



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 14, 2017 – 10:48 PM EST

PDB ID : 5CZP
Title : 70S termination complex containing E. coli RF2
Authors : Hoffer, E.D.; Dunham, C.M.
Deposited on : unknown
Resolution : 3.30 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

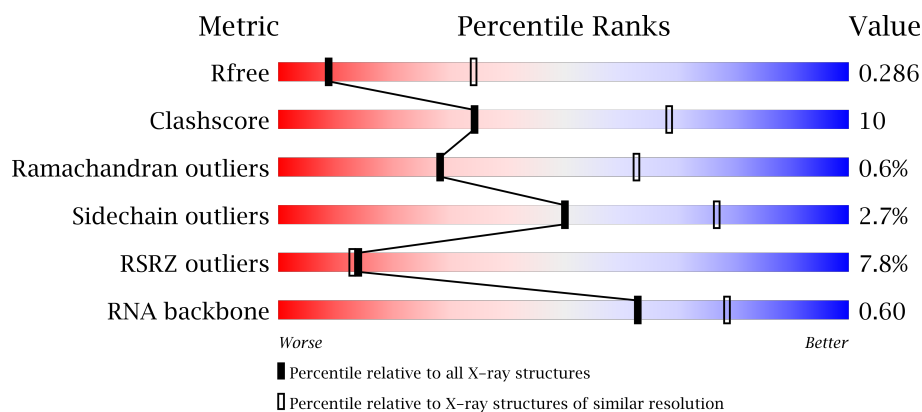
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



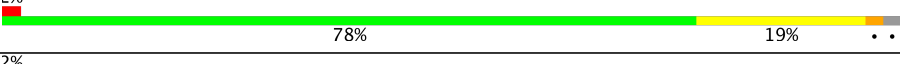
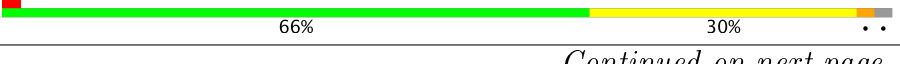
The reported resolution of this entry is 3.30 Å.

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}	100719	1034 (3.36-3.24)
Clashscore	112137	1100 (3.36-3.24)
Ramachandran outliers	110173	1081 (3.36-3.24)
Sidechain outliers	110143	1080 (3.36-3.24)
RSRZ outliers	101464	1039 (3.36-3.24)
RNA backbone	2435	1111 (3.80-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	RA	2915	
1	YA	2915	
2	RB	122	
2	YB	122	

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Mol	Chain	Length	Quality of chain
3	RD	276	
3	YD	276	
4	RE	206	
4	YE	206	
5	RF	210	
5	YF	210	
6	RG	182	
6	YG	182	
7	RH	180	
7	YH	180	
8	RI	148	
8	YI	148	
9	RN	140	
9	YN	140	
10	RO	122	
10	YO	122	
11	RP	150	
11	YP	150	
12	RQ	141	
12	YQ	141	
13	RR	118	
13	YR	118	
14	RS	112	
14	YS	112	
15	RT	146	

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Mol	Chain	Length	Quality of chain
15	YT	146	
16	RU	118	
16	YU	118	
17	RV	101	
17	YV	101	
18	RW	113	
18	YW	113	
19	RX	96	
19	YX	96	
20	RY	110	
20	YY	110	
21	RZ	206	
21	YZ	206	
22	R0	85	
22	Y0	85	
23	R1	98	
23	Y1	98	
24	R2	72	
24	Y2	72	
25	R3	60	
25	Y3	60	
26	R4	71	
26	Y4	71	
27	R5	60	
27	Y5	60	

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Mol	Chain	Length	Quality of chain
28	R6	54	<div>76%</div> <div>74%</div> <div>24%</div> <div>•</div>
28	Y6	54	<div>74%</div> <div>78%</div> <div>20%</div> <div>•</div>
29	R7	49	<div>6%</div> <div>80%</div> <div>16%</div> <div>• •</div>
29	Y7	49	<div>8%</div> <div>80%</div> <div>18%</div> <div>•</div>
30	R8	65	<div>3%</div> <div>69%</div> <div>23%</div> <div>6%</div> <div>•</div>
30	Y8	65	<div>74%</div> <div>22%</div> <div>• •</div>
31	R9	37	<div>54%</div> <div>86%</div> <div>14%</div>
31	Y9	37	<div>51%</div> <div>81%</div> <div>19%</div>
32	QA	1521	<div>2%</div> <div>58%</div> <div>35%</div> <div>6%</div> <div>•</div>
32	XA	1521	<div>2%</div> <div>58%</div> <div>34%</div> <div>6%</div> <div>•</div>
33	QB	256	<div>9%</div> <div>54%</div> <div>32%</div> <div>•</div> <div>10%</div>
33	XB	256	<div>9%</div> <div>52%</div> <div>32%</div> <div>5%</div> <div>•</div> <div>10%</div>
34	QC	239	<div>10%</div> <div>67%</div> <div>18%</div> <div>14%</div>
34	XC	239	<div>8%</div> <div>56%</div> <div>30%</div> <div>14%</div>
35	QD	209	<div>4%</div> <div>67%</div> <div>30%</div> <div>• •</div>
35	XD	209	<div>9%</div> <div>78%</div> <div>20%</div> <div>•</div>
36	QE	162	<div>6%</div> <div>65%</div> <div>25%</div> <div>• •</div> <div>9%</div>
36	XE	162	<div>6%</div> <div>64%</div> <div>27%</div> <div>•</div> <div>9%</div>
37	QF	101	<div>8%</div> <div>77%</div> <div>20%</div> <div>• •</div>
37	XF	101	<div>3%</div> <div>73%</div> <div>23%</div> <div>• • •</div>
38	QG	156	<div>15%</div> <div>71%</div> <div>28%</div> <div>• •</div>
38	XG	156	<div>10%</div> <div>76%</div> <div>21%</div> <div>• •</div>
39	QH	138	<div>10%</div> <div>67%</div> <div>30%</div> <div>• •</div>
39	XH	138	<div>7%</div> <div>75%</div> <div>21%</div> <div>• • •</div>
40	QI	128	<div>23%</div> <div>66%</div> <div>30%</div> <div>• • •</div>

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Mol	Chain	Length	Quality of chain
40	XI	128	
41	QJ	105	
41	XJ	105	
42	QK	129	
42	XK	129	
43	QL	132	
43	XL	132	
44	QM	126	
44	XM	126	
45	QN	61	
45	XN	61	
46	QO	89	
46	XO	89	
47	QP	88	
47	XP	88	
48	QQ	105	
48	XQ	105	
49	QR	88	
49	XR	88	
50	QS	93	
50	XS	93	
51	QT	106	
51	XT	106	
52	QU	27	
52	XU	27	

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Mol	Chain	Length	Quality of chain
53	QV	77	
53	XV	77	
54	QY	380	
54	XY	380	
55	QX	25	
55	XX	25	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	QA	1606	-	-	-	X
56	MG	QA	1610	-	-	-	X
56	MG	QA	1614	-	-	-	X
56	MG	QA	1616	-	-	-	X
56	MG	QA	1618	-	-	-	X
56	MG	QA	1619	-	-	-	X
56	MG	QA	1622	-	-	-	X
56	MG	QA	1623	-	-	-	X
56	MG	QA	1625	-	-	-	X
56	MG	QA	1626	-	-	-	X
56	MG	QA	1634	-	-	-	X
56	MG	QA	1638	-	-	-	X
56	MG	QA	1647	-	-	-	X
56	MG	QA	1654	-	-	-	X
56	MG	QA	1658	-	-	-	X
56	MG	QA	1671	-	-	-	X
56	MG	QA	1672	-	-	-	X
56	MG	QA	1680	-	-	-	X
56	MG	QA	1682	-	-	-	X
56	MG	QA	1691	-	-	-	X
56	MG	QA	1704	-	-	-	X
56	MG	QA	1706	-	-	-	X
56	MG	QA	1708	-	-	-	X
56	MG	QA	1711	-	-	-	X
56	MG	QA	1715	-	-	-	X
56	MG	QA	1724	-	-	-	X
56	MG	QA	1731	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	QA	1737	-	-	-	X
56	MG	QA	1759	-	-	-	X
56	MG	QA	1771	-	-	-	X
56	MG	QA	1773	-	-	-	X
56	MG	QA	1780	-	-	-	X
56	MG	QA	1802	-	-	-	X
56	MG	QA	1814	-	-	-	X
56	MG	QA	1823	-	-	-	X
56	MG	QA	1828	-	-	-	X
56	MG	QA	1829	-	-	-	X
56	MG	QA	1832	-	-	-	X
56	MG	QA	1835	-	-	-	X
56	MG	QA	1843	-	-	-	X
56	MG	QA	1849	-	-	-	X
56	MG	QA	1854	-	-	-	X
56	MG	QA	1857	-	-	-	X
56	MG	QA	1860	-	-	-	X
56	MG	QA	1872	-	-	-	X
56	MG	QA	1877	-	-	-	X
56	MG	QD	303	-	-	-	X
56	MG	QD	305	-	-	-	X
56	MG	QF	201	-	-	-	X
56	MG	QN	102	-	-	-	X
56	MG	QN	103	-	-	-	X
56	MG	QR	101	-	-	-	X
56	MG	QT	201	-	-	-	X
56	MG	QY	401	-	-	-	X
56	MG	R0	103	-	-	-	X
56	MG	R1	102	-	-	-	X
56	MG	R1	104	-	-	-	X
56	MG	R3	102	-	-	-	X
56	MG	R5	101	-	-	-	X
56	MG	R8	101	-	-	-	X
56	MG	RA	3006	-	-	-	X
56	MG	RA	3014	-	-	-	X
56	MG	RA	3020	-	-	-	X
56	MG	RA	3021	-	-	-	X
56	MG	RA	3022	-	-	-	X
56	MG	RA	3023	-	-	-	X
56	MG	RA	3027	-	-	-	X
56	MG	RA	3029	-	-	-	X
56	MG	RA	3030	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	RA	3032	-	-	-	X
56	MG	RA	3040	-	-	-	X
56	MG	RA	3041	-	-	-	X
56	MG	RA	3043	-	-	-	X
56	MG	RA	3045	-	-	-	X
56	MG	RA	3050	-	-	-	X
56	MG	RA	3064	-	-	-	X
56	MG	RA	3070	-	-	-	X
56	MG	RA	3073	-	-	-	X
56	MG	RA	3077	-	-	-	X
56	MG	RA	3082	-	-	-	X
56	MG	RA	3088	-	-	-	X
56	MG	RA	3092	-	-	-	X
56	MG	RA	3094	-	-	-	X
56	MG	RA	3098	-	-	-	X
56	MG	RA	3101	-	-	-	X
56	MG	RA	3102	-	-	-	X
56	MG	RA	3109	-	-	-	X
56	MG	RA	3113	-	-	-	X
56	MG	RA	3116	-	-	-	X
56	MG	RA	3117	-	-	-	X
56	MG	RA	3118	-	-	-	X
56	MG	RA	3119	-	-	-	X
56	MG	RA	3121	-	-	-	X
56	MG	RA	3122	-	-	-	X
56	MG	RA	3125	-	-	-	X
56	MG	RA	3128	-	-	-	X
56	MG	RA	3132	-	-	-	X
56	MG	RA	3136	-	-	-	X
56	MG	RA	3141	-	-	-	X
56	MG	RA	3142	-	-	-	X
56	MG	RA	3146	-	-	-	X
56	MG	RA	3148	-	-	-	X
56	MG	RA	3163	-	-	-	X
56	MG	RA	3165	-	-	-	X
56	MG	RA	3168	-	-	-	X
56	MG	RA	3170	-	-	-	X
56	MG	RA	3177	-	-	-	X
56	MG	RA	3178	-	-	-	X
56	MG	RA	3179	-	-	-	X
56	MG	RA	3185	-	-	-	X
56	MG	RA	3186	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	RA	3187	-	-	-	X
56	MG	RA	3197	-	-	-	X
56	MG	RA	3205	-	-	-	X
56	MG	RA	3208	-	-	-	X
56	MG	RA	3211	-	-	-	X
56	MG	RA	3217	-	-	-	X
56	MG	RA	3221	-	-	-	X
56	MG	RA	3226	-	-	-	X
56	MG	RA	3230	-	-	-	X
56	MG	RA	3231	-	-	-	X
56	MG	RA	3232	-	-	-	X
56	MG	RA	3234	-	-	-	X
56	MG	RA	3235	-	-	-	X
56	MG	RA	3241	-	-	-	X
56	MG	RA	3248	-	-	-	X
56	MG	RA	3251	-	-	-	X
56	MG	RA	3252	-	-	-	X
56	MG	RA	3265	-	-	-	X
56	MG	RA	3271	-	-	-	X
56	MG	RA	3275	-	-	-	X
56	MG	RA	3279	-	-	-	X
56	MG	RA	3290	-	-	-	X
56	MG	RA	3299	-	-	-	X
56	MG	RA	3300	-	-	-	X
56	MG	RA	3302	-	-	-	X
56	MG	RA	3307	-	-	-	X
56	MG	RA	3315	-	-	-	X
56	MG	RA	3321	-	-	-	X
56	MG	RA	3323	-	-	-	X
56	MG	RA	3328	-	-	-	X
56	MG	RA	3330	-	-	-	X
56	MG	RA	3332	-	-	-	X
56	MG	RA	3333	-	-	-	X
56	MG	RA	3335	-	-	-	X
56	MG	RA	3342	-	-	-	X
56	MG	RA	3348	-	-	-	X
56	MG	RA	3349	-	-	-	X
56	MG	RA	3352	-	-	-	X
56	MG	RA	3356	-	-	-	X
56	MG	RA	3359	-	-	-	X
56	MG	RA	3361	-	-	-	X
56	MG	RA	3364	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	RA	3366	-	-	-	X
56	MG	RA	3377	-	-	-	X
56	MG	RA	3379	-	-	-	X
56	MG	RA	3381	-	-	-	X
56	MG	RA	3382	-	-	-	X
56	MG	RA	3384	-	-	-	X
56	MG	RA	3385	-	-	-	X
56	MG	RA	3386	-	-	-	X
56	MG	RA	3387	-	-	-	X
56	MG	RA	3390	-	-	-	X
56	MG	RA	3391	-	-	-	X
56	MG	RA	3392	-	-	-	X
56	MG	RA	3394	-	-	-	X
56	MG	RA	3399	-	-	-	X
56	MG	RA	3401	-	-	-	X
56	MG	RA	3402	-	-	-	X
56	MG	RA	3404	-	-	-	X
56	MG	RA	3408	-	-	-	X
56	MG	RA	3409	-	-	-	X
56	MG	RA	3412	-	-	-	X
56	MG	RA	3419	-	-	-	X
56	MG	RA	3421	-	-	-	X
56	MG	RA	3424	-	-	-	X
56	MG	RA	3431	-	-	-	X
56	MG	RA	3436	-	-	-	X
56	MG	RA	3444	-	-	-	X
56	MG	RA	3452	-	-	-	X
56	MG	RA	3458	-	-	-	X
56	MG	RA	3462	-	-	-	X
56	MG	RA	3465	-	-	-	X
56	MG	RA	3466	-	-	-	X
56	MG	RA	3468	-	-	-	X
56	MG	RA	3470	-	-	-	X
56	MG	RA	3471	-	-	-	X
56	MG	RA	3472	-	-	-	X
56	MG	RA	3473	-	-	-	X
56	MG	RA	3476	-	-	-	X
56	MG	RA	3477	-	-	-	X
56	MG	RA	3479	-	-	-	X
56	MG	RA	3483	-	-	-	X
56	MG	RA	3484	-	-	-	X
56	MG	RA	3486	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	RA	3491	-	-	-	X
56	MG	RA	3496	-	-	-	X
56	MG	RA	3497	-	-	-	X
56	MG	RA	3501	-	-	-	X
56	MG	RA	3502	-	-	-	X
56	MG	RA	3505	-	-	-	X
56	MG	RA	3512	-	-	-	X
56	MG	RA	3514	-	-	-	X
56	MG	RA	3518	-	-	-	X
56	MG	RA	3521	-	-	-	X
56	MG	RA	3524	-	-	-	X
56	MG	RA	3526	-	-	-	X
56	MG	RA	3533	-	-	-	X
56	MG	RA	3535	-	-	-	X
56	MG	RA	3536	-	-	-	X
56	MG	RA	3537	-	-	-	X
56	MG	RA	3538	-	-	-	X
56	MG	RA	3539	-	-	-	X
56	MG	RA	3551	-	-	-	X
56	MG	RA	3566	-	-	-	X
56	MG	RA	3568	-	-	-	X
56	MG	RA	3572	-	-	-	X
56	MG	RA	3574	-	-	-	X
56	MG	RA	3588	-	-	-	X
56	MG	RA	3598	-	-	-	X
56	MG	RA	3601	-	-	-	X
56	MG	RA	3603	-	-	-	X
56	MG	RA	3607	-	-	-	X
56	MG	RA	3609	-	-	-	X
56	MG	RA	3611	-	-	-	X
56	MG	RA	3614	-	-	-	X
56	MG	RA	3616	-	-	-	X
56	MG	RA	3618	-	-	-	X
56	MG	RA	3623	-	-	-	X
56	MG	RA	3624	-	-	-	X
56	MG	RA	3630	-	-	-	X
56	MG	RA	3631	-	-	-	X
56	MG	RA	3634	-	-	-	X
56	MG	RA	3635	-	-	-	X
56	MG	RA	3638	-	-	-	X
56	MG	RA	3644	-	-	-	X
56	MG	RA	3656	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	RA	3659	-	-	-	X
56	MG	RA	3677	-	-	-	X
56	MG	RA	3679	-	-	-	X
56	MG	RA	3684	-	-	-	X
56	MG	RA	3696	-	-	-	X
56	MG	RA	3697	-	-	-	X
56	MG	RA	3707	-	-	-	X
56	MG	RA	3708	-	-	-	X
56	MG	RA	3709	-	-	-	X
56	MG	RA	3712	-	-	-	X
56	MG	RA	3713	-	-	-	X
56	MG	RA	3715	-	-	-	X
56	MG	RA	3717	-	-	-	X
56	MG	RA	3722	-	-	-	X
56	MG	RA	3724	-	-	-	X
56	MG	RA	3727	-	-	-	X
56	MG	RA	3733	-	-	-	X
56	MG	RA	3738	-	-	-	X
56	MG	RA	3742	-	-	-	X
56	MG	RA	3744	-	-	-	X
56	MG	RA	3746	-	-	-	X
56	MG	RA	3751	-	-	-	X
56	MG	RA	3754	-	-	-	X
56	MG	RA	3767	-	-	-	X
56	MG	RA	3770	-	-	-	X
56	MG	RA	3771	-	-	-	X
56	MG	RA	3773	-	-	-	X
56	MG	RA	3774	-	-	-	X
56	MG	RA	3786	-	-	-	X
56	MG	RA	3795	-	-	-	X
56	MG	RA	3803	-	-	-	X
56	MG	RA	3805	-	-	-	X
56	MG	RA	3807	-	-	-	X
56	MG	RA	3809	-	-	-	X
56	MG	RA	3812	-	-	-	X
56	MG	RA	3814	-	-	-	X
56	MG	RA	3821	-	-	-	X
56	MG	RA	3823	-	-	-	X
56	MG	RA	3827	-	-	-	X
56	MG	RA	3829	-	-	-	X
56	MG	RA	3839	-	-	-	X
56	MG	RA	3850	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	RA	3854	-	-	-	X
56	MG	RA	3856	-	-	-	X
56	MG	RA	3858	-	-	-	X
56	MG	RA	3862	-	-	-	X
56	MG	RA	3871	-	-	-	X
56	MG	RA	3874	-	-	-	X
56	MG	RA	3875	-	-	-	X
56	MG	RA	3882	-	-	-	X
56	MG	RA	3889	-	-	-	X
56	MG	RA	3892	-	-	-	X
56	MG	RA	3893	-	-	-	X
56	MG	RA	3900	-	-	-	X
56	MG	RA	3902	-	-	-	X
56	MG	RA	3903	-	-	-	X
56	MG	RA	3906	-	-	-	X
56	MG	RA	3911	-	-	-	X
56	MG	RA	3917	-	-	-	X
56	MG	RA	3924	-	-	-	X
56	MG	RA	3928	-	-	-	X
56	MG	RA	3938	-	-	-	X
56	MG	RA	3939	-	-	-	X
56	MG	RA	3941	-	-	-	X
56	MG	RA	3948	-	-	-	X
56	MG	RA	3952	-	-	-	X
56	MG	RA	3953	-	-	-	X
56	MG	RA	3959	-	-	-	X
56	MG	RA	3967	-	-	-	X
56	MG	RA	3969	-	-	-	X
56	MG	RA	3971	-	-	-	X
56	MG	RA	3981	-	-	-	X
56	MG	RA	3986	-	-	-	X
56	MG	RA	3990	-	-	-	X
56	MG	RA	4002	-	-	-	X
56	MG	RA	4003	-	-	-	X
56	MG	RA	4006	-	-	-	X
56	MG	RA	4008	-	-	-	X
56	MG	RA	4009	-	-	-	X
56	MG	RA	4012	-	-	-	X
56	MG	RA	4017	-	-	-	X
56	MG	RA	4018	-	-	-	X
56	MG	RA	4021	-	-	-	X
56	MG	RA	4023	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	RA	4024	-	-	-	X
56	MG	RA	4025	-	-	-	X
56	MG	RA	4026	-	-	-	X
56	MG	RA	4027	-	-	-	X
56	MG	RA	4028	-	-	-	X
56	MG	RA	4030	-	-	-	X
56	MG	RA	4032	-	-	-	X
56	MG	RA	4033	-	-	-	X
56	MG	RA	4034	-	-	-	X
56	MG	RA	4035	-	-	-	X
56	MG	RA	4036	-	-	-	X
56	MG	RA	4037	-	-	-	X
56	MG	RA	4040	-	-	-	X
56	MG	RA	4041	-	-	-	X
56	MG	RA	4042	-	-	-	X
56	MG	RA	4043	-	-	-	X
56	MG	RA	4044	-	-	-	X
56	MG	RA	4045	-	-	-	X
56	MG	RA	4046	-	-	-	X
56	MG	RA	4047	-	-	-	X
56	MG	RA	4048	-	-	-	X
56	MG	RA	4049	-	-	-	X
56	MG	RA	4050	-	-	-	X
56	MG	RA	4051	-	-	-	X
56	MG	RA	4052	-	-	-	X
56	MG	RA	4056	-	-	-	X
56	MG	RA	4057	-	-	-	X
56	MG	RA	4058	-	-	-	X
56	MG	RA	4059	-	-	-	X
56	MG	RA	4060	-	-	-	X
56	MG	RA	4061	-	-	-	X
56	MG	RA	4062	-	-	-	X
56	MG	RA	4063	-	-	-	X
56	MG	RA	4064	-	-	-	X
56	MG	RA	4065	-	-	-	X
56	MG	RA	4066	-	-	-	X
56	MG	RA	4067	-	-	-	X
56	MG	RA	4068	-	-	-	X
56	MG	RB	201	-	-	-	X
56	MG	RB	209	-	-	-	X
56	MG	RB	225	-	-	-	X
56	MG	RD	302	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	RD	303	-	-	-	X
56	MG	RD	305	-	-	-	X
56	MG	RD	306	-	-	-	X
56	MG	RD	308	-	-	-	X
56	MG	RD	309	-	-	-	X
56	MG	RD	312	-	-	-	X
56	MG	RD	313	-	-	-	X
56	MG	RE	302	-	-	-	X
56	MG	RE	306	-	-	-	X
56	MG	RE	307	-	-	-	X
56	MG	RF	301	-	-	-	X
56	MG	RF	303	-	-	-	X
56	MG	RF	304	-	-	-	X
56	MG	RF	305	-	-	-	X
56	MG	RF	306	-	-	-	X
56	MG	RF	308	-	-	-	X
56	MG	RF	309	-	-	-	X
56	MG	RF	311	-	-	-	X
56	MG	RN	201	-	-	-	X
56	MG	RP	201	-	-	-	X
56	MG	RQ	201	-	-	-	X
56	MG	RQ	204	-	-	-	X
56	MG	RR	201	-	-	-	X
56	MG	RR	202	-	-	-	X
56	MG	RU	203	-	-	-	X
56	MG	RV	202	-	-	-	X
56	MG	RV	203	-	-	-	X
56	MG	RX	101	-	-	-	X
56	MG	XA	1609	-	-	-	X
56	MG	XA	1611	-	-	-	X
56	MG	XA	1612	-	-	-	X
56	MG	XA	1616	-	-	-	X
56	MG	XA	1618	-	-	-	X
56	MG	XA	1623	-	-	-	X
56	MG	XA	1627	-	-	-	X
56	MG	XA	1628	-	-	-	X
56	MG	XA	1629	-	-	-	X
56	MG	XA	1631	-	-	-	X
56	MG	XA	1632	-	-	-	X
56	MG	XA	1633	-	-	-	X
56	MG	XA	1637	-	-	-	X
56	MG	XA	1645	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	XA	1658	-	-	-	X
56	MG	XA	1666	-	-	-	X
56	MG	XA	1673	-	-	-	X
56	MG	XA	1683	-	-	-	X
56	MG	XA	1688	-	-	-	X
56	MG	XA	1690	-	-	-	X
56	MG	XA	1696	-	-	-	X
56	MG	XA	1700	-	-	-	X
56	MG	XA	1707	-	-	-	X
56	MG	XA	1720	-	-	-	X
56	MG	XA	1723	-	-	-	X
56	MG	XA	1725	-	-	-	X
56	MG	XA	1727	-	-	-	X
56	MG	XA	1728	-	-	-	X
56	MG	XA	1731	-	-	-	X
56	MG	XA	1737	-	-	-	X
56	MG	XA	1738	-	-	-	X
56	MG	XA	1741	-	-	-	X
56	MG	XA	1744	-	-	-	X
56	MG	XA	1747	-	-	-	X
56	MG	XA	1758	-	-	-	X
56	MG	XA	1759	-	-	-	X
56	MG	XA	1760	-	-	-	X
56	MG	XA	1763	-	-	-	X
56	MG	XA	1770	-	-	-	X
56	MG	XA	1772	-	-	-	X
56	MG	XA	1774	-	-	-	X
56	MG	XA	1776	-	-	-	X
56	MG	XA	1777	-	-	-	X
56	MG	XA	1780	-	-	-	X
56	MG	XA	1781	-	-	-	X
56	MG	XA	1786	-	-	-	X
56	MG	XA	1792	-	-	-	X
56	MG	XA	1793	-	-	-	X
56	MG	XF	202	-	-	-	X
56	MG	XT	201	-	-	-	X
56	MG	Y0	101	-	-	-	X
56	MG	Y6	102	-	-	-	X
56	MG	Y8	101	-	-	-	X
56	MG	YA	3007	-	-	-	X
56	MG	YA	3008	-	-	-	X
56	MG	YA	3011	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	YA	3013	-	-	-	X
56	MG	YA	3019	-	-	-	X
56	MG	YA	3020	-	-	-	X
56	MG	YA	3027	-	-	-	X
56	MG	YA	3028	-	-	-	X
56	MG	YA	3030	-	-	-	X
56	MG	YA	3033	-	-	-	X
56	MG	YA	3036	-	-	-	X
56	MG	YA	3049	-	-	-	X
56	MG	YA	3053	-	-	-	X
56	MG	YA	3058	-	-	-	X
56	MG	YA	3071	-	-	-	X
56	MG	YA	3074	-	-	-	X
56	MG	YA	3077	-	-	-	X
56	MG	YA	3088	-	-	-	X
56	MG	YA	3089	-	-	-	X
56	MG	YA	3091	-	-	-	X
56	MG	YA	3092	-	-	-	X
56	MG	YA	3094	-	-	-	X
56	MG	YA	3102	-	-	-	X
56	MG	YA	3104	-	-	-	X
56	MG	YA	3107	-	-	-	X
56	MG	YA	3110	-	-	-	X
56	MG	YA	3112	-	-	-	X
56	MG	YA	3122	-	-	-	X
56	MG	YA	3129	-	-	-	X
56	MG	YA	3131	-	-	-	X
56	MG	YA	3133	-	-	-	X
56	MG	YA	3134	-	-	-	X
56	MG	YA	3146	-	-	-	X
56	MG	YA	3148	-	-	-	X
56	MG	YA	3150	-	-	-	X
56	MG	YA	3152	-	-	-	X
56	MG	YA	3153	-	-	-	X
56	MG	YA	3156	-	-	-	X
56	MG	YA	3166	-	-	-	X
56	MG	YA	3170	-	-	-	X
56	MG	YA	3174	-	-	-	X
56	MG	YA	3183	-	-	-	X
56	MG	YA	3192	-	-	-	X
56	MG	YA	3199	-	-	-	X
56	MG	YA	3201	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	YA	3209	-	-	-	X
56	MG	YA	3210	-	-	-	X
56	MG	YA	3216	-	-	-	X
56	MG	YA	3217	-	-	-	X
56	MG	YA	3237	-	-	-	X
56	MG	YA	3240	-	-	-	X
56	MG	YA	3247	-	-	-	X
56	MG	YA	3249	-	-	-	X
56	MG	YA	3268	-	-	-	X
56	MG	YA	3269	-	-	-	X
56	MG	YA	3270	-	-	-	X
56	MG	YA	3272	-	-	-	X
56	MG	YA	3284	-	-	-	X
56	MG	YA	3285	-	-	-	X
56	MG	YA	3291	-	-	-	X
56	MG	YA	3295	-	-	-	X
56	MG	YA	3297	-	-	-	X
56	MG	YA	3299	-	-	-	X
56	MG	YA	3303	-	-	-	X
56	MG	YA	3311	-	-	-	X
56	MG	YA	3314	-	-	-	X
56	MG	YA	3316	-	-	-	X
56	MG	YA	3317	-	-	-	X
56	MG	YA	3318	-	-	-	X
56	MG	YA	3320	-	-	-	X
56	MG	YA	3321	-	-	-	X
56	MG	YA	3323	-	-	-	X
56	MG	YA	3324	-	-	-	X
56	MG	YA	3325	-	-	-	X
56	MG	YA	3326	-	-	-	X
56	MG	YA	3328	-	-	-	X
56	MG	YA	3332	-	-	-	X
56	MG	YA	3335	-	-	-	X
56	MG	YA	3336	-	-	-	X
56	MG	YA	3339	-	-	-	X
56	MG	YA	3343	-	-	-	X
56	MG	YA	3345	-	-	-	X
56	MG	YA	3350	-	-	-	X
56	MG	YA	3351	-	-	-	X
56	MG	YA	3355	-	-	-	X
56	MG	YA	3360	-	-	-	X
56	MG	YA	3361	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	YA	3368	-	-	-	X
56	MG	YA	3374	-	-	-	X
56	MG	YA	3377	-	-	-	X
56	MG	YA	3378	-	-	-	X
56	MG	YA	3382	-	-	-	X
56	MG	YA	3384	-	-	-	X
56	MG	YA	3386	-	-	-	X
56	MG	YA	3387	-	-	-	X
56	MG	YA	3388	-	-	-	X
56	MG	YA	3391	-	-	-	X
56	MG	YA	3392	-	-	-	X
56	MG	YA	3397	-	-	-	X
56	MG	YA	3398	-	-	-	X
56	MG	YA	3401	-	-	-	X
56	MG	YA	3404	-	-	-	X
56	MG	YA	3409	-	-	-	X
56	MG	YA	3413	-	-	-	X
56	MG	YA	3415	-	-	-	X
56	MG	YA	3419	-	-	-	X
56	MG	YA	3420	-	-	-	X
56	MG	YA	3421	-	-	-	X
56	MG	YA	3429	-	-	-	X
56	MG	YA	3439	-	-	-	X
56	MG	YA	3440	-	-	-	X
56	MG	YA	3446	-	-	-	X
56	MG	YA	3447	-	-	-	X
56	MG	YA	3449	-	-	-	X
56	MG	YA	3456	-	-	-	X
56	MG	YA	3468	-	-	-	X
56	MG	YA	3474	-	-	-	X
56	MG	YA	3475	-	-	-	X
56	MG	YA	3476	-	-	-	X
56	MG	YA	3485	-	-	-	X
56	MG	YA	3488	-	-	-	X
56	MG	YA	3495	-	-	-	X
56	MG	YA	3499	-	-	-	X
56	MG	YA	3503	-	-	-	X
56	MG	YA	3509	-	-	-	X
56	MG	YA	3511	-	-	-	X
56	MG	YA	3514	-	-	-	X
56	MG	YA	3516	-	-	-	X
56	MG	YA	3517	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	YA	3518	-	-	-	X
56	MG	YA	3532	-	-	-	X
56	MG	YA	3538	-	-	-	X
56	MG	YA	3540	-	-	-	X
56	MG	YA	3550	-	-	-	X
56	MG	YA	3552	-	-	-	X
56	MG	YA	3554	-	-	-	X
56	MG	YA	3560	-	-	-	X
56	MG	YA	3570	-	-	-	X
56	MG	YA	3577	-	-	-	X
56	MG	YA	3578	-	-	-	X
56	MG	YA	3579	-	-	-	X
56	MG	YA	3580	-	-	-	X
56	MG	YA	3582	-	-	-	X
56	MG	YA	3587	-	-	-	X
56	MG	YA	3588	-	-	-	X
56	MG	YA	3600	-	-	-	X
56	MG	YA	3601	-	-	-	X
56	MG	YA	3606	-	-	-	X
56	MG	YA	3607	-	-	-	X
56	MG	YA	3610	-	-	-	X
56	MG	YA	3611	-	-	-	X
56	MG	YA	3612	-	-	-	X
56	MG	YA	3613	-	-	-	X
56	MG	YA	3614	-	-	-	X
56	MG	YA	3616	-	-	-	X
56	MG	YA	3621	-	-	-	X
56	MG	YA	3623	-	-	-	X
56	MG	YA	3630	-	-	-	X
56	MG	YA	3632	-	-	-	X
56	MG	YA	3633	-	-	-	X
56	MG	YA	3647	-	-	-	X
56	MG	YA	3648	-	-	-	X
56	MG	YA	3650	-	-	-	X
56	MG	YA	3656	-	-	-	X
56	MG	YA	3658	-	-	-	X
56	MG	YA	3660	-	-	-	X
56	MG	YA	3664	-	-	-	X
56	MG	YA	3665	-	-	-	X
56	MG	YA	3668	-	-	-	X
56	MG	YA	3679	-	-	-	X
56	MG	YA	3681	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	YA	3684	-	-	-	X
56	MG	YA	3685	-	-	-	X
56	MG	YA	3689	-	-	-	X
56	MG	YA	3691	-	-	-	X
56	MG	YA	3694	-	-	-	X
56	MG	YA	3699	-	-	-	X
56	MG	YA	3701	-	-	-	X
56	MG	YA	3702	-	-	-	X
56	MG	YA	3704	-	-	-	X
56	MG	YA	3705	-	-	-	X
56	MG	YA	3709	-	-	-	X
56	MG	YA	3710	-	-	-	X
56	MG	YA	3714	-	-	-	X
56	MG	YA	3715	-	-	-	X
56	MG	YA	3724	-	-	-	X
56	MG	YA	3727	-	-	-	X
56	MG	YA	3729	-	-	-	X
56	MG	YA	3733	-	-	-	X
56	MG	YA	3737	-	-	-	X
56	MG	YA	3740	-	-	-	X
56	MG	YA	3744	-	-	-	X
56	MG	YA	3745	-	-	-	X
56	MG	YA	3746	-	-	-	X
56	MG	YA	3747	-	-	-	X
56	MG	YA	3748	-	-	-	X
56	MG	YA	3749	-	-	-	X
56	MG	YA	3750	-	-	-	X
56	MG	YA	3751	-	-	-	X
56	MG	YA	3752	-	-	-	X
56	MG	YA	3753	-	-	-	X
56	MG	YA	3754	-	-	-	X
56	MG	YA	3755	-	-	-	X
56	MG	YA	3756	-	-	-	X
56	MG	YB	214	-	-	-	X
56	MG	YB	217	-	-	-	X
56	MG	YD	303	-	-	-	X
56	MG	YD	304	-	-	-	X
56	MG	YD	305	-	-	-	X
56	MG	YD	306	-	-	-	X
56	MG	YD	308	-	-	-	X
56	MG	YD	309	-	-	-	X
56	MG	YE	301	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	YE	302	-	-	-	X
56	MG	YE	303	-	-	-	X
56	MG	YE	305	-	-	-	X
56	MG	YF	301	-	-	-	X
56	MG	YF	303	-	-	-	X
56	MG	YQ	201	-	-	-	X
56	MG	YT	202	-	-	-	X
56	MG	YW	201	-	-	-	X
56	MG	YX	101	-	-	-	X
57	ZN	R4	101	-	-	-	X
57	ZN	Y4	101	-	-	-	X

2 Entry composition [i](#)

There are 58 unique types of molecules in this entry. The entry contains 296497 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 23S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	YA	2867	Total	C	N	O	P	0	0	0
			61758	27491	11552	19850	2865			
1	RA	2867	Total	C	N	O	P	0	0	0
			61758	27491	11552	19850	2865			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	YB	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			
2	RB	120	Total	C	N	O	P	0	0	0
			2572	1145	476	832	119			

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	YD	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			
3	RD	275	Total	C	N	O	S	0	0	0
			2131	1346	422	360	3			

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	YE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			
4	RE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	YF	203	Total	C	N	O	S	0	0	1
			1580	1007	297	274	2			
5	RF	203	Total	C	N	O	S	0	0	1
			1584	1009	298	275	2			

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	YG	181	Total	C	N	O	S	0	0	0
			1424	912	259	249	4			
6	RG	181	Total	C	N	O	S	0	0	0
			1426	916	253	253	4			

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	YH	173	Total	C	N	O	S	0	0	0
			1324	842	247	234	1			
7	RH	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	YI	146	Total	C	N	O	S	0	0	0
			1076	687	186	202	1			
8	RI	147	Total	C	N	O	S	0	0	0
			1094	699	191	203	1			

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	YN	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			
9	RN	140	Total	C	N	O	S	0	0	0
			1121	722	208	187	4			

- Molecule 10 is a protein called 50S ribosomal protein L14.

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

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

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	YP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			
11	RP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	YQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			
12	RQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	YR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			
13	RR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	YS	110	Total	C	N	O	0	0	0
			870	549	173	148			
14	RS	110	Total	C	N	O	0	0	0
			877	553	175	149			

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	YT	131	Total	C	N	O	0	0	0
			1083	675	224	183			
15	RT	131	Total	C	N	O	0	0	0
			1091	680	225	185			

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	YU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			
16	RU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	YV	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			
17	RV	101	Total	C	N	O	S	0	0	0
			775	498	141	135	1			

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	YW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			
18	RW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	YX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			
19	RX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	YY	107	Total	C	N	O	S	0	0	0
			810	519	153	132	6			
20	RY	107	Total	C	N	O	S	0	0	0
			810	520	153	131	6			

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	YZ	201	Total	C	N	O	S	0	0	0
			1557	995	274	286	2			
21	RZ	203	Total	C	N	O	S	0	0	0
			1587	1011	282	292	2			

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	Y0	77	Total	C	N	O	S	0	0	0
			608	375	129	103	1			
22	R0	77	Total	C	N	O	S	0	0	0
			608	375	129	103	1			

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	Y1	97	Total	C	N	O	S	0	0	0
			759	478	149	131	1			
23	R1	97	Total	C	N	O	S	0	0	0
			754	475	148	130	1			

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	Y2	70	Total	C	N	O	S	0	0	0
			592	368	119	103	2			
24	R2	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
25	Y3	59	Total	C	N	O	0	0	0
			464	296	90	78			
25	R3	59	Total	C	N	O	0	0	0
			469	298	90	81			

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	Y4	69	Total	C	N	O	S	0	0	0
			536	342	98	91	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	R4	69	Total	C	N	O	S	0	0	0
			546	346	96	99	5			

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	Y5	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			
27	R5	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	Y6	53	Total	C	N	O	S	0	0	0
			449	279	91	75	4			
28	R6	53	Total	C	N	O	S	0	0	0
			453	281	91	77	4			

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	Y7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			
29	R7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	Y8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			
30	R8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	Y9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
31	R9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 32 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	XA	1504	Total	C	N	O	P	0	0	0
			32331	14396	5990	10441	1504			
32	QA	1500	Total	C	N	O	P	0	0	0
			32246	14358	5975	10413	1500			

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	XB	231	Total	C	N	O	S	0	0	0
			1825	1167	326	327	5			
33	QB	231	Total	C	N	O	S	0	0	0
			1842	1175	330	332	5			

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	XC	206	Total	C	N	O	S	0	0	0
			1542	968	300	273	1			
34	QC	206	Total	C	N	O	S	0	0	0
			1558	979	305	273	1			

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	XD	208	Total	C	N	O	S	0	0	0
			1668	1047	330	284	7			
35	QD	208	Total	C	N	O	S	0	0	0
			1665	1043	329	286	7			

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	XE	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			
36	QE	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	XF	100	Total	C	N	O	S	0	0	0
			816	516	146	151	3			
37	QF	100	Total	C	N	O	S	0	0	0
			814	516	144	151	3			

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	XG	155	Total	C	N	O	S	0	0	0
			1229	766	241	216	6			
38	QG	155	Total	C	N	O	S	0	0	0
			1235	769	244	216	6			

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	XH	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			
39	QH	137	Total	C	N	O	S	0	0	0
			1098	694	210	192	2			

- Molecule 40 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	XI	126	Total	C	N	O		0	0	0
			966	613	186	167				
40	QI	127	Total	C	N	O		0	0	0
			986	625	193	168				

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	XJ	96	Total	C	N	O		0	0	0
			710	442	137	131				
41	QJ	97	Total	C	N	O		0	0	0
			719	446	142	131				

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	XK	114	Total	C	N	O	S	0	0	0
			833	519	156	155	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	QK	114	Total	C	N	O	S	0	0	0
			834	520	156	155	3			

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	XL	122	Total	C	N	O	S	0	0	0
			932	586	185	159	2			
43	QL	122	Total	C	N	O	S	0	0	0
			932	586	185	159	2			

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	XM	114	Total	C	N	O	S	0	0	0
			895	550	186	157	2			
44	QM	116	Total	C	N	O	S	0	0	0
			914	564	189	159	2			

- Molecule 45 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	XN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			
45	QN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

- Molecule 46 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	XO	88	Total	C	N	O	S	0	0	0
			728	456	144	126	2			
46	QO	88	Total	C	N	O	S	0	0	0
			728	456	144	126	2			

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	XP	82	Total	C	N	O	S	0	0	0
			677	430	133	113	1			
47	QP	82	Total	C	N	O	S	0	0	0
			681	433	134	113	1			

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	XQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			
48	QQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	XR	68	Total	C	N	O		0	0	0
			555	355	108	92				
49	QR	68	Total	C	N	O		0	0	0
			555	355	108	92				

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	XS	83	Total	C	N	O	S	0	0	0
			645	410	118	115	2			
50	QS	83	Total	C	N	O	S	0	0	0
			648	415	120	111	2			

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	XT	98	Total	C	N	O	S	0	0	0
			733	451	154	126	2			
51	QT	96	Total	C	N	O	S	0	0	0
			732	449	157	124	2			

- Molecule 52 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	XU	23	Total	C	N	O		0	0	0
			199	122	48	29				
52	QU	23	Total	C	N	O		0	0	0
			199	122	48	29				

- Molecule 53 is a RNA chain called P-site tRNA fMet.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	QV	77	Total	C	N	O	P	0	0	0
			1644	732	297	538	77			
53	XV	77	Total	C	N	O	P	0	0	0
			1644	732	297	538	77			

- Molecule 54 is a protein called Peptide chain release factor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	QY	357	Total	C	N	O	S	0	0	0
			2833	1742	498	583	10			
54	XY	357	Total	C	N	O	S	0	0	0
			2833	1742	498	583	10			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
QY	-14	MET	-	initiating methionine	UNP P07012
QY	-13	GLY	-	expression tag	UNP P07012
QY	-12	SER	-	expression tag	UNP P07012
QY	-11	SER	-	expression tag	UNP P07012
QY	-10	HIS	-	expression tag	UNP P07012
QY	-9	HIS	-	expression tag	UNP P07012
QY	-8	HIS	-	expression tag	UNP P07012
QY	-7	HIS	-	expression tag	UNP P07012
QY	-6	HIS	-	expression tag	UNP P07012
QY	-5	HIS	-	expression tag	UNP P07012
QY	-4	SER	-	expression tag	UNP P07012
QY	-3	GLU	-	expression tag	UNP P07012
QY	-2	ASP	-	expression tag	UNP P07012
QY	-1	PRO	-	expression tag	UNP P07012
QY	0	ALA	-	expression tag	UNP P07012
QY	298	VAL	LEU	conflict	UNP P07012
XY	-14	MET	-	initiating methionine	UNP P07012
XY	-13	GLY	-	expression tag	UNP P07012
XY	-12	SER	-	expression tag	UNP P07012
XY	-11	SER	-	expression tag	UNP P07012
XY	-10	HIS	-	expression tag	UNP P07012
XY	-9	HIS	-	expression tag	UNP P07012
XY	-8	HIS	-	expression tag	UNP P07012
XY	-7	HIS	-	expression tag	UNP P07012
XY	-6	HIS	-	expression tag	UNP P07012
XY	-5	HIS	-	expression tag	UNP P07012
XY	-4	SER	-	expression tag	UNP P07012

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Chain	Residue	Modelled	Actual	Comment	Reference
XY	-3	GLU	-	expression tag	UNP P07012
XY	-2	ASP	-	expression tag	UNP P07012
XY	-1	PRO	-	expression tag	UNP P07012
XY	0	ALA	-	expression tag	UNP P07012
XY	298	VAL	LEU	conflict	UNP P07012

- Molecule 55 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	XX	6	Total	C	N	O	P	0	0	0
			129	58	24	41	6			
55	QX	6	Total	C	N	O	P	0	0	0
			129	58	24	41	6			

- Molecule 56 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	QA	280	Total	Mg	0	0
			280	280		
56	YV	1	Total	Mg	0	0
			1	1		
56	RP	2	Total	Mg	0	0
			2	2		
56	R7	2	Total	Mg	0	0
			2	2		
56	YA	756	Total	Mg	0	0
			756	756		
56	Y5	1	Total	Mg	0	0
			1	1		
56	YR	1	Total	Mg	0	0
			1	1		
56	RT	3	Total	Mg	0	0
			3	3		
56	QD	4	Total	Mg	0	0
			4	4		
56	RN	3	Total	Mg	0	0
			3	3		
56	XE	2	Total	Mg	0	0
			2	2		
56	RG	4	Total	Mg	0	0
			4	4		
56	Y1	2	Total	Mg	0	0
			2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	YD	9	Total Mg 9 9	0	0
56	QV	4	Total Mg 4 4	0	0
56	RX	1	Total Mg 1 1	0	0
56	Y8	2	Total Mg 2 2	0	0
56	YO	2	Total Mg 2 2	0	0
56	XA	193	Total Mg 193 193	0	0
56	QI	1	Total Mg 1 1	0	0
56	RQ	4	Total Mg 4 4	0	0
56	R0	4	Total Mg 4 4	0	0
56	XT	1	Total Mg 1 1	0	0
56	QR	1	Total Mg 1 1	0	0
56	QL	2	Total Mg 2 2	0	0
56	RU	3	Total Mg 3 3	0	0
56	QG	3	Total Mg 3 3	0	0
56	RO	1	Total Mg 1 1	0	0
56	XJ	1	Total Mg 1 1	0	0
56	QO	1	Total Mg 1 1	0	0
56	Y0	1	Total Mg 1 1	0	0
56	YG	3	Total Mg 3 3	0	0
56	XY	1	Total Mg 1 1	0	0
56	YQ	2	Total Mg 2 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	YN	1	Total 1	Mg 1	0	0
56	XF	3	Total 3	Mg 3	0	0
56	YX	1	Total 1	Mg 1	0	0
56	RR	4	Total 4	Mg 4	0	0
56	RD	14	Total 14	Mg 14	0	0
56	R1	4	Total 4	Mg 4	0	0
56	Y7	1	Total 1	Mg 1	0	0
56	YT	3	Total 3	Mg 3	0	0
56	RV	4	Total 4	Mg 4	0	0
56	QF	1	Total 1	Mg 1	0	0
56	RH	2	Total 2	Mg 2	0	0
56	XK	1	Total 1	Mg 1	0	0
56	QH	2	Total 2	Mg 2	0	0
56	QQ	2	Total 2	Mg 2	0	0
56	RA	1069	Total 1069	Mg 1069	0	0
56	R4	1	Total 1	Mg 1	0	0
56	YF	3	Total 3	Mg 3	0	0
56	YP	1	Total 1	Mg 1	0	0
56	RZ	1	Total 1	Mg 1	0	0
56	QB	1	Total 1	Mg 1	0	0
56	QM	1	Total 1	Mg 1	0	0

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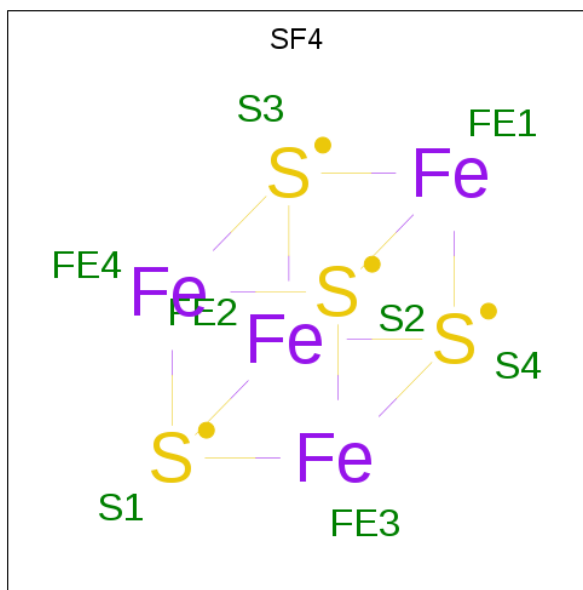
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	R9	2	Total	Mg	0	0
			2	2		
56	RE	7	Total	Mg	0	0
			7	7		
56	XL	1	Total	Mg	0	0
			1	1		
56	YB	19	Total	Mg	0	0
			19	19		
56	QT	1	Total	Mg	0	0
			1	1		
56	QN	2	Total	Mg	0	0
			2	2		
56	Y6	1	Total	Mg	0	0
			1	1		
56	YW	2	Total	Mg	0	0
			2	2		
56	RW	2	Total	Mg	0	0
			2	2		
56	QY	2	Total	Mg	0	0
			2	2		
56	XH	1	Total	Mg	0	0
			1	1		
56	XV	3	Total	Mg	0	0
			3	3		
56	RB	28	Total	Mg	0	0
			28	28		
56	YI	1	Total	Mg	0	0
			1	1		
56	QE	2	Total	Mg	0	0
			2	2		
56	R5	4	Total	Mg	0	0
			4	4		
56	R8	1	Total	Mg	0	0
			1	1		
56	RF	11	Total	Mg	0	0
			11	11		
56	R3	2	Total	Mg	0	0
			2	2		
56	YE	7	Total	Mg	0	0
			7	7		

- Molecule 57 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	Y9	1	Total Zn 1 1	0	0
57	QN	1	Total Zn 1 1	0	0
57	Y6	1	Total Zn 1 1	0	0
57	XN	1	Total Zn 1 1	0	0
57	R9	1	Total Zn 1 1	0	0
57	Y4	1	Total Zn 1 1	0	0
57	R6	1	Total Zn 1 1	0	0
57	Y5	1	Total Zn 1 1	0	0
57	R5	1	Total Zn 1 1	0	0
57	YY	1	Total Zn 1 1	0	0
57	R4	1	Total Zn 1 1	0	0
57	RY	1	Total Zn 1 1	0	0

- Molecule 58 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).

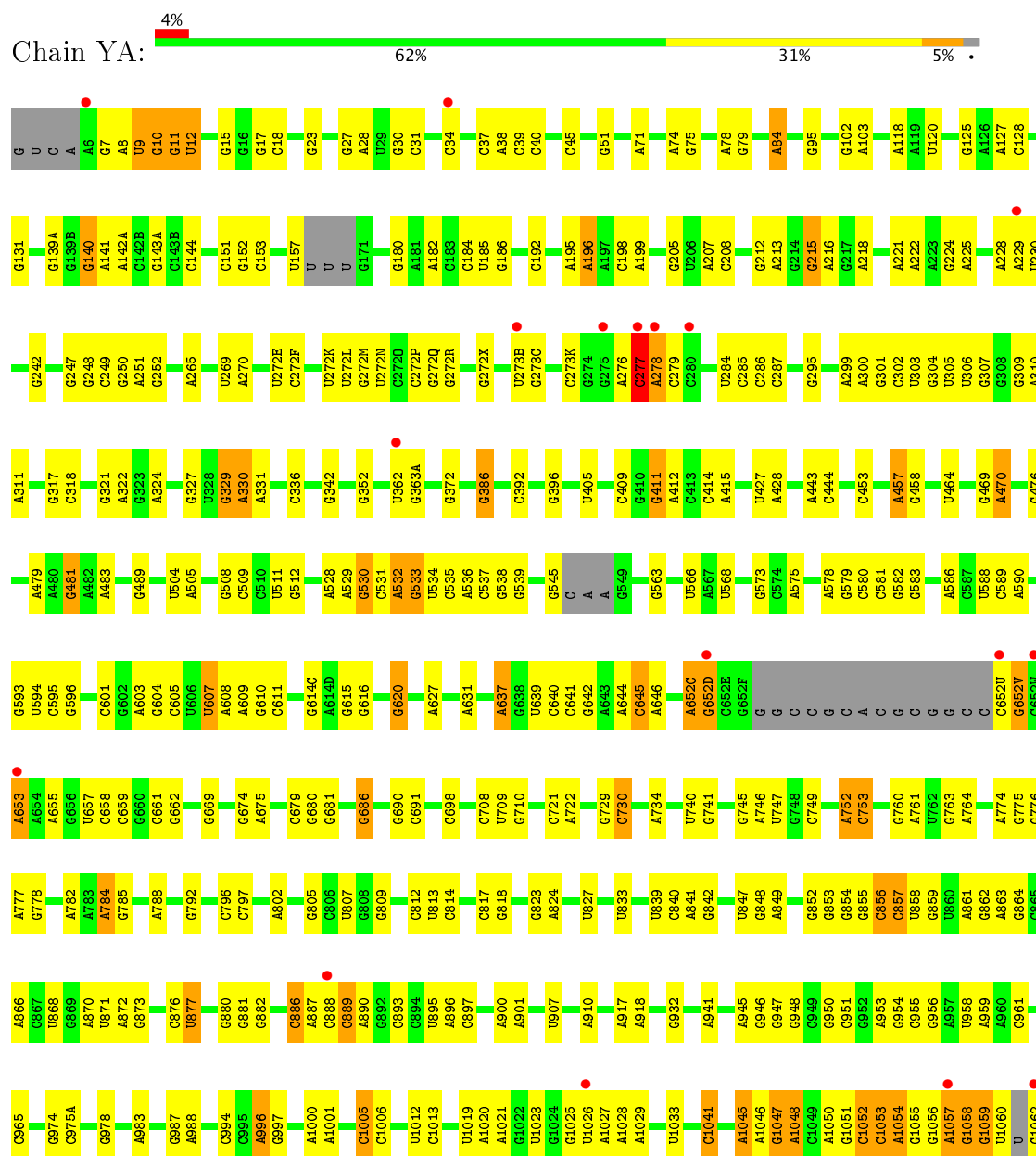


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
58	XD	1	Total 8	Fe 4	S 4	0	0
58	QD	1	Total 8	Fe 4	S 4	0	0

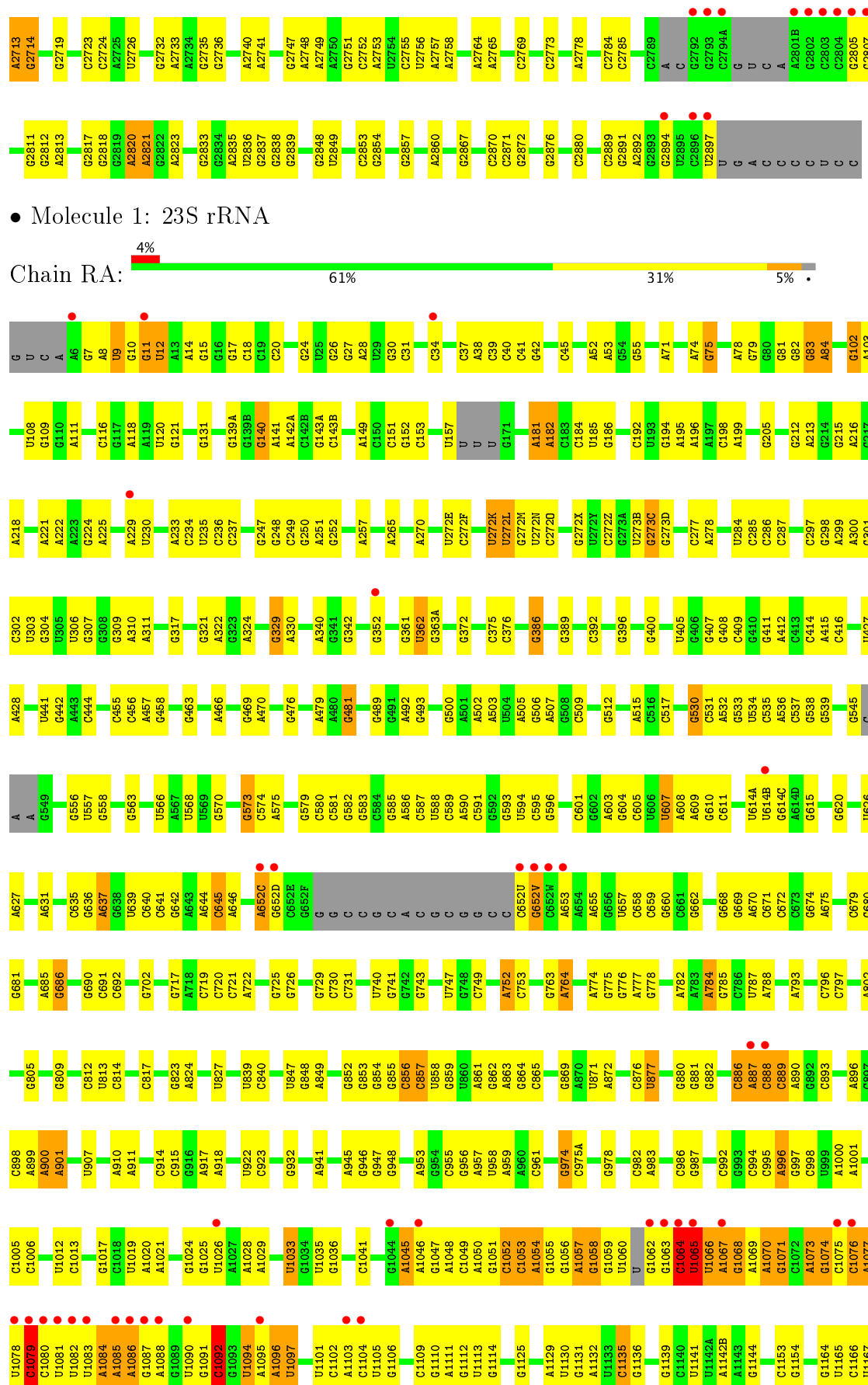
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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: 23S rRNA



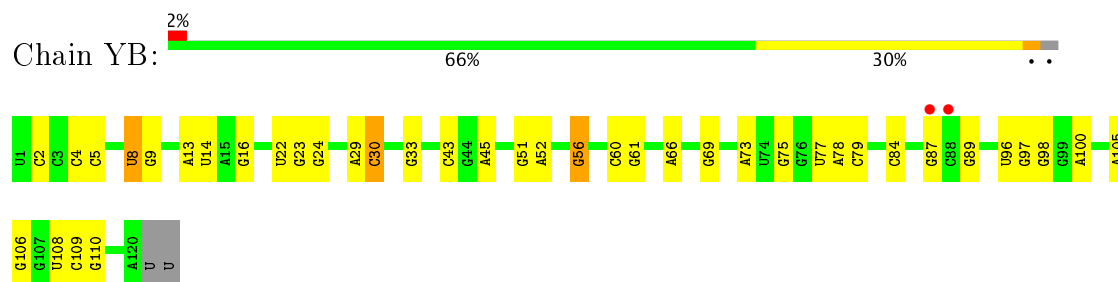
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U2603	C2359	G2270	G2166	G2106	G2012	A1876	U1757	G1622	A1509B	C1405	G1279	C1064
U2604	A2360	G2271	U2167	C2107	A2013	A1877	A1758	G1623	U1514	U1404	U1167	U1085
U2611	A2361	C2275	A2169	U2109	G2018	G1878	A1762	U1639	G1515	C1407	G1289	U1066
C2612	C2364	G2279	A2170	C2111	A2019	A1885	G1763	U1640	U1518	C1408	G1295	A1067
U2615	G2365	C2283	U2172	G2112	U2022	A1886	G1764	C1647	G1519	C1409	G1296	G1068
C2616	C2373	A2286	C2174	A2114	G2023	C1886	A1773	G1645	G1525	G1410	G1297	A1069
C2617	C2374	A2287	C2175	G2115	G2024	C1887	C1774	G1646	G1526	A1411	A	A1070
A2629	G2375	A2288	C2176	G2116	C2025	G1899	A1780	G1647	G1529	G1412	U	C1072
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C2635	G2379	U2290	U2180	U2119	A2031	G1906	A1786	C1649	C1630	G1414	C1178	G1075
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C2646	G2389	G2303	G2187	G2123	G2035	A1918	G1792	C1657	A	U420	G1184	C1080
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U2687	G2423	G2224	G2225	C2136	C2063	U1946	U1805	C1685	A1445A	C1445B	A1220	U1094
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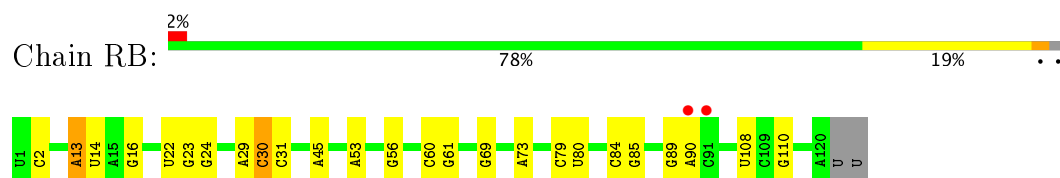
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C D C

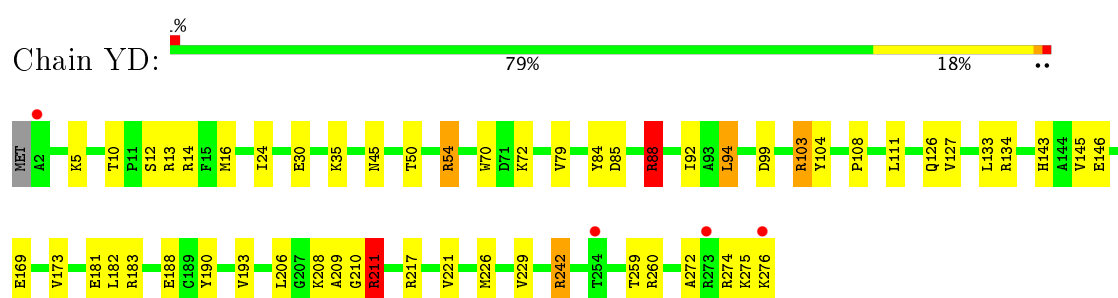
- Molecule 2: 5S rRNA



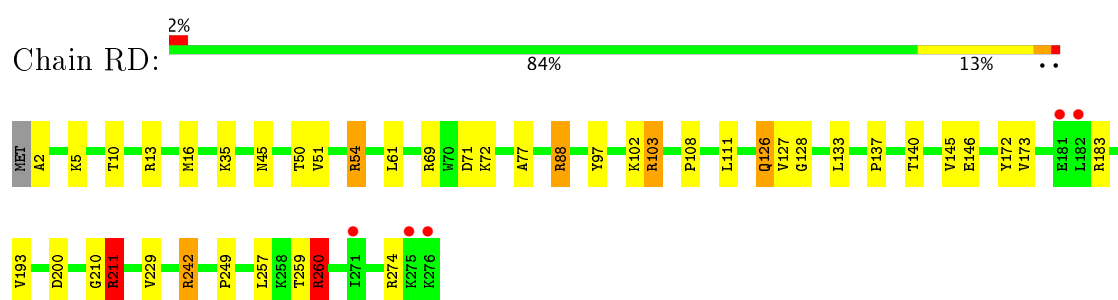
- Molecule 2: 5S rRNA



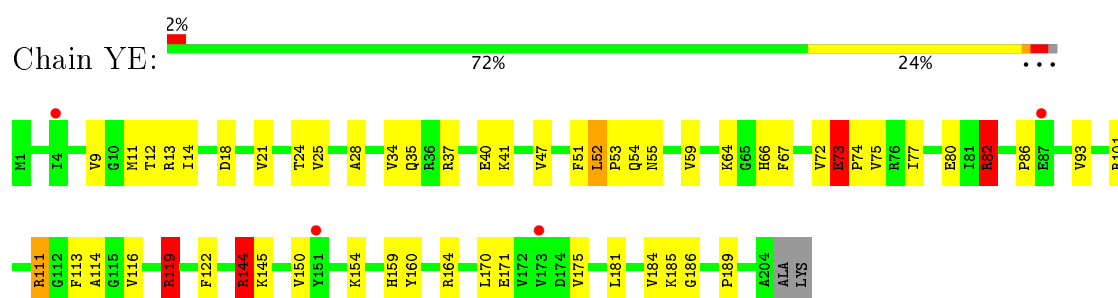
- Molecule 3: 50S ribosomal protein L2



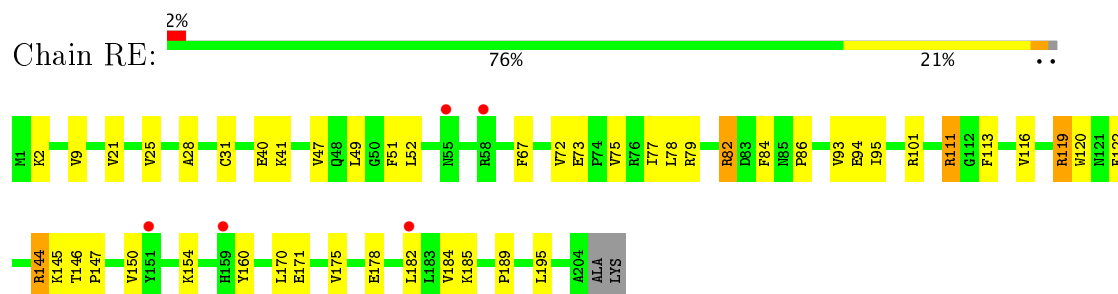
- Molecule 3: 50S ribosomal protein L2



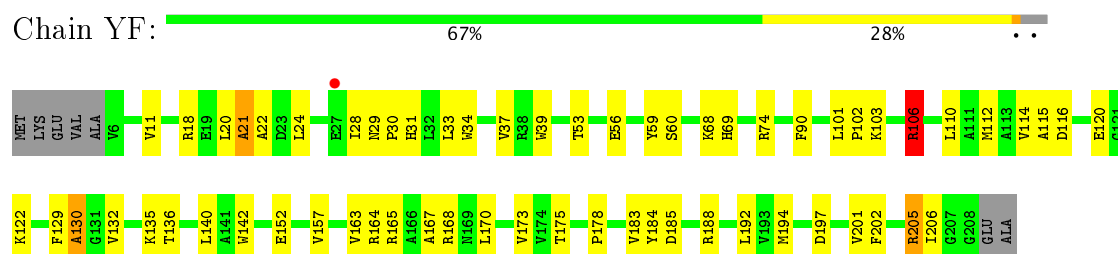
- Molecule 4: 50S ribosomal protein L3



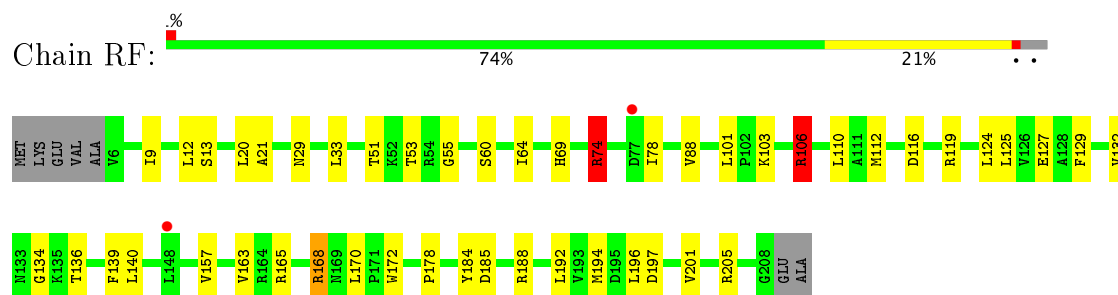
- Molecule 4: 50S ribosomal protein L3



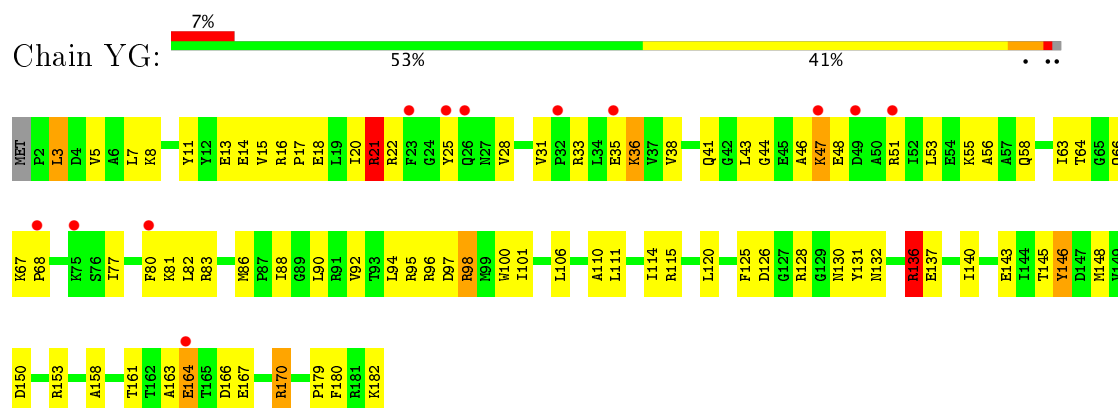
- Molecule 5: 50S ribosomal protein L4



- Molecule 5: 50S ribosomal protein L4

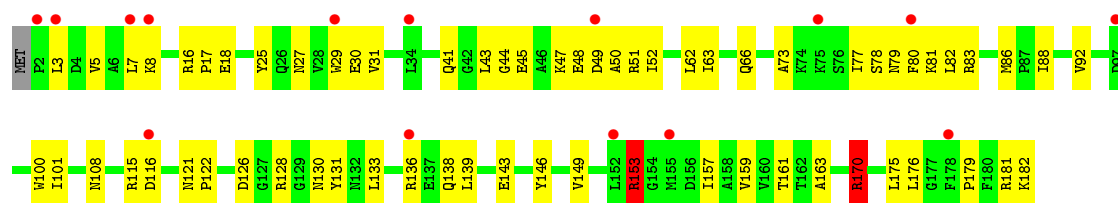


- Molecule 6: 50S ribosomal protein L5

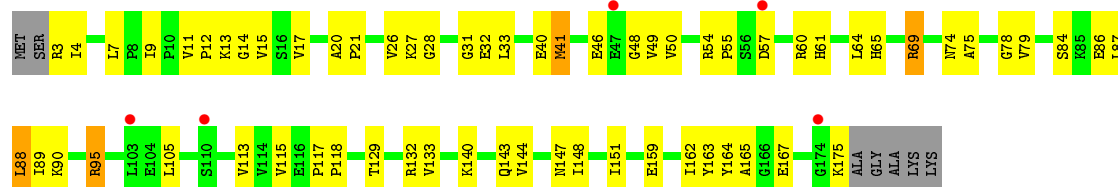


- Molecule 6: 50S ribosomal protein L5

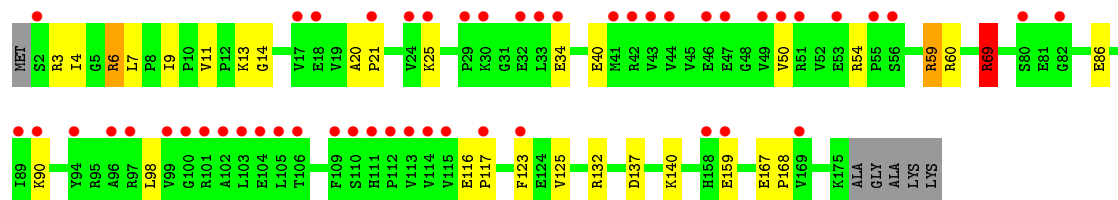
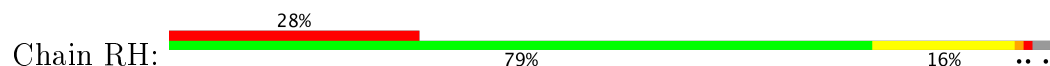




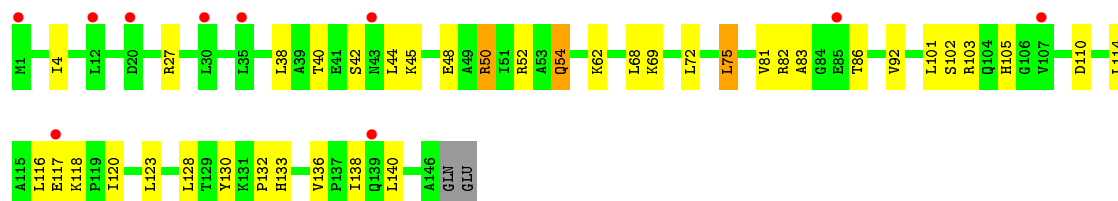
• Molecule 7: 50S ribosomal protein L6



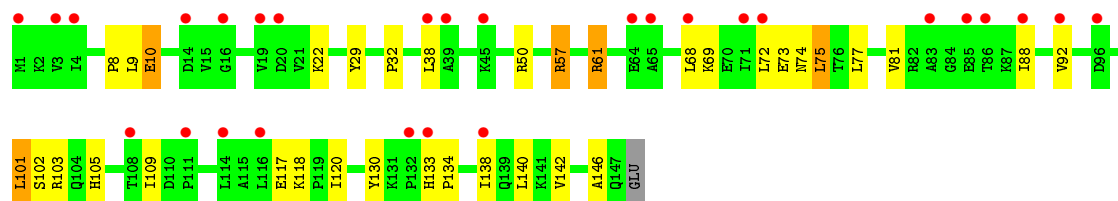
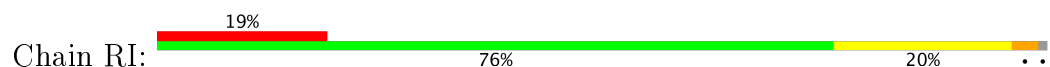
• Molecule 7: 50S ribosomal protein L6



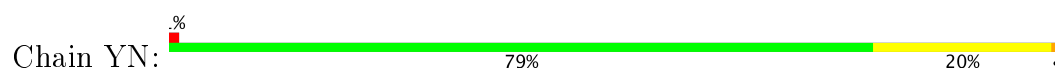
• Molecule 8: 50S ribosomal protein L9



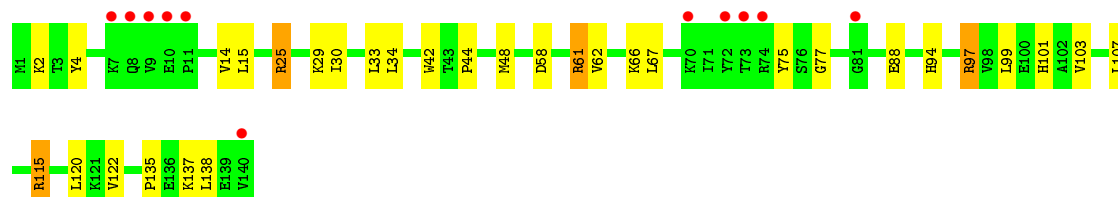
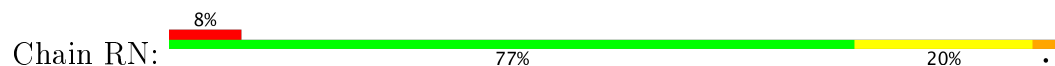
• Molecule 8: 50S ribosomal protein L9



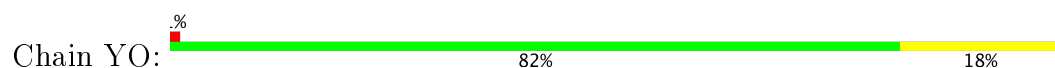
• Molecule 9: 50S ribosomal protein L13



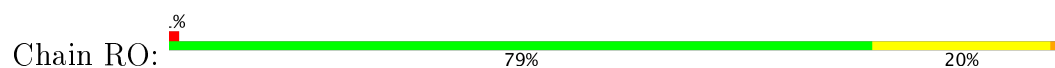
- Molecule 9: 50S ribosomal protein L13



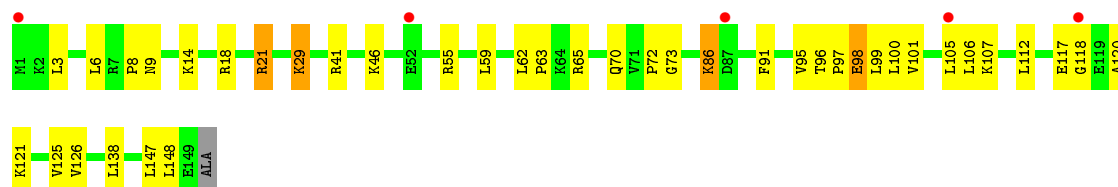
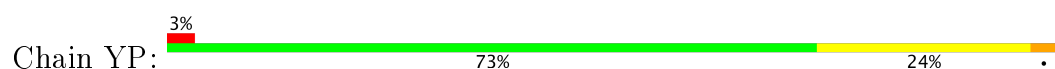
- Molecule 10: 50S ribosomal protein L14



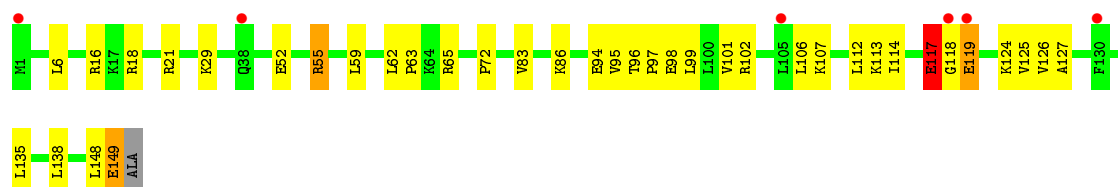
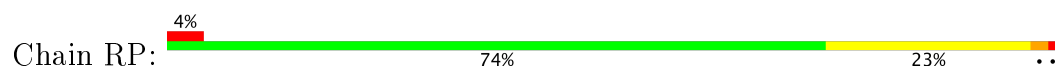
- Molecule 10: 50S ribosomal protein L14




- Molecule 11: 50S ribosomal protein L15

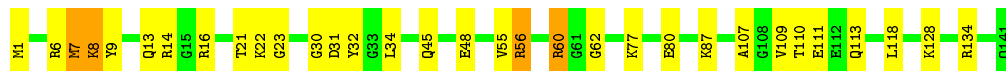


- Molecule 11: 50S ribosomal protein L15




- Molecule 12: 50S ribosomal protein L16

Chain YQ:  77% 20% .




- Molecule 12: 50S ribosomal protein L16

Chain RQ:  78% 19% .




- Molecule 13: 50S ribosomal protein L17

Chain YR:  71% 28% .



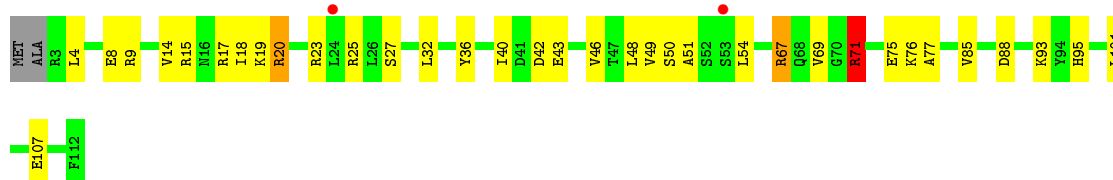
- Molecule 13: 50S ribosomal protein L17

Chain RR:  83% 15% .




- Molecule 14: 50S ribosomal protein L18

Chain YS:  67% 29% . . .



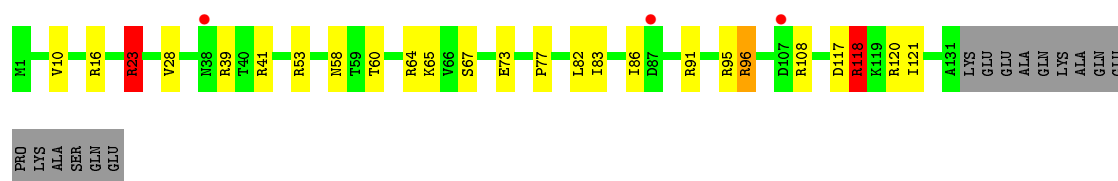
- Molecule 14: 50S ribosomal protein L18

Chain RS:  78% 17% . .

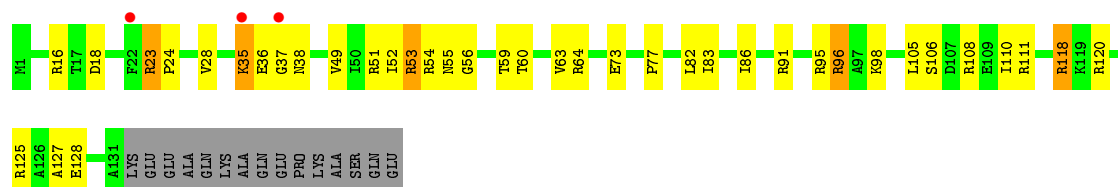


- Molecule 15: 50S ribosomal protein L19

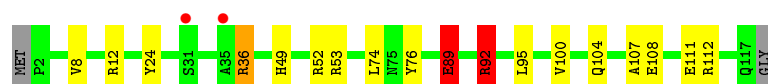
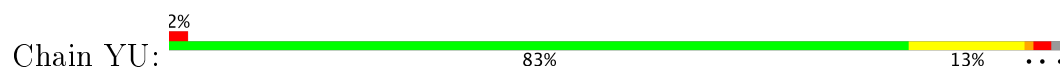
Chain YT:  73% 15% 10% . .



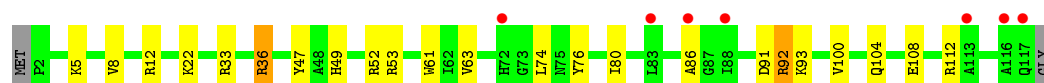
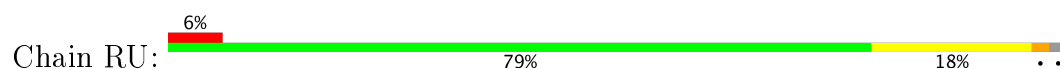
- Molecule 15: 50S ribosomal protein L19



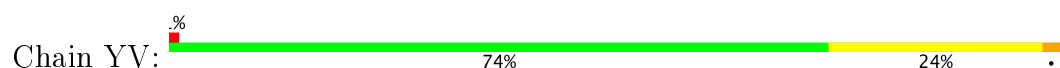
- Molecule 16: 50S ribosomal protein L20



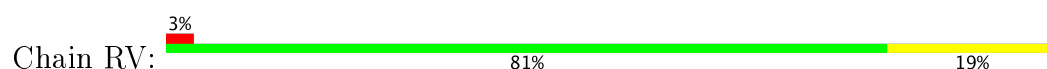
- Molecule 16: 50S ribosomal protein L20



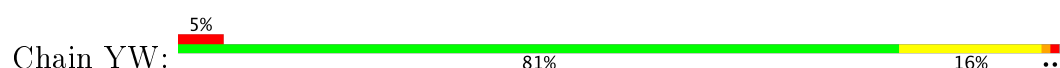
- Molecule 17: 50S ribosomal protein L21



- Molecule 17: 50S ribosomal protein L21

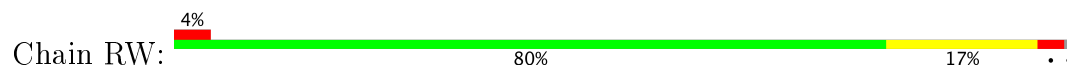


- Molecule 18: 50S ribosomal protein L22

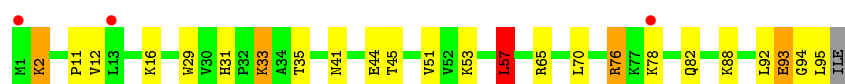
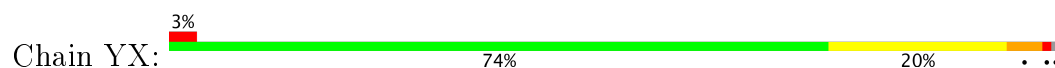




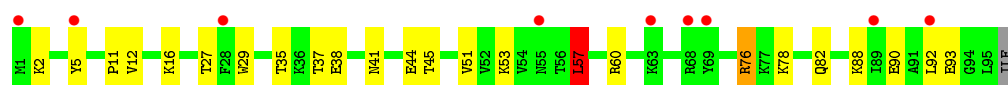
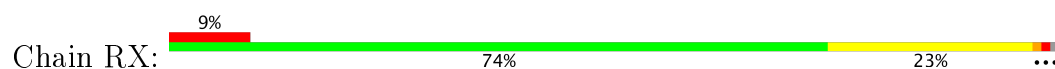
- Molecule 18: 50S ribosomal protein L22



- Molecule 19: 50S ribosomal protein L23



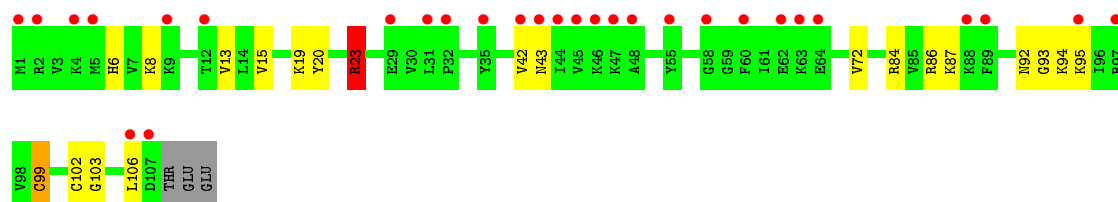
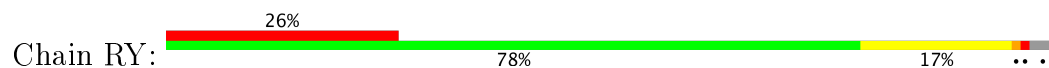
- Molecule 19: 50S ribosomal protein L23



- Molecule 20: 50S ribosomal protein L24

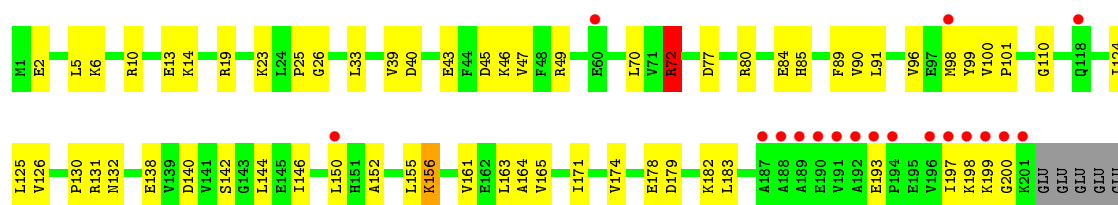


- Molecule 20: 50S ribosomal protein L24

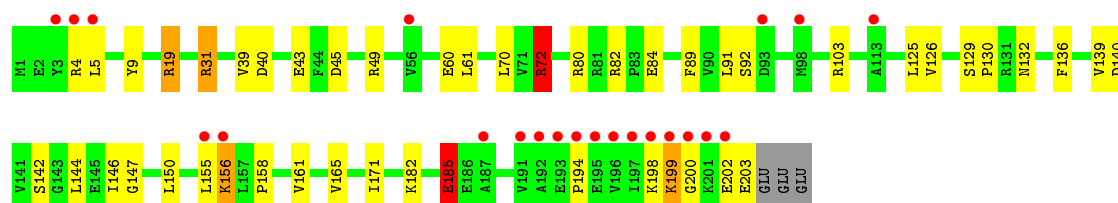
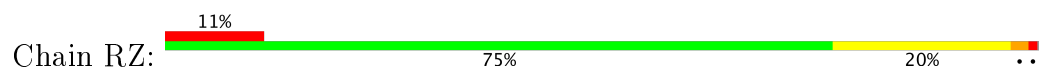


- Molecule 21: 50S ribosomal protein L25

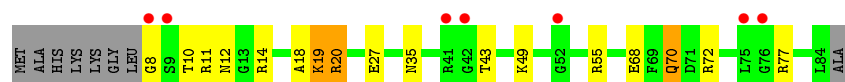
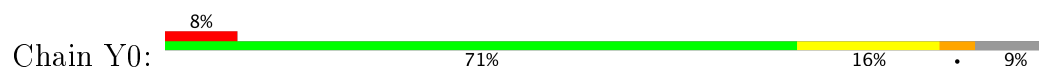




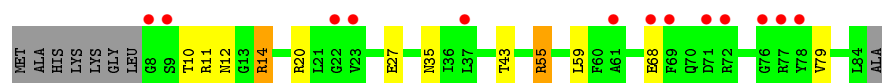
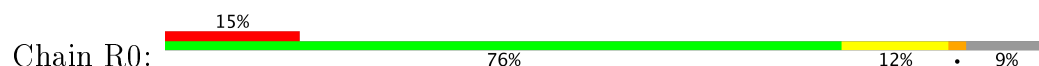
• Molecule 21: 50S ribosomal protein L25



• Molecule 22: 50S ribosomal protein L27



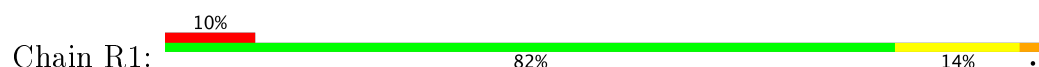
• Molecule 22: 50S ribosomal protein L27



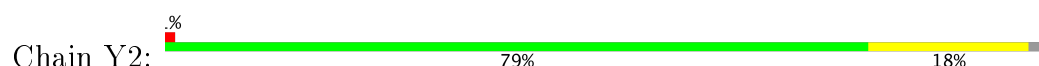
• Molecule 23: 50S ribosomal protein L28



• Molecule 23: 50S ribosomal protein L28

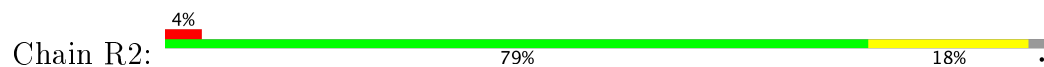


• Molecule 24: 50S ribosomal protein L29





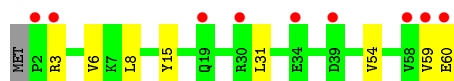
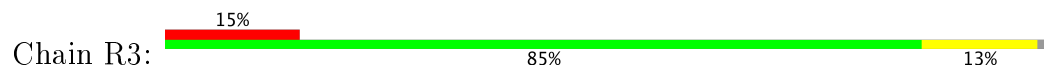
- Molecule 24: 50S ribosomal protein L29



- Molecule 25: 50S ribosomal protein L30



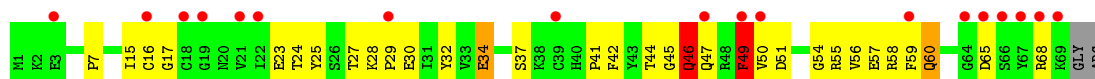
- Molecule 25: 50S ribosomal protein L30



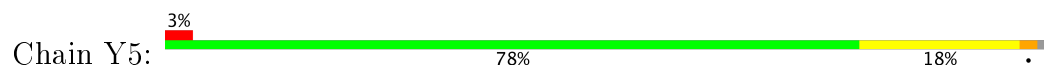
- Molecule 26: 50S ribosomal protein L31



- Molecule 26: 50S ribosomal protein L31



- Molecule 27: 50S ribosomal protein L32

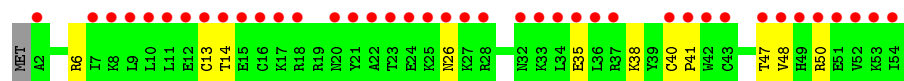
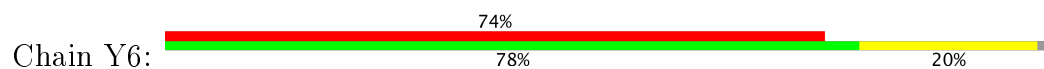


- Molecule 27: 50S ribosomal protein L32

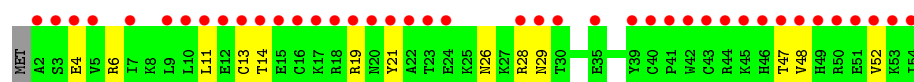
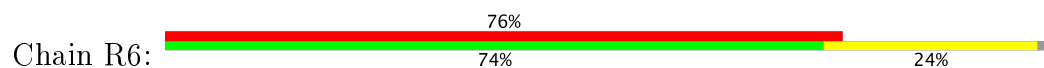




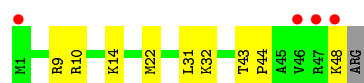
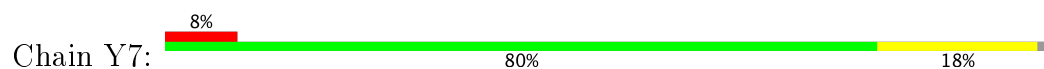
- Molecule 28: 50S ribosomal protein L33



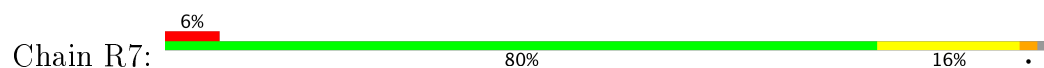
- Molecule 28: 50S ribosomal protein L33



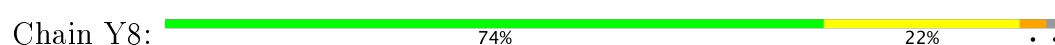
- Molecule 29: 50S ribosomal protein L34



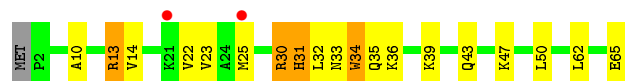
- Molecule 29: 50S ribosomal protein L34



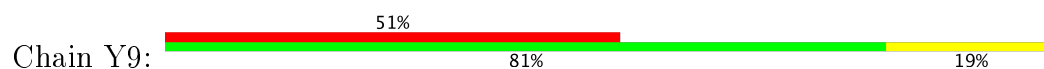
- Molecule 30: 50S ribosomal protein L35

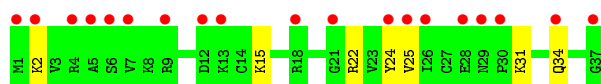


- Molecule 30: 50S ribosomal protein L35

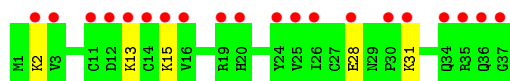
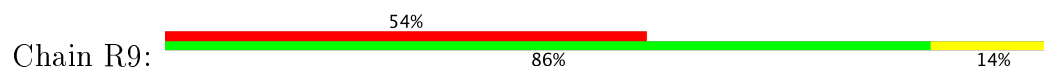


- Molecule 31: 50S ribosomal protein L36

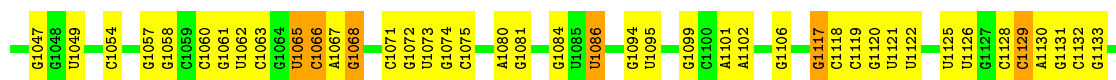
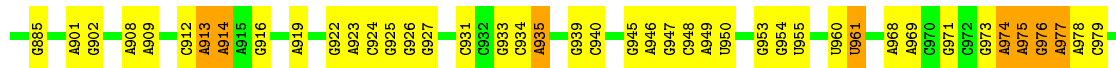
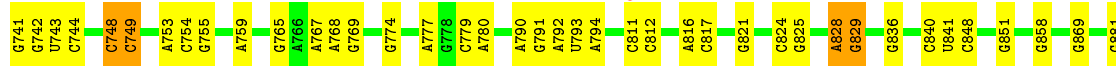
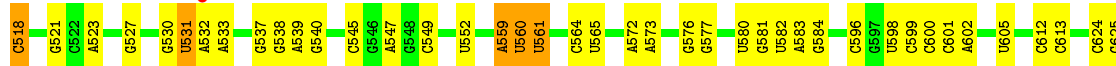
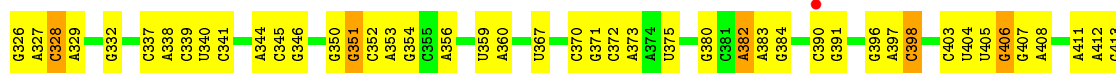
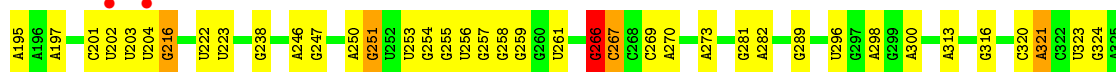
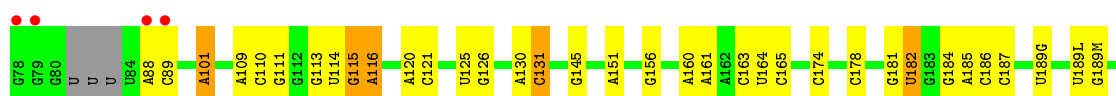
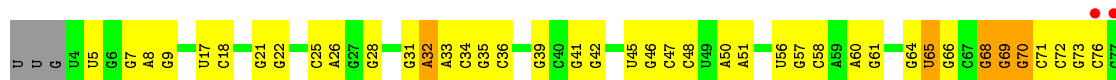




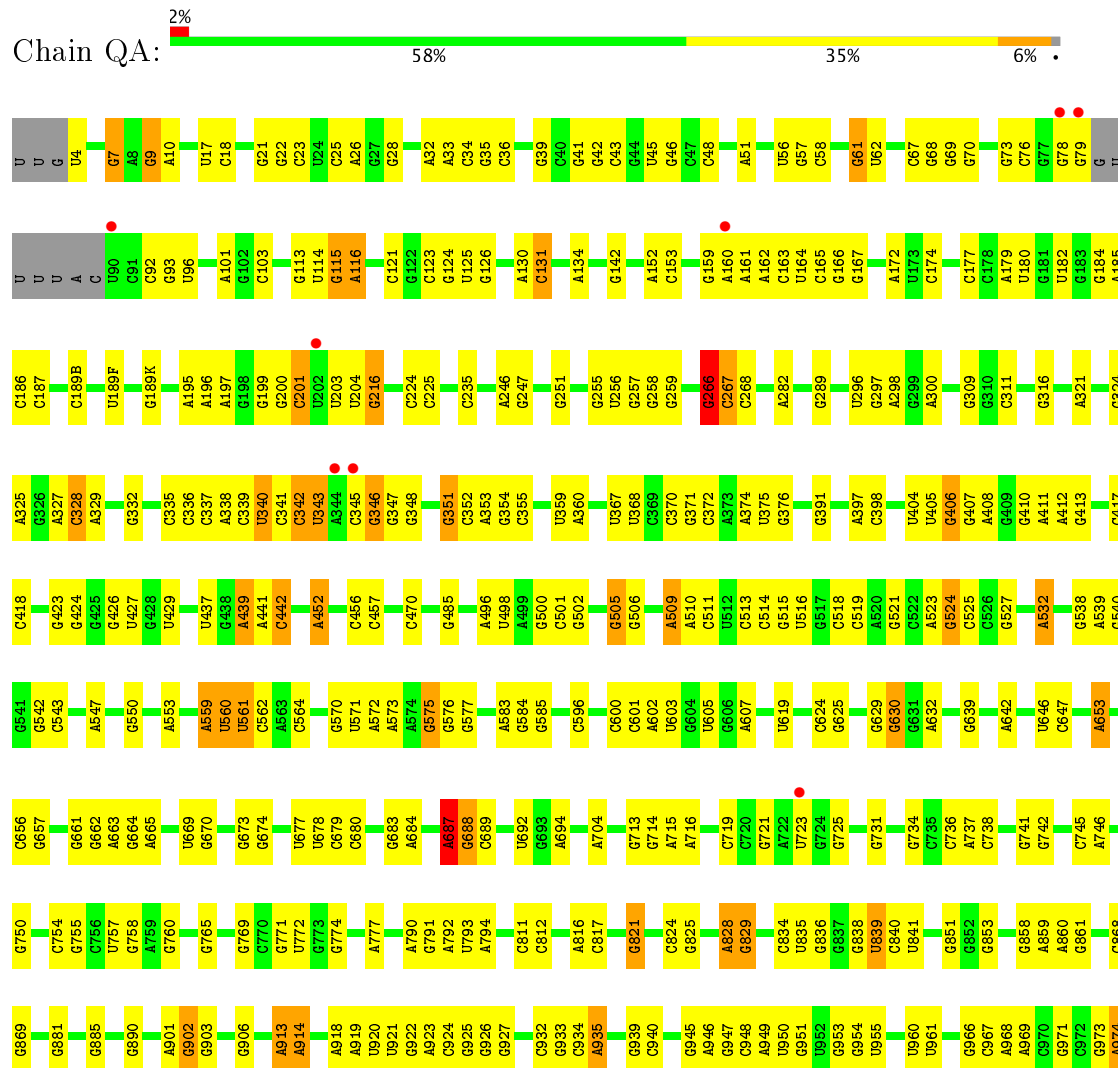
- Molecule 31: 50S ribosomal protein L36

