G	C4'-C3'-O3'	5.95	121.92	113.00
25	BA	1899	G	C4'-C3'-O3'	5.94	118.31	109.40
46	B5	3	LYS	CA-C-N	5.94	136.29	121.80
46	B5	3	LYS	C-N-CA	5.94	136.29	121.80
25	BA	1609	A	C3'-C2'-O2'	-5.94	105.69	114.60
43	BD	28	GLU	CA-C-N	-5.94	112.42	119.84
43	BD	28	GLU	C-N-CA	-5.94	112.42	119.84
25	BA	1989	G	C3'-C2'-O2'	5.93	119.60	110.70
25	BA	1395	A	C2'-C3'-O3'	-5.93	104.81	113.70
25	BA	518	G	C4'-C3'-O3'	-5.92	104.11	113.00
25	BA	1500	G	C2'-C3'-O3'	5.92	122.58	113.70
25	BA	2422	A	C4'-C3'-O3'	5.92	121.87	113.00
33	BT	80	SER	N-CA-C	5.92	122.88	109.81
23	AY	621	ILE	CB-CA-C	-5.91	104.16	112.14
25	BA	2081	C	C2'-C3'-O3'	-5.90	104.84	113.70
1	AA	242	C	C3'-C2'-O2'	5.90	119.55	110.70
1	AA	575	G	C1'-C2'-O2'	-5.90	102.95	111.80
52	BE	37	ARG	N-CA-C	-5.90	100.09	109.59
23	AY	493	VAL	N-CA-C	5.90	116.12	107.75
25	BA	298	G	C1'-C2'-O2'	5.89	117.24	108.40
25	BA	1426	G	C2'-C3'-O3'	5.89	122.54	113.70
25	BA	1511	C	C3'-C2'-O2'	5.89	119.54	110.70
25	BA	1539	G	C1'-C2'-O2'	-5.89	99.56	108.40
25	BA	1390	U	C4'-C3'-O3'	-5.89	104.17	113.00
25	BA	1798	U	C4'-C3'-O3'	-5.89	104.17	113.00
25	BA	90	U	C3'-C2'-O2'	5.89	119.53	110.70
26	BB	15	A	C4'-C3'-O3'	-5.89	100.57	109.40
29	BP	114	ILE	N-CA-C	-5.89	99.94	108.71
25	BA	36	G	C4'-C3'-O3'	-5.88	104.17	113.00
25	BA	951	C	C3'-C2'-O2'	5.88	119.52	110.70
53	BF	69	HIS	N-CA-C	5.88	123.32	110.80
34	BU	101	ARG	N-CA-C	-5.87	102.75	110.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1476	G	C1'-C2'-O2'	5.86	117.19	108.40
38	BY	6	HIS	N-CA-C	5.86	115.98	108.24
29	BP	67	MET	N-CA-C	-5.86	98.32	110.80
1	AA	62	U	C4'-C3'-O3'	-5.85	104.22	113.00
1	AA	1344	C	C3'-C2'-O2'	5.85	119.47	110.70
27	BN	76	SER	N-CA-C	-5.85	102.66	110.55
1	AA	712	A	C4'-C3'-O3'	-5.84	104.23	113.00
1	AA	560	U	C2'-C3'-O3'	5.84	118.26	109.50
25	BA	1961	C	C4'-C3'-O3'	-5.84	104.24	113.00
29	BP	53	GLY	N-CA-C	-5.84	106.96	113.79
52	BE	33	VAL	N-CA-CB	5.84	117.49	110.31
25	BA	1135	C	C4'-C3'-O3'	-5.84	104.25	113.00
1	AA	1502	A	C3'-C2'-O2'	-5.83	105.85	114.60
25	BA	1847	A	C2'-C3'-O3'	-5.83	100.75	109.50
25	BA	409	C	C3'-C2'-O2'	5.83	119.44	110.70
1	AA	34	C	C3'-C2'-O2'	5.83	119.44	110.70
1	AA	365	U	C2'-C3'-O3'	-5.83	104.96	113.70
25	BA	2823	A	C4'-C3'-O3'	-5.83	104.26	113.00
25	BA	1889	A	C4'-C3'-O3'	-5.83	104.26	113.00
25	BA	2597	G	C2'-C3'-O3'	-5.82	104.97	113.70
1	AA	1518	A	C3'-C2'-O2'	-5.82	101.97	110.70
25	BA	1658	C	C4'-C3'-O3'	-5.82	104.28	113.00
1	AA	68	G	C3'-C2'-O2'	5.81	119.42	110.70
2	AV	43	C	C2'-C3'-O3'	-5.81	104.98	113.70
1	AA	1530	G	C2'-C3'-O3'	-5.80	105.00	113.70
1	AA	9	G	C3'-C2'-O2'	5.80	119.40	110.70
31	BR	101	ALA	N-CA-C	-5.80	102.72	110.55
1	AA	1067	A	C3'-C2'-O2'	5.80	123.29	114.60
33	BT	49	VAL	CA-C-N	5.79	129.80	120.30
33	BT	49	VAL	C-N-CA	5.79	129.80	120.30
1	AA	1139	G	C2'-C3'-O3'	-5.79	100.81	109.50
25	BA	551	G	C2'-C3'-O3'	5.79	122.39	113.70
25	BA	565	C	C4'-C3'-O3'	-5.79	104.31	113.00
1	AA	348	G	C2'-C3'-O3'	5.79	122.38	113.70
1	AA	715	A	C3'-C2'-O2'	5.79	119.38	110.70
25	BA	537	C	C2'-C3'-O3'	5.79	122.38	113.70
25	BA	1386	C	C3'-C2'-O2'	5.78	119.37	110.70
25	BA	1436	G	C1'-C2'-O2'	5.78	117.07	108.40
43	BD	70	TRP	N-CA-C	5.78	119.43	112.38
25	BA	700	G	C2'-C3'-O3'	5.78	122.37	113.70
25	BA	333	G	C2'-C3'-O3'	-5.78	105.03	113.70
25	BA	1876	A	C3'-C2'-O2'	5.78	119.36	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	249	C	C1'-C2'-O2'	-5.77	103.14	111.80
25	BA	748	G	C2'-C3'-O3'	-5.77	105.05	113.70
25	BA	1308	A	C4'-C3'-O3'	-5.77	104.35	113.00
39	BZ	111	VAL	N-CA-C	-5.77	106.85	111.81
25	BA	1744	C	C2'-C3'-O3'	5.76	122.35	113.70
25	BA	2346	A	O4'-C1'-C2'	-5.76	100.04	105.80
1	AA	305	G	C2'-C3'-O3'	5.76	118.14	109.50
25	BA	785	G	C1'-C2'-O2'	5.76	117.04	108.40
53	BF	66	PRO	N-CA-C	5.76	124.33	112.47
1	AA	403	C	C3'-C2'-O2'	5.76	119.34	110.70
25	BA	1175	U	C2'-C3'-O3'	5.75	118.12	109.50
25	BA	1133	U	C2'-C3'-O3'	-5.75	105.08	113.70
38	BY	31	LEU	C-N-CD	-5.75	107.95	120.60
1	AA	38	G	C3'-C2'-O2'	5.75	119.32	110.70
51	BC	27	ARG	N-CA-C	-5.75	104.71	110.97
25	BA	1491	G	C4'-C3'-O3'	-5.74	104.39	113.00
46	B5	3	LYS	O-C-N	5.74	128.66	123.26
25	BA	2591	C	C2'-C3'-O3'	-5.74	105.10	113.70
26	BB	100	A	C3'-C2'-O2'	5.74	119.30	110.70
50	B9	28	GLU	N-CA-C	-5.74	105.17	111.82
21	AH	80	ILE	CB-CA-C	-5.73	106.14	112.68
1	AA	1053	G	C4'-C3'-O3'	-5.73	100.80	109.40
25	BA	295	G	C3'-C2'-O2'	5.73	119.30	110.70
29	BP	20	GLY	N-CA-C	-5.73	103.74	112.51
1	AA	1016	A	C1'-C2'-O2'	5.73	117.00	108.40
49	B8	48	PHE	N-CA-C	5.73	118.58	109.24
17	AD	171	GLY	CA-C-N	5.73	126.11	119.47
17	AD	171	GLY	C-N-CA	5.73	126.11	119.47
7	AM	111	LYS	N-CA-C	-5.72	101.27	110.14
1	AA	633	G	C1'-C2'-O2'	5.72	116.98	108.40
25	BA	2031	A	C5'-C4'-C3'	-5.72	106.62	115.20
1	AA	533	A	C4'-C3'-O3'	5.72	117.97	109.40
43	BD	271	ILE	N-CA-C	5.72	121.23	109.34
1	AA	732	C	C3'-C2'-O2'	5.71	119.27	110.70
41	B1	70	VAL	CB-CA-C	-5.71	104.42	112.14
25	BA	1947	C	C2'-C3'-O3'	5.71	122.27	113.70
25	BA	1888	G	O4'-C4'-C3'	-5.71	98.29	104.00
25	BA	2492	U	C4'-C3'-O3'	-5.71	104.43	113.00
25	BA	2706	G	C1'-C2'-O2'	5.71	116.97	108.40
1	AA	347	G	C3'-C2'-O2'	5.71	119.27	110.70
25	BA	1881	C	C2'-C3'-O3'	5.71	122.26	113.70
25	BA	2694	G	C2'-C3'-O3'	-5.71	105.14	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AV	1	G	C5'-C4'-C3'	5.71	124.56	116.00
16	AC	19	GLU	N-CA-C	-5.71	106.36	113.38
25	BA	1651	G	C4'-C3'-O3'	-5.71	104.44	113.00
25	BA	1654	A	C3'-C2'-O2'	5.71	119.26	110.70
25	BA	179	G	C3'-C2'-O2'	5.70	119.25	110.70
25	BA	1301	A	C1'-C2'-O2'	-5.70	103.25	111.80
25	BA	2683	C	C1'-C2'-O2'	5.70	116.95	108.40
12	AR	65	ILE	CB-CA-C	-5.69	104.59	112.04
25	BA	2643	G	C1'-C2'-O2'	5.69	116.93	108.40
50	B9	27	CYS	N-CA-C	-5.69	103.19	110.53
33	BT	77	PRO	N-CA-C	5.68	120.96	113.86
23	AY	548	GLU	N-CA-C	5.68	117.55	111.36
25	BA	706	A	C3'-C2'-O2'	-5.68	102.18	110.70
25	BA	1405	U	C3'-C2'-O2'	5.68	119.22	110.70
1	AA	1371	G	C3'-C2'-O2'	5.68	119.22	110.70
25	BA	2863	C	C4'-C3'-O3'	-5.68	104.48	113.00
5	AK	48	ILE	CB-CA-C	-5.68	101.98	111.29
19	AF	17	SER	N-CA-C	-5.67	104.79	110.97
1	AA	1134	G	C1'-C2'-O2'	5.67	116.90	108.40
1	AA	1204	A	C3'-C2'-O2'	5.67	119.20	110.70
25	BA	1227	G	C3'-C2'-O2'	5.67	119.20	110.70
25	BA	2027	G	C1'-C2'-O2'	5.67	116.90	108.40
25	BA	1693	U	P-O3'-C3'	5.67	128.70	120.20
43	BD	11	PRO	N-CA-C	-5.67	100.80	112.47
25	BA	1624	G	C4'-C3'-O3'	-5.66	104.51	113.00
25	BA	19	C	C3'-C2'-O2'	5.66	119.19	110.70
25	BA	2193	G	C1'-C2'-O2'	5.66	116.89	108.40
25	BA	2265	U	C4'-C3'-O3'	-5.66	104.51	113.00
25	BA	1210	A	C2'-C3'-O3'	5.65	117.98	109.50
1	AA	1363	C	C1'-C2'-O2'	5.65	116.87	108.40
25	BA	2454	G	C1'-C2'-O2'	5.65	116.88	108.40
5	AK	30	VAL	CB-CA-C	-5.65	102.27	110.63
1	AA	352	C	C4'-C3'-O3'	-5.64	104.54	113.00
25	BA	1168	G	C3'-C2'-O2'	5.64	119.16	110.70
25	BA	1879	C	C2'-C3'-O3'	5.64	122.16	113.70
25	BA	2414	G	C4'-C3'-O3'	-5.64	104.54	113.00
2	AV	75	C	C2'-C3'-O3'	-5.64	105.24	113.70
1	AA	1270	C	C3'-C2'-O2'	5.64	119.16	110.70
25	BA	1930	G	C3'-C2'-O2'	-5.63	106.15	114.60
1	AA	973	G	C2'-C3'-O3'	5.63	122.14	113.70
1	AA	981	U	C1'-C2'-O2'	5.63	116.84	108.40
25	BA	1658	C	C2'-C3'-O3'	-5.63	105.26	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	2445	G	C1'-C2'-O2'	5.63	116.84	108.40
1	AA	1488	G	C3'-C2'-O2'	5.62	119.14	110.70
25	BA	1388	G	C2'-C3'-O3'	5.62	122.14	113.70
46	B5	45	VAL	CB-CA-C	-5.62	102.15	111.32
1	AA	529	G	C1'-C2'-O2'	5.62	116.84	108.40
25	BA	2506	U	O4'-C4'-C3'	-5.62	100.48	106.10
25	BA	1881	C	C4'-C3'-O3'	-5.62	104.57	113.00
25	BA	1095	A	C3'-C2'-O2'	5.62	119.13	110.70
25	BA	2820	A	C1'-C2'-O2'	-5.62	103.37	111.80
25	BA	1655	A	C3'-C2'-O2'	5.62	119.12	110.70
25	BA	1079	C	C3'-C2'-O2'	5.62	119.12	110.70
25	BA	1142(A)	A	C2'-C3'-O3'	-5.62	101.08	109.50
25	BA	1161	C	C1'-C2'-O2'	5.62	116.82	108.40
1	AA	448	A	C3'-C2'-O2'	5.61	119.12	110.70
1	AA	547	A	C4'-C3'-O3'	5.61	117.81	109.40
1	AA	820	U	C2'-C3'-O3'	-5.61	101.09	109.50
1	AA	975	A	C2'-C3'-O3'	5.61	117.91	109.50
1	AA	1146	A	C1'-C2'-O2'	5.61	116.81	108.40
26	BB	71	C	C3'-C2'-O2'	5.60	119.10	110.70
25	BA	1040	C	C4'-C3'-O3'	5.60	117.80	109.40
25	BA	1119	C	C3'-C2'-O2'	5.60	119.10	110.70
52	BE	45	THR	CB-CA-C	-5.60	99.28	110.42
25	BA	1959	G	C4'-C3'-O3'	-5.60	104.60	113.00
25	BA	1895	C	C3'-C2'-O2'	5.59	119.09	110.70
25	BA	2686	G	C4'-C3'-O3'	-5.59	104.61	113.00
25	BA	585	G	C2'-C3'-O3'	-5.59	105.31	113.70
25	BA	2670	A	C1'-C2'-O2'	5.59	116.79	108.40
35	BV	89	GLN	CA-C-N	-5.59	114.00	119.76
35	BV	89	GLN	C-N-CA	-5.59	114.00	119.76
1	AA	13	U	C3'-C2'-O2'	-5.58	106.23	114.60
1	AA	108	G	C4'-C3'-O3'	5.58	121.38	113.00
1	AA	328	C	C3'-C2'-O2'	5.58	122.97	114.60
25	BA	2120	G	C3'-C2'-O2'	5.58	119.07	110.70
25	BA	516	C	C3'-C2'-O2'	5.57	119.06	110.70
1	AA	1456	G	C1'-C2'-O2'	-5.57	100.04	108.40
1	AA	785	G	C4'-C3'-O3'	-5.57	104.65	113.00
25	BA	81	G	C3'-C2'-O2'	5.57	119.05	110.70
1	AA	581	G	C1'-C2'-O2'	-5.57	100.05	108.40
25	BA	115	C	C4'-C3'-O3'	-5.57	104.65	113.00
57	BJ	110	ALA	N-CA-C	5.57	117.03	111.07
25	BA	1956	U	C1'-C2'-O2'	-5.56	100.06	108.40
29	BP	23	PRO	N-CA-C	5.56	123.92	112.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	117	G	C2'-C3'-O3'	-5.55	105.37	113.70
55	BH	167	GLU	N-CA-C	5.55	119.24	110.58
25	BA	1204	A	O4'-C1'-C2'	-5.55	100.25	105.80
30	BQ	140	ALA	N-CA-C	-5.55	102.69	110.35
25	BA	1914	C	C3'-C2'-O2'	5.55	119.02	110.70
1	AA	1340	A	C4'-C3'-O3'	-5.55	104.68	113.00
2	AV	50	U	C3'-C2'-O2'	5.55	119.02	110.70
25	BA	1000	A	C4'-C3'-O3'	-5.55	104.68	113.00
1	AA	409	G	C3'-C2'-O2'	5.55	119.02	110.70
25	BA	1865	G	C1'-C2'-O2'	5.55	116.72	108.40
25	BA	563	G	C2'-C3'-O3'	-5.54	105.39	113.70
25	BA	2414	G	C1'-C2'-O2'	5.54	116.72	108.40
25	BA	846	C	C3'-C2'-O2'	-5.54	106.29	114.60
25	BA	1196	C	C3'-C2'-O2'	5.54	119.01	110.70
25	BA	2041	U	C3'-C2'-O2'	5.54	119.01	110.70
29	BP	39	LYS	CB-CG-CD	5.54	124.03	111.30
36	BW	17	VAL	CB-CA-C	-5.53	104.83	112.24
1	AA	1126	U	C1'-C2'-O2'	-5.53	103.50	111.80
25	BA	1860	G	C4'-C3'-O3'	5.53	121.30	113.00
25	BA	2530	A	C2'-C3'-O3'	-5.53	105.40	113.70
25	BA	2619	C	C4'-C3'-O3'	-5.53	104.71	113.00
1	AA	836	G	C1'-C2'-O2'	5.53	116.69	108.40
25	BA	27	G	C2'-C3'-O3'	-5.53	101.21	109.50
1	AA	300	A	C2'-C3'-O3'	-5.53	105.41	113.70
25	BA	1680	U	C4'-C3'-O3'	-5.53	104.71	113.00
25	BA	1823	G	C3'-C2'-O2'	5.53	118.99	110.70
17	AD	19	LEU	N-CA-C	-5.52	101.80	110.36
51	BC	139	ASN	CA-C-N	-5.52	112.94	119.84
51	BC	139	ASN	C-N-CA	-5.52	112.94	119.84
1	AA	1198	G	C3'-C2'-O2'	5.52	118.97	110.70
25	BA	1188	U	C1'-C2'-O2'	-5.51	100.13	108.40
26	BB	22	U	C1'-C2'-O2'	5.51	116.67	108.40
1	AA	1517	G	C3'-C2'-O2'	5.51	118.97	110.70
25	BA	793	A	C4'-C3'-O3'	-5.51	101.14	109.40
1	AA	189(G)	G	C2'-C3'-O3'	-5.51	101.24	109.50
25	BA	269	U	C4'-C3'-O3'	-5.50	104.74	113.00
1	AA	1447	A	C4'-C3'-O3'	-5.50	104.74	113.00
25	BA	206	U	C4'-C3'-O3'	-5.50	104.75	113.00
25	BA	53	A	C4'-C3'-O3'	-5.50	104.75	113.00
25	BA	1545	A	C2'-C3'-O3'	5.50	121.95	113.70
4	AJ	55	LYS	N-CA-C	5.50	119.55	112.41
25	BA	889	C	C2'-C3'-O3'	5.50	117.74	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	925	C	C3'-C2'-O2'	5.50	118.94	110.70
23	AY	280	LEU	CA-C-N	5.49	125.44	119.78
23	AY	280	LEU	C-N-CA	5.49	125.44	119.78
1	AA	780	A	C4'-C3'-O3'	-5.49	104.76	113.00
25	BA	819	A	C3'-C2'-O2'	5.49	118.94	110.70
47	B6	12	GLU	N-CA-C	5.49	118.59	110.46
26	BB	12	C	C3'-C2'-O2'	5.49	122.83	114.60
55	BH	91	GLY	N-CA-C	5.49	117.16	111.95
25	BA	1879	C	C3'-C2'-O2'	5.48	118.93	110.70
50	B9	27	CYS	N-CA-CB	5.48	118.28	110.44
25	BA	2581	G	C2'-C3'-O3'	5.48	117.72	109.50
26	BB	108	U	C4'-C3'-O3'	-5.48	104.78	113.00
33	BT	90	GLN	N-CA-C	-5.48	99.13	110.80
25	BA	2349	G	C1'-C2'-O2'	5.48	116.62	108.40
25	BA	1772	G	C3'-C2'-O2'	5.48	118.92	110.70
1	AA	1013	G	O4'-C1'-C2'	-5.48	102.12	107.60
1	AA	1146	A	C2'-C3'-O3'	5.47	121.91	113.70
25	BA	1690	A	C1'-C2'-O2'	5.47	116.61	108.40
34	BU	102	GLU	N-CA-C	5.47	121.91	109.81
25	BA	1782	C	C3'-C2'-O2'	5.47	118.91	110.70
25	BA	1301	A	C2'-C3'-O3'	-5.47	101.30	109.50
34	BU	92	ARG	N-CA-C	-5.47	99.15	110.80
43	BD	245	PRO	CA-C-N	5.47	125.39	119.76
43	BD	245	PRO	C-N-CA	5.47	125.39	119.76
1	AA	611	A	C3'-C2'-O2'	5.46	118.90	110.70
14	AT	12	ALA	N-CA-C	-5.46	106.78	113.50
25	BA	127	A	C4'-C3'-O3'	-5.46	104.80	113.00
2	AV	64	A	C2'-C3'-O3'	5.46	121.89	113.70
33	BT	14	TYR	N-CA-C	-5.46	104.02	111.56
34	BU	58	ARG	N-CA-CB	5.46	118.25	110.06
1	AA	1131	G	C1'-C2'-O2'	5.46	116.59	108.40
1	AA	1133	G	N9-C1'-C2'	-5.46	103.81	112.00
4	AJ	16	LEU	N-CA-C	-5.46	104.97	111.03
5	AK	50	TYR	N-CA-C	5.46	117.74	110.53
25	BA	935	C	C2'-C3'-O3'	5.46	121.89	113.70
25	BA	2150	U	C3'-C2'-O2'	5.46	118.88	110.70
25	BA	1404	C	C4'-C3'-O3'	-5.45	104.82	113.00
25	BA	1764	G	C4'-C3'-O3'	-5.45	104.83	113.00
1	AA	374	A	C4'-C3'-O3'	-5.45	104.83	113.00
25	BA	271(O)	C	C4'-C3'-O3'	5.45	117.57	109.40
25	BA	1127	A	C4'-C3'-O3'	-5.44	104.83	113.00
25	BA	1086	A	C1'-C2'-O2'	5.44	116.56	108.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	1970	A	O4'-C1'-C2'	-5.44	100.36	105.80
25	BA	859	G	C4'-C3'-O3'	-5.44	101.24	109.40
25	BA	1697	G	C2'-C3'-O3'	-5.44	105.54	113.70
16	AC	167	TRP	N-CA-C	-5.44	101.37	109.96
25	BA	1653	G	C4'-C3'-O3'	5.44	117.56	109.40
1	AA	1176	A	C3'-C2'-O2'	5.44	118.85	110.70
25	BA	1092	C	C4'-C3'-O3'	5.43	121.15	113.00
25	BA	677	A	C4'-C3'-O3'	-5.43	104.85	113.00
25	BA	2374	C	C1'-C2'-O2'	5.43	116.55	108.40
25	BA	2166	G	C4'-C3'-O3'	-5.43	104.86	113.00
14	AT	96	GLY	N-CA-C	5.43	120.85	110.86
25	BA	2337	G	C3'-C2'-O2'	5.43	118.84	110.70
1	AA	574	A	C4'-C3'-O3'	-5.43	104.86	113.00
25	BA	2166	G	N9-C1'-C2'	5.43	120.14	112.00
1	AA	231	G	C4'-C3'-O3'	-5.42	104.86	113.00
25	BA	584	C	C3'-C2'-O2'	5.42	118.84	110.70
25	BA	1818	U	C3'-C2'-O2'	-5.42	106.46	114.60
25	BA	967	C	C3'-C2'-O2'	5.42	118.83	110.70
1	AA	7	G	C1'-C2'-O2'	-5.42	103.68	111.80
1	AA	918	A	C4'-C3'-O3'	-5.42	104.88	113.00
25	BA	2714	G	C5'-C4'-C3'	-5.41	107.88	116.00
25	BA	2714	G	C2'-C3'-O3'	5.41	121.82	113.70
25	BA	706	A	C1'-C2'-O2'	5.41	116.52	108.40
25	BA	1482	G	C3'-C2'-O2'	5.41	118.81	110.70
25	BA	2707	G	C4'-C3'-O3'	-5.41	104.89	113.00
49	B8	32	LEU	N-CA-C	-5.41	105.07	110.97
25	BA	1927	A	C2'-C3'-O3'	-5.41	105.59	113.70
41	B1	53	VAL	CB-CA-C	-5.41	102.42	111.29
25	BA	2231	C	C2'-C3'-O3'	5.40	121.81	113.70
7	AM	90	LEU	N-CA-C	-5.40	99.29	110.80
25	BA	1245	G	C2'-C3'-O3'	5.40	121.80	113.70
1	AA	666	G	C3'-C2'-O2'	5.40	118.80	110.70
25	BA	196	A	C2'-C3'-O3'	5.40	117.60	109.50
25	BA	857	C	C4'-C3'-O3'	-5.40	104.91	113.00
25	BA	1663	C	C4'-C3'-O3'	-5.40	104.90	113.00
1	AA	685	G	C3'-C2'-O2'	5.40	118.79	110.70
43	BD	256	GLY	N-CA-C	5.39	121.50	115.08
1	AA	518	C	C1'-C2'-O2'	-5.39	103.71	111.80
27	BN	110	GLY	CA-C-N	5.39	125.47	119.32
27	BN	110	GLY	C-N-CA	5.39	125.47	119.32
25	BA	2396	G	C4'-C3'-O3'	-5.39	104.92	113.00
25	BA	1182	A	C3'-C2'-O2'	5.39	118.78	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	747	U	C4'-C3'-O3'	-5.39	104.92	113.00
43	BD	71	ASP	CB-CA-C	-5.39	100.01	110.46
25	BA	2610	C	C4'-C3'-O3'	-5.38	101.32	109.40
2	AV	62	C	C4'-C3'-O3'	-5.38	104.93	113.00
25	BA	1162	G	C2'-C3'-O3'	5.38	121.77	113.70
1	AA	152	A	C1'-C2'-O2'	5.38	116.47	108.40
25	BA	2641	G	C1'-C2'-O2'	5.38	116.47	108.40
13	AS	70	LYS	N-CA-C	-5.38	103.79	110.41
25	BA	1248	G	C2'-C3'-O3'	-5.38	101.43	109.50
25	BA	1623	G	C1'-C2'-O2'	5.38	116.47	108.40
30	BQ	98	LYS	CA-C-N	5.38	125.69	119.93
30	BQ	98	LYS	C-N-CA	5.38	125.69	119.93
25	BA	1915	U	C4'-C3'-O3'	-5.38	104.94	113.00
25	BA	508	G	P-O5'-C5'	5.37	128.96	120.90
1	AA	931	C	C2'-C3'-O3'	5.37	121.75	113.70
25	BA	1847	A	C4'-C3'-O3'	5.37	117.45	109.40
1	AA	1151	A	C4'-C3'-O3'	-5.37	101.35	109.40
1	AA	1133	G	C3'-C2'-O2'	5.37	118.75	110.70
25	BA	2811	G	C2'-C3'-O3'	5.37	121.75	113.70
1	AA	1336	C	C3'-C2'-O2'	-5.37	106.55	114.60
6	AL	26	ALA	N-CA-C	-5.36	99.38	110.80
25	BA	1685	C	C3'-C2'-O2'	5.36	118.74	110.70
1	AA	1210	C	C3'-C2'-O2'	5.36	118.73	110.70
25	BA	2688	U	C4'-C3'-O3'	-5.36	104.97	113.00
25	BA	334	C	C2'-C3'-O3'	-5.36	105.67	113.70
1	AA	29	G	C4'-C3'-O3'	-5.35	104.98	113.00
1	AA	498	U	C3'-C2'-O2'	5.35	118.72	110.70
18	AE	11	ILE	N-CA-C	5.35	118.61	111.44
25	BA	1307	A	C1'-C2'-O2'	5.35	116.42	108.40
25	BA	2661	G	C4'-C3'-O3'	-5.35	104.98	113.00
1	AA	1279	A	N9-C1'-C2'	5.35	120.02	112.00
25	BA	1280	G	C2'-C3'-O3'	5.35	121.72	113.70
28	BO	38	VAL	CB-CA-C	-5.35	103.44	110.98
53	BF	46	ARG	CG-CD-NE	-5.35	100.23	112.00
1	AA	134	A	C3'-C2'-O2'	5.35	118.72	110.70
26	BB	35	U	C3'-C2'-O2'	5.35	118.72	110.70
25	BA	2248	C	C4'-C3'-O3'	-5.34	104.98	113.00
25	BA	1975	G	C4'-C3'-O3'	-5.34	104.98	113.00
53	BF	183	VAL	N-CA-C	5.34	116.07	110.62
25	BA	1710	C	C3'-C2'-O2'	5.34	118.71	110.70
25	BA	1186	G	C4'-C3'-O3'	-5.34	104.99	113.00
25	BA	1027	A	C2'-C3'-O3'	-5.33	105.70	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	1659	U	C1'-C2'-O2'	5.33	116.40	108.40
1	AA	266	G	P-O3'-C3'	5.33	128.20	120.20
1	AA	300	A	C1'-C2'-O2'	5.33	116.40	108.40
1	AA	1310	G	C3'-C2'-O2'	5.33	118.70	110.70
25	BA	326	G	C1'-C2'-O2'	5.33	116.40	108.40
25	BA	2763	G	C1'-C2'-O2'	5.33	116.40	108.40
25	BA	1527	G	C2'-C3'-O3'	-5.33	105.70	113.70
25	BA	444	C	C3'-C2'-O2'	5.33	118.69	110.70
55	BH	46	GLU	N-CA-C	5.33	117.09	108.41
25	BA	1936	A	O5'-C5'-C4'	-5.33	103.71	111.70
1	AA	748	C	C2'-C3'-O3'	5.33	117.49	109.50
47	B6	11	LEU	N-CA-CB	-5.33	101.49	110.49
1	AA	661	G	C1'-C2'-O2'	5.32	116.39	108.40
27	BN	46	VAL	N-CA-C	5.32	120.41	109.34
49	B8	62	LEU	N-CA-C	-5.32	105.22	112.35
25	BA	214	G	C2'-C3'-O3'	-5.32	105.72	113.70
1	AA	1502	A	N9-C1'-C2'	5.32	121.97	114.00
25	BA	767	U	C3'-C2'-O2'	5.32	118.67	110.70
41	B1	53	VAL	N-CA-C	5.32	120.40	109.34
2	AV	29	G	C2'-C3'-O3'	5.31	121.67	113.70
25	BA	740	U	C2'-C3'-O3'	-5.31	105.73	113.70
25	BA	807	U	P-O5'-C5'	-5.31	112.94	120.90
25	BA	363(E)	U	C1'-C2'-O2'	5.31	116.36	108.40
25	BA	1967	C	C4'-C3'-O3'	-5.31	105.04	113.00
25	BA	575	A	C3'-C2'-O2'	5.30	118.66	110.70
25	BA	2182	G	C3'-C2'-O2'	5.30	118.66	110.70
25	BA	2725	A	C2'-C3'-O3'	5.30	117.46	109.50
21	AH	100	ILE	CA-C-N	-5.30	114.52	120.14
21	AH	100	ILE	C-N-CA	-5.30	114.52	120.14
25	BA	1053	C	C2'-C3'-O3'	5.30	121.66	113.70
1	AA	118	U	C3'-C2'-O2'	5.30	118.65	110.70
43	BD	64	ILE	N-CA-CB	5.30	116.83	110.31
25	BA	372	G	C2'-C3'-O3'	-5.30	101.55	109.50
25	BA	2287	A	C1'-C2'-O2'	-5.30	103.85	111.80
43	BD	43	ARG	N-CA-C	5.30	119.50	113.19
25	BA	1462	C	C4'-C3'-O3'	-5.29	105.06	113.00
25	BA	2577	A	C1'-C2'-O2'	5.29	116.34	108.40
25	BA	2020	A	C2'-C3'-O3'	5.29	121.64	113.70
25	BA	2183	C	C4'-C3'-O3'	-5.29	105.06	113.00
1	AA	131	C	C3'-C2'-O2'	5.29	118.63	110.70
25	BA	796	C	C4'-C3'-O3'	-5.29	105.07	113.00
25	BA	1786	A	O4'-C1'-C2'	-5.28	100.52	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	326	G	N9-C1'-C2'	5.28	119.92	112.00
1	AA	1502	A	C4'-C3'-O3'	5.28	117.32	109.40
25	BA	2231	C	C4'-C3'-O3'	-5.28	105.08	113.00
25	BA	789	A	C2'-C3'-O3'	5.28	117.42	109.50
25	BA	1468	C	C3'-C2'-O2'	5.28	118.62	110.70
26	BB	5	C	C3'-C2'-O2'	5.28	118.62	110.70
2	AV	31	A	C3'-C2'-O2'	5.28	118.62	110.70
25	BA	584	C	C4'-C3'-O3'	-5.28	105.08	113.00
8	AN	42	ILE	CA-C-N	5.28	127.30	120.44
8	AN	42	ILE	C-N-CA	5.28	127.30	120.44
47	B6	48	VAL	CB-CA-C	-5.28	102.64	111.29
14	AT	49	ALA	N-CA-C	5.27	117.94	111.82
1	AA	1138	G	C1'-O4'-C4'	-5.27	104.43	109.70
25	BA	1579	A	C3'-C2'-O2'	5.27	118.61	110.70
1	AA	1512	U	C4'-C3'-O3'	-5.27	105.10	113.00
18	AE	33	VAL	CB-CA-C	-5.27	102.80	110.81
25	BA	249	C	C4'-C3'-O3'	-5.26	101.50	109.40
49	B8	47	LYS	N-CA-C	5.26	115.30	107.88
57	BJ	122	ALA	N-CA-C	5.26	116.88	108.41
25	BA	1546	C	C1'-C2'-O2'	5.26	116.29	108.40
25	BA	1564	C	C4'-C3'-O3'	-5.26	105.11	113.00
25	BA	2524	G	C1'-C2'-O2'	5.26	116.29	108.40
49	B8	49	VAL	CA-C-O	-5.26	116.04	121.93
1	AA	722	A	C3'-C2'-O2'	5.26	118.59	110.70
1	AA	1354	C	C3'-C2'-O2'	5.26	118.59	110.70
25	BA	1778	U	C4'-C3'-O3'	-5.26	105.11	113.00
35	BV	19	LYS	N-CA-C	5.26	122.00	110.80
1	AA	560	U	C4'-C3'-O3'	5.25	117.28	109.40
1	AA	1499	A	O5'-P-OP1	-5.25	92.25	108.00
25	BA	332	A	C2'-C3'-O3'	-5.25	101.62	109.50
1	AA	1372	U	C1'-C2'-O2'	5.25	116.28	108.40
1	AA	597	G	C3'-C2'-O2'	5.25	118.57	110.70
25	BA	1194	A	C4'-C3'-O3'	-5.25	105.13	113.00
53	BF	23	ASP	N-CA-C	-5.25	106.95	113.19
54	BG	82	LEU	N-CA-C	5.25	121.98	110.80
1	AA	682	G	C4'-C3'-O3'	-5.24	105.14	113.00
25	BA	1539	G	C3'-C2'-O2'	5.24	118.56	110.70
25	BA	385	C	C4'-C3'-O3'	-5.24	105.14	113.00
26	BB	101	G	C2'-C3'-O3'	5.24	121.56	113.70
25	BA	272(G)	C	C3'-C2'-O2'	5.24	118.56	110.70
25	BA	2607	G	C4'-C3'-O3'	-5.24	105.14	113.00
25	BA	2830	G	C4'-C3'-O3'	-5.24	105.14	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	102	G	C3'-C2'-O2'	-5.24	102.84	110.70
25	BA	1296	G	C3'-C2'-O2'	5.24	118.56	110.70
25	BA	2319	G	O4'-C4'-C3'	-5.24	100.86	106.10
1	AA	266	G	C4'-C3'-O3'	5.23	117.25	109.40
25	BA	1929	G	P-O5'-C5'	-5.23	113.05	120.90
1	AA	522	C	C3'-C2'-O2'	5.23	118.55	110.70
25	BA	2372	G	C3'-C2'-O2'	5.23	118.55	110.70
1	AA	18	C	C4'-C3'-O3'	-5.23	105.16	113.00
1	AA	1054	C	P-O5'-C5'	-5.23	113.05	120.90
22	AI	72	GLY	N-CA-C	-5.23	106.16	112.49
25	BA	1481	U	C2'-C3'-O3'	5.23	121.55	113.70
23	AY	404	VAL	CA-C-N	5.23	139.55	127.00
23	AY	404	VAL	C-N-CA	5.23	139.55	127.00
1	AA	1441	G	C3'-C2'-O2'	5.23	118.54	110.70
25	BA	1010	A	C2'-C3'-O3'	-5.23	105.86	113.70
31	BR	52	ILE	N-CA-C	-5.23	105.30	111.00
25	BA	2180	U	N1-C1'-C2'	5.23	119.84	112.00
25	BA	2425	A	C3'-C2'-O2'	-5.23	106.76	114.60
17	AD	13	ARG	N-CA-C	5.22	116.73	109.31
23	AY	634	MET	N-CA-C	5.22	116.55	107.93
25	BA	2285	C	C3'-C2'-O2'	5.22	118.54	110.70
25	BA	1686	C	C2'-C3'-O3'	5.22	121.53	113.70
25	BA	1982	C	C4'-C3'-O3'	-5.22	105.17	113.00
1	AA	811	C	C4'-C3'-O3'	-5.22	105.17	113.00
25	BA	2495	G	C4'-C3'-O3'	-5.22	105.17	113.00
1	AA	485	G	C4'-C3'-O3'	-5.22	101.57	109.40
25	BA	59	U	C4'-C3'-O3'	-5.22	105.17	113.00
53	BF	28	ILE	N-CA-C	5.22	115.61	107.99
25	BA	715	G	C4'-C3'-O3'	-5.22	105.18	113.00
25	BA	2431	U	C4'-C3'-O3'	-5.22	105.17	113.00
2	AV	72	C	C4'-C3'-C2'	-5.21	97.39	102.60
25	BA	55	G	C4'-C3'-O3'	-5.21	105.18	113.00
25	BA	2665	A	O4'-C4'-C3'	-5.21	98.78	104.00
1	AA	458	C	C1'-C2'-O2'	5.21	116.22	108.40
23	AY	132	ARG	N-CA-C	5.21	116.99	108.76
1	AA	776	G	C4'-C3'-O3'	-5.21	105.19	113.00
25	BA	45	C	C3'-C2'-O2'	5.21	118.52	110.70
25	BA	2068	U	C4'-C3'-O3'	-5.21	105.19	113.00
25	BA	1530	C	C4'-C3'-O3'	-5.21	105.19	113.00
25	BA	264	C	C3'-C2'-O2'	5.20	118.51	110.70
25	BA	1387	C	C2'-C3'-O3'	5.20	121.51	113.70
36	BW	18	ARG	N-CA-C	-5.20	105.04	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	355	C	C4'-C3'-O3'	-5.20	105.20	113.00
25	BA	623	G	C2'-C3'-O3'	5.20	121.50	113.70
25	BA	505	A	C2'-C3'-O3'	-5.20	105.90	113.70
25	BA	602	G	C3'-C2'-O2'	5.20	118.50	110.70
1	AA	1493	A	C2'-C3'-O3'	-5.19	105.91	113.70
1	AA	1293	G	C1'-C2'-O2'	5.19	116.19	108.40
1	AA	1342	C	C3'-C2'-O2'	5.19	118.49	110.70
30	BQ	134	ARG	N-CA-C	5.19	117.10	107.60
1	AA	487	A	C3'-C2'-O2'	5.19	118.48	110.70
2	AV	21	A	C4'-C3'-O3'	-5.19	105.22	113.00
25	BA	1678	G	C4'-C3'-O3'	-5.19	105.22	113.00
25	BA	2127	G	C3'-C2'-O2'	5.19	118.48	110.70
28	BO	69	ILE	CB-CA-C	-5.19	104.48	110.91
1	AA	705	U	C2'-C3'-O3'	-5.19	105.92	113.70
25	BA	526	A	C4'-C3'-O3'	-5.19	105.22	113.00
18	AE	102	ALA	N-CA-C	5.18	116.72	108.79
1	AA	200	G	C3'-C2'-O2'	5.18	118.47	110.70
1	AA	1484	C	C3'-C2'-O2'	5.18	118.47	110.70
25	BA	701	G	C3'-C2'-O2'	5.18	118.47	110.70
25	BA	2299	G	C4'-C3'-O3'	-5.18	105.23	113.00
1	AA	523	A	C4'-C3'-O3'	-5.18	105.23	113.00
25	BA	2781	A	C1'-C2'-O2'	5.18	116.17	108.40
1	AA	555	C	C3'-C2'-O2'	5.18	118.47	110.70
25	BA	494	G	C4'-C3'-O3'	-5.18	105.23	113.00
35	BV	34	GLU	N-CA-C	-5.18	102.02	110.20
52	BE	61	ARG	CA-C-N	-5.18	113.37	119.84
52	BE	61	ARG	C-N-CA	-5.18	113.37	119.84
1	AA	62	U	C3'-C2'-O2'	5.17	118.46	110.70
25	BA	627	A	C4'-C3'-O3'	5.17	117.16	109.40
31	BR	4	LEU	CA-C-N	5.17	128.04	119.35
31	BR	4	LEU	C-N-CA	5.17	128.04	119.35
1	AA	1490	C	C3'-C2'-O2'	5.17	118.46	110.70
1	AA	439	A	C3'-C2'-O2'	5.17	118.45	110.70
1	AA	1175	G	C3'-C2'-O2'	5.17	118.45	110.70
25	BA	1367	A	C2'-C3'-O3'	-5.17	105.95	113.70
25	BA	1863	G	C2'-C3'-O3'	5.17	121.45	113.70
1	AA	1222	G	C2'-C3'-O3'	5.17	121.45	113.70
25	BA	685	A	C2'-C3'-O3'	-5.17	101.75	109.50
25	BA	933	A	O4'-C4'-C3'	-5.17	98.83	104.00
25	BA	1769	G	C4'-C3'-O3'	-5.16	105.25	113.00
25	BA	2094	G	C3'-C2'-O2'	5.16	118.44	110.70
25	BA	536	A	C2'-C3'-O3'	5.16	121.44	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	828	U	N1-C1'-C2'	5.16	119.74	112.00
25	BA	2439	A	C2'-C3'-O3'	-5.16	101.76	109.50
1	AA	608	A	C1'-C2'-O2'	5.16	116.14	108.40
25	BA	435	C	C1'-C2'-O2'	5.16	116.14	108.40
1	AA	1199	U	C2'-C3'-O3'	-5.16	105.97	113.70
2	AV	76	A	C4'-C3'-C2'	-5.16	97.44	102.60
25	BA	271(V)	G	C1'-C2'-O2'	5.16	116.13	108.40
25	BA	1429	G	C3'-C2'-O2'	5.15	118.43	110.70
50	B9	23	VAL	CB-CA-C	-5.15	104.73	110.96
1	AA	1290	G	C3'-C2'-O2'	5.15	118.42	110.70
2	AV	13	C	C3'-C2'-O2'	5.15	118.43	110.70
25	BA	2182	G	C4'-C3'-O3'	-5.15	105.28	113.00
1	AA	1499	A	O5'-P-OP2	5.15	123.44	108.00
25	BA	15	G	C3'-C2'-O2'	5.15	118.42	110.70
25	BA	936	C	C3'-C2'-O2'	5.15	118.42	110.70
25	BA	1798	U	C2'-C3'-O3'	5.14	121.42	113.70
1	AA	826	C	C4'-C3'-O3'	-5.14	105.29	113.00
25	BA	118	A	C2'-C3'-O3'	-5.14	105.99	113.70
25	BA	2472	G	C1'-C2'-O2'	5.14	116.11	108.40
54	BG	20	ILE	N-CA-C	-5.14	105.31	110.30
35	BV	2	PHE	N-CA-CB	-5.14	101.80	110.49
1	AA	483	C	C4'-C3'-O3'	-5.14	105.29	113.00
6	AL	57	LYS	N-CA-C	-5.14	102.67	110.28
23	AY	685	GLU	N-CA-C	-5.14	105.57	111.07
25	BA	1475	G	C1'-C2'-O2'	5.14	116.11	108.40
39	BZ	155	LEU	N-CA-C	5.14	117.17	108.02
55	BH	158	HIS	N-CA-C	5.14	116.11	108.86
25	BA	777	A	C4'-C3'-O3'	-5.14	105.29	113.00
25	BA	2392	A	O4'-C4'-C3'	-5.13	98.87	104.00
29	BP	52	GLU	N-CA-C	5.13	121.74	110.80
23	AY	394	ALA	N-CA-C	5.13	116.03	110.13
26	BB	18	G	C2'-C3'-O3'	5.13	121.40	113.70
25	BA	2125	G	C2'-C3'-O3'	-5.13	106.00	113.70
29	BP	17	LYS	N-CA-C	5.13	121.73	110.80
1	AA	179	A	C2'-C3'-O3'	-5.13	106.01	113.70
1	AA	1152	A	C3'-C2'-O2'	5.13	118.39	110.70
25	BA	1358	G	C2'-C3'-O3'	-5.13	106.01	113.70
1	AA	1186	G	C3'-C2'-O2'	5.12	118.39	110.70
25	BA	2680	C	C3'-C2'-O2'	5.12	118.39	110.70
15	AB	186	ALA	N-CA-C	5.12	117.03	108.99
20	AG	145	ALA	N-CA-C	-5.12	99.89	110.80
25	BA	945	A	N9-C1'-C2'	5.12	121.68	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	934	G	C3'-C2'-O2'	5.12	118.38	110.70
25	BA	675	A	C3'-C2'-O2'	5.12	118.38	110.70
25	BA	2371	G	C3'-C2'-O2'	5.12	118.37	110.70
25	BA	2718	G	C4'-C3'-O3'	-5.12	105.33	113.00
1	AA	235	C	C3'-C2'-O2'	5.11	118.37	110.70
25	BA	700	G	C4'-C3'-O3'	-5.11	105.33	113.00
25	BA	1498	C	C1'-C2'-O2'	5.11	116.07	108.40
25	BA	1882	C	C4'-C3'-O3'	-5.11	105.33	113.00
1	AA	835	U	C1'-C2'-O2'	5.11	116.06	108.40
25	BA	443	A	C2'-C3'-O3'	-5.11	106.04	113.70
25	BA	722	A	C3'-C2'-O2'	5.10	118.35	110.70
25	BA	1902	C	C1'-C2'-O2'	-5.10	100.75	108.40
25	BA	1916	A	C2'-C3'-O3'	5.10	121.35	113.70
25	BA	2396	G	C2'-C3'-O3'	5.10	121.35	113.70
1	AA	936	C	C3'-C2'-O2'	5.10	118.35	110.70
18	AE	58	ALA	CA-C-N	5.10	125.75	119.99
18	AE	58	ALA	C-N-CA	5.10	125.75	119.99
37	BX	25	LYS	N-CA-C	5.10	117.94	107.69
1	AA	865	A	C3'-C2'-O2'	5.10	118.35	110.70
1	AA	1263	C	C3'-C2'-O2'	5.10	118.35	110.70
25	BA	731	C	C3'-C2'-O2'	5.10	118.35	110.70
25	BA	1462	C	C2'-C3'-O3'	5.10	121.35	113.70
25	BA	69	C	C2'-C3'-O3'	5.10	121.34	113.70
20	AG	87	VAL	N-CA-C	5.09	114.06	108.05
26	BB	29	A	C3'-C2'-O2'	5.09	118.34	110.70
1	AA	588	G	C2'-C3'-O3'	-5.09	106.06	113.70
25	BA	1278	A	C3'-C2'-O2'	5.09	118.33	110.70
30	BQ	72	LYS	CA-C-N	5.09	126.49	120.23
30	BQ	72	LYS	C-N-CA	5.09	126.49	120.23
25	BA	363(B)	G	C4'-C3'-O3'	-5.09	105.37	113.00
25	BA	773	U	C1'-C2'-O2'	5.08	116.03	108.40
57	BJ	59	ALA	N-CA-C	-5.08	103.63	110.24
25	BA	1501	C	C4'-C3'-O3'	-5.08	105.37	113.00
46	B5	46	CYS	CA-C-N	5.08	126.19	119.84
46	B5	46	CYS	C-N-CA	5.08	126.19	119.84
1	AA	1137	C	C2'-C3'-O3'	-5.08	106.08	113.70
25	BA	2025	C	C2'-C3'-O3'	5.08	121.32	113.70
25	BA	1694	C	C1'-C2'-O2'	5.08	119.42	111.80
25	BA	2713	A	C1'-C2'-O2'	-5.08	104.18	111.80
1	AA	1126	U	C3'-C2'-O2'	5.08	122.21	114.60
25	BA	1591	G	C1'-C2'-O2'	5.08	116.01	108.40
25	BA	1938	A	C4'-C3'-O3'	5.07	117.01	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AY	295	GLU	N-CA-C	-5.07	104.83	111.02
1	AA	853	G	C4'-C3'-O3'	-5.07	105.39	113.00
25	BA	906	G	C1'-C2'-O2'	5.07	116.00	108.40
1	AA	194	C	C4'-C3'-O3'	-5.06	105.41	113.00
1	AA	1504	G	P-O3'-C3'	5.06	127.79	120.20
25	BA	1467	C	C3'-C2'-O2'	5.06	118.29	110.70
39	BZ	194	PRO	N-CA-CB	5.06	108.56	103.25
1	AA	568	G	N9-C1'-C2'	5.06	119.58	112.00
25	BA	225	A	C4'-C3'-O3'	-5.06	105.42	113.00
25	BA	2639	A	C1'-C2'-O2'	5.05	115.98	108.40
25	BA	66	C	C2'-C3'-O3'	-5.05	106.12	113.70
25	BA	2022	U	C4'-C3'-O3'	5.05	116.97	109.40
25	BA	2333	A	C4'-C3'-O3'	-5.05	105.43	113.00
1	AA	804	U	C3'-C2'-O2'	5.05	118.27	110.70
17	AD	115	ARG	N-CA-C	-5.05	105.67	111.07
25	BA	933	A	C3'-C2'-O2'	5.05	118.27	110.70
25	BA	1019	U	C4'-C3'-O3'	-5.05	105.43	113.00
26	BB	47	C	C4'-C3'-O3'	-5.04	105.43	113.00
1	AA	250	A	C2'-C3'-O3'	5.04	117.07	109.50
25	BA	996	A	C3'-C2'-O2'	5.04	118.27	110.70
25	BA	1022	G	O4'-C1'-C2'	5.04	110.84	105.80
25	BA	1546	C	C2'-C3'-O3'	-5.04	106.13	113.70
25	BA	1426	G	C3'-C2'-O2'	5.04	118.26	110.70
18	AE	101	ILE	CB-CA-C	-5.04	106.94	112.68
1	AA	1401	G	C1'-C2'-O2'	5.04	115.95	108.40
2	AV	72	C	O4'-C4'-C3'	-5.04	98.97	104.00
25	BA	2672	G	C1'-C2'-O2'	5.04	115.95	108.40
1	AA	863	U	C1'-C2'-O2'	5.03	115.95	108.40
41	B1	83	GLU	N-CA-C	5.03	114.97	107.88
25	BA	958	U	C1'-C2'-O2'	5.03	115.94	108.40
25	BA	102	G	C1'-C2'-O2'	-5.02	100.87	108.40
25	BA	143	G	C3'-C2'-O2'	5.02	118.23	110.70
25	BA	2072	G	C1'-C2'-O2'	5.02	115.94	108.40
25	BA	125	G	C1'-C2'-O2'	-5.02	104.27	111.80
30	BQ	57	HIS	CA-C-N	-5.02	115.49	123.12
30	BQ	57	HIS	C-N-CA	-5.02	115.49	123.12
25	BA	946	G	O5'-P-OP1	-5.02	92.95	108.00
25	BA	1471	A	C2'-C3'-O3'	5.02	121.23	113.70
25	BA	1763	G	C2'-C3'-O3'	-5.02	106.17	113.70
25	BA	832	G	N9-C1'-C2'	5.02	119.52	112.00
52	BE	44	TYR	N-CA-C	5.02	121.48	110.80
25	BA	2726	U	C1'-C2'-O2'	-5.01	104.28	111.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	BJ	26	ALA	N-CA-C	5.01	117.14	109.07
1	AA	1276	G	C1'-C2'-O2'	5.01	115.92	108.40
25	BA	1600	C	C1'-C2'-O2'	5.01	115.92	108.40
25	BA	663	G	C1'-C2'-O2'	5.01	115.92	108.40
25	BA	691	C	C3'-C2'-O2'	5.01	118.21	110.70
25	BA	2328	A	C4'-C3'-O3'	-5.01	105.49	113.00
25	BA	2429	G	C2'-C3'-O3'	5.01	121.21	113.70
43	BD	240	ALA	CA-C-N	-5.01	113.58	119.84
43	BD	240	ALA	C-N-CA	-5.01	113.58	119.84
25	BA	996	A	O5'-P-OP2	5.01	123.02	108.00
25	BA	1544	A	C4'-C3'-O3'	-5.01	105.49	113.00
25	BA	2113	U	C2'-C3'-O3'	5.01	121.21	113.70
53	BF	46	ARG	N-CA-C	-5.01	106.86	113.12
25	BA	1916	A	C3'-C2'-O2'	5.00	118.21	110.70
25	BA	1957	C	C3'-C2'-O2'	5.00	118.21	110.70
25	BA	1843	C	C3'-C2'-O2'	5.00	118.21	110.70
51	BC	144	THR	N-CA-C	5.00	118.69	112.59
55	BH	47	GLU	N-CA-C	5.00	121.46	110.80
1	AA	853	G	C1'-C2'-O2'	5.00	115.90	108.40
1	AA	1362	C	C4'-C3'-O3'	-5.00	105.50	113.00
25	BA	1418	G	C1'-C2'-O2'	5.00	115.90	108.40

There are no chirality outliers.

All (72) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
17	AD	11	LEU	Peptide
17	AD	17	VAL	Peptide
4	AJ	54	PHE	Peptide
6	AL	28	LYS	Peptide
8	AN	13	THR	Peptide
14	AT	73	HIS	Peptide
14	AT	95	ALA	Peptide
23	AY	209	ALA	Peptide
23	AY	319	ASP	Peptide
23	AY	320	PRO	Peptide
23	AY	404	VAL	Peptide
41	B1	29	GLY	Peptide
41	B1	94	LEU	Peptide
46	B5	47	PRO	Peptide
46	B5	51	TYR	Peptide
47	B6	10	LEU	Peptide

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Mol	Chain	Res	Type	Group
47	B6	20	ASN	Peptide
47	B6	31	PRO	Peptide
51	BC	143	GLY	Peptide
51	BC	70	LYS	Peptide
43	BD	197	GLY	Peptide
43	BD	223	GLY	Peptide
43	BD	24	ILE	Peptide
43	BD	36	PRO	Peptide
52	BE	131	ALA	Peptide
52	BE	61	ARG	Peptide
52	BE	62	PRO	Peptide
52	BE	76	ARG	Peptide
52	BE	86	PRO	Peptide
53	BF	85	GLY	Peptide
55	BH	166	GLY	Peptide
58	BL	121	UNK	Peptide
27	BN	124	ALA	Peptide
27	BN	20	GLY	Peptide
29	BP	10	PRO	Peptide
29	BP	107	LYS	Peptide
29	BP	115	LEU	Peptide
29	BP	143	GLY	Peptide
29	BP	29	LYS	Peptide
29	BP	33	ARG	Peptide
29	BP	34	GLY	Peptide
29	BP	37	GLY	Peptide
29	BP	40	SER	Peptide
29	BP	44	GLY	Peptide
29	BP	51	PHE	Peptide
29	BP	57	THR	Peptide
29	BP	70	GLN	Peptide
29	BP	8	PRO	Peptide
29	BP	9	ASN	Peptide
30	BQ	17	LEU	Peptide
30	BQ	19	GLY	Peptide
31	BR	117	VAL	Peptide
31	BR	5	LYS	Peptide
32	BS	11	LYS	Peptide
33	BT	29	ARG	Peptide
33	BT	30	VAL	Peptide
33	BT	58	ASN	Peptide
33	BT	79	HIS	Peptide

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Mol	Chain	Res	Type	Group
33	BT	92	GLY	Peptide
33	BT	93	ARG	Peptide
34	BU	90	VAL	Peptide
34	BU	95	LEU	Peptide
34	BU	96	ALA	Peptide
35	BV	1	MET	Peptide
35	BV	18	LEU	Peptide
35	BV	42	GLY	Peptide
38	BY	16	ALA	Peptide
38	BY	17	SER	Peptide
38	BY	40	GLU	Peptide
38	BY	6	HIS	Peptide
38	BY	61	ILE	Peptide
38	BY	76	CYS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32529	0	16426	527	0
2	AV	1579	0	802	43	0
3	AX	125	0	64	2	0
4	AJ	795	0	840	30	0
5	AK	885	0	904	29	0
6	AL	971	0	1057	30	0
7	AM	988	0	1059	44	0
8	AN	492	0	529	21	0
9	AO	734	0	771	16	0
10	AP	701	0	720	15	0
11	AQ	824	0	891	19	0
12	AR	574	0	644	11	0
13	AS	630	0	652	30	0
14	AT	763	0	861	32	0
15	AB	1901	0	1951	90	0
16	AC	1613	0	1677	50	0
17	AD	1703	0	1763	73	0
18	AE	1147	0	1207	34	0
19	AF	843	0	857	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	AG	1257	0	1296	26	0
21	AH	1116	0	1177	27	0
22	AI	1011	0	1043	35	0
23	AY	4877	0	4964	176	0
24	AU	209	0	221	8	0
25	BA	61580	0	31049	1166	0
26	BB	2551	0	1295	57	0
27	BN	1104	0	1180	67	0
28	BO	933	0	996	38	0
29	BP	1114	0	1187	146	0
30	BQ	1122	0	1179	44	0
31	BR	960	0	1021	41	0
32	BS	770	0	832	43	0
33	BT	1141	0	1202	119	0
34	BU	958	0	1015	54	0
35	BV	779	0	852	49	0
36	BW	896	0	953	28	0
37	BX	725	0	778	17	0
38	BY	775	0	870	74	0
39	BZ	1508	0	1486	63	0
40	B0	662	0	688	23	0
41	B1	731	0	808	35	0
42	B2	598	0	653	33	0
43	BD	2104	0	2182	109	0
44	B3	467	0	523	6	0
45	B4	225	0	229	9	0
46	B5	459	0	477	32	0
47	B6	380	0	390	59	0
48	B7	418	0	467	12	0
49	B8	507	0	576	58	0
50	B9	299	0	323	10	0
51	BC	1718	0	1766	55	0
52	BE	1563	0	1629	91	0
53	BF	1623	0	1677	89	0
54	BG	1474	0	1535	61	0
55	BH	1303	0	1348	59	0
56	BK	936	0	970	67	0
57	BJ	651	0	649	17	0
58	BL	356	0	75	7	0
59	AA	45	0	0	0	0
59	AY	1	0	0	0	0
59	B8	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	BA	88	0	0	0	0
59	BD	1	0	0	0	0
59	BE	1	0	0	0	0
59	BF	1	0	0	0	0
60	AY	32	0	14	5	0
61	AY	4	0	0	1	0
All	All	151831	0	105250	3794	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 15.