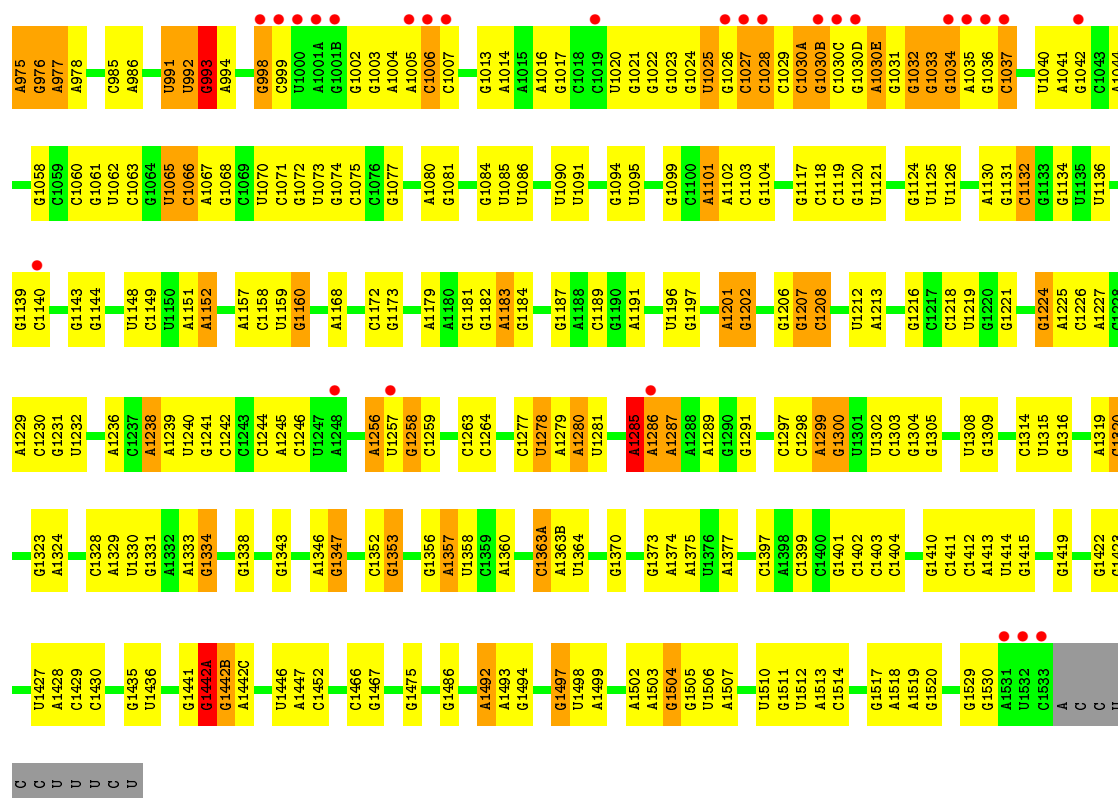


- Molecule 32: 16S rRNA

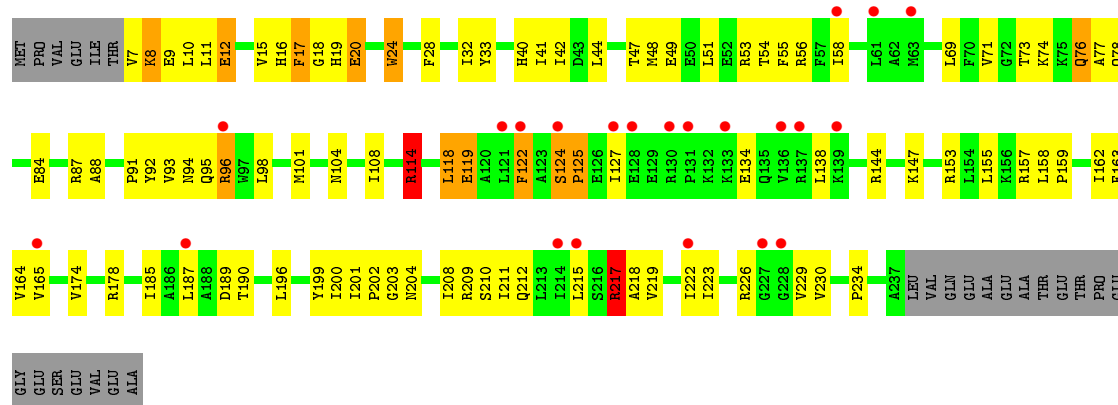


- Molecule 32: 16S rRNA

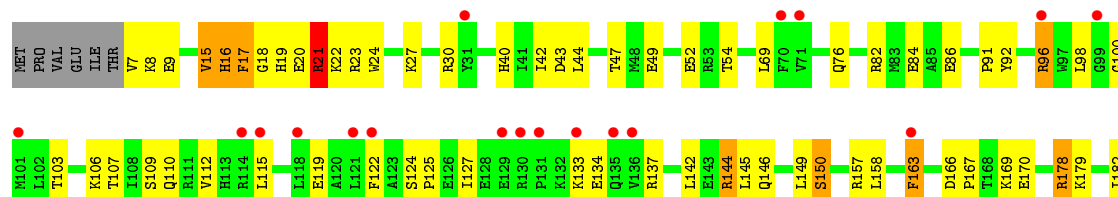


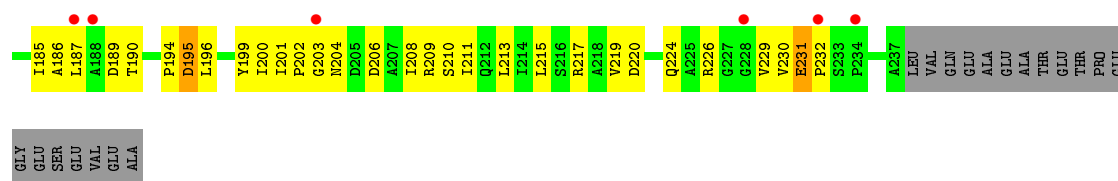


• Molecule 33: 30S ribosomal protein S2

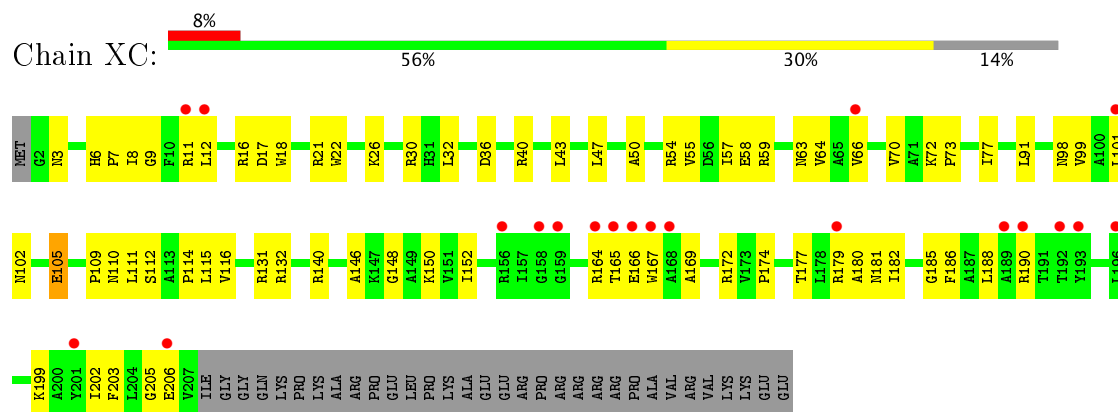


• Molecule 33: 30S ribosomal protein S2

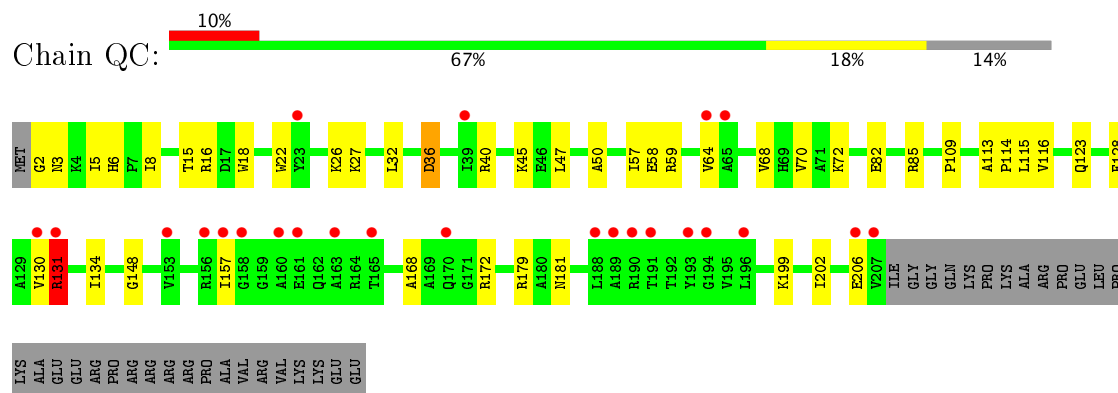




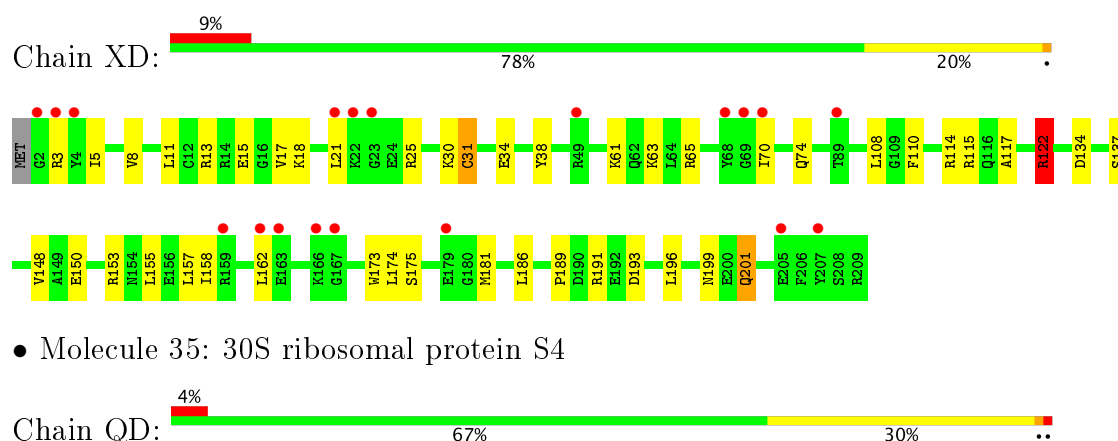
• Molecule 34: 30S ribosomal protein S3



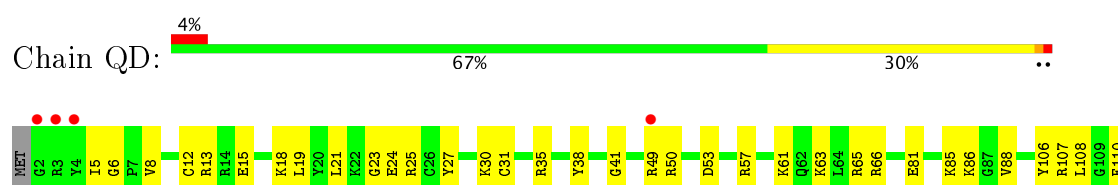
• Molecule 34: 30S ribosomal protein S3

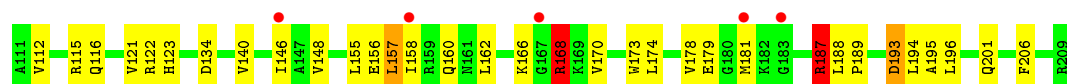


• Molecule 35: 30S ribosomal protein S4

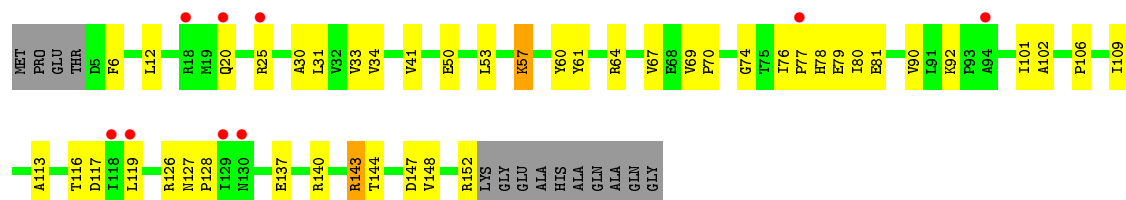


• Molecule 35: 30S ribosomal protein S4

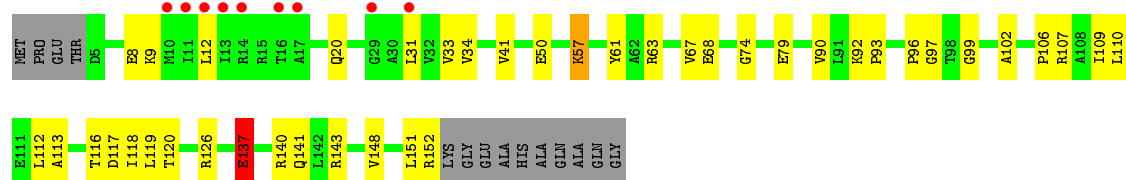




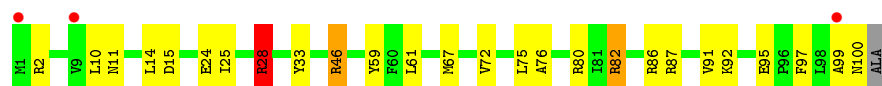
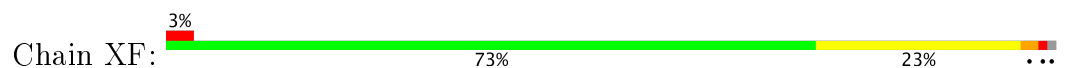
- Molecule 36: 30S ribosomal protein S5



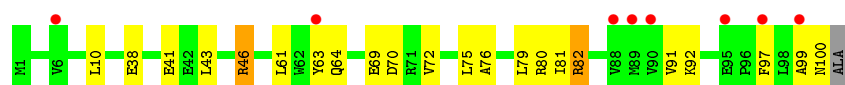
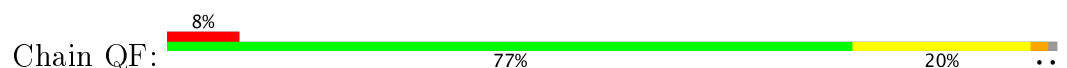
- Molecule 36: 30S ribosomal protein S5



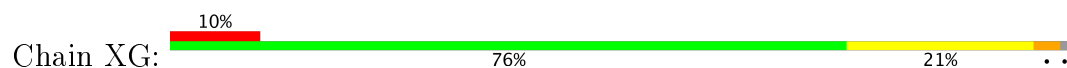
- Molecule 37: 30S ribosomal protein S6



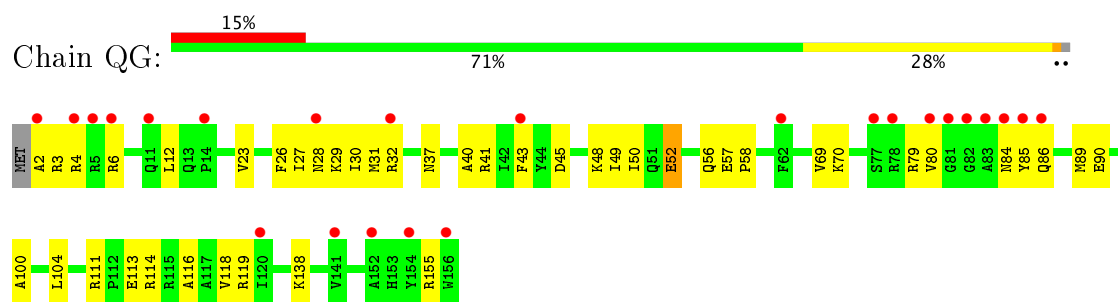
- Molecule 37: 30S ribosomal protein S6



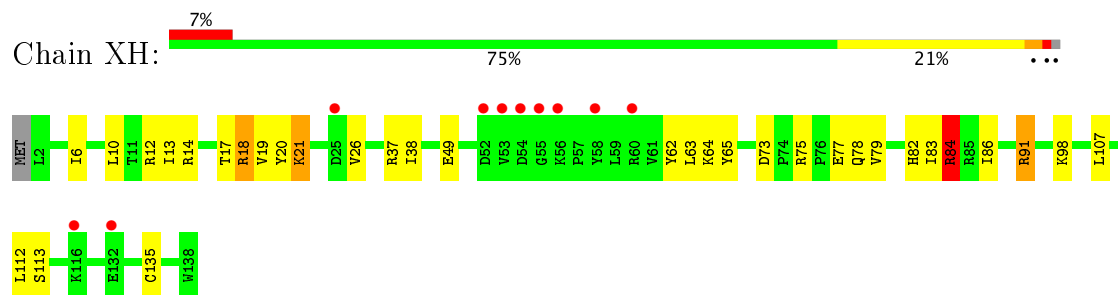
- Molecule 38: 30S ribosomal protein S7



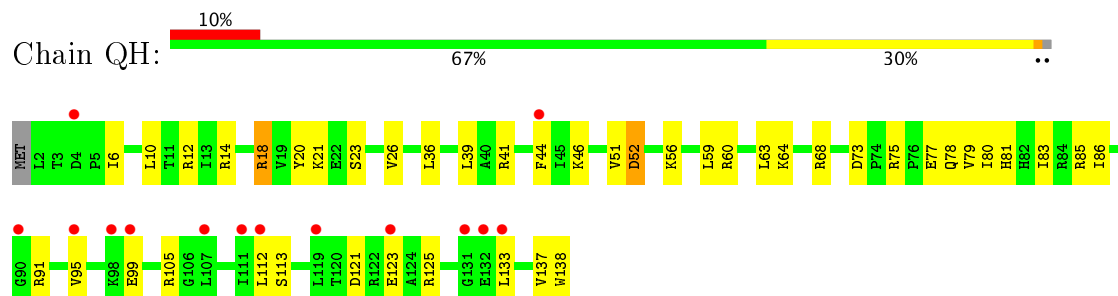
- Molecule 38: 30S ribosomal protein S7



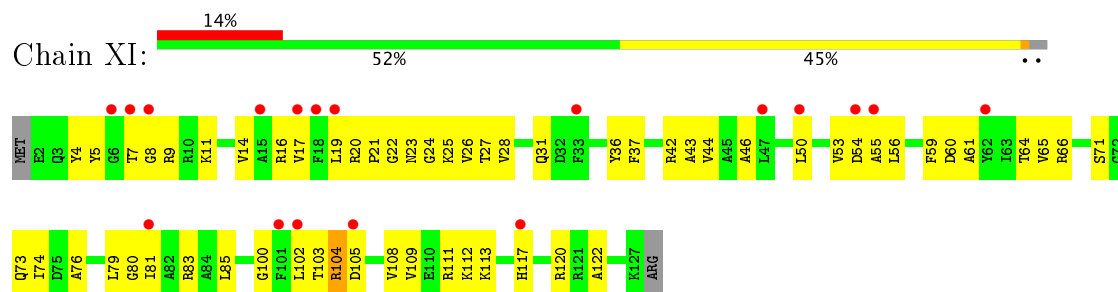
• Molecule 39: 30S ribosomal protein S8



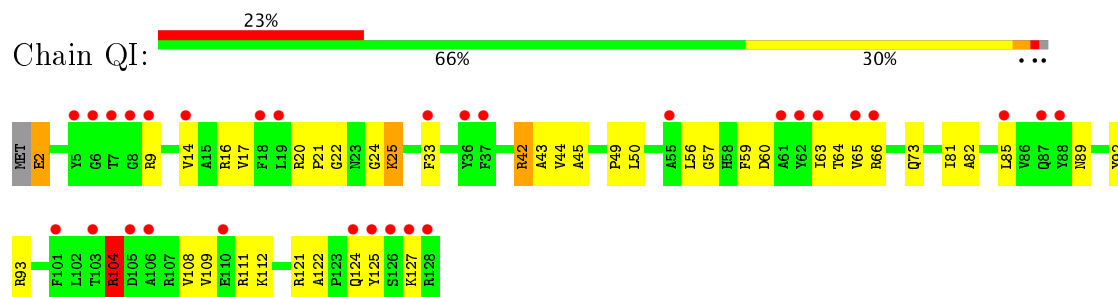
• Molecule 39: 30S ribosomal protein S8



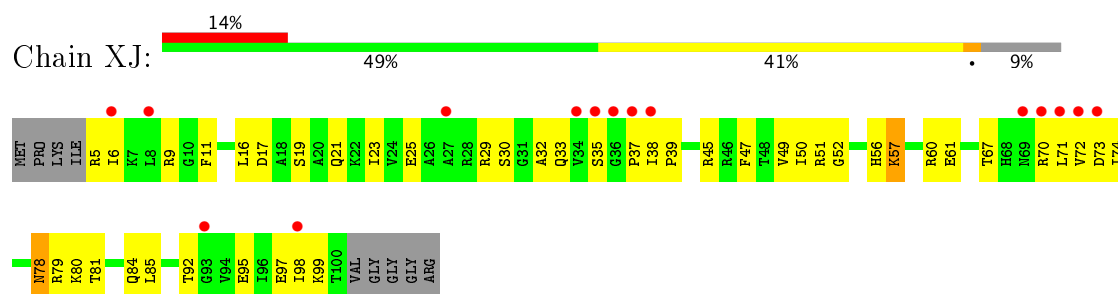
• Molecule 40: 30S ribosomal protein S9



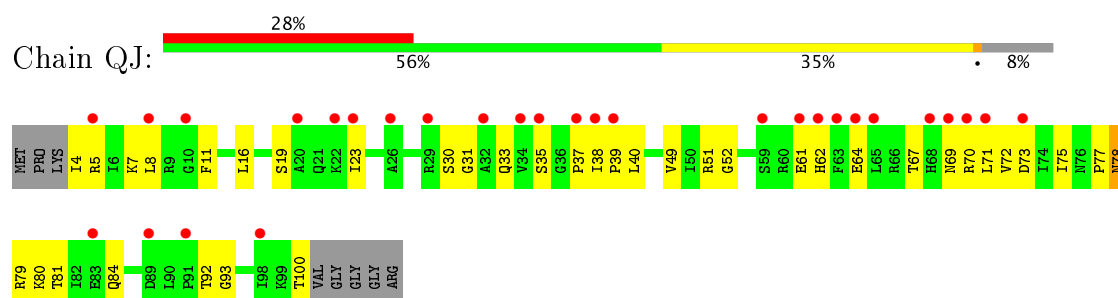
• Molecule 40: 30S ribosomal protein S9



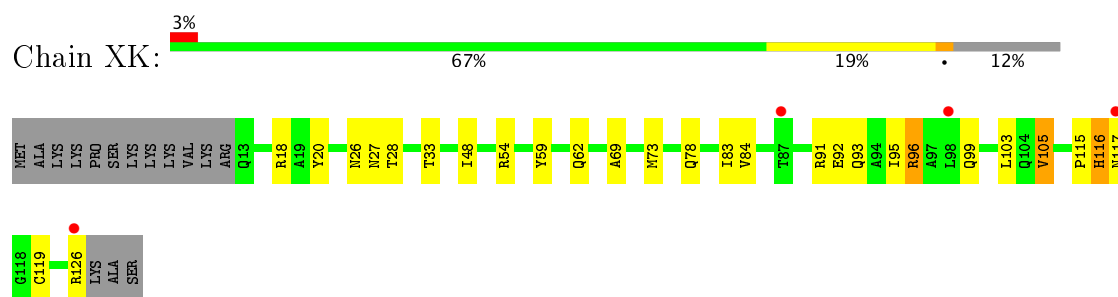
- Molecule 41: 30S ribosomal protein S10



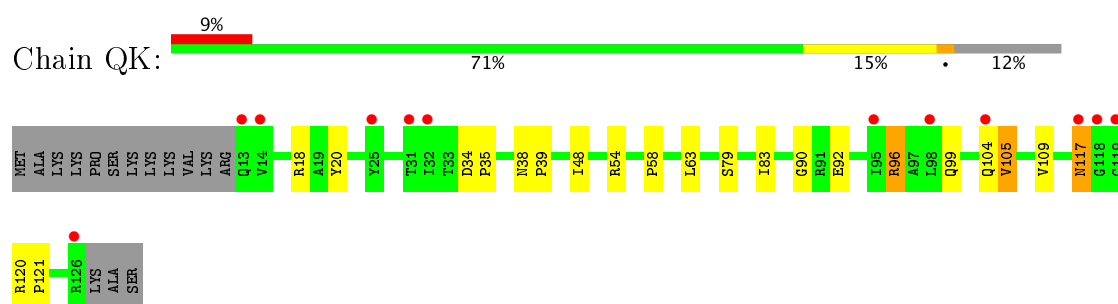
- Molecule 41: 30S ribosomal protein S10



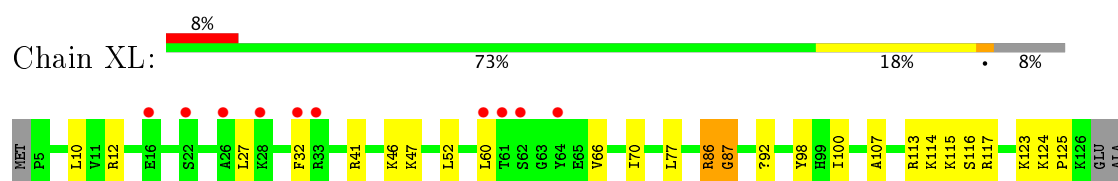
- Molecule 42: 30S ribosomal protein S11



- Molecule 42: 30S ribosomal protein S11




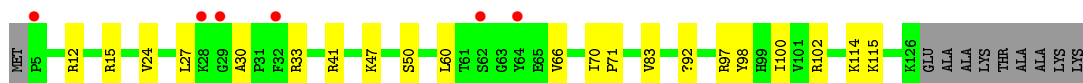
- Molecule 43: 30S ribosomal protein S12



ALA
LYS
THR
ALA
LYS
LYS

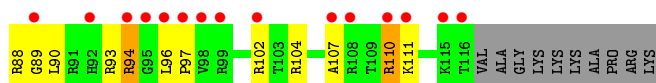
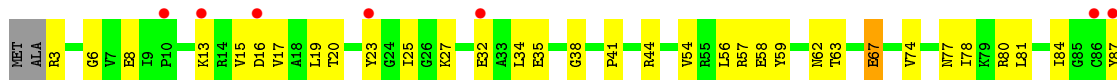
- Molecule 43: 30S ribosomal protein S12

Chain QL: 



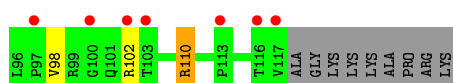
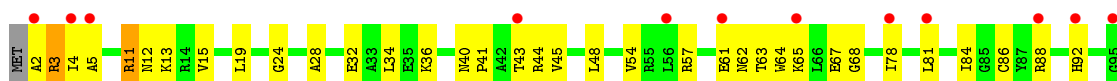
- Molecule 44: 30S ribosomal protein S13

Chain XM: 



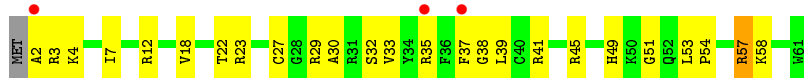
- Molecule 44: 30S ribosomal protein S13

Chain QM: 



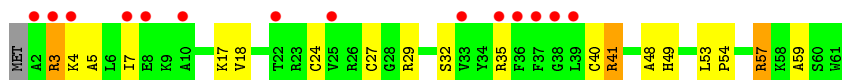
- Molecule 45: 30S ribosomal protein S14 type Z

Chain XN: 




- Molecule 45: 30S ribosomal protein S14 type Z

Chain QN: 

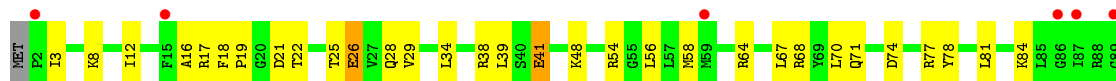


- Molecule 46: 30S ribosomal protein S15

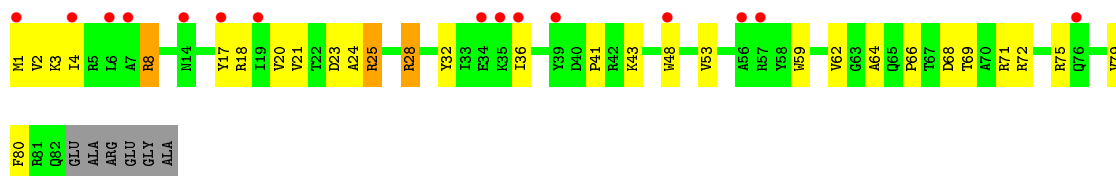
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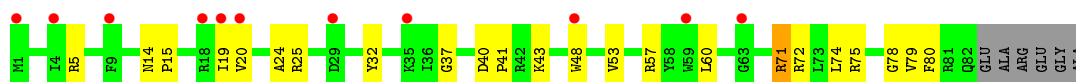
- Molecule 46: 30S ribosomal protein S15



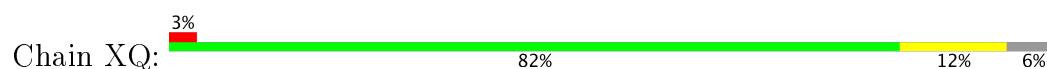
- Molecule 47: 30S ribosomal protein S16



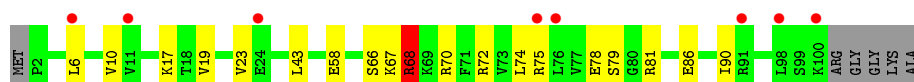
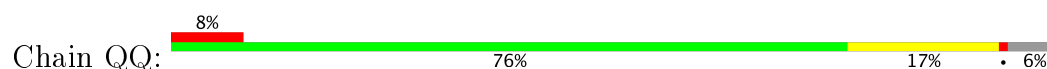
- Molecule 47: 30S ribosomal protein S16



- Molecule 48: 30S ribosomal protein S17



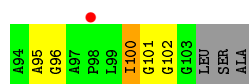
- Molecule 48: 30S ribosomal protein S17



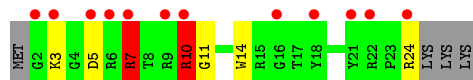
- Molecule 49: 30S ribosomal protein S18



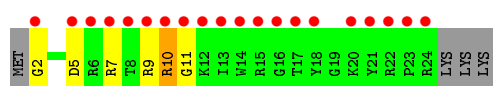
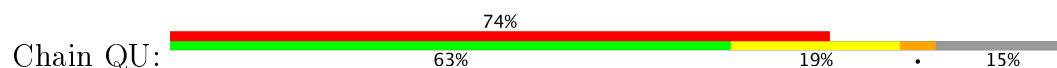
MET	L8	R8	N9	L10	S11	A12	L13	K14	Q18		R22	L36	S37		L42	Q43	L44	A44	Q45	E46	G47	K48		L63		M56	R57	K58	A59	E60	S61	L62	I63	D64	K65	A66		T71		A77		K81	L84	M85	R86		R89	Q90	L91	L92	E93
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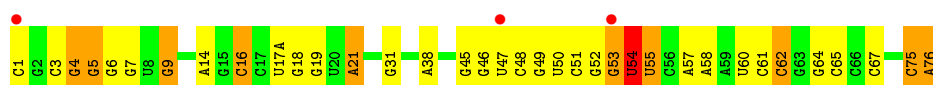
- Molecule 52: 30S ribosomal protein Thx



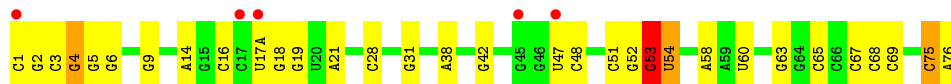
- Molecule 52: 30S ribosomal protein Thx



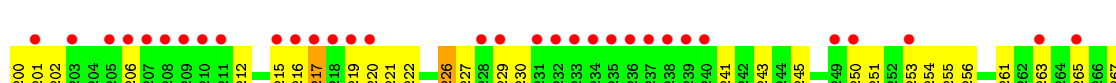
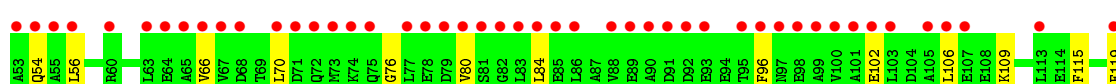
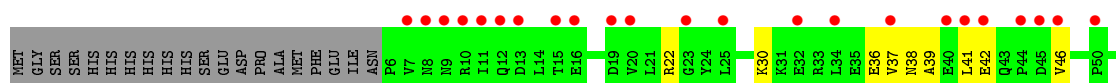
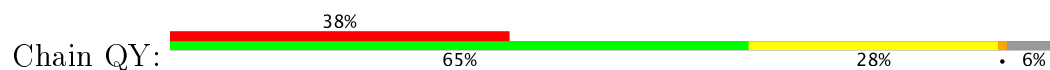
- Molecule 53: P-site tRNA fMet



- Molecule 53: P-site tRNA fMet



- Molecule 54: Peptide chain release factor 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	210.89Å 450.12Å 620.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.92 – 3.30 49.92 – 3.30	Depositor EDS
% Data completeness (in resolution range)	98.9 (49.92-3.30) 98.9 (49.92-3.30)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.23 (at 3.33Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.267 , 0.286 0.266 , 0.286	Depositor DCC
R_{free} test set	40126 reflections (4.63%)	DCC
Wilson B-factor (Å ²)	99.5	Xtriage
Anisotropy	0.175	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 39.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	296497	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.60% 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: 5MU, ZN, MEQ, OMG, MA6, SF4, 0TD, MG, 2MA, 2MU, 2MG, 5MC, UR3, 4OC, M2G, 7MG, PSU

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	RA	0.25	0/68901	0.81	30/107544 (0.0%)
1	YA	0.27	0/68901	0.81	39/107544 (0.0%)
2	RB	0.22	0/2876	0.78	0/4486
2	YB	0.23	0/2878	0.79	0/4490
3	RD	0.71	8/2181 (0.4%)	0.69	1/2940 (0.0%)
3	YD	0.75	13/2186 (0.6%)	0.66	0/2944
4	RE	1.10	19/1592 (1.2%)	0.65	0/2149
4	YE	1.36	19/1592 (1.2%)	0.69	3/2149 (0.1%)
5	RF	0.59	2/1619 (0.1%)	0.68	2/2193 (0.1%)
5	YF	0.50	2/1615 (0.1%)	0.62	0/2188
6	RG	0.69	9/1451 (0.6%)	0.59	0/1961
6	YG	0.71	9/1449 (0.6%)	0.56	0/1957
7	RH	0.77	8/1356 (0.6%)	0.56	0/1834
7	YH	0.62	6/1350 (0.4%)	0.59	1/1826 (0.1%)
8	RI	0.84	7/1109 (0.6%)	0.60	0/1512
8	YI	0.55	3/1091 (0.3%)	0.63	2/1490 (0.1%)
9	RN	0.76	6/1148 (0.5%)	0.67	1/1547 (0.1%)
9	YN	0.81	7/1144 (0.6%)	0.57	0/1543
10	RO	0.63	4/943 (0.4%)	0.67	1/1269 (0.1%)
10	YO	0.61	4/943 (0.4%)	0.62	1/1269 (0.1%)
11	RP	0.89	8/1152 (0.7%)	0.71	0/1533
11	YP	0.64	6/1152 (0.5%)	0.61	1/1533 (0.1%)
12	RQ	0.91	12/1143 (1.0%)	0.67	0/1527
12	YQ	0.81	9/1143 (0.8%)	0.60	0/1527
13	RR	0.97	8/982 (0.8%)	0.72	2/1312 (0.2%)
13	YR	0.81	7/982 (0.7%)	0.66	0/1312
14	RS	0.74	4/887 (0.5%)	0.61	0/1180
14	YS	0.87	9/880 (1.0%)	0.63	0/1172
15	RT	0.87	12/1105 (1.1%)	0.66	0/1477
15	YT	0.83	10/1097 (0.9%)	0.63	0/1468
16	RU	0.87	7/977 (0.7%)	0.67	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	YU	0.98	11/977 (1.1%)	0.66	2/1301 (0.2%)
17	RV	0.71	2/786 (0.3%)	0.62	0/1053
17	YV	0.63	0/782	0.63	0/1049
18	RW	0.89	9/897 (1.0%)	0.67	2/1205 (0.2%)
18	YW	0.71	6/897 (0.7%)	0.60	0/1205
19	RX	0.76	4/764 (0.5%)	0.65	1/1025 (0.1%)
19	YX	0.70	3/764 (0.4%)	0.65	1/1025 (0.1%)
20	RY	0.78	4/823 (0.5%)	0.66	0/1099
20	YY	0.49	0/823	0.59	0/1100
21	RZ	0.70	9/1620 (0.6%)	0.58	1/2200 (0.0%)
21	YZ	1.52	14/1590 (0.9%)	0.59	0/2162
22	R0	0.69	2/616 (0.3%)	0.68	1/821 (0.1%)
22	Y0	0.53	2/616 (0.3%)	0.55	0/821
23	R1	0.76	3/761 (0.4%)	0.61	0/1013
23	Y1	0.81	5/766 (0.7%)	0.62	0/1018
24	R2	0.40	0/590	0.55	0/781
24	Y2	0.44	0/594	0.51	0/785
25	R3	0.49	0/474	0.62	0/635
25	Y3	0.66	3/469 (0.6%)	0.62	0/630
26	R4	0.98	5/559 (0.9%)	0.74	0/754
26	Y4	1.29	10/549 (1.8%)	0.71	0/741
27	R5	0.65	2/473 (0.4%)	0.69	0/639
27	Y5	0.77	4/469 (0.9%)	0.58	0/635
28	R6	0.80	1/460 (0.2%)	0.59	0/613
28	Y6	0.56	0/456	0.54	0/608
29	R7	0.67	0/426	0.77	2/561 (0.4%)
29	Y7	0.69	2/426 (0.5%)	0.67	0/561
30	R8	0.83	4/525 (0.8%)	0.65	1/691 (0.1%)
30	Y8	0.82	4/525 (0.8%)	0.64	0/691
31	R9	0.44	0/310	0.58	0/407
31	Y9	0.37	0/310	0.54	0/407
32	QA	0.23	0/35795	0.79	14/55864 (0.0%)
32	XA	0.24	0/35890	0.80	20/56012 (0.0%)
33	QB	0.76	15/1876 (0.8%)	0.63	2/2533 (0.1%)
33	XB	1.13	25/1860 (1.3%)	0.62	0/2518
34	QC	0.51	3/1582 (0.2%)	0.54	0/2137
34	XC	0.60	4/1566 (0.3%)	0.55	0/2119
35	QD	0.63	7/1695 (0.4%)	0.58	0/2274
35	XD	0.58	8/1698 (0.5%)	0.53	0/2277
36	QE	0.62	3/1149 (0.3%)	0.58	0/1548
36	XE	0.77	6/1149 (0.5%)	0.56	0/1548
37	QF	0.63	4/827 (0.5%)	0.58	0/1120
37	XF	0.91	10/829 (1.2%)	0.57	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	QG	0.75	6/1254 (0.5%)	0.50	0/1683
38	XG	1.05	17/1248 (1.4%)	0.57	0/1676
39	QH	0.69	5/1118 (0.4%)	0.55	0/1506
39	XH	0.60	3/1108 (0.3%)	0.57	1/1494 (0.1%)
40	QI	0.82	8/1005 (0.8%)	0.58	0/1351
40	XI	0.49	0/985	0.58	1/1329 (0.1%)
41	QJ	0.52	2/732 (0.3%)	0.58	0/993
41	XJ	0.39	0/723	0.56	0/984
42	QK	0.76	6/849 (0.7%)	0.58	1/1150 (0.1%)
42	XK	0.65	4/848 (0.5%)	0.59	0/1149
43	QL	0.63	2/937 (0.2%)	0.57	1/1260 (0.1%)
43	XL	0.44	0/937	0.62	1/1260 (0.1%)
44	QM	0.69	5/924 (0.5%)	0.59	0/1242
44	XM	0.67	4/905 (0.4%)	0.60	0/1217
45	QN	0.76	4/501 (0.8%)	0.49	0/664
45	XN	1.04	9/501 (1.8%)	0.59	0/664
46	QO	0.81	7/739 (0.9%)	0.56	0/985
46	XO	0.78	7/739 (0.9%)	0.56	0/985
47	QP	0.57	2/697 (0.3%)	0.62	0/939
47	XP	0.94	7/693 (1.0%)	0.59	0/935
48	QQ	0.61	4/836 (0.5%)	0.56	0/1117
48	XQ	0.77	8/836 (1.0%)	0.58	1/1117 (0.1%)
49	QR	0.78	4/560 (0.7%)	0.64	0/746
49	XR	0.56	2/560 (0.4%)	0.57	0/746
50	QS	0.66	4/663 (0.6%)	0.59	0/895
50	XS	0.45	0/660	0.56	0/893
51	QT	0.61	2/734 (0.3%)	0.58	0/969
51	XT	0.53	2/736 (0.3%)	0.51	0/976
52	QU	1.23	7/203 (3.4%)	0.50	0/266
52	XU	1.42	8/203 (3.9%)	0.59	0/266
53	QV	0.36	1/1836 (0.1%)	0.86	9/2859 (0.3%)
53	XV	0.35	1/1836 (0.1%)	0.79	2/2859 (0.1%)
54	QY	0.38	0/2862	0.60	0/3854
54	XY	0.38	1/2862 (0.0%)	0.59	0/3854
55	QX	0.22	0/144	0.72	0/222
55	XX	0.19	0/144	0.70	0/222
All	All	0.47	554/317956 (0.2%)	0.75	148/474813 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
14	RS	0	1
19	RX	0	1
19	YX	0	1
33	QB	0	1
43	XL	0	1
54	XY	0	1
All	All	0	6

All (554) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	YZ	72	ARG	NE-CZ	-30.04	0.94	1.33
21	YZ	72	ARG	CZ-NH1	-26.71	0.98	1.33
21	YZ	72	ARG	CZ-NH2	-26.64	0.98	1.33
21	YZ	72	ARG	CD-NE	-22.76	1.07	1.46
4	YE	144	ARG	NE-CZ	-22.31	1.04	1.33
33	XB	119	GLU	CD-OE1	-20.82	1.02	1.25
4	YE	144	ARG	CZ-NH1	-20.56	1.06	1.33
4	YE	144	ARG	CZ-NH2	-16.65	1.11	1.33
33	XB	119	GLU	CD-OE2	-15.72	1.08	1.25
4	YE	144	ARG	CD-NE	-14.84	1.21	1.46
9	YN	137	LYS	CD-CE	-14.04	1.16	1.51
4	YE	111	ARG	NE-CZ	-13.64	1.15	1.33
4	RE	111	ARG	NE-CZ	-13.39	1.15	1.33
33	XB	119	GLU	CG-CD	-13.06	1.32	1.51
4	YE	111	ARG	CZ-NH2	-12.32	1.17	1.33
4	RE	111	ARG	CZ-NH1	-12.04	1.17	1.33
9	YN	137	LYS	CE-NZ	-11.75	1.19	1.49
4	RE	111	ARG	CZ-NH2	-11.64	1.18	1.33
13	RR	33	ARG	NE-CZ	-11.54	1.18	1.33
4	YE	111	ARG	CZ-NH1	-11.42	1.18	1.33
8	RI	57	ARG	NE-CZ	-11.07	1.18	1.33
4	YE	111	ARG	CD-NE	-10.93	1.27	1.46
38	XG	155	ARG	NE-CZ	-10.75	1.19	1.33
16	YU	92	ARG	CZ-NH2	-10.73	1.19	1.33
13	RR	33	ARG	CZ-NH1	-10.72	1.19	1.33
36	XE	79	GLU	CD-OE1	-10.69	1.13	1.25
11	RP	55	ARG	NE-CZ	-10.43	1.19	1.33
16	YU	92	ARG	NE-CZ	-10.41	1.19	1.33
53	QV	1	C	OP3-P	-10.34	1.48	1.61
20	RY	23	ARG	NE-CZ	-10.29	1.19	1.33
53	XV	1	C	OP3-P	-10.28	1.48	1.61
40	QI	104	ARG	CZ-NH1	-10.15	1.19	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	RI	57	ARG	CZ-NH1	-10.14	1.19	1.33
26	R4	30	GLU	CD-OE1	-10.06	1.14	1.25
21	YZ	131	ARG	CZ-NH1	-10.04	1.20	1.33
38	XG	155	ARG	CZ-NH1	-9.99	1.20	1.33
40	QI	104	ARG	NE-CZ	-9.86	1.20	1.33
11	RP	55	ARG	CZ-NH1	-9.78	1.20	1.33
4	RE	111	ARG	CD-NE	-9.74	1.29	1.46
11	RP	55	ARG	CZ-NH2	-9.73	1.20	1.33
38	QG	52	GLU	CD-OE1	-9.72	1.15	1.25
26	Y4	48	ARG	NE-CZ	-9.62	1.20	1.33
8	RI	57	ARG	CZ-NH2	-9.55	1.20	1.33
21	YZ	131	ARG	NE-CZ	-9.51	1.20	1.33
33	XB	217	ARG	NE-CZ	-9.44	1.20	1.33
13	RR	96	ARG	NE-CZ	-9.42	1.20	1.33
12	YQ	60	ARG	NE-CZ	-9.39	1.20	1.33
33	XB	157	ARG	NE-CZ	-9.39	1.20	1.33
26	Y4	61	ARG	CZ-NH2	-9.33	1.21	1.33
16	YU	92	ARG	CD-NE	-9.31	1.30	1.46
37	XF	46	ARG	CZ-NH2	-9.28	1.21	1.33
38	XG	155	ARG	CZ-NH2	-9.28	1.21	1.33
45	XN	12	ARG	CZ-NH1	-9.25	1.21	1.33
13	YR	96	ARG	CZ-NH1	-9.22	1.21	1.33
13	RR	96	ARG	CZ-NH1	-9.19	1.21	1.33
44	XM	32	GLU	CD-OE1	-9.16	1.15	1.25
11	RP	55	ARG	CD-NE	-9.16	1.30	1.46
15	YT	23	ARG	CZ-NH1	-9.16	1.21	1.33
48	XQ	72	ARG	NE-CZ	-9.15	1.21	1.33
12	RQ	6	ARG	CZ-NH1	-9.14	1.21	1.33
4	RE	82	ARG	NE-CZ	-9.13	1.21	1.33
16	RU	36	ARG	NE-CZ	-9.12	1.21	1.33
13	YR	96	ARG	NE-CZ	-9.02	1.21	1.33
15	YT	23	ARG	NE-CZ	-9.02	1.21	1.33
45	XN	12	ARG	NE-CZ	-8.99	1.21	1.33
4	YE	82	ARG	NE-CZ	-8.95	1.21	1.33
13	RR	33	ARG	CZ-NH2	-8.94	1.21	1.33
30	R8	30	ARG	NE-CZ	-8.90	1.21	1.33
26	Y4	48	ARG	CZ-NH1	-8.89	1.21	1.33
16	YU	36	ARG	NE-CZ	-8.84	1.21	1.33
16	YU	92	ARG	CZ-NH1	-8.80	1.21	1.33
46	QO	38	ARG	NE-CZ	-8.79	1.21	1.33
14	RS	20	ARG	NE-CZ	-8.79	1.21	1.33
20	RY	23	ARG	CZ-NH1	-8.77	1.21	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
37	XF	46	ARG	NE-CZ	-8.75	1.21	1.33
26	Y4	61	ARG	NE-CZ	-8.71	1.21	1.33
33	XB	157	ARG	CZ-NH1	-8.71	1.21	1.33
4	RE	94	GLU	CD-OE1	-8.70	1.16	1.25
7	RH	59	ARG	CZ-NH2	-8.69	1.21	1.33
12	YQ	60	ARG	CZ-NH1	-8.68	1.21	1.33
13	YR	33	ARG	CZ-NH1	-8.66	1.21	1.33
4	YE	82	ARG	CZ-NH2	-8.61	1.21	1.33
33	XB	217	ARG	CZ-NH1	-8.60	1.21	1.33
47	XP	25	ARG	NE-CZ	-8.57	1.22	1.33
42	QK	96	ARG	CZ-NH2	-8.50	1.22	1.33
19	YX	76	ARG	NE-CZ	-8.50	1.22	1.33
14	RS	20	ARG	CZ-NH1	-8.47	1.22	1.33
7	RH	59	ARG	NE-CZ	-8.45	1.22	1.33
47	XP	8	ARG	NE-CZ	-8.42	1.22	1.33
36	XE	79	GLU	CD-OE2	-8.41	1.16	1.25
39	QH	18	ARG	CZ-NH2	-8.39	1.22	1.33
3	YD	169	GLU	CD-OE1	-8.37	1.16	1.25
39	QH	18	ARG	NE-CZ	-8.35	1.22	1.33
16	RU	36	ARG	CZ-NH1	-8.34	1.22	1.33
48	XQ	72	ARG	CZ-NH1	-8.31	1.22	1.33
36	QE	68	GLU	CD-OE1	-8.24	1.16	1.25
21	RZ	72	ARG	NE-CZ	-8.23	1.22	1.33
38	XG	114	ARG	NE-CZ	-8.22	1.22	1.33
21	RZ	31	ARG	NE-CZ	-8.21	1.22	1.33
26	R4	30	GLU	CD-OE2	-8.21	1.16	1.25
30	Y8	30	ARG	CZ-NH1	-8.20	1.22	1.33
30	Y8	30	ARG	NE-CZ	-8.20	1.22	1.33
42	QK	96	ARG	NE-CZ	-8.20	1.22	1.33
4	RE	119	ARG	CZ-NH1	-8.19	1.22	1.33
17	RV	43	GLU	CD-OE1	-8.19	1.16	1.25
48	QQ	72	ARG	NE-CZ	-8.18	1.22	1.33
21	RZ	31	ARG	CZ-NH1	-8.17	1.22	1.33
23	Y1	83	GLU	CD-OE1	-8.17	1.16	1.25
4	RE	82	ARG	CZ-NH1	-8.15	1.22	1.33
20	RY	23	ARG	CZ-NH2	-8.14	1.22	1.33
44	XM	32	GLU	CD-OE2	-8.13	1.16	1.25
14	YS	67	ARG	NE-CZ	-8.12	1.22	1.33
6	RG	170	ARG	CZ-NH2	-8.12	1.22	1.33
13	YR	33	ARG	NE-CZ	-8.11	1.22	1.33
7	RH	69	ARG	NE-CZ	-8.11	1.22	1.33
18	RW	52	GLU	CD-OE1	-8.10	1.16	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	XG	10	ARG	NE-CZ	-8.10	1.22	1.33
30	R8	30	ARG	CZ-NH1	-8.10	1.22	1.33
51	QT	93	GLU	CD-OE1	-8.09	1.16	1.25
16	YU	36	ARG	CZ-NH1	-8.08	1.22	1.33
52	XU	10	ARG	NE-CZ	-8.06	1.22	1.33
12	RQ	6	ARG	NE-CZ	-8.05	1.22	1.33
7	RH	69	ARG	CZ-NH2	-8.05	1.22	1.33
14	YS	67	ARG	CZ-NH2	-8.04	1.22	1.33
12	RQ	56	ARG	CZ-NH2	-8.04	1.22	1.33
11	RP	117	GLU	CD-OE1	-8.03	1.16	1.25
26	Y4	61	ARG	CD-NE	-8.03	1.32	1.46
48	QQ	72	ARG	CZ-NH1	-8.02	1.22	1.33
38	XG	114	ARG	CZ-NH1	-8.01	1.22	1.33
23	R1	89	GLU	CD-OE1	-8.01	1.16	1.25
43	QL	41	ARG	CZ-NH2	-7.97	1.22	1.33
35	QD	187	ARG	NE-CZ	-7.95	1.22	1.33
19	YX	76	ARG	CZ-NH1	-7.95	1.22	1.33
52	XU	10	ARG	CZ-NH2	-7.95	1.22	1.33
19	RX	76	ARG	NE-CZ	-7.95	1.22	1.33
4	RE	144	ARG	CZ-NH1	-7.94	1.22	1.33
47	XP	8	ARG	CZ-NH1	-7.92	1.22	1.33
8	RI	57	ARG	CD-NE	-7.91	1.33	1.46
21	YZ	193	GLU	CD-OE1	-7.90	1.17	1.25
33	XB	49	GLU	CD-OE1	-7.90	1.17	1.25
44	QM	32	GLU	CD-OE1	-7.89	1.17	1.25
4	YE	82	ARG	CZ-NH1	-7.85	1.22	1.33
38	XG	155	ARG	CD-NE	-7.83	1.33	1.46
49	QR	28	GLU	CD-OE1	-7.83	1.17	1.25
11	YP	98	GLU	CD-OE1	-7.82	1.17	1.25
38	QG	52	GLU	CD-OE2	-7.79	1.17	1.25
47	XP	25	ARG	CZ-NH1	-7.79	1.23	1.33
41	QJ	84	GLN	CD-OE1	-7.79	1.06	1.24
6	RG	170	ARG	NE-CZ	-7.78	1.23	1.33
18	RW	11	ARG	CZ-NH2	-7.74	1.23	1.33
18	YW	52	GLU	CD-OE1	-7.73	1.17	1.25
7	RH	59	ARG	CZ-NH1	-7.73	1.23	1.33
21	RZ	72	ARG	CZ-NH1	-7.73	1.23	1.33
44	QM	110	ARG	NE-CZ	-7.72	1.23	1.33
42	XK	96	ARG	CZ-NH2	-7.70	1.23	1.33
43	QL	41	ARG	NE-CZ	-7.67	1.23	1.33
46	QO	38	ARG	CZ-NH1	-7.66	1.23	1.33
38	XG	10	ARG	CZ-NH2	-7.65	1.23	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	RT	118	ARG	NE-CZ	-7.65	1.23	1.33
19	RX	76	ARG	CZ-NH1	-7.63	1.23	1.33
13	RR	33	ARG	CD-NE	-7.62	1.33	1.46
8	YI	50	ARG	CZ-NH2	-7.61	1.23	1.33
42	XK	96	ARG	NE-CZ	-7.56	1.23	1.33
37	XF	46	ARG	CD-NE	-7.55	1.33	1.46
38	XG	113	GLU	CD-OE1	-7.51	1.17	1.25
6	RG	153	ARG	NE-CZ	-7.51	1.23	1.33
4	RE	144	ARG	NE-CZ	-7.50	1.23	1.33
8	RI	10	GLU	CD-OE1	-7.46	1.17	1.25
17	RV	43	GLU	CD-OE2	-7.46	1.17	1.25
4	RE	40	GLU	CD-OE1	-7.46	1.17	1.25
4	RE	94	GLU	CD-OE2	-7.44	1.17	1.25
4	RE	119	ARG	NE-CZ	-7.44	1.23	1.33
33	XB	144	ARG	NE-CZ	-7.43	1.23	1.33
30	Y8	30	ARG	CZ-NH2	-7.42	1.23	1.33
33	QB	96	ARG	NE-CZ	-7.40	1.23	1.33
40	QI	104	ARG	CZ-NH2	-7.39	1.23	1.33
6	YG	136	ARG	NE-CZ	-7.38	1.23	1.33
39	QH	18	ARG	CD-NE	-7.38	1.33	1.46
45	QN	3	ARG	NE-CZ	-7.38	1.23	1.33
35	XD	34	GLU	CD-OE1	-7.37	1.17	1.25
26	R4	23	GLU	CD-OE1	-7.37	1.17	1.25
26	Y4	48	ARG	CZ-NH2	-7.36	1.23	1.33
33	XB	12	GLU	CD-OE1	-7.36	1.17	1.25
37	XF	46	ARG	CZ-NH1	-7.35	1.23	1.33
38	XG	78	ARG	CZ-NH1	-7.34	1.23	1.33
12	RQ	56	ARG	NE-CZ	-7.34	1.23	1.33
38	XG	78	ARG	NE-CZ	-7.31	1.23	1.33
42	QK	96	ARG	CD-NE	-7.29	1.34	1.46
45	XN	57	ARG	CZ-NH1	-7.28	1.23	1.33
7	RH	59	ARG	CD-NE	-7.28	1.34	1.46
33	XB	96	ARG	NE-CZ	-7.27	1.23	1.33
4	RE	82	ARG	CZ-NH2	-7.25	1.23	1.33
44	QM	110	ARG	CZ-NH1	-7.23	1.23	1.33
33	XB	217	ARG	CZ-NH2	-7.20	1.23	1.33
47	QP	71	ARG	CZ-NH1	-7.19	1.23	1.33
3	YD	211	ARG	CZ-NH2	-7.18	1.23	1.33
33	QB	96	ARG	CZ-NH1	-7.17	1.23	1.33
35	QD	187	ARG	CZ-NH1	-7.17	1.23	1.33
7	RH	69	ARG	CD-NE	-7.17	1.34	1.46
21	YZ	131	ARG	CZ-NH2	-7.15	1.23	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	RG	153	ARG	CZ-NH2	-7.12	1.23	1.33
15	RT	96	ARG	NE-CZ	-7.10	1.23	1.33
20	RY	23	ARG	CD-NE	-7.10	1.34	1.46
7	RH	69	ARG	CZ-NH1	-7.10	1.23	1.33
18	RW	52	GLU	CD-OE2	-7.08	1.17	1.25
6	RG	170	ARG	CD-NE	-7.07	1.34	1.46
33	XB	144	ARG	CZ-NH1	-7.07	1.23	1.33
27	Y5	48	GLU	CD-OE1	-7.07	1.17	1.25
38	XG	10	ARG	CZ-NH1	-7.06	1.23	1.33
13	YR	96	ARG	CZ-NH2	-7.05	1.23	1.33
14	YS	67	ARG	CZ-NH1	-7.05	1.23	1.33
12	YQ	60	ARG	CZ-NH2	-7.04	1.24	1.33
4	YE	82	ARG	CD-NE	-7.04	1.34	1.46
39	QH	18	ARG	CZ-NH1	-7.03	1.24	1.33
4	YE	119	ARG	CZ-NH1	-7.03	1.24	1.33
42	QK	54	ARG	NE-CZ	-7.03	1.24	1.33
52	QU	7	ARG	NE-CZ	-7.03	1.24	1.33
8	YI	50	ARG	NE-CZ	-7.02	1.24	1.33
26	Y4	61	ARG	CZ-NH1	-7.02	1.24	1.33
50	QS	81	ARG	NE-CZ	-7.02	1.24	1.33
15	YT	118	ARG	CZ-NH2	-7.02	1.24	1.33
52	XU	10	ARG	CZ-NH1	-6.98	1.24	1.33
13	RR	96	ARG	CZ-NH2	-6.98	1.24	1.33
30	R8	30	ARG	CZ-NH2	-6.97	1.24	1.33
15	RT	96	ARG	CZ-NH1	-6.96	1.24	1.33
45	XN	57	ARG	NE-CZ	-6.96	1.24	1.33
11	RP	117	GLU	CD-OE2	-6.96	1.18	1.25
23	Y1	83	GLU	CD-OE2	-6.96	1.18	1.25
6	RG	45	GLU	CD-OE1	-6.96	1.18	1.25
45	QN	3	ARG	CD-NE	-6.96	1.34	1.46
42	QK	96	ARG	CZ-NH1	-6.95	1.24	1.33
52	XU	7	ARG	CZ-NH2	-6.94	1.24	1.33
52	XU	10	ARG	CD-NE	-6.92	1.34	1.46
36	XE	143	ARG	CZ-NH2	-6.91	1.24	1.33
45	QN	3	ARG	CZ-NH2	-6.91	1.24	1.33
38	QG	41	ARG	NE-CZ	-6.90	1.24	1.33
14	YS	67	ARG	CD-NE	-6.89	1.34	1.46
36	QE	68	GLU	CD-OE2	-6.88	1.18	1.25
3	YD	88	ARG	NE-CZ	-6.87	1.24	1.33
15	RT	23	ARG	CZ-NH2	-6.85	1.24	1.33
44	QM	32	GLU	CD-OE2	-6.84	1.18	1.25
15	RT	118	ARG	CZ-NH2	-6.84	1.24	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	RQ	59	ARG	CZ-NH2	-6.83	1.24	1.33
23	R1	89	GLU	CD-OE2	-6.83	1.18	1.25
4	YE	119	ARG	NE-CZ	-6.83	1.24	1.33
9	RN	115	ARG	CZ-NH1	-6.82	1.24	1.33
14	YS	20	ARG	NE-CZ	-6.81	1.24	1.33
15	RT	118	ARG	CZ-NH1	-6.80	1.24	1.33
33	XB	157	ARG	CZ-NH2	-6.79	1.24	1.33
29	Y7	9	ARG	CZ-NH1	-6.79	1.24	1.33
10	YO	23	ARG	NE-CZ	-6.79	1.24	1.33
15	YT	96	ARG	NE-CZ	-6.79	1.24	1.33
33	XB	96	ARG	CZ-NH1	-6.76	1.24	1.33
42	XK	96	ARG	CD-NE	-6.75	1.34	1.46
46	QO	38	ARG	CZ-NH2	-6.73	1.24	1.33
50	QS	81	ARG	CZ-NH1	-6.72	1.24	1.33
18	YW	11	ARG	CZ-NH2	-6.70	1.24	1.33
21	YZ	72	ARG	CG-CD	-6.70	1.35	1.51
36	XE	143	ARG	NE-CZ	-6.70	1.24	1.33
49	QR	32	ARG	CZ-NH1	-6.70	1.24	1.33
3	RD	54	ARG	NE-CZ	-6.69	1.24	1.33
15	YT	23	ARG	CZ-NH2	-6.69	1.24	1.33
4	YE	40	GLU	CD-OE1	-6.68	1.18	1.25
3	RD	103	ARG	CZ-NH1	-6.68	1.24	1.33
18	RW	11	ARG	CD-NE	-6.67	1.35	1.46
42	QK	54	ARG	CZ-NH1	-6.67	1.24	1.33
30	R8	30	ARG	CD-NE	-6.65	1.35	1.46
51	QT	93	GLU	CD-OE2	-6.64	1.18	1.25
12	YQ	16	ARG	NE-CZ	-6.64	1.24	1.33
41	QJ	84	GLN	CD-NE2	-6.64	1.16	1.32
3	YD	88	ARG	CZ-NH1	-6.63	1.24	1.33
18	RW	15	ARG	NE-CZ	-6.63	1.24	1.33
52	XU	7	ARG	NE-CZ	-6.63	1.24	1.33
37	XF	28	ARG	CZ-NH2	-6.62	1.24	1.33
22	R0	20	ARG	CZ-NH1	-6.62	1.24	1.33
51	XT	93	GLU	CD-OE1	-6.61	1.18	1.25
33	XB	114	ARG	NE-CZ	-6.58	1.24	1.33
36	QE	137	GLU	CD-OE1	-6.58	1.18	1.25
9	RN	97	ARG	CZ-NH1	-6.58	1.24	1.33
21	YZ	13	GLU	CD-OE1	-6.57	1.18	1.25
21	YZ	193	GLU	CD-OE2	-6.57	1.18	1.25
38	QG	41	ARG	CZ-NH1	-6.54	1.24	1.33
6	YG	136	ARG	CZ-NH1	-6.52	1.24	1.33
11	YP	21	ARG	CZ-NH2	-6.52	1.24	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	YD	54	ARG	CZ-NH1	-6.51	1.24	1.33
16	YU	89	GLU	CD-OE1	-6.50	1.18	1.25
5	RF	106	ARG	NE-CZ	-6.50	1.24	1.33
10	YO	23	ARG	CZ-NH2	-6.48	1.24	1.33
9	YN	68	GLU	CD-OE1	-6.47	1.18	1.25
38	XG	76	ARG	NE-CZ	-6.47	1.24	1.33
47	QP	71	ARG	NE-CZ	-6.47	1.24	1.33
6	RG	45	GLU	CD-OE2	-6.47	1.18	1.25
50	QS	81	ARG	CZ-NH2	-6.45	1.24	1.33
38	XG	10	ARG	CD-NE	-6.45	1.35	1.46
48	XQ	68	ARG	CZ-NH2	-6.44	1.24	1.33
34	QC	131	ARG	CZ-NH2	-6.42	1.24	1.33
14	YS	71	ARG	CZ-NH2	-6.42	1.24	1.33
8	YI	54	GLN	CD-OE1	-6.42	1.09	1.24
38	QG	41	ARG	CZ-NH2	-6.40	1.24	1.33
49	QR	28	GLU	CD-OE2	-6.39	1.18	1.25
33	XB	49	GLU	CD-OE2	-6.39	1.18	1.25
46	QO	41	GLU	CD-OE1	-6.39	1.18	1.25
46	XO	26	GLU	CD-OE1	-6.39	1.18	1.25
26	Y4	48	ARG	CD-NE	-6.39	1.35	1.46
10	RO	23	ARG	NE-CZ	-6.38	1.24	1.33
28	R6	4	GLU	CD-OE1	-6.38	1.18	1.25
35	XD	122	ARG	NE-CZ	-6.38	1.24	1.33
12	YQ	16	ARG	CZ-NH2	-6.38	1.24	1.33
5	YF	106	ARG	NE-CZ	-6.37	1.24	1.33
14	RS	20	ARG	CZ-NH2	-6.35	1.24	1.33
11	YP	98	GLU	CD-OE2	-6.34	1.18	1.25
47	XP	25	ARG	CZ-NH2	-6.34	1.24	1.33
11	YP	21	ARG	NE-CZ	-6.34	1.24	1.33
52	QU	7	ARG	CZ-NH1	-6.32	1.24	1.33
12	RQ	59	ARG	NE-CZ	-6.32	1.24	1.33
35	QD	168	ARG	CZ-NH1	-6.31	1.24	1.33
3	RD	103	ARG	NE-CZ	-6.31	1.24	1.33
26	Y4	34	GLU	CD-OE1	-6.30	1.18	1.25
9	RN	97	ARG	NE-CZ	-6.30	1.24	1.33
12	RQ	56	ARG	CZ-NH1	-6.30	1.24	1.33
38	XG	113	GLU	CD-OE2	-6.30	1.18	1.25
46	QO	26	GLU	CD-OE1	-6.30	1.18	1.25
37	XF	28	ARG	NE-CZ	-6.29	1.24	1.33
33	QB	170	GLU	CD-OE1	-6.29	1.18	1.25
10	RO	23	ARG	CZ-NH1	-6.29	1.24	1.33
10	RO	23	ARG	CZ-NH2	-6.29	1.24	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	YN	139	GLU	CD-OE1	-6.29	1.18	1.25
36	XE	143	ARG	CZ-NH1	-6.28	1.24	1.33
33	QB	144	ARG	CZ-NH2	-6.28	1.24	1.33
7	YH	95	ARG	NE-CZ	-6.27	1.25	1.33
10	YO	23	ARG	CZ-NH1	-6.27	1.25	1.33
3	YD	169	GLU	CD-OE2	-6.26	1.18	1.25
33	XB	217	ARG	CD-NE	-6.26	1.35	1.46
48	XQ	68	ARG	NE-CZ	-6.25	1.25	1.33
40	QI	104	ARG	CD-NE	-6.25	1.35	1.46
14	YS	20	ARG	CZ-NH1	-6.24	1.25	1.33
6	RG	170	ARG	CZ-NH1	-6.24	1.25	1.33
49	QR	32	ARG	NE-CZ	-6.23	1.25	1.33
33	QB	49	GLU	CD-OE1	-6.23	1.18	1.25
35	XD	122	ARG	CZ-NH2	-6.23	1.25	1.33
34	XC	105	GLU	CD-OE1	-6.23	1.18	1.25
40	QI	42	ARG	CZ-NH2	-6.23	1.25	1.33
18	RW	11	ARG	NE-CZ	-6.23	1.25	1.33
52	QU	7	ARG	CZ-NH2	-6.22	1.25	1.33
33	XB	114	ARG	CZ-NH1	-6.22	1.25	1.33
52	QU	9	ARG	CZ-NH2	-6.22	1.25	1.33
12	RQ	56	ARG	CD-NE	-6.22	1.35	1.46
3	YD	54	ARG	NE-CZ	-6.21	1.25	1.33
33	XB	12	GLU	CD-OE2	-6.21	1.18	1.25
6	YG	21	ARG	CZ-NH2	-6.21	1.25	1.33
9	YN	97	ARG	CZ-NH1	-6.21	1.25	1.33
16	RU	36	ARG	CZ-NH2	-6.21	1.25	1.33
3	YD	211	ARG	NE-CZ	-6.19	1.25	1.33
18	YW	52	GLU	CD-OE2	-6.18	1.18	1.25
9	RN	61	ARG	NE-CZ	-6.17	1.25	1.33
45	XN	3	ARG	NE-CZ	-6.17	1.25	1.33
45	XN	12	ARG	CZ-NH2	-6.17	1.25	1.33
9	YN	97	ARG	NE-CZ	-6.15	1.25	1.33
8	RI	10	GLU	CD-OE2	-6.15	1.18	1.25
27	Y5	35	GLU	CD-OE1	-6.14	1.18	1.25
35	QD	168	ARG	NE-CZ	-6.13	1.25	1.33
37	QF	46	ARG	CZ-NH2	-6.13	1.25	1.33
38	XG	76	ARG	CZ-NH1	-6.13	1.25	1.33
7	YH	95	ARG	CZ-NH1	-6.12	1.25	1.33
6	YG	164	GLU	CD-OE1	-6.12	1.19	1.25
33	QB	178	ARG	CZ-NH2	-6.12	1.25	1.33
5	YF	106	ARG	CZ-NH1	-6.11	1.25	1.33
3	RD	54	ARG	CZ-NH1	-6.10	1.25	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	XQ	72	ARG	CZ-NH2	-6.08	1.25	1.33
18	YW	11	ARG	NE-CZ	-6.07	1.25	1.33
6	YG	136	ARG	CZ-NH2	-6.06	1.25	1.33
34	QC	131	ARG	NE-CZ	-6.06	1.25	1.33
5	RF	106	ARG	CZ-NH1	-6.06	1.25	1.33
33	QB	21	ARG	NE-CZ	-6.06	1.25	1.33
44	XM	94	ARG	CZ-NH1	-6.05	1.25	1.33
3	YD	211	ARG	CD-NE	-6.05	1.36	1.46
18	RW	15	ARG	CZ-NH1	-6.04	1.25	1.33
26	R4	34	GLU	CD-OE1	-6.04	1.19	1.25
45	QN	3	ARG	CZ-NH1	-6.03	1.25	1.33
21	RZ	72	ARG	CZ-NH2	-6.03	1.25	1.33
33	QB	144	ARG	NE-CZ	-6.01	1.25	1.33
15	YT	118	ARG	NE-CZ	-6.00	1.25	1.33
52	QU	9	ARG	NE-CZ	-6.00	1.25	1.33
4	RE	40	GLU	CD-OE2	-5.99	1.19	1.25
21	RZ	19	ARG	CZ-NH1	-5.99	1.25	1.33
25	Y3	44	ARG	NE-CZ	-5.98	1.25	1.33
7	YH	69	ARG	CZ-NH2	-5.98	1.25	1.33
15	YT	96	ARG	CZ-NH1	-5.97	1.25	1.33
15	RT	23	ARG	NE-CZ	-5.96	1.25	1.33
12	YQ	60	ARG	CD-NE	-5.96	1.36	1.46
6	YG	21	ARG	NE-CZ	-5.96	1.25	1.33
16	RU	92	ARG	CZ-NH1	-5.96	1.25	1.33
11	YP	21	ARG	CD-NE	-5.95	1.36	1.46
11	RP	149	GLU	CD-OE1	-5.94	1.19	1.25
29	Y7	9	ARG	NE-CZ	-5.93	1.25	1.33
7	YH	69	ARG	NE-CZ	-5.93	1.25	1.33
44	XM	94	ARG	NE-CZ	-5.91	1.25	1.33
26	R4	23	GLU	CD-OE2	-5.91	1.19	1.25
9	RN	115	ARG	NE-CZ	-5.91	1.25	1.33
13	RR	96	ARG	CD-NE	-5.90	1.36	1.46
16	RU	92	ARG	NE-CZ	-5.89	1.25	1.33
21	YZ	138	GLU	CD-OE1	-5.88	1.19	1.25
46	QO	38	ARG	CD-NE	-5.87	1.36	1.46
48	XQ	68	ARG	CD-NE	-5.86	1.36	1.46
52	XU	7	ARG	CD-NE	-5.85	1.36	1.46
34	QC	131	ARG	CD-NE	-5.84	1.36	1.46
47	XP	25	ARG	CD-NE	-5.84	1.36	1.46
38	QG	41	ARG	CD-NE	-5.84	1.36	1.46
23	R1	83	GLU	CD-OE1	-5.83	1.19	1.25
12	RQ	59	ARG	CD-NE	-5.83	1.36	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	YD	103	ARG	NE-CZ	-5.82	1.25	1.33
16	RU	36	ARG	CD-NE	-5.82	1.36	1.46
42	XK	96	ARG	CZ-NH1	-5.82	1.25	1.33
46	XO	54	ARG	CZ-NH2	-5.80	1.25	1.33
30	Y8	30	ARG	CD-NE	-5.80	1.36	1.46
49	XR	32	ARG	CZ-NH1	-5.79	1.25	1.33
21	YZ	131	ARG	CD-NE	-5.79	1.36	1.46
4	RE	144	ARG	CD-NE	-5.79	1.36	1.46
15	YT	118	ARG	CD-NE	-5.78	1.36	1.46
27	Y5	35	GLU	CD-OE2	-5.78	1.19	1.25
49	XR	32	ARG	NE-CZ	-5.78	1.25	1.33
33	QB	21	ARG	CZ-NH2	-5.77	1.25	1.33
3	YD	103	ARG	CZ-NH1	-5.76	1.25	1.33
34	XC	131	ARG	CZ-NH2	-5.76	1.25	1.33
36	XE	143	ARG	CD-NE	-5.76	1.36	1.46
37	QF	46	ARG	NE-CZ	-5.74	1.25	1.33
14	RS	43	GLU	CD-OE1	-5.74	1.19	1.25
15	YT	23	ARG	CD-NE	-5.73	1.36	1.46
15	RT	96	ARG	CZ-NH2	-5.73	1.25	1.33
33	QB	178	ARG	NE-CZ	-5.73	1.25	1.33
22	R0	20	ARG	NE-CZ	-5.73	1.25	1.33
39	XH	91	ARG	NE-CZ	-5.71	1.25	1.33
22	Y0	20	ARG	CZ-NH1	-5.70	1.25	1.33
33	XB	157	ARG	CD-NE	-5.68	1.36	1.46
19	RX	76	ARG	CD-NE	-5.68	1.36	1.46
13	YR	96	ARG	CD-NE	-5.68	1.36	1.46
4	YE	73	GLU	CD-OE1	-5.67	1.19	1.25
46	XO	41	GLU	CD-OE1	-5.66	1.19	1.25
18	RW	15	ARG	CZ-NH2	-5.66	1.25	1.33
10	YO	23	ARG	CD-NE	-5.66	1.36	1.46
34	XC	131	ARG	NE-CZ	-5.65	1.25	1.33
15	RT	23	ARG	CZ-NH1	-5.65	1.25	1.33
48	XQ	72	ARG	CD-NE	-5.65	1.36	1.46
47	XP	8	ARG	CZ-NH2	-5.65	1.25	1.33
6	YG	21	ARG	CD-NE	-5.64	1.36	1.46
40	QI	2	GLU	CD-OE1	-5.63	1.19	1.25
3	RD	211	ARG	CD-NE	-5.62	1.36	1.46
37	XF	28	ARG	CD-NE	-5.62	1.36	1.46
12	YQ	16	ARG	CD-NE	-5.61	1.36	1.46
22	Y0	20	ARG	NE-CZ	-5.60	1.25	1.33
11	YP	21	ARG	CZ-NH1	-5.59	1.25	1.33
19	RX	76	ARG	CZ-NH2	-5.59	1.25	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	XN	3	ARG	CZ-NH2	-5.57	1.25	1.33
15	RT	23	ARG	CD-NE	-5.57	1.36	1.46
8	RI	61	ARG	CZ-NH2	-5.56	1.25	1.33
15	RT	118	ARG	CD-NE	-5.56	1.37	1.46
50	QS	81	ARG	CD-NE	-5.55	1.37	1.46
4	RE	119	ARG	CZ-NH2	-5.55	1.25	1.33
40	QI	42	ARG	NE-CZ	-5.55	1.25	1.33
33	XB	114	ARG	CZ-NH2	-5.54	1.25	1.33
21	RZ	19	ARG	NE-CZ	-5.53	1.25	1.33
35	XD	34	GLU	CD-OE2	-5.51	1.19	1.25
39	XH	91	ARG	CZ-NH2	-5.51	1.25	1.33
51	XT	93	GLU	CD-OE2	-5.51	1.19	1.25
33	QB	144	ARG	CD-NE	-5.51	1.37	1.46
12	RQ	6	ARG	CZ-NH2	-5.51	1.25	1.33
18	YW	11	ARG	CD-NE	-5.50	1.37	1.46
16	YU	36	ARG	CD-NE	-5.50	1.37	1.46
16	YU	36	ARG	CZ-NH2	-5.50	1.25	1.33
9	YN	68	GLU	CD-OE2	-5.49	1.19	1.25
4	RE	82	ARG	CD-NE	-5.49	1.37	1.46
37	XF	82	ARG	CZ-NH2	-5.48	1.25	1.33
9	RN	61	ARG	CZ-NH1	-5.48	1.25	1.33
11	RP	119	GLU	CD-OE1	-5.48	1.19	1.25
14	YS	71	ARG	NE-CZ	-5.47	1.25	1.33
48	QQ	72	ARG	CZ-NH2	-5.47	1.25	1.33
33	XB	144	ARG	CZ-NH2	-5.46	1.25	1.33
27	Y5	48	GLU	CD-OE2	-5.43	1.19	1.25
40	QI	42	ARG	CD-NE	-5.43	1.37	1.46
18	YW	11	ARG	CZ-NH1	-5.43	1.25	1.33
12	YQ	48	GLU	CD-OE1	-5.43	1.19	1.25
35	XD	65	ARG	NE-CZ	-5.43	1.25	1.33
35	XD	122	ARG	CD-NE	-5.43	1.37	1.46
39	XH	84	ARG	NE-CZ	-5.42	1.26	1.33
13	YR	33	ARG	CZ-NH2	-5.41	1.26	1.33
39	QH	91	ARG	CZ-NH2	-5.41	1.26	1.33
3	RD	211	ARG	CZ-NH2	-5.40	1.26	1.33
35	QD	187	ARG	CZ-NH2	-5.39	1.26	1.33
52	QU	9	ARG	CD-NE	-5.39	1.37	1.46
27	R5	59	GLU	CD-OE2	-5.39	1.19	1.25
37	QF	46	ARG	CD-NE	-5.38	1.37	1.46
7	YH	69	ARG	CZ-NH1	-5.37	1.26	1.33
10	RO	23	ARG	CD-NE	-5.37	1.37	1.46
44	QM	110	ARG	CZ-NH2	-5.36	1.26	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	RT	96	ARG	CD-NE	-5.35	1.37	1.46
46	QO	41	GLU	CD-OE2	-5.35	1.19	1.25
33	QB	49	GLU	CD-OE2	-5.35	1.19	1.25
35	XD	65	ARG	CZ-NH2	-5.34	1.26	1.33
46	XO	54	ARG	NE-CZ	-5.32	1.26	1.33
33	QB	178	ARG	CZ-NH1	-5.32	1.26	1.33
16	YU	104	GLN	CD-OE1	-5.31	1.12	1.24
23	Y1	21	ARG	NE-CZ	-5.29	1.26	1.33
35	QD	24	GLU	CD-OE1	-5.28	1.19	1.25
21	RZ	72	ARG	CD-NE	-5.28	1.37	1.46
16	RU	104	GLN	CD-OE1	-5.27	1.12	1.24
4	YE	40	GLU	CD-OE2	-5.25	1.19	1.25
18	RW	4	LYS	CD-CE	-5.24	1.38	1.51
52	QU	7	ARG	CD-NE	-5.24	1.37	1.46
25	Y3	44	ARG	CZ-NH2	-5.23	1.26	1.33
27	R5	59	GLU	CD-OE1	-5.23	1.20	1.25
3	YD	169	GLU	CG-CD	-5.22	1.44	1.51
45	XN	12	ARG	CD-NE	-5.22	1.37	1.46
46	XO	54	ARG	CD-NE	-5.22	1.37	1.46
33	QB	96	ARG	CZ-NH2	-5.22	1.26	1.33
3	RD	211	ARG	NE-CZ	-5.22	1.26	1.33
4	RE	178	GLU	CD-OE1	-5.21	1.20	1.25
3	YD	88	ARG	CZ-NH2	-5.21	1.26	1.33
33	XB	96	ARG	CZ-NH2	-5.21	1.26	1.33
26	Y4	34	GLU	CD-OE2	-5.20	1.20	1.25
33	QB	170	GLU	CD-OE2	-5.18	1.20	1.25
34	XC	131	ARG	CD-NE	-5.18	1.37	1.46
35	XD	122	ARG	CZ-NH1	-5.17	1.26	1.33
16	YU	89	GLU	CD-OE2	-5.17	1.20	1.25
15	YT	96	ARG	CZ-NH2	-5.17	1.26	1.33
3	RD	103	ARG	CZ-NH2	-5.17	1.26	1.33
38	XG	114	ARG	CZ-NH2	-5.16	1.26	1.33
46	XO	26	GLU	CD-OE2	-5.16	1.20	1.25
25	Y3	44	ARG	CZ-NH1	-5.15	1.26	1.33
14	YS	71	ARG	CD-NE	-5.14	1.37	1.46
37	XF	28	ARG	CZ-NH1	-5.14	1.26	1.33
12	RQ	59	ARG	CZ-NH1	-5.13	1.26	1.33
21	YZ	13	GLU	CD-OE2	-5.12	1.20	1.25
19	YX	76	ARG	CZ-NH2	-5.12	1.26	1.33
46	XO	41	GLU	CD-OE2	-5.11	1.20	1.25
12	RQ	60	ARG	CZ-NH2	-5.11	1.26	1.33
6	YG	167	GLU	CD-OE1	-5.11	1.20	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	Y1	21	ARG	CZ-NH1	-5.11	1.26	1.33
45	XN	3	ARG	CZ-NH1	-5.10	1.26	1.33
4	YE	73	GLU	CD-OE2	-5.10	1.20	1.25
23	Y1	52	ARG	CZ-NH2	-5.10	1.26	1.33
7	YH	69	ARG	CD-NE	-5.09	1.37	1.46
35	QD	65	ARG	CZ-NH2	-5.09	1.26	1.33
37	QF	82	ARG	CZ-NH2	-5.08	1.26	1.33
37	XF	82	ARG	NE-CZ	-5.08	1.26	1.33
48	QQ	72	ARG	CD-NE	-5.08	1.37	1.46
4	YE	144	ARG	CG-CD	-5.06	1.39	1.51
54	XY	214	HIS	CG-CD2	5.06	1.44	1.35
12	YQ	16	ARG	CZ-NH1	-5.05	1.26	1.33
33	XB	114	ARG	CD-NE	-5.05	1.37	1.46
48	XQ	68	ARG	CZ-NH1	-5.04	1.26	1.33
6	RG	153	ARG	CZ-NH1	-5.04	1.26	1.33
52	XU	7	ARG	CZ-NH1	-5.03	1.26	1.33
21	RZ	185	GLU	CD-OE1	-5.02	1.20	1.25
6	YG	136	ARG	CD-NE	-5.02	1.38	1.46

All (148) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	YA	1064	C	N1-C2-O2	9.58	124.65	118.90
1	RA	1064	C	N1-C2-O2	8.93	124.26	118.90
19	YX	57	LEU	CA-CB-CG	7.78	133.19	115.30
21	RZ	31	ARG	NE-CZ-NH1	-7.56	116.52	120.30
32	QA	639	G	N3-C4-N9	-7.37	121.58	126.00
10	RO	8	LEU	CA-CB-CG	7.27	132.02	115.30
1	RA	1079	C	C5-C6-N1	7.23	124.61	121.00
4	YE	52	LEU	CA-CB-CG	7.19	131.83	115.30
1	YA	1079	C	C5-C6-N1	7.12	124.56	121.00
32	XA	266	G	P-O3'-C3'	7.11	128.23	119.70
9	RN	25	ARG	NE-CZ-NH1	-7.08	116.76	120.30
1	RA	1065	U	O4'-C1'-N1	7.01	113.81	108.20
1	YA	1082	U	C2-N1-C1'	7.01	126.11	117.70
1	YA	847	U	C2-N1-C1'	7.00	126.11	117.70
1	YA	1092	C	N1-C2-O2	6.99	123.09	118.90
1	YA	1097	U	C2-N1-C1'	6.97	126.06	117.70
1	RA	847	U	C2-N1-C1'	6.97	126.06	117.70
32	XA	442	C	C2-N1-C1'	6.94	126.43	118.80
10	YO	8	LEU	CA-CB-CG	6.92	131.22	115.30
1	RA	1712	C	N3-C2-O2	-6.89	117.07	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	RF	74	ARG	NE-CZ-NH1	6.88	123.74	120.30
1	YA	1065	U	O4'-C1'-N1	6.88	113.70	108.20
1	RA	1092	C	N1-C2-O2	6.82	122.99	118.90
19	RX	57	LEU	CA-CB-CG	6.78	130.90	115.30
53	XV	53	G	OP1-P-O3'	6.73	120.02	105.20
53	QV	62	C	N3-C2-O2	-6.72	117.19	121.90
1	YA	1064	C	C2-N1-C1'	6.71	126.18	118.80
1	YA	277	C	N1-C2-O2	6.64	122.88	118.90
1	RA	1313	U	C2-N1-C1'	6.62	125.65	117.70
1	YA	1313	U	C2-N1-C1'	6.62	125.64	117.70
32	XA	1158	C	C2-N1-C1'	6.61	126.07	118.80
32	XA	1003	G	N7-C8-N9	6.61	116.41	113.10
1	YA	1092	C	C2-N1-C1'	6.53	125.98	118.80
53	QV	62	C	C6-N1-C2	-6.42	117.73	120.30
18	RW	11	ARG	NE-CZ-NH2	-6.42	117.09	120.30
5	RF	74	ARG	NE-CZ-NH2	-6.38	117.11	120.30
1	RA	1092	C	C2-N1-C1'	6.34	125.77	118.80
32	XA	1003	G	C8-N9-C4	-6.32	103.87	106.40
1	RA	1774	C	N3-C2-O2	-6.27	117.51	121.90
11	YP	147	LEU	CA-CB-CG	6.26	129.71	115.30
32	QA	600	C	C6-N1-C1'	6.20	128.24	120.80
8	YI	75	LEU	CA-CB-CG	6.18	129.50	115.30
18	RW	11	ARG	NE-CZ-NH1	6.17	123.39	120.30
3	RD	260	ARG	NE-CZ-NH1	6.16	123.38	120.30
32	XA	1003	G	C4-N9-C1'	6.15	134.49	126.50
29	R7	9	ARG	NE-CZ-NH1	6.12	123.36	120.30
1	YA	1052	C	C2-N1-C1'	6.10	125.51	118.80
32	XA	1183	A	P-O3'-C3'	6.08	127.00	119.70
1	YA	1097	U	N1-C2-O2	6.05	127.04	122.80
32	QA	993	G	N3-C4-N9	6.04	129.62	126.00
1	RA	1052	C	C2-N1-C1'	6.02	125.42	118.80
32	XA	1003	G	N3-C4-C5	-6.01	125.59	128.60
8	YI	50	ARG	NE-CZ-NH2	-5.98	117.31	120.30
1	YA	1531	C	C5-C6-N1	5.88	123.94	121.00
1	YA	1064	C	N3-C2-O2	-5.86	117.80	121.90
1	YA	1530	C	P-O3'-C3'	5.82	126.69	119.70
1	YA	277	C	C2-N1-C1'	5.82	125.20	118.80
1	YA	1097	U	N3-C2-O2	-5.81	118.13	122.20
32	XA	266	G	OP2-P-O3'	5.81	117.97	105.20
16	YU	36	ARG	NE-CZ-NH1	-5.80	117.40	120.30
1	RA	1097	U	C2-N1-C1'	5.78	124.64	117.70
32	XA	1025	U	O4'-C1'-N1	5.78	112.82	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	RA	1314	C	C2-N1-C1'	5.76	125.14	118.80
1	RA	1064	C	N3-C2-O2	-5.74	117.88	121.90
32	QA	991	U	P-O3'-C3'	5.74	126.59	119.70
30	R8	13	ARG	NE-CZ-NH2	-5.74	117.43	120.30
1	RA	1530	C	P-O3'-C3'	5.73	126.58	119.70
39	XH	84	ARG	NE-CZ-NH1	-5.72	117.44	120.30
1	RA	1064	C	C2-N1-C1'	5.72	125.09	118.80
53	QV	54	U	C6-N1-C1'	5.72	129.21	121.20
13	RR	33	ARG	NE-CZ-NH1	-5.71	117.45	120.30
32	QA	600	C	C5-C4-N4	5.68	124.17	120.20
22	R0	14	ARG	NE-CZ-NH2	-5.66	117.47	120.30
1	RA	1092	C	C5-C6-N1	5.65	123.82	121.00
1	YA	1314	C	C2-N1-C1'	5.65	125.01	118.80
48	XQ	72	ARG	NE-CZ-NH1	-5.64	117.48	120.30
43	QL	41	ARG	NE-CZ-NH2	-5.64	117.48	120.30
33	QB	178	ARG	NE-CZ-NH1	5.63	123.12	120.30
1	RA	1531	C	C5-C6-N1	5.62	123.81	121.00
1	RA	1092	C	C6-N1-C2	-5.62	118.05	120.30
42	QK	54	ARG	NE-CZ-NH1	-5.59	117.51	120.30
32	XA	754	C	C2-N1-C1'	5.58	124.94	118.80
1	YA	1712	C	N3-C2-O2	-5.58	118.00	121.90
1	YA	1712	C	N1-C2-N3	5.57	123.10	119.20
1	YA	2108	C	C6-N1-C2	-5.56	118.08	120.30
1	RA	1774	C	N1-C2-O2	5.54	122.22	118.90
1	YA	1914	C	C2-N1-C1'	5.54	124.89	118.80
32	QA	600	C	C2-N1-C1'	-5.53	112.72	118.80
53	QV	62	C	C2-N1-C1'	5.52	124.87	118.80
33	QB	178	ARG	NE-CZ-NH2	-5.52	117.54	120.30
1	RA	1747(B)	G	N3-C4-N9	-5.52	122.69	126.00
32	XA	1054	C	N1-C2-O2	5.51	122.21	118.90
1	YA	1774	C	N3-C2-O2	-5.50	118.05	121.90
1	YA	847	U	N1-C2-O2	5.50	126.65	122.80
1	RA	1712	C	C6-N1-C2	-5.46	118.11	120.30
53	QV	54	U	C2-N1-C1'	-5.46	111.15	117.70
1	YA	1082	U	C6-N1-C1'	-5.42	113.61	121.20
32	XA	442	C	C6-N1-C1'	-5.42	114.30	120.80
1	RA	2105	C	C2-N1-C1'	5.42	124.76	118.80
32	QA	639	G	C5-C6-O6	5.41	131.84	128.60
29	R7	9	ARG	NE-CZ-NH2	-5.39	117.61	120.30
1	YA	1065	U	P-O3'-C3'	5.38	126.16	119.70
1	RA	847	U	N1-C2-O2	5.35	126.55	122.80
1	YA	1092	C	C6-N1-C2	-5.35	118.16	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	YA	1064	C	C5-C6-N1	5.34	123.67	121.00
7	YH	88	LEU	CA-CB-CG	5.33	127.57	115.30
53	QV	54	U	N1-C2-O2	-5.33	119.07	122.80
1	YA	1092	C	C5-C6-N1	5.32	123.66	121.00
32	XA	1158	C	C5-C6-N1	5.32	123.66	121.00
53	XV	53	G	P-O3'-C3'	5.32	126.08	119.70
1	RA	847	U	N3-C2-O2	-5.30	118.49	122.20
53	QV	62	C	N1-C2-O2	5.30	122.08	118.90
32	QA	993	G	C4-N9-C1'	5.29	133.38	126.50
1	YA	1059	G	C5-C6-N1	5.29	114.14	111.50
32	QA	1442(A)	G	P-O3'-C3'	5.28	126.04	119.70
32	QA	991	U	OP2-P-O3'	5.28	116.82	105.20
1	YA	1092	C	N3-C2-O2	-5.28	118.21	121.90
32	XA	1224	G	C4-N9-C1'	-5.26	119.67	126.50
13	RR	96	ARG	NE-CZ-NH1	-5.26	117.67	120.30
4	YE	144	ARG	NE-CZ-NH1	-5.25	117.68	120.30
53	QV	53	G	O4'-C1'-N9	5.25	112.40	108.20
32	XA	1224	G	N3-C4-N9	-5.25	122.85	126.00
32	XA	1442(A)	G	OP1-P-O3'	5.24	116.74	105.20
32	QA	266	G	P-O3'-C3'	5.23	125.97	119.70
32	QA	687	A	P-O3'-C3'	5.22	125.97	119.70
32	XA	1183	A	OP1-P-O3'	5.21	116.67	105.20
1	RA	1065	U	P-O3'-C3'	5.21	125.95	119.70
1	YA	277	C	N3-C2-O2	-5.21	118.26	121.90
1	YA	269	U	C2-N1-C1'	5.18	123.92	117.70
32	XA	1442(A)	G	P-O3'-C3'	5.18	125.92	119.70
43	XL	87	GLY	N-CA-C	5.17	126.03	113.10
32	XA	1054	C	C2-N1-C1'	5.15	124.47	118.80
1	RA	2103	C	C5-C6-N1	5.14	123.57	121.00
1	RA	1092	C	N3-C2-O2	-5.13	118.31	121.90
53	QV	54	U	O4'-C1'-N1	-5.13	104.10	108.20
1	YA	1530	C	C2-N1-C1'	5.13	124.44	118.80
1	RA	140	G	O4'-C1'-N9	-5.11	104.11	108.20
1	YA	2105	C	C2-N1-C1'	5.10	124.41	118.80
1	RA	2108	C	C6-N1-C2	-5.10	118.26	120.30
1	RA	1097	U	N1-C2-O2	5.08	126.36	122.80
4	YE	111	ARG	NE-CZ-NH2	-5.06	117.77	120.30
1	YA	140	G	O4'-C1'-N9	-5.05	104.16	108.20
16	YU	92	ARG	NE-CZ-NH2	-5.05	117.78	120.30
32	QA	1285	A	P-O3'-C3'	5.04	125.75	119.70
40	XI	105	ASP	CB-CG-OD1	5.04	122.83	118.30
1	YA	1992	G	P-O3'-C3'	5.02	125.72	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	QA	754	C	C2-N1-C1'	5.01	124.31	118.80
1	YA	1531	C	C2-N1-C1'	5.01	124.31	118.80

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	QB	231	GLU	Peptide
14	RS	58	LEU	Peptide
19	RX	93	GLU	Peptide
43	XL	86	ARG	Peptide
54	XY	213	ARG	Peptide
19	YX	93	GLU	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	RA	61758	0	31146	667	0
1	YA	61758	0	31149	669	1
2	RB	2572	0	1305	12	0
2	YB	2573	0	1306	22	0
3	RD	2131	0	2207	48	0
3	YD	2136	0	2218	49	0
4	RE	1559	0	1618	36	0
4	YE	1559	0	1618	58	0
5	RF	1584	0	1625	43	0
5	YF	1580	0	1619	67	0
6	RG	1426	0	1445	61	0
6	YG	1424	0	1441	99	0
7	RH	1330	0	1407	26	0
7	YH	1324	0	1402	56	6
8	RI	1094	0	1127	33	0
8	YI	1076	0	1094	47	0
9	RN	1121	0	1195	27	0
9	YN	1117	0	1184	27	0
10	RO	933	0	996	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	YO	933	0	996	18	0
11	RP	1135	0	1212	39	0
11	YP	1135	0	1212	42	0
12	RQ	1122	0	1179	26	0
12	YQ	1122	0	1179	27	0
13	RR	968	0	1033	15	0
13	YR	968	0	1033	34	0
14	RS	877	0	938	15	0
14	YS	870	0	923	21	0
15	RT	1091	0	1151	38	0
15	YT	1083	0	1136	32	0
16	RU	959	0	1019	16	0
16	YU	959	0	1019	11	0
17	RV	775	0	841	22	0
17	YV	771	0	830	17	5
18	RW	886	0	940	18	1
18	YW	886	0	940	23	0
19	RX	750	0	814	26	0
19	YX	750	0	814	16	0
20	RY	810	0	892	16	0
20	YY	810	0	887	22	7
21	RZ	1587	0	1598	44	0
21	YZ	1557	0	1564	52	0
22	R0	608	0	622	8	0
22	Y0	608	0	622	16	0
23	R1	754	0	823	12	0
23	Y1	759	0	837	24	0
24	R2	588	0	643	16	1
24	Y2	592	0	654	7	0
25	R3	469	0	518	8	0
25	Y3	464	0	514	16	0
26	R4	546	0	522	55	0
26	Y4	536	0	514	58	0
27	R5	459	0	476	18	0
27	Y5	455	0	465	10	5
28	R6	453	0	473	9	0
28	Y6	449	0	469	6	0
29	R7	418	0	467	13	0
29	Y7	418	0	467	5	0
30	R8	517	0	582	24	0
30	Y8	517	0	582	20	0
31	R9	307	0	335	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	Y9	307	0	335	5	0
32	QA	32246	0	16293	408	0
32	XA	32331	0	16339	421	0
33	QB	1842	0	1862	86	0
33	XB	1825	0	1828	88	0
34	QC	1558	0	1557	44	0
34	XC	1542	0	1517	56	0
35	QD	1665	0	1687	71	0
35	XD	1668	0	1703	38	0
36	QE	1133	0	1191	47	0
36	XE	1133	0	1191	31	0
37	QF	814	0	808	18	0
37	XF	816	0	808	24	0
38	QG	1235	0	1249	37	0
38	XG	1229	0	1238	25	0
39	QH	1098	0	1143	42	0
39	XH	1088	0	1126	22	0
40	QI	986	0	990	44	0
40	XI	966	0	953	46	0
41	QJ	719	0	672	33	0
41	XJ	710	0	661	41	0
42	QK	834	0	838	16	0
42	XK	833	0	836	24	0
43	QL	932	0	981	17	0
43	XL	932	0	981	22	0
44	QM	914	0	954	53	0
44	XM	895	0	920	50	0
45	QN	492	0	529	20	0
45	XN	492	0	529	23	0
46	QO	728	0	760	27	0
46	XO	728	0	760	6	0
47	QP	681	0	697	20	0
47	XP	677	0	686	28	0
48	QQ	823	0	891	15	0
48	XQ	823	0	891	10	0
49	QR	555	0	618	16	0
49	XR	555	0	618	26	0
50	QS	648	0	658	29	0
50	XS	645	0	635	43	0
51	QT	732	0	809	34	0
51	XT	733	0	795	31	0
52	QU	199	0	208	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	XU	199	0	208	5	0
53	QV	1644	0	836	30	0
53	XV	1644	0	836	22	0
54	QY	2833	0	2729	96	0
54	XY	2833	0	2728	124	0
55	QX	129	0	64	1	0
55	XX	129	0	65	1	0
56	QA	280	0	0	0	0
56	QB	1	0	0	0	0
56	QD	4	0	0	0	0
56	QE	2	0	0	0	0
56	QF	1	0	0	0	0
56	QG	3	0	0	0	0
56	QH	2	0	0	0	0
56	QI	1	0	0	0	0
56	QL	2	0	0	0	0
56	QM	1	0	0	0	0
56	QN	2	0	0	0	0
56	QO	1	0	0	0	0
56	QQ	2	0	0	0	0
56	QR	1	0	0	0	0
56	QT	1	0	0	0	0
56	QV	4	0	0	0	0
56	QY	2	0	0	0	0
56	R0	4	0	0	0	0
56	R1	4	0	0	0	0
56	R3	2	0	0	0	0
56	R4	1	0	0	0	0
56	R5	4	0	0	0	0
56	R7	2	0	0	0	0
56	R8	1	0	0	0	0
56	R9	2	0	0	0	0
56	RA	1069	0	0	0	0
56	RB	28	0	0	0	0
56	RD	14	0	0	0	0
56	RE	7	0	0	0	0
56	RF	11	0	0	0	0
56	RG	4	0	0	0	0
56	RH	2	0	0	0	0
56	RN	3	0	0	0	0
56	RO	1	0	0	0	0
56	RP	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	RQ	4	0	0	0	0
56	RR	4	0	0	0	0
56	RT	3	0	0	0	0
56	RU	3	0	0	0	0
56	RV	4	0	0	0	0
56	RW	2	0	0	0	0
56	RX	1	0	0	0	0
56	RZ	1	0	0	0	0
56	XA	193	0	0	0	0
56	XE	2	0	0	0	0
56	XF	3	0	0	0	0
56	XH	1	0	0	0	0
56	XJ	1	0	0	0	0
56	XK	1	0	0	0	0
56	XL	1	0	0	0	0
56	XT	1	0	0	0	0
56	XV	3	0	0	0	0
56	XY	1	0	0	0	0
56	Y0	1	0	0	0	0
56	Y1	2	0	0	0	0
56	Y5	1	0	0	0	0
56	Y6	1	0	0	0	0
56	Y7	1	0	0	0	0
56	Y8	2	0	0	0	0
56	YA	756	0	0	0	0
56	YB	19	0	0	0	0
56	YD	9	0	0	0	0
56	YE	7	0	0	0	0
56	YF	3	0	0	0	0
56	YG	3	0	0	0	0
56	YI	1	0	0	0	0
56	YN	1	0	0	0	0
56	YO	2	0	0	0	0
56	YP	1	0	0	0	0
56	YQ	2	0	0	0	0
56	YR	1	0	0	0	0
56	YT	3	0	0	0	0
56	YV	1	0	0	0	0
56	YW	2	0	0	0	0
56	YX	1	0	0	0	0
57	QN	1	0	0	0	0
57	R4	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	R5	1	0	0	0	0
57	R6	1	0	0	0	0
57	R9	1	0	0	0	0
57	RY	1	0	0	0	0
57	XN	1	0	0	0	0
57	Y4	1	0	0	0	0
57	Y5	1	0	0	0	0
57	Y6	1	0	0	0	0
57	Y9	1	0	0	0	0
57	YY	1	0	0	0	0
58	QD	8	0	0	0	0
58	XD	8	0	0	0	0
All	All	296497	0	200048	4678	13

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 10.