All (3794) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2111:C:N3	25:BA:2147:G:N2	1.74	1.36
25:BA:1332:G:N2	25:BA:1609:A:O2'	1.62	1.26
47:B6:40:CYS:SG	47:B6:45:LYS:NZ	1.02	1.24
25:BA:90:U:O2'	25:BA:92:A:OP2	1.54	1.24
25:BA:1332:G:N2	25:BA:1609:A:HO2'	1.30	1.23
25:BA:2394:C:OP1	29:BP:63:PRO:HD2	1.41	1.20
23:AY:404:VAL:HG13	23:AY:405:PRO:HA	1.22	1.20
25:BA:1914:C:O2'	25:BA:1915:U:O5'	1.61	1.18
25:BA:271(H):G:C5'	41:B1:81:LYS:HE2	1.72	1.17
25:BA:271(G):C:O2'	41:B1:81:LYS:CE	1.95	1.14
47:B6:48:VAL:HG23	47:B6:49:HIS:N	1.53	1.14
25:BA:271(H):G:H5'	41:B1:81:LYS:CE	1.78	1.14
25:BA:1048:A:N6	25:BA:1107:G:O6	1.81	1.12
29:BP:7:ARG:HD3	53:BF:188:ARG:HA	1.30	1.11
47:B6:40:CYS:SG	47:B6:45:LYS:CE	2.39	1.09
47:B6:48:VAL:HG23	47:B6:49:HIS:H	1.02	1.09
38:BY:79:CYS:SG	38:BY:80:GLY:N	2.20	1.08
29:BP:48:PRO:O	29:BP:50:ARG:N	1.88	1.05
29:BP:7:ARG:HA	29:BP:7:ARG:HH11	1.14	1.05
47:B6:37:ARG:O	47:B6:48:VAL:O	1.76	1.03
2:AV:76:A:H4'	2:AV:76:A:OP1	1.57	1.03
29:BP:7:ARG:HA	29:BP:7:ARG:NH1	1.72	1.02
25:BA:271(G):C:O2'	41:B1:81:LYS:HE3	1.59	1.02
25:BA:811:U:OP2	29:BP:30:THR:O	1.78	1.02
25:BA:2419:U:O4	49:B8:30:ARG:CZ	2.08	1.01
25:BA:1540:U:H6	25:BA:1540:U:H5'	1.23	1.00
35:BV:24:LYS:HA	35:BV:92:THR:HG23	1.40	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BP:64:LYS:O	29:BP:66:GLY:N	1.95	0.99
1:AA:706:A:O4'	5:AK:29:ILE:HD11	1.63	0.99
1:AA:1054:C:O2	1:AA:1054:C:H3'	1.62	0.98
25:BA:242:G:H5''	49:B8:62:LEU:HD13	1.45	0.98
25:BA:2656:U:H3	25:BA:2665:A:H2	1.09	0.98
47:B6:48:VAL:CG2	47:B6:49:HIS:H	1.77	0.98
25:BA:676:A:H8	25:BA:2069:G:H21	1.05	0.97
25:BA:1100:C:H4'	25:BA:1100:C:OP1	1.63	0.97
17:AD:9:CYS:HA	17:AD:12:CYS:HB2	1.45	0.97
47:B6:47:THR:HG22	47:B6:48:VAL:N	1.76	0.97
1:AA:1502:A:H2	1:AA:1505:G:H1	1.02	0.96
1:AA:90:U:HO2'	1:AA:91:C:H5	1.09	0.96
8:AN:23:ARG:HD2	8:AN:28:GLY:O	1.63	0.96
25:BA:1899:G:H22	25:BA:1902:C:H41	1.09	0.96
27:BN:16:ILE:HD11	27:BN:26:LEU:HD11	1.46	0.96
46:B5:4:HIS:HB3	46:B5:5:PRO:CD	1.96	0.96
23:AY:404:VAL:HG13	23:AY:405:PRO:CA	1.95	0.96
43:BD:30:GLU:HG3	43:BD:63:ARG:NH2	1.81	0.96
25:BA:250:G:OP2	49:B8:13:ARG:NH2	1.98	0.95
47:B6:47:THR:CG2	47:B6:48:VAL:N	2.30	0.95
47:B6:48:VAL:CG2	47:B6:49:HIS:N	2.29	0.95
33:BT:85:LYS:NZ	33:BT:85:LYS:HB3	1.81	0.95
29:BP:56:SER:O	29:BP:58:THR:N	1.97	0.95
50:B9:29:ASN:HD21	50:B9:32:HIS:CE1	1.84	0.95
25:BA:2137:C:H3'	25:BA:2137:C:O2	1.67	0.95
29:BP:17:LYS:O	29:BP:19:VAL:N	1.99	0.95
29:BP:59:LEU:HA	29:BP:61:ARG:NH1	1.81	0.94
7:AM:65:LYS:HA	7:AM:66:LEU:HB2	1.50	0.94
25:BA:1771:C:HO2'	25:BA:1786:A:H8	0.99	0.94
52:BE:129:HIS:O	52:BE:130:GLY:O	1.86	0.94
17:AD:26:CYS:HA	17:AD:31:CYS:HB2	1.46	0.94
27:BN:58:ASP:O	27:BN:60:ILE:N	2.01	0.94
46:B5:50:GLY:O	46:B5:51:TYR:HD1	1.51	0.93
1:AA:159:G:N2	1:AA:162:A:OP2	2.00	0.93
25:BA:243:U:OP1	49:B8:6:THR:HG21	1.68	0.93
25:BA:2200:C:OP2	41:B1:50:ARG:NH2	2.02	0.93
39:BZ:19:ARG:NH1	39:BZ:84:GLU:O	2.01	0.93
23:AY:71:THR:HG22	23:AY:80:ASN:OD1	1.69	0.93
25:BA:1658:C:OP1	52:BE:132:HIS:CE1	2.22	0.93
29:BP:64:LYS:C	29:BP:66:GLY:N	2.25	0.93
25:BA:1779:U:H5	25:BA:1784:A:N7	1.66	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BZ:18:LEU:H	39:BZ:18:LEU:HD12	1.31	0.92
56:BK:109:LYS:HA	56:BK:112:MET:HE3	1.51	0.92
25:BA:807:U:OP2	29:BP:39:LYS:HG3	1.69	0.92
25:BA:1494:A:H3'	25:BA:1494:A:N3	1.84	0.92
25:BA:141:A:C8	25:BA:1408:C:O2'	2.22	0.92
25:BA:271(G):C:O2'	41:B1:81:LYS:NZ	2.02	0.92
1:AA:1321:C:H3'	1:AA:1322:C:H5''	1.49	0.91
4:AJ:34:VAL:HG22	4:AJ:74:ILE:HG22	1.52	0.91
25:BA:1910:G:H1	25:BA:1920:C:H5	1.16	0.91
1:AA:1138:G:O2'	1:AA:1139:G:OP1	1.88	0.91
25:BA:1447:G:O2'	25:BA:1544:A:H8	1.52	0.91
39:BZ:9:TYR:CE1	39:BZ:61:LEU:HD12	2.04	0.91
25:BA:259:G:H21	25:BA:621:A:H8	1.13	0.91
34:BU:91:ASP:OD1	34:BU:96:ALA:N	2.04	0.91
43:BD:2:ALA:O	43:BD:3:VAL:HB	1.71	0.91
25:BA:1538:G:H2'	25:BA:1539:G:H8	1.35	0.90
25:BA:1570:A:O4'	43:BD:38:LYS:HE2	1.70	0.90
15:AB:178:ARG:HG2	15:AB:178:ARG:HH11	1.34	0.90
25:BA:2111:C:C2	25:BA:2147:G:N2	2.38	0.90
43:BD:43:ARG:NH1	43:BD:44:ASN:OD1	2.04	0.90
56:BK:77:LEU:HD12	56:BK:107:ILE:HG23	1.54	0.90
38:BY:76:CYS:SG	38:BY:77:PRO:HD2	2.12	0.90
38:BY:96:ILE:HD12	38:BY:99:CYS:SG	2.12	0.90
34:BU:90:VAL:O	34:BU:92:ARG:N	2.05	0.90
46:B5:4:HIS:HB3	46:B5:5:PRO:HD3	1.52	0.90
1:AA:353:A:H8	1:AA:353:A:H5'	1.34	0.89
16:AC:154:SER:OG	16:AC:155:GLY:N	1.95	0.89
39:BZ:9:TYR:CZ	39:BZ:61:LEU:HD12	2.06	0.89
25:BA:330:A:H2	25:BA:1210:A:H2'	1.37	0.89
31:BR:11:ASN:OD1	31:BR:12:ARG:N	2.05	0.89
14:AT:73:HIS:HB3	14:AT:74:LYS:HG2	1.54	0.89
55:BH:41:MET:SD	55:BH:42:ARG:N	2.45	0.89
17:AD:9:CYS:HA	17:AD:12:CYS:CB	2.02	0.89
25:BA:1496:A:H8	25:BA:1577:C:HO2'	0.92	0.89
25:BA:1155:A:OP2	34:BU:58:ARG:NH1	2.05	0.89
25:BA:2068:U:N3	25:BA:2430:A:H2	1.70	0.89
38:BY:8:LYS:HB2	38:BY:28:LYS:NZ	1.88	0.89
47:B6:41:PRO:HD2	47:B6:46:HIS:H	1.36	0.89
50:B9:27:CYS:SG	50:B9:32:HIS:CD2	2.66	0.89
46:B5:46:CYS:SG	46:B5:47:PRO:N	2.46	0.88
17:AD:31:CYS:O	17:AD:31:CYS:SG	2.32	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:B6:41:PRO:HD2	47:B6:46:HIS:N	1.87	0.88
25:BA:242:G:C5'	49:B8:62:LEU:HD13	2.03	0.88
25:BA:1143:A:OP1	27:BN:25:ARG:NH2	2.07	0.88
25:BA:2068:U:H3	25:BA:2430:A:H2	1.00	0.88
25:BA:2445:G:OP1	53:BF:74:ARG:NH2	2.07	0.88
33:BT:50:ILE:HD11	33:BT:102:ILE:HD11	1.56	0.88
25:BA:2139:C:O2'	25:BA:2140:C:OP2	1.92	0.87
25:BA:993:G:OP1	34:BU:50:ARG:NH2	2.08	0.87
25:BA:1899:G:H22	25:BA:1902:C:N4	1.72	0.87
1:AA:250:A:H4'	1:AA:251:G:O5'	1.74	0.87
27:BN:2:LYS:O	27:BN:4:TYR:CZ	2.27	0.86
46:B5:33:CYS:HB2	46:B5:40:LYS:HE3	1.54	0.86
6:AL:27:LEU:O	6:AL:29:GLY:N	2.07	0.86
11:AQ:66:SER:O	11:AQ:70:ARG:NH1	2.08	0.86
47:B6:47:THR:CG2	47:B6:48:VAL:H	1.88	0.86
1:AA:1004:A:O2'	1:AA:1038:C:O2	1.91	0.86
25:BA:2394:C:OP1	29:BP:63:PRO:CD	2.23	0.86
39:BZ:102:LEU:HD11	39:BZ:124:ILE:HG12	1.56	0.86
1:AA:748:C:H4'	1:AA:749:C:O5'	1.74	0.86
47:B6:16:CYS:O	47:B6:18:ARG:NH2	2.09	0.86
49:B8:61:LEU:HD12	49:B8:62:LEU:HD12	1.58	0.86
43:BD:25:THR:O	43:BD:27:THR:N	2.08	0.86
47:B6:41:PRO:CD	47:B6:46:HIS:H	1.88	0.86
1:AA:975:A:H4'	1:AA:976:G:H5''	1.59	0.85
25:BA:141:A:H8	25:BA:1408:C:O2'	1.59	0.85
1:AA:692:U:OP1	5:AK:124:LYS:NZ	2.08	0.85
25:BA:1689:A:H62	25:BA:1698:A:H2	1.24	0.85
55:BH:19:VAL:HG11	55:BH:43:VAL:O	1.77	0.85
42:B2:22:GLU:HG3	42:B2:64:LEU:HD11	1.57	0.85
17:AD:2:GLY:O	17:AD:4:TYR:N	2.10	0.85
50:B9:27:CYS:SG	50:B9:32:HIS:HD2	1.99	0.85
36:BW:64:MET:O	36:BW:65:LEU:HB2	1.75	0.85
46:B5:50:GLY:O	46:B5:51:TYR:CD1	2.29	0.85
25:BA:1019:U:HO2'	25:BA:1021:A:H2	0.86	0.85
25:BA:1914:C:HO2'	25:BA:1915:U:P	1.98	0.85
25:BA:271(H):G:H5'	41:B1:81:LYS:HE2	0.90	0.84
23:AY:437:THR:HB	23:AY:454:MET:HE3	1.60	0.84
25:BA:1540:U:O2'	25:BA:1541:G:H5'	1.76	0.84
25:BA:2611:U:H5'	25:BA:2611:U:H6	1.42	0.84
29:BP:58:THR:O	29:BP:61:ARG:CZ	2.25	0.84
25:BA:528:A:C2	25:BA:2043:C:H4'	2.14	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AV:27:G:H1	2:AV:43:C:H5	1.21	0.83
4:AJ:23:ILE:HG22	4:AJ:23:ILE:O	1.77	0.83
1:AA:508:C:OP2	17:AD:209:ARG:NH2	2.11	0.83
1:AA:1539:C:H2'	1:AA:1540:U:O4'	1.77	0.83
1:AA:111:G:O6	1:AA:330:C:N4	2.12	0.83
33:BT:29:ARG:HB3	33:BT:30:VAL:HG22	1.59	0.83
33:BT:78:LEU:O	33:BT:79:HIS:CG	2.30	0.83
38:BY:2:ARG:O	38:BY:4:LYS:N	2.10	0.83
29:BP:64:LYS:C	29:BP:66:GLY:H	1.85	0.83
38:BY:76:CYS:SG	38:BY:77:PRO:CD	2.67	0.83
13:AS:44:MET:N	13:AS:44:MET:SD	2.51	0.82
25:BA:2187:G:H5'	25:BA:2188:C:OP2	1.79	0.82
29:BP:7:ARG:CD	53:BF:188:ARG:HA	2.08	0.82
23:AY:428:LEU:HD22	23:AY:451:ILE:HD11	1.61	0.82
25:BA:1447:G:O2'	25:BA:1544:A:C8	2.30	0.82
1:AA:1054:C:O2'	1:AA:1055:A:H5''	1.79	0.82
17:AD:8:VAL:O	17:AD:10:ARG:N	2.13	0.82
1:AA:1189:C:OP1	4:AJ:51:ARG:NH2	2.11	0.82
17:AD:30:LYS:O	17:AD:32:ALA:N	2.13	0.82
9:AO:26:GLU:OE2	9:AO:77:ARG:NH1	2.12	0.81
25:BA:2305:A:C2	25:BA:2306:C:H1'	2.15	0.81
43:BD:44:ASN:HB2	43:BD:48:ARG:O	1.79	0.81
25:BA:1022:G:H22	25:BA:1142(A):A:H2	1.24	0.81
35:BV:64:HIS:ND1	35:BV:92:THR:HG22	1.94	0.81
25:BA:607:U:OP1	53:BF:102:PRO:HA	1.80	0.81
25:BA:714:U:O2'	25:BA:716:A:N7	2.12	0.81
38:BY:97:ARG:O	38:BY:98:VAL:HB	1.78	0.81
17:AD:8:VAL:C	17:AD:10:ARG:H	1.88	0.81
1:AA:1008:C:O2	1:AA:1021:G:N2	2.13	0.81
25:BA:1169:G:N2	25:BA:1181:C:O2	2.14	0.81
25:BA:1980:G:O2'	25:BA:1982:C:OP2	1.98	0.81
29:BP:6:LEU:HG	29:BP:8:PRO:O	1.81	0.81
29:BP:47:ASP:HB3	29:BP:48:PRO:O	1.81	0.81
16:AC:180:ALA:O	16:AC:205:GLY:O	1.99	0.80
1:AA:1126:U:O2	1:AA:1280:A:H2'	1.80	0.80
38:BY:8:LYS:HB2	38:BY:28:LYS:CE	2.11	0.80
1:AA:1054:C:O2	1:AA:1054:C:C3'	2.28	0.80
29:BP:58:THR:O	29:BP:61:ARG:NE	2.14	0.80
25:BA:1047:G:OP2	25:BA:1047:G:H4'	1.79	0.80
25:BA:1048:A:H4'	25:BA:1049:C:OP1	1.82	0.80
25:BA:1782:C:H1'	25:BA:2609:U:H5''	1.64	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:BY:17:SER:OG	38:BY:18:GLY:N	2.09	0.80
47:B6:20:ASN:O	47:B6:21:TYR:CG	2.35	0.80
1:AA:1117:G:O3'	22:AI:104:ARG:HD3	1.82	0.80
25:BA:1093:G:OP2	25:BA:1093:G:H8	1.65	0.80
6:AL:117:ARG:HD2	6:AL:122:THR:HG22	1.64	0.80
25:BA:1915:U:H5''	25:BA:1916:A:OP2	1.82	0.79
39:BZ:151:HIS:HB2	39:BZ:170:THR:HA	1.64	0.79
25:BA:1019:U:O2'	25:BA:1021:A:H2	1.64	0.79
26:BB:8:U:O3'	32:BS:25:ARG:NH2	2.15	0.79
25:BA:2517:C:O2'	25:BA:2542:A:N1	2.14	0.79
33:BT:89:VAL:C	33:BT:91:ARG:H	1.91	0.79
25:BA:2808:U:O2	25:BA:2892:A:N6	2.16	0.78
57:BJ:26:ALA:HA	57:BJ:84:ALA:HA	1.65	0.78
1:AA:1134:G:C5	1:AA:1135:U:C5	2.71	0.78
15:AB:178:ARG:HH11	15:AB:178:ARG:CG	1.95	0.78
25:BA:860:U:H5	25:BA:917:A:N7	1.82	0.78
47:B6:12:GLU:HG3	47:B6:23:THR:HG22	1.64	0.78
2:AV:76:A:OP1	2:AV:76:A:C4'	2.31	0.78
25:BA:271(G):C:HO2'	41:B1:81:LYS:HE3	1.49	0.78
1:AA:1452:C:H4'	1:AA:1456:G:C2	2.19	0.78
25:BA:662:G:OP1	29:BP:18:ARG:HD2	1.84	0.78
25:BA:956:G:OP2	30:BQ:14:ARG:NH2	2.17	0.78
28:BO:4:PRO:O	28:BO:5:GLN:HB2	1.83	0.78
53:BF:24:LEU:HB3	53:BF:25:PRO:HD2	1.64	0.78
43:BD:44:ASN:HB3	43:BD:49:ILE:HA	1.66	0.77
55:BH:121:ILE:HD11	55:BH:140:LYS:HB3	1.66	0.77
13:AS:40:ILE:HG21	13:AS:62:ILE:HD11	1.66	0.77
25:BA:243:U:OP1	49:B8:6:THR:CG2	2.31	0.77
25:BA:1502:C:C6	25:BA:1502:C:H5''	2.20	0.77
43:BD:44:ASN:CB	43:BD:49:ILE:HA	2.15	0.77
25:BA:1022:G:N2	25:BA:1142(A):A:C2	2.50	0.77
23:AY:15:ILE:HA	23:AY:103:GLY:O	1.85	0.77
40:B0:23:VAL:HG22	40:B0:38:VAL:HG22	1.65	0.77
5:AK:84:VAL:HG11	5:AK:95:ILE:HD11	1.66	0.77
25:BA:881:G:N1	25:BA:895:U:O2	2.17	0.77
29:BP:84:ASN:HA	29:BP:115:LEU:O	1.84	0.77
35:BV:17:GLY:HA2	35:BV:96:ILE:O	1.84	0.77
25:BA:1539:G:C2'	25:BA:1540:U:H5''	2.15	0.77
33:BT:38:ASN:ND2	33:BT:40:THR:OG1	2.17	0.77
25:BA:2632:A:N3	52:BE:61:ARG:NH1	2.33	0.76
1:AA:254:G:OP1	11:AQ:67:LYS:O	2.02	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1368:G:OP2	22:AI:112:LYS:HD3	1.85	0.76
27:BN:56:ASN:C	27:BN:57:ALA:O	2.27	0.76
1:AA:426:G:OP1	17:AD:36:ARG:NH1	2.17	0.76
25:BA:1300:U:H4'	25:BA:1301:A:H5'	1.68	0.76
43:BD:25:THR:O	43:BD:26:LYS:C	2.28	0.76
43:BD:181:GLU:HA	43:BD:272:ALA:HB3	1.68	0.76
52:BE:117:MET:O	52:BE:118:LYS:HB2	1.84	0.76
25:BA:1058:G:H21	56:BK:126:MET:HE3	1.50	0.76
43:BD:137:PRO:O	43:BD:140:THR:OG1	2.03	0.76
52:BE:57:LYS:HD3	52:BE:57:LYS:N	2.01	0.76
25:BA:1063:G:N1	25:BA:1075:C:N4	2.34	0.76
23:AY:205:TYR:O	23:AY:209:ALA:N	2.18	0.76
35:BV:19:LYS:HG3	35:BV:20:LEU:N	1.99	0.76
43:BD:69:ARG:NH2	43:BD:128:GLY:O	2.19	0.76
55:BH:41:MET:CE	55:BH:43:VAL:HG13	2.16	0.76
1:AA:353:A:H5'	1:AA:353:A:C8	2.20	0.76
33:BT:85:LYS:HB3	33:BT:85:LYS:HZ2	1.49	0.76
25:BA:2287:A:N1	25:BA:2346:A:C2	2.54	0.75
46:B5:40:LYS:HE2	46:B5:46:CYS:HB3	1.66	0.75
25:BA:2392:A:H2	25:BA:2424:C:H42	1.31	0.75
1:AA:673:G:H2'	1:AA:674:G:C8	2.21	0.75
1:AA:632:A:H3'	1:AA:633:G:H5''	1.68	0.75
39:BZ:72:ARG:NH2	39:BZ:97:GLU:O	2.18	0.75
1:AA:1217:C:OP1	8:AN:9:LYS:NZ	2.19	0.75
25:BA:1089:G:H4'	25:BA:1090:U:OP1	1.85	0.75
47:B6:48:VAL:O	47:B6:49:HIS:HB2	1.87	0.75
15:AB:54:THR:HG21	15:AB:201:ILE:HD11	1.69	0.75
25:BA:2420:C:P	49:B8:33:ASN:O	2.45	0.75
11:AQ:95:TYR:HA	11:AQ:98:LEU:HD12	1.67	0.74
15:AB:17:PHE:O	15:AB:18:GLY:O	2.06	0.74
15:AB:67:THR:HG21	15:AB:155:LEU:HD21	1.69	0.74
25:BA:1540:U:H5'	25:BA:1540:U:C6	2.15	0.74
56:BK:30:HIS:HA	56:BK:59:ILE:HD12	1.69	0.74
1:AA:390:C:O3'	10:AP:28:ARG:NH2	2.20	0.74
1:AA:1138:G:H1'	1:AA:1139:G:OP1	1.88	0.74
25:BA:2068:U:N3	25:BA:2430:A:C2	2.47	0.74
43:BD:210:GLY:O	43:BD:212:SER:N	2.20	0.74
56:BK:99:ILE:HD12	56:BK:103:GLN:HB3	1.69	0.74
2:AV:34:G:H2'	2:AV:35:A:H5''	1.69	0.74
25:BA:943:U:OP2	29:BP:38:GLN:CD	2.30	0.74
49:B8:61:LEU:CD1	49:B8:62:LEU:HD12	2.17	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:528:A:N1	25:BA:2042:A:H2'	2.03	0.74
53:BF:22:ALA:O	53:BF:26:ALA:HB2	1.87	0.74
6:AL:26:ALA:O	6:AL:27:LEU:O	2.05	0.74
25:BA:774:A:O2'	25:BA:775:G:OP2	2.04	0.74
4:AJ:8:LEU:HD23	4:AJ:96:ILE:HG22	1.70	0.74
29:BP:47:ASP:HB3	29:BP:48:PRO:C	2.13	0.74
55:BH:41:MET:SD	55:BH:53:GLU:O	2.46	0.74
56:BK:106:GLU:HA	56:BK:109:LYS:HD3	1.68	0.74
39:BZ:151:HIS:CB	39:BZ:170:THR:HA	2.18	0.73
53:BF:167:ALA:HB1	53:BF:173:VAL:HG11	1.67	0.73
56:BK:100:THR:HA	56:BK:139:VAL:HB	1.68	0.73
9:AO:17:ARG:HH11	9:AO:17:ARG:HG3	1.54	0.73
41:B1:51:VAL:O	41:B1:57:GLU:O	2.06	0.73
23:AY:210:ARG:O	23:AY:212:TYR:N	2.18	0.73
25:BA:2849:U:OP2	33:BT:95:ARG:NH1	2.22	0.73
4:AJ:49:VAL:HG22	8:AN:41:ARG:HB2	1.69	0.73
25:BA:956:G:H4'	30:BQ:83:MET:HE1	1.70	0.73
25:BA:1091:G:O6	25:BA:1100:C:N4	2.15	0.73
31:BR:87:TYR:O	31:BR:89:ASP:N	2.22	0.73
6:AL:8:ASN:O	6:AL:12:ARG:HG3	1.89	0.73
25:BA:1899:G:N2	25:BA:1902:C:H5	1.86	0.73
52:BE:60:ASN:HD22	52:BE:60:ASN:N	1.85	0.73
23:AY:264:LEU:HB2	60:AY:702:GCP:C6	2.19	0.72
25:BA:1899:G:N2	25:BA:1902:C:C5	2.57	0.72
52:BE:129:HIS:O	52:BE:130:GLY:C	2.31	0.72
1:AA:1446:U:O2'	1:AA:1447:A:H3'	1.89	0.72
25:BA:1786:A:C2	25:BA:2606:C:H1'	2.24	0.72
25:BA:2079:U:OP1	41:B1:21:ARG:NH1	2.19	0.72
1:AA:1305:G:OP2	24:AU:2:GLY:N	2.22	0.72
29:BP:16:ARG:C	29:BP:16:ARG:HD3	2.14	0.72
38:BY:74:PRO:O	38:BY:80:GLY:HA3	1.88	0.72
55:BH:89:ILE:C	55:BH:89:ILE:HD12	2.15	0.72
25:BA:1064:C:H2'	25:BA:1065:U:O4'	1.89	0.72
43:BD:3:VAL:HG13	43:BD:17:THR:HB	1.70	0.72
2:AV:74:C:O2'	2:AV:75:C:OP2	2.06	0.72
25:BA:2810:A:H2'	52:BE:61:ARG:NH2	2.05	0.72
43:BD:10:THR:OG1	43:BD:13:ARG:HB2	1.89	0.72
7:AM:89:GLY:C	7:AM:90:LEU:O	2.31	0.72
33:BT:7:ILE:HG23	52:BE:181:LEU:HD21	1.72	0.72
29:BP:51:PHE:HB3	29:BP:52:GLU:OE2	1.89	0.71
9:AO:39:LEU:CD1	9:AO:56:LEU:HB2	2.20	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AB:115:LEU:HD13	15:AB:145:LEU:HB3	1.71	0.71
23:AY:679:VAL:HB	23:AY:680:PRO:CD	2.20	0.71
25:BA:2137:C:O2	25:BA:2137:C:C3'	2.37	0.71
25:BA:1899:G:N2	25:BA:1902:C:H41	1.85	0.71
33:BT:89:VAL:HG11	33:BT:91:ARG:HG3	1.72	0.71
38:BY:26:LYS:O	38:BY:27:VAL:O	2.07	0.71
39:BZ:10:ARG:NH2	39:BZ:26:GLY:O	2.23	0.71
54:BG:96:ARG:O	54:BG:99:MET:N	2.21	0.71
33:BT:23:ARG:O	33:BT:25:GLY:N	2.23	0.71
51:BC:131:LEU:HB3	51:BC:137:LEU:HD23	1.73	0.71
1:AA:633:G:H5''	1:AA:633:G:H8	1.56	0.71
6:AL:53:ARG:HG2	6:AL:93:LEU:HD11	1.73	0.71
12:AR:22:VAL:O	12:AR:25:THR:HB	1.91	0.71
25:BA:2139:C:O2'	25:BA:2140:C:P	2.48	0.71
25:BA:2180:U:C6	25:BA:2180:U:C5'	2.74	0.71
56:BK:81:ALA:HB1	56:BK:99:ILE:HD11	1.73	0.71
56:BK:99:ILE:HG23	56:BK:103:GLN:HB2	1.72	0.71
28:BO:20:MET:HE3	28:BO:44:LYS:HE2	1.73	0.71
34:BU:92:ARG:NH1	34:BU:94:ASN:HD22	1.89	0.71
25:BA:259:G:N2	25:BA:621:A:H8	1.86	0.71
25:BA:1538:G:H2'	25:BA:1539:G:C8	2.25	0.71
34:BU:92:ARG:O	34:BU:94:ASN:N	2.24	0.71
47:B6:20:ASN:C	47:B6:21:TYR:CG	2.69	0.71
53:BF:66:PRO:O	53:BF:67:GLN:CB	2.39	0.71
25:BA:1396:U:O2	25:BA:1396:U:H2'	1.89	0.70
1:AA:953:G:H5'	1:AA:965:A:H61	1.56	0.70
25:BA:1847:A:N3	25:BA:1847:A:H2'	2.06	0.70
25:BA:1887:C:H2'	25:BA:1888:G:H5'	1.73	0.70
25:BA:613:G:H5''	25:BA:613:G:H8	1.56	0.70
25:BA:2317:C:H2'	25:BA:2318:G:H5'	1.72	0.70
38:BY:39:VAL:C	38:BY:40:GLU:OE1	2.34	0.70
25:BA:271(J):C:H5'	25:BA:271(K):U:OP2	1.90	0.70
38:BY:8:LYS:HB2	38:BY:28:LYS:HZ3	1.57	0.70
25:BA:2646:C:OP2	25:BA:2732:G:O2'	2.08	0.70
51:BC:42:GLU:CG	51:BC:215:THR:HG23	2.21	0.70
1:AA:1144:G:O2'	1:AA:1145:C:H5'	1.92	0.70
1:AA:1533:C:H2'	1:AA:1534:A:O4'	1.92	0.70
23:AY:25:LYS:NZ	60:AY:702:GCP:O3G	2.25	0.70
25:BA:662:G:OP1	29:BP:18:ARG:NH1	2.24	0.70
42:B2:42:GLY:O	42:B2:44:LEU:N	2.25	0.70
13:AS:42:PRO:O	13:AS:44:MET:SD	2.50	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:AE:6:PHE:CE1	18:AE:66:MET:HE1	2.27	0.70
23:AY:212:TYR:HA	23:AY:215:LYS:HB3	1.72	0.70
25:BA:330:A:C2	25:BA:1210:A:H2'	2.25	0.70
2:AV:33:U:H5	2:AV:36:A:OP2	1.75	0.70
33:BT:16:ARG:NH2	33:BT:82:LEU:O	2.21	0.70
1:AA:1136:U:H3'	1:AA:1137:C:H5''	1.74	0.69
25:BA:2317:C:C2'	25:BA:2318:G:H5'	2.22	0.69
47:B6:41:PRO:HD3	47:B6:46:HIS:HA	1.74	0.69
1:AA:975:A:H5'	1:AA:975:A:H8	1.56	0.69
25:BA:1079:C:H41	25:BA:1088:A:H5''	1.56	0.69
25:BA:2683:C:OP1	33:BT:53:ARG:NH2	2.25	0.69
1:AA:1133:G:C8	1:AA:1133:G:H3'	2.27	0.69
14:AT:73:HIS:O	14:AT:76:ALA:HB3	1.92	0.69
25:BA:1092:C:H2'	25:BA:1093:G:H5'	1.75	0.69
43:BD:221:VAL:HG22	43:BD:226:MET:HE2	1.73	0.69
47:B6:47:THR:HG23	47:B6:48:VAL:H	1.54	0.69
1:AA:1392:G:N2	1:AA:1502:A:H8	1.90	0.69
23:AY:162:VAL:HG21	23:AY:255:ILE:HG12	1.74	0.69
51:BC:185:LEU:O	51:BC:188:ASN:N	2.25	0.69
23:AY:61:ARG:NH2	23:AY:460:GLU:OE2	2.25	0.69
10:AP:8:ARG:HG2	10:AP:8:ARG:HH11	1.58	0.69
1:AA:460:G:O6	1:AA:470:C:H5'	1.93	0.69
1:AA:979:C:H2'	1:AA:980:C:H5'	1.73	0.69
25:BA:1100:C:C5'	25:BA:1100:C:H6	2.06	0.69
25:BA:2167:U:H3	25:BA:2171:A:H2	1.41	0.69
37:BX:11:PRO:HB3	37:BX:92:LEU:HD21	1.75	0.69
45:B4:60:GLU:O	54:BG:113:ARG:NH2	2.26	0.69
7:AM:90:LEU:O	7:AM:92:HIS:N	2.26	0.69
23:AY:19:ALA:HB3	23:AY:25:LYS:HE3	1.75	0.69
17:AD:25:ARG:C	17:AD:27:TYR:H	2.00	0.69
25:BA:587:C:OP2	29:BP:33:ARG:NH2	2.26	0.69
25:BA:1918:A:HO2'	25:BA:1919:A:H2	1.38	0.69
27:BN:2:LYS:O	27:BN:4:TYR:CE1	2.45	0.69
29:BP:7:ARG:HB2	29:BP:8:PRO:HD2	1.75	0.69
1:AA:62:U:H2'	1:AA:63:C:H5''	1.75	0.68
1:AA:1138:G:C2'	1:AA:1139:G:OP1	2.41	0.68
15:AB:195:ASP:O	21:AH:68:ARG:NH2	2.26	0.68
25:BA:1093:G:OP2	25:BA:1093:G:C8	2.46	0.68
26:BB:50:G:OP1	32:BS:63:THR:HG23	1.93	0.68
46:B5:46:CYS:SG	46:B5:47:PRO:CD	2.81	0.68
25:BA:2476:A:N1	25:BA:2477:C:C6	2.61	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BO:88:ASN:C	28:BO:88:ASN:HD22	2.01	0.68
51:BC:42:GLU:HG3	51:BC:215:THR:HG23	1.75	0.68
1:AA:1293:G:H8	1:AA:1293:G:H5''	1.58	0.68
40:B0:43:THR:HG23	40:B0:43:THR:O	1.91	0.68
2:AV:34:G:C2'	2:AV:35:A:H5''	2.23	0.68
15:AB:88:ALA:HB2	15:AB:219:VAL:HG13	1.75	0.68
27:BN:46:VAL:O	27:BN:47:ALA:HB3	1.92	0.68
1:AA:1243:C:OP2	24:AU:10:ARG:NH2	2.27	0.68
5:AK:61:ALA:HB1	5:AK:94:ALA:HB2	1.76	0.68
25:BA:1266:G:O5'	36:BW:15:ARG:NH2	2.26	0.68
25:BA:1496:A:H8	25:BA:1577:C:O2'	1.71	0.68
52:BE:64:LYS:O	52:BE:73:GLU:OE1	2.11	0.68
55:BH:175:LYS:N	55:BH:176:ALA:HB2	2.08	0.68
1:AA:530:G:O2'	1:AA:531:U:OP1	2.10	0.68
25:BA:9:U:C5	25:BA:2629:A:N6	2.62	0.68
27:BN:3:THR:O	27:BN:5:VAL:HG12	1.93	0.68
56:BK:4:VAL:HG12	56:BK:5:VAL:H	1.59	0.68
29:BP:51:PHE:CB	29:BP:52:GLU:HG2	2.24	0.68
43:BD:223:GLY:C	43:BD:224:ALA:O	2.33	0.68
2:AV:73:A:H2'	2:AV:74:C:H5'	1.76	0.68
25:BA:847:U:OP2	25:BA:928:G:O6	2.11	0.68
25:BA:1502:C:H5''	25:BA:1502:C:H6	1.56	0.68
14:AT:73:HIS:CB	14:AT:74:LYS:HG2	2.23	0.67
25:BA:684:G:OP1	48:B7:16:HIS:HD2	1.76	0.67
33:BT:30:VAL:HG21	33:BT:84:GLN:HG3	1.74	0.67
17:AD:11:LEU:C	17:AD:13:ARG:N	2.51	0.67
25:BA:271(H):G:C4'	41:B1:81:LYS:HE2	2.25	0.67
35:BV:47:VAL:O	35:BV:49:THR:O	2.12	0.67
25:BA:2287:A:N1	25:BA:2346:A:H2	1.92	0.67
38:BY:7:VAL:HB	38:BY:8:LYS:CE	2.24	0.67
56:BK:57:ILE:HA	56:BK:66:THR:O	1.94	0.67
1:AA:17:U:H2'	1:AA:18:C:C6	2.28	0.67
7:AM:97:PRO:HA	7:AM:110:ARG:HD3	1.76	0.67
23:AY:255:ILE:HG23	23:AY:257:PRO:HD3	1.77	0.67
25:BA:2632:A:O2'	52:BE:61:ARG:NH2	2.27	0.67
29:BP:9:ASN:HA	29:BP:11:GLY:H	1.60	0.67
30:BQ:97:VAL:HG11	30:BQ:103:MET:HE3	1.76	0.67
38:BY:39:VAL:HG12	38:BY:40:GLU:H	1.59	0.67
1:AA:100:C:H2'	1:AA:101:A:C8	2.29	0.67
25:BA:517:C:OP1	46:B5:16:ARG:NH2	2.28	0.67
25:BA:2506:U:C6	25:BA:2506:U:H5'	2.30	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:BJ:34:ALA:HA	57:BJ:37:ALA:HB3	1.75	0.67
1:AA:1138:G:C1'	1:AA:1139:G:OP1	2.42	0.67
23:AY:94:VAL:O	23:AY:96:ARG:N	2.28	0.67
23:AY:404:VAL:CG1	23:AY:405:PRO:HA	2.15	0.67
25:BA:1076:C:O2'	25:BA:1077:A:O5'	2.12	0.67
25:BA:2439:A:H5'	25:BA:2439:A:C8	2.29	0.67
51:BC:66:HIS:CD2	51:BC:184:LYS:HG3	2.30	0.67
54:BG:54:GLU:HA	54:BG:57:ALA:HB3	1.77	0.67
25:BA:1053:C:H2'	25:BA:1054:A:H5''	1.75	0.67
34:BU:65:ILE:HD11	34:BU:93:LYS:HA	1.76	0.67
35:BV:21:ARG:O	35:BV:22:VAL:HG13	1.95	0.67
36:BW:73:ALA:HB3	36:BW:106:ILE:HG12	1.75	0.67
25:BA:142:A:H8	25:BA:1595:G:H21	1.44	0.66
25:BA:1858:G:O2'	25:BA:1883:G:N2	2.26	0.66
26:BB:20:C:H2'	26:BB:21:G:H5'	1.75	0.66
25:BA:2681:C:H5	25:BA:2725:A:H62	1.41	0.66
25:BA:2850:A:OP2	25:BA:2866:U:H5	1.77	0.66
56:BK:6:ALA:HB3	56:BK:59:ILE:HG22	1.77	0.66
1:AA:376:G:OP2	10:AP:67:THR:HG21	1.95	0.66
16:AC:154:SER:O	16:AC:157:ILE:HD11	1.95	0.66
34:BU:90:VAL:O	34:BU:91:ASP:C	2.37	0.66
55:BH:41:MET:HE3	55:BH:43:VAL:HG13	1.77	0.66
23:AY:357:ARG:NH1	23:AY:373:ASP:OD2	2.28	0.66
39:BZ:18:LEU:H	39:BZ:18:LEU:CD1	2.08	0.66
1:AA:1101:A:H4'	1:AA:1102:A:O5'	1.96	0.66
1:AA:1143:G:H5''	1:AA:1144:G:OP2	1.94	0.66
25:BA:943:U:OP2	29:BP:38:GLN:NE2	2.29	0.66
53:BF:65:TRP:CZ3	53:BF:73:ALA:O	2.49	0.66
56:BK:75:SER:O	56:BK:79:ARG:HG3	1.96	0.66
25:BA:1019:U:H3	25:BA:1142(A):A:H62	1.44	0.66
27:BN:126:PRO:O	27:BN:127:ASP:O	2.13	0.66
30:BQ:82:ARG:HH22	40:B0:2:ALA:HB1	1.61	0.66
15:AB:33:TYR:HB3	15:AB:41:ILE:HG22	1.78	0.66
15:AB:67:THR:HG21	15:AB:155:LEU:CD2	2.26	0.66
25:BA:1779:U:C5	25:BA:1784:A:N7	2.57	0.66
25:BA:1887:C:C2'	25:BA:1888:G:H5'	2.25	0.66
55:BH:83:TYR:HB3	55:BH:134:SER:HA	1.78	0.66
1:AA:79:G:O2'	1:AA:80:G:O5'	2.14	0.65
17:AD:30:LYS:C	17:AD:32:ALA:H	2.03	0.65
25:BA:661:C:O2'	29:BP:16:ARG:O	2.10	0.65
33:BT:28:VAL:HG12	33:BT:29:ARG:HD3	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BW:5:ALA:HB3	36:BW:50:VAL:HG23	1.76	0.65
56:BK:17:ALA:HB3	56:BK:38:VAL:HG22	1.78	0.65
1:AA:975:A:H5'	1:AA:975:A:C8	2.31	0.65
14:AT:100:ILE:O	14:AT:102:GLY:N	2.29	0.65
29:BP:51:PHE:O	29:BP:52:GLU:HB2	1.95	0.65
46:B5:51:TYR:HB3	46:B5:52:TYR:O	1.97	0.65
25:BA:252:G:OP2	29:BP:50:ARG:NH1	2.24	0.65
43:BD:70:TRP:CH2	43:BD:150:LYS:HA	2.31	0.65
1:AA:36:C:O2'	1:AA:501:C:OP1	2.12	0.65
1:AA:328:C:O2	1:AA:328:C:H2'	1.97	0.65
15:AB:28:PHE:CD1	15:AB:190:THR:HA	2.31	0.65
17:AD:10:ARG:CG	17:AD:10:ARG:O	2.43	0.65
25:BA:71:A:H5'	25:BA:71:A:C8	2.31	0.65
29:BP:7:ARG:HB2	29:BP:8:PRO:CD	2.27	0.65
33:BT:50:ILE:CD1	33:BT:102:ILE:HD11	2.27	0.65
39:BZ:94:GLU:O	39:BZ:130:PRO:HD3	1.97	0.65
1:AA:1149:C:OP1	22:AI:9:ARG:NH1	2.26	0.65
15:AB:17:PHE:HB3	15:AB:44:LEU:HD21	1.78	0.65
33:BT:54:ARG:HA	33:BT:59:THR:HB	1.79	0.65
47:B6:41:PRO:CD	47:B6:46:HIS:N	2.55	0.65
14:AT:53:LEU:HB2	14:AT:100:ILE:CG2	2.27	0.65
25:BA:1046:A:N7	57:BJ:5:ALA:HB3	2.11	0.65
25:BA:1962:C:O2'	25:BA:1964:G:OP2	2.12	0.65
29:BP:55:ARG:HG2	29:BP:56:SER:H	1.60	0.65
47:B6:19:ARG:HG3	47:B6:20:ASN:N	2.09	0.65
49:B8:63:PRO:O	49:B8:64:TYR:O	2.12	0.65
53:BF:66:PRO:O	53:BF:67:GLN:HB3	1.97	0.65
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.12	0.65
1:AA:1307:U:OP1	7:AM:101:GLN:OE1	2.14	0.65
12:AR:32:ARG:HA	12:AR:69:THR:HG21	1.77	0.65
22:AI:17:VAL:HG22	22:AI:63:ILE:HG12	1.77	0.65
4:AJ:16:LEU:HD13	4:AJ:70:ARG:HG2	1.79	0.65
14:AT:104:LEU:HD23	14:AT:104:LEU:C	2.22	0.65
25:BA:1956:U:H1'	25:BA:2552:U:OP1	1.96	0.65
25:BA:2602:A:OP2	25:BA:2602:A:H4'	1.96	0.65
33:BT:13:ARG:NH1	33:BT:13:ARG:HA	2.11	0.65
1:AA:1004:A:OP1	1:AA:1024:G:N2	2.30	0.65
25:BA:1899:G:H21	25:BA:1902:C:H5	1.45	0.65
25:BA:896:A:C8	39:BZ:146:ILE:HD13	2.32	0.65
25:BA:1141:U:OP2	27:BN:63:THR:OG1	2.15	0.65
25:BA:2420:C:OP2	49:B8:33:ASN:O	2.15	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2787:C:O2	52:BE:61:ARG:NH1	2.30	0.65
52:BE:1:MET:HB3	52:BE:200:GLU:OE1	1.96	0.65
52:BE:132:HIS:CD2	52:BE:135:HIS:CE1	2.84	0.65
23:AY:681:LYS:C	23:AY:684:GLN:HE22	2.05	0.64
42:B2:47:ASN:O	42:B2:49:LYS:N	2.30	0.64
43:BD:270:ILE:C	43:BD:271:ILE:HG13	2.21	0.64
12:AR:26:LEU:O	19:AF:100:ASN:ND2	2.30	0.64
23:AY:603:GLU:O	23:AY:605:ILE:HD12	1.96	0.64
33:BT:78:LEU:O	33:BT:79:HIS:ND1	2.30	0.64
53:BF:28:ILE:HD13	53:BF:28:ILE:H	1.62	0.64
4:AJ:58:ASP:O	4:AJ:59:SER:C	2.40	0.64
25:BA:548:A:O2'	25:BA:549:G:OP1	2.13	0.64
47:B6:11:LEU:HD22	47:B6:12:GLU:N	2.11	0.64
23:AY:122:TRP:CD2	23:AY:157:LEU:HD12	2.33	0.64
1:AA:975:A:H4'	1:AA:976:G:C5'	2.26	0.64
25:BA:9:U:C4	25:BA:2629:A:N6	2.65	0.64
29:BP:85:LEU:HD23	29:BP:85:LEU:H	1.62	0.64
33:BT:27:THR:O	33:BT:28:VAL:HG23	1.98	0.64
43:BD:24:ILE:O	43:BD:26:LYS:N	2.31	0.64
1:AA:1013:G:N2	1:AA:1015:A:H3'	2.12	0.64
1:AA:1464:G:OP2	33:BT:111:ARG:NH2	2.31	0.64
8:AN:23:ARG:CD	8:AN:28:GLY:O	2.43	0.64
25:BA:118:A:N3	25:BA:178:G:H1'	2.12	0.64
25:BA:250:G:P	49:B8:13:ARG:HH22	2.21	0.64
25:BA:860:U:C5	25:BA:917:A:N7	2.65	0.64
40:B0:36:ILE:C	40:B0:36:ILE:HD12	2.22	0.64
43:BD:209:ALA:C	43:BD:210:GLY:O	2.37	0.64
56:BK:42:ASN:O	56:BK:46:ALA:HB2	1.98	0.64
1:AA:542:G:OP1	17:AD:10:ARG:NH2	2.29	0.64
25:BA:1100:C:C5'	25:BA:1100:C:C6	2.81	0.64
43:BD:11:PRO:O	43:BD:13:ARG:N	2.29	0.64
54:BG:124:SER:HB2	54:BG:131:TYR:CE1	2.33	0.64
1:AA:737:A:H1'	19:AF:73:ASN:OD1	1.98	0.64
29:BP:48:PRO:O	29:BP:49:ARG:C	2.40	0.64
15:AB:97:TRP:CZ3	15:AB:176:GLU:OE2	2.50	0.64
23:AY:272:LEU:O	23:AY:276:VAL:HG23	1.97	0.64
25:BA:1458:C:H4'	25:BA:1459:G:O5'	1.97	0.64
27:BN:3:THR:O	27:BN:5:VAL:N	2.31	0.64
29:BP:136:GLU:O	29:BP:139:LYS:N	2.31	0.64
30:BQ:12:GLN:HG2	30:BQ:73:PRO:HD2	1.80	0.64
32:BS:52:SER:HB2	32:BS:55:ALA:HB3	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:BC:119:VAL:HB	51:BC:123:VAL:HG23	1.79	0.64
52:BE:77:ILE:HG22	52:BE:78:LEU:H	1.62	0.64
43:BD:13:ARG:HD2	43:BD:16:MET:HE3	1.80	0.63
52:BE:70:ALA:O	52:BE:72:VAL:N	2.31	0.63
1:AA:1323:G:H2'	1:AA:1324:A:C8	2.33	0.63
4:AJ:23:ILE:O	4:AJ:23:ILE:CG2	2.46	0.63
33:BT:85:LYS:HB3	33:BT:85:LYS:HZ3	1.63	0.63
25:BA:1538:G:C4	25:BA:1539:G:C8	2.87	0.63
13:AS:40:ILE:CG2	13:AS:62:ILE:HD11	2.28	0.63
33:BT:27:THR:HA	33:BT:87:ASP:HB2	1.81	0.63
1:AA:472:A:H2'	1:AA:473:G:O4'	1.99	0.63
1:AA:1277:C:O2'	1:AA:1279:A:H8	1.82	0.63
25:BA:2611:U:H5'	25:BA:2611:U:C6	2.31	0.63
41:B1:52:ARG:O	41:B1:56:GLN:O	2.15	0.63
1:AA:974:A:OP2	8:AN:41:ARG:NH1	2.32	0.63
33:BT:28:VAL:O	33:BT:29:ARG:CB	2.45	0.63
14:AT:36:LEU:HD12	14:AT:55:ILE:HG23	1.80	0.63
34:BU:88:ILE:HD13	34:BU:109:LEU:HD22	1.81	0.63
47:B6:26:ASN:ND2	47:B6:32:ASN:OD1	2.32	0.63
1:AA:1075:C:OP1	15:AB:179:LYS:NZ	2.26	0.63
25:BA:90:U:O2'	25:BA:92:A:P	2.57	0.63
25:BA:1407:C:C6	25:BA:1407:C:H5''	2.32	0.63
25:BA:2517:C:O2'	25:BA:2542:A:C2	2.48	0.63
26:BB:45:A:OP2	54:BG:96:ARG:NH2	2.32	0.63
30:BQ:16:ARG:C	30:BQ:17:LEU:HD23	2.24	0.63
33:BT:93:ARG:HG3	33:BT:93:ARG:HH11	1.63	0.63
43:BD:27:THR:CG2	43:BD:83:GLU:HB3	2.28	0.63
1:AA:509:A:H5'	17:AD:55:ALA:HB2	1.79	0.63
23:AY:616:TYR:OH	23:AY:666:ARG:NH1	2.32	0.63
25:BA:1494:A:H2'	25:BA:1495:A:H5''	1.81	0.63
33:BT:89:VAL:CG1	33:BT:91:ARG:HG3	2.28	0.63
1:AA:1452:C:H4'	1:AA:1456:G:N2	2.13	0.62
25:BA:1539:G:C3'	25:BA:1540:U:H5''	2.29	0.62
28:BO:4:PRO:O	28:BO:5:GLN:CB	2.47	0.62
33:BT:106:SER:C	33:BT:107:ASP:OD1	2.42	0.62
53:BF:24:LEU:O	53:BF:26:ALA:N	2.32	0.62
43:BD:27:THR:HG21	43:BD:83:GLU:OE2	1.99	0.62
53:BF:133:ASN:HA	53:BF:162:LEU:HD23	1.80	0.62
4:AJ:85:LEU:O	4:AJ:87:THR:N	2.32	0.62
47:B6:28:ARG:HA	47:B6:32:ASN:HB3	1.80	0.62
52:BE:87:GLU:O	52:BE:89:ASP:N	2.31	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AY:153:MET:HA	23:AY:157:LEU:HD21	1.80	0.62
25:BA:1332:G:N2	25:BA:1610:A:H8	1.96	0.62
25:BA:1403:C:H5''	25:BA:1471:A:H1'	1.80	0.62
25:BA:2849:U:O4	33:BT:23:ARG:NH2	2.30	0.62
25:BA:2850:A:OP2	25:BA:2866:U:C5	2.52	0.62
1:AA:1401:G:C2	1:AA:1402:C:H1'	2.33	0.62
6:AL:27:LEU:C	6:AL:29:GLY:H	2.07	0.62
10:AP:20:VAL:HG21	10:AP:32:TYR:CD1	2.34	0.62
25:BA:1906:G:H2'	25:BA:1907:G:O4'	2.00	0.62
25:BA:2180:U:C6	25:BA:2180:U:H5''	2.34	0.62
47:B6:40:CYS:HG	47:B6:45:LYS:NZ	0.94	0.62
51:BC:119:VAL:O	51:BC:121:GLY:N	2.33	0.62
13:AS:5:LEU:HG	13:AS:10:PHE:HD1	1.65	0.62
25:BA:252:G:P	29:BP:50:ARG:HH11	2.23	0.62
25:BA:806:C:P	29:BP:39:LYS:HB3	2.40	0.62
25:BA:2296:U:H4'	25:BA:2297:C:OP1	1.98	0.62
26:BB:77:U:OP1	39:BZ:19:ARG:NH2	2.32	0.62
1:AA:1305:G:H5''	24:AU:4:GLY:HA3	1.82	0.62
25:BA:27:G:O2'	25:BA:28:A:OP2	2.16	0.62
25:BA:140:G:N3	25:BA:142:A:N1	2.47	0.62
29:BP:107:LYS:O	29:BP:109:GLY:N	2.28	0.62
38:BY:55:TYR:O	38:BY:56:PRO:C	2.41	0.62
14:AT:38:LYS:O	14:AT:41:ILE:HG12	2.00	0.62
25:BA:1040:C:O2'	25:BA:1041:C:OP2	2.15	0.62
38:BY:55:TYR:O	38:BY:57:GLN:O	2.17	0.62
54:BG:57:ALA:HA	54:BG:90:LEU:HD21	1.81	0.62
6:AL:115:LYS:O	6:AL:117:ARG:N	2.32	0.62
23:AY:683:VAL:O	23:AY:686:LYS:N	2.32	0.62
29:BP:146:VAL:HG13	29:BP:147:LEU:N	2.14	0.62
33:BT:30:VAL:CG2	33:BT:84:GLN:O	2.48	0.62
7:AM:14:ARG:NH2	7:AM:16:ASP:OD2	2.32	0.62
25:BA:271(H):G:H4'	41:B1:81:LYS:HG2	1.82	0.62
25:BA:2734:A:H5'	25:BA:2735:G:OP2	2.00	0.62
58:BL:67:UNK:O	58:BL:69:UNK:N	2.33	0.62
1:AA:460:G:C6	1:AA:470:C:H5''	2.35	0.61
1:AA:680:C:O2'	43:BD:166:GLN:HG3	2.00	0.61
1:AA:1057:G:H5''	16:AC:154:SER:HB2	1.81	0.61
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.34	0.61
2:AV:72:C:H3'	2:AV:72:C:C6	2.35	0.61
17:AD:189:PRO:HB2	17:AD:194:LEU:HD21	1.80	0.61
23:AY:437:THR:HB	23:AY:454:MET:CE	2.27	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2419:U:O4	49:B8:30:ARG:NH2	2.32	0.61
25:BA:2801:A:N3	25:BA:2801:A:H2'	2.14	0.61
27:BN:90:MET:O	27:BN:93:THR:O	2.18	0.61
38:BY:73:ARG:NH2	38:BY:81:LYS:HA	2.14	0.61
51:BC:53:ARG:O	51:BC:54:SER:C	2.43	0.61
55:BH:144:VAL:O	55:BH:148:ILE:HG12	2.00	0.61
1:AA:967:C:H4'	22:AI:125:TYR:HE1	1.65	0.61
25:BA:2476:A:N1	25:BA:2477:C:C5	2.69	0.61
25:BA:2602:A:H2'	25:BA:2602:A:N3	2.15	0.61
34:BU:95:LEU:O	34:BU:98:LEU:HG	1.99	0.61
36:BW:60:ASN:OD1	36:BW:61:ASN:ND2	2.33	0.61
53:BF:132:VAL:O	53:BF:138:GLU:OE1	2.18	0.61
55:BH:89:ILE:HD11	55:BH:94:TYR:O	1.99	0.61
4:AJ:5:ARG:HD3	4:AJ:73:ASP:OD1	2.01	0.61
25:BA:1246:A:OP1	29:BP:16:ARG:NH2	2.33	0.61
25:BA:2163:C:O2	25:BA:2163:C:O4'	2.15	0.61
25:BA:2179:C:O2'	25:BA:2180:U:OP2	2.17	0.61
29:BP:24:GLY:O	29:BP:25:SER:HB3	1.99	0.61
29:BP:112:LEU:CD1	29:BP:114:ILE:HG22	2.30	0.61
33:BT:13:ARG:HA	33:BT:13:ARG:CZ	2.30	0.61
45:B4:62:CYS:SG	45:B4:63:SER:N	2.73	0.61
46:B5:46:CYS:SG	46:B5:47:PRO:HD2	2.39	0.61
1:AA:1136:U:H3'	1:AA:1137:C:C5'	2.31	0.61
23:AY:683:VAL:HG23	23:AY:684:GLN:H	1.62	0.61
25:BA:910:A:H62	30:BQ:12:GLN:HA	1.65	0.61
42:B2:47:ASN:O	42:B2:48:HIS:C	2.43	0.61
2:AV:73:A:C2'	2:AV:74:C:H5'	2.30	0.61
23:AY:230:LYS:HG2	23:AY:235:GLU:O	2.00	0.61
27:BN:131:GLN:OE1	27:BN:131:GLN:HA	1.99	0.61
38:BY:97:ARG:O	38:BY:98:VAL:CB	2.47	0.61
23:AY:354:ARG:HG2	23:AY:378:VAL:HG22	1.83	0.61
25:BA:996:A:O2'	34:BU:92:ARG:HG3	2.01	0.61
47:B6:9:LEU:O	47:B6:25:LYS:HB2	2.00	0.61
25:BA:1332:G:H5'	25:BA:1332:G:H8	1.66	0.61
26:BB:105:A:H2'	26:BB:106:G:O4'	2.01	0.61
18:AE:9:LYS:HB2	18:AE:112:LEU:HD11	1.83	0.61
25:BA:1952:A:OP1	28:BO:44:LYS:NZ	2.30	0.61
42:B2:38:GLN:HB3	42:B2:44:LEU:HB3	1.82	0.61
49:B8:63:PRO:O	49:B8:64:TYR:C	2.43	0.61
1:AA:580:U:H2'	1:AA:581:G:O4'	2.01	0.61
1:AA:889:A:H4'	1:AA:890:G:OP1	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AM:88:ARG:HG3	7:AM:98:VAL:HG13	1.83	0.61
19:AF:1:MET:HE2	19:AF:68:PRO:HD3	1.83	0.61
25:BA:2168:G:H22	25:BA:2171:A:H5'	1.65	0.61
1:AA:1158:C:O2'	1:AA:1160:G:OP1	2.17	0.60
20:AG:120:ILE:O	20:AG:124:LEU:HG	2.00	0.60
23:AY:409:ILE:HG12	23:AY:656:ALA:HB3	1.82	0.60
25:BA:1263:U:H1'	46:B5:10:LYS:HG3	1.83	0.60
25:BA:1915:U:C5'	25:BA:1916:A:OP2	2.48	0.60
39:BZ:45:ASP:OD2	39:BZ:49:ARG:HD2	2.00	0.60
22:AI:118:LYS:O	22:AI:119:ALA:HB3	2.00	0.60
25:BA:607:U:N3	25:BA:621:A:C2	2.63	0.60
25:BA:2019:A:N7	46:B5:9:LYS:HE3	2.16	0.60
31:BR:102:GLU:OE1	36:BW:37:ARG:NH1	2.34	0.60
7:AM:65:LYS:HA	7:AM:66:LEU:CB	2.30	0.60
18:AE:10:MET:SD	18:AE:13:ILE:HG13	2.41	0.60
20:AG:5:ARG:NH1	20:AG:5:ARG:HB2	2.15	0.60
25:BA:652:C:O2	25:BA:652:C:C2'	2.48	0.60
25:BA:860:U:O2	25:BA:860:U:O4'	2.14	0.60
25:BA:1495:A:H2'	25:BA:1495:A:N3	2.15	0.60
30:BQ:134:ARG:HA	30:BQ:137:TYR:CD1	2.36	0.60
35:BV:49:THR:HB	35:BV:50:PRO:CD	2.31	0.60
15:AB:97:TRP:HH2	15:AB:176:GLU:CD	2.09	0.60
17:AD:10:ARG:O	17:AD:10:ARG:HG2	1.99	0.60
25:BA:996:A:H4'	34:BU:92:ARG:NE	2.16	0.60
25:BA:1100:C:H6	25:BA:1100:C:H5''	1.66	0.60
25:BA:1504:C:O2'	25:BA:1505:C:P	2.59	0.60
25:BA:2140:C:O2	25:BA:2140:C:O4'	2.18	0.60
32:BS:14:VAL:HG12	32:BS:15:ARG:N	2.15	0.60
43:BD:24:ILE:O	43:BD:25:THR:C	2.43	0.60
47:B6:20:ASN:O	47:B6:21:TYR:CD2	2.53	0.60
25:BA:2406:U:H2'	25:BA:2406:U:OP2	2.01	0.60
26:BB:2:C:O2	26:BB:2:C:H2'	2.02	0.60
26:BB:20:C:C2'	26:BB:21:G:H5'	2.31	0.60
29:BP:51:PHE:HB2	29:BP:52:GLU:HG2	1.84	0.60
25:BA:2585:U:O2	25:BA:2585:U:O4'	2.19	0.60
33:BT:89:VAL:HG21	33:BT:91:ARG:NE	2.17	0.60
43:BD:224:ALA:O	43:BD:225:ALA:HB3	2.00	0.60
49:B8:32:LEU:HB3	49:B8:36:LYS:NZ	2.17	0.60
1:AA:976:G:OP2	1:AA:1358:U:O2'	2.18	0.60
25:BA:483:A:H5''	38:BY:49:VAL:HG22	1.84	0.60
25:BA:2690:C:OP2	31:BR:14:SER:HB2	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1118:C:OP1	22:AI:104:ARG:HD2	2.01	0.60
6:AL:24:VAL:O	6:AL:24:VAL:HG12	2.02	0.60
15:AB:97:TRP:HZ3	15:AB:176:GLU:OE2	1.85	0.60
16:AC:36:ASP:OD2	16:AC:59:ARG:NH2	2.34	0.60
25:BA:900:A:OP1	25:BA:900:A:H4'	2.02	0.60
25:BA:994:C:OP1	34:BU:53:ARG:NH2	2.35	0.60
25:BA:2681:C:H5	25:BA:2725:A:N6	2.00	0.60
28:BO:76:ALA:HB3	33:BT:75:ILE:HD12	1.82	0.60
43:BD:34:VAL:O	43:BD:64:ILE:HG23	2.01	0.60
1:AA:116:A:OP2	1:AA:116:A:C8	2.55	0.60
1:AA:149:A:O2'	1:AA:150:C:C6	2.55	0.60
4:AJ:30:SER:HB2	4:AJ:81:THR:OG1	2.01	0.60
9:AO:70:LEU:HD23	9:AO:78:TYR:HA	1.84	0.60
25:BA:1169:G:N2	25:BA:1181:C:C2	2.70	0.60
30:BQ:27:VAL:O	30:BQ:28:ALA:HB3	2.01	0.60
32:BS:104:GLY:O	32:BS:106:ARG:N	2.29	0.60
42:B2:43:GLN:O	42:B2:44:LEU:HB2	2.00	0.60
52:BE:68:ALA:C	52:BE:70:ALA:H	2.10	0.60
26:BB:92:C:OP1	30:BQ:19:GLY:HA2	2.01	0.60
43:BD:71:ASP:HB2	43:BD:103:ARG:HH22	1.67	0.60
52:BE:128:SER:OG	52:BE:129:HIS:N	2.35	0.60
1:AA:1218:C:H2'	1:AA:1219:U:C6	2.37	0.59
1:AA:1346:A:O4'	1:AA:1348:U:C6	2.54	0.59
17:AD:9:CYS:HA	17:AD:12:CYS:HB3	1.83	0.59
22:AI:42:ARG:NH1	22:AI:71:SER:OG	2.34	0.59
23:AY:264:LEU:HD12	60:AY:702:GCP:C2	2.32	0.59
25:BA:247:G:H4'	25:BA:386:G:C5	2.37	0.59
25:BA:330:A:HO2'	25:BA:331:A:H8	1.48	0.59
25:BA:969:U:H2'	25:BA:970:C:C6	2.37	0.59
25:BA:2392:A:OP1	49:B8:32:LEU:CD2	2.50	0.59
25:BA:2590:A:OP2	43:BD:238:GLY:HA2	2.01	0.59
27:BN:41:ASP:O	27:BN:42:TRP:C	2.43	0.59
36:BW:20:VAL:CG2	36:BW:47:VAL:HG21	2.32	0.59
51:BC:104:LEU:N	51:BC:105:ASP:HA	2.17	0.59
55:BH:41:MET:HE3	55:BH:43:VAL:N	2.16	0.59
55:BH:98:LEU:HD13	55:BH:125:VAL:HG23	1.82	0.59
55:BH:171:LEU:O	55:BH:173:PRO:HD3	2.02	0.59
1:AA:979:C:C3'	1:AA:980:C:H5'	2.31	0.59
23:AY:618:GLY:HA3	25:BA:1095:A:OP1	2.01	0.59
25:BA:1448:G:H1'	25:BA:1528:A:H62	1.65	0.59
29:BP:47:ASP:OD2	29:BP:50:ARG:NH2	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BV:45:THR:O	35:BV:46:VAL:HG12	2.02	0.59
39:BZ:18:LEU:HD12	39:BZ:18:LEU:N	2.12	0.59
1:AA:263:A:OP2	14:AT:79:ARG:NH1	2.35	0.59
25:BA:2092:U:C5	25:BA:2226:C:OP2	2.55	0.59
33:BT:1:MET:O	33:BT:2:ASN:C	2.44	0.59
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.18	0.59
23:AY:110:SER:OG	23:AY:137:ASN:O	2.14	0.59
25:BA:994:C:OP2	34:BU:54:LYS:NZ	2.36	0.59
25:BA:1449:A:H5'	25:BA:1450:G:OP2	2.03	0.59
25:BA:2306:C:C5	25:BA:2307:G:H1'	2.37	0.59
26:BB:21:G:H2'	26:BB:22:U:O4'	2.02	0.59
27:BN:134:ARG:HD2	27:BN:134:ARG:O	2.01	0.59
42:B2:38:GLN:OE1	42:B2:44:LEU:HD22	2.02	0.59
51:BC:30:LYS:NZ	51:BC:180:PHE:O	2.27	0.59
1:AA:1138:G:H1'	1:AA:1139:G:P	2.42	0.59
23:AY:10:LYS:N	23:AY:282:SER:HG	1.99	0.59
25:BA:1063:G:H1	25:BA:1075:C:N4	1.98	0.59
25:BA:1217:C:OP2	34:BU:15:LYS:NZ	2.34	0.59
25:BA:1539:G:C2	25:BA:1540:U:C2	2.90	0.59
25:BA:2097:C:O2'	25:BA:2098:U:H5'	2.03	0.59
25:BA:2476:A:C2	25:BA:2477:C:C6	2.90	0.59
26:BB:71:C:H2'	26:BB:72:G:O4'	2.03	0.59
1:AA:46:G:O2'	1:AA:365:U:H1'	2.02	0.59
1:AA:375:U:C4	1:AA:376:G:N7	2.70	0.59
16:AC:64:VAL:HB	16:AC:99:VAL:HG12	1.84	0.59
18:AE:143:ARG:NH1	21:AH:77:GLU:OE2	2.34	0.59
25:BA:1239:G:H2'	25:BA:1240:U:O4'	2.03	0.59
25:BA:2682:U:C6	52:BE:11:MET:HE2	2.37	0.59
25:BA:2875:C:HO2'	33:BT:3:ARG:HB2	1.68	0.59
27:BN:3:THR:C	27:BN:5:VAL:N	2.61	0.59
38:BY:9:LYS:O	38:BY:11:ASP:N	2.33	0.59
52:BE:115:GLY:C	52:BE:116:VAL:O	2.42	0.59
9:AO:39:LEU:HD11	9:AO:56:LEU:HB2	1.84	0.59
25:BA:154(A):C:O2	25:BA:154(A):C:O4'	2.21	0.59
51:BC:70:LYS:HG2	51:BC:71:GLN:HE21	1.67	0.59
12:AR:44:LEU:HD22	12:AR:79:LEU:HD22	1.85	0.59
25:BA:881:G:H2'	25:BA:882:G:O4'	2.03	0.59
25:BA:2688:U:H5	25:BA:2720:U:OP2	1.86	0.59
25:BA:2793:G:O2'	25:BA:2794:C:OP2	2.20	0.59
31:BR:103:ARG:NH1	31:BR:108:GLY:O	2.36	0.59
14:AT:99:LEU:O	14:AT:101:GLY:N	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1742:G:H8	25:BA:1742:G:H3'	1.68	0.59
25:BA:1796:U:H2'	25:BA:1797:C:C6	2.37	0.59
28:BO:111:PHE:HB3	28:BO:114:ILE:HD13	1.83	0.59
38:BY:40:GLU:HB3	38:BY:64:GLU:OE2	2.01	0.59
53:BF:65:TRP:HZ3	53:BF:73:ALA:O	1.85	0.59
1:AA:1446:U:N3	1:AA:1452:C:N3	2.51	0.59
25:BA:639:U:H2'	25:BA:640:C:C6	2.37	0.59
25:BA:900:A:H3'	25:BA:901:A:H8	1.68	0.59
25:BA:1054:A:C5'	25:BA:1054:A:H8	2.16	0.59
25:BA:2138:C:H6	25:BA:2138:C:C5'	2.15	0.59
25:BA:2319:G:OP1	25:BA:2319:G:C4'	2.51	0.59
29:BP:23:PRO:O	29:BP:33:ARG:HD2	2.03	0.59
55:BH:174:GLY:C	55:BH:176:ALA:HB2	2.27	0.59
25:BA:662:G:P	29:BP:18:ARG:HD2	2.43	0.58
25:BA:2096:U:C4'	25:BA:2096:U:OP1	2.51	0.58
42:B2:45:SER:O	42:B2:46:GLN:NE2	2.36	0.58
1:AA:509:A:C5'	17:AD:55:ALA:HB2	2.33	0.58
1:AA:979:C:C2'	1:AA:980:C:H5'	2.32	0.58
2:AV:73:A:C3'	2:AV:74:C:H5'	2.33	0.58
25:BA:1312:U:H4'	25:BA:1313:U:O5'	2.03	0.58
25:BA:1531:C:H6	25:BA:1531:C:O5'	1.86	0.58
29:BP:64:LYS:O	29:BP:66:GLY:CA	2.50	0.58
29:BP:105:LEU:O	29:BP:106:LEU:CB	2.51	0.58
35:BV:18:LEU:HD22	35:BV:19:LYS:HA	1.84	0.58
35:BV:29:PRO:O	35:BV:61:VAL:O	2.20	0.58
52:BE:36:ARG:NH1	52:BE:85:ASN:OD1	2.35	0.58
56:BK:59:ILE:HG12	56:BK:60:TYR:N	2.18	0.58
1:AA:1013:G:C8	1:AA:1013:G:H5''	2.39	0.58
1:AA:1392:G:N2	1:AA:1502:A:C8	2.69	0.58
17:AD:26:CYS:CA	17:AD:31:CYS:HB2	2.28	0.58
25:BA:1174:A:OP1	25:BA:1175:U:OP1	2.20	0.58
25:BA:1418:G:OP1	25:BA:1588:C:O2'	2.22	0.58
25:BA:1528:A:C2	25:BA:1541:G:C2	2.91	0.58
25:BA:2422:A:H4'	25:BA:2423:U:OP1	2.02	0.58
26:BB:50:G:H2'	26:BB:51:G:O4'	2.02	0.58
29:BP:81:GLN:OE1	29:BP:106:LEU:HA	2.03	0.58
35:BV:2:PHE:O	35:BV:14:VAL:O	2.21	0.58
39:BZ:74:VAL:HG22	39:BZ:86:VAL:HG13	1.84	0.58
51:BC:185:LEU:O	51:BC:187:ASP:N	2.36	0.58
55:BH:41:MET:HE2	55:BH:52:VAL:HA	1.86	0.58
1:AA:1228:C:OP1	7:AM:108:ARG:NH2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AC:92:ALA:O	16:AC:95:THR:O	2.20	0.58
23:AY:683:VAL:O	23:AY:685:GLU:N	2.36	0.58
25:BA:2789:C:N3	25:BA:2894:G:O6	2.36	0.58
43:BD:77:ALA:HB2	43:BD:97:TYR:CD2	2.37	0.58
1:AA:60:A:H4'	1:AA:61:G:O5'	2.02	0.58
1:AA:978:A:C5	1:AA:1319:A:C2	2.92	0.58
22:AI:42:ARG:NH2	22:AI:75:ASP:OD2	2.35	0.58
43:BD:26:LYS:HD3	43:BD:113:VAL:HG21	1.85	0.58
47:B6:48:VAL:O	47:B6:49:HIS:CB	2.48	0.58
1:AA:432:A:C8	1:AA:433:C:C5	2.92	0.58
16:AC:55:VAL:O	16:AC:55:VAL:HG12	2.02	0.58
34:BU:92:ARG:NH1	35:BV:11:GLN:O	2.36	0.58
6:AL:23:LYS:C	6:AL:24:VAL:HG23	2.28	0.58
6:AL:37:CYS:O	6:AL:79:GLU:O	2.20	0.58
15:AB:109:SER:O	15:AB:111:ARG:N	2.36	0.58
25:BA:90:U:H1'	25:BA:92:A:N7	2.19	0.58
25:BA:385:C:O2'	25:BA:388:G:N2	2.36	0.58
25:BA:662:G:H5'	29:BP:18:ARG:HA	1.86	0.58
25:BA:2681:C:C5	25:BA:2725:A:N6	2.71	0.58
38:BY:76:CYS:O	38:BY:96:ILE:CD1	2.51	0.58
1:AA:158:G:N2	1:AA:163:C:O2	2.33	0.58
1:AA:1442(A):G:N3	1:AA:1442(A):G:H2'	2.18	0.58
26:BB:1:U:O2	26:BB:1:U:H2'	2.03	0.58
28:BO:64:ARG:NH1	28:BO:81:ASP:OD2	2.37	0.58
31:BR:11:ASN:CG	31:BR:12:ARG:H	2.12	0.58
46:B5:40:LYS:CE	46:B5:46:CYS:HB3	2.33	0.58
55:BH:157:TYR:CE1	55:BH:171:LEU:HD22	2.38	0.58
25:BA:1210:A:H5'	25:BA:1210:A:H8	1.68	0.58
25:BA:1970:A:H5''	25:BA:1971:A:OP1	2.02	0.58
25:BA:2315:G:OP1	54:BG:36:LYS:NZ	2.35	0.58
25:BA:2529:G:O6	50:B9:31:LYS:NZ	2.37	0.58
25:BA:2836:U:H2'	25:BA:2837:G:C8	2.39	0.58
30:BQ:138:ASP:OD2	30:BQ:138:ASP:N	2.37	0.58
42:B2:35:LEU:HD12	42:B2:53:LEU:HD12	1.86	0.58
56:BK:103:GLN:O	56:BK:106:GLU:HG2	2.03	0.58
57:BJ:55:ALA:O	57:BJ:56:ALA:C	2.46	0.58
6:AL:53:ARG:NH1	6:AL:92:ASP:OD2	2.36	0.58
8:AN:26:ARG:NH1	8:AN:47:LEU:HD21	2.19	0.58
23:AY:428:LEU:CD2	23:AY:451:ILE:HD11	2.32	0.58
25:BA:685:A:OP1	48:B7:11:LYS:NZ	2.36	0.58
25:BA:2542:A:H2'	25:BA:2542:A:N3	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:607:U:H3	25:BA:621:A:H2	1.44	0.57
33:BT:7:ILE:O	33:BT:11:GLU:OE1	2.21	0.57
33:BT:123:GLN:HA	33:BT:126:ALA:HB3	1.86	0.57
34:BU:105:VAL:HG11	35:BV:40:LEU:HD11	1.86	0.57
51:BC:39:GLU:OE1	51:BC:216:THR:HB	2.04	0.57
56:BK:14:ALA:HA	56:BK:41:PHE:CE2	2.39	0.57
1:AA:269:C:H2'	1:AA:270:A:C8	2.39	0.57
1:AA:814:A:H2'	1:AA:816:A:H5''	1.86	0.57
25:BA:705:A:H2'	25:BA:706:A:O4'	2.03	0.57
25:BA:1434:A:H61	25:BA:1558:A:H62	1.52	0.57
25:BA:2662:A:H2'	25:BA:2663:G:O4'	2.04	0.57
40:B0:2:ALA:O	40:B0:4:LYS:N	2.34	0.57
49:B8:51:ALA:N	49:B8:53:PRO:HD2	2.19	0.57
1:AA:59:A:H2'	1:AA:60:A:OP1	2.04	0.57
13:AS:47:HIS:O	13:AS:62:ILE:HG22	2.04	0.57
25:BA:2165:G:C2'	25:BA:2166:G:H5''	2.34	0.57
27:BN:1:MET:HE2	27:BN:2:LYS:N	2.19	0.57
32:BS:15:ARG:O	32:BS:18:ILE:HG22	2.04	0.57
58:BL:100:UNK:O	58:BL:101:UNK:CB	2.52	0.57
1:AA:986:A:H2'	1:AA:987:G:O4'	2.04	0.57
1:AA:1054:C:C2'	1:AA:1055:A:H5''	2.34	0.57
9:AO:15:PHE:CZ	9:AO:85:LEU:HD13	2.39	0.57
9:AO:54:ARG:HG2	9:AO:58:MET:HE2	1.85	0.57
15:AB:84:GLU:HB3	15:AB:219:VAL:HG21	1.86	0.57
25:BA:1058:G:H5''	25:BA:1058:G:C8	2.40	0.57
25:BA:1742:G:C8	25:BA:1743:C:C6	2.93	0.57
29:BP:97:PRO:HB3	29:BP:112:LEU:HB2	1.86	0.57
33:BT:27:THR:OG1	33:BT:28:VAL:N	2.36	0.57
35:BV:39:LEU:HA	35:BV:47:VAL:HG11	1.85	0.57
52:BE:1:MET:HB3	52:BE:200:GLU:CD	2.29	0.57
1:AA:838:G:N2	1:AA:849:C:C2	2.72	0.57
2:AV:43:C:O2	2:AV:43:C:O4'	2.21	0.57
6:AL:41:ARG:HB3	6:AL:41:ARG:HH11	1.68	0.57
17:AD:31:CYS:C	17:AD:33:MET:H	2.12	0.57
25:BA:956:G:C4'	30:BQ:83:MET:HE1	2.34	0.57
25:BA:1982:C:H5''	25:BA:1983:C:OP2	2.04	0.57
26:BB:76:G:O3'	39:BZ:19:ARG:NH2	2.33	0.57
36:BW:6:ILE:HA	36:BW:103:ILE:O	2.04	0.57
53:BF:167:ALA:O	53:BF:169:ASN:N	2.38	0.57
57:BJ:14:ALA:O	57:BJ:18:ALA:HB3	2.05	0.57
1:AA:416:G:C5	1:AA:417:C:C4	2.93	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AB:97:TRP:CH2	15:AB:176:GLU:CD	2.83	0.57
17:AD:25:ARG:O	17:AD:27:TYR:N	2.37	0.57
25:BA:470:A:OP1	53:BF:59:TYR:HE2	1.87	0.57
25:BA:1062:G:P	25:BA:1070:A:H4'	2.45	0.57
25:BA:1496:A:C8	25:BA:1577:C:O2'	2.52	0.57
25:BA:1688:U:H1'	25:BA:1701:A:C6	2.39	0.57
25:BA:2208:A:H1'	25:BA:2219:G:C5	2.39	0.57
25:BA:2602:A:OP2	25:BA:2602:A:C4'	2.52	0.57
25:BA:2688:U:O2	25:BA:2688:U:O5'	2.23	0.57
1:AA:343:U:O2'	1:AA:346:G:O6	2.13	0.57
1:AA:1181:G:O2'	1:AA:1182:G:H5'	2.03	0.57
11:AQ:45:HIS:HB2	11:AQ:65:ILE:HD13	1.86	0.57
25:BA:1918:A:O2'	25:BA:1919:A:H2	1.87	0.57
29:BP:58:THR:O	29:BP:61:ARG:NH2	2.37	0.57
33:BT:89:VAL:C	33:BT:91:ARG:N	2.52	0.57
35:BV:18:LEU:HD13	35:BV:19:LYS:N	2.19	0.57
49:B8:50:LEU:HA	49:B8:53:PRO:CD	2.35	0.57
56:BK:19:PRO:HB3	56:BK:34:ILE:HD12	1.87	0.57
15:AB:121:LEU:HB3	15:AB:127:ILE:HD11	1.86	0.57
27:BN:3:THR:C	27:BN:5:VAL:H	2.13	0.57
27:BN:4:TYR:N	27:BN:4:TYR:CD1	2.71	0.57
33:BT:28:VAL:HG13	33:BT:46:GLU:HA	1.87	0.57
39:BZ:15:PRO:HA	39:BZ:18:LEU:HD13	1.87	0.57
43:BD:30:GLU:HG3	43:BD:63:ARG:CZ	2.34	0.57
1:AA:1452:C:C4'	1:AA:1456:G:N2	2.67	0.57
13:AS:79:THR:O	13:AS:80:TYR:O	2.22	0.57
60:AY:702:GCP:PG	61:AY:803:HOH:O	2.62	0.57
25:BA:523:C:H4'	25:BA:540:C:O2	2.04	0.57
25:BA:2320:A:N3	25:BA:2320:A:H2'	2.20	0.57
25:BA:2845:G:O2'	25:BA:2846:G:H5'	2.05	0.57
55:BH:106:THR:HG22	55:BH:112:PRO:HG3	1.87	0.57
56:BK:121:GLU:CD	56:BK:121:GLU:H	2.12	0.57
2:AV:74:C:O2'	2:AV:75:C:P	2.63	0.57