All (4678) 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)
33:XB:114:ARG:NH1	33:XB:118:LEU:HG	1.41	1.36
42:QK:48:ILE:HD12	42:QK:63:LEU:CB	1.60	1.29
7:YH:7:LEU:O	7:YH:69:ARG:NH1	1.63	1.29
42:QK:48:ILE:CD1	42:QK:63:LEU:HB2	1.66	1.25
26:Y4:59:PHE:CE1	50:XS:64:GLU:HB2	1.73	1.23
26:Y4:58:ARG:NH1	50:XS:65:ASN:O	1.71	1.21
34:XC:152:ILE:HG22	34:XC:167:TRP:CB	1.74	1.16
40:XI:16:ARG:HB2	40:XI:64:THR:HG22	1.26	1.16
4:YE:119:ARG:HD3	4:YE:160:TYR:HB2	1.27	1.15
6:RG:7:LEU:CD1	6:RG:100:TRP:HE3	1.59	1.14
8:YI:72:LEU:HA	8:YI:75:LEU:HD22	1.23	1.13
6:RG:7:LEU:CD1	6:RG:100:TRP:CE3	2.32	1.13
51:XT:56:MET:CE	51:XT:84:LEU:HD22	1.77	1.13
15:YT:118:ARG:HH22	15:YT:121:ILE:HG21	1.01	1.13
6:YG:56:ALA:HA	6:YG:153:ARG:NH2	1.64	1.12
8:YI:72:LEU:O	8:YI:75:LEU:HD23	1.49	1.12
8:YI:40:THR:O	8:YI:44:LEU:HD22	1.46	1.11
9:YN:120:LEU:HD11	9:YN:122:VAL:HG23	1.33	1.11
42:QK:48:ILE:HD12	42:QK:63:LEU:HB2	1.10	1.10
44:QM:64:TRP:C	26:R4:50:VAL:HG21	1.69	1.10
21:RZ:126:VAL:HG11	21:RZ:161:VAL:CG2	1.81	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:YF:178:PRO:HB2	5:YF:201:VAL:HG21	1.35	1.09
21:RZ:126:VAL:CG1	21:RZ:161:VAL:HG23	1.83	1.09
40:QI:17:VAL:HG21	40:QI:81:ILE:HG22	1.33	1.08
14:RS:59:LYS:HD2	14:RS:60:GLY:H	1.03	1.08
9:YN:120:LEU:CD1	9:YN:122:VAL:HG23	1.82	1.08
34:XC:152:ILE:HG22	34:XC:167:TRP:HB2	1.36	1.07
8:YI:72:LEU:O	8:YI:75:LEU:CD2	2.01	1.07
44:QM:65:LYS:HA	26:R4:50:VAL:HG11	1.35	1.07
14:YS:50:SER:O	14:YS:76:LYS:NZ	1.89	1.06
33:XB:122:PHE:CG	33:XB:127:ILE:HD12	1.90	1.05
9:YN:120:LEU:HD11	9:YN:122:VAL:CG2	1.88	1.04
40:QI:16:ARG:HB2	40:QI:64:THR:HG22	1.37	1.04
15:RT:55:ASN:H	15:RT:59:THR:HG22	1.19	1.04
7:YH:41:MET:HE1	7:YH:64:LEU:HB2	1.35	1.03
6:YG:136:ARG:H	6:YG:136:ARG:HD3	1.21	1.03
46:QO:3:ILE:HD11	46:QO:34:LEU:HD21	1.37	1.03
46:QO:71:GLN:NE2	46:QO:78:TYR:CE2	2.26	1.03
51:XT:56:MET:HE3	51:XT:84:LEU:HD22	1.05	1.02
40:QI:89:ASN:OD1	40:QI:92:TYR:CD1	2.13	1.02
26:Y4:59:PHE:CZ	50:XS:64:GLU:HB2	1.94	1.01
32:QA:1422:G:H5''	10:RO:48:PRO:HB3	1.41	1.01
6:YG:146:TYR:HD2	44:XM:8:GLU:CD	1.63	1.00
33:XB:114:ARG:NH1	33:XB:118:LEU:CG	2.23	1.00
25:R3:8:LEU:HD12	25:R3:31:LEU:HA	1.39	1.00
32:XA:1003:G:H2'	32:XA:1004:A:H4'	1.42	0.99
6:YG:16:ARG:HH21	6:YG:31:VAL:HG22	1.28	0.98
6:RG:7:LEU:HD12	6:RG:100:TRP:HE3	1.28	0.98
6:YG:16:ARG:NH2	6:YG:31:VAL:HG22	1.77	0.98
6:YG:56:ALA:CA	6:YG:153:ARG:NH2	2.27	0.98
3:RD:108:PRO:HD2	3:RD:111:LEU:CD1	1.93	0.98
8:YI:72:LEU:CA	8:YI:75:LEU:HD22	1.94	0.97
40:XI:23:ASN:OD1	40:XI:25:LYS:HE3	1.64	0.97
8:YI:92:VAL:HG23	8:YI:120:ILE:HB	1.43	0.97
26:Y4:59:PHE:HE1	50:XS:64:GLU:HB2	1.27	0.97
4:YE:12:THR:HG22	4:YE:13:ARG:H	1.29	0.97
1:RA:2131:G:H5''	1:RA:2132:U:H5'	1.47	0.97
51:QT:89:ARG:O	51:QT:93:GLU:HG2	1.66	0.96
33:XB:114:ARG:HH11	33:XB:118:LEU:HG	1.01	0.96
26:Y4:59:PHE:HA	26:Y4:61:ARG:N	1.80	0.96
51:XT:56:MET:HE3	51:XT:84:LEU:CD2	1.95	0.96
15:YT:118:ARG:NH2	15:YT:121:ILE:HG21	1.79	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:QO:3:ILE:HD11	46:QO:34:LEU:CD2	1.95	0.95
44:QM:64:TRP:CA	26:R4:50:VAL:HG21	1.95	0.95
10:YO:48:PRO:HB3	32:XA:1422:G:H5"	1.45	0.95
1:YA:2131:G:H5"	1:YA:2132:U:H5'	1.49	0.95
7:YH:33:LEU:HD11	7:YH:75:ALA:HB1	1.48	0.95
15:YT:118:ARG:HH21	15:YT:121:ILE:CD1	1.79	0.95
34:XC:152:ILE:HG22	34:XC:167:TRP:HB3	1.45	0.95
35:QD:88:VAL:HG22	36:QE:96:PRO:HB2	1.48	0.95
25:R3:8:LEU:HD11	25:R3:31:LEU:HD22	1.50	0.94
6:YG:44:GLY:O	6:YG:47:LYS:HD2	1.68	0.94
4:RE:175:VAL:HG12	4:RE:182:LEU:HD12	1.50	0.93
8:RI:140:LEU:CD1	8:RI:142:VAL:CG2	2.45	0.93
8:RI:140:LEU:CD1	8:RI:142:VAL:HG22	1.98	0.93
8:YI:72:LEU:HA	8:YI:75:LEU:CD2	1.98	0.93
37:QF:99:ALA:HB2	49:QR:31:LEU:HD21	1.47	0.93
21:YZ:126:VAL:HG11	21:YZ:161:VAL:HG13	1.47	0.92
6:RG:179:PRO:HB2	26:R4:42:PHE:HE2	1.31	0.92
9:RN:120:LEU:HD22	9:RN:122:VAL:HG23	1.51	0.92
44:XM:96:LEU:O	44:XM:110:ARG:NH1	2.02	0.92
7:YH:41:MET:HE1	7:YH:64:LEU:CB	2.00	0.92
35:QD:108:LEU:HD22	35:QD:174:LEU:HD13	1.49	0.91
46:QO:3:ILE:CD1	46:QO:34:LEU:HD21	2.00	0.91
21:RZ:126:VAL:CG1	21:RZ:161:VAL:CG2	2.42	0.91
9:RN:29:LYS:O	9:RN:33:LEU:HD22	1.69	0.91
25:Y3:8:LEU:CD1	25:Y3:31:LEU:HD22	2.01	0.91
3:RD:108:PRO:HD2	3:RD:111:LEU:HD12	1.50	0.90
13:RR:36:THR:HG22	13:RR:37:THR:H	1.35	0.90
51:QT:57:ARG:HH12	51:QT:100:ILE:HD12	1.36	0.90
33:QB:96:ARG:HD2	33:QB:98:LEU:HD23	1.54	0.90
8:YI:75:LEU:HD12	8:YI:105:HIS:ND1	1.87	0.90
34:QC:59:ARG:O	41:QJ:92:THR:CG2	2.19	0.89
42:QK:48:ILE:HD12	42:QK:63:LEU:HB3	1.52	0.89
13:YR:55:ALA:CB	13:YR:79:LEU:HD22	2.02	0.89
1:YA:250:G:OP2	30:Y8:13:ARG:NH2	2.06	0.89
33:XB:122:PHE:CE1	33:XB:127:ILE:HD11	2.06	0.89
6:YG:56:ALA:HA	6:YG:153:ARG:HH22	1.35	0.89
32:XA:582:U:OP1	46:XO:68:ARG:NH2	2.06	0.89
33:QB:15:VAL:CG2	33:QB:209:ARG:HG2	2.02	0.88
25:Y3:8:LEU:HD11	25:Y3:31:LEU:HD22	1.53	0.88
29:R7:34:ARG:NH1	29:R7:41:ARG:O	2.07	0.88
8:RI:140:LEU:HD11	8:RI:142:VAL:HG22	1.55	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:2602:A:N6	54:QY:253:HIS:O	2.06	0.88
15:RT:55:ASN:N	15:RT:59:THR:HG22	1.89	0.88
6:YG:36:LYS:HE2	6:YG:95:ARG:NH1	1.89	0.88
51:QT:10:LEU:HD23	51:QT:11:SER:H	1.39	0.88
14:RS:59:LYS:CD	14:RS:60:GLY:H	1.85	0.88
28:R6:14:THR:HG21	28:R6:48:VAL:HG13	1.53	0.88
50:XS:50:ALA:HB1	50:XS:57:HIS:HB3	1.55	0.87
8:YI:40:THR:O	8:YI:44:LEU:CD2	2.22	0.87
40:QI:89:ASN:OD1	40:QI:92:TYR:HD1	1.53	0.87
46:QO:3:ILE:CD1	46:QO:34:LEU:CD2	2.52	0.87
21:RZ:126:VAL:HG11	21:RZ:161:VAL:HG23	1.48	0.87
33:XB:15:VAL:HB	33:XB:209:ARG:HB3	1.53	0.87
8:RI:109:ILE:HG13	8:RI:130:TYR:CZ	2.09	0.87
7:YH:7:LEU:C	7:YH:69:ARG:HH12	1.78	0.87
25:R3:8:LEU:CD1	25:R3:31:LEU:HD22	2.04	0.87
6:YG:56:ALA:CB	6:YG:153:ARG:NH2	2.37	0.86
41:XJ:49:VAL:HG23	45:XN:41:ARG:HB2	1.57	0.86
1:YA:1041:C:H42	1:YA:1114:G:H1	1.24	0.86
13:YR:18:LEU:HD11	13:YR:22:ARG:CZ	2.05	0.86
33:QB:96:ARG:HD2	33:QB:98:LEU:CD2	2.05	0.86
13:YR:55:ALA:HB2	13:YR:79:LEU:HD22	1.57	0.86
34:QC:59:ARG:O	41:QJ:92:THR:HG22	1.75	0.86
5:RF:178:PRO:HB2	5:RF:201:VAL:HG21	1.57	0.86
6:RG:7:LEU:HD13	6:RG:100:TRP:CE3	2.08	0.85
14:RS:59:LYS:HD2	14:RS:60:GLY:N	1.89	0.85
26:Y4:58:ARG:CZ	44:XM:80:ARG:NH2	2.39	0.85
5:RF:165:ARG:HA	5:RF:168:ARG:HD2	1.58	0.85
7:RH:116:GLU:OE1	7:RH:117:PRO:HD2	1.76	0.85
17:RV:72:VAL:HG13	17:RV:85:LYS:HB3	1.58	0.85
18:RW:11:ARG:HG3	18:RW:11:ARG:O	1.75	0.85
53:XV:75:C:OP2	54:XY:278:ARG:NH2	2.09	0.85
33:QB:82:ARG:NH1	33:QB:86:GLU:OE2	2.10	0.85
35:XD:18:LYS:NZ	35:XD:31:CYS:SG	2.50	0.85
4:RE:51:PHE:H	4:RE:75:VAL:HG11	1.41	0.84
6:YG:16:ARG:HH21	6:YG:31:VAL:CG2	1.89	0.84
5:YF:178:PRO:HB2	5:YF:201:VAL:CG2	2.05	0.84
27:R5:47:PRO:O	27:R5:60:VAL:HG21	1.76	0.84
6:RG:41:GLN:HB3	6:RG:43:LEU:HD13	1.60	0.84
33:XB:88:ALA:HB1	33:XB:222:ILE:HD11	1.59	0.84
34:QC:6:HIS:CE1	34:QC:8:ILE:HB	2.12	0.84
40:QI:16:ARG:HD3	40:QI:64:THR:HG21	1.58	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:XM:107:ALA:HB3	44:XM:111:LYS:HD2	1.60	0.84
10:YO:24:VAL:HG23	10:YO:33:ALA:HB2	1.60	0.84
38:QG:89:MET:HE1	38:QG:155:ARG:HB2	1.60	0.83
12:RQ:80:GLU:OE1	54:QY:281:HIS:CD2	2.31	0.83
40:XI:16:ARG:HD3	40:XI:64:THR:HG21	1.58	0.83
7:YH:9:ILE:HG12	7:YH:69:ARG:HD3	1.58	0.83
1:RA:2103:C:N3	1:RA:2104:G:N2	2.27	0.83
5:RF:178:PRO:HB2	5:RF:201:VAL:CG2	2.08	0.83
7:YH:41:MET:CE	7:YH:64:LEU:HB2	2.09	0.83
40:QI:16:ARG:HB2	40:QI:64:THR:CG2	2.07	0.83
26:R4:41:PRO:HG3	26:R4:49:PHE:CE1	2.13	0.83
26:Y4:59:PHE:HA	26:Y4:61:ARG:H	1.40	0.83
9:YN:94:HIS:CB	9:YN:97:ARG:HD3	2.08	0.83
9:YN:94:HIS:HB3	9:YN:97:ARG:HD3	1.57	0.83
1:RA:1310:G:OP2	29:R7:9:ARG:NH1	2.10	0.83
12:YQ:34:LEU:HB2	12:YQ:118:LEU:HD22	1.60	0.83
1:RA:250:G:OP2	30:R8:13:ARG:NH2	2.09	0.83
33:QB:15:VAL:CG1	33:QB:213:LEU:HD12	2.08	0.82
40:XI:53:VAL:O	40:XI:55:ALA:N	2.11	0.82
39:QH:51:VAL:HG12	39:QH:52:ASP:H	1.43	0.82
39:XH:12:ARG:HD2	39:XH:26:VAL:HG12	1.61	0.82
26:Y4:58:ARG:NH1	44:XM:80:ARG:HH21	1.76	0.82
4:RE:51:PHE:H	4:RE:75:VAL:CG1	1.92	0.82
44:QM:15:VAL:O	44:QM:19:LEU:HD13	1.80	0.82
18:YW:11:ARG:HG3	18:YW:11:ARG:O	1.80	0.82
36:XE:50:GLU:HB2	36:XE:53:LEU:HD13	1.62	0.82
6:YG:146:TYR:CD2	44:XM:8:GLU:CD	2.53	0.81
5:YF:39:TRP:CZ2	5:YF:106:ARG:NH2	2.48	0.81
6:YG:16:ARG:NH2	6:YG:31:VAL:CG2	2.43	0.81
1:YA:2103:C:N3	1:YA:2104:G:N2	2.29	0.81
33:QB:15:VAL:HG23	33:QB:209:ARG:CG	2.11	0.81
15:YT:118:ARG:HH22	15:YT:121:ILE:CG2	1.89	0.81
15:YT:118:ARG:HH21	15:YT:121:ILE:HD12	1.43	0.81
15:YT:118:ARG:NH2	15:YT:121:ILE:CD1	2.42	0.81
19:RX:88:LYS:NZ	19:RX:90:GLU:OE1	2.13	0.81
13:RR:24:GLN:HB3	13:RR:44:LEU:HD11	1.61	0.81
21:RZ:72:ARG:CG	21:RZ:89:PHE:HB2	2.11	0.81
32:XA:559:A:H4'	32:XA:560:U:H3'	1.62	0.81
1:RA:587:C:OP2	11:RP:21:ARG:NH2	2.13	0.81
41:XJ:35:SER:HB3	41:XJ:73:ASP:H	1.45	0.81
13:YR:62:ALA:HA	13:YR:65:LEU:HD23	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:QI:108:VAL:HG12	40:QI:109:VAL:H	1.45	0.81
27:R5:40:LYS:NZ	27:R5:44:THR:O	2.13	0.81
50:XS:20:LEU:HD23	50:XS:23:ASN:HD22	1.46	0.81
5:RF:20:LEU:HD13	5:RF:21:ALA:N	1.96	0.80
40:QI:50:LEU:HD13	40:QI:56:LEU:HA	1.62	0.80
6:YG:56:ALA:CB	6:YG:153:ARG:HH21	1.93	0.80
13:YR:61:HIS:O	13:YR:65:LEU:HD22	1.80	0.80
11:YP:97:PRO:HA	11:YP:112:LEU:HD12	1.64	0.80
40:XI:16:ARG:HB2	40:XI:64:THR:CG2	2.08	0.80
54:XY:203:ARG:HD3	54:XY:328:LEU:HD12	1.64	0.80
7:YH:9:ILE:HG12	7:YH:69:ARG:CD	2.12	0.80
48:QQ:66:SER:O	48:QQ:70:ARG:NH1	2.15	0.80
33:XB:47:THR:HA	33:XB:202:PRO:HG2	1.64	0.80
33:XB:114:ARG:HH12	33:XB:118:LEU:HG	1.45	0.80
5:YF:24:LEU:HD23	5:YF:115:ALA:HA	1.64	0.80
15:RT:95:ARG:HH11	15:RT:95:ARG:HG2	1.47	0.80
22:R0:10:THR:HG22	22:R0:12:ASN:H	1.45	0.79
6:RG:161:THR:HG22	6:RG:163:ALA:H	1.47	0.79
6:YG:36:LYS:HE2	6:YG:95:ARG:HH12	1.45	0.79
40:QI:16:ARG:CB	40:QI:64:THR:HG22	2.11	0.79
33:XB:122:PHE:CG	33:XB:127:ILE:CD1	2.66	0.79
7:YH:9:ILE:CG1	7:YH:69:ARG:HD3	2.12	0.79
6:RG:179:PRO:HB2	26:R4:42:PHE:CE2	2.18	0.79
25:Y3:8:LEU:HD12	25:Y3:31:LEU:HA	1.62	0.79
4:YE:119:ARG:CD	4:YE:160:TYR:HB2	2.09	0.79
32:QA:532:A:N6	32:QA:1206:G:O2'	2.16	0.79
4:YE:47:VAL:HG11	4:YE:86:PRO:HD2	1.65	0.79
27:R5:47:PRO:O	27:R5:60:VAL:CG2	2.30	0.79
4:RE:47:VAL:HG21	4:RE:86:PRO:HD2	1.64	0.79
34:QC:6:HIS:HE1	34:QC:8:ILE:HB	1.46	0.79
1:RA:140:G:N2	1:RA:142(A):A:N6	2.31	0.79
33:QB:200:ILE:HG22	33:QB:202:PRO:HD3	1.65	0.78
8:RI:140:LEU:HD12	8:RI:142:VAL:CG2	2.11	0.78
4:YE:12:THR:HG22	4:YE:13:ARG:N	1.98	0.78
37:XF:33:TYR:HB2	37:XF:75:LEU:HD23	1.65	0.78
21:YZ:45:ASP:OD1	21:YZ:49:ARG:NH1	2.17	0.78
1:RA:1530:C:O2'	1:RA:1531:C:O5'	2.01	0.78
18:RW:23:LEU:HD11	27:R5:25:LEU:HB2	1.63	0.78
1:YA:1530:C:O2'	1:YA:1531:C:O5'	2.00	0.78
51:QT:10:LEU:CD2	51:QT:11:SER:H	1.97	0.78
9:RN:120:LEU:CD2	9:RN:122:VAL:HG23	2.13	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:RT:35:LYS:HD2	15:RT:36:GLU:N	1.98	0.78
54:XY:203:ARG:HH12	54:XY:206:PRO:HD3	1.49	0.78
7:YH:41:MET:CE	7:YH:64:LEU:CB	2.61	0.78
13:YR:100:LEU:HD22	13:YR:112:ALA:HA	1.65	0.78
33:XB:229:VAL:HG12	33:XB:230:VAL:H	1.49	0.78
1:YA:1069:A:H5'	1:YA:1096:A:H5'	1.66	0.78
5:YF:39:TRP:CH2	5:YF:106:ARG:NH2	2.52	0.78
33:QB:15:VAL:HG23	33:QB:209:ARG:HG2	1.64	0.78
32:QA:1492:A:O4'	43:QL:47:LYS:NZ	2.17	0.78
35:QD:166:LYS:N	35:QD:168:ARG:HH21	1.82	0.77
33:XB:8:LYS:HG2	33:XB:9:GLU:H	1.49	0.77
1:RA:272(K):U:H1'	8:RI:50:ARG:HH21	1.48	0.77
32:XA:1402:4OC:HM22	32:XA:1403:C:H5'	1.67	0.77
33:XB:18:GLY:HA2	33:XB:42:ILE:HD12	1.66	0.77
1:YA:2640:G:O3'	9:YN:74:ARG:NH2	2.13	0.77
8:YI:92:VAL:CG2	8:YI:120:ILE:HB	2.14	0.77
32:QA:1189:C:OP1	41:QJ:51:ARG:NH2	2.17	0.77
1:RA:994:C:OP1	16:RU:53:ARG:NH2	2.16	0.77
32:QA:673:G:H2'	32:QA:674:G:C8	2.19	0.77
44:QM:65:LYS:HG2	26:R4:50:VAL:HG13	1.67	0.77
8:YI:72:LEU:O	8:YI:75:LEU:HD22	1.83	0.77
5:RF:53:THR:HG22	5:RF:55:GLY:H	1.50	0.77
33:XB:185:ILE:HD12	33:XB:199:TYR:HB2	1.66	0.77
32:XA:975:A:H4'	32:XA:976:G:H5''	1.67	0.77
10:RO:24:VAL:HG23	10:RO:33:ALA:HB2	1.67	0.77
11:RP:101:VAL:HG23	11:RP:106:LEU:HD12	1.66	0.77
13:RR:55:ALA:CB	13:RR:79:LEU:HD22	2.15	0.76
46:QO:84:LYS:O	46:QO:84:LYS:HD3	1.85	0.76
9:RN:29:LYS:O	9:RN:33:LEU:CD2	2.33	0.76
32:XA:673:G:H2'	32:XA:674:G:C8	2.20	0.76
1:YA:2748:A:H5'	7:YH:4:ILE:HD12	1.67	0.76
10:YO:35:VAL:HG11	10:YO:103:ALA:HB3	1.67	0.76
32:QA:538:G:H5''	43:QL:114:LYS:HB2	1.66	0.76
33:QB:185:ILE:HG22	33:QB:199:TYR:HB2	1.67	0.76
6:YG:35:GLU:HG3	6:YG:36:LYS:HE3	1.67	0.76
44:QM:3:ARG:HG3	44:QM:4:ILE:H	1.50	0.76
21:RZ:144:LEU:HD21	21:RZ:150:LEU:HD13	1.67	0.76
46:XO:17:ARG:HD3	46:XO:26:GLU:OE1	1.85	0.76
15:YT:118:ARG:NH2	15:YT:121:ILE:HD13	1.99	0.76
32:XA:390:C:O3'	47:XP:28:ARG:NH2	2.18	0.76
10:RO:35:VAL:HG11	10:RO:103:ALA:HB3	1.66	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:677:U:H3	32:QA:713:G:H22	1.34	0.76
11:RP:63:PRO:HG2	30:R8:25:MET:HB2	1.68	0.76
1:YA:2602:A:N6	54:XY:253:HIS:O	2.18	0.76
44:XM:15:VAL:O	44:XM:19:LEU:HD13	1.85	0.76
1:YA:2785:C:OP1	4:YE:41:LYS:NZ	2.19	0.76
6:YG:56:ALA:HB2	6:YG:153:ARG:NH2	2.00	0.76
22:Y0:10:THR:HG22	22:Y0:12:ASN:H	1.51	0.75
33:XB:122:PHE:CD1	33:XB:127:ILE:CD1	2.69	0.75
21:YZ:72:ARG:CG	21:YZ:89:PHE:HB2	2.17	0.75
23:Y1:75:GLU:HA	23:Y1:78:LYS:HE2	1.68	0.75
20:YY:23:ARG:HG2	20:YY:42:VAL:HG22	1.67	0.75
25:Y3:8:LEU:CD1	25:Y3:31:LEU:HA	2.16	0.75
6:YG:161:THR:HG22	6:YG:163:ALA:H	1.49	0.75
32:QA:1402:4OC:HM22	32:QA:1403:C:H5'	1.68	0.75
44:QM:68:GLY:HA3	6:RG:116:ASP:OD1	1.87	0.75
6:YG:136:ARG:H	6:YG:136:ARG:CD	1.98	0.75
6:YG:56:ALA:HA	6:YG:153:ARG:HH21	1.52	0.75
32:QA:370:C:O2	32:QA:391:G:N2	2.18	0.75
32:QA:975:A:H4'	32:QA:976:G:H5''	1.67	0.75
1:RA:1073:A:H2'	1:RA:1074:G:H8	1.50	0.75
15:YT:16:ARG:NH2	15:YT:83:ILE:O	2.20	0.75
13:RR:55:ALA:HB2	13:RR:79:LEU:HD22	1.69	0.75
11:RP:98:GLU:OE1	11:RP:102:ARG:NH1	2.16	0.74
21:RZ:72:ARG:HG2	21:RZ:89:PHE:HB2	1.69	0.74
23:R1:50:ARG:HG2	23:R1:59:THR:HG22	1.69	0.74
51:QT:57:ARG:NH1	51:QT:100:ILE:HD12	2.03	0.74
1:RA:956:G:OP2	12:RQ:14:ARG:NH2	2.18	0.74
33:QB:15:VAL:HG21	33:QB:209:ARG:HG2	1.69	0.74
44:QM:65:LYS:N	26:R4:50:VAL:HG21	2.02	0.74
28:Y6:13:CYS:SG	28:Y6:47:THR:HG21	2.27	0.74
9:YN:120:LEU:HD13	9:YN:122:VAL:HG23	1.66	0.74
32:XA:1302:U:OP1	44:XM:13:LYS:NZ	2.20	0.74
54:XY:334:LYS:HG2	54:XY:341:GLU:HG2	1.69	0.74
32:QA:1124:G:N2	32:QA:1125:U:O4	2.19	0.74
41:QJ:35:SER:HB3	41:QJ:73:ASP:HB2	1.69	0.74
3:RD:69:ARG:NH2	3:RD:128:GLY:O	2.20	0.74
11:RP:112:LEU:HD12	11:RP:127:ALA:CB	2.18	0.74
1:RA:2748:A:H5'	7:RH:4:ILE:HD12	1.69	0.74
49:XR:56:THR:HB	49:XR:58:LEU:HD23	1.70	0.74
21:YZ:10:ARG:NH2	21:YZ:26:GLY:O	2.21	0.74
21:YZ:126:VAL:CG1	21:YZ:161:VAL:HG13	2.17	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:1250:G:N7	11:RP:18:ARG:NH2	2.35	0.74
32:XA:501:C:H2'	32:XA:502:G:H8	1.53	0.74
26:Y4:59:PHE:CE1	50:XS:64:GLU:CB	2.65	0.74
54:QY:162:LYS:HB2	54:QY:184:SER:HB3	1.70	0.74
39:QH:14:ARG:O	39:QH:18:ARG:HG2	1.87	0.73
44:QM:65:LYS:CA	26:R4:50:VAL:HG11	2.15	0.73
32:XA:1060:C:HO2'	41:XJ:56:HIS:HD1	1.34	0.73
5:YF:110:LEU:HD13	5:YF:202:PHE:HE1	1.52	0.73
33:XB:122:PHE:CZ	33:XB:127:ILE:HD11	2.23	0.73
21:RZ:9:TYR:OH	21:RZ:61:LEU:HD23	1.89	0.73
53:XV:75:C:H5	54:XY:278:ARG:HH12	1.37	0.73
44:QM:64:TRP:HA	26:R4:50:VAL:HG21	1.70	0.73
1:RA:83:G:OP1	20:RY:95:LYS:NZ	2.19	0.73
3:RD:72:LYS:HG3	3:RD:103:ARG:NH2	2.02	0.73
39:QH:20:TYR:CE1	39:QH:78:GLN:NE2	2.55	0.73
3:YD:30:GLU:HG3	3:YD:94:LEU:HD21	1.71	0.73
7:YH:69:ARG:HD2	7:YH:69:ARG:O	1.88	0.73
6:YG:136:ARG:HG2	6:YG:137:GLU:HG3	1.71	0.73
44:QM:4:ILE:HD12	44:QM:57:ARG:HA	1.71	0.73
6:YG:101:ILE:HD13	26:Y4:25:TYR:HB2	1.69	0.73
11:RP:59:LEU:HD11	30:R8:10:ALA:HB2	1.70	0.73
49:XR:58:LEU:HD12	49:XR:62:GLU:HG3	1.69	0.73
40:QI:25:LYS:HE2	40:QI:25:LYS:HA	1.71	0.73
50:QS:64:GLU:HG3	26:R4:59:PHE:CE1	2.23	0.73
32:XA:1318:A:H5''	50:XS:3:ARG:HH22	1.53	0.73
28:R6:14:THR:HG21	28:R6:48:VAL:CG1	2.18	0.72
38:XG:151:TYR:OH	42:XK:54:ARG:NH1	2.21	0.72
32:XA:109:A:C6	32:XA:326:G:C6	2.77	0.72
32:XA:978:A:OP2	32:XA:1363(A):C:N4	2.21	0.72
32:QA:946:A:H2'	32:QA:947:G:C8	2.24	0.72
32:XA:1456:G:O6	51:XT:54:LYS:NZ	2.22	0.72
26:Y4:18:CYS:SG	26:Y4:39:CYS:HB3	2.28	0.72
1:YA:1266:G:O5'	18:YW:15:ARG:NH2	2.22	0.72
21:YZ:179:ASP:O	21:YZ:182:LYS:HG2	1.89	0.72
32:QA:159:G:N2	32:QA:162:A:OP2	2.17	0.72
21:RZ:126:VAL:HG13	21:RZ:161:VAL:HG23	1.70	0.72
32:XA:677:U:H3	32:XA:713:G:H22	1.36	0.72
35:XD:108:LEU:CD1	35:XD:174:LEU:HD13	2.19	0.72
44:XM:58:GLU:O	44:XM:62:ASN:ND2	2.23	0.72
41:XJ:17:ASP:OD1	41:XJ:70:ARG:NH1	2.22	0.72
8:YI:50:ARG:O	8:YI:54:GLN:NE2	2.23	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:1356:G:H2'	32:QA:1357:A:C8	2.24	0.72
41:QJ:49:VAL:HG23	45:QN:41:ARG:HB2	1.70	0.72
44:QM:4:ILE:CD1	44:QM:57:ARG:HA	2.20	0.72
6:RG:63:ILE:HA	6:RG:143:GLU:HG3	1.71	0.72
15:RT:16:ARG:NH2	15:RT:83:ILE:O	2.22	0.72
1:RA:2126:A:H4'	1:RA:2127:G:O5'	1.90	0.72
26:Y4:58:ARG:CZ	44:XM:80:ARG:HH21	2.02	0.72
13:YR:36:THR:HG22	13:YR:37:THR:H	1.54	0.72
35:QD:148:VAL:HG11	35:QD:158:ILE:HD12	1.69	0.72
1:RA:1971:A:OP2	3:RD:242:ARG:NH2	2.23	0.72
21:RZ:126:VAL:HG11	21:RZ:161:VAL:HG21	1.70	0.72
41:XJ:38:ILE:CG1	41:XJ:71:LEU:HB3	2.20	0.72
34:QC:59:ARG:H	41:QJ:92:THR:HG21	1.53	0.72
54:QY:138:GLY:O	54:QY:140:GLU:N	2.22	0.72
27:Y5:16:ARG:NH1	27:Y5:17:ASP:OD1	2.23	0.72
10:YO:24:VAL:CG2	10:YO:33:ALA:HB2	2.20	0.72
32:QA:339:C:OP2	10:RO:97:ARG:NH1	2.23	0.71
35:QD:88:VAL:CG2	36:QE:96:PRO:HB2	2.20	0.71
37:XF:67:MET:SD	37:XF:72:VAL:HG12	2.30	0.71
40:XI:16:ARG:CB	40:XI:64:THR:HG22	2.14	0.71
26:Y4:58:ARG:HH12	50:XS:66:MET:HA	1.55	0.71
32:QA:343:U:O2'	32:QA:346:G:O6	2.06	0.71
33:QB:229:VAL:HG12	33:QB:230:VAL:H	1.54	0.71
39:QH:112:LEU:HD23	39:QH:133:LEU:HA	1.72	0.71
7:RH:116:GLU:OE1	7:RH:117:PRO:CD	2.38	0.71
11:RP:112:LEU:CD1	11:RP:127:ALA:CB	2.69	0.71
54:XY:201:LEU:HD21	54:XY:203:ARG:HE	1.53	0.71
26:Y4:16:CYS:SG	26:Y4:17:GLY:N	2.63	0.71
8:YI:72:LEU:C	8:YI:75:LEU:HD22	2.09	0.71
33:QB:21:ARG:H	33:QB:21:ARG:CD	2.03	0.71
35:QD:50:ARG:NH1	36:QE:9:LYS:HZ3	1.88	0.71
32:XA:1086:U:H3	32:XA:1099:G:H22	1.38	0.71
32:QA:56:U:H2'	32:QA:57:G:H8	1.55	0.71
44:QM:3:ARG:HG3	44:QM:4:ILE:N	2.05	0.71
1:RA:631:A:OP1	11:RP:65:ARG:NH1	2.22	0.71
32:XA:1356:G:H2'	32:XA:1357:A:C8	2.25	0.71
4:YE:11:MET:HG2	4:YE:24:THR:HG22	1.71	0.71
50:QS:41:VAL:HG12	50:QS:44:MET:HG3	1.71	0.71
34:XC:6:HIS:HD2	34:XC:9:GLY:H	1.38	0.71
50:XS:41:VAL:HG12	50:XS:44:MET:HG3	1.71	0.71
35:QD:106:TYR:HE2	35:QD:107:ARG:HH11	1.38	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:R6:13:CYS:SG	28:R6:47:THR:HG21	2.31	0.71
5:RF:33:LEU:HD13	5:RF:112:MET:CE	2.21	0.71
1:RA:1041:C:H42	1:RA:1114:G:H1	1.38	0.71
13:RR:36:THR:HG22	13:RR:37:THR:N	2.04	0.71
32:QA:974:A:OP2	45:QN:29:ARG:NH2	2.24	0.70
35:QD:57:ARG:NH2	36:QE:107:ARG:CD	2.55	0.70
53:QV:75:C:OP2	54:QY:278:ARG:NH2	2.24	0.70
1:YA:1073:A:H2'	1:YA:1074:G:H8	1.55	0.70
33:XB:91:PRO:HG3	33:XB:155:LEU:HD23	1.74	0.70
6:YG:41:GLN:HB3	6:YG:43:LEU:HD13	1.73	0.70
7:YH:33:LEU:CD1	7:YH:75:ALA:HB1	2.19	0.70
15:YT:118:ARG:HH21	15:YT:121:ILE:HD13	1.52	0.70
33:QB:15:VAL:HG11	33:QB:213:LEU:HD12	1.73	0.70
1:YA:1064:C:H3'	1:YA:1065:U:C5'	2.22	0.70
1:YA:2406:U:N3	11:YP:73:GLY:O	2.23	0.70
51:QT:60:GLU:HG3	51:QT:81:LYS:HD2	1.72	0.70
25:R3:3:ARG:NH1	25:R3:60:GLU:OE2	2.24	0.70
6:YG:63:ILE:HA	6:YG:143:GLU:HG3	1.73	0.70
10:RO:10:VAL:CG2	10:RO:16:ALA:O	2.40	0.70
8:YI:86:THR:HA	8:YI:123:LEU:HD23	1.73	0.70
19:YX:57:LEU:HD12	19:YX:78:LYS:HG2	1.73	0.70
33:QB:21:ARG:H	33:QB:21:ARG:HD2	1.57	0.69
18:YW:51:LEU:C	18:YW:51:LEU:HD13	2.13	0.69
35:QD:88:VAL:HG13	36:QE:97:GLY:HA2	1.72	0.69
32:QA:1298:C:C4	38:QG:114:ARG:HD2	2.27	0.69
54:QY:22:ARG:HG2	54:QY:70:LEU:HD13	1.71	0.69
29:R7:9:ARG:NH2	29:R7:47:ARG:HB3	2.07	0.69
6:RG:115:ARG:HB3	6:RG:136:ARG:HH22	1.58	0.69
8:RI:140:LEU:CD1	8:RI:142:VAL:HG23	2.22	0.69
54:XY:130:LEU:HD12	54:XY:192:LEU:HD13	1.73	0.69
24:Y2:35:LEU:HD21	24:Y2:49:LYS:HE2	1.74	0.69
19:YX:29:TRP:CZ2	19:YX:76:ARG:NH2	2.59	0.69
40:QI:108:VAL:HG12	40:QI:109:VAL:N	2.07	0.69
44:QM:2:ALA:O	26:R4:34:GLU:OE1	2.10	0.69
34:QC:59:ARG:O	41:QJ:92:THR:HG23	1.91	0.69
1:RA:1064:C:H3'	1:RA:1065:U:C5'	2.22	0.69
33:XB:122:PHE:CD1	33:XB:127:ILE:HD12	2.26	0.69
32:QA:1492:A:H2'	54:QY:319:TRP:HE1	1.56	0.69
32:QA:992:U:H4'	32:QA:993:G:H5'	1.75	0.69
35:QD:18:LYS:NZ	35:QD:31:CYS:SG	2.65	0.69
1:RA:20:C:OP1	16:RU:22:LYS:NZ	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Y4:59:PHE:CZ	50:XS:64:GLU:CB	2.75	0.69
32:QA:1304:G:OP1	52:QU:2:GLY:N	2.25	0.69
3:RD:108:PRO:HD2	3:RD:111:LEU:CG	2.21	0.69
34:XC:109:PRO:HB3	34:XC:115:LEU:HD23	1.74	0.69
10:YO:10:VAL:CG2	10:YO:16:ALA:O	2.40	0.69
47:QP:53:VAL:HG13	47:QP:79:VAL:HG12	1.74	0.69
32:XA:17:U:H2'	32:XA:18:C:C6	2.28	0.69
26:Y4:59:PHE:HZ	50:XS:64:GLU:OE1	1.75	0.69
12:YQ:80:GLU:OE1	54:XY:281:HIS:ND1	2.26	0.69
21:YZ:72:ARG:HG3	21:YZ:89:PHE:HB2	1.74	0.69
19:RX:5:TYR:O	24:R2:36:ARG:NH2	2.25	0.69
32:XA:946:A:H2'	32:XA:947:G:C8	2.28	0.69
32:QA:1025:U:C2	32:QA:1036:G:O6	2.46	0.69
1:YA:1721:G:H8	1:YA:1741:A:H62	1.39	0.69
15:YT:118:ARG:NH2	15:YT:121:ILE:CG2	2.54	0.69
32:QA:1030(A):C:N4	32:QA:1032:G:O6	2.27	0.68
35:QD:57:ARG:HH22	36:QE:107:ARG:CD	2.06	0.68
10:RO:24:VAL:CG2	10:RO:33:ALA:HB2	2.22	0.68
32:XA:1189:C:OP1	41:XJ:51:ARG:NH2	2.23	0.68
26:Y4:61:ARG:HG2	50:XS:42:PRO:CG	2.23	0.68
38:QG:89:MET:CE	38:QG:155:ARG:HB2	2.23	0.68
20:RY:92:ASN:HB2	20:RY:94:LYS:H	1.59	0.68
1:YA:641:C:O2'	1:YA:2350:C:OP1	2.12	0.68
7:YH:33:LEU:HD11	7:YH:75:ALA:CB	2.23	0.68
1:RA:140:G:H22	1:RA:1596:A:H4'	1.57	0.68
4:RE:51:PHE:N	4:RE:75:VAL:HG11	2.07	0.68
32:XA:1360:A:OP2	45:YN:35:ARG:NH2	2.26	0.68
54:XY:228:ASP:HB3	54:XY:230:ILE:HG13	1.75	0.68
17:YV:72:VAL:HG13	17:YV:85:LYS:HB3	1.75	0.68
1:YA:857:C:OP2	22:Y0:77:ARG:NH2	2.26	0.68
15:YT:108:ARG:NH1	32:XA:1464:G:OP1	2.27	0.68
18:YW:23:LEU:HD11	27:Y5:25:LEU:HB2	1.76	0.68
32:XA:642:A:N3	39:XH:113:SER:OG	2.26	0.68
32:XA:946:A:H2'	32:XA:947:G:H8	1.58	0.68
37:XF:100:ASN:ND2	49:XR:23:LYS:HE2	2.09	0.68
32:QA:1158:C:H5	32:QA:1181:G:H1	1.42	0.68
33:XB:114:ARG:HH12	33:XB:118:LEU:CG	2.04	0.68
47:XP:66:PRO:HG2	47:XP:71:ARG:NH1	2.09	0.68
35:QD:50:ARG:NH1	36:QE:9:LYS:NZ	2.41	0.68
54:QY:115:PHE:HB3	54:QY:119:PHE:HD2	1.57	0.68
21:RZ:45:ASP:OD1	21:RZ:49:ARG:NH1	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:XB:96:ARG:HD2	33:XB:98:LEU:HD23	1.74	0.68
21:YZ:198:LYS:NZ	53:XV:52:G:H2'	2.08	0.68
6:YG:146:TYR:HE2	44:XM:8:GLU:HB3	1.58	0.68
33:QB:21:ARG:HH22	33:QB:23:ARG:HH21	1.39	0.68
6:RG:3:LEU:HD22	26:R4:25:TYR:CE2	2.28	0.68
42:XK:99:GLN:HG2	42:XK:105:VAL:HG21	1.75	0.68
32:XA:581:G:OP1	46:XO:65:ARG:NH2	2.27	0.68
6:YG:21:ARG:HE	6:YG:22:ARG:HG2	1.59	0.68
32:XA:1182:G:H4'	32:XA:1183:A:H3'	1.75	0.68
36:XE:137:GLU:HG2	36:XE:140:ARG:HH11	1.59	0.68
30:Y8:6:THR:HG22	30:Y8:63:PRO:HD2	1.76	0.68
3:YD:134:ARG:NH1	3:YD:188:GLU:OE2	2.25	0.68
23:Y1:50:ARG:HG2	23:Y1:59:THR:HG22	1.76	0.67
33:QB:96:ARG:CD	33:QB:98:LEU:HD23	2.23	0.67
21:RZ:72:ARG:HG3	21:RZ:89:PHE:HB2	1.75	0.67
32:XA:559:A:OP1	36:XE:126:ARG:NH2	2.26	0.67
33:XB:122:PHE:HA	33:XB:127:ILE:HD12	1.76	0.67
54:QY:168:GLU:HG2	54:QY:179:VAL:HG12	1.76	0.67
7:RH:9:ILE:HD11	7:RH:69:ARG:HD2	1.74	0.67
54:XY:162:LYS:HB2	54:XY:184:SER:HB3	1.75	0.67
18:YW:14:PRO:HG2	18:YW:78:GLU:HG2	1.77	0.67
1:YA:2126:A:H4'	1:YA:2127:G:O5'	1.93	0.67
32:QA:559:A:OP1	36:QE:126:ARG:NH2	2.28	0.67
5:RF:165:ARG:HA	5:RF:168:ARG:CD	2.24	0.67
53:XV:53:G:H4'	53:XV:54:U:OP1	1.93	0.67
1:YA:2753:A:N3	31:Y9:15:LYS:NZ	2.42	0.67
1:RA:2115:G:N1	1:RA:2119:A:OP2	2.27	0.67
11:RP:112:LEU:HD12	11:RP:127:ALA:HB2	1.77	0.67
41:XJ:11:PHE:HE1	41:XJ:67:THR:HG22	1.57	0.67
54:XY:21:LEU:HD23	54:XY:70:LEU:HD21	1.76	0.67
6:YG:66:GLN:HG3	26:Y4:1:MET:HE3	1.75	0.67
32:QA:1492:A:H3'	32:QA:1493:A:H8	1.60	0.67
33:QB:8:LYS:NZ	33:QB:52:GLU:HA	2.09	0.67
4:YE:12:THR:HG23	15:YT:58:ASN:HD21	1.60	0.67
19:RX:5:TYR:HB3	24:R2:33:MET:HB2	1.77	0.67
33:XB:122:PHE:CD2	33:XB:127:ILE:HD12	2.28	0.67
19:YX:11:PRO:HB3	19:YX:92:LEU:HD11	1.76	0.67
33:QB:106:LYS:H	33:QB:106:LYS:HD3	1.59	0.67
6:RG:16:ARG:NH2	6:RG:31:VAL:HG22	2.10	0.67
1:YA:1971:A:OP2	3:YD:242:ARG:NH2	2.27	0.67
33:QB:21:ARG:O	33:QB:23:ARG:N	2.26	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:QS:45:VAL:HG21	26:R4:59:PHE:HZ	1.60	0.67
6:RG:25:TYR:CD2	6:RG:31:VAL:HG12	2.30	0.67
1:YA:2689:U:H4'	1:YA:2690:C:H5'	1.76	0.67
38:QG:69:VAL:HG21	38:QG:104:LEU:HD21	1.77	0.66
41:QJ:61:GLU:OE2	45:QN:49:HIS:NE2	2.27	0.66
46:QO:3:ILE:CD1	46:QO:34:LEU:HD23	2.24	0.66
1:RA:1405:U:H2'	1:RA:1406:U:H6	1.60	0.66
6:YG:3:LEU:HD12	26:Y4:25:TYR:CE1	2.30	0.66
1:RA:102:G:OP1	24:R2:7:ARG:NH2	2.28	0.66
1:RA:1405:U:H2'	1:RA:1406:U:C6	2.30	0.66
1:RA:84:A:H5''	20:RY:8:LYS:HE2	1.75	0.66
5:YF:185:ASP:HA	5:YF:188:ARG:HD3	1.77	0.66
5:YF:31:HIS:HB2	11:YP:9:ASN:OD1	1.95	0.66
7:YH:143:GLN:NE2	7:YH:147:ASN:OD1	2.28	0.66
4:RE:116:VAL:HG22	4:RE:122:PHE:CD2	2.29	0.66
32:XA:1031:G:H2'	32:XA:1032:G:C8	2.30	0.66
32:XA:452:A:N3	47:XP:72:ARG:NH1	2.43	0.66
11:YP:100:LEU:HD12	11:YP:112:LEU:HD11	1.76	0.66
12:YQ:21:THR:CG2	12:YQ:23:GLY:O	2.44	0.66
32:QA:56:U:H2'	32:QA:57:G:C8	2.30	0.66
23:R1:3:LYS:HG3	23:R1:4:VAL:H	1.61	0.66
4:RE:77:ILE:HD13	4:RE:195:LEU:HD13	1.77	0.66
5:YF:110:LEU:CD1	5:YF:202:PHE:HE1	2.08	0.66
1:RA:2218:U:O4'	23:R1:52:ARG:NH2	2.29	0.66
9:RN:94:HIS:HB2	9:RN:97:ARG:HD3	1.77	0.66
32:XA:1278:U:H5''	32:XA:1279:A:H5'	1.77	0.66
54:XY:161:PHE:HD1	54:XY:185:GLY:HA3	1.59	0.66
32:QA:1013:G:N2	32:QA:1016:A:OP2	2.27	0.66
41:QJ:33:GLN:O	41:QJ:75:ILE:N	2.28	0.66
5:RF:140:LEU:HD21	5:RF:170:LEU:HD11	1.78	0.66
18:RW:14:PRO:HG2	18:RW:78:GLU:HG2	1.78	0.66
32:XA:664:G:H22	32:XA:741:G:H1	1.43	0.66
1:YA:140:G:N2	1:YA:142(A):A:N6	2.43	0.66
34:QC:58:GLU:O	34:QC:64:VAL:HG23	1.96	0.66
6:RG:7:LEU:CD1	6:RG:100:TRP:CZ3	2.78	0.66
11:RP:112:LEU:HD11	11:RP:114:ILE:HD11	1.76	0.66
32:XA:1128:C:H1'	32:XA:1147:C:H42	1.59	0.66
33:XB:122:PHE:CD2	33:XB:127:ILE:CD1	2.78	0.66
33:QB:42:ILE:HD12	33:QB:203:GLY:HA2	1.78	0.66
34:QC:59:ARG:N	41:QJ:92:THR:HG21	2.11	0.66
35:XD:175:SER:HB3	35:XD:186:LEU:HD11	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:QB:15:VAL:HG23	33:QB:209:ARG:HB3	1.78	0.66
37:QF:10:LEU:HD21	37:QF:61:LEU:HD22	1.78	0.66
50:QS:3:ARG:HH21	50:QS:7:LYS:HE2	1.60	0.66
1:RA:2140:C:H2'	1:RA:2141:G:H8	1.61	0.66
1:RA:574:C:N3	4:RE:145:LYS:NZ	2.39	0.66
1:YA:1405:U:H2'	1:YA:1406:U:C6	2.31	0.66
5:YF:21:ALA:HB3	5:YF:22:ALA:HA	1.78	0.66
35:QD:50:ARG:HH12	36:QE:9:LYS:NZ	1.93	0.66
1:RA:2206:G:H5''	1:RA:2207:G:C8	2.31	0.66
36:XE:102:ALA:HB1	36:XE:106:PRO:HG2	1.78	0.66
1:YA:1385:G:O2'	1:YA:1396:U:O2	2.13	0.66
1:YA:1607:C:N4	1:YA:1622:G:OP2	2.27	0.66
1:YA:631:A:OP1	11:YP:65:ARG:NH1	2.28	0.66
9:RN:94:HIS:CB	9:RN:97:ARG:HD3	2.25	0.65
1:YA:1405:U:H2'	1:YA:1406:U:H6	1.61	0.65
1:YA:530:G:N1	1:YA:2023:G:OP1	2.25	0.65
32:QA:560:U:O2'	32:QA:561:U:OP2	2.13	0.65
33:XB:101:MET:HA	33:XB:108:ILE:HG13	1.78	0.65
12:YQ:21:THR:HG21	12:YQ:23:GLY:O	1.97	0.65
1:RA:2102:U:H2'	1:RA:2103:C:C6	2.31	0.65
41:XJ:38:ILE:HG12	41:XJ:71:LEU:HB3	1.78	0.65
32:XA:790:A:OP1	53:XV:38:A:O2'	2.13	0.65
24:Y2:32:LEU:HD12	24:Y2:57:ILE:CD1	2.27	0.65
32:QA:664:G:H22	32:QA:741:G:H1	1.42	0.65
33:QB:15:VAL:HG13	33:QB:213:LEU:HD12	1.77	0.65
6:RG:77:ILE:N	6:RG:82:LEU:O	2.25	0.65
19:RX:29:TRP:CZ2	19:RX:76:ARG:NH2	2.64	0.65
1:YA:529:A:OP2	9:YN:114:ARG:NH2	2.30	0.65
4:YE:170:LEU:HD23	4:YE:184:VAL:HG11	1.78	0.65
32:QA:1510:U:H2'	32:QA:1511:G:C8	2.32	0.65
32:QA:376:G:H5''	47:QP:5:ARG:HD3	1.78	0.65
53:QV:58:A:O2'	53:QV:60:U:OP2	2.13	0.65
44:XM:20:THR:HG21	44:XM:27:LYS:NZ	2.10	0.65
1:YA:139(A):G:O6	1:YA:140:G:O2'	2.13	0.65
6:YG:3:LEU:H	6:YG:3:LEU:HD23	1.62	0.65
36:QE:8:GLU:OE2	36:QE:63:ARG:NH2	2.29	0.65
37:QF:99:ALA:HB2	49:QR:31:LEU:CD2	2.25	0.65
8:RI:92:VAL:HG13	8:RI:120:ILE:HB	1.79	0.65
54:XY:22:ARG:HG2	54:XY:70:LEU:HD13	1.79	0.65
26:Y4:58:ARG:HH22	50:XS:69:HIS:CD2	2.15	0.65
1:YA:2102:U:H2'	1:YA:2103:C:C6	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:QM:64:TRP:CA	26:R4:50:VAL:CG2	2.74	0.65
28:R6:14:THR:CG2	28:R6:48:VAL:HG13	2.27	0.65
4:YE:51:PHE:N	4:YE:75:VAL:HG21	2.11	0.65
33:XB:122:PHE:CD1	33:XB:127:ILE:HD11	2.30	0.65
33:XB:77:ALA:HB2	33:XB:211:ILE:HD13	1.78	0.65
37:XF:10:LEU:HD21	37:XF:61:LEU:HD22	1.79	0.65
40:XI:9:ARG:HG2	40:XI:14:VAL:HG12	1.79	0.65
23:Y1:76:ARG:HH22	23:Y1:97:LEU:HB3	1.61	0.65
5:RF:185:ASP:HA	5:RF:188:ARG:HD3	1.79	0.65
19:RX:5:TYR:HD1	24:R2:33:MET:SD	2.19	0.65
32:QA:17:U:H2'	32:QA:18:C:C6	2.32	0.65
1:RA:301:G:OP2	20:RY:84:ARG:NH2	2.30	0.65
38:XG:15:ASP:OD1	38:XG:20:ASP:N	2.28	0.65
47:XP:20:VAL:HG21	47:XP:32:TYR:CG	2.31	0.65
54:XY:338:THR:HG23	54:XY:339:GLY:HA2	1.79	0.65
18:YW:29:LEU:HD11	18:YW:51:LEU:HD11	1.78	0.65
21:YZ:5:LEU:HD11	21:YZ:39:VAL:HB	1.79	0.65
35:QD:194:LEU:HD12	35:QD:195:ALA:H	1.62	0.64
38:QG:100:ALA:O	38:QG:104:LEU:HD23	1.96	0.64
19:RX:57:LEU:HD12	19:RX:78:LYS:HG2	1.79	0.64
40:XI:42:ARG:NH1	40:XI:71:SER:O	2.30	0.64
42:XK:62:GLN:HB2	42:XK:93:GLN:HG3	1.80	0.64
37:XF:97:PHE:HB2	49:XR:32:ARG:NH1	2.12	0.64
23:Y1:3:LYS:HB2	23:Y1:61:ARG:NH1	2.12	0.64
1:YA:2304:G:H22	1:YA:2312:U:H3	1.45	0.64
35:QD:57:ARG:NH2	36:QE:107:ARG:HD3	2.13	0.64
44:QM:13:LYS:HA	44:QM:44:ARG:HH11	1.60	0.64
54:QY:250:GLY:HA3	54:QY:254:VAL:HB	1.78	0.64
1:RA:997:G:H5''	16:RU:92:ARG:HH21	1.62	0.64
34:QC:59:ARG:H	41:QJ:92:THR:CG2	2.10	0.64
44:QM:64:TRP:C	26:R4:50:VAL:CG2	2.58	0.64
36:XE:69:VAL:HG11	36:XE:113:ALA:HB1	1.78	0.64
32:QA:201:C:H42	32:QA:216:G:H1	1.46	0.64
25:R3:8:LEU:CD1	25:R3:31:LEU:HA	2.22	0.64
50:QS:64:GLU:HG3	26:R4:59:PHE:HE1	1.62	0.64
30:R8:23:VAL:HG11	30:R8:47:LYS:HD3	1.79	0.64
1:YA:2646:C:OP2	1:YA:2732:G:O2'	2.12	0.64
11:YP:59:LEU:HD11	30:Y8:10:ALA:HB2	1.77	0.64
32:XA:1001(A):A:H2'	32:XA:1001(B):G:C8	2.32	0.64
4:YE:72:VAL:HG12	4:YE:73:GLU:O	1.97	0.64
6:YG:136:ARG:N	6:YG:136:ARG:HD3	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:YV:62:LEU:HD21	17:YV:95:LEU:HB2	1.78	0.64
37:XF:95:GLU:O	49:XR:32:ARG:NH2	2.30	0.64
32:XA:1353:G:OP1	52:XU:10:ARG:NH1	2.30	0.64
54:XY:25:LEU:O	54:XY:30:LYS:NZ	2.25	0.64
54:XY:219:SER:HB3	54:XY:317:ILE:HG12	1.79	0.64
5:YF:33:LEU:HD13	5:YF:112:MET:CE	2.27	0.64
1:RA:1075:C:OP1	12:RQ:59:ARG:NH2	2.31	0.64
1:RA:1568:G:H5''	3:RD:61:LEU:HD13	1.80	0.64
21:RZ:126:VAL:HG13	21:RZ:161:VAL:CG2	2.26	0.64
23:Y1:3:LYS:HB2	23:Y1:61:ARG:HH12	1.63	0.64
35:QD:85:LYS:HD3	35:QD:86:LYS:N	2.12	0.64
44:QM:4:ILE:HD12	44:QM:57:ARG:CA	2.28	0.64
6:RG:7:LEU:HD21	6:RG:176:LEU:HD22	1.80	0.64
6:YG:25:TYR:CD2	6:YG:31:VAL:HG12	2.31	0.64
34:QC:131:ARG:HH12	36:QE:50:GLU:CG	2.11	0.64
51:QT:86:ARG:O	51:QT:90:GLN:NE2	2.31	0.64
6:RG:108:ASN:O	26:R4:37:SER:N	2.30	0.64
4:YE:116:VAL:HG22	4:YE:122:PHE:CD2	2.33	0.64
5:YF:110:LEU:CD1	5:YF:202:PHE:CE1	2.81	0.64
5:YF:37:VAL:HG21	11:YP:6:LEU:CD1	2.28	0.64
36:QE:41:VAL:HG13	36:QE:113:ALA:HA	1.80	0.64
32:XA:370:C:H2'	32:XA:371:G:H8	1.63	0.64
23:Y1:4:VAL:HG11	23:Y1:11:ARG:NH1	2.13	0.64
4:YE:73:GLU:OE1	4:YE:74:PRO:HD2	1.98	0.64
9:YN:42:TRP:HA	9:YN:48:MET:CE	2.28	0.64
35:QD:13:ARG:NH1	35:QD:38:TYR:O	2.30	0.63
13:RR:41:ALA:HB1	13:RR:114:VAL:HG22	1.79	0.63
32:XA:56:U:H2'	32:XA:57:G:H8	1.63	0.63
34:XC:58:GLU:HB3	41:XJ:92:THR:HG21	1.78	0.63
1:YA:1712:C:O2	1:YA:1747(B):G:N2	2.31	0.63
39:QH:64:LYS:HG2	39:QH:79:VAL:HG21	1.80	0.63
36:XE:144:THR:H	36:XE:147:ASP:HB2	1.63	0.63
40:XI:108:VAL:HG12	40:XI:109:VAL:H	1.62	0.63
41:XJ:52:GLY:O	45:XN:41:ARG:NH2	2.30	0.63
54:XY:144:TRP:HE3	54:XY:147:MET:HE3	1.63	0.63
1:YA:833:U:O2	11:YP:55:ARG:NH2	2.27	0.63
34:QC:131:ARG:NH1	36:QE:50:GLU:CD	2.51	0.63
34:QC:131:ARG:HH12	36:QE:50:GLU:HG3	1.63	0.63
1:YA:1920:4OC:HM22	1:YA:1921:G:H5'	1.79	0.63
32:QA:45:U:H2'	32:QA:46:G:C8	2.34	0.63
32:QA:1191:A:OP2	34:QC:3:ASN:ND2	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:1244:C:H2'	32:XA:1245:A:C8	2.34	0.63
1:YA:140:G:H22	1:YA:1596:A:H4'	1.63	0.63
1:YA:947:G:H2'	1:YA:948:G:H8	1.62	0.63
4:YE:52:LEU:HB3	4:YE:53:PRO:HD2	1.80	0.63
8:YI:72:LEU:C	8:YI:75:LEU:CD2	2.65	0.63
32:QA:790:A:OP1	53:QV:38:A:O2'	2.16	0.63
36:QE:143:ARG:NH1	39:QH:77:GLU:OE2	2.31	0.63
32:XA:406:G:H5'	35:XD:5:ILE:HD11	1.81	0.63
35:XD:8:VAL:HG22	35:XD:21:LEU:HD13	1.78	0.63
17:YV:6:LYS:HB2	17:YV:38:LEU:HD21	1.79	0.63
33:QB:195:ASP:O	39:QH:68:ARG:NH2	2.31	0.63
32:XA:501:C:H2'	32:XA:502:G:C8	2.33	0.63
48:XQ:66:SER:O	48:XQ:70:ARG:NH1	2.31	0.63
35:QD:173:TRP:CD2	35:QD:189:PRO:HG3	2.34	0.63
37:QF:38:GLU:OE1	37:QF:64:GLN:NE2	2.30	0.63
34:QC:22:TRP:CZ2	45:QN:54:PRO:HG2	2.33	0.63
53:QV:16:C:O2'	53:QV:61:C:OP1	2.16	0.63
1:RA:2452:C:H4'	54:QY:256:ARG:HG3	1.80	0.63
1:RA:1094:U:OP1	1:RA:1096:A:N6	2.32	0.63
9:RN:103:VAL:HG11	9:RN:120:LEU:HD12	1.81	0.63
11:RP:112:LEU:CD1	11:RP:127:ALA:HB2	2.28	0.63
19:RX:53:LYS:HB3	19:RX:82:GLN:HB3	1.80	0.63
1:YA:1316:U:H2'	1:YA:1317:A:H8	1.63	0.63
3:RD:108:PRO:HD2	3:RD:111:LEU:HG	1.80	0.63
4:RE:175:VAL:HG12	4:RE:182:LEU:CD1	2.26	0.63
11:RP:52:GLU:OE1	11:RP:55:ARG:NH1	2.32	0.63
43:XL:70:ILE:HG12	43:XL:100:ILE:HD12	1.81	0.63
22:Y0:27:GLU:HG3	22:Y0:68:GLU:HA	1.81	0.63
1:YA:994:C:OP1	16:YU:53:ARG:NH2	2.31	0.63
6:YG:55:LYS:HD3	6:YG:150:ASP:OD2	1.99	0.63
8:YI:40:THR:C	8:YI:44:LEU:CD2	2.67	0.63
1:YA:1064:C:H3'	1:YA:1065:U:H5'	1.81	0.63
1:YA:2379:G:O2'	14:YS:17:ARG:NH2	2.20	0.63
1:YA:2012:G:OP1	18:YW:11:ARG:NH2	2.31	0.63
21:YZ:19:ARG:NH1	21:YZ:84:GLU:O	2.32	0.63
32:QA:1286:A:H2'	32:QA:1287:A:H4'	1.79	0.62
37:QF:69:GLU:O	37:QF:72:VAL:HG12	1.99	0.62
1:RA:139(A):G:O6	1:RA:140:G:O2'	2.17	0.62
32:XA:316:G:OP2	32:XA:351:G:O2'	2.15	0.62
40:XI:108:VAL:HG12	40:XI:109:VAL:N	2.14	0.62
7:YH:41:MET:CE	7:YH:64:LEU:HB3	2.28	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:QG:27:ILE:HD12	38:QG:40:ALA:HA	1.81	0.62
42:QK:92:GLU:O	42:QK:96:ARG:HG2	1.99	0.62
1:RA:1266:G:O5'	18:RW:15:ARG:NH2	2.33	0.62
1:RA:947:G:H2'	1:RA:948:G:H8	1.64	0.62
4:RE:175:VAL:CG1	4:RE:182:LEU:HD12	2.27	0.62
21:RZ:139:VAL:CG1	21:RZ:150:LEU:HD23	2.29	0.62
34:XC:6:HIS:CD2	34:XC:9:GLY:H	2.17	0.62
44:XM:59:TYR:CE1	44:XM:63:THR:HG21	2.35	0.62
1:YA:38:A:H2'	1:YA:39:C:C6	2.34	0.62
13:YR:100:LEU:CD2	13:YR:112:ALA:HA	2.29	0.62
5:YF:110:LEU:HD12	5:YF:206:ILE:CG2	2.29	0.62
39:QH:51:VAL:HG12	39:QH:52:ASP:N	2.11	0.62
54:QY:161:PHE:HD1	54:QY:185:GLY:HA3	1.63	0.62
44:QM:65:LYS:HD3	26:R4:51:ASP:CB	2.29	0.62
1:RA:1721:G:H8	1:RA:1741:A:H62	1.48	0.62
34:XC:152:ILE:HG13	34:XC:199:LYS:HB2	1.82	0.62
26:Y4:58:ARG:HH11	50:XS:65:ASN:C	2.02	0.62
33:QB:69:LEU:HD13	33:QB:91:PRO:HB2	1.80	0.62
37:QF:97:PHE:HB2	49:QR:32:ARG:HH11	1.65	0.62
1:RA:1101:U:H2'	1:RA:1102:C:H6	1.64	0.62
1:RA:793:A:OP2	1:RA:2071:A:O2'	2.16	0.62
1:RA:2850:A:N7	1:RA:2868:A:O2'	2.29	0.62
1:YA:2334:G:H5'	14:YS:9:ARG:HG2	1.82	0.62
32:QA:1033:G:H2'	32:QA:1034:G:H8	1.64	0.62
33:QB:15:VAL:HG23	33:QB:209:ARG:CB	2.29	0.62
46:QO:71:GLN:HB2	46:QO:78:TYR:CG	2.35	0.62
32:XA:1119:C:H2'	32:XA:1120:G:H8	1.64	0.62
40:XI:46:ALA:HB2	40:XI:74:ILE:HG23	1.82	0.62
34:XC:12:LEU:HD11	45:YN:51:GLY:HA2	1.80	0.62
1:YA:2140:C:H2'	1:YA:2141:G:H8	1.63	0.62
1:YA:2218:U:O2	23:Y1:52:ARG:NH2	2.32	0.62
1:YA:2328:A:H2'	1:YA:2329:G:C8	2.34	0.62
36:QE:74:GLY:HA3	36:QE:116:THR:HG22	1.82	0.62
37:QF:97:PHE:HB2	49:QR:32:ARG:HD2	1.82	0.62
54:QY:150:ARG:HB3	54:QY:154:ARG:NH1	2.14	0.62
11:RP:59:LEU:HD21	30:R8:10:ALA:HA	1.82	0.62
1:RA:1165:U:H2'	1:RA:1166:C:C6	2.35	0.62
18:YW:29:LEU:CD1	18:YW:51:LEU:HD11	2.29	0.62
33:QB:76:GLN:NE2	33:QB:206:ASP:OD1	2.33	0.62
32:XA:1510:U:H2'	32:XA:1511:G:C8	2.35	0.62
32:XA:689:C:OP1	42:XK:27:ASN:ND2	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1165:U:H2'	1:YA:1166:C:C6	2.34	0.62
1:YA:848:G:H2'	1:YA:849:A:C8	2.35	0.62
1:YA:1340:U:OP1	19:YX:16:LYS:NZ	2.31	0.62
35:QD:8:VAL:HG22	35:QD:21:LEU:HD13	1.82	0.62
1:RA:140:G:N2	1:RA:142(A):A:H62	1.95	0.62
1:RA:140:G:C2	1:RA:142(A):A:N6	2.67	0.62
1:RA:309:G:N3	1:RA:329:G:O2'	2.33	0.62
1:RA:37:C:H2'	1:RA:38:A:C8	2.35	0.62
11:RP:112:LEU:CD1	11:RP:127:ALA:HB1	2.29	0.62
17:RV:40:LEU:HD12	17:RV:46:VAL:CG1	2.30	0.62
1:YA:1816:G:O6	3:YD:35:LYS:NZ	2.24	0.62
1:YA:2206:G:H5''	1:YA:2207:G:C8	2.34	0.62
32:QA:266:G:H5'	32:QA:268:C:H41	1.65	0.62
1:RA:1064:C:H3'	1:RA:1065:U:H5'	1.82	0.62
3:RD:72:LYS:HG3	3:RD:103:ARG:HH22	1.63	0.62
6:RG:7:LEU:HD11	6:RG:100:TRP:CE3	2.31	0.62
32:XA:1002:G:N3	32:XA:1003:G:H8	1.97	0.62
32:QA:922:G:H2'	32:QA:923:A:C8	2.35	0.61
38:QG:69:VAL:HG21	38:QG:104:LEU:CD2	2.30	0.61
1:RA:2478:A:OP2	31:R9:2:LYS:NZ	2.29	0.61
1:RA:517:C:OP1	27:R5:16:ARG:NH2	2.33	0.61
11:RP:112:LEU:HD13	11:RP:127:ALA:HB1	1.82	0.61
32:XA:390:C:H4'	47:XP:28:ARG:HH21	1.65	0.61
32:QA:501:C:H2'	32:QA:502:G:H8	1.64	0.61
32:QA:410:G:OP1	35:QD:30:LYS:NZ	2.23	0.61
51:QT:57:ARG:HH12	51:QT:100:ILE:CD1	2.12	0.61
1:RA:2573:C:N4	54:QY:245:ARG:HE	1.98	0.61
9:RN:14:VAL:HG11	9:RN:138:LEU:HD12	1.81	0.61
40:XI:50:LEU:HD23	40:XI:85:LEU:HD11	1.83	0.61
26:Y4:20:ASN:HD21	26:Y4:38:LYS:HG3	1.64	0.61
32:QA:1492:A:H3'	32:QA:1493:A:C8	2.34	0.61
42:QK:48:ILE:CD1	42:QK:63:LEU:CB	2.42	0.61
13:RR:83:ILE:O	13:RR:86:ARG:HG2	1.99	0.61
32:XA:41:G:H2'	32:XA:42:G:H8	1.64	0.61
54:XY:14:LEU:HD21	54:XY:107:GLU:HG3	1.82	0.61
44:QM:34:LEU:HD13	44:QM:41:PRO:HA	1.82	0.61
12:RQ:7:MET:HE1	21:RZ:194:PRO:HB2	1.80	0.61
19:RX:41:ASN:O	19:RX:45:THR:HG23	2.00	0.61
32:XA:68:G:H8	32:XA:68:G:C5'	2.14	0.61
54:XY:106:LEU:HD23	54:XY:109:LYS:HD2	1.81	0.61
1:YA:2343:C:HO2'	1:YA:2373:G:HO2'	1.41	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:2724:C:OP1	4:YE:111:ARG:NH1	2.34	0.61
7:YH:88:LEU:CD2	7:YH:165:ALA:HA	2.31	0.61
1:RA:2684:U:O2'	10:RO:68:GLU:OE1	2.17	0.61
3:RD:108:PRO:CD	3:RD:111:LEU:HD12	2.29	0.61
8:RI:92:VAL:CG1	8:RI:120:ILE:HB	2.31	0.61
15:RT:64:ARG:HB2	15:RT:73:GLU:HG2	1.81	0.61
32:XA:370:C:H2'	32:XA:371:G:C8	2.36	0.61
54:QY:243:VAL:HG12	54:QY:261:VAL:HG12	1.83	0.61
38:XG:113:GLU:HG2	38:XG:119:ARG:HG2	1.81	0.61
32:QA:341:C:H2'	32:QA:342:C:C6	2.36	0.61
39:QH:112:LEU:CD2	39:QH:133:LEU:HA	2.30	0.61
44:QM:2:ALA:C	26:R4:34:GLU:OE1	2.38	0.61
24:R2:23:LYS:O	24:R2:27:GLU:HG3	2.00	0.61
1:RA:856:C:H2'	1:RA:857:C:C6	2.35	0.61
11:RP:83:VAL:HG12	11:RP:112:LEU:HD21	1.83	0.61
27:Y5:40:LYS:HD3	27:Y5:41:PRO:O	2.01	0.61
1:YA:2074:U:H2'	1:YA:2075:U:C6	2.35	0.61
2:YB:66:A:H61	2:YB:109:C:H5'	1.66	0.61
3:YD:108:PRO:HB3	3:YD:143:HIS:CE1	2.35	0.61
5:YF:101:LEU:HD12	5:YF:102:PRO:HD2	1.82	0.61
34:QC:82:GLU:OE1	34:QC:85:ARG:NH2	2.33	0.61
33:XB:114:ARG:HH11	33:XB:118:LEU:CG	1.93	0.61
54:XY:203:ARG:NH1	54:XY:206:PRO:HD3	2.15	0.61
1:YA:1076:C:H4'	1:YA:1077:A:OP1	2.00	0.61
21:YZ:91:LEU:HD11	21:YZ:96:VAL:HG11	1.83	0.61
32:QA:1005:A:OP1	32:QA:1006:C:N4	2.34	0.61
54:QY:156:ALA:HB1	54:QY:161:PHE:HB2	1.83	0.61
32:XA:1244:C:H2'	32:XA:1245:A:H8	1.63	0.61
32:XA:1513:A:H2'	32:XA:1514:C:C6	2.36	0.61
32:XA:1073:U:O2'	33:XB:104:ASN:OD1	2.16	0.61
43:XL:60:LEU:HD21	43:XL:66:VAL:HG22	1.81	0.61
1:YA:589:C:H2'	1:YA:590:A:H8	1.65	0.61
32:QA:1238:A:H2	32:QA:1241:G:N3	1.99	0.60
32:QA:45:U:H2'	32:QA:46:G:H8	1.65	0.60
53:QV:4:G:HO2'	53:QV:5:G:H8	1.48	0.60
19:RX:5:TYR:CD1	24:R2:33:MET:CE	2.84	0.60
32:XA:501:C:OP1	43:XL:117:ARG:NH2	2.26	0.60
27:Y5:40:LYS:CD	27:Y5:41:PRO:O	2.49	0.60
7:YH:12:PRO:O	7:YH:15:VAL:HG22	2.01	0.60
32:QA:1216:G:H5''	45:QN:5:ALA:HB2	1.84	0.60
46:QO:26:GLU:OE1	46:QO:77:ARG:NE	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:QT:47:GLY:HA2	51:QT:48:LYS:HB2	1.81	0.60
1:RA:987:G:O2'	1:RA:1000:A:N3	2.32	0.60
40:XI:50:LEU:HB2	40:XI:56:LEU:HD23	1.82	0.60
54:XY:342:THR:HG22	54:XY:344:ASN:H	1.65	0.60
24:Y2:16:LEU:O	24:Y2:67:LYS:NZ	2.34	0.60
1:YA:956:G:OP2	12:YQ:14:ARG:NH2	2.34	0.60
13:YR:100:LEU:CD2	13:YR:112:ALA:CA	2.79	0.60
44:QM:15:VAL:HG11	44:QM:48:LEU:HD21	1.82	0.60
22:R0:11:ARG:O	22:R0:14:ARG:NH2	2.25	0.60
1:RA:1024:G:HO2'	1:RA:1144:G:HO2'	1.45	0.60
6:RG:139:LEU:HD21	6:RG:149:VAL:HG11	1.81	0.60
35:XD:13:ARG:NH1	35:XD:38:TYR:O	2.34	0.60
49:XR:58:LEU:HD12	49:XR:62:GLU:CG	2.31	0.60
1:YA:458:G:O2'	1:YA:469:G:O6	2.15	0.60
4:YE:170:LEU:HD23	4:YE:184:VAL:CG1	2.30	0.60
18:YW:23:LEU:CD1	27:Y5:25:LEU:HB2	2.31	0.60
54:XY:129:TYR:HE1	54:XY:182:LYS:HG3	1.66	0.60
1:YA:947:G:H2'	1:YA:948:G:C8	2.36	0.60
32:QA:824:C:H2'	32:QA:825:G:H8	1.65	0.60
41:QJ:38:ILE:HG12	41:QJ:71:LEU:HB3	1.82	0.60
1:RA:1101:U:H2'	1:RA:1102:C:C6	2.36	0.60
6:RG:170:ARG:O	6:RG:170:ARG:HD3	2.01	0.60
10:YO:115:VAL:HG13	10:YO:121:VAL:HG21	1.82	0.60
36:XE:57:LYS:HG2	36:XE:61:TYR:HE2	1.66	0.60
26:R4:24:THR:OG1	26:R4:25:TYR:N	2.35	0.60
21:RZ:203:GLU:C	53:QV:53:G:H4'	2.20	0.60
33:XB:84:GLU:HB3	33:XB:219:VAL:HG21	1.84	0.60
34:XC:40:ARG:NH2	34:XC:55:VAL:O	2.34	0.60
34:XC:57:ILE:HG12	34:XC:66:VAL:HG22	1.84	0.60
49:XR:47:THR:HG23	49:XR:49:LYS:HG3	1.82	0.60
1:YA:2659:G:O2'	7:YH:175:LYS:HE2	2.02	0.60
21:YZ:72:ARG:HG2	21:YZ:89:PHE:HB2	1.83	0.60
54:QY:84:LEU:HD22	54:QY:96:PHE:HD1	1.67	0.60
1:RA:1076:C:H4'	1:RA:1077:A:OP1	2.00	0.60
46:XO:35:ARG:HH21	46:XO:59:MET:HE2	1.66	0.60
26:Y4:24:THR:OG1	26:Y4:25:TYR:N	2.34	0.60
1:YA:140:G:C2	1:YA:142(A):A:N6	2.70	0.60
1:YA:2478:A:OP2	31:Y9:2:LYS:NZ	2.29	0.60
1:YA:307:G:N1	1:YA:310:A:OP2	2.31	0.60
32:QA:407:G:H2'	32:QA:408:A:C8	2.37	0.60
43:QL:83:VAL:HG13	43:QL:100:ILE:HG23	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:1385:G:O2'	1:RA:1396:U:O2	2.19	0.60
1:RA:530:G:N1	1:RA:2023:G:OP1	2.32	0.60
1:RA:674:G:H1'	5:RF:74:ARG:HD3	1.81	0.60
32:XA:404:U:H2'	32:XA:405:U:H6	1.67	0.60
41:XJ:9:ARG:NH2	41:XJ:95:GLU:OE1	2.35	0.60
22:Y0:11:ARG:O	22:Y0:14:ARG:NH2	2.30	0.60
6:YG:18:GLU:OE1	6:YG:21:ARG:NH2	2.35	0.60
36:QE:57:LYS:HG2	36:QE:61:TYR:CE2	2.37	0.60
1:RA:1507:A:O2'	1:RA:1508:A:O5'	2.17	0.60
33:XB:16:HIS:CG	33:XB:210:SER:HB3	2.37	0.60
54:XY:265:HIS:HB2	54:XY:291:MET:HE1	1.84	0.60
1:YA:140:G:N2	1:YA:1596:A:H4'	2.17	0.60
5:YF:103:LYS:HA	5:YF:106:ARG:HD3	1.83	0.60
6:YG:5:VAL:HG12	26:Y4:25:TYR:CE1	2.37	0.60
33:QB:115:LEU:O	33:QB:119:GLU:HG2	2.02	0.59
49:QR:32:ARG:HA	49:QR:69:THR:HG21	1.83	0.59
54:QY:149:GLU:OE2	54:QY:179:VAL:HG11	2.02	0.59
54:QY:241:ILE:HG12	54:QY:263:ILE:HG12	1.83	0.59
54:QY:326:TYR:CD1	54:QY:333:ILE:HG23	2.37	0.59
33:XB:229:VAL:HG12	33:XB:230:VAL:N	2.16	0.59
32:XA:1292:U:OP2	38:XG:41:ARG:NH2	2.35	0.59
1:YA:987:G:O2'	1:YA:1000:A:N3	2.30	0.59
1:YA:1019:U:H2'	1:YA:1020:A:H8	1.67	0.59
1:YA:1059:G:O6	1:YA:1079:C:N4	2.35	0.59
15:YT:95:ARG:HG2	15:YT:95:ARG:HH11	1.66	0.59
1:RA:856:C:H2'	1:RA:857:C:H6	1.67	0.59
12:RQ:21:THR:HG21	12:RQ:101:ARG:HB2	1.84	0.59
32:XA:1410:G:H2'	32:XA:1411:C:C6	2.36	0.59
33:XB:78:GLN:O	33:XB:94:ASN:ND2	2.34	0.59
33:XB:88:ALA:HB2	33:XB:219:VAL:HG13	1.83	0.59
1:YA:1066:U:O2'	1:YA:1068:G:OP2	2.16	0.59
1:YA:11:G:H2'	1:YA:12:U:H5'	1.84	0.59
5:YF:132:VAL:HG21	5:YF:163:VAL:HG22	1.84	0.59
1:YA:2752:C:OP2	7:YH:4:ILE:HD11	2.02	0.59
33:QB:19:HIS:NE2	33:QB:189:ASP:OD2	2.33	0.59
35:QD:196:LEU:HD12	35:QD:196:LEU:H	1.67	0.59
34:QC:131:ARG:HH12	36:QE:50:GLU:CD	2.05	0.59
40:QI:25:LYS:CE	40:QI:25:LYS:HA	2.28	0.59
27:R5:40:LYS:CD	27:R5:41:PRO:O	2.50	0.59
1:RA:192:C:O2'	1:RA:802:A:N3	2.30	0.59
8:YI:72:LEU:CA	8:YI:75:LEU:CD2	2.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:1027:C:H2'	32:QA:1028:C:C5	2.36	0.59
54:QY:335:ASP:O	54:QY:337:ARG:N	2.31	0.59
1:RA:2064:C:H2'	1:RA:2065:C:C6	2.36	0.59
1:RA:642:G:N2	1:RA:644:A:H3'	2.17	0.59
1:RA:848:G:H2'	1:RA:849:A:C8	2.37	0.59
32:XA:1005:A:H5''	32:XA:1006:C:C5	2.37	0.59
40:XI:4:TYR:HB2	40:XI:19:LEU:HB2	1.84	0.59
54:XY:204:LYS:NZ	54:XY:211:GLY:O	2.34	0.59
27:Y5:16:ARG:HH11	27:Y5:16:ARG:HG2	1.67	0.59
1:YA:1379:A:H4'	1:YA:1380:G:OP2	2.02	0.59
15:YT:39:ARG:NH2	32:XA:345:C:OP2	2.34	0.59
1:RA:589:C:H2'	1:RA:590:A:H8	1.68	0.59
33:XB:114:ARG:NH1	33:XB:118:LEU:CD1	2.65	0.59
32:QA:946:A:O2'	32:QA:1333:A:N3	2.33	0.59
44:QM:11:ARG:HA	44:QM:45:VAL:HB	1.84	0.59
1:RA:947:G:H2'	1:RA:948:G:C8	2.37	0.59
5:RF:12:LEU:HD13	5:RF:124:LEU:HD11	1.84	0.59
6:RG:131:TYR:HB3	6:RG:159:VAL:CG1	2.32	0.59
7:RH:25:LYS:HG3	7:RH:34:GLU:HG2	1.83	0.59
21:RZ:144:LEU:HD21	21:RZ:150:LEU:CD1	2.31	0.59
1:YA:2156:G:N7	1:YA:2157:G:N2	2.51	0.59
1:YA:855:G:O2'	22:Y0:27:GLU:OE2	2.20	0.59
35:QD:162:LEU:HD13	35:QD:181:MET:HG2	1.85	0.59
35:QD:8:VAL:HG22	35:QD:21:LEU:CD1	2.33	0.59
48:QQ:78:GLU:HG2	48:QQ:79:SER:H	1.68	0.59
42:QK:109:VAL:HG23	49:QR:85:LEU:O	2.03	0.59
50:QS:52:TYR:HB2	50:QS:57:HIS:CE1	2.36	0.59
1:RA:1936:A:OP2	1:RA:1962:5MC:N4	2.34	0.59
1:RA:538:G:H2'	1:RA:539:G:H8	1.67	0.59
8:RI:140:LEU:HD13	8:RI:140:LEU:C	2.23	0.59
32:XA:1414:U:H2'	32:XA:1415:G:H8	1.67	0.59
32:XA:992:U:H4'	32:XA:993:G:O5'	2.03	0.59
32:XA:539:A:OP2	43:XL:115:LYS:NZ	2.35	0.59
2:YB:84:C:OP1	25:Y3:15:TYR:OH	2.18	0.59
1:YA:2823:A:OP1	4:YE:159:HIS:NE2	2.35	0.59
32:QA:1360:A:OP2	45:QN:35:ARG:NH2	2.36	0.59
35:QD:170:VAL:HG12	35:QD:174:LEU:HB2	1.85	0.59
8:RI:130:TYR:HB3	8:RI:138:ILE:HB	1.84	0.59
15:RT:24:PRO:HA	15:RT:49:VAL:HG23	1.85	0.59
32:XA:976:G:H5'	32:XA:1358:U:O2'	2.02	0.59
32:XA:922:G:H2'	32:XA:923:A:C8	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:XF:25:ILE:HD13	37:XF:82:ARG:HE	1.68	0.59
54:XY:270:ILE:HD11	54:XY:298:VAL:HG21	1.85	0.59
50:QS:41:VAL:HG22	50:QS:42:PRO:HD2	1.84	0.59
26:R4:41:PRO:HG3	26:R4:49:PHE:CD1	2.37	0.59
1:RA:1036:G:OP2	7:RH:59:ARG:NH1	2.36	0.59
11:RP:101:VAL:CG2	11:RP:106:LEU:HD12	2.32	0.59
1:YA:2128:C:H5'	1:YA:2129:C:OP2	2.02	0.59
1:YA:309:G:N3	1:YA:329:G:O2'	2.35	0.59
1:YA:637:A:H8	11:YP:117:GLU:HG3	1.66	0.59
32:QA:1003:G:H2'	32:QA:1004:A:H4'	1.83	0.59
32:QA:339:C:H2'	32:QA:340:U:C6	2.38	0.59
1:RA:1073:A:H2'	1:RA:1074:G:C8	2.36	0.59
1:RA:1530:C:O2'	1:RA:1531:C:H6	1.86	0.59
9:RN:34:LEU:HD23	9:RN:107:LEU:HD11	1.85	0.59
10:RO:80:ASP:OD1	15:RT:64:ARG:NH2	2.34	0.59
18:RW:23:LEU:CD1	27:R5:25:LEU:HB2	2.33	0.59
32:XA:28:G:O2'	32:XA:296:U:OP1	2.20	0.59
41:XJ:57:LYS:HE2	41:XJ:60:ARG:NH2	2.18	0.59
1:YA:1796:U:H2'	1:YA:1797:C:C6	2.38	0.59
1:YA:538:G:H2'	1:YA:539:G:H8	1.68	0.59
1:YA:581:C:H2'	1:YA:582:G:H8	1.68	0.59
4:YE:51:PHE:C	4:YE:75:VAL:HG22	2.23	0.59
33:QB:40:HIS:HB3	33:QB:190:THR:HG21	1.83	0.58
36:QE:57:LYS:HG2	36:QE:61:TYR:HE2	1.68	0.58
32:XA:68:G:O5'	32:XA:68:G:H8	1.85	0.58
3:YD:79:VAL:HG21	3:YD:111:LEU:HD11	1.85	0.58
27:R5:16:ARG:HH11	27:R5:16:ARG:HG2	1.68	0.58
1:RA:641:C:O2'	1:RA:2350:C:OP1	2.15	0.58
5:RF:101:LEU:O	5:RF:106:ARG:NH1	2.36	0.58
26:Y4:57:GLU:CB	26:Y4:58:ARG:HD2	2.33	0.58
1:YA:1514:U:H2'	1:YA:1515:G:H8	1.68	0.58
1:YA:854:G:H2'	1:YA:855:G:H8	1.67	0.58
7:YH:11:VAL:HG21	7:YH:50:VAL:HG23	1.85	0.58
13:YR:18:LEU:HD11	13:YR:22:ARG:NE	2.18	0.58
9:RN:120:LEU:CD2	9:RN:122:VAL:CG2	2.79	0.58
32:XA:1435:G:H2'	32:XA:1436:U:C6	2.38	0.58
32:XA:411:A:OP2	35:XD:25:ARG:NH2	2.36	0.58
32:XA:986:A:H2'	32:XA:987:G:C8	2.38	0.58
48:XQ:74:LEU:CD1	48:XQ:75:ARG:HG2	2.33	0.58
49:XR:52:PRO:HB2	49:XR:54:ARG:HG2	1.85	0.58
11:YP:59:LEU:HD21	30:Y8:10:ALA:HA	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:856:C:H2'	1:YA:857:C:C6	2.37	0.58
6:YG:66:GLN:OE1	6:YG:98:ARG:NE	2.34	0.58
32:QA:1143:G:H2'	32:QA:1144:G:H8	1.68	0.58
32:QA:22:G:H4'	32:QA:885:G:C8	2.38	0.58
1:RA:1711:C:H2'	1:RA:1712:C:C6	2.39	0.58
1:RA:2328:A:H2'	1:RA:2329:G:C8	2.38	0.58
1:RA:2853:C:H2'	1:RA:2854:G:H8	1.68	0.58
1:RA:272(K):U:H1'	8:RI:50:ARG:NH2	2.17	0.58
32:XA:1422:G:H2'	32:XA:1423:G:H8	1.67	0.58
32:QA:976:G:H5'	32:QA:1358:U:O2'	2.03	0.58
36:QE:33:VAL:HG21	36:QE:109:ILE:HA	1.84	0.58
38:QG:111:ARG:NH1	38:QG:113:GLU:OE1	2.35	0.58
40:QI:49:PRO:HD2	40:QI:81:ILE:HD11	1.84	0.58
1:RA:2246:G:H2'	1:RA:2247:A:H8	1.69	0.58
1:RA:2291:U:H2'	1:RA:2292:C:C6	2.37	0.58
33:XB:16:HIS:HB2	33:XB:204:ASN:HB3	1.84	0.58
1:YA:1062:G:N7	1:YA:1070:A:H1'	2.18	0.58
1:YA:184:C:H2'	1:YA:185:U:C6	2.39	0.58
1:YA:2074:U:HO2'	1:YA:2597:G:HO2'	1.52	0.58
11:YP:126:VAL:HG12	11:YP:148:LEU:HD22	1.84	0.58
19:YX:53:LYS:HB3	19:YX:82:GLN:HB3	1.85	0.58
35:QD:108:LEU:CD2	35:QD:174:LEU:HD13	2.28	0.58
49:QR:47:THR:HG23	49:QR:49:LYS:HG3	1.85	0.58
54:QY:324:ARG:HG3	54:QY:335:ASP:HA	1.86	0.58
54:QY:338:THR:HG23	54:QY:339:GLY:HA2	1.85	0.58
1:RA:1779:U:OP2	1:RA:1784:A:N6	2.29	0.58
1:RA:463:G:N2	1:RA:466:A:OP2	2.27	0.58
4:RE:119:ARG:HD3	4:RE:160:TYR:HB2	1.85	0.58
6:RG:50:ALA:C	6:RG:52:ILE:H	2.07	0.58
9:RN:4:TYR:CD2	16:RU:100:VAL:HG11	2.39	0.58
32:XA:21:G:H2'	32:XA:22:G:C8	2.39	0.58
32:XA:474:G:H2'	32:XA:475:G:H8	1.68	0.58
32:XA:68:G:C8	32:XA:68:G:C5'	2.86	0.58
34:XC:9:GLY:HA3	45:XN:49:HIS:HA	1.86	0.58
54:XY:136:SER:O	54:XY:138:GLY:N	2.32	0.58
54:XY:34:LEU:HD13	54:XY:63:LEU:HB2	1.85	0.58
1:YA:2321:G:O2'	1:YA:2322:A:OP1	2.21	0.58
1:YA:589:C:H2'	1:YA:590:A:C8	2.38	0.58
36:QE:8:GLU:HG2	36:QE:34:VAL:HG22	1.84	0.58
32:XA:1129:C:H2'	32:XA:1139:G:N7	2.19	0.58
32:XA:126:G:OP1	32:XA:605:U:O2'	2.14	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:473:G:OP2	47:XP:75:ARG:HD3	2.03	0.58
50:XS:27:GLU:OE1	50:XS:47:HIS:NE2	2.36	0.58
26:Y4:58:ARG:NH2	44:XM:80:ARG:NH2	2.51	0.58
1:YA:1316:U:H2'	1:YA:1317:A:C8	2.38	0.58
47:QP:20:VAL:HG21	47:QP:32:TYR:CG	2.38	0.58
1:RA:1062:G:N7	1:RA:1070:A:H1'	2.19	0.58
1:RA:1296:G:OP1	1:RA:2709:G:O2'	2.11	0.58
1:RA:2074:U:H2'	1:RA:2075:U:C6	2.38	0.58
1:RA:2446:G:N2	1:RA:2449:U:O2	2.35	0.58
1:RA:299:A:N1	1:RA:322:A:O2'	2.30	0.58
1:RA:2839:G:H5'	13:RR:46:GLY:HA2	1.85	0.58
14:RS:15:ARG:O	14:RS:19:LYS:HG2	2.03	0.58
30:Y8:23:VAL:HG11	30:Y8:47:LYS:HD3	1.86	0.58
1:YA:1065:U:H4'	1:YA:1066:U:H5'	1.85	0.58
3:YD:10:THR:OG1	3:YD:13:ARG:HG2	2.04	0.58
21:YZ:144:LEU:HD21	21:YZ:150:LEU:HD13	1.85	0.58
21:RZ:198:LYS:NZ	53:QV:52:G:H2'	2.18	0.58
17:RV:61:VAL:HG23	17:RV:92:THR:CG2	2.34	0.58
32:XA:266:G:O2'	32:XA:267:C:OP2	2.18	0.58
32:XA:674:G:H2'	32:XA:675:A:H8	1.68	0.58
33:XB:54:THR:HG21	33:XB:201:ILE:HD11	1.86	0.58
35:XD:122:ARG:NH1	35:XD:134:ASP:O	2.37	0.58
1:YA:140:G:N2	1:YA:142(A):A:H62	2.02	0.58
1:YA:2724:C:P	4:YE:111:ARG:NH1	2.77	0.58
6:YG:83:ARG:O	6:YG:86:MET:HB2	2.04	0.58
7:YH:69:ARG:HD2	7:YH:69:ARG:C	2.23	0.58
21:RZ:158:PRO:HG2	21:RZ:161:VAL:HG11	1.86	0.58
1:RA:1353:A:H2'	1:RA:1354:A:C8	2.38	0.57
15:YT:41:ARG:NH2	32:XA:346:G:OP1	2.29	0.57
32:XA:922:G:H4'	36:XE:20:GLN:HA	1.86	0.57
51:XT:100:ILE:HG22	51:XT:101:GLY:H	1.68	0.57
1:YA:2749:A:OP1	7:YH:3:ARG:NH2	2.30	0.57
32:QA:1086:U:H3	32:QA:1099:G:H22	1.52	0.57
35:QD:108:LEU:HD21	35:QD:174:LEU:HD22	1.85	0.57
1:RA:918:A:N3	2:RB:80:U:O2'	2.32	0.57
32:XA:979:C:H42	45:YN:18:VAL:HG12	1.69	0.57
34:XC:179:ARG:NH1	34:XC:206:GLU:OE1	2.36	0.57
54:XY:201:LEU:HD21	54:XY:203:ARG:NE	2.18	0.57
32:QA:370:C:H2'	32:QA:371:G:C8	2.39	0.57
51:QT:53:LEU:CD1	51:QT:100:ILE:HG13	2.34	0.57
1:RA:1316:U:H2'	1:RA:1317:A:H8	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:XG:50:ILE:HD11	38:XG:58:PRO:HA	1.86	0.57
48:XQ:41:LYS:HZ3	48:XQ:92:ARG:HH21	1.52	0.57
1:YA:1530:C:O2'	1:YA:1531:C:H6	1.87	0.57
1:YA:2359:C:H2'	1:YA:2360:A:O4'	2.05	0.57
5:YF:33:LEU:HD13	5:YF:112:MET:HE2	1.85	0.57
17:YV:52:VAL:HG23	17:YV:55:ALA:HB3	1.85	0.57
33:QB:76:GLN:HE21	33:QB:206:ASP:HA	1.69	0.57
39:QH:95:VAL:HB	39:QH:99:GLU:HB2	1.86	0.57
12:RQ:21:THR:CG2	12:RQ:101:ARG:HB2	2.34	0.57
32:XA:380:G:N2	32:XA:383:A:OP2	2.37	0.57
21:YZ:198:LYS:HZ1	53:XV:52:G:H2'	1.69	0.57
21:YZ:91:LEU:HG	21:YZ:130:PRO:HG3	1.85	0.57
30:R8:14:VAL:HG13	30:R8:22:VAL:HG13	1.85	0.57
5:RF:51:THR:HB	5:RF:88:VAL:HG11	1.87	0.57
17:RV:40:LEU:HB2	17:RV:46:VAL:HG12	1.87	0.57
1:YA:1786:A:H1'	1:YA:1938:A:N6	2.19	0.57
1:RA:1141:U:OP1	9:RN:25:ARG:NH1	2.38	0.57
9:RN:15:LEU:HB2	9:RN:135:PRO:HB2	1.84	0.57
11:RP:95:VAL:HG22	11:RP:125:VAL:HG12	1.86	0.57
11:RP:126:VAL:HG12	11:RP:148:LEU:HD21	1.86	0.57
32:XA:1001(A):A:H2'	32:XA:1001(B):G:H8	1.69	0.57
32:XA:1456:G:N1	51:XT:51:GLU:OE1	2.36	0.57
1:YA:2698:U:H2'	1:YA:2699:C:C6	2.40	0.57
1:YA:2836:U:H2'	1:YA:2837:G:C8	2.39	0.57
7:YH:113:VAL:HG11	7:YH:151:ILE:HD13	1.86	0.57
17:YV:40:LEU:HB2	17:YV:46:VAL:HG12	1.86	0.57
53:QV:21:A:H61	53:QV:46:G:H2'	1.70	0.57
32:XA:1002:G:H2'	32:XA:1003:G:C8	2.40	0.57
31:Y9:25:VAL:HB	31:Y9:34:GLN:HB2	1.85	0.57
1:YA:2853:C:H2'	1:YA:2854:G:H8	1.70	0.57
2:YB:14:U:O3'	2:YB:108:U:O2'	2.23	0.57
1:YA:1815:A:OP2	3:YD:54:ARG:NH2	2.37	0.57
32:QA:1513:A:H2'	32:QA:1514:C:C6	2.40	0.57
34:QC:32:LEU:HD22	34:QC:59:ARG:NH1	2.20	0.57
35:QD:57:ARG:NH2	36:QE:107:ARG:NE	2.52	0.57
36:QE:12:LEU:HB3	36:QE:31:LEU:HB2	1.86	0.57
40:QI:17:VAL:HG23	40:QI:63:ILE:HG12	1.85	0.57
54:QY:135:GLY:HA2	54:QY:317:ILE:HD12	1.87	0.57
12:RQ:80:GLU:OE1	54:QY:281:HIS:HD2	1.82	0.57
1:RA:414:C:H2'	1:RA:415:A:H8	1.70	0.57
32:XA:1399:C:O2	32:XA:1502:A:N6	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:164:U:H2'	32:XA:165:C:C6	2.40	0.57
40:XI:24:GLY:HA2	40:XI:59:PHE:O	2.05	0.57
1:YA:144:C:H5'	19:YX:2:LYS:HE2	1.87	0.57
14:YS:15:ARG:O	14:YS:19:LYS:HG2	2.03	0.57
20:YY:82:PRO:O	20:YY:101:LYS:NZ	2.27	0.57
32:QA:519:C:OP2	43:QL:50:SER:OG	2.20	0.57
1:RA:2384:G:OP2	22:R0:55:ARG:NH1	2.38	0.57
19:RX:5:TYR:HD1	24:R2:33:MET:CE	2.18	0.57
1:RA:2081:C:H2'	1:RA:2082:A:H8	1.70	0.57
32:XA:1027:C:H3'	32:XA:1028:C:C6	2.39	0.57
54:XY:176:ILE:HG21	54:XY:179:VAL:HG13	1.87	0.57
4:YE:24:THR:HG23	4:YE:186:GLY:O	2.04	0.57
26:R4:44:THR:O	26:R4:46:GLN:N	2.38	0.57
5:YF:110:LEU:HD11	5:YF:202:PHE:CD1	2.39	0.57
11:YP:86:LYS:HB3	11:YP:118:GLY:HA3	1.86	0.57
36:QE:137:GLU:OE1	36:QE:141:GLN:NE2	2.35	0.56
32:QA:1279:A:H5''	41:QJ:7:LYS:NZ	2.20	0.56
1:RA:1796:U:H2'	1:RA:1797:C:C6	2.40	0.56
1:RA:2138:C:H2'	1:RA:2139:C:C6	2.40	0.56
32:XA:189(L):U:H2'	32:XA:189(M):G:C8	2.39	0.56
1:YA:2261:C:OP1	22:Y0:19:LYS:NZ	2.37	0.56
1:YA:1353:A:H2'	1:YA:1354:A:C8	2.40	0.56
1:YA:2065:C:H2'	1:YA:2066:C:H6	1.70	0.56
4:YE:51:PHE:N	4:YE:75:VAL:CG2	2.68	0.56
9:YN:15:LEU:HB2	9:YN:135:PRO:HB2	1.87	0.56
21:YZ:198:LYS:HE3	53:XV:52:G:N3	2.20	0.56
34:QC:70:VAL:HG22	34:QC:72:LYS:H	1.69	0.56
45:QN:48:ALA:HB2	45:QN:53:LEU:HD12	1.88	0.56
1:RA:2573:C:N4	54:QY:255:ASN:O	2.37	0.56
53:QV:75:C:H5	54:QY:278:ARG:HH12	1.53	0.56
54:QY:270:ILE:HD11	54:QY:298:VAL:HG21	1.86	0.56
1:RA:140:G:N2	1:RA:1596:A:H4'	2.20	0.56
1:RA:1816:G:O6	3:RD:35:LYS:NZ	2.29	0.56
1:RA:2010:G:H5''	18:RW:42:ARG:HB2	1.86	0.56
47:XP:59:TRP:HA	47:XP:62:VAL:HG12	1.87	0.56
32:QA:411:A:OP2	35:QD:25:ARG:NH2	2.38	0.56
54:QY:330:ASP:OD2	54:QY:332:ARG:NH2	2.37	0.56
1:RA:1102:C:H2'	1:RA:1103:A:C8	2.40	0.56
7:RH:3:ARG:HD3	7:RH:54:ARG:HH12	1.70	0.56
32:XA:1238:A:N7	32:XA:1303:C:H1'	2.20	0.56
32:XA:45:U:H2'	32:XA:46:G:C8	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:XH:37:ARG:NH2	39:XH:38:ILE:HD11	2.20	0.56
54:XY:315:SER:HB3	54:XY:316:ASP:HB3	1.87	0.56
1:YA:2115:G:H21	1:YA:2171:A:H61	1.54	0.56
1:YA:321:G:OP2	5:YF:135:LYS:HD3	2.05	0.56
7:YH:33:LEU:HD12	7:YH:33:LEU:O	2.05	0.56
32:QA:1030(D):G:N7	32:QA:1031:G:N2	2.53	0.56
32:QA:945:G:C2	32:QA:946:A:C8	2.93	0.56
1:RA:2406:U:C4	11:RP:72:PRO:HD2	2.41	0.56
1:RA:675:A:N3	1:RA:2443:C:O2'	2.37	0.56
1:RA:813:U:H2'	1:RA:814:C:C6	2.41	0.56
15:YT:39:ARG:HH22	32:XA:344:A:H4'	1.71	0.56
32:QA:742:G:H5'	46:QO:58:MET:HE3	1.86	0.56
6:RG:7:LEU:HD12	6:RG:100:TRP:CE3	2.20	0.56
32:XA:41:G:H2'	32:XA:42:G:C8	2.40	0.56
41:XJ:61:GLU:OE1	45:XN:58:LYS:NZ	2.34	0.56
23:Y1:64:ALA:HA	23:Y1:67:ILE:HG13	1.88	0.56
1:YA:1019:U:H2'	1:YA:1020:A:C8	2.40	0.56
1:YA:1798:U:H5'	3:YD:259:THR:HG22	1.86	0.56
11:YP:97:PRO:CA	11:YP:112:LEU:HD12	2.33	0.56
16:YU:92:ARG:HA	16:YU:95:LEU:HB2	1.88	0.56
33:QB:7:VAL:HG12	33:QB:217:ARG:HD2	1.88	0.56
54:QY:315:SER:HB3	54:QY:316:ASP:HB3	1.87	0.56
35:XD:173:TRP:CD1	35:XD:174:LEU:HG	2.40	0.56
39:XH:20:TYR:CE1	39:XH:78:GLN:NE2	2.74	0.56
32:XA:101:A:H5'	51:XT:10:LEU:HD21	1.87	0.56
1:YA:1471:A:OP2	1:YA:1519:G:N2	2.30	0.56
1:YA:2111:C:H42	1:YA:2147:G:H22	1.52	0.56
1:YA:2683:C:OP1	15:YT:53:ARG:NH2	2.38	0.56
3:YD:145:VAL:HG12	3:YD:146:GLU:O	2.05	0.56
7:YH:48:GLY:O	7:YH:49:VAL:HG23	2.05	0.56
32:QA:1062:U:H2'	32:QA:1063:C:C6	2.40	0.56
50:QS:27:GLU:CB	50:QS:28:LYS:HE3	2.35	0.56
50:QS:45:VAL:HG21	26:R4:59:PHE:CZ	2.39	0.56
1:RA:1316:U:H2'	1:RA:1317:A:C8	2.40	0.56
1:RA:1453:U:OP1	13:RR:77:ARG:NH1	2.36	0.56
32:XA:404:U:H5'	35:XD:122:ARG:HD3	1.88	0.56
1:YA:2246:G:H2'	1:YA:2247:A:H8	1.69	0.56
1:YA:2291:U:H2'	1:YA:2292:C:C6	2.40	0.56
1:YA:2693:A:H2'	1:YA:2694:G:H8	1.71	0.56
1:YA:639:U:H2'	1:YA:640:C:C6	2.41	0.56
4:YE:82:ARG:HH11	4:YE:82:ARG:CG	2.17	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:123:C:OP1	32:QA:311:C:O2'	2.22	0.56
32:XA:1352:C:OP1	52:XU:3:LYS:NZ	2.21	0.56
1:YA:301:G:OP2	20:YY:84:ARG:NH2	2.39	0.56
1:YA:489:G:N7	18:YW:49:LYS:NZ	2.54	0.56
6:YG:146:TYR:HD2	44:XM:8:GLU:CG	2.18	0.56
12:YQ:6:ARG:NH2	21:YZ:197:ILE:HG12	2.20	0.56
32:QA:339:C:H2'	32:QA:340:U:H6	1.71	0.56
32:QA:946:A:H2'	32:QA:947:G:H8	1.67	0.56
48:QQ:74:LEU:HD13	48:QQ:75:ARG:HG2	1.87	0.56
26:R4:54:GLY:O	26:R4:56:VAL:HA	2.06	0.56
1:RA:1827:C:O2'	1:RA:1970:A:N3	2.35	0.56
41:XJ:38:ILE:CD1	41:XJ:71:LEU:HD22	2.36	0.56
41:XJ:38:ILE:HG12	41:XJ:71:LEU:CD2	2.36	0.56
32:XA:1047:G:H5''	45:XN:4:LYS:HD3	1.88	0.56
33:QB:106:LYS:N	33:QB:106:LYS:HD3	2.20	0.56
51:QT:18:GLN:O	51:QT:22:ARG:HG3	2.05	0.56
1:RA:2698:U:H2'	1:RA:2699:C:C6	2.40	0.56
1:RA:37:C:H2'	1:RA:38:A:H8	1.71	0.56
16:RU:108:GLU:O	16:RU:112:ARG:HG2	2.06	0.56
32:XA:769:G:H4'	32:XA:1513:A:H4'	1.88	0.56
33:XB:187:LEU:HA	33:XB:201:ILE:HB	1.87	0.56
1:YA:1429:G:H2'	1:YA:1430:C:C6	2.41	0.56
7:YH:28:GLY:HA3	7:YH:79:VAL:HB	1.88	0.56
32:QA:1399:C:O2	32:QA:1502:A:N6	2.39	0.56
35:QD:178:VAL:HG12	35:QD:179:GLU:H	1.71	0.56
35:QD:53:ASP:HB3	35:QD:57:ARG:HH12	1.69	0.56
54:QY:176:ILE:HG21	54:QY:179:VAL:HG13	1.87	0.56
1:RA:1084:A:C8	1:RA:1085:A:H4'	2.41	0.56
1:RA:2094:G:P	8:RI:22:LYS:HD2	2.46	0.56
1:RA:2336:A:H61	22:R0:43:THR:HG22	1.70	0.56
5:RF:184:TYR:O	5:RF:188:ARG:HG3	2.06	0.56
32:XA:1030(D):G:H2'	32:XA:1030(E):A:C8	2.41	0.56
32:XA:1286:A:H2'	32:XA:1287:A:H4'	1.87	0.56
33:XB:185:ILE:CD1	33:XB:199:TYR:HD2	2.18	0.56
33:XB:58:ILE:CG2	33:XB:222:ILE:HG22	2.36	0.56
40:XI:53:VAL:C	40:XI:55:ALA:H	2.06	0.56
44:XM:54:VAL:HA	44:XM:57:ARG:HB3	1.87	0.56
48:XQ:74:LEU:HD13	48:XQ:75:ARG:HG2	1.88	0.56
54:XY:261:VAL:HG21	54:XY:284:LYS:HA	1.88	0.56
1:YA:581:C:H2'	1:YA:582:G:C8	2.41	0.56
3:YD:133:LEU:HB3	3:YD:173:VAL:HG21	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:297:G:N2	32:QA:300:A:OP2	2.33	0.55
32:QA:514:C:H2'	32:QA:515:G:H8	1.70	0.55
32:QA:811:C:O2'	32:QA:901:A:N1	2.38	0.55
33:QB:200:ILE:HG22	33:QB:202:PRO:CD	2.34	0.55
51:QT:10:LEU:HD13	51:QT:12:ALA:HB2	1.87	0.55
1:RA:2102:U:O2	1:RA:2187:G:O6	2.24	0.55
1:RA:414:C:H2'	1:RA:415:A:C8	2.40	0.55
3:RD:16:MET:CG	3:RD:211:ARG:HH21	2.19	0.55
6:RG:16:ARG:CZ	6:RG:31:VAL:CG2	2.84	0.55
32:XA:1003:G:H3'	32:XA:1003:G:N3	2.21	0.55
42:XK:92:GLU:O	42:XK:96:ARG:HG2	2.06	0.55
1:YA:2336:A:H61	22:Y0:43:THR:HG22	1.71	0.55
1:YA:2420:C:OP1	30:Y8:34:TRP:HB3	2.06	0.55
3:YD:206:LEU:HD22	3:YD:211:ARG:HG2	1.86	0.55
4:YE:101:ARG:CZ	4:YE:171:GLU:HB2	2.37	0.55
5:YF:122:LYS:NZ	5:YF:152:GLU:OE2	2.32	0.55
10:YO:64:ARG:NH1	10:YO:81:ASP:OD1	2.38	0.55
1:YA:483:A:O2'	20:YY:49:VAL:O	2.15	0.55
32:QA:1030(D):G:H2'	32:QA:1030(E):A:C8	2.41	0.55
51:QT:57:ARG:HH22	51:QT:100:ILE:HD12	1.71	0.55
1:RA:2689:U:H4'	1:RA:2690:C:H5'	1.88	0.55
21:RZ:129:SER:HB3	21:RZ:132:ASN:HB2	1.87	0.55
36:XE:74:GLY:HA3	36:XE:116:THR:HG22	1.87	0.55
54:XY:333:ILE:HG13	54:XY:345:THR:HG22	1.88	0.55
1:YA:2150:U:H2'	1:YA:2151:G:C8	2.42	0.55
1:YA:2206:G:H3'	1:YA:2207:G:H8	1.70	0.55
1:YA:2648:C:H2'	1:YA:2649:U:H6	1.71	0.55
6:YG:80:PHE:O	6:YG:82:LEU:N	2.40	0.55
35:QD:166:LYS:HB2	35:QD:168:ARG:NH2	2.22	0.55
32:XA:69:G:H2'	32:XA:70:G:H8	1.72	0.55
38:XG:10:ARG:NH1	38:XG:10:ARG:HG3	2.21	0.55
54:XY:144:TRP:HH2	54:XY:326:TYR:CD2	2.23	0.55
1:YA:1429:G:H2'	1:YA:1430:C:H6	1.72	0.55
1:YA:2647:U:H2'	1:YA:2648:C:C6	2.41	0.55
2:YB:43:C:H5''	26:Y4:1:MET:HG2	1.87	0.55
3:YD:30:GLU:HG2	3:YD:94:LEU:HD11	1.88	0.55
14:YS:43:GLU:OE1	22:Y0:49:LYS:HE3	2.07	0.55
21:YZ:198:LYS:CE	53:XV:52:G:H2'	2.36	0.55
39:QH:112:LEU:CD2	39:QH:133:LEU:HG	2.36	0.55
39:QH:51:VAL:HG11	39:QH:60:ARG:HH12	1.71	0.55
53:QV:3:C:H2'	53:QV:4:G:H5'	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:11:G:H2'	1:RA:12:U:H5'	1.87	0.55
1:RA:652(U):C:H2'	1:RA:652(V):G:C8	2.42	0.55
6:RG:50:ALA:O	6:RG:52:ILE:N	2.40	0.55
1:RA:566:U:H5''	11:RP:29:LYS:HE3	1.89	0.55
32:XA:1005:A:OP2	32:XA:1024:G:N2	2.39	0.55
32:XA:678:U:H2'	32:XA:679:C:C6	2.41	0.55
32:XA:945:G:C2	32:XA:946:A:C8	2.94	0.55
1:YA:2189:U:H2'	1:YA:2190:G:C8	2.41	0.55
1:YA:881:G:H2'	1:YA:882:G:C8	2.42	0.55
3:YD:221:VAL:HG13	3:YD:226:MET:CE	2.36	0.55
9:YN:42:TRP:HA	9:YN:48:MET:HE1	1.87	0.55
54:QY:200:ARG:HD3	54:QY:322:GLN:HE21	1.71	0.55
23:R1:40:ARG:HD3	23:R1:40:ARG:C	2.27	0.55
1:RA:2064:C:H2'	1:RA:2065:C:H6	1.72	0.55
33:XB:87:ARG:HD3	33:XB:234:PRO:HD2	1.88	0.55
32:XA:545:C:OP1	35:XD:61:LYS:NZ	2.40	0.55
2:YB:105:A:OP1	21:YZ:72:ARG:NH1	2.39	0.55
13:YR:18:LEU:CD1	13:YR:22:ARG:HD2	2.36	0.55
1:RA:1053:C:H2'	1:RA:1054:A:C8	2.41	0.55
1:RA:392:C:H5''	1:RA:409:C:H5''	1.88	0.55
4:RE:170:LEU:HB3	4:RE:184:VAL:HG22	1.89	0.55
5:RF:51:THR:HB	5:RF:88:VAL:CG1	2.37	0.55
6:RG:16:ARG:NH2	6:RG:31:VAL:CG2	2.69	0.55
7:RH:116:GLU:HA	7:RH:116:GLU:OE1	2.06	0.55
13:RR:21:TYR:OH	13:RR:43:GLU:HG2	2.06	0.55
32:XA:539:A:H2'	32:XA:540:G:C8	2.41	0.55
33:XB:76:GLN:HB2	33:XB:208:ILE:HG12	1.88	0.55
45:XN:32:SER:OG	45:XN:41:ARG:HG2	2.06	0.55
1:YA:2134:A:N6	1:YA:2156:G:O2'	2.39	0.55
1:YA:579:G:H2'	1:YA:580:C:C6	2.42	0.55
1:RA:143(A):G:H4'	19:RX:35:THR:HG21	1.88	0.55
6:RG:77:ILE:HB	6:RG:82:LEU:HB3	1.88	0.55
15:RT:108:ARG:HA	15:RT:111:ARG:NH1	2.21	0.55
1:YA:1050:A:H2'	1:YA:1051:G:H8	1.72	0.55
1:YA:1614:A:C2	18:YW:93:ALA:HB2	2.41	0.55
1:YA:2461:C:H2'	1:YA:2462:U:C6	2.41	0.55
17:YV:43:GLU:N	17:YV:43:GLU:OE2	2.40	0.55
32:QA:924:C:H2'	32:QA:925:G:H8	1.71	0.55
33:QB:229:VAL:HG12	33:QB:230:VAL:N	2.19	0.55
35:QD:85:LYS:HD3	35:QD:86:LYS:H	1.71	0.55
32:QA:1279:A:H5''	41:QJ:7:LYS:HZ1	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:QY:166:ILE:HG22	54:QY:167:GLU:HG3	1.88	0.55
1:RA:2137:C:H2'	1:RA:2138:C:C6	2.41	0.55
1:RA:265:A:N1	1:RA:427:U:O2'	2.38	0.55
1:RA:881:G:H2'	1:RA:882:G:C8	2.42	0.55
51:XT:18:GLN:O	51:XT:22:ARG:HG3	2.06	0.55
54:XY:196:THR:HG22	54:XY:222:VAL:H	1.70	0.55
1:YA:1709:U:H2'	1:YA:1710:C:C6	2.41	0.55
1:YA:1823:G:OP1	3:YD:54:ARG:NH1	2.40	0.55
1:YA:265:A:N1	1:YA:427:U:O2'	2.35	0.55
8:YI:82:ARG:HD2	32:QA:368:U:O4	2.06	0.55
33:QB:84:GLU:HB3	33:QB:219:VAL:HG21	1.89	0.55
33:QB:8:LYS:HZ1	33:QB:52:GLU:HA	1.70	0.55
1:RA:2180:U:H2'	1:RA:2181:G:C8	2.42	0.55
32:XA:427:U:OP1	35:XD:13:ARG:NH2	2.39	0.55
32:XA:624:C:H2'	32:XA:625:G:H8	1.72	0.55
53:XV:51:C:H2'	53:XV:52:G:O4'	2.07	0.55
1:YA:306:U:H2'	1:YA:307:G:O4'	2.07	0.55
1:YA:813:U:H2'	1:YA:814:C:C6	2.42	0.55
5:YF:164:ARG:HD2	5:YF:175:THR:HG23	1.89	0.55
8:YI:130:TYR:HB3	8:YI:138:ILE:HB	1.88	0.55
32:QA:539:A:H2'	32:QA:540:G:C8	2.42	0.55
1:RA:24:G:O2'	18:RW:78:GLU:O	2.24	0.55
6:RG:170:ARG:C	6:RG:170:ARG:HD3	2.27	0.55
9:RN:67:LEU:O	9:RN:88:GLU:HG3	2.07	0.55
34:XC:32:LEU:HD12	34:XC:59:ARG:NH1	2.22	0.55
36:XE:12:LEU:HD12	36:XE:128:PRO:HB2	1.89	0.55
38:XG:132:GLY:O	38:XG:136:LYS:HG2	2.06	0.55
54:XY:121:GLY:O	54:XY:123:TYR:N	2.39	0.55
1:YA:2110:G:H5''	1:YA:2111:C:H5	1.72	0.55
6:YG:146:TYR:CD2	44:XM:8:GLU:CG	2.90	0.55
11:YP:101:VAL:HA	11:YP:106:LEU:O	2.07	0.55
32:QA:316:G:OP2	32:QA:351:G:O2'	2.24	0.54
33:QB:158:LEU:HG	33:QB:182:ILE:HD11	1.89	0.54
1:RA:1639:U:H2'	1:RA:1640:C:H5''	1.89	0.54
1:RA:2059:A:O2'	5:RF:69:HIS:ND1	2.38	0.54
1:RA:752:A:H3'	29:R7:1:MET:CE	2.37	0.54
3:RD:126:GLN:O	3:RD:193:VAL:CG2	2.54	0.54
13:RR:102:GLU:OE2	18:RW:37:ARG:NH2	2.36	0.54
16:RU:8:VAL:HG11	16:RU:12:ARG:CZ	2.37	0.54
32:XA:954:G:H21	32:XA:1227:A:H62	1.53	0.54
32:XA:56:U:H2'	32:XA:57:G:C8	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:1187:G:H4'	40:XI:111:ARG:HH11	1.72	0.54
47:XP:68:ASP:O	47:XP:71:ARG:HG2	2.07	0.54
21:YZ:198:LYS:HD3	53:XV:53:G:O4'	2.07	0.54
1:YA:1101:U:H2'	1:YA:1102:C:C6	2.42	0.54
4:YE:150:VAL:CG1	4:YE:154:LYS:HG3	2.37	0.54
6:YG:46:ALA:HB2	6:YG:53:LEU:HD12	1.89	0.54
34:QC:148:GLY:HA3	34:QC:172:ARG:O	2.07	0.54
35:QD:15:GLU:HG3	35:QD:63:LYS:HD3	1.89	0.54
41:QJ:78:ASN:O	41:QJ:80:LYS:N	2.39	0.54
32:QA:881:G:P	43:QL:12:ARG:HH22	2.30	0.54
1:RA:2689:U:OP2	1:RA:2719:G:N2	2.28	0.54
1:RA:911:A:H2'	12:RQ:9:TYR:OH	2.08	0.54
11:RP:126:VAL:CG1	11:RP:148:LEU:HD21	2.38	0.54
17:RV:62:LEU:HD11	17:RV:95:LEU:HB2	1.89	0.54
32:XA:1309:G:O2'	44:XM:77:ASN:ND2	2.39	0.54
32:XA:338:A:H2'	32:XA:339:C:H6	1.73	0.54
41:XJ:38:ILE:HG12	41:XJ:71:LEU:HD22	1.89	0.54
49:XR:26:LEU:HD11	49:XR:42:ARG:NE	2.22	0.54
54:XY:203:ARG:HH12	54:XY:206:PRO:CD	2.20	0.54
6:YG:5:VAL:HG12	26:Y4:25:TYR:HE1	1.72	0.54
26:Y4:20:ASN:ND2	26:Y4:38:LYS:HG3	2.21	0.54
32:QA:407:G:H2'	32:QA:408:A:H8	1.71	0.54
35:QD:57:ARG:HH22	36:QE:107:ARG:HD3	1.69	0.54
1:RA:582:G:H2'	1:RA:583:G:C8	2.42	0.54
6:RG:7:LEU:HD11	6:RG:100:TRP:CZ3	2.41	0.54
17:RV:21:ARG:NH2	17:RV:91:TYR:OH	2.40	0.54
32:XA:1410:G:H2'	32:XA:1411:C:H6	1.72	0.54
32:XA:201:C:H42	32:XA:216:G:H1	1.55	0.54
35:XD:8:VAL:HG22	35:XD:21:LEU:CD1	2.38	0.54
41:XJ:37:PRO:HA	41:XJ:72:VAL:HG12	1.89	0.54
44:XM:6:GLY:HA3	44:XM:67:GLU:HG3	1.89	0.54
51:XT:60:GLU:HG3	51:XT:81:LYS:HD2	1.88	0.54
55:XX:21:A:H62	54:XY:215:THR:HG1	1.51	0.54
1:YA:414:C:H2'	1:YA:415:A:C8	2.41	0.54
32:QA:126:G:OP1	32:QA:605:U:O2'	2.17	0.54
41:QJ:19:SER:O	41:QJ:23:ILE:HG12	2.08	0.54
41:QJ:37:PRO:HA	41:QJ:72:VAL:HG12	1.89	0.54
1:RA:1065:U:H4'	1:RA:1066:U:H5'	1.89	0.54
1:RA:876:C:H2'	1:RA:877:U:O4'	2.08	0.54
7:RH:11:VAL:HG21	7:RH:50:VAL:HG23	1.88	0.54
34:XC:63:ASN:HB2	34:XC:98:ASN:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:1346:A:OP1	40:XI:120:ARG:NH1	2.38	0.54
54:XY:166:ILE:HG22	54:XY:167:GLU:HG3	1.90	0.54
1:YA:1430:C:H2'	1:YA:1431:U:C6	2.42	0.54
1:YA:1444:G:H2'	1:YA:1445(B):C:C5	2.43	0.54
1:YA:2162:G:O3'	1:YA:2172:U:O2'	2.24	0.54
1:YA:752:A:H4'	1:YA:753:C:O5'	2.08	0.54
36:QE:41:VAL:HG11	36:QE:113:ALA:HB2	1.90	0.54
53:QV:51:C:H2'	53:QV:52:G:O4'	2.08	0.54
29:R7:9:ARG:HH22	29:R7:47:ARG:HD3	1.71	0.54
1:RA:2243:U:H2'	1:RA:2244:U:C6	2.42	0.54
1:RA:270:A:OP2	1:RA:272(X):G:N1	2.30	0.54
32:XA:1391:U:H2'	32:XA:1392:G:C8	2.43	0.54
54:XY:129:TYR:HD2	54:XY:223:TYR:HE1	1.56	0.54
1:YA:1101:U:H2'	1:YA:1102:C:H6	1.71	0.54
1:YA:566:U:H5''	11:YP:29:LYS:HE3	1.88	0.54
7:YH:41:MET:HE2	7:YH:64:LEU:HB3	1.90	0.54
17:YV:52:VAL:CG2	17:YV:55:ALA:HB3	2.38	0.54
32:QA:1244:C:H2'	32:QA:1245:A:H8	1.72	0.54
35:QD:50:ARG:HH12	36:QE:9:LYS:HZ2	1.55	0.54
1:RA:140:G:H21	1:RA:142(A):A:N6	2.05	0.54
32:XA:25:C:H2'	32:XA:26:A:C8	2.43	0.54
33:XB:33:TYR:N	33:XB:41:ILE:O	2.36	0.54
38:XG:45:ASP:O	38:XG:49:ILE:HG13	2.07	0.54
1:YA:1296:G:OP1	1:YA:2709:G:O2'	2.15	0.54
1:YA:1388:G:H2'	1:YA:1389:G:H8	1.72	0.54
1:YA:151:C:H2'	1:YA:152:G:H8	1.72	0.54
1:YA:476:G:N1	1:YA:479:A:OP2	2.40	0.54
9:YN:120:LEU:HD11	9:YN:122:VAL:HG21	1.81	0.54
32:QA:1414:U:H3	32:QA:1486:G:H1	1.54	0.54
32:QA:404:U:H2'	32:QA:405:U:H6	1.71	0.54
35:QD:53:ASP:HB3	35:QD:57:ARG:NH1	2.23	0.54
41:QJ:11:PHE:HE1	41:QJ:67:THR:HG22	1.71	0.54
48:QQ:74:LEU:CD1	48:QQ:75:ARG:HG2	2.38	0.54
1:RA:1406:U:H2'	1:RA:1407:C:C6	2.42	0.54
1:RA:1794:U:H2'	1:RA:1795:C:H6	1.73	0.54
1:RA:595:C:H2'	1:RA:596:G:H8	1.72	0.54
1:RA:1799:G:OP1	3:RD:260:ARG:NH2	2.39	0.54
21:RZ:156:LYS:HD2	21:RZ:156:LYS:O	2.08	0.54
32:XA:662:G:H2'	32:XA:663:A:C8	2.43	0.54
54:XY:324:ARG:HD2	54:XY:326:TYR:HE1	1.73	0.54
1:YA:1073:A:H2'	1:YA:1074:G:C8	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:2375:G:N2	1:YA:2378:A:OP2	2.39	0.54
4:YE:51:PHE:H	4:YE:75:VAL:CG2	2.20	0.54
33:QB:16:HIS:HB2	33:QB:204:ASN:HB3	1.90	0.54
32:QA:562:C:H1'	43:QL:15:ARG:HD2	1.89	0.54
46:QO:17:ARG:HD3	46:QO:26:GLU:OE1	2.07	0.54
48:QQ:86:GLU:O	48:QQ:90:ILE:HG12	2.07	0.54
44:QM:61:GLU:OE1	26:R4:49:PHE:HE2	1.90	0.54
1:RA:637:A:H8	11:RP:117:GLU:HG3	1.72	0.54
42:XK:27:ASN:OD1	42:XK:28:THR:N	2.38	0.54
46:XO:25:THR:HG21	46:XO:70:LEU:HB2	1.89	0.54
54:XY:136:SER:OG	54:XY:317:ILE:O	2.17	0.54
1:YA:2648:C:H2'	1:YA:2649:U:C6	2.43	0.54
1:YA:764:A:H5'	3:YD:210:GLY:HA2	1.90	0.54
5:YF:11:VAL:HB	5:YF:18:ARG:HB3	1.90	0.54
19:YX:88:LYS:HE2	19:YX:93:GLU:HG3	1.89	0.54
32:QA:1518:MA6:N6	32:QA:1519:MA6:H103	2.23	0.54
32:QA:256:U:OP1	48:QQ:17:LYS:NZ	2.38	0.54
6:RG:101:ILE:HD13	26:R4:25:TYR:HB2	1.90	0.54
1:RA:1019:U:H2'	1:RA:1020:A:H8	1.73	0.54
1:RA:2030:A:H4'	1:RA:2031:A:H8	1.72	0.54
8:RI:109:ILE:HG13	8:RI:130:TYR:OH	2.08	0.54
37:XF:33:TYR:CB	37:XF:75:LEU:HD23	2.38	0.54
1:YA:1094:U:OP1	1:YA:1096:A:N6	2.41	0.54
1:YA:2064:C:H2'	1:YA:2065:C:C6	2.43	0.54
1:YA:2071:A:H2'	1:YA:2072:G:H8	1.72	0.54
1:YA:594:U:H2'	1:YA:595:C:C6	2.43	0.54
1:YA:994:C:O2'	1:YA:996:A:OP1	2.17	0.54
11:YP:91:PHE:CE2	11:YP:99:LEU:HD21	2.43	0.54
32:QA:1435:G:H2'	32:QA:1436:U:C6	2.42	0.54
32:QA:669:U:H2'	32:QA:670:G:C8	2.43	0.54
50:QS:64:GLU:HA	26:R4:59:PHE:HE1	1.73	0.54
54:QY:84:LEU:HD22	54:QY:96:PHE:CD1	2.43	0.54
1:RA:152:G:H2'	1:RA:153:C:C6	2.43	0.54
1:RA:2246:G:H2'	1:RA:2247:A:C8	2.43	0.54
1:RA:749:C:H5'	1:RA:1271:G:H1'	1.90	0.54
1:RA:854:G:H2'	1:RA:855:G:H8	1.72	0.54
9:RN:62:VAL:CG1	9:RN:66:LYS:HB2	2.38	0.54
32:XA:1118:C:OP1	40:XI:104:ARG:NH1	2.39	0.54
32:XA:45:U:H2'	32:XA:46:G:H8	1.73	0.54
34:XC:152:ILE:CG2	34:XC:167:TRP:HB3	2.27	0.54
25:Y3:23:LEU:HD22	25:Y3:50:VAL:HG11	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:YF:184:TYR:CE2	5:YF:188:ARG:HD2	2.43	0.54
15:YT:65:LYS:HE3	15:YT:67:SER:HB2	1.90	0.54
32:QA:28:G:O2'	32:QA:296:U:OP1	2.26	0.53
41:QJ:35:SER:N	41:QJ:73:ASP:O	2.32	0.53
44:QM:40:ASN:HB3	44:QM:43:THR:HG23	1.89	0.53
34:QC:22:TRP:CH2	45:QN:54:PRO:HG2	2.43	0.53
26:R4:16:CYS:SG	26:R4:17:GLY:N	2.81	0.53
1:RA:1019:U:OP1	1:RA:1035:U:O2'	2.21	0.53
1:RA:1406:U:H2'	1:RA:1407:C:H6	1.73	0.53
1:RA:974:G:OP1	1:RA:1187:G:O2'	2.22	0.53
5:RF:136:THR:O	5:RF:140:LEU:HD23	2.08	0.53
5:RF:64:ILE:HG21	5:RF:78:ILE:HG23	1.90	0.53
37:XF:97:PHE:CB	49:XR:32:ARG:HD3	2.38	0.53
32:XA:1492:A:O4'	43:XL:47:LYS:HD3	2.08	0.53
47:XP:20:VAL:HG21	47:XP:32:TYR:CD2	2.43	0.53
25:Y3:6:VAL:HG12	25:Y3:54:VAL:CG2	2.38	0.53
1:YA:2096:U:H3	1:YA:2193:G:H1	1.56	0.53
1:YA:2329:G:H2'	1:YA:2330:G:H8	1.73	0.53
1:YA:249:C:O2	30:Y8:12:LYS:NZ	2.30	0.53
33:QB:21:ARG:CD	33:QB:21:ARG:N	2.67	0.53
32:QA:922:G:H4'	36:QE:20:GLN:HA	1.89	0.53
1:RA:1223:G:N2	1:RA:1226:A:OP2	2.39	0.53
1:RA:2030:A:H4'	1:RA:2031:A:C8	2.44	0.53
6:RG:108:ASN:HA	26:R4:37:SER:HB3	1.90	0.53
15:RT:56:GLY:O	15:RT:59:THR:HG23	2.08	0.53
15:RT:91:ARG:HD2	15:RT:120:ARG:NH1	2.23	0.53
32:XA:1006:C:H2'	32:XA:1007:C:C6	2.43	0.53
33:XB:71:VAL:HG12	33:XB:93:VAL:HG22	1.89	0.53
54:XY:148:LEU:HD21	54:XY:199:HIS:HD2	1.72	0.53
1:YA:2641:G:P	9:YN:74:ARG:HH22	2.29	0.53
11:YP:100:LEU:HD22	11:YP:105:LEU:HD12	1.89	0.53
1:YA:863:A:P	12:YQ:22:LYS:HG3	2.48	0.53
32:QA:1065:U:H4'	32:QA:1066:C:O5'	2.08	0.53
54:QY:41:LEU:HD23	54:QY:46:VAL:HG21	1.89	0.53
1:RA:871:U:OP1	12:RQ:5:ARG:HD3	2.07	0.53
33:XB:69:LEU:HB3	33:XB:162:ILE:HG22	1.89	0.53
39:XH:12:ARG:CD	39:XH:26:VAL:HG12	2.37	0.53
40:XI:100:GLY:O	40:XI:103:THR:HG22	2.09	0.53
41:XJ:11:PHE:CE1	41:XJ:67:THR:HG22	2.40	0.53
54:XY:144:TRP:CE3	54:XY:201:LEU:HD22	2.43	0.53
1:YA:1068:G:H1	54:XY:58:LYS:HB2	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1341:U:OP1	1:YA:1397:U:N3	2.39	0.53
1:YA:2110:G:OP1	1:YA:2118:U:N3	2.40	0.53
1:YA:2246:G:H2'	1:YA:2247:A:C8	2.43	0.53
1:YA:23:G:OP1	1:YA:504:U:N3	2.39	0.53
5:YF:33:LEU:HB3	11:YP:6:LEU:HD21	1.89	0.53
32:QA:1006:C:H2'	32:QA:1007:C:C6	2.44	0.53
32:QA:673:G:H2'	32:QA:674:G:H8	1.73	0.53
32:QA:1187:G:H4'	40:QI:111:ARG:NH1	2.23	0.53
1:RA:2693:A:H2'	1:RA:2694:G:H8	1.74	0.53
32:XA:407:G:H2'	32:XA:408:A:C8	2.42	0.53
1:YA:2291:U:H2'	1:YA:2292:C:H6	1.74	0.53
1:YA:2329:G:H2'	1:YA:2330:G:C8	2.42	0.53
21:YZ:156:LYS:O	21:YZ:156:LYS:HD2	2.07	0.53
32:QA:1058:G:OP1	34:QC:199:LYS:HE3	2.08	0.53
19:RX:5:TYR:CE2	24:R2:30:ARG:HB2	2.44	0.53
30:R8:23:VAL:CG1	30:R8:47:LYS:HD3	2.39	0.53
1:RA:1847:A:H3'	1:RA:1848:A:H5'	1.90	0.53
1:RA:2753:A:N3	31:R9:15:LYS:NZ	2.55	0.53
5:RF:184:TYR:CE2	5:RF:188:ARG:HD2	2.43	0.53
20:RY:87:LYS:HB3	20:RY:95:LYS:HD3	1.90	0.53
54:XY:326:TYR:CD1	54:XY:333:ILE:HG23	2.43	0.53
54:XY:344:ASN:HB3	54:XY:347:ALA:HB3	1.89	0.53
1:YA:2838:G:C4	1:YA:2839:G:C8	2.97	0.53
1:YA:652(U):C:H2'	1:YA:652(V):G:C8	2.44	0.53
6:YG:16:ARG:NH2	6:YG:28:VAL:O	2.41	0.53
8:YI:110:ASP:N	8:YI:130:TYR:OH	2.31	0.53
34:QC:179:ARG:NH1	34:QC:206:GLU:OE1	2.42	0.53
1:RA:1019:U:H2'	1:RA:1020:A:C8	2.44	0.53
1:RA:2478:A:H5'	31:R9:31:LYS:HE2	1.89	0.53
34:XC:164:ARG:NH1	34:XC:166:GLU:OE1	2.42	0.53
39:XH:64:LYS:HG2	39:XH:79:VAL:HG21	1.89	0.53
1:YA:1165:U:H2'	1:YA:1166:C:H6	1.71	0.53
6:YG:47:LYS:HG2	6:YG:48:GLU:N	2.22	0.53
13:YR:100:LEU:CD2	13:YR:112:ALA:C	2.77	0.53
13:YR:61:HIS:O	13:YR:65:LEU:CD2	2.55	0.53
54:QY:202:VAL:HG22	54:QY:215:THR:HG23	1.90	0.53
30:R8:62:LEU:HB3	30:R8:65:GLU:HG2	1.90	0.53
1:RA:1066:U:O2'	1:RA:1068:G:OP2	2.18	0.53
1:RA:1657:C:H2'	1:RA:1658:C:H6	1.74	0.53
1:RA:579:G:O2'	1:RA:2019:A:OP1	2.21	0.53
15:RT:35:LYS:C	15:RT:35:LYS:HE2	2.29	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:950:U:OP2	44:XM:102:ARG:HD3	2.08	0.53
49:XR:32:ARG:HA	49:XR:69:THR:HG21	1.90	0.53
1:YA:1796:U:H2'	1:YA:1797:C:H6	1.74	0.53
1:YA:1859:A:N6	1:YA:1883:G:O2'	2.40	0.53
5:YF:103:LYS:O	5:YF:106:ARG:HG2	2.09	0.53
9:YN:94:HIS:HB2	9:YN:97:ARG:HD3	1.88	0.53
32:QA:1297:C:O2'	38:QG:114:ARG:NH2	2.42	0.53
32:QA:1410:G:H2'	32:QA:1411:C:C6	2.44	0.53
33:QB:167:PRO:HG3	33:QB:186:ALA:HB1	1.91	0.53
54:QY:217:PHE:CE2	54:QY:319:TRP:HA	2.43	0.53
1:RA:1657:C:H2'	1:RA:1658:C:C6	2.44	0.53
5:RF:33:LEU:HD13	5:RF:112:MET:HE2	1.90	0.53
9:RN:75:TYR:CE2	9:RN:77:GLY:HA2	2.43	0.53
15:RT:95:ARG:HH11	15:RT:95:ARG:CG	2.20	0.53
21:RZ:139:VAL:HG11	21:RZ:150:LEU:HD23	1.91	0.53
32:XA:437:U:H5'	35:XD:155:LEU:HD21	1.90	0.53
35:XD:15:GLU:HG3	35:XD:63:LYS:HD3	1.91	0.53
26:Y4:59:PHE:HE1	50:XS:64:GLU:CB	2.12	0.53
1:YA:1102:C:H2'	1:YA:1103:A:C8	2.44	0.53
1:YA:1507:A:O2'	1:YA:1508:A:O5'	2.26	0.53
1:YA:1514:U:H2'	1:YA:1515:G:C8	2.44	0.53
1:YA:2115:G:N1	1:YA:2119:A:OP2	2.41	0.53
1:YA:856:C:H2'	1:YA:857:C:H6	1.73	0.53
2:YB:45:A:OP2	6:YG:96:ARG:NH2	2.37	0.53
3:YD:108:PRO:HB3	3:YD:143:HIS:HE1	1.72	0.53
3:YD:92:ILE:HD12	3:YD:104:TYR:CD1	2.43	0.53
6:YG:66:GLN:HB3	6:YG:92:VAL:HG21	1.90	0.53
7:YH:40:GLU:OE1	7:YH:60:ARG:NH1	2.42	0.53
13:YR:41:ALA:HB1	13:YR:114:VAL:HG22	1.91	0.53
32:QA:41:G:H2'	32:QA:42:G:H8	1.74	0.53
34:QC:109:PRO:CB	34:QC:115:LEU:HD23	2.39	0.53
34:QC:18:TRP:HZ2	45:QN:57:ARG:HB3	1.74	0.53
35:QD:166:LYS:H	35:QD:168:ARG:HH21	1.52	0.53
54:QY:80:VAL:HG22	54:QY:102:GLU:OE1	2.09	0.53
1:RA:1050:A:H2'	1:RA:1051:G:H8	1.73	0.53
1:RA:7:G:H2'	1:RA:8:A:C8	2.44	0.53
32:XA:1009:G:H1	32:XA:1020:U:H3	1.57	0.53
32:XA:1221:G:OP1	32:XA:1320:C:N4	2.42	0.53
38:XG:9:VAL:HG11	38:XG:94:ARG:HD3	1.91	0.53
51:XT:57:ARG:HH12	51:XT:100:ILE:HB	1.74	0.53
51:XT:97:ALA:O	51:XT:99:LEU:HD13	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:XY:217:PHE:CE2	54:XY:319:TRP:HA	2.44	0.53
1:YA:1798:U:H5'	3:YD:259:THR:CG2	2.39	0.53
12:YQ:45:GLN:N	12:YQ:45:GLN:OE1	2.41	0.53
32:QA:501:C:H2'	32:QA:502:G:C8	2.43	0.53
40:QI:24:GLY:HA2	40:QI:59:PHE:O	2.09	0.53
49:QR:33:ASP:OD2	49:QR:36:ASN:HB2	2.09	0.53
1:RA:639:U:H2'	1:RA:640:C:C6	2.44	0.53
17:RV:21:ARG:NH2	17:RV:91:TYR:CZ	2.77	0.53
32:XA:811:C:O2'	32:XA:901:A:N1	2.41	0.53
54:XY:241:ILE:HG21	54:XY:284:LYS:HE2	1.90	0.53
11:YP:62:LEU:O	30:Y8:13:ARG:HD3	2.08	0.53
1:YA:184:C:H2'	1:YA:185:U:H6	1.72	0.53
1:YA:2817:G:OP1	13:YR:42:LYS:NZ	2.29	0.53
4:YE:21:VAL:HG23	4:YE:185:LYS:HD2	1.91	0.53
5:YF:165:ARG:HG2	5:YF:168:ARG:NH2	2.24	0.53
32:QA:1143:G:H2'	32:QA:1144:G:C8	2.44	0.52
32:QA:791:G:N2	32:QA:1497:G:O3'	2.41	0.52
44:QM:65:LYS:HA	26:R4:50:VAL:CG1	2.24	0.52
48:QQ:78:GLU:HG2	48:QQ:79:SER:N	2.23	0.52
1:RA:1059:G:O6	1:RA:1079:C:N4	2.42	0.52
1:RA:1429:G:H2'	1:RA:1430:C:C6	2.44	0.52
1:RA:2025:C:H2'	1:RA:2026:C:C6	2.44	0.52
1:RA:2836:U:H2'	1:RA:2837:G:C8	2.43	0.52
6:RG:5:VAL:HG22	6:RG:8:LYS:HB3	1.91	0.52
15:RT:54:ARG:HA	15:RT:59:THR:HB	1.91	0.52
32:XA:160:A:H2'	32:XA:161:A:O4'	2.08	0.52
32:XA:976:G:OP2	32:XA:1358:U:O2'	2.22	0.52
33:XB:200:ILE:HG22	33:XB:202:PRO:HD3	1.90	0.52
41:XJ:78:ASN:O	41:XJ:80:LYS:N	2.42	0.52
37:XF:99:ALA:HB2	49:XR:31:LEU:HD21	1.92	0.52
1:YA:1164:G:H2'	1:YA:1165:U:C6	2.44	0.52
1:YA:1936:A:OP2	1:YA:1962:5MC:N4	2.39	0.52
1:YA:2022:U:O2'	1:YA:2617:C:H5'	2.08	0.52
1:YA:38:A:H2'	1:YA:39:C:H6	1.75	0.52
1:YA:777:A:H2'	1:YA:778:G:H8	1.73	0.52
5:YF:130:ALA:HB3	5:YF:142:TRP:HD1	1.75	0.52
32:QA:1316:G:N1	32:QA:1319:A:OP2	2.42	0.52
36:QE:151:LEU:HD11	39:QH:77:GLU:CD	2.30	0.52
44:QM:62:ASN:O	26:R4:50:VAL:HA	2.09	0.52
27:R5:40:LYS:HD3	27:R5:41:PRO:O	2.09	0.52
32:QA:1475:G:H4'	1:RA:1689:A:H4'	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:1314:C:OP2	50:XS:4:SER:OG	2.13	0.52
32:XA:337:C:H2'	32:XA:338:A:C8	2.43	0.52
32:XA:503:C:OP2	43:XL:116:SER:HB3	2.09	0.52
1:YA:1047:G:H21	1:YA:1111:A:H62	1.56	0.52
1:YA:1991:U:H2'	1:YA:1992:G:H5''	1.91	0.52
32:QA:1003:G:N2	32:QA:1004:A:N3	2.57	0.52
32:QA:255:G:H2'	32:QA:256:U:C6	2.44	0.52
32:QA:998:G:H2'	32:QA:999:C:C6	2.44	0.52
43:QL:60:LEU:HD21	43:QL:66:VAL:HG22	1.90	0.52
22:R0:27:GLU:HG3	22:R0:68:GLU:HA	1.90	0.52
28:R6:6:ARG:NH1	28:R6:26:ASN:HB2	2.25	0.52
1:RA:2189:U:H2'	1:RA:2190:G:C8	2.44	0.52
1:RA:38:A:H2'	1:RA:39:C:C6	2.45	0.52
1:RA:579:G:H2'	1:RA:580:C:C6	2.44	0.52
1:RA:752:A:H3'	29:R7:1:MET:HE1	1.91	0.52
18:RW:17:VAL:CG2	18:RW:76:VAL:HG11	2.39	0.52
20:RY:92:ASN:N	20:RY:93:GLY:HA2	2.24	0.52
33:XB:16:HIS:O	33:XB:18:GLY:N	2.42	0.52
36:XE:12:LEU:HB3	36:XE:31:LEU:HB2	1.92	0.52
1:YA:2839:G:H5'	13:YR:46:GLY:HA2	1.91	0.52
1:YA:414:C:H2'	1:YA:415:A:H8	1.74	0.52
1:YA:746:A:O2'	1:YA:2611:U:O2'	2.23	0.52
3:YD:85:ASP:OD2	3:YD:88:ARG:HD2	2.09	0.52
32:QA:370:C:H2'	32:QA:371:G:H8	1.74	0.52
41:QJ:38:ILE:CG1	41:QJ:71:LEU:HB3	2.39	0.52
1:RA:2156:G:N7	1:RA:2157:G:N2	2.56	0.52
54:XY:241:ILE:HG12	54:XY:263:ILE:HG12	1.90	0.52
1:YA:185:U:H4'	1:YA:218:A:H4'	1.92	0.52
2:YB:29:A:H2'	2:YB:30:C:C6	2.44	0.52
32:QA:500:G:H2'	32:QA:501:C:C6	2.45	0.52
40:QI:33:PHE:HE1	40:QI:43:ALA:HB1	1.75	0.52
45:QN:4:LYS:O	45:QN:7:ILE:HG12	2.10	0.52
47:QP:43:LYS:HG2	47:QP:48:TRP:CE2	2.45	0.52
54:QY:130:LEU:HD12	54:QY:192:LEU:HD13	1.91	0.52
1:RA:1794:U:H2'	1:RA:1795:C:C6	2.45	0.52
1:RA:2591:C:H2'	1:RA:2592:G:C8	2.44	0.52
35:XD:70:ILE:HD11	35:XD:74:GLN:HB3	1.91	0.52
26:Y4:15:ILE:HD12	26:Y4:21:VAL:HG22	1.92	0.52
3:YD:108:PRO:HG2	3:YD:111:LEU:HB2	1.90	0.52
6:YG:56:ALA:CA	6:YG:153:ARG:HH21	2.06	0.52
6:YG:5:VAL:HG22	6:YG:8:LYS:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:YG:77:ILE:HG21	6:YG:80:PHE:CD2	2.44	0.52
9:YN:34:LEU:HD23	9:YN:107:LEU:HD11	1.91	0.52
14:YS:93:LYS:HD2	14:YS:95:HIS:HB2	1.90	0.52
21:YZ:125:LEU:HB3	21:YZ:165:VAL:HG13	1.89	0.52
32:QA:1412:C:H2'	32:QA:1413:A:C8	2.45	0.52
32:QA:939:G:H2'	32:QA:940:C:C6	2.44	0.52
32:QA:1073:U:OP1	36:QE:57:LYS:NZ	2.40	0.52
40:QI:65:VAL:HG21	40:QI:73:GLN:HB3	1.92	0.52
47:QP:74:LEU:O	47:QP:79:VAL:HG22	2.09	0.52
1:RA:2115:G:H21	1:RA:2171:A:H61	1.55	0.52
1:RA:302:C:H2'	1:RA:303:U:H6	1.73	0.52
3:RD:16:MET:HG3	3:RD:211:ARG:HH21	1.74	0.52
4:RE:2:LYS:HB2	4:RE:95:ILE:HD12	1.92	0.52
5:RF:157:VAL:HB	5:RF:194:MET:HG2	1.91	0.52
7:RH:98:LEU:HD13	7:RH:125:VAL:HG23	1.92	0.52
34:XC:8:ILE:HG23	34:XC:16:ARG:HG2	1.91	0.52
41:XJ:19:SER:O	41:XJ:23:ILE:HG12	2.10	0.52
1:YA:286:C:H2'	1:YA:287:C:C6	2.45	0.52
1:YA:2659:G:H4'	7:YH:175:LYS:HD3	1.92	0.52
32:QA:1025:U:O2	32:QA:1036:G:O6	2.28	0.52
32:QA:1241:G:H2'	32:QA:1242:C:C6	2.44	0.52
32:QA:838:G:H2'	32:QA:839:U:H2'	1.91	0.52
37:QF:82:ARG:HG2	37:QF:82:ARG:HH11	1.72	0.52
1:RA:1467:C:C5	1:RA:1546:C:H2'	2.43	0.52
32:XA:184:G:H2'	32:XA:185:A:H8	1.75	0.52
35:XD:150:GLU:HA	35:XD:153:ARG:HE	1.75	0.52
37:XF:100:ASN:HD21	49:XR:23:LYS:HE2	1.73	0.52
50:XS:41:VAL:HG22	50:XS:42:PRO:HD2	1.91	0.52
1:YA:1404:C:H2'	1:YA:1405:U:H6	1.74	0.52
1:YA:2206:G:H8	1:YA:2207:G:N7	2.07	0.52
1:YA:2243:U:H2'	1:YA:2244:U:C6	2.45	0.52
7:YH:90:LYS:HD2	7:YH:163:TYR:CD1	2.45	0.52
1:YA:272(P):C:H5"	8:YI:45:LYS:HD2	1.91	0.52
32:XA:1062:U:H2'	32:XA:1063:C:C6	2.45	0.52
32:XA:113:G:H2'	32:XA:114:U:H6	1.74	0.52
32:XA:269:C:H2'	32:XA:270:A:C8	2.45	0.52
45:XN:4:LYS:HG3	45:XN:7:ILE:HD11	1.92	0.52
54:XY:217:PHE:HD1	54:XY:217:PHE:N	2.08	0.52
1:YA:1079:C:N4	1:YA:1080:C:C2	2.78	0.52
1:YA:1711:C:H2'	1:YA:1712:C:C6	2.44	0.52
32:QA:34:C:H2'	32:QA:35:G:H8	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:924:C:H2'	32:QA:925:G:C8	2.45	0.52
38:QG:113:GLU:HG2	38:QG:119:ARG:HG2	1.90	0.52
44:QM:61:GLU:OE1	26:R4:49:PHE:CE2	2.62	0.52
1:RA:2304:G:H22	1:RA:2312:U:H3	1.56	0.52
1:RA:2646:C:OP2	1:RA:2732:G:O2'	2.21	0.52
32:XA:674:G:H2'	32:XA:675:A:C8	2.45	0.52
32:XA:881:G:P	43:XL:12:ARG:HH22	2.32	0.52
36:XE:57:LYS:HG2	36:XE:61:TYR:CE2	2.44	0.52
38:XG:10:ARG:HH11	38:XG:10:ARG:HG3	1.74	0.52
54:XY:141:ALA:HA	54:XY:144:TRP:HB3	1.92	0.52
54:XY:251:GLY:O	54:XY:254:VAL:HG12	2.09	0.52
1:YA:27:G:N2	1:YA:512:G:H1'	2.25	0.52
1:YA:1187:G:H5'	17:YV:81:TYR:CE1	2.45	0.52
32:QA:341:C:H2'	32:QA:342:C:H6	1.74	0.52
32:QA:973:G:H3'	32:QA:974:A:H5''	1.92	0.52
36:QE:92:LYS:HB3	36:QE:119:LEU:HB2	1.91	0.52
50:QS:22:LEU:HD22	50:QS:28:LYS:HA	1.90	0.52
1:RA:1079:C:N4	1:RA:1080:C:C2	2.78	0.52
1:RA:2206:G:H5''	1:RA:2207:G:N7	2.24	0.52
8:RI:77:LEU:CD1	8:RI:101:LEU:HG	2.40	0.52
11:RP:125:VAL:HG22	11:RP:138:LEU:HD21	1.92	0.52
33:XB:40:HIS:HB3	33:XB:190:THR:HG21	1.91	0.52
49:XR:56:THR:CB	49:XR:58:LEU:HD23	2.39	0.52
54:XY:212:ARG:HB2	54:XY:214:HIS:CD2	2.45	0.52
25:Y3:8:LEU:HD12	25:Y3:31:LEU:CA	2.37	0.52
1:YA:579:G:O2'	1:YA:2019:A:OP1	2.25	0.52
3:YD:182:LEU:HB2	3:YD:272:ALA:HB3	1.92	0.52
32:QA:1034:G:H3'	32:QA:1035:A:C8	2.45	0.51
32:QA:25:C:H2'	32:QA:26:A:C8	2.45	0.51
54:QY:200:ARG:HB2	54:QY:322:GLN:HG2	1.91	0.51
19:RX:5:TYR:CD1	24:R2:33:MET:HE2	2.45	0.51
1:RA:1475:G:H2'	1:RA:1476:C:C6	2.46	0.51
1:RA:1709:U:H2'	1:RA:1710:C:C6	2.44	0.51
1:RA:1864:U:OP1	1:RA:2410:G:O2'	2.20	0.51
1:RA:249:C:OP2	1:RA:2394:C:O2'	2.27	0.51
1:RA:862:G:H2'	1:RA:863:A:O4'	2.10	0.51
53:XV:3:C:H2'	53:XV:4:G:H5'	1.91	0.51
54:XY:314:LYS:HG3	54:XY:315:SER:H	1.75	0.51
22:Y0:8:GLY:N	53:XV:2:G:H4'	2.24	0.51
1:YA:1250:G:N7	11:YP:18:ARG:NH2	2.57	0.51
1:YA:2171:A:H4'	1:YA:2172:U:OP1	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:958:U:OP2	12:YQ:14:ARG:NH1	2.42	0.51
1:YA:2635:C:O2'	4:YE:80:GLU:OE1	2.21	0.51
5:YF:33:LEU:CD1	5:YF:112:MET:HE2	2.40	0.51
5:YF:39:TRP:CZ2	5:YF:106:ARG:CZ	2.93	0.51
6:YG:56:ALA:HB2	6:YG:153:ARG:CZ	2.39	0.51
14:YS:14:VAL:O	14:YS:18:ILE:HG12	2.10	0.51
17:YV:15:GLU:O	17:YV:18:LEU:HB2	2.09	0.51
19:YX:57:LEU:HD12	19:YX:78:LYS:CG	2.39	0.51
32:QA:1072:G:H2'	32:QA:1073:U:C6	2.45	0.51
32:QA:324:G:N1	32:QA:327:A:OP2	2.42	0.51
32:QA:769:G:H4'	32:QA:1513:A:H4'	1.92	0.51
1:RA:1028:A:N3	1:RA:2486:G:O2'	2.35	0.51
1:RA:2334:G:H5'	14:RS:9:ARG:HG2	1.91	0.51
9:RN:103:VAL:HG11	9:RN:120:LEU:CD1	2.40	0.51
32:XA:443:C:H2'	32:XA:444:C:C6	2.44	0.51
46:XO:26:GLU:OE1	46:XO:77:ARG:HD2	2.10	0.51
54:XY:134:ALA:O	54:XY:317:ILE:HG21	2.09	0.51
54:XY:324:ARG:HD2	54:XY:326:TYR:CE1	2.45	0.51
1:YA:2025:C:H2'	1:YA:2026:C:C6	2.45	0.51
1:YA:207:A:H2'	1:YA:208:C:O4'	2.10	0.51
1:YA:2138:C:H2'	1:YA:2139:C:C6	2.44	0.51
1:YA:2711:A:H5''	1:YA:2712(A):U:H5''	1.91	0.51
1:YA:784:A:C6	3:YD:229:VAL:HG11	2.45	0.51
5:YF:110:LEU:HD11	5:YF:202:PHE:CE1	2.45	0.51
20:YY:38:ILE:HD11	20:YY:66:PRO:HG3	1.91	0.51
20:YY:87:LYS:HB3	20:YY:95:LYS:HD3	1.91	0.51
21:YZ:152:ALA:O	21:YZ:155:LEU:HB2	2.10	0.51
33:QB:115:LEU:HD13	33:QB:145:LEU:HB3	1.90	0.51
40:QI:16:ARG:HH11	40:QI:64:THR:HG21	1.75	0.51
53:QV:50:U:H3	53:QV:64:G:H1	1.58	0.51
32:QA:1492:A:H2'	54:QY:319:TRP:NE1	2.22	0.51
27:R5:45:VAL:HG11	27:R5:58:LEU:HD12	1.92	0.51
1:RA:900:A:H2'	1:RA:901:A:O4'	2.10	0.51
32:XA:692:U:O2'	32:XA:694:A:N7	2.37	0.51
33:XB:222:ILE:HG13	33:XB:223:ILE:N	2.26	0.51
37:XF:24:GLU:HG3	37:XF:28:ARG:HD3	1.92	0.51
1:YA:1047:G:H2'	1:YA:1110:G:H22	1.76	0.51
1:YA:277:C:O2'	1:YA:278:A:OP1	2.27	0.51
1:YA:616:G:H5'	5:YF:205:ARG:HD2	1.92	0.51
5:YF:34:TRP:CZ3	11:YP:8:PRO:HB3	2.46	0.51
7:YH:164:TYR:HB2	7:YH:167:GLU:HB2	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:YP:106:LEU:HD13	11:YP:107:LYS:O	2.10	0.51
21:YZ:198:LYS:NZ	53:XV:53:G:O5'	2.43	0.51
21:YZ:23:LYS:NZ	21:YZ:40:ASP:OD2	2.44	0.51
38:QG:50:ILE:HD11	38:QG:58:PRO:HA	1.93	0.51
54:QY:265:HIS:CD2	54:QY:267:PRO:HD2	2.45	0.51
29:R7:9:ARG:NH2	29:R7:47:ARG:CB	2.73	0.51
1:RA:1378:A:OP1	29:R7:10:ARG:NH2	2.43	0.51
1:RA:1430:C:H2'	1:RA:1431:U:C6	2.45	0.51
1:RA:273(C):G:H2'	1:RA:273(D):G:H8	1.75	0.51
1:RA:286:C:H2'	1:RA:287:C:C6	2.45	0.51
3:RD:257:LEU:C	3:RD:257:LEU:HD13	2.31	0.51
32:XA:34:C:H2'	32:XA:35:G:H8	1.76	0.51
32:XA:474:G:H2'	32:XA:475:G:C8	2.45	0.51
32:XA:828:A:H2'	32:XA:829:G:O4'	2.09	0.51
25:Y3:6:VAL:CG1	25:Y3:54:VAL:HG21	2.41	0.51
3:YD:242:ARG:HD3	3:YD:242:ARG:N	2.25	0.51
6:YG:67:LYS:HE3	6:YG:68:PRO:O	2.10	0.51
11:YP:91:PHE:O	11:YP:121:LYS:NZ	2.39	0.51
35:QD:108:LEU:HB3	35:QD:110:PHE:CE1	2.45	0.51
51:QT:10:LEU:HD22	51:QT:12:ALA:H	1.75	0.51
1:RA:2122:U:H2'	1:RA:2123:G:C8	2.46	0.51
1:RA:2266:A:H4'	1:RA:2267:A:N3	2.26	0.51
1:RA:589:C:H2'	1:RA:590:A:C8	2.44	0.51
4:RE:78:LEU:O	4:RE:79:ARG:NH1	2.38	0.51
1:RA:587:C:P	11:RP:21:ARG:HH22	2.33	0.51
12:RQ:32:TYR:OH	12:RQ:111:GLU:OE1	2.21	0.51
14:RS:27:SER:HA	14:RS:88:ASP:HB3	1.91	0.51
19:RX:60:ARG:HH12	29:R7:47:ARG:HH22	1.59	0.51
32:XA:1047:G:OP1	45:XN:4:LYS:NZ	2.43	0.51
32:XA:977:A:N6	32:XA:1224:G:OP1	2.35	0.51
32:XA:1458:G:H5''	51:XT:31:SER:HB2	1.93	0.51
32:XA:737:A:H2'	32:XA:738:C:C6	2.45	0.51
1:YA:1057:A:N7	1:YA:1086:A:H2'	2.26	0.51
1:YA:1789:A:H2'	1:YA:1790:C:O4'	2.11	0.51
1:YA:675:A:N3	1:YA:2443:C:O2'	2.39	0.51
4:YE:116:VAL:CG2	4:YE:122:PHE:CD2	2.93	0.51
1:RA:1113:U:H2'	1:RA:1114:G:H8	1.76	0.51
1:RA:2641:G:H2'	1:RA:2642:G:H8	1.76	0.51
1:RA:536:A:H2'	1:RA:537:C:C6	2.46	0.51
1:RA:581:C:H2'	1:RA:582:G:H8	1.74	0.51
5:RF:170:LEU:HD23	5:RF:172:TRP:CZ2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:RO:10:VAL:HG22	10:RO:16:ALA:O	2.10	0.51
1:RA:1029:A:OP1	12:RQ:128:LYS:NZ	2.43	0.51
17:RV:40:LEU:HD12	17:RV:46:VAL:HG11	1.91	0.51
32:XA:411:A:OP1	35:XD:30:LYS:NZ	2.38	0.51
33:XB:119:GLU:OE2	33:XB:153:ARG:NH1	2.42	0.51
33:XB:16:HIS:CD2	33:XB:210:SER:HB3	2.46	0.51
44:XM:3:ARG:HG3	44:XM:8:GLU:HG3	1.91	0.51
1:YA:1430:C:H2'	1:YA:1431:U:H6	1.75	0.51
19:YX:31:HIS:CE1	19:YX:33:LYS:HB2	2.46	0.51
32:QA:1071:C:H2'	32:QA:1072:G:H8	1.75	0.51
32:QA:1077:G:N2	32:QA:1080:A:OP2	2.40	0.51
32:QA:1187:G:H4'	40:QI:111:ARG:HH11	1.76	0.51
32:QA:1375:A:H4'	38:QG:29:LYS:HE2	1.92	0.51
32:QA:160:A:H2'	32:QA:161:A:O4'	2.10	0.51
27:R5:16:ARG:NH1	27:R5:17:ASP:OD1	2.44	0.51
1:RA:140:G:N2	1:RA:142(A):A:C6	2.79	0.51
32:XA:1118:C:P	40:XI:104:ARG:HH11	2.33	0.51
32:XA:407:G:H2'	32:XA:408:A:H8	1.74	0.51
34:XC:70:VAL:HG22	34:XC:72:LYS:H	1.76	0.51
1:YA:1184:G:OP1	25:Y3:30:ARG:HD2	2.09	0.51
1:YA:272(P):C:O2'	8:YI:42:SER:OG	2.26	0.51
6:YG:97:ASP:HA	6:YG:100:TRP:HD1	1.75	0.51
6:YG:11:TYR:HA	6:YG:15:VAL:HB	1.91	0.51
8:YI:101:LEU:HD11	8:YI:140:LEU:HD11	1.92	0.51
15:YT:60:THR:HG22	15:YT:77:PRO:HA	1.92	0.51
16:YU:108:GLU:O	16:YU:112:ARG:HG2	2.11	0.51
32:QA:1323:G:H2'	32:QA:1324:A:C8	2.46	0.51
32:QA:624:C:H2'	32:QA:625:G:H8	1.76	0.51
32:QA:1117:G:O3'	40:QI:104:ARG:NH1	2.43	0.51
50:QS:64:GLU:HG3	26:R4:59:PHE:CD1	2.46	0.51
1:RA:1131:G:HO2'	1:RA:1132:A:H8	1.59	0.51
1:RA:1444:G:H2'	1:RA:1445(B):C:C5	2.45	0.51
2:RB:84:C:OP1	25:R3:15:TYR:OH	2.23	0.51
5:RF:33:LEU:HD13	5:RF:112:MET:HE3	1.91	0.51
32:XA:404:U:C5'	35:XD:122:ARG:HD3	2.41	0.51
54:XY:138:GLY:O	54:XY:141:ALA:N	2.44	0.51
54:XY:238:ASP:HB2	54:XY:267:PRO:HD3	1.93	0.51
32:QA:765:G:N1	32:QA:812:C:O2'	2.42	0.51
33:QB:163:PHE:CD2	33:QB:185:ILE:HD11	2.46	0.51
39:QH:51:VAL:HG21	39:QH:60:ARG:HH11	1.76	0.51
47:QP:20:VAL:HG21	47:QP:32:TYR:CD2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:376:G:H5''	47:QP:5:ARG:CD	2.40	0.51
47:QP:79:VAL:HG23	47:QP:80:PHE:CD1	2.46	0.51
1:RA:1514:U:H2'	1:RA:1515:G:H8	1.76	0.51
1:RA:184:C:H2'	1:RA:185:U:C6	2.46	0.51
1:RA:306:U:H2'	1:RA:307:G:O4'	2.11	0.51
1:RA:321:G:O2'	1:RA:340:A:N3	2.41	0.51
21:RZ:92:SER:O	21:RZ:130:PRO:HG2	2.11	0.51
32:XA:1187:G:OP1	40:XI:113:LYS:NZ	2.43	0.51
32:XA:69:G:H8	32:XA:69:G:OP2	1.93	0.51
49:XR:33:ASP:OD2	49:XR:36:ASN:HB2	2.10	0.51
1:YA:1794:U:H2'	1:YA:1795:C:H6	1.76	0.51
21:YZ:40:ASP:HB3	21:YZ:43:GLU:HB2	1.92	0.51
35:QD:201:GLN:HE22	36:QE:99:GLY:HA2	1.76	0.51
39:QH:10:LEU:HD22	39:QH:83:ILE:HD11	1.93	0.51
50:QS:64:GLU:HA	26:R4:59:PHE:CE1	2.46	0.51
1:RA:1053:C:H2'	1:RA:1054:A:H8	1.75	0.51
1:RA:1942:5MC:O2'	54:QY:290:GLN:NE2	2.44	0.51
32:XA:1309:G:OP1	44:XM:88:ARG:HD2	2.11	0.51
33:XB:42:ILE:HD13	33:XB:203:GLY:HA2	1.93	0.51
33:XB:55:PHE:CE1	33:XB:218:ALA:HA	2.46	0.51
32:XA:538:G:H5''	43:XL:114:LYS:HB2	1.93	0.51
51:XT:100:ILE:HG22	51:XT:101:GLY:N	2.25	0.51
1:YA:1478:G:O2'	1:YA:1558:A:N7	2.43	0.51
1:YA:1525:G:H2'	1:YA:1526:G:C8	2.45	0.51
1:YA:2134:A:H8	1:YA:2156:G:H21	1.57	0.51
6:YG:68:PRO:HB2	6:YG:90:LEU:HB3	1.93	0.51
1:YA:997:G:OP1	16:YU:92:ARG:HG2	2.11	0.51
21:YZ:150:LEU:HB3	21:YZ:171:ILE:HD11	1.93	0.51
32:QA:1036:G:H5''	32:QA:1037:C:C5	2.46	0.50
32:QA:678:U:H2'	32:QA:679:C:C6	2.46	0.50
39:QH:6:ILE:O	39:QH:10:LEU:HG	2.10	0.50
46:QO:74:ASP:OD2	46:QO:77:ARG:HG3	2.11	0.50
54:QY:121:GLY:O	54:QY:123:TYR:N	2.44	0.50
54:QY:215:THR:HG22	54:QY:217:PHE:HE1	1.76	0.50
23:R1:51:VAL:HG11	23:R1:74:VAL:HG21	1.93	0.50
27:R5:47:PRO:O	27:R5:60:VAL:HG23	2.09	0.50
1:RA:307:G:N1	1:RA:310:A:OP2	2.35	0.50
1:RA:586:A:N1	1:RA:809:G:O2'	2.37	0.50
4:RE:116:VAL:CG2	4:RE:122:PHE:CD2	2.93	0.50
9:RN:15:LEU:HD12	9:RN:137:LYS:HG2	1.92	0.50
15:RT:28:VAL:HG13	15:RT:86:ILE:HG23	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:919:A:O2'	32:XA:1080:A:N1	2.38	0.50
32:XA:1343:G:H4'	40:XI:122:ALA:HB3	1.93	0.50
1:YA:2612:C:OP2	27:Y5:2:ALA:N	2.44	0.50
1:YA:2687:U:H2'	1:YA:2688:U:O4'	2.12	0.50
9:YN:62:VAL:CG1	9:YN:66:LYS:HB2	2.41	0.50
32:QA:115:G:H4'	32:QA:116:A:O5'	2.11	0.50
32:QA:1218:C:H2'	32:QA:1219:U:C6	2.47	0.50
32:QA:179:A:H2'	32:QA:180:U:H6	1.75	0.50
40:QI:108:VAL:CG1	40:QI:109:VAL:H	2.21	0.50
41:QJ:30:SER:OG	41:QJ:81:THR:HG22	2.11	0.50
6:RG:62:LEU:HD13	26:R4:28:LYS:NZ	2.25	0.50
26:R4:7:PRO:HB2	26:R4:27:THR:HG21	1.94	0.50
1:RA:2206:G:H8	1:RA:2207:G:N7	2.09	0.50
1:RA:817:C:O2'	1:RA:839:U:H5''	2.11	0.50
7:RH:7:LEU:O	7:RH:69:ARG:NH1	2.43	0.50
12:RQ:109:VAL:HG13	12:RQ:113:GLN:CB	2.41	0.50
32:XA:113:G:H2'	32:XA:114:U:C6	2.46	0.50
32:XA:973:G:H3'	32:XA:974:A:H5''	1.93	0.50
33:XB:95:GLN:HG3	33:XB:147:LYS:O	2.11	0.50
33:XB:53:ARG:HH22	33:XB:199:TYR:HE1	1.59	0.50
39:XH:19:VAL:HG23	39:XH:21:LYS:HD3	1.91	0.50
26:Y4:13:ARG:NH2	26:Y4:21:VAL:HG11	2.25	0.50
1:YA:2099:U:H2'	1:YA:2100:G:C8	2.45	0.50
6:YG:18:GLU:O	6:YG:21:ARG:HG3	2.12	0.50
12:YQ:32:TYR:OH	12:YQ:111:GLU:OE1	2.23	0.50
37:QF:97:PHE:O	49:QR:31:LEU:N	2.33	0.50
39:QH:86:ILE:HG13	39:QH:133:LEU:HD22	1.92	0.50
50:QS:3:ARG:NH1	50:QS:10:PHE:HB2	2.25	0.50
53:QV:53:G:H1'	53:QV:54:U:H5'	1.93	0.50
1:RA:1354:A:H3'	1:RA:1355:G:H8	1.77	0.50
1:RA:813:U:H2'	1:RA:814:C:H6	1.77	0.50
6:RG:7:LEU:HD13	6:RG:100:TRP:CZ3	2.43	0.50
23:Y1:77:ALA:O	23:Y1:80:LEU:HB2	2.12	0.50
25:Y3:29:ARG:HB2	25:Y3:30:ARG:HD3	1.91	0.50
30:Y8:46:ARG:HB2	30:Y8:46:ARG:HH21	1.76	0.50
1:YA:2647:U:H2'	1:YA:2648:C:H6	1.76	0.50
2:YB:22:U:H2'	2:YB:23:G:C8	2.46	0.50
4:YE:11:MET:CG	4:YE:24:THR:HG22	2.39	0.50
32:QA:1256:A:H5'	34:QC:27:LYS:HE2	1.92	0.50
32:QA:646:U:H2'	32:QA:647:C:C6	2.47	0.50
39:QH:23:SER:HA	39:QH:63:LEU:HD22	1.91	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R8:31:HIS:CE1	30:R8:32:LEU:CD2	2.94	0.50
1:RA:1798:U:H5'	3:RD:259:THR:CG2	2.41	0.50
1:RA:2138:C:H2'	1:RA:2139:C:H6	1.76	0.50
1:RA:2398:U:H2'	1:RA:2399:G:H8	1.76	0.50
1:RA:30:G:H2'	1:RA:31:C:C6	2.47	0.50
38:XG:149:ARG:HG2	42:XK:59:TYR:CE1	2.47	0.50
1:YA:192:C:O2'	1:YA:802:A:N3	2.41	0.50
3:YD:275:LYS:HG3	3:YD:276:LYS:HA	1.94	0.50
32:QA:69:G:H2'	32:QA:70:G:H8	1.77	0.50
32:QA:836:G:OP1	49:QR:61:LYS:NZ	2.31	0.50
33:QB:15:VAL:CG2	33:QB:209:ARG:CG	2.76	0.50
33:QB:16:HIS:CG	33:QB:17:PHE:N	2.78	0.50
35:QD:8:VAL:CG2	35:QD:21:LEU:HD13	2.42	0.50
39:QH:12:ARG:HD2	39:QH:26:VAL:HG12	1.92	0.50
51:QT:10:LEU:CD2	51:QT:11:SER:N	2.70	0.50
22:R0:59:LEU:HD23	22:R0:79:VAL:HB	1.94	0.50
1:RA:1113:U:H2'	1:RA:1114:G:C8	2.46	0.50
1:RA:1588:C:H2'	1:RA:1589:C:C6	2.46	0.50
1:RA:1786:A:H1'	1:RA:1938:A:N6	2.26	0.50
1:RA:2321:G:O2'	1:RA:2322:A:OP1	2.22	0.50
1:RA:956:G:H5''	12:RQ:77:LYS:HD2	1.92	0.50
39:XH:63:LEU:HD23	39:XH:65:TYR:OH	2.11	0.50
1:YA:1406:U:H2'	1:YA:1407:C:C6	2.46	0.50
1:YA:2361:A:P	30:Y8:26:LYS:NZ	2.84	0.50
1:YA:876:C:H2'	1:YA:877:U:O4'	2.12	0.50
32:QA:1442(A):G:N3	32:QA:1442(A):G:H2'	2.27	0.50
32:QA:539:A:OP2	43:QL:115:LYS:NZ	2.44	0.50
32:QA:918:A:H2'	32:QA:919:A:C8	2.46	0.50
32:QA:978:A:OP2	32:QA:1363(A):C:N4	2.41	0.50
36:QE:79:GLU:HG3	36:QE:93:PRO:HD2	1.93	0.50
26:R4:57:GLU:HB2	26:R4:58:ARG:HA	1.94	0.50
1:RA:1629:U:H2'	1:RA:1630:G:C8	2.47	0.50
1:RA:2128:C:H5'	1:RA:2129:C:OP2	2.12	0.50
1:RA:2171:A:H4'	1:RA:2172:U:OP1	2.12	0.50
1:RA:2853:C:H2'	1:RA:2854:G:C8	2.47	0.50
1:RA:581:C:H2'	1:RA:582:G:C8	2.46	0.50
1:RA:858:U:O2	1:RA:2268:A:H2'	2.12	0.50
6:RG:66:GLN:HB3	6:RG:92:VAL:HG21	1.93	0.50
19:RX:57:LEU:HD12	19:RX:78:LYS:CG	2.41	0.50
32:XA:1426:C:H2'	32:XA:1427:U:C6	2.46	0.50
32:XA:382:A:H2'	32:XA:383:A:H8	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:XJ:16:LEU:HD13	41:XJ:70:ARG:HG2	1.94	0.50
54:XY:202:VAL:HG22	54:XY:215:THR:HG23	1.94	0.50
7:YH:89:ILE:O	7:YH:129:THR:HG23	2.11	0.50
10:YO:10:VAL:HG22	10:YO:16:ALA:O	2.12	0.50
32:QA:258:G:H2'	32:QA:259:G:H8	1.76	0.50
33:QB:54:THR:HG21	33:QB:201:ILE:HD11	1.93	0.50
44:QM:57:ARG:O	44:QM:61:GLU:HG3	2.11	0.50
44:QM:63:THR:O	26:R4:50:VAL:HG23	2.11	0.50
32:QA:1316:G:H5''	45:QN:17:LYS:NZ	2.27	0.50
54:QY:41:LEU:HA	54:QY:46:VAL:HG21	1.94	0.50
1:RA:1278:A:H2'	1:RA:1279:G:C8	2.47	0.50
1:RA:1824:G:O3'	3:RD:249:PRO:HD3	2.11	0.50
1:RA:302:C:H2'	1:RA:303:U:C6	2.46	0.50
1:RA:635:C:H2'	1:RA:636:G:O4'	2.12	0.50
4:RE:111:ARG:HG3	4:RE:160:TYR:CD2	2.46	0.50
5:RF:20:LEU:HD13	5:RF:21:ALA:H	1.75	0.50
5:RF:33:LEU:CD1	5:RF:112:MET:HE2	2.42	0.50
34:XC:116:VAL:HG21	34:XC:202:ILE:HD11	1.93	0.50
37:XF:97:PHE:HB2	49:XR:32:ARG:HD3	1.94	0.50
50:XS:20:LEU:HD23	50:XS:23:ASN:ND2	2.22	0.50
1:YA:1068:G:H3'	1:YA:1096:A:OP2	2.12	0.50
1:YA:2127:G:H2'	1:YA:2128:C:O4'	2.11	0.50
1:YA:690:G:H2'	1:YA:691:C:C6	2.47	0.50
4:YE:14:ILE:HG13	4:YE:21:VAL:HG13	1.92	0.50
8:YI:27:ARG:HD3	23:Y1:71:TYR:CE1	2.46	0.50
32:QA:1410:G:H2'	32:QA:1411:C:H6	1.77	0.50
32:QA:881:G:OP2	43:QL:12:ARG:NH2	2.44	0.50
1:RA:1165:U:H2'	1:RA:1166:C:H6	1.76	0.50
1:RA:1166:C:H2'	1:RA:1167:U:C6	2.47	0.50
1:RA:2111:C:H42	1:RA:2147:G:H22	1.59	0.50
1:RA:2291:U:H2'	1:RA:2292:C:H6	1.76	0.50
32:XA:1148:U:O2'	40:XI:66:ARG:NH1	2.40	0.50
32:XA:1159:U:O4'	32:XA:1182:G:N2	2.45	0.50
33:XB:124:SER:HB2	33:XB:125:PRO:HD3	1.94	0.50
34:XC:111:LEU:HD22	34:XC:146:ALA:HB2	1.93	0.50
36:XE:6:PHE:HB2	36:XE:34:VAL:HG13	1.93	0.50
40:XI:8:GLY:HA2	40:XI:79:LEU:HD23	1.92	0.50
50:XS:30:LEU:HD11	50:XS:50:ALA:HB2	1.92	0.50
54:XY:324:ARG:HG3	54:XY:335:ASP:HA	1.93	0.50
1:YA:1453:U:O2'	1:YA:1455:G:N7	2.40	0.50
1:YA:1657:C:H2'	1:YA:1658:C:H6	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1266:G:O2'	1:YA:2012:G:O6	2.23	0.50
7:YH:54:ARG:HD3	7:YH:65:HIS:ND1	2.27	0.50
32:QA:560:U:HO2'	32:QA:561:U:P	2.31	0.50
32:QA:920:U:H2'	32:QA:921:U:C6	2.47	0.50
33:QB:115:LEU:HD12	33:QB:142:LEU:HD12	1.93	0.50
33:QB:8:LYS:HZ3	33:QB:52:GLU:HA	1.77	0.50
32:QA:1492:A:C4'	43:QL:47:LYS:NZ	2.75	0.50
23:R1:64:ALA:HA	23:R1:67:ILE:HG13	1.94	0.50
5:RF:13:SER:OG	5:RF:127:GLU:OE2	2.29	0.50
8:RI:68:LEU:O	8:RI:68:LEU:HD13	2.11	0.50
17:RV:52:VAL:CG2	17:RV:55:ALA:HB3	2.42	0.50
32:XA:1030(C):C:H41	32:XA:1030(D):G:H21	1.60	0.50
32:XA:1218:C:H2'	32:XA:1219:U:C6	2.46	0.50
32:XA:580:U:H2'	32:XA:581:G:O4'	2.12	0.50
32:XA:678:U:H2'	32:XA:679:C:H6	1.77	0.50
41:XJ:51:ARG:O	45:XN:45:ARG:NH1	2.45	0.50
44:XM:20:THR:CG2	44:XM:27:LYS:HZ3	2.25	0.50
32:XA:273:A:H1'	48:XQ:16:GLN:NE2	2.26	0.50
1:YA:2086:U:H2'	1:YA:2087:G:C8	2.46	0.50
1:YA:2109:U:H2'	1:YA:2110:G:C8	2.47	0.50
1:YA:302:C:H2'	1:YA:303:U:C6	2.47	0.50
8:YI:114:LEU:HD12	8:YI:116:LEU:HB2	1.93	0.50
18:YW:23:LEU:O	18:YW:27:LYS:NZ	2.45	0.50
32:QA:1352:C:H2'	32:QA:1353:G:C8	2.46	0.49
32:QA:35:G:H2'	32:QA:36:C:C6	2.47	0.49
35:QD:194:LEU:HD12	35:QD:195:ALA:N	2.25	0.49
51:QT:57:ARG:NH2	51:QT:100:ILE:HD12	2.27	0.49
1:RA:1797:C:O3'	3:RD:259:THR:HG22	2.12	0.49
1:RA:2022:U:O2'	1:RA:2617:C:H5'	2.12	0.49
1:RA:2164:C:H3'	1:RA:2165:G:H8	1.76	0.49
1:RA:2629:A:H1'	1:RA:2630:G:H5"	1.94	0.49
4:RE:21:VAL:HG23	4:RE:185:LYS:HD2	1.94	0.49
32:XA:328:C:H4'	32:XA:329:A:H5'	1.94	0.49
36:XE:92:LYS:HB3	36:XE:119:LEU:HB2	1.93	0.49
6:YG:146:TYR:HE2	44:XM:8:GLU:CB	2.23	0.49
54:XY:132:ILE:HD11	54:XY:152:TYR:HD2	1.76	0.49
26:Y4:48:ARG:HG3	26:Y4:52:THR:HG23	1.94	0.49
1:YA:1073:A:O2'	1:YA:1074:G:O5'	2.29	0.49
1:YA:2206:G:H3'	1:YA:2207:G:C8	2.47	0.49
32:QA:328:C:H4'	32:QA:329:A:H5'	1.94	0.49
33:QB:231:GLU:HB3	33:QB:232:PRO:HD3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:QC:36:ASP:OD1	34:QC:57:ILE:HG21	2.12	0.49
38:QG:70:LYS:O	38:QG:138:LYS:HE2	2.12	0.49
39:QH:14:ARG:O	39:QH:18:ARG:CG	2.58	0.49
40:QI:121:ARG:NH1	40:QI:122:ALA:O	2.46	0.49
41:QJ:8:LEU:HB2	41:QJ:70:ARG:HB2	1.93	0.49
46:QO:39:LEU:HD13	46:QO:56:LEU:HB2	1.94	0.49
1:RA:1068:G:H3'	1:RA:1096:A:OP2	2.12	0.49
1:RA:662:G:H5''	11:RP:16:ARG:HG3	1.93	0.49
17:RV:40:LEU:HB2	17:RV:46:VAL:CG1	2.43	0.49
32:XA:1002:G:N3	32:XA:1003:G:C8	2.79	0.49
32:XA:22:G:H4'	32:XA:885:G:C8	2.47	0.49
54:XY:335:ASP:O	54:XY:337:ARG:N	2.45	0.49
54:XY:334:LYS:NZ	54:XY:341:GLU:OE2	2.42	0.49
1:YA:1639:U:H2'	1:YA:1640:C:H5''	1.94	0.49
6:YG:146:TYR:CD2	44:XM:8:GLU:OE1	2.65	0.49
6:YG:5:VAL:CG2	6:YG:8:LYS:HB3	2.43	0.49
32:QA:692:U:O2'	32:QA:694:A:N7	2.33	0.49
34:QC:59:ARG:N	41:QJ:92:THR:CG2	2.74	0.49
46:QO:18:PHE:HB2	46:QO:19:PRO:HD2	1.94	0.49
49:QR:65:ILE:O	49:QR:69:THR:HG23	2.12	0.49
30:R8:23:VAL:HG13	30:R8:47:LYS:HB3	1.93	0.49
1:RA:2696:U:H2'	1:RA:2697:G:C8	2.47	0.49
1:RA:75:G:H22	1:RA:111:A:H2	1.60	0.49
1:RA:78:A:H2'	1:RA:79:G:H8	1.78	0.49
1:RA:922:U:H2'	1:RA:923:C:C6	2.47	0.49
8:RI:81:VAL:O	8:RI:146:ALA:HA	2.11	0.49
32:XA:1131:G:H2'	32:XA:1132:C:C6	2.47	0.49
35:XD:162:LEU:HD13	35:XD:181:MET:HG2	1.94	0.49
40:XI:21:PRO:HA	40:XI:59:PHE:HA	1.93	0.49
40:XI:22:GLY:HA3	40:XI:60:ASP:OD1	2.13	0.49
51:XT:42:GLN:O	51:XT:45:GLN:HB3	2.12	0.49
1:YA:2137:C:H2'	1:YA:2138:C:C6	2.46	0.49
1:YA:2591:C:H2'	1:YA:2592:G:C8	2.47	0.49
1:YA:528:A:OP2	9:YN:114:ARG:NH1	2.44	0.49
4:YE:51:PHE:O	4:YE:77:ILE:N	2.42	0.49
15:YT:117:ASP:OD2	15:YT:120:ARG:NE	2.39	0.49
18:YW:12:ILE:HD13	18:YW:17:VAL:HG13	1.94	0.49
20:YY:37:VAL:HG21	20:YY:72:VAL:HG21	1.94	0.49
32:QA:1003:G:C2'	32:QA:1004:A:H4'	2.43	0.49
32:QA:1239:A:O2'	38:QG:114:ARG:O	2.27	0.49
1:RA:2238:G:H2'	1:RA:2238:G:N3	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:RG:126:ASP:HB3	6:RG:128:ARG:H	1.77	0.49
32:XA:1426:C:H2'	32:XA:1427:U:H6	1.77	0.49
32:XA:17:U:H2'	32:XA:18:C:H6	1.75	0.49
33:XB:122:PHE:CE2	33:XB:127:ILE:CD1	2.95	0.49
41:XJ:25:GLU:O	41:XJ:29:ARG:HG2	2.11	0.49
45:YN:27:CYS:SG	45:YN:29:ARG:HB2	2.52	0.49
54:XY:141:ALA:O	54:XY:145:ALA:N	2.40	0.49
54:XY:150:ARG:HG3	54:XY:154:ARG:HH12	1.77	0.49
1:YA:1798:U:OP2	3:YD:274:ARG:NH2	2.45	0.49
1:YA:2266:A:H4'	1:YA:2267:A:N3	2.27	0.49
1:YA:2693:A:H2'	1:YA:2694:G:C8	2.47	0.49
1:YA:862:G:H2'	1:YA:863:A:O4'	2.11	0.49
7:YH:87:LEU:HD23	7:YH:164:TYR:HA	1.95	0.49
7:YH:55:PRO:HG2	7:YH:61:HIS:CE1	2.48	0.49
1:YA:300:A:OP1	20:YY:86:ARG:NH2	2.46	0.49
32:QA:1020:U:H2'	32:QA:1021:G:C8	2.47	0.49
32:QA:1060:C:H2'	32:QA:1061:G:H8	1.77	0.49
32:QA:1172:C:H2'	32:QA:1173:G:H8	1.78	0.49
35:QD:81:GLU:O	35:QD:85:LYS:HB2	2.11	0.49
39:QH:36:LEU:HD12	39:QH:59:LEU:HD13	1.92	0.49
41:QJ:38:ILE:O	41:QJ:38:ILE:HG13	2.11	0.49
1:RA:2119:A:H61	1:RA:2168:G:H21	1.61	0.49
1:RA:861:A:N3	2:RB:79:C:O2'	2.39	0.49
3:RD:126:GLN:O	3:RD:193:VAL:HG22	2.13	0.49
17:RV:28:GLU:O	17:RV:61:VAL:HG11	2.12	0.49
19:RX:5:TYR:CG	24:R2:30:ARG:HA	2.48	0.49
32:XA:1427:U:H2'	32:XA:1428:A:C8	2.48	0.49
32:XA:35:G:H2'	32:XA:36:C:C6	2.47	0.49
54:XY:166:ILE:HD11	54:XY:182:LYS:HE3	1.94	0.49
1:YA:1057:A:O2'	1:YA:1058:G:OP1	2.30	0.49
1:YA:601:C:O2'	1:YA:605:C:OP1	2.31	0.49
3:YD:72:LYS:HG3	3:YD:103:ARG:HH22	1.77	0.49
18:YW:86:LEU:HD22	18:YW:96:ILE:HD11	1.94	0.49
32:QA:868:C:H2'	32:QA:869:G:O4'	2.13	0.49
32:QA:9:G:H2'	32:QA:10:A:H8	1.78	0.49
40:QI:43:ALA:O	40:QI:45:ALA:N	2.45	0.49
50:QS:65:ASN:O	26:R4:58:ARG:HD2	2.13	0.49
1:RA:1085:A:H2'	1:RA:1086:A:C2	2.46	0.49
4:RE:119:ARG:HG2	4:RE:120:TRP:CE2	2.47	0.49
32:XA:246:A:C2	32:XA:282:A:C5	3.00	0.49
34:XC:152:ILE:CG2	34:XC:167:TRP:HB2	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:XC:174:PRO:HD2	34:XC:182:ILE:HD11	1.94	0.49
40:XI:8:GLY:HA3	40:XI:76:ALA:O	2.13	0.49
1:YA:2119:A:H61	1:YA:2168:G:H21	1.58	0.49
1:YA:2773:C:OP1	4:YE:164:ARG:NE	2.38	0.49
1:YA:2853:C:H2'	1:YA:2854:G:C8	2.46	0.49
1:YA:303:U:H2'	1:YA:304:G:H8	1.77	0.49
1:YA:863:A:H2'	1:YA:864:G:H8	1.77	0.49
9:YN:131:GLN:CD	9:YN:131:GLN:H	2.15	0.49
19:YX:41:ASN:O	19:YX:45:THR:HG23	2.13	0.49
21:YZ:198:LYS:HZ1	53:XV:52:G:C2'	2.26	0.49
32:QA:21:G:H2'	32:QA:22:G:C8	2.48	0.49
32:QA:34:C:H2'	32:QA:35:G:C8	2.47	0.49
32:QA:714:G:H2'	32:QA:715:A:C8	2.47	0.49
37:QF:76:ALA:O	37:QF:80:ARG:HG3	2.12	0.49
46:QO:25:THR:HG21	46:QO:70:LEU:HB2	1.94	0.49
1:RA:1614:A:C2	18:RW:93:ALA:HB2	2.47	0.49
3:RD:77:ALA:HB2	3:RD:97:TYR:CD2	2.48	0.49
10:RO:10:VAL:HG21	10:RO:16:ALA:HB3	1.95	0.49
17:RV:28:GLU:O	17:RV:61:VAL:CG1	2.61	0.49
32:XA:1346:A:N1	32:XA:1374:A:H5''	2.28	0.49
32:XA:8:A:H5'	36:XE:101:ILE:HG22	1.93	0.49
33:XB:189:ASP:OD1	33:XB:189:ASP:N	2.43	0.49
36:XE:60:TYR:CZ	36:XE:64:ARG:HD3	2.48	0.49
38:XG:65:ALA:HB1	38:XG:127:ALA:HB3	1.94	0.49
42:XK:20:TYR:CE1	42:XK:83:ILE:HD12	2.48	0.49
47:XP:18:ARG:NH1	47:XP:32:TYR:OH	2.45	0.49
54:XY:264:THR:HG22	54:XY:271:VAL:HG12	1.94	0.49
27:Y5:16:ARG:NH1	27:Y5:16:ARG:HG2	2.27	0.49
1:YA:212:G:H2'	1:YA:213:A:O4'	2.13	0.49
5:YF:167:ALA:O	5:YF:170:LEU:HD23	2.13	0.49
8:YI:116:LEU:CD2	8:YI:118:LYS:O	2.61	0.49
32:QA:1244:C:H2'	32:QA:1245:A:C8	2.48	0.49
32:QA:1278:U:H5'	32:QA:1279:A:O4'	2.13	0.49
39:QH:81:HIS:N	39:QH:138:TRP:O	2.45	0.49
33:QB:178:ARG:HH22	39:QH:68:ARG:HH12	1.61	0.49
32:QA:1343:G:H4'	40:QI:122:ALA:HB3	1.95	0.49
40:QI:16:ARG:H	40:QI:64:THR:HG22	1.77	0.49
44:QM:65:LYS:HG2	26:R4:50:VAL:CG1	2.39	0.49
30:R8:31:HIS:CG	30:R8:32:LEU:HD22	2.47	0.49
1:RA:601:C:O2'	1:RA:605:C:OP1	2.29	0.49
8:RI:77:LEU:HD12	8:RI:101:LEU:HG	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1918:A:O2'	1:YA:1920:4OC:N4	2.45	0.49
1:YA:1827:C:O2'	1:YA:1970:A:N3	2.36	0.49
1:YA:2820:A:O2'	1:YA:2821:A:OP1	2.29	0.49
6:YG:46:ALA:HB2	6:YG:53:LEU:CD1	2.43	0.49
12:YQ:21:THR:HG22	12:YQ:23:GLY:O	2.13	0.49
32:QA:235:C:H5'	48:QQ:70:ARG:HG2	1.95	0.49
1:RA:1829:A:H3'	1:RA:1830:C:H6	1.77	0.49
1:RA:1853:A:H2'	1:RA:1854:A:C8	2.48	0.49
1:RA:212:G:H2'	1:RA:213:A:O4'	2.13	0.49
1:RA:2555:U:O2	54:QY:245:ARG:NH1	2.41	0.49
1:RA:881:G:H2'	1:RA:882:G:H8	1.76	0.49
4:RE:150:VAL:CG1	4:RE:154:LYS:HG3	2.43	0.49
38:XG:26:PHE:O	38:XG:30:ILE:HG13	2.12	0.49
31:Y9:2:LYS:HE2	31:Y9:31:LYS:O	2.12	0.49
1:YA:1210:A:H5''	1:YA:1212:G:O4'	2.13	0.49
1:YA:1467:C:C5	1:YA:1546:C:H2'	2.47	0.49
1:YA:2115:G:N1	1:YA:2117:A:N7	2.61	0.49
1:YA:272(E):U:H2'	1:YA:272(F):C:C6	2.48	0.49
4:YE:12:THR:CG2	4:YE:13:ARG:H	2.11	0.49
32:QA:524:G:H2'	32:QA:525:C:C6	2.48	0.49
34:QC:130:VAL:HG21	34:QC:157:ILE:HG23	1.95	0.49
45:QN:32:SER:HB3	45:QN:41:ARG:HG2	1.94	0.49
50:QS:27:GLU:CB	50:QS:28:LYS:CE	2.90	0.49
1:RA:108:U:H2'	1:RA:109:G:C8	2.48	0.49
1:RA:1656:C:H2'	1:RA:1657:C:H6	1.78	0.49
1:RA:2075:U:OP2	1:RA:2238:G:O2'	2.30	0.49
1:RA:2547:U:H2'	1:RA:2548:G:H8	1.77	0.49
1:RA:372:G:O2'	1:RA:400:G:O6	2.29	0.49
5:RF:136:THR:HG22	5:RF:140:LEU:CD2	2.43	0.49
7:RH:90:LYS:HD3	7:RH:159:GLU:HG2	1.95	0.49
12:RQ:14:ARG:HG2	12:RQ:41:TRP:HH2	1.78	0.49
21:RZ:155:LEU:HD11	21:RZ:171:ILE:HD13	1.94	0.49
32:XA:441:A:H3'	32:XA:442:C:H6	1.78	0.49
32:XA:715:A:H2'	32:XA:716:A:C8	2.48	0.49
34:XC:164:ARG:HG2	34:XC:165:THR:H	1.77	0.49
40:XI:31:GLN:HG3	40:XI:36:TYR:HB2	1.95	0.49
37:XF:91:VAL:HG11	49:XR:72:ARG:NH1	2.27	0.49
54:XY:217:PHE:N	54:XY:217:PHE:CD1	2.81	0.49
1:YA:2079:U:OP1	23:Y1:21:ARG:NH2	2.46	0.49
26:Y4:15:ILE:HB	26:Y4:32:TYR:CD1	2.48	0.49
1:YA:1475:G:H2'	1:YA:1476:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1791:A:H8	1:YA:1791:A:OP2	1.96	0.49
1:YA:2138:C:H2'	1:YA:2139:C:H6	1.77	0.49
1:YA:950:G:H2'	1:YA:951:C:C6	2.48	0.49
2:YB:75:G:H21	21:YZ:85:HIS:CE1	2.31	0.49
3:YD:127:VAL:HA	3:YD:193:VAL:HG23	1.94	0.49
21:YZ:10:ARG:HH21	21:YZ:26:GLY:H	1.60	0.49
44:QM:63:THR:C	26:R4:50:VAL:HG23	2.34	0.48
1:RA:121:G:H4'	1:RA:149:A:H5'	1.93	0.48
1:RA:2489:G:N2	1:RA:2491:U:O4	2.43	0.48
1:RA:2502:G:H5''	1:RA:2503:2MA:H5''	1.95	0.48
1:RA:721:C:H2'	1:RA:722:A:H8	1.78	0.48
32:XA:256:U:H2'	32:XA:257:G:C8	2.48	0.48
32:XA:382:A:H2'	32:XA:383:A:C8	2.48	0.48
43:XL:77:LEU:HD21	43:XL:107:ALA:HA	1.95	0.48
54:XY:168:GLU:HG2	54:XY:179:VAL:HG12	1.95	0.48
54:XY:291:MET:HE3	54:XY:295:LEU:HG	1.95	0.48
26:Y4:59:PHE:CA	26:Y4:61:ARG:H	2.20	0.48
1:YA:1866:C:H2'	1:YA:1876:A:O4'	2.13	0.48
6:YG:11:TYR:OH	6:YG:33:ARG:HG3	2.13	0.48
1:YA:1005:C:O2'	9:YN:28:THR:HG21	2.13	0.48
20:YY:20:TYR:CE1	20:YY:43:ASN:HA	2.48	0.48
32:QA:736:C:H2'	32:QA:737:A:C8	2.48	0.48
34:QC:8:ILE:HG23	34:QC:16:ARG:HG2	1.95	0.48
40:QI:25:LYS:HE2	40:QI:25:LYS:CA	2.35	0.48
1:RA:152:G:H2'	1:RA:153:C:H6	1.78	0.48
1:RA:2849:U:O4	15:RT:23:ARG:NH2	2.46	0.48
1:RA:729:G:O2'	1:RA:763:G:H4'	2.14	0.48
8:RI:140:LEU:HD12	8:RI:142:VAL:HG23	1.86	0.48
32:XA:1422:G:H2'	32:XA:1423:G:C8	2.46	0.48
32:XA:1438:G:H2'	32:XA:1439:C:H6	1.78	0.48
32:XA:601:C:H2'	32:XA:602:A:C8	2.48	0.48
41:XJ:32:ALA:HB1	41:XJ:33:GLN:CD	2.34	0.48
54:XY:265:HIS:CD2	54:XY:267:PRO:HD2	2.48	0.48
1:YA:2328:A:H2'	1:YA:2329:G:H8	1.74	0.48
1:YA:708:C:H2'	1:YA:709:U:C6	2.49	0.48
32:QA:166:G:H2'	32:QA:167:G:C8	2.47	0.48
32:QA:559:A:H4'	32:QA:560:U:H5''	1.96	0.48
34:QC:15:THR:HG21	34:QC:181:ASN:HA	1.95	0.48
1:RA:1057:A:O2'	1:RA:1058:G:OP1	2.31	0.48
1:RA:2816:C:O2	1:RA:2883:A:O2'	2.30	0.48
8:RI:109:ILE:CG1	8:RI:130:TYR:CZ	2.91	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:1952:A:N3	10:RO:22:ILE:HD12	2.27	0.48
32:XA:115:G:H4'	32:XA:116:A:O5'	2.12	0.48
33:XB:8:LYS:HG2	33:XB:9:GLU:N	2.25	0.48
30:Y8:63:PRO:HG2	30:Y8:64:TYR:CE2	2.48	0.48
1:YA:1000:A:H2'	1:YA:1001:A:C8	2.48	0.48
1:YA:2164:C:H3'	1:YA:2165:G:H8	1.78	0.48
1:YA:1805:U:O2	3:YD:50:THR:HB	2.13	0.48
6:YG:115:ARG:HG2	6:YG:136:ARG:HH21	1.77	0.48
10:YO:16:ALA:HB2	10:YO:52:VAL:HG21	1.95	0.48
20:YY:56:PRO:O	20:YY:57:GLN:HB2	2.14	0.48
21:YZ:110:GLY:HA3	21:YZ:174:VAL:HG11	1.95	0.48
1:RA:2130:U:H2'	1:RA:2158:A:H61	1.78	0.48
2:RB:14:U:O3'	2:RB:108:U:O2'	2.31	0.48
1:RA:1812:A:O2'	3:RD:45:ASN:N	2.46	0.48
11:RP:97:PRO:HD3	11:RP:126:VAL:O	2.13	0.48
19:RX:11:PRO:HB3	19:RX:92:LEU:HD11	1.95	0.48
32:XA:1025:U:H3	32:XA:1036:G:H1	1.60	0.48
32:XA:1120:G:H2'	32:XA:1121:U:C6	2.49	0.48
32:XA:1179:A:H2'	32:XA:1180:A:O4'	2.12	0.48
32:XA:939:G:H2'	32:XA:940:C:C6	2.49	0.48
49:XR:56:THR:O	49:XR:58:LEU:HD22	2.13	0.48
1:YA:854:G:H2'	1:YA:855:G:C8	2.46	0.48
4:YE:150:VAL:HG13	4:YE:154:LYS:HG3	1.95	0.48
5:YF:110:LEU:HA	5:YF:183:VAL:HG12	1.95	0.48
32:QA:1314:C:H2'	32:QA:1315:U:C6	2.49	0.48
32:QA:142:G:O2'	32:QA:196:A:N1	2.47	0.48
32:QA:966:M2G:HM13	32:QA:967:5MC:H1'	1.95	0.48
1:RA:1866:C:H2'	1:RA:1876:A:O4'	2.14	0.48
1:RA:2153:G:H2'	1:RA:2154:G:C8	2.48	0.48
1:RA:2168:G:O2'	1:RA:2170:A:N7	2.38	0.48
5:RF:9:ILE:HG21	5:RF:125:LEU:CD2	2.44	0.48
7:RH:40:GLU:OE1	7:RH:60:ARG:NH1	2.47	0.48
11:RP:94:GLU:HG3	11:RP:124:LYS:HD3	1.96	0.48
19:RX:5:TYR:CZ	24:R2:30:ARG:HG3	2.48	0.48
20:RY:13:VAL:HB	20:RY:72:VAL:HG13	1.95	0.48
32:XA:978:A:OP1	32:XA:1361:G:N2	2.39	0.48
34:XC:164:ARG:HG2	34:XC:165:THR:N	2.29	0.48
38:XG:70:LYS:O	38:XG:138:LYS:HE2	2.14	0.48
1:YA:2747:G:O6	1:YA:2755:C:H5''	2.12	0.48
1:YA:753:C:O5'	1:YA:753:C:H6	1.96	0.48
1:YA:956:G:H5''	12:YQ:77:LYS:HD2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YE:18:ASP:HB3	15:YT:82:LEU:HD21	1.96	0.48
5:YF:34:TRP:CH2	11:YP:8:PRO:HB3	2.48	0.48
7:YH:9:ILE:HG12	7:YH:69:ARG:NE	2.28	0.48
32:QA:1240:U:C2	38:QG:32:ARG:HD3	2.49	0.48
32:QA:1277:C:O2'	32:QA:1279:A:H1'	2.13	0.48
32:QA:437:U:H5'	35:QD:155:LEU:HD21	1.94	0.48
32:QA:679:C:H2'	32:QA:680:C:H6	1.78	0.48
33:QB:215:LEU:O	33:QB:219:VAL:HG23	2.14	0.48
33:QB:82:ARG:HG3	33:QB:92:TYR:CZ	2.49	0.48
35:QD:173:TRP:CE3	35:QD:174:LEU:HG	2.49	0.48
1:RA:679:C:H2'	1:RA:680:G:H8	1.78	0.48
1:RA:864:G:H2'	1:RA:865:C:C6	2.47	0.48
3:RD:2:ALA:N	3:RD:200:ASP:OD2	2.46	0.48
4:RE:101:ARG:CZ	4:RE:171:GLU:HB2	2.43	0.48
6:RG:133:LEU:HD11	6:RG:157:ILE:HD12	1.95	0.48
33:XB:71:VAL:HG12	33:XB:93:VAL:CG2	2.43	0.48
35:XD:114:ARG:HA	35:XD:117:ALA:HB3	1.96	0.48
42:XK:84:VAL:HG11	42:XK:91:ARG:HD2	1.94	0.48
44:XM:81:LEU:HD13	44:XM:88:ARG:HG2	1.95	0.48
52:XU:5:ASP:O	52:XU:11:GLY:HA3	2.14	0.48
54:XY:129:TYR:HB2	54:XY:223:TYR:CE1	2.48	0.48
54:XY:132:ILE:HD11	54:XY:152:TYR:CD2	2.48	0.48
1:YA:2233:U:H2'	1:YA:2234:G:C8	2.49	0.48
5:YF:120:GLU:HB2	5:YF:122:LYS:HG2	1.95	0.48
7:YH:115:VAL:HG11	7:YH:148:ILE:HD11	1.95	0.48
8:YI:40:THR:C	8:YI:44:LEU:HD22	2.23	0.48
13:YR:18:LEU:HD13	13:YR:18:LEU:C	2.34	0.48
32:QA:1245:A:H2'	32:QA:1246:C:C6	2.49	0.48
39:QH:41:ARG:NH2	39:QH:123:GLU:OE2	2.44	0.48
41:QJ:40:LEU:HB2	41:QJ:69:ASN:HB2	1.96	0.48
1:RA:1055:G:H2'	1:RA:1056:G:O4'	2.13	0.48
1:RA:1263:U:C4	1:RA:1264:G:C6	3.02	0.48
1:RA:1739:U:HO2'	1:RA:1740:G:H8	1.61	0.48
1:RA:1802:A:H2'	1:RA:1803:A:C8	2.49	0.48
1:RA:534:U:H2'	1:RA:535:C:C6	2.48	0.48
1:RA:595:C:H2'	1:RA:596:G:C8	2.47	0.48
10:RO:64:ARG:HB2	10:RO:83:ALA:HB3	1.95	0.48
1:RA:489:G:N7	18:RW:49:LYS:NZ	2.62	0.48
19:RX:44:GLU:HG3	19:RX:51:VAL:HG23	1.96	0.48
32:XA:1027:C:H3'	32:XA:1028:C:H6	1.78	0.48
32:XA:1072:G:H2'	32:XA:1073:U:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:255:G:H2'	32:XA:256:U:C6	2.49	0.48
32:XA:501:C:H1'	32:XA:549:C:H1'	1.96	0.48
36:XE:78:HIS:HE1	36:XE:80:ILE:HD13	1.79	0.48
32:XA:738:C:OP1	37:XF:2:ARG:NH1	2.45	0.48
44:XM:17:VAL:HA	44:XM:27:LYS:NZ	2.29	0.48
1:YA:1525:G:H2'	1:YA:1526:G:H8	1.79	0.48
1:YA:270:A:OP2	1:YA:272(X):G:N1	2.37	0.48
1:YA:30:G:H2'	1:YA:31:C:C6	2.48	0.48
8:YI:27:ARG:CD	23:Y1:71:TYR:CE1	2.96	0.48
18:YW:9:TYR:HA	18:YW:100:THR:CG2	2.44	0.48
32:QA:1377:A:HO2'	38:QG:2:ALA:N	2.12	0.48
32:QA:553:A:H5"	43:QL:24:VAL:HG21	1.96	0.48
32:QA:452:A:H4'	47:QP:72:ARG:NH1	2.28	0.48
1:RA:2573:C:N4	54:QY:256:ARG:HA	2.29	0.48
1:RA:590:A:H2'	1:RA:591:C:C6	2.49	0.48
3:RD:108:PRO:CD	3:RD:111:LEU:CD1	2.81	0.48
10:RO:10:VAL:HG21	10:RO:16:ALA:O	2.13	0.48
17:RV:72:VAL:CG1	17:RV:85:LYS:HB3	2.37	0.48
21:RZ:70:LEU:HG	21:RZ:91:LEU:HD21	1.95	0.48
32:XA:71:C:H2'	32:XA:72:C:C6	2.48	0.48
32:XA:935:A:C2	38:XG:3:ARG:NH2	2.82	0.48
34:XC:114:PRO:HA	34:XC:185:GLY:HA3	1.95	0.48
35:XD:108:LEU:HD13	35:XD:174:LEU:HD13	1.95	0.48
44:XM:74:VAL:O	44:XM:78:ILE:HG13	2.13	0.48
50:XS:23:ASN:HA	50:XS:27:GLU:OE2	2.14	0.48
54:XY:189:TYR:CE2	54:XY:193:ARG:HD3	2.49	0.48
1:YA:2070:G:H2'	1:YA:2071:A:C8	2.49	0.48
1:YA:2115:G:N2	1:YA:2171:A:H61	2.12	0.48
2:YB:96:U:H2'	2:YB:97:G:C8	2.48	0.48
17:YV:40:LEU:HB2	17:YV:46:VAL:CG1	2.43	0.48
32:QA:1119:C:H2'	32:QA:1120:G:H8	1.78	0.48
32:QA:1256:A:OP2	34:QC:26:LYS:NZ	2.44	0.48
33:QB:185:ILE:HG22	33:QB:199:TYR:CD2	2.48	0.48
1:RA:251:A:C5	1:RA:252:G:H1'	2.49	0.48
6:RG:73:ALA:HB1	6:RG:82:LEU:HD11	1.94	0.48
21:RZ:5:LEU:HD11	21:RZ:39:VAL:HG11	1.96	0.48
21:RZ:4:ARG:NE	21:RZ:60:GLU:OE1	2.36	0.48
32:XA:1342:C:H2'	32:XA:1343:G:H8	1.79	0.48
32:XA:181:G:N2	32:XA:182:U:O4	2.43	0.48
32:XA:184:G:H2'	32:XA:185:A:C8	2.49	0.48
32:XA:64:G:H4'	32:XA:65:U:H3'	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:743:U:H2'	32:XA:744:C:C6	2.49	0.48
33:XB:71:VAL:HG23	33:XB:164:VAL:HA	1.95	0.48
34:XC:36:ASP:O	34:XC:40:ARG:HG3	2.14	0.48
40:XI:26:VAL:HA	40:XI:61:ALA:O	2.13	0.48
44:XM:20:THR:HG21	44:XM:27:LYS:HZ3	1.79	0.48
1:YA:1802:A:H2'	1:YA:1803:A:C8	2.49	0.48
1:YA:2364:C:H2'	1:YA:2365:G:O4'	2.14	0.48
4:YE:181:LEU:HD23	15:YT:10:VAL:CG2	2.43	0.48
32:QA:9:G:H2'	32:QA:10:A:C8	2.49	0.48
33:QB:134:GLU:HG3	33:QB:137:ARG:NH2	2.28	0.48
1:RA:1075:C:H2'	1:RA:1076:C:H3'	1.95	0.48
1:RA:1514:U:H2'	1:RA:1515:G:C8	2.49	0.48
1:RA:2650:U:H2'	1:RA:2651:C:H6	1.79	0.48
1:RA:2740:A:H2'	1:RA:2741:A:C8	2.49	0.48
32:XA:512:U:H2'	32:XA:513:C:C6	2.49	0.48
32:XA:669:U:H2'	32:XA:670:G:C8	2.48	0.48
44:XM:34:LEU:HD13	44:XM:41:PRO:HA	1.96	0.48
26:Y4:61:ARG:HG2	50:XS:42:PRO:HG3	1.95	0.48
54:XY:215:THR:HG22	54:XY:217:PHE:CE1	2.49	0.48
1:YA:1364:G:P	23:Y1:3:LYS:HG3	2.53	0.48
1:YA:2106:G:C4	1:YA:2107:C:H1'	2.49	0.48
1:YA:37:C:H2'	1:YA:38:A:H8	1.78	0.48
1:YA:39:C:H2'	1:YA:40:C:C6	2.49	0.48
1:YA:588:U:H1'	5:YF:90:PHE:HB3	1.95	0.48
1:YA:674:G:H1'	5:YF:74:ARG:HD3	1.96	0.48
7:YH:105:LEU:HD21	7:YH:162:ILE:HD11	1.96	0.48
21:YZ:140:ASP:OD1	21:YZ:142:SER:OG	2.32	0.48
35:QD:156:GLU:O	35:QD:160:GLN:HG2	2.14	0.47
53:QV:7:G:O2'	53:QV:49:G:H5'	2.13	0.47
54:QY:37:VAL:HG13	54:QY:56:LEU:HB3	1.96	0.47
1:RA:1164:G:H2'	1:RA:1165:U:C6	2.49	0.47
1:RA:1791:A:H8	1:RA:1791:A:OP2	1.96	0.47
1:RA:2206:G:H3'	1:RA:2207:G:C8	2.49	0.47
1:RA:690:G:H2'	1:RA:691:C:C6	2.48	0.47
5:RF:132:VAL:HG11	5:RF:139:PHE:HA	1.95	0.47
14:RS:66:ALA:O	14:RS:69:VAL:HG22	2.14	0.47
15:RT:51:ARG:HG3	15:RT:98:LYS:HE3	1.95	0.47
32:XA:1010:G:H2'	32:XA:1011:G:H8	1.79	0.47
32:XA:1352:C:H2'	32:XA:1353:G:C8	2.48	0.47
32:XA:912:C:OP1	43:XL:46:LYS:NZ	2.45	0.47
1:YA:1068:G:N1	54:XY:58:LYS:HB2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1025:G:C4	1:YA:1135:C:H1'	2.49	0.47
1:YA:247:G:H4'	1:YA:386:G:C5	2.49	0.47
3:YD:72:LYS:HG3	3:YD:103:ARG:NH2	2.28	0.47
1:YA:1649:G:O2'	13:YR:107:ASP:OD2	2.27	0.47
32:QA:683:G:H2'	32:QA:684:A:C8	2.50	0.47
37:QF:91:VAL:HG12	37:QF:92:LYS:O	2.14	0.47
40:QI:16:ARG:CD	40:QI:64:THR:HG21	2.37	0.47
45:QN:4:LYS:HG3	45:QN:7:ILE:HD11	1.96	0.47
44:QM:64:TRP:HA	26:R4:50:VAL:CG2	2.40	0.47
1:RA:585:G:H2'	1:RA:1251:C:H42	1.78	0.47
1:RA:1899:G:N3	1:RA:1899:G:H2'	2.29	0.47
1:RA:1949:G:H2'	1:RA:1950:G:C8	2.49	0.47
1:RA:2735:G:H2'	1:RA:2736:G:H8	1.77	0.47
6:RG:77:ILE:HG21	6:RG:80:PHE:CD2	2.49	0.47
7:RH:86:GLU:OE2	7:RH:132:ARG:NH2	2.44	0.47
7:RH:9:ILE:HG12	7:RH:69:ARG:CD	2.45	0.47
15:RT:16:ARG:HD3	15:RT:18:ASP:OD1	2.14	0.47
32:XA:1004:A:N7	32:XA:1037:C:H2'	2.30	0.47
32:XA:338:A:H2'	32:XA:339:C:C6	2.49	0.47
23:Y1:4:VAL:HG12	23:Y1:11:ARG:HB3	1.96	0.47
1:YA:1657:C:H2'	1:YA:1658:C:C6	2.48	0.47
1:YA:2502:G:H5''	1:YA:2503:2MA:H5''	1.96	0.47
6:YG:106:LEU:HA	6:YG:110:ALA:HB3	1.96	0.47
6:YG:170:ARG:NH2	6:YG:182:LYS:O	2.47	0.47
14:YS:51:ALA:HB1	14:YS:69:VAL:HG23	1.96	0.47
17:YV:29:PRO:HA	17:YV:61:VAL:HG23	1.95	0.47
32:QA:266:G:H5''	32:QA:267:C:C5	2.49	0.47
33:QB:16:HIS:HB3	33:QB:210:SER:HB2	1.95	0.47
50:QS:12:ASP:O	50:QS:14:HIS:N	2.45	0.47
1:RA:2109:U:N3	1:RA:2110:G:O6	2.48	0.47
1:RA:2648:C:H2'	1:RA:2649:U:H6	1.79	0.47
6:RG:50:ALA:C	6:RG:52:ILE:N	2.67	0.47
12:RQ:35:VAL:CG1	12:RQ:130:LYS:HB3	2.44	0.47
19:RX:5:TYR:CE1	24:R2:30:ARG:HG3	2.50	0.47
32:XA:1010:G:H2'	32:XA:1011:G:C8	2.50	0.47
32:XA:1412:C:H2'	32:XA:1413:A:C8	2.49	0.47
41:XJ:38:ILE:O	41:XJ:38:ILE:HG13	2.13	0.47
54:XY:338:THR:CG2	54:XY:339:GLY:HA2	2.44	0.47
28:Y6:35:GLU:OE2	28:Y6:50:ARG:NH1	2.47	0.47
1:YA:1113:U:H2'	1:YA:1114:G:C8	2.50	0.47
1:YA:1412:A:H2'	1:YA:1413:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1683:C:H2'	1:YA:1684:C:C6	2.49	0.47
1:YA:2152:G:H2'	1:YA:2153:G:C8	2.48	0.47
1:YA:2870:C:H2'	1:YA:2871:C:O4'	2.14	0.47
1:YA:745:G:O6	1:YA:746:A:N6	2.47	0.47
1:YA:196:A:O4'	11:YP:46:LYS:HD2	2.14	0.47
15:YT:64:ARG:HB2	15:YT:73:GLU:HG2	1.96	0.47
1:YA:336:C:H5''	20:YY:6:HIS:ND1	2.29	0.47
32:QA:164:U:H2'	32:QA:165:C:C6	2.49	0.47
33:QB:200:ILE:HD12	33:QB:200:ILE:N	2.29	0.47
38:QG:113:GLU:HG3	38:QG:118:VAL:HG12	1.96	0.47
48:QQ:6:LEU:HG	48:QQ:23:VAL:HG11	1.97	0.47
51:QT:56:MET:CG	51:QT:84:LEU:HD22	2.44	0.47
54:QY:216:SER:C	54:QY:217:PHE:HD1	2.17	0.47
54:QY:217:PHE:N	54:QY:217:PHE:CD1	2.82	0.47
1:RA:250:G:P	30:R8:13:ARG:HH22	2.35	0.47
1:RA:2223:G:OP1	3:RD:172:TYR:OH	2.24	0.47
1:RA:247:G:H4'	1:RA:386:G:C5	2.49	0.47
1:RA:2647:U:H2'	1:RA:2648:C:C6	2.49	0.47
32:XA:222:U:H2'	32:XA:223:U:C6	2.49	0.47
32:XA:552:U:O3'	43:XL:87:GLY:HA2	2.14	0.47
32:XA:961:U:OP2	32:XA:1223:C:O2'	2.22	0.47
36:XE:148:VAL:HG21	39:XH:107:LEU:HD13	1.95	0.47
48:XQ:74:LEU:HD13	48:XQ:75:ARG:CG	2.43	0.47
1:YA:2543:G:H2'	1:YA:2544:G:C8	2.49	0.47
1:YA:2590:A:H2'	1:YA:2591:C:C6	2.50	0.47
1:YA:392:C:H5''	1:YA:409:C:H5''	1.96	0.47
1:YA:1799:G:O2'	3:YD:181:GLU:OE2	2.23	0.47
1:YA:2443:C:OP1	5:YF:68:LYS:HD3	2.13	0.47
7:YH:9:ILE:N	7:YH:50:VAL:O	2.30	0.47
8:YI:102:SER:OG	8:YI:103:ARG:N	2.46	0.47
32:QA:679:C:H2'	32:QA:680:C:C6	2.50	0.47
32:QA:404:U:H5'	35:QD:122:ARG:HD3	1.96	0.47
42:QK:20:TYR:CE1	42:QK:83:ILE:HD12	2.50	0.47
1:RA:1388:G:H2'	1:RA:1389:G:H8	1.79	0.47
1:RA:184:C:H2'	1:RA:185:U:H6	1.79	0.47
1:RA:2243:U:H2'	1:RA:2244:U:H6	1.80	0.47
1:RA:2567:G:H2'	1:RA:2568:C:C6	2.50	0.47
1:RA:721:C:H2'	1:RA:722:A:C8	2.50	0.47
4:RE:51:PHE:O	4:RE:75:VAL:HG13	2.15	0.47
32:XA:1118:C:H1'	32:XA:1179:A:C4	2.50	0.47
34:XC:150:LYS:HG3	34:XC:169:ALA:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:XC:6:HIS:NE2	34:XC:8:ILE:HB	2.29	0.47
40:XI:50:LEU:HD11	40:XI:81:ILE:HD11	1.96	0.47
1:YA:1029:A:OP1	12:YQ:128:LYS:NZ	2.45	0.47
1:YA:2065:C:H2'	1:YA:2066:C:C6	2.49	0.47
1:YA:855:G:H2'	1:YA:856:C:C6	2.50	0.47
1:YA:2314:C:H5'	6:YG:38:VAL:HG11	1.95	0.47
7:YH:88:LEU:HD22	7:YH:165:ALA:HA	1.96	0.47
5:YF:37:VAL:HG21	11:YP:6:LEU:HD11	1.97	0.47
21:YZ:146:ILE:HA	21:YZ:174:VAL:HG12	1.95	0.47
2:YB:77:U:OP1	21:YZ:19:ARG:NH2	2.47	0.47
32:QA:514:C:H2'	32:QA:515:G:C8	2.48	0.47
32:QA:985:C:H2'	32:QA:986:A:C8	2.50	0.47
39:QH:121:ASP:HB2	39:QH:125:ARG:NH2	2.30	0.47
41:QJ:52:GLY:O	45:QN:41:ARG:NH2	2.48	0.47
51:QT:14:LYS:HE3	51:QT:18:GLN:NE2	2.30	0.47
1:RA:610:G:H2'	1:RA:611:C:C6	2.50	0.47
1:RA:784:A:C6	3:RD:229:VAL:HG11	2.50	0.47
1:RA:823:G:H2'	1:RA:824:A:C8	2.48	0.47
1:RA:1805:U:O2	3:RD:50:THR:HB	2.14	0.47
32:XA:1060:C:OP1	45:XN:45:ARG:NH2	2.39	0.47
32:XA:1074:G:H2'	32:XA:1075:C:H6	1.80	0.47
32:XA:1342:C:H2'	32:XA:1343:G:C8	2.50	0.47
32:XA:765:G:N1	32:XA:812:C:O2'	2.43	0.47
36:XE:116:THR:HG23	36:XE:117:ASP:OD2	2.14	0.47
39:XH:14:ARG:O	39:XH:18:ARG:HD3	2.15	0.47
36:XE:143:ARG:NH1	39:XH:77:GLU:OE2	2.43	0.47
37:XF:97:PHE:HB2	49:XR:32:ARG:HH11	1.78	0.47
22:Y0:70:GLN:HE21	22:Y0:72:ARG:CG	2.28	0.47
1:YA:1411:C:H2'	1:YA:1412:A:C8	2.50	0.47
1:YA:251:A:C5	1:YA:252:G:H1'	2.50	0.47
1:YA:747:U:O2	1:YA:2014:A:H1'	2.14	0.47
17:YV:98:GLU:OE1	17:YV:100:ARG:NH1	2.48	0.47
18:YW:11:ARG:O	18:YW:11:ARG:CG	2.55	0.47
32:QA:1020:U:H2'	32:QA:1021:G:H8	1.79	0.47
32:QA:1263:C:H2'	32:QA:1264:C:C6	2.49	0.47
32:QA:134:A:H1'	32:QA:325:A:C5	2.50	0.47
32:QA:678:U:H2'	32:QA:679:C:H6	1.78	0.47
33:QB:185:ILE:HG22	33:QB:199:TYR:HD2	1.80	0.47
1:RA:1056:G:H5''	1:RA:1057:A:H5'	1.96	0.47
1:RA:2461:C:H2'	1:RA:2462:U:C6	2.49	0.47
1:RA:679:C:H2'	1:RA:680:G:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:680:G:H2'	1:RA:681:G:C8	2.50	0.47
32:XA:324:G:N1	32:XA:327:A:OP2	2.45	0.47
32:XA:518:C:C4	32:XA:530:G:C6	3.02	0.47
41:XJ:38:ILE:HG13	41:XJ:71:LEU:HB3	1.96	0.47
1:YA:1263:U:C4	1:YA:1264:G:C6	3.03	0.47
1:YA:2812:G:H2'	1:YA:2813:A:H8	1.80	0.47
1:YA:284:U:H2'	1:YA:285:C:H6	1.79	0.47
1:YA:680:G:H2'	1:YA:681:G:C8	2.49	0.47
1:YA:861:A:N3	2:YB:79:C:O2'	2.46	0.47
32:QA:113:G:H2'	32:QA:114:U:H6	1.80	0.47
32:QA:417:C:H2'	32:QA:418:C:H6	1.80	0.47
32:QA:757:U:H2'	32:QA:758:G:O4'	2.15	0.47
32:QA:948:C:H2'	32:QA:949:A:H8	1.79	0.47
33:QB:9:GLU:CD	33:QB:217:ARG:HH22	2.18	0.47
39:QH:23:SER:HA	39:QH:63:LEU:CD2	2.45	0.47
46:QO:29:VAL:HG11	46:QO:67:LEU:HD21	1.97	0.47
1:RA:108:U:H2'	1:RA:109:G:H8	1.79	0.47
1:RA:1278:A:H2'	1:RA:1279:G:H8	1.78	0.47
1:RA:1991:U:H2'	1:RA:1992:G:H5''	1.97	0.47
1:RA:2106:G:C4	1:RA:2107:C:H1'	2.50	0.47
1:RA:2320:A:N3	1:RA:2320:A:H2'	2.30	0.47
1:RA:2462:U:H2'	1:RA:2463:C:C6	2.49	0.47
1:RA:2648:C:H2'	1:RA:2649:U:C6	2.50	0.47
1:RA:272(E):U:H2'	1:RA:272(F):C:C6	2.50	0.47
1:RA:593:G:H2'	1:RA:594:U:C6	2.50	0.47
10:RO:2:ILE:HG21	10:RO:8:LEU:HD21	1.97	0.47
11:RP:112:LEU:HD11	11:RP:114:ILE:CD1	2.42	0.47
15:RT:54:ARG:HA	15:RT:59:THR:CG2	2.45	0.47
32:XA:340:U:H2'	32:XA:341:C:H6	1.80	0.47
32:XA:537:G:OP1	43:XL:113:ARG:NH2	2.42	0.47
39:XH:73:ASP:OD1	39:XH:75:ARG:HD3	2.15	0.47
40:XI:5:TYR:OH	40:XI:16:ARG:HG2	2.15	0.47
47:XP:43:LYS:HA	47:XP:48:TRP:HB3	1.96	0.47
54:XY:127:ASP:HB2	54:XY:225:GLU:OE1	2.15	0.47
1:YA:1166:C:H2'	1:YA:1167:U:C6	2.50	0.47
1:YA:1614:A:P	1:YA:1614:A:H8	2.37	0.47
1:YA:1794:U:H2'	1:YA:1795:C:C6	2.50	0.47
1:YA:1899:G:N3	1:YA:1899:G:H2'	2.30	0.47
32:QA:335:C:H2'	32:QA:336:C:C6	2.50	0.47
32:QA:509:A:N3	32:QA:543:C:O2'	2.40	0.47
35:QD:173:TRP:CG	35:QD:189:PRO:HG3	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:QD:6:GLY:O	35:QD:115:ARG:NH1	2.35	0.47
39:QH:44:PHE:HB3	39:QH:80:ILE:HD11	1.96	0.47
41:QJ:49:VAL:HG21	45:QN:41:ARG:O	2.15	0.47
54:QY:106:LEU:HD23	54:QY:109:LYS:HD2	1.97	0.47
54:QY:200:ARG:HD3	54:QY:322:GLN:NE2	2.30	0.47
1:RA:1000:A:H2'	1:RA:1001:A:C8	2.49	0.47
1:RA:1210:A:H5''	1:RA:1212:G:O4'	2.14	0.47
1:RA:1939:5MU:OP1	1:RA:2604:U:O2'	2.32	0.47
1:RA:2537:U:H2'	1:RA:2538:C:C6	2.50	0.47
1:RA:886:C:O2'	1:RA:889:C:N4	2.43	0.47
4:RE:73:GLU:CD	4:RE:73:GLU:H	2.18	0.47
8:RI:109:ILE:HD11	8:RI:130:TYR:CE2	2.50	0.47
8:RI:117:GLU:HG3	8:RI:118:LYS:N	2.30	0.47
20:RY:20:TYR:O	20:RY:23:ARG:HB2	2.15	0.47
32:XA:500:G:H2'	32:XA:501:C:C6	2.50	0.47
32:XA:677:U:H2'	32:XA:678:U:H6	1.80	0.47
35:XD:173:TRP:CD1	35:XD:189:PRO:HG3	2.49	0.47
51:XT:33:ILE:O	51:XT:37:SER:OG	2.19	0.47
54:XY:141:ALA:HB2	54:XY:216:SER:HB2	1.97	0.47
54:XY:129:TYR:CD2	54:XY:223:TYR:HE1	2.33	0.47
1:YA:2889:C:H3'	1:YA:2891:G:C8	2.49	0.47
1:YA:330:A:N7	1:YA:1210:A:O2'	2.35	0.47
1:YA:7:G:H2'	1:YA:8:A:C8	2.50	0.47
4:YE:9:VAL:HG22	4:YE:25:VAL:O	2.14	0.47
20:YY:13:VAL:HG12	20:YY:74:PRO:HA	1.97	0.47
32:QA:1074:G:O2'	32:QA:1101:A:N1	2.42	0.47
32:QA:953:G:H2'	32:QA:954:G:O4'	2.15	0.47
35:QD:88:VAL:HG13	36:QE:97:GLY:CA	2.42	0.47
40:QI:125:TYR:OH	40:QI:127:LYS:HD3	2.14	0.47
43:QL:70:ILE:HG12	43:QL:100:ILE:HD12	1.97	0.47
1:RA:1581:G:H2'	1:RA:1582:C:O4'	2.14	0.47
1:RA:1914:C:H41	54:QY:221:PHE:HB2	1.79	0.47
1:RA:321:G:H5'	5:RF:134:GLY:O	2.15	0.47
18:RW:4:LYS:HB2	18:RW:106:ILE:HG12	1.97	0.47
32:XA:1347:G:N2	32:XA:1373:G:H2'	2.30	0.47
32:XA:417:C:H2'	32:XA:418:C:H6	1.80	0.47
40:XI:31:GLN:NE2	40:XI:36:TYR:HD1	2.13	0.47
1:YA:125:G:N3	29:Y7:48:LYS:HE2	2.30	0.47
1:YA:1164:G:H2'	1:YA:1165:U:H6	1.78	0.47
1:YA:1720:U:H2'	1:YA:1721:G:O4'	2.15	0.47
1:YA:858:U:O2	1:YA:2268:A:H2'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:2688:U:OP1	1:YA:2713:A:N6	2.48	0.47
1:YA:536:A:H2'	1:YA:537:C:C6	2.50	0.47
1:YA:729:G:O2'	1:YA:763:G:H4'	2.15	0.47
3:YD:5:LYS:HB3	3:YD:5:LYS:HE3	1.66	0.47
6:YG:35:GLU:HG3	6:YG:36:LYS:CE	2.40	0.47
32:QA:1118:C:H1'	32:QA:1179:A:C4	2.49	0.47
32:QA:1329:A:P	44:QM:28:ALA:HB3	2.54	0.47
54:QY:161:PHE:CD1	54:QY:185:GLY:HA3	2.48	0.47
54:QY:30:LYS:HD2	54:QY:66:VAL:HG11	1.97	0.47
1:RA:2206:G:H3'	1:RA:2207:G:H8	1.80	0.47
1:RA:26:G:H1'	1:RA:515:A:H61	1.80	0.47
1:RA:273(C):G:H2'	1:RA:273(D):G:C8	2.49	0.47
32:XA:1258:G:H2'	32:XA:1259:C:C6	2.50	0.47
32:XA:1333:A:H2'	32:XA:1334:G:O4'	2.15	0.47
32:XA:1106:G:H5''	34:XC:172:ARG:HG2	1.96	0.47
51:XT:14:LYS:O	51:XT:18:GLN:HG3	2.15	0.47
1:YA:1952:A:OP1	10:YO:42:SER:OG	2.27	0.47
1:YA:2033:A:O2'	1:YA:2035:G:OP2	2.23	0.47
1:YA:2327:A:H2'	1:YA:2328:A:C8	2.50	0.47
13:YR:18:LEU:HD13	13:YR:18:LEU:O	2.15	0.47
32:QA:656:C:O2'	46:QO:28:GLN:OE1	2.19	0.46
53:QV:54:U:C4	53:QV:58:A:C8	3.03	0.46
30:R8:31:HIS:NE2	30:R8:32:LEU:CD2	2.78	0.46
1:RA:743:G:O2'	1:RA:1659:U:OP1	2.31	0.46
1:RA:2047:U:H2'	1:RA:2048:G:H8	1.80	0.46
1:RA:2695:C:H2'	1:RA:2696:U:C6	2.50	0.46
1:RA:286:C:H2'	1:RA:287:C:H6	1.80	0.46
1:RA:855:G:H2'	1:RA:856:C:C6	2.50	0.46
5:RF:170:LEU:CD2	5:RF:172:TRP:CZ2	2.99	0.46
32:XA:1241:G:H2'	32:XA:1242:C:C6	2.50	0.46
32:XA:824:C:H2'	32:XA:825:G:H8	1.80	0.46
34:XC:43:LEU:O	34:XC:47:LEU:HB2	2.14	0.46
44:XM:20:THR:HA	44:XM:25:ILE:O	2.15	0.46
54:XY:319:TRP:O	54:XY:321:SER:N	2.46	0.46
1:YA:2857:G:N2	1:YA:2860:A:OP2	2.43	0.46
3:YD:221:VAL:HG13	3:YD:226:MET:HE3	1.96	0.46
4:YE:114:ALA:HB3	4:YE:119:ARG:CG	2.45	0.46
6:YG:55:LYS:HA	6:YG:58:GLN:HB3	1.96	0.46
18:YW:4:LYS:HE2	18:YW:6:ILE:HD11	1.97	0.46
32:QA:932:C:H4'	38:QG:4:ARG:NH2	2.30	0.46
33:QB:200:ILE:HD12	33:QB:200:ILE:H	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:QB:15:VAL:CG2	33:QB:209:ARG:HB3	2.45	0.46
33:QB:18:GLY:HA3	33:QB:42:ILE:HG13	1.97	0.46
36:QE:102:ALA:HB1	36:QE:106:PRO:HG2	1.97	0.46
37:QF:100:ASN:HD22	49:QR:27:GLY:C	2.18	0.46
38:QG:79:ARG:HA	38:QG:84:ASN:HA	1.96	0.46
52:QU:5:ASP:O	52:QU:11:GLY:HA3	2.15	0.46
1:RA:2133:G:N2	1:RA:2157:G:H2'	2.31	0.46
1:RA:2233:U:H2'	1:RA:2234:G:C8	2.51	0.46
1:RA:747:U:O2	1:RA:2014:A:H1'	2.14	0.46
1:RA:888:C:H2'	1:RA:889:C:C2	2.49	0.46
11:RP:99:LEU:HD23	11:RP:102:ARG:HH21	1.80	0.46
14:RS:84:GLN:HA	14:RS:111:GLU:HB2	1.96	0.46
32:XA:1057:G:H2'	32:XA:1058:G:O4'	2.14	0.46
32:XA:531:U:OP1	54:XY:213:ARG:NH2	2.48	0.46
32:XA:582:U:H2'	32:XA:583:A:C8	2.51	0.46
32:XA:71:C:H2'	32:XA:72:C:H6	1.80	0.46
33:XB:134:GLU:O	33:XB:138:LEU:HG	2.15	0.46
40:XI:26:VAL:HG13	40:XI:61:ALA:HB3	1.96	0.46
42:XK:20:TYR:CZ	42:XK:83:ILE:HD12	2.49	0.46
49:XR:59:SER:OG	49:XR:62:GLU:HG2	2.15	0.46
1:YA:152:G:H2'	1:YA:153:C:C6	2.50	0.46
1:YA:2347:C:OP1	28:Y6:38:LYS:NZ	2.33	0.46
1:YA:2712(A):U:H2'	1:YA:2714:G:H5''	1.97	0.46
1:YA:37:C:H2'	1:YA:38:A:C8	2.50	0.46
7:YH:41:MET:HE2	7:YH:64:LEU:CB	2.42	0.46
14:YS:25:ARG:HD3	14:YS:42:ASP:OD2	2.15	0.46
15:YT:118:ARG:NH2	15:YT:121:ILE:CB	2.79	0.46
32:QA:456:C:H2'	32:QA:457:C:C6	2.50	0.46
1:RA:1095:A:N6	54:QY:54:GLN:OE1	2.30	0.46
26:R4:68:ARG:HA	26:R4:68:ARG:NH2	2.30	0.46
1:RA:1430:C:H2'	1:RA:1431:U:H6	1.79	0.46
1:RA:2150:U:H2'	1:RA:2151:G:C8	2.50	0.46
1:RA:764:A:H5'	3:RD:210:GLY:HA2	1.97	0.46
1:RA:78:A:H2'	1:RA:79:G:C8	2.51	0.46
6:RG:181:ARG:HG3	6:RG:182:LYS:N	2.30	0.46
13:RR:67:LEU:HD13	13:RR:76:VAL:HG21	1.97	0.46
21:RZ:182:LYS:O	21:RZ:185:GLU:HG3	2.15	0.46
32:XA:258:G:H2'	32:XA:259:G:H8	1.80	0.46
32:XA:109:A:N1	32:XA:326:G:C6	2.82	0.46
24:Y2:38:GLN:HB3	24:Y2:44:LEU:HB2	1.97	0.46
1:YA:1073:A:HO2'	1:YA:1074:G:C5'	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:2361:A:OP2	30:Y8:26:LYS:NZ	2.47	0.46
1:YA:534:U:H2'	1:YA:535:C:C6	2.51	0.46
1:YA:813:U:H2'	1:YA:814:C:H6	1.80	0.46
4:YE:93:VAL:HB	4:YE:175:VAL:CG2	2.45	0.46
32:QA:985:C:H2'	32:QA:986:A:H8	1.79	0.46
33:QB:189:ASP:OD1	33:QB:189:ASP:N	2.38	0.46
33:QB:208:ILE:HA	33:QB:211:ILE:HD12	1.97	0.46
32:QA:1060:C:C4	34:QC:2:GLY:HA3	2.50	0.46
34:QC:50:ALA:HB1	34:QC:70:VAL:HG21	1.98	0.46
35:QD:15:GLU:OE2	35:QD:66:ARG:NH1	2.48	0.46
44:QM:3:ARG:O	44:QM:57:ARG:NH2	2.38	0.46
1:RA:458:G:O2'	1:RA:469:G:O6	2.23	0.46
1:RA:955:C:OP1	12:RQ:87:LYS:HE2	2.14	0.46
7:RH:9:ILE:CG1	7:RH:69:ARG:CD	2.94	0.46
32:XA:1003:G:H1	32:XA:1035:A:N6	2.13	0.46
32:XA:1312:G:H5'	50:XS:5:LEU:CD2	2.45	0.46
32:XA:1376:U:H2'	32:XA:1377:A:H8	1.80	0.46
32:XA:514:C:H2'	32:XA:515:G:H8	1.81	0.46
32:XA:560:U:H4'	32:XA:561:U:O5'	2.15	0.46
32:XA:583:A:H2'	32:XA:584:G:O4'	2.15	0.46
35:XD:108:LEU:HB3	35:XD:110:PHE:CE1	2.50	0.46
42:XK:115:PRO:C	42:XK:117:ASN:HA	2.36	0.46
43:XL:32:PHE:CD2	43:XL:86:ARG:HB3	2.51	0.46
54:XY:251:GLY:O	54:XY:254:VAL:N	2.40	0.46
23:Y1:8:SER:HB3	23:Y1:66:HIS:CD2	2.50	0.46
1:YA:1386:C:H2'	1:YA:1387:C:C6	2.51	0.46
1:YA:2134:A:O2'	1:YA:2159:G:H1'	2.16	0.46
1:YA:1759:A:H1'	1:YA:2711:A:C2	2.51	0.46
10:YO:10:VAL:HG21	10:YO:16:ALA:HB3	1.98	0.46
32:QA:1333:A:H3'	32:QA:1334:G:H8	1.80	0.46
32:QA:1347:G:H22	32:QA:1374:A:P	2.39	0.46
32:QA:159:G:O2'	32:QA:161:A:N7	2.47	0.46
32:QA:266:G:H2'	32:QA:266:G:N3	2.30	0.46
32:QA:677:U:H2'	32:QA:678:U:H6	1.79	0.46
35:QD:178:VAL:HG12	35:QD:179:GLU:N	2.31	0.46
1:RA:1429:G:H2'	1:RA:1430:C:H6	1.79	0.46
1:RA:2115:G:N2	1:RA:2171:A:H61	2.14	0.46
1:RA:740:U:H2'	1:RA:741:G:C8	2.51	0.46
32:XA:35:G:H2'	32:XA:36:C:H6	1.79	0.46
42:XK:99:GLN:HG3	42:XK:105:VAL:HG11	1.98	0.46
53:XV:68:C:H2'	53:XV:69:C:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1397:U:OP2	1:YA:1398:C:N4	2.37	0.46
1:YA:17:G:H2'	1:YA:18:C:C6	2.50	0.46
1:YA:2462:U:H2'	1:YA:2463:C:C6	2.51	0.46
1:YA:2735:G:H2'	1:YA:2736:G:H8	1.81	0.46
6:YG:111:LEU:O	6:YG:114:ILE:HB	2.15	0.46
7:YH:17:VAL:HG22	7:YH:26:VAL:HG22	1.97	0.46
21:YZ:70:LEU:HD11	21:YZ:98:MET:SD	2.56	0.46
32:QA:1314:C:H2'	32:QA:1315:U:H6	1.80	0.46
32:QA:337:C:H2'	32:QA:338:A:C8	2.50	0.46
32:QA:61:G:H2'	32:QA:62:U:C6	2.51	0.46
32:QA:669:U:H2'	32:QA:670:G:H8	1.79	0.46
33:QB:166:ASP:OD2	33:QB:169:LYS:HB2	2.16	0.46
39:QH:112:LEU:HD21	39:QH:133:LEU:HG	1.97	0.46
40:QI:33:PHE:CE1	40:QI:43:ALA:HB1	2.51	0.46
45:QN:27:CYS:SG	45:QN:29:ARG:HB2	2.56	0.46
50:QS:50:ALA:HB1	50:QS:57:HIS:HB3	1.97	0.46
1:RA:1064:C:N4	1:RA:1065:U:C2	2.84	0.46
37:QF:81:ILE:HD11	3:RD:137:PRO:HG2	1.98	0.46
1:RA:2312:U:H5'	6:RG:88:ILE:HD11	1.97	0.46
9:RN:94:HIS:HB3	9:RN:97:ARG:HD3	1.94	0.46
32:XA:986:A:H2'	32:XA:987:G:H8	1.81	0.46
1:YA:1028:A:N6	1:YA:1125:G:H2'	2.31	0.46
1:YA:2099:U:H3	1:YA:2190:G:H1	1.64	0.46
1:YA:2650:U:H2'	1:YA:2651:C:H6	1.79	0.46
3:YD:126:GLN:O	3:YD:193:VAL:CG2	2.64	0.46
9:YN:75:TYR:CE2	9:YN:77:GLY:HA2	2.51	0.46
21:YZ:77:ASP:OD2	21:YZ:80:ARG:NH1	2.48	0.46
32:QA:1073:U:H2'	32:QA:1074:G:H8	1.81	0.46
32:QA:1466:C:H2'	32:QA:1467:G:O4'	2.16	0.46
32:QA:189(B):C:H42	32:QA:189(K):G:H1	1.64	0.46
32:QA:57:G:H2'	32:QA:58:C:C6	2.51	0.46
33:QB:96:ARG:HD2	33:QB:98:LEU:HD21	1.92	0.46
32:QA:542:G:H5'	35:QD:41:GLY:HA3	1.98	0.46
36:QE:110:LEU:HD13	36:QE:118:ILE:HG21	1.97	0.46
51:QT:57:ARG:HH22	51:QT:100:ILE:CD1	2.27	0.46
53:QV:61:C:H2'	53:QV:62:C:H6	1.80	0.46
1:RA:1292:U:H2'	1:RA:1293:C:C6	2.51	0.46
1:RA:1431:U:H2'	1:RA:1432:C:C6	2.50	0.46
1:RA:1853:A:N3	1:RA:2233:U:O2'	2.40	0.46
1:RA:303:U:H2'	1:RA:304:G:H8	1.81	0.46
2:RB:89:G:H2'	2:RB:90:A:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:RD:137:PRO:O	3:RD:140:THR:HG23	2.15	0.46
7:RH:13:LYS:HA	7:RH:14:GLY:HA2	1.75	0.46
21:RZ:125:LEU:HB3	21:RZ:165:VAL:HG13	1.98	0.46
26:Y4:67:TYR:CB	50:XS:16:LEU:HD11	2.46	0.46
54:XY:11:ILE:HG12	54:XY:103:LEU:HD11	1.96	0.46
54:XY:144:TRP:CH2	54:XY:326:TYR:CD2	3.03	0.46
26:Y4:47:GLN:C	26:Y4:48:ARG:HG2	2.36	0.46
1:YA:1557:C:H5''	1:YA:1558:A:OP2	2.16	0.46
1:YA:1587:A:H2'	1:YA:1588:C:C6	2.51	0.46
1:YA:1683:C:H2'	1:YA:1684:C:H6	1.80	0.46
1:YA:2130:U:H2'	1:YA:2158:A:H61	1.81	0.46
1:YA:78:A:H2'	1:YA:79:G:H8	1.80	0.46
6:YG:8:LYS:HD2	6:YG:100:TRP:CD1	2.51	0.46
16:YU:76:TYR:OH	16:YU:92:ARG:NH1	2.49	0.46
19:YX:65:ARG:HB3	19:YX:70:LEU:HD23	1.97	0.46
21:YZ:33:LEU:HD11	21:YZ:90:VAL:HG21	1.97	0.46
32:QA:1182:G:H4'	32:QA:1183:A:H5'	1.97	0.46
32:QA:1429:C:H2'	32:QA:1430:C:C6	2.50	0.46
35:QD:12:CYS:SG	35:QD:19:LEU:HB2	2.55	0.46
54:QY:212:ARG:NH1	55:QX:21:A:H3'	2.31	0.46
1:RA:1166:C:H2'	1:RA:1167:U:H6	1.81	0.46
1:RA:2001:A:H2'	1:RA:2002:G:C8	2.51	0.46
1:RA:2650:U:H2'	1:RA:2651:C:C6	2.51	0.46
1:RA:272(L):U:H5'	8:RI:50:ARG:HH12	1.81	0.46
1:RA:557:U:H2'	1:RA:558:G:H8	1.81	0.46
1:RA:652(C):A:H61	1:RA:655:A:H1'	1.81	0.46
7:RH:69:ARG:HD2	7:RH:69:ARG:O	2.16	0.46
1:RA:626:U:O4	11:RP:107:LYS:HE2	2.16	0.46
21:RZ:139:VAL:CG1	21:RZ:150:LEU:CD2	2.94	0.46
32:XA:1223:C:P	50:XS:78:ARG:HH22	2.38	0.46
32:XA:736:C:H2'	32:XA:737:A:C8	2.51	0.46
34:XC:180:ALA:HB1	34:XC:203:PHE:HE1	1.81	0.46
30:Y8:6:THR:HG23	30:Y8:64:TYR:HD2	1.80	0.46
1:YA:1475:G:H2'	1:YA:1476:C:H6	1.80	0.46
1:YA:285:C:H2'	1:YA:286:C:C6	2.50	0.46
1:YA:852:G:H2'	1:YA:853:G:C8	2.51	0.46
2:YB:60:C:H2'	2:YB:61:G:H8	1.80	0.46
32:QA:1330:U:H2'	32:QA:1331:G:H5'	1.98	0.46
32:QA:662:G:H2'	32:QA:663:A:C8	2.51	0.46
37:QF:82:ARG:NH1	37:QF:82:ARG:HG2	2.31	0.46
46:QO:16:ALA:HB1	46:QO:21:ASP:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:R1:3:LYS:HG2	23:R1:61:ARG:NH1	2.30	0.46
26:R4:56:VAL:HB	26:R4:60:GLN:HG2	1.97	0.46
1:RA:1073:A:HO2'	1:RA:1074:G:C5'	2.28	0.46
1:RA:1198:U:H2'	1:RA:1199:U:H6	1.81	0.46
1:RA:671:C:H2'	1:RA:672:C:C6	2.51	0.46
3:RD:5:LYS:HB3	3:RD:5:LYS:HE3	1.71	0.46
8:RI:72:LEU:C	8:RI:74:ASN:H	2.18	0.46
18:RW:68:ARG:HH12	18:RW:112:GLY:H	1.62	0.46
18:RW:4:LYS:HG2	18:RW:5:ALA:N	2.31	0.46
32:XA:1288:A:N3	32:XA:1352:C:O2'	2.42	0.46
32:XA:1295:G:O2'	32:XA:1302:U:O4	2.20	0.46
35:XD:8:VAL:HG21	35:XD:21:LEU:HB3	1.96	0.46
39:XH:82:HIS:NE2	39:XH:84:ARG:HG2	2.30	0.46
1:YA:180:G:N2	1:YA:215:G:O6	2.48	0.46
1:YA:1667:G:O2'	1:YA:1991:U:O4	2.27	0.46
1:YA:2740:A:H2'	1:YA:2741:A:C8	2.50	0.46
1:YA:579:G:H2'	1:YA:580:C:H6	1.80	0.46
7:YH:105:LEU:HD21	7:YH:162:ILE:CD1	2.45	0.46
14:YS:36:TYR:OH	14:YS:54:LEU:HD22	2.16	0.46
32:QA:1330:U:OP1	44:QM:24:GLY:N	2.43	0.46
32:QA:407:G:OP1	35:QD:115:ARG:NH2	2.49	0.46
32:QA:715:A:H2'	32:QA:716:A:C8	2.50	0.46
32:QA:824:C:H2'	32:QA:825:G:C8	2.47	0.46
32:QA:1232:U:H5''	40:QI:124:GLN:O	2.16	0.46
44:QM:11:ARG:C	44:QM:13:LYS:H	2.19	0.46
44:QM:86:CYS:HB2	50:QS:73:GLU:HB3	1.98	0.46
54:QY:217:PHE:N	54:QY:217:PHE:HD1	2.14	0.46
30:R8:33:ASN:HA	30:R8:36:LYS:HD2	1.98	0.46
1:RA:2838:G:C4	1:RA:2839:G:C8	3.04	0.46
1:RA:580:C:H2'	1:RA:581:C:C6	2.51	0.46
1:RA:594:U:H2'	1:RA:595:C:C6	2.50	0.46
1:RA:657:U:H2'	1:RA:658:C:C6	2.51	0.46
1:RA:995:C:N4	9:RN:2:LYS:HD2	2.31	0.46
3:RD:127:VAL:HA	3:RD:193:VAL:HG23	1.98	0.46
3:RD:10:THR:OG1	3:RD:13:ARG:HG2	2.15	0.46
4:RE:28:ALA:HB3	4:RE:93:VAL:CG1	2.46	0.46
8:RI:101:LEU:HD23	8:RI:101:LEU:HA	1.79	0.46
14:RS:110:LEU:HA	14:RS:110:LEU:HD12	1.78	0.46
1:RA:2849:U:P	15:RT:95:ARG:HH12	2.39	0.46
1:RA:1187:G:H5'	17:RV:81:TYR:CE1	2.51	0.46
32:XA:1181:G:O2'	32:XA:1182:G:N7	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:1438:G:H2'	32:XA:1439:C:C6	2.50	0.46
32:XA:359:U:H2'	32:XA:360:A:C8	2.51	0.46
32:XA:632:A:H5'	32:XA:633:G:OP2	2.15	0.46
33:XB:200:ILE:HG22	33:XB:202:PRO:CD	2.46	0.46
38:XG:149:ARG:HG2	42:XK:59:TYR:CZ	2.50	0.46
44:XM:80:ARG:O	44:XM:84:ILE:HG23	2.16	0.46
11:YP:63:PRO:HD3	30:Y8:27:THR:HG22	1.98	0.46
1:YA:2206:G:H5''	1:YA:2207:G:N7	2.31	0.46
1:YA:2317:C:H2'	1:YA:2318:G:H5'	1.98	0.46
1:YA:840:C:H2'	1:YA:841:A:H8	1.80	0.46
5:YF:140:LEU:HD21	5:YF:170:LEU:HD11	1.96	0.46
7:YH:20:ALA:HB1	7:YH:21:PRO:HD2	1.98	0.46
9:YN:4:TYR:CD2	16:YU:100:VAL:HG11	2.51	0.46
13:YR:87:TYR:OH	13:YR:117:VAL:O	2.20	0.46
32:QA:935:A:C2	38:QG:3:ARG:NH2	2.84	0.45
38:QG:28:ASN:HA	38:QG:31:MET:HE2	1.98	0.45
44:QM:81:LEU:HD13	44:QM:88:ARG:HG2	1.98	0.45
44:QM:86:CYS:HA	50:QS:73:GLU:O	2.16	0.45
21:RZ:198:LYS:HZ3	53:QV:52:G:H2'	1.79	0.45
44:QM:2:ALA:CA	26:R4:34:GLU:OE1	2.64	0.45
1:RA:2443:C:H2'	1:RA:2444:G:C8	2.51	0.45
1:RA:2712(A):U:H1'	1:RA:2712(B):A:C8	2.51	0.45
1:RA:2823:A:OP1	4:RE:113:PHE:HB2	2.16	0.45
1:RA:659:C:H2'	1:RA:660:G:H8	1.79	0.45
15:RT:49:VAL:HG12	15:RT:63:VAL:HG22	1.98	0.45
32:XA:1015:A:H2'	32:XA:1016:A:C8	2.51	0.45
32:XA:1151:A:O2'	32:XA:1152:A:O5'	2.28	0.45
32:XA:1191:A:OP2	34:XC:3:ASN:ND2	2.49	0.45
32:XA:1442(A):G:N3	32:XA:1442(A):G:H2'	2.31	0.45
32:XA:68:G:C8	32:XA:68:G:H5''	2.51	0.45
32:XA:933:G:O6	38:XG:3:ARG:NH2	2.49	0.45
48:XQ:6:LEU:O	48:XQ:58:GLU:HA	2.16	0.45
54:XY:43:GLN:HG2	54:XY:45:ASP:H	1.81	0.45
1:YA:1182:A:H2'	1:YA:1183:G:C8	2.51	0.45
1:YA:2078:C:H2'	1:YA:2079:U:C6	2.52	0.45
1:YA:483:A:O2'	20:YY:59:GLY:N	2.49	0.45
1:YA:1812:A:O2'	3:YD:45:ASN:N	2.48	0.45
15:YT:28:VAL:HG13	15:YT:86:ILE:HG23	1.98	0.45
1:YA:2012:G:P	18:YW:11:ARG:HH22	2.39	0.45
32:QA:1131:G:H2'	32:QA:1132:C:H6	1.80	0.45
32:QA:1263:C:H2'	32:QA:1264:C:H6	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:725:G:OP1	32:QA:853:G:N2	2.36	0.45
40:QI:22:GLY:HA3	40:QI:60:ASP:OD1	2.16	0.45
46:QO:8:LYS:O	46:QO:12:ILE:HG13	2.16	0.45
1:RA:1587:A:H2'	1:RA:1588:C:C6	2.50	0.45
1:RA:2785:C:OP1	4:RE:41:LYS:NZ	2.48	0.45
1:RA:610:G:H2'	1:RA:611:C:H6	1.81	0.45
15:RT:60:THR:HG22	15:RT:77:PRO:HA	1.98	0.45
32:XA:1305:G:H22	32:XA:1331:G:H1'	1.81	0.45
33:XB:44:LEU:H	33:XB:44:LEU:HD22	1.80	0.45
36:XE:33:VAL:HG21	36:XE:109:ILE:HA	1.98	0.45
41:XJ:21:GLN:O	41:XJ:25:GLU:HG2	2.17	0.45
41:XJ:5:ARG:N	41:XJ:99:LYS:O	2.48	0.45
1:YA:1364:G:OP2	23:Y1:3:LYS:HG3	2.15	0.45
1:YA:2180:U:H2'	1:YA:2181:G:C8	2.50	0.45
1:YA:2251:OMG:HM23	1:YA:2251:OMG:H1'	1.80	0.45
1:YA:840:C:H2'	1:YA:841:A:C8	2.51	0.45
6:YG:179:PRO:HB2	26:Y4:42:PHE:HE2	1.81	0.45
32:QA:340:U:H2'	32:QA:341:C:C6	2.51	0.45
32:QA:41:G:H2'	32:QA:42:G:C8	2.50	0.45
33:QB:54:THR:HG23	33:QB:199:TYR:HB3	1.99	0.45
38:QG:26:PHE:O	38:QG:30:ILE:HG13	2.16	0.45
54:QY:197:GLY:HA3	54:QY:323:ILE:HD13	1.97	0.45
54:QY:338:THR:CG2	54:QY:339:GLY:HA2	2.45	0.45
54:QY:333:ILE:HG13	54:QY:345:THR:HG22	1.98	0.45
1:RA:1067:A:H4'	1:RA:1068:G:OP2	2.15	0.45
1:RA:1073:A:O2'	1:RA:1074:G:O5'	2.35	0.45
6:RG:3:LEU:HD22	26:R4:25:TYR:CZ	2.50	0.45
8:RI:38:LEU:HD12	8:RI:38:LEU:H	1.81	0.45
8:RI:81:VAL:HG21	8:RI:88:ILE:HD13	1.99	0.45
9:RN:42:TRP:CH2	9:RN:44:PRO:HB3	2.51	0.45
10:RO:8:LEU:HD13	10:RO:82:ASN:HB3	1.97	0.45
12:RQ:137:TYR:HE2	21:RZ:49:ARG:NH1	2.14	0.45
32:XA:1120:G:H2'	32:XA:1121:U:H6	1.80	0.45
32:XA:57:G:H2'	32:XA:58:C:C6	2.51	0.45
32:XA:881:G:OP2	43:XL:12:ARG:NH2	2.48	0.45
33:XB:185:ILE:CD1	33:XB:199:TYR:CD2	2.99	0.45
39:XH:20:TYR:HA	39:XH:65:TYR:CZ	2.51	0.45
40:XI:17:VAL:HG11	40:XI:80:GLY:C	2.37	0.45
44:XM:13:LYS:HA	44:XM:44:ARG:HH11	1.81	0.45
51:XT:50:GLU:HG3	51:XT:100:ILE:HD11	1.97	0.45
54:XY:161:PHE:CD1	54:XY:185:GLY:HA3	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1048:A:N1	1:YA:1112:G:O2'	2.46	0.45
1:YA:1231:G:H2'	1:YA:1232:G:H8	1.81	0.45
1:YA:1411:C:H2'	1:YA:1412:A:H8	1.81	0.45
1:YA:2103:C:C4	1:YA:2104:G:N2	2.85	0.45
1:YA:2889:C:H3'	1:YA:2891:G:H8	1.81	0.45
1:YA:679:C:H2'	1:YA:680:G:H8	1.81	0.45
1:YA:886:C:O2'	1:YA:889:C:N4	2.48	0.45
6:YG:46:ALA:HB2	6:YG:53:LEU:HG	1.98	0.45
7:YH:117:PRO:HA	7:YH:118:PRO:HD3	1.85	0.45
8:YI:27:ARG:HD2	23:Y1:71:TYR:CZ	2.51	0.45
8:YI:38:LEU:HD22	8:YI:40:THR:HG22	1.98	0.45
8:YI:50:ARG:HB3	8:YI:50:ARG:HE	1.42	0.45
21:RZ:202:GLU:OE2	53:QV:62:C:O2	2.34	0.45
54:QY:324:ARG:HD2	54:QY:326:TYR:CE1	2.52	0.45
28:R6:19:ARG:NH2	28:R6:52:VAL:HG11	2.31	0.45
30:R8:39:LYS:O	30:R8:43:GLN:HG3	2.16	0.45
1:RA:1252:G:N3	16:RU:33:ARG:HG2	2.32	0.45
1:RA:2070:G:H2'	1:RA:2071:A:C8	2.50	0.45
1:RA:2103:C:C2	1:RA:2104:G:N2	2.84	0.45
1:RA:2507:C:H5'	54:QY:256:ARG:HD2	1.98	0.45
32:XA:1305:G:N2	32:XA:1331:G:H1'	2.32	0.45
32:XA:1376:U:H2'	32:XA:1377:A:C8	2.52	0.45
32:XA:396:G:O2'	32:XA:398:C:OP1	2.21	0.45
32:XA:691:G:P	42:XK:26:ASN:HD22	2.38	0.45
35:XD:25:ARG:NH1	35:XD:30:LYS:O	2.49	0.45
41:XJ:30:SER:OG	41:XJ:81:THR:HG22	2.17	0.45
26:Y4:59:PHE:CZ	50:XS:64:GLU:OE1	2.61	0.45
54:XY:215:THR:HG22	54:XY:217:PHE:HE1	1.79	0.45
26:Y4:13:ARG:CZ	26:Y4:21:VAL:HG11	2.47	0.45
1:YA:1539:G:H2'	1:YA:1540:U:O4'	2.17	0.45
1:YA:2849:U:P	15:YT:95:ARG:HH12	2.40	0.45
1:YA:839:U:H2'	1:YA:840:C:C6	2.52	0.45
2:YB:24:G:N7	2:YB:56:G:H2'	2.31	0.45
5:YF:39:TRP:CH2	5:YF:106:ARG:CZ	2.99	0.45
1:YA:2059:A:O2'	5:YF:69:HIS:ND1	2.48	0.45
8:YI:130:TYR:CE2	8:YI:132:PRO:HB3	2.52	0.45
1:YA:139(A):G:H1'	19:YX:41:ASN:ND2	2.31	0.45
20:YY:13:VAL:HB	20:YY:72:VAL:HG13	1.97	0.45
21:YZ:99:TYR:HA	21:YZ:124:ILE:O	2.17	0.45
33:QB:100:GLY:HA2	33:QB:103:THR:OG1	2.17	0.45
33:QB:196:LEU:HA	33:QB:196:LEU:HD12	1.83	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:QC:47:LEU:HD13	34:QC:68:VAL:HG11	1.97	0.45
51:QT:10:LEU:HD22	51:QT:12:ALA:N	2.32	0.45
6:RG:78:SER:OG	53:QV:57:A:O4'	2.32	0.45
53:QV:54:U:C4	53:QV:58:A:H8	2.35	0.45
53:QV:9:G:N3	53:QV:45:G:H2'	2.31	0.45
1:RA:1796:U:H2'	1:RA:1797:C:H6	1.79	0.45
13:RR:36:THR:CG2	13:RR:37:THR:H	2.18	0.45
37:XF:86:ARG:O	37:XF:87:ARG:HG2	2.16	0.45
54:XY:216:SER:C	54:XY:217:PHE:HD1	2.19	0.45
1:YA:2279:G:N7	22:Y0:14:ARG:NH1	2.65	0.45
1:YA:1693:U:O2'	3:YD:14:ARG:NH2	2.50	0.45
32:QA:187:C:O2'	51:QT:89:ARG:NH2	2.40	0.45
32:QA:359:U:H2'	32:QA:360:A:H8	1.82	0.45
39:QH:73:ASP:OD1	39:QH:75:ARG:HD3	2.17	0.45
44:QM:54:VAL:HA	44:QM:57:ARG:HB3	1.99	0.45
44:QM:78:ILE:HD13	44:QM:92:HIS:CE1	2.51	0.45
27:R5:40:LYS:HD2	27:R5:41:PRO:O	2.15	0.45
1:RA:1028:A:N6	1:RA:1125:G:H2'	2.32	0.45
1:RA:2590:A:H2'	1:RA:2591:C:C6	2.51	0.45
18:RW:20:VAL:O	18:RW:23:LEU:HB2	2.16	0.45
21:RZ:72:ARG:HG2	21:RZ:89:PHE:CB	2.42	0.45
32:XA:1366:C:O2'	41:XJ:60:ARG:NH2	2.29	0.45
32:XA:1226:C:N4	44:XM:104:ARG:HD2	2.32	0.45
22:Y0:11:ARG:NH2	53:XV:63:G:H4'	2.32	0.45
1:YA:2611:U:C4	27:Y5:3:LYS:HG2	2.52	0.45
1:YA:1336:A:H2'	1:YA:1337:G:C8	2.51	0.45
1:YA:1530:C:HO2'	1:YA:1531:C:P	2.34	0.45
1:YA:1688:U:O2	1:YA:1700:A:H5'	2.17	0.45
1:YA:2119:A:H61	1:YA:2168:G:N2	2.14	0.45
1:YA:2649:U:H2'	1:YA:2650:U:H6	1.81	0.45
1:YA:2695:C:H2'	1:YA:2696:U:C6	2.51	0.45
1:YA:284:U:H2'	1:YA:285:C:C6	2.51	0.45
1:YA:595:C:H2'	1:YA:596:G:H8	1.81	0.45
1:YA:881:G:H2'	1:YA:882:G:H8	1.79	0.45
5:YF:184:TYR:O	5:YF:188:ARG:HG3	2.15	0.45
12:YQ:109:VAL:HG13	12:YQ:113:GLN:CB	2.46	0.45
32:QA:1040:U:H2'	32:QA:1041:A:H8	1.80	0.45
32:QA:1239:A:C4	32:QA:1298:C:N4	2.85	0.45
32:QA:505:G:H2'	32:QA:506:G:C8	2.51	0.45
32:QA:624:C:H2'	32:QA:625:G:C8	2.51	0.45
42:QK:20:TYR:CZ	42:QK:83:ILE:HD12	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:QQ:67:LYS:O	48:QQ:68:ARG:HB3	2.17	0.45
53:QV:58:A:H2	53:QV:60:U:HO2'	1.63	0.45
25:R3:6:VAL:HG13	25:R3:54:VAL:CG1	2.47	0.45
1:RA:1817:G:OP1	3:RD:88:ARG:NH2	2.37	0.45
1:RA:2398:U:H2'	1:RA:2399:G:C8	2.51	0.45
6:RG:83:ARG:O	6:RG:86:MET:HB2	2.16	0.45
17:RV:62:LEU:CD1	17:RV:95:LEU:HB2	2.45	0.45
32:XA:340:U:H2'	32:XA:341:C:C6	2.51	0.45
38:XG:90:GLU:OE2	38:XG:90:GLU:N	2.43	0.45
43:XL:117:ARG:NH2	43:XL:124:LYS:HB2	2.32	0.45
32:XA:1319:A:OP2	50:XS:3:ARG:NH2	2.49	0.45
53:XV:53:G:HO2'	53:XV:54:U:H5	1.64	0.45
54:XY:197:GLY:HA3	54:XY:323:ILE:HD13	1.97	0.45
30:Y8:63:PRO:HG2	30:Y8:64:TYR:CD2	2.52	0.45
1:YA:2506:U:H4'	54:XY:256:ARG:NH1	2.31	0.45
1:YA:2650:U:H2'	1:YA:2651:C:C6	2.52	0.45
1:YA:302:C:H2'	1:YA:303:U:H6	1.80	0.45
13:YR:18:LEU:HD11	13:YR:22:ARG:NH1	2.30	0.45
21:YZ:125:LEU:HG	21:YZ:164:ALA:HB3	1.98	0.45
32:QA:1241:G:H2'	32:QA:1242:C:H6	1.81	0.45
32:QA:1427:U:H2'	32:QA:1428:A:C8	2.52	0.45
32:QA:500:G:H2'	32:QA:501:C:H6	1.80	0.45
32:QA:584:G:H2'	32:QA:585:G:H8	1.81	0.45
32:QA:923:A:H2'	32:QA:924:C:C6	2.51	0.45
32:QA:933:G:O6	38:QG:3:ARG:NH2	2.45	0.45
42:QK:18:ARG:NH2	42:QK:35:PRO:O	2.50	0.45
44:QM:13:LYS:HA	44:QM:44:ARG:NH1	2.30	0.45
30:R8:31:HIS:CD2	30:R8:32:LEU:HD22	2.52	0.45
1:RA:2547:U:H2'	1:RA:2548:G:C8	2.51	0.45
1:RA:2696:U:H2'	1:RA:2697:G:H8	1.80	0.45
1:RA:588:U:H2'	1:RA:589:C:C6	2.51	0.45
1:RA:608:A:H2'	1:RA:609:A:C8	2.52	0.45
1:RA:691:C:H2'	1:RA:692:C:H6	1.82	0.45
6:RG:108:ASN:HA	26:R4:37:SER:CB	2.46	0.45
20:RY:15:VAL:HG21	20:RY:42:VAL:HG11	1.97	0.45
21:RZ:80:ARG:O	21:RZ:82:ARG:HG3	2.17	0.45
32:XA:1074:G:H2'	32:XA:1075:C:C6	2.51	0.45
32:XA:767:A:H2'	32:XA:768:A:O4'	2.16	0.45
38:XG:151:TYR:CZ	42:XK:54:ARG:NH1	2.85	0.45
26:Y4:14:ILE:HB	26:Y4:22:ILE:HD13	1.99	0.45
26:Y4:44:THR:O	26:Y4:46:GLN:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Y4:58:ARG:NH1	50:XS:65:ASN:C	2.61	0.45
1:YA:1097:U:H2'	1:YA:1097:U:O2	2.17	0.45
1:YA:1406:U:H2'	1:YA:1407:C:H6	1.82	0.45
1:YA:1414:G:H2'	1:YA:1415:U:C6	2.52	0.45
1:YA:1297:C:OP1	1:YA:2710:C:H4'	2.16	0.45
1:YA:285:C:H2'	1:YA:286:C:H6	1.82	0.45
1:YA:295:G:OP1	20:YY:1:MET:HB2	2.16	0.45
1:YA:749:C:H5'	1:YA:1271:G:H1'	1.97	0.45
1:YA:84:A:C2	1:YA:103:A:C5	3.05	0.45
6:YG:14:GLU:C	6:YG:17:PRO:HD2	2.37	0.45
7:YH:84:SER:HA	7:YH:133:VAL:O	2.17	0.45
11:YP:96:THR:OG1	11:YP:98:GLU:HG2	2.17	0.45
13:YR:38:VAL:HB	13:YR:39:PRO:HD3	1.98	0.45
14:YS:4:LEU:HD22	14:YS:8:GLU:HB3	1.99	0.45
17:YV:35:LEU:HB2	17:YV:57:VAL:HG22	1.99	0.45
32:QA:1221:G:OP1	32:QA:1320:C:N4	2.45	0.45
32:QA:1239:A:H62	32:QA:1299:A:H61	1.64	0.45
33:QB:178:ARG:HH22	39:QH:68:ARG:NH1	2.15	0.45
33:QB:220:ASP:O	33:QB:224:GLN:HB3	2.17	0.45
37:QF:97:PHE:HB3	49:QR:31:LEU:HB2	1.99	0.45
32:QA:950:U:OP2	44:QM:102:ARG:HD2	2.17	0.45
54:QY:286:GLN:O	54:QY:290:GLN:HG3	2.17	0.45
1:RA:1446:C:H2'	1:RA:1447:G:H8	1.82	0.45
1:RA:1475:G:H2'	1:RA:1476:C:H6	1.80	0.45
1:RA:1831:G:H2'	1:RA:1832:C:C6	2.52	0.45
1:RA:686:G:N2	1:RA:788:A:H61	2.15	0.45
9:RN:42:TRP:CE3	16:RU:63:VAL:HG11	2.52	0.45
11:RP:83:VAL:CG1	11:RP:112:LEU:HD21	2.45	0.45
15:RT:24:PRO:HD3	15:RT:52:ILE:HD12	1.99	0.45
21:RZ:103:ARG:HD2	21:RZ:136:PHE:CD2	2.52	0.45
32:XA:1318:A:O2'	50:XS:37:ARG:HD2	2.17	0.45
32:XA:1427:U:H2'	32:XA:1428:A:H8	1.82	0.45
32:XA:1503:A:H5'	32:XA:1531:A:H1'	1.99	0.45
32:XA:32:A:H2'	32:XA:33:A:C8	2.52	0.45
33:XB:200:ILE:HG22	33:XB:202:PRO:N	2.32	0.45
33:XB:7:VAL:O	33:XB:217:ARG:NE	2.43	0.45
32:XA:1256:A:OP2	34:XC:26:LYS:NZ	2.50	0.45
39:XH:49:GLU:OE2	39:XH:62:TYR:OH	2.19	0.45
41:XJ:5:ARG:O	41:XJ:98:ILE:HA	2.17	0.45
29:Y7:10:ARG:HG2	29:Y7:14:LYS:HD2	1.98	0.45
1:YA:582:G:H2'	1:YA:583:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:2680:C:H5'	4:YE:189:PRO:HA	1.99	0.45
5:YF:116:ASP:O	5:YF:120:GLU:HG3	2.17	0.45
11:YP:97:PRO:HD3	11:YP:126:VAL:O	2.16	0.45
32:QA:1036:G:H5'	32:QA:1037:C:C6	2.52	0.45
32:QA:1258:G:H2'	32:QA:1259:C:C6	2.52	0.45
34:QC:116:VAL:HG21	34:QC:202:ILE:HD11	1.98	0.45
35:QD:155:LEU:O	35:QD:158:ILE:HG12	2.17	0.45
41:QJ:39:PRO:HA	41:QJ:70:ARG:HD3	1.99	0.45
46:QO:3:ILE:HD12	46:QO:34:LEU:CD2	2.40	0.45
1:RA:195:A:H61	1:RA:198:C:H3'	1.82	0.45
1:RA:2286:A:H4'	1:RA:2287:A:O4'	2.17	0.45
1:RA:2677:G:H2'	1:RA:2678:C:C6	2.51	0.45
1:RA:414:C:H1'	1:RA:1864:U:H1'	1.99	0.45
1:RA:557:U:H2'	1:RA:558:G:C8	2.52	0.45
3:RD:51:VAL:HG11	3:RD:54:ARG:HH11	1.81	0.45
21:RZ:19:ARG:NH1	21:RZ:84:GLU:O	2.50	0.45
32:XA:1006:C:H2'	32:XA:1007:C:H6	1.82	0.45
44:XM:87:TYR:HA	44:XM:90:LEU:HD12	1.99	0.45
54:XY:148:LEU:HD21	54:XY:199:HIS:CD2	2.52	0.45
54:XY:150:ARG:HD3	54:XY:154:ARG:HH22	1.82	0.45
54:XY:200:ARG:HD3	54:XY:322:GLN:HE21	1.81	0.45
1:YA:1317:A:H2'	1:YA:1318:C:C6	2.52	0.45
1:YA:1685:C:H2'	1:YA:1686:C:H6	1.81	0.45
1:YA:195:A:H61	1:YA:198:C:H3'	1.82	0.45
1:YA:2452:C:H2'	1:YA:2453:A:C8	2.52	0.45
1:YA:863:A:H2'	1:YA:864:G:C8	2.52	0.45
4:YE:67:PHE:CE1	4:YE:75:VAL:HG12	2.52	0.45
13:YR:29:LEU:HB3	13:YR:75:LEU:HD21	1.99	0.45
18:YW:17:VAL:HG23	18:YW:76:VAL:HG21	1.99	0.45
18:YW:51:LEU:CD1	18:YW:51:LEU:C	2.84	0.45
32:QA:1201:A:H1'	32:QA:1202:G:OP2	2.17	0.44
32:QA:1512:U:H2'	32:QA:1513:A:H8	1.82	0.44
32:QA:359:U:H2'	32:QA:360:A:C8	2.52	0.44
33:QB:109:SER:O	33:QB:112:VAL:HG22	2.16	0.44
33:QB:21:ARG:HD3	33:QB:21:ARG:N	2.32	0.44
1:RA:2583:G:H21	54:QY:255:ASN:ND2	2.16	0.44
1:RA:2165:G:H2'	1:RA:2166:G:O4'	2.17	0.44
1:RA:635:C:O2'	1:RA:639:U:OP1	2.32	0.44
32:XA:1071:C:H2'	32:XA:1072:G:H8	1.82	0.44
32:XA:1431:C:H2'	32:XA:1432:G:O4'	2.17	0.44
32:XA:1513:A:H2'	32:XA:1514:C:H6	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:337:C:H2'	32:XA:338:A:H8	1.80	0.44
34:XC:50:ALA:O	34:XC:72:LYS:HB2	2.17	0.44
42:XK:78:GLN:O	42:XK:103:LEU:HA	2.18	0.44
6:YG:146:TYR:CE2	44:XM:8:GLU:HB3	2.45	0.44
45:XN:22:THR:HB	45:XN:33:VAL:HG11	1.98	0.44
49:XR:76:LEU:HA	49:XR:76:LEU:HD12	1.79	0.44
1:YA:2452:C:O2'	54:XY:256:ARG:NH1	2.50	0.44
25:Y3:6:VAL:CG1	25:Y3:54:VAL:CG2	2.95	0.44
28:Y6:14:THR:HB	28:Y6:48:VAL:HG13	1.98	0.44
1:YA:1791:A:H3'	1:YA:1792:G:H8	1.82	0.44
1:YA:1829:A:H3'	1:YA:1830:C:H6	1.83	0.44
1:YA:1949:G:H2'	1:YA:1950:G:C8	2.51	0.44
1:YA:224:G:H2'	1:YA:225:A:O4'	2.18	0.44
1:YA:276:A:H5''	1:YA:277:C:H5'	1.99	0.44
1:YA:27:G:O2'	1:YA:28:A:OP2	2.33	0.44
1:YA:870:A:H2'	1:YA:871:U:O4'	2.17	0.44
6:YG:120:LEU:HB3	6:YG:131:TYR:OH	2.17	0.44
12:YQ:31:ASP:OD1	12:YQ:134:ARG:NH1	2.38	0.44
1:YA:143(A):G:H4'	19:YX:35:THR:HG21	1.99	0.44
21:YZ:33:LEU:HD21	21:YZ:90:VAL:HG11	1.98	0.44
32:QA:713:G:H2'	32:QA:714:G:C8	2.52	0.44
36:QE:116:THR:HG23	36:QE:117:ASP:OD2	2.17	0.44
38:QG:89:MET:CE	38:QG:155:ARG:CB	2.94	0.44
40:QI:16:ARG:CB	40:QI:64:THR:CG2	2.83	0.44
47:QP:57:ARG:NH2	47:QP:78:GLY:O	2.50	0.44
49:QR:58:LEU:HG	49:QR:62:GLU:HB2	1.98	0.44
54:QY:324:ARG:HD2	54:QY:326:TYR:HE1	1.83	0.44
1:RA:2420:C:OP1	30:R8:34:TRP:HB3	2.16	0.44
1:RA:1057:A:N6	1:RA:1087:G:OP1	2.51	0.44
1:RA:2375:G:N2	1:RA:2377:A:H3'	2.33	0.44
1:RA:2461:C:H2'	1:RA:2462:U:H6	1.82	0.44
1:RA:725:G:C6	1:RA:726:G:N1	2.85	0.44
6:RG:79:ASN:OD1	6:RG:79:ASN:N	2.50	0.44
32:XA:130:A:O2'	32:XA:131:C:O5'	2.33	0.44
33:XB:92:TYR:CE1	33:XB:94:ASN:HB2	2.53	0.44
1:YA:1092:C:O2	1:YA:1092:C:H2'	2.17	0.44
1:YA:2144:U:O2'	1:YA:2147:G:N1	2.45	0.44
1:YA:2389:G:H5''	1:YA:2390:U:O4'	2.17	0.44
1:YA:538:G:H2'	1:YA:539:G:C8	2.50	0.44
4:YE:82:ARG:HG3	4:YE:82:ARG:HH11	1.80	0.44
5:YF:167:ALA:HB1	5:YF:173:VAL:HG11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:YF:184:TYR:CD2	5:YF:188:ARG:HD2	2.52	0.44
10:YO:120:GLU:HG2	10:YO:122:LEU:HG	1.99	0.44
20:YY:102:CYS:SG	20:YY:103:GLY:N	2.91	0.44
32:QA:1084:G:C5	32:QA:1085:U:C4	3.06	0.44
32:QA:1157:A:C2	32:QA:1181:G:C4	3.05	0.44
32:QA:977:A:N6	32:QA:1224:G:H5'	2.32	0.44
32:QA:1299:A:O2'	32:QA:1300:G:H4'	2.18	0.44
32:QA:22:G:H2'	32:QA:23:C:C6	2.52	0.44
32:QA:35:G:H2'	32:QA:36:C:H6	1.83	0.44
32:QA:370:C:N3	32:QA:391:G:N1	2.41	0.44
35:QD:140:VAL:HG11	35:QD:146:ILE:HD11	2.00	0.44
46:QO:54:ARG:HG2	46:QO:58:MET:HE2	1.99	0.44
54:QY:159:ARG:NH2	54:QY:354:ASP:OD2	2.48	0.44
1:RA:1474:C:H2'	1:RA:1475:G:H8	1.82	0.44
1:RA:2134:A:N6	1:RA:2156:G:O2'	2.50	0.44
1:RA:1815:A:OP2	3:RD:54:ARG:NH2	2.49	0.44
15:RT:54:ARG:HA	15:RT:59:THR:HG22	2.00	0.44
17:RV:61:VAL:HG23	17:RV:92:THR:HG23	2.00	0.44
17:RV:72:VAL:HG11	17:RV:85:LYS:HD2	1.99	0.44
32:XA:1060:C:H2'	32:XA:1061:G:H8	1.82	0.44
32:XA:685:G:O2'	32:XA:686:U:H5'	2.18	0.44
33:XB:114:ARG:O	33:XB:118:LEU:N	2.48	0.44
34:XC:30:ARG:NH2	45:XN:38:GLY:HA2	2.33	0.44
36:XE:41:VAL:HG13	36:XE:113:ALA:HA	1.97	0.44
54:XY:272:THR:HG21	54:XY:291:MET:HB2	2.00	0.44
23:Y1:83:GLU:HA	23:Y1:84:GLY:HA2	1.68	0.44
24:Y2:67:LYS:HA	24:Y2:70:GLN:OE1	2.16	0.44
1:YA:2152:G:H2'	1:YA:2153:G:H8	1.82	0.44
1:YA:242:G:C8	30:Y8:3:LYS:HG3	2.53	0.44
1:YA:679:C:H2'	1:YA:680:G:C8	2.53	0.44
7:YH:144:VAL:O	7:YH:148:ILE:HG12	2.18	0.44
7:YH:74:ASN:O	7:YH:78:GLY:N	2.50	0.44
21:YZ:199:LYS:HG3	21:YZ:200:GLY:N	2.32	0.44
32:QA:1512:U:H2'	32:QA:1513:A:C8	2.52	0.44
44:QM:11:ARG:O	44:QM:13:LYS:N	2.50	0.44
46:QO:64:ARG:HH11	46:QO:68:ARG:HH21	1.65	0.44
1:RA:1322:A:C5	1:RA:1323:U:C5	3.06	0.44
1:RA:2024:G:H2'	1:RA:2025:C:C6	2.53	0.44
1:RA:2647:U:H2'	1:RA:2648:C:H6	1.82	0.44
1:RA:361:G:O2'	1:RA:362:U:H5'	2.18	0.44
32:XA:1355:G:H2'	32:XA:1356:G:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:34:C:H2'	32:XA:35:G:C8	2.51	0.44
32:XA:683:G:H2'	32:XA:684:A:C8	2.52	0.44
32:XA:687:A:C2	32:XA:704:A:C6	3.05	0.44
32:XA:719:C:O2'	49:XR:49:LYS:HB3	2.17	0.44
51:XT:59:ALA:O	51:XT:63:ILE:HG13	2.17	0.44
1:YA:2602:A:C5	54:XY:278:ARG:HG2	2.52	0.44
54:XY:280:GLN:HG2	54:XY:281:HIS:CD2	2.53	0.44
1:YA:1317:A:H2'	1:YA:1318:C:H6	1.82	0.44
1:YA:657:U:H2'	1:YA:658:C:C6	2.52	0.44
4:YE:59:VAL:HG12	4:YE:64:LYS:HG3	2.00	0.44
5:YF:132:VAL:CG2	5:YF:163:VAL:HG22	2.47	0.44
32:QA:1158:C:C4	32:QA:1160:G:C8	3.06	0.44
32:QA:309:G:O2'	32:QA:607:A:N1	2.50	0.44
47:QP:75:ARG:HG3	47:QP:80:PHE:HD2	1.81	0.44
51:QT:57:ARG:CZ	51:QT:100:ILE:HD12	2.47	0.44
51:QT:37:SER:O	51:QT:41:ILE:HG13	2.18	0.44
54:QY:226:VAL:HG23	54:QY:227:ASP:H	1.82	0.44
54:QY:241:ILE:HG21	54:QY:284:LYS:HE2	1.98	0.44
27:R5:37:LYS:HD3	27:R5:37:LYS:HA	1.82	0.44
1:RA:1084:A:H3'	1:RA:1085:A:C4'	2.48	0.44
1:RA:1630:G:H2'	1:RA:1631(A):C:C6	2.52	0.44
1:RA:1935:G:H1'	1:RA:1964:G:N2	2.32	0.44
1:RA:2443:C:H2'	1:RA:2444:G:H8	1.82	0.44
1:RA:2453:A:H5''	54:QY:256:ARG:HH21	1.82	0.44
1:RA:2683:C:OP1	15:RT:53:ARG:NH2	2.51	0.44
32:XA:1256:A:H61	32:XA:1278:U:H1'	1.83	0.44
32:XA:1492:A:H3'	32:XA:1493:A:H8	1.83	0.44
32:XA:69:G:OP2	32:XA:69:G:C8	2.70	0.44
32:XA:748:C:H4'	32:XA:749:C:O5'	2.17	0.44
33:XB:9:GLU:O	33:XB:12:GLU:OE1	2.35	0.44
33:XB:174:VAL:O	33:XB:178:ARG:HB2	2.17	0.44
34:XC:91:LEU:HD22	34:XC:101:LEU:HD22	1.98	0.44
34:XC:110:ASN:OD1	34:XC:140:ARG:NH2	2.50	0.44
34:XC:32:LEU:HD12	34:XC:59:ARG:HH12	1.83	0.44
47:XP:43:LYS:HA	47:XP:48:TRP:CB	2.48	0.44
1:YA:2279:G:O6	22:Y0:14:ARG:HD2	2.18	0.44
1:YA:1064:C:N4	1:YA:1065:U:C2	2.86	0.44
1:YA:1645:G:H5''	1:YA:1646:C:H5'	2.00	0.44
1:YA:2591:C:H2'	1:YA:2592:G:H8	1.83	0.44
1:YA:532:A:H4'	1:YA:533:G:C8	2.52	0.44
1:YA:607:U:OP1	5:YF:102:PRO:HA	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:698:C:O2'	1:YA:734:A:N6	2.51	0.44
2:YB:78:A:C2	2:YB:100:A:C4	3.06	0.44
1:YA:1803:A:O2'	3:YD:259:THR:HG21	2.18	0.44
1:YA:2724:C:OP2	4:YE:111:ARG:NH1	2.51	0.44
1:YA:2303:G:O2'	6:YG:132:ASN:HB2	2.18	0.44
7:YH:90:LYS:HD3	7:YH:159:GLU:HG2	2.00	0.44
21:YZ:198:LYS:HE3	53:XV:52:G:H2'	1.98	0.44
32:QA:737:A:H2'	32:QA:738:C:C6	2.52	0.44
32:QA:860:A:H2'	32:QA:861:G:O4'	2.17	0.44
34:QC:22:TRP:CD1	34:QC:59:ARG:HD2	2.52	0.44
40:QI:49:PRO:HB3	40:QI:82:ALA:HB2	1.99	0.44
54:QY:150:ARG:HB3	54:QY:154:ARG:HH12	1.82	0.44
26:R4:15:ILE:HB	26:R4:32:TYR:CD1	2.53	0.44
1:RA:1658:C:H2'	1:RA:1659:U:C6	2.53	0.44
1:RA:2612:C:OP2	27:R5:2:ALA:N	2.51	0.44
1:RA:39:C:H2'	1:RA:40:C:C6	2.53	0.44
1:RA:854:G:H2'	1:RA:855:G:C8	2.52	0.44
4:RE:119:ARG:HG2	4:RE:120:TRP:NE1	2.32	0.44
7:RH:117:PRO:HG3	7:RH:123:PHE:CD2	2.53	0.44
32:XA:601:C:H2'	32:XA:602:A:H8	1.82	0.44
32:XA:73:G:H2'	32:XA:76:C:C6	2.53	0.44
33:XB:48:MET:HA	33:XB:51:LEU:HD12	2.00	0.44
34:XC:6:HIS:HA	34:XC:7:PRO:HD3	1.80	0.44
36:XE:81:GLU:HG2	36:XE:90:VAL:HG13	1.99	0.44
45:XN:4:LYS:O	45:XN:7:ILE:HG12	2.17	0.44
1:YA:1210:A:H4'	1:YA:1211:U:O5'	2.18	0.44
1:YA:1308:A:H2'	1:YA:1309:G:O4'	2.18	0.44
1:YA:2074:U:H2'	1:YA:2075:U:H6	1.81	0.44
1:YA:760:G:H2'	1:YA:761:A:O4'	2.18	0.44
1:YA:1803:A:H4'	3:YD:259:THR:HG23	2.00	0.44
6:YG:146:TYR:CE2	44:XM:8:GLU:CB	3.00	0.44
16:YU:107:ALA:O	16:YU:111:GLU:HG2	2.18	0.44
19:YX:44:GLU:HG3	19:YX:51:VAL:HG23	1.99	0.44
32:QA:1030(A):C:C4	32:QA:1030(B):G:H1'	2.52	0.44
32:QA:1073:U:P	36:QE:57:LYS:NZ	2.90	0.44
32:QA:103:C:O2'	32:QA:172:A:N1	2.40	0.44
39:QH:51:VAL:CG1	39:QH:52:ASP:H	2.22	0.44
44:QM:4:ILE:HA	44:QM:5:ALA:HA	1.63	0.44
29:R7:43:THR:HG23	29:R7:44:PRO:HD2	1.99	0.44
1:RA:2099:U:H3	1:RA:2190:G:H1	1.65	0.44
1:RA:476:G:H4'	1:RA:502:A:N1	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:RO:73:ASP:HB2	15:RT:82:LEU:HD13	2.00	0.44
32:XA:1157:A:C2	32:XA:1181:G:C4	3.06	0.44
32:XA:1429:C:H2'	32:XA:1430:C:C6	2.53	0.44
34:XC:8:ILE:HD12	34:XC:16:ARG:HD3	2.00	0.44
44:XM:90:LEU:HD23	44:XM:93:ARG:HH21	1.83	0.44
47:XP:66:PRO:HG2	47:XP:71:ARG:HH12	1.82	0.44
51:XT:43:LEU:HA	51:XT:43:LEU:HD23	1.88	0.44
54:XY:265:HIS:CE1	54:XY:268:THR:HG1	2.35	0.44
1:YA:1359:A:N3	1:YA:1359:A:H5'	2.32	0.44
1:YA:823:G:H2'	1:YA:824:A:C8	2.53	0.44
1:YA:817:C:O2'	1:YA:839:U:H5''	2.18	0.44
2:YB:8:U:O2'	14:YS:40:ILE:HD13	2.17	0.44
8:YI:48:GLU:HG3	8:YI:52:ARG:HH11	1.82	0.44
15:YT:91:ARG:HD2	15:YT:120:ARG:NH1	2.32	0.44
32:QA:1016:A:H2'	32:QA:1017:G:O4'	2.17	0.44
32:QA:1073:U:C2	32:QA:1074:G:C8	3.06	0.44
32:QA:166:G:H2'	32:QA:167:G:H8	1.83	0.44
32:QA:25:C:H2'	32:QA:26:A:H8	1.82	0.44
32:QA:771:G:H2'	32:QA:772:U:C6	2.53	0.44
33:QB:44:LEU:HD12	33:QB:44:LEU:HA	1.79	0.44
32:QA:427:U:OP1	35:QD:13:ARG:NH2	2.51	0.44
35:QD:31:CYS:O	35:QD:35:ARG:HG3	2.18	0.44
42:QK:120:ARG:HA	42:QK:121:PRO:HD3	1.82	0.44
53:QV:3:C:C2'	53:QV:4:G:H5'	2.48	0.44
53:QV:21:A:N6	53:QV:46:G:H2'	2.31	0.44
54:QY:196:THR:HG22	54:QY:222:VAL:H	1.83	0.44
54:QY:334:LYS:NZ	54:QY:341:GLU:OE2	2.51	0.44
44:QM:61:GLU:HB3	26:R4:49:PHE:CE2	2.53	0.44
1:RA:1266:G:OP2	27:R5:20:ARG:NE	2.34	0.44
1:RA:1404:C:H2'	1:RA:1405:U:H6	1.82	0.44
1:RA:1945:G:H2'	1:RA:1946:U:C6	2.53	0.44
1:RA:2110:G:H5''	1:RA:2111:C:H5	1.83	0.44
1:RA:2282:G:H4'	1:RA:2389:G:O2'	2.17	0.44
1:RA:2747:G:O6	1:RA:2755:C:H5''	2.17	0.44
12:RQ:35:VAL:HG12	12:RQ:130:LYS:O	2.18	0.44
32:XA:1016:A:H2'	32:XA:1017:G:O4'	2.18	0.44
32:XA:1286:A:N6	32:XA:1354:C:O3'	2.51	0.44
32:XA:443:C:H2'	32:XA:444:C:H6	1.82	0.44
34:XC:148:GLY:HA3	34:XC:172:ARG:O	2.17	0.44
50:XS:40:ILE:HB	50:XS:67:VAL:O	2.18	0.44
54:XY:127:ASP:HB3	54:XY:184:SER:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1946:U:H2'	1:YA:1947:C:C6	2.53	0.44
1:YA:2455:G:H2'	1:YA:2456:C:C6	2.53	0.44
1:YA:2590:A:H2'	1:YA:2591:C:H6	1.81	0.44
1:YA:305:U:H2'	1:YA:306:U:C6	2.53	0.44
1:YA:607:U:C5	1:YA:620:G:C5	3.06	0.44
5:YF:188:ARG:HA	11:YP:3:LEU:HD13	2.00	0.44
8:YI:62:LYS:HG2	8:YI:133:HIS:NE2	2.33	0.44
32:QA:1033:G:H2'	32:QA:1034:G:C8	2.49	0.44
32:QA:452:A:H4'	47:QP:72:ARG:CZ	2.48	0.44
1:RA:2285:C:OP2	28:R6:6:ARG:NH1	2.51	0.44
1:RA:2262:U:H4'	1:RA:2328:A:C2	2.53	0.44
1:RA:2692:C:H2'	1:RA:2693:A:H8	1.83	0.44
1:RA:2812:G:H2'	1:RA:2813:A:H8	1.83	0.44
1:RA:52:A:H2'	1:RA:53:A:C8	2.53	0.44
1:RA:887:A:O2'	1:RA:888:C:H3'	2.18	0.44
1:RA:958:U:O2	2:RB:90:A:O2'	2.29	0.44
4:RE:31:CYS:HB3	4:RE:49:LEU:HG	1.99	0.44
15:RT:35:LYS:HE3	15:RT:36:GLU:O	2.18	0.44
32:XA:1151:A:O2'	32:XA:1152:A:H8	2.01	0.44
32:XA:791:G:N2	32:XA:1497:G:O3'	2.51	0.44
32:XA:73:G:H2'	32:XA:76:C:H6	1.83	0.44
32:XA:948:C:H2'	32:XA:949:A:H8	1.82	0.44
35:XD:11:LEU:O	35:XD:15:GLU:HB2	2.18	0.44
40:XI:111:ARG:O	40:XI:113:LYS:HD2	2.17	0.44
42:XK:18:ARG:HB2	42:XK:33:THR:OG1	2.17	0.44
54:XY:251:GLY:O	54:XY:253:HIS:N	2.51	0.44
54:XY:64:GLU:O	54:XY:68:ASP:HB2	2.18	0.44
28:Y6:6:ARG:NH1	28:Y6:26:ASN:HB2	2.33	0.44
1:YA:1322:A:C5	1:YA:1323:U:C5	3.06	0.44
1:YA:1756:G:H4'	1:YA:1758:G:O4'	2.18	0.44
1:YA:185:U:H2'	1:YA:186:G:H8	1.82	0.44
1:YA:330:A:HO2'	1:YA:331:A:H8	1.65	0.44
1:YA:721:C:H2'	1:YA:722:A:C8	2.53	0.44
32:QA:629:G:H2'	32:QA:630:G:O4'	2.17	0.43
32:QA:67:C:H2'	32:QA:68:G:C8	2.52	0.43
32:QA:73:G:H1	32:QA:96:U:H3	1.66	0.43
32:QA:73:G:H2'	32:QA:76:C:C6	2.53	0.43
33:QB:107:THR:O	33:QB:110:GLN:HB2	2.18	0.43
23:R1:51:VAL:HG12	23:R1:53:VAL:HG23	2.00	0.43
24:R2:65:ASN:O	24:R2:69:ARG:HB2	2.18	0.43
25:R3:59:VAL:O	25:R3:60:GLU:HG2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:1386:C:H2'	1:RA:1387:C:C6	2.53	0.43
1:RA:1482:G:C6	1:RA:1507:A:C6	3.05	0.43
1:RA:17:G:H2'	1:RA:18:C:C6	2.53	0.43
1:RA:1952:A:OP1	10:RO:42:SER:OG	2.28	0.43
1:RA:2051:A:H5'	1:RA:2578:G:O4'	2.17	0.43
1:RA:2590:A:H2'	1:RA:2591:C:H6	1.83	0.43
1:RA:27:G:N2	1:RA:512:G:H1'	2.33	0.43
6:RG:47:LYS:HG3	6:RG:48:GLU:H	1.83	0.43
13:RR:41:ALA:HB1	13:RR:114:VAL:CG2	2.47	0.43
18:RW:46:PHE:O	18:RW:50:VAL:HG23	2.18	0.43
18:RW:68:ARG:NH1	18:RW:112:GLY:H	2.16	0.43
1:YA:1171:G:N2	1:YA:1178:C:O2	2.50	0.43
1:YA:1371:G:HO2'	1:YA:1372:U:H5	1.65	0.43
1:YA:1999:C:H5''	1:YA:2723:C:O2'	2.18	0.43
1:YA:2290:G:H2'	1:YA:2291:U:C6	2.53	0.43
1:YA:2443:C:H2'	1:YA:2444:G:H8	1.82	0.43
1:YA:2461:C:H2'	1:YA:2462:U:H6	1.81	0.43
4:YE:54:GLN:OE1	4:YE:55:ASN:N	2.48	0.43
8:YI:69:LYS:HB2	8:YI:138:ILE:HG12	1.99	0.43
1:YA:1669:A:C8	10:YO:5:GLN:HG3	2.53	0.43
11:YP:63:PRO:HB2	30:Y8:30:ARG:NH2	2.34	0.43
12:YQ:109:VAL:HG13	12:YQ:113:GLN:HB2	1.99	0.43
38:QG:90:GLU:N	38:QG:90:GLU:OE2	2.37	0.43
51:QT:100:ILE:HB	51:QT:101:GLY:H	1.63	0.43
1:RA:1164:G:H2'	1:RA:1165:U:H6	1.83	0.43
1:RA:1685:C:H2'	1:RA:1686:C:H6	1.82	0.43
1:RA:2693:A:H2'	1:RA:2694:G:C8	2.51	0.43
1:RA:2698:U:H2'	1:RA:2699:C:H6	1.82	0.43
1:RA:2812:G:H2'	1:RA:2813:A:C8	2.53	0.43
1:RA:2845:G:H2'	1:RA:2846:G:C8	2.53	0.43
1:RA:852:G:H2'	1:RA:853:G:C8	2.54	0.43
7:RH:137:ASP:HB3	7:RH:140:LYS:HB3	2.00	0.43
15:RT:35:LYS:C	15:RT:35:LYS:CD	2.86	0.43
32:XA:1119:C:H2'	32:XA:1120:G:C8	2.49	0.43
32:XA:438:G:O2'	32:XA:494:U:O4	2.28	0.43
32:XA:913:A:H4'	32:XA:914:A:O5'	2.18	0.43
33:XB:211:ILE:O	33:XB:215:LEU:HB2	2.17	0.43
34:XC:22:TRP:CD1	34:XC:59:ARG:HD2	2.53	0.43
40:XI:112:LYS:HE2	40:XI:117:HIS:O	2.18	0.43
47:XP:21:VAL:HG11	47:XP:59:TRP:NE1	2.33	0.43
1:YA:1790:C:O2'	3:YD:209:ALA:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:2047:U:H2'	1:YA:2048:G:H8	1.82	0.43
3:YD:24:ILE:HD13	3:YD:84:TYR:HB2	1.99	0.43
5:YF:192:LEU:CD2	5:YF:194:MET:HG3	2.48	0.43
13:YR:18:LEU:HD13	13:YR:22:ARG:HD2	2.00	0.43
32:QA:1280:A:O2'	32:QA:1281:U:H5'	2.19	0.43
35:QD:107:ARG:HG3	35:QD:173:TRP:HH2	1.84	0.43
37:QF:41:GLU:HG2	37:QF:43:LEU:HD12	2.00	0.43
54:QY:76:GLY:O	54:QY:80:VAL:HG23	2.17	0.43
1:RA:2110:G:OP1	1:RA:2118:U:N3	2.51	0.43
2:RB:13:A:N1	2:RB:69:G:O2'	2.44	0.43
3:RD:242:ARG:HD3	3:RD:242:ARG:N	2.32	0.43
7:RH:167:GLU:HA	7:RH:168:PRO:HD3	1.90	0.43
19:RX:5:TYR:CE1	24:R2:33:MET:CE	3.01	0.43
32:XA:1005:A:H1'	32:XA:1025:U:C2	2.53	0.43
32:XA:323:U:H2'	32:XA:324:G:O4'	2.19	0.43
32:XA:669:U:H2'	32:XA:670:G:H8	1.84	0.43
32:XA:923:A:H2'	32:XA:924:C:C6	2.53	0.43
41:XJ:45:ARG:HG2	41:XJ:47:PHE:CZ	2.54	0.43
51:XT:14:LYS:HE3	51:XT:18:GLN:NE2	2.33	0.43
54:XY:286:GLN:O	54:XY:290:GLN:HG3	2.18	0.43
1:YA:1275:A:N1	1:YA:1295:C:O2'	2.41	0.43
1:YA:2102:U:O2	1:YA:2187:G:O6	2.36	0.43
1:YA:2286:A:H4'	1:YA:2287:A:O4'	2.18	0.43
1:YA:272(Q):G:H2'	1:YA:272(R):G:C8	2.54	0.43
13:YR:44:LEU:CD2	13:YR:48:VAL:HG23	2.48	0.43
14:YS:75:GLU:OE1	14:YS:75:GLU:HA	2.17	0.43
32:QA:1308:U:H2'	32:QA:1309:G:H8	1.84	0.43
32:QA:7:G:H5''	32:QA:298:A:O4'	2.18	0.43
1:RA:1446:C:H2'	1:RA:1447:G:C8	2.54	0.43
1:RA:729:G:OP2	3:RD:13:ARG:HD3	2.18	0.43
1:RA:992:C:OP1	16:RU:47:TYR:OH	2.26	0.43
1:RA:2572:A:N7	4:RE:144:ARG:HG2	2.33	0.43
6:RG:181:ARG:HG3	6:RG:182:LYS:H	1.83	0.43
6:RG:41:GLN:HB3	6:RG:43:LEU:CD1	2.40	0.43
7:RH:9:ILE:CD1	7:RH:69:ARG:HD2	2.46	0.43
11:RP:112:LEU:HD22	11:RP:113:LYS:N	2.34	0.43
14:RS:14:VAL:O	14:RS:18:ILE:HG12	2.18	0.43
16:RU:86:ALA:O	17:RV:49:THR:HG23	2.18	0.43
21:RZ:203:GLU:OE2	53:QV:54:U:C5'	2.66	0.43
32:XA:116:A:H61	32:XA:313:A:H1'	1.83	0.43
32:XA:417:C:H2'	32:XA:418:C:C6	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:448:A:P	32:XA:485:G:H22	2.41	0.43
34:XC:186:PHE:HZ	34:XC:188:LEU:HD13	1.83	0.43
38:XG:137:LYS:NZ	38:XG:141:VAL:CG2	2.82	0.43
47:XP:43:LYS:HG2	47:XP:48:TRP:CD2	2.52	0.43
51:XT:58:LYS:HA	51:XT:58:LYS:HD2	1.87	0.43
52:XU:3:LYS:HB3	52:XU:14:TRP:CG	2.53	0.43
1:YA:1833:U:O2'	1:YA:1969:A:N1	2.44	0.43
1:YA:2070:G:C2	1:YA:2442:C:C2	3.06	0.43
1:YA:453:C:O2	1:YA:457:A:O2'	2.35	0.43
5:YF:192:LEU:HD22	5:YF:194:MET:HG3	2.01	0.43
5:YF:29:ASN:H	5:YF:112:MET:CE	2.32	0.43
6:YG:36:LYS:HG3	6:YG:38:VAL:HG23	1.99	0.43
7:YH:55:PRO:HG2	7:YH:61:HIS:ND1	2.34	0.43
8:YI:4:ILE:HD11	8:YI:44:LEU:HD13	2.00	0.43
10:YO:80:ASP:OD1	15:YT:64:ARG:NH2	2.51	0.43
32:QA:1148:U:H2'	32:QA:1149:C:O4'	2.19	0.43
32:QA:1148:U:O3'	40:QI:14:VAL:HG11	2.19	0.43
32:QA:113:G:H2'	32:QA:114:U:C6	2.53	0.43
32:QA:130:A:O2'	32:QA:131:C:O5'	2.35	0.43
32:QA:745:C:H2'	32:QA:746:A:C8	2.53	0.43
34:QC:5:ILE:HG13	34:QC:6:HIS:N	2.34	0.43
40:QI:111:ARG:HG2	40:QI:112:LYS:N	2.33	0.43
54:QY:219:SER:HB3	54:QY:317:ILE:HG22	1.99	0.43
54:QY:38:ASN:O	54:QY:42:GLU:HB2	2.18	0.43
24:R2:63:VAL:O	24:R2:66:GLU:HB2	2.18	0.43
29:R7:16:HIS:HB2	29:R7:44:PRO:HG2	2.00	0.43
29:R7:9:ARG:HH22	29:R7:47:ARG:CD	2.31	0.43
1:RA:823:G:H2'	1:RA:824:A:H8	1.83	0.43
4:RE:67:PHE:O	4:RE:72:VAL:HG12	2.18	0.43
8:RI:8:PRO:O	8:RI:9:LEU:HD22	2.18	0.43
1:RA:2674:G:O2'	10:RO:29:ASN:OD1	2.28	0.43
32:XA:1238:A:H2	32:XA:1241:G:N3	2.16	0.43
32:XA:125:U:H2'	32:XA:126:G:C8	2.53	0.43
32:XA:1512:U:H2'	32:XA:1513:A:H8	1.84	0.43
33:XB:88:ALA:CB	33:XB:222:ILE:HD11	2.40	0.43
35:XD:108:LEU:HD12	35:XD:174:LEU:HD13	1.98	0.43
38:XG:101:LEU:O	38:XG:105:VAL:HG23	2.18	0.43
42:XK:84:VAL:HG21	42:XK:95:ILE:HD11	2.00	0.43
1:YA:1604:C:O2'	1:YA:1610:A:N1	2.45	0.43
1:YA:1885:A:H2'	1:YA:1886:C:O4'	2.18	0.43
1:YA:2649:U:H2'	1:YA:2650:U:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:817:C:H2'	1:YA:818:G:O4'	2.19	0.43
4:YE:170:LEU:HB3	4:YE:184:VAL:HG13	2.00	0.43
6:YG:64:THR:HB	6:YG:94:LEU:HD21	2.00	0.43
7:YH:13:LYS:HA	7:YH:14:GLY:HA2	1.80	0.43
12:YQ:62:GLY:CA	12:YQ:109:VAL:HG23	2.48	0.43
16:YU:49:HIS:HA	16:YU:52:ARG:HB3	1.99	0.43
19:YX:12:VAL:HG22	19:YX:29:TRP:CE2	2.53	0.43
32:QA:1422:G:H2'	32:QA:1423:G:H8	1.83	0.43
34:QC:123:GLN:O	34:QC:128:PHE:HB2	2.18	0.43
32:QA:4:U:O4	39:QH:105:ARG:HD3	2.18	0.43
39:QH:46:LYS:HG3	39:QH:64:LYS:HB2	2.00	0.43
44:QM:88:ARG:HG3	44:QM:98:VAL:HG11	2.00	0.43
50:QS:79:THR:CG2	50:QS:81:ARG:NH1	2.82	0.43
51:QT:59:ALA:O	51:QT:63:ILE:HG13	2.19	0.43
54:QY:335:ASP:C	54:QY:337:ARG:H	2.17	0.43
1:RA:1431:U:H2'	1:RA:1432:C:H6	1.82	0.43
1:RA:236:C:H2'	1:RA:237:C:H6	1.84	0.43
1:RA:607:U:C5	1:RA:620:G:C5	3.07	0.43
3:RD:145:VAL:HG12	3:RD:146:GLU:O	2.18	0.43
1:RA:956:G:P	12:RQ:14:ARG:HH22	2.39	0.43
32:XA:1492:A:P	43:XL:47:LYS:HG3	2.58	0.43
43:XL:27:LEU:HD13	43:XL:98:TYR:CE1	2.54	0.43
44:XM:20:THR:HG21	44:XM:27:LYS:HZ1	1.83	0.43
22:Y0:19:LYS:HD2	22:Y0:19:LYS:N	2.34	0.43
1:YA:2130:U:H2'	1:YA:2158:A:N1	2.33	0.43
1:YA:796:C:H2'	1:YA:797:C:C6	2.53	0.43
1:YA:868:U:O2	12:YQ:8:LYS:NZ	2.52	0.43
1:YA:978:G:O4'	1:YA:1001:A:H2	2.01	0.43
1:YA:637:A:H5''	11:YP:117:GLU:HG2	2.00	0.43
13:YR:36:THR:HG22	13:YR:37:THR:N	2.27	0.43
14:YS:27:SER:HA	14:YS:88:ASP:HB3	1.99	0.43
32:QA:426:G:OP1	35:QD:38:TYR:OH	2.37	0.43
32:QA:437:U:O2'	35:QD:123:HIS:ND1	2.31	0.43
32:QA:441:A:H3'	32:QA:442:C:H6	1.84	0.43
32:QA:570:G:H2'	32:QA:571:U:C6	2.52	0.43
32:QA:978:A:C4	32:QA:1319:A:C2	3.07	0.43
32:QA:406:G:H5'	35:QD:5:ILE:HD11	2.01	0.43
48:QQ:10:VAL:HG13	48:QQ:19:VAL:HB	2.01	0.43
54:QY:196:THR:HA	54:QY:220:ALA:O	2.18	0.43
11:RP:62:LEU:O	30:R8:13:ARG:HD3	2.19	0.43
1:RA:1005:C:H2'	1:RA:1006:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:2149:G:H2'	1:RA:2150:U:O4'	2.19	0.43
1:RA:2070:G:C2	1:RA:2442:C:C2	3.07	0.43
16:RU:76:TYR:CZ	16:RU:80:ILE:HG13	2.53	0.43
32:XA:1030(C):C:H41	32:XA:1030(D):G:N2	2.16	0.43
32:XA:1263:C:H2'	32:XA:1264:C:C6	2.53	0.43
32:XA:1355:G:H2'	32:XA:1356:G:C8	2.53	0.43
32:XA:1512:U:H2'	32:XA:1513:A:C8	2.54	0.43
41:XJ:6:ILE:HB	41:XJ:72:VAL:HG22	2.01	0.43
44:XM:110:ARG:HG2	44:XM:110:ARG:HH11	1.83	0.43
51:XT:37:SER:O	51:XT:41:ILE:HG12	2.19	0.43
51:XT:56:MET:CE	51:XT:84:LEU:CD2	2.70	0.43
53:XV:28:C:H42	53:XV:42:G:H1	1.66	0.43
54:XY:129:TYR:CE1	54:XY:182:LYS:HG3	2.50	0.43
1:YA:1790:C:H5''	1:YA:1791:A:OP1	2.18	0.43
1:YA:686:G:N2	1:YA:788:A:H61	2.16	0.43
4:YE:144:ARG:HB3	4:YE:145:LYS:H	1.52	0.43
7:YH:54:ARG:NE	7:YH:57:ASP:OD1	2.47	0.43
32:QA:1101:A:H4'	32:QA:1102:A:O5'	2.19	0.43
32:QA:657:G:H4'	46:QO:28:GLN:HG2	1.99	0.43
32:QA:750:G:O2'	46:QO:22:THR:O	2.16	0.43
26:R4:57:GLU:CB	26:R4:58:ARG:HA	2.49	0.43
30:R8:31:HIS:CD2	30:R8:32:LEU:CD2	3.02	0.43
1:RA:1092:C:O2	1:RA:1092:C:H2'	2.19	0.43
1:RA:1688:U:O2	1:RA:1700:A:H5'	2.19	0.43
1:RA:2513:G:H2'	1:RA:2514:U:C6	2.54	0.43
1:RA:2515:C:H2'	1:RA:2516:G:H8	1.84	0.43
1:RA:668:G:C2	1:RA:670:A:C6	3.07	0.43
1:RA:863:A:H2'	1:RA:864:G:H8	1.84	0.43
8:RI:75:LEU:HD22	8:RI:105:HIS:ND1	2.33	0.43
13:RR:118:GLU:CD	13:RR:118:GLU:H	2.22	0.43
32:XA:476:G:H2'	32:XA:477:A:C8	2.54	0.43
32:XA:69:G:H2'	32:XA:70:G:C8	2.53	0.43
32:XA:985:C:H2'	32:XA:986:A:C8	2.54	0.43
36:XE:127:ASN:HA	36:XE:128:PRO:HD3	1.87	0.43
38:XG:10:ARG:HH11	38:XG:10:ARG:CG	2.29	0.43
44:XM:19:LEU:HD21	44:XM:56:LEU:HD21	2.00	0.43
23:Y1:53:VAL:HG22	23:Y1:74:VAL:HG13	2.00	0.43
1:YA:1614:A:N1	18:YW:93:ALA:HB2	2.33	0.43
1:YA:2271:G:OP1	22:Y0:18:ALA:HB1	2.19	0.43
1:YA:2320:A:N3	1:YA:2320:A:H2'	2.33	0.43
1:YA:586:A:N1	1:YA:809:G:O2'	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:652(D):G:N2	1:YA:653:A:H1'	2.33	0.43
1:YA:729:G:C8	3:YD:208:LYS:HD2	2.54	0.43
1:YA:740:U:H2'	1:YA:741:G:C8	2.54	0.43
1:YA:848:G:H2'	1:YA:849:A:H8	1.81	0.43
32:QA:1238:A:N7	32:QA:1303:C:H1'	2.33	0.43
32:QA:1328:C:H2'	32:QA:1329:A:O4'	2.18	0.43
36:QE:137:GLU:HG2	36:QE:140:ARG:HH11	1.84	0.43
45:QN:24:CYS:HB2	45:QN:40:CYS:HB3	2.01	0.43
46:QO:3:ILE:HD12	46:QO:34:LEU:HD21	1.93	0.43
48:QQ:67:LYS:O	48:QQ:68:ARG:CB	2.65	0.43
50:QS:22:LEU:HD12	50:QS:31:ILE:HD11	2.00	0.43
1:RA:2507:C:O4'	54:QY:255:ASN:HB3	2.19	0.43
54:QY:332:ARG:NH1	54:QY:334:LYS:HE2	2.33	0.43
29:R7:9:ARG:HH21	29:R7:47:ARG:HB3	1.79	0.43
1:RA:2394:C:OP2	30:R8:30:ARG:HD2	2.18	0.43
1:RA:1669:A:C8	10:RO:5:GLN:HG3	2.54	0.43
1:RA:272(Z):C:H1'	1:RA:273(D):G:H1'	1.99	0.43
1:RA:297:C:H2'	1:RA:298:G:O4'	2.19	0.43
2:RB:22:U:H2'	2:RB:23:G:C8	2.54	0.43
1:RA:1798:U:H5'	3:RD:259:THR:HG22	2.00	0.43
6:RG:43:LEU:HB3	6:RG:44:GLY:H	1.67	0.43
7:RH:20:ALA:HB1	7:RH:21:PRO:HD2	2.00	0.43
8:RI:140:LEU:HD13	8:RI:142:VAL:HG23	2.01	0.43
10:RO:63:VAL:HG12	10:RO:106:LEU:HD11	1.99	0.43
16:RU:8:VAL:CG1	16:RU:12:ARG:CZ	2.97	0.43
19:RX:5:TYR:OH	24:R2:30:ARG:HD2	2.19	0.43
32:XA:110:C:H2'	32:XA:111:G:O4'	2.19	0.43
32:XA:1354:C:H2'	32:XA:1355:G:H8	1.84	0.43
32:XA:514:C:H2'	32:XA:515:G:C8	2.54	0.43
33:XB:28:PHE:CD1	33:XB:190:THR:HA	2.54	0.43
33:XB:96:ARG:CD	33:XB:98:LEU:HD23	2.44	0.43
37:XF:10:LEU:HB2	37:XF:59:TYR:HB3	2.01	0.43
54:XY:132:ILE:HA	54:XY:219:SER:O	2.19	0.43
26:Y4:61:ARG:HG2	50:XS:42:PRO:HG2	1.98	0.43
1:YA:1005:C:H2'	1:YA:1006:C:C6	2.54	0.43
1:YA:1045:A:N3	1:YA:1045:A:H2'	2.33	0.43
1:YA:185:U:H2'	1:YA:186:G:C8	2.54	0.43
1:YA:2153:G:H2'	1:YA:2154:G:C8	2.54	0.43
1:YA:610:G:H2'	1:YA:611:C:C6	2.54	0.43
5:YF:39:TRP:HZ2	5:YF:106:ARG:NH2	2.12	0.43
12:YQ:7:MET:HG3	12:YQ:9:TYR:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:YR:100:LEU:HD22	13:YR:112:ALA:CA	2.40	0.43
32:QA:1120:G:H2'	32:QA:1121:U:H6	1.83	0.43
32:QA:1131:G:H2'	32:QA:1132:C:C6	2.54	0.43
32:QA:246:A:C2	32:QA:282:A:C5	3.07	0.43
32:QA:687:A:H1'	32:QA:688:G:OP2	2.19	0.43
50:QS:64:GLU:CA	26:R4:59:PHE:HE1	2.32	0.43
1:RA:1946:U:H2'	1:RA:1947:C:C6	2.53	0.43
1:RA:2086:U:H2'	1:RA:2087:G:C8	2.53	0.43
1:RA:2300:G:H2'	1:RA:2301:C:C6	2.54	0.43
1:RA:2848:G:O2'	1:RA:2867:G:N2	2.44	0.43
1:RA:685:A:N1	1:RA:787:U:H1'	2.34	0.43
5:RF:168:ARG:HD3	5:RF:168:ARG:HH11	1.69	0.43
5:RF:29:ASN:HB3	5:RF:112:MET:HE1	2.00	0.43
11:RP:96:THR:H	11:RP:99:LEU:HD12	1.82	0.43
12:RQ:62:GLY:CA	12:RQ:109:VAL:HG23	2.49	0.43
15:RT:106:SER:O	15:RT:110:ILE:HG13	2.18	0.43
19:RX:2:LYS:NZ	19:RX:38:GLU:OE2	2.30	0.43
20:RY:102:CYS:SG	20:RY:103:GLY:N	2.92	0.43
20:RY:92:ASN:CB	20:RY:94:LYS:H	2.30	0.43
21:RZ:146:ILE:HA	21:RZ:147:GLY:HA2	1.79	0.43
32:XA:1014:A:C2	32:XA:1219:U:H1'	2.54	0.43
32:XA:1273:G:H3'	32:XA:1274:G:H8	1.82	0.43
32:XA:253:U:H2'	32:XA:254:G:H8	1.83	0.43
32:XA:691:G:H2'	32:XA:692:U:C6	2.54	0.43
32:XA:908:A:H2'	32:XA:909:A:C8	2.54	0.43
35:XD:173:TRP:CZ3	35:XD:193:ASP:HB3	2.54	0.43
37:XF:76:ALA:O	37:XF:80:ARG:HG3	2.19	0.43
40:XI:9:ARG:H	40:XI:79:LEU:HD23	1.83	0.43
47:XP:20:VAL:CG2	47:XP:32:TYR:CG	3.00	0.43
1:YA:1021:A:N3	1:YA:1021:A:H3'	2.34	0.43
1:YA:2287:A:O2'	1:YA:2288:A:H3'	2.19	0.43
1:YA:2355:C:H2'	1:YA:2356:C:O4'	2.19	0.43
1:YA:2848:G:O2'	1:YA:2867:G:N2	2.49	0.43
1:YA:511:U:O4	1:YA:512:G:N1	2.51	0.43
12:YQ:62:GLY:O	21:YZ:178:GLU:HG2	2.19	0.43
15:YT:118:ARG:NH2	15:YT:121:ILE:HD12	2.17	0.43
32:QA:1075:C:OP1	33:QB:179:LYS:NZ	2.51	0.42
32:QA:1411:C:H2'	32:QA:1412:C:C6	2.53	0.42
32:QA:1504:G:OP1	32:QA:1507:A:H4'	2.19	0.42
32:QA:859:A:H2'	32:QA:860:A:O4'	2.19	0.42
36:QE:148:VAL:O	36:QE:152:ARG:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:QG:48:LYS:O	38:QG:52:GLU:HG2	2.19	0.42
39:QH:41:ARG:NH1	39:QH:123:GLU:OE2	2.48	0.42
39:QH:51:VAL:HG11	39:QH:60:ARG:NH1	2.33	0.42
32:QA:1316:G:O2'	45:QN:18:VAL:HG11	2.19	0.42
54:QY:141:ALA:HA	54:QY:144:TRP:HB3	2.01	0.42
23:R1:3:LYS:HG3	23:R1:4:VAL:N	2.32	0.42
30:R8:14:VAL:CG1	30:R8:22:VAL:HG13	2.47	0.42
1:RA:2153:G:H2'	1:RA:2154:G:H8	1.84	0.42
7:RH:3:ARG:HB3	7:RH:6:ARG:HG2	2.01	0.42
9:RN:58:ASP:N	9:RN:58:ASP:OD1	2.51	0.42
12:RQ:110:THR:HG23	12:RQ:113:GLN:OE1	2.19	0.42
17:RV:62:LEU:HD11	17:RV:95:LEU:CB	2.49	0.42
21:RZ:40:ASP:HB3	21:RZ:43:GLU:HB2	2.01	0.42
33:XB:32:ILE:HD13	33:XB:40:HIS:CD2	2.54	0.42
32:XA:406:G:O2'	35:XD:3:ARG:NH2	2.52	0.42
44:XM:20:THR:CG2	44:XM:27:LYS:NZ	2.78	0.42
53:XV:58:A:O2'	53:XV:60:U:OP2	2.22	0.42
54:XY:100:VAL:HA	54:XY:103:LEU:HB3	2.01	0.42
1:YA:1408:C:H2'	1:YA:1409:C:C6	2.54	0.42
1:YA:2365:G:N7	30:Y8:39:LYS:NZ	2.64	0.42
1:YA:709:U:H2'	1:YA:710:G:C8	2.54	0.42
1:YA:774:A:N3	1:YA:774:A:H2'	2.34	0.42
15:YT:118:ARG:NE	15:YT:118:ARG:HA	2.34	0.42
32:QA:1285:A:H1'	32:QA:1286:A:OP2	2.19	0.42
32:QA:902:G:H2'	32:QA:903:G:H8	1.83	0.42
35:QD:108:LEU:HB3	35:QD:110:PHE:CD1	2.55	0.42
32:QA:1148:U:O4'	40:QI:16:ARG:HD2	2.18	0.42
42:QK:99:GLN:HG2	42:QK:105:VAL:HG21	2.01	0.42
46:QO:17:ARG:HG3	46:QO:17:ARG:HH11	1.84	0.42
48:QQ:58:GLU:OE2	48:QQ:75:ARG:NH2	2.52	0.42
51:QT:101:GLY:HA2	51:QT:102:GLY:HA2	1.72	0.42
1:RA:1025:G:C4	1:RA:1135:C:H1'	2.54	0.42
1:RA:1053:C:O2'	1:RA:1054:A:O5'	2.32	0.42
1:RA:1406:U:C2	1:RA:1407:C:C5	3.07	0.42
1:RA:185:U:H4'	1:RA:218:A:H4'	2.02	0.42
1:RA:2543:G:H2'	1:RA:2544:G:C8	2.54	0.42
4:RE:47:VAL:HG23	4:RE:84:PHE:O	2.19	0.42
32:XA:320:C:H2'	32:XA:321:A:C8	2.54	0.42
32:XA:955:U:HO2'	50:XS:83:HIS:CE1	2.37	0.42
33:XB:158:LEU:HA	33:XB:159:PRO:HD3	1.83	0.42
32:XA:677:U:H1'	42:XK:119:CYS:SG	2.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:XK:84:VAL:CG1	42:XK:91:ARG:HD2	2.49	0.42
47:XP:3:LYS:O	47:XP:21:VAL:HA	2.19	0.42
32:XA:130:A:H5'	48:XQ:63:ARG:HE	1.83	0.42
51:XT:100:ILE:CG2	51:XT:101:GLY:H	2.30	0.42
54:XY:260:ALA:CB	54:XY:275:GLN:HG2	2.49	0.42
1:YA:2064:C:H2'	1:YA:2065:C:H6	1.82	0.42
1:YA:304:G:H2'	1:YA:305:U:C6	2.54	0.42
1:YA:588:U:H2'	1:YA:589:C:C6	2.54	0.42
1:YA:841:A:H2'	1:YA:842:G:C8	2.55	0.42
1:YA:2784:C:H1'	4:YE:37:ARG:HH12	1.83	0.42
6:YG:145:THR:CG2	6:YG:148:MET:HG2	2.50	0.42
7:YH:27:LYS:HD3	7:YH:32:GLU:HB2	2.01	0.42
13:YR:95:THR:HG22	13:YR:116:LEU:HD23	1.99	0.42
14:YS:71:ARG:NH1	14:YS:107:GLU:OE1	2.52	0.42
18:YW:12:ILE:HD13	18:YW:17:VAL:CG1	2.49	0.42
32:QA:1151:A:O2'	32:QA:1152:A:O5'	2.33	0.42
32:QA:33:A:H2'	32:QA:34:C:C6	2.54	0.42
43:QL:97:ARG:HB2	43:QL:98:TYR:CE1	2.54	0.42
32:QA:719:C:O2'	49:QR:49:LYS:HB3	2.20	0.42
27:R5:35:GLU:HG3	27:R5:51:TYR:CB	2.49	0.42
1:RA:2065:C:H2'	1:RA:2066:C:H6	1.84	0.42
1:RA:2643:G:H2'	1:RA:2644:G:O4'	2.18	0.42
1:RA:702:G:C2	1:RA:731:C:C2	3.07	0.42
3:RD:13:ARG:HD2	3:RD:16:MET:HE3	2.02	0.42
14:RS:24:LEU:HA	14:RS:24:LEU:HD23	1.85	0.42
15:RT:95:ARG:NH1	15:RT:95:ARG:CG	2.82	0.42
17:RV:28:GLU:HG3	17:RV:29:PRO:HD2	2.00	0.42
32:XA:1226:C:H4'	50:XS:80:TYR:OH	2.20	0.42
32:XA:390:C:H4'	47:XP:28:ARG:NH2	2.31	0.42
33:XB:74:LYS:HD3	33:XB:165:VAL:HG12	2.02	0.42
34:XC:73:PRO:O	34:XC:77:ILE:HG12	2.20	0.42
35:XD:17:VAL:HG12	35:XD:18:LYS:N	2.34	0.42
54:XY:134:ALA:O	54:XY:317:ILE:HD13	2.20	0.42
1:YA:1053:C:H2'	1:YA:1054:A:C8	2.54	0.42
1:YA:1357:U:H2'	1:YA:1358:G:O4'	2.18	0.42
2:YB:4:C:H2'	2:YB:5:C:H6	1.84	0.42
3:YD:276:LYS:HG3	3:YD:276:LYS:H	1.45	0.42
5:YF:53:THR:HG22	5:YF:56:GLU:OE2	2.18	0.42
6:YG:3:LEU:HD23	6:YG:97:ASP:OD2	2.20	0.42
1:YA:2312:U:H5'	6:YG:88:ILE:HD11	1.99	0.42
10:YO:10:VAL:HG21	10:YO:16:ALA:O	2.15	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:84:A:H5''	20:YY:8:LYS:HE3	2.00	0.42
32:QA:834:C:H2'	32:QA:835:U:C6	2.54	0.42
35:QD:23:GLY:HA3	35:QD:112:VAL:HB	2.01	0.42
38:QG:69:VAL:CG2	38:QG:104:LEU:HD21	2.48	0.42
39:QH:6:ILE:HB	39:QH:85:ARG:NH1	2.33	0.42
44:QM:84:ILE:HD12	50:QS:74:PHE:CE2	2.55	0.42
54:QY:115:PHE:HB3	54:QY:119:PHE:CD2	2.46	0.42
54:QY:140:GLU:OE1	54:QY:206:PRO:HD2	2.19	0.42
54:QY:310:MET:O	54:QY:314:LYS:HG3	2.19	0.42
1:RA:1021:A:H3'	1:RA:1021:A:N3	2.35	0.42
1:RA:1379:A:H4'	1:RA:1380:G:OP2	2.20	0.42
1:RA:2117:A:H4'	1:RA:2148:G:OP1	2.20	0.42
1:RA:218:A:C2	1:RA:235:U:H4'	2.54	0.42
1:RA:2250:G:O2'	1:RA:2496:C:OP1	2.31	0.42
1:RA:300:A:OP1	20:RY:86:ARG:NH2	2.52	0.42
1:RA:774:A:H2'	1:RA:774:A:N3	2.34	0.42
6:RG:16:ARG:CZ	6:RG:31:VAL:HG21	2.49	0.42
36:XE:12:LEU:O	36:XE:30:ALA:HA	2.19	0.42
41:XJ:57:LYS:HE2	41:XJ:60:ARG:HH21	1.83	0.42
41:XJ:80:LYS:O	41:XJ:84:GLN:HB2	2.20	0.42
54:XY:18:SER:O	54:XY:22:ARG:HG3	2.19	0.42
54:XY:326:TYR:HA	54:XY:333:ILE:HG12	2.02	0.42
1:YA:1427:A:H4'	1:YA:1428:C:O4'	2.19	0.42
1:YA:2342:C:O2'	1:YA:2374:C:H5''	2.19	0.42
1:YA:2352:A:N6	1:YA:2365:G:O2'	2.53	0.42
1:YA:2521:C:H2'	1:YA:2522:U:C6	2.55	0.42
1:YA:272(P):C:H2'	1:YA:272(Q):G:C8	2.54	0.42
1:YA:300:A:O2'	1:YA:318:C:O2	2.34	0.42
5:YF:24:LEU:HD21	5:YF:114:VAL:HG12	2.01	0.42
6:YG:38:VAL:HB	6:YG:158:ALA:HB3	2.02	0.42
7:YH:86:GLU:OE2	7:YH:132:ARG:NH2	2.52	0.42
12:YQ:55:VAL:HG11	21:YZ:183:LEU:HD21	2.02	0.42
13:YR:118:GLU:H	13:YR:118:GLU:CD	2.21	0.42
32:QA:1030(A):C:N3	32:QA:1031:G:N2	2.68	0.42
32:QA:922:G:H2'	32:QA:923:A:H8	1.80	0.42
51:QT:53:LEU:HD13	51:QT:100:ILE:HG13	2.00	0.42
53:QV:54:U:N3	53:QV:58:A:C8	2.88	0.42
1:RA:1637:A:H4'	1:RA:2711:A:O2'	2.19	0.42
1:RA:777:A:H2'	1:RA:778:G:H8	1.85	0.42
1:RA:81:G:H2'	1:RA:82:G:O4'	2.19	0.42
1:RA:839:U:H2'	1:RA:840:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:998:C:P	16:RU:92:ARG:HH22	2.43	0.42
2:RB:16:G:N2	2:RB:69:G:H1'	2.34	0.42
14:RS:25:ARG:HD3	14:RS:42:ASP:OD2	2.19	0.42
1:RA:1188:U:H4'	17:RV:79:VAL:HG22	2.02	0.42
32:XA:1429:C:H2'	32:XA:1430:C:H6	1.83	0.42
34:XC:18:TRP:NE1	45:XN:53:LEU:O	2.52	0.42
51:XT:38:LYS:HE2	51:XT:38:LYS:HB3	1.70	0.42
51:XT:43:LEU:HD13	51:XT:51:GLU:HB3	2.00	0.42
54:XY:243:VAL:HG11	54:XY:280:GLN:NE2	2.35	0.42
54:XY:34:LEU:HD11	54:XY:64:GLU:HG3	2.01	0.42
11:YP:63:PRO:HB2	30:Y8:30:ARG:HH21	1.84	0.42
1:YA:1070:A:H2'	1:YA:1071:G:C8	2.54	0.42
1:YA:2692:C:H2'	1:YA:2693:A:H8	1.84	0.42
1:YA:608:A:H2'	1:YA:609:A:C8	2.54	0.42
1:YA:616:G:OP2	5:YF:106:ARG:NH2	2.51	0.42
1:YA:652(C):A:H61	1:YA:655:A:H1'	1.84	0.42
1:YA:729:G:H5'	1:YA:730:C:H5''	2.01	0.42
1:YA:777:A:H2'	1:YA:778:G:C8	2.53	0.42
3:YD:12:SER:HB3	3:YD:208:LYS:HB3	2.01	0.42
4:YE:119:ARG:CG	4:YE:160:TYR:HB2	2.50	0.42
10:YO:97:ARG:HE	10:YO:97:ARG:HB2	1.57	0.42
14:YS:49:VAL:HG21	14:YS:77:ALA:HA	2.01	0.42
15:YT:118:ARG:HG2	32:XA:1442(B):G:C8	2.54	0.42
20:YY:40:GLU:O	20:YY:42:VAL:HG23	2.19	0.42
21:YZ:14:LYS:HB3	21:YZ:14:LYS:HE2	1.81	0.42
40:QI:16:ARG:H	40:QI:64:THR:CG2	2.32	0.42
1:RA:2080:G:H5'	23:R1:35:THR:HG23	2.01	0.42
28:R6:11:LEU:HB2	28:R6:21:TYR:HB2	2.01	0.42
1:RA:1630:G:H2'	1:RA:1631(A):C:H6	1.85	0.42
1:RA:2122:U:H2'	1:RA:2123:G:H8	1.84	0.42
1:RA:2134:A:C5	1:RA:2157:G:H5'	2.54	0.42
1:RA:2591:C:H2'	1:RA:2592:G:H8	1.82	0.42
1:RA:538:G:H2'	1:RA:539:G:C8	2.51	0.42
3:RD:133:LEU:HB3	3:RD:173:VAL:HG21	2.02	0.42
5:RF:125:LEU:CD1	5:RF:194:MET:HB2	2.50	0.42
1:RA:1141:U:P	9:RN:25:ARG:HH12	2.43	0.42
32:QA:339:C:P	10:RO:97:ARG:HH11	2.43	0.42
20:RY:92:ASN:HB3	20:RY:94:LYS:HG2	2.00	0.42
32:XA:403:C:OP1	35:XD:137:SER:OG	2.26	0.42
32:XA:624:C:H2'	32:XA:625:G:C8	2.51	0.42
32:XA:741:G:H2'	32:XA:742:G:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:924:C:H2'	32:XA:925:G:H8	1.84	0.42
44:XM:17:VAL:HA	44:XM:27:LYS:HZ2	1.85	0.42
45:YN:37:PHE:HB3	45:YN:39:LEU:HD12	2.02	0.42
37:XF:97:PHE:HB3	49:XR:32:ARG:HD3	2.01	0.42
49:XR:65:ILE:O	49:XR:69:THR:HG23	2.19	0.42
26:Y4:59:PHE:HZ	50:XS:64:GLU:HB2	1.71	0.42
29:Y7:22:MET:SD	29:Y7:31:LEU:HD12	2.59	0.42
1:YA:151:C:H2'	1:YA:152:G:C8	2.52	0.42
1:YA:2812:G:H2'	1:YA:2813:A:C8	2.54	0.42
1:YA:303:U:H2'	1:YA:304:G:C8	2.54	0.42
1:YA:578:A:OP1	1:YA:1255:U:O2'	2.28	0.42
3:YD:70:TRP:HB3	3:YD:190:TYR:CE1	2.54	0.42
5:YF:129:PHE:O	5:YF:132:VAL:HG22	2.18	0.42
5:YF:157:VAL:HB	5:YF:194:MET:HG2	2.01	0.42
1:YA:1952:A:N3	10:YO:22:ILE:HD12	2.34	0.42
17:YV:61:VAL:HG12	17:YV:94:LEU:CD2	2.50	0.42
32:QA:124:G:H2'	32:QA:125:U:C6	2.55	0.42
32:QA:159:G:N2	32:QA:161:A:H3'	2.35	0.42
39:QH:12:ARG:CD	39:QH:26:VAL:HG12	2.49	0.42
43:QL:102:ARG:HD2	43:QL:102:ARG:HA	1.90	0.42
51:QT:77:ALA:O	51:QT:81:LYS:HG3	2.20	0.42
23:R1:80:LEU:HB3	23:R1:82:LEU:HG	2.02	0.42
31:R9:2:LYS:HE2	31:R9:31:LYS:O	2.19	0.42
1:RA:1076:C:H1'	1:RA:1077:A:H5'	2.01	0.42
1:RA:1588:C:H2'	1:RA:1589:C:H6	1.83	0.42
1:RA:1798:U:OP2	3:RD:274:ARG:NH2	2.40	0.42
1:RA:2109:U:H2'	1:RA:2110:G:C8	2.54	0.42
1:RA:2285:C:OP1	28:R6:29:ASN:ND2	2.43	0.42
1:RA:570:G:H2'	1:RA:2030:A:C5	2.55	0.42
10:RO:115:VAL:HG13	10:RO:121:VAL:HG21	2.02	0.42
20:RY:6:HIS:HE1	20:RY:72:VAL:O	2.02	0.42
32:XA:1002:G:C2	32:XA:1003:G:C8	3.08	0.42
32:XA:1032:G:H2'	32:XA:1033:G:H8	1.84	0.42
32:XA:1068:G:H8	32:XA:1068:G:OP2	2.02	0.42
32:XA:1279:A:H2'	32:XA:1279:A:N3	2.35	0.42
32:XA:953:G:N7	44:XM:104:ARG:NH2	2.53	0.42
33:XB:114:ARG:HH12	33:XB:118:LEU:CD2	2.33	0.42
33:XB:9:GLU:C	33:XB:11:LEU:H	2.23	0.42
41:XJ:33:GLN:O	41:XJ:74:ILE:HA	2.19	0.42
49:XR:61:LYS:O	49:XR:65:ILE:HG12	2.20	0.42
26:Y4:18:CYS:HB2	26:Y4:20:ASN:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1278:A:H2'	1:YA:1279:G:C8	2.55	0.42
1:YA:152:G:H2'	1:YA:153:C:H6	1.84	0.42
1:YA:1479:G:H5''	1:YA:1560:G:H4'	2.01	0.42
1:YA:2224:G:H4'	1:YA:2226:C:C2	2.55	0.42
4:YE:119:ARG:HD3	4:YE:160:TYR:CB	2.20	0.42
4:YE:28:ALA:HB3	4:YE:93:VAL:CG1	2.49	0.42
6:YG:110:ALA:O	6:YG:140:ILE:HG23	2.19	0.42
6:YG:36:LYS:CE	6:YG:95:ARG:HH12	2.24	0.42
9:YN:42:TRP:CD1	9:YN:48:MET:HE2	2.55	0.42
11:YP:120:ALA:HB1	11:YP:138:LEU:HD12	2.02	0.42
32:QA:1414:U:H2'	32:QA:1415:G:H8	1.84	0.42
32:QA:224:C:H2'	32:QA:225:C:C6	2.55	0.42
32:QA:950:U:H2'	32:QA:951:G:C8	2.55	0.42
32:QA:955:U:P	54:QY:154:ARG:HH21	2.43	0.42
33:QB:200:ILE:CG2	33:QB:202:PRO:HD3	2.44	0.42
34:QC:22:TRP:HA	41:QJ:93:GLY:HA2	2.01	0.42
38:QG:12:LEU:HD12	38:QG:12:LEU:H	1.84	0.42
32:QA:1149:C:P	40:QI:9:ARG:HH21	2.42	0.42
42:QK:79:SER:HA	42:QK:104:GLN:HB2	2.01	0.42
47:QP:14:ASN:N	47:QP:15:PRO:HD3	2.35	0.42
32:QA:1289:A:OP1	52:QU:10:ARG:NH2	2.53	0.42
53:QV:76:A:H3'	54:QY:251:GLY:HA3	2.01	0.42
54:QY:36:GLU:HA	54:QY:39:ALA:HB3	2.01	0.42
1:RA:1045:A:N3	1:RA:1045:A:H2'	2.35	0.42
1:RA:1709:U:H2'	1:RA:1710:C:H6	1.85	0.42
1:RA:2101:G:C5	1:RA:2102:U:C4	3.07	0.42
1:RA:2247:A:H2'	1:RA:2248:C:H6	1.85	0.42
1:RA:224:G:H2'	1:RA:225:A:O4'	2.19	0.42
1:RA:307:G:N2	1:RA:309:G:H3'	2.35	0.42
4:RE:119:ARG:HG2	4:RE:120:TRP:CD1	2.54	0.42
21:RZ:202:GLU:OE2	53:QV:62:C:H1'	2.20	0.42
32:XA:145:G:C2	32:XA:178:C:C2	3.07	0.42
32:XA:33:A:H2'	32:XA:34:C:C6	2.54	0.42
32:XA:433:C:H2'	32:XA:434:U:H6	1.84	0.42
34:XC:112:SER:O	34:XC:116:VAL:HG23	2.19	0.42
38:XG:137:LYS:HD3	38:XG:137:LYS:O	2.20	0.42
40:XI:65:VAL:HG21	40:XI:73:GLN:HB3	2.00	0.42
41:XJ:49:VAL:HG22	41:XJ:50:ILE:O	2.19	0.42
45:YN:23:ARG:NH1	45:YN:30:ALA:HB2	2.35	0.42
54:XY:196:THR:HA	54:XY:220:ALA:O	2.20	0.42
25:Y3:19:GLN:OE1	25:Y3:52:HIS:NE2	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Y8:23:VAL:HG13	30:Y8:47:LYS:HB3	2.01	0.42
1:YA:1231:G:H2'	1:YA:1232:G:C8	2.55	0.42
1:YA:1593:G:H2'	1:YA:1594:G:C8	2.55	0.42
1:YA:2576:G:O2'	1:YA:2579:C:OP2	2.29	0.42
1:YA:299:A:N1	1:YA:322:A:O2'	2.37	0.42
1:YA:658:C:H2'	1:YA:659:C:C6	2.55	0.42
2:YB:16:G:N2	2:YB:69:G:H1'	2.34	0.42
6:YG:126:ASP:HB2	6:YG:130:ASN:O	2.20	0.42
14:YS:101:LEU:C	14:YS:101:LEU:HD23	2.40	0.42
32:QA:1333:A:H2'	32:QA:1334:G:O4'	2.20	0.42
32:QA:601:C:H2'	32:QA:602:A:H8	1.85	0.42
37:QF:61:LEU:HD23	37:QF:63:TYR:OH	2.20	0.42
42:QK:38:ASN:HA	42:QK:39:PRO:HD3	1.88	0.42
50:QS:79:THR:HG21	50:QS:81:ARG:NH1	2.34	0.42
1:RA:1449:A:N3	1:RA:1529:G:H1'	2.35	0.42
1:RA:185:U:H2'	1:RA:186:G:H8	1.84	0.42
1:RA:2182:G:H2'	1:RA:2183:C:C6	2.55	0.42
1:RA:2445:G:OP1	5:RF:74:ARG:NH2	2.41	0.42
1:RA:9:U:O4	1:RA:2629:A:H2	2.02	0.42
5:RF:196:LEU:HA	5:RF:196:LEU:HD23	1.87	0.42
12:RQ:55:VAL:HG12	12:RQ:64:ILE:HD12	2.02	0.42
32:XA:1206:G:H2'	32:XA:1207:2MG:O4'	2.19	0.42
33:XB:24:TRP:HB3	33:XB:40:HIS:CE1	2.54	0.42
33:XB:73:THR:HG22	33:XB:95:GLN:O	2.20	0.42
34:XC:181:ASN:N	34:XC:205:GLY:O	2.40	0.42
34:XC:91:LEU:HA	34:XC:91:LEU:HD12	1.93	0.42
39:XH:37:ARG:NH2	39:XH:38:ILE:CD1	2.83	0.42
40:XI:7:THR:O	40:XI:83:ARG:HD2	2.20	0.42
32:XA:1151:A:O4'	41:XJ:39:PRO:HB2	2.20	0.42
49:XR:26:LEU:HD11	49:XR:42:ARG:CD	2.49	0.42
54:XY:126:ALA:O	54:XY:128:CYS:N	2.52	0.42
1:YA:1050:A:H2'	1:YA:1051:G:C8	2.53	0.42
1:YA:1431:U:H2'	1:YA:1432:C:C6	2.55	0.42
1:YA:1721:G:H2'	1:YA:1740:G:O6	2.20	0.42
1:YA:1946:U:H2'	1:YA:1947:C:H6	1.85	0.42
1:YA:2077:A:H2'	1:YA:2078:C:C6	2.54	0.42
1:YA:2113:U:H2'	1:YA:2114:A:O4'	2.20	0.42
1:YA:2695:C:H2'	1:YA:2696:U:H6	1.85	0.42
2:YB:96:U:H2'	2:YB:97:G:H8	1.84	0.42
8:YI:83:ALA:CB	8:YI:123:LEU:HD21	2.50	0.42
33:QB:187:LEU:HA	33:QB:201:ILE:HB	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:QE:41:VAL:HG13	36:QE:113:ALA:CA	2.48	0.42
48:QQ:43:LEU:HD12	48:QQ:68:ARG:HG2	2.02	0.42
49:QR:58:LEU:HD23	49:QR:63:GLN:HA	2.01	0.42
51:QT:53:LEU:HD12	51:QT:100:ILE:HG13	2.02	0.42
54:QY:141:ALA:HB2	54:QY:216:SER:HB2	2.02	0.42
30:R8:31:HIS:CE1	30:R8:32:LEU:HD22	2.54	0.42
31:R9:13:LYS:HD3	31:R9:13:LYS:HA	1.87	0.42
1:RA:1353:A:H62	1:RA:1377:G:H2'	1.85	0.42
1:RA:233:A:H2'	1:RA:234:C:O4'	2.20	0.42
1:RA:2389:G:H5''	1:RA:2390:U:O4'	2.19	0.42
1:RA:2748:A:H5'	7:RH:4:ILE:CD1	2.45	0.42
1:RA:41:C:H2'	1:RA:42:G:H8	1.85	0.42
1:RA:479:A:O2'	1:RA:481:G:H5'	2.20	0.42
1:RA:796:C:H2'	1:RA:797:C:C6	2.54	0.42
1:RA:871:U:H2'	1:RA:872:A:C8	2.55	0.42
6:RG:16:ARG:HB2	6:RG:17:PRO:HD3	2.02	0.42
1:RA:996:A:H4'	16:RU:91:ASP:OD2	2.20	0.42
32:XA:500:G:H2'	32:XA:501:C:H6	1.85	0.42
32:XA:582:U:H2'	32:XA:583:A:H8	1.85	0.42
32:XA:581:G:N1	32:XA:759:A:OP2	2.33	0.42
32:XA:779:C:H2'	32:XA:780:A:O4'	2.20	0.42
33:XB:53:ARG:HG2	33:XB:56:ARG:HH21	1.85	0.42
34:XC:54:ARG:HB3	34:XC:54:ARG:HH11	1.85	0.42
37:XF:11:ASN:HB3	37:XF:14:LEU:HG	2.01	0.42
32:XA:391:G:P	47:XP:28:ARG:HH22	2.43	0.42
1:YA:1412:A:H2'	1:YA:1413:G:H8	1.85	0.42
1:YA:78:A:H2'	1:YA:79:G:C8	2.54	0.42
5:YF:165:ARG:HG2	5:YF:168:ARG:HH21	1.83	0.42
20:YY:7:VAL:CG1	20:YY:27:VAL:HG21	2.50	0.42
32:QA:1003:G:N2	32:QA:1004:A:H1'	2.35	0.41
32:QA:515:G:H2'	32:QA:516:PSU:O4'	2.20	0.41
34:QC:134:ILE:HG22	34:QC:168:ALA:HB3	2.02	0.41
38:QG:111:ARG:HB3	38:QG:113:GLU:OE2	2.20	0.41
39:QH:83:ILE:HG13	39:QH:137:VAL:HG22	2.02	0.41
47:QP:5:ARG:HH21	47:QP:24:ALA:HA	1.85	0.41
51:QT:43:LEU:HD22	51:QT:48:LYS:HD2	2.00	0.41
53:QV:55:U:O5'	53:QV:55:U:H6	2.03	0.41
23:R1:3:LYS:CG	23:R1:4:VAL:H	2.23	0.41
1:RA:1198:U:C2	1:RA:1199:U:C5	3.08	0.41
1:RA:194:G:H2'	1:RA:195:A:O4'	2.20	0.41
1:RA:2328:A:H2'	1:RA:2329:G:H8	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:2455:G:H2'	1:RA:2456:C:C6	2.55	0.41
1:RA:582:G:H2'	1:RA:583:G:H8	1.84	0.41
1:RA:956:G:H2'	1:RA:957:A:H2'	2.03	0.41
1:RA:978:G:C2	1:RA:986:C:C2	3.08	0.41
4:RE:9:VAL:CG2	4:RE:25:VAL:HG12	2.50	0.41
8:RI:133:HIS:ND1	8:RI:134:PRO:O	2.49	0.41
12:RQ:21:THR:HG21	12:RQ:101:ARG:CB	2.49	0.41
20:RY:99:CYS:HB2	20:RY:106:LEU:HD21	2.02	0.41
32:XA:1117:G:H5'	32:XA:1118:C:OP2	2.20	0.41
32:XA:1138:G:H2'	32:XA:1140:C:H5'	2.02	0.41
32:XA:64:G:H5''	32:XA:65:U:H3'	2.02	0.41
33:XB:196:LEU:HA	33:XB:196:LEU:HD12	1.81	0.41
34:XC:54:ARG:NH1	34:XC:54:ARG:HB3	2.34	0.41
35:XD:191:ARG:HA	35:XD:191:ARG:HD2	1.79	0.41
37:XF:15:ASP:OD2	35:QD:27:TYR:OH	2.33	0.41
32:XA:523:A:N1	43:XL:92:0TD:H6	2.35	0.41
44:XM:97:PRO:HA	44:XM:110:ARG:HH11	1.85	0.41
47:XP:4:ILE:HG23	47:XP:36:ILE:HD11	2.02	0.41
54:XY:26:ASP:HB3	54:XY:29:ALA:HB3	2.02	0.41
1:YA:1449:A:N3	1:YA:1529:G:H1'	2.34	0.41
1:YA:39:C:H2'	1:YA:40:C:H6	1.85	0.41
2:YB:87:G:N2	2:YB:89:G:H3'	2.35	0.41
4:YE:82:ARG:NH1	4:YE:82:ARG:CG	2.69	0.41
6:YG:170:ARG:HH21	6:YG:180:PHE:HB2	1.85	0.41
6:YG:41:GLN:HB3	6:YG:43:LEU:CD1	2.43	0.41
32:QA:1207:2MG:H2'	32:QA:1208:C:C6	2.55	0.41
32:QA:177:C:OP1	51:QT:65:LYS:NZ	2.44	0.41
32:QA:417:C:H2'	32:QA:418:C:C6	2.55	0.41
32:QA:513:C:H2'	32:QA:514:C:C6	2.55	0.41
32:QA:688:G:H2'	32:QA:689:C:C6	2.55	0.41
32:QA:913:A:H4'	32:QA:914:A:O5'	2.20	0.41
33:QB:8:LYS:HZ3	33:QB:52:GLU:CA	2.33	0.41
34:QC:36:ASP:O	34:QC:40:ARG:HG3	2.20	0.41
46:QO:26:GLU:HG3	46:QO:81:LEU:HD22	2.03	0.41
50:QS:58:VAL:HA	50:QS:59:PRO:HD3	1.87	0.41
54:QY:128:CYS:HB3	54:QY:189:TYR:HB2	2.02	0.41
1:RA:2615:U:C2	27:R5:7:PRO:HA	2.55	0.41
21:RZ:140:ASP:OD1	21:RZ:142:SER:OG	2.34	0.41
32:XA:1084:G:H5'	32:XA:1102:A:OP2	2.20	0.41
32:XA:439:A:C5	32:XA:441:A:H1'	2.55	0.41
39:XH:10:LEU:HD22	39:XH:83:ILE:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:XJ:85:LEU:HA	41:XJ:85:LEU:HD23	1.86	0.41
45:YN:53:LEU:HA	45:YN:54:PRO:HD2	1.90	0.41
28:Y6:40:CYS:HA	28:Y6:41:PRO:HD3	1.82	0.41
1:YA:1055:G:H2'	1:YA:1056:G:O4'	2.20	0.41
1:YA:180:G:OP2	29:Y7:32:LYS:HE3	2.20	0.41
1:YA:2316:C:H2'	1:YA:2317:C:C6	2.55	0.41
1:YA:2469:A:H2'	1:YA:2470:G:O4'	2.20	0.41
1:YA:642:G:N2	1:YA:645:C:OP2	2.51	0.41
1:YA:807:U:OP2	11:YP:41:ARG:NH2	2.53	0.41
1:YA:1800:C:OP2	3:YD:183:ARG:NH2	2.53	0.41
6:YG:125:PHE:CE1	6:YG:131:TYR:HB2	2.56	0.41
7:YH:28:GLY:N	7:YH:31:GLY:O	2.53	0.41
8:YI:68:LEU:HD13	8:YI:68:LEU:O	2.20	0.41
1:YA:1665:A:H4'	10:YO:67:LYS:HB2	2.02	0.41
11:YP:21:ARG:HD2	11:YP:21:ARG:HH11	1.66	0.41
1:YA:411:G:C5	11:YP:72:PRO:HB3	2.55	0.41
32:QA:1347:G:N2	32:QA:1373:G:H2'	2.36	0.41
32:QA:374:A:C6	32:QA:375:U:C4	3.07	0.41
33:QB:146:GLN:O	33:QB:150:SER:HB3	2.20	0.41
33:QB:231:GLU:HG3	33:QB:232:PRO:HD3	2.03	0.41
36:QE:33:VAL:HG13	36:QE:112:LEU:HD12	2.03	0.41
37:QF:75:LEU:O	37:QF:79:LEU:HG	2.20	0.41
47:QP:43:LYS:HG2	47:QP:48:TRP:NE1	2.35	0.41
47:QP:60:LEU:HA	47:QP:60:LEU:HD13	1.90	0.41
1:RA:1070:A:H2'	1:RA:1071:G:C8	2.56	0.41
1:RA:1086:A:OP1	1:RA:1104:C:O2'	2.27	0.41
1:RA:1756:G:H4'	1:RA:1758:G:O4'	2.21	0.41
1:RA:2630:G:H2'	1:RA:2631:G:H8	1.85	0.41
1:RA:2704:C:H2'	1:RA:2705:A:O4'	2.21	0.41
1:RA:2819:G:H2'	1:RA:2821:A:N7	2.35	0.41
9:RN:30:ILE:HA	9:RN:33:LEU:HD23	2.01	0.41
10:RO:22:ILE:HG21	10:RO:22:ILE:HD13	1.83	0.41
33:XB:122:PHE:CZ	33:XB:127:ILE:CD1	2.99	0.41
36:XE:152:ARG:NH1	39:XH:107:LEU:O	2.43	0.41
39:XH:13:ILE:O	39:XH:17:THR:HG23	2.20	0.41
42:XK:84:VAL:HG11	42:XK:91:ARG:HH11	1.85	0.41
50:XS:12:ASP:OD2	50:XS:35:SER:HB3	2.19	0.41
50:XS:20:LEU:HA	50:XS:23:ASN:HD22	1.86	0.41
26:Y4:59:PHE:HZ	50:XS:64:GLU:CB	2.32	0.41
31:Y9:22:ARG:HB2	31:Y9:24:TYR:CE1	2.54	0.41
1:YA:1842:G:H2'	1:YA:1843:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:2805:G:H2'	1:YA:2807:G:C8	2.54	0.41
1:YA:918:A:H5''	2:YB:98:G:O2'	2.19	0.41
4:YE:114:ALA:HB3	4:YE:119:ARG:HG3	2.02	0.41
5:YF:167:ALA:HA	5:YF:170:LEU:HD23	2.02	0.41
6:YG:126:ASP:HB3	6:YG:128:ARG:H	1.86	0.41
6:YG:46:ALA:O	6:YG:51:ARG:HA	2.21	0.41
13:YR:96:ARG:HD2	13:YR:96:ARG:HH11	1.62	0.41
14:YS:23:ARG:NH1	14:YS:85:VAL:O	2.53	0.41
21:YZ:100:VAL:HA	21:YZ:101:PRO:HD3	1.96	0.41
32:QA:1240:U:OP2	38:QG:116:ALA:N	2.39	0.41
32:QA:257:G:H2'	32:QA:258:G:H8	1.86	0.41
32:QA:688:G:H2'	32:QA:689:C:H6	1.84	0.41
44:QM:3:ARG:HH21	44:QM:11:ARG:HG2	1.85	0.41
41:QJ:64:GLU:HB3	45:QN:59:ALA:HB2	2.03	0.41
48:QQ:81:ARG:HA	48:QQ:81:ARG:HD2	1.79	0.41
1:RA:1084:A:H3'	1:RA:1085:A:H4'	2.02	0.41
1:RA:2127:G:H2'	1:RA:2128:C:O4'	2.20	0.41
1:RA:2134:A:H8	1:RA:2156:G:H21	1.66	0.41
1:RA:407:G:H2'	1:RA:408:G:C8	2.55	0.41
3:RD:16:MET:HG2	3:RD:211:ARG:HH21	1.85	0.41
32:XA:1201:A:H4'	32:XA:1202:G:H5''	2.02	0.41
37:XF:91:VAL:HG12	37:XF:92:LYS:O	2.20	0.41
38:XG:23:VAL:O	38:XG:27:ILE:HG12	2.21	0.41
39:XH:86:ILE:HG12	39:XH:135:CYS:HA	2.03	0.41
41:XJ:38:ILE:CG1	41:XJ:71:LEU:HD22	2.50	0.41
23:Y1:67:ILE:N	23:Y1:68:PRO:HD2	2.35	0.41
1:YA:1027:A:C2	1:YA:2488:A:H5'	2.54	0.41
1:YA:1053:C:O2'	1:YA:1054:A:O5'	2.33	0.41
1:YA:1141:U:OP2	9:YN:63:THR:OG1	2.36	0.41
1:YA:127:A:H5''	1:YA:128:C:C6	2.55	0.41
1:YA:2065:C:C2	1:YA:2066:C:C5	3.09	0.41
1:YA:2525:G:H2'	1:YA:2526:G:H8	1.86	0.41
1:YA:709:U:H2'	1:YA:710:G:H8	1.85	0.41
2:YB:30:C:OP2	14:YS:32:LEU:HD11	2.20	0.41
1:YA:1791:A:H5'	3:YD:206:LEU:HD12	2.01	0.41
4:YE:111:ARG:HD2	4:YE:111:ARG:HH11	1.50	0.41
4:YE:34:VAL:HG12	4:YE:72:VAL:HG21	2.01	0.41
6:YG:16:ARG:O	6:YG:20:ILE:HG13	2.20	0.41
9:YN:58:ASP:N	9:YN:58:ASP:OD1	2.52	0.41
12:YQ:56:ARG:HH11	21:YZ:183:LEU:HD12	1.85	0.41
13:YR:100:LEU:HD23	13:YR:112:ALA:CA	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:YS:46:VAL:HG12	14:YS:48:LEU:HD22	2.01	0.41
20:YY:23:ARG:NH1	20:YY:23:ARG:HB2	2.35	0.41
32:QA:677:U:H2'	32:QA:678:U:C6	2.55	0.41
35:QD:61:LYS:HD3	35:QD:206:PHE:CE2	2.55	0.41
40:QI:81:ILE:O	40:QI:85:LEU:HG	2.21	0.41
42:QK:34:ASP:OD2	42:QK:38:ASN:HB2	2.21	0.41
43:QL:27:LEU:HD23	43:QL:30:ALA:O	2.21	0.41
51:QT:42:GLN:O	51:QT:45:GLN:HB3	2.20	0.41
32:QA:1493:A:H4'	54:QY:138:GLY:H	1.85	0.41
1:RA:1139:G:OP1	9:RN:101:HIS:ND1	2.43	0.41
1:RA:143(A):G:H2'	1:RA:143(B):C:C6	2.56	0.41
1:RA:1614:A:H8	1:RA:1614:A:P	2.43	0.41
1:RA:2277:G:OP2	22:R0:10:THR:HG21	2.21	0.41
1:RA:301:G:H1'	1:RA:302:C:C6	2.55	0.41
1:RA:441:U:H2'	1:RA:442:G:C8	2.54	0.41
14:RS:76:LYS:O	14:RS:80:LEU:HD22	2.20	0.41
32:XA:1126:U:O4'	32:XA:1281:U:H1'	2.20	0.41
32:XA:600:C:H2'	32:XA:601:C:C6	2.55	0.41
32:XA:985:C:H2'	32:XA:986:A:H8	1.85	0.41
34:XC:180:ALA:HA	34:XC:206:GLU:HA	2.01	0.41
51:XT:50:GLU:HB2	51:XT:99:LEU:CD2	2.50	0.41
22:Y0:11:ARG:HH22	53:XV:63:G:H4'	1.84	0.41
6:YG:101:ILE:CD1	26:Y4:25:TYR:HB2	2.46	0.41
1:YA:1197:G:H2'	1:YA:1198:U:H6	1.85	0.41
1:YA:1431:U:H2'	1:YA:1432:C:H6	1.85	0.41
1:YA:1656:C:H2'	1:YA:1657:C:H6	1.86	0.41
1:YA:2448:A:HO2'	1:YA:2449:U:H5	1.66	0.41
1:YA:593:G:H2'	1:YA:594:U:C6	2.55	0.41
5:YF:34:TRP:N	11:YP:6:LEU:HD22	2.35	0.41
8:YI:48:GLU:HG3	8:YI:52:ARG:NH1	2.35	0.41
1:YA:954:G:H5"	12:YQ:13:GLN:HB3	2.02	0.41
17:YV:14:VAL:HA	17:YV:18:LEU:HD12	2.03	0.41
18:YW:17:VAL:CG2	18:YW:76:VAL:HG11	2.51	0.41
20:YY:5:MET:HE1	20:YY:32:PRO:HA	2.03	0.41
32:QA:584:G:H2'	32:QA:585:G:C8	2.55	0.41
32:QA:858:G:O6	32:QA:869:G:H3'	2.20	0.41
32:QA:932:C:H5"	38:QG:4:ARG:CZ	2.50	0.41
33:QB:145:LEU:HD12	33:QB:149:LEU:HD12	2.03	0.41
33:QB:27:LYS:O	33:QB:30:ARG:NH1	2.54	0.41
1:RA:2390:U:P	30:R8:35:GLN:HE22	2.44	0.41
1:RA:1057:A:H2'	1:RA:1058:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:1080:C:H2'	1:RA:1081:U:C6	2.55	0.41
1:RA:2854:G:H2'	1:RA:2855:C:C6	2.55	0.41
1:RA:2849:U:H4'	1:RA:2868:A:C2	2.55	0.41
1:RA:500:G:N1	1:RA:503:A:OP2	2.54	0.41
1:RA:644:A:H4'	1:RA:645:C:H5	1.85	0.41
1:RA:2572:A:H62	4:RE:145:LYS:HD2	1.85	0.41
1:RA:2680:C:H5'	4:RE:189:PRO:HA	2.02	0.41
6:RG:5:VAL:CG2	6:RG:8:LYS:HB3	2.51	0.41
12:RQ:109:VAL:HG13	12:RQ:113:GLN:HB2	2.02	0.41
15:RT:37:GLY:HA2	15:RT:38:ASN:HA	1.75	0.41
15:RT:95:ARG:NH1	15:RT:95:ARG:HG2	2.25	0.41
17:RV:49:THR:HG22	17:RV:49:THR:O	2.19	0.41
32:XA:375:U:OP1	47:XP:69:THR:HG21	2.21	0.41
35:XD:148:VAL:HG11	35:XD:158:ILE:HG21	2.01	0.41
36:XE:76:ILE:HB	36:XE:77:PRO:HD2	2.02	0.41
43:XL:124:LYS:HA	43:XL:125:PRO:HD3	1.98	0.41
48:XQ:41:LYS:NZ	48:XQ:92:ARG:HH21	2.15	0.41
21:YZ:198:LYS:HD3	53:XV:53:G:H5'	2.02	0.41
54:XY:37:VAL:HG11	54:XY:60:ARG:HB2	2.03	0.41
25:Y3:6:VAL:HG12	25:Y3:54:VAL:HG21	2.02	0.41
26:Y4:28:LYS:HA	26:Y4:29:PRO:HD3	1.91	0.41
1:YA:1075:C:H2'	1:YA:1076:C:H3'	2.03	0.41
1:YA:2125:G:H22	1:YA:2172:U:H3'	1.85	0.41
1:YA:2314:C:H5''	6:YG:38:VAL:HG21	2.03	0.41
1:YA:272(P):C:H5''	8:YI:45:LYS:CD	2.50	0.41
3:YD:16:MET:HG3	3:YD:206:LEU:O	2.21	0.41
3:YD:217:ARG:HD3	3:YD:217:ARG:HH11	1.71	0.41
8:YI:133:HIS:HD2	8:YI:136:VAL:HG23	1.86	0.41
8:YI:27:ARG:HD2	23:Y1:71:TYR:CE1	2.56	0.41
9:YN:104:LYS:HE3	9:YN:117:PHE:CZ	2.56	0.41
11:YP:95:VAL:HG22	11:YP:125:VAL:HG12	2.03	0.41
16:YU:89:GLU:HB2	17:YV:50:PRO:HB3	2.03	0.41
32:QA:1040:U:H2'	32:QA:1041:A:C8	2.56	0.41
32:QA:199:G:H2'	32:QA:200:G:H8	1.85	0.41
32:QA:42:G:H2'	32:QA:43:C:C6	2.56	0.41
32:QA:57:G:H2'	32:QA:58:C:H6	1.85	0.41
32:QA:92:C:H2'	32:QA:93:G:C8	2.55	0.41
34:QC:113:ALA:HB3	34:QC:114:PRO:HD3	2.03	0.41
35:QD:187:ARG:NH2	35:QD:193:ASP:OD2	2.53	0.41
36:QE:41:VAL:CG1	36:QE:113:ALA:HB2	2.50	0.41
36:QE:31:LEU:HA	36:QE:31:LEU:HD23	1.77	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:QM:15:VAL:HG13	44:QM:43:THR:O	2.20	0.41
47:QP:71:ARG:HD2	47:QP:71:ARG:HH11	1.63	0.41
31:R9:13:LYS:HG3	31:R9:28:GLU:OE2	2.19	0.41
1:RA:1096:A:H2'	1:RA:1097:U:H6	1.85	0.41
1:RA:2602:A:C5	54:QY:278:ARG:HG2	2.56	0.41
1:RA:375:C:H2'	1:RA:376:C:C6	2.56	0.41
1:RA:407:G:H2'	1:RA:408:G:H8	1.86	0.41
2:RB:60:C:H2'	2:RB:61:G:H8	1.86	0.41
4:RE:146:THR:HA	4:RE:147:PRO:HA	1.91	0.41
6:RG:138:GLN:HE22	6:RG:153:ARG:HD2	1.85	0.41
14:RS:3:ARG:HA	14:RS:3:ARG:HE	1.85	0.41
15:RT:127:ALA:O	15:RT:128:GLU:HB3	2.21	0.41
15:RT:18:ASP:N	15:RT:18:ASP:OD1	2.48	0.41
32:XA:1030(B):G:H2'	32:XA:1030(C):C:H5''	2.02	0.41
32:XA:1350:A:H2'	32:XA:1351:U:O4'	2.21	0.41
32:XA:1428:A:H2'	32:XA:1429:C:C6	2.56	0.41
32:XA:238:G:OP1	48:XQ:25:ARG:NH2	2.53	0.41
32:XA:858:G:O6	32:XA:869:G:H3'	2.20	0.41
34:XC:16:ARG:HG3	34:XC:17:ASP:N	2.36	0.41
36:XE:20:GLN:OE1	36:XE:25:ARG:HD2	2.21	0.41
38:XG:23:VAL:HG13	38:XG:43:PHE:CE2	2.56	0.41
40:XI:50:LEU:HD21	40:XI:81:ILE:HG12	2.01	0.41
50:XS:66:MET:HB2	50:XS:74:PHE:CZ	2.55	0.41
24:Y2:32:LEU:HD12	24:Y2:57:ILE:HD12	1.98	0.41
1:YA:1057:A:H2'	1:YA:1058:G:H8	1.85	0.41
1:YA:1069:A:H2'	1:YA:1073:A:N7	2.35	0.41
1:YA:1518:U:H2'	1:YA:1519:G:O4'	2.21	0.41
1:YA:2100:G:C6	1:YA:2190:G:C6	3.08	0.41
1:YA:2564:A:C2	1:YA:2647:U:H4'	2.55	0.41
1:YA:610:G:H2'	1:YA:611:C:H6	1.86	0.41
1:YA:639:U:H2'	1:YA:640:C:H6	1.85	0.41
1:YA:662:G:H5'	11:YP:14:LYS:O	2.21	0.41
5:YF:136:THR:HG22	5:YF:140:LEU:CD2	2.51	0.41
6:YG:164:GLU:OE2	6:YG:164:GLU:N	2.53	0.41
12:YQ:30:GLY:HA2	12:YQ:107:ALA:HB2	2.02	0.41
13:YR:2:ARG:HG2	13:YR:5:LYS:HB2	2.02	0.41
32:QA:1230:C:H2'	32:QA:1231:G:H8	1.86	0.41
32:QA:184:G:H2'	32:QA:185:A:H8	1.85	0.41
32:QA:602:A:H2'	32:QA:603:U:C6	2.56	0.41
32:QA:828:A:H2'	32:QA:829:G:O4'	2.21	0.41
32:QA:890:G:O2'	32:QA:906:G:O6	2.23	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:QH:39:LEU:HA	39:QH:39:LEU:HD12	1.88	0.41
32:QA:1131:G:OP1	40:QI:20:ARG:NH2	2.53	0.41
44:QM:65:LYS:CD	26:R4:51:ASP:CB	2.98	0.41
1:RA:181:A:H3'	1:RA:182:A:H8	1.85	0.41
1:RA:185:U:H2'	1:RA:186:G:C8	2.56	0.41
1:RA:2626:C:H2'	1:RA:2627:G:O4'	2.20	0.41
1:RA:1800:C:OP2	3:RD:183:ARG:NH2	2.54	0.41
6:RG:27:ASN:HB3	6:RG:30:GLU:HG3	2.02	0.41
7:RH:69:ARG:HH11	7:RH:69:ARG:HD3	1.65	0.41
9:RN:120:LEU:HD22	9:RN:122:VAL:CG2	2.32	0.41
11:RP:86:LYS:HB3	11:RP:118:GLY:HA3	2.03	0.41
16:RU:49:HIS:HA	16:RU:52:ARG:HB3	2.02	0.41
32:XA:1065:U:H1'	32:XA:1066:C:OP2	2.21	0.41
32:XA:1183:A:H1'	32:XA:1184:G:OP1	2.20	0.41
32:XA:978:A:C2	32:XA:1319:A:C4	3.09	0.41
32:XA:1441:G:H5''	32:XA:1442(A):G:O5'	2.20	0.41
32:XA:186:C:H2'	32:XA:187:C:C6	2.56	0.41
32:XA:512:U:H2'	32:XA:513:C:H6	1.85	0.41
32:XA:598:U:H2'	32:XA:599:C:H6	1.85	0.41
34:XC:64:VAL:O	34:XC:99:VAL:HA	2.20	0.41
35:XD:199:ASN:OD1	35:XD:201:GLN:HB2	2.21	0.41
37:XF:25:ILE:CD1	37:XF:82:ARG:HE	2.33	0.41
40:XI:27:THR:HG23	40:XI:31:GLN:O	2.21	0.41
40:XI:37:PHE:HB3	40:XI:43:ALA:CB	2.51	0.41
51:XT:39:LYS:HB2	51:XT:39:LYS:HE3	1.83	0.41
51:XT:57:ARG:HH22	51:XT:100:ILE:CD1	2.34	0.41
51:XT:77:ALA:O	51:XT:81:LYS:HG3	2.20	0.41
52:XU:7:ARG:HD2	52:XU:7:ARG:HH11	1.67	0.41
43:XL:52:LEU:HD21	54:XY:320:GLY:O	2.21	0.41
23:Y1:40:ARG:C	23:Y1:40:ARG:HD3	2.41	0.41
24:Y2:9:GLN:HE22	24:Y2:56:GLN:HB3	1.85	0.41
1:YA:1441:G:H2'	1:YA:1442:G:H8	1.85	0.41
1:YA:2103:C:C2	1:YA:2104:G:N2	2.89	0.41
1:YA:2165:G:H2'	1:YA:2166:G:O4'	2.20	0.41
1:YA:2513:G:H2'	1:YA:2514:U:C6	2.56	0.41
1:YA:2646:C:H2'	1:YA:2647:U:O4'	2.20	0.41
1:YA:470:A:OP1	5:YF:59:TYR:HE1	2.03	0.41
6:YG:13:GLU:O	6:YG:17:PRO:HG2	2.20	0.41
6:YG:3:LEU:CD2	6:YG:97:ASP:OD2	2.69	0.41
9:YN:129:PRO:HA	9:YN:131:GLN:HE22	1.85	0.41
21:YZ:163:LEU:HD12	21:YZ:163:LEU:HA	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:1201:A:H4'	32:QA:1202:G:O5'	2.21	0.41
32:QA:1225:A:H2'	32:QA:1226:C:C5	2.55	0.41
32:QA:1427:U:H2'	32:QA:1428:A:H8	1.86	0.41
32:QA:933:G:OP2	38:QG:3:ARG:HB2	2.20	0.41
36:QE:41:VAL:HG23	36:QE:67:VAL:CG1	2.51	0.41
39:QH:18:ARG:HH11	39:QH:18:ARG:HD2	1.64	0.41
40:QI:56:LEU:HD13	40:QI:57:GLY:N	2.36	0.41
42:QK:58:PRO:HA	42:QK:90:GLY:HA2	2.03	0.41
26:R4:28:LYS:HA	26:R4:29:PRO:HD3	1.89	0.41
1:RA:1057:A:H2'	1:RA:1058:G:C8	2.55	0.41
1:RA:11:G:C2'	1:RA:12:U:H5'	2.51	0.41
1:RA:1798:U:H5''	3:RD:260:ARG:HB3	2.03	0.41
1:RA:2100:G:C6	1:RA:2190:G:C6	3.09	0.41
1:RA:2462:U:H2'	1:RA:2463:C:H6	1.85	0.41
1:RA:2514:U:H2'	1:RA:2515:C:C6	2.56	0.41
1:RA:2532:G:O2'	1:RA:2657:A:N1	2.50	0.41
1:RA:415:A:H2'	1:RA:416:C:H6	1.86	0.41
5:RF:9:ILE:CG2	5:RF:125:LEU:CD2	2.99	0.41
15:RT:35:LYS:C	15:RT:35:LYS:HD2	2.38	0.41
32:XA:1030(B):G:H1'	32:XA:1030(D):G:C5	2.56	0.41
32:XA:1040:U:H2'	32:XA:1041:A:O4'	2.21	0.41
32:XA:1121:U:H2'	32:XA:1122:U:C6	2.56	0.41
32:XA:1314:C:H2'	32:XA:1315:U:C6	2.56	0.41
32:XA:1327:C:H2'	32:XA:1328:C:C6	2.56	0.41
32:XA:1437:C:H2'	32:XA:1438:G:H8	1.85	0.41
32:XA:452:A:HO2'	32:XA:453:A:H8	1.65	0.41
40:XI:20:ARG:HA	40:XI:21:PRO:HD3	1.95	0.41
41:XJ:6:ILE:HA	41:XJ:97:GLU:O	2.21	0.41
42:XK:69:ALA:O	42:XK:73:MET:HG3	2.21	0.41
26:Y4:58:ARG:NH2	44:XM:80:ARG:HH22	2.18	0.41
47:XP:1:MET:SD	47:XP:1:MET:N	2.87	0.41
32:XA:261:U:OP2	51:XT:79:ARG:NH2	2.54	0.41
25:Y3:8:LEU:HD13	25:Y3:31:LEU:HA	2.00	0.41
26:Y4:47:GLN:C	26:Y4:49:PHE:H	2.24	0.41
26:Y4:64:GLY:C	26:Y4:66:SER:N	2.74	0.41
1:YA:9:U:O2'	1:YA:10:G:OP1	2.35	0.41
1:YA:1853:A:H2'	1:YA:1854:A:C8	2.56	0.41
1:YA:2293:C:H2'	1:YA:2294:C:C6	2.56	0.41
1:YA:2397:G:H5'	23:Y1:28:GLY:O	2.20	0.41
1:YA:2443:C:H2'	1:YA:2444:G:C8	2.55	0.41
1:YA:2023:G:H5'	1:YA:2617:C:H4'	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:823:G:H2'	1:YA:824:A:H8	1.85	0.41
6:YG:170:ARG:HH21	6:YG:180:PHE:CB	2.34	0.41
6:YG:56:ALA:CA	6:YG:153:ARG:HH22	2.09	0.41
8:YI:62:LYS:HE2	8:YI:133:HIS:NE2	2.36	0.41
1:YA:661:C:HO2'	11:YP:14:LYS:H	1.66	0.41
5:YF:34:TRP:CA	11:YP:6:LEU:HD22	2.50	0.41
32:QA:1428:A:H2'	32:QA:1429:C:C6	2.56	0.41
32:QA:186:C:H2'	32:QA:187:C:C6	2.56	0.41
33:QB:30:ARG:HH22	33:QB:194:PRO:HB2	1.85	0.41
35:QD:166:LYS:HB2	35:QD:168:ARG:HH22	1.85	0.41
41:QJ:16:LEU:HD21	41:QJ:70:ARG:HG2	2.03	0.41
41:QJ:62:HIS:HB3	45:QN:59:ALA:HB3	2.02	0.41
54:QY:215:THR:HG22	54:QY:217:PHE:CE1	2.54	0.41
30:R8:50:LEU:HD23	30:R8:50:LEU:HA	1.87	0.41
1:RA:2077:A:H2'	1:RA:2078:C:H6	1.85	0.41
1:RA:2162:G:O3'	1:RA:2172:U:O2'	2.31	0.41
1:RA:2290:G:H2'	1:RA:2291:U:C6	2.56	0.41
1:RA:2627:G:O2'	1:RA:2781:A:N1	2.43	0.41
1:RA:2802:G:H2'	1:RA:2803:C:O4'	2.21	0.41
1:RA:2805:G:H2'	1:RA:2807:G:C8	2.56	0.41
1:RA:492:A:H2'	1:RA:493:G:O4'	2.20	0.41
4:RE:170:LEU:HB3	4:RE:184:VAL:CG2	2.50	0.41
5:RF:33:LEU:HB3	11:RP:6:LEU:HD21	2.02	0.41
6:RG:18:GLU:CG	6:RG:175:LEU:HD21	2.51	0.41
19:RX:12:VAL:HG21	19:RX:27:THR:HG22	2.02	0.41
21:RZ:199:LYS:HG3	21:RZ:200:GLY:N	2.35	0.41
32:XA:256:U:H2'	32:XA:257:G:H8	1.86	0.41
32:XA:612:C:H2'	32:XA:613:C:C6	2.55	0.41
36:XE:41:VAL:HG23	36:XE:67:VAL:CG1	2.51	0.41
42:XK:48:ILE:HD13	42:XK:48:ILE:HA	1.85	0.41
29:Y7:43:THR:HG23	29:Y7:44:PRO:HD2	2.03	0.41
1:YA:1057:A:O2'	1:YA:1058:G:P	2.79	0.41
1:YA:1263:U:H1'	27:Y5:10:LYS:HG3	2.03	0.41
1:YA:1354:A:H3'	1:YA:1355:G:H8	1.86	0.41
1:YA:2063:C:C4	1:YA:2064:C:C5	3.09	0.41
1:YA:2641:G:H2'	1:YA:2642:G:H8	1.85	0.41
1:YA:595:C:H2'	1:YA:596:G:C8	2.56	0.41
4:YE:35:GLN:OE1	4:YE:66:HIS:HE1	2.03	0.41
8:YI:81:VAL:HG11	8:YI:92:VAL:HG13	2.03	0.41
16:YU:8:VAL:HG11	16:YU:12:ARG:CZ	2.50	0.41
32:QA:1120:G:H2'	32:QA:1121:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:1207:2MG:O2'	32:QA:1208:C:OP1	2.35	0.41
32:QA:1236:A:H4'	32:QA:1304:G:H4'	2.02	0.41
32:QA:1442(A):G:H1'	32:QA:1442(B):G:OP1	2.20	0.41
32:QA:583:A:H2'	32:QA:584:G:O4'	2.21	0.41
32:QA:642:A:N3	39:QH:113:SER:OG	2.42	0.41
32:QA:687:A:C2	32:QA:704:A:C6	3.09	0.41
34:QC:109:PRO:HB3	34:QC:115:LEU:HD23	2.02	0.41
38:QG:80:VAL:HB	38:QG:85:TYR:CD2	2.56	0.41
40:QI:20:ARG:HA	40:QI:21:PRO:HD3	1.96	0.41
54:QY:144:TRP:CE3	54:QY:201:LEU:HD22	2.56	0.41
22:R0:43:THR:O	22:R0:43:THR:HG23	2.21	0.41
1:RA:2077:A:H2'	1:RA:2078:C:C6	2.56	0.41
1:RA:2078:C:H2'	1:RA:2079:U:C6	2.56	0.41
1:RA:2317:C:H2'	1:RA:2318:G:H5'	2.03	0.41
1:RA:2593:U:H2'	1:RA:2594:C:C6	2.56	0.41
1:RA:2726:U:O2'	1:RA:2727:G:H8	2.04	0.41
1:RA:303:U:H2'	1:RA:304:G:C8	2.56	0.41
1:RA:415:A:H2'	1:RA:416:C:C6	2.57	0.41
1:RA:479:A:N3	1:RA:481:G:H5''	2.36	0.41
1:RA:506:G:O3'	1:RA:507:A:H8	2.03	0.41
1:RA:573:G:O2'	1:RA:574:C:H3'	2.21	0.41
1:RA:640:C:H2'	1:RA:641:C:C6	2.56	0.41
1:RA:863:A:H2'	1:RA:864:G:C8	2.56	0.41
8:RI:102:SER:OG	8:RI:103:ARG:N	2.54	0.41
11:RP:135:LEU:HD23	11:RP:135:LEU:HA	1.73	0.41
12:RQ:16:ARG:HG3	12:RQ:17:LEU:H	1.85	0.41
15:RT:23:ARG:HD3	15:RT:23:ARG:HH11	1.69	0.41
21:RZ:31:ARG:HG2	21:RZ:31:ARG:H	1.49	0.41
32:XA:1049:U:HO2'	45:XN:2:ALA:N	2.19	0.41
32:XA:1285:A:H4'	32:XA:1286:A:H5'	2.02	0.41
32:XA:518:C:N4	32:XA:530:G:O6	2.54	0.41
32:XA:70:G:H2'	32:XA:71:C:H6	1.86	0.41
35:XD:196:LEU:H	35:XD:196:LEU:HD12	1.86	0.41
40:XI:28:VAL:N	40:XI:31:GLN:O	2.52	0.41
1:YA:1588:C:H2'	1:YA:1589:C:C6	2.56	0.41
1:YA:1668:A:H4'	1:YA:1669:A:O5'	2.20	0.41
1:YA:2018:G:C6	1:YA:2019:A:C6	3.09	0.41
1:YA:2689:U:P	1:YA:2719:G:H22	2.44	0.41
1:YA:301:G:C6	1:YA:317:G:C6	3.09	0.41
12:YQ:110:THR:HG23	12:YQ:113:GLN:OE1	2.20	0.41
1:YA:955:C:OP1	12:YQ:87:LYS:HE2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:1090:U:H2'	32:QA:1091:U:C6	2.56	0.40
32:QA:953:G:C6	32:QA:1229:A:C6	3.09	0.40
32:QA:1363(B):A:H4'	32:QA:1364:U:H2'	2.04	0.40
32:QA:653:A:OP1	39:QH:56:LYS:NZ	2.54	0.40
33:QB:133:LYS:HD2	33:QB:133:LYS:HA	1.95	0.40
34:QC:32:LEU:HD22	34:QC:59:ARG:HH11	1.86	0.40
35:QD:188:LEU:HA	35:QD:189:PRO:HD3	1.63	0.40
38:QG:45:ASP:O	38:QG:49:ILE:HG13	2.22	0.40
47:QP:25:ARG:HH11	47:QP:25:ARG:HG3	1.86	0.40
54:QY:326:TYR:N	54:QY:326:TYR:CD1	2.87	0.40
1:RA:1153:C:H2'	1:RA:1154:G:O4'	2.22	0.40
1:RA:1636:C:H2'	1:RA:1637:A:C8	2.56	0.40
3:RD:102:LYS:O	3:RD:103:ARG:HG2	2.20	0.40
3:RD:71:ASP:OD2	3:RD:103:ARG:NH1	2.53	0.40
5:RF:129:PHE:CD2	5:RF:163:VAL:HG21	2.56	0.40
18:RW:17:VAL:HG23	18:RW:76:VAL:HG11	2.02	0.40
32:XA:1132:C:C2	32:XA:1133:G:C8	3.09	0.40
32:XA:253:U:H2'	32:XA:254:G:C8	2.55	0.40
32:XA:993:G:O2'	32:XA:994:A:N7	2.54	0.40
39:XH:91:ARG:HD3	39:XH:91:ARG:HH11	1.64	0.40
40:XI:5:TYR:HE1	40:XI:16:ARG:HB3	1.86	0.40
43:XL:10:LEU:HA	43:XL:10:LEU:HD23	1.97	0.40
34:XC:12:LEU:CD1	45:XN:51:GLY:HA2	2.49	0.40
47:XP:17:TYR:HE1	47:XP:41:PRO:HG3	1.85	0.40
47:XP:23:ASP:OD1	47:XP:25:ARG:HD3	2.21	0.40
47:XP:3:LYS:HD2	47:XP:24:ALA:HB2	2.03	0.40
47:XP:53:VAL:HG13	47:XP:79:VAL:HA	2.04	0.40
54:XY:326:TYR:CD1	54:XY:326:TYR:N	2.89	0.40
54:XY:335:ASP:C	54:XY:337:ARG:H	2.23	0.40
1:YA:1068:G:H22	54:XY:58:LYS:HD2	1.86	0.40
1:YA:1084:A:N6	1:YA:1086:A:C8	2.89	0.40
1:YA:1388:G:H2'	1:YA:1389:G:C8	2.52	0.40
1:YA:1721:G:N1	1:YA:1739:U:OP2	2.54	0.40
1:YA:644:A:H4'	1:YA:645:C:H5	1.86	0.40
1:YA:708:C:H2'	1:YA:709:U:H6	1.84	0.40
4:YE:52:LEU:HB3	4:YE:53:PRO:CD	2.50	0.40
13:YR:67:LEU:HD12	13:YR:67:LEU:HA	1.97	0.40
19:YX:94:GLY:HA3	19:YX:95:LEU:O	2.21	0.40
32:QA:1014:A:C2	32:QA:1219:U:H1'	2.55	0.40
32:QA:152:A:H3'	32:QA:153:C:C6	2.56	0.40
32:QA:439:A:C5	32:QA:441:A:H1'	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:513:C:H2'	32:QA:514:C:H6	1.86	0.40
33:QB:124:SER:HA	33:QB:125:PRO:HA	1.77	0.40
33:QB:47:THR:HA	33:QB:202:PRO:HG2	2.02	0.40
35:QD:116:GLN:NE2	35:QD:157:LEU:HD11	2.36	0.40
36:QE:90:VAL:O	36:QE:120:THR:HA	2.21	0.40
40:QI:65:VAL:HG22	40:QI:73:GLN:HG2	2.03	0.40
41:QJ:4:ILE:N	41:QJ:100:THR:HG22	2.37	0.40
43:QL:71:PRO:O	43:QL:102:ARG:NH1	2.54	0.40
32:QA:523:A:N1	43:QL:92:0TD:H6	2.36	0.40
53:QV:4:G:O2'	53:QV:5:G:H8	2.03	0.40
1:RA:1049:C:O2	1:RA:1113:U:H4'	2.21	0.40
1:RA:1092:C:H6	1:RA:1092:C:OP2	2.04	0.40
1:RA:1105:U:H2'	1:RA:1106:G:C8	2.56	0.40
1:RA:1201:C:H2'	1:RA:1202:C:C6	2.56	0.40
1:RA:1417:C:H2'	1:RA:1418:G:O4'	2.22	0.40
1:RA:2144:U:O2'	1:RA:2147:G:N1	2.49	0.40
1:RA:225:A:O2'	1:RA:257:A:H4'	2.22	0.40
1:RA:284:U:H2'	1:RA:285:C:H6	1.84	0.40
1:RA:27:G:O2'	1:RA:28:A:OP2	2.35	0.40
1:RA:84:A:C2	1:RA:103:A:C5	3.09	0.40
1:RA:898:C:H2'	1:RA:899:A:O4'	2.21	0.40
6:RG:121:ASN:HA	6:RG:122:PRO:HD3	1.80	0.40
12:RQ:84:GLY:O	12:RQ:85:LYS:HB2	2.21	0.40
14:RS:3:ARG:CA	14:RS:3:ARG:HE	2.34	0.40
32:XA:1143:G:H2'	32:XA:1144:G:C8	2.55	0.40
32:XA:1516:G:H2'	32:XA:1518:MA6:OP2	2.21	0.40
32:XA:390:C:H2'	32:XA:391:G:C8	2.55	0.40
33:XB:118:LEU:HD23	33:XB:118:LEU:HA	1.89	0.40
33:XB:19:HIS:O	33:XB:20:GLU:HB2	2.21	0.40
33:XB:33:TYR:HB3	33:XB:41:ILE:HG22	2.03	0.40
34:XC:11:ARG:NH2	34:XC:177:THR:O	2.50	0.40
32:XA:407:G:H5''	35:XD:115:ARG:HB3	2.03	0.40
36:XE:31:LEU:HD23	36:XE:31:LEU:HA	1.93	0.40
36:XE:69:VAL:HA	36:XE:70:PRO:HD3	1.64	0.40
47:XP:75:ARG:HG3	47:XP:80:PHE:HD2	1.86	0.40
50:XS:20:LEU:HA	50:XS:23:ASN:HB2	2.03	0.40
26:Y4:61:ARG:NH2	50:XS:9:VAL:HG11	2.37	0.40
54:XY:265:HIS:HB2	54:XY:291:MET:CE	2.48	0.40
23:Y1:70:VAL:O	23:Y1:74:VAL:HG23	2.21	0.40
26:Y4:14:ILE:HB	26:Y4:22:ILE:HB	2.03	0.40
26:Y4:48:ARG:HB3	26:Y4:52:THR:HA	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:2182:G:H2'	1:YA:2183:C:C6	2.56	0.40
1:YA:2059:A:C8	1:YA:2503:2MA:HM23	2.57	0.40
3:YD:275:LYS:HA	3:YD:276:LYS:C	2.41	0.40
6:YG:5:VAL:CG2	6:YG:8:LYS:CB	2.99	0.40
6:YG:82:LEU:HA	6:YG:86:MET:SD	2.61	0.40
8:YI:114:LEU:HD11	8:YI:128:LEU:HD13	2.04	0.40
12:YQ:55:VAL:HG23	21:YZ:178:GLU:HB3	2.02	0.40
1:YA:483:A:O4'	20:YY:48:ALA:HB1	2.21	0.40
32:QA:1103:C:H2'	32:QA:1104:G:O4'	2.21	0.40
32:QA:575:G:HO2'	32:QA:821:G:H5'	1.86	0.40
54:QY:315:SER:HA	54:QY:316:ASP:HA	1.65	0.40
1:RA:151:C:H2'	1:RA:152:G:H8	1.87	0.40
1:RA:2144:U:H5''	1:RA:2145:C:C5	2.57	0.40
1:RA:2168:G:H2'	1:RA:2170:A:OP2	2.22	0.40
6:RG:126:ASP:HB2	6:RG:130:ASN:H	1.86	0.40
2:RB:31:C:H4'	6:RG:29:TRP:CH2	2.57	0.40
15:RT:35:LYS:O	15:RT:35:LYS:HE2	2.22	0.40
16:RU:61:TRP:CH2	16:RU:93:LYS:HB2	2.57	0.40
32:XA:300:A:H1'	32:XA:565:U:O2	2.20	0.40
32:XA:476:G:H2'	32:XA:477:A:H8	1.86	0.40
32:XA:721:G:H4'	32:XA:722:A:O4'	2.22	0.40
44:XM:89:GLY:O	44:XM:93:ARG:HG3	2.22	0.40
26:Y4:58:ARG:NH1	50:XS:66:MET:HA	2.29	0.40
54:XY:217:PHE:CZ	54:XY:319:TRP:HA	2.57	0.40
26:Y4:58:ARG:HH12	50:XS:66:MET:CA	2.30	0.40
1:YA:443:A:H1'	1:YA:1201:C:O4'	2.20	0.40
1:YA:2243:U:H2'	1:YA:2244:U:H6	1.86	0.40
1:YA:872:A:H2'	1:YA:873:G:C8	2.56	0.40
5:YF:28:ILE:O	5:YF:30:PRO:HD3	2.22	0.40
8:YI:117:GLU:HG3	8:YI:118:LYS:N	2.37	0.40
13:YR:21:TYR:OH	13:YR:43:GLU:HG2	2.21	0.40
1:YA:533:G:H5'	16:YU:24:TYR:CE1	2.57	0.40
17:YV:5:VAL:HG11	17:YV:57:VAL:HG21	2.04	0.40
32:QA:1158:C:H5	32:QA:1181:G:H22	1.69	0.40
32:QA:923:A:O2'	32:QA:1399:C:OP2	2.23	0.40
32:QA:1441:G:H5''	32:QA:1442(A):G:H5'	2.03	0.40
38:QG:23:VAL:HG13	38:QG:43:PHE:CE2	2.57	0.40
38:QG:56:GLN:O	38:QG:58:PRO:HD3	2.21	0.40
50:QS:12:ASP:OD2	50:QS:35:SER:HB3	2.21	0.40
1:RA:55:G:C2	1:RA:116:C:C2	3.10	0.40
1:RA:2065:C:C2	1:RA:2066:C:C5	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:2071:A:H2'	1:RA:2072:G:H8	1.86	0.40
1:RA:2321:G:N3	1:RA:2321:G:H2'	2.36	0.40
1:RA:2649:U:H2'	1:RA:2650:U:C6	2.56	0.40
1:RA:2741:A:H2'	1:RA:2742:C:O4'	2.22	0.40
1:RA:476:G:N1	1:RA:479:A:OP2	2.51	0.40
1:RA:614(A):U:H2'	1:RA:614(B):U:O4'	2.22	0.40
2:RB:29:A:H2'	2:RB:30:C:C6	2.56	0.40
5:RF:103:LYS:O	5:RF:106:ARG:HG2	2.22	0.40
5:RF:136:THR:O	5:RF:140:LEU:CD2	2.70	0.40
5:RF:170:LEU:HD23	5:RF:172:TRP:CE2	2.56	0.40
10:RO:23:ARG:HG3	10:RO:24:VAL:N	2.35	0.40
10:RO:64:ARG:NH2	10:RO:99:PHE:O	2.55	0.40
15:RT:105:LEU:HD23	15:RT:105:LEU:HA	1.85	0.40
19:RX:35:THR:HG22	19:RX:37:THR:H	1.85	0.40
32:XA:250:A:H4'	32:XA:251:G:O5'	2.20	0.40
32:XA:70:G:H2'	32:XA:71:C:C6	2.56	0.40
42:XK:116:HIS:N	42:XK:117:ASN:HA	2.37	0.40
44:XM:16:ASP:OD1	44:XM:16:ASP:N	2.53	0.40
32:XA:1330:U:H4'	44:XM:23:TYR:CE1	2.57	0.40
44:XM:35:GLU:O	44:XM:38:GLY:N	2.52	0.40
47:XP:2:VAL:HG13	47:XP:64:ALA:HA	2.03	0.40
1:YA:1939:5MU:OP1	1:YA:2604:U:O2'	2.38	0.40
1:YA:2193:G:H2'	1:YA:2194:G:C8	2.56	0.40
1:YA:479:A:HO2'	1:YA:481:G:H8	1.65	0.40
1:YA:987:G:H2'	1:YA:988:A:O4'	2.22	0.40
1:YA:2784:C:H1'	4:YE:37:ARG:NH1	2.35	0.40
6:YG:166:ASP:O	6:YG:170:ARG:N	2.45	0.40
14:YS:69:VAL:HG13	14:YS:101:LEU:HD12	2.03	0.40
32:QA:1065:U:H1'	32:QA:1066:C:OP2	2.22	0.40
32:QA:1291:G:OP1	38:QG:37:ASN:ND2	2.55	0.40
32:QA:1498:UR3:O5'	32:QA:1498:UR3:H6	2.21	0.40
33:QB:211:ILE:HG13	33:QB:211:ILE:H	1.73	0.40
35:QD:121:VAL:O	35:QD:134:ASP:HA	2.22	0.40
47:QP:19:ILE:HG22	47:QP:37:GLY:C	2.42	0.40
47:QP:40:ASP:HA	47:QP:41:PRO:HD2	1.91	0.40
50:QS:65:ASN:O	26:R4:58:ARG:CD	2.70	0.40
50:QS:71:LEU:HD23	50:QS:71:LEU:HA	1.83	0.40
51:QT:36:LEU:HD12	51:QT:62:LEU:HD12	2.04	0.40
51:QT:92:LEU:O	51:QT:96:GLY:N	2.45	0.40
1:RA:1033:U:O2'	1:RA:2750:A:N6	2.54	0.40
1:RA:1340:U:OP1	19:RX:16:LYS:NZ	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:2024:G:H2'	1:RA:2025:C:H6	1.85	0.40
1:RA:2329:G:H2'	1:RA:2330:G:C8	2.56	0.40
1:RA:2630:G:H2'	1:RA:2631:G:C8	2.57	0.40
1:RA:479:A:HO2'	1:RA:481:G:H8	1.65	0.40
1:RA:536:A:H2'	1:RA:537:C:H6	1.87	0.40
1:RA:719:C:H2'	1:RA:720:C:C6	2.57	0.40
5:RF:116:ASP:OD1	5:RF:119:ARG:NH2	2.48	0.40
8:RI:29:TYR:O	8:RI:32:PRO:HD2	2.21	0.40
20:RY:19:LYS:HE2	20:RY:19:LYS:HB3	1.84	0.40
32:XA:687:A:H1'	32:XA:688:G:OP2	2.22	0.40
35:XD:122:ARG:HD2	35:XD:122:ARG:HH11	1.67	0.40
39:XH:6:ILE:O	39:XH:10:LEU:HG	2.21	0.40
32:XA:36:C:OP1	43:XL:123:LYS:HE2	2.21	0.40
54:XY:129:TYR:HD1	54:XY:182:LYS:HA	1.87	0.40
25:Y3:3:ARG:NH1	25:Y3:60:GLU:HA	2.36	0.40
1:YA:1588:C:H2'	1:YA:1589:C:H6	1.86	0.40
1:YA:1629:U:H2'	1:YA:1630:G:C8	2.56	0.40
1:YA:2247:A:H2'	1:YA:2248:C:H6	1.85	0.40
1:YA:2262:U:H4'	1:YA:2328:A:C2	2.57	0.40
1:YA:642:G:N2	1:YA:644:A:H3'	2.36	0.40
9:YN:138:LEU:HA	9:YN:138:LEU:HD23	1.97	0.40
15:YT:23:ARG:HG3	15:YT:120:ARG:NH1	2.37	0.40
21:YZ:5:LEU:HD23	21:YZ:47:VAL:HG21	2.04	0.40
21:YZ:25:PRO:O	21:YZ:85:HIS:HA	2.22	0.40

All (13) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:YH:46:GLU:OE1	20:YY:22:GLY:C[4_445]	0.78	1.42
7:YH:46:GLU:OE1	20:YY:22:GLY:O[4_445]	1.12	1.08
7:YH:46:GLU:OE1	20:YY:23:ARG:N[4_445]	1.56	0.64
17:YV:49:THR:O	27:Y5:60:VAL:O[4_445]	1.77	0.43
17:YV:53:GLU:OE2	27:Y5:59:GLU:CA[4_445]	1.88	0.32
20:YY:92:ASN:ND2	18:RW:59:VAL:O[3_545]	1.95	0.25
7:YH:46:GLU:CD	20:YY:22:GLY:C[4_445]	1.97	0.23
17:YV:53:GLU:CD	27:Y5:59:GLU:CG[4_445]	1.99	0.21
7:YH:46:GLU:OE1	20:YY:22:GLY:CA[4_445]	2.00	0.20
1:YA:277:C:O2'	24:R2:46:GLN:OE1[3_545]	2.00	0.20
17:YV:53:GLU:OE1	27:Y5:59:GLU:CB[4_445]	2.02	0.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:YH:46:GLU:OE2	20:YY:23:ARG:CA[4_445]	2.02	0.18
17:YV:53:GLU:OE2	27:Y5:59:GLU:C[4_445]	2.18	0.02