12:AR:31:LEU:HD22	19:AF:97:PHE:O	2.05	0.57
26:BB:80:U:H2'	26:BB:81:G:H21	1.68	0.57
27:BN:119:ARG:HH11	27:BN:119:ARG:HG3	1.69	0.57
38:BY:2:ARG:C	38:BY:4:LYS:H	2.11	0.57
38:BY:76:CYS:HB3	38:BY:96:ILE:HD11	1.87	0.57
11:AQ:27:PHE:CZ	11:AQ:36:ILE:HD11	2.40	0.56
14:AT:96:GLY:O	14:AT:97:ALA:HB3	2.05	0.56
16:AC:156:ARG:NE	16:AC:160:ALA:O	2.34	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AY:680:PRO:HD2	23:AY:683:VAL:HG22	1.87	0.56
25:BA:8:A:H2'	25:BA:9:U:C5	2.39	0.56
43:BD:136:ILE:HG22	43:BD:140:THR:OG1	2.05	0.56
53:BF:23:ASP:N	53:BF:23:ASP:OD1	2.38	0.56
1:AA:250:A:C4'	1:AA:251:G:O5'	2.51	0.56
25:BA:102:G:C4'	25:BA:102:G:OP1	2.53	0.56
27:BN:32:THR:O	27:BN:35:ARG:O	2.23	0.56
29:BP:6:LEU:HD12	29:BP:8:PRO:HG2	1.86	0.56
34:BU:90:VAL:HG22	35:BV:39:LEU:CB	2.36	0.56
46:B5:34:PRO:O	46:B5:35:GLU:HG2	2.04	0.56
1:AA:432:A:N7	1:AA:433:C:C5	2.73	0.56
1:AA:664:G:H22	1:AA:741:G:H1	1.52	0.56
1:AA:975:A:C4'	1:AA:976:G:H5''	2.34	0.56
1:AA:1104:G:OP1	15:AB:111:ARG:NE	2.38	0.56
7:AM:79:LYS:O	7:AM:82:MET:SD	2.63	0.56
15:AB:239:VAL:O	15:AB:239:VAL:HG12	2.06	0.56
16:AC:165:THR:HG23	16:AC:165:THR:O	2.05	0.56
23:AY:418:LYS:O	23:AY:419:ALA:HB3	2.05	0.56
25:BA:272(J):C:C2'	25:BA:274:G:OP1	2.53	0.56
25:BA:1210:A:H8	25:BA:1210:A:C5'	2.17	0.56
25:BA:1494:A:N3	25:BA:1494:A:C3'	2.65	0.56
25:BA:1786:A:N1	25:BA:2606:C:H1'	2.20	0.56
28:BO:80:ASP:OD2	33:BT:64:ARG:NH2	2.37	0.56
33:BT:106:SER:HA	33:BT:110:ILE:HG13	1.86	0.56
38:BY:76:CYS:SG	38:BY:77:PRO:HD3	2.45	0.56
43:BD:182:LEU:O	43:BD:271:ILE:N	2.38	0.56
55:BH:167:GLU:HB3	55:BH:168:PRO:CD	2.35	0.56
1:AA:417:C:H2'	1:AA:418:C:H6	1.70	0.56
2:AV:46:G:H3'	2:AV:47:U:C5'	2.35	0.56
14:AT:53:LEU:HB2	14:AT:100:ILE:HG22	1.86	0.56
25:BA:252:G:P	29:BP:50:ARG:NH1	2.78	0.56
25:BA:1877:A:H5''	25:BA:1878:G:OP2	2.05	0.56
34:BU:108:GLU:OE2	34:BU:112:ARG:NH1	2.38	0.56
39:BZ:8:TYR:O	39:BZ:37:VAL:HB	2.05	0.56
1:AA:838:G:C2	1:AA:849:C:C2	2.94	0.56
15:AB:109:SER:C	15:AB:111:ARG:H	2.12	0.56
23:AY:70:THR:HA	23:AY:358:MET:O	2.06	0.56
25:BA:650:C:OP1	49:B8:48:PHE:CZ	2.58	0.56
25:BA:658:C:H2'	25:BA:659:C:C6	2.40	0.56
25:BA:1075:C:OP1	25:BA:1075:C:H4'	2.06	0.56
25:BA:1538:G:O2'	25:BA:1539:G:O5'	2.24	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2180:U:C6	25:BA:2180:U:H5'	2.39	0.56
25:BA:2238:G:H2'	25:BA:2238:G:N3	2.20	0.56
32:BS:89:ARG:HB3	32:BS:92:TYR:HB3	1.87	0.56
38:BY:17:SER:HB2	38:BY:71:LYS:HE2	1.87	0.56
51:BC:113:VAL:HG21	51:BC:131:LEU:HD11	1.88	0.56
1:AA:1014:A:H4'	13:AS:14:HIS:CE1	2.40	0.56
13:AS:63:THR:OG1	13:AS:65:ASN:OD1	2.23	0.56
29:BP:16:ARG:NH1	29:BP:16:ARG:HB2	2.20	0.56
33:BT:24:PRO:HB3	33:BT:99:LEU:HD21	1.88	0.56
38:BY:90:LEU:HG	38:BY:91:GLU:HG3	1.87	0.56
15:AB:80:ILE:HD12	15:AB:80:ILE:N	2.20	0.56
23:AY:108:PHE:CE1	23:AY:114:VAL:HG22	2.41	0.56
25:BA:17:G:H4'	34:BU:25:TRP:CH2	2.41	0.56
53:BF:65:TRP:HB2	53:BF:66:PRO:HD2	1.87	0.56
54:BG:55:LYS:O	54:BG:59:GLU:HB2	2.06	0.56
56:BK:23:VAL:HG13	56:BK:27:LEU:HD22	1.87	0.56
23:AY:98:MET:HG3	23:AY:130:VAL:HG21	1.88	0.56
23:AY:215:LYS:HA	23:AY:218:GLU:HB3	1.88	0.56
25:BA:821:A:H2'	25:BA:946:G:H5''	1.88	0.56
25:BA:1022:G:N2	25:BA:1142(A):A:H2	1.97	0.56
29:BP:51:PHE:HB3	29:BP:52:GLU:HG2	1.87	0.56
33:BT:12:SER:O	33:BT:13:ARG:NE	2.38	0.56
33:BT:29:ARG:HD2	33:BT:30:VAL:HG13	1.87	0.56
23:AY:168:ILE:HD11	23:AY:178:ILE:CD1	2.35	0.56
23:AY:493:VAL:HG23	23:AY:512:ILE:HD11	1.87	0.56
25:BA:1448:G:H4'	25:BA:1542:A:OP1	2.06	0.56
25:BA:1584:C:O2	25:BA:1584:C:C2'	2.54	0.56
31:BR:113:LEU:HD23	31:BR:113:LEU:C	2.31	0.56
1:AA:149:A:O2'	1:AA:150:C:H6	1.89	0.56
1:AA:1133:G:C8	1:AA:1133:G:C3'	2.89	0.56
7:AM:82:MET:SD	7:AM:83:ASP:N	2.79	0.56
17:AD:17:VAL:O	17:AD:17:VAL:HG12	2.06	0.56
25:BA:528:A:C2	25:BA:2043:C:C5'	2.89	0.56
25:BA:810:U:O5'	25:BA:810:U:H6	1.89	0.56
25:BA:1504:C:HO2'	25:BA:1505:C:P	2.28	0.56
25:BA:1538:G:C5	25:BA:1539:G:N7	2.73	0.56
25:BA:2894:G:H2'	25:BA:2894:G:N3	2.21	0.56
33:BT:58:ASN:C	33:BT:58:ASN:HD22	2.14	0.56
4:AJ:85:LEU:C	4:AJ:87:THR:H	2.14	0.55
25:BA:762:U:H4'	25:BA:763:G:O5'	2.06	0.55
28:BO:68:GLU:H	28:BO:68:GLU:CD	2.13	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:BY:65:ALA:HB1	38:BY:66:PRO:CD	2.35	0.55
42:B2:9:GLN:HE22	42:B2:56:GLN:HG2	1.72	0.55
51:BC:58:VAL:HG13	51:BC:199:HIS:HB3	1.87	0.55
56:BK:56:GLU:O	56:BK:67:PHE:HA	2.06	0.55
23:AY:204:GLU:C	23:AY:206:LEU:H	2.14	0.55
25:BA:102:G:OP1	25:BA:102:G:O4'	2.23	0.55
25:BA:528:A:O2'	25:BA:529:A:H5'	2.06	0.55
25:BA:1778:U:H2'	25:BA:1784:A:N6	2.20	0.55
25:BA:2444:G:OP2	53:BF:68:LYS:HE2	2.06	0.55
27:BN:1:MET:HE2	27:BN:1:MET:C	2.31	0.55
31:BR:104:ARG:NH1	31:BR:107:ASP:OD1	2.39	0.55
38:BY:65:ALA:HB1	38:BY:66:PRO:HD3	1.88	0.55
1:AA:1392:G:H21	1:AA:1502:A:H8	1.52	0.55
5:AK:54:ARG:O	5:AK:57:THR:HG22	2.06	0.55
16:AC:7:PRO:O	16:AC:11:ARG:HG2	2.06	0.55
16:AC:180:ALA:O	16:AC:181:ASN:HB3	2.06	0.55
23:AY:404:VAL:HG22	23:AY:405:PRO:O	2.07	0.55
23:AY:556:ILE:HD11	23:AY:601:ILE:HD13	1.88	0.55
25:BA:456:C:O2'	37:BX:68:ARG:NH1	2.40	0.55
25:BA:1754:C:OP1	33:BT:96:ARG:NH1	2.40	0.55
25:BA:2262:U:H4'	25:BA:2328:A:H2	1.71	0.55
43:BD:209:ALA:O	43:BD:210:GLY:O	2.24	0.55
52:BE:77:ILE:HG22	52:BE:78:LEU:N	2.21	0.55
11:AQ:9:VAL:HG12	11:AQ:56:VAL:HG22	1.88	0.55
25:BA:1188:U:H4'	35:BV:79:VAL:HG22	1.88	0.55
25:BA:1315:C:C2	25:BA:1338:G:N2	2.74	0.55
25:BA:1952:A:OP1	28:BO:42:SER:OG	2.25	0.55
25:BA:1996:C:OP1	28:BO:31:LYS:HE2	2.06	0.55
25:BA:2243:U:H2'	25:BA:2244:U:C6	2.41	0.55
28:BO:7:TYR:CZ	28:BO:44:LYS:HG3	2.42	0.55
38:BY:7:VAL:HB	38:BY:8:LYS:CD	2.36	0.55
38:BY:73:ARG:HH21	38:BY:81:LYS:HA	1.71	0.55
44:B3:50:VAL:HG23	44:B3:54:VAL:HG21	1.88	0.55
15:AB:45:GLN:O	15:AB:48:MET:HE2	2.06	0.55
23:AY:58:GLU:HG2	23:AY:63:ILE:O	2.05	0.55
25:BA:1054:A:C5'	25:BA:1054:A:C8	2.89	0.55
27:BN:5:VAL:O	27:BN:5:VAL:HG13	2.06	0.55
35:BV:2:PHE:CB	35:BV:42:GLY:HA3	2.36	0.55
36:BW:18:ARG:NH1	36:BW:76:VAL:O	2.40	0.55
56:BK:6:ALA:O	56:BK:58:THR:HG23	2.07	0.55
1:AA:694:A:N1	1:AA:787:A:O2'	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1140:C:O2'	1:AA:1141:C:H5'	2.06	0.55
1:AA:1192:C:OP2	16:AC:4:LYS:NZ	2.40	0.55
2:AV:34:G:C3'	2:AV:35:A:H5''	2.36	0.55
5:AK:111:ASP:HA	12:AR:84:LYS:HG3	1.87	0.55
11:AQ:12:SER:HB3	11:AQ:20:THR:HB	1.88	0.55
25:BA:2584:U:H2'	25:BA:2585:U:H2'	1.88	0.55
48:B7:43:THR:O	48:B7:44:PRO:C	2.49	0.55
1:AA:1311:G:N2	1:AA:1327:C:C2	2.74	0.55
19:AF:37:VAL:HG12	19:AF:38:GLU:O	2.07	0.55
20:AG:137:LYS:O	20:AG:141:VAL:HG23	2.07	0.55
23:AY:519:ARG:NE	23:AY:519:ARG:HA	2.21	0.55
23:AY:652:MET:HG2	23:AY:671:MET:SD	2.47	0.55
25:BA:1054:A:H5''	25:BA:1054:A:H8	1.72	0.55
25:BA:2365:G:O6	49:B8:39:LYS:HE3	2.07	0.55
27:BN:24:GLY:HA2	27:BN:27:ALA:HB3	1.87	0.55
32:BS:96:GLY:O	32:BS:98:VAL:N	2.39	0.55
33:BT:106:SER:O	33:BT:107:ASP:CG	2.50	0.55
45:B4:62:CYS:C	45:B4:64:LYS:H	2.14	0.55
52:BE:103:ASP:OD2	52:BE:168:MET:HE2	2.07	0.55
1:AA:1178:G:N7	22:AI:97:LYS:NZ	2.48	0.55
7:AM:39:ILE:HD12	7:AM:56:LEU:HD23	1.88	0.55
20:AG:144:MET:C	20:AG:145:ALA:O	2.43	0.55
22:AI:47:LEU:C	22:AI:49:PRO:HD2	2.32	0.55
23:AY:488:THR:OG1	23:AY:598:ASP:O	2.24	0.55
25:BA:372:G:O2'	25:BA:373:U:P	2.65	0.55
25:BA:1272:A:H4'	25:BA:1272:A:OP1	2.05	0.55
25:BA:1300:U:O2'	25:BA:1635:G:OP1	2.22	0.55
25:BA:2095:C:H6	25:BA:2095:C:H5''	1.72	0.55
29:BP:10:PRO:O	53:BF:34:TRP:CD1	2.60	0.55
29:BP:99:LEU:HD23	29:BP:99:LEU:O	2.07	0.55
56:BK:34:ILE:O	56:BK:35:MET:HE2	2.07	0.55
56:BK:109:LYS:O	56:BK:112:MET:HG2	2.06	0.55
1:AA:1014:A:H5''	13:AS:14:HIS:CG	2.42	0.55
1:AA:1292:U:H2'	1:AA:1293:G:H5''	1.88	0.55
1:AA:1399:C:C2	1:AA:1502:A:N6	2.74	0.55
7:AM:108:ARG:O	7:AM:111:LYS:O	2.25	0.55
23:AY:212:TYR:O	23:AY:215:LYS:N	2.40	0.55
25:BA:36:G:O2'	25:BA:450:G:H2'	2.07	0.55
25:BA:111:A:O3'	42:B2:69:ARG:NH2	2.39	0.55
25:BA:583:G:P	34:BU:10:ARG:HH11	2.29	0.55
25:BA:1332:G:N2	25:BA:1610:A:C8	2.75	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BB:73:A:C4	26:BB:105:A:C2	2.94	0.55
29:BP:18:ARG:NH1	29:BP:18:ARG:O	2.40	0.55
31:BR:101:ALA:O	31:BR:102:GLU:HB2	2.07	0.55
49:B8:32:LEU:HB2	49:B8:36:LYS:HE2	1.88	0.55
51:BC:53:ARG:O	51:BC:55:ASP:OD1	2.25	0.55
52:BE:89:ASP:O	52:BE:90:THR:O	2.24	0.55
54:BG:17:PRO:HA	54:BG:20:ILE:HD12	1.89	0.55
1:AA:408:A:H4'	17:AD:112:VAL:HG11	1.88	0.55
1:AA:630:G:C8	1:AA:630:G:H5''	2.42	0.55
2:AV:33:U:C5	2:AV:36:A:OP2	2.59	0.55
17:AD:25:ARG:C	17:AD:27:TYR:N	2.65	0.55
23:AY:71:THR:CG2	23:AY:80:ASN:OD1	2.48	0.55
25:BA:2097:C:C2'	25:BA:2098:U:H5'	2.36	0.55
34:BU:98:LEU:O	34:BU:101:ARG:O	2.24	0.55
38:BY:42:VAL:HG12	38:BY:65:ALA:HB3	1.88	0.55
51:BC:42:GLU:HG2	51:BC:215:THR:HG23	1.87	0.55
53:BF:9:ILE:O	53:BF:128:ALA:HB2	2.07	0.55
1:AA:1036:G:H3'	1:AA:1037:C:C6	2.42	0.54
23:AY:212:TYR:HA	23:AY:215:LYS:CB	2.35	0.54
25:BA:1713:U:O2'	25:BA:1714:G:H5'	2.07	0.54
25:BA:2031:A:C6	25:BA:2498:C:H1'	2.43	0.54
25:BA:2095:C:H6	25:BA:2095:C:C5'	2.20	0.54
28:BO:18:LYS:HB2	28:BO:45:GLU:HG3	1.89	0.54
29:BP:97:PRO:O	29:BP:98:GLU:CG	2.55	0.54
42:B2:38:GLN:O	42:B2:41:ILE:HG12	2.06	0.54
47:B6:20:ASN:CG	47:B6:21:TYR:H	2.13	0.54
53:BF:53:THR:HG23	53:BF:55:GLY:H	1.71	0.54
1:AA:1003:G:H2'	1:AA:1004:A:H4'	1.89	0.54
5:AK:48:ILE:HG22	5:AK:49:GLY:N	2.23	0.54
23:AY:679:VAL:HB	23:AY:680:PRO:HD2	1.88	0.54
25:BA:1539:G:H2'	25:BA:1540:U:C5'	2.37	0.54
25:BA:2136:C:C2	25:BA:2137:C:C5	2.96	0.54
26:BB:42:C:O2'	26:BB:43:C:O5'	2.21	0.54
26:BB:91:C:OP2	30:BQ:16:ARG:NH1	2.39	0.54
29:BP:8:PRO:O	29:BP:10:PRO:HD3	2.06	0.54
51:BC:180:PHE:C	51:BC:181:PRO:O	2.50	0.54
52:BE:74:PRO:O	52:BE:75:VAL:O	2.26	0.54
54:BG:116:ASP:O	54:BG:117:PHE:CB	2.55	0.54
13:AS:70:LYS:N	13:AS:70:LYS:HE3	2.22	0.54
22:AI:118:LYS:O	22:AI:119:ALA:CB	2.55	0.54
25:BA:607:U:O2	25:BA:621:A:N1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1639:U:O2'	25:BA:1640:C:H5'	2.08	0.54
25:BA:2492:U:H2'	25:BA:2493:U:C6	2.42	0.54
27:BN:46:VAL:O	27:BN:47:ALA:CB	2.55	0.54
31:BR:9:LYS:O	31:BR:10:LEU:HD23	2.06	0.54
33:BT:3:ARG:HG3	33:BT:6:LEU:HB3	1.89	0.54
33:BT:30:VAL:HG12	33:BT:44:ASP:OD1	2.08	0.54
35:BV:62:LEU:CD2	35:BV:95:LEU:HB2	2.37	0.54
43:BD:27:THR:HG23	43:BD:83:GLU:HB3	1.87	0.54
47:B6:20:ASN:O	47:B6:21:TYR:CD1	2.60	0.54
53:BF:81:PRO:CB	53:BF:89:VAL:HG23	2.37	0.54
53:BF:202:PHE:O	53:BF:206:ILE:HG12	2.08	0.54
56:BK:37:PHE:O	56:BK:41:PHE:HB3	2.07	0.54
16:AC:167:TRP:O	16:AC:168:ALA:HB2	2.08	0.54
25:BA:528:A:C2	25:BA:2043:C:C4'	2.88	0.54
25:BA:1721:G:C2	25:BA:1739:U:OP2	2.61	0.54
28:BO:1:MET:HG3	28:BO:67:LYS:HG2	1.90	0.54
35:BV:19:LYS:HG3	35:BV:20:LEU:C	2.32	0.54
42:B2:38:GLN:CD	42:B2:44:LEU:HD13	2.33	0.54
47:B6:41:PRO:CD	47:B6:46:HIS:HA	2.37	0.54
51:BC:84:LYS:HA	51:BC:87:GLU:HG3	1.89	0.54
52:BE:65:GLY:O	52:BE:67:PHE:N	2.40	0.54
1:AA:977:A:O2'	1:AA:979:C:OP2	2.26	0.54
1:AA:1080:A:C5'	18:AE:16:THR:HG21	2.37	0.54
25:BA:242:G:H5'	49:B8:62:LEU:HD13	1.88	0.54
25:BA:598:G:H2'	25:BA:599:G:O4'	2.07	0.54
25:BA:900:A:H3'	25:BA:901:A:C8	2.42	0.54
25:BA:1539:G:H2'	25:BA:1540:U:H5''	1.87	0.54
25:BA:2312:U:O2'	54:BG:71:THR:HG21	2.08	0.54
36:BW:92:ARG:O	36:BW:93:ALA:HB3	2.05	0.54
1:AA:134:A:H1'	1:AA:325:A:C5	2.43	0.54
1:AA:1226:C:H4'	1:AA:1227:A:OP1	2.08	0.54
1:AA:1504:G:OP1	1:AA:1507:A:H4'	2.08	0.54
2:AV:33:U:O4'	2:AV:33:U:O2	2.23	0.54
25:BA:213:A:H2'	25:BA:214:G:O4'	2.07	0.54
25:BA:524:U:H4'	25:BA:555:U:H4'	1.88	0.54
25:BA:1539:G:C3'	25:BA:1540:U:C5'	2.86	0.54
25:BA:1689:A:N7	25:BA:1698:A:N1	2.55	0.54
29:BP:7:ARG:HA	29:BP:7:ARG:CZ	2.36	0.54
29:BP:23:PRO:HB2	29:BP:33:ARG:CD	2.38	0.54
39:BZ:6:LYS:HG2	39:BZ:8:TYR:OH	2.07	0.54
52:BE:4:ILE:HD13	52:BE:28:ALA:HB1	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:BH:117:PRO:HB3	55:BH:123:PHE:CE2	2.42	0.54
1:AA:1133:G:H2'	1:AA:1134:G:O4'	2.08	0.54
1:AA:1202:G:C2	8:AN:42:ILE:HG21	2.43	0.54
26:BB:66:A:O2'	26:BB:67:G:OP2	2.19	0.54
29:BP:135:LEU:HD21	29:BP:144:GLU:HG3	1.89	0.54
42:B2:53:LEU:O	42:B2:57:ILE:HG13	2.07	0.54
55:BH:136:ILE:HD12	55:BH:136:ILE:H	1.71	0.54
2:AV:73:A:H2'	2:AV:74:C:C5'	2.37	0.54
16:AC:60:ALA:O	16:AC:62:ASP:N	2.41	0.54
21:AH:96:GLY:N	21:AH:99:GLU:OE1	2.41	0.54
25:BA:219:G:H2'	25:BA:220:G:O4'	2.07	0.54
25:BA:1131:G:OP2	25:BA:2515:C:H4'	2.07	0.54
25:BA:2743:C:H2'	25:BA:2744:G:O5'	2.08	0.54
35:BV:49:THR:HB	35:BV:50:PRO:HD2	1.90	0.54
42:B2:45:SER:O	42:B2:46:GLN:CD	2.51	0.54
54:BG:7:LEU:HD22	54:BG:176:LEU:HD22	1.89	0.54
7:AM:10:PRO:HB2	7:AM:18:ALA:HB1	1.89	0.54
15:AB:77:ALA:HB2	15:AB:211:ILE:HD13	1.89	0.54
25:BA:918:A:H1'	26:BB:80:U:O2'	2.08	0.54
25:BA:2019:A:C2'	25:BA:2020:A:O5'	2.56	0.54
29:BP:7:ARG:CB	29:BP:8:PRO:CD	2.84	0.54
29:BP:65:ARG:O	29:BP:66:GLY:C	2.51	0.54
31:BR:2:ARG:C	31:BR:3:HIS:O	2.50	0.54
56:BK:77:LEU:HD23	56:BK:77:LEU:H	1.72	0.54
1:AA:991:U:O2	1:AA:991:U:H2'	2.08	0.54
2:AV:57:G:H8	2:AV:57:G:H5''	1.73	0.54
4:AJ:49:VAL:O	4:AJ:60:ARG:HB2	2.09	0.54
17:AD:30:LYS:C	17:AD:32:ALA:N	2.64	0.54
23:AY:148:LEU:O	23:AY:152:THR:OG1	2.15	0.54
23:AY:210:ARG:C	23:AY:212:TYR:H	2.10	0.54
25:BA:684:G:OP1	48:B7:16:HIS:CD2	2.61	0.54
25:BA:1478:G:O2'	25:BA:1558:A:C2	2.60	0.54
25:BA:2477:C:C5	50:B9:4:ARG:NH2	2.76	0.54
25:BA:2609:U:OP1	25:BA:2609:U:H4'	2.07	0.54
2:AV:18:G:O2'	2:AV:57:G:N2	2.31	0.53
15:AB:31:TYR:CE1	15:AB:200:ILE:HD12	2.42	0.53
25:BA:646:A:H2'	25:BA:647:G:O5'	2.08	0.53
25:BA:1100:C:C6	25:BA:1100:C:H5'	2.43	0.53
25:BA:1818:U:O4	43:BD:154:LYS:HE3	2.09	0.53
30:BQ:84:GLY:O	30:BQ:85:LYS:HB2	2.06	0.53
33:BT:56:GLY:C	33:BT:57:PHE:O	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BZ:11:GLU:O	39:BZ:36:LYS:NZ	2.28	0.53
41:B1:57:GLU:O	41:B1:58:ILE:HG23	2.07	0.53
51:BC:53:ARG:O	51:BC:55:ASP:N	2.41	0.53
15:AB:109:SER:C	15:AB:111:ARG:N	2.66	0.53
21:AH:38:ILE:CD1	21:AH:118:VAL:HG12	2.37	0.53
23:AY:151:ARG:O	23:AY:154:GLN:HG2	2.08	0.53
25:BA:1763:G:H4'	25:BA:1763:G:OP1	2.07	0.53
25:BA:2287:A:C2	25:BA:2346:A:N1	2.76	0.53
29:BP:62:LEU:HD11	49:B8:30:ARG:HG2	1.90	0.53
30:BQ:6:ARG:HA	39:BZ:195:GLU:O	2.07	0.53
30:BQ:21:THR:O	30:BQ:22:LYS:CB	2.55	0.53
32:BS:98:VAL:HG12	32:BS:100:ALA:N	2.23	0.53
35:BV:5:VAL:HG21	35:BV:35:LEU:HD23	1.90	0.53
42:B2:46:GLN:OE1	42:B2:46:GLN:HA	2.08	0.53
1:AA:1360:A:H8	1:AA:1360:A:OP1	1.90	0.53
23:AY:484:ARG:HB2	23:AY:602:LEU:HB2	1.89	0.53
25:BA:2032:G:H21	52:BE:146:THR:HG23	1.74	0.53
25:BA:2052:G:H4'	52:BE:143:ASN:O	2.07	0.53
25:BA:2134:A:C2	25:BA:2158:A:C5	2.95	0.53
46:B5:52:TYR:CD1	46:B5:52:TYR:C	2.86	0.53
1:AA:671:G:C2'	1:AA:672:U:H5'	2.39	0.53
1:AA:978:A:C4	1:AA:1319:A:C2	2.97	0.53
14:AT:100:ILE:O	14:AT:100:ILE:HG23	2.07	0.53
34:BU:91:ASP:O	34:BU:95:LEU:HB2	2.08	0.53
39:BZ:98:MET:HE2	39:BZ:100:VAL:HG22	1.90	0.53
43:BD:30:GLU:CG	43:BD:63:ARG:NH2	2.65	0.53
51:BC:92:ASP:N	51:BC:92:ASP:OD1	2.41	0.53
52:BE:116:VAL:HB	52:BE:122:PHE:CD2	2.43	0.53
55:BH:155:SER:CB	55:BH:156:ALA:HA	2.39	0.53
1:AA:633:G:C5'	1:AA:633:G:C8	2.92	0.53
10:AP:3:LYS:O	10:AP:21:VAL:HA	2.08	0.53
25:BA:2165:G:H2'	25:BA:2166:G:H5''	1.90	0.53
55:BH:41:MET:HE2	55:BH:43:VAL:HG13	1.91	0.53
56:BK:19:PRO:HD3	56:BK:35:MET:HE3	1.91	0.53
1:AA:396:G:O2'	1:AA:398:C:OP1	2.19	0.53
1:AA:973:G:H2'	1:AA:974:A:OP1	2.08	0.53
1:AA:1068:G:OP2	1:AA:1068:G:H8	1.91	0.53
20:AG:6:ARG:O	20:AG:7:ALA:HB3	2.07	0.53
23:AY:117:GLN:HA	23:AY:120:THR:OG1	2.08	0.53
23:AY:157:LEU:N	23:AY:157:LEU:HD23	2.23	0.53
25:BA:661:C:H4'	29:BP:16:ARG:NH1	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1024:G:H3'	25:BA:1025:G:H5''	1.91	0.53
25:BA:1570:A:H5'	43:BD:38:LYS:HG3	1.90	0.53
25:BA:2206:G:N3	25:BA:2206:G:H5''	2.24	0.53
25:BA:2298:A:H62	25:BA:2318:G:H8	1.55	0.53
28:BO:104:ARG:HH21	33:BT:33:LYS:HE2	1.74	0.53
29:BP:16:ARG:CZ	29:BP:18:ARG:HG3	2.39	0.53
29:BP:85:LEU:HA	29:BP:88:LEU:HD22	1.90	0.53
37:BX:27:THR:HA	37:BX:79:ALA:O	2.09	0.53
38:BY:96:ILE:CD1	38:BY:99:CYS:SG	2.92	0.53
56:BK:79:ARG:HD2	56:BK:85:GLU:O	2.09	0.53
1:AA:353:A:H2'	1:AA:354:G:OP2	2.09	0.53
1:AA:518:C:H5	1:AA:530:G:O5'	1.92	0.53
1:AA:1533:C:H4'	1:AA:1533:C:OP1	2.09	0.53
20:AG:26:PHE:CE2	20:AG:30:ILE:HD11	2.43	0.53
23:AY:250:THR:N	23:AY:255:ILE:HG22	2.23	0.53
25:BA:686:G:H1	48:B7:16:HIS:CE1	2.27	0.53
25:BA:1204:A:N1	25:BA:1241:A:C2	2.76	0.53
25:BA:1538:G:C4	25:BA:1539:G:N7	2.76	0.53
25:BA:1720:U:O2	25:BA:1742:G:O6	2.26	0.53
25:BA:1920:C:O2	25:BA:1920:C:O4'	2.23	0.53
25:BA:2019:A:H2'	25:BA:2020:A:O5'	2.08	0.53
25:BA:2109:U:H1'	25:BA:2181:G:N2	2.24	0.53
25:BA:2875:C:O2'	33:BT:3:ARG:HB2	2.09	0.53
31:BR:4:LEU:O	31:BR:5:LYS:HG2	2.09	0.53
32:BS:52:SER:CB	32:BS:55:ALA:HB3	2.38	0.53
34:BU:81:HIS:NE2	34:BU:117:GLN:HG3	2.23	0.53
51:BC:137:LEU:HD22	51:BC:138:PRO:HD2	1.89	0.53
1:AA:460:G:O6	1:AA:470:C:C5'	2.55	0.53
4:AJ:90:LEU:N	4:AJ:91:PRO:HD3	2.24	0.53
25:BA:8:A:H2'	25:BA:9:U:C6	2.44	0.53
25:BA:661:C:H4'	29:BP:16:ARG:HH12	1.74	0.53
25:BA:1364:G:N7	41:B1:3:LYS:HE2	2.24	0.53
25:BA:1833:U:O2	25:BA:1969:A:H2	1.90	0.53
29:BP:100:LEU:O	29:BP:105:LEU:O	2.26	0.53
31:BR:78:LYS:HE2	31:BR:83:ILE:HD11	1.90	0.53
50:B9:29:ASN:ND2	50:B9:32:HIS:CE1	2.66	0.53
54:BG:114:ILE:HG12	54:BG:140:ILE:HG21	1.90	0.53
57:BJ:106:ALA:O	57:BJ:107:ALA:CB	2.57	0.53
1:AA:1118:C:H1'	1:AA:1179:A:C4	2.44	0.53
25:BA:1742:G:H3'	25:BA:1742:G:C8	2.44	0.53
31:BR:2:ARG:CZ	52:BE:111:ARG:HG3	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:BC:76:ALA:HB3	51:BC:94:VAL:HG22	1.90	0.53
1:AA:602:A:H2'	1:AA:603:U:O4'	2.09	0.53
1:AA:1278:U:O2	1:AA:1278:U:O4'	2.26	0.53
15:AB:145:LEU:CD1	15:AB:149:LEU:HD12	2.39	0.53
17:AD:3:ARG:HG2	17:AD:118:ARG:CD	2.39	0.53
17:AD:11:LEU:HA	17:AD:13:ARG:O	2.09	0.53
25:BA:185:U:H4'	25:BA:218:A:H4'	1.91	0.53
25:BA:2138:C:O2	25:BA:2154:G:C2	2.62	0.53
31:BR:117:VAL:O	31:BR:117:VAL:HG12	2.09	0.53
43:BD:238:GLY:O	43:BD:239:ARG:O	2.26	0.53
46:B5:33:CYS:HB2	46:B5:40:LYS:CE	2.34	0.53
52:BE:55:ASN:C	52:BE:57:LYS:H	2.16	0.53
1:AA:421:U:O2	1:AA:421:U:O4'	2.27	0.52
1:AA:552:U:O2'	6:AL:86:ARG:O	2.27	0.52
1:AA:633:G:H8	1:AA:633:G:C5'	2.19	0.52
23:AY:201:ILE:H	23:AY:201:ILE:HD12	1.74	0.52
25:BA:613:G:H8	25:BA:613:G:C5'	2.20	0.52
25:BA:1243:G:H2'	25:BA:1244:G:O4'	2.09	0.52
25:BA:2063:C:O2	25:BA:2451:A:C2	2.62	0.52
29:BP:5:ASP:N	53:BF:116:ASP:OD2	2.42	0.52
29:BP:35:HIS:C	29:BP:36:LYS:HG3	2.33	0.52
29:BP:112:LEU:HD13	29:BP:114:ILE:HG22	1.90	0.52
30:BQ:68:ILE:HD13	30:BQ:103:MET:HE2	1.91	0.52
32:BS:66:ALA:HA	32:BS:69:VAL:HG12	1.91	0.52
43:BD:221:VAL:CG2	43:BD:226:MET:HE2	2.38	0.52
2:AV:10:G:H2'	2:AV:11:C:C6	2.43	0.52
25:BA:657:U:H2'	25:BA:658:C:C6	2.45	0.52
25:BA:1858:G:H8	25:BA:1858:G:OP2	1.92	0.52
25:BA:2096:U:OP1	25:BA:2096:U:H4'	2.09	0.52
25:BA:2306:C:H5	25:BA:2307:G:H1'	1.71	0.52
38:BY:42:VAL:CG1	38:BY:65:ALA:HB3	2.39	0.52
52:BE:1:MET:HG3	52:BE:83:ASP:HB2	1.92	0.52
1:AA:104:G:N7	14:AT:14:LYS:NZ	2.57	0.52
1:AA:427:U:OP2	17:AD:36:ARG:NH2	2.42	0.52
1:AA:539:A:H2'	1:AA:540:G:C8	2.44	0.52
1:AA:706:A:H2'	5:AK:31:THR:HG21	1.91	0.52
1:AA:986:A:C2	1:AA:1220:G:C2	2.98	0.52
16:AC:134:ILE:CG2	16:AC:168:ALA:HB3	2.39	0.52
25:BA:612:C:H2'	25:BA:613:G:H5''	1.91	0.52
25:BA:715:G:H2'	25:BA:716:A:O4'	2.08	0.52
25:BA:2305:A:H5''	54:BG:134:GLY:HA3	1.89	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2556:C:H2'	25:BA:2557:G:O4'	2.09	0.52
29:BP:17:LYS:C	29:BP:19:VAL:H	2.14	0.52
32:BS:99:LYS:C	32:BS:101:LEU:H	2.16	0.52
33:BT:24:PRO:HA	33:BT:49:VAL:O	2.08	0.52
37:BX:40:LYS:HG3	37:BX:51:VAL:HB	1.91	0.52
38:BY:79:CYS:HG	38:BY:80:GLY:N	2.02	0.52
52:BE:24:THR:CG2	52:BE:187:ALA:H	2.22	0.52
52:BE:117:MET:O	52:BE:118:LYS:CB	2.56	0.52
17:AD:28:SER:O	17:AD:30:LYS:N	2.36	0.52
25:BA:247:G:H4'	25:BA:386:G:C6	2.45	0.52
25:BA:889:C:H1'	25:BA:890:A:O4'	2.10	0.52
25:BA:1332:G:H5'	25:BA:1332:G:C8	2.44	0.52
25:BA:2111:C:H42	25:BA:2147:G:H1	1.56	0.52
25:BA:2492:U:H2'	25:BA:2493:U:H6	1.75	0.52
29:BP:13:ASN:OD1	53:BF:31:HIS:HB2	2.09	0.52
29:BP:59:LEU:HA	29:BP:61:ARG:CZ	2.39	0.52
30:BQ:21:THR:HG23	30:BQ:101:ARG:HB2	1.90	0.52
33:BT:82:LEU:N	33:BT:82:LEU:HD12	2.24	0.52
39:BZ:22:GLY:C	39:BZ:23:LYS:HD2	2.35	0.52
52:BE:47:VAL:HG13	52:BE:47:VAL:O	2.09	0.52
52:BE:55:ASN:O	52:BE:57:LYS:N	2.41	0.52
55:BH:173:PRO:O	55:BH:174:GLY:C	2.52	0.52
7:AM:54:VAL:O	7:AM:55:ARG:C	2.53	0.52
25:BA:652:C:C6	25:BA:652:C:OP2	2.62	0.52
25:BA:771:G:OP1	48:B7:10:ARG:NH1	2.42	0.52
25:BA:1506:C:O2	25:BA:1506:C:H2'	2.08	0.52
29:BP:51:PHE:HB3	29:BP:52:GLU:CG	2.39	0.52
43:BD:30:GLU:HB2	43:BD:35:LYS:HE3	1.90	0.52
45:B4:64:LYS:C	45:B4:65:CYS:SG	2.93	0.52
54:BG:5:VAL:HG12	54:BG:6:ALA:H	1.74	0.52
55:BH:6:ARG:CB	55:BH:65:HIS:NE2	2.73	0.52
12:AR:25:THR:HG22	12:AR:26:LEU:HG	1.92	0.52
15:AB:80:ILE:HD11	15:AB:208:ILE:HG23	1.92	0.52
15:AB:146:GLN:O	15:AB:150:SER:OG	2.27	0.52
16:AC:73:PRO:HB3	16:AC:103:VAL:HG11	1.91	0.52
25:BA:528:A:H2	25:BA:2043:C:H5'	1.74	0.52
25:BA:1403:C:H5''	25:BA:1471:A:C1'	2.40	0.52
25:BA:2415:G:H4'	29:BP:67:MET:N	2.24	0.52
37:BX:35:THR:O	37:BX:39:ILE:HG13	2.10	0.52
49:B8:6:THR:HB	49:B8:63:PRO:HG3	1.91	0.52
52:BE:2:LYS:HA	52:BE:84:PHE:CD2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BZ:24:LEU:CD2	39:BZ:25:PRO:O	2.57	0.52
47:B6:18:ARG:HG3	47:B6:19:ARG:N	2.25	0.52
49:B8:50:LEU:O	49:B8:51:ALA:CB	2.58	0.52
50:B9:10:ILE:HB	50:B9:32:HIS:CD2	2.44	0.52
55:BH:85:LYS:HE3	55:BH:145:ALA:HB1	1.92	0.52
56:BK:17:ALA:O	56:BK:35:MET:HE1	2.10	0.52
1:AA:187:C:O2'	14:AT:89:ARG:NH2	2.40	0.52
18:AE:12:LEU:HB3	18:AE:31:LEU:HB2	1.92	0.52
20:AG:23:VAL:HG13	20:AG:43:PHE:CE2	2.45	0.52
25:BA:1771:C:H1'	25:BA:1786:A:C8	2.44	0.52
25:BA:2141:G:H2'	25:BA:2142:C:C6	2.45	0.52
25:BA:2164:C:O2	25:BA:2164:C:O4'	2.25	0.52
25:BA:2611:U:H6	25:BA:2611:U:C5'	2.18	0.52
32:BS:42:ASP:O	32:BS:43:GLU:HB2	2.10	0.52
32:BS:88:ASP:OD2	32:BS:89:ARG:N	2.42	0.52
43:BD:24:ILE:O	43:BD:26:LYS:HB3	2.09	0.52
55:BH:23:ARG:C	55:BH:24:VAL:HG12	2.35	0.52
56:BK:41:PHE:CE1	56:BK:45:THR:HG21	2.45	0.52
1:AA:1074:G:O2'	1:AA:1101:A:N1	2.39	0.52
1:AA:1080:A:H5''	18:AE:16:THR:HG21	1.92	0.52
1:AA:1309:G:OP1	7:AM:88:ARG:NH1	2.42	0.52
25:BA:301:G:C4	25:BA:302:C:C5	2.98	0.52
25:BA:613:G:C5'	25:BA:613:G:C8	2.93	0.52
25:BA:2063:C:O2	25:BA:2450:A:N1	2.43	0.52
25:BA:2619:C:OP1	52:BE:152:LYS:NZ	2.39	0.52
33:BT:93:ARG:HH11	33:BT:93:ARG:CG	2.23	0.52
39:BZ:108:PRO:HA	39:BZ:142:SER:HA	1.91	0.52
57:BJ:21:ALA:H	57:BJ:88:ALA:HB1	1.73	0.52
1:AA:1020:U:H2'	1:AA:1021:G:C8	2.45	0.52
25:BA:84:A:N1	25:BA:98:G:O2'	2.35	0.52
25:BA:195:A:H61	25:BA:198:C:H3'	1.75	0.52
25:BA:807:U:OP2	29:BP:39:LYS:CG	2.51	0.52
25:BA:1170:G:N2	25:BA:1180:C:N3	2.58	0.52
25:BA:1667:G:O2'	25:BA:1991:U:O4	2.26	0.52
25:BA:1963:U:H4'	25:BA:1964:G:OP1	2.10	0.52
25:BA:2262:U:H4'	25:BA:2328:A:C2	2.45	0.52
26:BB:14:U:OP2	26:BB:70:C:O2'	2.25	0.52
29:BP:130:PHE:CB	29:BP:135:LEU:HD23	2.39	0.52
31:BR:55:ALA:HB2	31:BR:79:LEU:HD13	1.91	0.52
39:BZ:153:SER:HA	39:BZ:155:LEU:HD23	1.91	0.52
49:B8:61:LEU:HD23	49:B8:61:LEU:H	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:BK:7:VAL:HG13	56:BK:7:VAL:O	2.08	0.52
18:AE:37:ARG:C	18:AE:38:GLN:HG2	2.34	0.51
18:AE:91:LEU:HG	18:AE:118:ILE:HD11	1.92	0.51
19:AF:60:PHE:C	19:AF:61:LEU:HD12	2.34	0.51
23:AY:493:VAL:HG23	23:AY:512:ILE:CD1	2.40	0.51
25:BA:1430:C:H2'	25:BA:1431:U:C6	2.45	0.51
25:BA:2518:A:H5'	25:BA:2518:A:C8	2.44	0.51
43:BD:166:GLN:HB2	43:BD:174:ILE:HG22	1.91	0.51
56:BK:58:THR:O	56:BK:66:THR:HG22	2.09	0.51
56:BK:99:ILE:HG23	56:BK:103:GLN:CB	2.39	0.51
1:AA:757:U:H2'	1:AA:758:G:O4'	2.10	0.51
1:AA:992:U:H4'	1:AA:993:G:O5'	2.09	0.51
1:AA:1531:A:O3'	1:AA:1532:U:H6	1.92	0.51
17:AD:36:ARG:HG2	17:AD:36:ARG:HH11	1.75	0.51
25:BA:271(O):C:O2'	25:BA:271(P):C:P	2.68	0.51
25:BA:1296:G:OP1	25:BA:2709:G:O2'	2.23	0.51
25:BA:1299:G:H5'	25:BA:1301:A:O4'	2.10	0.51
25:BA:2261:C:O2'	25:BA:2262:U:H5'	2.10	0.51
32:BS:59:LYS:HB3	32:BS:65:VAL:HG22	1.92	0.51
33:BT:32:TYR:HD2	33:BT:81:PRO:O	1.92	0.51
43:BD:44:ASN:HB2	43:BD:49:ILE:HA	1.90	0.51
43:BD:77:ALA:HB2	43:BD:97:TYR:CE2	2.44	0.51
52:BE:75:VAL:O	52:BE:77:ILE:N	2.43	0.51
55:BH:19:VAL:HG11	55:BH:44:VAL:HA	1.93	0.51
1:AA:633:G:H5''	1:AA:633:G:C8	2.43	0.51
5:AK:82:VAL:O	5:AK:109:VAL:HG23	2.10	0.51
11:AQ:40:LYS:HD3	11:AQ:42:TYR:CZ	2.46	0.51
22:AI:16:ARG:HB2	22:AI:64:THR:HG22	1.92	0.51
23:AY:603:GLU:HG2	23:AY:679:VAL:HG13	1.92	0.51
25:BA:614:U:O2	25:BA:614:U:O4'	2.25	0.51
25:BA:1156:A:OP1	34:BU:55:ARG:NH1	2.43	0.51
25:BA:1385:G:H4'	25:BA:1386:C:OP1	2.10	0.51
25:BA:1681:G:O2'	25:BA:1762:A:N3	2.40	0.51
25:BA:2469:A:H2	25:BA:2481:G:H21	1.58	0.51
25:BA:2579:C:H2'	25:BA:2580:U:O4'	2.11	0.51
28:BO:64:ARG:HG2	28:BO:79:PHE:CG	2.45	0.51
33:BT:45:PHE:CE2	33:BT:63:VAL:HG12	2.45	0.51
34:BU:92:ARG:O	34:BU:93:LYS:C	2.54	0.51
1:AA:552:U:H4'	6:AL:86:ARG:HG2	1.93	0.51
1:AA:939:G:C6	1:AA:940:C:N4	2.78	0.51
1:AA:1140:C:C2	1:AA:1141:C:C5	2.98	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AB:211:ILE:HG23	15:AB:215:LEU:HD23	1.92	0.51
23:AY:211:GLU:O	23:AY:215:LYS:HB2	2.10	0.51
25:BA:958:U:O2	26:BB:90:A:H4'	2.11	0.51
25:BA:1847:A:C5'	25:BA:1848:A:OP2	2.59	0.51
25:BA:2116:G:H3'	25:BA:2117:A:C8	2.45	0.51
25:BA:2391:G:OP1	49:B8:32:LEU:HD12	2.11	0.51
26:BB:78:A:C2	26:BB:100:A:C4	2.98	0.51
43:BD:43:ARG:HB2	43:BD:54:ARG:HB2	1.91	0.51
49:B8:50:LEU:O	49:B8:51:ALA:HB3	2.10	0.51
53:BF:64:ILE:HD12	53:BF:64:ILE:O	2.11	0.51
56:BK:112:MET:CE	56:BK:120:LEU:HD21	2.41	0.51
1:AA:680:C:O2'	43:BD:166:GLN:CG	2.59	0.51
1:AA:1371:G:C5	1:AA:1372:U:C5	2.99	0.51
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.46	0.51
2:AV:72:C:C6	2:AV:72:C:C3'	2.94	0.51
15:AB:166:ASP:HB3	15:AB:169:LYS:HB3	1.93	0.51
25:BA:285:C:O2'	25:BA:286:C:H5'	2.09	0.51
25:BA:479:A:H4'	25:BA:480:A:OP1	2.11	0.51
25:BA:1021:A:H3'	25:BA:1021:A:C8	2.45	0.51
25:BA:1447:G:HO2'	25:BA:1544:A:H8	0.69	0.51
25:BA:1478:G:O2'	25:BA:1558:A:N1	2.43	0.51
25:BA:1789:A:C2'	25:BA:1790:C:H5'	2.39	0.51
25:BA:2291:U:O2'	25:BA:2374:C:O2	2.28	0.51
25:BA:2822:G:OP2	52:BE:110:GLY:O	2.28	0.51
26:BB:40:U:H3'	26:BB:41:U:C5'	2.41	0.51
26:BB:117:G:H5'	32:BS:55:ALA:HB1	1.92	0.51
42:B2:9:GLN:NE2	42:B2:56:GLN:HG2	2.26	0.51
53:BF:101:LEU:O	53:BF:106:ARG:NH1	2.36	0.51
56:BK:77:LEU:HD13	56:BK:110:GLN:OE1	2.11	0.51
1:AA:685:G:O2'	1:AA:686:U:H5'	2.10	0.51
1:AA:1293:G:H8	1:AA:1293:G:C5'	2.22	0.51
25:BA:566:U:H2'	25:BA:567:A:O4'	2.10	0.51
25:BA:1039:G:C2'	25:BA:1040:C:H5'	2.41	0.51
25:BA:2136:C:N3	25:BA:2137:C:H5	2.07	0.51
25:BA:2199:A:H3'	25:BA:2200:C:H6	1.76	0.51
28:BO:64:ARG:HG2	28:BO:79:PHE:CD2	2.46	0.51
33:BT:28:VAL:O	33:BT:29:ARG:HB2	2.10	0.51
55:BH:148:ILE:O	55:BH:162:ILE:HD11	2.11	0.51
1:AA:1269:A:H5''	1:AA:1270:C:OP2	2.10	0.51
10:AP:20:VAL:HG21	10:AP:32:TYR:CE1	2.45	0.51
25:BA:221:A:H2'	25:BA:266:G:N7	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:832:G:O2'	29:BP:52:GLU:HB3	2.11	0.51
25:BA:1281:G:C8	25:BA:1281:G:H5''	2.45	0.51
25:BA:2098:U:O2'	25:BA:2099:U:OP2	2.22	0.51
25:BA:2887:U:H2'	25:BA:2888:C:C6	2.46	0.51
28:BO:77:ILE:CD1	33:BT:74:ARG:HD3	2.41	0.51
34:BU:90:VAL:C	34:BU:92:ARG:N	2.69	0.51
38:BY:98:VAL:O	38:BY:98:VAL:CG1	2.58	0.51
39:BZ:124:ILE:HD13	39:BZ:155:LEU:HD11	1.91	0.51
39:BZ:151:HIS:HA	39:BZ:171:ILE:HG12	1.93	0.51
41:B1:68:PRO:O	41:B1:69:LYS:C	2.52	0.51
51:BC:66:HIS:CD2	51:BC:184:LYS:CG	2.94	0.51
5:AK:48:ILE:HD13	5:AK:48:ILE:N	2.26	0.51
7:AM:52:GLU:O	7:AM:56:LEU:HB2	2.11	0.51
9:AO:54:ARG:O	9:AO:58:MET:HG3	2.10	0.51
17:AD:61:LYS:HA	17:AD:203:VAL:HG22	1.92	0.51
23:AY:463:VAL:C	23:AY:465:ARG:H	2.19	0.51
25:BA:528:A:C2	25:BA:2043:C:H5'	2.46	0.51
25:BA:1046:A:C8	57:BJ:5:ALA:HB3	2.45	0.51
25:BA:1126:A:H8	25:BA:1126:A:OP1	1.93	0.51
25:BA:1281:G:H5''	25:BA:1281:G:H8	1.76	0.51
25:BA:1678:G:H22	25:BA:1989:G:H22	1.59	0.51
25:BA:2586:C:H6	25:BA:2586:C:O5'	1.93	0.51
29:BP:57:THR:HB	29:BP:59:LEU:N	2.26	0.51
33:BT:28:VAL:HG22	33:BT:46:GLU:HA	1.93	0.51
35:BV:15:GLU:O	35:BV:16:PRO:C	2.53	0.51
41:B1:3:LYS:HB3	41:B1:61:ARG:NH2	2.26	0.51
1:AA:1285:A:H4'	1:AA:1286:A:O5'	2.11	0.51
1:AA:1347:G:OP2	22:AI:107:ARG:HG2	2.10	0.51
5:AK:40:ILE:HG23	5:AK:75:TYR:CD2	2.46	0.51
6:AL:18:VAL:HG23	6:AL:19:ARG:N	2.26	0.51
15:AB:7:VAL:O	15:AB:11:LEU:HD12	2.10	0.51
15:AB:168:THR:CG2	15:AB:192:SER:HA	2.41	0.51
23:AY:461:ILE:C	23:AY:461:ILE:HD12	2.36	0.51
25:BA:319:C:H2'	25:BA:320:A:O5'	2.11	0.51
25:BA:806:C:OP1	29:BP:39:LYS:HB3	2.11	0.51
25:BA:1187:G:H8	25:BA:1187:G:O5'	1.92	0.51
25:BA:2312:U:H4'	54:BG:71:THR:CG2	2.40	0.51
25:BA:2387:U:OP1	40:B0:55:ARG:NH2	2.44	0.51
26:BB:75:G:H5''	26:BB:76:G:OP2	2.11	0.51
28:BO:115:VAL:HG13	28:BO:121:VAL:HG21	1.93	0.51
38:BY:39:VAL:O	38:BY:40:GLU:OE1	2.29	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:B6:19:ARG:CG	47:B6:20:ASN:N	2.70	0.51
52:BE:128:SER:O	52:BE:129:HIS:C	2.53	0.51
1:AA:1532:U:H3'	1:AA:1533:C:H5''	1.92	0.51
25:BA:537:C:H4'	27:BN:3:THR:HG21	1.92	0.51
25:BA:1210:A:C5'	25:BA:1210:A:C8	2.94	0.51
25:BA:2134:A:H8	25:BA:2159:G:HO2'	1.57	0.51
29:BP:18:ARG:HB3	29:BP:18:ARG:CZ	2.41	0.51
41:B1:82:LEU:O	41:B1:83:GLU:OE1	2.29	0.51
51:BC:82:LYS:O	51:BC:83:ILE:C	2.53	0.51
1:AA:148:G:O2'	1:AA:149:A:H5'	2.11	0.50
1:AA:1015:A:H2'	1:AA:1016:A:C8	2.46	0.50
1:AA:1135:U:O2	1:AA:1135:U:H2'	2.10	0.50
1:AA:1436:U:OP1	14:AT:23:ARG:NH2	2.43	0.50
12:AR:32:ARG:HD2	12:AR:65:ILE:CG2	2.42	0.50
23:AY:180:VAL:O	23:AY:182:ARG:N	2.44	0.50
23:AY:342:TYR:CE1	23:AY:347:GLY:HA2	2.46	0.50
25:BA:857:C:N4	25:BA:858:U:O4	2.44	0.50
25:BA:2678:C:H2'	25:BA:2679:A:O4'	2.11	0.50
27:BN:56:ASN:O	27:BN:57:ALA:O	2.29	0.50
31:BR:83:ILE:O	31:BR:86:ARG:HB2	2.12	0.50
32:BS:34:HIS:HB3	32:BS:53:SER:HB3	1.93	0.50
33:BT:28:VAL:CG2	33:BT:46:GLU:HG3	2.41	0.50
38:BY:8:LYS:HE2	38:BY:72:VAL:O	2.10	0.50
56:BK:71:THR:HB	56:BK:72:PRO:HD2	1.92	0.50
1:AA:1293:G:C5'	1:AA:1293:G:C8	2.95	0.50
1:AA:1352:C:O2	1:AA:1371:G:C2	2.64	0.50
2:AV:27:G:N1	2:AV:43:C:H5	2.00	0.50
23:AY:377:VAL:CG2	23:AY:380:LEU:HD22	2.41	0.50
25:BA:285:C:H2'	25:BA:286:C:H6	1.75	0.50
25:BA:1025:G:C4	25:BA:1135:C:H1'	2.47	0.50
25:BA:1054:A:H4'	25:BA:1054:A:OP1	2.12	0.50
25:BA:1477:A:C2	25:BA:1515:G:C2	3.00	0.50
25:BA:2137:C:H5'	25:BA:2138:C:OP2	2.11	0.50
25:BA:2252:G:O6	40:B0:4:LYS:HB3	2.10	0.50
40:B0:43:THR:O	40:B0:43:THR:CG2	2.57	0.50
1:AA:310:G:H5''	10:AP:31:LYS:HB2	1.93	0.50
1:AA:706:A:C1'	5:AK:29:ILE:HD11	2.39	0.50
1:AA:1125:U:O2'	1:AA:1126:U:OP2	2.20	0.50
1:AA:1187:G:H5''	1:AA:1187:G:H8	1.76	0.50
1:AA:1212:U:C6	1:AA:1212:U:H5'	2.46	0.50
15:AB:15:VAL:H	15:AB:16:HIS:CD2	2.30	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:628:G:H4'	25:BA:651:G:O2'	2.10	0.50
25:BA:686:G:C4	48:B7:11:LYS:HG2	2.47	0.50
25:BA:813:U:O2'	25:BA:1225:G:H1'	2.10	0.50
25:BA:1048:A:C4'	25:BA:1049:C:OP1	2.57	0.50
25:BA:1449:A:H5''	25:BA:1449:A:H8	1.75	0.50
25:BA:1709:U:H2'	25:BA:1710:C:C6	2.47	0.50
25:BA:2331:G:C4'	40:B0:42:GLY:HA3	2.42	0.50
25:BA:2441:C:OP2	25:BA:2586:C:O2'	2.29	0.50
26:BB:40:U:C2	26:BB:43:C:OP2	2.63	0.50
33:BT:91:ARG:O	33:BT:117:ASP:HB2	2.11	0.50
37:BX:27:THR:HB	37:BX:80:ILE:HB	1.94	0.50
47:B6:18:ARG:CG	47:B6:19:ARG:N	2.74	0.50
52:BE:67:PHE:O	52:BE:70:ALA:N	2.44	0.50
55:BH:64:LEU:O	55:BH:68:THR:OG1	2.18	0.50
55:BH:83:TYR:HB3	55:BH:134:SER:CA	2.41	0.50
2:AV:52:G:C2	2:AV:63:G:C2	2.99	0.50
25:BA:590:A:OP1	53:BF:95:ARG:NH1	2.44	0.50
25:BA:848:G:H2'	25:BA:849:A:C8	2.46	0.50
25:BA:1817:G:H2'	25:BA:1818:U:H5'	1.93	0.50
33:BT:3:ARG:HG3	33:BT:6:LEU:CB	2.40	0.50
39:BZ:166:SER:OG	39:BZ:167:PRO:C	2.55	0.50
21:AH:114:THR:HG21	21:AH:119:LEU:HD12	1.94	0.50
23:AY:78:ARG:C	23:AY:79:ILE:HD12	2.36	0.50
25:BA:336:C:H5''	38:BY:7:VAL:HG21	1.94	0.50
25:BA:1504:C:O2'	25:BA:1505:C:O5'	2.30	0.50
25:BA:1668:A:O2'	25:BA:1674:G:N7	2.39	0.50
25:BA:2121:G:H2'	25:BA:2122:U:C6	2.47	0.50
25:BA:2420:C:OP1	49:B8:34:TRP:HB2	2.11	0.50
29:BP:17:LYS:O	29:BP:19:VAL:HG22	2.12	0.50
29:BP:33:ARG:O	29:BP:34:GLY:C	2.54	0.50
35:BV:39:LEU:HB3	35:BV:47:VAL:HG21	1.93	0.50
53:BF:138:GLU:O	53:BF:141:ALA:HB3	2.12	0.50
54:BG:81:LYS:O	54:BG:82:LEU:O	2.28	0.50
1:AA:979:C:H3'	1:AA:980:C:H5'	1.94	0.50
1:AA:1060:C:C5	16:AC:2:GLY:HA2	2.46	0.50
1:AA:1302:U:C5	7:AM:17:VAL:HG21	2.46	0.50
1:AA:1531:A:H2'	1:AA:1532:U:C5	2.46	0.50
17:AD:7:PRO:HB2	17:AD:10:ARG:HD2	1.93	0.50
18:AE:50:GLU:CD	18:AE:51:VAL:H	2.19	0.50
25:BA:910:A:C6	25:BA:911:A:C6	2.99	0.50
25:BA:1260:G:H2'	25:BA:1261:C:O4'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2355:C:H4'	40:B0:36:ILE:HD11	1.94	0.50
29:BP:108:LYS:C	29:BP:110:TYR:H	2.20	0.50
30:BQ:78:PRO:HG2	30:BQ:81:VAL:HG11	1.92	0.50
33:BT:23:ARG:C	33:BT:25:GLY:N	2.69	0.50
51:BC:77:ILE:HG22	51:BC:119:VAL:HG21	1.94	0.50
1:AA:63:C:C5'	1:AA:63:C:H6	2.24	0.50
1:AA:160:A:H2'	1:AA:161:A:O4'	2.12	0.50
1:AA:530:G:H3'	1:AA:531:U:C5'	2.41	0.50
1:AA:630:G:H5''	1:AA:630:G:H8	1.74	0.50
1:AA:738:C:OP1	19:AF:2:ARG:NH1	2.45	0.50
1:AA:1169:A:H2'	1:AA:1170:A:C8	2.47	0.50
2:AV:4:C:O2'	25:BA:1850:G:H4'	2.12	0.50
13:AS:31:ILE:O	13:AS:31:ILE:HG23	2.11	0.50
23:AY:138:LYS:HE2	60:AY:702:GCP:C4	2.42	0.50
25:BA:1241:A:C2'	25:BA:1242:A:O5'	2.60	0.50
25:BA:1721:G:N1	25:BA:1739:U:OP2	2.45	0.50
25:BA:1901:A:OP2	25:BA:1901:A:H4'	2.12	0.50
25:BA:2206:G:N3	25:BA:2206:G:H3'	2.27	0.50
27:BN:132:ALA:C	27:BN:133:GLN:O	2.54	0.50
33:BT:55:ASN:O	33:BT:57:PHE:O	2.29	0.50
40:B0:11:ARG:O	40:B0:14:ARG:NH2	2.45	0.50
42:B2:39:ALA:HA	42:B2:45:SER:HB3	1.94	0.50
58:BL:113:UNK:HA	58:BL:117:UNK:O	2.12	0.50
1:AA:583:A:H2'	1:AA:584:G:O4'	2.12	0.50
1:AA:1138:G:OP1	1:AA:1140:C:C1'	2.60	0.50
1:AA:1269:A:C2	1:AA:1313:U:O4'	2.64	0.50
1:AA:1351:U:O4'	20:AG:33:ASP:HB3	2.11	0.50
6:AL:90:VAL:O	6:AL:92:ASP:N	2.41	0.50
16:AC:42:LEU:HD22	16:AC:94:LEU:HD23	1.93	0.50
25:BA:1658:C:OP1	52:BE:132:HIS:ND1	2.44	0.50
25:BA:2136:C:N3	25:BA:2137:C:C5	2.80	0.50
25:BA:2789:C:OP1	25:BA:2789:C:H4'	2.12	0.50
29:BP:130:PHE:CG	29:BP:135:LEU:HD23	2.46	0.50
30:BQ:14:ARG:HG2	30:BQ:41:TRP:HH2	1.77	0.50
38:BY:96:ILE:HG21	38:BY:99:CYS:SG	2.51	0.50
1:AA:961:U:OP2	1:AA:1223:C:H1'	2.12	0.50
1:AA:1037:C:C4	1:AA:1038:C:N4	2.80	0.50
1:AA:1143:G:H8	1:AA:1143:G:O5'	1.94	0.50
8:AN:15:LYS:O	8:AN:16:PHE:O	2.30	0.50
14:AT:89:ARG:CZ	14:AT:104:LEU:HD21	2.42	0.50
25:BA:7:G:H2'	25:BA:8:A:O4'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:316:C:H2'	25:BA:317:G:O5'	2.11	0.50
25:BA:1058:G:H5''	25:BA:1058:G:H8	1.75	0.50
25:BA:1418:G:H8	25:BA:1418:G:O5'	1.95	0.50
25:BA:1615:C:C2	36:BW:87:PRO:HG2	2.47	0.50
25:BA:2824:C:H2'	25:BA:2825:C:O4'	2.12	0.50
26:BB:13:A:N1	26:BB:69:G:O2'	2.39	0.50
27:BN:131:GLN:HE22	27:BN:134:ARG:HH21	1.59	0.50
38:BY:13:VAL:HG13	38:BY:72:VAL:HB	1.94	0.50
51:BC:65:PRO:O	51:BC:188:ASN:OD1	2.30	0.50
53:BF:18:ARG:NH2	53:BF:20:LEU:HD12	2.27	0.50
54:BG:96:ARG:O	54:BG:97:ASP:C	2.55	0.50
56:BK:134:MET:HG3	56:BK:136:VAL:HG12	1.94	0.50
1:AA:1147:C:O2	22:AI:16:ARG:NH1	2.44	0.49
1:AA:1367:C:OP2	22:AI:112:LYS:NZ	2.45	0.49
25:BA:94:C:H5'	25:BA:94(A):G:OP2	2.11	0.49
25:BA:467:G:OP1	48:B7:33:ARG:NH1	2.44	0.49
25:BA:2821:A:OP2	52:BE:110:GLY:O	2.30	0.49
26:BB:12:C:O2'	40:B0:74:ARG:HG2	2.12	0.49
26:BB:77:U:P	39:BZ:19:ARG:NH2	2.85	0.49
35:BV:47:VAL:HB	35:BV:49:THR:O	2.12	0.49
49:B8:50:LEU:HA	49:B8:53:PRO:HD3	1.94	0.49
52:BE:132:HIS:CD2	52:BE:135:HIS:NE2	2.80	0.49
53:BF:53:THR:HB	53:BF:56:GLU:OE2	2.12	0.49
55:BH:89:ILE:HD13	55:BH:94:TYR:CB	2.42	0.49
55:BH:89:ILE:HD13	55:BH:94:TYR:HB3	1.93	0.49
1:AA:1263:C:C2	1:AA:1273:G:N2	2.81	0.49
14:AT:100:ILE:C	14:AT:102:GLY:N	2.70	0.49
16:AC:95:THR:C	16:AC:97:LYS:H	2.19	0.49
23:AY:162:VAL:CG2	23:AY:255:ILE:HG12	2.41	0.49
23:AY:286:ILE:O	23:AY:287:PRO:C	2.55	0.49
25:BA:664:C:H4'	25:BA:941:A:OP1	2.11	0.49
25:BA:907:U:OP1	30:BQ:24:GLY:N	2.42	0.49
25:BA:2814:C:O2'	46:B5:29:THR:HG21	2.12	0.49
26:BB:81:G:O6	26:BB:96:U:C2	2.66	0.49
31:BR:2:ARG:NE	52:BE:111:ARG:HA	2.27	0.49
35:BV:69:LYS:HA	35:BV:87:HIS:O	2.12	0.49
43:BD:32:SER:O	43:BD:36:PRO:HD3	2.12	0.49
43:BD:83:GLU:OE1	43:BD:104:TYR:OH	2.27	0.49
1:AA:1293:G:H5''	1:AA:1293:G:C8	2.44	0.49
4:AJ:54:PHE:CZ	4:AJ:55:LYS:HE3	2.47	0.49
7:AM:40:ASN:HB3	7:AM:43:THR:HG23	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AM:87:TYR:O	7:AM:91:ARG:HG2	2.12	0.49
15:AB:32:ILE:HD11	15:AB:40:HIS:CG	2.47	0.49
15:AB:167:PRO:HG3	15:AB:188:ALA:HB2	1.94	0.49
15:AB:211:ILE:CG2	15:AB:215:LEU:HD23	2.43	0.49
20:AG:44:TYR:O	20:AG:45:ASP:C	2.55	0.49
20:AG:116:ALA:O	20:AG:120:ILE:HD12	2.12	0.49
23:AY:98:MET:HA	23:AY:98:MET:CE	2.42	0.49
25:BA:1204:A:N1	25:BA:1241:A:N1	2.61	0.49
25:BA:2420:C:OP1	49:B8:34:TRP:CB	2.60	0.49
26:BB:4:C:H2'	26:BB:5:C:O4'	2.11	0.49
33:BT:83:ILE:HG13	33:BT:84:GLN:H	1.76	0.49
52:BE:67:PHE:O	52:BE:68:ALA:C	2.55	0.49
54:BG:60:LEU:HD13	54:BG:60:LEU:C	2.37	0.49
1:AA:652:U:O4	1:AA:752:G:O2'	2.24	0.49
1:AA:1173:G:H2'	1:AA:1174:G:O4'	2.11	0.49
1:AA:1541:U:H2'	1:AA:1542:U:H4'	1.94	0.49
15:AB:17:PHE:CB	15:AB:44:LEU:HD21	2.42	0.49
15:AB:165:VAL:HG23	15:AB:166:ASP:N	2.27	0.49
18:AE:32:VAL:HB	18:AE:58:ALA:HB1	1.93	0.49
23:AY:546:ILE:HG12	23:AY:590:ILE:HG13	1.95	0.49
25:BA:1644:C:H2'	25:BA:1645:G:H5'	1.94	0.49
25:BA:2291:U:OP1	25:BA:2381:C:H5'	2.13	0.49
25:BA:2334:G:N3	32:BS:18:ILE:HD12	2.27	0.49
25:BA:2787:C:H1'	52:BE:61:ARG:HD3	1.94	0.49
26:BB:1:U:O2	26:BB:1:U:C2'	2.61	0.49
43:BD:13:ARG:HD2	43:BD:16:MET:CE	2.43	0.49
51:BC:23:ASP:O	51:BC:24:GLU:C	2.56	0.49
51:BC:84:LYS:C	51:BC:86:ALA:H	2.20	0.49
1:AA:1486:G:H2'	1:AA:1487:G:O4'	2.12	0.49
13:AS:19:VAL:O	13:AS:22:LEU:HB2	2.13	0.49
15:AB:33:TYR:HB2	15:AB:43:ASP:HB2	1.94	0.49
15:AB:223:ILE:O	15:AB:224:GLN:C	2.55	0.49
25:BA:582:G:H2'	25:BA:583:G:C8	2.48	0.49
25:BA:2165:G:H2'	25:BA:2166:G:C5'	2.42	0.49
25:BA:2285:C:OP2	47:B6:27:LYS:HB3	2.12	0.49
33:BT:28:VAL:O	33:BT:29:ARG:CG	2.60	0.49
38:BY:77:PRO:O	38:BY:78:ALA:CB	2.61	0.49
52:BE:46:ALA:HA	52:BE:82:ARG:O	2.13	0.49
52:BE:60:ASN:N	52:BE:60:ASN:ND2	2.50	0.49
53:BF:103:LYS:HA	53:BF:106:ARG:HG3	1.94	0.49
1:AA:706:A:C4'	5:AK:29:ILE:HD11	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AN:47:LEU:O	8:AN:48:ALA:C	2.56	0.49
15:AB:165:VAL:O	15:AB:187:LEU:O	2.30	0.49
25:BA:1058:G:OP1	25:BA:1058:G:H4'	2.11	0.49
43:BD:24:ILE:HD13	43:BD:25:THR:N	2.27	0.49
47:B6:41:PRO:O	47:B6:42:TRP:C	2.55	0.49
54:BG:4:ASP:HB2	54:BG:8:LYS:HG2	1.95	0.49
57:BJ:6:ALA:O	57:BJ:7:ALA:HB3	2.13	0.49
1:AA:33:A:N3	6:AL:32:PHE:HE2	2.10	0.49
1:AA:1066:C:O2'	1:AA:1067:A:H5'	2.13	0.49
1:AA:1152:A:H2'	1:AA:1153:C:C6	2.46	0.49
13:AS:9:VAL:O	13:AS:11:VAL:N	2.45	0.49
23:AY:413:ILE:HG21	23:AY:451:ILE:HD12	1.95	0.49
25:BA:90:U:C2'	25:BA:92:A:OP2	2.55	0.49
25:BA:1150:C:H2'	25:BA:1151:G:O4'	2.13	0.49
25:BA:1299:G:H5''	25:BA:1301:A:H5''	1.94	0.49
25:BA:2151:G:H5''	25:BA:2151:G:C8	2.48	0.49
26:BB:50:G:OP1	32:BS:62:LYS:HB2	2.12	0.49
27:BN:42:TRP:O	34:BU:64:ARG:NH1	2.38	0.49
28:BO:1:MET:HE2	28:BO:32:TYR:CE2	2.48	0.49
28:BO:23:ARG:HG3	28:BO:24:VAL:N	2.27	0.49
29:BP:23:PRO:O	29:BP:33:ARG:NH1	2.46	0.49
29:BP:66:GLY:O	29:BP:67:MET:HB3	2.12	0.49
31:BR:45:ARG:HA	31:BR:95:THR:HG21	1.94	0.49
32:BS:89:ARG:HG2	32:BS:92:TYR:HA	1.93	0.49
38:BY:28:LYS:O	38:BY:29:GLU:C	2.56	0.49
46:B5:50:GLY:O	46:B5:51:TYR:CB	2.60	0.49
47:B6:15:GLU:HG2	47:B6:18:ARG:HE	1.78	0.49
56:BK:17:ALA:HB3	56:BK:38:VAL:HG13	1.93	0.49
57:BJ:124:ALA:HB3	57:BJ:127:ALA:HB3	1.93	0.49
1:AA:790:A:H2'	1:AA:791:G:C8	2.47	0.49
1:AA:1118:C:H1'	1:AA:1179:A:C5	2.48	0.49
1:AA:1297:C:N3	20:AG:115:ARG:NH2	2.61	0.49
16:AC:180:ALA:O	16:AC:181:ASN:CB	2.56	0.49
21:AH:112:LEU:N	21:AH:112:LEU:HD23	2.27	0.49
25:BA:263:C:O2'	25:BA:429:A:N3	2.40	0.49
25:BA:492:A:H2'	25:BA:493:G:O4'	2.13	0.49
25:BA:570:G:C6	25:BA:2030:A:C2	3.00	0.49
25:BA:638:G:C5	25:BA:651:G:C2	3.00	0.49
25:BA:748:G:C8	36:BW:89:ALA:HB1	2.48	0.49
25:BA:1076:C:O2'	25:BA:1076:C:O2	2.31	0.49
25:BA:1451:C:N3	25:BA:1459:G:O6	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2103:C:C3'	25:BA:2104:G:H5''	2.42	0.49
25:BA:2327:A:H2'	25:BA:2328:A:C8	2.48	0.49
33:BT:5:ALA:O	33:BT:6:LEU:C	2.55	0.49
39:BZ:23:LYS:HD2	39:BZ:23:LYS:N	2.27	0.49
41:B1:8:SER:HB3	41:B1:66:HIS:CD2	2.48	0.49
41:B1:40:ARG:HD3	41:B1:40:ARG:C	2.38	0.49
49:B8:50:LEU:HD12	49:B8:51:ALA:H	1.78	0.49
51:BC:138:PRO:HA	51:BC:144:THR:OG1	2.13	0.49
1:AA:1277:C:O2'	1:AA:1279:A:C8	2.63	0.49
6:AL:60:LEU:HB2	6:AL:64:TYR:O	2.12	0.49
23:AY:129:LYS:HB3	23:AY:253:LEU:HD11	1.95	0.49
23:AY:343:ASN:HD22	23:AY:343:ASN:C	2.20	0.49
25:BA:637:A:H4'	25:BA:638:G:O5'	2.13	0.49
25:BA:674:G:O2'	53:BF:74:ARG:HD3	2.13	0.49
25:BA:1241:A:H2'	25:BA:1242:A:O5'	2.13	0.49
29:BP:62:LEU:CD1	49:B8:30:ARG:HG2	2.42	0.49
35:BV:64:HIS:CE1	35:BV:92:THR:HG22	2.47	0.49
47:B6:19:ARG:NH1	47:B6:43:CYS:SG	2.81	0.49
52:BE:69:LYS:C	52:BE:71:GLY:H	2.20	0.49
56:BK:57:ILE:HD12	56:BK:57:ILE:N	2.28	0.49
1:AA:59:A:C2'	1:AA:60:A:OP1	2.61	0.49
1:AA:946:A:H2'	1:AA:947:G:C8	2.48	0.49
4:AJ:24:VAL:O	4:AJ:25:GLU:C	2.56	0.49
17:AD:32:ALA:O	17:AD:36:ARG:N	2.46	0.49
23:AY:179:ASP:C	23:AY:180:VAL:O	2.56	0.49
25:BA:196:A:O2'	25:BA:805:G:O6	2.21	0.49
30:BQ:42:ILE:HD13	30:BQ:97:VAL:HB	1.95	0.49
36:BW:5:ALA:CB	36:BW:50:VAL:HG23	2.43	0.49
37:BX:57:LEU:HD22	37:BX:78:LYS:HG2	1.94	0.49
39:BZ:188:ALA:O	39:BZ:189:ALA:C	2.55	0.49
49:B8:51:ALA:O	49:B8:54:GLU:HB2	2.13	0.49
52:BE:14:ILE:HD11	52:BE:173:VAL:HG11	1.94	0.49
52:BE:16:ARG:O	52:BE:18:ASP:N	2.46	0.49
52:BE:201:THR:OG1	52:BE:202:LYS:N	2.46	0.49
53:BF:185:ASP:OD1	53:BF:188:ARG:NH1	2.41	0.49
1:AA:45:U:H2'	1:AA:46:G:C8	2.47	0.48
1:AA:1226:C:OP1	13:AS:81:ARG:HD2	2.13	0.48
2:AV:56:C:H2'	2:AV:57:G:H5''	1.94	0.48
15:AB:91:PRO:HG3	15:AB:155:LEU:HB2	1.94	0.48
25:BA:1356:G:N2	25:BA:1376:C:C2	2.81	0.48
25:BA:1632:A:C5	25:BA:1633:G:C6	3.01	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1914:C:O2'	25:BA:1915:U:O4'	2.30	0.48
25:BA:2836:U:C4	25:BA:2883:A:N6	2.81	0.48
29:BP:116:GLY:H	29:BP:134:ALA:HB2	1.78	0.48
34:BU:9:VAL:O	34:BU:13:LYS:HE3	2.12	0.48
52:BE:132:HIS:ND1	52:BE:132:HIS:O	2.46	0.48
1:AA:791:G:C6	1:AA:792:A:N7	2.81	0.48
2:AV:43:C:H4'	2:AV:44:G:OP1	2.13	0.48
16:AC:164:ARG:O	16:AC:165:THR:HB	2.13	0.48
25:BA:1379:A:H4'	25:BA:1380:G:OP2	2.13	0.48
25:BA:1584:C:O2	25:BA:1584:C:O2'	2.28	0.48
25:BA:2875:C:O2'	33:BT:5:ALA:HB3	2.12	0.48
26:BB:48:A:OP1	32:BS:92:TYR:O	2.31	0.48
46:B5:4:HIS:CB	46:B5:5:PRO:HD3	2.35	0.48
1:AA:192:U:O2'	14:AT:57:ARG:HG2	2.13	0.48
16:AC:124:ILE:HG12	16:AC:130:VAL:HG22	1.95	0.48
23:AY:517:LEU:HD11	23:AY:564:LYS:HB2	1.94	0.48
25:BA:272(J):C:H2'	25:BA:274:G:OP1	2.13	0.48
25:BA:500:G:N2	25:BA:502:A:H3'	2.28	0.48
25:BA:1002:G:H2'	25:BA:1003:G:O5'	2.13	0.48
25:BA:1021:A:H3'	25:BA:1021:A:H8	1.78	0.48
25:BA:2140:C:H5	25:BA:2151:G:H1	1.61	0.48
33:BT:106:SER:O	33:BT:107:ASP:CB	2.61	0.48
37:BX:12:VAL:HG12	37:BX:29:TRP:CE2	2.48	0.48
49:B8:50:LEU:HG	49:B8:51:ALA:N	2.28	0.48
53:BF:9:ILE:O	53:BF:9:ILE:HG22	2.13	0.48
53:BF:9:ILE:HG23	53:BF:13:SER:O	2.13	0.48
1:AA:29:G:O2'	1:AA:30:U:H5'	2.13	0.48
1:AA:376:G:P	10:AP:67:THR:HG21	2.53	0.48
1:AA:714:G:H2'	1:AA:715:A:C8	2.48	0.48
1:AA:760:G:O2'	11:AQ:98:LEU:HD23	2.12	0.48
1:AA:975:A:N6	1:AA:1367:C:O4'	2.47	0.48
1:AA:1346:A:C8	20:AG:10:ARG:NH2	2.81	0.48
8:AN:41:ARG:HG2	8:AN:41:ARG:HH11	1.79	0.48
16:AC:12:LEU:HD13	16:AC:18:TRP:CE2	2.48	0.48
23:AY:301:ILE:HG22	23:AY:332:SER:HB2	1.96	0.48
25:BA:118:A:C8	25:BA:119:A:C8	3.00	0.48
25:BA:244:A:C2	25:BA:255:A:C4	3.01	0.48
25:BA:330:A:H2	25:BA:1210:A:C2'	2.17	0.48
25:BA:1224:C:O2'	35:BV:85:LYS:HA	2.13	0.48
25:BA:2114:A:H2'	25:BA:2167:U:O2'	2.13	0.48
25:BA:2262:U:OP1	25:BA:2387:U:O2'	2.23	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2467:C:H4'	30:BQ:123:HIS:CD2	2.48	0.48
25:BA:2477:C:H1'	25:BA:2481:G:O6	2.14	0.48
25:BA:2801(A):A:H4'	25:BA:2802:G:H5'	1.95	0.48
25:BA:2849:U:P	33:BT:95:ARG:HH12	2.36	0.48
35:BV:47:VAL:O	35:BV:48:GLY:C	2.56	0.48
47:B6:33:LYS:HE2	47:B6:33:LYS:HA	1.94	0.48
1:AA:299:G:H2'	1:AA:300:A:C8	2.49	0.48
1:AA:738:C:H5''	19:AF:69:GLU:HB2	1.95	0.48
1:AA:1061:G:OP1	4:AJ:59:SER:OG	2.23	0.48
1:AA:1132:C:N3	1:AA:1142:G:N2	2.59	0.48
1:AA:1445:C:C4	1:AA:1446:U:C4	3.01	0.48
9:AO:16:ALA:HB1	9:AO:21:ASP:HB3	1.94	0.48