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	
3	RD	273/276 (99%)	262 (96%)	11 (4%)	0	100	100
3	YD	273/276 (99%)	260 (95%)	13 (5%)	0	100	100
4	RE	202/206 (98%)	195 (96%)	6 (3%)	1 (0%)	32	66
4	YE	202/206 (98%)	196 (97%)	6 (3%)	0	100	100
5	RF	201/210 (96%)	197 (98%)	4 (2%)	0	100	100
5	YF	201/210 (96%)	196 (98%)	3 (2%)	2 (1%)	18	53
6	RG	179/182 (98%)	167 (93%)	11 (6%)	1 (1%)	28	63
6	YG	179/182 (98%)	170 (95%)	8 (4%)	1 (1%)	28	63
7	RH	172/180 (96%)	167 (97%)	5 (3%)	0	100	100
7	YH	171/180 (95%)	165 (96%)	6 (4%)	0	100	100
8	RI	145/148 (98%)	133 (92%)	11 (8%)	1 (1%)	25	60
8	YI	144/148 (97%)	135 (94%)	9 (6%)	0	100	100
9	RN	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
9	YN	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
10	RO	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
10	YO	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
11	RP	147/150 (98%)	141 (96%)	6 (4%)	0	100	100
11	YP	147/150 (98%)	141 (96%)	5 (3%)	1 (1%)	25	60
12	RQ	139/141 (99%)	134 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	YQ	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
13	RR	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
13	YR	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
14	RS	108/112 (96%)	104 (96%)	3 (3%)	1 (1%)	20	55
14	YS	108/112 (96%)	105 (97%)	3 (3%)	0	100	100
15	RT	129/146 (88%)	124 (96%)	5 (4%)	0	100	100
15	YT	129/146 (88%)	125 (97%)	4 (3%)	0	100	100
16	RU	114/118 (97%)	114 (100%)	0	0	100	100
16	YU	114/118 (97%)	114 (100%)	0	0	100	100
17	RV	99/101 (98%)	97 (98%)	2 (2%)	0	100	100
17	YV	99/101 (98%)	96 (97%)	3 (3%)	0	100	100
18	RW	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
18	YW	110/113 (97%)	110 (100%)	0	0	100	100
19	RX	93/96 (97%)	92 (99%)	1 (1%)	0	100	100
19	YX	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
20	RY	105/110 (96%)	99 (94%)	6 (6%)	0	100	100
20	YY	105/110 (96%)	101 (96%)	4 (4%)	0	100	100
21	RZ	201/206 (98%)	196 (98%)	5 (2%)	0	100	100
21	YZ	199/206 (97%)	194 (98%)	5 (2%)	0	100	100
22	R0	75/85 (88%)	73 (97%)	2 (3%)	0	100	100
22	Y0	75/85 (88%)	73 (97%)	2 (3%)	0	100	100
23	R1	95/98 (97%)	94 (99%)	0	1 (1%)	17	52
23	Y1	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	17	52
24	R2	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
24	Y2	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
25	R3	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
25	Y3	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
26	R4	67/71 (94%)	55 (82%)	6 (9%)	6 (9%)	1	6
26	Y4	67/71 (94%)	53 (79%)	11 (16%)	3 (4%)	3	20
27	R5	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
27	Y5	57/60 (95%)	56 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	R6	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
28	Y6	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
29	R7	46/49 (94%)	46 (100%)	0	0	100	100
29	Y7	46/49 (94%)	46 (100%)	0	0	100	100
30	R8	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
30	Y8	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
31	R9	35/37 (95%)	35 (100%)	0	0	100	100
31	Y9	35/37 (95%)	35 (100%)	0	0	100	100
33	QB	229/256 (90%)	202 (88%)	20 (9%)	7 (3%)	5	30
33	XB	229/256 (90%)	205 (90%)	19 (8%)	5 (2%)	8	37
34	QC	204/239 (85%)	190 (93%)	14 (7%)	0	100	100
34	XC	204/239 (85%)	187 (92%)	17 (8%)	0	100	100
35	QD	206/209 (99%)	197 (96%)	9 (4%)	0	100	100
35	XD	206/209 (99%)	199 (97%)	7 (3%)	0	100	100
36	QE	146/162 (90%)	144 (99%)	2 (1%)	0	100	100
36	XE	146/162 (90%)	145 (99%)	1 (1%)	0	100	100
37	QF	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
37	XF	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
38	QG	153/156 (98%)	148 (97%)	5 (3%)	0	100	100
38	XG	153/156 (98%)	148 (97%)	4 (3%)	1 (1%)	25	60
39	QH	135/138 (98%)	133 (98%)	2 (2%)	0	100	100
39	XH	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
40	QI	125/128 (98%)	115 (92%)	9 (7%)	1 (1%)	22	57
40	XI	124/128 (97%)	113 (91%)	8 (6%)	3 (2%)	7	35
41	QJ	95/105 (90%)	83 (87%)	8 (8%)	4 (4%)	3	22
41	XJ	94/105 (90%)	85 (90%)	7 (7%)	2 (2%)	8	38
42	QK	112/129 (87%)	103 (92%)	7 (6%)	2 (2%)	10	42
42	XK	112/129 (87%)	106 (95%)	5 (4%)	1 (1%)	20	55
43	QL	119/132 (90%)	117 (98%)	2 (2%)	0	100	100
43	XL	119/132 (90%)	116 (98%)	3 (2%)	0	100	100
44	QM	114/126 (90%)	105 (92%)	7 (6%)	2 (2%)	10	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	XM	112/126 (89%)	105 (94%)	6 (5%)	1 (1%)	20	55
45	QN	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
45	XN	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
46	QO	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
46	XO	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
47	QP	80/88 (91%)	77 (96%)	3 (4%)	0	100	100
47	XP	80/88 (91%)	76 (95%)	4 (5%)	0	100	100
48	QQ	97/105 (92%)	94 (97%)	2 (2%)	1 (1%)	18	53
48	XQ	97/105 (92%)	95 (98%)	2 (2%)	0	100	100
49	QR	66/88 (75%)	65 (98%)	1 (2%)	0	100	100
49	XR	66/88 (75%)	65 (98%)	1 (2%)	0	100	100
50	QS	81/93 (87%)	78 (96%)	3 (4%)	0	100	100
50	XS	81/93 (87%)	79 (98%)	2 (2%)	0	100	100
51	QT	94/106 (89%)	86 (92%)	6 (6%)	2 (2%)	8	38
51	XT	96/106 (91%)	88 (92%)	6 (6%)	2 (2%)	8	38
52	QU	21/27 (78%)	19 (90%)	2 (10%)	0	100	100
52	XU	21/27 (78%)	19 (90%)	1 (5%)	1 (5%)	2	18
54	QY	354/380 (93%)	309 (87%)	37 (10%)	8 (2%)	7	36
54	XY	354/380 (93%)	309 (87%)	36 (10%)	9 (2%)	6	34
All	All	12148/12888 (94%)	11573 (95%)	504 (4%)	71 (1%)	28	63

All (71) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
23	Y1	3	LYS
33	XB	17	PHE
33	XB	20	GLU
33	XB	124	SER
40	XI	44	VAL
40	XI	54	ASP
33	QB	16	HIS
33	QB	17	PHE
33	QB	22	LYS
51	QT	95	ALA
26	R4	49	PHE

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Mol	Chain	Res	Type
54	QY	127	ASP
54	QY	139	THR
54	XY	127	ASP
54	XY	336	LEU
6	YG	81	LYS
26	Y4	60	GLN
33	XB	10	LEU
41	XJ	79	ARG
44	XM	67	GLU
51	XT	95	ALA
40	QI	44	VAL
41	QJ	31	GLY
41	QJ	78	ASN
41	QJ	79	ARG
6	RG	51	ARG
14	RS	60	GLY
26	R4	45	GLY
26	R4	47	GLN
54	QY	122	GLU
54	QY	229	ASP
54	QY	336	LEU
54	XY	122	GLU
54	XY	134	ALA
5	YF	21	ALA
26	Y4	45	GLY
33	XB	125	PRO
41	XJ	78	ASN
44	QM	12	ASN
4	RE	52	LEU
54	XY	319	TRP
38	XG	7	ALA
33	QB	20	GLU
44	QM	67	GLU
26	R4	46	GLN
26	R4	55	ARG
54	QY	226	VAL
54	XY	137	GLY
54	XY	230	ILE
5	YF	130	ALA
26	Y4	55	ARG
51	XT	100	ILE
52	XU	7	ARG

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Mol	Chain	Res	Type
33	QB	43	ASP
33	QB	127	ILE
42	QK	117	ASN
8	RI	73	GLU
23	R1	3	LYS
26	R4	60	GLN
54	XY	121	GLY
11	YP	29	LYS
40	XI	11	LYS
48	QQ	68	ARG
51	QT	100	ILE
54	QY	121	GLY
54	QY	230	ILE
54	XY	320	GLY
42	XK	105	VAL
42	QK	105	VAL
33	QB	15	VAL
41	QJ	77	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	
3	RD	214/218 (98%)	209 (98%)	5 (2%)	56	79
3	YD	215/218 (99%)	209 (97%)	6 (3%)	49	76
4	RE	164/166 (99%)	163 (99%)	1 (1%)	89	93
4	YE	164/166 (99%)	159 (97%)	5 (3%)	46	75
5	RF	160/166 (96%)	152 (95%)	8 (5%)	28	64
5	YF	159/166 (96%)	154 (97%)	5 (3%)	45	75
6	RG	144/156 (92%)	139 (96%)	5 (4%)	41	72
6	YG	142/156 (91%)	133 (94%)	9 (6%)	21	56
7	RH	144/148 (97%)	142 (99%)	2 (1%)	71	85
7	YH	143/148 (97%)	140 (98%)	3 (2%)	59	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	RI	111/124 (90%)	105 (95%)	6 (5%)	26	62
8	YI	108/124 (87%)	108 (100%)	0	100	100
9	RN	119/119 (100%)	115 (97%)	4 (3%)	42	73
9	YN	118/119 (99%)	115 (98%)	3 (2%)	53	78
10	RO	100/100 (100%)	100 (100%)	0	100	100
10	YO	100/100 (100%)	100 (100%)	0	100	100
11	RP	115/116 (99%)	112 (97%)	3 (3%)	51	77
11	YP	115/116 (99%)	113 (98%)	2 (2%)	66	83
12	RQ	111/111 (100%)	107 (96%)	4 (4%)	40	72
12	YQ	111/111 (100%)	106 (96%)	5 (4%)	32	67
13	RR	101/101 (100%)	99 (98%)	2 (2%)	60	81
13	YR	101/101 (100%)	101 (100%)	0	100	100
14	RS	87/88 (99%)	84 (97%)	3 (3%)	42	73
14	YS	85/88 (97%)	82 (96%)	3 (4%)	41	72
15	RT	115/127 (91%)	110 (96%)	5 (4%)	33	68
15	YT	113/127 (89%)	110 (97%)	3 (3%)	50	77
16	RU	93/94 (99%)	90 (97%)	3 (3%)	44	74
16	YU	93/94 (99%)	89 (96%)	4 (4%)	33	68
17	RV	81/82 (99%)	80 (99%)	1 (1%)	75	87
17	YV	80/82 (98%)	78 (98%)	2 (2%)	53	78
18	RW	90/92 (98%)	86 (96%)	4 (4%)	33	67
18	YW	90/92 (98%)	88 (98%)	2 (2%)	57	80
19	RX	77/78 (99%)	76 (99%)	1 (1%)	73	86
19	YX	77/78 (99%)	74 (96%)	3 (4%)	37	70
20	RY	86/91 (94%)	83 (96%)	3 (4%)	41	72
20	YY	86/91 (94%)	82 (95%)	4 (5%)	30	66
21	RZ	169/179 (94%)	165 (98%)	4 (2%)	54	79
21	YZ	165/179 (92%)	159 (96%)	6 (4%)	40	72
22	R0	61/67 (91%)	59 (97%)	2 (3%)	43	74
22	Y0	61/67 (91%)	56 (92%)	5 (8%)	13	44
23	R1	79/83 (95%)	77 (98%)	2 (2%)	53	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	Y1	81/83 (98%)	79 (98%)	2 (2%)	53	78
24	R2	65/67 (97%)	63 (97%)	2 (3%)	45	75
24	Y2	66/67 (98%)	64 (97%)	2 (3%)	46	75
25	R3	51/52 (98%)	51 (100%)	0	100	100
25	Y3	50/52 (96%)	47 (94%)	3 (6%)	22	58
26	R4	58/63 (92%)	55 (95%)	3 (5%)	27	63
26	Y4	54/63 (86%)	47 (87%)	7 (13%)	5	22
27	R5	51/52 (98%)	50 (98%)	1 (2%)	60	81
27	Y5	50/52 (96%)	49 (98%)	1 (2%)	60	81
28	R6	51/52 (98%)	50 (98%)	1 (2%)	60	81
28	Y6	50/52 (96%)	50 (100%)	0	100	100
29	R7	41/42 (98%)	41 (100%)	0	100	100
29	Y7	41/42 (98%)	41 (100%)	0	100	100
30	R8	54/55 (98%)	52 (96%)	2 (4%)	39	71
30	Y8	54/55 (98%)	52 (96%)	2 (4%)	39	71
31	R9	34/34 (100%)	34 (100%)	0	100	100
31	Y9	34/34 (100%)	34 (100%)	0	100	100
33	QB	191/220 (87%)	182 (95%)	9 (5%)	30	66
33	XB	187/220 (85%)	176 (94%)	11 (6%)	23	58
34	QC	144/188 (77%)	141 (98%)	3 (2%)	59	81
34	XC	140/188 (74%)	135 (96%)	5 (4%)	40	72
35	QD	171/181 (94%)	166 (97%)	5 (3%)	48	75
35	XD	172/181 (95%)	168 (98%)	4 (2%)	56	79
36	QE	114/123 (93%)	112 (98%)	2 (2%)	64	83
36	XE	114/123 (93%)	113 (99%)	1 (1%)	82	90
37	QF	85/90 (94%)	83 (98%)	2 (2%)	54	79
37	XF	85/90 (94%)	83 (98%)	2 (2%)	54	79
38	QG	120/127 (94%)	117 (98%)	3 (2%)	53	78
38	XG	119/127 (94%)	116 (98%)	3 (2%)	53	78
39	QH	116/119 (98%)	114 (98%)	2 (2%)	66	83
39	XH	114/119 (96%)	109 (96%)	5 (4%)	33	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	QI	91/99 (92%)	85 (93%)	6 (7%)	19	54
40	XI	88/99 (89%)	86 (98%)	2 (2%)	56	79
41	QJ	68/92 (74%)	67 (98%)	1 (2%)	70	85
41	XJ	68/92 (74%)	67 (98%)	1 (2%)	70	85
42	QK	83/99 (84%)	82 (99%)	1 (1%)	75	87
42	XK	83/99 (84%)	81 (98%)	2 (2%)	54	79
43	QL	96/108 (89%)	95 (99%)	1 (1%)	80	88
43	XL	96/108 (89%)	95 (99%)	1 (1%)	80	88
44	QM	90/101 (89%)	86 (96%)	4 (4%)	33	67
44	XM	87/101 (86%)	85 (98%)	2 (2%)	56	79
45	QN	49/50 (98%)	46 (94%)	3 (6%)	22	57
45	XN	49/50 (98%)	48 (98%)	1 (2%)	60	81
46	QO	78/80 (98%)	76 (97%)	2 (3%)	51	77
46	XO	78/80 (98%)	75 (96%)	3 (4%)	38	70
47	QP	69/74 (93%)	69 (100%)	0	100	100
47	XP	68/74 (92%)	66 (97%)	2 (3%)	48	75
48	QQ	94/97 (97%)	93 (99%)	1 (1%)	78	88
48	XQ	94/97 (97%)	94 (100%)	0	100	100
49	QR	59/77 (77%)	58 (98%)	1 (2%)	66	83
49	XR	59/77 (77%)	58 (98%)	1 (2%)	66	83
50	QS	68/80 (85%)	65 (96%)	3 (4%)	33	67
50	XS	67/80 (84%)	67 (100%)	0	100	100
51	QT	71/82 (87%)	70 (99%)	1 (1%)	71	85
51	XT	70/82 (85%)	70 (100%)	0	100	100
52	QU	18/22 (82%)	17 (94%)	1 (6%)	25	60
52	XU	18/22 (82%)	16 (89%)	2 (11%)	7	29
54	QY	303/323 (94%)	301 (99%)	2 (1%)	87	92
54	XY	303/323 (94%)	301 (99%)	2 (1%)	87	92
All	All	9969/10710 (93%)	9702 (97%)	267 (3%)	50	77

All (267) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	YD	88	ARG
3	YD	94	LEU
3	YD	99	ASP
3	YD	211	ARG
3	YD	242	ARG
3	YD	260	ARG
4	YE	73	GLU
4	YE	82	ARG
4	YE	113	PHE
4	YE	119	ARG
4	YE	144	ARG
5	YF	20	LEU
5	YF	60	SER
5	YF	106	ARG
5	YF	197	ASP
5	YF	205	ARG
6	YG	3	LEU
6	YG	7	LEU
6	YG	21	ARG
6	YG	36	LYS
6	YG	47	LYS
6	YG	98	ARG
6	YG	136	ARG
6	YG	146	TYR
6	YG	170	ARG
7	YH	41	MET
7	YH	95	ARG
7	YH	140	LYS
9	YN	90	MET
9	YN	99	LEU
9	YN	131	GLN
11	YP	70	GLN
11	YP	86	LYS
12	YQ	1	MET
12	YQ	7	MET
12	YQ	8	LYS
12	YQ	56	ARG
12	YQ	60	ARG
14	YS	20	ARG
14	YS	67	ARG
14	YS	71	ARG
15	YT	23	ARG
15	YT	96	ARG

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Mol	Chain	Res	Type
15	YT	118	ARG
16	YU	36	ARG
16	YU	74	LEU
16	YU	89	GLU
16	YU	92	ARG
17	YV	6	LYS
17	YV	18	LEU
18	YW	11	ARG
18	YW	15	ARG
19	YX	2	LYS
19	YX	33	LYS
19	YX	57	LEU
20	YY	6	HIS
20	YY	23	ARG
20	YY	57	GLN
20	YY	99	CYS
21	YZ	2	GLU
21	YZ	6	LYS
21	YZ	46	LYS
21	YZ	72	ARG
21	YZ	132	ASN
21	YZ	156	LYS
22	Y0	19	LYS
22	Y0	20	ARG
22	Y0	35	ASN
22	Y0	55	ARG
22	Y0	70	GLN
23	Y1	40	ARG
23	Y1	52	ARG
24	Y2	52	ASP
24	Y2	53	LEU
25	Y3	3	ARG
25	Y3	30	ARG
25	Y3	55	ARG
26	Y4	8	LYS
26	Y4	34	GLU
26	Y4	48	ARG
26	Y4	60	GLN
26	Y4	62	ARG
26	Y4	63	TYR
26	Y4	69	LYS
27	Y5	40	LYS

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Mol	Chain	Res	Type
30	Y8	31	HIS
30	Y8	34	TRP
33	XB	8	LYS
33	XB	17	PHE
33	XB	24	TRP
33	XB	76	GLN
33	XB	114	ARG
33	XB	118	LEU
33	XB	122	PHE
33	XB	163	PHE
33	XB	212	GLN
33	XB	217	ARG
33	XB	226	ARG
34	XC	21	ARG
34	XC	102	ASN
34	XC	105	GLU
34	XC	132	ARG
34	XC	190	ARG
35	XD	31	CYS
35	XD	122	ARG
35	XD	157	LEU
35	XD	201	GLN
36	XE	57	LYS
37	XF	28	ARG
37	XF	46	ARG
38	XG	15	ASP
38	XG	78	ARG
38	XG	115	ARG
39	XH	18	ARG
39	XH	21	LYS
39	XH	84	ARG
39	XH	98	LYS
39	XH	112	LEU
40	XI	102	LEU
40	XI	104	ARG
41	XJ	57	LYS
42	XK	116	HIS
42	XK	126	ARG
43	XL	41	ARG
44	XM	94	ARG
44	XM	110	ARG
45	XN	57	ARG

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Mol	Chain	Res	Type
46	XO	38	ARG
46	XO	39	LEU
46	XO	41	GLU
47	XP	8	ARG
47	XP	28	ARG
49	XR	41	LYS
52	XU	10	ARG
52	XU	24	ARG
33	QB	21	ARG
33	QB	24	TRP
33	QB	122	PHE
33	QB	144	ARG
33	QB	150	SER
33	QB	157	ARG
33	QB	163	PHE
33	QB	195	ASP
33	QB	226	ARG
34	QC	36	ASP
34	QC	45	LYS
34	QC	131	ARG
35	QD	49	ARG
35	QD	157	LEU
35	QD	168	ARG
35	QD	187	ARG
35	QD	193	ASP
36	QE	57	LYS
36	QE	137	GLU
37	QF	46	ARG
37	QF	70	ASP
38	QG	6	ARG
38	QG	57	GLU
38	QG	86	GLN
39	QH	21	LYS
39	QH	52	ASP
40	QI	2	GLU
40	QI	25	LYS
40	QI	42	ARG
40	QI	66	ARG
40	QI	93	ARG
40	QI	104	ARG
41	QJ	5	ARG
42	QK	117	ASN

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Mol	Chain	Res	Type
43	QL	33	ARG
44	QM	3	ARG
44	QM	11	ARG
44	QM	36	LYS
44	QM	110	ARG
45	QN	3	ARG
45	QN	41	ARG
45	QN	57	ARG
46	QO	41	GLU
46	QO	48	LYS
48	QQ	68	ARG
49	QR	35	ARG
50	QS	5	LEU
50	QS	65	ASN
50	QS	81	ARG
51	QT	90	GLN
52	QU	10	ARG
3	RD	88	ARG
3	RD	126	GLN
3	RD	211	ARG
3	RD	242	ARG
3	RD	260	ARG
4	RE	82	ARG
5	RF	60	SER
5	RF	74	ARG
5	RF	106	ARG
5	RF	110	LEU
5	RF	168	ARG
5	RF	192	LEU
5	RF	197	ASP
5	RF	205	ARG
6	RG	49	ASP
6	RG	81	LYS
6	RG	146	TYR
6	RG	153	ARG
6	RG	170	ARG
7	RH	6	ARG
7	RH	69	ARG
8	RI	10	GLU
8	RI	57	ARG
8	RI	61	ARG
8	RI	69	LYS

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Mol	Chain	Res	Type
8	RI	75	LEU
8	RI	101	LEU
9	RN	48	MET
9	RN	61	ARG
9	RN	99	LEU
9	RN	115	ARG
11	RP	117	GLU
11	RP	119	GLU
11	RP	149	GLU
12	RQ	16	ARG
12	RQ	18	LYS
12	RQ	56	ARG
12	RQ	60	ARG
13	RR	44	LEU
13	RR	86	ARG
14	RS	20	ARG
14	RS	43	GLU
14	RS	59	LYS
15	RT	35	LYS
15	RT	53	ARG
15	RT	96	ARG
15	RT	118	ARG
15	RT	125	ARG
16	RU	5	LYS
16	RU	36	ARG
16	RU	74	LEU
17	RV	44	LYS
18	RW	4	LYS
18	RW	11	ARG
18	RW	15	ARG
18	RW	67	ASP
19	RX	57	LEU
20	RY	23	ARG
20	RY	43	ASN
20	RY	99	CYS
21	RZ	72	ARG
21	RZ	156	LYS
21	RZ	185	GLU
21	RZ	199	LYS
22	R0	35	ASN
22	R0	55	ARG
23	R1	40	ARG

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Mol	Chain	Res	Type
23	R1	52	ARG
24	R2	52	ASP
24	R2	53	LEU
26	R4	46	GLN
26	R4	49	PHE
26	R4	65	ASP
27	R5	40	LYS
28	R6	28	ARG
30	R8	31	HIS
30	R8	34	TRP
54	QY	217	PHE
54	QY	326	TYR
54	XY	217	PHE
54	XY	326	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
9	YN	131	GLN
21	YZ	85	HIS
34	XC	6	HIS
50	XS	23	ASN
33	QB	76	GLN
38	QG	56	GLN
50	QS	57	HIS
50	QS	65	ASN
54	QY	281	HIS
54	QY	290	GLN
54	QY	308	GLN
54	XY	54	GLN
54	XY	286	GLN
54	XY	290	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	RA	2855/2915 (97%)	427 (14%)	21 (0%)
1	YA	2855/2915 (97%)	430 (15%)	24 (0%)
2	RB	119/122 (97%)	10 (8%)	0
2	YB	119/122 (97%)	12 (10%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	QA	1494/1521 (98%)	220 (14%)	14 (0%)
32	XA	1498/1521 (98%)	232 (15%)	18 (1%)
53	QV	76/77 (98%)	19 (25%)	1 (1%)
53	XV	76/77 (98%)	18 (23%)	1 (1%)
55	QX	5/25 (20%)	1 (20%)	0
55	XX	5/25 (20%)	1 (20%)	0
All	All	9102/9320 (97%)	1370 (15%)	79 (0%)

All (1370) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	YA	10	G
1	YA	11	G
1	YA	12	U
1	YA	15	G
1	YA	34	C
1	YA	45	C
1	YA	51	G
1	YA	71	A
1	YA	74	A
1	YA	75	G
1	YA	84	A
1	YA	95	G
1	YA	102	G
1	YA	118	A
1	YA	120	U
1	YA	131	G
1	YA	141	A
1	YA	157	U
1	YA	182	A
1	YA	196	A
1	YA	199	A
1	YA	205	G
1	YA	215	G
1	YA	216	A
1	YA	221	A
1	YA	222	A
1	YA	228	A
1	YA	229	A
1	YA	230	U
1	YA	248	G
1	YA	272(K)	U

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Mol	Chain	Res	Type
1	YA	272(L)	U
1	YA	272(M)	G
1	YA	272(N)	U
1	YA	273(B)	U
1	YA	273(C)	G
1	YA	273(K)	C
1	YA	277	C
1	YA	278	A
1	YA	279	C
1	YA	311	A
1	YA	324	A
1	YA	327	G
1	YA	329	G
1	YA	330	A
1	YA	342	G
1	YA	352	G
1	YA	362	U
1	YA	363(A)	G
1	YA	372	G
1	YA	386	G
1	YA	396	G
1	YA	405	U
1	YA	411	G
1	YA	412	A
1	YA	428	A
1	YA	444	C
1	YA	457	A
1	YA	464	U
1	YA	470	A
1	YA	481	G
1	YA	505	A
1	YA	508	G
1	YA	509	C
1	YA	530	G
1	YA	531	C
1	YA	532	A
1	YA	533	G
1	YA	545	G
1	YA	563	G
1	YA	568	U
1	YA	573	G
1	YA	575	A

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Mol	Chain	Res	Type
1	YA	603	A
1	YA	604	G
1	YA	607	U
1	YA	614(C)	G
1	YA	615	G
1	YA	620	G
1	YA	627	A
1	YA	637	A
1	YA	645	C
1	YA	646	A
1	YA	652(C)	A
1	YA	652(D)	G
1	YA	652(V)	G
1	YA	653	A
1	YA	669	G
1	YA	686	G
1	YA	730	C
1	YA	753	C
1	YA	775	G
1	YA	776	G
1	YA	782	A
1	YA	784	A
1	YA	785	G
1	YA	792	G
1	YA	805	G
1	YA	812	C
1	YA	827	U
1	YA	857	C
1	YA	859	G
1	YA	866	A
1	YA	877	U
1	YA	880	G
1	YA	886	C
1	YA	887	A
1	YA	888	C
1	YA	889	C
1	YA	890	A
1	YA	893	C
1	YA	895	U
1	YA	896	A
1	YA	897	C
1	YA	900	A

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Mol	Chain	Res	Type
1	YA	901	A
1	YA	907	U
1	YA	910	A
1	YA	917	A
1	YA	932	G
1	YA	941	A
1	YA	945	A
1	YA	946	G
1	YA	953	A
1	YA	959	A
1	YA	961	C
1	YA	965	C
1	YA	974	G
1	YA	975(A)	C
1	YA	983	A
1	YA	996	A
1	YA	1005	C
1	YA	1012	U
1	YA	1013	C
1	YA	1023	U
1	YA	1026	U
1	YA	1033	U
1	YA	1041	C
1	YA	1045	A
1	YA	1046	A
1	YA	1047	G
1	YA	1048	A
1	YA	1052	C
1	YA	1053	C
1	YA	1054	A
1	YA	1058	G
1	YA	1060	U
1	YA	1063	G
1	YA	1064	C
1	YA	1065	U
1	YA	1066	U
1	YA	1067	A
1	YA	1068	G
1	YA	1069	A
1	YA	1070	A
1	YA	1071	G
1	YA	1073	A

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Mol	Chain	Res	Type
1	YA	1074	G
1	YA	1076	C
1	YA	1077	A
1	YA	1078	U
1	YA	1079	C
1	YA	1082	U
1	YA	1083	U
1	YA	1084	A
1	YA	1085	A
1	YA	1086	A
1	YA	1088	A
1	YA	1090	U
1	YA	1091	G
1	YA	1092	C
1	YA	1094	U
1	YA	1098	A
1	YA	1109	C
1	YA	1110	G
1	YA	1111	A
1	YA	1112	G
1	YA	1129	A
1	YA	1130	U
1	YA	1135	C
1	YA	1136	G
1	YA	1142(B)	A
1	YA	1171	G
1	YA	1206	G
1	YA	1211	U
1	YA	1220	A
1	YA	1230	C
1	YA	1236	G
1	YA	1248	G
1	YA	1252	G
1	YA	1253	A
1	YA	1256	G
1	YA	1271	G
1	YA	1272	A
1	YA	1273	U
1	YA	1289	C
1	YA	1300	U
1	YA	1301	A
1	YA	1314	C

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Mol	Chain	Res	Type
1	YA	1341	U
1	YA	1352	U
1	YA	1359	A
1	YA	1365	A
1	YA	1368	G
1	YA	1380	G
1	YA	1384	A
1	YA	1385	G
1	YA	1416	G
1	YA	1417	C
1	YA	1420	U
1	YA	1421	G
1	YA	1428	C
1	YA	1445(A)	A
1	YA	1450(A)	G
1	YA	1455	G
1	YA	1459	G
1	YA	1467	C
1	YA	1471	A
1	YA	1482	G
1	YA	1493	C
1	YA	1497	U
1	YA	1508	A
1	YA	1509(A)	C
1	YA	1509(B)	A
1	YA	1531	C
1	YA	1542	A
1	YA	1543	C
1	YA	1558	A
1	YA	1566	A
1	YA	1569	A
1	YA	1578	U
1	YA	1580	A
1	YA	1584	C
1	YA	1586	A
1	YA	1608	A
1	YA	1609	A
1	YA	1610	A
1	YA	1640	C
1	YA	1648	C
1	YA	1651	G
1	YA	1674	G