16:AC:24:ALA:HB1	16:AC:28:GLN:HB2	1.95	0.48
21:AH:83:ILE:HG13	21:AH:137:VAL:HG22	1.95	0.48
22:AI:95:LYS:NZ	22:AI:96:LEU:HD13	2.29	0.48
25:BA:620:G:H4'	25:BA:621:A:H5''	1.95	0.48
25:BA:1380:G:C2	25:BA:1381:G:C8	3.01	0.48
25:BA:2155:G:C6	25:BA:2156:G:C4	3.01	0.48
25:BA:2272:U:H5''	25:BA:2273:A:OP1	2.14	0.48
25:BA:2600:A:O2'	25:BA:2601:C:H5'	2.13	0.48
31:BR:33:ARG:HD2	46:B5:55:ARG:HG2	1.94	0.48
39:BZ:7:ALA:C	39:BZ:8:TYR:CD1	2.91	0.48
58:BL:61:UNK:O	58:BL:62:UNK:CB	2.61	0.48
1:AA:149:A:O2'	1:AA:150:C:P	2.71	0.48
1:AA:389:A:C6	1:AA:390:C:H1'	2.48	0.48
1:AA:986:A:H1'	13:AS:54:GLY:O	2.13	0.48
25:BA:848:G:C4	25:BA:933:A:H8	2.32	0.48
25:BA:1278:A:H4'	31:BR:34:ILE:HD12	1.96	0.48
25:BA:1329:U:H5''	25:BA:1330:C:H5	1.78	0.48
25:BA:1332:G:C2	25:BA:1609:A:O2'	2.54	0.48
25:BA:1977:A:H2'	25:BA:1978:A:O5'	2.13	0.48
25:BA:2023:G:H4'	25:BA:2617:C:O3'	2.14	0.48
25:BA:2123:G:H2'	25:BA:2124:G:O4'	2.13	0.48
1:AA:1004:A:C8	1:AA:1036:G:O6	2.67	0.48
14:AT:75:ASN:O	14:AT:79:ARG:HB2	2.14	0.48
17:AD:23:GLY:HA3	17:AD:112:VAL:HG22	1.96	0.48
23:AY:458:HIS:O	23:AY:461:ILE:HG13	2.13	0.48
25:BA:518:G:H4'	36:BW:18:ARG:NH1	2.29	0.48
25:BA:1199:U:H2'	25:BA:1200:C:O4'	2.14	0.48
25:BA:1449:A:H5''	25:BA:1449:A:C8	2.48	0.48
25:BA:1546:C:H5''	25:BA:1546:C:H6	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BB:13:A:OP2	40:B0:74:ARG:NH2	2.45	0.48
30:BQ:39:PRO:HA	30:BQ:97:VAL:O	2.13	0.48
38:BY:7:VAL:HB	38:BY:8:LYS:HD2	1.96	0.48
43:BD:176:ARG:HA	43:BD:182:LEU:HD23	1.95	0.48
49:B8:62:LEU:N	49:B8:63:PRO:CD	2.76	0.48
53:BF:164:ARG:HG3	53:BF:175:THR:OG1	2.14	0.48
1:AA:155:C:H2'	1:AA:156:G:C8	2.49	0.48
1:AA:345:C:H4'	1:AA:346:G:O5'	2.14	0.48
1:AA:428:G:H4'	1:AA:429:U:O5'	2.13	0.48
1:AA:460:G:C6	1:AA:470:C:C5'	2.96	0.48
1:AA:520:A:N1	1:AA:536:C:H1'	2.29	0.48
1:AA:1456:G:O4'	1:AA:1456:G:OP1	2.31	0.48
21:AH:107:LEU:N	21:AH:107:LEU:HD23	2.29	0.48
25:BA:528:A:C2	25:BA:2042:A:H2'	2.48	0.48
25:BA:819:A:H2'	25:BA:820:A:H5'	1.95	0.48
25:BA:958:U:OP2	30:BQ:14:ARG:HD3	2.12	0.48
25:BA:1528:A:H2	25:BA:1542:A:H62	1.58	0.48
25:BA:1637:A:H5'	25:BA:1760:A:O2'	2.14	0.48
25:BA:2155:G:H2'	25:BA:2156:G:O5'	2.14	0.48
25:BA:2392:A:N1	25:BA:2424:C:N3	2.61	0.48
25:BA:2649:U:H2'	25:BA:2650:U:C6	2.48	0.48
27:BN:30:ILE:HG23	27:BN:52:VAL:HG11	1.96	0.48
27:BN:67:LEU:O	27:BN:68:GLU:HB2	2.13	0.48
27:BN:93:THR:OG1	27:BN:94:HIS:CD2	2.67	0.48
33:BT:28:VAL:CG1	33:BT:46:GLU:HB2	2.44	0.48
47:B6:15:GLU:OE2	47:B6:41:PRO:CB	2.62	0.48
49:B8:23:VAL:CG1	49:B8:46:ARG:HD3	2.44	0.48
52:BE:116:VAL:O	52:BE:117:MET:HB3	2.13	0.48
53:BF:107:LYS:HD2	53:BF:205:ARG:O	2.14	0.48
1:AA:62:U:H5''	1:AA:385:C:O2'	2.13	0.48
1:AA:441:A:OP2	1:AA:441:A:H8	1.96	0.48
16:AC:174:PRO:HD2	16:AC:182:ILE:HD11	1.95	0.48
25:BA:1364:G:OP2	41:B1:61:ARG:NH2	2.45	0.48
32:BS:106:ARG:HD2	32:BS:107:GLU:O	2.14	0.48
36:BW:20:VAL:HG22	36:BW:47:VAL:HG21	1.96	0.48
39:BZ:196:VAL:O	39:BZ:197:ILE:C	2.56	0.48
52:BE:55:ASN:O	52:BE:57:LYS:HD3	2.14	0.48
53:BF:65:TRP:HB2	53:BF:66:PRO:CD	2.43	0.48
56:BK:105:LEU:CD2	56:BK:120:LEU:HD13	2.44	0.48
1:AA:1013:G:H22	1:AA:1015:A:H3'	1.79	0.48
4:AJ:22:LYS:C	4:AJ:24:VAL:H	2.21	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AK:105:VAL:O	5:AK:105:VAL:HG23	2.13	0.48
15:AB:62:ALA:C	15:AB:64:ARG:H	2.21	0.48
18:AE:107:ARG:O	18:AE:108:ALA:C	2.56	0.48
20:AG:5:ARG:HB2	20:AG:5:ARG:HH11	1.77	0.48
22:AI:48:GLU:N	22:AI:49:PRO:HD2	2.28	0.48
23:AY:242:LEU:O	23:AY:245:ALA:N	2.46	0.48
25:BA:551:G:O2'	25:BA:1220:A:N3	2.31	0.48
25:BA:784:A:C6	43:BD:229:VAL:HG11	2.49	0.48
25:BA:1488:G:C5	25:BA:1489:U:C5	3.02	0.48
25:BA:1494:A:C2'	25:BA:1495:A:H5''	2.43	0.48
25:BA:2517:C:C6	25:BA:2542:A:C2	3.01	0.48
27:BN:66:LYS:O	27:BN:70:LYS:HB3	2.14	0.48
29:BP:146:VAL:O	29:BP:148:LEU:HG	2.14	0.48
34:BU:65:ILE:HG12	34:BU:96:ALA:HB3	1.96	0.48
38:BY:13:VAL:O	38:BY:24:VAL:HA	2.14	0.48
43:BD:10:THR:C	43:BD:11:PRO:O	2.55	0.48
43:BD:27:THR:CG2	43:BD:83:GLU:OE2	2.62	0.48
52:BE:76:ARG:HA	52:BE:77:ILE:HG12	1.95	0.48
55:BH:154:PRO:HB3	55:BH:163:TYR:CZ	2.49	0.48
1:AA:881:G:P	6:AL:12:ARG:HH22	2.37	0.47
1:AA:1202:G:H1'	8:AN:29:ARG:HD2	1.96	0.47
15:AB:142:LEU:HD21	15:AB:146:GLN:OE1	2.13	0.47
15:AB:155:LEU:HD12	15:AB:157:ARG:O	2.14	0.47
16:AC:40:ARG:O	16:AC:44:GLU:HB2	2.14	0.47
17:AD:11:LEU:O	17:AD:13:ARG:O	2.32	0.47
25:BA:364:C:OP2	25:BA:365:C:OP2	2.32	0.47
25:BA:652:C:O2	25:BA:652:C:O2'	2.28	0.47
25:BA:1301:A:C8	25:BA:1303:G:C8	3.02	0.47
25:BA:2870:C:H2'	25:BA:2871:C:O4'	2.14	0.47
27:BN:115:ARG:O	27:BN:119:ARG:HG2	2.14	0.47
56:BK:13:PRO:HA	56:BK:52:ILE:HA	1.94	0.47
1:AA:264:U:H2'	1:AA:265:G:O4'	2.14	0.47
1:AA:731:G:H5'	1:AA:766:A:H4'	1.96	0.47
1:AA:1059:C:O3'	8:AN:45:ARG:NH2	2.47	0.47
13:AS:66:MET:HE3	13:AS:74:PHE:CE2	2.49	0.47
14:AT:49:ALA:HB2	14:AT:92:LEU:HD22	1.96	0.47
15:AB:165:VAL:HG23	15:AB:166:ASP:H	1.79	0.47
25:BA:470:A:H2'	25:BA:471:A:O4'	2.14	0.47
25:BA:882:G:H2'	25:BA:883:G:C8	2.48	0.47
25:BA:883:G:N2	25:BA:893:C:O2	2.47	0.47
25:BA:1905:C:H2'	25:BA:1930:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BO:114:ILE:H	28:BO:114:ILE:HD12	1.79	0.47
30:BQ:27:VAL:O	30:BQ:28:ALA:CB	2.62	0.47
30:BQ:116:GLU:OE1	30:BQ:116:GLU:HA	2.13	0.47
32:BS:24:LEU:O	32:BS:85:VAL:HB	2.14	0.47
35:BV:2:PHE:O	35:BV:3:ALA:O	2.31	0.47
52:BE:59:VAL:C	52:BE:60:ASN:HD22	2.21	0.47
53:BF:3:GLU:O	53:BF:19:GLU:HA	2.14	0.47
53:BF:152:GLU:OE1	53:BF:191:ARG:HD2	2.15	0.47
54:BG:4:ASP:CB	54:BG:8:LYS:HG2	2.43	0.47
1:AA:756:C:H2'	1:AA:757:U:O4'	2.15	0.47
2:AV:35:A:C5'	2:AV:35:A:H8	2.27	0.47
15:AB:145:LEU:HD12	15:AB:149:LEU:HD12	1.96	0.47
17:AD:134:ASP:OD2	17:AD:135:LEU:HD13	2.13	0.47
23:AY:162:VAL:HG21	23:AY:255:ILE:CG1	2.42	0.47
23:AY:401:SER:OG	23:AY:402:ILE:N	2.47	0.47
25:BA:239:U:H2'	25:BA:240:G:O4'	2.14	0.47
25:BA:636:G:N7	29:BP:113:LYS:NZ	2.54	0.47
25:BA:714:U:H2'	25:BA:716:A:OP2	2.15	0.47
25:BA:1078:U:H4'	25:BA:1078:U:OP1	2.15	0.47
25:BA:2023:G:H5'	25:BA:2617:C:H4'	1.95	0.47
25:BA:2316:C:O2'	54:BG:128:ARG:NH2	2.47	0.47
25:BA:2876:G:O5'	33:BT:3:ARG:HB3	2.14	0.47
30:BQ:27:VAL:HG12	30:BQ:28:ALA:N	2.29	0.47
31:BR:11:ASN:CG	31:BR:12:ARG:N	2.70	0.47
32:BS:89:ARG:O	32:BS:92:TYR:HB3	2.14	0.47
32:BS:97:ARG:HH21	32:BS:98:VAL:HA	1.79	0.47
33:BT:30:VAL:HG23	33:BT:30:VAL:O	2.14	0.47
34:BU:64:ARG:O	34:BU:65:ILE:C	2.57	0.47
53:BF:5:ALA:O	53:BF:6:VAL:CG2	2.62	0.47
1:AA:659:U:O2'	1:AA:660:G:H5'	2.14	0.47
1:AA:750:G:N3	9:AO:23:GLY:HA3	2.28	0.47
1:AA:1203:C:OP1	8:AN:3:ARG:HD3	2.13	0.47
18:AE:93:PRO:HG2	21:AH:105:ARG:NH2	2.29	0.47
25:BA:71:A:H5'	25:BA:71:A:H8	1.76	0.47
25:BA:271(L):U:H4'	25:BA:271(M):G:C5	2.50	0.47
25:BA:558:G:H1'	27:BN:45:ASN:HB3	1.95	0.47
25:BA:1539:G:N2	25:BA:1540:U:C2	2.82	0.47
25:BA:1899:G:O2'	25:BA:1900:A:OP2	2.27	0.47
27:BN:47:ALA:HB2	27:BN:112:LEU:HD11	1.96	0.47
33:BT:125:ARG:C	33:BT:127:ALA:H	2.22	0.47
38:BY:7:VAL:HG13	38:BY:83:THR:HG21	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BZ:51:ALA:HB1	39:BZ:57:ILE:HD11	1.95	0.47
51:BC:84:LYS:C	51:BC:86:ALA:N	2.72	0.47
54:BG:59:GLU:HA	54:BG:62:LEU:HD22	1.95	0.47
55:BH:6:ARG:CB	55:BH:65:HIS:CD2	2.97	0.47
55:BH:17:VAL:O	55:BH:45:VAL:HG13	2.14	0.47
1:AA:393:A:OP2	10:AP:12:LYS:NZ	2.32	0.47
1:AA:571:U:O5'	1:AA:571:U:H6	1.97	0.47
15:AB:15:VAL:C	15:AB:16:HIS:CG	2.92	0.47
15:AB:98:LEU:HG	15:AB:101:MET:HE3	1.95	0.47
22:AI:54:ASP:O	22:AI:56:LEU:N	2.45	0.47
24:AU:12:LYS:O	24:AU:13:ILE:C	2.58	0.47
25:BA:9:U:O2'	25:BA:10:G:P	2.73	0.47
25:BA:285:C:H2'	25:BA:286:C:C6	2.50	0.47
25:BA:478:A:N1	25:BA:500:G:H4'	2.29	0.47
25:BA:889:C:O4'	25:BA:889:C:O2	2.29	0.47
25:BA:1429:G:H2'	25:BA:1430:C:C6	2.50	0.47
25:BA:2308:G:N7	25:BA:2310:A:H5'	2.30	0.47
25:BA:2492:U:O2'	25:BA:2493:U:H5'	2.13	0.47
29:BP:146:VAL:HG13	29:BP:147:LEU:H	1.78	0.47
31:BR:34:ILE:HD13	31:BR:34:ILE:HA	1.78	0.47
32:BS:56:LEU:HD23	32:BS:56:LEU:O	2.15	0.47
35:BV:47:VAL:C	35:BV:49:THR:O	2.58	0.47
43:BD:32:SER:O	43:BD:36:PRO:CD	2.62	0.47
43:BD:147:LEU:HD12	43:BD:155:LEU:HD21	1.96	0.47
52:BE:111:ARG:HD2	52:BE:160:TYR:CE1	2.50	0.47
1:AA:673:G:OP1	19:AF:87:ARG:HD3	2.15	0.47
1:AA:779:C:H2'	1:AA:780:A:O4'	2.14	0.47
1:AA:1318:A:H1'	13:AS:37:ARG:HH21	1.79	0.47
1:AA:1333:A:H2'	1:AA:1334:G:O4'	2.13	0.47
1:AA:1465:C:H2'	1:AA:1466:C:O4'	2.15	0.47
4:AJ:35:SER:OG	4:AJ:73:ASP:HB2	2.15	0.47
23:AY:250:THR:HA	23:AY:255:ILE:HG22	1.97	0.47
23:AY:319:ASP:OD1	23:AY:322:VAL:HG22	2.15	0.47
23:AY:377:VAL:HG21	23:AY:380:LEU:HD22	1.96	0.47
25:BA:71:A:OP2	25:BA:71:A:H3'	2.14	0.47
25:BA:220:G:O2'	25:BA:233:A:N3	2.44	0.47
25:BA:309:G:N3	25:BA:329:G:O2'	2.48	0.47
25:BA:806:C:OP2	29:BP:39:LYS:HB3	2.15	0.47
25:BA:814:C:H2'	25:BA:815:C:H6	1.79	0.47
25:BA:1406:U:H2'	25:BA:1407:C:C6	2.49	0.47
25:BA:1407:C:H5'	25:BA:1408:C:OP2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1464:C:HO2'	25:BA:1528:A:H8	1.59	0.47
25:BA:1786:A:H2	25:BA:2606:C:H1'	1.76	0.47
25:BA:2134:A:C8	25:BA:2159:G:O2'	2.63	0.47
25:BA:2591:C:OP2	43:BD:239:ARG:HB3	2.14	0.47
33:BT:28:VAL:HG21	33:BT:46:GLU:HG3	1.97	0.47
35:BV:2:PHE:HB3	35:BV:42:GLY:HA3	1.96	0.47
36:BW:9:TYR:H	36:BW:102:HIS:HD2	1.62	0.47
36:BW:69:LEU:HA	36:BW:108:GLY:O	2.15	0.47
38:BY:2:ARG:O	38:BY:4:LYS:HG3	2.14	0.47
41:B1:29:GLY:O	41:B1:30:VAL:HG13	2.14	0.47
54:BG:18:GLU:O	54:BG:22:ARG:N	2.47	0.47
56:BK:59:ILE:HG12	56:BK:60:TYR:H	1.78	0.47
57:BJ:46:ALA:O	57:BJ:47:ALA:HB2	2.14	0.47
1:AA:148:G:C2	1:AA:175:C:C2	3.03	0.47
1:AA:264:U:O2'	11:AQ:64:PRO:O	2.32	0.47
1:AA:298:A:H2'	1:AA:299:G:O4'	2.14	0.47
1:AA:456:C:H2'	1:AA:457:C:C6	2.49	0.47
1:AA:547:A:H4'	1:AA:548:G:O5'	2.14	0.47
1:AA:590:C:OP1	21:AH:30:ARG:N	2.46	0.47
1:AA:938:A:N6	1:AA:939:G:C6	2.83	0.47
1:AA:1307:U:H2'	1:AA:1308:U:O4'	2.13	0.47
1:AA:1368:G:OP2	22:AI:112:LYS:CD	2.61	0.47
5:AK:97:ALA:O	5:AK:101:SER:HB3	2.13	0.47
17:AD:81:GLU:OE1	17:AD:139:ARG:NH2	2.46	0.47
18:AE:76:ILE:O	18:AE:93:PRO:HB3	2.15	0.47
18:AE:84:PHE:HB3	18:AE:134:ALA:HB2	1.95	0.47
21:AH:38:ILE:HD11	21:AH:118:VAL:HG12	1.96	0.47
23:AY:92:ILE:O	23:AY:96:ARG:HB2	2.15	0.47
23:AY:94:VAL:C	23:AY:96:ARG:N	2.72	0.47
23:AY:218:GLU:O	23:AY:221:ALA:HB3	2.15	0.47
23:AY:438:PHE:CZ	23:AY:451:ILE:HG12	2.49	0.47
25:BA:129:C:H6	25:BA:129:C:H5''	1.79	0.47
25:BA:295:G:H5''	25:BA:295:G:C8	2.50	0.47
25:BA:479:A:N3	25:BA:481:G:H5''	2.30	0.47
25:BA:647:G:O5'	25:BA:647:G:H8	1.97	0.47
25:BA:1283:G:N2	25:BA:1285:G:H3'	2.30	0.47
25:BA:1653:G:H4'	25:BA:1654:A:O5'	2.15	0.47
25:BA:1809:A:H2'	25:BA:1810:A:C8	2.50	0.47
25:BA:2181:G:H2'	25:BA:2182:G:O5'	2.15	0.47
25:BA:2370:G:H2'	25:BA:2371:G:O4'	2.14	0.47
25:BA:2521:C:O2'	25:BA:2564:A:N3	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2688:U:C5	25:BA:2720:U:OP2	2.67	0.47
25:BA:2712:U:H2'	25:BA:2712:U:O2	2.14	0.47
30:BQ:137:TYR:OH	39:BZ:81:ARG:HD3	2.15	0.47
33:BT:121:ILE:O	33:BT:124:ASP:HB2	2.14	0.47
42:B2:44:LEU:O	42:B2:45:SER:CB	2.62	0.47
43:BD:26:LYS:HG2	43:BD:81:ALA:HA	1.97	0.47
43:BD:32:SER:HA	43:BD:35:LYS:NZ	2.30	0.47
47:B6:16:CYS:O	47:B6:18:ARG:CZ	2.62	0.47
49:B8:23:VAL:HA	49:B8:47:LYS:O	2.15	0.47
51:BC:185:LEU:O	51:BC:186:ALA:C	2.57	0.47
53:BF:129:PHE:CD2	53:BF:163:VAL:HG21	2.50	0.47
54:BG:82:LEU:HD23	54:BG:83:ARG:H	1.79	0.47
1:AA:407:G:OP1	17:AD:3:ARG:NH1	2.48	0.47
1:AA:437:U:H5''	17:AD:155:LEU:HD21	1.97	0.47
1:AA:515:G:H2'	1:AA:516:U:O4'	2.15	0.47
1:AA:712:A:H2'	1:AA:713:G:O4'	2.14	0.47
1:AA:863:U:O2'	1:AA:865:A:N7	2.33	0.47
1:AA:1152:A:H5''	4:AJ:13:HIS:CD2	2.50	0.47
1:AA:1277:C:C2'	1:AA:1279:A:H8	2.27	0.47
15:AB:238:LEU:O	15:AB:240:GLN:N	2.47	0.47
17:AD:187:ARG:NH2	17:AD:193:ASP:OD2	2.48	0.47
25:BA:669:G:C2'	25:BA:669:G:N3	2.77	0.47
25:BA:1053:C:H2'	25:BA:1054:A:C5'	2.45	0.47
25:BA:1540:U:H2'	25:BA:1541:G:O4'	2.15	0.47
25:BA:1932:A:H2'	25:BA:1933:G:O4'	2.14	0.47
26:BB:101:G:H2'	26:BB:102:A:O4'	2.15	0.47
29:BP:61:ARG:H	29:BP:61:ARG:HD2	1.80	0.47
34:BU:91:ASP:O	34:BU:92:ARG:HB3	2.13	0.47
37:BX:55:ASN:HD22	37:BX:55:ASN:N	2.12	0.47
38:BY:20:TYR:O	38:BY:23:ARG:HB2	2.15	0.47
38:BY:74:PRO:O	38:BY:80:GLY:CA	2.60	0.47
53:BF:132:VAL:HG22	53:BF:133:ASN:H	1.80	0.47
56:BK:112:MET:HE2	56:BK:120:LEU:HD21	1.95	0.47
1:AA:538:G:H2'	1:AA:539:A:H8	1.80	0.47
1:AA:997:U:O5'	1:AA:997:U:H6	1.97	0.47
1:AA:1063:C:H3'	1:AA:1064:G:H2'	1.96	0.47
1:AA:1397:C:O4'	1:AA:1397:C:O2	2.33	0.47
8:AN:25:VAL:HB	8:AN:38:GLY:O	2.15	0.47
10:AP:8:ARG:HH11	10:AP:8:ARG:CG	2.26	0.47
19:AF:69:GLU:O	19:AF:72:VAL:HG12	2.15	0.47
20:AG:116:ALA:O	20:AG:120:ILE:CD1	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AY:380:LEU:HD21	23:AY:389:LEU:HD21	1.97	0.47
25:BA:1407:C:H5''	25:BA:1407:C:H6	1.76	0.47
25:BA:1794:U:H2'	25:BA:1795:C:C6	2.50	0.47
25:BA:1906:G:N7	25:BA:1929:G:C8	2.82	0.47
26:BB:2:C:O2	26:BB:2:C:C2'	2.62	0.47
26:BB:32:C:C2	26:BB:51:G:N2	2.83	0.47
31:BR:28:LEU:HD12	31:BR:48:VAL:HG21	1.96	0.47
32:BS:53:SER:O	32:BS:55:ALA:N	2.47	0.47
6:AL:111:LYS:O	6:AL:112:ASP:HB2	2.16	0.47
7:AM:2:ALA:N	7:AM:9:ILE:HG23	2.30	0.47
23:AY:10:LYS:O	23:AY:10:LYS:HD3	2.15	0.47
23:AY:21:ILE:HD13	25:BA:2661:G:H5'	1.97	0.47
25:BA:494:G:O2'	36:BW:5:ALA:O	2.23	0.47
27:BN:17:ASP:OD2	27:BN:56:ASN:ND2	2.44	0.47
33:BT:28:VAL:HG13	33:BT:46:GLU:CA	2.45	0.47
38:BY:30:VAL:HG12	38:BY:31:LEU:N	2.29	0.47
56:BK:17:ALA:CB	56:BK:38:VAL:HG22	2.43	0.47
21:AH:44:PHE:CE2	21:AH:109:ILE:HG21	2.50	0.46
25:BA:607:U:C2	25:BA:621:A:N1	2.83	0.46
25:BA:1386:C:OP2	25:BA:1396:U:H5	1.97	0.46
25:BA:1742:G:C8	25:BA:1742:G:C3'	2.98	0.46
25:BA:1790:C:H2'	25:BA:1791:A:C5	2.50	0.46
25:BA:1865:G:C5'	25:BA:1865:G:H8	2.29	0.46
31:BR:28:LEU:O	31:BR:28:LEU:HD22	2.15	0.46
32:BS:28:VAL:HB	32:BS:89:ARG:HB2	1.97	0.46
33:BT:28:VAL:HG13	33:BT:46:GLU:HB2	1.96	0.46
34:BU:92:ARG:NH1	34:BU:94:ASN:ND2	2.61	0.46
35:BV:23:GLU:O	35:BV:24:LYS:C	2.57	0.46
36:BW:17:VAL:O	36:BW:18:ARG:C	2.55	0.46
53:BF:84:VAL:O	53:BF:86:GLY:N	2.48	0.46
53:BF:117:ARG:HA	53:BF:117:ARG:HD3	1.57	0.46
1:AA:710:G:OP1	19:AF:54:LYS:CE	2.63	0.46
5:AK:99:GLN:HA	5:AK:105:VAL:HG13	1.97	0.46
13:AS:50:ALA:HB1	13:AS:57:HIS:HB3	1.98	0.46
17:AD:162:LEU:HD13	17:AD:181:MET:HG2	1.97	0.46
25:BA:379:G:O2'	25:BA:2232:U:OP1	2.28	0.46
25:BA:391:G:H1'	25:BA:411:G:O4'	2.14	0.46
25:BA:806:C:OP2	29:BP:39:LYS:HD3	2.15	0.46
25:BA:1177:A:H4'	25:BA:1178:C:C6	2.50	0.46
29:BP:7:ARG:NH1	29:BP:7:ARG:CA	2.62	0.46
32:BS:16:ASN:O	32:BS:19:LYS:CB	2.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:BF:65:TRP:CB	53:BF:66:PRO:CD	2.94	0.46
55:BH:41:MET:HE3	55:BH:43:VAL:CA	2.44	0.46
1:AA:162:A:H3'	1:AA:163:C:O4'	2.16	0.46
1:AA:538:G:H2'	1:AA:539:A:C8	2.49	0.46
1:AA:722:A:H3'	1:AA:722:A:N3	2.30	0.46
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.80	0.46
7:AM:56:LEU:O	7:AM:59:TYR:N	2.49	0.46
23:AY:89:ASP:HA	23:AY:454:MET:HB3	1.96	0.46
25:BA:527:C:OP2	25:BA:2779:U:H5	1.98	0.46
25:BA:1448:G:O2'	25:BA:1528(A):A:N1	2.47	0.46
25:BA:1959:G:H2'	25:BA:1960:A:O5'	2.15	0.46
25:BA:2086:U:H2'	25:BA:2087:G:C8	2.49	0.46
25:BA:2341:G:H2'	25:BA:2342:C:C6	2.50	0.46
27:BN:133:GLN:HG2	27:BN:134:ARG:N	2.30	0.46
33:BT:23:ARG:O	33:BT:24:PRO:C	2.58	0.46
38:BY:7:VAL:HB	38:BY:8:LYS:HE3	1.96	0.46
43:BD:58:HIS:HD2	43:BD:59:LYS:O	1.99	0.46
47:B6:39:TYR:HB3	47:B6:49:HIS:CD2	2.49	0.46
53:BF:3:GLU:HA	53:BF:24:LEU:HB3	1.96	0.46
53:BF:101:LEU:HD12	53:BF:102:PRO:HD2	1.97	0.46
1:AA:263:A:P	14:AT:79:ARG:HH11	2.38	0.46
1:AA:629:G:H2'	1:AA:630:G:O4'	2.15	0.46
1:AA:938:A:C6	1:AA:939:G:C5	3.04	0.46
1:AA:1446:U:H4'	1:AA:1447:A:C5	2.51	0.46
1:AA:1507:A:C2	1:AA:1508:G:C4	3.03	0.46
2:AV:15:G:H8	2:AV:15:G:OP2	1.98	0.46
8:AN:28:GLY:O	8:AN:29:ARG:C	2.58	0.46
23:AY:684:GLN:O	23:AY:688:ILE:N	2.41	0.46
25:BA:215:G:O3'	25:BA:216:A:H4'	2.15	0.46
25:BA:250:G:H2'	25:BA:251:A:C8	2.51	0.46
25:BA:476:G:H4'	25:BA:502:A:N1	2.30	0.46
25:BA:528:A:N1	25:BA:2043:C:O5'	2.48	0.46
33:BT:57:PHE:O	33:BT:58:ASN:C	2.59	0.46
33:BT:108:ARG:HB3	33:BT:111:ARG:NH1	2.31	0.46
43:BD:68:LYS:HB2	43:BD:70:TRP:CH2	2.51	0.46
51:BC:222:VAL:O	51:BC:224:ILE:HG23	2.14	0.46
54:BG:148:MET:HA	54:BG:148:MET:HE3	1.97	0.46
1:AA:328:C:O2	1:AA:328:C:C2'	2.58	0.46
1:AA:499:A:C6	1:AA:547:A:C8	3.03	0.46
1:AA:1226:C:H5''	13:AS:81:ARG:HB3	1.96	0.46
1:AA:1237:C:C2'	1:AA:1238:A:OP1	2.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AJ:90:LEU:HG	4:AJ:90:LEU:O	2.15	0.46
15:AB:84:GLU:HG3	15:AB:215:LEU:HB3	1.96	0.46
16:AC:54:ARG:NH1	16:AC:56:ASP:OD1	2.35	0.46
23:AY:162:VAL:HG21	23:AY:255:ILE:CD1	2.45	0.46
25:BA:1115:G:H2'	25:BA:1116:C:C6	2.51	0.46
25:BA:1353:A:H4'	43:BD:38:LYS:HE3	1.96	0.46
25:BA:1865:G:H8	25:BA:1865:G:H5''	1.80	0.46
25:BA:2290:G:C2	25:BA:2343:C:O2	2.69	0.46
25:BA:2316:C:OP2	25:BA:2316:C:H6	1.99	0.46
25:BA:2477:C:O2	25:BA:2481:G:O6	2.33	0.46
25:BA:2533:A:H5''	25:BA:2665:A:O2'	2.16	0.46
25:BA:2612:C:H2'	25:BA:2613:U:H5'	1.98	0.46
26:BB:27:C:O3'	32:BS:36:TYR:OH	2.31	0.46
33:BT:11:GLU:N	33:BT:11:GLU:CD	2.74	0.46
33:BT:106:SER:O	33:BT:107:ASP:OD1	2.34	0.46
38:BY:28:LYS:HE3	38:BY:30:VAL:HG22	1.98	0.46
43:BD:65:ILE:HD11	43:BD:67:PHE:CZ	2.51	0.46
53:BF:24:LEU:HB3	53:BF:25:PRO:CD	2.38	0.46
54:BG:82:LEU:HD22	54:BG:87:PRO:HB3	1.97	0.46
54:BG:135:LEU:HD22	54:BG:140:ILE:HD11	1.97	0.46
1:AA:807:A:H2'	1:AA:808:C:O4'	2.16	0.46
7:AM:83:ASP:OD1	7:AM:84:ILE:N	2.49	0.46
7:AM:120:LYS:HE3	7:AM:121:LYS:O	2.16	0.46
9:AO:56:LEU:O	9:AO:60:VAL:HG23	2.16	0.46
22:AI:50:LEU:HB3	22:AI:56:LEU:HA	1.96	0.46
25:BA:651:G:H4'	49:B8:18:ALA:HB3	1.98	0.46
25:BA:1021:A:OP2	27:BN:65:LYS:NZ	2.48	0.46
25:BA:1050:A:H2'	25:BA:1051:G:H8	1.79	0.46
25:BA:1086:A:H3'	25:BA:1086:A:N3	2.31	0.46
25:BA:1434:A:O2'	25:BA:1435:G:H5'	2.16	0.46
25:BA:1914:C:OP1	25:BA:1914:C:H2'	2.15	0.46
25:BA:2125:G:H5''	25:BA:2126:A:OP1	2.16	0.46
25:BA:2134:A:H8	25:BA:2159:G:O2'	1.98	0.46
25:BA:2503:A:N3	25:BA:2503:A:H5'	2.31	0.46
31:BR:56:LYS:NZ	31:BR:90:ARG:O	2.48	0.46
39:BZ:73:GLN:HB3	39:BZ:87:ASP:HB2	1.96	0.46
40:B0:24:LYS:HG3	40:B0:36:ILE:HD11	1.98	0.46
51:BC:17:ASN:O	51:BC:18:LYS:C	2.59	0.46
52:BE:2:LYS:HD2	52:BE:95:ILE:HG23	1.96	0.46
53:BF:157:VAL:HG23	53:BF:198:ALA:HB1	1.96	0.46
54:BG:48:GLU:O	54:BG:49:ASP:CB	2.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:706:A:C2'	5:AK:31:THR:HG21	2.46	0.46
1:AA:973:G:C2'	1:AA:974:A:OP1	2.64	0.46
1:AA:1265:G:H2'	1:AA:1266:G:O4'	2.16	0.46
1:AA:1349:A:C2	1:AA:1374:A:C4	3.04	0.46
1:AA:1521:G:H2'	1:AA:1522:U:C6	2.50	0.46
4:AJ:85:LEU:C	4:AJ:87:THR:N	2.74	0.46
6:AL:27:LEU:C	6:AL:29:GLY:N	2.67	0.46
17:AD:2:GLY:C	17:AD:4:TYR:N	2.73	0.46
23:AY:293:THR:HG22	23:AY:297:GLU:O	2.15	0.46
25:BA:197:A:H2'	25:BA:198:C:H5'	1.98	0.46
25:BA:586:A:H2	25:BA:809:G:N3	2.14	0.46
25:BA:1328:G:H8	25:BA:1328:G:O5'	1.98	0.46
25:BA:2340:G:O2'	25:BA:2341:G:H5'	2.16	0.46
29:BP:6:LEU:HD23	29:BP:6:LEU:H	1.81	0.46
36:BW:73:ALA:HB3	36:BW:106:ILE:CG1	2.44	0.46
37:BX:52:VAL:O	37:BX:52:VAL:HG12	2.16	0.46
39:BZ:166:SER:OG	39:BZ:167:PRO:HA	2.16	0.46
52:BE:5:LEU:HD12	52:BE:51:PHE:HB2	1.96	0.46
53:BF:113:ALA:HB1	53:BF:186:ILE:HG21	1.98	0.46
54:BG:39:ILE:HD11	54:BG:94:LEU:HD11	1.96	0.46
56:BK:14:ALA:HA	56:BK:41:PHE:CZ	2.50	0.46
1:AA:55:A:H1'	23:AY:321:TYR:HB3	1.97	0.46
1:AA:120:A:O2'	1:AA:121:C:H5'	2.16	0.46
1:AA:673:G:H5''	19:AF:87:ARG:CZ	2.45	0.46
1:AA:1031:G:H2'	1:AA:1032:G:O4'	2.16	0.46
1:AA:1234:C:H1'	1:AA:1364:U:O2	2.15	0.46
1:AA:1452:C:O4'	1:AA:1456:G:N2	2.49	0.46
2:AV:47:U:H3'	2:AV:48:C:C5'	2.46	0.46
14:AT:93:GLU:OE1	14:AT:93:GLU:C	2.59	0.46
21:AH:86:ILE:HB	21:AH:133:LEU:O	2.16	0.46
23:AY:435:ASP:OD1	23:AY:435:ASP:C	2.58	0.46
25:BA:64:A:C2	37:BX:66:LEU:HD22	2.50	0.46
25:BA:89:G:OP2	25:BA:90:U:H2'	2.16	0.46
25:BA:991:C:H6	25:BA:991:C:H5'	1.80	0.46
25:BA:1741:A:N7	25:BA:1742:G:C2	2.84	0.46
25:BA:1789:A:H2'	25:BA:1790:C:H5'	1.96	0.46
25:BA:2144:U:O2	25:BA:2147:G:O6	2.34	0.46
25:BA:2297:C:O2'	25:BA:2322:A:N3	2.43	0.46
25:BA:2298:A:N6	25:BA:2318:G:C8	2.82	0.46
28:BO:77:ILE:HD12	33:BT:74:ARG:HD3	1.97	0.46
33:BT:125:ARG:O	33:BT:128:GLU:HG3	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BU:90:VAL:HG12	34:BU:91:ASP:N	2.31	0.46
39:BZ:166:SER:OG	39:BZ:167:PRO:CA	2.64	0.46
47:B6:11:LEU:HD21	47:B6:51:GLU:HB2	1.97	0.46
53:BF:81:PRO:HB3	53:BF:89:VAL:HG23	1.98	0.46
57:BJ:100:ALA:O	57:BJ:104:ALA:HB3	2.16	0.46
1:AA:1190:G:OP1	16:AC:4:LYS:HA	2.15	0.46
1:AA:1319:A:C8	1:AA:1323:G:C5	3.04	0.46
1:AA:1508:G:O2'	1:AA:1509:C:H5'	2.16	0.46
7:AM:45:VAL:HA	7:AM:48:LEU:HD22	1.98	0.46
14:AT:26:ASN:OD1	14:AT:71:THR:OG1	2.27	0.46
14:AT:94:ALA:O	14:AT:95:ALA:CB	2.64	0.46
15:AB:114:ARG:NH1	15:AB:118:LEU:HD21	2.31	0.46
15:AB:235:SER:OG	15:AB:236:TYR:CD1	2.69	0.46
18:AE:7:GLU:O	18:AE:8:GLU:HB3	2.16	0.46
25:BA:796:C:H2'	25:BA:797:C:C6	2.51	0.46
25:BA:889:C:O2'	25:BA:890:A:OP2	2.32	0.46
25:BA:1051:G:H2'	25:BA:1052:C:O4'	2.16	0.46
25:BA:1055:G:H5'	25:BA:1056:G:OP2	2.16	0.46
32:BS:97:ARG:NH2	32:BS:98:VAL:HA	2.30	0.46
43:BD:134:ARG:HG3	43:BD:135:PHE:CD1	2.51	0.46
43:BD:158:ALA:O	43:BD:159:ALA:C	2.59	0.46
45:B4:38:ALA:O	45:B4:49:GLU:HG2	2.16	0.46
51:BC:46:LYS:NZ	51:BC:168:THR:O	2.48	0.46
51:BC:215:THR:OG1	51:BC:216:THR:N	2.48	0.46
57:BJ:37:ALA:C	57:BJ:39:ALA:H	2.23	0.46
1:AA:503:C:O2	1:AA:510:A:H2	1.98	0.46
1:AA:1128:C:C2'	1:AA:1129:C:H5'	2.45	0.46
1:AA:1158:C:O2	1:AA:1158:C:C2'	2.64	0.46
7:AM:70:LEU:O	7:AM:71:ARG:C	2.59	0.46
17:AD:31:CYS:C	17:AD:33:MET:N	2.73	0.46
19:AF:89:MET:HG2	19:AF:91:VAL:HG23	1.98	0.46
21:AH:113:SER:O	21:AH:131:GLY:HA3	2.16	0.46
25:BA:309:G:O3'	38:BY:18:GLY:HA2	2.16	0.46
25:BA:451:C:H4'	53:BF:52:LYS:HE2	1.97	0.46
25:BA:814:C:H2'	25:BA:815:C:C6	2.51	0.46
25:BA:1208:C:C4	25:BA:1209:G:N7	2.84	0.46
25:BA:2151:G:C6	25:BA:2152:G:C5	3.03	0.46
27:BN:119:ARG:HH11	27:BN:119:ARG:CG	2.29	0.46
29:BP:64:LYS:O	29:BP:65:ARG:C	2.56	0.46
34:BU:65:ILE:HG12	34:BU:96:ALA:CB	2.46	0.46
38:BY:8:LYS:C	38:BY:28:LYS:HE2	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:BD:169:GLU:OE1	43:BD:169:GLU:HA	2.16	0.46
55:BH:64:LEU:HD23	55:BH:67:LEU:HD23	1.98	0.46
1:AA:503:C:O5'	1:AA:503:C:H6	1.99	0.45
1:AA:979:C:C3'	1:AA:980:C:C5'	2.93	0.45
18:AE:28:PHE:O	18:AE:47:LYS:HA	2.17	0.45
25:BA:35:G:C2'	25:BA:36:G:O5'	2.64	0.45
25:BA:428:A:H5'	25:BA:429:A:OP2	2.16	0.45
25:BA:2512:C:H2'	25:BA:2513:G:O4'	2.15	0.45
26:BB:41:U:C6	54:BG:69:ALA:HB1	2.51	0.45
29:BP:23:PRO:HB2	29:BP:33:ARG:HD2	1.97	0.45
38:BY:42:VAL:HG23	38:BY:67:LEU:HD13	1.99	0.45
53:BF:20:LEU:HD23	53:BF:21:ALA:N	2.31	0.45
1:AA:1134:G:C5	1:AA:1135:U:C6	3.04	0.45
1:AA:1149:C:P	22:AI:9:ARG:HH11	2.38	0.45
7:AM:58:GLU:O	7:AM:62:ASN:ND2	2.50	0.45
16:AC:35:GLU:O	16:AC:36:ASP:C	2.59	0.45
20:AG:152:ALA:O	20:AG:155:ARG:NE	2.49	0.45
23:AY:551:GLN:O	23:AY:559:PRO:HA	2.15	0.45
25:BA:299:A:C5	25:BA:322:A:C2	3.05	0.45
25:BA:401:A:H2'	25:BA:402:A:O4'	2.16	0.45
25:BA:613:G:H5''	25:BA:613:G:C8	2.43	0.45
25:BA:659:C:H4'	53:BF:100:THR:O	2.16	0.45
25:BA:995:C:O2	27:BN:4:TYR:OH	2.28	0.45
25:BA:1499:C:O2'	25:BA:1500:G:H5'	2.16	0.45
25:BA:1761:C:H2'	25:BA:1762:A:H5'	1.98	0.45
25:BA:2388:A:H5'	25:BA:2389:G:OP2	2.16	0.45
25:BA:2654:A:O4'	25:BA:2656:U:C6	2.69	0.45
33:BT:92:GLY:O	33:BT:115:ARG:O	2.35	0.45
34:BU:66:ASN:O	34:BU:70:ARG:HB2	2.16	0.45
34:BU:81:HIS:CD2	34:BU:117:GLN:HG3	2.52	0.45
38:BY:76:CYS:O	38:BY:96:ILE:HD13	2.16	0.45
41:B1:3:LYS:C	41:B1:46:LEU:HD21	2.41	0.45
43:BD:70:TRP:HZ3	43:BD:146:GLU:CD	2.24	0.45
43:BD:226:MET:O	43:BD:234:GLY:HA2	2.16	0.45
53:BF:20:LEU:HD23	53:BF:21:ALA:H	1.81	0.45
54:BG:72:ARG:HB3	54:BG:87:PRO:HD3	1.97	0.45
54:BG:149:VAL:HG13	54:BG:149:VAL:O	2.17	0.45
55:BH:105:LEU:CD2	55:BH:113:VAL:HB	2.46	0.45
1:AA:288:A:H2'	1:AA:289:G:H4'	1.98	0.45
1:AA:1013:G:H5''	1:AA:1013:G:H8	1.78	0.45
2:AV:73:A:H3'	2:AV:74:C:H5'	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AB:7:VAL:O	15:AB:11:LEU:HB2	2.16	0.45
15:AB:178:ARG:HG2	15:AB:178:ARG:NH1	2.13	0.45
17:AD:16:GLY:C	17:AD:17:VAL:HG23	2.41	0.45
23:AY:90:PHE:O	23:AY:91:THR:C	2.59	0.45
23:AY:409:ILE:HD13	23:AY:409:ILE:HA	1.86	0.45
25:BA:306:U:H2'	25:BA:307:G:O4'	2.16	0.45
25:BA:308:G:C8	25:BA:501:A:O4'	2.69	0.45
25:BA:387:U:H4'	25:BA:388:G:O5'	2.16	0.45
25:BA:1394:U:C6	25:BA:1394:U:H3'	2.52	0.45
25:BA:1426:G:C6	25:BA:1427:A:C6	3.04	0.45
25:BA:1918:A:O2'	25:BA:1919:A:C2	2.64	0.45
25:BA:2137:C:N4	25:BA:2154:G:O6	2.49	0.45
25:BA:2506:U:H4'	25:BA:2507:C:OP1	2.14	0.45
27:BN:134:ARG:O	27:BN:134:ARG:CD	2.64	0.45
30:BQ:76:LYS:HB3	30:BQ:91:GLU:HG2	1.99	0.45
46:B5:51:TYR:CD2	46:B5:52:TYR:CE2	3.05	0.45
51:BC:131:LEU:HD12	51:BC:137:LEU:HA	1.98	0.45
1:AA:33:A:O2'	1:AA:363:A:H1'	2.16	0.45
1:AA:35:G:H2'	1:AA:36:C:C6	2.51	0.45
1:AA:141:A:H1'	1:AA:182:U:O2	2.17	0.45
1:AA:353:A:C2'	1:AA:354:G:OP2	2.65	0.45
1:AA:501:C:H1'	1:AA:549:C:H1'	1.98	0.45
1:AA:695:A:H2'	1:AA:696:A:C8	2.51	0.45
1:AA:981:U:O4	1:AA:1222:G:O6	2.33	0.45
1:AA:1003:G:C2'	1:AA:1004:A:H4'	2.45	0.45
4:AJ:30:SER:CB	4:AJ:81:THR:OG1	2.65	0.45
17:AD:28:SER:C	17:AD:30:LYS:N	2.75	0.45
18:AE:41:VAL:HG23	18:AE:67:VAL:HG13	1.99	0.45
23:AY:72:CYS:SG	23:AY:81:ILE:HD11	2.56	0.45
23:AY:289:ILE:HD11	23:AY:331:TYR:CD2	2.51	0.45
25:BA:30:G:H2'	25:BA:31:C:C6	2.51	0.45
25:BA:94:C:O2	25:BA:94:C:H2'	2.17	0.45
25:BA:271(A):A:N1	25:BA:272(D):G:O2'	2.46	0.45
25:BA:2138:C:H6	25:BA:2138:C:H5''	1.82	0.45
25:BA:2461:C:H2'	25:BA:2462:U:C6	2.51	0.45
25:BA:2517:C:C2'	25:BA:2542:A:C2	2.99	0.45
25:BA:2746:U:H2'	25:BA:2747:G:H5'	1.99	0.45
25:BA:2757:A:N1	55:BH:67:LEU:HD22	2.31	0.45
29:BP:38:GLN:HG3	29:BP:39:LYS:H	1.81	0.45
31:BR:38:VAL:HB	31:BR:39:PRO:CD	2.45	0.45
38:BY:38:ILE:CG2	38:BY:39:VAL:N	2.78	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:BY:41:GLY:O	38:BY:42:VAL:C	2.59	0.45
41:B1:4:VAL:HG13	41:B1:4:VAL:O	2.15	0.45
51:BC:99:ILE:HD13	51:BC:99:ILE:H	1.81	0.45
1:AA:737:A:O2'	19:AF:72:VAL:CG1	2.65	0.45
16:AC:40:ARG:HG3	16:AC:40:ARG:NH1	2.30	0.45
23:AY:212:TYR:O	23:AY:216:LEU:N	2.40	0.45
25:BA:1421:G:C2	25:BA:1422:G:C8	3.05	0.45
25:BA:1562:A:H2'	25:BA:1563:G:O4'	2.17	0.45
25:BA:1910:G:N1	25:BA:1920:C:H5	1.98	0.45
25:BA:2302:G:C3'	25:BA:2303:G:H5'	2.47	0.45
25:BA:2302:G:H2'	25:BA:2303:G:H5'	1.99	0.45
25:BA:2371:G:C6	25:BA:2372:G:N7	2.85	0.45
25:BA:2506:U:H5'	25:BA:2506:U:H6	1.79	0.45
34:BU:66:ASN:CG	34:BU:76:TYR:HB2	2.41	0.45
35:BV:40:LEU:HD23	35:BV:46:VAL:HG23	1.98	0.45
35:BV:79:VAL:O	35:BV:79:VAL:HG13	2.16	0.45
38:BY:17:SER:HB2	38:BY:71:LYS:HB3	1.97	0.45
38:BY:28:LYS:HB3	38:BY:37:VAL:HB	1.97	0.45
42:B2:38:GLN:HB3	42:B2:44:LEU:CB	2.45	0.45
48:B7:5:TRP:CD1	48:B7:7:PRO:HD3	2.51	0.45
49:B8:33:ASN:HA	49:B8:36:LYS:CG	2.47	0.45
51:BC:193:ILE:HD12	51:BC:193:ILE:H	1.80	0.45
52:BE:134:ILE:C	52:BE:134:ILE:HD12	2.42	0.45
53:BF:114:VAL:HG21	53:BF:202:PHE:CE1	2.51	0.45
1:AA:262:A:C6	1:AA:263:A:C6	3.04	0.45
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.98	0.45
1:AA:1230:C:O2'	1:AA:1231:G:H5'	2.17	0.45
1:AA:1349:A:H2'	1:AA:1350:A:O5'	2.16	0.45
2:AV:19:G:C5	25:BA:2169:A:H1'	2.52	0.45
17:AD:22:LYS:O	17:AD:24:GLU:N	2.49	0.45
17:AD:28:SER:C	17:AD:30:LYS:H	2.24	0.45
21:AH:83:ILE:HG23	21:AH:83:ILE:O	2.17	0.45
21:AH:111:ILE:C	21:AH:112:LEU:HD23	2.42	0.45
25:BA:338:G:C5	25:BA:339:U:C5	3.05	0.45
25:BA:780:G:H2'	25:BA:782:A:N7	2.31	0.45
25:BA:1209:G:O2'	25:BA:1237:A:N1	2.45	0.45
25:BA:2142:C:H5''	25:BA:2143:C:OP2	2.16	0.45
25:BA:2164:C:C4	25:BA:2165:G:C8	3.05	0.45
29:BP:47:ASP:HB3	29:BP:48:PRO:CA	2.46	0.45
31:BR:4:LEU:O	31:BR:5:LYS:HD3	2.17	0.45
38:BY:85:VAL:HG13	38:BY:92:ASN:OD1	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:BD:24:ILE:O	43:BD:26:LYS:CB	2.65	0.45
47:B6:15:GLU:OE2	47:B6:41:PRO:HB2	2.16	0.45
53:BF:61:GLY:O	53:BF:62:ARG:C	2.59	0.45
53:BF:88:VAL:HG11	53:BF:91:GLY:HA3	1.98	0.45
55:BH:85:LYS:O	55:BH:85:LYS:NZ	2.42	0.45
1:AA:1371:G:C6	1:AA:1372:U:C4	3.04	0.45
6:AL:27:LEU:HB2	6:AL:62:SER:HB2	1.98	0.45
22:AI:112:LYS:HG2	22:AI:118:LYS:HA	1.98	0.45
23:AY:20:HIS:CG	23:AY:21:ILE:N	2.85	0.45
23:AY:490:PRO:O	23:AY:491:VAL:HG23	2.17	0.45
23:AY:627:ARG:NH1	23:AY:651:GLU:O	2.50	0.45
25:BA:529:A:N3	25:BA:529:A:O4'	2.50	0.45
25:BA:833:U:H5''	29:BP:48:PRO:HB3	1.97	0.45
25:BA:2592:G:H2'	25:BA:2593:U:O4'	2.17	0.45
41:B1:44:PRO:HB2	41:B1:46:LEU:HD13	1.98	0.45
45:B4:37:PRO:HA	45:B4:51:TYR:CD2	2.52	0.45
52:BE:98:PRO:HD3	52:BE:175:VAL:CG1	2.47	0.45
58:BL:79:UNK:C	58:BL:81:UNK:N	2.78	0.45
9:AO:78:TYR:O	9:AO:82:ILE:HG22	2.17	0.45
15:AB:31:TYR:CZ	15:AB:200:ILE:HD12	2.52	0.45
18:AE:51:VAL:O	18:AE:55:VAL:HG23	2.16	0.45
23:AY:114:VAL:HG11	23:AY:157:LEU:HD22	1.98	0.45
25:BA:26:G:C6	25:BA:27:G:N1	2.85	0.45
25:BA:27:G:O2'	25:BA:28:A:P	2.73	0.45
25:BA:363(E):U:H5'	25:BA:363(F):A:OP2	2.17	0.45
25:BA:864:G:N7	30:BQ:22:LYS:NZ	2.62	0.45
25:BA:1063:G:C6	25:BA:1075:C:N4	2.84	0.45
25:BA:1449:A:C4	25:BA:1528(A):A:C2	3.05	0.45
25:BA:1569:A:O2'	43:BD:38:LYS:HG2	2.17	0.45
25:BA:2575:C:H6	25:BA:2575:C:O5'	1.99	0.45
25:BA:2645:G:N2	25:BA:2767:C:OP2	2.49	0.45
34:BU:74:LEU:HD23	34:BU:78:THR:HG22	1.98	0.45
38:BY:55:TYR:O	38:BY:57:GLN:N	2.50	0.45
39:BZ:188:ALA:O	39:BZ:190:GLU:N	2.50	0.45
51:BC:28:LEU:HD12	51:BC:28:LEU:O	2.17	0.45
54:BG:85:GLY:O	54:BG:86:MET:C	2.59	0.45
1:AA:918:A:H2'	1:AA:919:A:C8	2.51	0.45
1:AA:1028:C:N4	1:AA:1033:G:O6	2.49	0.45
1:AA:1100:C:OP2	15:AB:96:ARG:NE	2.50	0.45
6:AL:41:ARG:HB3	6:AL:41:ARG:NH1	2.32	0.45
16:AC:91:LEU:HD11	16:AC:101:LEU:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:AG:113:GLU:HG2	20:AG:119:ARG:HG2	1.99	0.45
22:AI:95:LYS:C	22:AI:95:LYS:HE2	2.42	0.45
23:AY:470:PHE:O	23:AY:471:LYS:HG3	2.17	0.45
25:BA:270:A:N1	25:BA:366:C:O2'	2.43	0.45
25:BA:571:A:H5'	25:BA:2030:A:N7	2.32	0.45
25:BA:1057:A:C6	25:BA:1086:A:C2	3.05	0.45
25:BA:1078:U:O2	25:BA:1088:A:H5'	2.17	0.45
25:BA:1089:G:C4'	25:BA:1090:U:OP1	2.63	0.45
25:BA:1204:A:C2	25:BA:1241:A:N1	2.85	0.45
25:BA:1775:U:H2'	25:BA:1776:G:O5'	2.16	0.45
25:BA:1805:U:O2	43:BD:50:THR:HB	2.16	0.45
25:BA:2208:A:O2'	25:BA:2219:G:C8	2.70	0.45
25:BA:2447:G:N7	25:BA:2501:C:O4'	2.50	0.45
26:BB:82:G:H2'	26:BB:83:G:O5'	2.16	0.45
30:BQ:35:VAL:HG11	30:BQ:130:LYS:HE3	1.99	0.45
33:BT:32:TYR:O	33:BT:41:ARG:O	2.35	0.45
37:BX:21:PHE:O	37:BX:23:GLU:O	2.35	0.45
39:BZ:152:ALA:HB1	39:BZ:167:PRO:HB2	1.98	0.45
43:BD:125:ILE:HD11	43:BD:131:LEU:HD22	1.98	0.45
1:AA:62:U:C2'	1:AA:63:C:H5''	2.45	0.45
1:AA:927:G:OP2	1:AA:927:G:H4'	2.17	0.45
7:AM:13:LYS:O	7:AM:44:ARG:HA	2.16	0.45
15:AB:166:ASP:HB3	15:AB:169:LYS:CB	2.46	0.45
15:AB:178:ARG:CG	15:AB:178:ARG:NH1	2.65	0.45
18:AE:148:VAL:O	18:AE:152:ARG:HG3	2.17	0.45
23:AY:58:GLU:HG3	23:AY:65:ILE:HG22	1.98	0.45
23:AY:180:VAL:HG23	23:AY:181:LEU:N	2.31	0.45
23:AY:224:ASP:HB2	23:AY:227:ILE:HD12	1.98	0.45
23:AY:685:GLU:HA	23:AY:688:ILE:HG22	1.99	0.45
25:BA:251:A:H5''	29:BP:51:PHE:HZ	1.82	0.45
25:BA:301:G:H1'	25:BA:302:C:C6	2.52	0.45
25:BA:854:G:H5''	25:BA:855:G:OP2	2.17	0.45
25:BA:1076:C:O2'	25:BA:1077:A:O4'	2.34	0.45
25:BA:1914:C:C2'	25:BA:1915:U:O5'	2.59	0.45
25:BA:2637:U:C2'	25:BA:2638:G:H5'	2.46	0.45
27:BN:15:LEU:O	27:BN:136:GLU:HA	2.17	0.45
28:BO:88:ASN:C	28:BO:88:ASN:ND2	2.73	0.45
29:BP:57:THR:HB	29:BP:59:LEU:HB2	1.99	0.45
33:BT:30:VAL:HG12	33:BT:44:ASP:CG	2.41	0.45
38:BY:26:LYS:O	38:BY:27:VAL:C	2.59	0.45
47:B6:11:LEU:HD22	47:B6:11:LEU:C	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:BE:68:ALA:O	52:BE:70:ALA:N	2.50	0.45
54:BG:28:VAL:O	54:BG:31:VAL:HG12	2.17	0.45
57:BJ:21:ALA:HB3	57:BJ:88:ALA:HA	1.98	0.45
1:AA:711:G:O2'	1:AA:712:A:H5'	2.17	0.44
1:AA:1138:G:O2'	1:AA:1139:G:P	2.75	0.44
2:AV:55:U:O2	2:AV:55:U:O4'	2.35	0.44
13:AS:66:MET:HE3	13:AS:74:PHE:CZ	2.52	0.44
25:BA:316:C:C2'	25:BA:317:G:O5'	2.65	0.44
25:BA:861:A:H2'	25:BA:862:G:O4'	2.17	0.44
25:BA:1246:A:P	29:BP:16:ARG:NH2	2.90	0.44
25:BA:1367:A:H5''	25:BA:1368:G:OP2	2.17	0.44
25:BA:1458:C:C4'	25:BA:1459:G:O5'	2.64	0.44
25:BA:1462:C:H4'	25:BA:2703:C:H5'	1.98	0.44
25:BA:1527:G:H2'	25:BA:1544:A:C2	2.52	0.44
25:BA:1817:G:C6	25:BA:1818:U:C4	3.04	0.44
25:BA:1943:U:H4'	25:BA:1944:U:OP1	2.17	0.44
25:BA:2166:G:O2'	25:BA:2167:U:H5'	2.17	0.44
25:BA:2179:C:O2	25:BA:2179:C:O4'	2.35	0.44
29:BP:120:ALA:HB1	29:BP:138:LEU:HD12	1.99	0.44
31:BR:44:LEU:HD22	31:BR:48:VAL:HG23	1.98	0.44
33:BT:82:LEU:HD12	33:BT:82:LEU:H	1.80	0.44
37:BX:66:LEU:HD23	37:BX:66:LEU:O	2.16	0.44
41:B1:3:LYS:HG2	41:B1:4:VAL:H	1.82	0.44
42:B2:35:LEU:CD1	42:B2:53:LEU:HD12	2.46	0.44
43:BD:270:ILE:C	43:BD:271:ILE:CG1	2.89	0.44
1:AA:180:U:H2'	1:AA:181:G:H5'	1.99	0.44
1:AA:452:A:HO2'	1:AA:453:A:H8	1.65	0.44
1:AA:1037:C:H2'	1:AA:1038:C:C6	2.52	0.44
1:AA:1533:C:H3'	1:AA:1534:A:H5''	1.98	0.44
15:AB:215:LEU:HA	15:AB:215:LEU:HD13	1.76	0.44
17:AD:22:LYS:HE2	17:AD:25:ARG:HD2	1.98	0.44
23:AY:79:ILE:HD12	23:AY:79:ILE:N	2.32	0.44
25:BA:852:G:O2'	25:BA:853:G:H5'	2.17	0.44
25:BA:1903:G:OP1	43:BD:241:PRO:HB2	2.17	0.44
25:BA:2343:C:O2'	25:BA:2344:U:H5'	2.17	0.44
25:BA:2685:G:P	33:BT:51:ARG:HH12	2.40	0.44
28:BO:104:ARG:HH11	28:BO:107:ARG:HH12	1.63	0.44
29:BP:51:PHE:HB3	29:BP:52:GLU:CD	2.42	0.44
30:BQ:55:VAL:O	30:BQ:56:ARG:C	2.58	0.44
31:BR:78:LYS:CE	31:BR:83:ILE:HD11	2.47	0.44
49:B8:54:GLU:O	49:B8:58:ILE:HG13	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:BE:75:VAL:C	52:BE:77:ILE:H	2.25	0.44
53:BF:22:ALA:HB1	53:BF:26:ALA:CB	2.47	0.44
54:BG:32:PRO:HB2	54:BG:172:LEU:HD13	1.99	0.44
1:AA:501:C:H2'	1:AA:502:G:C8	2.53	0.44
5:AK:38:ASN:HA	5:AK:39:PRO:HD3	1.91	0.44
7:AM:65:LYS:O	7:AM:65:LYS:CG	2.65	0.44
9:AO:18:PHE:O	9:AO:19:PRO:C	2.58	0.44
13:AS:62:ILE:C	13:AS:63:THR:HG22	2.41	0.44
15:AB:19:HIS:HB2	15:AB:204:ASN:HD22	1.83	0.44
18:AE:7:GLU:OE1	18:AE:37:ARG:NE	2.49	0.44
18:AE:126:ARG:O	18:AE:127:ASN:C	2.60	0.44
23:AY:26:THR:HA	23:AY:83:ASP:OD2	2.16	0.44
23:AY:325:LEU:HD21	23:AY:358:MET:CE	2.47	0.44
23:AY:403:GLU:O	23:AY:404:VAL:C	2.60	0.44
23:AY:632:LEU:HD11	23:AY:646:PHE:CD2	2.52	0.44
25:BA:370:G:O5'	25:BA:370:G:C8	2.70	0.44
25:BA:1268:A:C2	25:BA:2013:A:C4	3.05	0.44
25:BA:1899:G:HO2'	25:BA:1900:A:P	2.38	0.44
25:BA:2469:A:H2'	25:BA:2470:G:O4'	2.18	0.44
26:BB:84:C:OP1	44:B3:15:TYR:OH	2.35	0.44
28:BO:9:GLU:O	28:BO:83:ALA:HA	2.18	0.44
34:BU:88:ILE:HD13	34:BU:109:LEU:CD2	2.44	0.44
38:BY:52:SER:O	38:BY:54:LYS:N	2.50	0.44
49:B8:32:LEU:CB	49:B8:36:LYS:NZ	2.80	0.44
49:B8:33:ASN:HA	49:B8:36:LYS:HG2	2.00	0.44
51:BC:103:ILE:O	51:BC:104:LEU:C	2.60	0.44
55:BH:23:ARG:O	55:BH:24:VAL:HG12	2.18	0.44
56:BK:3:LYS:HD3	56:BK:29:GLN:HG2	2.00	0.44
1:AA:684:A:C6	1:AA:685:G:C6	3.05	0.44
1:AA:702:A:H4'	1:AA:703:G:OP2	2.17	0.44
15:AB:51:LEU:O	15:AB:55:PHE:HB2	2.17	0.44
15:AB:92:TYR:O	15:AB:151:GLY:HA3	2.18	0.44
15:AB:126:GLU:O	15:AB:130:ARG:HG3	2.18	0.44
23:AY:86:GLY:O	23:AY:117:GLN:CG	2.66	0.44
23:AY:281:PRO:HB2	23:AY:286:ILE:HD11	2.00	0.44
23:AY:495:GLY:O	23:AY:510:VAL:N	2.51	0.44
25:BA:92:A:C2	25:BA:93:G:H1'	2.52	0.44
25:BA:358:U:O2	25:BA:358:U:H2'	2.18	0.44
25:BA:484:C:H2'	25:BA:485:C:C6	2.52	0.44
25:BA:1491:G:OP2	25:BA:1494:A:C6	2.71	0.44
25:BA:2287:A:N1	25:BA:2346:A:N1	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2743:C:C2'	25:BA:2744:G:O5'	2.65	0.44
27:BN:134:ARG:HD2	27:BN:134:ARG:N	2.32	0.44
28:BO:63:VAL:HG11	28:BO:85:VAL:HG23	1.99	0.44
29:BP:143:GLY:HA3	29:BP:145:PRO:HD3	1.99	0.44
32:BS:53:SER:OG	32:BS:54:LEU:N	2.50	0.44
33:BT:80:SER:HB3	33:BT:81:PRO:HD3	1.98	0.44
35:BV:19:LYS:CG	35:BV:20:LEU:O	2.65	0.44
39:BZ:151:HIS:HB3	39:BZ:170:THR:HA	1.99	0.44
41:B1:51:VAL:HG21	41:B1:74:VAL:HG21	2.00	0.44
53:BF:24:LEU:HD13	53:BF:118:ALA:HB1	1.98	0.44
54:BG:48:GLU:O	54:BG:49:ASP:HB3	2.17	0.44
1:AA:685:G:C2	1:AA:686:U:C4	3.05	0.44
7:AM:86:CYS:HA	13:AS:73:GLU:O	2.18	0.44
12:AR:22:VAL:O	12:AR:23:LYS:C	2.58	0.44
15:AB:12:GLU:C	15:AB:14:GLY:N	2.74	0.44
16:AC:101:LEU:HD23	16:AC:101:LEU:C	2.43	0.44
19:AF:72:VAL:HG13	19:AF:73:ASN:N	2.31	0.44
25:BA:95:G:O2'	42:B2:48:HIS:ND1	2.40	0.44
25:BA:510:C:OP1	25:BA:511:U:OP2	2.36	0.44
25:BA:603:A:O4'	25:BA:603:A:N3	2.50	0.44
25:BA:1692:U:O2'	25:BA:1693:U:H2'	2.18	0.44
25:BA:1835:G:H1'	25:BA:1931:U:C2	2.53	0.44
25:BA:2025:C:H2'	25:BA:2026:C:C6	2.52	0.44
25:BA:2151:G:C2	25:BA:2152:G:C4	3.05	0.44
25:BA:2392:A:OP1	49:B8:32:LEU:HD21	2.16	0.44
25:BA:2401:U:O2'	25:BA:2402:C:H5''	2.17	0.44
25:BA:2557:G:H2'	25:BA:2558:C:C6	2.52	0.44
27:BN:35:ARG:O	27:BN:37:LYS:N	2.50	0.44
32:BS:99:LYS:N	32:BS:99:LYS:HD3	2.27	0.44
33:BT:96:ARG:CZ	33:BT:96:ARG:HB3	2.47	0.44
47:B6:20:ASN:C	47:B6:21:TYR:CD1	2.96	0.44
55:BH:157:TYR:CE1	55:BH:173:PRO:HB3	2.53	0.44
56:BK:19:PRO:CB	56:BK:34:ILE:HD12	2.47	0.44
56:BK:77:LEU:HD23	56:BK:77:LEU:N	2.32	0.44
1:AA:96:U:O2'	1:AA:97:G:P	2.76	0.44
1:AA:909:A:H2'	1:AA:910:C:O4'	2.18	0.44
19:AF:72:VAL:CG2	19:AF:90:VAL:HG11	2.48	0.44
22:AI:10:ARG:CZ	22:AI:105:ASP:OD2	2.65	0.44
22:AI:48:GLU:N	22:AI:49:PRO:CD	2.80	0.44
23:AY:491:VAL:O	23:AY:513:LYS:HA	2.17	0.44
23:AY:512:ILE:CD1	23:AY:589:ALA:HB1	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:104:U:C5	25:BA:105:C:C5	3.05	0.44
25:BA:264:C:O2'	25:BA:265:A:H2'	2.18	0.44
25:BA:271(O):C:O2'	25:BA:271(P):C:OP2	2.31	0.44
25:BA:445:C:OP1	34:BU:2:PRO:HA	2.18	0.44
25:BA:614:U:O2	25:BA:614:U:O5'	2.35	0.44
25:BA:774:A:HO2'	25:BA:775:G:P	2.32	0.44
25:BA:2115:G:H2'	25:BA:2117:A:N7	2.33	0.44
25:BA:2165:G:C5	25:BA:2166:G:C6	3.05	0.44
25:BA:2266:A:H4'	25:BA:2267:A:O5'	2.18	0.44
25:BA:2667:C:H1'	55:BH:109:PHE:CD1	2.52	0.44
25:BA:2689:U:O2	25:BA:2713:A:O5'	2.36	0.44
28:BO:43:VAL:HG21	28:BO:52:VAL:CG1	2.47	0.44
29:BP:55:ARG:CG	29:BP:56:SER:H	2.30	0.44
29:BP:68:GLN:HE21	29:BP:68:GLN:HB2	1.61	0.44
33:BT:83:ILE:HG13	33:BT:84:GLN:N	2.33	0.44
35:BV:3:ALA:HA	35:BV:40:LEU:O	2.18	0.44
38:BY:23:ARG:O	38:BY:24:VAL:O	2.35	0.44
39:BZ:30:ASN:O	39:BZ:31:ARG:C	2.60	0.44
47:B6:14:THR:O	47:B6:49:HIS:HA	2.17	0.44
49:B8:61:LEU:H	49:B8:61:LEU:CD2	2.22	0.44
54:BG:16:ARG:NE	54:BG:31:VAL:HG11	2.33	0.44
54:BG:37:VAL:HG22	54:BG:159:VAL:HA	2.00	0.44
54:BG:130:ASN:OD1	54:BG:130:ASN:N	2.50	0.44
56:BK:21:PRO:HA	56:BK:23:VAL:N	2.33	0.44
1:AA:452:A:O2'	1:AA:453:A:H8	2.00	0.44
1:AA:804:U:H5''	1:AA:805:C:OP2	2.17	0.44
1:AA:926:G:H5''	1:AA:927:G:O5'	2.17	0.44
1:AA:1085:U:C2	1:AA:1094:G:O6	2.71	0.44
1:AA:1119:C:OP2	22:AI:9:ARG:NH2	2.50	0.44
2:AV:35:A:H5''	2:AV:35:A:H8	1.82	0.44
15:AB:15:VAL:O	15:AB:16:HIS:ND1	2.51	0.44
21:AH:31:PHE:O	21:AH:35:ILE:HG13	2.18	0.44
23:AY:321:TYR:CD1	23:AY:321:TYR:N	2.86	0.44
23:AY:627:ARG:O	23:AY:628:ARG:CB	2.66	0.44
25:BA:1375:C:H2'	25:BA:1376:C:H6	1.83	0.44
25:BA:2097:C:H2'	25:BA:2098:U:H5'	1.99	0.44
25:BA:2648:C:H2'	25:BA:2649:U:C6	2.52	0.44
25:BA:2681:C:O2	25:BA:2681:C:H2'	2.17	0.44
25:BA:2712:U:O2'	25:BA:2712(A):A:OP2	2.29	0.44
25:BA:2769:C:H2'	25:BA:2770:G:O4'	2.17	0.44
29:BP:17:LYS:C	29:BP:19:VAL:N	2.69	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:BS:35:ILE:HG23	32:BS:69:VAL:HG11	1.98	0.44
34:BU:25:TRP:CD1	34:BU:25:TRP:C	2.94	0.44
42:B2:47:ASN:C	42:B2:49:LYS:N	2.74	0.44
43:BD:27:THR:CG2	43:BD:81:ALA:HB1	2.47	0.44
54:BG:64:THR:HG23	54:BG:66:GLN:H	1.83	0.44
54:BG:116:ASP:O	54:BG:117:PHE:HB3	2.18	0.44
1:AA:72:C:H2'	1:AA:73:G:C8	2.53	0.44
15:AB:191:ASP:OD1	15:AB:191:ASP:O	2.35	0.44
16:AC:91:LEU:CB	16:AC:99:VAL:HG21	2.48	0.44
18:AE:84:PHE:CB	18:AE:134:ALA:HB2	2.48	0.44
21:AH:44:PHE:HE2	21:AH:109:ILE:HG21	1.82	0.44
25:BA:485:C:C2	25:BA:496:G:N2	2.86	0.44
25:BA:508:G:N3	25:BA:508:G:H2'	2.32	0.44
25:BA:1599:C:OP1	37:BX:36:LYS:N	2.45	0.44
25:BA:2189:U:O5'	25:BA:2189:U:H6	2.00	0.44
25:BA:2302:G:C2'	25:BA:2303:G:H5'	2.47	0.44
25:BA:2451:A:H5'	40:B0:2:ALA:HB2	1.99	0.44
26:BB:40:U:H3'	26:BB:41:U:H5'	1.98	0.44
27:BN:58:ASP:O	27:BN:60:ILE:HG13	2.17	0.44
31:BR:94:TYR:O	31:BR:117:VAL:HB	2.18	0.44
33:BT:128:GLU:CD	33:BT:129:ARG:N	2.76	0.44
34:BU:102:GLU:OE2	35:BV:13:ARG:NH2	2.51	0.44
54:BG:80:PHE:C	54:BG:81:LYS:HG2	2.42	0.44
1:AA:241:C:O2'	1:AA:242:C:H5'	2.18	0.44
1:AA:786:G:C2	1:AA:797:C:C2	3.06	0.44
1:AA:926:G:H2'	1:AA:1505:G:N3	2.33	0.44
1:AA:1499:A:H1'	1:AA:1520:G:H5'	2.00	0.44
4:AJ:51:ARG:HG3	4:AJ:60:ARG:HA	1.99	0.44
5:AK:114:VAL:HA	5:AK:115:PRO:HD2	1.88	0.44
11:AQ:66:SER:OG	11:AQ:69:LYS:HB2	2.17	0.44
17:AD:61:LYS:HD2	17:AD:207:TYR:OH	2.17	0.44
17:AD:81:GLU:CD	17:AD:139:ARG:HH22	2.26	0.44
21:AH:9:MET:O	21:AH:13:ILE:HG12	2.18	0.44
25:BA:171:G:H2'	25:BA:172:C:O4'	2.18	0.44
25:BA:236:C:O2'	25:BA:431:U:H4'	2.17	0.44
25:BA:1538:G:C2'	25:BA:1539:G:O5'	2.66	0.44
25:BA:1676:A:H2'	25:BA:1677:A:O4'	2.18	0.44
25:BA:1859:A:C2	25:BA:1884:A:H1'	2.52	0.44
25:BA:1881:C:C6	25:BA:1881:C:H5''	2.53	0.44
25:BA:2193:G:C4	25:BA:2194:G:C8	3.06	0.44
25:BA:2762:G:H5''	25:BA:2762:G:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2789:C:O2'	25:BA:2790:A:H1'	2.17	0.44
29:BP:143:GLY:CA	29:BP:145:PRO:HD3	2.48	0.44
35:BV:36:PRO:HA	35:BV:56:SER:CB	2.48	0.44
36:BW:88:ARG:HG3	36:BW:94:ASP:OD1	2.17	0.44
38:BY:3:VAL:O	38:BY:3:VAL:HG12	2.18	0.44
39:BZ:40:ASP:HB3	39:BZ:43:GLU:HB2	1.99	0.44
50:B9:29:ASN:HA	50:B9:30:PRO:HD3	1.77	0.44
53:BF:65:TRP:CH2	53:BF:73:ALA:O	2.70	0.44
1:AA:116:A:OP2	1:AA:116:A:H8	2.01	0.43
1:AA:243:A:C2	1:AA:246:A:C8	3.06	0.43
1:AA:325:A:H2'	1:AA:326:G:O4'	2.18	0.43
1:AA:693:G:C8	3:AX:15:A:H1'	2.52	0.43
1:AA:1317:C:C2	8:AN:16:PHE:CE1	3.06	0.43
1:AA:1423:G:H2'	1:AA:1424:C:O4'	2.19	0.43
1:AA:1442:G:C8	1:AA:1442(B):A:C2	3.06	0.43
1:AA:1531:A:O3'	1:AA:1532:U:C6	2.70	0.43
5:AK:33:THR:HG22	5:AK:39:PRO:HA	2.01	0.43
11:AQ:50:LYS:HG3	11:AQ:51:TYR:CE1	2.53	0.43
15:AB:166:ASP:CG	15:AB:169:LYS:HB2	2.43	0.43
16:AC:10:PHE:CE2	16:AC:178:LEU:HD13	2.52	0.43
17:AD:176:LEU:HD12	17:AD:182:LYS:O	2.18	0.43
25:BA:105:C:H2'	25:BA:106:C:C6	2.53	0.43
25:BA:445:C:H2'	25:BA:446:G:O4'	2.18	0.43
25:BA:601:C:O2	25:BA:605:C:H4'	2.17	0.43
25:BA:1058:G:C8	25:BA:1058:G:C5'	3.01	0.43
25:BA:1168:G:H2'	25:BA:1169:G:O4'	2.17	0.43
25:BA:1344:G:H4'	25:BA:1384:A:C5	2.53	0.43
25:BA:2077:A:C2'	25:BA:2434:A:O2'	2.66	0.43
25:BA:2180:U:OP2	25:BA:2180:U:H3'	2.18	0.43
25:BA:2821:A:OP1	52:BE:110:GLY:N	2.47	0.43
29:BP:57:THR:CB	29:BP:59:LEU:HB2	2.47	0.43
33:BT:26:ASP:C	33:BT:26:ASP:OD2	2.61	0.43
33:BT:93:ARG:HD2	33:BT:93:ARG:HA	1.83	0.43
39:BZ:8:TYR:CD1	39:BZ:8:TYR:N	2.86	0.43
43:BD:2:ALA:O	43:BD:3:VAL:CB	2.54	0.43
43:BD:100:GLY:O	43:BD:101:GLU:C	2.62	0.43
46:B5:4:HIS:O	46:B5:5:PRO:C	2.60	0.43
47:B6:12:GLU:HB2	47:B6:52:VAL:HG13	1.99	0.43
47:B6:30:THR:O	47:B6:31:PRO:C	2.61	0.43
53:BF:5:ALA:C	53:BF:6:VAL:HG23	2.43	0.43
53:BF:8:GLN:HE21	53:BF:8:GLN:C	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:BG:6:ALA:HB3	54:BG:104:GLU:CD	2.43	0.43
54:BG:54:GLU:HA	54:BG:57:ALA:CB	2.44	0.43
1:AA:416:G:C6	1:AA:417:C:C4	3.06	0.43
1:AA:706:A:O2'	5:AK:31:THR:CG2	2.67	0.43
1:AA:985:C:C2	1:AA:1221:G:N2	2.86	0.43
1:AA:1069:C:C2'	1:AA:1070:U:O5'	2.66	0.43
1:AA:1158:C:O2	1:AA:1158:C:H2'	2.17	0.43
1:AA:1288:A:H2'	1:AA:1289:A:O4'	2.17	0.43
11:AQ:100:LYS:HD3	11:AQ:100:LYS:N	2.33	0.43
16:AC:155:GLY:O	16:AC:156:ARG:HB2	2.18	0.43
23:AY:190:ASN:ND2	23:AY:194:THR:OG1	2.44	0.43
25:BA:336:C:O3'	38:BY:7:VAL:CG2	2.66	0.43
25:BA:998:C:H2'	25:BA:999:U:O5'	2.18	0.43
25:BA:1210:A:H5'	25:BA:1210:A:C8	2.50	0.43
25:BA:1569:A:O4'	43:BD:59:LYS:NZ	2.51	0.43
25:BA:1684:C:O2'	25:BA:1685:C:H5'	2.18	0.43
25:BA:2103:C:H3'	25:BA:2104:G:H5''	2.00	0.43
25:BA:2113:U:H5''	25:BA:2114:A:OP2	2.18	0.43
25:BA:2746:U:C2'	25:BA:2747:G:H5'	2.48	0.43
25:BA:2810:A:C2'	52:BE:61:ARG:NH2	2.79	0.43
25:BA:2876:G:H4'	33:BT:3:ARG:HE	1.83	0.43
33:BT:26:ASP:OD2	33:BT:26:ASP:O	2.35	0.43
33:BT:107:ASP:OD1	33:BT:107:ASP:N	2.51	0.43
42:B2:12:GLU:HA	42:B2:15:LYS:HE2	2.01	0.43
43:BD:102:LYS:C	43:BD:103:ARG:HG2	2.43	0.43
43:BD:108:PRO:HD2	43:BD:111:LEU:HD12	2.00	0.43
51:BC:131:LEU:CB	51:BC:137:LEU:HD23	2.46	0.43
53:BF:157:VAL:O	53:BF:157:VAL:CG2	2.65	0.43
53:BF:194:MET:C	53:BF:195:ASP:O	2.61	0.43
1:AA:178:C:C2	1:AA:179:A:C8	3.06	0.43
1:AA:795:C:H5''	1:AA:796:C:OP2	2.18	0.43
1:AA:1034:G:H2'	1:AA:1035:A:C8	2.53	0.43
1:AA:1053:G:H4'	1:AA:1054:C:H5'	2.00	0.43