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Mol	Chain	Res	Type
1	YA	1696	G
1	YA	1700	A
1	YA	1701	A
1	YA	1721	G
1	YA	1722	A
1	YA	1750	G
1	YA	1756	G
1	YA	1762	A
1	YA	1763	G
1	YA	1764	G
1	YA	1773	A
1	YA	1780	A
1	YA	1786	A
1	YA	1791	A
1	YA	1800	C
1	YA	1801	G
1	YA	1816	G
1	YA	1829	A
1	YA	1835	G
1	YA	1847	A
1	YA	1848	A
1	YA	1877	A
1	YA	1878	G
1	YA	1900	A
1	YA	1906	G
1	YA	1913	A
1	YA	1914	C
1	YA	1915	5MU
1	YA	1929	G
1	YA	1930	G
1	YA	1936	A
1	YA	1955	U
1	YA	1963	U
1	YA	1967	C
1	YA	1970	A
1	YA	1971	A
1	YA	1972	A
1	YA	1993	U
1	YA	1997	G
1	YA	2023	G
1	YA	2031	A
1	YA	2032	G

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Mol	Chain	Res	Type
1	YA	2033	A
1	YA	2043	C
1	YA	2055	C
1	YA	2056	G
1	YA	2060	A
1	YA	2061	G
1	YA	2062	A
1	YA	2069	G
1	YA	2096	U
1	YA	2099	U
1	YA	2103	C
1	YA	2104	G
1	YA	2105	C
1	YA	2107	C
1	YA	2108	C
1	YA	2109	U
1	YA	2110	G
1	YA	2111	C
1	YA	2112	G
1	YA	2115	G
1	YA	2116	G
1	YA	2117	A
1	YA	2118	U
1	YA	2119	A
1	YA	2121	G
1	YA	2123	G
1	YA	2126	A
1	YA	2127	G
1	YA	2129	C
1	YA	2131	G
1	YA	2132	U
1	YA	2133	G
1	YA	2134	A
1	YA	2136	C
1	YA	2138	C
1	YA	2145	C
1	YA	2146	C
1	YA	2147	G
1	YA	2148	G
1	YA	2151	G
1	YA	2158	A
1	YA	2159	G

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Mol	Chain	Res	Type
1	YA	2161	C
1	YA	2165	G
1	YA	2172	U
1	YA	2173	A
1	YA	2180	U
1	YA	2186	G
1	YA	2189	U
1	YA	2192	G
1	YA	2198	A
1	YA	2206	G
1	YA	2207	G
1	YA	2208	A
1	YA	2218	U
1	YA	2225	A
1	YA	2238	G
1	YA	2239	G
1	YA	2269	A
1	YA	2275	C
1	YA	2279	G
1	YA	2283	C
1	YA	2287	A
1	YA	2291	U
1	YA	2292	C
1	YA	2305	A
1	YA	2308	G
1	YA	2312	U
1	YA	2319	G
1	YA	2320	A
1	YA	2321	G
1	YA	2322	A
1	YA	2325	G
1	YA	2334	G
1	YA	2335	A
1	YA	2336	A
1	YA	2343	C
1	YA	2347	C
1	YA	2350	C
1	YA	2354	G
1	YA	2383	G
1	YA	2385	C
1	YA	2406	U
1	YA	2410	G

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Mol	Chain	Res	Type
1	YA	2414	G
1	YA	2422	A
1	YA	2424	C
1	YA	2425	A
1	YA	2429	G
1	YA	2430	A
1	YA	2435	A
1	YA	2439	A
1	YA	2441	C
1	YA	2446	G
1	YA	2448	A
1	YA	2474	C
1	YA	2476	A
1	YA	2478	A
1	YA	2502	G
1	YA	2504	U
1	YA	2505	G
1	YA	2506	U
1	YA	2518	A
1	YA	2529	G
1	YA	2554	U
1	YA	2566	A
1	YA	2567	G
1	YA	2573	C
1	YA	2574	G
1	YA	2585	U
1	YA	2586	C
1	YA	2602	A
1	YA	2611	U
1	YA	2612	C
1	YA	2615	U
1	YA	2629	A
1	YA	2630	G
1	YA	2654	A
1	YA	2663	G
1	YA	2689	U
1	YA	2690	C
1	YA	2702	U
1	YA	2703	C
1	YA	2712(B)	A
1	YA	2713	A
1	YA	2714	G

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Mol	Chain	Res	Type
1	YA	2726	U
1	YA	2733	A
1	YA	2751	G
1	YA	2757	A
1	YA	2758	A
1	YA	2764	A
1	YA	2765	A
1	YA	2769	C
1	YA	2778	A
1	YA	2811	G
1	YA	2818	G
1	YA	2820	A
1	YA	2821	A
1	YA	2833	G
1	YA	2835	A
1	YA	2872	G
1	YA	2876	G
1	YA	2880	C
1	YA	2892	A
1	YA	2894	G
1	YA	2897	U
2	YB	2	C
2	YB	8	U
2	YB	9	G
2	YB	13	A
2	YB	30	C
2	YB	33	G
2	YB	51	G
2	YB	52	A
2	YB	56	G
2	YB	73	A
2	YB	106	G
2	YB	110	G
32	XA	5	U
32	XA	7	G
32	XA	9	G
32	XA	31	G
32	XA	32	A
32	XA	39	G
32	XA	47	C
32	XA	48	C
32	XA	50	A

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Mol	Chain	Res	Type
32	XA	51	A
32	XA	61	G
32	XA	66	G
32	XA	68	G
32	XA	69	G
32	XA	70	G
32	XA	88	A
32	XA	89	C
32	XA	101	A
32	XA	116	A
32	XA	120	A
32	XA	121	C
32	XA	131	C
32	XA	151	A
32	XA	156	G
32	XA	163	C
32	XA	174	C
32	XA	182	U
32	XA	189(G)	U
32	XA	195	A
32	XA	197	A
32	XA	202	U
32	XA	203	U
32	XA	204	U
32	XA	216	G
32	XA	247	G
32	XA	251	G
32	XA	266	G
32	XA	267	C
32	XA	281	G
32	XA	289	G
32	XA	298	A
32	XA	321	A
32	XA	328	C
32	XA	332	G
32	XA	350	G
32	XA	351	G
32	XA	352	C
32	XA	353	A
32	XA	354	G
32	XA	356	A
32	XA	367	U

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Mol	Chain	Res	Type
32	XA	372	C
32	XA	373	A
32	XA	382	A
32	XA	384	G
32	XA	397	A
32	XA	398	C
32	XA	406	G
32	XA	412	A
32	XA	413	G
32	XA	424	G
32	XA	429	U
32	XA	439	A
32	XA	442	C
32	XA	452	A
32	XA	458	C
32	XA	470	C
32	XA	476	G
32	XA	482	A
32	XA	485	G
32	XA	496	A
32	XA	498	U
32	XA	505	G
32	XA	509	A
32	XA	510	A
32	XA	511	C
32	XA	518	C
32	XA	521	G
32	XA	527	7MG
32	XA	531	U
32	XA	532	A
32	XA	533	A
32	XA	547	A
32	XA	559	A
32	XA	560	U
32	XA	561	U
32	XA	564	C
32	XA	572	A
32	XA	573	A
32	XA	576	G
32	XA	577	G
32	XA	596	C
32	XA	630	G

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Mol	Chain	Res	Type
32	XA	632	A
32	XA	653	A
32	XA	661	G
32	XA	665	A
32	XA	687	A
32	XA	688	G
32	XA	695	A
32	XA	723	U
32	XA	731	G
32	XA	749	C
32	XA	753	A
32	XA	755	G
32	XA	774	G
32	XA	777	A
32	XA	792	A
32	XA	793	U
32	XA	794	A
32	XA	816	A
32	XA	817	C
32	XA	821	G
32	XA	828	A
32	XA	829	G
32	XA	836	G
32	XA	840	C
32	XA	841	U
32	XA	848	C
32	XA	851	G
32	XA	902	G
32	XA	914	A
32	XA	916	G
32	XA	926	G
32	XA	927	G
32	XA	931	C
32	XA	934	C
32	XA	935	A
32	XA	960	U
32	XA	961	U
32	XA	968	A
32	XA	969	A
32	XA	971	G
32	XA	974	A
32	XA	975	A

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Mol	Chain	Res	Type
32	XA	976	G
32	XA	977	A
32	XA	989	C
32	XA	992	U
32	XA	993	G
32	XA	994	A
32	XA	999	C
32	XA	1003	G
32	XA	1004	A
32	XA	1005	A
32	XA	1006	C
32	XA	1009	G
32	XA	1020	U
32	XA	1022	G
32	XA	1023	G
32	XA	1025	U
32	XA	1026	G
32	XA	1027	C
32	XA	1028	C
32	XA	1029	C
32	XA	1030(B)	G
32	XA	1030(C)	C
32	XA	1038	C
32	XA	1041	A
32	XA	1043	C
32	XA	1044	A
32	XA	1065	U
32	XA	1066	C
32	XA	1068	G
32	XA	1081	G
32	XA	1086	U
32	XA	1094	G
32	XA	1095	U
32	XA	1101	A
32	XA	1117	G
32	XA	1125	U
32	XA	1129	C
32	XA	1130	A
32	XA	1136	U
32	XA	1137	C
32	XA	1139	G
32	XA	1140	C

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Mol	Chain	Res	Type
32	XA	1147	C
32	XA	1152	A
32	XA	1159	U
32	XA	1160	G
32	XA	1183	A
32	XA	1184	G
32	XA	1196	U
32	XA	1197	G
32	XA	1211	U
32	XA	1213	A
32	XA	1224	G
32	XA	1227	A
32	XA	1228	C
32	XA	1238	A
32	XA	1250	A
32	XA	1256	A
32	XA	1257	U
32	XA	1258	G
32	XA	1260	C
32	XA	1270	C
32	XA	1278	U
32	XA	1279	A
32	XA	1280	A
32	XA	1281	U
32	XA	1282	C
32	XA	1286	A
32	XA	1287	A
32	XA	1300	G
32	XA	1305	G
32	XA	1320	C
32	XA	1346	A
32	XA	1347	G
32	XA	1353	G
32	XA	1363(A)	C
32	XA	1370	G
32	XA	1380	U
32	XA	1397	C
32	XA	1401	G
32	XA	1419	G
32	XA	1442(A)	G
32	XA	1442(B)	G
32	XA	1447	A

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Mol	Chain	Res	Type
32	XA	1456	G
32	XA	1487	G
32	XA	1491	G
32	XA	1492	A
32	XA	1493	A
32	XA	1497	G
32	XA	1503	A
32	XA	1504	G
32	XA	1506	U
32	XA	1517	G
32	XA	1520	G
32	XA	1529	G
32	XA	1530	G
32	QA	7	G
32	QA	9	G
32	QA	32	A
32	QA	39	G
32	QA	48	C
32	QA	51	A
32	QA	61	G
32	QA	78	G
32	QA	79	G
32	QA	101	A
32	QA	116	A
32	QA	121	C
32	QA	131	C
32	QA	163	C
32	QA	174	C
32	QA	182	U
32	QA	189(F)	U
32	QA	195	A
32	QA	197	A
32	QA	201	C
32	QA	203	U
32	QA	204	U
32	QA	216	G
32	QA	247	G
32	QA	251	G
32	QA	266	G
32	QA	267	C
32	QA	289	G
32	QA	321	A

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Mol	Chain	Res	Type
32	QA	328	C
32	QA	332	G
32	QA	340	U
32	QA	342	C
32	QA	343	U
32	QA	345	C
32	QA	346	G
32	QA	347	G
32	QA	348	G
32	QA	351	G
32	QA	352	C
32	QA	353	A
32	QA	354	G
32	QA	355	C
32	QA	367	U
32	QA	372	C
32	QA	397	A
32	QA	398	C
32	QA	406	G
32	QA	412	A
32	QA	413	G
32	QA	423	G
32	QA	424	G
32	QA	429	U
32	QA	439	A
32	QA	442	C
32	QA	452	A
32	QA	470	C
32	QA	485	G
32	QA	496	A
32	QA	498	U
32	QA	505	G
32	QA	509	A
32	QA	510	A
32	QA	511	C
32	QA	518	C
32	QA	521	G
32	QA	524	G
32	QA	527	7MG
32	QA	532	A
32	QA	547	A
32	QA	550	G

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Mol	Chain	Res	Type
32	QA	559	A
32	QA	561	U
32	QA	564	C
32	QA	572	A
32	QA	573	A
32	QA	575	G
32	QA	576	G
32	QA	577	G
32	QA	596	C
32	QA	619	U
32	QA	630	G
32	QA	632	A
32	QA	653	A
32	QA	661	G
32	QA	665	A
32	QA	687	A
32	QA	688	G
32	QA	721	G
32	QA	723	U
32	QA	731	G
32	QA	734	G
32	QA	755	G
32	QA	760	G
32	QA	774	G
32	QA	777	A
32	QA	792	A
32	QA	793	U
32	QA	794	A
32	QA	816	A
32	QA	817	C
32	QA	821	G
32	QA	828	A
32	QA	829	G
32	QA	839	U
32	QA	840	C
32	QA	841	U
32	QA	851	G
32	QA	902	G
32	QA	913	A
32	QA	914	A
32	QA	926	G
32	QA	927	G

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Mol	Chain	Res	Type
32	QA	934	C
32	QA	935	A
32	QA	960	U
32	QA	961	U
32	QA	968	A
32	QA	969	A
32	QA	971	G
32	QA	974	A
32	QA	975	A
32	QA	976	G
32	QA	977	A
32	QA	992	U
32	QA	993	G
32	QA	994	A
32	QA	998	G
32	QA	1002	G
32	QA	1006	C
32	QA	1022	G
32	QA	1023	G
32	QA	1024	G
32	QA	1025	U
32	QA	1026	G
32	QA	1027	C
32	QA	1028	C
32	QA	1029	C
32	QA	1030(A)	C
32	QA	1030(B)	G
32	QA	1030(C)	C
32	QA	1030(E)	A
32	QA	1032	G
32	QA	1033	G
32	QA	1034	G
32	QA	1037	C
32	QA	1042	G
32	QA	1044	A
32	QA	1065	U
32	QA	1066	C
32	QA	1068	G
32	QA	1070	U
32	QA	1081	G
32	QA	1094	G
32	QA	1095	U

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Mol	Chain	Res	Type
32	QA	1101	A
32	QA	1126	U
32	QA	1130	A
32	QA	1132	C
32	QA	1134	G
32	QA	1136	U
32	QA	1139	G
32	QA	1140	C
32	QA	1152	A
32	QA	1159	U
32	QA	1160	G
32	QA	1168	A
32	QA	1183	A
32	QA	1184	G
32	QA	1196	U
32	QA	1197	G
32	QA	1202	G
32	QA	1208	C
32	QA	1212	U
32	QA	1213	A
32	QA	1224	G
32	QA	1227	A
32	QA	1238	A
32	QA	1256	A
32	QA	1257	U
32	QA	1258	G
32	QA	1278	U
32	QA	1280	A
32	QA	1286	A
32	QA	1287	A
32	QA	1299	A
32	QA	1300	G
32	QA	1302	U
32	QA	1305	G
32	QA	1320	C
32	QA	1334	G
32	QA	1338	G
32	QA	1346	A
32	QA	1347	G
32	QA	1353	G
32	QA	1357	A
32	QA	1363(A)	C

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Mol	Chain	Res	Type
32	QA	1370	G
32	QA	1397	C
32	QA	1401	G
32	QA	1404	5MC
32	QA	1419	G
32	QA	1442(A)	G
32	QA	1442(B)	G
32	QA	1442(C)	A
32	QA	1446	U
32	QA	1447	A
32	QA	1452	C
32	QA	1492	A
32	QA	1494	G
32	QA	1497	G
32	QA	1499	A
32	QA	1503	A
32	QA	1504	G
32	QA	1505	G
32	QA	1506	U
32	QA	1517	G
32	QA	1520	G
32	QA	1529	G
32	QA	1530	G
1	RA	10	G
1	RA	11	G
1	RA	12	U
1	RA	14	A
1	RA	15	G
1	RA	34	C
1	RA	45	C
1	RA	71	A
1	RA	74	A
1	RA	75	G
1	RA	83	G
1	RA	84	A
1	RA	102	G
1	RA	118	A
1	RA	120	U
1	RA	131	G
1	RA	141	A
1	RA	157	U
1	RA	181	A

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Mol	Chain	Res	Type
1	RA	182	A
1	RA	196	A
1	RA	199	A
1	RA	205	G
1	RA	215	G
1	RA	216	A
1	RA	221	A
1	RA	222	A
1	RA	229	A
1	RA	230	U
1	RA	248	G
1	RA	272(K)	U
1	RA	272(L)	U
1	RA	272(M)	G
1	RA	272(N)	U
1	RA	272(O)	C
1	RA	273(B)	U
1	RA	273(C)	G
1	RA	277	C
1	RA	278	A
1	RA	311	A
1	RA	317	G
1	RA	324	A
1	RA	329	G
1	RA	330	A
1	RA	342	G
1	RA	352	G
1	RA	362	U
1	RA	363(A)	G
1	RA	386	G
1	RA	389	G
1	RA	396	G
1	RA	405	U
1	RA	411	G
1	RA	412	A
1	RA	428	A
1	RA	444	C
1	RA	455	C
1	RA	456	C
1	RA	457	A
1	RA	470	A
1	RA	481	G

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Mol	Chain	Res	Type
1	RA	505	A
1	RA	509	C
1	RA	530	G
1	RA	531	C
1	RA	532	A
1	RA	533	G
1	RA	545	G
1	RA	556	G
1	RA	563	G
1	RA	568	U
1	RA	573	G
1	RA	575	A
1	RA	603	A
1	RA	604	G
1	RA	607	U
1	RA	614(C)	G
1	RA	615	G
1	RA	627	A
1	RA	637	A
1	RA	645	C
1	RA	646	A
1	RA	652(C)	A
1	RA	652(D)	G
1	RA	652(V)	G
1	RA	653	A
1	RA	669	G
1	RA	686	G
1	RA	717	G
1	RA	730	C
1	RA	753	C
1	RA	764	A
1	RA	775	G
1	RA	776	G
1	RA	782	A
1	RA	784	A
1	RA	785	G
1	RA	805	G
1	RA	812	C
1	RA	827	U
1	RA	857	C
1	RA	859	G
1	RA	869	G

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Mol	Chain	Res	Type
1	RA	877	U
1	RA	880	G
1	RA	886	C
1	RA	887	A
1	RA	888	C
1	RA	889	C
1	RA	890	A
1	RA	893	C
1	RA	896	A
1	RA	900	A
1	RA	901	A
1	RA	907	U
1	RA	910	A
1	RA	914	C
1	RA	915	C
1	RA	917	A
1	RA	932	G
1	RA	941	A
1	RA	945	A
1	RA	946	G
1	RA	953	A
1	RA	959	A
1	RA	961	C
1	RA	974	G
1	RA	975(A)	C
1	RA	982	C
1	RA	983	A
1	RA	996	A
1	RA	1012	U
1	RA	1013	C
1	RA	1017	G
1	RA	1026	U
1	RA	1033	U
1	RA	1045	A
1	RA	1046	A
1	RA	1047	G
1	RA	1048	A
1	RA	1052	C
1	RA	1053	C
1	RA	1054	A
1	RA	1058	G
1	RA	1060	U

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Mol	Chain	Res	Type
1	RA	1063	G
1	RA	1064	C
1	RA	1065	U
1	RA	1066	U
1	RA	1067	A
1	RA	1068	G
1	RA	1069	A
1	RA	1070	A
1	RA	1071	G
1	RA	1073	A
1	RA	1074	G
1	RA	1076	C
1	RA	1077	A
1	RA	1078	U
1	RA	1079	C
1	RA	1082	U
1	RA	1083	U
1	RA	1084	A
1	RA	1085	A
1	RA	1086	A
1	RA	1088	A
1	RA	1090	U
1	RA	1091	G
1	RA	1092	C
1	RA	1094	U
1	RA	1096	A
1	RA	1109	C
1	RA	1110	G
1	RA	1111	A
1	RA	1112	G
1	RA	1129	A
1	RA	1130	U
1	RA	1135	C
1	RA	1136	G
1	RA	1142(B)	A
1	RA	1171	G
1	RA	1206	G
1	RA	1211	U
1	RA	1212	G
1	RA	1220	A
1	RA	1236	G
1	RA	1253	A

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Mol	Chain	Res	Type
1	RA	1256	G
1	RA	1271	G
1	RA	1272	A
1	RA	1273	U
1	RA	1300	U
1	RA	1301	A
1	RA	1302	A
1	RA	1313	U
1	RA	1314	C
1	RA	1341	U
1	RA	1352	U
1	RA	1359	A
1	RA	1365	A
1	RA	1368	G
1	RA	1384	A
1	RA	1385	G
1	RA	1395	A
1	RA	1416	G
1	RA	1417	C
1	RA	1421	G
1	RA	1428	C
1	RA	1445(A)	A
1	RA	1450(A)	G
1	RA	1455	G
1	RA	1459	G
1	RA	1460	A
1	RA	1467	C
1	RA	1471	A
1	RA	1482	G
1	RA	1493	C
1	RA	1497	U
1	RA	1508	A
1	RA	1509(A)	C
1	RA	1509(B)	A
1	RA	1531	C
1	RA	1542	A
1	RA	1543	C
1	RA	1558	A
1	RA	1566	A
1	RA	1569	A
1	RA	1578	U
1	RA	1580	A

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Mol	Chain	Res	Type
1	RA	1584	C
1	RA	1586	A
1	RA	1608	A
1	RA	1609	A
1	RA	1610	A
1	RA	1640	C
1	RA	1647	G
1	RA	1648	C
1	RA	1674	G
1	RA	1696	G
1	RA	1700	A
1	RA	1701	A
1	RA	1721	G
1	RA	1722	A
1	RA	1756	G
1	RA	1762	A
1	RA	1763	G
1	RA	1764	G
1	RA	1773	A
1	RA	1780	A
1	RA	1782	C
1	RA	1786	A
1	RA	1791	A
1	RA	1800	C
1	RA	1801	G
1	RA	1811	G
1	RA	1812	A
1	RA	1816	G
1	RA	1829	A
1	RA	1835	G
1	RA	1847	A
1	RA	1848	A
1	RA	1877	A
1	RA	1878	G
1	RA	1889	A
1	RA	1900	A
1	RA	1906	G
1	RA	1914	C
1	RA	1916	A
1	RA	1929	G
1	RA	1930	G
1	RA	1936	A

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Mol	Chain	Res	Type
1	RA	1938	A
1	RA	1955	U
1	RA	1963	U
1	RA	1967	C
1	RA	1970	A
1	RA	1971	A
1	RA	1972	A
1	RA	1993	U
1	RA	1997	G
1	RA	2021	C
1	RA	2023	G
1	RA	2031	A
1	RA	2032	G
1	RA	2033	A
1	RA	2043	C
1	RA	2055	C
1	RA	2056	G
1	RA	2060	A
1	RA	2061	G
1	RA	2062	A
1	RA	2069	G
1	RA	2096	U
1	RA	2103	C
1	RA	2104	G
1	RA	2105	C
1	RA	2107	C
1	RA	2108	C
1	RA	2109	U
1	RA	2110	G
1	RA	2112	G
1	RA	2115	G
1	RA	2116	G
1	RA	2117	A
1	RA	2118	U
1	RA	2119	A
1	RA	2121	G
1	RA	2123	G
1	RA	2126	A
1	RA	2127	G
1	RA	2129	C
1	RA	2131	G
1	RA	2132	U

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Mol	Chain	Res	Type
1	RA	2133	G
1	RA	2134	A
1	RA	2136	C
1	RA	2145	C
1	RA	2146	C
1	RA	2147	G
1	RA	2148	G
1	RA	2151	G
1	RA	2158	A
1	RA	2159	G
1	RA	2161	C
1	RA	2163	C
1	RA	2165	G
1	RA	2172	U
1	RA	2173	A
1	RA	2174	C
1	RA	2180	U
1	RA	2186	G
1	RA	2189	U
1	RA	2192	G
1	RA	2198	A
1	RA	2206	G
1	RA	2207	G
1	RA	2208	A
1	RA	2218	U
1	RA	2225	A
1	RA	2239	G
1	RA	2269	A
1	RA	2275	C
1	RA	2279	G
1	RA	2283	C
1	RA	2287	A
1	RA	2291	U
1	RA	2292	C
1	RA	2305	A
1	RA	2308	G
1	RA	2311	A
1	RA	2312	U
1	RA	2320	A
1	RA	2321	G
1	RA	2322	A
1	RA	2325	G

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Mol	Chain	Res	Type
1	RA	2334	G
1	RA	2335	A
1	RA	2336	A
1	RA	2343	C
1	RA	2345	G
1	RA	2347	C
1	RA	2350	C
1	RA	2383	G
1	RA	2385	C
1	RA	2406	U
1	RA	2410	G
1	RA	2422	A
1	RA	2425	A
1	RA	2429	G
1	RA	2430	A
1	RA	2435	A
1	RA	2439	A
1	RA	2441	C
1	RA	2448	A
1	RA	2474	C
1	RA	2476	A
1	RA	2478	A
1	RA	2502	G
1	RA	2504	U
1	RA	2505	G
1	RA	2518	A
1	RA	2520	C
1	RA	2525	G
1	RA	2529	G
1	RA	2549	G
1	RA	2554	U
1	RA	2555	U
1	RA	2566	A
1	RA	2567	G
1	RA	2572	A
1	RA	2585	U
1	RA	2602	A
1	RA	2603	G
1	RA	2611	U
1	RA	2612	C
1	RA	2615	U
1	RA	2629	A

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Mol	Chain	Res	Type
1	RA	2630	G
1	RA	2654	A
1	RA	2663	G
1	RA	2689	U
1	RA	2690	C
1	RA	2691	C
1	RA	2703	C
1	RA	2712(B)	A
1	RA	2713	A
1	RA	2714	G
1	RA	2726	U
1	RA	2732	G
1	RA	2733	A
1	RA	2758	A
1	RA	2764	A
1	RA	2765	A
1	RA	2769	C
1	RA	2778	A
1	RA	2780	G
1	RA	2818	G
1	RA	2820	A
1	RA	2821	A
1	RA	2833	G
1	RA	2849	U
1	RA	2872	G
1	RA	2880	C
1	RA	2886	G
1	RA	2892	A
1	RA	2894	G
1	RA	2897	U
2	RB	2	C
2	RB	13	A
2	RB	24	G
2	RB	30	C
2	RB	45	A
2	RB	53	A
2	RB	56	G
2	RB	73	A
2	RB	85	G
2	RB	110	G
53	QV	4	G
53	QV	5	G

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Mol	Chain	Res	Type
53	QV	6	G
53	QV	9	G
53	QV	14	A
53	QV	16	C
53	QV	17(A)	U
53	QV	18	G
53	QV	19	G
53	QV	21	A
53	QV	31	G
53	QV	47	U
53	QV	48	C
53	QV	54	U
53	QV	55	U
53	QV	65	C
53	QV	67	C
53	QV	75	C
53	QV	76	A
53	XV	4	G
53	XV	5	G
53	XV	6	G
53	XV	9	G
53	XV	14	A
53	XV	16	C
53	XV	17(A)	U
53	XV	18	G
53	XV	19	G
53	XV	21	A
53	XV	31	G
53	XV	47	U
53	XV	48	C
53	XV	54	U
53	XV	65	C
53	XV	67	C
53	XV	75	C
53	XV	76	A
55	XX	21	A
55	QX	21	A

All (79) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	YA	9	U

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Mol	Chain	Res	Type
1	YA	272(M)	G
1	YA	277	C
1	YA	752	A
1	YA	827	U
1	YA	856	C
1	YA	900	A
1	YA	1053	C
1	YA	1057	A
1	YA	1065	U
1	YA	1067	A
1	YA	1073	A
1	YA	1210	A
1	YA	1379	A
1	YA	1420	U
1	YA	1530	C
1	YA	1992	G
1	YA	2126	A
1	YA	2171	A
1	YA	2172	U
1	YA	2321	G
1	YA	2585	U
1	YA	2689	U
1	YA	2756	U
32	XA	60	A
32	XA	65	U
32	XA	69	G
32	XA	115	G
32	XA	266	G
32	XA	509	A
32	XA	560	U
32	XA	687	A
32	XA	748	C
32	XA	840	C
32	XA	913	A
32	XA	991	U
32	XA	992	U
32	XA	1065	U
32	XA	1067	A
32	XA	1183	A
32	XA	1256	A
32	XA	1442(A)	G
32	QA	115	G

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Mol	Chain	Res	Type
32	QA	266	G
32	QA	509	A
32	QA	560	U
32	QA	687	A
32	QA	839	U
32	QA	913	A
32	QA	991	U
32	QA	1065	U
32	QA	1067	A
32	QA	1201	A
32	QA	1207	2MG
32	QA	1285	A
32	QA	1442(A)	G
1	RA	9	U
1	RA	272(M)	G
1	RA	277	C
1	RA	752	A
1	RA	856	C
1	RA	900	A
1	RA	1053	C
1	RA	1057	A
1	RA	1065	U
1	RA	1067	A
1	RA	1073	A
1	RA	1076	C
1	RA	1210	A
1	RA	1420	U
1	RA	1530	C
1	RA	1992	G
1	RA	2126	A
1	RA	2171	A
1	RA	2172	U
1	RA	2321	G
1	RA	2689	U
53	QV	54	U
53	XV	53	G

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

50 non-standard protein/DNA/RNA residues are modelled in this entry.

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
32	2MG	QA	1207	32	19,26,27	1.30	2 (10%)	20,38,41	2.35	7 (35%)
32	5MC	QA	1400	32	15,22,23	1.41	1 (6%)	17,32,35	1.06	2 (11%)
32	4OC	QA	1402	32	16,23,24	0.66	0	19,32,35	1.07	1 (5%)
32	5MC	QA	1404	32	15,22,23	1.43	1 (6%)	17,32,35	1.11	2 (11%)
32	5MC	QA	1407	32	15,22,23	1.42	1 (6%)	17,32,35	1.12	2 (11%)
32	UR3	QA	1498	32	14,22,23	0.80	0	16,32,35	0.61	0
32	MA6	QA	1518	32	16,26,27	1.01	1 (6%)	18,38,41	2.36	6 (33%)
32	MA6	QA	1519	32	16,26,27	1.05	1 (6%)	18,38,41	2.26	6 (33%)
32	PSU	QA	516	32,56	16,21,22	1.34	2 (12%)	20,30,33	3.43	6 (30%)
32	7MG	QA	527	32,56	20,26,27	1.66	2 (10%)	22,39,42	2.81	5 (22%)
32	M2G	QA	966	32	20,27,28	1.42	3 (15%)	21,40,43	2.18	5 (23%)
32	5MC	QA	967	32	15,22,23	1.44	1 (6%)	17,32,35	0.97	2 (11%)
43	0TD	QL	92	43	5,9,10	4.66	4 (80%)	3,11,13	4.40	3 (100%)
54	MEQ	QY	252	54	9,9,10	0.97	0	7,10,12	1.24	1 (14%)
1	PSU	RA	1911	1	16,21,22	1.38	1 (6%)	20,30,33	3.51	7 (35%)
1	5MU	RA	1915	1,56	14,22,23	0.72	0	16,32,35	2.44	2 (12%)
1	PSU	RA	1917	1	16,21,22	1.36	1 (6%)	20,30,33	3.59	6 (30%)
1	4OC	RA	1920	1	15,22,24	0.67	0	19,31,35	0.80	1 (5%)
1	5MU	RA	1939	1	14,22,23	0.70	0	16,32,35	2.26	3 (18%)
1	5MC	RA	1942	1	15,22,23	1.39	1 (6%)	17,32,35	1.06	2 (11%)
1	5MC	RA	1962	1,56	15,22,23	1.40	1 (6%)	17,32,35	1.11	2 (11%)
1	OMG	RA	2251	1,56,53	18,26,27	1.26	2 (11%)	22,38,41	2.06	6 (27%)
1	2MA	RA	2503	1,56	18,25,26	1.61	3 (16%)	17,37,40	1.87	2 (11%)
1	2MU	RA	2552	1,56	14,22,24	0.92	0	18,31,36	1.97	1 (5%)
1	PSU	RA	2605	1	16,21,22	1.49	1 (6%)	20,30,33	3.55	6 (30%)
32	2MG	XA	1207	32	19,26,27	1.30	2 (10%)	20,38,41	2.31	8 (40%)
32	5MC	XA	1400	32	15,22,23	1.42	1 (6%)	17,32,35	0.99	2 (11%)
32	4OC	XA	1402	32	16,23,24	0.68	0	19,32,35	1.16	1 (5%)
32	5MC	XA	1404	32	15,22,23	1.39	1 (6%)	17,32,35	1.13	2 (11%)
32	5MC	XA	1407	32	15,22,23	1.37	1 (6%)	17,32,35	1.13	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	UR3	XA	1498	32,56	14,22,23	0.83	1 (7%)	16,32,35	0.65	0
32	MA6	XA	1518	32	16,26,27	0.99	1 (6%)	18,38,41	2.37	7 (38%)
32	MA6	XA	1519	32	16,26,27	1.01	1 (6%)	18,38,41	2.43	7 (38%)
32	PSU	XA	516	32	16,21,22	1.29	2 (12%)	20,30,33	3.46	6 (30%)
32	7MG	XA	527	32,56	20,26,27	1.63	2 (10%)	22,39,42	2.78	6 (27%)
32	M2G	XA	966	32	20,27,28	1.45	3 (15%)	21,40,43	2.22	5 (23%)
32	5MC	XA	967	32	15,22,23	1.46	1 (6%)	17,32,35	0.99	2 (11%)
43	0TD	XL	92	43	5,9,10	3.10	2 (40%)	3,11,13	2.71	1 (33%)
54	MEQ	XY	252	54	9,9,10	1.17	1 (11%)	7,10,12	1.82	1 (14%)
1	PSU	YA	1911	1	16,21,22	1.37	1 (6%)	20,30,33	3.53	7 (35%)
1	5MU	YA	1915	1	14,22,23	0.63	0	16,32,35	2.52	2 (12%)
1	PSU	YA	1917	1	16,21,22	1.34	1 (6%)	20,30,33	3.57	6 (30%)
1	4OC	YA	1920	1	15,22,24	0.75	0	19,31,35	0.86	1 (5%)
1	5MU	YA	1939	1,56	14,22,23	0.72	1 (7%)	16,32,35	2.27	3 (18%)
1	5MC	YA	1942	1	15,22,23	1.36	1 (6%)	17,32,35	1.09	1 (5%)
1	5MC	YA	1962	1,56	15,22,23	1.38	1 (6%)	17,32,35	1.08	2 (11%)
1	OMG	YA	2251	1,56,53	18,26,27	1.28	2 (11%)	22,38,41	2.03	6 (27%)
1	2MA	YA	2503	1,56	18,25,26	1.61	3 (16%)	17,37,40	1.93	2 (11%)
1	2MU	YA	2552	1,56	14,22,24	0.93	0	18,31,36	1.96	1 (5%)
1	PSU	YA	2605	1	16,21,22	1.46	2 (12%)	20,30,33	3.60	6 (30%)

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
32	2MG	QA	1207	32	-	0/5/27/28	0/3/3/3
32	5MC	QA	1400	32	-	0/3/25/26	0/2/2/2
32	4OC	QA	1402	32	-	0/7/29/30	0/2/2/2
32	5MC	QA	1404	32	-	0/3/25/26	0/2/2/2
32	5MC	QA	1407	32	-	0/3/25/26	0/2/2/2
32	UR3	QA	1498	32	-	0/3/25/26	0/2/2/2
32	MA6	QA	1518	32	-	0/7/29/30	0/3/3/3
32	MA6	QA	1519	32	-	0/7/29/30	0/3/3/3
32	PSU	QA	516	32,56	-	0/7/25/26	0/2/2/2
32	7MG	QA	527	32,56	-	0/7/37/38	0/3/3/3
32	M2G	QA	966	32	-	0/7/29/30	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	5MC	QA	967	32	-	0/3/25/26	0/2/2/2
43	0TD	QL	92	43	-	0/2/12/14	0/0/0/0
54	MEQ	QY	252	54	-	0/7/9/11	0/0/0/0
1	PSU	RA	1911	1	-	0/7/25/26	0/2/2/2
1	5MU	RA	1915	1,56	-	0/3/25/26	0/2/2/2
1	PSU	RA	1917	1	-	0/7/25/26	0/2/2/2
1	4OC	RA	1920	1	-	0/5/27/30	0/2/2/2
1	5MU	RA	1939	1	-	0/3/25/26	0/2/2/2
1	5MC	RA	1942	1	-	0/3/25/26	0/2/2/2
1	5MC	RA	1962	1,56	-	0/3/25/26	0/2/2/2
1	OMG	RA	2251	1,56,53	-	0/5/27/28	0/3/3/3
1	2MA	RA	2503	1,56	-	0/3/25/26	0/3/3/3
1	2MU	RA	2552	1,56	-	0/5/27/28	0/2/2/2
1	PSU	RA	2605	1	-	0/7/25/26	0/2/2/2
32	2MG	XA	1207	32	-	0/5/27/28	0/3/3/3
32	5MC	XA	1400	32	-	0/3/25/26	0/2/2/2
32	4OC	XA	1402	32	-	0/7/29/30	0/2/2/2
32	5MC	XA	1404	32	-	0/3/25/26	0/2/2/2
32	5MC	XA	1407	32	-	0/3/25/26	0/2/2/2
32	UR3	XA	1498	32,56	-	0/3/25/26	0/2/2/2
32	MA6	XA	1518	32	-	0/7/29/30	0/3/3/3
32	MA6	XA	1519	32	-	0/7/29/30	0/3/3/3
32	PSU	XA	516	32	-	0/7/25/26	0/2/2/2
32	7MG	XA	527	32,56	-	0/7/37/38	0/3/3/3
32	M2G	XA	966	32	-	0/7/29/30	0/3/3/3
32	5MC	XA	967	32	-	0/3/25/26	0/2/2/2
43	0TD	XL	92	43	-	0/2/12/14	0/0/0/0
54	MEQ	XY	252	54	-	0/7/9/11	0/0/0/0
1	PSU	YA	1911	1	-	0/7/25/26	0/2/2/2
1	5MU	YA	1915	1	-	0/3/25/26	0/2/2/2
1	PSU	YA	1917	1	-	0/7/25/26	0/2/2/2
1	4OC	YA	1920	1	-	0/5/27/30	0/2/2/2
1	5MU	YA	1939	1,56	-	0/3/25/26	0/2/2/2
1	5MC	YA	1942	1	-	0/3/25/26	0/2/2/2
1	5MC	YA	1962	1,56	-	0/3/25/26	0/2/2/2
1	OMG	YA	2251	1,56,53	-	0/5/27/28	0/3/3/3
1	2MA	YA	2503	1,56	-	0/3/25/26	0/3/3/3
1	2MU	YA	2552	1,56	-	0/5/27/28	0/2/2/2
1	PSU	YA	2605	1	-	0/7/25/26	0/2/2/2

All (60) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	QL	92	0TD	CB-SB	-7.70	1.64	1.84
43	XL	92	0TD	CB-SB	-5.88	1.69	1.84
1	RA	2605	PSU	C5-C1'	-4.57	1.48	1.52
1	YA	2605	PSU	C5-C1'	-4.39	1.48	1.52
1	RA	1911	PSU	C5-C1'	-4.07	1.48	1.52
1	RA	1917	PSU	C5-C1'	-4.01	1.48	1.52
1	YA	1911	PSU	C5-C1'	-3.96	1.48	1.52
32	QA	516	PSU	C5-C1'	-3.92	1.48	1.52
1	YA	1917	PSU	C5-C1'	-3.82	1.48	1.52
32	XA	516	PSU	C5-C1'	-3.64	1.49	1.52
43	QL	92	0TD	CA-N	-2.93	1.37	1.47
43	QL	92	0TD	CSB-SB	-2.51	1.74	1.79
32	QA	516	PSU	O4'-C1'	-2.08	1.41	1.44
1	YA	1939	5MU	C2-N3	-2.02	1.34	1.38
1	YA	2605	PSU	C2-N3	-2.02	1.34	1.38
32	XA	516	PSU	O4'-C1'	-2.00	1.41	1.44
32	XA	1498	UR3	C4-N3	2.05	1.41	1.38
54	XY	252	MEQ	CA-C	2.60	1.53	1.50
32	QA	1207	2MG	C5-C4	3.04	1.47	1.40
1	YA	2503	2MA	C5-C4	3.04	1.47	1.40
1	RA	2503	2MA	C5-C4	3.05	1.47	1.40
1	RA	2251	OMG	C5-C4	3.06	1.47	1.40
43	XL	92	0TD	CA-C	3.06	1.54	1.50
32	XA	966	M2G	C5-C4	3.09	1.47	1.40
32	XA	1207	2MG	C5-C4	3.09	1.47	1.40
32	QA	966	M2G	C5-C4	3.12	1.47	1.40
32	XA	1518	MA6	C5-C4	3.14	1.47	1.40
1	YA	2251	OMG	C5-C4	3.15	1.47	1.40
32	QA	527	7MG	C5-C4	3.17	1.47	1.39
32	XA	527	7MG	C5-C4	3.18	1.47	1.39
32	XA	1519	MA6	C5-C4	3.19	1.47	1.40
32	QA	1519	MA6	C5-C4	3.26	1.47	1.40
32	QA	1518	MA6	C5-C4	3.27	1.47	1.40
32	QA	966	M2G	C2-N2	3.39	1.40	1.34
1	YA	2503	2MA	C6-N6	3.57	1.35	1.27
32	XA	966	M2G	C2-N2	3.58	1.40	1.34
1	RA	2503	2MA	C6-N6	3.62	1.35	1.27
1	RA	2251	OMG	C6-C5	3.68	1.48	1.41
32	QA	966	M2G	C6-C5	3.71	1.48	1.41
1	YA	2251	OMG	C6-C5	3.72	1.48	1.41
32	XA	966	M2G	C6-C5	3.79	1.48	1.41
32	QA	1207	2MG	C6-C5	3.81	1.48	1.41
32	XA	1207	2MG	C6-C5	4.03	1.49	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	RA	2503	2MA	C6-C5	4.35	1.48	1.41
1	YA	2503	2MA	C6-C5	4.36	1.48	1.41
32	XA	1407	5MC	C5-C4	4.75	1.48	1.41
1	YA	1942	5MC	C5-C4	4.80	1.48	1.41
32	XA	1404	5MC	C5-C4	4.84	1.48	1.41
1	YA	1962	5MC	C5-C4	4.87	1.48	1.41
1	RA	1942	5MC	C5-C4	4.89	1.48	1.41
1	RA	1962	5MC	C5-C4	4.91	1.48	1.41
32	QA	1407	5MC	C5-C4	4.94	1.48	1.41
32	QA	1400	5MC	C5-C4	4.97	1.48	1.41
32	QA	1404	5MC	C5-C4	5.00	1.48	1.41
32	XA	1400	5MC	C5-C4	5.01	1.48	1.41
32	QA	967	5MC	C5-C4	5.12	1.48	1.41
32	XA	967	5MC	C5-C4	5.20	1.49	1.41
32	XA	527	7MG	C6-C5	5.64	1.48	1.41
32	QA	527	7MG	C6-C5	5.79	1.48	1.41
43	QL	92	0TD	CA-C	5.88	1.58	1.50

All (172) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	YA	2605	PSU	N1-C2-N3	-9.50	121.56	128.40
1	RA	1917	PSU	N1-C2-N3	-9.41	121.63	128.40
32	XA	516	PSU	N1-C2-N3	-9.37	121.66	128.40
1	YA	1917	PSU	N1-C2-N3	-9.36	121.67	128.40
1	YA	1911	PSU	N1-C2-N3	-9.28	121.72	128.40
1	RA	1911	PSU	N1-C2-N3	-9.07	121.88	128.40
1	RA	2605	PSU	N1-C2-N3	-9.01	121.92	128.40
32	QA	516	PSU	N1-C2-N3	-9.01	121.92	128.40
1	RA	1911	PSU	C5-C4-N3	-8.53	118.43	125.43
1	RA	2605	PSU	C5-C4-N3	-8.49	118.46	125.43
1	YA	1917	PSU	C5-C4-N3	-8.47	118.48	125.43
1	YA	1911	PSU	C5-C4-N3	-8.47	118.48	125.43
32	QA	516	PSU	C5-C4-N3	-8.40	118.54	125.43
1	YA	2605	PSU	C5-C4-N3	-8.34	118.59	125.43
1	RA	1917	PSU	C5-C4-N3	-8.26	118.65	125.43
32	XA	516	PSU	C5-C4-N3	-8.18	118.72	125.43
1	YA	1915	5MU	C5-C4-N3	-6.18	118.43	125.24
32	QA	1518	MA6	N3-C2-N1	-6.14	123.51	128.86
1	RA	1915	5MU	C5-C4-N3	-5.99	118.64	125.24
32	XA	1519	MA6	N3-C2-N1	-5.93	123.69	128.86
32	XA	1518	MA6	N3-C2-N1	-5.84	123.77	128.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	YA	1939	5MU	C5-C4-N3	-5.75	118.90	125.24
1	RA	1939	5MU	C5-C4-N3	-5.66	119.00	125.24
32	QA	1519	MA6	N3-C2-N1	-5.61	123.97	128.86
32	QA	527	7MG	C5-C4-N3	-5.29	117.64	126.47
32	XA	527	7MG	C5-C4-N3	-5.15	117.88	126.47
32	QA	527	7MG	C5-C6-N1	-4.83	115.80	123.37
32	XA	527	7MG	C5-C6-N1	-4.73	115.94	123.37
54	XY	252	MEQ	CB-CA-C	-4.53	104.19	111.65
1	RA	1917	PSU	C5-C1'-C2'	-4.10	108.48	115.55
32	QA	516	PSU	C5-C6-N1	-4.09	119.09	124.39
1	RA	2251	OMG	C5-C6-N1	-3.97	117.83	123.48
1	RA	1911	PSU	C5-C6-N1	-3.96	119.26	124.39
1	RA	2605	PSU	C5-C6-N1	-3.95	119.26	124.39
32	QA	966	M2G	C5-C6-N1	-3.94	117.87	123.48
32	XA	966	M2G	C5-C6-N1	-3.92	117.90	123.48
32	XA	1402	4OC	CM4-N4-C4	-3.91	119.56	122.94
1	RA	1917	PSU	C5-C6-N1	-3.91	119.32	124.39
32	XA	516	PSU	C5-C6-N1	-3.91	119.32	124.39
1	YA	2251	OMG	C5-C6-N1	-3.90	117.94	123.48
32	XA	1207	2MG	C5-C6-N1	-3.87	117.98	123.48
1	RA	2605	PSU	C5-C1'-C2'	-3.83	108.94	115.55
1	YA	1911	PSU	C5-C6-N1	-3.82	119.44	124.39
32	QA	1207	2MG	C5-C6-N1	-3.80	118.07	123.48
1	YA	2605	PSU	C5-C6-N1	-3.80	119.46	124.39
32	QA	1207	2MG	C6-C5-C4	-3.79	117.08	120.84
1	YA	2605	PSU	C5-C1'-C2'	-3.76	109.05	115.55
1	YA	1917	PSU	C5-C6-N1	-3.74	119.53	124.39
32	XA	1207	2MG	C6-C5-C4	-3.73	117.14	120.84
32	QA	1518	MA6	C4-C5-N7	-3.72	105.81	109.41
32	XA	966	M2G	C6-C5-C4	-3.69	117.17	120.84
32	XA	1207	2MG	CM2-N2-C2	-3.62	119.22	123.63
32	XA	1518	MA6	C4-C5-N7	-3.60	105.93	109.41
32	XA	1519	MA6	C4-C5-N7	-3.59	105.94	109.41
32	QA	966	M2G	C6-C5-C4	-3.54	117.32	120.84
32	QA	1519	MA6	C4-C5-N7	-3.38	106.14	109.41
32	QA	1518	MA6	C9-N6-C6	-3.38	109.27	119.51
32	XA	1519	MA6	C10-N6-C6	-3.36	109.33	119.51
32	QA	1402	4OC	CM4-N4-C4	-3.34	120.06	122.94
32	XA	1518	MA6	C9-N6-C6	-3.33	109.43	119.51
1	YA	1917	PSU	C5-C1'-C2'	-3.30	109.86	115.55
1	RA	2251	OMG	C6-C5-C4	-3.27	117.59	120.84
32	XA	1207	2MG	C4-C5-N7	-3.21	106.31	109.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	QA	1207	2MG	CM2-N2-C2	-3.13	119.82	123.63
1	RA	2251	OMG	N3-C2-N1	-3.12	122.90	127.46
1	YA	2251	OMG	C6-C5-C4	-3.11	117.75	120.84
32	QA	1519	MA6	C9-N6-C6	-3.05	110.29	119.51
1	YA	2503	2MA	C4-C5-N7	-3.01	106.50	109.41
1	RA	2503	2MA	C4-C5-N7	-3.00	106.51	109.41
1	YA	2251	OMG	N3-C2-N1	-2.99	123.09	127.46
32	XA	1519	MA6	C9-N6-C6	-2.98	110.50	119.51
1	RA	1911	PSU	C5-C1'-C2'	-2.92	110.50	115.55
54	QY	252	MEQ	CB-CA-C	-2.91	106.85	111.65
32	XA	1519	MA6	C10-N6-C9	-2.89	106.67	116.03
32	XA	966	M2G	C4-C5-N7	-2.87	106.63	109.41
1	RA	1939	5MU	C5-C6-N1	-2.86	119.05	122.15
32	QA	1207	2MG	C4-C5-N7	-2.80	106.71	109.41
1	YA	2251	OMG	C4-C5-N7	-2.78	106.72	109.41
32	QA	966	M2G	C4-C5-N7	-2.73	106.77	109.41
1	RA	2251	OMG	C4-C5-N7	-2.71	106.79	109.41
1	YA	1939	5MU	C5-C6-N1	-2.69	119.23	122.15
1	YA	1911	PSU	C5-C1'-C2'	-2.56	111.14	115.55
32	XA	1518	MA6	C10-N6-C9	-2.55	107.77	116.03
32	XA	1518	MA6	C10-N6-C6	-2.52	111.89	119.51
32	QA	1404	5MC	C5-C6-N1	-2.39	119.56	122.15
1	RA	1962	5MC	C5-C6-N1	-2.38	119.57	122.15
32	QA	1518	MA6	C10-N6-C9	-2.37	108.35	116.03
32	QA	1207	2MG	N3-C2-N1	-2.25	122.84	126.23
32	QA	967	5MC	C5-C6-N1	-2.24	119.73	122.15
43	QL	92	0TD	O-C-CA	-2.21	120.00	125.15
32	XA	1404	5MC	C5-C6-N1	-2.20	119.77	122.15
32	QA	1519	MA6	C10-N6-C6	-2.16	112.98	119.51
1	YA	1962	5MC	C5-C6-N1	-2.15	119.83	122.15
1	RA	1942	5MC	C5-C6-N1	-2.11	119.86	122.15
32	QA	1400	5MC	C5-C6-N1	-2.10	119.88	122.15
32	XA	1207	2MG	N3-C2-N1	-2.07	123.10	126.23
32	QA	1407	5MC	C5-C6-N1	-2.06	119.92	122.15
32	XA	527	7MG	C5-C4-N9	-2.06	103.32	106.31
32	QA	1518	MA6	C10-N6-C6	-2.05	113.30	119.51
32	XA	1400	5MC	C5-C6-N1	-2.04	119.94	122.15
32	XA	967	5MC	C5-C6-N1	-2.04	119.94	122.15
1	YA	1911	PSU	O4'-C1'-C2'	2.03	107.70	104.45
1	RA	1911	PSU	O4'-C1'-C2'	2.03	107.71	104.45
32	QA	967	5MC	N4-C4-N3	2.14	120.17	117.00
1	RA	1920	4OC	N4-C4-N3	2.14	120.25	116.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	XA	527	7MG	C2-N3-C4	2.15	119.99	113.95
32	XA	1207	2MG	N2-C2-N1	2.17	119.06	116.95
32	QA	527	7MG	C2-N3-C4	2.20	120.12	113.95
32	XA	967	5MC	N4-C4-N3	2.22	120.28	117.00
32	XA	516	PSU	O4'-C1'-C2'	2.23	108.03	104.45
1	YA	1920	4OC	N4-C4-N3	2.35	120.59	116.64
32	QA	516	PSU	O4'-C1'-C2'	2.35	108.22	104.45
32	XA	1400	5MC	N4-C4-N3	2.43	120.60	117.00
32	QA	1404	5MC	N4-C4-N3	2.51	120.70	117.00
32	QA	1400	5MC	N4-C4-N3	2.51	120.72	117.00
1	YA	1962	5MC	N4-C4-N3	2.52	120.73	117.00
1	YA	1942	5MC	N4-C4-N3	2.54	120.75	117.00
32	QA	1407	5MC	N4-C4-N3	2.54	120.76	117.00
1	RA	1942	5MC	N4-C4-N3	2.58	120.81	117.00
1	RA	1962	5MC	N4-C4-N3	2.58	120.82	117.00
32	XA	1404	5MC	N4-C4-N3	2.66	120.93	117.00
32	XA	1407	5MC	N4-C4-N3	2.74	121.04	117.00
32	XA	1519	MA6	N1-C6-N6	2.97	120.15	117.00
32	XA	1518	MA6	N1-C6-N6	3.00	120.18	117.00
43	QL	92	0TD	C-CA-N	3.31	116.53	109.86
32	QA	1519	MA6	N1-C6-N6	3.40	120.61	117.00
32	XA	1207	2MG	C6-N1-C2	3.89	122.15	115.18
32	QA	1207	2MG	C6-N1-C2	3.97	122.29	115.18
1	RA	2605	PSU	C6-N1-C2	4.13	121.97	115.36
32	QA	1519	MA6	C2-N1-C6	4.17	122.06	111.82
1	YA	1911	PSU	C6-N1-C2	4.23	122.12	115.36
1	YA	2251	OMG	C6-N1-C2	4.23	122.14	116.06
1	RA	1911	PSU	C6-N1-C2	4.24	122.14	115.36
32	QA	516	PSU	C6-N1-C2	4.24	122.15	115.36
1	YA	1917	PSU	C6-N1-C2	4.25	122.16	115.36
1	YA	2605	PSU	C6-N1-C2	4.27	122.19	115.36
32	XA	1518	MA6	C2-N1-C6	4.28	122.32	111.82
1	RA	1917	PSU	C6-N1-C2	4.28	122.22	115.36
32	XA	516	PSU	C6-N1-C2	4.29	122.23	115.36
32	XA	1519	MA6	C2-N1-C6	4.30	122.36	111.82
1	RA	2251	OMG	C6-N1-C2	4.37	122.34	116.06
32	QA	1518	MA6	C2-N1-C6	4.44	122.71	111.82
43	XL	92	0TD	CSB-SB-CB	4.50	109.99	101.60
32	QA	527	7MG	C6-N1-C2	4.64	122.74	116.06
32	XA	527	7MG	C6-N1-C2	4.65	122.74	116.06
32	QA	966	M2G	C2-N3-C4	5.01	120.83	115.11
32	QA	1207	2MG	C2-N3-C4	5.01	120.83	115.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	RA	2251	OMG	C2-N3-C4	5.08	121.09	115.16
1	YA	2251	OMG	C2-N3-C4	5.10	121.11	115.16
32	XA	1207	2MG	C2-N3-C4	5.13	120.97	115.11
32	XA	966	M2G	C2-N3-C4	5.16	121.00	115.11
32	QA	966	M2G	C6-N1-C2	5.21	122.39	116.18
32	XA	966	M2G	C6-N1-C2	5.29	122.48	116.18
1	RA	1939	5MU	C4-N3-C2	6.02	120.42	115.16
1	YA	1939	5MU	C4-N3-C2	6.09	120.49	115.16
32	QA	516	PSU	C4-N3-C2	6.16	120.55	115.16
32	XA	516	PSU	C4-N3-C2	6.34	120.71	115.16
1	RA	1911	PSU	C4-N3-C2	6.34	120.71	115.16
1	RA	2605	PSU	C4-N3-C2	6.38	120.74	115.16
1	RA	1917	PSU	C4-N3-C2	6.43	120.78	115.16
43	QL	92	0TD	CSB-SB-CB	6.51	113.73	101.60
1	RA	2503	2MA	C2-N3-C4	6.53	121.05	115.41
1	YA	1911	PSU	C4-N3-C2	6.57	120.90	115.16
1	YA	2605	PSU	C4-N3-C2	6.58	120.91	115.16
1	YA	1917	PSU	C4-N3-C2	6.60	120.93	115.16
1	YA	2503	2MA	C2-N3-C4	6.81	121.30	115.41
1	YA	1915	5MU	C4-N3-C2	7.11	121.38	115.16
1	RA	1915	5MU	C4-N3-C2	7.18	121.44	115.16
1	YA	2552	2MU	C4-N3-C2	7.77	120.80	114.13
1	RA	2552	2MU	C4-N3-C2	7.80	120.83	114.13
32	XA	527	7MG	N3-C4-N9	9.25	138.79	126.98
32	QA	527	7MG	N3-C4-N9	9.32	138.88	126.98

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

22 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	QA	1207	2MG	2	0
32	QA	1402	4OC	1	0
32	QA	1498	UR3	1	0
32	QA	1518	MA6	1	0
32	QA	1519	MA6	1	0
32	QA	516	PSU	1	0
32	QA	966	M2G	1	0
32	QA	967	5MC	1	0
43	QL	92	0TD	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	RA	1939	5MU	1	0
1	RA	1942	5MC	1	0
1	RA	1962	5MC	1	0
1	RA	2503	2MA	1	0
32	XA	1207	2MG	1	0
32	XA	1402	4OC	1	0
32	XA	1518	MA6	1	0
43	XL	92	0TD	1	0
1	YA	1920	4OC	2	0
1	YA	1939	5MU	1	0
1	YA	1962	5MC	1	0
1	YA	2251	OMG	1	0
1	YA	2503	2MA	2	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2534 ligands modelled in this entry, 2532 are monoatomic - leaving 2 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	$\# Z > 2$
58	SF4	QD	302	35	0,12,12	0.00	-	0,24,24	0.00	-
58	SF4	XD	301	35	0,12,12	0.00	-	0,24,24	0.00	-

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
58	SF4	QD	302	35	-	0/0/48/48	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	SF4	XD	301	35	-	0/0/48/48	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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	RA	2856/2915 (97%)	0.33	130 (4%) 33 31	76, 86, 96, 102	0
1	YA	2856/2915 (97%)	0.44	117 (4%) 38 35	71, 83, 96, 100	0
2	RB	120/122 (98%)	-0.10	2 (1%) 70 67	84, 90, 93, 96	0
2	YB	120/122 (98%)	-0.17	2 (1%) 70 67	80, 87, 91, 94	0
3	RD	275/276 (99%)	0.47	5 (1%) 69 66	77, 85, 89, 96	0
3	YD	275/276 (99%)	0.50	4 (1%) 74 70	76, 83, 89, 90	0
4	RE	204/206 (99%)	0.50	5 (2%) 58 54	78, 86, 91, 93	0
4	YE	204/206 (99%)	0.54	4 (1%) 65 63	77, 86, 90, 94	0
5	RF	203/210 (96%)	0.32	2 (0%) 82 81	81, 87, 92, 95	0
5	YF	203/210 (96%)	0.34	1 (0%) 90 90	76, 85, 91, 94	0
6	RG	181/182 (99%)	0.48	15 (8%) 12 11	87, 91, 94, 97	0
6	YG	181/182 (99%)	0.32	12 (6%) 19 18	85, 89, 93, 95	0
7	RH	174/180 (96%)	1.30	50 (28%) 1 1	86, 92, 95, 97	0
7	YH	173/180 (96%)	0.32	5 (2%) 52 50	82, 88, 92, 95	0
8	RI	147/148 (99%)	0.91	28 (19%) 1 1	85, 91, 94, 97	0
8	YI	146/148 (98%)	0.53	10 (6%) 18 18	84, 90, 94, 96	0
9	RN	140/140 (100%)	0.63	11 (7%) 13 12	83, 88, 92, 96	0
9	YN	140/140 (100%)	0.53	1 (0%) 87 87	80, 86, 91, 94	0
10	RO	122/122 (100%)	0.45	1 (0%) 86 85	79, 85, 90, 91	0
10	YO	122/122 (100%)	0.42	1 (0%) 86 85	78, 85, 89, 92	0
11	RP	149/150 (99%)	0.77	6 (4%) 39 36	78, 88, 92, 95	0
11	YP	149/150 (99%)	0.62	5 (3%) 46 42	77, 85, 90, 94	0
12	RQ	141/141 (100%)	0.26	2 (1%) 75 73	82, 87, 91, 93	0
12	YQ	141/141 (100%)	0.36	0 100 100	77, 85, 89, 91	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	RR	118/118 (100%)	0.47	2 (1%) 70 67	81, 86, 89, 91	0
13	YR	118/118 (100%)	0.52	3 (2%) 58 54	80, 85, 89, 92	0
14	RS	110/112 (98%)	0.56	9 (8%) 12 12	84, 89, 93, 95	0
14	YS	110/112 (98%)	0.46	2 (1%) 69 66	82, 88, 91, 94	0
15	RT	131/146 (89%)	0.29	3 (2%) 61 58	82, 87, 91, 95	0
15	YT	131/146 (89%)	0.34	3 (2%) 61 58	82, 86, 92, 95	0
16	RU	116/118 (98%)	0.44	7 (6%) 23 21	82, 87, 92, 93	0
16	YU	116/118 (98%)	0.45	2 (1%) 70 67	78, 84, 90, 91	0
17	RV	101/101 (100%)	0.21	3 (2%) 51 49	81, 89, 92, 95	0
17	YV	101/101 (100%)	0.50	1 (0%) 82 81	80, 86, 91, 93	0
18	RW	112/113 (99%)	0.61	4 (3%) 43 40	80, 85, 90, 95	0
18	YW	112/113 (99%)	0.59	6 (5%) 26 25	78, 84, 90, 95	0
19	RX	95/96 (98%)	0.70	9 (9%) 9 8	83, 87, 90, 93	0
19	YX	95/96 (98%)	0.44	3 (3%) 48 46	79, 84, 89, 94	0
20	RY	107/110 (97%)	1.49	29 (27%) 1 1	85, 90, 93, 100	0
20	YY	107/110 (97%)	0.73	11 (10%) 7 6	82, 88, 92, 98	0
21	RZ	203/206 (98%)	0.92	22 (10%) 6 5	87, 90, 94, 99	0
21	YZ	201/206 (97%)	0.50	18 (8%) 10 10	83, 89, 94, 96	0
22	R0	77/85 (90%)	1.16	13 (16%) 2 1	83, 87, 90, 95	0
22	Y0	77/85 (90%)	0.72	7 (9%) 10 10	80, 85, 90, 95	0
23	R1	97/98 (98%)	0.78	10 (10%) 7 6	82, 86, 92, 94	0
23	Y1	97/98 (98%)	0.81	6 (6%) 21 21	78, 85, 91, 94	0
24	R2	70/72 (97%)	0.38	3 (4%) 36 34	83, 89, 92, 94	0
24	Y2	70/72 (97%)	0.40	1 (1%) 75 73	79, 86, 90, 97	0
25	R3	59/60 (98%)	1.13	9 (15%) 2 2	82, 88, 93, 98	0
25	Y3	59/60 (98%)	0.87	4 (6%) 18 18	79, 85, 91, 95	0
26	R4	69/71 (97%)	1.27	18 (26%) 1 1	89, 93, 96, 97	0
26	Y4	69/71 (97%)	0.70	12 (17%) 2 1	87, 92, 96, 97	0
27	R5	59/60 (98%)	0.41	2 (3%) 46 42	78, 86, 92, 95	0
27	Y5	59/60 (98%)	0.38	2 (3%) 46 42	78, 85, 92, 97	0
28	R6	53/54 (98%)	3.35	41 (77%) 0 0	89, 93, 96, 100	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	Y6	53/54 (98%)	3.02	40 (75%) 0 0	88, 92, 95, 97	0
29	R7	48/49 (97%)	0.74	3 (6%) 21 20	79, 84, 91, 93	0
29	Y7	48/49 (97%)	1.05	4 (8%) 12 11	76, 81, 88, 93	0
30	R8	64/65 (98%)	0.78	2 (3%) 49 48	81, 86, 90, 91	0
30	Y8	64/65 (98%)	0.64	0 100 100	76, 83, 89, 90	0
31	R9	37/37 (100%)	2.40	20 (54%) 0 0	88, 90, 94, 97	0
31	Y9	37/37 (100%)	2.14	19 (51%) 0 0	84, 89, 91, 91	0
32	QA	1488/1521 (97%)	0.10	35 (2%) 59 56	83, 90, 96, 103	0
32	XA	1492/1521 (98%)	0.10	37 (2%) 58 54	78, 90, 96, 101	0
33	QB	231/256 (90%)	0.62	24 (10%) 7 6	88, 92, 95, 97	0
33	XB	231/256 (90%)	0.46	22 (9%) 9 8	87, 91, 95, 98	0
34	QC	206/239 (86%)	0.58	24 (11%) 5 4	88, 91, 94, 96	0
34	XC	206/239 (86%)	0.58	20 (9%) 8 8	87, 90, 93, 96	0
35	QD	208/209 (99%)	0.34	9 (4%) 36 34	85, 89, 93, 97	0
35	XD	208/209 (99%)	0.52	19 (9%) 10 10	85, 90, 94, 97	0
36	QE	148/162 (91%)	0.38	9 (6%) 22 21	85, 90, 93, 95	0
36	XE	148/162 (91%)	0.52	9 (6%) 22 21	85, 88, 92, 94	0
37	QF	100/101 (99%)	0.32	8 (8%) 13 12	87, 90, 93, 95	0
37	XF	100/101 (99%)	0.16	3 (3%) 51 49	83, 89, 93, 95	0
38	QG	155/156 (99%)	0.90	24 (15%) 2 2	88, 91, 94, 96	0
38	XG	155/156 (99%)	0.66	15 (9%) 8 8	87, 91, 95, 96	0
39	QH	137/138 (99%)	0.63	14 (10%) 7 6	86, 89, 92, 94	0
39	XH	137/138 (99%)	0.62	10 (7%) 16 15	82, 89, 92, 94	0
40	QI	127/128 (99%)	1.33	30 (23%) 1 1	86, 92, 95, 96	0
40	XI	126/128 (98%)	0.89	18 (14%) 3 3	85, 92, 95, 98	0
41	QJ	97/105 (92%)	1.33	29 (29%) 1 1	86, 92, 95, 97	0
41	XJ	96/105 (91%)	0.96	15 (15%) 2 2	87, 91, 94, 96	0
42	QK	114/129 (88%)	0.75	12 (10%) 7 6	86, 90, 93, 94	0
42	XK	114/129 (88%)	0.51	4 (3%) 44 41	82, 88, 92, 95	0
43	QL	121/132 (91%)	0.51	6 (4%) 30 27	81, 87, 90, 92	0
43	XL	121/132 (91%)	0.66	10 (8%) 12 11	83, 87, 91, 93	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	QM	116/126 (92%)	0.76	19 (16%) 2 2	88, 92, 95, 97	0
44	XM	114/126 (90%)	0.97	22 (19%) 1 1	87, 91, 94, 95	0
45	QN	60/61 (98%)	1.46	14 (23%) 1 1	87, 91, 94, 95	0
45	XN	60/61 (98%)	0.51	3 (5%) 30 27	88, 90, 93, 95	0
46	QO	88/89 (98%)	0.50	6 (6%) 18 18	86, 89, 93, 94	0
46	XO	88/89 (98%)	0.59	6 (6%) 18 18	84, 89, 92, 94	0
47	QP	82/88 (93%)	1.02	11 (13%) 4 3	84, 89, 91, 93	0
47	XP	82/88 (93%)	0.96	15 (18%) 1 1	86, 90, 92, 95	0
48	QQ	99/105 (94%)	0.70	8 (8%) 13 12	85, 89, 93, 95	0
48	XQ	99/105 (94%)	0.44	3 (3%) 51 49	85, 88, 91, 93	0
49	QR	68/88 (77%)	1.23	14 (20%) 1 1	87, 90, 94, 96	0
49	XR	68/88 (77%)	0.67	3 (4%) 35 33	83, 89, 92, 93	0
50	QS	83/93 (89%)	1.55	27 (32%) 0 1	88, 92, 95, 97	0
50	XS	83/93 (89%)	1.50	24 (28%) 1 1	89, 92, 94, 96	0
51	QT	96/106 (90%)	0.65	5 (5%) 28 26	84, 89, 91, 93	0
51	XT	98/106 (92%)	1.18	17 (17%) 2 1	86, 90, 93, 94	0
52	QU	23/27 (85%)	3.02	20 (86%) 0 0	88, 92, 94, 95	0
52	XU	23/27 (85%)	2.17	12 (52%) 0 0	89, 91, 93, 93	0
53	QV	77/77 (100%)	0.22	3 (3%) 40 37	85, 91, 96, 98	0
53	XV	77/77 (100%)	0.41	5 (6%) 20 19	83, 90, 96, 100	0
54	QY	356/380 (93%)	1.86	144 (40%) 0 0	86, 92, 96, 99	0
54	XY	356/380 (93%)	1.63	119 (33%) 0 1	84, 91, 96, 99	0
55	QX	6/25 (24%)	0.64	0 100 100	87, 90, 91, 92	0
55	XX	6/25 (24%)	0.63	0 100 100	85, 88, 91, 91	0
All	All	21446/22208 (96%)	0.54	1678 (7%) 14 13	71, 88, 95, 103	0

All (1678) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
28	R6	20	ASN	11.6
21	YZ	192	ALA	10.7
20	YY	1	MET	9.1
31	R9	37	GLY	8.8
25	R3	60	GLU	8.8

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Mol	Chain	Res	Type	RSRZ
20	RY	1	MET	8.7
54	QY	81	SER	8.5
1	YA	2141	G	8.4
26	R4	69	LYS	8.3
1	RA	1067	A	7.9
1	YA	2140	C	7.8
1	RA	229	A	7.6
43	QL	64	TYR	7.5
21	RZ	200	GLY	7.4
21	RZ	191	VAL	7.3
22	Y0	8	GLY	7.2
21	YZ	193	GLU	7.2
1	YA	2154	G	7.1
28	R6	43	CYS	7.0
54	QY	330	ASP	7.0
21	RZ	192	ALA	6.9
1	RA	2146	C	6.9
32	QA	1036	G	6.9
1	RA	1064	C	6.8
54	QY	66	VAL	6.7
25	Y3	60	GLU	6.5
40	QI	127	LYS	6.5
52	QU	18	TYR	6.5
1	YA	2139	C	6.5
1	RA	2125	G	6.4
7	RH	105	LEU	6.4
1	YA	2153	G	6.4
21	YZ	197	ILE	6.4
21	RZ	201	LYS	6.3
28	R6	42	TRP	6.2
1	YA	2804	C	6.2
21	RZ	194	PRO	6.2
21	RZ	195	GLU	6.2
28	Y6	20	ASN	6.1
1	YA	2116	G	6.1
54	QY	102	GLU	6.1
1	RA	1509(A)	C	6.1
1	RA	2142	C	6.0
22	R0	8	GLY	6.0
32	QA	1030(C)	C	6.0
21	RZ	202	GLU	5.9
54	XY	46	VAL	5.9

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Mol	Chain	Res	Type	RSRZ
21	RZ	199	LYS	5.9
1	RA	2116	G	5.9
28	R6	14	THR	5.9
28	Y6	42	TRP	5.9
52	QU	5	ASP	5.8
28	Y6	15	GLU	5.8
38	QG	78	ARG	5.7
28	R6	54	ILE	5.6
54	XY	50	PRO	5.6
31	R9	13	LYS	5.6
1	YA	2142	C	5.6
1	YA	2155	G	5.6
41	XJ	38	ILE	5.6
28	R6	4	GLU	5.6
54	QY	216	SER	5.6
1	YA	2805	G	5.5
35	XD	163	GLU	5.5
8	RI	83	ALA	5.5
54	XY	66	VAL	5.5
54	QY	163	THR	5.5
24	R2	1	MET	5.4
32	XA	88	A	5.4
28	R6	11	LEU	5.4
54	QY	77	LEU	5.4
51	XT	11	SER	5.4
54	QY	175	GLY	5.4
1	RA	2110	G	5.4
1	RA	2144	U	5.3
50	XS	4	SER	5.3
54	XY	216	SER	5.3
21	YZ	194	PRO	5.3
1	RA	2793	G	5.3
26	R4	68	ARG	5.3
7	RH	43	VAL	5.3
1	RA	2155	G	5.3
1	YA	1095	A	5.2
28	Y6	14	THR	5.2
1	YA	2793	G	5.2
1	RA	2169	A	5.2
1	RA	2153	G	5.2
1	RA	2162	G	5.2
21	YZ	201	LYS	5.2

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Mol	Chain	Res	Type	RSRZ
54	QY	174	ALA	5.2
54	XY	84	LEU	5.2
1	YA	1083	U	5.2
1	RA	2140	C	5.1
1	RA	2896	C	5.1
28	Y6	35	GLU	5.1
31	Y9	28	GLU	5.1
32	XA	1030(C)	C	5.1
7	RH	103	LEU	5.1
1	YA	1509(A)	C	5.1
1	RA	1076	C	5.1
21	YZ	191	VAL	5.1
28	R6	19	ARG	5.1
1	RA	2801(B)	A	5.1
38	QG	156	TRP	5.1
1	YA	2152	G	5.1
1	RA	2141	G	5.1
1	RA	2804	C	5.1
7	RH	2	SER	5.1
7	RH	159	GLU	5.0
1	RA	1083	U	5.0
1	YA	2147	G	5.0
54	QY	101	ALA	5.0
1	RA	2154	G	5.0
54	QY	96	PHE	5.0
54	QY	71	ASP	5.0
54	QY	91	ASP	5.0
38	QG	82	GLY	5.0
20	RY	45	VAL	5.0
32	QA	1001(A)	A	5.0
54	QY	44	PRO	5.0
7	RH	101	ARG	4.9
38	QG	80	VAL	4.9
1	RA	2143	C	4.9
54	QY	93	GLU	4.9
34	QC	189	ALA	4.9
54	QY	236	PRO	4.9
21	YZ	200	GLY	4.9
32	QA	1531	A	4.9
1	YA	1075	C	4.9
28	Y6	32	ASN	4.9
54	XY	41	LEU	4.9

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Mol	Chain	Res	Type	RSRZ
43	XL	64	TYR	4.9
32	QA	1532	U	4.9
38	QG	6	ARG	4.8
54	QY	341	GLU	4.8
7	RH	115	VAL	4.8
6	RG	2	PRO	4.8
38	QG	81	GLY	4.8
7	RH	102	ALA	4.8
21	RZ	193	GLU	4.8
28	R6	39	TYR	4.8
49	QR	62	GLU	4.8
1	RA	2120	G	4.8
1	RA	2124	G	4.8
3	RD	276	LYS	4.8
54	QY	73	MET	4.8
1	YA	1076	C	4.8
54	XY	345	THR	4.7
1	RA	2159	G	4.7
54	QY	25	LEU	4.7
40	QI	36	TYR	4.7
28	Y6	49	HIS	4.7
34	QC	160	ALA	4.7
1	RA	2138	C	4.7
1	RA	2139	C	4.7
28	Y6	54	ILE	4.7
20	RY	5	MET	4.7
54	QY	74	LYS	4.7
43	XL	61	THR	4.7
54	QY	88	VAL	4.7
22	R0	9	SER	4.7
19	RX	1	MET	4.6
40	QI	128	ARG	4.6
28	R6	21	TYR	4.6
1	RA	2147	G	4.6
31	Y9	1	MET	4.6
1	YA	2108	C	4.6
54	QY	70	LEU	4.6
42	QK	117	ASN	4.6
40	QI	33	PHE	4.6
1	YA	2125	G	4.6
41	XJ	71	LEU	4.6
1	RA	2131	G	4.6

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Mol	Chain	Res	Type	RSRZ
1	RA	2894	G	4.6
54	QY	332	ARG	4.5
38	QG	85	TYR	4.5
33	XB	227	GLY	4.5
54	QY	82	GLY	4.5
41	QJ	89	ASP	4.5
28	Y6	21	TYR	4.5
1	RA	2145	C	4.5
54	XY	88	VAL	4.5
20	RY	43	ASN	4.5
1	RA	2137	C	4.5
21	YZ	196	VAL	4.5
1	YA	2151	G	4.5
28	Y6	43	CYS	4.5
1	RA	2122	U	4.5
1	YA	2143	C	4.5
20	RY	62	GLU	4.4
1	RA	2165	G	4.4
54	QY	218	SER	4.4
54	XY	42	GLU	4.4
1	YA	2807	G	4.4
38	QG	86	GLN	4.4
54	XY	231	ASP	4.4
32	XA	1257	U	4.4
34	XC	196	LEU	4.4
6	RG	75	LYS	4.4
54	QY	176	ILE	4.4
39	QH	131	GLY	4.4
1	YA	2138	C	4.4
1	RA	2174	C	4.4
22	R0	71	ASP	4.4
31	Y9	29	ASN	4.4
54	XY	44	PRO	4.4
1	RA	1085	A	4.3
54	QY	140	GLU	4.3
52	QU	17	THR	4.3
28	R6	5	VAL	4.3
34	XC	193	TYR	4.3
1	RA	2805	G	4.3
54	QY	164	GLU	4.3
54	XY	78	GLU	4.3
31	Y9	37	GLY	4.3

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Mol	Chain	Res	Type	RSRZ
54	QY	235	ASN	4.3
9	RN	8	GLN	4.3
21	RZ	198	LYS	4.3
49	QR	43	PHE	4.3
28	Y6	26	ASN	4.3
38	XG	85	TYR	4.3
1	RA	888	C	4.3
1	RA	2802	G	4.3
9	RN	140	VAL	4.3
52	XU	2	GLY	4.3
54	QY	7	VAL	4.3
28	Y6	50	ARG	4.3
40	QI	5	TYR	4.3
42	QK	13	GLN	4.3
54	XY	71	ASP	4.3
32	QA	1286	A	4.2
38	XG	82	GLY	4.2
50	QS	65	ASN	4.2
1	YA	2132	U	4.2
28	R6	40	CYS	4.2
8	RI	138	ILE	4.2
28	R6	12	GLU	4.2
54	QY	68	ASP	4.2
47	QP	19	ILE	4.2
34	XC	206	GLU	4.2
54	XY	85	GLU	4.2
28	Y6	10	LEU	4.2
54	QY	72	GLN	4.2
44	XM	107	ALA	4.2
1	YA	2803	C	4.2
38	QG	154	TYR	4.2
9	YN	140	VAL	4.2
1	RA	1062	G	4.2
7	YH	57	ASP	4.2
1	RA	2105	C	4.1
38	QG	77	SER	4.2
29	Y7	1	MET	4.1
1	YA	2162	G	4.1
28	R6	23	THR	4.1
20	RY	55	TYR	4.1
44	XM	97	PRO	4.1
28	Y6	36	LEU	4.1

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Mol	Chain	Res	Type	RSRZ
1	RA	2156	G	4.1
28	R6	24	GLU	4.1
28	R6	9	LEU	4.1
54	XY	47	TRP	4.1
1	YA	1081	U	4.1
22	R0	72	ARG	4.1
54	XY	12	GLN	4.1
54	XY	61	SER	4.1
28	Y6	41	PRO	4.1
34	QC	207	VAL	4.1
20	RY	2	ARG	4.1
32	QA	344	A	4.1
36	XE	118	ILE	4.1
54	XY	63	LEU	4.0
54	QY	78	GLU	4.0
4	RE	151	TYR	4.0
9	RN	74	ARG	4.0
44	QM	102	ARG	4.0
11	YP	1	MET	4.0
1	YA	1091	G	4.0
50	QS	30	LEU	4.0
38	QG	4	ARG	4.0
41	QJ	32	ALA	4.0
25	R3	59	VAL	4.0
1	RA	2172	U	4.0
28	R6	18	ARG	4.0
54	XY	21	LEU	4.0
54	XY	69	THR	4.0
1	YA	2165	G	4.0
1	RA	2133	G	4.0
7	RH	112	PRO	4.0
44	XM	98	VAL	4.0
45	QN	38	GLY	4.0
41	QJ	20	ALA	4.0
54	QY	201	LEU	4.0
32	QA	1030(B)	G	4.0
23	R1	23	LYS	4.0
18	YW	112	GLY	3.9
23	R1	22	GLY	3.9
31	R9	31	LYS	3.9
54	XY	38	ASN	3.9
54	QY	165	ILE	3.9

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Mol	Chain	Res	Type	RSRZ
38	XG	156	TRP	3.9
43	XL	28	LYS	3.9
54	QY	238	ASP	3.9
20	RY	29	GLU	3.9
34	QC	196	LEU	3.9
54	QY	172	GLU	3.9
1	RA	2126	A	3.9
1	RA	2176	A	3.9
52	QU	22	ARG	3.9
8	RI	92	VAL	3.9
52	QU	13	ILE	3.9
43	XL	62	SER	3.9
29	Y7	47	ARG	3.9
34	XC	166	GLU	3.9
54	XY	95	THR	3.9
52	QU	11	GLY	3.9
50	XS	49	ILE	3.9
7	RH	113	VAL	3.8
1	YA	2146	C	3.8
54	QY	103	LEU	3.8
54	XY	28	ASP	3.8
1	RA	2127	G	3.8
23	Y1	2	SER	3.8
28	R6	41	PRO	3.8
1	YA	2801(B)	A	3.8
1	RA	1046	A	3.8
54	XY	98	GLU	3.8
1	RA	2111	C	3.8
54	QY	83	LEU	3.8
54	XY	72	GLN	3.8
28	Y6	25	LYS	3.8
41	QJ	26	ALA	3.8
1	YA	1080	C	3.8
40	QI	66	ARG	3.8
54	QY	63	LEU	3.8
54	QY	113	LEU	3.8
1	YA	1064	C	3.8
1	YA	1087	G	3.8
1	RA	2180	U	3.8
31	R9	28	GLU	3.8
1	RA	2173	A	3.8
32	XA	1286	A	3.8

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Mol	Chain	Res	Type	RSRZ
54	QY	253	HIS	3.8
32	XA	1001(B)	G	3.8
40	QI	88	TYR	3.8
52	XU	9	ARG	3.8
1	RA	2792	G	3.8
1	YA	2173	A	3.8
1	RA	2170	A	3.8
21	RZ	4	ARG	3.8
32	XA	1030(A)	C	3.8
53	XV	1	C	3.8
1	YA	2172	U	3.7
1	YA	2133	G	3.7
1	RA	2168	G	3.7
20	RY	35	TYR	3.7
31	R9	36	GLN	3.7
54	QY	9	ASN	3.7
54	QY	263	ILE	3.7
45	QN	22	THR	3.7
1	RA	652(D)	G	3.7
54	XY	205	SER	3.7
50	QS	16	LEU	3.7
1	RA	1086	A	3.7
31	R9	26	ILE	3.7
1	RA	2164	C	3.7
1	RA	2100	G	3.7
32	QA	345	C	3.7
39	QH	107	LEU	3.7
28	Y6	53	LYS	3.7
1	YA	2897	U	3.7
1	YA	2131	G	3.7
54	QY	8	ASN	3.7
7	RH	114	VAL	3.7
40	QI	65	VAL	3.7
53	QV	1	C	3.7
1	RA	2121	G	3.7
8	RI	1	MET	3.7
8	RI	39	ALA	3.7
38	QG	83	ALA	3.7
45	QN	2	ALA	3.7
28	Y6	16	CYS	3.7
38	XG	78	ARG	3.7
44	QM	78	ILE	3.7

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Mol	Chain	Res	Type	RSRZ
8	RI	16	GLY	3.7
41	QJ	37	PRO	3.7
39	XH	25	ASP	3.7
21	RZ	197	ILE	3.7
54	QY	205	SER	3.6
26	R4	49	PHE	3.6
33	XB	228	GLY	3.6
21	YZ	187	ALA	3.6
54	QY	92	ASP	3.6
1	RA	1026	U	3.6
1	YA	2145	C	3.6
1	RA	2803	C	3.6
54	XY	65	ALA	3.6
51	XT	52	ALA	3.6
41	QJ	70	ARG	3.6
1	YA	2174	C	3.6
1	YA	2894	G	3.6
40	XI	7	THR	3.6
49	XR	31	LEU	3.6
54	QY	228	ASP	3.6
54	XY	40	GLU	3.6
7	RH	99	VAL	3.6
28	Y6	51	GLU	3.6
44	QM	4	ILE	3.6
26	R4	67	TYR	3.6
45	QN	39	LEU	3.6
38	QG	84	ASN	3.6
28	Y6	11	LEU	3.6
1	YA	2144	U	3.6
1	YA	653	A	3.6
7	RH	55	PRO	3.6
50	XS	38	SER	3.6
33	QB	114	ARG	3.5
1	RA	1075	C	3.5
28	Y6	27	LYS	3.5
31	Y9	30	PRO	3.5
42	XK	117	ASN	3.5
28	R6	16	CYS	3.5
28	R6	53	LYS	3.5
28	Y6	52	VAL	3.5
54	XY	341	GLU	3.5
54	XY	308	GLN	3.5

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Mol	Chain	Res	Type	RSRZ
9	RN	72	TYR	3.5
38	XG	58	PRO	3.5
52	XU	24	ARG	3.5
33	QB	163	PHE	3.5
1	YA	1085	A	3.5
26	R4	47	GLN	3.5
28	R6	44	ARG	3.5
29	Y7	48	LYS	3.5
26	Y4	59	PHE	3.5
50	XS	74	PHE	3.5
20	RY	64	GLU	3.5
8	RI	88	ILE	3.5
54	XY	56	LEU	3.5
28	Y6	13	CYS	3.5
1	RA	2123	G	3.5
7	RH	97	ARG	3.5
54	XY	73	MET	3.5
6	YG	32	PRO	3.5
54	QY	55	ALA	3.5
7	YH	47	GLU	3.5
28	R6	50	ARG	3.5
33	QB	70	PHE	3.5
52	XU	18	TYR	3.5
54	XY	89	GLU	3.5
41	XJ	6	ILE	3.5
50	XS	69	HIS	3.5
31	Y9	34	GLN	3.5
41	XJ	36	GLY	3.5
52	QU	16	GLY	3.5
54	QY	146	SER	3.5
2	YB	88	C	3.5
1	RA	653	A	3.5
4	RE	159	HIS	3.5
28	R6	10	LEU	3.5
1	YA	2130	U	3.5
45	QN	8	GLU	3.5
51	XT	100	ILE	3.5
24	Y2	1	MET	3.5
54	QY	265	HIS	3.5
41	XJ	70	ARG	3.5
50	XS	50	ALA	3.5
41	QJ	23	ILE	3.4

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Mol	Chain	Res	Type	RSRZ
49	QR	57	GLY	3.4
31	Y9	9	ARG	3.4
7	RH	123	PHE	3.4
6	YG	75	LYS	3.4
28	R6	51	GLU	3.4
54	QY	99	ALA	3.4
39	QH	95	VAL	3.4
54	QY	80	VAL	3.4
40	QI	105	ASP	3.4
1	RA	1079	C	3.4
1	RA	1090	U	3.4
42	QK	126	ARG	3.4
46	XO	88	ARG	3.4
28	Y6	22	ALA	3.4
1	YA	1067	A	3.4
22	R0	22	GLY	3.4
54	XY	30	LYS	3.4
1	RA	1080	C	3.4
32	QA	1533	C	3.4
1	RA	2119	A	3.4
54	QY	53	ALA	3.4
1	RA	2152	G	3.4
40	XI	81	ILE	3.4
54	XY	96	PHE	3.4
1	YA	2794(A)	C	3.4
1	YA	1082	U	3.4
1	RA	2807	G	3.4
33	QB	31	TYR	3.4
54	QY	183	ILE	3.4
34	QC	190	ARG	3.4
1	YA	2123	G	3.4
38	XG	83	ALA	3.4
54	QY	100	VAL	3.4
34	XC	192	THR	3.4
32	XA	1001(A)	A	3.3
54	QY	65	ALA	3.3
54	XY	207	PHE	3.3
1	YA	888	C	3.3
1	RA	2161	C	3.3
1	YA	2166	G	3.3
31	R9	30	PRO	3.3
1	YA	2167	U	3.3

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Mol	Chain	Res	Type	RSRZ
1	RA	2117	A	3.3
26	Y4	66	SER	3.3
1	RA	2136	C	3.3
28	R6	13	CYS	3.3
32	XA	1036	G	3.3
28	R6	49	HIS	3.3
54	XY	144	TRP	3.3
38	XG	59	LEU	3.3
38	XG	86	GLN	3.3
54	QY	56	LEU	3.3
42	XK	87	THR	3.3
7	RH	24	VAL	3.3
27	R5	60	VAL	3.3
35	XD	166	LYS	3.3
32	XA	77	G	3.3
3	RD	275	LYS	3.3
49	QR	85	LEU	3.3
21	RZ	196	VAL	3.3
54	XY	67	VAL	3.3
1	RA	1082	U	3.3
34	QC	206	GLU	3.3
1	YA	2160	G	3.3
1	YA	2802	G	3.3
1	RA	2897	U	3.3
54	QY	274	CYS	3.3
34	QC	130	VAL	3.3
54	QY	11	ILE	3.3
33	QB	203	GLY	3.3
54	XY	53	ALA	3.3
1	YA	2168	G	3.3
26	Y4	62	ARG	3.3
28	Y6	24	GLU	3.3
33	XB	133	LYS	3.3
54	XY	208	ASP	3.3
40	QI	125	TYR	3.3
50	QS	4	SER	3.3
50	QS	69	HIS	3.3
1	RA	1095	A	3.2
38	QG	32	ARG	3.2
1	RA	2132	U	3.2
1	RA	2106	G	3.2
28	R6	15	GLU	3.2

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Mol	Chain	Res	Type	RSRZ
40	XI	19	LEU	3.2
44	QM	116	THR	3.2
54	QY	15	THR	3.2
26	Y4	68	ARG	3.2
44	XM	102	ARG	3.2
23	R1	57	GLU	3.2
54	XY	167	GLU	3.2
9	RN	7	LYS	3.2
28	R6	45	LYS	3.2
13	YR	69	ASP	3.2
26	R4	18	CYS	3.2
48	QQ	98	LEU	3.2
52	QU	12	LYS	3.2
23	R1	2	SER	3.2
33	XB	136	VAL	3.2
50	QS	41	VAL	3.2
54	XY	81	SER	3.2
1	RA	2109	U	3.2
32	XA	1040	U	3.2
15	RT	35	LYS	3.2
20	YY	63	LYS	3.2
50	XS	40	ILE	3.2
51	XT	55	ILE	3.2
51	XT	56	MET	3.2
1	RA	2128	C	3.2
1	YA	2124	G	3.2
1	RA	11	G	3.2
7	RH	29	PRO	3.2
33	QB	234	PRO	3.2
20	RY	63	LYS	3.2
54	XY	49	GLU	3.2
42	XK	126	ARG	3.2
7	RH	21	PRO	3.2
33	QB	232	PRO	3.2
40	QI	106	ALA	3.2
11	RP	119	GLU	3.2
1	YA	1536	C	3.2
41	QJ	63	PHE	3.2
44	XM	111	LYS	3.2
19	YX	1	MET	3.2
20	RY	107	ASP	3.2
40	QI	37	PHE	3.2

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Mol	Chain	Res	Type	RSRZ
54	XY	281	HIS	3.2
45	QN	3	ARG	3.2
28	Y6	34	LEU	3.2
1	RA	652(U)	C	3.2
6	YG	35	GLU	3.2
11	RP	118	GLY	3.2
54	QY	84	LEU	3.2
54	XY	276	ASN	3.2
1	YA	2149	G	3.2
33	XB	128	GLU	3.2
54	QY	329	ASP	3.2
32	QA	1257	U	3.1
41	QJ	5	ARG	3.1
54	XY	203	ARG	3.1
28	R6	47	THR	3.1
1	YA	2156	G	3.1
1	RA	2107	C	3.1
26	R4	66	SER	3.1
8	RI	86	THR	3.1
41	QJ	71	LEU	3.1
50	XS	71	LEU	3.1
54	QY	229	ASP	3.1
54	QY	173	VAL	3.1
45	XN	2	ALA	3.1
51	XT	18	GLN	3.1
53	QV	53	G	3.1
6	YG	51	ARG	3.1
11	RP	105	LEU	3.1
54	QY	219	SER	3.1
17	YV	1	MET	3.1
6	YG	164	GLU	3.1
1	YA	1065	U	3.1
1	RA	1078	U	3.1
49	QR	87	ARG	3.1
8	RI	38	LEU	3.1
47	XP	1	MET	3.1
53	QV	47	U	3.1
54	QY	234	ILE	3.1
13	YR	118	GLU	3.1
50	QS	43	GLU	3.1
1	YA	1026	U	3.1
31	R9	25	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
38	QG	28	ASN	3.1
54	QY	206	PRO	3.1
54	QY	331	SER	3.1
1	YA	2117	A	3.1
42	QK	31	THR	3.1
11	YP	105	LEU	3.1
2	YB	87	G	3.1
41	QJ	29	ARG	3.1
25	Y3	2	PRO	3.1
22	Y0	75	LEU	3.1
38	QG	2	ALA	3.1
1	YA	2107	C	3.1
7	YH	174	GLY	3.1
54	QY	60	ARG	3.1
33	QB	133	LYS	3.1
21	YZ	188	ALA	3.1
34	XC	168	ALA	3.1
38	QG	5	ARG	3.1
1	YA	652(U)	C	3.1
14	RS	57	LYS	3.1
39	XH	54	ASP	3.1
31	Y9	7	VAL	3.1
1	YA	2169	A	3.1
1	RA	2163	C	3.1
8	RI	65	ALA	3.1
18	YW	94	ASP	3.0
20	YY	92	ASN	3.0
34	QC	193	TYR	3.0
34	QC	157	ILE	3.0
35	XD	2	GLY	3.0
40	XI	105	ASP	3.0
20	YY	2	ARG	3.0
52	QU	24	ARG	3.0
1	YA	2129	C	3.0
1	RA	2171	A	3.0
33	XB	122	PHE	3.0
47	QP	9	PHE	3.0
41	QJ	38	ILE	3.0
52	XU	3	LYS	3.0
54	XY	45	ASP	3.0
1	RA	1065	U	3.0
45	QN	35	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
54	QY	34	LEU	3.0
1	YA	2115	G	3.0
32	QA	1001(B)	G	3.0
25	Y3	59	VAL	3.0
32	QA	1028	C	3.0
46	XO	49	ASP	3.0
1	RA	2895	U	3.0
7	RH	33	LEU	3.0
28	Y6	9	LEU	3.0
54	QY	119	PHE	3.0
19	RX	89	ILE	3.0
54	QY	211	GLY	3.0
54	QY	64	GLU	3.0
47	XP	76	GLN	3.0
54	QY	144	TRP	3.0
1	RA	2148	G	3.0
54	QY	209	SER	3.0
28	R6	22	ALA	3.0
54	QY	207	PHE	3.0
26	R4	39	CYS	3.0
43	QL	28	LYS	3.0
20	RY	60	PHE	3.0
1	YA	2137	C	3.0
31	R9	24	TYR	3.0
50	QS	49	ILE	3.0
35	QD	183	GLY	3.0
47	XP	17	TYR	3.0
45	QN	25	VAL	3.0
26	Y4	69	LYS	3.0
28	Y6	17	LYS	3.0
50	QS	15	LEU	3.0
54	XY	83	LEU	3.0
31	Y9	18	ARG	3.0
40	QI	18	PHE	3.0
20	RY	4	LYS	3.0
14	RS	37	ALA	3.0
21	RZ	187	ALA	3.0
43	QL	29	GLY	3.0
54	QY	127	ASP	3.0
3	RD	182	LEU	3.0
39	QH	119	LEU	3.0
26	Y4	64	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
46	XO	87	ILE	3.0
31	R9	16	VAL	3.0
34	XC	11	ARG	3.0
29	R7	48	LYS	3.0
32	QA	1030(D)	G	3.0
54	XY	346	GLN	3.0
35	XD	49	ARG	3.0
33	QB	118	LEU	3.0
49	QR	61	LYS	3.0
1	YA	1090	U	2.9
45	QN	33	VAL	2.9
54	QY	67	VAL	2.9
44	QM	65	LYS	2.9
47	XP	4	ILE	2.9
18	RW	51	LEU	2.9
21	RZ	56	VAL	2.9
32	XA	1456	G	2.9
40	QI	110	GLU	2.9
54	XY	325	SER	2.9
20	YY	46	LYS	2.9
54	QY	50	PRO	2.9
34	QC	65	ALA	2.9
39	QH	112	LEU	2.9
1	RA	1081	U	2.9
35	XD	3	ARG	2.9
15	RT	37	GLY	2.9
54	QY	32	GLU	2.9
53	XV	45	G	2.9
54	QY	75	GLN	2.9
49	QR	58	LEU	2.9
54	XY	70	LEU	2.9
32	QA	1027	C	2.9
7	RH	90	LYS	2.9
40	QI	6	GLY	2.9
14	RS	58	LEU	2.9
33	XB	127	ILE	2.9
35	XD	162	LEU	2.9
47	XP	36	ILE	2.9
32	XA	1030(D)	G	2.9
52	QU	6	ARG	2.9
54	QY	16	GLU	2.9
12	RQ	92	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
8	YI	35	LEU	2.9
41	XJ	72	VAL	2.9
7	RH	111	HIS	2.9
28	Y6	8	LYS	2.9
28	Y6	23	THR	2.9
31	Y9	4	ARG	2.9
39	XH	60	ARG	2.9
44	XM	96	LEU	2.9
54	XY	29	ALA	2.9
8	RI	108	THR	2.9
20	RY	42	VAL	2.9
1	YA	2164	C	2.9
8	YI	85	GLU	2.9
53	XV	47	U	2.9
7	RH	82	GLY	2.9
8	RI	68	LEU	2.9
54	QY	41	LEU	2.9
33	QB	122	PHE	2.9
54	QY	54	GLN	2.9
32	XA	1029	C	2.9
39	QH	123	GLU	2.9
1	RA	2112	G	2.9
51	XT	101	GLY	2.9
32	XA	1531	A	2.9
50	QS	51	VAL	2.9
16	RU	86	ALA	2.9
40	XI	18	PHE	2.9
44	QM	5	ALA	2.9
8	RI	20	ASP	2.9
54	QY	89	GLU	2.9
54	XY	250	GLY	2.9
1	YA	2792	G	2.9
26	Y4	67	TYR	2.9
35	XD	68	TYR	2.9
44	XM	99	ARG	2.9
28	R6	17	LYS	2.9
31	R9	15	LYS	2.9
47	QP	35	LYS	2.9
40	QI	8	GLY	2.9
54	QY	86	LEU	2.9
28	Y6	18	ARG	2.8
40	QI	55	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
50	QS	79	THR	2.8
44	XM	13	LYS	2.8
31	R9	12	ASP	2.8
1	RA	1087	G	2.8
39	XH	55	GLY	2.8
47	XP	6	LEU	2.8
46	QO	87	ILE	2.8
26	R4	59	PHE	2.8
1	RA	2179	C	2.8
26	Y4	52	THR	2.8
54	XY	164	GLU	2.8
31	R9	11	CYS	2.8
35	XD	167	GLY	2.8
1	YA	229	A	2.8
1	YA	1077	A	2.8
10	RO	1	MET	2.8
31	R9	34	GLN	2.8
52	QU	8	THR	2.8
54	QY	95	THR	2.8
1	YA	2118	U	2.8
54	QY	210	GLY	2.8
44	XM	108	ARG	2.8
18	YW	13	SER	2.8
4	RE	58	ARG	2.8
36	QE	29	GLY	2.8
7	RH	89	ILE	2.8
34	XC	66	VAL	2.8
45	QN	7	ILE	2.8
50	XS	62	ILE	2.8
54	XY	80	VAL	2.8
3	YD	2	ALA	2.8
6	YG	26	GLN	2.8
54	XY	27	TYR	2.8
20	RY	58	GLY	2.8
29	R7	47	ARG	2.8
43	QL	5	PRO	2.8
40	QI	124	GLN	2.8
44	XM	95	GLY	2.8
50	QS	35	SER	2.8
54	XY	62	SER	2.8
25	R3	2	PRO	2.8
34	XC	201	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
34	QC	188	LEU	2.8
38	QG	152	ALA	2.8
47	QP	18	ARG	2.8
54	QY	13	ASP	2.8
41	QJ	65	LEU	2.8
41	XJ	98	ILE	2.8
43	QL	62	SER	2.8
8	YI	1	MET	2.8
51	XT	17	ARG	2.8
54	XY	60	ARG	2.8
1	RA	2167	U	2.8
21	RZ	113	ALA	2.8
36	XE	94	ALA	2.8
40	XI	15	ALA	2.8
50	XS	15	LEU	2.8
54	XY	39	ALA	2.8
32	QA	1006	C	2.8
50	QS	36	ARG	2.8
44	QM	103	THR	2.8
50	QS	39	THR	2.8
1	YA	1088	A	2.8
38	QG	11	GLN	2.8
22	R0	77	ARG	2.8
35	QD	49	ARG	2.8
36	QE	11	ILE	2.8
17	RV	1	MET	2.8
21	YZ	190	GLU	2.8
50	QS	6	LYS	2.8
22	Y0	9	SER	2.8
41	QJ	69	ASN	2.8
33	QB	131	PRO	2.8
54	XY	79	ASP	2.8
34	XC	179	ARG	2.8
1	RA	2118	U	2.8
7	RH	104	GLU	2.8
20	RY	106	LEU	2.8
32	XA	1039	C	2.8
33	QB	71	VAL	2.8
52	QU	10	ARG	2.8
32	XA	204	U	2.7
50	QS	38	SER	2.7
44	QM	92	HIS	2.7

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Mol	Chain	Res	Type	RSRZ
49	QR	56	THR	2.7
46	XO	83	GLU	2.7
1	RA	34	C	2.7
28	R6	2	ALA	2.7
28	R6	7	ILE	2.7
38	XG	153	HIS	2.7
1	RA	2808	U	2.7
23	R1	60	PHE	2.7
52	QU	21	TYR	2.7
52	QU	23	PRO	2.7
28	Y6	33	LYS	2.7
54	QY	79	ASP	2.7
28	Y6	40	CYS	2.7
54	XY	256	ARG	2.7
10	YO	91	LEU	2.7
28	R6	30	THR	2.7
32	XA	78	G	2.7
1	YA	2896	C	2.7
41	XJ	35	SER	2.7
19	RX	55	ASN	2.7
41	XJ	93	GLY	2.7
7	RH	17	VAL	2.7
39	XH	58	TYR	2.7
52	QU	9	ARG	2.7
51	XT	98	PRO	2.7
22	R0	76	GLY	2.7
6	RG	49	ASP	2.7
44	QM	117	VAL	2.7
52	XU	21	TYR	2.7
54	QY	240	ARG	2.7
21	RZ	155	LEU	2.7
1	YA	1103	A	2.7
6	YG	80	PHE	2.7
1	YA	2112	G	2.7
32	QA	78	G	2.7
35	XD	69	GLY	2.7
35	QD	167	GLY	2.7
48	QQ	11	VAL	2.7
54	XY	175	GLY	2.7
1	YA	2161	C	2.7
1	RA	2108	C	2.7
1	RA	2794(A)	C	2.7