1:AA:1206:G:H2'	1:AA:1207:G:O4'	2.17	0.43
1:AA:1245:A:H2'	1:AA:1246:C:O4'	2.18	0.43
1:AA:1328:C:H5''	7:AM:28:ALA:CB	2.48	0.43
1:AA:1534:A:H2'	1:AA:1535:C:C6	2.53	0.43
16:AC:141:VAL:HG11	16:AC:149:ALA:HB2	2.00	0.43
19:AF:16:GLN:HE21	19:AF:16:GLN:HB3	1.64	0.43
20:AG:15:ASP:O	20:AG:19:GLY:HA2	2.18	0.43
22:AI:49:PRO:HG2	22:AI:81:ILE:HG22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AY:485:GLU:O	23:AY:560:VAL:HA	2.18	0.43
25:BA:128:C:H3'	25:BA:128:C:C6	2.53	0.43
25:BA:2137:C:H3'	25:BA:2138:C:H5''	2.00	0.43
25:BA:2291:U:H2'	25:BA:2292:C:C6	2.53	0.43
25:BA:2419:U:O4	49:B8:30:ARG:NH1	2.48	0.43
25:BA:2577:A:H5''	25:BA:2578:G:H5'	1.99	0.43
26:BB:81:G:O6	26:BB:96:U:O2	2.36	0.43
29:BP:7:ARG:NH1	29:BP:7:ARG:O	2.52	0.43
33:BT:16:ARG:HG2	33:BT:79:HIS:HA	1.99	0.43
33:BT:31:SER:HB2	33:BT:32:TYR:CD2	2.54	0.43
36:BW:33:ARG:NH2	36:BW:52:GLU:OE1	2.42	0.43
39:BZ:71:VAL:HG11	39:BZ:74:VAL:HG23	2.00	0.43
47:B6:41:PRO:HG2	47:B6:44:ARG:O	2.18	0.43
52:BE:68:ALA:C	52:BE:70:ALA:N	2.76	0.43
57:BJ:118:ALA:O	57:BJ:119:ALA:HB3	2.18	0.43
2:AV:35:A:C5'	2:AV:35:A:C8	3.01	0.43
23:AY:605:ILE:HD13	23:AY:677:GLN:HB3	1.99	0.43
25:BA:128:C:H4'	25:BA:129:C:OP1	2.19	0.43
25:BA:336:C:H4'	38:BY:7:VAL:HG21	2.00	0.43
25:BA:607:U:C5'	53:BF:103:LYS:HE2	2.48	0.43
25:BA:631:A:N3	25:BA:2415:G:O2'	2.50	0.43
25:BA:742:G:H4'	25:BA:1676:A:H5'	2.00	0.43
25:BA:1021:A:O2'	25:BA:1123:C:OP1	2.33	0.43
25:BA:1430:C:H2'	25:BA:1431:U:H6	1.83	0.43
25:BA:1644:C:C2'	25:BA:1645:G:H5'	2.48	0.43
25:BA:1762:A:H8	25:BA:1762:A:O5'	2.01	0.43
25:BA:1820:U:H4'	25:BA:1821:A:OP2	2.18	0.43
25:BA:2392:A:H2	25:BA:2424:C:N4	2.06	0.43
25:BA:2740:A:C6	25:BA:2741:A:C6	3.06	0.43
25:BA:2774:C:H2'	25:BA:2775:A:O4'	2.17	0.43
28:BO:43:VAL:HG12	28:BO:54:GLU:HA	2.01	0.43
29:BP:16:ARG:HD3	29:BP:17:LYS:N	2.33	0.43
33:BT:29:ARG:HE	33:BT:86:ILE:HG22	1.83	0.43
35:BV:28:GLU:HG3	35:BV:29:PRO:HD3	2.00	0.43
52:BE:61:ARG:HA	52:BE:63:LEU:HB2	1.99	0.43
53:BF:135:LYS:O	53:BF:136:THR:C	2.61	0.43
1:AA:1378:C:OP1	20:AG:6:ARG:O	2.36	0.43
6:AL:18:VAL:CG2	6:AL:19:ARG:N	2.82	0.43
8:AN:57:ARG:NH2	16:AC:13:GLY:HA3	2.33	0.43
13:AS:78:ARG:HD2	13:AS:81:ARG:HH12	1.83	0.43
18:AE:11:ILE:HG22	18:AE:31:LEU:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:AE:36:ASP:O	18:AE:37:ARG:HB2	2.17	0.43
23:AY:169:GLY:HA3	23:AY:173:THR:O	2.18	0.43
25:BA:543:C:C5'	25:BA:543:C:H6	2.32	0.43
25:BA:623:G:H2'	25:BA:624:C:C6	2.53	0.43
25:BA:1881:C:H5''	25:BA:1881:C:H6	1.83	0.43
32:BS:99:LYS:C	32:BS:101:LEU:N	2.77	0.43
33:BT:65:LYS:HE3	33:BT:67:SER:HB2	2.01	0.43
41:B1:3:LYS:CG	41:B1:4:VAL:N	2.80	0.43
42:B2:63:VAL:O	42:B2:64:LEU:C	2.60	0.43
43:BD:43:ARG:CB	43:BD:54:ARG:HB2	2.47	0.43
1:AA:310:G:OP2	10:AP:27:LYS:HE2	2.18	0.43
1:AA:689:C:H2'	1:AA:690:G:O4'	2.18	0.43
1:AA:812:C:OP1	1:AA:903:G:H1'	2.19	0.43
1:AA:1157:A:H4'	1:AA:1158:C:O5'	2.19	0.43
7:AM:59:TYR:O	7:AM:63:THR:OG1	2.15	0.43
9:AO:82:ILE:HG13	9:AO:88:ARG:HB2	2.01	0.43
11:AQ:45:HIS:CB	11:AQ:65:ILE:HD13	2.46	0.43
11:AQ:59:ILE:HA	11:AQ:59:ILE:HD13	1.75	0.43
14:AT:100:ILE:C	14:AT:102:GLY:H	2.25	0.43
15:AB:200:ILE:HB	15:AB:202:PRO:HD3	2.01	0.43
23:AY:181:LEU:HD23	23:AY:182:ARG:NH1	2.34	0.43
23:AY:205:TYR:HA	23:AY:208:GLN:HB3	2.00	0.43
23:AY:264:LEU:HD13	23:AY:265:LYS:HE3	2.01	0.43
23:AY:684:GLN:N	23:AY:687:LEU:HB2	2.33	0.43
25:BA:228:A:H3'	25:BA:229:A:C5'	2.48	0.43
25:BA:579:G:H2'	25:BA:580:C:C6	2.54	0.43
25:BA:876:C:H2'	25:BA:877:U:O4'	2.19	0.43
25:BA:1073:A:H2'	25:BA:1074:G:O4'	2.18	0.43
25:BA:1131:G:N2	27:BN:73:THR:HG23	2.33	0.43
25:BA:1674:G:H1'	25:BA:1676:A:N6	2.33	0.43
25:BA:2009:G:OP1	36:BW:41:LYS:HE2	2.19	0.43
25:BA:2352:A:C4	25:BA:2366:A:C2	3.06	0.43
26:BB:84:C:H2'	26:BB:85:G:O5'	2.18	0.43
27:BN:39:ARG:HD3	27:BN:41:ASP:OD1	2.18	0.43
27:BN:67:LEU:O	27:BN:68:GLU:CB	2.65	0.43
43:BD:30:GLU:CD	43:BD:63:ARG:HH21	2.27	0.43
47:B6:51:GLU:HG3	47:B6:52:VAL:N	2.32	0.43
49:B8:62:LEU:O	49:B8:64:TYR:N	2.49	0.43
51:BC:177:LYS:C	51:BC:179:SER:H	2.27	0.43
1:AA:1134:G:C4	1:AA:1135:U:C6	3.06	0.43
2:AV:1:G:C2	2:AV:73:A:C8	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AV:36:A:C2	3:AX:19:U:C2	3.06	0.43
15:AB:23:ARG:HG3	15:AB:23:ARG:O	2.18	0.43
17:AD:28:SER:HB3	17:AD:30:LYS:HG3	2.01	0.43
18:AE:50:GLU:OE1	18:AE:50:GLU:HA	2.18	0.43
19:AF:3:ARG:CZ	19:AF:3:ARG:HB2	2.49	0.43
23:AY:86:GLY:O	23:AY:117:GLN:HG2	2.19	0.43
25:BA:385:C:O2	29:BP:71:VAL:HG21	2.18	0.43
25:BA:983:A:C6	25:BA:984:A:N1	2.87	0.43
25:BA:1181:C:C2'	25:BA:1182:A:H5'	2.48	0.43
25:BA:1722:A:C6	25:BA:1741:A:N1	2.87	0.43
25:BA:2056:G:N2	46:B5:5:PRO:HA	2.34	0.43
25:BA:2712:U:O2	25:BA:2712:U:H5'	2.19	0.43
25:BA:2815:C:O2'	46:B5:42:PRO:HG2	2.19	0.43
26:BB:13:A:O2'	26:BB:15:A:OP2	2.31	0.43
26:BB:42:C:C5'	54:BG:69:ALA:HB2	2.49	0.43
29:BP:13:ASN:OD1	53:BF:31:HIS:CB	2.67	0.43
30:BQ:16:ARG:O	30:BQ:17:LEU:HD23	2.18	0.43
36:BW:43:GLY:O	36:BW:44:ALA:C	2.62	0.43
39:BZ:23:LYS:O	39:BZ:25:PRO:HD3	2.19	0.43
54:BG:131:TYR:HB3	54:BG:159:VAL:CG1	2.49	0.43
55:BH:26:VAL:O	55:BH:32:GLU:HA	2.18	0.43
55:BH:37:VAL:HG13	55:BH:68:THR:HG21	2.00	0.43
56:BK:29:GLN:O	56:BK:59:ILE:HD12	2.19	0.43
1:AA:504:C:C2	1:AA:542:G:N2	2.87	0.43
21:AH:50:ARG:O	21:AH:51:VAL:CG1	2.67	0.43
23:AY:395:PRO:O	23:AY:397:VAL:N	2.51	0.43
25:BA:422:A:C6	25:BA:423:A:C6	3.06	0.43
25:BA:702:G:C2	25:BA:731:C:C2	3.06	0.43
25:BA:2035:G:H4'	25:BA:2036:C:OP2	2.18	0.43
25:BA:2298:A:H2'	25:BA:2299:G:O4'	2.17	0.43
25:BA:2305:A:C2	25:BA:2306:C:C1'	2.95	0.43
25:BA:2734:A:C5'	25:BA:2735:G:OP2	2.65	0.43
28:BO:66:LYS:HD2	28:BO:80:ASP:O	2.18	0.43
29:BP:16:ARG:C	29:BP:16:ARG:CD	2.84	0.43
29:BP:136:GLU:O	29:BP:138:LEU:N	2.51	0.43
43:BD:224:ALA:N	43:BD:233:HIS:HB2	2.32	0.43
49:B8:26:LYS:HB2	49:B8:44:LYS:HG3	2.00	0.43
49:B8:32:LEU:HB3	49:B8:36:LYS:HZ3	1.82	0.43
54:BG:37:VAL:HG22	54:BG:159:VAL:HG23	2.01	0.43
1:AA:789:U:O2'	1:AA:791:G:N7	2.46	0.43
1:AA:1030:C:N4	1:AA:1032:G:C2	2.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1303:C:H2'	1:AA:1304:G:H5'	2.01	0.43
1:AA:1326:C:OP1	24:AU:12:LYS:NZ	2.25	0.43
6:AL:118:SER:C	6:AL:119:LYS:O	2.56	0.43
15:AB:80:ILE:HD12	15:AB:80:ILE:H	1.84	0.43
23:AY:122:TRP:CZ2	23:AY:159:ALA:HB2	2.53	0.43
25:BA:27:G:HO2'	25:BA:28:A:P	2.41	0.43
25:BA:508:G:C5'	25:BA:509:C:OP1	2.67	0.43
25:BA:760:G:H4'	25:BA:1776:G:OP1	2.19	0.43
25:BA:1174:A:OP1	25:BA:1175:U:H5''	2.17	0.43
25:BA:1322:A:C5	25:BA:1323:U:C5	3.06	0.43
25:BA:1504:C:H1'	25:BA:1505:C:H5''	2.01	0.43
25:BA:1512:U:H2'	25:BA:1513:C:C6	2.53	0.43
25:BA:1975:G:H2'	25:BA:1976:U:O4'	2.19	0.43
25:BA:2151:G:H5''	25:BA:2151:G:H8	1.84	0.43
29:BP:10:PRO:O	29:BP:11:GLY:C	2.61	0.43
29:BP:144:GLU:N	29:BP:145:PRO:HD3	2.33	0.43
31:BR:9:LYS:C	31:BR:10:LEU:HG	2.44	0.43
32:BS:89:ARG:HG2	32:BS:92:TYR:CA	2.49	0.43
33:BT:12:SER:O	33:BT:13:ARG:CZ	2.67	0.43
37:BX:90:GLU:O	37:BX:91:ALA:C	2.59	0.43
42:B2:63:VAL:O	42:B2:66:GLU:HG2	2.18	0.43
52:BE:61:ARG:H	52:BE:62:PRO:CD	2.32	0.43
52:BE:144:ARG:HB3	52:BE:145:LYS:H	1.62	0.43
53:BF:83:PHE:O	53:BF:84:VAL:C	2.62	0.43
54:BG:56:ALA:CB	54:BG:153:ARG:NH1	2.82	0.43
1:AA:428:G:C4'	1:AA:429:U:O5'	2.66	0.43
1:AA:1237:C:H2'	1:AA:1238:A:OP1	2.18	0.43
2:AV:47:U:H3'	2:AV:48:C:H5''	2.01	0.43
4:AJ:24:VAL:HG22	4:AJ:34:VAL:HG11	2.00	0.43
7:AM:31:LYS:O	7:AM:35:GLU:HG2	2.18	0.43
17:AD:24:GLU:CD	17:AD:24:GLU:C	2.86	0.43
25:BA:362:U:H6	25:BA:362:U:H5''	1.84	0.43
25:BA:459:U:H5''	48:B7:40:TRP:CD2	2.54	0.43
25:BA:464:U:O2'	48:B7:16:HIS:CE1	2.72	0.43
25:BA:1039:G:H1'	25:BA:1117:G:N2	2.34	0.43
25:BA:1786:A:N1	25:BA:2606:C:C1'	2.82	0.43
25:BA:1799:G:H5'	25:BA:1819:A:N6	2.34	0.43
25:BA:1858:G:HO2'	25:BA:1883:G:N2	2.16	0.43
25:BA:2623:G:H4'	25:BA:2825:C:O2	2.19	0.43
25:BA:2741:A:H2'	25:BA:2742:C:O4'	2.18	0.43
26:BB:46:A:C5	26:BB:47:C:C4	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BN:89:LYS:O	27:BN:93:THR:HG22	2.18	0.43
29:BP:83:VAL:CG1	29:BP:112:LEU:HD21	2.49	0.43
33:BT:61:PHE:CE2	33:BT:76:PHE:HB2	2.54	0.43
36:BW:68:ARG:O	36:BW:110:LYS:HB3	2.19	0.43
51:BC:215:THR:HB	51:BC:221:SER:HA	2.01	0.43
53:BF:114:VAL:HG21	53:BF:202:PHE:CZ	2.53	0.43
54:BG:72:ARG:HA	54:BG:87:PRO:HD2	2.00	0.43
56:BK:57:ILE:HD12	56:BK:57:ILE:H	1.84	0.43
1:AA:155:C:H2'	1:AA:156:G:O4'	2.19	0.42
1:AA:1013:G:H5'	1:AA:1014:A:OP2	2.19	0.42
5:AK:84:VAL:HG22	5:AK:110:ASP:HA	2.01	0.42
6:AL:60:LEU:HB3	6:AL:62:SER:H	1.84	0.42
16:AC:179:ARG:HG3	16:AC:207:VAL:H	1.84	0.42
17:AD:162:LEU:HD13	17:AD:181:MET:HE2	2.01	0.42
21:AH:13:ILE:O	21:AH:17:THR:HG23	2.19	0.42
22:AI:4:TYR:CD2	22:AI:88:TYR:HB2	2.54	0.42
25:BA:387:U:O5'	25:BA:387:U:H6	2.01	0.42
25:BA:638:G:H2'	25:BA:639:U:O4'	2.19	0.42
25:BA:832:G:H21	29:BP:53:GLY:HA3	1.83	0.42
25:BA:973:A:O4'	25:BA:1188:U:C6	2.72	0.42
25:BA:1094:U:H6	25:BA:1094:U:C5'	2.32	0.42
25:BA:1445:A:N3	25:BA:1445:A:C2'	2.82	0.42
25:BA:1817:G:H5''	43:BD:88:ARG:NH2	2.34	0.42
25:BA:1876:A:H2'	25:BA:1877:A:C8	2.54	0.42
25:BA:2134:A:C8	25:BA:2135:A:C8	3.06	0.42
25:BA:2139:C:O2'	25:BA:2140:C:O2	2.36	0.42
25:BA:2174:C:O2	51:BC:218:MET:SD	2.77	0.42
25:BA:2261:C:H3'	40:B0:16:SER:OG	2.19	0.42
25:BA:2864:G:H2'	25:BA:2865:U:O4'	2.19	0.42
26:BB:65:C:H2'	26:BB:66:A:H5'	2.01	0.42
33:BT:1:MET:O	33:BT:3:ARG:N	2.52	0.42
34:BU:31:SER:C	34:BU:33:ARG:H	2.27	0.42
46:B5:33:CYS:SG	46:B5:34:PRO:O	2.76	0.42
46:B5:52:TYR:O	46:B5:52:TYR:CG	2.72	0.42
54:BG:6:ALA:HB3	54:BG:104:GLU:OE2	2.19	0.42
57:BJ:94:ALA:O	57:BJ:97:ALA:HB3	2.19	0.42
1:AA:269:C:H2'	1:AA:270:A:H8	1.81	0.42
16:AC:12:LEU:O	16:AC:16:ARG:O	2.37	0.42
16:AC:29:TYR:O	16:AC:30:ARG:C	2.62	0.42
25:BA:370:G:O5'	25:BA:370:G:H8	2.02	0.42
25:BA:642:G:O3'	47:B6:42:TRP:CZ2	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1050:A:H2'	25:BA:1051:G:C8	2.54	0.42
25:BA:1313:U:O2	25:BA:1313:U:C2'	2.66	0.42
25:BA:1494:A:O2'	25:BA:1495:A:OP1	2.19	0.42
25:BA:1777:U:O2'	25:BA:1778:U:H5'	2.19	0.42
25:BA:1847:A:H5'	25:BA:1848:A:OP2	2.19	0.42
25:BA:2219:G:H8	25:BA:2219:G:O5'	2.02	0.42
25:BA:2273:A:H2'	25:BA:2274:A:C8	2.54	0.42
25:BA:2392:A:OP1	49:B8:32:LEU:HD22	2.19	0.42
27:BN:16:ILE:HD11	27:BN:26:LEU:CD1	2.34	0.42
27:BN:132:ALA:O	27:BN:133:GLN:O	2.37	0.42
29:BP:146:VAL:HG22	29:BP:147:LEU:H	1.83	0.42
30:BQ:98:LYS:HB3	30:BQ:99:PRO:HD2	2.00	0.42
35:BV:18:LEU:O	35:BV:19:LYS:O	2.37	0.42
37:BX:10:ALA:HB1	37:BX:11:PRO:HD2	2.01	0.42
46:B5:34:PRO:O	46:B5:35:GLU:CB	2.67	0.42
1:AA:149:A:HO2'	1:AA:150:C:H6	1.52	0.42
1:AA:1051:C:O5'	1:AA:1051:C:H6	2.02	0.42
2:AV:30:G:H5''	2:AV:30:G:H8	1.84	0.42
4:AJ:61:GLU:OE2	8:AN:45:ARG:NH1	2.47	0.42
15:AB:59:GLU:HB2	15:AB:221:LEU:HD11	2.00	0.42
16:AC:87:LEU:O	16:AC:91:LEU:HG	2.18	0.42
16:AC:108:ASN:HA	16:AC:109:PRO:HD2	1.88	0.42
18:AE:100:VAL:O	18:AE:107:ARG:NH2	2.50	0.42
22:AI:99:LEU:HD13	22:AI:99:LEU:N	2.33	0.42
23:AY:483:TYR:CE1	23:AY:603:GLU:HB3	2.54	0.42
25:BA:437:G:H8	25:BA:437:G:O5'	2.01	0.42
25:BA:1945:G:H2'	25:BA:1946:U:C6	2.55	0.42
25:BA:2001:A:H2'	25:BA:2002:G:C8	2.54	0.42
25:BA:2078:C:C4	25:BA:2079:U:C4	3.07	0.42
25:BA:2287:A:H62	25:BA:2344:U:H3	1.67	0.42
34:BU:92:ARG:HD2	35:BV:11:GLN:HB2	2.01	0.42
39:BZ:189:ALA:O	39:BZ:190:GLU:C	2.62	0.42
53:BF:40:GLN:O	53:BF:44:ARG:HG2	2.19	0.42
53:BF:139:PHE:CZ	53:BF:156:LEU:HD22	2.54	0.42
1:AA:120:A:C6	1:AA:122:G:C2	3.07	0.42
1:AA:222:U:H2'	1:AA:223:U:C6	2.54	0.42
1:AA:417:C:H2'	1:AA:418:C:C6	2.51	0.42
1:AA:679:C:H2'	1:AA:680:C:C6	2.54	0.42
1:AA:1128:C:O2'	1:AA:1129:C:H5'	2.19	0.42
1:AA:1286:A:C8	1:AA:1287:A:H4'	2.55	0.42
6:AL:25:PRO:C	6:AL:27:LEU:N	2.78	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AM:84:ILE:O	7:AM:84:ILE:HG22	2.20	0.42
13:AS:44:MET:HA	13:AS:44:MET:HE3	2.02	0.42
18:AE:102:ALA:HB2	18:AE:120:THR:HG21	2.01	0.42
20:AG:37:ASN:O	20:AG:38:LEU:C	2.61	0.42
20:AG:138:LYS:O	20:AG:142:GLU:HG3	2.19	0.42
23:AY:181:LEU:HD23	23:AY:182:ARG:HG3	2.00	0.42
25:BA:185:U:C2	25:BA:212:G:N2	2.87	0.42
25:BA:300:A:H2'	25:BA:334:C:H1'	2.01	0.42
25:BA:954:G:N3	25:BA:2274:A:C2	2.88	0.42
25:BA:1532:C:O2	25:BA:1532:C:H2'	2.17	0.42
25:BA:1578:U:C2'	25:BA:1579:A:H5'	2.49	0.42
25:BA:1833:U:O2	25:BA:1969:A:C2	2.71	0.42
25:BA:1952:A:C4	28:BO:22:ILE:HG13	2.55	0.42
25:BA:1977:A:C2'	25:BA:1978:A:O5'	2.67	0.42
25:BA:2095:C:H2'	25:BA:2096:U:O4'	2.19	0.42
25:BA:2331:G:O4'	40:B0:42:GLY:HA3	2.19	0.42
26:BB:33:G:N3	26:BB:50:G:C2	2.88	0.42
27:BN:42:TRP:CD1	34:BU:63:VAL:HG11	2.55	0.42
27:BN:128:HIS:ND1	27:BN:128:HIS:C	2.77	0.42
33:BT:89:VAL:HG21	33:BT:91:ARG:CZ	2.49	0.42
33:BT:125:ARG:C	33:BT:127:ALA:N	2.77	0.42
35:BV:8:GLY:O	35:BV:10:LYS:HE3	2.19	0.42
42:B2:42:GLY:O	42:B2:44:LEU:O	2.37	0.42
1:AA:427:U:C4	1:AA:428:G:C6	3.08	0.42
1:AA:990:C:C4	1:AA:991:U:C5	3.07	0.42
1:AA:1342:C:H2'	1:AA:1343:G:C8	2.54	0.42
4:AJ:13:HIS:CD2	4:AJ:13:HIS:C	2.97	0.42
25:BA:300:A:H1'	25:BA:319:C:O4'	2.20	0.42
25:BA:562:U:C4	25:BA:2036:C:O4'	2.72	0.42
25:BA:586:A:C2	25:BA:809:G:N3	2.87	0.42
25:BA:588:U:H2'	25:BA:589:C:C6	2.54	0.42
25:BA:714:U:O2'	25:BA:716:A:C8	2.66	0.42
25:BA:1006:C:O2'	27:BN:106:MET:HB3	2.20	0.42
25:BA:2754:U:H2'	25:BA:2756:U:OP1	2.18	0.42
25:BA:2820:A:C8	52:BE:109:LYS:HE2	2.54	0.42
30:BQ:76:LYS:HB3	30:BQ:91:GLU:CG	2.50	0.42
32:BS:16:ASN:OD1	32:BS:17:ARG:N	2.52	0.42
34:BU:112:ARG:NH2	35:BV:46:VAL:CG1	2.82	0.42
39:BZ:61:LEU:CD2	39:BZ:61:LEU:N	2.82	0.42
41:B1:44:PRO:HB2	41:B1:46:LEU:CD1	2.48	0.42
42:B2:21:LEU:HD23	42:B2:21:LEU:HA	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:BD:65:ILE:HD11	43:BD:67:PHE:CE1	2.55	0.42
43:BD:171:ASP:OD2	43:BD:171:ASP:N	2.53	0.42
43:BD:270:ILE:O	43:BD:270:ILE:HD12	2.20	0.42
44:B3:19:GLN:NE2	44:B3:52:HIS:NE2	2.67	0.42
47:B6:15:GLU:OE1	47:B6:18:ARG:HD2	2.19	0.42
52:BE:13:ARG:HD2	52:BE:20:ALA:HB1	2.01	0.42
55:BH:41:MET:CE	55:BH:42:ARG:C	2.93	0.42
56:BK:99:ILE:O	56:BK:139:VAL:N	2.52	0.42
1:AA:559:A:OP1	18:AE:126:ARG:NH2	2.48	0.42
1:AA:620:C:C2	17:AD:135:LEU:HG	2.55	0.42
1:AA:1078:U:H1'	18:AE:130:ASN:OD1	2.20	0.42
1:AA:1273:G:H8	1:AA:1273:G:H5''	1.83	0.42
5:AK:21:ILE:HG12	5:AK:30:VAL:CG1	2.50	0.42
11:AQ:45:HIS:HB2	11:AQ:65:ILE:CD1	2.49	0.42
14:AT:96:GLY:O	14:AT:97:ALA:CB	2.68	0.42
18:AE:131:ILE:HD13	18:AE:131:ILE:HA	1.93	0.42
23:AY:115:GLU:HB3	23:AY:116:PRO:CD	2.49	0.42
23:AY:204:GLU:C	23:AY:206:LEU:N	2.78	0.42
25:BA:304:G:H2'	25:BA:305:U:C6	2.55	0.42
25:BA:334:C:H2'	25:BA:335:C:OP1	2.19	0.42
25:BA:1394:U:H4'	25:BA:1603:A:H4'	2.00	0.42
26:BB:81:G:C6	26:BB:82:G:C5	3.07	0.42
27:BN:36:GLY:CA	27:BN:49:GLY:HA2	2.48	0.42
27:BN:93:THR:HG1	27:BN:94:HIS:CD2	2.38	0.42
27:BN:108:PRO:O	27:BN:113:GLY:HA3	2.19	0.42
29:BP:18:ARG:NH1	29:BP:18:ARG:HB3	2.35	0.42
31:BR:44:LEU:CD2	31:BR:48:VAL:HG23	2.49	0.42
40:B0:50:ASN:HB3	40:B0:63:VAL:HG22	2.02	0.42
43:BD:130:ALA:C	43:BD:131:LEU:HD12	2.45	0.42
47:B6:42:TRP:CE3	47:B6:42:TRP:HA	2.55	0.42
49:B8:36:LYS:HD2	49:B8:41:ILE:HG22	2.02	0.42
52:BE:52:LEU:C	52:BE:74:PRO:HB3	2.45	0.42
55:BH:15:VAL:HG23	55:BH:15:VAL:O	2.18	0.42
55:BH:157:TYR:HD1	55:BH:173:PRO:HG3	1.84	0.42
1:AA:346:G:H5'	33:BT:41:ARG:CZ	2.50	0.42
1:AA:1092:A:C6	1:AA:1093:A:C6	3.08	0.42
1:AA:1118:C:C1'	1:AA:1179:A:C4	3.02	0.42
1:AA:1179:A:H2'	1:AA:1180:A:O4'	2.18	0.42
1:AA:1241:G:H2'	1:AA:1242:C:C6	2.55	0.42
8:AN:9:LYS:O	8:AN:9:LYS:HG2	2.19	0.42
8:AN:23:ARG:NH1	8:AN:30:ALA:HB2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AS:4:SER:C	13:AS:5:LEU:O	2.62	0.42
15:AB:8:LYS:HD3	15:AB:8:LYS:HA	1.92	0.42
15:AB:39:ILE:HG22	15:AB:41:ILE:CD1	2.50	0.42
15:AB:47:THR:HG22	15:AB:51:LEU:HD12	2.00	0.42
16:AC:167:TRP:O	16:AC:168:ALA:CB	2.68	0.42
17:AD:31:CYS:O	17:AD:33:MET:N	2.47	0.42
23:AY:335:LEU:HD11	23:AY:352:VAL:HG11	2.00	0.42
23:AY:587:SER:O	23:AY:591:LYS:HB2	2.20	0.42
25:BA:548:A:O2'	25:BA:549:G:P	2.77	0.42
25:BA:572:A:OP2	35:BV:78:LYS:HE2	2.19	0.42
25:BA:979:G:H3'	25:BA:980:A:H5''	2.02	0.42
25:BA:1090:U:H3	25:BA:1101:U:H3	1.67	0.42
25:BA:1329:U:H3'	25:BA:1330:C:H6	1.84	0.42
25:BA:1416:G:C4	25:BA:1417:C:C5	3.07	0.42
25:BA:1721:G:N2	25:BA:1739:U:OP2	2.53	0.42
25:BA:2151:G:N1	25:BA:2152:G:C5	2.88	0.42
25:BA:2811:G:H2'	25:BA:2812:G:O4'	2.20	0.42
33:BT:32:TYR:CD2	33:BT:81:PRO:O	2.72	0.42
33:BT:62:THR:HA	33:BT:74:ARG:O	2.20	0.42
43:BD:27:THR:HG22	43:BD:81:ALA:HB1	2.01	0.42
43:BD:45:ASN:ND2	43:BD:46:GLN:N	2.68	0.42
44:B3:31:LEU:C	44:B3:33:GLN:H	2.27	0.42
44:B3:50:VAL:CG2	44:B3:54:VAL:HG21	2.50	0.42
56:BK:105:LEU:HD21	56:BK:120:LEU:HD13	2.01	0.42
56:BK:136:VAL:O	56:BK:136:VAL:HG13	2.20	0.42
1:AA:73:G:H2'	1:AA:76:C:O4'	2.19	0.42
1:AA:339:C:OP2	28:BO:97:ARG:NH1	2.52	0.42
1:AA:355:C:H2'	1:AA:356:A:O4'	2.20	0.42
1:AA:920:U:H2'	1:AA:921:U:C6	2.54	0.42
7:AM:99:ARG:HB2	7:AM:101:GLN:HE21	1.84	0.42
15:AB:155:LEU:HD22	15:AB:155:LEU:HA	1.87	0.42
17:AD:11:LEU:O	17:AD:12:CYS:C	2.61	0.42
17:AD:71:SER:OG	17:AD:74:GLN:HB2	2.20	0.42
19:AF:23:LYS:O	19:AF:27:GLN:HG2	2.19	0.42
23:AY:209:ALA:O	23:AY:210:ARG:HB2	2.20	0.42
23:AY:344:THR:HG23	23:AY:390:VAL:HG22	2.02	0.42
25:BA:122:G:H2'	25:BA:123:G:O5'	2.20	0.42
25:BA:271(F):C:H2'	25:BA:271(G):C:C6	2.55	0.42
25:BA:832:G:N3	29:BP:53:GLY:HA2	2.35	0.42
25:BA:962:G:H4'	25:BA:2496:C:O2'	2.19	0.42
25:BA:1005:C:H2'	25:BA:1006:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1299:G:H8	25:BA:1299:G:O5'	2.02	0.42
25:BA:1816:G:H8	43:BD:62:TYR:OH	2.02	0.42
25:BA:1959:G:C2'	25:BA:1960:A:O5'	2.68	0.42
25:BA:2135:A:H2'	25:BA:2136:C:O4'	2.19	0.42
25:BA:2702:U:H4'	25:BA:2703:C:OP1	2.20	0.42
30:BQ:27:VAL:O	30:BQ:105:GLU:OE1	2.37	0.42
31:BR:10:LEU:HD22	31:BR:17:ARG:CD	2.50	0.42
34:BU:92:ARG:HD3	34:BU:94:ASN:HB3	2.02	0.42
35:BV:39:LEU:HD13	35:BV:39:LEU:N	2.34	0.42
41:B1:3:LYS:HG2	41:B1:4:VAL:N	2.34	0.42
46:B5:40:LYS:HE2	46:B5:40:LYS:HB3	1.70	0.42
1:AA:684:A:N6	1:AA:685:G:C6	2.88	0.42
1:AA:836:G:C6	1:AA:851:G:C6	3.08	0.42
7:AM:83:ASP:OD1	7:AM:85:GLY:N	2.48	0.42
22:AI:71:SER:HA	22:AI:74:ILE:HD12	2.02	0.42
23:AY:418:LYS:O	23:AY:419:ALA:CB	2.67	0.42
23:AY:689:LYS:HG3	23:AY:689:LYS:O	2.19	0.42
25:BA:26:G:OP1	36:BW:80:PRO:HB3	2.20	0.42
25:BA:97:C:H5''	42:B2:2:LYS:HB2	2.02	0.42
25:BA:453:C:O2	25:BA:457:A:O2'	2.35	0.42
25:BA:764:A:N1	25:BA:1789:A:O2'	2.46	0.42
25:BA:813:U:H2'	25:BA:814:C:C6	2.54	0.42
25:BA:996:A:OP2	34:BU:92:ARG:NH2	2.53	0.42
25:BA:1058:G:N2	56:BK:126:MET:HE3	2.26	0.42
25:BA:1857:G:C6	25:BA:1858:G:N1	2.88	0.42
25:BA:2230:G:C6	25:BA:2231:C:C4	3.07	0.42
25:BA:2420:C:O5'	25:BA:2420:C:H6	2.01	0.42
25:BA:2690:C:OP2	31:BR:14:SER:CB	2.67	0.42
25:BA:2795:G:H2'	25:BA:2795:G:N3	2.35	0.42
27:BN:28:THR:HG22	27:BN:29:LYS:N	2.34	0.42
28:BO:10:VAL:CG1	28:BO:17:ARG:C	2.93	0.42
29:BP:97:PRO:O	29:BP:98:GLU:CB	2.68	0.42
33:BT:29:ARG:HE	33:BT:86:ILE:CG2	2.32	0.42
37:BX:14:SER:O	37:BX:15:GLU:C	2.63	0.42
43:BD:129:ASN:O	43:BD:193:VAL:HG12	2.19	0.42
49:B8:52:LYS:N	49:B8:53:PRO:CD	2.82	0.42
51:BC:88:GLU:O	51:BC:89:ALA:CB	2.68	0.42
53:BF:184:TYR:O	53:BF:188:ARG:HG2	2.19	0.42
54:BG:60:LEU:C	54:BG:62:LEU:H	2.28	0.42
55:BH:171:LEU:O	55:BH:173:PRO:CD	2.67	0.42
56:BK:99:ILE:HD12	56:BK:103:GLN:CB	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:302:G:O3'	6:AL:17:LYS:HE2	2.20	0.42
1:AA:346:G:OP1	33:BT:35:LYS:NZ	2.52	0.42
1:AA:1146:A:N3	1:AA:1146:A:H2'	2.33	0.42
1:AA:1458:G:OP1	14:AT:35:THR:OG1	2.36	0.42
5:AK:59:TYR:O	5:AK:62:GLN:HB3	2.19	0.42
12:AR:61:LYS:O	12:AR:65:ILE:HG12	2.20	0.42
15:AB:37:ASN:HD22	15:AB:37:ASN:HA	1.68	0.42
17:AD:3:ARG:NE	17:AD:5:ILE:HG13	2.35	0.42
20:AG:108:ALA:O	20:AG:119:ARG:HD2	2.19	0.42
23:AY:85:PRO:HG2	23:AY:90:PHE:HB2	2.02	0.42
25:BA:280:C:N4	25:BA:281:G:C6	2.88	0.42
25:BA:530:G:N3	25:BA:530:G:O4'	2.52	0.42
25:BA:785:G:O2'	25:BA:1779:U:H5'	2.19	0.42
25:BA:864:G:C6	25:BA:865:C:N4	2.88	0.42
25:BA:1364:G:P	41:B1:61:ARG:HH22	2.43	0.42
25:BA:1470:G:H5''	25:BA:1471:A:OP1	2.20	0.42
25:BA:2324:C:H5''	25:BA:2325:G:H5'	2.01	0.42
25:BA:2584:U:O2	25:BA:2584:U:O4'	2.37	0.42
25:BA:2801:A:H2'	25:BA:2895:U:H4'	2.01	0.42
29:BP:106:LEU:O	29:BP:107:LYS:O	2.38	0.42
32:BS:56:LEU:HD23	32:BS:58:LEU:HB2	2.01	0.42
33:BT:4:GLY:HA2	52:BE:9:VAL:HG23	2.02	0.42
34:BU:74:LEU:CD2	34:BU:78:THR:HG22	2.50	0.42
42:B2:65:ASN:HB3	42:B2:69:ARG:NH2	2.35	0.42
43:BD:26:LYS:CD	43:BD:113:VAL:HG21	2.50	0.42
43:BD:33:LEU:HD23	43:BD:34:VAL:HG13	2.02	0.42
50:B9:32:HIS:O	50:B9:34:GLN:HG3	2.20	0.42
54:BG:85:GLY:C	54:BG:87:PRO:HD3	2.45	0.42
1:AA:90:U:O2'	1:AA:91:C:H5	1.86	0.41
1:AA:126:G:H5'	1:AA:633:G:N2	2.35	0.41
1:AA:264:U:H4'	11:AQ:63:ARG:HD3	2.02	0.41
1:AA:640:A:N3	21:AH:115:SER:HB3	2.35	0.41
1:AA:745:C:OP1	1:AA:851:G:O2'	2.38	0.41
1:AA:950:U:H2'	1:AA:951:G:C8	2.55	0.41
1:AA:1226:C:H2'	7:AM:103:THR:OG1	2.20	0.41
1:AA:1319:A:OP2	13:AS:5:LEU:HD23	2.19	0.41
1:AA:1325:C:P	24:AU:6:ARG:HH12	2.43	0.41
1:AA:1517:G:H1'	25:BA:1919:A:O3'	2.20	0.41
16:AC:113:ALA:HB3	16:AC:114:PRO:HD3	2.01	0.41
17:AD:78:LEU:HB3	17:AD:93:PHE:HE2	1.85	0.41
17:AD:194:LEU:HD22	17:AD:194:LEU:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:AG:13:GLN:O	20:AG:24:THR:HG21	2.20	0.41
21:AH:17:THR:OG1	21:AH:18:ARG:NH1	2.53	0.41
22:AI:53:VAL:HG13	22:AI:95:LYS:NZ	2.35	0.41
23:AY:343:ASN:O	23:AY:347:GLY:N	2.53	0.41
23:AY:349:LYS:H	23:AY:349:LYS:HD3	1.85	0.41
25:BA:435:C:C2'	25:BA:436:C:H5'	2.50	0.41
25:BA:881:G:C2	25:BA:882:G:H1'	2.55	0.41
25:BA:1019:U:C2'	25:BA:1021:A:C2	3.03	0.41
25:BA:1168:G:C2	25:BA:1182:A:C2	3.08	0.41
25:BA:1275:A:N1	25:BA:1295:C:O2'	2.49	0.41
25:BA:1417:C:H2'	25:BA:1418:G:O4'	2.20	0.41
25:BA:1475:G:C8	25:BA:1475:G:H5''	2.54	0.41
25:BA:2287:A:C2	25:BA:2346:A:C2	3.08	0.41
27:BN:56:ASN:H	27:BN:125:GLY:HA3	1.85	0.41
29:BP:16:ARG:HB2	29:BP:16:ARG:CZ	2.50	0.41
29:BP:127:ALA:HB3	29:BP:130:PHE:CE2	2.55	0.41
33:BT:29:ARG:CB	33:BT:30:VAL:HG22	2.41	0.41
35:BV:18:LEU:HD13	35:BV:19:LYS:H	1.85	0.41
39:BZ:17:ALA:O	39:BZ:20:ARG:HB3	2.19	0.41
39:BZ:24:LEU:HD23	39:BZ:24:LEU:C	2.45	0.41
39:BZ:54:HIS:CE1	39:BZ:123:ASP:OD1	2.73	0.41
39:BZ:98:MET:HE2	39:BZ:100:VAL:CG2	2.50	0.41
46:B5:4:HIS:CB	46:B5:5:PRO:CD	2.82	0.41
55:BH:44:VAL:O	55:BH:45:VAL:C	2.63	0.41
1:AA:232:G:H1'	1:AA:262:A:N1	2.34	0.41
1:AA:367:U:H4'	23:AY:351:ARG:NE	2.35	0.41
1:AA:782:A:C6	1:AA:801:U:C2	3.08	0.41
1:AA:1187:G:C5'	1:AA:1187:G:C8	3.03	0.41
10:AP:58:TYR:O	10:AP:62:VAL:HG22	2.20	0.41
17:AD:26:CYS:CB	17:AD:31:CYS:HB2	2.50	0.41
17:AD:155:LEU:O	17:AD:156:GLU:C	2.62	0.41
22:AI:9:ARG:CG	22:AI:14:VAL:HG13	2.50	0.41
23:AY:120:THR:O	23:AY:124:GLN:HG3	2.20	0.41
25:BA:228:A:H2'	25:BA:230:U:O4'	2.21	0.41
25:BA:414:C:OP1	25:BA:1879:C:O2'	2.38	0.41
25:BA:1156:A:C8	34:BU:51:LYS:HD2	2.54	0.41
25:BA:2286:A:H4'	25:BA:2287:A:O4'	2.20	0.41
25:BA:2430:A:H8	25:BA:2431:U:H5	1.68	0.41
26:BB:39:A:N3	26:BB:39:A:H2'	2.35	0.41
33:BT:56:GLY:O	33:BT:59:THR:HG23	2.19	0.41
49:B8:14:VAL:CG2	49:B8:22:VAL:HG13	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:BF:24:LEU:O	53:BF:25:PRO:C	2.63	0.41
55:BH:105:LEU:H	55:BH:105:LEU:HD22	1.84	0.41
1:AA:390:C:H2'	1:AA:391:G:C8	2.55	0.41
1:AA:665:A:N3	1:AA:732:C:H2'	2.35	0.41
1:AA:1260:C:OP1	1:AA:1284:C:H4'	2.20	0.41
2:AV:73:A:C2'	2:AV:74:C:C5'	2.98	0.41
6:AL:23:LYS:C	6:AL:24:VAL:CG2	2.93	0.41
14:AT:63:ILE:HG22	14:AT:77:ALA:HB1	2.02	0.41
16:AC:196:LEU:CD2	16:AC:196:LEU:N	2.84	0.41
19:AF:76:ALA:HB1	19:AF:80:ARG:NH2	2.35	0.41
25:BA:629:G:OP1	25:BA:650:C:O2'	2.36	0.41
25:BA:896:A:N7	39:BZ:146:ILE:HD13	2.36	0.41
25:BA:945:A:C4	25:BA:2448:A:C2	3.08	0.41
25:BA:1286:A:N1	25:BA:1329:U:O2'	2.46	0.41
25:BA:2016:U:O5'	25:BA:2016:U:H6	2.03	0.41
25:BA:2055:C:H5'	25:BA:2056:G:O5'	2.19	0.41
25:BA:2219:G:C2	25:BA:2220:G:C8	3.08	0.41
29:BP:28:GLY:HA3	29:BP:29:LYS:HD2	2.02	0.41
31:BR:2:ARG:HD2	52:BE:111:ARG:HG3	2.02	0.41
32:BS:12:PHE:O	32:BS:12:PHE:CD1	2.74	0.41
33:BT:57:PHE:O	33:BT:59:THR:N	2.54	0.41
36:BW:51:LEU:HD23	36:BW:105:VAL:HG11	2.02	0.41
48:B7:34:ARG:HB3	48:B7:39:ARG:HG3	2.02	0.41
52:BE:63:LEU:O	52:BE:64:LYS:C	2.62	0.41
53:BF:123:LEU:HD12	53:BF:124:LEU:N	2.35	0.41
1:AA:1135:U:O2	1:AA:1135:U:C2'	2.67	0.41
13:AS:5:LEU:HG	13:AS:10:PHE:CD1	2.51	0.41
15:AB:169:LYS:O	15:AB:169:LYS:HD3	2.20	0.41
17:AD:191:ARG:NH1	17:AD:200:GLU:OE1	2.54	0.41
18:AE:80:ILE:CD1	18:AE:138:ALA:HB1	2.50	0.41
21:AH:75:ARG:HA	21:AH:76:PRO:HD2	1.88	0.41
21:AH:97:VAL:HG13	21:AH:98:LYS:N	2.35	0.41
23:AY:75:LYS:O	23:AY:76:ASP:C	2.63	0.41
23:AY:404:VAL:HG13	23:AY:405:PRO:C	2.43	0.41
25:BA:259:G:C2'	25:BA:621:A:O2'	2.68	0.41
25:BA:319:C:C2'	25:BA:320:A:O5'	2.68	0.41
25:BA:535:C:O2'	25:BA:536:A:H5'	2.20	0.41
25:BA:923:C:H2'	25:BA:924:C:C6	2.56	0.41
25:BA:1151:G:H5'	34:BU:81:HIS:CE1	2.54	0.41
25:BA:1290:C:O2'	25:BA:1291:C:H5'	2.20	0.41
25:BA:1570:A:OP1	43:BD:36:PRO:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1839:G:H1'	25:BA:1927:A:O5'	2.20	0.41
31:BR:55:ALA:HA	31:BR:80:PHE:CZ	2.55	0.41
31:BR:58:GLY:HA2	31:BR:80:PHE:CE1	2.56	0.41
43:BD:26:LYS:HG2	43:BD:113:VAL:HG21	2.02	0.41
46:B5:20:ARG:HG2	46:B5:23:HIS:CD2	2.56	0.41
49:B8:2:PRO:O	49:B8:3:LYS:CB	2.68	0.41
49:B8:32:LEU:HB2	49:B8:36:LYS:CE	2.48	0.41
52:BE:182:LEU:C	52:BE:183:LEU:HD12	2.46	0.41
56:BK:41:PHE:C	56:BK:43:ALA:H	2.28	0.41
56:BK:130:SER:HA	56:BK:133:SER:OG	2.21	0.41
57:BJ:25:ALA:O	57:BJ:85:ALA:N	2.53	0.41
1:AA:266:G:O3'	11:AQ:67:LYS:HB2	2.20	0.41
1:AA:859:A:H2	21:AH:19:VAL:HG11	1.83	0.41
1:AA:1213:A:C8	1:AA:1215:G:C5	3.08	0.41
1:AA:1228:C:P	7:AM:108:ARG:NH2	2.94	0.41
1:AA:1326:C:O2'	1:AA:1327:C:H5'	2.20	0.41
14:AT:89:ARG:NH1	14:AT:105:SER:O	2.49	0.41
15:AB:11:LEU:HD13	15:AB:217:ARG:NH2	2.36	0.41
15:AB:19:HIS:CD2	15:AB:189:ASP:OD2	2.73	0.41
15:AB:40:HIS:HB3	15:AB:190:THR:HG21	2.01	0.41
23:AY:156:ARG:HB3	23:AY:156:ARG:HH11	1.85	0.41
23:AY:169:GLY:O	23:AY:170:ARG:C	2.62	0.41
23:AY:250:THR:CA	23:AY:255:ILE:HG22	2.50	0.41
25:BA:30:G:H2'	25:BA:31:C:O4'	2.21	0.41
25:BA:103:A:H8	25:BA:103:A:O5'	2.03	0.41
25:BA:475:U:C4	25:BA:481:G:O6	2.73	0.41
25:BA:660:G:C6	25:BA:661:C:C4	3.08	0.41
25:BA:783:A:C8	25:BA:783:A:H3'	2.55	0.41
25:BA:1021:A:H62	25:BA:1141:U:H3	1.67	0.41
25:BA:1039:G:O6	25:BA:1116:C:N3	2.53	0.41
25:BA:1446:C:C2	25:BA:1466:G:N2	2.87	0.41
25:BA:1876:A:H2'	25:BA:1877:A:H8	1.85	0.41
25:BA:2141:G:N2	25:BA:2151:G:H1'	2.36	0.41
25:BA:2154:G:C5'	25:BA:2154:G:C8	3.04	0.41
25:BA:2419:U:O4	49:B8:30:ARG:NE	2.52	0.41
25:BA:2592:G:C5	25:BA:2593:U:C4	3.09	0.41
25:BA:2695:C:H2'	25:BA:2696:U:C6	2.55	0.41
27:BN:119:ARG:HG3	27:BN:119:ARG:NH1	2.34	0.41
31:BR:96:ARG:NH1	31:BR:115:GLU:OE1	2.46	0.41
49:B8:39:LYS:O	49:B8:43:GLN:HB2	2.20	0.41
51:BC:64:LEU:HD23	51:BC:64:LEU:HA	1.95	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:BG:19:LEU:HA	54:BG:22:ARG:HB2	2.03	0.41
55:BH:41:MET:HE3	55:BH:42:ARG:C	2.46	0.41
55:BH:72:ILE:O	55:BH:75:ALA:HB3	2.19	0.41
1:AA:130:A:N6	1:AA:234:C:O4'	2.53	0.41
1:AA:242:C:H2'	1:AA:243:A:H5'	2.03	0.41
1:AA:1048:G:OP1	8:AN:4:LYS:HB2	2.20	0.41
1:AA:1119:C:O2'	1:AA:1120:G:H5'	2.21	0.41
1:AA:1256:A:H4'	1:AA:1258:G:C4	2.56	0.41
1:AA:1347:G:C6	22:AI:107:ARG:NH2	2.89	0.41
2:AV:46:G:H3'	2:AV:47:U:H5''	2.02	0.41
10:AP:70:ALA:O	10:AP:74:LEU:HD12	2.21	0.41
20:AG:66:VAL:HG12	20:AG:70:LYS:HE3	2.03	0.41
20:AG:74:GLU:HG2	20:AG:91:VAL:HG22	2.01	0.41
20:AG:143:ARG:HG2	20:AG:143:ARG:O	2.21	0.41
23:AY:18:ALA:O	23:AY:106:VAL:HA	2.20	0.41
23:AY:79:ILE:N	23:AY:79:ILE:CD1	2.83	0.41
25:BA:83:G:H22	25:BA:102:G:H2'	1.84	0.41
25:BA:122:G:C2'	25:BA:123:G:O5'	2.69	0.41
25:BA:332:A:O2'	25:BA:334:C:OP2	2.29	0.41
25:BA:569:U:O2'	25:BA:983:A:N1	2.51	0.41
25:BA:631:A:O2'	29:BP:67:MET:HB3	2.20	0.41
25:BA:994:C:O2'	25:BA:996:A:OP1	2.35	0.41
25:BA:1437:C:H6	25:BA:1437:C:H5''	1.86	0.41
25:BA:1655:A:H3'	25:BA:1656:C:H6	1.86	0.41
25:BA:2123:G:O6	25:BA:2175:C:N3	2.53	0.41
25:BA:2173:A:H5''	25:BA:2174:C:OP2	2.19	0.41
25:BA:2637:U:O2'	25:BA:2638:G:H5'	2.20	0.41
25:BA:2689:U:H5''	25:BA:2690:C:H5'	2.03	0.41
27:BN:47:ALA:HB2	27:BN:112:LEU:CD1	2.50	0.41
27:BN:93:THR:OG1	27:BN:94:HIS:NE2	2.53	0.41
32:BS:74:ALA:HB1	32:BS:103:GLU:CB	2.51	0.41
34:BU:65:ILE:CG1	34:BU:96:ALA:HB3	2.49	0.41
38:BY:28:LYS:C	38:BY:38:ILE:HG22	2.46	0.41
40:B0:14:ARG:HB2	40:B0:14:ARG:NH1	2.36	0.41
42:B2:2:LYS:O	42:B2:3:LEU:C	2.63	0.41
43:BD:44:ASN:ND2	43:BD:44:ASN:C	2.79	0.41
43:BD:124:PRO:HB2	43:BD:126:GLN:HG2	2.02	0.41
52:BE:55:ASN:C	52:BE:57:LYS:N	2.78	0.41
52:BE:101:ARG:NH1	52:BE:169:ASN:O	2.49	0.41
54:BG:7:LEU:O	54:BG:11:TYR:HB3	2.20	0.41
56:BK:115:LEU:HD13	56:BK:126:MET:SD	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:401:C:H1'	1:AA:622:A:H1'	2.03	0.41
1:AA:600:C:C2	1:AA:639:G:C2	3.09	0.41
1:AA:620:C:H2'	1:AA:621:A:O4'	2.19	0.41
1:AA:781:A:H5'	1:AA:782:A:OP2	2.20	0.41
1:AA:979:C:OP1	1:AA:981:U:O4	2.38	0.41
1:AA:1071:C:H2'	1:AA:1072:G:C8	2.55	0.41
1:AA:1134:G:C6	1:AA:1135:U:C5	3.09	0.41
1:AA:1144:G:C2'	1:AA:1145:C:H5'	2.50	0.41
1:AA:1411:C:O2'	1:AA:1412:C:H5'	2.20	0.41
2:AV:76:A:H2'	25:BA:2395:C:C2	2.56	0.41
5:AK:65:ALA:HB1	5:AK:98:LEU:CD2	2.50	0.41
14:AT:50:GLU:HG3	14:AT:100:ILE:HB	2.03	0.41
15:AB:62:ALA:O	15:AB:64:ARG:N	2.54	0.41
15:AB:172:ILE:HD12	15:AB:172:ILE:H	1.85	0.41
15:AB:239:VAL:O	15:AB:239:VAL:CG1	2.69	0.41
17:AD:2:GLY:C	17:AD:4:TYR:H	2.26	0.41
23:AY:673:PHE:CD1	23:AY:673:PHE:C	2.99	0.41
25:BA:685:A:C4'	25:BA:686:G:O5'	2.69	0.41
25:BA:957:A:N1	25:BA:2458:G:H4'	2.35	0.41
25:BA:1054:A:C8	25:BA:1054:A:H5'	2.56	0.41
25:BA:1190:G:H5''	29:BP:35:HIS:H	1.84	0.41
25:BA:1477:A:H2'	25:BA:1478:G:O4'	2.21	0.41
25:BA:1668:A:N3	25:BA:1670:C:C4	2.89	0.41
25:BA:1682:G:C5	25:BA:1683:C:C4	3.09	0.41
25:BA:2100:G:N3	25:BA:2100:G:H2'	2.35	0.41
25:BA:2176:A:N3	51:BC:44:HIS:HE1	2.18	0.41
26:BB:31:C:N4	32:BS:32:LEU:HD22	2.36	0.41
39:BZ:24:LEU:CD2	39:BZ:24:LEU:C	2.94	0.41
39:BZ:54:HIS:HB3	39:BZ:101:PRO:HD3	2.02	0.41
45:B4:36:VAL:HB	45:B4:37:PRO:HD2	2.03	0.41
55:BH:43:VAL:HG12	55:BH:46:GLU:OE2	2.20	0.41
56:BK:24:GLY:H	56:BK:25:PRO:HD2	1.86	0.41
1:AA:596:C:O2	1:AA:596:C:H2'	2.20	0.41
1:AA:693:G:H2'	1:AA:694:A:O4'	2.19	0.41
1:AA:801:U:H2'	1:AA:802:A:O5'	2.21	0.41
1:AA:859:A:H2'	1:AA:860:A:O4'	2.20	0.41
1:AA:1021:G:H2'	1:AA:1022:G:O4'	2.20	0.41
1:AA:1253:G:H1'	1:AA:1355:G:O2'	2.20	0.41
4:AJ:54:PHE:CE2	4:AJ:55:LYS:HE3	2.56	0.41
7:AM:36:LYS:O	7:AM:37:THR:HG23	2.21	0.41
7:AM:56:LEU:O	7:AM:57:ARG:C	2.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AB:235:SER:OG	15:AB:236:TYR:N	2.54	0.41
23:AY:242:LEU:O	23:AY:243:VAL:C	2.64	0.41
23:AY:294:PRO:O	23:AY:295:GLU:C	2.64	0.41
23:AY:606:MET:HE3	23:AY:671:MET:HG2	2.02	0.41
24:AU:12:LYS:HG2	24:AU:22:ARG:HB3	2.01	0.41
25:BA:729:G:H2'	25:BA:1775:U:H1'	2.02	0.41
25:BA:1069:A:N7	25:BA:1073:A:N6	2.68	0.41
25:BA:1396:U:O2	25:BA:1396:U:C2'	2.60	0.41
25:BA:1538:G:H8	25:BA:1538:G:H5'	1.85	0.41
25:BA:2061:G:H5''	25:BA:2503:A:C2	2.55	0.41
25:BA:2167:U:H2'	25:BA:2168:G:O4'	2.20	0.41
25:BA:2466:C:H5''	50:B9:6:SER:HB3	2.02	0.41
32:BS:83:LYS:HB3	32:BS:105:ALA:HB3	2.03	0.41
35:BV:64:HIS:CE1	35:BV:92:THR:CG2	3.04	0.41
38:BY:82:PRO:HD2	38:BY:97:ARG:HD3	2.03	0.41
39:BZ:168:GLU:O	39:BZ:169:GLU:C	2.63	0.41
41:B1:58:ILE:HD11	41:B1:60:PHE:CZ	2.56	0.41
42:B2:11:GLU:O	42:B2:15:LYS:HG3	2.21	0.41
52:BE:72:VAL:O	52:BE:73:GLU:C	2.64	0.41
55:BH:24:VAL:CG1	55:BH:37:VAL:HG21	2.51	0.41
55:BH:67:LEU:HD12	55:BH:71:LEU:HD13	2.03	0.41
1:AA:123:C:OP1	1:AA:312:C:H5'	2.21	0.41
1:AA:192:U:H4'	14:AT:57:ARG:HD2	2.03	0.41
1:AA:575:G:H4'	1:AA:575:G:OP1	2.21	0.41
1:AA:731:G:N2	1:AA:732:C:C2	2.89	0.41
1:AA:1003:G:N2	1:AA:1039:C:N4	2.69	0.41
1:AA:1140:C:H2'	1:AA:1141:C:H6	1.86	0.41
2:AV:55:U:H5	2:AV:58:A:OP2	2.04	0.41
5:AK:12:ARG:NH2	5:AK:34:ASP:OD1	2.53	0.41
5:AK:96:ARG:O	5:AK:97:ALA:C	2.63	0.41
7:AM:74:VAL:O	7:AM:77:ASN:HB2	2.20	0.41
9:AO:39:LEU:HD12	9:AO:56:LEU:HB2	2.01	0.41
15:AB:19:HIS:O	15:AB:39:ILE:HG23	2.21	0.41
17:AD:2:GLY:O	17:AD:3:ARG:C	2.64	0.41
20:AG:50:ILE:O	20:AG:54:THR:HG23	2.21	0.41
25:BA:57:C:H2'	25:BA:58:G:O4'	2.21	0.41
25:BA:408:G:O2'	25:BA:409:C:H5'	2.21	0.41
25:BA:536:A:H2'	25:BA:537:C:C6	2.55	0.41
25:BA:673:C:H5''	53:BF:81:PRO:HD2	2.03	0.41
25:BA:893:C:H2'	25:BA:894:C:C6	2.55	0.41
25:BA:901:A:H2'	25:BA:902:C:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:991:C:O2'	25:BA:992:C:H5'	2.21	0.41
25:BA:1245:G:OP1	29:BP:16:ARG:HG2	2.20	0.41
25:BA:1299:G:H4'	25:BA:1300:U:H5''	2.02	0.41
25:BA:1405:U:H2'	25:BA:1406:U:C6	2.55	0.41
25:BA:1742:G:N7	25:BA:1743:C:C6	2.89	0.41
25:BA:1848:A:H2'	25:BA:1849:G:O4'	2.21	0.41
25:BA:2135:A:H4'	25:BA:2160:G:H4'	2.03	0.41
25:BA:2155:G:C2'	25:BA:2156:G:O5'	2.69	0.41
25:BA:2164:C:C4	25:BA:2165:G:H8	2.39	0.41
25:BA:2346:A:H5'	25:BA:2383:G:O4'	2.21	0.41
25:BA:2524:G:O2'	25:BA:2741:A:N1	2.52	0.41
25:BA:2680:C:O2'	25:BA:2681:C:H5'	2.21	0.41
25:BA:2766:G:N3	25:BA:2766:G:H2'	2.36	0.41
25:BA:2811:G:OP1	52:BE:60:ASN:CB	2.68	0.41
26:BB:104:U:C5'	30:BQ:141:GLN:HB3	2.50	0.41
26:BB:105:A:OP1	39:BZ:72:ARG:NH1	2.54	0.41
28:BO:10:VAL:O	28:BO:10:VAL:HG22	2.21	0.41
28:BO:35:VAL:CG2	28:BO:69:ILE:HD11	2.51	0.41
29:BP:85:LEU:H	29:BP:85:LEU:CD2	2.33	0.41
29:BP:144:GLU:N	29:BP:145:PRO:CD	2.84	0.41
30:BQ:21:THR:OG1	30:BQ:99:PRO:O	2.35	0.41
32:BS:58:LEU:O	32:BS:59:LYS:O	2.38	0.41
35:BV:55:ALA:HA	35:BV:100:ARG:O	2.20	0.41
38:BY:95:LYS:HD3	38:BY:99:CYS:O	2.21	0.41
40:B0:48:GLY:O	40:B0:49:LYS:C	2.64	0.41
43:BD:89:SER:HB2	43:BD:159:ALA:HB2	2.02	0.41
45:B4:36:VAL:HG22	45:B4:52:SER:O	2.21	0.41
51:BC:96:GLY:O	51:BC:97:GLU:HG3	2.20	0.41
51:BC:103:ILE:HG23	51:BC:105:ASP:OD2	2.21	0.41
53:BF:33:LEU:HD12	53:BF:33:LEU:HA	1.89	0.41
54:BG:83:ARG:O	54:BG:85:GLY:N	2.54	0.41
1:AA:500:G:H2'	1:AA:501:C:C6	2.56	0.41
1:AA:684:A:O3'	5:AK:12:ARG:NH1	2.54	0.41
1:AA:955:U:H2'	1:AA:956:U:O4'	2.21	0.41
1:AA:1053:G:N7	1:AA:1200:C:H5''	2.36	0.41
1:AA:1181:G:H8	1:AA:1181:G:H5''	1.86	0.41
5:AK:29:ILE:HG21	5:AK:29:ILE:HD13	1.75	0.41
6:AL:84:LEU:HD23	6:AL:84:LEU:HA	1.95	0.41
23:AY:320:PRO:O	23:AY:320:PRO:CD	2.67	0.41
23:AY:325:LEU:HD21	23:AY:358:MET:HE1	2.03	0.41
25:BA:507:A:H5''	25:BA:508:G:H5'	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:572:A:H3'	25:BA:573:G:O4'	2.21	0.41
25:BA:1451:C:H4'	25:BA:1452:A:C8	2.55	0.41
28:BO:1:MET:HE2	28:BO:32:TYR:CD2	2.56	0.41
28:BO:87:ILE:HA	28:BO:87:ILE:HD13	1.82	0.41
29:BP:23:PRO:O	29:BP:33:ARG:CZ	2.69	0.41
31:BR:4:LEU:O	31:BR:5:LYS:CG	2.68	0.41
34:BU:91:ASP:OD1	34:BU:96:ALA:HB2	2.20	0.41
40:B0:23:VAL:HG22	40:B0:38:VAL:CG2	2.44	0.41
44:B3:8:LEU:HD13	44:B3:31:LEU:HD23	2.03	0.41
47:B6:22:ALA:HB2	47:B6:39:TYR:CZ	2.56	0.41
51:BC:30:LYS:NZ	51:BC:30:LYS:HB3	2.36	0.41
53:BF:28:ILE:H	53:BF:28:ILE:CD1	2.31	0.41
55:BH:86:GLU:HB3	55:BH:132:ARG:HB2	2.01	0.41
55:BH:137:ASP:HB3	55:BH:140:LYS:HB2	2.02	0.41
56:BK:121:GLU:O	56:BK:125:ARG:NE	2.53	0.41
1:AA:36:C:H2'	1:AA:37:U:O4'	2.21	0.40
1:AA:109:A:C6	1:AA:327:A:C6	3.09	0.40
1:AA:735:C:O2'	1:AA:736:C:H5'	2.21	0.40
1:AA:963:G:H21	4:AJ:55:LYS:HE3	1.86	0.40
16:AC:65:ALA:HA	16:AC:100:ALA:HB3	2.02	0.40
16:AC:85:ARG:HH12	16:AC:88:ARG:NH1	2.18	0.40
16:AC:91:LEU:HB2	16:AC:99:VAL:HG21	2.03	0.40
18:AE:11:ILE:HD12	18:AE:33:VAL:CG2	2.51	0.40
22:AI:8:GLY:O	22:AI:15:ALA:N	2.46	0.40
23:AY:61:ARG:NH1	25:BA:2663:G:OP1	2.54	0.40
25:BA:41:C:H2'	25:BA:42:G:O4'	2.21	0.40
25:BA:52:A:O2'	25:BA:53:A:H5'	2.21	0.40
25:BA:1046:A:O5'	25:BA:1047:G:OP1	2.39	0.40
25:BA:1086:A:C5'	25:BA:1087:G:OP1	2.69	0.40
25:BA:1461:G:C6	25:BA:1462:C:C4	3.10	0.40
25:BA:1668:A:H4'	25:BA:1669:A:O5'	2.20	0.40
25:BA:1680:U:O2	25:BA:1763:G:H3'	2.21	0.40
25:BA:2313:C:H4'	54:BG:91:ARG:HG3	2.02	0.40
25:BA:2356:C:O3'	40:B0:20:ARG:HD3	2.21	0.40
25:BA:2472:G:H3'	25:BA:2475:C:H42	1.86	0.40
27:BN:5:VAL:O	27:BN:5:VAL:CG1	2.68	0.40
27:BN:30:ILE:HG22	27:BN:34:LEU:HD22	2.03	0.40
33:BT:91:ARG:HG2	33:BT:116:ALA:HA	2.03	0.40
38:BY:10:GLY:HA2	38:BY:27:VAL:HG13	2.03	0.40
38:BY:77:PRO:O	38:BY:78:ALA:HB2	2.20	0.40
43:BD:148:GLU:OE1	43:BD:151:LYS:NZ	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:B6:10:LEU:H	47:B6:10:LEU:CD2	2.34	0.40
51:BC:39:GLU:OE1	51:BC:216:THR:CB	2.69	0.40
53:BF:3:GLU:HA	53:BF:24:LEU:CB	2.51	0.40
53:BF:13:SER:HB2	53:BF:14:PRO:CD	2.50	0.40
53:BF:110:LEU:HA	53:BF:110:LEU:HD23	1.86	0.40
54:BG:54:GLU:O	54:BG:58:GLN:HG3	2.21	0.40
1:AA:375:U:O3'	10:AP:6:LEU:HB2	2.21	0.40
1:AA:488:C:O5'	1:AA:488:C:H6	2.04	0.40
1:AA:524:G:H2'	1:AA:525:C:C6	2.56	0.40
1:AA:1026:G:H2'	1:AA:1026:G:N3	2.36	0.40
7:AM:49:THR:O	7:AM:53:VAL:HG23	2.20	0.40
7:AM:121:LYS:O	7:AM:122:LYS:HG2	2.21	0.40
13:AS:22:LEU:HD13	13:AS:27:GLU:HB2	2.02	0.40
17:AD:15:GLU:OE1	17:AD:59:ARG:NE	2.43	0.40
18:AE:91:LEU:HD12	18:AE:91:LEU:HA	1.86	0.40
23:AY:128:TYR:OH	23:AY:402:ILE:O	2.36	0.40
23:AY:446:THR:O	23:AY:446:THR:HG23	2.21	0.40
24:AU:9:ARG:HH21	24:AU:22:ARG:HA	1.86	0.40
25:BA:565:C:H2'	25:BA:566:U:O4'	2.21	0.40
25:BA:570:G:C5	25:BA:2030:A:C2	3.09	0.40
25:BA:1285:G:C5	25:BA:1329:U:C4	3.09	0.40
25:BA:1338:G:N3	25:BA:1393:A:H2	2.19	0.40
25:BA:1491:G:C6	25:BA:1500:G:C2	3.09	0.40
25:BA:2519:U:C5	25:BA:2541:A:C6	3.09	0.40
36:BW:46:PHE:O	36:BW:50:VAL:HG12	2.20	0.40
43:BD:39:LYS:HB2	43:BD:62:TYR:HB2	2.03	0.40
45:B4:51:TYR:O	54:BG:105:LYS:NZ	2.52	0.40
47:B6:20:ASN:CG	47:B6:21:TYR:N	2.79	0.40
53:BF:136:THR:HA	53:BF:166:ALA:O	2.22	0.40
53:BF:167:ALA:CB	53:BF:173:VAL:HG11	2.43	0.40
56:BK:58:THR:HB	56:BK:66:THR:CG2	2.52	0.40
1:AA:441:A:H3'	1:AA:442:C:H6	1.87	0.40
1:AA:1236:A:H4'	1:AA:1304:G:H4'	2.02	0.40
1:AA:1373:G:O5'	1:AA:1373:G:H8	2.04	0.40
4:AJ:26:ALA:O	4:AJ:27:ALA:HB2	2.22	0.40
7:AM:87:TYR:N	13:AS:73:GLU:O	2.54	0.40
21:AH:10:LEU:HD22	21:AH:83:ILE:HD11	2.03	0.40
25:BA:535:C:C2'	25:BA:536:A:H5'	2.52	0.40
25:BA:644:A:C2	25:BA:2369:A:H1'	2.56	0.40
25:BA:1645:G:OP1	25:BA:1646:C:H5'	2.20	0.40
25:BA:1814:G:OP2	25:BA:1815:A:O2'	2.32	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2250:G:OP1	30:BQ:85:LYS:NZ	2.52	0.40
25:BA:2279:G:N7	40:B0:14:ARG:NH1	2.64	0.40
25:BA:2408:U:H2'	25:BA:2409:G:C8	2.56	0.40
25:BA:2468:G:H5'	30:BQ:120:ILE:HD12	2.03	0.40
25:BA:2810:A:H2'	52:BE:61:ARG:HH21	1.81	0.40
30:BQ:104:PHE:HE1	30:BQ:125:LEU:HD11	1.86	0.40
39:BZ:24:LEU:HD23	39:BZ:25:PRO:O	2.21	0.40
39:BZ:69:THR:HG22	39:BZ:90:VAL:HA	2.04	0.40
41:B1:58:ILE:HD11	41:B1:60:PHE:CE2	2.56	0.40
43:BD:26:LYS:HG2	43:BD:82:ILE:H	1.86	0.40
43:BD:32:SER:HA	43:BD:35:LYS:HZ2	1.85	0.40
51:BC:19:VAL:HG22	51:BC:223:ARG:HG3	2.02	0.40
58:BL:81:UNK:O	58:BL:85:UNK:C	2.69	0.40
1:AA:157:G:C6	1:AA:158:G:C5	3.10	0.40
1:AA:327:A:O3'	1:AA:328:C:H4'	2.21	0.40
1:AA:619:U:O2	17:AD:133:VAL:HA	2.21	0.40
11:AQ:26:GLN:HA	11:AQ:36:ILE:O	2.22	0.40
12:AR:40:LEU:C	12:AR:42:ARG:N	2.79	0.40
16:AC:19:GLU:O	16:AC:56:ASP:HA	2.22	0.40
17:AD:64:LEU:O	17:AD:67:ILE:HB	2.22	0.40
17:AD:150:GLU:CD	17:AD:151:LYS:H	2.29	0.40
23:AY:329:ARG:HH21	23:AY:372:GLY:HA2	1.86	0.40
23:AY:486:THR:HG21	23:AY:519:ARG:HH12	1.86	0.40
25:BA:526:A:N3	25:BA:2044:C:H1'	2.36	0.40
25:BA:647:G:H2'	25:BA:648:G:O4'	2.21	0.40
25:BA:774:A:O2'	25:BA:775:G:P	2.78	0.40
25:BA:1263:U:O3'	46:B5:11:THR:OG1	2.39	0.40
25:BA:1684:C:H2'	25:BA:1685:C:C6	2.57	0.40
25:BA:1787:A:O4'	25:BA:2589:A:H4'	2.21	0.40
25:BA:2139:C:C2'	25:BA:2140:C:OP2	2.68	0.40
25:BA:2250:G:C8	25:BA:2496:C:H5''	2.57	0.40
25:BA:2392:A:OP1	49:B8:32:LEU:CD1	2.70	0.40
26:BB:24:G:N7	26:BB:56:G:H2'	2.37	0.40
27:BN:57:ALA:C	27:BN:58:ASP:O	2.61	0.40
31:BR:2:ARG:CD	52:BE:111:ARG:HG3	2.52	0.40
41:B1:87:PRO:O	41:B1:88:LYS:C	2.64	0.40
43:BD:131:LEU:HB2	43:BD:136:ILE:HD11	2.03	0.40
43:BD:245:PRO:HA	43:BD:246:PRO:HD3	1.87	0.40
52:BE:72:VAL:O	52:BE:74:PRO:N	2.53	0.40
52:BE:74:PRO:O	52:BE:75:VAL:C	2.63	0.40
53:BF:5:ALA:O	53:BF:6:VAL:HG23	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:BK:61:ALA:C	56:BK:63:ARG:H	2.30	0.40
56:BK:104:VAL:CG2	56:BK:127:ILE:HB	2.51	0.40
56:BK:115:LEU:HB3	56:BK:126:MET:HE1	2.03	0.40
58:BL:70:UNK:O	58:BL:74:UNK:N	2.54	0.40
1:AA:152:A:N6	1:AA:170:U:C2	2.89	0.40
1:AA:175:C:H2'	1:AA:176:C:C6	2.57	0.40
1:AA:1003:G:N2	1:AA:1038:C:C4	2.89	0.40
1:AA:1091:U:O2	1:AA:1093:A:C8	2.74	0.40
1:AA:1141:C:C2	1:AA:1142:G:C8	3.09	0.40
1:AA:1237:C:C4'	1:AA:1334:G:N2	2.84	0.40
1:AA:1299:A:O3'	1:AA:1300:G:H4'	2.21	0.40
9:AO:27:VAL:HG12	9:AO:31:LEU:HD22	2.04	0.40
10:AP:33:ILE:HD13	10:AP:33:ILE:N	2.36	0.40
15:AB:70:PHE:O	15:AB:92:TYR:HA	2.21	0.40
17:AD:137:SER:O	17:AD:138:TYR:C	2.65	0.40
23:AY:168:ILE:HD11	23:AY:178:ILE:HD12	2.03	0.40
25:BA:435:C:H2'	25:BA:436:C:H5'	2.04	0.40
25:BA:732:C:H2'	25:BA:733:G:O4'	2.22	0.40
25:BA:1002:G:H2'	25:BA:1003:G:O4'	2.21	0.40
25:BA:1771:C:C1'	25:BA:1786:A:C8	3.05	0.40
25:BA:2092:U:C6	25:BA:2225:A:O2'	2.75	0.40
25:BA:2285:C:C5	47:B6:27:LYS:HE3	2.57	0.40
25:BA:2310:A:N3	25:BA:2310:A:H2'	2.36	0.40
25:BA:2550:G:C2'	25:BA:2551:C:H5'	2.51	0.40
25:BA:2731:G:OP1	52:BE:169:ASN:ND2	2.37	0.40
30:BQ:10:ARG:O	30:BQ:10:ARG:HG3	2.21	0.40
30:BQ:35:VAL:HG21	39:BZ:81:ARG:HH21	1.86	0.40
39:BZ:4:ARG:O	39:BZ:5:LEU:HB2	2.21	0.40
41:B1:57:GLU:C	41:B1:58:ILE:HG23	2.45	0.40
42:B2:12:GLU:O	42:B2:15:LYS:HE3	2.22	0.40
51:BC:53:ARG:HG3	51:BC:55:ASP:OD1	2.21	0.40
51:BC:162:GLU:HG2	51:BC:163:PHE:N	2.37	0.40
53:BF:123:LEU:HD12	53:BF:124:LEU:H	1.86	0.40
54:BG:77:ILE:O	54:BG:81:LYS:O	2.39	0.40
54:BG:103:LEU:HD22	54:BG:178:PHE:HZ	1.87	0.40
56:BK:121:GLU:CD	56:BK:121:GLU:N	2.79	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AJ	96/98 (98%)	80 (83%)	10 (10%)	6 (6%)	1	2
5	AK	117/119 (98%)	105 (90%)	9 (8%)	3 (3%)	4	9
6	AL	122/124 (98%)	107 (88%)	10 (8%)	5 (4%)	2	4
7	AM	122/124 (98%)	82 (67%)	32 (26%)	8 (7%)	1	1
8	AN	58/60 (97%)	48 (83%)	8 (14%)	2 (3%)	3	6
9	AO	86/88 (98%)	79 (92%)	6 (7%)	1 (1%)	10	22
10	AP	81/83 (98%)	74 (91%)	7 (9%)	0	100	100
11	AQ	97/99 (98%)	92 (95%)	4 (4%)	1 (1%)	12	25
12	AR	68/70 (97%)	60 (88%)	5 (7%)	3 (4%)	2	3
13	AS	76/78 (97%)	60 (79%)	8 (10%)	8 (10%)	0	0
14	AT	97/99 (98%)	86 (89%)	5 (5%)	6 (6%)	1	2
15	AB	232/234 (99%)	191 (82%)	32 (14%)	9 (4%)	2	4
16	AC	204/206 (99%)	173 (85%)	22 (11%)	9 (4%)	2	3
17	AD	206/208 (99%)	171 (83%)	25 (12%)	10 (5%)	1	3
18	AE	148/150 (99%)	141 (95%)	5 (3%)	2 (1%)	9	19
19	AF	99/101 (98%)	91 (92%)	8 (8%)	0	100	100
20	AG	153/155 (99%)	132 (86%)	17 (11%)	4 (3%)	4	9
21	AH	136/138 (99%)	127 (93%)	6 (4%)	3 (2%)	5	12
22	AI	125/127 (98%)	99 (79%)	17 (14%)	9 (7%)	1	1
23	AY	612/680 (90%)	520 (85%)	72 (12%)	20 (3%)	3	7
24	AU	22/24 (92%)	17 (77%)	5 (23%)	0	100	100
27	BN	136/140 (97%)	113 (83%)	17 (12%)	6 (4%)	2	3
28	BO	120/122 (98%)	113 (94%)	3 (2%)	4 (3%)	3	7
29	BP	144/150 (96%)	90 (62%)	21 (15%)	33 (23%)	0	0
30	BQ	139/141 (99%)	117 (84%)	17 (12%)	5 (4%)	2	5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	BR	115/118 (98%)	101 (88%)	9 (8%)	5 (4%)	2	4
32	BS	96/112 (86%)	61 (64%)	20 (21%)	15 (16%)	0	0
33	BT	135/146 (92%)	96 (71%)	24 (18%)	15 (11%)	0	0
34	BU	115/118 (98%)	101 (88%)	10 (9%)	4 (4%)	3	6
35	BV	99/101 (98%)	75 (76%)	9 (9%)	15 (15%)	0	0
36	BW	111/113 (98%)	101 (91%)	4 (4%)	6 (5%)	1	2
37	BX	90/96 (94%)	83 (92%)	7 (8%)	0	100	100
38	BY	98/110 (89%)	58 (59%)	18 (18%)	22 (22%)	0	0
39	BZ	194/206 (94%)	146 (75%)	32 (16%)	16 (8%)	0	1
40	B0	82/85 (96%)	71 (87%)	8 (10%)	3 (4%)	2	5
41	B1	91/98 (93%)	76 (84%)	12 (13%)	3 (3%)	3	7
42	B2	69/72 (96%)	58 (84%)	4 (6%)	7 (10%)	0	0
43	BD	269/276 (98%)	231 (86%)	24 (9%)	14 (5%)	1	2
44	B3	57/60 (95%)	54 (95%)	2 (4%)	1 (2%)	6	15
45	B4	28/71 (39%)	21 (75%)	4 (14%)	3 (11%)	0	0
46	B5	57/60 (95%)	47 (82%)	4 (7%)	6 (10%)	0	0
47	B6	42/54 (78%)	20 (48%)	15 (36%)	7 (17%)	0	0
48	B7	46/49 (94%)	43 (94%)	2 (4%)	1 (2%)	5	12
49	B8	61/65 (94%)	45 (74%)	11 (18%)	5 (8%)	0	1
50	B9	34/37 (92%)	32 (94%)	2 (6%)	0	100	100
51	BC	219/229 (96%)	166 (76%)	35 (16%)	18 (8%)	0	1
52	BE	202/206 (98%)	145 (72%)	30 (15%)	27 (13%)	0	0
53	BF	205/210 (98%)	165 (80%)	24 (12%)	16 (8%)	1	1
54	BG	179/182 (98%)	123 (69%)	44 (25%)	12 (7%)	1	1
55	BH	171/180 (95%)	128 (75%)	26 (15%)	17 (10%)	0	0
56	BK	121/147 (82%)	84 (69%)	30 (25%)	7 (6%)	1	2
57	BJ	128/130 (98%)	84 (66%)	31 (24%)	13 (10%)	0	0
All	All	6610/6949 (95%)	5383 (81%)	812 (12%)	415 (6%)	1	2

All (415) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AJ	23	ILE

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Mol	Chain	Res	Type
4	AJ	59	SER
4	AJ	86	MET
5	AK	117	ASN
5	AK	128	ALA
6	AL	27	LEU
7	AM	46	LYS
7	AM	83	ASP
7	AM	90	LEU
8	AN	16	PHE
11	AQ	49	GLU
12	AR	25	THR
13	AS	5	LEU
13	AS	10	PHE
13	AS	26	GLY
13	AS	28	LYS
13	AS	80	TYR
14	AT	95	ALA
15	AB	18	GLY
15	AB	237	ALA
16	AC	154	SER
16	AC	165	THR
16	AC	168	ALA
17	AD	3	ARG
17	AD	31	CYS
20	AG	155	ARG
22	AI	55	ALA
22	AI	89	ASN
22	AI	118	LYS
22	AI	119	ALA
23	AY	34	TYR
23	AY	95	GLU
23	AY	171	GLU
23	AY	180	VAL
23	AY	215	LYS
23	AY	683	VAL
23	AY	684	GLN
27	BN	4	TYR
27	BN	57	ALA
27	BN	59	LYS
27	BN	127	ASP
27	BN	133	GLN
29	BP	14	LYS

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Mol	Chain	Res	Type
29	BP	18	ARG
29	BP	23	PRO
29	BP	25	SER
29	BP	47	ASP
29	BP	49	ARG
29	BP	52	GLU
29	BP	57	THR
29	BP	65	ARG
29	BP	106	LEU
29	BP	107	LYS
30	BQ	18	LYS
30	BQ	22	LYS
31	BR	4	LEU
32	BS	59	LYS
32	BS	89	ARG
32	BS	97	ARG
32	BS	105	ALA
33	BT	24	PRO
33	BT	30	VAL
33	BT	80	SER
33	BT	91	ARG
33	BT	107	ASP
34	BU	91	ASP
34	BU	93	LYS
35	BV	3	ALA
35	BV	16	PRO
35	BV	19	LYS
35	BV	22	VAL
35	BV	24	LYS
35	BV	46	VAL
36	BW	63	ASP
38	BY	3	VAL
38	BY	10	GLY
38	BY	24	VAL
38	BY	27	VAL
38	BY	31	LEU
38	BY	42	VAL
38	BY	56	PRO
38	BY	62	GLU
38	BY	77	PRO
38	BY	78	ALA
38	BY	98	VAL

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Mol	Chain	Res	Type
39	BZ	21	ALA
39	BZ	146	ILE
39	BZ	189	ALA
40	B0	3	HIS
41	B1	53	VAL
42	B2	43	GLN
42	B2	44	LEU
42	B2	70	GLN
43	BD	3	VAL
43	BD	12	SER
43	BD	26	LYS
46	B5	4	HIS
46	B5	35	GLU
46	B5	49	CYS
46	B5	51	TYR
46	B5	52	TYR
46	B5	57	VAL
47	B6	19	ARG
47	B6	31	PRO
47	B6	46	HIS
49	B8	34	TRP
49	B8	61	LEU
51	BC	54	SER
51	BC	55	ASP
51	BC	80	GLY
51	BC	83	ILE
51	BC	109	ASP
51	BC	186	ALA
52	BE	60	ASN
52	BE	66	HIS
52	BE	69	LYS
52	BE	72	VAL
52	BE	75	VAL
52	BE	77	ILE
52	BE	82	ARG
52	BE	87	GLU
52	BE	88	GLY
52	BE	90	THR
52	BE	118	LYS
53	BF	21	ALA
53	BF	67	GLN
53	BF	168	ARG

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Mol	Chain	Res	Type
53	BF	195	ASP
54	BG	82	LEU
54	BG	87	PRO
54	BG	97	ASP
55	BH	9	ILE
55	BH	10	PRO
55	BH	13	LYS
55	BH	45	VAL
55	BH	83	TYR
55	BH	85	LYS
55	BH	92	ILE
55	BH	138	LYS
56	BK	115	LEU
57	BJ	47	ALA
57	BJ	50	ALA
57	BJ	56	ALA
57	BJ	61	ALA
57	BJ	73	ALA
57	BJ	107	ALA
57	BJ	128	ALA
4	AJ	27	ALA
6	AL	91	LYS
7	AM	66	LEU
8	AN	14	PRO
12	AR	28	GLU
14	AT	75	ASN
14	AT	101	GLY
15	AB	14	GLY
15	AB	110	GLN
16	AC	12	LEU
16	AC	61	ALA
16	AC	156	ARG
17	AD	9	CYS
17	AD	17	VAL
17	AD	23	GLY
17	AD	26	CYS
22	AI	105	ASP
23	AY	196	ILE
23	AY	211	GLU
23	AY	396	ARG
23	AY	551	GLN
28	BO	5	GLN

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Mol	Chain	Res	Type
29	BP	11	GLY
29	BP	26	GLY
29	BP	33	ARG
29	BP	34	GLY
29	BP	66	GLY
29	BP	67	MET
29	BP	98	GLU
29	BP	109	GLY
30	BQ	27	VAL
30	BQ	28	ALA
32	BS	14	VAL
32	BS	102	ALA
33	BT	2	ASN
33	BT	81	PRO
33	BT	126	ALA
33	BT	129	ARG
35	BV	37	VAL
35	BV	40	LEU
36	BW	65	LEU
38	BY	29	GLU
38	BY	39	VAL
39	BZ	142	SER
39	BZ	165	VAL
39	BZ	168	GLU
39	BZ	190	GLU
41	B1	58	ILE
42	B2	9	GLN
43	BD	11	PRO
43	BD	25	THR
43	BD	210	GLY
43	BD	224	ALA
43	BD	238	GLY
43	BD	239	ARG
45	B4	61	VAL
47	B6	23	THR
51	BC	85	GLU
51	BC	86	ALA
51	BC	89	ALA
51	BC	97	GLU
52	BE	45	THR
52	BE	63	LEU
52	BE	71	GLY

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Mol	Chain	Res	Type
52	BE	74	PRO
52	BE	95	ILE
52	BE	130	GLY
53	BF	3	GLU
53	BF	5	ALA
53	BF	6	VAL
53	BF	11	VAL
53	BF	25	PRO
53	BF	134	GLY
54	BG	61	ALA
54	BG	84	LYS
54	BG	117	PHE
55	BH	55	PRO
55	BH	84	SER
55	BH	172	LYS
56	BK	82	ALA
57	BJ	7	ALA
57	BJ	72	ALA
57	BJ	120	ALA
4	AJ	58	ASP
6	AL	28	LYS
7	AM	124	PRO
12	AR	87	ARG
13	AS	6	LYS
13	AS	76	PRO
14	AT	99	LEU
15	AB	153	ARG
15	AB	236	TYR
16	AC	4	LYS
16	AC	181	ASN
17	AD	18	LYS
18	AE	68	GLU
23	AY	96	ARG
23	AY	181	LEU
23	AY	403	GLU
23	AY	404	VAL
23	AY	581	ALA
27	BN	47	ALA
28	BO	29	ASN
29	BP	17	LYS
29	BP	35	HIS
29	BP	36	LYS

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Mol	Chain	Res	Type
29	BP	39	LYS
29	BP	42	SER
29	BP	108	LYS
29	BP	136	GLU
29	BP	146	VAL
32	BS	19	LYS
32	BS	53	SER
32	BS	88	ASP
32	BS	92	TYR
32	BS	103	GLU
33	BT	27	THR
33	BT	58	ASN
35	BV	2	PHE
35	BV	20	LEU
35	BV	23	GLU
35	BV	47	VAL
35	BV	48	GLY
38	BY	67	LEU
38	BY	82	PRO
38	BY	90	LEU
39	BZ	140	ASP
42	B2	45	SER
42	B2	48	HIS
43	BD	32	SER
43	BD	101	GLU
44	B3	51	ALA
45	B4	63	SER
47	B6	22	ALA
47	B6	28	ARG
49	B8	51	ALA
51	BC	141	LYS
52	BE	17	ASP
52	BE	61	ARG
52	BE	128	SER
53	BF	10	PRO
53	BF	141	ALA
54	BG	49	ASP
54	BG	64	THR
54	BG	142	PRO
55	BH	126	PRO
56	BK	51	ALA
57	BJ	84	ALA

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Mol	Chain	Res	Type
6	AL	19	ARG
7	AM	67	GLU
14	AT	97	ALA
15	AB	15	VAL
15	AB	130	ARG
15	AB	131	PRO
16	AC	36	ASP
17	AD	4	TYR
20	AG	81	GLY
21	AH	2	LEU
22	AI	92	TYR
28	BO	26	LYS
29	BP	43	GLY
29	BP	48	PRO
29	BP	122	PRO
29	BP	147	LEU
30	BQ	59	ARG
31	BR	3	HIS
31	BR	106	GLY
32	BS	54	LEU
33	BT	31	SER
33	BT	32	TYR
34	BU	33	ARG
36	BW	6	ILE
38	BY	32	PRO
38	BY	99	CYS
39	BZ	14	LYS
39	BZ	80	ARG
39	BZ	199	LYS
40	B0	6	GLY
40	B0	9	SER
41	B1	85	LEU
48	B7	47	ARG
49	B8	33	ASN
49	B8	53	PRO
51	BC	185	LEU
52	BE	18	ASP
52	BE	187	ALA
53	BF	131	GLY
54	BG	122	PRO
55	BH	168	PRO
56	BK	42	ASN

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Mol	Chain	Res	Type
57	BJ	93	ALA
7	AM	7	VAL
7	AM	55	ARG
9	AO	24	SER
14	AT	100	ILE
17	AD	5	ILE
18	AE	8	GLU
20	AG	54	THR
22	AI	54	ASP
22	AI	127	LYS
23	AY	136	ALA
29	BP	38	GLN
31	BR	86	ARG
31	BR	117	VAL
32	BS	13	ARG
33	BT	57	PHE
35	BV	44	LYS
39	BZ	156	LYS
47	B6	44	ARG
51	BC	140	PRO
51	BC	227	HIS
52	BE	44	TYR
53	BF	26	ALA
54	BG	43	LEU
55	BH	24	VAL
55	BH	137	ASP
55	BH	171	LEU
56	BK	62	ASP
57	BJ	38	ALA
4	AJ	90	LEU
13	AS	29	ARG
20	AG	7	ALA
21	AH	51	VAL
29	BP	9	ASN
32	BS	95	HIS
32	BS	107	GLU
35	BV	79	VAL
36	BW	11	ARG
36	BW	93	ALA
38	BY	81	LYS
39	BZ	78	LYS
39	BZ	147	GLY

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Mol	Chain	Res	Type
42	B2	17	SER
43	BD	35	LYS
45	B4	54	LYS
51	BC	118	ASP
51	BC	181	PRO
52	BE	129	HIS
54	BG	86	MET
55	BH	47	GLU
56	BK	10	LEU
22	AI	44	VAL
6	AL	121	GLY
17	AD	29	PRO
23	AY	243	VAL
23	AY	299	VAL
28	BO	48	PRO
34	BU	90	VAL
38	BY	53	PRO
38	BY	66	PRO
39	BZ	197	ILE
51	BC	96	GLY
52	BE	73	GLU
53	BF	84	VAL
5	AK	48	ILE
23	AY	516	PRO
43	BD	271	ILE
21	AH	73	ASP
33	BT	88	ILE
36	BW	112	GLY
38	BY	80	GLY
43	BD	28	GLU
51	BC	103	ILE
52	BE	116	VAL
53	BF	24	LEU
39	BZ	166	SER
52	BE	53	PRO
56	BK	4	VAL

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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	AJ	88/88 (100%)	70 (80%)	18 (20%)	1	1
5	AK	90/90 (100%)	69 (77%)	21 (23%)	1	0
6	AL	104/104 (100%)	80 (77%)	24 (23%)	1	0
7	AM	99/99 (100%)	80 (81%)	19 (19%)	1	2
8	AN	49/49 (100%)	37 (76%)	12 (24%)	1	0
9	AO	79/79 (100%)	67 (85%)	12 (15%)	3	5
10	AP	72/72 (100%)	61 (85%)	11 (15%)	3	5
11	AQ	94/94 (100%)	79 (84%)	15 (16%)	2	4
12	AR	61/61 (100%)	49 (80%)	12 (20%)	1	2
13	AS	69/69 (100%)	51 (74%)	18 (26%)	0	0
14	AT	76/76 (100%)	64 (84%)	12 (16%)	2	4
15	AB	202/202 (100%)	168 (83%)	34 (17%)	2	3
16	AC	160/160 (100%)	121 (76%)	39 (24%)	1	0
17	AD	180/180 (100%)	143 (79%)	37 (21%)	1	1
18	AE	115/115 (100%)	102 (89%)	13 (11%)	5	11
19	AF	90/90 (100%)	76 (84%)	14 (16%)	2	4
20	AG	126/126 (100%)	110 (87%)	16 (13%)	4	8
21	AH	119/119 (100%)	94 (79%)	25 (21%)	1	1
22	AI	98/98 (100%)	79 (81%)	19 (19%)	1	2
23	AY	528/573 (92%)	412 (78%)	116 (22%)	1	1
24	AU	19/19 (100%)	12 (63%)	7 (37%)	0	0
27	BN	117/119 (98%)	83 (71%)	34 (29%)	0	0
28	BO	100/100 (100%)	79 (79%)	21 (21%)	1	1
29	BP	112/116 (97%)	79 (70%)	33 (30%)	0	0
30	BQ	111/111 (100%)	97 (87%)	14 (13%)	4	8
31	BR	100/101 (99%)	77 (77%)	23 (23%)	1	0
32	BS	77/88 (88%)	63 (82%)	14 (18%)	2	2
33	BT	120/127 (94%)	90 (75%)	30 (25%)	0	0
34	BU	92/94 (98%)	75 (82%)	17 (18%)	1	2
35	BV	82/82 (100%)	56 (68%)	26 (32%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	BW	91/92 (99%)	72 (79%)	19 (21%)	1	1
37	BX	74/78 (95%)	58 (78%)	16 (22%)	1	1
38	BY	84/91 (92%)	63 (75%)	21 (25%)	0	0
39	BZ	154/179 (86%)	125 (81%)	29 (19%)	1	2
40	B0	66/67 (98%)	56 (85%)	10 (15%)	3	5
41	B1	78/83 (94%)	62 (80%)	16 (20%)	1	1
42	B2	66/67 (98%)	52 (79%)	14 (21%)	1	1
43	BD	213/218 (98%)	168 (79%)	45 (21%)	1	1
44	B3	51/52 (98%)	38 (74%)	13 (26%)	0	0
45	B4	27/63 (43%)	23 (85%)	4 (15%)	3	5
46	B5	51/52 (98%)	43 (84%)	8 (16%)	2	4
47	B6	43/52 (83%)	31 (72%)	12 (28%)	0	0
48	B7	41/42 (98%)	35 (85%)	6 (15%)	3	5
49	B8	53/55 (96%)	34 (64%)	19 (36%)	0	0
50	B9	33/34 (97%)	24 (73%)	9 (27%)	0	0
51	BC	177/181 (98%)	149 (84%)	28 (16%)	2	4
52	BE	165/166 (99%)	132 (80%)	33 (20%)	1	2
53	BF	165/166 (99%)	129 (78%)	36 (22%)	1	1
54	BG	155/156 (99%)	126 (81%)	29 (19%)	1	2
55	BH	136/148 (92%)	106 (78%)	30 (22%)	1	1
56	BK	96/111 (86%)	82 (85%)	14 (15%)	3	5
All	All	5448/5654 (96%)	4331 (80%)	1117 (20%)	1	1

All (1117) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	AJ	3	LYS
4	AJ	4	ILE
4	AJ	5	ARG
4	AJ	6	ILE
4	AJ	14	LYS
4	AJ	16	LEU
4	AJ	38	ILE
4	AJ	46	ARG
4	AJ	49	VAL

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Mol	Chain	Res	Type
4	AJ	76	ASN
4	AJ	78	ASN
4	AJ	79	ARG
4	AJ	80	LYS
4	AJ	81	THR
4	AJ	86	MET
4	AJ	96	ILE
4	AJ	98	ILE
4	AJ	99	LYS
5	AK	11	LYS
5	AK	14	VAL
5	AK	28	THR
5	AK	29	ILE
5	AK	30	VAL
5	AK	31	THR
5	AK	41	THR
5	AK	48	ILE
5	AK	51	LYS
5	AK	53	SER
5	AK	87	THR
5	AK	92	GLU
5	AK	96	ARG
5	AK	103	LEU
5	AK	109	VAL
5	AK	112	THR
5	AK	114	VAL
5	AK	117	ASN
5	AK	122	LYS
5	AK	124	LYS
5	AK	126	ARG
6	AL	7	ILE
6	AL	13	LYS
6	AL	18	VAL
6	AL	20	LYS
6	AL	27	LEU
6	AL	33	ARG
6	AL	38	THR
6	AL	39	VAL
6	AL	41	ARG
6	AL	42	THR
6	AL	53	ARG
6	AL	55	VAL

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Mol	Chain	Res	Type
6	AL	57	LYS
6	AL	60	LEU
6	AL	67	THR
6	AL	78	GLN
6	AL	83	VAL
6	AL	84	LEU
6	AL	85	ILE
6	AL	89	ARG
6	AL	91	LYS
6	AL	92	ASP
6	AL	111	LYS
6	AL	126	LYS
7	AM	4	ILE
7	AM	13	LYS
7	AM	47	ASP
7	AM	49	THR
7	AM	56	LEU
7	AM	64	TRP
7	AM	70	LEU
7	AM	79	LYS
7	AM	82	MET
7	AM	86	CYS
7	AM	90	LEU
7	AM	93	ARG
7	AM	94	ARG
7	AM	102	ARG
7	AM	108	ARG
7	AM	109	THR
7	AM	111	LYS
7	AM	115	LYS
7	AM	120	LYS
8	AN	4	LYS
8	AN	7	ILE
8	AN	9	LYS
8	AN	18	VAL
8	AN	25	VAL
8	AN	26	ARG
8	AN	27	CYS
8	AN	33	VAL
8	AN	35	ARG
8	AN	41	ARG
8	AN	44	LEU

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Mol	Chain	Res	Type
8	AN	60	SER
9	AO	10	LYS
9	AO	17	ARG
9	AO	24	SER
9	AO	26	GLU
9	AO	31	LEU
9	AO	39	LEU
9	AO	45	VAL
9	AO	65	ARG
9	AO	66	LEU
9	AO	82	ILE
9	AO	83	GLU
9	AO	87	ILE
10	AP	2	VAL
10	AP	4	ILE
10	AP	8	ARG
10	AP	20	VAL
10	AP	21	VAL
10	AP	25	ARG
10	AP	27	LYS
10	AP	28	ARG
10	AP	33	ILE
10	AP	45	THR
10	AP	54	GLU
11	AQ	7	THR
11	AQ	9	VAL
11	AQ	14	LYS
11	AQ	36	ILE
11	AQ	38	ARG
11	AQ	48	GLU
11	AQ	50	LYS
11	AQ	52	LYS
11	AQ	59	ILE
11	AQ	74	LEU
11	AQ	87	LYS
11	AQ	92	ARG
11	AQ	93	GLN
11	AQ	97	SER
11	AQ	100	LYS
12	AR	25	THR
12	AR	31	LEU
12	AR	32	ARG

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Mol	Chain	Res	Type
12	AR	37	VAL
12	AR	44	LEU
12	AR	45	SER
12	AR	47	THR
12	AR	54	ARG
12	AR	65	ILE
12	AR	76	LEU
12	AR	84	LYS
12	AR	85	LEU
13	AS	5	LEU
13	AS	6	LYS
13	AS	7	LYS
13	AS	9	VAL
13	AS	11	VAL
13	AS	15	LEU
13	AS	16	LEU
13	AS	18	LYS
13	AS	22	LEU
13	AS	30	LEU
13	AS	37	ARG
13	AS	44	MET
13	AS	60	VAL
13	AS	63	THR
13	AS	64	GLU
13	AS	70	LYS
13	AS	73	GLU
13	AS	80	TYR
14	AT	24	LEU
14	AT	27	LYS
14	AT	30	LYS
14	AT	35	THR
14	AT	38	LYS
14	AT	51	GLU
14	AT	54	LYS
14	AT	65	LYS
14	AT	75	ASN
14	AT	85	MET
14	AT	86	ARG
14	AT	104	LEU
15	AB	7	VAL
15	AB	15	VAL
15	AB	17	PHE

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Mol	Chain	Res	Type
15	AB	30	ARG
15	AB	32	ILE
15	AB	36	ARG
15	AB	37	ASN
15	AB	39	ILE
15	AB	41	ILE
15	AB	42	ILE
15	AB	43	ASP
15	AB	52	GLU
15	AB	67	THR
15	AB	76	GLN
15	AB	83	MET
15	AB	96	ARG
15	AB	117	GLU
15	AB	119	GLU
15	AB	128	GLU
15	AB	133	LYS
15	AB	137	ARG
15	AB	139	LYS
15	AB	140	HIS
15	AB	155	LEU
15	AB	156	LYS
15	AB	170	GLU
15	AB	178	ARG
15	AB	187	LEU
15	AB	196	LEU
15	AB	200	ILE
15	AB	215	LEU
15	AB	221	LEU
15	AB	223	ILE
15	AB	239	VAL
16	AC	5	ILE
16	AC	12	LEU
16	AC	14	ILE
16	AC	16	ARG
16	AC	21	ARG
16	AC	27	LYS
16	AC	34	LEU
16	AC	36	ASP
16	AC	37	GLN
16	AC	38	ARG
16	AC	45	LYS

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Mol	Chain	Res	Type
16	AC	46	GLU
16	AC	47	LEU
16	AC	49	SER
16	AC	52	LEU
16	AC	54	ARG
16	AC	56	ASP
16	AC	62	ASP
16	AC	68	VAL
16	AC	72	LYS
16	AC	76	VAL
16	AC	82	GLU
16	AC	83	ARG
16	AC	85	ARG
16	AC	86	VAL
16	AC	94	LEU
16	AC	99	VAL
16	AC	104	GLN
16	AC	131	ARG
16	AC	132	ARG
16	AC	136	GLN
16	AC	154	SER
16	AC	166	GLU
16	AC	167	TRP
16	AC	179	ARG
16	AC	188	LEU
16	AC	196	LEU
16	AC	202	ILE
16	AC	207	VAL
17	AD	3	ARG
17	AD	5	ILE
17	AD	8	VAL
17	AD	9	CYS
17	AD	10	ARG
17	AD	11	LEU
17	AD	15	GLU
17	AD	18	LYS
17	AD	19	LEU
17	AD	22	LYS
17	AD	33	MET
17	AD	34	GLU
17	AD	36	ARG
17	AD	58	LEU

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Mol	Chain	Res	Type
17	AD	73	ARG
17	AD	78	LEU
17	AD	80	GLU
17	AD	86	LYS
17	AD	91	SER
17	AD	96	LEU
17	AD	103	ASN
17	AD	108	LEU
17	AD	127	THR
17	AD	131	ARG
17	AD	132	ARG
17	AD	135	LEU
17	AD	139	ARG
17	AD	145	GLU
17	AD	150	GLU
17	AD	155	LEU
17	AD	162	LEU
17	AD	170	VAL
17	AD	175	SER
17	AD	179	GLU
17	AD	187	ARG
17	AD	194	LEU
17	AD	201	GLN
18	AE	11	ILE
18	AE	31	LEU
18	AE	32	VAL
18	AE	34	VAL
18	AE	41	VAL
18	AE	47	LYS
18	AE	50	GLU
18	AE	66	MET
18	AE	67	VAL
18	AE	76	ILE
18	AE	80	ILE
18	AE	91	LEU
18	AE	100	VAL
19	AF	3	ARG
19	AF	10	LEU
19	AF	16	GLN
19	AF	24	GLU
19	AF	25	ILE
19	AF	28	ARG

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Mol	Chain	Res	Type
19	AF	43	LEU
19	AF	45	LEU
19	AF	46	ARG
19	AF	54	LYS
19	AF	65	VAL
19	AF	83	ASP
19	AF	92	LYS
19	AF	100	ASN
20	AG	5	ARG
20	AG	8	GLU
20	AG	13	GLN
20	AG	22	LEU
20	AG	30	ILE
20	AG	32	ARG
20	AG	54	THR
20	AG	61	VAL
20	AG	63	LYS
20	AG	67	GLU
20	AG	72	ARG
20	AG	84	ASN
20	AG	104	LEU
20	AG	113	GLU
20	AG	131	LYS
20	AG	137	LYS
21	AH	1	MET
21	AH	6	ILE
21	AH	21	LYS
21	AH	24	THR
21	AH	26	VAL
21	AH	35	ILE
21	AH	39	LEU
21	AH	41	ARG
21	AH	52	ASP
21	AH	56	LYS
21	AH	80	ILE
21	AH	88	LYS
21	AH	91	ARG
21	AH	92	ARG
21	AH	98	LYS
21	AH	99	GLU
21	AH	102	ARG
21	AH	104	ARG

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Mol	Chain	Res	Type
21	AH	107	LEU
21	AH	109	ILE
21	AH	112	LEU
21	AH	115	SER
21	AH	125	ARG
21	AH	126	LYS
21	AH	127	LEU
22	AI	10	ARG
22	AI	14	VAL
22	AI	20	ARG
22	AI	42	ARG
22	AI	44	VAL
22	AI	47	LEU
22	AI	56	LEU
22	AI	64	THR
22	AI	65	VAL
22	AI	66	ARG
22	AI	79	LEU
22	AI	86	VAL
22	AI	95	LYS
22	AI	97	LYS
22	AI	99	LEU
22	AI	111	ARG
22	AI	112	LYS
22	AI	118	LYS
22	AI	128	ARG
23	AY	10	LYS
23	AY	12	LEU
23	AY	15	ILE
23	AY	25	LYS
23	AY	30	GLU
23	AY	31	ARG
23	AY	33	LEU
23	AY	39	ILE
23	AY	56	GLU
23	AY	61	ARG
23	AY	65	ILE
23	AY	69	VAL
23	AY	70	THR
23	AY	77	HIS
23	AY	81	ILE
23	AY	91	THR

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Mol	Chain	Res	Type
23	AY	98	MET
23	AY	120	THR
23	AY	123	ARG
23	AY	146	LEU
23	AY	148	LEU
23	AY	152	THR
23	AY	156	ARG
23	AY	157	LEU
23	AY	165	GLN
23	AY	175	SER
23	AY	178	ILE
23	AY	187	THR
23	AY	197	ARG
23	AY	201	ILE
23	AY	206	LEU
23	AY	214	GLU
23	AY	217	VAL
23	AY	224	ASP
23	AY	225	GLU
23	AY	232	LEU
23	AY	254	LYS
23	AY	255	ILE
23	AY	260	LEU
23	AY	264	LEU
23	AY	280	LEU
23	AY	284	LEU
23	AY	286	ILE
23	AY	290	LYS
23	AY	292	THR
23	AY	295	GLU
23	AY	298	VAL
23	AY	306	ASN
23	AY	312	LEU
23	AY	316	ILE
23	AY	319	ASP
23	AY	337	SER
23	AY	346	LYS
23	AY	348	ARG
23	AY	349	LYS
23	AY	355	LEU
23	AY	356	LEU
23	AY	363	ARG

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Mol	Chain	Res	Type
23	AY	368	GLU
23	AY	369	LEU
23	AY	377	VAL
23	AY	378	VAL
23	AY	385	THR
23	AY	396	ARG
23	AY	399	LEU
23	AY	400	GLU
23	AY	402	ILE
23	AY	403	GLU
23	AY	409	ILE
23	AY	414	GLU
23	AY	422	GLU
23	AY	423	LYS
23	AY	426	GLN
23	AY	431	LEU
23	AY	440	VAL
23	AY	446	THR
23	AY	450	ILE
23	AY	451	ILE
23	AY	452	SER
23	AY	457	LEU
23	AY	459	LEU
23	AY	465	ARG
23	AY	472	VAL
23	AY	473	ASP
23	AY	476	VAL
23	AY	481	VAL
23	AY	485	GLU
23	AY	488	THR
23	AY	492	ASP
23	AY	493	VAL
23	AY	512	ILE
23	AY	515	GLU
23	AY	517	LEU
23	AY	544	LYS
23	AY	546	ILE
23	AY	548	GLU
23	AY	556	ILE
23	AY	566	THR
23	AY	584	ILE
23	AY	590	ILE

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Mol	Chain	Res	Type
23	AY	591	LYS
23	AY	603	GLU
23	AY	605	ILE
23	AY	610	VAL
23	AY	612	THR
23	AY	623	ASP
23	AY	628	ARG
23	AY	634	MET
23	AY	637	ARG
23	AY	647	VAL
23	AY	649	LEU
23	AY	679	VAL
23	AY	681	LYS
23	AY	684	GLN
23	AY	686	LYS
23	AY	687	LEU
24	AU	6	ARG
24	AU	7	ARG
24	AU	9	ARG
24	AU	12	LYS
24	AU	13	ILE
24	AU	15	ARG
24	AU	25	LYS
27	BN	1	MET
27	BN	2	LYS
27	BN	3	THR
27	BN	4	TYR
27	BN	9	VAL
27	BN	12	ARG
27	BN	15	LEU
27	BN	16	ILE
27	BN	19	GLU
27	BN	28	THR
27	BN	33	LEU
27	BN	34	LEU
27	BN	37	LYS
27	BN	41	ASP
27	BN	43	THR
27	BN	48	MET
27	BN	55	VAL
27	BN	58	ASP
27	BN	60	ILE

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Mol	Chain	Res	Type
27	BN	62	VAL
27	BN	63	THR
27	BN	65	LYS
27	BN	67	LEU
27	BN	68	GLU
27	BN	73	THR
27	BN	87	LEU
27	BN	89	LYS
27	BN	93	THR
27	BN	99	LEU
27	BN	119	ARG
27	BN	120	LEU
27	BN	133	GLN
27	BN	134	ARG
27	BN	136	GLU
28	BO	3	GLN
28	BO	8	LEU
28	BO	10	VAL
28	BO	20	MET
28	BO	22	ILE
28	BO	23	ARG
28	BO	24	VAL
28	BO	45	GLU
28	BO	47	ILE
28	BO	48	PRO
28	BO	49	ARG
28	BO	66	LYS
28	BO	70	LYS
28	BO	87	ILE
28	BO	88	ASN
28	BO	91	LEU
28	BO	94	ARG
28	BO	98	VAL
28	BO	104	ARG
28	BO	108	GLU
28	BO	113	LYS
29	BP	6	LEU
29	BP	13	ASN
29	BP	16	ARG
29	BP	17	LYS
29	BP	27	HIS
29	BP	39	LYS

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Mol	Chain	Res	Type
29	BP	42	SER
29	BP	45	LEU
29	BP	55	ARG
29	BP	56	SER
29	BP	57	THR
29	BP	58	THR
29	BP	61	ARG
29	BP	62	LEU
29	BP	67	MET
29	BP	68	GLN
29	BP	85	LEU
29	BP	88	LEU
29	BP	91	PHE
29	BP	95	VAL
29	BP	98	GLU
29	BP	100	LEU
29	BP	105	LEU
29	BP	107	LYS
29	BP	110	TYR
29	BP	112	LEU
29	BP	114	ILE
29	BP	115	LEU
29	BP	125	VAL
29	BP	135	LEU
29	BP	136	GLU
29	BP	138	LEU
29	BP	144	GLU
30	BQ	10	ARG
30	BQ	18	LYS
30	BQ	45	GLN
30	BQ	55	VAL
30	BQ	58	PHE
30	BQ	59	ARG
30	BQ	75	THR
30	BQ	76	LYS
30	BQ	96	VAL
30	BQ	112	GLU
30	BQ	115	MET
30	BQ	131	ILE
30	BQ	133	ARG
30	BQ	138	ASP
31	BR	4	LEU

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Mol	Chain	Res	Type
31	BR	18	LEU
31	BR	28	LEU
31	BR	29	LEU
31	BR	33	ARG
31	BR	34	ILE
31	BR	36	THR
31	BR	44	LEU
31	BR	51	LEU
31	BR	54	LEU
31	BR	63	ARG
31	BR	65	LEU
31	BR	67	LEU
31	BR	74	LYS
31	BR	75	LEU
31	BR	79	LEU
31	BR	88	ARG
31	BR	100	LEU
31	BR	105	ARG
31	BR	113	LEU
31	BR	116	LEU
31	BR	117	VAL
31	BR	118	GLU
32	BS	18	ILE
32	BS	20	ARG
32	BS	27	SER
32	BS	30	ARG
32	BS	31	SER
32	BS	46	VAL
32	BS	49	VAL
32	BS	54	LEU
32	BS	73	LEU
32	BS	80	LEU
32	BS	92	TYR
32	BS	97	ARG
32	BS	99	LYS
32	BS	107	GLU
33	BT	6	LEU
33	BT	11	GLU
33	BT	13	ARG
33	BT	15	VAL
33	BT	27	THR
33	BT	29	ARG

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Mol	Chain	Res	Type
33	BT	32	TYR
33	BT	43	GLN
33	BT	49	VAL
33	BT	50	ILE
33	BT	58	ASN
33	BT	59	THR
33	BT	62	THR
33	BT	63	VAL
33	BT	64	ARG
33	BT	65	LYS
33	BT	70	VAL
33	BT	78	LEU
33	BT	82	LEU
33	BT	86	ILE
33	BT	87	ASP
33	BT	89	VAL
33	BT	90	GLN
33	BT	93	ARG
33	BT	96	ARG
33	BT	99	LEU
33	BT	112	ARG
33	BT	118	ARG
33	BT	119	LYS
33	BT	128	GLU
34	BU	8	VAL
34	BU	13	LYS
34	BU	15	LYS
34	BU	16	LYS
34	BU	19	LYS
34	BU	27	LEU
34	BU	31	SER
34	BU	34	LYS
34	BU	60	LEU
34	BU	74	LEU
34	BU	83	LEU
34	BU	85	LYS
34	BU	88	ILE
34	BU	92	ARG
34	BU	95	LEU
34	BU	108	GLU
34	BU	114	LYS
35	BV	5	VAL

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Mol	Chain	Res	Type
35	BV	6	LYS
35	BV	13	ARG
35	BV	16	PRO
35	BV	18	LEU
35	BV	19	LYS
35	BV	20	LEU
35	BV	21	ARG
35	BV	28	GLU
35	BV	32	THR
35	BV	33	VAL
35	BV	35	LEU
35	BV	39	LEU
35	BV	40	LEU
35	BV	46	VAL
35	BV	47	VAL
35	BV	57	VAL
35	BV	61	VAL
35	BV	62	LEU
35	BV	66	ARG
35	BV	72	VAL
35	BV	73	SER
35	BV	79	VAL
35	BV	85	LYS
35	BV	95	LEU
35	BV	99	ILE
36	BW	11	ARG
36	BW	17	VAL
36	BW	19	LEU
36	BW	20	VAL
36	BW	23	LEU
36	BW	41	LYS
36	BW	50	VAL
36	BW	51	LEU
36	BW	52	GLU
36	BW	60	ASN
36	BW	63	ASP
36	BW	65	LEU
36	BW	76	VAL
36	BW	95	ILE
36	BW	96	ILE
36	BW	100	THR
36	BW	106	ILE

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Mol	Chain	Res	Type
36	BW	107	LEU
36	BW	110	LYS
37	BX	12	VAL
37	BX	27	THR
37	BX	39	ILE
37	BX	48	LYS
37	BX	55	ASN
37	BX	57	LEU
37	BX	60	ARG
37	BX	64	LYS
37	BX	66	LEU
37	BX	68	ARG
37	BX	70	LEU
37	BX	72	LYS
37	BX	77	LYS
37	BX	80	ILE
37	BX	90	GLU
37	BX	92	LEU
38	BY	4	LYS
38	BY	6	HIS
38	BY	9	LYS
38	BY	13	VAL
38	BY	31	LEU
38	BY	34	LYS
38	BY	38	ILE
38	BY	40	GLU
38	BY	44	ILE
38	BY	45	VAL
38	BY	49	VAL
38	BY	71	LYS
38	BY	75	ILE
38	BY	81	LYS
38	BY	83	THR
38	BY	85	VAL
38	BY	88	LYS
38	BY	89	PHE
38	BY	97	ARG
38	BY	98	VAL
38	BY	99	CYS
39	BZ	5	LEU
39	BZ	6	LYS
39	BZ	16	SER

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Mol	Chain	Res	Type
39	BZ	18	LEU
39	BZ	23	LYS
39	BZ	24	LEU
39	BZ	31	ARG
39	BZ	33	LEU
39	BZ	34	ASN
39	BZ	42	VAL
39	BZ	46	LYS
39	BZ	61	LEU
39	BZ	63	ASP
39	BZ	72	ARG
39	BZ	73	GLN
39	BZ	80	ARG
39	BZ	82	ARG
39	BZ	86	VAL
39	BZ	90	VAL
39	BZ	105	VAL
39	BZ	107	THR
39	BZ	111	VAL
39	BZ	112	ARG
39	BZ	118	GLN
39	BZ	132	ASN
39	BZ	144	LEU
39	BZ	146	ILE
39	BZ	150	LEU
39	BZ	156	LYS
40	B0	7	LEU
40	B0	11	ARG
40	B0	19	LYS
40	B0	20	ARG
40	B0	30	VAL
40	B0	41	ARG
40	B0	43	THR
40	B0	49	LYS
40	B0	68	GLU
40	B0	84	LEU
41	B1	7	ILE
41	B1	30	VAL
41	B1	38	SER
41	B1	39	LYS
41	B1	40	ARG
41	B1	46	LEU

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Mol	Chain	Res	Type
41	B1	48	LYS
41	B1	52	ARG
41	B1	58	ILE
41	B1	59	THR
41	B1	61	ARG
41	B1	72	GLU
41	B1	75	GLU
41	B1	82	LEU
41	B1	83	GLU
41	B1	95	LEU
42	B2	3	LEU
42	B2	8	LYS
42	B2	15	LYS
42	B2	16	LEU
42	B2	17	SER
42	B2	30	ARG
42	B2	32	LEU
42	B2	44	LEU
42	B2	51	ARG
42	B2	52	ASP
42	B2	53	LEU
42	B2	57	ILE
42	B2	64	LEU
42	B2	68	ARG
43	BD	3	VAL
43	BD	4	LYS
43	BD	24	ILE
43	BD	26	LYS
43	BD	28	GLU
43	BD	33	LEU
43	BD	34	VAL
43	BD	35	LYS
43	BD	43	ARG
43	BD	45	ASN
43	BD	49	ILE
43	BD	61	LEU
43	BD	64	ILE
43	BD	65	ILE
43	BD	69	ARG
43	BD	75	ILE
43	BD	89	SER
43	BD	94	LEU

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Mol	Chain	Res	Type
43	BD	103	ARG
43	BD	111	LEU
43	BD	117	VAL
43	BD	138	VAL
43	BD	140	THR
43	BD	141	VAL
43	BD	155	LEU
43	BD	166	GLN
43	BD	169	GLU
43	BD	171	ASP
43	BD	173	VAL
43	BD	174	ILE
43	BD	176	ARG
43	BD	192	THR
43	BD	193	VAL
43	BD	204	ILE
43	BD	211	ARG
43	BD	218	ARG
43	BD	221	VAL
43	BD	229	VAL
43	BD	232	PRO
43	BD	252	TRP
43	BD	257	LEU
43	BD	260	ARG
43	BD	262	ARG
43	BD	266	SER
43	BD	271	ILE
44	B3	3	ARG
44	B3	6	VAL
44	B3	8	LEU
44	B3	10	LYS
44	B3	17	LYS
44	B3	18	ASP
44	B3	29	ARG
44	B3	30	ARG
44	B3	31	LEU
44	B3	36	VAL
44	B3	37	LEU
44	B3	40	THR
44	B3	56	VAL
45	B4	48	ILE
45	B4	49	GLU

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Mol	Chain	Res	Type
45	B4	50	THR
45	B4	62	CYS
46	B5	3	LYS
46	B5	4	HIS
46	B5	6	VAL
46	B5	11	THR
46	B5	29	THR
46	B5	37	LYS
46	B5	48	GLU
46	B5	49	CYS
47	B6	9	LEU
47	B6	10	LEU
47	B6	11	LEU
47	B6	17	LYS
47	B6	18	ARG
47	B6	25	LYS
47	B6	32	ASN
47	B6	33	LYS
47	B6	42	TRP
47	B6	44	ARG
47	B6	50	ARG
47	B6	51	GLU
48	B7	11	LYS
48	B7	23	ARG
48	B7	24	THR
48	B7	41	ARG
48	B7	43	THR
48	B7	48	LYS
49	B8	6	THR
49	B8	11	LYS
49	B8	13	ARG
49	B8	14	VAL
49	B8	15	LYS
49	B8	23	VAL
49	B8	30	ARG
49	B8	32	LEU
49	B8	33	ASN
49	B8	34	TRP
49	B8	35	GLN
49	B8	36	LYS
49	B8	44	LYS
49	B8	47	LYS

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Mol	Chain	Res	Type
49	B8	49	VAL
49	B8	52	LYS
49	B8	56	GLU
49	B8	61	LEU
49	B8	64	TYR
50	B9	2	LYS
50	B9	4	ARG
50	B9	6	SER
50	B9	9	ARG
50	B9	14	CYS
50	B9	20	HIS
50	B9	22	ARG
50	B9	26	ILE
50	B9	29	ASN
51	BC	5	LYS
51	BC	23	ASP
51	BC	24	GLU
51	BC	27	ARG
51	BC	30	LYS
51	BC	42	GLU
51	BC	53	ARG
51	BC	63	SER
51	BC	68	LEU
51	BC	70	LYS
51	BC	71	GLN
51	BC	72	VAL
51	BC	73	ARG
51	BC	81	GLU
51	BC	84	LYS
51	BC	92	ASP
51	BC	98	GLU
51	BC	99	ILE
51	BC	104	LEU
51	BC	113	VAL
51	BC	130	ILE
51	BC	131	LEU
51	BC	137	LEU
51	BC	141	LYS
51	BC	184	LYS
51	BC	205	LYS
51	BC	217	THR
51	BC	227	HIS

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Mol	Chain	Res	Type
52	BE	7	VAL
52	BE	9	VAL
52	BE	12	THR
52	BE	18	ASP
52	BE	24	THR
52	BE	33	VAL
52	BE	34	VAL
52	BE	40	GLU
52	BE	54	GLN
52	BE	55	ASN
52	BE	57	LYS
52	BE	60	ASN
52	BE	66	HIS
52	BE	79	ARG
52	BE	87	GLU
52	BE	92	THR
52	BE	93	VAL
52	BE	94	GLU
52	BE	111	ARG
52	BE	118	LYS
52	BE	144	ARG
52	BE	145	LYS
52	BE	146	THR
52	BE	152	LYS
52	BE	154	LYS
52	BE	175	VAL
52	BE	181	LEU
52	BE	185	LYS
52	BE	188	VAL
52	BE	195	LEU
52	BE	197	ILE
52	BE	202	LYS
52	BE	203	LYS
53	BF	1	MET
53	BF	4	VAL
53	BF	8	GLN
53	BF	18	ARG
53	BF	19	GLU
53	BF	20	LEU
53	BF	23	ASP
53	BF	24	LEU
53	BF	27	GLU

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Mol	Chain	Res	Type
53	BF	28	ILE
53	BF	33	LEU
53	BF	43	LYS
53	BF	53	THR
53	BF	57	VAL
53	BF	64	ILE
53	BF	66	PRO
53	BF	68	LYS
53	BF	72	ARG
53	BF	74	ARG
53	BF	78	ILE
53	BF	88	VAL
53	BF	102	PRO
53	BF	103	LYS
53	BF	106	ARG
53	BF	110	LEU
53	BF	117	ARG
53	BF	126	VAL
53	BF	157	VAL
53	BF	164	ARG
53	BF	170	LEU
53	BF	175	THR
53	BF	176	LEU
53	BF	183	VAL
53	BF	192	LEU
53	BF	199	TRP
53	BF	200	GLU
54	BG	5	VAL
54	BG	8	LYS
54	BG	21	ARG
54	BG	22	ARG
54	BG	28	VAL
54	BG	34	LEU
54	BG	39	ILE
54	BG	43	LEU
54	BG	45	GLU
54	BG	59	GLU
54	BG	60	LEU
54	BG	62	LEU
54	BG	71	THR
54	BG	82	LEU
54	BG	83	ARG

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Mol	Chain	Res	Type
54	BG	86	MET
54	BG	98	ARG
54	BG	123	ASN
54	BG	126	ASP
54	BG	128	ARG
54	BG	130	ASN
54	BG	133	LEU
54	BG	139	LEU
54	BG	143	GLU
54	BG	146	TYR
54	BG	148	MET
54	BG	152	LEU
54	BG	161	THR
54	BG	174	GLU
55	BH	23	ARG
55	BH	24	VAL
55	BH	25	LYS
55	BH	34	GLU
55	BH	36	PRO
55	BH	43	VAL
55	BH	46	GLU
55	BH	53	GLU
55	BH	69	ARG
55	BH	71	LEU
55	BH	80	SER
55	BH	85	LYS
55	BH	89	ILE
55	BH	98	LEU
55	BH	101	ARG
55	BH	105	LEU
55	BH	107	VAL
55	BH	114	VAL
55	BH	119	GLU
55	BH	122	THR
55	BH	132	ARG
55	BH	139	GLN
55	BH	143	GLN
55	BH	151	ILE
55	BH	153	LYS
55	BH	155	SER
55	BH	162	ILE
55	BH	168	PRO

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Mol	Chain	Res	Type
55	BH	171	LEU
55	BH	173	PRO
56	BK	2	LYS
56	BK	3	LYS
56	BK	4	VAL
56	BK	5	VAL
56	BK	29	GLN
56	BK	30	HIS
56	BK	38	VAL
56	BK	57	ILE
56	BK	59	ILE
56	BK	65	PHE
56	BK	70	LYS
56	BK	77	LEU
56	BK	99	ILE
56	BK	117	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (78) such sidechains are listed below:

Mol	Chain	Res	Type
4	AJ	13	HIS
4	AJ	84	GLN
5	AK	26	ASN
5	AK	93	GLN
7	AM	101	GLN
8	AN	49	HIS
9	AO	9	GLN
9	AO	50	HIS
11	AQ	93	GLN
15	AB	37	ASN
15	AB	95	GLN
15	AB	135	GLN
15	AB	224	GLN
16	AC	69	HIS
16	AC	118	GLN
17	AD	45	GLN
17	AD	62	GLN
19	AF	7	ASN
19	AF	16	GLN
20	AG	97	GLN
20	AG	110	GLN
20	AG	148	ASN

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Mol	Chain	Res	Type
20	AG	153	HIS
22	AI	31	GLN
22	AI	38	GLN
23	AY	124	GLN
23	AY	154	GLN
23	AY	343	ASN
23	AY	443	HIS
23	AY	448	GLN
23	AY	684	GLN
28	BO	3	GLN
28	BO	88	ASN
29	BP	38	GLN
30	BQ	12	GLN
30	BQ	45	GLN
30	BQ	57	HIS
31	BR	13	HIS
31	BR	23	ASN
32	BS	68	GLN
32	BS	95	HIS
33	BT	38	ASN
33	BT	58	ASN
33	BT	90	GLN
34	BU	81	HIS
34	BU	94	ASN
36	BW	61	ASN
36	BW	102	HIS
37	BX	55	ASN
38	BY	43	ASN
39	BZ	32	HIS
39	BZ	34	ASN
40	B0	70	GLN
42	B2	70	GLN
43	BD	45	ASN
43	BD	58	HIS
43	BD	96	HIS
43	BD	116	GLN
44	B3	19	GLN
47	B6	26	ASN
47	B6	49	HIS
48	B7	16	HIS
49	B8	43	GLN
50	B9	29	ASN

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Mol	Chain	Res	Type
50	B9	32	HIS
51	BC	66	HIS
51	BC	71	GLN
52	BE	60	ASN
52	BE	132	HIS
52	BE	180	ASN
53	BF	31	HIS
53	BF	169	ASN
54	BG	26	GLN
54	BG	41	GLN
54	BG	132	ASN
56	BK	29	GLN
56	BK	33	ASN
56	BK	47	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1512/1516 (99%)	322 (21%)	65 (4%)
2	AV	73/76 (96%)	29 (39%)	9 (12%)
25	BA	2850/2915 (97%)	770 (27%)	130 (4%)
26	BB	119/122 (97%)	34 (28%)	4 (3%)
3	AX	5/25 (20%)	0	0
All	All	4559/4654 (97%)	1155 (25%)	208 (4%)

All (1155) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	6	G
1	AA	9	G
1	AA	13	U
1	AA	30	U
1	AA	31	G
1	AA	32	A
1	AA	39	G
1	AA	48	C
1	AA	49	U
1	AA	50	A
1	AA	51	A
1	AA	60	A
1	AA	61	G

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Mol	Chain	Res	Type
1	AA	63	C
1	AA	76	C
1	AA	79	G
1	AA	80	G
1	AA	81	U
1	AA	88	A
1	AA	90	U
1	AA	91	C
1	AA	92	C
1	AA	97	G
1	AA	101	A
1	AA	105	G
1	AA	108	G
1	AA	109	A
1	AA	110	C
1	AA	116	A
1	AA	121	C
1	AA	131	C
1	AA	144	G
1	AA	146	G
1	AA	147	G
1	AA	150	C
1	AA	160	A
1	AA	163	C
1	AA	179	A
1	AA	189(G)	G
1	AA	195	A
1	AA	197	A
1	AA	203	U
1	AA	204	U
1	AA	216	G
1	AA	217	C
1	AA	220	G
1	AA	221	C
1	AA	231	G
1	AA	244	U
1	AA	247	G
1	AA	251	G
1	AA	252	U
1	AA	266	G
1	AA	267	C
1	AA	289	G

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Mol	Chain	Res	Type
1	AA	301	G
1	AA	319	G
1	AA	321	A
1	AA	328	C
1	AA	329	A
1	AA	331	G
1	AA	332	G
1	AA	346	G
1	AA	347	G
1	AA	352	C
1	AA	353	A
1	AA	354	G
1	AA	367	U
1	AA	372	C
1	AA	373	A
1	AA	374	A
1	AA	381	C
1	AA	384	G
1	AA	398	C
1	AA	406	G
1	AA	409	G
1	AA	412	A
1	AA	413	G
1	AA	414	A
1	AA	422	C
1	AA	423	G
1	AA	424	G
1	AA	428	G
1	AA	429	U
1	AA	436	C
1	AA	439	A
1	AA	441	A
1	AA	443	C
1	AA	452	A
1	AA	470	C
1	AA	485	G
1	AA	492	G
1	AA	495	A
1	AA	496	A
1	AA	498	U
1	AA	501	C
1	AA	505	G

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Mol	Chain	Res	Type
1	AA	509	A
1	AA	510	A
1	AA	511	C
1	AA	518	C
1	AA	519	C
1	AA	522	C
1	AA	527	G
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	534	U
1	AA	539	A
1	AA	545	C
1	AA	547	A
1	AA	559	A
1	AA	561	U
1	AA	562	C
1	AA	572	A
1	AA	573	A
1	AA	576	G
1	AA	577	G
1	AA	582	U
1	AA	592	G
1	AA	596	C
1	AA	617	G
1	AA	630	G
1	AA	631	G
1	AA	632	A
1	AA	633	G
1	AA	649	G
1	AA	653	A
1	AA	665	A
1	AA	671	G
1	AA	673	G
1	AA	688	G
1	AA	731	G
1	AA	734	G
1	AA	749	C
1	AA	755	G
1	AA	765	G
1	AA	773	G
1	AA	777	A

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Mol	Chain	Res	Type
1	AA	785	G
1	AA	793	U
1	AA	794	A
1	AA	801	U
1	AA	802	A
1	AA	816	A
1	AA	817	C
1	AA	827	U
1	AA	828	A
1	AA	838	G
1	AA	839	U
1	AA	840	C
1	AA	841	U
1	AA	848	C
1	AA	851	G
1	AA	853	G
1	AA	859	A
1	AA	876	G
1	AA	890	G
1	AA	902	G
1	AA	913	A
1	AA	914	A
1	AA	919	A
1	AA	926	G
1	AA	927	G
1	AA	934	C
1	AA	935	A
1	AA	947	G
1	AA	960	U
1	AA	961	U
1	AA	966	G
1	AA	968	A
1	AA	969	A
1	AA	973	G
1	AA	974	A
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	980	C
1	AA	981	U
1	AA	984	C
1	AA	991	U

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Mol	Chain	Res	Type
1	AA	992	U
1	AA	993	G
1	AA	994	A
1	AA	1001(A)	G
1	AA	1004	A
1	AA	1005	A
1	AA	1009	G
1	AA	1013	G
1	AA	1016	A
1	AA	1021	G
1	AA	1024	G
1	AA	1025	U
1	AA	1026	G
1	AA	1027	C
1	AA	1030	C
1	AA	1030(D)	A
1	AA	1031	G
1	AA	1044	A
1	AA	1046	A
1	AA	1050	G
1	AA	1053	G
1	AA	1054	C
1	AA	1055	A
1	AA	1065	U
1	AA	1067	A
1	AA	1068	G
1	AA	1081	G
1	AA	1086	U
1	AA	1087	G
1	AA	1089	G
1	AA	1094	G
1	AA	1095	U
1	AA	1101	A
1	AA	1124	G
1	AA	1125	U
1	AA	1126	U
1	AA	1127	G
1	AA	1132	C
1	AA	1133	G
1	AA	1134	G
1	AA	1135	U
1	AA	1136	U

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Mol	Chain	Res	Type
1	AA	1137	C
1	AA	1138	G
1	AA	1139	G
1	AA	1140	C
1	AA	1143	G
1	AA	1146	A
1	AA	1147	C
1	AA	1152	A
1	AA	1159	U
1	AA	1160	G
1	AA	1171	G
1	AA	1181	G
1	AA	1182	G
1	AA	1184	G
1	AA	1187	G
1	AA	1192	C
1	AA	1196	U
1	AA	1197	G
1	AA	1212	U
1	AA	1213	A
1	AA	1214	C
1	AA	1215	G
1	AA	1218	C
1	AA	1225	A
1	AA	1226	C
1	AA	1227	A
1	AA	1238	A
1	AA	1256	A
1	AA	1257	U
1	AA	1258	G
1	AA	1259	C
1	AA	1260	C
1	AA	1269	A
1	AA	1273	G
1	AA	1281	U
1	AA	1285	A
1	AA	1286	A
1	AA	1287	A
1	AA	1288	A
1	AA	1290	G
1	AA	1293	G
1	AA	1299	A

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Mol	Chain	Res	Type
1	AA	1300	G
1	AA	1301	U
1	AA	1302	U
1	AA	1305	G
1	AA	1310	G
1	AA	1317	C
1	AA	1319	A
1	AA	1320	C
1	AA	1322	C
1	AA	1323	G
1	AA	1328	C
1	AA	1332	A
1	AA	1336	C
1	AA	1337	G
1	AA	1338	G
1	AA	1346	A
1	AA	1347	G
1	AA	1350	A
1	AA	1353	G
1	AA	1364	U
1	AA	1378	C
1	AA	1397	C
1	AA	1398	A
1	AA	1402	C
1	AA	1407	C
1	AA	1419	G
1	AA	1422	G
1	AA	1442	G
1	AA	1442(A)	G
1	AA	1443	G
1	AA	1446	U
1	AA	1447	A
1	AA	1452	C
1	AA	1456	G
1	AA	1457	G
1	AA	1472	U
1	AA	1492	A
1	AA	1493	A
1	AA	1494	G
1	AA	1499	A
1	AA	1502	A
1	AA	1504	G

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Mol	Chain	Res	Type
1	AA	1505	G
1	AA	1506	U
1	AA	1507	A
1	AA	1517	G
1	AA	1519	A
1	AA	1520	G
1	AA	1529	G
1	AA	1530	G
1	AA	1532	U
1	AA	1533	C
1	AA	1534	A
1	AA	1535	C
1	AA	1536	C
1	AA	1542	U
1	AA	1543	C
2	AV	4	C
2	AV	13	C
2	AV	15	G
2	AV	19	G
2	AV	20	U
2	AV	21	A
2	AV	22	G
2	AV	23	A
2	AV	26	A
2	AV	27	G
2	AV	30	G
2	AV	34	G
2	AV	35	A
2	AV	36	A
2	AV	38	A
2	AV	44	G
2	AV	46	G
2	AV	47	U
2	AV	48	C
2	AV	51	U
2	AV	52	G
2	AV	53	G
2	AV	57	G
2	AV	61	C
2	AV	72	C
2	AV	73	A
2	AV	74	C

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Mol	Chain	Res	Type
2	AV	75	C
2	AV	76	A
25	BA	9	U
25	BA	10	G
25	BA	34	C
25	BA	35	G
25	BA	36	G
25	BA	41	C
25	BA	45	C
25	BA	49	A
25	BA	50	U
25	BA	55	G
25	BA	63	U
25	BA	71	A
25	BA	72	U
25	BA	74	A
25	BA	75	G
25	BA	86	C
25	BA	88	G
25	BA	90	U
25	BA	92	A
25	BA	94	C
25	BA	95	G
25	BA	99	U
25	BA	100	G
25	BA	102	G
25	BA	103	A
25	BA	110	G
25	BA	118	A
25	BA	119	A
25	BA	120	U
25	BA	123	G
25	BA	128	C
25	BA	129	C
25	BA	131	G
25	BA	141	A
25	BA	154	G
25	BA	154(A)	C
25	BA	157	U
25	BA	158	U
25	BA	171	G
25	BA	173	G

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Mol	Chain	Res	Type
25	BA	174	C
25	BA	175	G
25	BA	181	A
25	BA	182	A
25	BA	196	A
25	BA	197	A
25	BA	199	A
25	BA	200	U
25	BA	204	A
25	BA	205	G
25	BA	214	G
25	BA	215	G
25	BA	216	A
25	BA	217	G
25	BA	221	A
25	BA	222	A
25	BA	224	G
25	BA	228	A
25	BA	229	A
25	BA	233	A
25	BA	248	G
25	BA	250	G
25	BA	252	G
25	BA	259	G
25	BA	264	C
25	BA	265	A
25	BA	271(C)	C
25	BA	271(D)	G
25	BA	271(J)	C
25	BA	271(K)	U
25	BA	271(L)	U
25	BA	271(M)	G
25	BA	271(N)	U
25	BA	271(P)	C
25	BA	271(T)	C
25	BA	271(U)	G
25	BA	271(Y)	U
25	BA	271(Z)	C
25	BA	272	G
25	BA	272(G)	C
25	BA	272(H)	C
25	BA	272(I)	U

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Mol	Chain	Res	Type
25	BA	272(J)	C
25	BA	274	G
25	BA	275	G
25	BA	280	C
25	BA	288	C
25	BA	289	A
25	BA	298	G
25	BA	310	A
25	BA	311	A
25	BA	320	A
25	BA	324	A
25	BA	327	G
25	BA	329	G
25	BA	330	A
25	BA	333	G
25	BA	334	C
25	BA	335	C
25	BA	342	G
25	BA	345	A
25	BA	346	A
25	BA	349	G
25	BA	352	G
25	BA	353	G
25	BA	358	U
25	BA	360	G
25	BA	362	U
25	BA	363	G
25	BA	363(A)	A
25	BA	363(B)	G
25	BA	363(E)	U
25	BA	372	G
25	BA	374	A
25	BA	386	G
25	BA	387	U
25	BA	388	G
25	BA	389	G
25	BA	396	G
25	BA	405	U
25	BA	407	G
25	BA	411	G
25	BA	416	C
25	BA	428	A

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Mol	Chain	Res	Type
25	BA	438	G
25	BA	441	U
25	BA	442	G
25	BA	443	A
25	BA	444	C
25	BA	448	U
25	BA	452	G
25	BA	454	A
25	BA	457	A
25	BA	470	A
25	BA	473	G
25	BA	479	A
25	BA	480	A
25	BA	481	G
25	BA	488	G
25	BA	494	G
25	BA	504	U
25	BA	505	A
25	BA	508	G
25	BA	510	C
25	BA	513	A
25	BA	517	C
25	BA	528	A
25	BA	529	A
25	BA	530	G
25	BA	531	C
25	BA	532	A
25	BA	533	G
25	BA	543	C
25	BA	548	A
25	BA	549	G
25	BA	551	G
25	BA	563	G
25	BA	565	C
25	BA	571	A
25	BA	573	G
25	BA	574	C
25	BA	575	A
25	BA	584	C
25	BA	586	A
25	BA	587	C
25	BA	592	G

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Mol	Chain	Res	Type
25	BA	593	G
25	BA	604	G
25	BA	606	U
25	BA	607	U
25	BA	609	A
25	BA	613	G
25	BA	614	U
25	BA	614(B)	G
25	BA	615	G
25	BA	620	G
25	BA	621	A
25	BA	622	G
25	BA	624	C
25	BA	627	A
25	BA	631	A
25	BA	637	A
25	BA	645	C
25	BA	646	A
25	BA	647	G
25	BA	652	C
25	BA	669	G
25	BA	685	A
25	BA	686	G
25	BA	708	C
25	BA	715	G
25	BA	721	C
25	BA	722	A
25	BA	729	G
25	BA	730	C
25	BA	738	G
25	BA	746	A
25	BA	747	U
25	BA	764	A
25	BA	765	G
25	BA	775	G
25	BA	776	G
25	BA	777	A
25	BA	782	A
25	BA	784	A
25	BA	785	G
25	BA	790	C
25	BA	791	C

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Mol	Chain	Res	Type
25	BA	792	G
25	BA	805	G
25	BA	812	C
25	BA	819	A
25	BA	827	U
25	BA	828	U
25	BA	830	G
25	BA	836	G
25	BA	854	G
25	BA	858	U
25	BA	859	G
25	BA	878	A
25	BA	886	C
25	BA	888	C
25	BA	890	A
25	BA	896	A
25	BA	897	C
25	BA	900	A
25	BA	901	A
25	BA	906	G
25	BA	907	U
25	BA	910	A
25	BA	917	A
25	BA	919	G
25	BA	932	G
25	BA	933	A
25	BA	934	G
25	BA	941	A
25	BA	945	A
25	BA	946	G
25	BA	958	U
25	BA	961	C
25	BA	973	A
25	BA	974	G
25	BA	975	C
25	BA	983	A
25	BA	991	C
25	BA	996	A
25	BA	997	G
25	BA	999	U
25	BA	1012	U
25	BA	1013	C

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Mol	Chain	Res	Type
25	BA	1022	G
25	BA	1023	U
25	BA	1025	G
25	BA	1026	U
25	BA	1027	A
25	BA	1033	U
25	BA	1034	G
25	BA	1038	C
25	BA	1039	G
25	BA	1040	C
25	BA	1042	G
25	BA	1045	A
25	BA	1046	A
25	BA	1047	G
25	BA	1048	A
25	BA	1049	C
25	BA	1050	A
25	BA	1053	C
25	BA	1054	A
25	BA	1055	G
25	BA	1057	A
25	BA	1058	G
25	BA	1059	G
25	BA	1060	U
25	BA	1063	G
25	BA	1071	G
25	BA	1072	C
25	BA	1073	A
25	BA	1074	G
25	BA	1075	C
25	BA	1076	C
25	BA	1077	A
25	BA	1078	U
25	BA	1079	C
25	BA	1083	U
25	BA	1087	G
25	BA	1088	A
25	BA	1089	G
25	BA	1090	U
25	BA	1092	C
25	BA	1093	G
25	BA	1094	U

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Mol	Chain	Res	Type
25	BA	1096	A
25	BA	1097	U
25	BA	1098	A
25	BA	1099	G
25	BA	1100	C
25	BA	1101	U
25	BA	1106	G
25	BA	1107	G
25	BA	1110	G
25	BA	1111	A
25	BA	1112	G
25	BA	1113	U
25	BA	1114	G
25	BA	1115	G
25	BA	1116	C
25	BA	1122	G
25	BA	1128	A
25	BA	1129	A
25	BA	1135	C
25	BA	1136	G
25	BA	1139	G
25	BA	1142	U
25	BA	1142(A)	A
25	BA	1143	A
25	BA	1148	A
25	BA	1151	G
25	BA	1155	A
25	BA	1168	G
25	BA	1171	G
25	BA	1173	G
25	BA	1174	A
25	BA	1175	U
25	BA	1176	G
25	BA	1177	A
25	BA	1179	C
25	BA	1180	C
25	BA	1187	G
25	BA	1193	G
25	BA	1194	A
25	BA	1195	G
25	BA	1210	A
25	BA	1211	U

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Mol	Chain	Res	Type
25	BA	1218	C
25	BA	1220	A
25	BA	1235	G
25	BA	1237	A
25	BA	1238	G
25	BA	1242	A
25	BA	1244	G
25	BA	1246	A
25	BA	1247	A
25	BA	1249	U
25	BA	1253	A
25	BA	1256	G
25	BA	1263	U
25	BA	1271	G
25	BA	1272	A
25	BA	1273	U
25	BA	1281	G
25	BA	1284	A
25	BA	1288	U
25	BA	1289	C
25	BA	1300	U
25	BA	1301	A
25	BA	1302	A
25	BA	1306	C
25	BA	1308	A
25	BA	1329	U
25	BA	1338	G
25	BA	1344	G
25	BA	1345	C
25	BA	1347	G
25	BA	1349	A
25	BA	1350	C
25	BA	1358	G
25	BA	1359	A
25	BA	1365	A
25	BA	1372	U
25	BA	1380	G
25	BA	1384	A
25	BA	1385	G
25	BA	1390	U
25	BA	1392	A
25	BA	1396	U

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Mol	Chain	Res	Type
25	BA	1397	U
25	BA	1406	U
25	BA	1407	C
25	BA	1415	U
25	BA	1416	G
25	BA	1420	U
25	BA	1428	C
25	BA	1437	C
25	BA	1445	A
25	BA	1449	A
25	BA	1450	G
25	BA	1453	U
25	BA	1459	G
25	BA	1467	C
25	BA	1471	A
25	BA	1474	C
25	BA	1475	G
25	BA	1478	G
25	BA	1480	G
25	BA	1482	G
25	BA	1485	G
25	BA	1488	G
25	BA	1490	A
25	BA	1491	G
25	BA	1493	C
25	BA	1494	A
25	BA	1495	A
25	BA	1496	A
25	BA	1497	U
25	BA	1498	C
25	BA	1502	C
25	BA	1503	U
25	BA	1505	C
25	BA	1506	C
25	BA	1508	A
25	BA	1509	C
25	BA	1509(A)	A
25	BA	1512	U
25	BA	1514	U
25	BA	1519	G
25	BA	1523	U
25	BA	1525	G

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Mol	Chain	Res	Type
25	BA	1532	C
25	BA	1539	G
25	BA	1540	U
25	BA	1541	G
25	BA	1542	A
25	BA	1543	C
25	BA	1544	A
25	BA	1545	A
25	BA	1547	C
25	BA	1549	C
25	BA	1554	A
25	BA	1558	A
25	BA	1559	G
25	BA	1566	A
25	BA	1569	A
25	BA	1572	A
25	BA	1578	U
25	BA	1579	A
25	BA	1580	A
25	BA	1581	G
25	BA	1582	C
25	BA	1584	C
25	BA	1587	A
25	BA	1588	C
25	BA	1598	C
25	BA	1608	A
25	BA	1609	A
25	BA	1610	A
25	BA	1616	A
25	BA	1617	C
25	BA	1618	A
25	BA	1622	G
25	BA	1624	G
25	BA	1647	G
25	BA	1648	C
25	BA	1652	A
25	BA	1653	G
25	BA	1654	A
25	BA	1655	A
25	BA	1672	C
25	BA	1674	G
25	BA	1678	G

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Mol	Chain	Res	Type
25	BA	1681	G
25	BA	1686	C
25	BA	1695	G
25	BA	1696	G
25	BA	1701	A
25	BA	1722	A
25	BA	1739	U
25	BA	1740	G
25	BA	1741	A
25	BA	1742	G
25	BA	1744	C
25	BA	1745	C
25	BA	1745(A)	C
25	BA	1747	G
25	BA	1750	G
25	BA	1756	G
25	BA	1762	A
25	BA	1763	G
25	BA	1764	G
25	BA	1769	G
25	BA	1773	A
25	BA	1780	A
25	BA	1786	A
25	BA	1791	A
25	BA	1799	G
25	BA	1800	C
25	BA	1801	G
25	BA	1802	A
25	BA	1810	A
25	BA	1816	G
25	BA	1819	A
25	BA	1820	U
25	BA	1829	A
25	BA	1834	U
25	BA	1835	G
25	BA	1838	C
25	BA	1839	G
25	BA	1843	C
25	BA	1847	A
25	BA	1848	A
25	BA	1858	G
25	BA	1859	A

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Mol	Chain	Res	Type
25	BA	1864	U
25	BA	1865	G
25	BA	1876	A
25	BA	1877	A
25	BA	1878	G
25	BA	1880	C
25	BA	1881	C
25	BA	1882	C
25	BA	1885	A
25	BA	1888	G
25	BA	1889	A
25	BA	1900	A
25	BA	1907	G
25	BA	1913	A
25	BA	1914	C
25	BA	1915	U
25	BA	1919	A
25	BA	1924	C
25	BA	1925	C
25	BA	1930	G
25	BA	1936	A
25	BA	1938	A
25	BA	1944	U
25	BA	1947	C
25	BA	1955	U
25	BA	1963	U
25	BA	1964	G
25	BA	1965	C
25	BA	1967	C
25	BA	1969	A
25	BA	1970	A
25	BA	1971	A
25	BA	1972	A
25	BA	1978	A
25	BA	1982	C
25	BA	1987	G
25	BA	1991	U
25	BA	1992	G
25	BA	1993	U
25	BA	1996	C
25	BA	1997	G
25	BA	2020	A

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Mol	Chain	Res	Type
25	BA	2021	C
25	BA	2023	G
25	BA	2026	C
25	BA	2027	G
25	BA	2031	A
25	BA	2032	G
25	BA	2033	A
25	BA	2036	C
25	BA	2039	C
25	BA	2043	C
25	BA	2049	G
25	BA	2051	A
25	BA	2055	C
25	BA	2056	G
25	BA	2060	A
25	BA	2061	G
25	BA	2062	A
25	BA	2069	G
25	BA	2070	G
25	BA	2095	C
25	BA	2096	U
25	BA	2100	G
25	BA	2101	G
25	BA	2102	U
25	BA	2103	C
25	BA	2104	G
25	BA	2106	G
25	BA	2107	C
25	BA	2108	C
25	BA	2113	U
25	BA	2115	G
25	BA	2116	G
25	BA	2122	U
25	BA	2123	G
25	BA	2126	A
25	BA	2127	G
25	BA	2131	G
25	BA	2137	C
25	BA	2138	C
25	BA	2140	C
25	BA	2141	G
25	BA	2142	C

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Mol	Chain	Res	Type
25	BA	2145	C
25	BA	2146	C
25	BA	2147	G
25	BA	2148	G
25	BA	2151	G
25	BA	2152	G
25	BA	2153	G
25	BA	2154	G
25	BA	2156	G
25	BA	2158	A
25	BA	2159	G
25	BA	2163	C
25	BA	2172	U
25	BA	2173	A
25	BA	2178	C
25	BA	2179	C
25	BA	2180	U
25	BA	2182	G
25	BA	2183	C
25	BA	2186	G
25	BA	2187	G
25	BA	2191	G
25	BA	2192	G
25	BA	2193	G
25	BA	2194	G
25	BA	2198	A
25	BA	2199	A
25	BA	2201	C
25	BA	2202	C
25	BA	2206	G
25	BA	2207	G
25	BA	2208	A
25	BA	2218	U
25	BA	2219	G
25	BA	2225	A
25	BA	2226	C
25	BA	2232	U
25	BA	2238	G
25	BA	2239	G
25	BA	2243	U
25	BA	2267	A
25	BA	2268	A

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Mol	Chain	Res	Type
25	BA	2275	C
25	BA	2276	G
25	BA	2283	C
25	BA	2287	A
25	BA	2297	C
25	BA	2301	C
25	BA	2302	G
25	BA	2303	G
25	BA	2305	A
25	BA	2307	G
25	BA	2308	G
25	BA	2309	A
25	BA	2310	A
25	BA	2312	U
25	BA	2316	C
25	BA	2318	G
25	BA	2319	G
25	BA	2320	A
25	BA	2321	G
25	BA	2324	C
25	BA	2325	G
25	BA	2334	G
25	BA	2336	A
25	BA	2342	C
25	BA	2347	C
25	BA	2350	C
25	BA	2361	A
25	BA	2372	G
25	BA	2383	G
25	BA	2385	C
25	BA	2386	C
25	BA	2393	A
25	BA	2394	C
25	BA	2402	C
25	BA	2406	U
25	BA	2410	G
25	BA	2418	A
25	BA	2423	U
25	BA	2424	C
25	BA	2425	A
25	BA	2429	G
25	BA	2430	A

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Mol	Chain	Res	Type
25	BA	2431	U
25	BA	2434	A
25	BA	2435	A
25	BA	2439	A
25	BA	2440	C
25	BA	2441	C
25	BA	2442	C
25	BA	2447	G
25	BA	2448	A
25	BA	2469	A
25	BA	2470	G
25	BA	2471	C
25	BA	2472	G
25	BA	2476	A
25	BA	2477	C
25	BA	2478	A
25	BA	2491	U
25	BA	2496	C
25	BA	2502	G
25	BA	2505	G
25	BA	2508	G
25	BA	2515	C
25	BA	2518	A
25	BA	2520	C
25	BA	2529	G
25	BA	2542	A
25	BA	2543	G
25	BA	2552	U
25	BA	2554	U
25	BA	2556	C
25	BA	2564	A
25	BA	2566	A
25	BA	2567	G
25	BA	2572	A
25	BA	2573	C
25	BA	2576	G
25	BA	2581	G
25	BA	2582	G
25	BA	2585	U
25	BA	2586	C
25	BA	2602	A
25	BA	2603	G

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Mol	Chain	Res	Type
25	BA	2604	U
25	BA	2609	U
25	BA	2610	C
25	BA	2611	U
25	BA	2612	C
25	BA	2615	U
25	BA	2630	G
25	BA	2634	G
25	BA	2655	G
25	BA	2656	U
25	BA	2669	G
25	BA	2670	A
25	BA	2673	G
25	BA	2690	C
25	BA	2691	C
25	BA	2712	U
25	BA	2712(A)	A
25	BA	2713	A
25	BA	2726	U
25	BA	2730	C
25	BA	2733	A
25	BA	2748	A
25	BA	2755	C
25	BA	2757	A
25	BA	2758	A
25	BA	2760	C
25	BA	2762	G
25	BA	2764	A
25	BA	2765	A
25	BA	2766	G
25	BA	2778	A
25	BA	2779	U
25	BA	2780	G
25	BA	2789	C
25	BA	2790	A
25	BA	2791	C
25	BA	2793	G
25	BA	2794	C
25	BA	2795	G
25	BA	2801(A)	A
25	BA	2802	G
25	BA	2803	C

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Mol	Chain	Res	Type
25	BA	2804	C
25	BA	2808	U
25	BA	2820	A
25	BA	2821	A
25	BA	2835	A
25	BA	2842	G
25	BA	2843	G
25	BA	2854	G
25	BA	2863	C
25	BA	2872	G
25	BA	2880	C
25	BA	2883	A
25	BA	2889	C
25	BA	2893	G
25	BA	2894	G
25	BA	2896	C
26	BB	2	C
26	BB	3	C
26	BB	5	C
26	BB	9	G
26	BB	12	C
26	BB	13	A
26	BB	15	A
26	BB	16	G
26	BB	17	C
26	BB	25	A
26	BB	26	A
26	BB	29	A
26	BB	32	C
26	BB	34	U
26	BB	40	U
26	BB	41	U
26	BB	42	C
26	BB	43	C
26	BB	44	G
26	BB	47	C
26	BB	50	G
26	BB	53	A
26	BB	56	G
26	BB	67	G
26	BB	73	A
26	BB	75	G

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Mol	Chain	Res	Type
26	BB	81	G
26	BB	99	G
26	BB	102	A
26	BB	106	G
26	BB	109	C
26	BB	110	G
26	BB	116	G
26	BB	118	G

All (208) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	5	U
1	AA	30	U
1	AA	49	U
1	AA	60	A
1	AA	79	G
1	AA	108	G
1	AA	109	A
1	AA	115	G
1	AA	121	C
1	AA	149	A
1	AA	173	U
1	AA	243	A
1	AA	250	A
1	AA	251	G
1	AA	266	G
1	AA	305	G
1	AA	328	C
1	AA	353	A
1	AA	428	G
1	AA	496	A
1	AA	509	A
1	AA	533	A
1	AA	560	U
1	AA	575	G
1	AA	576	G
1	AA	587	G
1	AA	687	A
1	AA	748	C
1	AA	766	A
1	AA	785	G

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Mol	Chain	Res	Type
1	AA	793	U
1	AA	913	A
1	AA	931	C
1	AA	971	G
1	AA	973	G
1	AA	983	A
1	AA	992	U
1	AA	1049	U
1	AA	1067	A
1	AA	1086	U
1	AA	1124	G
1	AA	1133	G
1	AA	1135	U
1	AA	1136	U
1	AA	1138	G
1	AA	1139	G
1	AA	1145	C
1	AA	1181	G
1	AA	1212	U
1	AA	1225	A
1	AA	1257	U
1	AA	1280	A
1	AA	1285	A
1	AA	1300	G
1	AA	1319	A
1	AA	1332	A
1	AA	1337	G
1	AA	1397	C
1	AA	1442	G
1	AA	1447	A
1	AA	1498	U
1	AA	1503	A
1	AA	1504	G
1	AA	1505	G
1	AA	1533	C
2	AV	7	A
2	AV	18	G
2	AV	19	G
2	AV	28	G
2	AV	34	G
2	AV	35	A
2	AV	43	C

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Mol	Chain	Res	Type
2	AV	57	G
2	AV	72	C
25	BA	27	G
25	BA	49	A
25	BA	71	A
25	BA	74	A
25	BA	102	G
25	BA	119	A
25	BA	128	C
25	BA	196	A
25	BA	199	A
25	BA	221	A
25	BA	249	C
25	BA	271(U)	G
25	BA	271(Y)	U
25	BA	272(J)	C
25	BA	310	A
25	BA	311	A
25	BA	333	G
25	BA	370	G
25	BA	372	G
25	BA	387	U
25	BA	405	U
25	BA	479	A
25	BA	542	C
25	BA	549	G
25	BA	551	G
25	BA	603	A
25	BA	614(C)	A
25	BA	615	G
25	BA	627	A
25	BA	685	A
25	BA	686	G
25	BA	746	A
25	BA	752	A
25	BA	764	A
25	BA	776	G
25	BA	790	C
25	BA	805	G
25	BA	827	U
25	BA	858	U
25	BA	889	C

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Mol	Chain	Res	Type
25	BA	906	G
25	BA	933	A
25	BA	974	G
25	BA	989	G
25	BA	1022	G
25	BA	1026	U
25	BA	1033	U
25	BA	1048	A
25	BA	1053	C
25	BA	1054	A
25	BA	1057	A
25	BA	1058	G
25	BA	1076	C
25	BA	1087	G
25	BA	1089	G
25	BA	1100	C
25	BA	1128	A
25	BA	1142(A)	A
25	BA	1151	G
25	BA	1162	G
25	BA	1181	C
25	BA	1210	A
25	BA	1237	A
25	BA	1253	A
25	BA	1286	A
25	BA	1300	U
25	BA	1301	A
25	BA	1349	A
25	BA	1379	A
25	BA	1396	U
25	BA	1403	C
25	BA	1494	A
25	BA	1497	U
25	BA	1540	U
25	BA	1543	C
25	BA	1558	A
25	BA	1559	G
25	BA	1608	A
25	BA	1609	A
25	BA	1610	A
25	BA	1617	C
25	BA	1653	G

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Mol	Chain	Res	Type
25	BA	1740	G
25	BA	1763	G
25	BA	1780	A
25	BA	1784	A
25	BA	1786	A
25	BA	1799	G
25	BA	1819	A
25	BA	1847	A
25	BA	1858	G
25	BA	1888	G
25	BA	1913	A
25	BA	1914	C
25	BA	1943	U
25	BA	1962	C
25	BA	1963	U
25	BA	1970	A
25	BA	1992	G
25	BA	2019	A
25	BA	2031	A
25	BA	2141	G
25	BA	2146	C
25	BA	2179	C
25	BA	2180	U
25	BA	2191	G
25	BA	2207	G
25	BA	2225	A
25	BA	2275	C
25	BA	2282	G
25	BA	2296	U
25	BA	2311	A
25	BA	2318	G
25	BA	2319	G
25	BA	2320	A
25	BA	2402	C
25	BA	2422	A
25	BA	2439	A
25	BA	2497	A
25	BA	2542	A
25	BA	2566	A
25	BA	2581	G
25	BA	2602	A
25	BA	2609	U

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Mol	Chain	Res	Type
25	BA	2611	U
25	BA	2655	G
25	BA	2665	A
25	BA	2689	U
25	BA	2778	A
25	BA	2802	G
26	BB	1	U
26	BB	44	G
26	BB	66	A
26	BB	109	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 139 ligands modelled in this entry, 138 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
60	GCP	AY	702	59	32,34,34	2.04	10 (31%)	49,54,54	2.10	19 (38%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	GCP	AY	702	59	-	2/19/38/38	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	AY	702	GCP	PA-O3A	4.15	1.64	1.59
60	AY	702	GCP	PB-O2B	-4.07	1.46	1.56
60	AY	702	GCP	C2'-C3'	-4.02	1.42	1.53
60	AY	702	GCP	PG-O2G	-3.66	1.46	1.55
60	AY	702	GCP	PG-O3G	-3.29	1.47	1.55
60	AY	702	GCP	PB-O3A	3.03	1.61	1.58
60	AY	702	GCP	C5-C6	-2.94	1.33	1.44
60	AY	702	GCP	C5-N7	-2.82	1.33	1.39
60	AY	702	GCP	C4-N9	-2.16	1.32	1.38
60	AY	702	GCP	PB-O1B	-2.05	1.46	1.51

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	AY	702	GCP	O4'-C4'-C5'	-4.85	93.80	109.33
60	AY	702	GCP	C2-N3-C4	4.79	120.56	112.30
60	AY	702	GCP	O1G-PG-C3B	-3.82	103.03	111.37
60	AY	702	GCP	C5-C4-N3	-3.67	122.55	128.39
60	AY	702	GCP	C2'-C3'-C4'	-3.67	95.53	102.61
60	AY	702	GCP	O2B-PB-O1B	2.99	119.68	109.95
60	AY	702	GCP	N2-C2-N1	2.97	123.02	116.76
60	AY	702	GCP	C2-N1-C6	-2.90	119.85	125.11
60	AY	702	GCP	N9-C8-N7	-2.76	108.28	113.40
60	AY	702	GCP	N1-C2-N3	-2.75	118.28	123.32
60	AY	702	GCP	C1'-N9-C4	-2.73	118.43	126.49
60	AY	702	GCP	O4'-C1'-N9	2.68	114.43	108.36
60	AY	702	GCP	O2'-C2'-C3'	-2.68	103.24	111.82
60	AY	702	GCP	O3G-PG-O2G	2.54	115.20	107.96
60	AY	702	GCP	C1'-N9-C8	2.49	133.80	126.73
60	AY	702	GCP	O3'-C3'-C2'	-2.46	103.92	111.82
60	AY	702	GCP	C8-N7-C5	2.15	108.08	104.26
60	AY	702	GCP	PB-O3A-PA	-2.10	125.52	132.37
60	AY	702	GCP	O4'-C1'-C2'	-2.09	102.14	106.62

There are no chirality outliers.

All (2) torsion outliers are listed below:

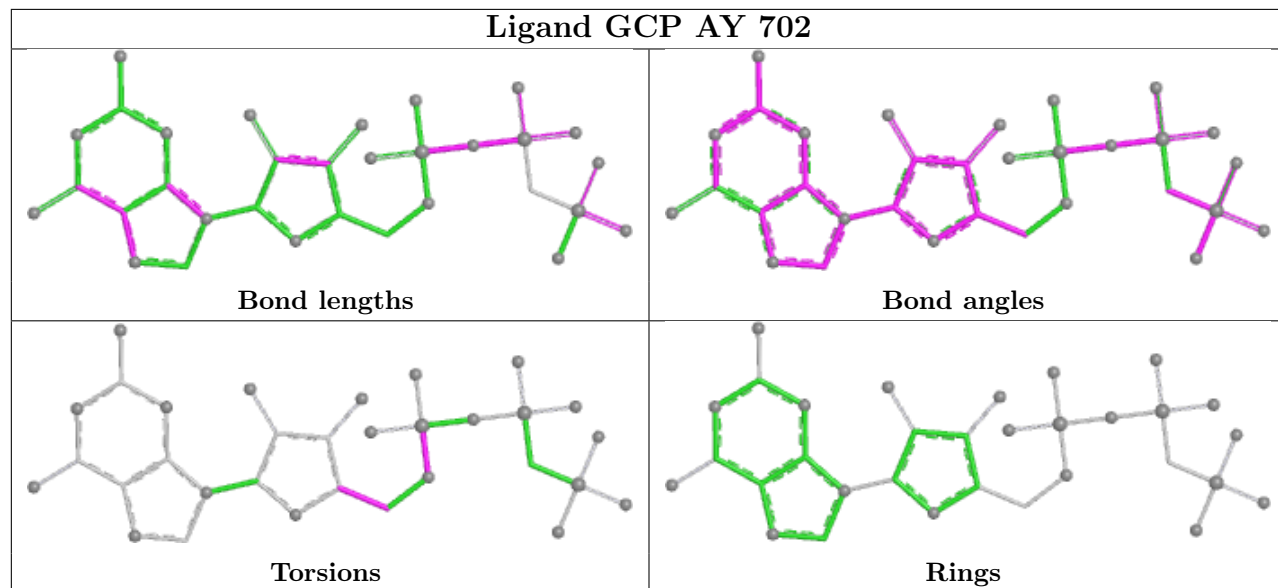
Mol	Chain	Res	Type	Atoms
60	AY	702	GCP	C5'-O5'-PA-O1A
60	AY	702	GCP	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	AY	702	GCP	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
25	BA	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BA	2506:U	O3'	2507:C	P	1.76

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AA	1514/1516 (99%)	-0.28	52 (3%) 48 38	9, 32, 113, 247	0
2	AV	74/76 (97%)	0.23	3 (4%) 41 32	23, 54, 91, 134	0
3	AX	6/25 (24%)	0.09	1 (16%) 4 3	18, 22, 53, 75	0
4	AJ	98/98 (100%)	1.09	24 (24%) 2 1	22, 49, 98, 108	0
5	AK	119/119 (100%)	0.46	6 (5%) 34 27	18, 41, 65, 104	0
6	AL	124/124 (100%)	0.37	12 (9%) 13 10	16, 32, 64, 107	0
7	AM	124/124 (100%)	1.56	34 (27%) 1 1	31, 69, 118, 161	0
8	AN	60/60 (100%)	0.49	7 (11%) 9 7	21, 33, 69, 83	0
9	AO	88/88 (100%)	0.26	2 (2%) 61 52	24, 41, 67, 73	0
10	AP	83/83 (100%)	0.35	0 100 100	29, 40, 60, 112	0
11	AQ	99/99 (100%)	-0.03	0 100 100	20, 34, 53, 59	0
12	AR	70/70 (100%)	0.26	4 (5%) 29 22	23, 41, 75, 92	0
13	AS	78/78 (100%)	1.29	17 (21%) 2 2	39, 69, 107, 121	0
14	AT	99/99 (100%)	0.63	14 (14%) 6 4	24, 39, 78, 90	0
15	AB	234/234 (100%)	0.89	43 (18%) 3 3	21, 55, 117, 134	0
16	AC	206/206 (100%)	0.27	10 (4%) 35 27	22, 41, 67, 103	0
17	AD	208/208 (100%)	0.64	15 (7%) 21 15	26, 49, 75, 90	0
18	AE	150/150 (100%)	-0.10	0 100 100	19, 30, 54, 81	0
19	AF	101/101 (100%)	0.41	5 (4%) 34 27	28, 52, 75, 87	0
20	AG	155/155 (100%)	0.90	25 (16%) 4 4	31, 53, 104, 148	0
21	AH	138/138 (100%)	-0.08	2 (1%) 73 67	19, 32, 55, 84	0
22	AI	127/127 (100%)	0.67	9 (7%) 22 16	21, 51, 82, 108	0
23	AY	622/680 (91%)	0.60	46 (7%) 20 14	30, 55, 97, 131	0
24	AU	24/24 (100%)	1.24	4 (16%) 4 3	33, 48, 65, 83	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	BA	2859/2915 (98%)	-0.35	107 (3%) 45 35	7, 27, 90, 267	0
26	BB	119/122 (97%)	0.42	3 (2%) 58 49	26, 63, 95, 134	0
27	BN	138/140 (98%)	0.53	16 (11%) 9 7	18, 35, 66, 80	0
28	BO	122/122 (100%)	-0.08	0 100 100	18, 31, 49, 60	0
29	BP	146/150 (97%)	1.71	43 (29%) 1 1	18, 55, 94, 127	0
30	BQ	141/141 (100%)	0.32	10 (7%) 22 16	23, 35, 64, 112	0
31	BR	117/118 (99%)	0.35	10 (8%) 16 12	15, 33, 58, 75	0
32	BS	98/112 (87%)	2.10	44 (44%) 0 0	50, 80, 106, 125	0
33	BT	137/146 (93%)	1.27	37 (27%) 1 1	23, 50, 135, 151	0
34	BU	117/118 (99%)	0.36	13 (11%) 10 8	16, 29, 58, 85	0
35	BV	101/101 (100%)	0.85	16 (15%) 5 4	15, 49, 77, 97	0
36	BW	113/113 (100%)	0.17	5 (4%) 39 30	18, 29, 67, 122	0
37	BX	92/96 (95%)	0.23	5 (5%) 31 23	20, 34, 54, 61	0
38	BY	100/110 (90%)	2.24	47 (47%) 0 0	29, 56, 122, 168	0
39	BZ	198/206 (96%)	1.00	29 (14%) 6 4	33, 59, 92, 103	0
40	B0	84/85 (98%)	0.69	10 (11%) 9 7	26, 41, 96, 133	0
41	B1	93/98 (94%)	0.52	9 (9%) 13 10	18, 33, 72, 121	0
42	B2	71/72 (98%)	0.55	5 (7%) 22 16	30, 49, 82, 100	0
43	BD	271/276 (98%)	0.02	17 (6%) 26 19	9, 20, 46, 89	0
44	B3	59/60 (98%)	0.39	4 (6%) 23 17	24, 40, 76, 137	0
45	B4	30/71 (42%)	2.87	23 (76%) 0 0	102, 130, 156, 174	0
46	B5	59/60 (98%)	1.12	15 (25%) 1 1	10, 35, 98, 134	0
47	B6	44/54 (81%)	2.55	23 (52%) 0 0	34, 59, 99, 109	0
48	B7	48/49 (97%)	0.17	5 (10%) 11 9	10, 19, 59, 101	0
49	B8	63/65 (96%)	1.27	12 (19%) 3 3	22, 37, 61, 118	0
50	B9	36/37 (97%)	1.06	6 (16%) 4 3	26, 44, 69, 77	0
51	BC	225/229 (98%)	0.96	29 (12%) 7 5	36, 64, 111, 132	0
52	BE	204/206 (99%)	0.57	34 (16%) 4 3	14, 32, 85, 109	0
53	BF	207/210 (98%)	0.68	29 (14%) 6 5	15, 37, 103, 187	0
54	BG	181/182 (99%)	2.23	96 (53%) 0 0	67, 101, 130, 147	0
55	BH	173/180 (96%)	1.22	27 (15%) 5 4	35, 60, 95, 159	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
56	BK	127/147 (86%)	3.74	119 (93%) 0 0	127, 181, 237, 263	0
57	BJ	130/130 (100%)	3.08	105 (80%) 0 0	74, 106, 140, 195	0
58	BL	0/125	-	-	-	-
All	All	11304/11728 (96%)	0.37	1288 (11%) 10 8	7, 40, 108, 267	0

All (1288) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
38	BY	3	VAL	11.3
56	BK	74	ALA	10.9
7	AM	123	ALA	10.6
53	BF	12	LEU	10.3
55	BH	44	VAL	10.3
46	B5	54	GLY	9.4
47	B6	42	TRP	9.1
56	BK	136	VAL	9.1
32	BS	54	LEU	8.8
53	BF	11	VAL	8.7
56	BK	134	MET	8.6
53	BF	24	LEU	8.4
38	BY	28	LYS	8.3
49	B8	64	TYR	8.2
56	BK	52	ILE	8.0
52	BE	76	ARG	7.8
56	BK	135	GLY	7.8
17	AD	9	CYS	7.7
57	BJ	87	ALA	7.5
46	B5	53	ALA	7.3
7	AM	122	LYS	7.3
5	AK	128	ALA	7.3
8	AN	2	ALA	7.2
7	AM	124	PRO	7.2
55	BH	45	VAL	7.2
38	BY	51	VAL	7.1
57	BJ	88	ALA	7.1
7	AM	84	ILE	7.1
47	B6	43	CYS	7.1
40	B0	7	LEU	6.9
56	BK	105	LEU	6.9
13	AS	10	PHE	6.8
35	BV	36	PRO	6.8

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Mol	Chain	Res	Type	RSRZ
29	BP	27	HIS	6.8
33	BT	105	LEU	6.8
6	AL	28	LYS	6.7
49	B8	34	TRP	6.7
38	BY	53	PRO	6.7
54	BG	3	LEU	6.7
56	BK	77	LEU	6.6
30	BQ	140	ALA	6.6
57	BJ	86	ALA	6.6
45	B4	36	VAL	6.6
27	BN	3	THR	6.5
20	AG	83	ALA	6.5
33	BT	32	TYR	6.4
29	BP	33	ARG	6.4
41	B1	95	LEU	6.3
56	BK	13	PRO	6.3
57	BJ	30	ALA	6.3
56	BK	84	LEU	6.3
17	AD	26	CYS	6.3
32	BS	30	ARG	6.3
53	BF	7	TYR	6.2
46	B5	58	LEU	6.2
40	B0	4	LYS	6.2
57	BJ	52	ALA	6.2
49	B8	63	PRO	6.2
53	BF	25	PRO	6.1
30	BQ	141	GLN	6.1
20	AG	82	GLY	6.1
43	BD	35	LYS	6.1
25	BA	547	A	6.0
54	BG	129	GLY	6.0
4	AJ	55	LYS	6.0
15	AB	133	LYS	6.0
21	AH	1	MET	6.0
48	B7	47	ARG	6.0
47	B6	39	TYR	6.0
56	BK	101	TRP	5.9
53	BF	10	PRO	5.9
17	AD	12	CYS	5.9
48	B7	48	LYS	5.9
56	BK	11	GLN	5.9
38	BY	60	PHE	5.9

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Mol	Chain	Res	Type	RSRZ
46	B5	2	ALA	5.9
57	BJ	66	ALA	5.9
40	B0	5	LYS	5.9
35	BV	20	LEU	5.8
7	AM	121	LYS	5.7
56	BK	12	LEU	5.7
27	BN	4	TYR	5.7
29	BP	110	TYR	5.7
38	BY	61	ILE	5.7
41	B1	85	LEU	5.7
38	BY	58	GLY	5.7
27	BN	68	GLU	5.6
15	AB	237	ALA	5.6
56	BK	130	SER	5.6
56	BK	53	VAL	5.6
56	BK	133	SER	5.6
57	BJ	7	ALA	5.6
57	BJ	89	ALA	5.6
57	BJ	8	ALA	5.6
55	BH	172	LYS	5.5
32	BS	14	VAL	5.5
29	BP	65	ARG	5.5
38	BY	17	SER	5.5
38	BY	49	VAL	5.4
52	BE	75	VAL	5.4
32	BS	12	PHE	5.4
55	BH	43	VAL	5.4
7	AM	7	VAL	5.4
20	AG	81	GLY	5.4
23	AY	582	PHE	5.4
32	BS	11	LYS	5.4
31	BR	105	ARG	5.4
38	BY	82	PRO	5.4
5	AK	127	LYS	5.3
57	BJ	55	ALA	5.3
34	BU	91	ASP	5.3
38	BY	2	ARG	5.3
57	BJ	50	ALA	5.3
57	BJ	53	ALA	5.3
56	BK	26	ALA	5.3
43	BD	25	THR	5.3
40	B0	3	HIS	5.2

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Mol	Chain	Res	Type	RSRZ
37	BX	94	GLY	5.2
47	B6	22	ALA	5.2
56	BK	78	ILE	5.2
29	BP	107	LYS	5.2
56	BK	132	ARG	5.2
5	AK	129	SER	5.2
57	BJ	51	ALA	5.2
31	BR	11	ASN	5.1
56	BK	75	SER	5.1
57	BJ	37	ALA	5.1
39	BZ	166	SER	5.1
52	BE	54	GLN	5.1
25	BA	2803	C	5.0
56	BK	81	ALA	5.0
57	BJ	54	ALA	5.0
56	BK	140	GLY	5.0
15	AB	15	VAL	5.0
38	BY	52	SER	5.0
8	AN	13	THR	5.0
45	B4	53	THR	5.0
52	BE	61	ARG	5.0
32	BS	16	ASN	5.0
55	BH	170	ARG	5.0
55	BH	168	PRO	5.0
29	BP	62	LEU	5.0
56	BK	10	LEU	4.9
56	BK	76	TYR	4.9
52	BE	77	ILE	4.9
7	AM	10	PRO	4.9
54	BG	12	TYR	4.9
49	B8	35	GLN	4.9
56	BK	82	ALA	4.9
45	B4	37	PRO	4.9
56	BK	22	PRO	4.9
41	B1	84	GLY	4.8
55	BH	169	VAL	4.8
29	BP	16	ARG	4.8
54	BG	141	PHE	4.8
32	BS	58	LEU	4.8
56	BK	107	ILE	4.8
25	BA	2801(A)	A	4.8
15	AB	239	VAL	4.8

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Mol	Chain	Res	Type	RSRZ
54	BG	84	LYS	4.7
25	BA	1076	C	4.7
51	BC	71	GLN	4.7
52	BE	73	GLU	4.7
1	AA	1456	G	4.7
56	BK	68	VAL	4.7
1	AA	532	A	4.7
25	BA	1070	A	4.7
56	BK	16	LYS	4.7
47	B6	36	LEU	4.7
57	BJ	98	ALA	4.7
54	BG	5	VAL	4.7
49	B8	48	PHE	4.7
33	BT	31	SER	4.7
33	BT	91	ARG	4.6
1	AA	1442(A)	G	4.6
20	AG	156	TRP	4.6
47	B6	23	THR	4.6
38	BY	81	LYS	4.6
55	BH	85	LYS	4.6
49	B8	32	LEU	4.6
56	BK	122	ALA	4.6
56	BK	116	ASN	4.6
43	BD	36	PRO	4.6
31	BR	3	HIS	4.6
25	BA	1847	A	4.6
54	BG	156	ASP	4.6
56	BK	72	PRO	4.6
38	BY	98	VAL	4.6
38	BY	4	LYS	4.6
23	AY	39	ILE	4.5
53	BF	207	GLY	4.5
17	AD	31	CYS	4.5
31	BR	2	ARG	4.5
45	B4	50	THR	4.5
57	BJ	59	ALA	4.5
56	BK	115	LEU	4.5
56	BK	111	LYS	4.5
38	BY	5	MET	4.5
25	BA	1495	A	4.5
50	B9	26	ILE	4.4
4	AJ	91	PRO	4.4

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Mol	Chain	Res	Type	RSRZ
52	BE	56	PRO	4.4
57	BJ	26	ALA	4.4
7	AM	8	GLU	4.4
29	BP	18	ARG	4.4
57	BJ	49	ALA	4.4
15	AB	16	HIS	4.4
53	BF	13	SER	4.4
45	B4	61	VAL	4.4
29	BP	15	ARG	4.4
14	AT	74	LYS	4.4
54	BG	2	PRO	4.4
56	BK	19	PRO	4.4
57	BJ	41	ALA	4.4
57	BJ	75	ALA	4.4
57	BJ	84	ALA	4.4
52	BE	72	VAL	4.4
25	BA	508	G	4.4
4	AJ	90	LEU	4.4
29	BP	51	PHE	4.4
52	BE	68	ALA	4.3
57	BJ	116	ALA	4.3
14	AT	75	ASN	4.3
56	BK	120	LEU	4.3
25	BA	275	G	4.3
26	BB	119	G	4.3
33	BT	135	ALA	4.3
56	BK	73	PRO	4.3
54	BG	52	ILE	4.3
25	BA	2602	A	4.3
29	BP	147	LEU	4.3
54	BG	139	LEU	4.3
54	BG	88	ILE	4.3
56	BK	54	PRO	4.3
54	BG	157	ILE	4.3
34	BU	58	ARG	4.3
52	BE	204	ALA	4.3
51	BC	124	GLY	4.3
1	AA	89	C	4.2
15	AB	19	HIS	4.2
57	BJ	83	ALA	4.2
36	BW	112	GLY	4.2
33	BT	38	ASN	4.2

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Mol	Chain	Res	Type	RSRZ
56	BK	126	MET	4.2
1	AA	1138	G	4.2
20	AG	32	ARG	4.2
56	BK	104	VAL	4.2
57	BJ	101	ALA	4.2
43	BD	262	ARG	4.2
6	AL	128	ALA	4.2
39	BZ	168	GLU	4.2
39	BZ	6	LYS	4.2
16	AC	167	TRP	4.2
14	AT	99	LEU	4.2
15	AB	7	VAL	4.2
20	AG	80	VAL	4.2
25	BA	1048	A	4.2
27	BN	138	LEU	4.2
32	BS	101	LEU	4.2
47	B6	52	VAL	4.2
57	BJ	73	ALA	4.2
1	AA	839	U	4.1
25	BA	1060	U	4.1
40	B0	2	ALA	4.1
25	BA	2402	C	4.1
32	BS	92	TYR	4.1
54	BG	146	TYR	4.1
7	AM	6	GLY	4.1
54	BG	80	PHE	4.1
31	BR	8	ARG	4.1
15	AB	155	LEU	4.1
52	BE	53	PRO	4.1
57	BJ	24	ALA	4.1
57	BJ	25	ALA	4.1
54	BG	42	GLY	4.1
56	BK	34	ILE	4.1
38	BY	50	ARG	4.1
25	BA	2790	A	4.1
13	AS	5	LEU	4.1
56	BK	51	ALA	4.1
32	BS	89	ARG	4.1
54	BG	82	LEU	4.0
47	B6	27	LYS	4.0
52	BE	67	PHE	4.0
1	AA	470	C	4.0

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Mol	Chain	Res	Type	RSRZ
55	BH	6	ARG	4.0
2	AV	20	U	4.0
50	B9	20	HIS	4.0
56	BK	21	PRO	4.0
57	BJ	28	ALA	4.0
57	BJ	34	ALA	4.0
46	B5	60	VAL	4.0
53	BF	9	ILE	4.0
56	BK	127	ILE	4.0
32	BS	107	GLU	4.0
30	BQ	18	LYS	4.0
41	B1	81	LYS	4.0
54	BG	86	MET	4.0
30	BQ	136	ALA	3.9
25	BA	2892	A	3.9
15	AB	232	PRO	3.9
14	AT	100	ILE	3.9
57	BJ	82	ALA	3.9
54	BG	67	LYS	3.9
45	B4	58	TYR	3.9
37	BX	3	THR	3.9
56	BK	128	ALA	3.9
45	B4	65	CYS	3.9
1	AA	81	U	3.9
52	BE	70	ALA	3.9
56	BK	79	ARG	3.9
57	BJ	17	ALA	3.9
33	BT	25	GLY	3.9
15	AB	23	ARG	3.9
35	BV	101	GLY	3.8
47	B6	33	LYS	3.8
38	BY	89	PHE	3.8
15	AB	234	PRO	3.8
33	BT	29	ARG	3.8
52	BE	132	HIS	3.8
6	AL	26	ALA	3.8
57	BJ	6	ALA	3.8
38	BY	88	LYS	3.8
25	BA	2179	C	3.8
51	BC	12	GLU	3.8
46	B5	57	VAL	3.8
56	BK	38	VAL	3.8

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Mol	Chain	Res	Type	RSRZ
15	AB	137	ARG	3.8
53	BF	18	ARG	3.8
57	BJ	57	ALA	3.8
55	BH	175	LYS	3.8
15	AB	122	PHE	3.8
25	BA	274	G	3.8
26	BB	2	C	3.8
1	AA	1447	A	3.8
52	BE	69	LYS	3.8
57	BJ	29	ALA	3.8
52	BE	63	LEU	3.8
25	BA	889	C	3.8
25	BA	1532	C	3.8
33	BT	118	ARG	3.7
53	BF	21	ALA	3.7
57	BJ	10	ALA	3.7
54	BG	128	ARG	3.7
39	BZ	149	SER	3.7
54	BG	106	LEU	3.7
54	BG	117	PHE	3.7
56	BK	117	THR	3.7
56	BK	137	GLU	3.7
32	BS	106	ARG	3.7
47	B6	44	ARG	3.7
29	BP	76	LYS	3.7
47	B6	31	PRO	3.7
51	BC	109	ASP	3.7
57	BJ	103	ALA	3.7
40	B0	6	GLY	3.7
47	B6	45	LYS	3.7
32	BS	98	VAL	3.7
25	BA	1111	A	3.7
53	BF	14	PRO	3.7
22	AI	3	GLN	3.7
33	BT	130	ALA	3.7
57	BJ	42	ALA	3.7
22	AI	128	ARG	3.7
16	AC	207	VAL	3.7
34	BU	90	VAL	3.7
56	BK	18	THR	3.7
56	BK	138	VAL	3.7
29	BP	72	PRO	3.6

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Mol	Chain	Res	Type	RSRZ
7	AM	120	LYS	3.6
40	B0	74	ARG	3.6
56	BK	113	PRO	3.6
25	BA	2896	C	3.6
15	AB	14	GLY	3.6
56	BK	83	GLY	3.6
22	AI	88	TYR	3.6
56	BK	99	ILE	3.6
25	BA	2207	G	3.6
25	BA	2795	G	3.6
33	BT	6	LEU	3.6
42	B2	43	GLN	3.6
56	BK	61	ALA	3.6
56	BK	119	ASP	3.6
25	BA	2310	A	3.6
56	BK	56	GLU	3.6
14	AT	73	HIS	3.6
47	B6	46	HIS	3.6
38	BY	87	LYS	3.6
29	BP	61	ARG	3.6
22	AI	126	SER	3.6
14	AT	101	GLY	3.6
17	AD	5	ILE	3.6
52	BE	17	ASP	3.6
1	AA	1492	A	3.6
54	BG	115	ARG	3.5
25	BA	1742	G	3.5
25	BA	2894	G	3.5
38	BY	27	VAL	3.5
39	BZ	202	GLU	3.5
13	AS	32	LYS	3.5
38	BY	101	LYS	3.5
56	BK	20	ALA	3.5
57	BJ	56	ALA	3.5
17	AD	23	GLY	3.5
54	BG	144	ILE	3.5
25	BA	363	G	3.5
38	BY	95	LYS	3.5
15	AB	236	TYR	3.5
57	BJ	85	ALA	3.5
57	BJ	104	ALA	3.5
25	BA	6	A	3.5

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Mol	Chain	Res	Type	RSRZ
55	BH	174	GLY	3.5
56	BK	64	SER	3.5
54	BG	142	PRO	3.5
1	AA	80	G	3.5
25	BA	2166	G	3.5
27	BN	132	ALA	3.5
32	BS	29	PHE	3.5
54	BG	125	PHE	3.5
25	BA	1046	A	3.5
25	BA	1494	A	3.5
35	BV	19	LYS	3.5
43	BD	38	LYS	3.5
51	BC	104	LEU	3.5
4	AJ	35	SER	3.5
54	BG	72	ARG	3.5
23	AY	213	HIS	3.5
30	BQ	74	TYR	3.5
57	BJ	40	ALA	3.5
57	BJ	61	ALA	3.5
33	BT	1	MET	3.4
33	BT	37	GLY	3.4
56	BK	5	VAL	3.4
54	BG	53	LEU	3.4
38	BY	77	PRO	3.4
23	AY	581	ALA	3.4
56	BK	40	ALA	3.4
57	BJ	15	ALA	3.4
46	B5	56	LYS	3.4
51	BC	141	LYS	3.4
48	B7	46	VAL	3.4
56	BK	4	VAL	3.4
56	BK	7	VAL	3.4
54	BG	35	GLU	3.4
1	AA	91	C	3.4
56	BK	50	ASP	3.4
15	AB	136	VAL	3.4
15	AB	238	LEU	3.4
56	BK	121	GLU	3.4
54	BG	50	ALA	3.4
57	BJ	4	ALA	3.4
1	AA	1452	C	3.4
6	AL	91	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
32	BS	61	ASN	3.4
49	B8	49	VAL	3.4
52	BE	88	GLY	3.4
53	BF	132	VAL	3.4
54	BG	111	LEU	3.4
33	BT	115	ARG	3.4
32	BS	105	ALA	3.4
57	BJ	27	ALA	3.4
33	BT	137	LYS	3.4
52	BE	64	LYS	3.4
33	BT	27	THR	3.4
55	BH	83	TYR	3.4
56	BK	67	PHE	3.4
1	AA	1493	A	3.4
5	AK	117	ASN	3.3
39	BZ	191	VAL	3.3
29	BP	48	PRO	3.3
54	BG	87	PRO	3.3
4	AJ	99	LYS	3.3
4	AJ	75	ILE	3.3
23	AY	196	ILE	3.3
57	BJ	105	ALA	3.3
57	BJ	119	ALA	3.3
44	B3	1	MET	3.3
29	BP	71	VAL	3.3
7	AM	125	ARG	3.3
15	AB	132	LYS	3.3
39	BZ	146	ILE	3.3
43	BD	272	ALA	3.3
45	B4	40	ILE	3.3
56	BK	44	ALA	3.3
57	BJ	58	ALA	3.3
13	AS	30	LEU	3.3
56	BK	23	VAL	3.3
20	AG	85	TYR	3.3
41	B1	79	GLY	3.3
56	BK	97	GLY	3.3
20	AG	8	GLU	3.3
56	BK	46	ALA	3.3
25	BA	1063	G	3.3
25	BA	2893	G	3.3
52	BE	59	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
53	BF	205	ARG	3.3
16	AC	154	SER	3.3
25	BA	2180	U	3.3
56	BK	62	ASP	3.3
33	BT	134	GLU	3.3
37	BX	23	GLU	3.3
24	AU	25	LYS	3.3
46	B5	3	LYS	3.3
56	BK	9	LYS	3.3
35	BV	50	PRO	3.3
25	BA	1177	A	3.3
20	AG	153	HIS	3.3
51	BC	142	ALA	3.3
56	BK	123	ALA	3.3
57	BJ	20	ALA	3.3
57	BJ	31	ALA	3.3
32	BS	24	LEU	3.3
47	B6	34	LEU	3.3
1	AA	1039	C	3.3
33	BT	3	ARG	3.3
7	AM	117	VAL	3.3
25	BA	2802	G	3.3
35	BV	48	GLY	3.3
51	BC	121	GLY	3.3
13	AS	28	LYS	3.2
15	AB	22	LYS	3.2
20	AG	57	GLU	3.2
25	BA	271(K)	U	3.2
26	BB	1	U	3.2
24	AU	7	ARG	3.2
33	BT	39	ARG	3.2
55	BH	82	GLY	3.2
56	BK	66	THR	3.2
1	AA	82	U	3.2
56	BK	25	PRO	3.2
55	BH	4	ILE	3.2
53	BF	26	ALA	3.2
57	BJ	13	ALA	3.2
45	B4	47	VAL	3.2
12	AR	88	LYS	3.2
25	BA	548	A	3.2
25	BA	887	A	3.2

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Mol	Chain	Res	Type	RSRZ
50	B9	13	LYS	3.2
4	AJ	100	THR	3.2
1	AA	1532	U	3.2
30	BQ	59	ARG	3.2
25	BA	11	G	3.2
20	AG	13	GLN	3.2
14	AT	96	GLY	3.2
15	AB	18	GLY	3.2
46	B5	50	GLY	3.2
46	B5	59	GLU	3.2
56	BK	48	MET	3.2
8	AN	3	ARG	3.2
19	AF	101	ALA	3.2
25	BA	614(A)	U	3.2
57	BJ	90	ALA	3.2
56	BK	2	LYS	3.2
56	BK	29	GLN	3.2
25	BA	1106	G	3.2
32	BS	108	GLY	3.2
35	BV	49	THR	3.2
7	AM	11	ARG	3.1
23	AY	229	LEU	3.1
47	B6	21	TYR	3.1
56	BK	60	TYR	3.1
57	BJ	5	ALA	3.1
15	AB	230	VAL	3.1
56	BK	85	GLU	3.1
23	AY	567	LEU	3.1
53	BF	128	ALA	3.1
55	BH	176	ALA	3.1
57	BJ	18	ALA	3.1
4	AJ	76	ASN	3.1
15	AB	191	ASP	3.1
51	BC	105	ASP	3.1
56	BK	37	PHE	3.1
54	BG	41	GLN	3.1
35	BV	42	GLY	3.1
7	AM	69	GLU	3.1
29	BP	30	THR	3.1
39	BZ	97	GLU	3.1
54	BG	140	ILE	3.1
33	BT	24	PRO	3.1

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Mol	Chain	Res	Type	RSRZ
46	B5	55	ARG	3.1
51	BC	167	LYS	3.1
7	AM	5	ALA	3.1
57	BJ	23	ALA	3.1
57	BJ	81	ALA	3.1
55	BH	111	HIS	3.1
39	BZ	180	VAL	3.1
54	BG	102	PHE	3.1
25	BA	614(B)	G	3.1
56	BK	31	GLY	3.1
22	AI	12	GLU	3.1
43	BD	271	ILE	3.1
13	AS	81	ARG	3.1
15	AB	21	ARG	3.1
15	AB	96	ARG	3.1
25	BA	645	C	3.1
56	BK	27	LEU	3.1
56	BK	131	ALA	3.1
57	BJ	102	ALA	3.1
45	B4	59	VAL	3.1
56	BK	15	GLY	3.1
1	AA	841	U	3.1
9	AO	88	ARG	3.1
15	AB	10	LEU	3.1
36	BW	113	LYS	3.1
25	BA	34	C	3.1
57	BJ	77	ALA	3.0
20	AG	154	TYR	3.0
27	BN	1	MET	3.0
4	AJ	78	ASN	3.0
5	AK	102	GLY	3.0
45	B4	41	ILE	3.0
17	AD	150	GLU	3.0
33	BT	36	GLU	3.0
43	BD	237	GLU	3.0
1	AA	204	U	3.0
25	BA	1045	A	3.0
57	BJ	132	ALA	3.0
56	BK	41	PHE	3.0
30	BQ	137	TYR	3.0
7	AM	119	GLY	3.0
20	AG	79	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
52	BE	57	LYS	3.0
54	BG	39	ILE	3.0
4	AJ	85	LEU	3.0
32	BS	43	GLU	3.0
39	BZ	190	GLU	3.0
57	BJ	48	ALA	3.0
57	BJ	74	ALA	3.0
56	BK	139	VAL	3.0
25	BA	1062	G	3.0
54	BG	29	TRP	3.0
25	BA	652	C	3.0
25	BA	1075	C	3.0
25	BA	2477	C	3.0
39	BZ	4	ARG	3.0
45	B4	54	LYS	3.0
7	AM	66	LEU	3.0
30	BQ	138	ASP	3.0
47	B6	30	THR	3.0
1	AA	90	U	3.0
57	BJ	63	ALA	3.0
33	BT	33	LYS	3.0
23	AY	201	ILE	3.0
23	AY	563	ILE	3.0
29	BP	148	LEU	3.0
50	B9	12	ASP	3.0
56	BK	114	ASP	3.0
32	BS	100	ALA	3.0
15	AB	140	HIS	3.0
32	BS	15	ARG	2.9
25	BA	2801	A	2.9
14	AT	98	PRO	2.9
35	BV	16	PRO	2.9
43	BD	30	GLU	2.9
45	B4	55	PRO	2.9
32	BS	53	SER	2.9
23	AY	183	MET	2.9
25	BA	352	G	2.9
45	B4	42	CYS	2.9
49	B8	51	ALA	2.9
57	BJ	107	ALA	2.9
1	AA	1086	U	2.9
13	AS	80	TYR	2.9

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Mol	Chain	Res	Type	RSRZ
46	B5	52	TYR	2.9
25	BA	1069	A	2.9
4	AJ	86	MET	2.9
30	BQ	135	ASP	2.9
41	B1	86	SER	2.9
54	BG	4	ASP	2.9
34	BU	96	ALA	2.9
33	BT	35	LYS	2.9
56	BK	118	THR	2.9
43	BD	244	ARG	2.9
23	AY	688	ILE	2.9
56	BK	24	GLY	2.9
46	B5	51	TYR	2.9
52	BE	203	LYS	2.9
56	BK	70	LYS	2.9
4	AJ	92	THR	2.9
23	AY	255	ILE	2.9
25	BA	1026	U	2.9
32	BS	68	GLN	2.9
5	AK	11	LYS	2.9
12	AR	84	LYS	2.9
27	BN	2	LYS	2.9
54	BG	130	ASN	2.9
57	BJ	112	ALA	2.9
57	BJ	129	ALA	2.9
4	AJ	88	LEU	2.9
31	BR	4	LEU	2.9
4	AJ	36	GLY	2.8
38	BY	56	PRO	2.8
54	BG	47	LYS	2.8
1	AA	1001(A)	G	2.8
1	AA	1024	G	2.8
45	B4	38	ALA	2.8
56	BK	47	ASN	2.8
36	BW	111	HIS	2.8
32	BS	82	ILE	2.8
39	BZ	183	LEU	2.8
56	BK	100	THR	2.8
32	BS	96	GLY	2.8
34	BU	118	GLY	2.8
52	BE	65	GLY	2.8
56	BK	49	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
23	AY	686	LYS	2.8
4	AJ	46	ARG	2.8
15	AB	229	VAL	2.8
25	BA	272(J)	C	2.8
54	BG	118	ARG	2.8
57	BJ	19	ALA	2.8
38	BY	38	ILE	2.8
51	BC	130	ILE	2.8
42	B2	45	SER	2.8
1	AA	1030(C)	G	2.8
25	BA	1047	G	2.8
54	BG	127	GLY	2.8
47	B6	17	LYS	2.8
38	BY	57	GLN	2.8
20	AG	114	ARG	2.8
36	BW	92	ARG	2.8
51	BC	123	VAL	2.8
31	BR	10	LEU	2.8
29	BP	87	ASP	2.8
54	BG	78	SER	2.8
38	BY	59	GLY	2.8
1	AA	1032	G	2.8
25	BA	1174	A	2.8
41	B1	27	GLU	2.8
29	BP	7	ARG	2.8
29	BP	79	ARG	2.8
54	BG	113	ARG	2.8
56	BK	125	ARG	2.8
54	BG	149	VAL	2.8
39	BZ	192	ALA	2.8
57	BJ	62	ALA	2.8
38	BY	90	LEU	2.8
43	BD	105	ILE	2.8
29	BP	35	HIS	2.8
33	BT	40	THR	2.8
55	BH	41	MET	2.8
20	AG	55	GLY	2.8
32	BS	90	GLY	2.8
55	BH	21	PRO	2.8
34	BU	117	GLN	2.7
47	B6	40	CYS	2.7
54	BG	70	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
25	BA	2116	G	2.7
51	BC	77	ILE	2.7
53	BF	20	LEU	2.7
6	AL	17	LYS	2.7
15	AB	8	LYS	2.7
56	BK	28	GLY	2.7
54	BG	83	ARG	2.7
1	AA	1030(B)	C	2.7
56	BK	106	GLU	2.7
15	AB	127	ILE	2.7
45	B4	48	ILE	2.7
54	BG	114	ILE	2.7
25	BA	12	U	2.7
25	BA	2833	G	2.7
53	BF	133	ASN	2.7
29	BP	43	GLY	2.7
29	BP	143	GLY	2.7
34	BU	73	GLY	2.7
23	AY	320	PRO	2.7
14	AT	11	SER	2.7
24	AU	9	ARG	2.7
55	BH	60	ARG	2.7
15	AB	17	PHE	2.7
35	BV	38	LEU	2.7
56	BK	65	PHE	2.7
27	BN	42	TRP	2.7
32	BS	99	LYS	2.7
13	AS	61	TYR	2.7
1	AA	161	A	2.7
32	BS	22	GLY	2.7
54	BG	85	GLY	2.7
54	BG	126	ASP	2.7
2	AV	19	G	2.7
25	BA	2792	G	2.7
20	AG	129	GLU	2.7
54	BG	143	GLU	2.7
52	BE	52	LEU	2.7
54	BG	62	LEU	2.7
54	BG	152	LEU	2.7
55	BH	171	LEU	2.7
54	BG	178	PHE	2.7
29	BP	132	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
54	BG	11	TYR	2.7
7	AM	12	ASN	2.7
46	B5	47	PRO	2.7
53	BF	131	GLY	2.7
54	BG	179	PRO	2.7
25	BA	90	U	2.7
25	BA	890	A	2.7
27	BN	131	GLN	2.7
47	B6	12	GLU	2.7
54	BG	99	MET	2.6
1	AA	1027	C	2.6
25	BA	1509	C	2.6
1	AA	1025	U	2.6
4	AJ	22	LYS	2.6
20	AG	86	GLN	2.6
22	AI	53	VAL	2.6
46	B5	37	LYS	2.6
47	B6	24	GLU	2.6
55	BH	159	GLU	2.6
25	BA	229	A	2.6
52	BE	1	MET	2.6
23	AY	302	HIS	2.6
52	BE	66	HIS	2.6
7	AM	115	LYS	2.6
13	AS	6	LYS	2.6
16	AC	45	LYS	2.6
25	BA	888	C	2.6
54	BG	107	LEU	2.6
15	AB	48	MET	2.6
25	BA	1078	U	2.6
56	BK	124	ALA	2.6
57	BJ	126	ALA	2.6
25	BA	1077	A	2.6
32	BS	34	HIS	2.6
51	BC	227	HIS	2.6
24	AU	24	ARG	2.6
7	AM	85	GLY	2.6
7	AM	100	GLY	2.6
33	BT	81	PRO	2.6
23	AY	583	LYS	2.6
25	BA	2206	G	2.6
44	B3	59	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
55	BH	49	VAL	2.6
23	AY	55	MET	2.6
27	BN	8	GLN	2.6
53	BF	1	MET	2.6
33	BT	131	ALA	2.6
51	BC	147	PHE	2.6
54	BG	116	ASP	2.6
57	BJ	12	ALA	2.6
57	BJ	106	ALA	2.6
7	AM	113	PRO	2.6
31	BR	5	LYS	2.6
51	BC	205	LYS	2.6
49	B8	50	LEU	2.6
35	BV	37	VAL	2.6
56	BK	58	THR	2.6
56	BK	71	THR	2.6
54	BG	46	ALA	2.6
57	BJ	79	ALA	2.6
1	AA	78	G	2.5
51	BC	53	ARG	2.5
25	BA	2791	C	2.5
8	AN	14	PRO	2.5
32	BS	104	GLY	2.5
38	BY	18	GLY	2.5
13	AS	45	VAL	2.5
23	AY	402	ILE	2.5
13	AS	43	GLU	2.5
29	BP	149	GLU	2.5
34	BU	89	GLU	2.5
41	B1	83	GLU	2.5
47	B6	15	GLU	2.5
32	BS	55	ALA	2.5
57	BJ	11	ALA	2.5
57	BJ	110	ALA	2.5
19	AF	100	ASN	2.5
27	BN	127	ASP	2.5
33	BT	13	ARG	2.5
34	BU	15	LYS	2.5
25	BA	1176	G	2.5
29	BP	10	PRO	2.5
38	BY	66	PRO	2.5
39	BZ	95	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
33	BT	4	GLY	2.5
38	BY	45	VAL	2.5
54	BG	63	ILE	2.5
56	BK	112	MET	2.5
54	BG	131	TYR	2.5
32	BS	63	THR	2.5
55	BH	53	GLU	2.5
56	BK	110	GLN	2.5
57	BJ	14	ALA	2.5
20	AG	84	ASN	2.5
47	B6	37	ARG	2.5
51	BC	2	LYS	2.5
17	AD	11	LEU	2.5
49	B8	61	LEU	2.5
38	BY	10	GLY	2.5
38	BY	96	ILE	2.5
43	BD	42	GLY	2.5
56	BK	129	GLY	2.5
25	BA	530	G	2.5
39	BZ	84	GLU	2.5
4	AJ	87	THR	2.5
32	BS	102	ALA	2.5
51	BC	122	ALA	2.5
54	BG	158	ALA	2.5
57	BJ	35	ALA	2.5
57	BJ	69	ALA	2.5
57	BJ	91	ALA	2.5
25	BA	1460	A	2.5
38	BY	97	ARG	2.5
39	BZ	80	ARG	2.5
51	BC	27	ARG	2.5
13	AS	65	ASN	2.5
29	BP	39	LYS	2.5
32	BS	33	LYS	2.5
51	BC	126	LYS	2.5
4	AJ	74	ILE	2.5
15	AB	235	SER	2.5
23	AY	584	ILE	2.5
25	BA	1175	U	2.5
33	BT	89	VAL	2.5
56	BK	8	VAL	2.5
7	AM	61	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
45	B4	51	TYR	2.5
54	BG	164	GLU	2.5
32	BS	97	ARG	2.5
38	BY	86	ARG	2.5
44	B3	29	ARG	2.5
57	BJ	45	ALA	2.5
57	BJ	95	ALA	2.5
57	BJ	100	ALA	2.5
6	AL	47	LYS	2.5
6	AL	126	LYS	2.5
7	AM	65	LYS	2.5
38	BY	47	LYS	2.5
53	BF	144	LYS	2.5
1	AA	1503	A	2.5
23	AY	181	LEU	2.4
54	BG	43	LEU	2.4
54	BG	173	LEU	2.4
15	AB	131	PRO	2.4
6	AL	18	VAL	2.4
45	B4	43	GLY	2.4
33	BT	106	SER	2.4
22	AI	2	GLU	2.4
23	AY	59	ARG	2.4
29	BP	41	ARG	2.4
39	BZ	13	GLU	2.4
51	BC	52	ARG	2.4
29	BP	14	LYS	2.4
33	BT	132	LYS	2.4
23	AY	334	THR	2.4
7	AM	82	MET	2.4
8	AN	27	CYS	2.4
15	AB	11	LEU	2.4
49	B8	62	LEU	2.4
25	BA	1068	G	2.4
45	B4	57	ILE	2.4
49	B8	41	ILE	2.4
23	AY	404	VAL	2.4
29	BP	82	GLY	2.4
34	BU	92	ARG	2.4
54	BG	170	ARG	2.4
1	AA	1541	U	2.4
51	BC	202	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
15	AB	13	ALA	2.4
16	AC	48	TYR	2.4
29	BP	99	LEU	2.4
1	AA	840	C	2.4
27	BN	125	GLY	2.4
39	BZ	93	ASP	2.4
55	BH	5	GLY	2.4
1	AA	1030(D)	A	2.4
1	AA	1030(A)	G	2.4
25	BA	1888	G	2.4
54	BG	137	GLU	2.4
25	BA	1963	U	2.4
25	BA	2506	U	2.4
25	BA	2895	U	2.4
56	BK	35	MET	2.4
42	B2	44	LEU	2.4
56	BK	42	ASN	2.4
7	AM	60	VAL	2.4
51	BC	119	VAL	2.4
31	BR	69	ASP	2.4
36	BW	110	LYS	2.4
54	BG	98	ARG	2.4
25	BA	886	C	2.4
1	AA	412	A	2.4
53	BF	127	GLU	2.4
54	BG	73	ALA	2.4
56	BK	14	ALA	2.4
57	BJ	68	ALA	2.4
57	BJ	96	ALA	2.4
57	BJ	124	ALA	2.4
1	AA	1003	G	2.4
25	BA	958	U	2.4
25	BA	2099	U	2.4
25	BA	2793	G	2.4
38	BY	6	HIS	2.4
38	BY	31	LEU	2.4
54	BG	135	LEU	2.4
55	BH	92	ILE	2.4
14	AT	8	ARG	2.3
16	AC	80	GLY	2.3
16	AC	85	ARG	2.3
27	BN	134	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
33	BT	2	ASN	2.3
39	BZ	112	ARG	2.3
43	BD	43	ARG	2.3
54	BG	28	VAL	2.3
7	AM	83	ASP	2.3
23	AY	223	PHE	2.3
45	B4	44	CYS	2.3
14	AT	93	GLU	2.3
57	BJ	38	ALA	2.3
57	BJ	78	ALA	2.3
25	BA	1181	C	2.3
3	AX	15	A	2.3
25	BA	2629	A	2.3
7	AM	31	LYS	2.3
38	BY	8	LYS	2.3
54	BG	105	LYS	2.3
25	BA	7	G	2.3
33	BT	34	VAL	2.3
37	BX	12	VAL	2.3
35	BV	17	GLY	2.3
15	AB	128	GLU	2.3
38	BY	99	CYS	2.3
53	BF	22	ALA	2.3
7	AM	20	THR	2.3
25	BA	279	C	2.3
39	BZ	9	TYR	2.3
43	BD	40	THR	2.3
54	BG	64	THR	2.3
23	AY	681	LYS	2.3
44	B3	2	PRO	2.3
54	BG	181	ARG	2.3
54	BG	109	VAL	2.3
1	AA	79	G	2.3
14	AT	97	ALA	2.3
25	BA	2307	G	2.3
35	BV	43	GLU	2.3
57	BJ	21	ALA	2.3
57	BJ	60	ALA	2.3
57	BJ	111	ALA	2.3
57	BJ	133	ALA	2.3
53	BF	23	ASP	2.3
23	AY	232	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
15	AB	156	LYS	2.3
32	BS	52	SER	2.3
7	AM	102	ARG	2.3
20	AG	72	ARG	2.3
20	AG	115	ARG	2.3
30	BQ	60	ARG	2.3
50	B9	9	ARG	2.3
23	AY	683	VAL	2.3
25	BA	8	A	2.3
32	BS	69	VAL	2.3
52	BE	74	PRO	2.3
23	AY	379	GLY	2.3
29	BP	24	GLY	2.3
16	AC	61	ALA	2.3
23	AY	236	GLU	2.3
39	BZ	187	ALA	2.3
39	BZ	188	ALA	2.3
42	B2	72	ALA	2.3
57	BJ	108	ALA	2.3
39	BZ	5	LEU	2.3
43	BD	33	LEU	2.3
20	AG	136	LYS	2.3
27	BN	109	LYS	2.3
54	BG	81	LYS	2.3
56	BK	63	ARG	2.3
56	BK	98	ARG	2.3
23	AY	231	TYR	2.3
33	BT	28	VAL	2.3
1	AA	1533	C	2.2
25	BA	899	A	2.2
25	BA	1178	C	2.2
4	AJ	25	GLU	2.2
54	BG	121	ASN	2.2
32	BS	48	LEU	2.2
15	AB	135	GLN	2.2
22	AI	16	ARG	2.2
31	BR	33	ARG	2.2
56	BK	55	VAL	2.2
2	AV	15	G	2.2
25	BA	2165	G	2.2
52	BE	71	GLY	2.2
34	BU	32	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
54	BG	180	PHE	2.2
15	AB	231	GLU	2.2
23	AY	214	GLU	2.2
39	BZ	185	GLU	2.2
57	BJ	131	ALA	2.2
23	AY	689	LYS	2.2
38	BY	43	ASN	2.2
56	BK	80	LYS	2.2
52	BE	89	ASP	2.2
13	AS	9	VAL	2.2
27	BN	93	THR	2.2
20	AG	151	TYR	2.2
29	BP	118	GLY	2.2
52	BE	29	GLY	2.2
23	AY	617	MET	2.2
17	AD	30	LYS	2.2
6	AL	127	GLU	2.2
22	AI	55	ALA	2.2
53	BF	2	LYS	2.2
54	BG	8	LYS	2.2
54	BG	36	LYS	2.2
56	BK	3	LYS	2.2
25	BA	1171	G	2.2
57	BJ	9	ALA	2.2
57	BJ	36	ALA	2.2
57	BJ	80	ALA	2.2
57	BJ	99	ALA	2.2
57	BJ	114	ALA	2.2
57	BJ	125	ALA	2.2
52	BE	55	ASN	2.2
16	AC	14	ILE	2.2
34	BU	59	ARG	2.2
42	B2	46	GLN	2.2
54	BG	77	ILE	2.2
1	AA	1006	C	2.2
4	AJ	89	ASP	2.2
6	AL	25	PRO	2.2
51	BC	72	VAL	2.2
54	BG	15	VAL	2.2
7	AM	64	TRP	2.2
29	BP	109	GLY	2.2
54	BG	25	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
35	BV	2	PHE	2.2
19	AF	95	GLU	2.2
23	AY	203	GLU	2.2
8	AN	7	ILE	2.2
21	AH	102	ARG	2.2
25	BA	2808	U	2.2
29	BP	90	ARG	2.2
29	BP	102	ARG	2.2
25	BA	10	G	2.2
23	AY	510	VAL	2.2
25	BA	1848	A	2.2
32	BS	49	VAL	2.2
32	BS	91	PRO	2.2
53	BF	4	VAL	2.2
1	AA	1137	C	2.2
13	AS	68	GLY	2.2
20	AG	132	GLY	2.2
53	BF	134	GLY	2.2
6	AL	27	LEU	2.2
29	BP	106	LEU	2.2
54	BG	94	LEU	2.2
19	AF	99	ALA	2.2
23	AY	240	GLU	2.2
23	AY	685	GLU	2.2
40	B0	85	ALA	2.2
56	BK	6	ALA	2.2
56	BK	43	ALA	2.2
57	BJ	32	ALA	2.2
57	BJ	97	ALA	2.2
4	AJ	5	ARG	2.1
17	AD	47	ARG	2.1
17	AD	76	ARG	2.1
43	BD	270	ILE	2.1
56	BK	57	ILE	2.1
25	BA	1065	U	2.1
33	BT	104	ASN	2.1
1	AA	1004	A	2.1
1	AA	1029	C	2.1
13	AS	4	SER	2.1
38	BY	76	CYS	2.1
23	AY	585	ALA	2.1
54	BG	6	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
54	BG	163	ALA	2.1
56	BK	17	ALA	2.1
57	BJ	118	ALA	2.1
4	AJ	83	GLU	2.1
12	AR	28	GLU	2.1
45	B4	39	ARG	2.1
23	AY	289	ILE	2.1
40	B0	17	GLN	2.1
56	BK	103	GLN	2.1
15	AB	37	ASN	2.1
1	AA	1446	U	2.1
25	BA	271(N)	U	2.1
32	BS	59	LYS	2.1
39	BZ	14	LYS	2.1
54	BG	182	LYS	2.1
23	AY	473	ASP	2.1
33	BT	107	ASP	2.1
52	BE	186	GLY	2.1
54	BG	145	THR	2.1
1	AA	160	A	2.1
29	BP	150	ALA	2.1
48	B7	45	ALA	2.1
1	AA	631	G	2.1
7	AM	4	ILE	2.1
7	AM	9	ILE	2.1
23	AY	409	ILE	2.1
25	BA	1059	G	2.1
34	BU	88	ILE	2.1
43	BD	169	GLU	2.1
45	B4	60	GLU	2.1
50	B9	27	CYS	2.1
56	BK	36	GLU	2.1
13	AS	25	LYS	2.1
27	BN	21	LYS	2.1
48	B7	1	MET	2.1
54	BG	38	VAL	2.1
55	BH	10	PRO	2.1
25	BA	9	U	2.1
9	AO	23	GLY	2.1
19	AF	21	LEU	2.1
23	AY	102	ASP	2.1
29	BP	57	THR	2.1

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Mol	Chain	Res	Type	RSRZ
20	AG	94	ARG	2.1
37	BX	65	ARG	2.1
29	BP	12	ALA	2.1
29	BP	141	ALA	2.1
51	BC	103	ILE	2.1
57	BJ	47	ALA	2.1
57	BJ	117	ALA	2.1
57	BJ	123	ALA	2.1
7	AM	87	TYR	2.1
16	AC	193	TYR	2.1
52	BE	40	GLU	2.1
52	BE	151	TYR	2.1
1	AA	88	A	2.1
39	BZ	153	SER	2.1
23	AY	565	VAL	2.1
23	AY	596	LYS	2.1
25	BA	1907	G	2.1
25	BA	1914	C	2.1
54	BG	37	VAL	2.1
54	BG	112	PRO	2.1
14	AT	9	ASN	2.1
15	AB	154	LEU	2.1
40	B0	84	LEU	2.1
54	BG	34	LEU	2.1
17	AD	109	GLY	2.1
35	BV	54	GLY	2.1
51	BC	95	GLY	2.1
15	AB	209	ARG	2.1
17	AD	3	ARG	2.1
41	B1	26	ARG	2.1
54	BG	61	ALA	2.1
57	BJ	93	ALA	2.1
12	AR	46	GLU	2.1
23	AY	211	GLU	2.1
54	BG	48	GLU	2.1
32	BS	94	TYR	2.1
38	BY	55	TYR	2.1
32	BS	62	LYS	2.0
54	BG	68	PRO	2.0
25	BA	2306	C	2.0
35	BV	18	LEU	2.0
47	B6	32	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
1	AA	93	G	2.0
1	AA	1002	G	2.0
14	AT	102	GLY	2.0
25	BA	271(M)	G	2.0
25	BA	1091	G	2.0
1	AA	1542	U	2.0
4	AJ	6	ILE	2.0
23	AY	178	ILE	2.0
33	BT	88	ILE	2.0
13	AS	24	ALA	2.0
17	AD	32	ALA	2.0
39	BZ	189	ALA	2.0
39	BZ	11	GLU	2.0
53	BF	27	GLU	2.0
8	AN	4	LYS	2.0
51	BC	102	LYS	2.0
39	BZ	165	VAL	2.0
29	BP	23	PRO	2.0
1	AA	1286	A	2.0
4	AJ	79	ARG	2.0
6	AL	19	ARG	2.0
32	BS	20	ARG	2.0
54	BG	132	ASN	2.0
56	BK	33	ASN	2.0
51	BC	48	GLY	2.0
1	AA	163	C	2.0
17	AD	48	ALA	2.0
20	AG	150	ALA	2.0
15	AB	12	GLU	2.0
25	BA	882	G	2.0
25	BA	1173	G	2.0
38	BY	54	LYS	2.0
38	BY	91	GLU	2.0
45	B4	49	GLU	2.0
53	BF	65	TRP	2.0
38	BY	42	VAL	2.0
55	BH	24	VAL	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
59	MG	AA	1636	1/1	0.79	0.16	24,24,24,24	0
59	MG	BA	3004	1/1	0.80	0.17	46,46,46,46	0
59	MG	BA	3011	1/1	0.85	0.23	30,30,30,30	0
59	MG	BA	3039	1/1	0.85	0.26	24,24,24,24	0
59	MG	BF	301	1/1	0.85	0.11	27,27,27,27	0
59	MG	AA	1644	1/1	0.86	0.30	33,33,33,33	0
59	MG	BA	3012	1/1	0.87	0.09	10,10,10,10	0
59	MG	AA	1640	1/1	0.88	0.22	21,21,21,21	0
59	MG	BA	3065	1/1	0.88	0.31	24,24,24,24	0
59	MG	BA	3073	1/1	0.88	0.23	14,14,14,14	0
59	MG	AA	1642	1/1	0.88	0.24	30,30,30,30	0
59	MG	BA	3059	1/1	0.89	0.18	9,9,9,9	0
59	MG	AA	1635	1/1	0.89	0.15	24,24,24,24	0
59	MG	AA	1645	1/1	0.89	0.33	35,35,35,35	0
59	MG	BA	3052	1/1	0.89	0.22	19,19,19,19	0
59	MG	BA	3027	1/1	0.90	0.24	30,30,30,30	0
59	MG	BA	3056	1/1	0.90	0.15	18,18,18,18	0
59	MG	BA	3086	1/1	0.90	0.20	26,26,26,26	0
59	MG	BA	3051	1/1	0.90	0.27	24,24,24,24	0
59	MG	BA	3029	1/1	0.91	0.23	28,28,28,28	0
59	MG	BA	3060	1/1	0.91	0.24	22,22,22,22	0
59	MG	BA	3008	1/1	0.91	0.24	13,13,13,13	0
59	MG	BA	3072	1/1	0.91	0.19	19,19,19,19	0
59	MG	AA	1619	1/1	0.91	0.20	27,27,27,27	0
59	MG	BA	3001	1/1	0.91	0.34	32,32,32,32	0
59	MG	B8	101	1/1	0.91	0.09	15,15,15,15	0
59	MG	AA	1641	1/1	0.91	0.15	25,25,25,25	0
59	MG	BA	3071	1/1	0.92	0.29	29,29,29,29	0
59	MG	BA	3013	1/1	0.92	0.26	26,26,26,26	0
59	MG	AA	1643	1/1	0.92	0.17	31,31,31,31	0
59	MG	BA	3080	1/1	0.92	0.19	16,16,16,16	0
59	MG	BA	3082	1/1	0.92	0.21	21,21,21,21	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
59	MG	AA	1633	1/1	0.92	0.15	27,27,27,27	0
59	MG	BA	3087	1/1	0.92	0.22	26,26,26,26	0
59	MG	AA	1618	1/1	0.92	0.20	22,22,22,22	0
59	MG	AA	1603	1/1	0.92	0.23	23,23,23,23	0
59	MG	BA	3017	1/1	0.93	0.21	16,16,16,16	0
59	MG	BA	3020	1/1	0.93	0.20	6,6,6,6	0
59	MG	BA	3074	1/1	0.93	0.17	16,16,16,16	0
59	MG	AA	1626	1/1	0.93	0.19	19,19,19,19	0
59	MG	AA	1637	1/1	0.93	0.20	34,34,34,34	0
59	MG	BA	3030	1/1	0.93	0.25	12,12,12,12	0
59	MG	BA	3033	1/1	0.93	0.20	12,12,12,12	0
59	MG	BA	3067	1/1	0.93	0.18	16,16,16,16	0
59	MG	BE	301	1/1	0.93	0.21	16,16,16,16	0
59	MG	BA	3014	1/1	0.93	0.30	27,27,27,27	0
59	MG	BA	3078	1/1	0.94	0.15	15,15,15,15	0
59	MG	AA	1638	1/1	0.94	0.18	22,22,22,22	0
59	MG	BA	3081	1/1	0.94	0.18	17,17,17,17	0
59	MG	BA	3023	1/1	0.94	0.19	9,9,9,9	0
59	MG	BA	3070	1/1	0.94	0.23	24,24,24,24	0
59	MG	AA	1617	1/1	0.94	0.20	21,21,21,21	0
59	MG	AA	1625	1/1	0.94	0.26	25,25,25,25	0
59	MG	AA	1601	1/1	0.94	0.21	13,13,13,13	0
59	MG	AA	1629	1/1	0.94	0.19	38,38,38,38	0
59	MG	BA	3048	1/1	0.95	0.17	9,9,9,9	0
59	MG	AA	1622	1/1	0.95	0.17	25,25,25,25	0
59	MG	BA	3002	1/1	0.95	0.16	17,17,17,17	0
59	MG	BA	3054	1/1	0.95	0.15	9,9,9,9	0
59	MG	BA	3075	1/1	0.95	0.17	12,12,12,12	0
59	MG	BA	3076	1/1	0.95	0.17	8,8,8,8	0
59	MG	BA	3032	1/1	0.95	0.16	21,21,21,21	0
59	MG	BA	3079	1/1	0.95	0.18	14,14,14,14	0
59	MG	AA	1610	1/1	0.95	0.24	14,14,14,14	0
59	MG	AA	1605	1/1	0.95	0.11	25,25,25,25	0
59	MG	BA	3063	1/1	0.95	0.24	22,22,22,22	0
59	MG	BA	3041	1/1	0.95	0.19	11,11,11,11	0
59	MG	BA	3066	1/1	0.95	0.16	15,15,15,15	0
59	MG	BA	3043	1/1	0.95	0.20	7,7,7,7	0
59	MG	BA	3069	1/1	0.95	0.19	14,14,14,14	0
59	MG	BA	3045	1/1	0.95	0.19	16,16,16,16	0
59	MG	BA	3061	1/1	0.96	0.18	8,8,8,8	0
59	MG	BA	3031	1/1	0.96	0.19	16,16,16,16	0
59	MG	AA	1624	1/1	0.96	0.14	14,14,14,14	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
59	MG	AA	1609	1/1	0.96	0.23	16,16,16,16	0
59	MG	BA	3034	1/1	0.96	0.18	5,5,5,5	0
59	MG	BA	3068	1/1	0.96	0.15	7,7,7,7	0
59	MG	BA	3035	1/1	0.96	0.27	18,18,18,18	0
59	MG	BA	3037	1/1	0.96	0.19	7,7,7,7	0
59	MG	AA	1602	1/1	0.96	0.30	16,16,16,16	0
59	MG	BA	3040	1/1	0.96	0.20	10,10,10,10	0
59	MG	AA	1611	1/1	0.96	0.23	7,7,7,7	0
59	MG	BA	3018	1/1	0.96	0.15	12,12,12,12	0
59	MG	BA	3044	1/1	0.96	0.17	15,15,15,15	0
59	MG	BA	3019	1/1	0.96	0.24	16,16,16,16	0
59	MG	BA	3077	1/1	0.96	0.17	17,17,17,17	0
59	MG	BA	3047	1/1	0.96	0.35	27,27,27,27	0
59	MG	AA	1639	1/1	0.96	0.14	20,20,20,20	0
59	MG	AA	1630	1/1	0.96	0.29	29,29,29,29	0
59	MG	BA	3025	1/1	0.96	0.18	16,16,16,16	0
59	MG	BA	3053	1/1	0.96	0.19	7,7,7,7	0
59	MG	BA	3083	1/1	0.96	0.21	37,37,37,37	0
59	MG	BA	3084	1/1	0.96	0.20	22,22,22,22	0
59	MG	BA	3085	1/1	0.96	0.18	18,18,18,18	0
59	MG	BA	3026	1/1	0.96	0.18	19,19,19,19	0
59	MG	AA	1632	1/1	0.96	0.19	22,22,22,22	0
59	MG	BA	3088	1/1	0.96	0.23	26,26,26,26	0
59	MG	BD	301	1/1	0.96	0.19	7,7,7,7	0
59	MG	BA	3057	1/1	0.96	0.14	8,8,8,8	0
59	MG	BA	3009	1/1	0.96	0.28	31,31,31,31	0
59	MG	AA	1613	1/1	0.96	0.15	6,6,6,6	0
59	MG	BA	3024	1/1	0.97	0.18	2,2,2,2	0
59	MG	AA	1615	1/1	0.97	0.21	24,24,24,24	0
59	MG	BA	3010	1/1	0.97	0.24	14,14,14,14	0
59	MG	BA	3064	1/1	0.97	0.21	22,22,22,22	0
59	MG	AA	1621	1/1	0.97	0.18	14,14,14,14	0
59	MG	AA	1616	1/1	0.97	0.14	5,5,5,5	0
59	MG	AA	1631	1/1	0.97	0.19	13,13,13,13	0
59	MG	AA	1623	1/1	0.97	0.17	15,15,15,15	0
59	MG	BA	3003	1/1	0.97	0.19	2,2,2,2	0
59	MG	AA	1606	1/1	0.97	0.23	15,15,15,15	0
59	MG	BA	3005	1/1	0.97	0.25	12,12,12,12	0
59	MG	BA	3007	1/1	0.97	0.21	4,4,4,4	0
59	MG	BA	3055	1/1	0.97	0.16	5,5,5,5	0
59	MG	BA	3036	1/1	0.97	0.26	20,20,20,20	0
59	MG	BA	3021	1/1	0.97	0.25	25,25,25,25	0

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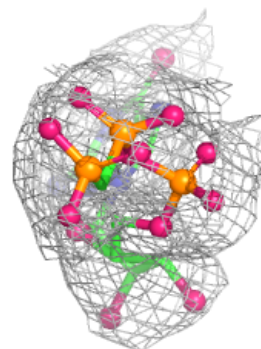
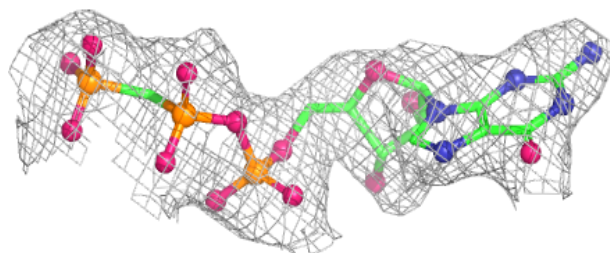
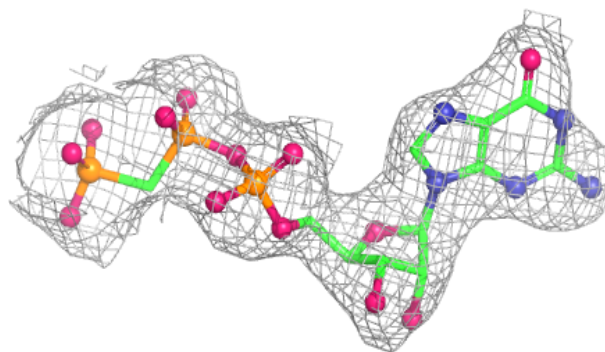
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
59	MG	AA	1607	1/1	0.97	0.11	24,24,24,24	0
60	GCP	AY	702	32/32	0.97	0.07	27,42,47,49	0
59	MG	AA	1628	1/1	0.98	0.09	18,18,18,18	0
59	MG	AA	1634	1/1	0.98	0.08	6,6,6,6	0
59	MG	BA	3016	1/1	0.98	0.07	15,15,15,15	0
59	MG	BA	3042	1/1	0.98	0.23	11,11,11,11	0
59	MG	AA	1604	1/1	0.98	0.08	3,3,3,3	0
59	MG	AA	1620	1/1	0.98	0.25	18,18,18,18	0
59	MG	BA	3058	1/1	0.98	0.09	3,3,3,3	0
59	MG	AA	1614	1/1	0.98	0.19	11,11,11,11	0
59	MG	BA	3046	1/1	0.98	0.18	14,14,14,14	0
59	MG	BA	3028	1/1	0.98	0.23	23,23,23,23	0
59	MG	BA	3062	1/1	0.98	0.19	18,18,18,18	0
59	MG	AA	1612	1/1	0.98	0.14	14,14,14,14	0
59	MG	BA	3050	1/1	0.98	0.18	10,10,10,10	0
59	MG	BA	3038	1/1	0.98	0.25	19,19,19,19	0
59	MG	AY	701	1/1	0.99	0.03	41,41,41,41	0
59	MG	BA	3022	1/1	0.99	0.22	13,13,13,13	0
59	MG	AA	1608	1/1	0.99	0.29	23,23,23,23	0
59	MG	AA	1627	1/1	0.99	0.17	15,15,15,15	0
59	MG	BA	3049	1/1	0.99	0.17	2,2,2,2	0
59	MG	BA	3006	1/1	0.99	0.25	13,13,13,13	0
59	MG	BA	3015	1/1	0.99	0.19	10,10,10,10	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around GCP AY 702:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.