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Mol	Chain	Res	Type	RSRZ
43	XL	26	ALA	2.7
54	XY	140	GLU	2.7
50	QS	31	ILE	2.7
33	QB	121	LEU	2.7
7	RH	41	MET	2.7
7	RH	49	VAL	2.7
23	R1	28	GLY	2.7
40	QI	101	PHE	2.7
50	XS	42	PRO	2.7
37	QF	88	VAL	2.7
52	XU	16	GLY	2.7
54	QY	20	VAL	2.7
54	XY	94	GLU	2.7
6	YG	25	TYR	2.7
1	YA	652(D)	G	2.7
1	YA	2128	C	2.7
1	RA	652(V)	G	2.7
34	QC	194	GLY	2.7
40	XI	8	GLY	2.7
54	XY	20	VAL	2.7
51	XT	12	ALA	2.7
54	XY	90	ALA	2.7
26	R4	65	ASP	2.7
54	QY	294	LYS	2.7
44	XM	116	THR	2.7
44	XM	10	PRO	2.7
7	RH	96	ALA	2.7
33	XB	61	LEU	2.6
38	XG	77	SER	2.6
43	XL	33	ARG	2.6
54	XY	77	LEU	2.6
54	XY	330	ASP	2.6
54	XY	119	PHE	2.6
1	YA	2135	A	2.6
35	QD	2	GLY	2.6
7	RH	47	GLU	2.6
39	XH	132	GLU	2.6
42	QK	104	GLN	2.6
22	R0	78	TYR	2.6
35	QD	4	TYR	2.6
54	XY	209	SER	2.6
34	QC	64	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
54	QY	290	GLN	2.6
8	RI	114	LEU	2.6
18	YW	111	HIS	2.6
28	R6	46	HIS	2.6
49	XR	29	PHE	2.6
20	YY	5	MET	2.6
47	QP	20	VAL	2.6
54	QY	45	ASP	2.6
1	YA	2150	U	2.6
49	QR	66	LEU	2.6
32	QA	160	A	2.6
26	Y4	45	GLY	2.6
50	XS	56	GLN	2.6
44	QM	81	LEU	2.6
1	RA	2151	G	2.6
50	QS	80	TYR	2.6
54	XY	217	PHE	2.6
1	RA	1508	A	2.6
8	RI	3	VAL	2.6
28	R6	52	VAL	2.6
34	XC	158	GLY	2.6
44	QM	100	GLY	2.6
54	QY	107	GLU	2.6
54	XY	329	ASP	2.6
39	XH	56	LYS	2.6
50	XS	77	THR	2.6
34	XC	164	ARG	2.6
45	QN	36	PHE	2.6
49	QR	29	PHE	2.6
1	YA	1063	G	2.6
1	YA	1074	G	2.6
35	XD	4	TYR	2.6
54	XY	8	ASN	2.6
35	XD	159	ARG	2.6
40	QI	7	THR	2.6
54	QY	40	GLU	2.6
21	YZ	199	LYS	2.6
36	XE	20	GLN	2.6
50	QS	71	LEU	2.6
1	RA	6	A	2.6
28	Y6	12	GLU	2.6
48	QQ	100	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
40	QI	85	LEU	2.6
34	XC	189	ALA	2.6
54	QY	277	ASP	2.6
11	YP	118	GLY	2.6
34	QC	161	GLU	2.6
1	RA	652(W)	C	2.6
28	R6	28	ARG	2.6
32	QA	1019	C	2.6
15	RT	22	PHE	2.6
14	RS	33	LYS	2.6
42	QK	14	VAL	2.6
14	RS	97	ARG	2.6
35	QD	146	ILE	2.6
1	RA	2104	G	2.6
47	XP	39	TYR	2.6
33	XB	165	VAL	2.6
47	QP	63	GLY	2.6
20	RY	31	LEU	2.6
20	RY	44	ILE	2.6
40	QI	63	ILE	2.6
54	QY	268	THR	2.6
6	RG	178	PHE	2.5
13	YR	41	ALA	2.5
54	XY	101	ALA	2.5
5	YF	27	GLU	2.5
1	YA	2120	G	2.5
32	QA	1037	C	2.5
38	XG	141	VAL	2.5
50	QS	12	ASP	2.5
41	XJ	37	PRO	2.5
42	QK	95	ILE	2.5
9	RN	10	GLU	2.5
40	XI	55	ALA	2.5
29	Y7	46	VAL	2.5
37	QF	6	VAL	2.5
32	QA	1000	U	2.5
34	XC	101	LEU	2.5
1	YA	277	C	2.5
3	RD	271	ILE	2.5
26	R4	29	PRO	2.5
48	XQ	27	PHE	2.5
54	QY	334	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
32	XA	1042	G	2.5
16	RU	117	GLN	2.5
31	Y9	24	TYR	2.5
40	QI	61	ALA	2.5
44	XM	86	CYS	2.5
6	YG	47	LYS	2.5
11	RP	130	PHE	2.5
41	QJ	39	PRO	2.5
7	RH	53	GLU	2.5
8	YI	117	GLU	2.5
1	YA	1099	G	2.5
7	RH	109	PHE	2.5
40	XI	33	PHE	2.5
48	QQ	75	ARG	2.5
32	QA	90	U	2.5
33	QB	188	ALA	2.5
1	YA	6	A	2.5
47	XP	48	TRP	2.5
50	QS	45	VAL	2.5
14	RS	56	LEU	2.5
49	QR	51	LEU	2.5
1	RA	352	G	2.5
46	QO	15	PHE	2.5
3	RD	181	GLU	2.5
20	RY	46	LYS	2.5
23	Y1	81	LYS	2.5
54	QY	46	VAL	2.5
8	YI	12	LEU	2.5
1	RA	652(C)	A	2.5
54	QY	270	ILE	2.5
37	QF	90	VAL	2.5
43	XL	60	LEU	2.5
7	RH	30	LYS	2.5
1	YA	1079	C	2.5
1	RA	2129	C	2.5
37	QF	95	GLU	2.5
12	RQ	6	ARG	2.5
39	XH	53	VAL	2.5
40	XI	62	TYR	2.5
50	XS	16	LEU	2.5
54	XY	253	HIS	2.5
54	XY	275	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
54	QY	217	PHE	2.5
28	Y6	7	ILE	2.5
41	QJ	64	GLU	2.5
7	RH	169	VAL	2.5
23	R1	98	LEU	2.5
35	XD	23	GLY	2.5
50	XS	20	LEU	2.5
21	YZ	118	GLN	2.5
54	QY	12	GLN	2.5
6	RG	8	LYS	2.5
47	XP	19	ILE	2.5
52	XU	7	ARG	2.5
26	R4	19	GLY	2.5
32	QA	998	G	2.5
1	YA	2105	C	2.5
28	R6	3	SER	2.5
32	QA	1035	A	2.5
34	XC	167	TRP	2.5
36	QE	14	ARG	2.5
20	RY	12	THR	2.5
39	QH	90	GLY	2.5
54	QY	139	THR	2.5
51	XT	14	LYS	2.5
54	XY	204	LYS	2.5
1	RA	1063	G	2.5
39	QH	99	GLU	2.5
32	XA	1037	C	2.4
1	YA	2171	A	2.4
6	RG	3	LEU	2.4
19	RX	92	LEU	2.4
34	XC	12	LEU	2.4
34	XC	159	GLY	2.4
7	RH	94	TYR	2.4
40	QI	62	TYR	2.4
48	XQ	7	THR	2.4
52	XU	5	ASP	2.4
54	XY	166	ILE	2.4
7	RH	56	SER	2.4
54	XY	214	HIS	2.4
23	Y1	23	LYS	2.4
1	YA	2157	G	2.4
26	R4	50	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
54	XY	76	GLY	2.4
4	YE	151	TYR	2.4
28	R6	35	GLU	2.4
49	QR	63	GLN	2.4
30	R8	21	LYS	2.4
39	QH	4	ASP	2.4
41	XJ	8	LEU	2.4
51	XT	20	LEU	2.4
54	QY	184	SER	2.4
21	YZ	189	ALA	2.4
42	QK	32	ILE	2.4
28	Y6	48	VAL	2.4
42	QK	98	LEU	2.4
52	QU	2	GLY	2.4
54	XY	110	LEU	2.4
28	Y6	28	ARG	2.4
3	YD	276	LYS	2.4
25	R3	19	GLN	2.4
1	YA	1078	U	2.4
20	YY	14	LEU	2.4
22	R0	23	VAL	2.4
32	XA	1260	C	2.4
32	QA	1140	C	2.4
41	QJ	8	LEU	2.4
8	RI	14	ASP	2.4
8	RI	133	HIS	2.4
20	YY	107	ASP	2.4
54	XY	82	GLY	2.4
54	XY	228	ASP	2.4
20	YY	47	LYS	2.4
54	XY	352	SER	2.4
33	XB	214	ILE	2.4
9	RN	9	VAL	2.4
28	R6	48	VAL	2.4
33	XB	63	MET	2.4
36	XE	18	ARG	2.4
46	QO	2	PRO	2.4
51	XT	10	LEU	2.4
1	YA	2109	U	2.4
1	YA	2178	C	2.4
31	R9	14	CYS	2.4
38	QG	62	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
1	RA	887	A	2.4
1	RA	2134	A	2.4
1	RA	2160	G	2.4
33	XB	58	ILE	2.4
38	QG	120	ILE	2.4
51	XT	84	LEU	2.4
34	XC	165	THR	2.4
18	RW	3	ALA	2.4
47	XP	7	ALA	2.4
52	QU	14	TRP	2.4
54	QY	152	TYR	2.4
1	RA	2175	C	2.4
34	XC	190	ARG	2.4
51	XT	41	ILE	2.4
54	QY	150	ARG	2.4
33	QB	115	LEU	2.4
33	QB	136	VAL	2.4
34	QC	153	VAL	2.4
1	YA	1062	G	2.4
32	QA	1026	G	2.4
54	XY	97	ASN	2.4
47	XP	56	ALA	2.4
54	QY	10	ARG	2.4
54	QY	98	GLU	2.4
54	XY	297	GLU	2.4
1	RA	2177	C	2.4
13	RR	6	SER	2.4
24	R2	56	GLN	2.4
29	R7	1	MET	2.4
31	Y9	21	GLY	2.4
40	QI	87	GLN	2.4
41	QJ	10	GLY	2.4
46	QO	59	MET	2.4
50	QS	66	MET	2.4
54	XY	75	GLN	2.4
9	RN	73	THR	2.4
14	RS	8	GLU	2.4
25	R3	30	ARG	2.4
27	Y5	52	TYR	2.4
31	R9	19	ARG	2.4
35	XD	205	GLU	2.4
54	XY	172	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
6	RG	29	TRP	2.4
23	Y1	98	LEU	2.4
31	Y9	25	VAL	2.4
54	QY	318	GLY	2.4
52	XU	22	ARG	2.4
7	RH	106	THR	2.4
22	R0	61	ALA	2.4
16	RU	88	ILE	2.4
28	Y6	47	THR	2.4
37	QF	99	ALA	2.4
54	XY	338	THR	2.4
54	XY	344	ASN	2.4
54	XY	109	LYS	2.4
6	RG	97	ASP	2.4
33	XB	187	LEU	2.4
54	QY	19	ASP	2.4
40	QI	14	VAL	2.4
1	RA	2150	U	2.4
31	Y9	6	SER	2.4
43	XL	22	SER	2.4
45	XN	37	PHE	2.4
54	QY	120	SER	2.4
47	XP	34	GLU	2.4
54	XY	206	PRO	2.4
36	QE	12	LEU	2.4
54	XY	103	LEU	2.4
8	RI	19	VAL	2.3
20	RY	97	ARG	2.3
25	R3	3	ARG	2.3
33	QB	101	MET	2.3
7	RH	80	SER	2.3
26	R4	16	CYS	2.3
54	XY	106	LEU	2.3
4	YE	173	VAL	2.3
34	QC	156	ARG	2.3
6	RG	116	ASP	2.3
1	YA	2062	A	2.3
28	Y6	2	ALA	2.3
19	RX	28	PHE	2.3
32	QA	79	G	2.3
45	QN	4	LYS	2.3
54	XY	135	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
32	QA	1007	C	2.3
37	XF	1	MET	2.3
1	YA	2126	A	2.3
16	RU	83	LEU	2.3
33	XB	130	ARG	2.3
36	QE	31	LEU	2.3
37	QF	89	MET	2.3
31	Y9	12	ASP	2.3
54	QY	231	ASP	2.3
32	QA	1034	G	2.3
7	RH	25	LYS	2.3
54	QY	90	ALA	2.3
54	XY	87	ALA	2.3
8	YI	107	VAL	2.3
41	QJ	34	VAL	2.3
32	XA	1532	U	2.3
7	RH	34	GLU	2.3
21	YZ	98	MET	2.3
50	XS	73	GLU	2.3
33	QB	135	GLN	2.3
37	XF	99	ALA	2.3
40	XI	47	LEU	2.3
22	R0	69	PHE	2.3
37	XF	9	VAL	2.3
1	YA	2121	G	2.3
33	QB	99	GLY	2.3
32	QA	723	U	2.3
40	QI	9	ARG	2.3
53	XV	17(A)	U	2.3
32	QA	1005	A	2.3
44	QM	43	THR	2.3
54	QY	239	LEU	2.3
3	YD	273	ARG	2.3
2	RB	91	C	2.3
54	XY	218	SER	2.3
51	QT	56	MET	2.3
1	YA	273(B)	U	2.3
1	RA	2157	G	2.3
8	RI	116	LEU	2.3
40	QI	19	LEU	2.3
34	QC	165	THR	2.3
39	XH	52	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
54	QY	215	THR	2.3
54	XY	296	TYR	2.3
7	RH	44	VAL	2.3
8	RI	45	LYS	2.3
41	QJ	98	ILE	2.3
18	RW	39	THR	2.3
1	RA	1103	A	2.3
54	XY	107	GLU	2.3
8	RI	132	PRO	2.3
18	YW	74	ALA	2.3
31	R9	35	ARG	2.3
41	QJ	62	HIS	2.3
50	XS	57	HIS	2.3
38	XG	127	ALA	2.3
42	QK	25	TYR	2.3
15	YT	38	ASN	2.3
46	QO	86	GLY	2.3
25	Y3	57	GLU	2.3
54	XY	9	ASN	2.3
1	RA	2115	G	2.3
39	QH	133	LEU	2.3
7	YH	110	SER	2.3
7	RH	110	SER	2.3
8	RI	4	ILE	2.3
14	YS	53	SER	2.3
23	R1	21	ARG	2.3
38	XG	6	ARG	2.3
44	XM	110	ARG	2.3
7	RH	50	VAL	2.3
34	QC	163	ALA	2.3
54	QY	250	GLY	2.3
34	QC	191	THR	2.3
41	QJ	73	ASP	2.3
54	XY	342	THR	2.3
21	YZ	198	LYS	2.3
43	XL	32	PHE	2.3
47	QP	4	ILE	2.3
1	RA	1088	A	2.3
31	R9	20	HIS	2.3
40	XI	17	VAL	2.3
41	QJ	35	SER	2.3
33	XB	137	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
41	XJ	69	ASN	2.2
50	QS	44	MET	2.2
52	QU	7	ARG	2.2
54	QY	344	ASN	2.2
20	RY	95	LYS	2.2
32	QA	202	U	2.2
54	XY	163	THR	2.2
8	RI	111	PRO	2.2
20	RY	89	PHE	2.2
31	Y9	26	ILE	2.2
33	XB	131	PRO	2.2
44	QM	97	PRO	2.2
20	RY	48	ALA	2.2
34	QC	170	GLN	2.2
44	XM	32	GLU	2.2
44	QM	61	GLU	2.2
54	QY	105	ALA	2.2
8	YI	30	LEU	2.2
33	XB	121	LEU	2.2
44	XM	16	ASP	2.2
54	QY	208	ASP	2.2
54	QY	313	ASN	2.2
37	QF	97	PHE	2.2
44	QM	113	PRO	2.2
54	QY	340	VAL	2.2
1	YA	280	C	2.2
7	RH	18	GLU	2.2
44	XM	92	HIS	2.2
36	QE	10	MET	2.2
35	QD	158	ILE	2.2
6	YG	68	PRO	2.2
25	R3	58	VAL	2.2
40	QI	103	THR	2.2
47	XP	14	ASN	2.2
6	RG	136	ARG	2.2
48	QQ	24	GLU	2.2
50	XS	30	LEU	2.2
45	QN	37	PHE	2.2
6	YG	49	ASP	2.2
36	XE	130	ASN	2.2
49	QR	86	VAL	2.2
9	RN	11	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
31	Y9	2	LYS	2.2
31	Y9	5	ALA	2.2
32	QA	1248	A	2.2
41	QJ	22	LYS	2.2
42	XK	98	LEU	2.2
1	YA	2127	G	2.2
1	RA	1719	G	2.2
32	XA	1024	G	2.2
39	QH	44	PHE	2.2
50	XS	45	VAL	2.2
54	QY	166	ILE	2.2
26	Y4	51	ASP	2.2
34	QC	158	GLY	2.2
35	XD	207	TYR	2.2
44	XM	115	LYS	2.2
54	QY	123	TYR	2.2
41	QJ	68	HIS	2.2
14	RS	20	ARG	2.2
20	YY	34	LYS	2.2
31	Y9	13	LYS	2.2
31	R9	2	LYS	2.2
33	XB	139	LYS	2.2
1	RA	2166	G	2.2
13	RR	107	ASP	2.2
40	XI	54	ASP	2.2
6	RG	34	LEU	2.2
22	R0	37	LEU	2.2
54	QY	280	GLN	2.2
24	R2	29	LYS	2.2
34	QC	39	ILE	2.2
36	QE	13	ILE	2.2
11	YP	52	GLU	2.2
26	Y4	54	GLY	2.2
40	XI	6	GLY	2.2
54	QY	249	ALA	2.2
8	YI	139	GLN	2.2
17	RV	29	PRO	2.2
40	XI	102	LEU	2.2
9	RN	70	LYS	2.2
19	RX	68	ARG	2.2
39	XH	116	LYS	2.2
7	RH	158	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
11	RP	1	MET	2.2
27	Y5	60	VAL	2.2
47	QP	59	TRP	2.2
50	XS	11	VAL	2.2
54	XY	102	GLU	2.2
7	RH	100	GLY	2.2
1	RA	2135	A	2.2
8	RI	72	LEU	2.2
28	Y6	37	ARG	2.2
36	XE	25	ARG	2.2
1	YA	652(W)	C	2.2
4	RE	55	ASN	2.2
32	XA	390	C	2.2
41	QJ	83	GLU	2.2
22	Y0	42	GLY	2.2
20	RY	47	LYS	2.2
33	XB	124	SER	2.2
36	QE	17	ALA	2.2
41	XJ	27	ALA	2.2
44	XM	87	TYR	2.2
1	YA	1057	A	2.2
1	RA	2892	A	2.2
11	YP	87	ASP	2.2
15	YT	87	ASP	2.2
54	XY	186	ASP	2.2
39	QH	111	ILE	2.2
54	QY	272	THR	2.2
54	XY	215	THR	2.2
21	RZ	3	TYR	2.2
45	QN	10	ALA	2.2
54	QY	106	LEU	2.2
54	QY	237	ALA	2.2
1	RA	2181	G	2.2
32	XA	1030(B)	G	2.2
54	XY	355	GLN	2.2
18	RW	94	ASP	2.2
42	QK	119	CYS	2.2
39	QH	132	GLU	2.2
54	XY	68	ASP	2.2
33	QB	130	ARG	2.2
44	QM	88	ARG	2.2
51	QT	71	THR	2.2

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Mol	Chain	Res	Type	RSRZ
46	XO	85	LEU	2.1
54	XY	25	LEU	2.1
50	XS	76	PRO	2.1
7	RH	42	ARG	2.1
14	RS	59	LYS	2.1
15	YT	107	ASP	2.1
54	QY	42	GLU	2.1
1	YA	275	G	2.1
17	RV	67	GLY	2.1
32	XA	79	G	2.1
44	QM	95	GLY	2.1
48	QQ	6	LEU	2.1
1	YA	2163	C	2.1
4	YE	87	GLU	2.1
34	QC	131	ARG	2.1
54	XY	340	VAL	2.1
51	XT	36	LEU	2.1
54	XY	295	LEU	2.1
16	RU	72	HIS	2.1
19	RX	5	TYR	2.1
51	QT	66	ALA	2.1
1	YA	2148	G	2.1
8	RI	85	GLU	2.1
23	Y1	21	ARG	2.1
23	Y1	76	ARG	2.1
23	R1	10	LYS	2.1
26	R4	3	GLU	2.1
52	XU	10	ARG	2.1
38	QG	141	VAL	2.1
38	XG	89	MET	2.1
38	QG	14	PRO	2.1
42	QK	118	GLY	2.1
1	RA	2130	U	2.1
54	XY	312	ASP	2.1
3	YD	254	THR	2.1
35	XD	22	LYS	2.1
36	QE	16	THR	2.1
47	QP	48	TRP	2.1
54	QY	319	TRP	2.1
22	R0	68	GLU	2.1
25	R3	34	GLU	2.1
54	QY	167	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
20	RY	32	PRO	2.1
30	R8	25	MET	2.1
4	RE	182	LEU	2.1
7	YH	103	LEU	2.1
21	RZ	5	LEU	2.1
32	XA	1004	A	2.1
33	XB	215	LEU	2.1
8	RI	96	ASP	2.1
21	RZ	93	ASP	2.1
21	RZ	156	LYS	2.1
32	XA	1137	C	2.1
54	QY	203	ARG	2.1
54	XY	117	ARG	2.1
33	QB	187	LEU	2.1
46	XO	31	LEU	2.1
52	QU	20	LYS	2.1
1	YA	1093	G	2.1
1	YA	2159	G	2.1
8	YI	20	ASP	2.1
41	XJ	34	VAL	2.1
54	QY	233	GLU	2.1
8	RI	71	ILE	2.1
54	QY	232	ILE	2.1
54	XY	173	VAL	2.1
5	RF	148	LEU	2.1
54	QY	23	GLY	2.1
39	QH	98	LYS	2.1
34	QC	23	TYR	2.1
25	R3	39	ASP	2.1
54	XY	298	VAL	2.1
1	YA	362	U	2.1
1	YA	1089	G	2.1
1	RA	1044	G	2.1
22	Y0	76	GLY	2.1
35	XD	89	THR	2.1
35	QD	3	ARG	2.1
44	XM	94	ARG	2.1
44	QM	56	LEU	2.1
47	XP	35	LYS	2.1
50	XS	44	MET	2.1
43	QL	32	PHE	2.1
16	YU	35	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
16	RU	116	ALA	2.1
50	QS	50	ALA	2.1
50	QS	64	GLU	2.1
20	YY	45	VAL	2.1
26	R4	22	ILE	2.1
40	XI	117	HIS	2.1
19	YX	13	LEU	2.1
44	XM	89	GLY	2.1
2	RB	90	A	2.1
47	QP	1	MET	2.1
27	R5	28	PRO	2.1
32	XA	1028	C	2.1
32	QA	999	C	2.1
4	YE	4	ILE	2.1
33	XB	222	ILE	2.1
52	QU	15	ARG	2.1
14	YS	24	LEU	2.1
35	XD	21	LEU	2.1
38	XG	81	GLY	2.1
48	QQ	76	LEU	2.1
6	RG	155	MET	2.1
6	RG	80	PHE	2.1
50	XS	39	THR	2.1
54	QY	97	ASN	2.1
7	RH	46	GLU	2.1
16	RU	113	ALA	2.1
33	XB	96	ARG	2.1
33	QB	96	ARG	2.1
43	XL	16	GLU	2.1
54	QY	220	ALA	2.1
1	RA	1104	C	2.1
32	XA	89	C	2.1
26	Y4	65	ASP	2.1
32	QA	1042	G	2.1
40	XI	50	LEU	2.1
41	XJ	73	ASP	2.1
46	QO	89	GLY	2.1
54	XY	227	ASP	2.1
11	RP	38	GLN	2.1
8	YI	43	ASN	2.1
18	YW	92	ARG	2.1
20	RY	88	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
32	XA	1000	U	2.1
47	XP	57	ARG	2.1
54	QY	85	GLU	2.1
35	XD	70	ILE	2.1
54	QY	130	LEU	2.1
34	XC	156	ARG	2.0
45	XN	35	ARG	2.0
48	XQ	58	GLU	2.0
48	QQ	91	ARG	2.0
52	XU	6	ARG	2.0
31	R9	3	VAL	2.0
51	QT	41	ILE	2.0
33	QB	228	GLY	2.0
54	QY	153	LEU	2.0
16	YU	31	SER	2.0
19	YX	78	LYS	2.0
20	RY	9	LYS	2.0
7	RH	51	ARG	2.0
32	XA	1447	A	2.0
35	QD	181	MET	2.0
50	QS	47	HIS	2.0
8	RI	64	GLU	2.0
41	QJ	61	GLU	2.0
44	QM	2	ALA	2.0
6	RG	152	LEU	2.0
36	XE	77	PRO	2.0
36	XE	129	ILE	2.0
1	YA	2122	U	2.0
32	XA	1034	G	2.0
50	QS	82	GLY	2.0
22	Y0	41	ARG	2.0
38	QG	43	PHE	2.0
5	RF	77	ASP	2.0
23	R1	19	GLN	2.0
41	QJ	59	SER	2.0
32	XA	532	A	2.0
49	QR	60	ALA	2.0
54	QY	37	VAL	2.0
1	YA	34	C	2.0
6	RG	7	LEU	2.0
19	RX	63	LYS	2.0
36	XE	119	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
53	XV	17	C	2.0
26	R4	64	GLY	2.0
1	RA	614(B)	U	2.0
21	RZ	98	MET	2.0
32	XA	202	U	2.0
21	YZ	60	GLU	2.0
51	XT	45	GLN	2.0
19	RX	69	TYR	2.0
26	R4	21	VAL	2.0
37	QF	63	TYR	2.0
47	QP	29	ASP	2.0
54	XY	11	ILE	2.0
54	XY	121	GLY	2.0
54	XY	269	GLY	2.0
7	RH	117	PRO	2.0
28	R6	29	ASN	2.0
32	XA	811	C	2.0
40	XI	101	PHE	2.0
51	QT	98	PRO	2.0
7	RH	32	GLU	2.0
35	XD	179	GLU	2.0
21	YZ	150	LEU	2.0
40	QI	126	SER	2.0
49	XR	54	ARG	2.0
54	XY	350	ASP	2.0
9	RN	81	GLY	2.0
22	Y0	52	GLY	2.0
6	YG	23	PHE	2.0
41	QJ	91	PRO	2.0
1	YA	278	A	2.0
32	XA	1044	A	2.0
33	QB	129	GLU	2.0
32	XA	76	C	2.0
50	XS	63	THR	2.0
44	XM	23	TYR	2.0

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
32	UR3	XA	1498	21/22	0.96	0.22	-	74,83,87,88	0
1	5MC	RA	1942	21/22	0.94	0.23	-	81,85,88,90	0
1	5MC	YA	1942	21/22	0.93	0.23	-	76,81,87,88	0
43	0TD	XL	92	10/11	0.95	0.26	-	85,89,93,95	0
32	2MG	QA	1207	24/25	0.92	0.19	-	89,91,96,97	0
1	5MU	YA	1915	21/22	0.86	0.21	-	85,89,92,95	0
32	5MC	XA	1407	21/22	0.94	0.22	-	81,84,89,91	0
1	PSU	RA	1917	20/21	0.92	0.16	-	84,87,91,91	0
32	MA6	QA	1519	24/25	0.94	0.28	-	82,85,85,87	0
1	2MU	RA	2552	21/23	0.95	0.27	-	75,82,84,87	0
1	4OC	YA	1920	21/23	0.94	0.23	-	81,83,85,87	0
32	5MC	XA	1400	21/22	0.95	0.21	-	78,85,86,88	0
54	MEQ	XY	252	10/11	0.94	0.33	-	86,87,91,91	0
32	PSU	XA	516	20/21	0.91	0.16	-	89,90,93,94	0
32	M2G	XA	966	25/26	0.92	0.19	-	83,87,94,94	0
1	PSU	YA	1911	20/21	0.95	0.18	-	79,85,88,90	0
1	5MU	YA	1939	21/22	0.95	0.27	-	72,77,82,84	0
1	2MA	RA	2503	23/24	0.95	0.25	-	75,81,83,84	0
32	5MC	XA	1404	21/22	0.96	0.18	-	79,84,85,87	0
1	2MU	YA	2552	21/23	0.93	0.29	-	74,78,86,87	0
1	4OC	RA	1920	21/23	0.93	0.20	-	83,85,89,92	0
43	0TD	QL	92	10/11	0.94	0.20	-	87,90,94,95	0
32	MA6	QA	1518	24/25	0.93	0.27	-	82,86,88,89	0
32	5MC	QA	967	21/22	0.94	0.20	-	83,87,90,93	0
54	MEQ	QY	252	10/11	0.93	0.32	-	85,87,90,90	0
32	4OC	XA	1402	22/23	0.90	0.28	-	83,85,87,89	0
32	PSU	QA	516	20/21	0.90	0.15	-	87,89,91,91	0
1	5MC	YA	1962	21/22	0.96	0.19	-	73,81,85,85	0
32	4OC	QA	1402	22/23	0.89	0.24	-	84,87,89,90	0
1	PSU	RA	1911	20/21	0.95	0.14	-	82,85,88,89	0
32	5MC	QA	1404	21/22	0.94	0.20	-	83,86,88,88	0
32	2MG	XA	1207	24/25	0.90	0.22	-	88,90,95,97	0
32	MA6	XA	1518	24/25	0.96	0.29	-	70,82,82,83	0
1	2MA	YA	2503	23/24	0.94	0.29	-	72,78,79,81	0
1	PSU	YA	2605	20/21	0.94	0.28	-	69,77,81,83	0
32	7MG	XA	527	24/25	0.93	0.24	-	83,86,87,88	0
32	M2G	QA	966	25/26	0.93	0.18	-	85,87,91,93	0
32	MA6	XA	1519	24/25	0.96	0.27	-	76,83,84,86	0
1	5MU	RA	1939	21/22	0.95	0.23	-	76,82,84,85	0
1	PSU	RA	2605	20/21	0.93	0.25	-	72,79,84,84	0
1	PSU	YA	1917	20/21	0.93	0.18	-	81,86,88,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	5MC	QA	1400	21/22	0.94	0.24	-	85,89,90,90	0
32	UR3	QA	1498	21/22	0.90	0.27	-	80,84,87,92	0
32	5MC	QA	1407	21/22	0.96	0.16	-	80,83,85,86	0
1	5MC	RA	1962	21/22	0.94	0.18	-	76,84,87,87	0
32	5MC	XA	967	21/22	0.93	0.25	-	87,88,89,89	0
1	5MU	RA	1915	21/22	0.89	0.13	-	84,89,93,97	0
32	7MG	QA	527	24/25	0.93	0.21	-	85,87,87,88	0
1	OMG	YA	2251	24/25	0.97	0.28	-	72,78,83,84	0
1	OMG	RA	2251	24/25	0.95	0.27	-	80,83,85,85	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3324	1/1	0.92	1.09	154.64	62,62,62,62	0
56	MG	XA	1781	1/1	0.84	1.36	87.52	79,79,79,79	0
56	MG	YA	3360	1/1	0.94	1.11	82.31	62,62,62,62	0
56	MG	YA	3343	1/1	0.94	0.83	71.35	62,62,62,62	0
56	MG	YA	3247	1/1	0.40	0.74	65.95	80,80,80,80	0
56	MG	RA	3444	1/1	0.90	1.29	64.47	62,62,62,62	0
56	MG	RA	3122	1/1	0.43	1.93	64.04	102,102,102,102	0
56	MG	RA	3854	1/1	0.61	1.73	63.73	87,87,87,87	0
56	MG	YA	3102	1/1	0.55	1.80	60.80	101,101,101,101	0
56	MG	YA	3295	1/1	0.80	1.09	59.63	62,62,62,62	0
56	MG	YA	3131	1/1	0.60	1.26	58.98	105,105,105,105	0
56	MG	RA	3697	1/1	0.72	2.04	58.95	101,101,101,101	0
56	MG	YA	3582	1/1	0.74	1.24	57.95	74,74,74,74	0
56	MG	QA	1704	1/1	0.24	0.78	57.72	89,89,89,89	0
56	MG	YA	3058	1/1	0.40	1.08	55.29	93,93,93,93	0
56	MG	QA	1771	1/1	-0.14	1.08	55.04	93,93,93,93	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	XA	1780	1/1	0.51	1.11	52.98	74,74,74,74	0
56	MG	YA	3710	1/1	0.25	1.19	50.96	80,80,80,80	0
56	MG	RA	3588	1/1	0.79	1.02	50.37	76,76,76,76	0
56	MG	YA	3374	1/1	0.76	0.98	49.44	75,75,75,75	0
56	MG	RA	3394	1/1	0.97	0.91	47.40	62,62,62,62	0
56	MG	XA	1623	1/1	-0.04	0.50	47.17	83,83,83,83	0
56	MG	RA	3754	1/1	0.88	0.82	46.82	62,62,62,62	0
56	MG	RA	3029	1/1	0.69	1.46	46.68	104,104,104,104	0
56	MG	YA	3320	1/1	0.26	1.08	44.91	87,87,87,87	0
56	MG	RA	3205	1/1	0.23	1.13	44.88	87,87,87,87	0
56	MG	RA	3631	1/1	0.32	1.07	43.28	94,94,94,94	0
56	MG	YA	3745	1/1	0.82	0.96	42.51	104,104,104,104	0
56	MG	RA	3773	1/1	0.97	0.76	42.15	70,70,70,70	0
56	MG	RA	3829	1/1	-0.04	1.51	42.13	96,96,96,96	0
56	MG	RA	3221	1/1	0.83	1.14	41.66	92,92,92,92	0
56	MG	RA	3141	1/1	0.65	1.21	41.13	92,92,92,92	0
56	MG	YA	3166	1/1	0.72	0.96	40.74	109,109,109,109	0
56	MG	YA	3705	1/1	0.38	1.20	40.41	78,78,78,78	0
56	MG	YA	3419	1/1	0.87	0.74	39.71	77,77,77,77	0
56	MG	RA	3882	1/1	0.77	1.20	39.12	87,87,87,87	0
56	MG	RA	3751	1/1	0.49	1.29	38.87	83,83,83,83	0
56	MG	YA	3401	1/1	0.94	0.69	38.86	62,62,62,62	0
56	MG	YA	3409	1/1	0.42	1.29	38.17	95,95,95,95	0
56	MG	RA	3537	1/1	-0.03	1.01	37.60	84,84,84,84	0
56	MG	YA	3647	1/1	0.74	1.16	37.47	62,62,62,62	0
56	MG	RA	3116	1/1	0.63	1.16	37.42	104,104,104,104	0
56	MG	RA	3094	1/1	0.86	1.24	35.97	85,85,85,85	0
56	MG	YD	303	1/1	0.78	1.07	35.16	84,84,84,84	0
56	MG	RA	3850	1/1	0.44	0.56	35.15	72,72,72,72	0
56	MG	RA	3572	1/1	0.36	0.56	35.03	81,81,81,81	0
56	MG	QA	1780	1/1	0.33	1.33	34.95	80,80,80,80	0
56	MG	YA	3316	1/1	0.83	0.62	34.86	62,62,62,62	0
56	MG	RA	3738	1/1	0.40	0.61	34.81	93,93,93,93	0
56	MG	YA	3630	1/1	0.89	0.86	34.59	66,66,66,66	0
56	MG	RA	3436	1/1	0.80	1.11	34.43	63,63,63,63	0
56	MG	RA	3088	1/1	0.82	1.03	34.14	98,98,98,98	0
56	MG	RA	3486	1/1	0.47	0.78	33.57	83,83,83,83	0
56	MG	RA	3118	1/1	0.80	0.72	33.04	96,96,96,96	0
56	MG	XA	1611	1/1	0.75	0.65	32.98	81,81,81,81	0
56	MG	YA	3314	1/1	0.66	0.60	31.85	69,69,69,69	0
56	MG	YA	3518	1/1	0.13	0.88	31.84	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
56	MG	YA	3694	1/1	0.23	0.89	31.80	82,82,82,82	0
56	MG	RA	3101	1/1	0.69	0.82	31.60	95,95,95,95	0
56	MG	QA	1625	1/1	0.71	0.53	31.18	88,88,88,88	0
56	MG	RA	3142	1/1	0.39	0.49	31.13	85,85,85,85	0
56	MG	YA	3633	1/1	0.23	1.20	30.47	95,95,95,95	0
56	MG	QA	1614	1/1	0.78	0.80	30.42	85,85,85,85	0
56	MG	RA	3408	1/1	0.96	0.76	30.36	62,62,62,62	0
56	MG	RA	3208	1/1	0.59	0.68	30.23	89,89,89,89	0
56	MG	YA	3509	1/1	-0.35	0.79	30.11	97,97,97,97	0
56	MG	XA	1627	1/1	0.74	0.97	30.10	80,80,80,80	0
56	MG	YA	3747	1/1	0.74	1.25	29.96	98,98,98,98	0
56	MG	RA	3889	1/1	0.88	0.66	29.90	62,62,62,62	0
56	MG	YA	3350	1/1	0.79	0.58	29.33	76,76,76,76	0
56	MG	RA	3677	1/1	-0.04	1.12	28.86	86,86,86,86	0
56	MG	YA	3476	1/1	0.93	0.93	28.80	62,62,62,62	0
56	MG	RA	3634	1/1	0.60	0.61	28.68	79,79,79,79	0
56	MG	YA	3648	1/1	0.84	0.63	28.66	62,62,62,62	0
56	MG	RA	3903	1/1	0.95	0.47	28.50	79,79,79,79	0
56	MG	RA	3470	1/1	0.95	0.80	28.47	62,62,62,62	0
56	MG	QA	1849	1/1	0.51	1.44	28.34	76,76,76,76	0
56	MG	RA	3302	1/1	0.91	0.77	28.10	91,91,91,91	0
56	MG	RA	3163	1/1	0.85	1.46	27.99	88,88,88,88	0
56	MG	RA	3603	1/1	0.17	1.55	27.87	90,90,90,90	0
56	MG	RA	3132	1/1	0.71	0.39	27.65	95,95,95,95	0
56	MG	RA	3364	1/1	0.70	0.95	27.27	74,74,74,74	0
56	MG	YA	3391	1/1	0.93	0.79	26.90	62,62,62,62	0
56	MG	RA	3027	1/1	0.15	0.84	26.83	112,112,112,112	0
56	MG	RA	3924	1/1	0.47	0.66	26.76	89,89,89,89	0
56	MG	XA	1645	1/1	0.97	0.64	26.66	82,82,82,82	0
56	MG	RA	3252	1/1	0.95	0.68	26.56	89,89,89,89	0
56	MG	YA	3611	1/1	0.95	1.04	26.52	62,62,62,62	0
56	MG	QA	1814	1/1	0.72	0.89	25.95	89,89,89,89	0
56	MG	RA	3392	1/1	0.87	0.80	25.93	62,62,62,62	0
56	MG	RA	3290	1/1	0.69	1.46	25.71	99,99,99,99	0
56	MG	RA	3412	1/1	0.90	0.46	25.59	62,62,62,62	0
56	MG	RA	3839	1/1	0.94	0.86	25.57	62,62,62,62	0
56	MG	RA	3419	1/1	0.92	0.78	25.48	62,62,62,62	0
56	MG	RA	3941	1/1	0.23	0.78	25.44	87,87,87,87	0
56	MG	RB	201	1/1	0.78	0.76	25.27	104,104,104,104	0
56	MG	YA	3650	1/1	0.67	0.90	25.08	76,76,76,76	0
56	MG	RA	3917	1/1	0.54	0.49	24.90	92,92,92,92	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3552	1/1	0.78	0.68	24.88	65,65,65,65	0
56	MG	RA	3022	1/1	0.72	0.85	24.82	98,98,98,98	0
56	MG	RA	3616	1/1	0.89	0.86	24.52	62,62,62,62	0
56	MG	RD	313	1/1	0.75	0.86	24.48	84,84,84,84	0
56	MG	YA	3088	1/1	0.84	0.97	24.43	90,90,90,90	0
56	MG	YA	3570	1/1	0.92	0.77	24.42	62,62,62,62	0
56	MG	YF	303	1/1	0.80	0.97	24.33	108,108,108,108	0
56	MG	YA	3323	1/1	0.75	0.64	24.30	62,62,62,62	0
56	MG	YA	3681	1/1	0.89	0.62	24.28	62,62,62,62	0
56	MG	RA	3384	1/1	0.91	0.62	24.21	67,67,67,67	0
56	MG	YA	3030	1/1	0.26	0.59	24.21	88,88,88,88	0
56	MG	QA	1854	1/1	0.23	0.97	24.13	94,94,94,94	0
56	MG	YA	3355	1/1	0.92	0.97	23.99	62,62,62,62	0
56	MG	YA	3387	1/1	0.78	0.71	23.99	62,62,62,62	0
56	MG	RA	3165	1/1	0.79	1.06	23.90	103,103,103,103	0
56	MG	RP	201	1/1	0.48	1.10	23.88	86,86,86,86	0
56	MG	YA	3378	1/1	0.89	0.65	23.47	62,62,62,62	0
56	MG	RA	4044	1/1	0.75	1.12	23.40	106,106,106,106	0
56	MG	RA	3483	1/1	0.84	0.66	23.28	62,62,62,62	0
56	MG	QA	1724	1/1	0.47	1.89	23.12	85,85,85,85	0
56	MG	RA	3805	1/1	0.71	0.61	23.10	97,97,97,97	0
56	MG	RA	3521	1/1	0.68	0.47	23.10	69,69,69,69	0
56	MG	RA	4012	1/1	0.72	2.56	23.06	103,103,103,103	0
56	MG	RA	3512	1/1	-0.35	0.93	22.61	94,94,94,94	0
56	MG	RA	3696	1/1	0.58	0.92	22.54	82,82,82,82	0
56	MG	RA	3893	1/1	0.81	0.59	22.49	76,76,76,76	0
56	MG	RA	3113	1/1	0.47	1.02	22.48	90,90,90,90	0
56	MG	XA	1612	1/1	0.64	0.51	22.47	84,84,84,84	0
56	MG	YA	3724	1/1	0.41	0.53	22.47	71,71,71,71	0
56	MG	RA	3497	1/1	0.93	0.70	22.39	62,62,62,62	0
56	MG	RA	3611	1/1	0.49	0.50	22.39	95,95,95,95	0
56	MG	RA	3226	1/1	0.83	0.81	22.34	113,113,113,113	0
56	MG	RA	4062	1/1	0.57	1.38	22.16	98,98,98,98	0
56	MG	RA	3624	1/1	0.81	0.81	22.16	75,75,75,75	0
56	MG	YA	3183	1/1	0.53	0.66	21.97	88,88,88,88	0
56	MG	YA	3514	1/1	0.91	0.62	21.80	62,62,62,62	0
56	MG	RA	3708	1/1	0.72	0.98	21.60	77,77,77,77	0
56	MG	YA	3027	1/1	0.23	0.92	21.22	83,83,83,83	0
56	MG	RA	3742	1/1	0.59	0.35	21.18	88,88,88,88	0
56	MG	YA	3623	1/1	0.82	0.55	21.11	65,65,65,65	0
56	MG	RA	3366	1/1	0.76	0.41	21.03	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3186	1/1	0.86	0.93	21.02	98,98,98,98	0
56	MG	RA	3077	1/1	0.62	0.53	20.65	80,80,80,80	0
56	MG	RA	3713	1/1	0.74	1.84	20.61	89,89,89,89	0
56	MG	YA	3456	1/1	0.47	0.77	20.39	84,84,84,84	0
56	MG	RD	303	1/1	0.72	1.20	20.39	88,88,88,88	0
56	MG	YA	3170	1/1	0.06	0.52	20.37	92,92,92,92	0
56	MG	Y0	101	1/1	-0.08	1.09	20.33	78,78,78,78	0
56	MG	RA	3484	1/1	0.93	0.84	20.23	62,62,62,62	0
56	MG	RA	4060	1/1	0.84	1.10	20.11	109,109,109,109	0
56	MG	YA	3715	1/1	0.78	0.42	19.97	83,83,83,83	0
56	MG	RA	3618	1/1	0.15	0.82	19.79	88,88,88,88	0
56	MG	RA	3786	1/1	0.85	0.69	19.72	89,89,89,89	0
56	MG	YA	3270	1/1	0.42	0.90	19.69	79,79,79,79	0
56	MG	YA	3328	1/1	0.87	0.59	19.69	62,62,62,62	0
56	MG	XA	1658	1/1	0.42	0.67	19.61	86,86,86,86	0
56	MG	RA	3767	1/1	0.47	0.91	19.52	63,63,63,63	0
56	MG	RA	3707	1/1	0.67	0.46	19.39	73,73,73,73	0
56	MG	RA	4049	1/1	0.93	0.94	19.38	99,99,99,99	0
56	MG	RA	3185	1/1	0.87	0.73	19.25	85,85,85,85	0
56	MG	QA	1711	1/1	0.86	0.50	19.24	78,78,78,78	0
56	MG	RA	3458	1/1	0.27	0.90	19.24	84,84,84,84	0
56	MG	RA	3536	1/1	0.38	0.66	19.23	86,86,86,86	0
56	MG	RA	3332	1/1	0.48	0.52	19.17	93,93,93,93	0
56	MG	YA	3033	1/1	0.03	0.52	19.11	99,99,99,99	0
56	MG	YA	3361	1/1	0.45	0.63	18.90	88,88,88,88	0
56	MG	YA	3269	1/1	0.46	0.54	18.84	75,75,75,75	0
56	MG	YA	3475	1/1	0.72	0.56	18.76	65,65,65,65	0
56	MG	RA	3858	1/1	0.96	0.54	18.73	70,70,70,70	0
56	MG	RA	3526	1/1	0.07	0.84	18.67	89,89,89,89	0
56	MG	RA	3117	1/1	0.76	0.66	18.64	96,96,96,96	0
56	MG	XA	1738	1/1	0.85	0.61	18.60	64,64,64,64	0
56	MG	RA	3468	1/1	0.91	0.46	18.46	63,63,63,63	0
56	MG	RA	3348	1/1	0.95	0.59	18.38	74,74,74,74	0
56	MG	YA	3614	1/1	0.94	0.53	18.35	68,68,68,68	0
56	MG	YA	3291	1/1	0.25	0.84	18.29	88,88,88,88	0
56	MG	RA	3524	1/1	0.42	0.69	18.22	85,85,85,85	0
56	MG	YW	201	1/1	0.59	0.94	18.19	98,98,98,98	0
56	MG	YA	3091	1/1	0.76	0.47	18.15	76,76,76,76	0
56	MG	RA	3939	1/1	0.42	2.08	18.14	95,95,95,95	0
56	MG	RE	302	1/1	0.45	0.95	18.08	97,97,97,97	0
56	MG	YA	3192	1/1	0.42	0.44	18.05	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
56	MG	RA	3952	1/1	0.18	0.52	18.03	96,96,96,96	0
56	MG	YA	3612	1/1	0.95	0.59	18.01	64,64,64,64	0
56	MG	RA	3241	1/1	0.79	0.62	18.00	91,91,91,91	0
56	MG	RA	3948	1/1	0.72	0.58	17.98	64,64,64,64	0
56	MG	RA	3187	1/1	0.49	0.57	17.95	90,90,90,90	0
56	MG	RA	3568	1/1	0.27	0.54	17.91	89,89,89,89	0
56	MG	RA	3197	1/1	0.23	0.56	17.89	100,100,100,100	0
56	MG	RA	3574	1/1	0.84	1.32	17.83	90,90,90,90	0
56	MG	RR	201	1/1	0.36	0.77	17.76	98,98,98,98	0
56	MG	YA	3249	1/1	0.45	0.69	17.72	94,94,94,94	0
56	MG	XA	1720	1/1	0.46	0.65	17.71	96,96,96,96	0
56	MG	QA	1860	1/1	0.13	0.83	17.69	92,92,92,92	0
56	MG	RA	4030	1/1	0.85	1.21	17.55	103,103,103,103	0
56	MG	RA	3496	1/1	0.95	0.70	17.33	63,63,63,63	0
56	MG	RF	303	1/1	0.39	1.36	17.30	98,98,98,98	0
56	MG	XA	1725	1/1	0.75	0.50	17.04	85,85,85,85	0
56	MG	XA	1774	1/1	0.94	0.65	17.03	80,80,80,80	0
56	MG	RA	3121	1/1	0.66	0.95	17.02	100,100,100,100	0
56	MG	YA	3709	1/1	0.69	0.43	16.99	71,71,71,71	0
56	MG	RA	3386	1/1	0.85	0.71	16.97	76,76,76,76	0
56	MG	RA	3082	1/1	0.84	0.95	16.97	100,100,100,100	0
56	MG	RA	3109	1/1	0.41	0.72	16.88	97,97,97,97	0
56	MG	RA	3045	1/1	0.72	0.89	16.77	86,86,86,86	0
56	MG	RA	3125	1/1	0.94	0.52	16.75	93,93,93,93	0
56	MG	XA	1673	1/1	0.59	0.46	16.64	89,89,89,89	0
56	MG	RA	3659	1/1	0.84	0.76	16.52	95,95,95,95	0
56	MG	YA	3107	1/1	0.81	0.43	16.39	74,74,74,74	0
56	MG	YA	3134	1/1	0.72	0.62	16.29	73,73,73,73	0
56	MG	XA	1786	1/1	0.54	0.71	16.27	89,89,89,89	0
56	MG	R5	101	1/1	0.77	1.50	16.13	105,105,105,105	0
56	MG	RA	3856	1/1	0.81	0.54	16.13	77,77,77,77	0
56	MG	YA	3112	1/1	0.02	0.72	16.09	85,85,85,85	0
56	MG	RA	3098	1/1	0.62	0.54	16.03	68,68,68,68	0
56	MG	YA	3272	1/1	0.90	0.76	15.98	77,77,77,77	0
56	MG	YD	305	1/1	0.58	0.70	15.95	92,92,92,92	0
56	MG	RA	4052	1/1	0.83	1.03	15.92	90,90,90,90	0
56	MG	YA	3753	1/1	0.82	1.13	15.76	81,81,81,81	0
56	MG	RA	4034	1/1	0.81	0.97	15.70	88,88,88,88	0
56	MG	RA	3566	1/1	0.68	0.56	15.67	67,67,67,67	0
56	MG	RA	4065	1/1	0.17	1.02	15.63	91,91,91,91	0
56	MG	RA	3476	1/1	0.88	0.72	15.61	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3468	1/1	0.86	0.59	15.54	62,62,62,62	0
56	MG	RA	3409	1/1	0.81	0.45	15.52	65,65,65,65	0
56	MG	RA	3265	1/1	0.81	0.77	15.50	94,94,94,94	0
56	MG	YA	3074	1/1	0.64	0.65	15.50	68,68,68,68	0
56	MG	RA	3356	1/1	0.97	0.82	15.46	78,78,78,78	0
56	MG	YA	3325	1/1	0.96	0.51	15.45	62,62,62,62	0
56	MG	QA	1715	1/1	0.90	0.52	15.43	71,71,71,71	0
56	MG	QA	1654	1/1	0.59	0.43	15.41	77,77,77,77	0
56	MG	YA	3656	1/1	0.95	0.43	15.40	78,78,78,78	0
56	MG	YA	3660	1/1	0.67	0.61	15.31	69,69,69,69	0
56	MG	RA	4051	1/1	0.92	0.72	15.29	105,105,105,105	0
56	MG	RA	4043	1/1	0.64	1.09	15.28	92,92,92,92	0
56	MG	YA	3129	1/1	0.71	0.47	15.26	77,77,77,77	0
56	MG	YA	3668	1/1	0.93	0.74	15.25	62,62,62,62	0
56	MG	XA	1747	1/1	0.94	0.67	15.25	63,63,63,63	0
56	MG	RA	3712	1/1	0.66	0.78	15.15	83,83,83,83	0
56	MG	RA	3385	1/1	0.97	1.01	15.13	62,62,62,62	0
56	MG	YA	3750	1/1	0.88	0.98	15.09	92,92,92,92	0
56	MG	YA	3388	1/1	0.90	0.54	15.05	62,62,62,62	0
56	MG	YA	3440	1/1	0.92	0.55	15.03	64,64,64,64	0
56	MG	RA	3814	1/1	0.93	0.49	14.98	73,73,73,73	0
56	MG	RD	302	1/1	0.82	0.82	14.96	71,71,71,71	0
56	MG	RF	306	1/1	0.67	1.38	14.91	106,106,106,106	0
56	MG	RA	3401	1/1	0.73	0.70	14.86	62,62,62,62	0
56	MG	RA	4026	1/1	0.89	0.69	14.82	105,105,105,105	0
56	MG	RA	4024	1/1	0.56	1.50	14.78	98,98,98,98	0
56	MG	YA	3447	1/1	0.26	0.56	14.74	80,80,80,80	0
56	MG	RA	4064	1/1	0.81	1.09	14.73	84,84,84,84	0
56	MG	YA	3122	1/1	0.79	0.55	14.70	82,82,82,82	0
56	MG	RA	3466	1/1	0.85	0.70	14.70	62,62,62,62	0
56	MG	YA	3733	1/1	0.91	0.82	14.67	89,89,89,89	0
56	MG	QA	1857	1/1	0.81	0.34	14.63	83,83,83,83	0
56	MG	RV	203	1/1	0.70	0.76	14.54	83,83,83,83	0
56	MG	RA	3502	1/1	0.92	1.11	14.50	64,64,64,64	0
56	MG	RA	3462	1/1	0.61	0.75	14.47	86,86,86,86	0
56	MG	RA	3279	1/1	0.59	0.71	14.42	98,98,98,98	0
56	MG	XA	1633	1/1	0.59	0.80	14.30	66,66,66,66	0
56	MG	XA	1744	1/1	0.84	0.91	14.27	63,63,63,63	0
56	MG	RA	4063	1/1	0.75	1.57	14.22	100,100,100,100	0
56	MG	RA	4028	1/1	0.55	1.02	14.19	108,108,108,108	0
56	MG	YA	3421	1/1	0.26	0.54	14.18	82,82,82,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	4048	1/1	0.70	1.12	14.17	103,103,103,103	0
56	MG	RA	3119	1/1	0.92	1.27	14.16	94,94,94,94	0
56	MG	RA	3827	1/1	0.32	0.69	14.13	81,81,81,81	0
56	MG	YA	3077	1/1	0.84	0.80	14.09	107,107,107,107	0
56	MG	YA	3495	1/1	0.61	0.69	14.04	77,77,77,77	0
56	MG	RA	3551	1/1	0.46	0.46	13.96	79,79,79,79	0
56	MG	YA	3485	1/1	0.91	0.56	13.96	62,62,62,62	0
56	MG	YA	3377	1/1	0.94	0.52	13.90	62,62,62,62	0
56	MG	YA	3299	1/1	0.36	0.49	13.88	64,64,64,64	0
56	MG	RA	3404	1/1	0.92	0.48	13.83	71,71,71,71	0
56	MG	RA	3251	1/1	0.17	0.88	13.81	82,82,82,82	0
56	MG	RA	4058	1/1	0.09	0.92	13.81	96,96,96,96	0
56	MG	XA	1760	1/1	0.88	0.49	13.78	67,67,67,67	0
56	MG	RA	3727	1/1	0.35	0.55	13.74	78,78,78,78	0
56	MG	YA	3744	1/1	0.90	0.85	13.72	98,98,98,98	0
56	MG	RA	3990	1/1	0.65	0.73	13.68	68,68,68,68	0
56	MG	YA	3540	1/1	0.83	0.59	13.61	82,82,82,82	0
56	MG	YA	3511	1/1	0.85	0.56	13.60	62,62,62,62	0
56	MG	RA	3871	1/1	0.93	0.66	13.56	62,62,62,62	0
56	MG	QA	1623	1/1	0.79	0.33	13.45	86,86,86,86	0
56	MG	QA	1731	1/1	0.87	0.62	13.42	76,76,76,76	0
56	MG	RA	3379	1/1	0.75	0.52	13.40	62,62,62,62	0
56	MG	RA	3021	1/1	0.81	0.95	13.33	103,103,103,103	0
56	MG	RA	3465	1/1	0.73	0.46	13.32	69,69,69,69	0
56	MG	YA	3632	1/1	0.82	0.56	13.29	67,67,67,67	0
56	MG	RA	3323	1/1	0.63	0.44	13.22	69,69,69,69	0
56	MG	RA	3020	1/1	0.87	0.72	13.21	95,95,95,95	0
56	MG	RA	3911	1/1	0.93	0.44	13.15	71,71,71,71	0
56	MG	RA	3359	1/1	0.65	0.58	13.13	89,89,89,89	0
56	MG	RA	4041	1/1	0.87	0.76	13.12	109,109,109,109	0
56	MG	YA	3752	1/1	0.34	1.10	13.06	100,100,100,100	0
56	MG	RF	305	1/1	0.80	0.93	13.01	101,101,101,101	0
56	MG	RA	3902	1/1	0.90	0.58	13.01	62,62,62,62	0
56	MG	YA	3020	1/1	0.85	0.59	12.91	96,96,96,96	0
56	MG	YA	3398	1/1	0.93	0.84	12.76	63,63,63,63	0
56	MG	RA	3823	1/1	0.72	0.56	12.73	73,73,73,73	0
56	MG	RA	3424	1/1	0.98	0.54	12.70	62,62,62,62	0
56	MG	XA	1777	1/1	0.91	0.45	12.70	74,74,74,74	0
56	MG	YA	3499	1/1	0.78	0.42	12.69	65,65,65,65	0
56	MG	RA	3179	1/1	0.07	0.99	12.68	105,105,105,105	0
56	MG	YD	309	1/1	0.52	0.69	12.65	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3387	1/1	0.96	0.48	12.64	75,75,75,75	0
56	MG	YA	3209	1/1	0.53	0.84	12.63	85,85,85,85	0
56	MG	YA	3413	1/1	0.66	0.80	12.63	85,85,85,85	0
56	MG	YA	3699	1/1	0.71	0.50	12.62	77,77,77,77	0
56	MG	RA	3146	1/1	0.57	0.37	12.58	68,68,68,68	0
56	MG	R0	103	1/1	0.45	0.82	12.52	70,70,70,70	0
56	MG	YA	3351	1/1	0.69	0.55	12.49	68,68,68,68	0
56	MG	YA	3156	1/1	0.73	0.47	12.39	103,103,103,103	0
56	MG	RA	3967	1/1	0.77	0.48	12.39	97,97,97,97	0
56	MG	QA	1828	1/1	0.45	0.55	12.39	86,86,86,86	0
56	MG	YA	3318	1/1	0.95	0.48	12.34	62,62,62,62	0
56	MG	RA	4003	1/1	0.36	0.81	12.34	92,92,92,92	0
56	MG	QA	1872	1/1	0.67	0.85	12.26	70,70,70,70	0
56	MG	RA	3452	1/1	0.93	0.60	12.24	62,62,62,62	0
56	MG	YA	3664	1/1	0.98	0.65	12.03	72,72,72,72	0
56	MG	RA	3684	1/1	0.17	0.52	11.98	93,93,93,93	0
56	MG	XA	1690	1/1	0.29	0.79	11.92	94,94,94,94	0
56	MG	XA	1696	1/1	0.75	0.90	11.90	67,67,67,67	0
56	MG	RA	3006	1/1	0.95	0.35	11.79	73,73,73,73	0
56	MG	RA	3771	1/1	0.99	0.61	11.70	72,72,72,72	0
56	MG	YA	3532	1/1	0.90	0.47	11.65	84,84,84,84	0
56	MG	RA	3679	1/1	0.77	0.40	11.62	72,72,72,72	0
56	MG	YA	3684	1/1	0.85	0.52	11.59	63,63,63,63	0
56	MG	YA	3691	1/1	0.69	0.49	11.52	82,82,82,82	0
56	MG	RA	3744	1/1	0.82	0.58	11.51	73,73,73,73	0
56	MG	YA	3321	1/1	0.88	0.51	11.42	62,62,62,62	0
56	MG	YA	3152	1/1	0.10	1.07	11.39	83,83,83,83	0
56	MG	RA	3539	1/1	0.87	0.45	11.38	98,98,98,98	0
56	MG	YA	3749	1/1	0.65	0.99	11.34	90,90,90,90	0
56	MG	YA	3240	1/1	0.62	0.47	11.29	93,93,93,93	0
56	MG	RA	4045	1/1	0.93	0.72	11.24	101,101,101,101	0
56	MG	YA	3336	1/1	0.69	0.75	11.24	62,62,62,62	0
56	MG	RA	3231	1/1	0.87	0.82	11.17	89,89,89,89	0
56	MG	YA	3679	1/1	0.89	0.58	11.17	65,65,65,65	0
56	MG	YA	3600	1/1	0.80	0.68	11.17	65,65,65,65	0
56	MG	XA	1683	1/1	0.42	0.56	11.08	76,76,76,76	0
56	MG	RA	3638	1/1	0.87	0.88	11.08	85,85,85,85	0
56	MG	RA	3535	1/1	0.41	0.57	11.07	97,97,97,97	0
56	MG	RA	3607	1/1	0.92	0.92	11.05	91,91,91,91	0
56	MG	YD	308	1/1	0.94	0.61	11.04	97,97,97,97	0
56	MG	QA	1682	1/1	0.09	0.53	10.99	87,87,87,87	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3248	1/1	0.65	0.58	10.95	89,89,89,89	0
56	MG	RA	3900	1/1	0.39	0.59	10.92	92,92,92,92	0
56	MG	XA	1629	1/1	0.69	0.42	10.92	68,68,68,68	0
56	MG	RV	202	1/1	0.38	0.47	10.82	86,86,86,86	0
56	MG	YA	3216	1/1	0.50	0.47	10.71	80,80,80,80	0
56	MG	RA	4035	1/1	0.77	1.19	10.71	90,90,90,90	0
56	MG	RA	4059	1/1	0.91	0.84	10.67	98,98,98,98	0
56	MG	YA	3658	1/1	0.59	0.70	10.65	87,87,87,87	0
56	MG	YA	3577	1/1	0.94	0.65	10.65	62,62,62,62	0
56	MG	RA	3501	1/1	0.88	0.84	10.63	63,63,63,63	0
56	MG	RA	3377	1/1	0.80	0.32	10.63	69,69,69,69	0
56	MG	YA	3013	1/1	0.50	0.55	10.62	72,72,72,72	0
56	MG	RA	3623	1/1	0.93	0.70	10.62	65,65,65,65	0
56	MG	QA	1680	1/1	0.37	0.52	10.61	84,84,84,84	0
56	MG	YA	3579	1/1	0.91	0.69	10.60	62,62,62,62	0
56	MG	YA	3665	1/1	0.96	0.49	10.52	63,63,63,63	0
56	MG	RA	4066	1/1	0.80	0.77	10.48	86,86,86,86	0
56	MG	RA	3232	1/1	0.90	0.82	10.48	100,100,100,100	0
56	MG	YA	3011	1/1	0.76	0.42	10.41	70,70,70,70	0
56	MG	RA	3421	1/1	0.90	0.52	10.25	62,62,62,62	0
56	MG	RA	4057	1/1	0.14	1.28	10.24	97,97,97,97	0
56	MG	RA	4017	1/1	0.80	0.97	10.13	92,92,92,92	0
56	MG	RA	3361	1/1	0.79	0.48	10.12	82,82,82,82	0
56	MG	YA	3701	1/1	0.83	0.62	10.11	62,62,62,62	0
56	MG	YA	3740	1/1	0.84	0.86	10.10	96,96,96,96	0
56	MG	RA	3812	1/1	0.57	0.38	10.02	76,76,76,76	0
56	MG	RA	3391	1/1	0.98	0.42	10.02	74,74,74,74	0
56	MG	RA	3275	1/1	0.64	0.56	10.01	110,110,110,110	0
56	MG	YA	3397	1/1	0.27	0.65	9.99	75,75,75,75	0
56	MG	RA	3330	1/1	0.83	0.41	9.97	68,68,68,68	0
56	MG	YA	3110	1/1	0.80	0.45	9.93	62,62,62,62	0
56	MG	RA	3170	1/1	0.71	0.38	9.90	86,86,86,86	0
56	MG	QA	1626	1/1	0.80	0.33	9.88	87,87,87,87	0
56	MG	YA	3415	1/1	0.86	0.79	9.80	68,68,68,68	0
56	MG	RA	4023	1/1	0.92	0.66	9.76	101,101,101,101	0
56	MG	YA	3368	1/1	0.89	0.63	9.73	62,62,62,62	0
56	MG	YA	3049	1/1	0.67	0.49	9.71	85,85,85,85	0
56	MG	RA	3953	1/1	0.92	0.33	9.71	81,81,81,81	0
56	MG	YA	3335	1/1	0.88	0.67	9.66	62,62,62,62	0
56	MG	RA	3307	1/1	0.76	1.83	9.65	99,99,99,99	0
56	MG	RF	301	1/1	-0.24	0.83	9.61	99,99,99,99	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	4036	1/1	0.90	1.05	9.61	99,99,99,99	0
56	MG	RA	3382	1/1	0.89	0.52	9.59	76,76,76,76	0
56	MG	YA	3268	1/1	0.91	0.62	9.57	83,83,83,83	0
56	MG	RN	201	1/1	0.45	1.15	9.57	91,91,91,91	0
56	MG	RA	4037	1/1	0.73	0.69	9.54	95,95,95,95	0
56	MG	XA	1707	1/1	0.79	0.27	9.40	80,80,80,80	0
56	MG	QA	1843	1/1	0.82	0.50	9.34	68,68,68,68	0
56	MG	RA	3538	1/1	0.49	0.89	9.33	95,95,95,95	0
56	MG	QA	1835	1/1	0.53	0.52	9.33	72,72,72,72	0
56	MG	RA	3390	1/1	0.93	0.42	9.24	65,65,65,65	0
56	MG	XA	1616	1/1	0.56	0.43	9.21	81,81,81,81	0
56	MG	YA	3449	1/1	0.87	0.46	9.19	66,66,66,66	0
56	MG	YA	3446	1/1	0.42	0.64	9.17	89,89,89,89	0
56	MG	RA	3630	1/1	0.49	0.58	9.16	68,68,68,68	0
56	MG	RA	3148	1/1	0.47	0.47	9.09	81,81,81,81	0
56	MG	QN	103	1/1	0.75	1.01	9.05	81,81,81,81	0
56	MG	YA	3751	1/1	0.76	0.71	8.98	102,102,102,102	0
56	MG	RA	3168	1/1	0.80	0.51	8.91	91,91,91,91	0
56	MG	RD	305	1/1	0.83	0.84	8.90	102,102,102,102	0
56	MG	YA	3737	1/1	0.96	0.61	8.88	63,63,63,63	0
56	MG	YT	202	1/1	0.47	0.90	8.87	80,80,80,80	0
56	MG	RA	4032	1/1	0.67	0.87	8.86	89,89,89,89	0
56	MG	RA	3795	1/1	0.80	0.60	8.84	75,75,75,75	0
56	MG	RA	3533	1/1	0.68	0.35	8.83	89,89,89,89	0
56	MG	QA	1877	1/1	0.30	0.70	8.83	92,92,92,92	0
56	MG	YA	3326	1/1	0.95	0.46	8.78	65,65,65,65	0
56	MG	RA	3471	1/1	0.96	0.64	8.78	74,74,74,74	0
56	MG	RA	3040	1/1	0.36	0.71	8.78	97,97,97,97	0
56	MG	RA	3892	1/1	0.65	0.49	8.77	78,78,78,78	0
56	MG	RA	3321	1/1	0.97	0.50	8.77	63,63,63,63	0
56	MG	YD	304	1/1	0.97	0.55	8.76	104,104,104,104	0
56	MG	RA	3518	1/1	0.56	0.57	8.75	96,96,96,96	0
56	MG	RA	3342	1/1	0.66	0.45	8.73	79,79,79,79	0
56	MG	XA	1700	1/1	0.97	0.55	8.68	65,65,65,65	0
56	MG	YA	3488	1/1	0.76	0.46	8.67	77,77,77,77	0
56	MG	RA	3023	1/1	0.79	0.36	8.60	78,78,78,78	0
56	MG	YA	3754	1/1	0.88	0.42	8.51	84,84,84,84	0
56	MG	XA	1776	1/1	0.91	0.32	8.37	80,80,80,80	0
56	MG	YA	3538	1/1	0.92	0.44	8.32	64,64,64,64	0
56	MG	YA	3284	1/1	0.77	0.51	8.32	63,63,63,63	0
56	MG	YA	3606	1/1	0.96	0.50	8.25	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3070	1/1	0.84	0.76	8.19	85,85,85,85	0
56	MG	RA	3300	1/1	0.55	0.65	8.15	100,100,100,100	0
56	MG	RA	3715	1/1	0.96	0.46	8.05	65,65,65,65	0
56	MG	RD	309	1/1	0.79	0.64	8.03	100,100,100,100	0
56	MG	R1	102	1/1	0.31	0.92	8.02	83,83,83,83	0
56	MG	RF	309	1/1	-0.42	0.84	8.01	103,103,103,103	0
56	MG	RA	3479	1/1	0.84	0.39	7.99	80,80,80,80	0
56	MG	RA	3073	1/1	0.92	0.67	7.99	96,96,96,96	0
56	MG	RA	3807	1/1	0.59	0.60	7.97	91,91,91,91	0
56	MG	YA	3621	1/1	0.97	0.53	7.86	62,62,62,62	0
56	MG	YA	3146	1/1	0.59	0.50	7.86	83,83,83,83	0
56	MG	XA	1759	1/1	0.89	0.45	7.86	68,68,68,68	0
56	MG	YE	302	1/1	0.73	0.69	7.85	95,95,95,95	0
56	MG	RA	4025	1/1	0.68	0.82	7.82	97,97,97,97	0
56	MG	YA	3748	1/1	0.92	0.64	7.81	93,93,93,93	0
56	MG	RA	3477	1/1	0.81	0.50	7.79	63,63,63,63	0
56	MG	YB	217	1/1	0.84	0.33	7.78	84,84,84,84	0
56	MG	RF	311	1/1	0.17	0.69	7.68	94,94,94,94	0
56	MG	QA	1708	1/1	0.82	0.44	7.64	69,69,69,69	0
56	MG	YA	3153	1/1	0.72	0.51	7.64	68,68,68,68	0
56	MG	RA	3050	1/1	0.41	0.77	7.58	89,89,89,89	0
56	MG	YA	3610	1/1	0.81	0.55	7.57	64,64,64,64	0
56	MG	RF	308	1/1	0.45	0.79	7.56	92,92,92,92	0
56	MG	YA	3392	1/1	0.94	0.65	7.48	62,62,62,62	0
56	MG	RA	4061	1/1	0.46	0.65	7.47	105,105,105,105	0
56	MG	YA	3580	1/1	0.70	0.51	7.44	70,70,70,70	0
56	MG	YA	3237	1/1	0.84	0.90	7.42	95,95,95,95	0
56	MG	RA	3862	1/1	0.56	0.38	7.42	75,75,75,75	0
56	MG	YA	3217	1/1	0.84	0.34	7.38	98,98,98,98	0
56	MG	RA	3178	1/1	0.81	0.44	7.33	107,107,107,107	0
56	MG	YA	3028	1/1	0.75	0.41	7.27	85,85,85,85	0
56	MG	YA	3613	1/1	0.83	0.40	7.19	75,75,75,75	0
56	MG	YA	3439	1/1	0.60	0.90	7.13	88,88,88,88	0
56	MG	RA	3821	1/1	0.96	0.34	7.05	76,76,76,76	0
56	MG	XA	1763	1/1	0.80	0.41	7.05	70,70,70,70	0
56	MG	RA	3724	1/1	0.86	0.25	6.98	82,82,82,82	0
56	MG	RA	3874	1/1	0.92	0.51	6.96	63,63,63,63	0
56	MG	YA	3702	1/1	0.95	0.44	6.95	66,66,66,66	0
56	MG	QF	201	1/1	0.90	0.45	6.93	75,75,75,75	0
56	MG	YA	3384	1/1	0.87	0.60	6.92	64,64,64,64	0
56	MG	QA	1773	1/1	0.71	0.27	6.91	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3491	1/1	0.78	0.28	6.87	85,85,85,85	0
56	MG	RA	3230	1/1	0.85	0.58	6.86	106,106,106,106	0
56	MG	RA	3349	1/1	0.73	0.38	6.80	68,68,68,68	0
56	MG	RA	3335	1/1	0.78	0.33	6.78	75,75,75,75	0
56	MG	RA	3969	1/1	0.57	0.52	6.75	97,97,97,97	0
56	MG	QA	1737	1/1	0.61	0.47	6.71	88,88,88,88	0
56	MG	RE	307	1/1	0.47	0.59	6.65	86,86,86,86	0
56	MG	RA	3136	1/1	0.97	0.47	6.59	94,94,94,94	0
56	MG	RA	3299	1/1	0.66	0.45	6.58	68,68,68,68	0
56	MG	RA	3809	1/1	0.55	0.54	6.57	89,89,89,89	0
56	MG	YA	3382	1/1	0.97	0.63	6.53	62,62,62,62	0
56	MG	YA	3104	1/1	0.72	0.28	6.50	69,69,69,69	0
56	MG	YA	3404	1/1	0.93	0.60	6.48	62,62,62,62	0
56	MG	RA	3928	1/1	0.86	0.43	6.47	90,90,90,90	0
56	MG	YA	3210	1/1	0.85	0.39	6.43	70,70,70,70	0
56	MG	YA	3311	1/1	0.22	0.86	6.41	73,73,73,73	0
56	MG	YA	3588	1/1	0.90	0.42	6.40	64,64,64,64	0
56	MG	RA	3609	1/1	0.15	1.11	6.38	90,90,90,90	0
56	MG	RA	3472	1/1	0.96	0.48	6.29	78,78,78,78	0
56	MG	YA	3550	1/1	0.86	0.39	6.22	80,80,80,80	0
56	MG	XA	1737	1/1	0.92	0.29	6.22	78,78,78,78	0
56	MG	RA	3717	1/1	0.65	0.40	6.20	65,65,65,65	0
56	MG	RA	4033	1/1	0.88	0.68	6.18	96,96,96,96	0
56	MG	RA	3128	1/1	0.89	0.41	6.15	85,85,85,85	0
56	MG	YA	3386	1/1	0.75	0.40	6.09	82,82,82,82	0
56	MG	RA	3875	1/1	0.87	0.65	6.06	62,62,62,62	0
56	MG	YA	3516	1/1	0.74	1.26	6.05	85,85,85,85	0
56	MG	YA	3345	1/1	0.95	0.35	5.97	62,62,62,62	0
56	MG	YA	3587	1/1	0.82	0.39	5.88	68,68,68,68	0
56	MG	RA	3635	1/1	0.63	0.41	5.84	96,96,96,96	0
56	MG	QA	1832	1/1	0.17	0.40	5.83	84,84,84,84	0
56	MG	RA	3938	1/1	0.65	0.39	5.80	78,78,78,78	0
56	MG	XA	1770	1/1	0.88	0.51	5.79	87,87,87,87	0
56	MG	YA	3201	1/1	0.36	0.29	5.76	90,90,90,90	0
56	MG	RA	4047	1/1	0.39	0.70	5.74	97,97,97,97	0
56	MG	RA	3644	1/1	0.51	0.56	5.73	91,91,91,91	0
56	MG	RA	3315	1/1	0.91	0.32	5.71	82,82,82,82	0
56	MG	YA	3019	1/1	0.58	0.57	5.68	102,102,102,102	0
56	MG	YA	3317	1/1	0.77	0.69	5.66	69,69,69,69	0
56	MG	YA	3285	1/1	0.93	0.33	5.63	76,76,76,76	0
56	MG	RA	3803	1/1	0.73	1.18	5.63	101,101,101,101	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3746	1/1	0.89	0.47	5.59	62,62,62,62	0
56	MG	QA	1706	1/1	0.70	0.34	5.58	76,76,76,76	0
56	MG	QA	1829	1/1	0.86	0.32	5.51	81,81,81,81	0
56	MG	RA	3399	1/1	0.91	0.53	5.51	62,62,62,62	0
56	MG	YA	3474	1/1	0.26	0.44	5.50	78,78,78,78	0
56	MG	RD	308	1/1	0.09	0.60	5.50	83,83,83,83	0
56	MG	R3	102	1/1	0.01	0.87	5.45	102,102,102,102	0
56	MG	XA	1741	1/1	0.87	0.34	5.43	78,78,78,78	0
56	MG	YA	3503	1/1	0.63	0.28	5.41	67,67,67,67	0
56	MG	YA	3092	1/1	0.56	0.42	5.39	85,85,85,85	0
56	MG	RA	3770	1/1	0.95	0.44	5.33	66,66,66,66	0
56	MG	YA	3714	1/1	0.13	0.63	5.30	85,85,85,85	0
56	MG	RA	4002	1/1	0.92	0.42	5.24	74,74,74,74	0
56	MG	RA	3177	1/1	0.50	0.53	5.24	83,83,83,83	0
56	MG	RA	3381	1/1	0.83	0.41	5.23	64,64,64,64	0
56	MG	XA	1637	1/1	0.54	0.19	5.21	86,86,86,86	0
56	MG	QA	1638	1/1	0.94	0.25	5.15	75,75,75,75	0
56	MG	QA	1622	1/1	0.79	0.48	5.15	89,89,89,89	0
56	MG	RA	4027	1/1	0.88	0.59	5.14	88,88,88,88	0
56	MG	YA	3303	1/1	0.90	0.36	5.13	62,62,62,62	0
56	MG	YD	306	1/1	0.93	0.50	5.12	81,81,81,81	0
56	MG	YA	3036	1/1	0.87	0.33	5.10	76,76,76,76	0
56	MG	RA	4021	1/1	0.77	0.63	5.07	78,78,78,78	0
56	MG	YF	301	1/1	-0.11	0.45	5.05	94,94,94,94	0
56	MG	R8	101	1/1	0.21	0.87	5.04	90,90,90,90	0
56	MG	YA	3560	1/1	0.88	0.26	5.03	64,64,64,64	0
56	MG	XA	1631	1/1	0.64	0.47	5.00	88,88,88,88	0
56	MG	XT	201	1/1	0.50	0.66	4.94	93,93,93,93	0
56	MG	RU	203	1/1	0.89	0.39	4.89	81,81,81,81	0
56	MG	RA	3774	1/1	0.98	0.32	4.89	64,64,64,64	0
56	MG	RA	3959	1/1	-0.25	0.92	4.85	97,97,97,97	0
56	MG	RA	4056	1/1	0.94	0.79	4.81	112,112,112,112	0
56	MG	R1	104	1/1	0.47	0.68	4.77	88,88,88,88	0
56	MG	RA	3234	1/1	0.70	0.51	4.75	101,101,101,101	0
56	MG	RA	3431	1/1	0.84	0.48	4.74	63,63,63,63	0
56	MG	QA	1634	1/1	0.88	0.28	4.73	68,68,68,68	0
56	MG	QA	1671	1/1	0.97	0.37	4.73	85,85,85,85	0
56	MG	RA	3733	1/1	0.91	0.27	4.67	79,79,79,79	0
56	MG	XA	1728	1/1	-0.32	0.41	4.66	84,84,84,84	0
56	MG	YA	3007	1/1	0.69	0.35	4.66	69,69,69,69	0
56	MG	YA	3339	1/1	0.93	0.36	4.62	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	QA	1759	1/1	0.45	0.75	4.62	77,77,77,77	0
56	MG	RA	3514	1/1	0.76	0.34	4.57	63,63,63,63	0
56	MG	RA	4042	1/1	0.55	0.55	4.54	81,81,81,81	0
56	MG	RA	3102	1/1	0.80	0.83	4.51	88,88,88,88	0
56	MG	RA	3217	1/1	0.92	0.53	4.51	97,97,97,97	0
56	MG	RA	4046	1/1	0.68	0.53	4.46	91,91,91,91	0
56	MG	QA	1616	1/1	0.89	0.30	4.45	101,101,101,101	0
56	MG	RA	3614	1/1	0.80	0.37	4.44	68,68,68,68	0
56	MG	RA	3709	1/1	0.30	0.57	4.43	91,91,91,91	0
56	MG	XF	202	1/1	0.62	0.63	4.42	96,96,96,96	0
56	MG	RA	3352	1/1	-0.12	0.79	4.42	97,97,97,97	0
56	MG	YA	3517	1/1	0.90	0.51	4.42	97,97,97,97	0
56	MG	YA	3607	1/1	0.97	0.34	4.37	65,65,65,65	0
56	MG	YA	3729	1/1	0.93	0.50	4.30	69,69,69,69	0
56	MG	YA	3071	1/1	0.99	0.44	4.22	90,90,90,90	0
56	MG	XA	1628	1/1	0.78	0.27	4.20	79,79,79,79	0
56	MG	QA	1802	1/1	0.91	0.24	4.19	82,82,82,82	0
56	MG	QA	1647	1/1	0.31	0.25	4.17	101,101,101,101	0
56	MG	RA	3333	1/1	0.91	0.46	4.15	64,64,64,64	0
56	MG	RA	3235	1/1	0.57	0.55	4.15	93,93,93,93	0
56	MG	QY	401	1/1	0.31	0.68	4.13	90,90,90,90	0
56	MG	RB	209	1/1	0.38	0.29	4.13	76,76,76,76	0
56	MG	XA	1772	1/1	0.91	0.33	4.12	76,76,76,76	0
56	MG	RA	4050	1/1	0.68	0.38	4.11	98,98,98,98	0
56	MG	YA	3148	1/1	0.81	0.34	4.09	63,63,63,63	0
56	MG	RA	4009	1/1	0.70	0.54	4.01	84,84,84,84	0
56	MG	XA	1792	1/1	0.53	0.59	4.00	95,95,95,95	0
56	MG	QD	303	1/1	0.54	0.55	3.99	94,94,94,94	0
56	MG	YX	101	1/1	0.80	0.41	3.97	69,69,69,69	0
56	MG	RA	3598	1/1	0.94	0.37	3.95	69,69,69,69	0
56	MG	YE	305	1/1	0.51	0.40	3.91	82,82,82,82	0
56	MG	XA	1609	1/1	0.78	0.26	3.87	87,87,87,87	0
56	MG	RA	3473	1/1	0.73	0.25	3.84	80,80,80,80	0
56	MG	Y8	101	1/1	0.77	0.79	3.84	72,72,72,72	0
56	MG	RR	202	1/1	-0.01	0.60	3.81	87,87,87,87	0
56	MG	QA	1619	1/1	0.91	0.37	3.77	95,95,95,95	0
56	MG	RA	4040	1/1	0.88	0.57	3.76	99,99,99,99	0
56	MG	YA	3133	1/1	0.92	1.09	3.70	87,87,87,87	0
56	MG	RA	3971	1/1	0.94	0.47	3.69	63,63,63,63	0
56	MG	QA	1658	1/1	0.79	0.30	3.66	88,88,88,88	0
56	MG	RA	3656	1/1	0.96	0.36	3.65	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3328	1/1	0.69	0.29	3.64	73,73,73,73	0
56	MG	YA	3755	1/1	0.96	0.36	3.64	74,74,74,74	0
56	MG	YA	3199	1/1	0.93	0.34	3.63	71,71,71,71	0
56	MG	RA	4008	1/1	0.59	0.48	3.63	92,92,92,92	0
56	MG	XA	1688	1/1	0.84	0.43	3.62	97,97,97,97	0
56	MG	YA	3746	1/1	0.90	0.42	3.60	85,85,85,85	0
56	MG	YA	3578	1/1	0.87	0.62	3.60	101,101,101,101	0
56	MG	XA	1793	1/1	0.54	0.59	3.60	94,94,94,94	0
56	MG	RA	3092	1/1	0.86	0.39	3.55	91,91,91,91	0
56	MG	RE	306	1/1	0.42	0.41	3.53	63,63,63,63	0
56	MG	RA	3041	1/1	0.80	0.20	3.51	70,70,70,70	0
56	MG	YA	3601	1/1	0.98	0.36	3.51	62,62,62,62	0
56	MG	QN	102	1/1	0.00	0.88	3.38	90,90,90,90	0
56	MG	XA	1731	1/1	0.70	0.24	3.37	82,82,82,82	0
56	MG	QA	1672	1/1	0.72	0.55	3.32	85,85,85,85	0
56	MG	RB	225	1/1	0.60	0.34	3.32	80,80,80,80	0
56	MG	XA	1758	1/1	0.91	0.42	3.31	68,68,68,68	0
56	MG	YA	3616	1/1	0.84	0.34	3.31	65,65,65,65	0
56	MG	XA	1666	1/1	0.87	0.31	3.30	92,92,92,92	0
56	MG	YA	3332	1/1	0.59	0.28	3.27	62,62,62,62	0
56	MG	RD	306	1/1	0.81	0.52	3.20	84,84,84,84	0
56	MG	QA	1618	1/1	0.88	0.21	3.20	101,101,101,101	0
56	MG	YA	3704	1/1	0.81	0.36	3.14	66,66,66,66	0
56	MG	RA	3271	1/1	0.86	0.38	3.13	97,97,97,97	0
56	MG	YA	3297	1/1	0.26	0.35	3.13	70,70,70,70	0
56	MG	YE	301	1/1	0.53	0.50	3.11	66,66,66,66	0
56	MG	RA	3043	1/1	0.70	0.23	3.09	67,67,67,67	0
56	MG	RA	3064	1/1	0.86	0.27	3.09	81,81,81,81	0
56	MG	QT	201	1/1	0.77	0.54	3.09	77,77,77,77	0
56	MG	RF	304	1/1	0.88	0.40	3.09	74,74,74,74	0
56	MG	YA	3554	1/1	0.79	0.32	3.03	79,79,79,79	0
56	MG	RA	3030	1/1	0.89	0.74	3.03	94,94,94,94	0
56	MG	YE	303	1/1	0.26	0.44	2.99	93,93,93,93	0
56	MG	RA	3014	1/1	0.95	0.31	2.96	68,68,68,68	0
56	MG	QA	1823	1/1	0.53	0.66	2.95	94,94,94,94	0
56	MG	RA	3402	1/1	0.61	0.33	2.93	80,80,80,80	0
56	MG	RA	3986	1/1	0.82	0.56	2.93	79,79,79,79	0
56	MG	YA	3429	1/1	0.81	0.41	2.89	73,73,73,73	0
56	MG	YQ	201	1/1	0.53	0.34	2.88	69,69,69,69	0
56	MG	YA	3756	1/1	0.39	0.72	2.84	96,96,96,96	0
56	MG	YA	3174	1/1	0.80	0.21	2.84	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3008	1/1	0.69	0.65	2.81	66,66,66,66	0
56	MG	YA	3689	1/1	0.78	0.32	2.80	78,78,78,78	0
56	MG	QA	1610	1/1	0.83	0.27	2.80	93,93,93,93	0
56	MG	QD	305	1/1	0.55	0.32	2.76	99,99,99,99	0
56	MG	RD	312	1/1	0.55	0.51	2.72	90,90,90,90	0
56	MG	RX	101	1/1	0.82	0.41	2.60	78,78,78,78	0
56	MG	RA	3601	1/1	0.65	0.49	2.60	83,83,83,83	0
56	MG	RQ	201	1/1	0.47	0.39	2.57	87,87,87,87	0
56	MG	YA	3089	1/1	0.83	0.29	2.56	80,80,80,80	0
56	MG	YB	214	1/1	0.82	0.25	2.52	78,78,78,78	0
56	MG	XA	1618	1/1	0.86	0.30	2.51	81,81,81,81	0
56	MG	RA	3032	1/1	0.51	0.29	2.50	92,92,92,92	0
56	MG	XA	1723	1/1	0.48	0.28	2.46	91,91,91,91	0
56	MG	RA	4068	1/1	0.58	0.58	2.36	91,91,91,91	0
56	MG	RQ	204	1/1	0.72	0.65	2.29	89,89,89,89	0
56	MG	RA	4018	1/1	0.92	0.38	2.28	106,106,106,106	0
56	MG	XA	1727	1/1	0.86	0.23	2.23	79,79,79,79	0
56	MG	QA	1606	1/1	0.68	0.20	2.23	88,88,88,88	0
57	ZN	Y4	101	1/1	0.56	0.40	2.20	176,176,176,176	0
56	MG	YA	3053	1/1	0.82	0.23	2.19	62,62,62,62	0
56	MG	YA	3420	1/1	0.89	0.30	2.18	68,68,68,68	0
56	MG	RA	4006	1/1	0.86	0.30	2.15	74,74,74,74	0
56	MG	RA	3906	1/1	0.93	0.42	2.15	62,62,62,62	0
56	MG	YA	3094	1/1	0.21	0.25	2.14	77,77,77,77	0
56	MG	RA	3505	1/1	0.79	0.31	2.13	68,68,68,68	0
56	MG	YA	3727	1/1	0.94	0.36	2.12	62,62,62,62	0
56	MG	RA	3211	1/1	0.89	0.29	2.10	78,78,78,78	0
56	MG	XA	1632	1/1	0.97	0.58	2.09	84,84,84,84	0
56	MG	YA	3685	1/1	0.49	0.60	2.07	87,87,87,87	0
56	MG	RA	3981	1/1	0.96	0.23	2.01	78,78,78,78	0
57	ZN	R4	101	1/1	0.65	0.51	1.95	177,177,177,177	0
56	MG	QA	1621	1/1	0.64	0.28	1.93	85,85,85,85	0
56	MG	YA	3060	1/1	0.79	0.34	1.92	68,68,68,68	0
56	MG	YA	3407	1/1	0.91	0.33	1.90	62,62,62,62	0
56	MG	YA	3039	1/1	0.87	0.19	1.87	67,67,67,67	0
56	MG	QA	1635	1/1	0.41	0.19	1.86	77,77,77,77	0
56	MG	RA	4001	1/1	0.73	0.34	1.85	62,62,62,62	0
56	MG	RA	4067	1/1	0.98	0.41	1.83	72,72,72,72	0
56	MG	RA	3625	1/1	0.83	0.30	1.83	73,73,73,73	0
56	MG	XF	201	1/1	0.54	0.29	1.81	68,68,68,68	0
56	MG	YA	3252	1/1	0.67	0.24	1.72	96,96,96,96	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3571	1/1	0.83	0.17	1.69	74,74,74,74	0
56	MG	YA	3669	1/1	0.89	0.37	1.65	65,65,65,65	0
56	MG	QB	301	1/1	0.60	0.35	1.65	81,81,81,81	0
56	MG	QA	1645	1/1	0.80	0.25	1.62	76,76,76,76	0
56	MG	QA	1656	1/1	0.74	0.25	1.59	78,78,78,78	0
56	MG	YA	3012	1/1	0.82	0.26	1.59	70,70,70,70	0
56	MG	YA	3221	1/1	0.87	0.17	1.58	80,80,80,80	0
56	MG	YA	3281	1/1	0.58	0.33	1.57	62,62,62,62	0
56	MG	RA	4029	1/1	0.66	0.36	1.56	62,62,62,62	0
56	MG	YA	3139	1/1	0.85	0.30	1.53	63,63,63,63	0
56	MG	XA	1697	1/1	0.08	0.21	1.48	87,87,87,87	0
56	MG	YA	3150	1/1	0.86	0.40	1.43	79,79,79,79	0
56	MG	RA	3157	1/1	0.80	0.24	1.37	84,84,84,84	0
56	MG	QA	1717	1/1	0.92	0.17	1.36	92,92,92,92	0
56	MG	RB	206	1/1	0.76	0.15	1.31	80,80,80,80	0
56	MG	XL	201	1/1	0.70	0.40	1.31	82,82,82,82	0
56	MG	RA	3396	1/1	0.77	0.25	1.29	67,67,67,67	0
56	MG	RA	3722	1/1	0.80	0.42	1.25	83,83,83,83	0
56	MG	RA	3867	1/1	0.88	0.15	1.24	81,81,81,81	0
56	MG	QQ	202	1/1	0.84	0.24	1.17	92,92,92,92	0
56	MG	QA	1620	1/1	0.90	0.20	1.11	69,69,69,69	0
56	MG	RA	3532	1/1	0.78	0.27	1.07	63,63,63,63	0
56	MG	RB	205	1/1	0.70	0.21	1.01	92,92,92,92	0
56	MG	RA	4004	1/1	0.87	0.34	0.97	64,64,64,64	0
56	MG	QA	1691	1/1	0.76	0.41	0.94	96,96,96,96	0
56	MG	RA	3084	1/1	0.91	0.26	0.89	76,76,76,76	0
56	MG	YA	3111	1/1	0.92	0.26	0.86	88,88,88,88	0
56	MG	RB	219	1/1	0.93	0.21	0.84	73,73,73,73	0
56	MG	QR	101	1/1	0.60	0.41	0.82	93,93,93,93	0
56	MG	YA	3730	1/1	0.92	0.28	0.80	80,80,80,80	0
56	MG	XA	1753	1/1	0.94	0.25	0.78	81,81,81,81	0
56	MG	RG	201	1/1	0.81	0.33	0.73	89,89,89,89	0
56	MG	QA	1655	1/1	0.82	0.31	0.71	93,93,93,93	0
56	MG	RE	303	1/1	0.45	0.39	0.71	102,102,102,102	0
56	MG	QA	1742	1/1	0.83	0.18	0.69	92,92,92,92	0
56	MG	YA	3725	1/1	0.85	0.35	0.69	62,62,62,62	0
56	MG	RA	3131	1/1	0.38	0.14	0.68	88,88,88,88	0
56	MG	YA	3337	1/1	0.92	0.26	0.67	76,76,76,76	0
56	MG	RA	3075	1/1	0.78	0.24	0.67	76,76,76,76	0
56	MG	RA	3585	1/1	0.57	0.21	0.59	77,77,77,77	0
56	MG	RA	3530	1/1	0.93	0.30	0.59	62,62,62,62	0
56	MG	RA	3508	1/1	0.93	0.19	0.56	89,89,89,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3305	1/1	0.71	0.29	0.55	73,73,73,73	0
56	MG	YA	3565	1/1	0.91	0.39	0.54	64,64,64,64	0
56	MG	QA	1665	1/1	0.86	0.29	0.50	95,95,95,95	0
56	MG	YA	3448	1/1	0.72	0.17	0.47	80,80,80,80	0
56	MG	YA	3535	1/1	0.92	0.28	0.47	69,69,69,69	0
56	MG	RA	3784	1/1	0.95	0.24	0.46	88,88,88,88	0
56	MG	XA	1764	1/1	0.90	0.23	0.41	73,73,73,73	0
56	MG	Y6	102	1/1	0.56	0.48	0.40	102,102,102,102	0
56	MG	YG	202	1/1	0.86	0.20	0.31	92,92,92,92	0
56	MG	QA	1781	1/1	0.88	0.28	0.26	95,95,95,95	0
56	MG	RA	3312	1/1	0.39	0.34	0.20	96,96,96,96	0
56	MG	RA	3852	1/1	0.74	0.20	0.19	90,90,90,90	0
56	MG	Y1	101	1/1	0.73	0.31	0.12	62,62,62,62	0
56	MG	XA	1659	1/1	0.73	0.21	0.06	88,88,88,88	0
56	MG	QA	1770	1/1	0.85	0.15	0.04	91,91,91,91	0
56	MG	RA	3326	1/1	0.94	0.29	0.03	63,63,63,63	0
56	MG	YA	3085	1/1	0.82	0.18	-0.01	85,85,85,85	0
56	MG	RA	4039	1/1	0.91	0.23	-0.02	92,92,92,92	0
56	MG	RB	215	1/1	0.54	0.18	-0.03	81,81,81,81	0
57	ZN	RY	201	1/1	0.84	0.24	-0.04	158,158,158,158	0
56	MG	RA	3654	1/1	0.91	0.19	-0.05	71,71,71,71	0
56	MG	RA	3025	1/1	0.72	0.21	-0.07	69,69,69,69	0
56	MG	RA	3455	1/1	0.85	0.22	-0.09	81,81,81,81	0
56	MG	XA	1654	1/1	0.81	0.28	-0.11	87,87,87,87	0
57	ZN	YY	201	1/1	0.56	0.23	-0.13	167,167,167,167	0
56	MG	QA	1874	1/1	0.67	0.23	-0.15	93,93,93,93	0
56	MG	RA	3901	1/1	0.91	0.24	-0.18	71,71,71,71	0
56	MG	YE	304	1/1	0.77	0.29	-0.22	71,71,71,71	0
56	MG	RA	3008	1/1	0.17	0.22	-0.23	83,83,83,83	0
56	MG	YA	3151	1/1	0.92	0.23	-0.24	87,87,87,87	0
56	MG	YA	3283	1/1	0.62	0.14	-0.31	74,74,74,74	0
56	MG	YA	3115	1/1	0.72	0.17	-0.51	77,77,77,77	0
56	MG	RD	307	1/1	0.81	0.26	-0.54	72,72,72,72	0
56	MG	RA	4038	1/1	0.63	0.23	-0.57	75,75,75,75	0
56	MG	QV	101	1/1	0.69	0.17	-0.62	86,86,86,86	0
58	SF4	QD	302	8/8	0.99	0.17	-0.64	71,79,94,101	0
56	MG	RA	3702	1/1	0.94	0.20	-0.64	83,83,83,83	0
56	MG	RA	3357	1/1	0.95	0.21	-0.84	62,62,62,62	0
56	MG	YA	3453	1/1	0.87	0.17	-0.85	79,79,79,79	0
56	MG	RA	3062	1/1	0.68	0.13	-0.88	84,84,84,84	0
56	MG	YF	302	1/1	0.62	0.24	-0.95	75,75,75,75	0
58	SF4	XD	301	8/8	0.98	0.15	-0.97	65,79,98,112	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	XA	1636	1/1	0.74	0.22	-0.98	68,68,68,68	0
56	MG	XK	201	1/1	0.75	0.18	-1.05	87,87,87,87	0
56	MG	RA	3868	1/1	0.82	0.14	-1.06	83,83,83,83	0
57	ZN	XN	101	1/1	0.98	0.13	-1.09	91,91,91,91	0
56	MG	XA	1644	1/1	0.88	0.13	-1.12	94,94,94,94	0
56	MG	QA	1631	1/1	0.87	0.17	-1.13	73,73,73,73	0
56	MG	RG	204	1/1	0.24	0.18	-1.17	84,84,84,84	0
56	MG	YG	203	1/1	0.65	0.15	-1.17	91,91,91,91	0
56	MG	RA	3671	1/1	0.86	0.12	-1.23	79,79,79,79	0
56	MG	YA	3021	1/1	0.86	0.20	-1.32	66,66,66,66	0
57	ZN	Y6	101	1/1	0.82	0.37	-1.34	156,156,156,156	0
57	ZN	R6	101	1/1	0.80	0.32	-1.43	159,159,159,159	0
56	MG	QA	1845	1/1	0.60	0.12	-1.44	79,79,79,79	0
57	ZN	QN	101	1/1	0.96	0.12	-1.48	110,110,110,110	0
56	MG	RA	3965	1/1	0.81	0.18	-1.50	73,73,73,73	0
56	MG	YA	3430	1/1	0.94	0.27	-1.58	80,80,80,80	0
57	ZN	R9	102	1/1	0.94	0.10	-1.59	125,125,125,125	0
57	ZN	R5	103	1/1	0.88	0.04	-1.59	135,135,135,135	0
57	ZN	Y9	101	1/1	0.94	0.06	-1.67	116,116,116,116	0
57	ZN	Y5	102	1/1	0.89	0.06	-1.73	144,144,144,144	0
56	MG	QA	1871	1/1	0.58	0.12	-1.82	77,77,77,77	0
56	MG	RA	3966	1/1	0.88	0.20	-1.98	71,71,71,71	0
56	MG	XA	1621	1/1	0.70	0.13	-2.09	83,83,83,83	0
56	MG	YA	3184	1/1	0.91	0.15	-2.24	78,78,78,78	0
56	MG	XV	101	1/1	0.79	0.11	-2.60	87,87,87,87	0
56	MG	QA	1650	1/1	0.96	0.08	-3.90	93,93,93,93	0
56	MG	YA	3187	1/1	0.95	0.07	-5.88	89,89,89,89	0
56	MG	RA	3562	1/1	0.61	0.69	-	82,82,82,82	0
56	MG	YA	3241	1/1	0.89	0.65	-	91,91,91,91	0
56	MG	RA	3678	1/1	0.82	0.87	-	78,78,78,78	0
56	MG	YA	3670	1/1	0.64	0.55	-	85,85,85,85	0
56	MG	RA	3848	1/1	0.02	1.03	-	91,91,91,91	0
56	MG	QA	1840	1/1	0.25	0.60	-	88,88,88,88	0
56	MG	XA	1625	1/1	0.54	0.77	-	90,90,90,90	0
56	MG	RA	4005	1/1	0.83	0.21	-	80,80,80,80	0
56	MG	RA	3681	1/1	0.71	0.88	-	72,72,72,72	0
56	MG	RA	3266	1/1	0.80	0.13	-	106,106,106,106	0
56	MG	YA	3273	1/1	0.82	0.36	-	84,84,84,84	0
56	MG	RB	208	1/1	0.30	0.34	-	95,95,95,95	0
56	MG	YA	3399	1/1	0.46	0.80	-	76,76,76,76	0
56	MG	RA	3346	1/1	0.85	0.62	-	83,83,83,83	0
56	MG	RD	304	1/1	0.48	0.52	-	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	XA	1716	1/1	0.63	0.56	-	79,79,79,79	0
56	MG	YA	3417	1/1	0.83	0.68	-	69,69,69,69	0
56	MG	XA	1619	1/1	0.46	0.82	-	76,76,76,76	0
56	MG	YB	207	1/1	0.94	0.35	-	97,97,97,97	0
56	MG	YA	3334	1/1	0.80	0.57	-	66,66,66,66	0
56	MG	QA	1782	1/1	0.55	0.28	-	98,98,98,98	0
56	MG	RA	3292	1/1	0.79	0.66	-	93,93,93,93	0
56	MG	RA	4020	1/1	0.71	0.45	-	91,91,91,91	0
56	MG	YA	3348	1/1	0.77	0.59	-	88,88,88,88	0
56	MG	XA	1694	1/1	0.76	0.37	-	77,77,77,77	0
56	MG	QA	1727	1/1	0.65	0.47	-	86,86,86,86	0
56	MG	RA	3222	1/1	0.76	0.64	-	88,88,88,88	0
56	MG	RA	3842	1/1	0.87	0.68	-	75,75,75,75	0
56	MG	RA	3220	1/1	0.95	0.29	-	82,82,82,82	0
56	MG	QA	1769	1/1	-0.54	1.08	-	99,99,99,99	0
56	MG	RA	3055	1/1	0.89	0.94	-	112,112,112,112	0
56	MG	YA	3016	1/1	0.47	0.63	-	89,89,89,89	0
56	MG	QA	1661	1/1	0.58	0.90	-	85,85,85,85	0
56	MG	RA	3374	1/1	0.54	0.75	-	72,72,72,72	0
56	MG	RA	3553	1/1	0.70	0.23	-	100,100,100,100	0
56	MG	YA	3687	1/1	0.62	0.72	-	62,62,62,62	0
56	MG	YA	3403	1/1	0.20	0.35	-	81,81,81,81	0
56	MG	RA	3993	1/1	0.48	0.83	-	85,85,85,85	0
56	MG	RA	3622	1/1	0.78	0.43	-	87,87,87,87	0
56	MG	XA	1657	1/1	0.25	0.97	-	91,91,91,91	0
56	MG	RA	3420	1/1	0.93	0.64	-	62,62,62,62	0
56	MG	XA	1742	1/1	0.56	0.42	-	78,78,78,78	0
56	MG	QA	1690	1/1	0.43	0.32	-	68,68,68,68	0
56	MG	YA	3465	1/1	0.44	0.58	-	85,85,85,85	0
56	MG	QA	1818	1/1	-0.00	0.58	-	93,93,93,93	0
56	MG	YA	3657	1/1	0.81	0.67	-	81,81,81,81	0
56	MG	RA	3887	1/1	0.52	0.57	-	91,91,91,91	0
56	MG	RA	3324	1/1	0.85	0.65	-	62,62,62,62	0
56	MG	RA	3564	1/1	0.33	0.76	-	91,91,91,91	0
56	MG	YA	3287	1/1	0.93	0.52	-	78,78,78,78	0
56	MG	RA	3797	1/1	0.01	0.44	-	109,109,109,109	0
56	MG	QA	1644	1/1	0.82	0.39	-	95,95,95,95	0
56	MG	YA	3219	1/1	0.36	0.60	-	95,95,95,95	0
56	MG	YA	3472	1/1	0.59	0.66	-	82,82,82,82	0
56	MG	RA	3528	1/1	0.37	1.11	-	81,81,81,81	0
56	MG	YA	3742	1/1	0.85	0.27	-	85,85,85,85	0
56	MG	RA	3437	1/1	0.35	1.16	-	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
56	MG	RA	3570	1/1	0.79	0.57	-	71,71,71,71	0
56	MG	YA	3507	1/1	0.20	0.79	-	80,80,80,80	0
56	MG	YA	3274	1/1	0.93	0.85	-	62,62,62,62	0
56	MG	RA	3256	1/1	0.84	0.88	-	96,96,96,96	0
56	MG	RA	3227	1/1	0.20	1.13	-	103,103,103,103	0
56	MG	RA	3072	1/1	0.86	1.18	-	110,110,110,110	0
56	MG	RD	301	1/1	0.81	1.08	-	93,93,93,93	0
56	MG	YA	3347	1/1	0.86	0.23	-	79,79,79,79	0
56	MG	RA	3670	1/1	-0.72	1.68	-	103,103,103,103	0
56	MG	QA	1746	1/1	0.68	0.42	-	80,80,80,80	0
56	MG	RA	3400	1/1	0.07	0.79	-	101,101,101,101	0
56	MG	QA	1851	1/1	0.79	0.67	-	78,78,78,78	0
56	MG	YA	3090	1/1	0.26	0.32	-	100,100,100,100	0
56	MG	YA	3005	1/1	0.73	0.42	-	85,85,85,85	0
56	MG	RA	3563	1/1	0.45	0.37	-	87,87,87,87	0
56	MG	QA	1744	1/1	0.93	0.38	-	77,77,77,77	0
56	MG	YA	3246	1/1	0.76	0.57	-	81,81,81,81	0
56	MG	YA	3052	1/1	0.94	0.10	-	80,80,80,80	0
56	MG	YA	3576	1/1	0.85	0.76	-	74,74,74,74	0
56	MG	YA	3383	1/1	0.94	0.61	-	63,63,63,63	0
56	MG	RA	3130	1/1	0.84	0.17	-	85,85,85,85	0
56	MG	QA	1743	1/1	0.86	0.27	-	71,71,71,71	0
56	MG	RW	201	1/1	0.45	0.54	-	83,83,83,83	0
56	MG	YV	201	1/1	0.47	0.54	-	84,84,84,84	0
56	MG	YA	3307	1/1	0.68	0.71	-	71,71,71,71	0
56	MG	RA	3443	1/1	0.94	0.99	-	62,62,62,62	0
56	MG	RA	3613	1/1	0.56	1.04	-	75,75,75,75	0
56	MG	YA	3605	1/1	0.84	0.33	-	84,84,84,84	0
56	MG	YA	3549	1/1	0.15	0.71	-	90,90,90,90	0
56	MG	RA	3645	1/1	0.70	0.74	-	85,85,85,85	0
56	MG	YA	3534	1/1	0.53	0.34	-	85,85,85,85	0
56	MG	QA	1880	1/1	0.64	0.39	-	102,102,102,102	0
56	MG	QA	1681	1/1	0.26	1.12	-	92,92,92,92	0
56	MG	RA	3144	1/1	0.77	0.69	-	86,86,86,86	0
56	MG	YA	3666	1/1	0.77	0.45	-	63,63,63,63	0
56	MG	YA	3003	1/1	0.93	0.68	-	70,70,70,70	0
56	MG	RA	3378	1/1	0.82	0.54	-	66,66,66,66	0
56	MG	YA	3536	1/1	0.93	0.47	-	63,63,63,63	0
56	MG	RA	3581	1/1	0.63	0.69	-	97,97,97,97	0
56	MG	RA	3034	1/1	0.87	0.69	-	97,97,97,97	0
56	MG	YA	3176	1/1	0.82	0.34	-	78,78,78,78	0
56	MG	RA	3704	1/1	0.70	0.56	-	82,82,82,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	QA	1786	1/1	0.55	0.58	-	80,80,80,80	0
56	MG	YD	302	1/1	0.80	0.84	-	81,81,81,81	0
56	MG	RA	3257	1/1	0.78	0.52	-	100,100,100,100	0
56	MG	RA	3510	1/1	0.91	0.98	-	71,71,71,71	0
56	MG	YA	3707	1/1	0.74	0.56	-	82,82,82,82	0
56	MG	XY	401	1/1	-0.02	1.97	-	97,97,97,97	0
56	MG	R0	101	1/1	0.84	0.74	-	77,77,77,77	0
56	MG	QA	1808	1/1	0.24	0.39	-	74,74,74,74	0
56	MG	XH	201	1/1	-0.10	0.60	-	99,99,99,99	0
56	MG	RA	3273	1/1	0.41	1.22	-	99,99,99,99	0
56	MG	XA	1669	1/1	0.18	0.62	-	106,106,106,106	0
56	MG	QA	1637	1/1	0.29	0.82	-	85,85,85,85	0
56	MG	RA	3869	1/1	0.40	0.93	-	88,88,88,88	0
56	MG	XA	1736	1/1	0.88	0.87	-	70,70,70,70	0
56	MG	YA	3341	1/1	0.40	0.37	-	91,91,91,91	0
56	MG	RA	3788	1/1	0.64	0.55	-	90,90,90,90	0
56	MG	RA	3647	1/1	0.64	1.10	-	102,102,102,102	0
56	MG	YA	3477	1/1	0.60	0.59	-	77,77,77,77	0
56	MG	RA	3904	1/1	0.22	0.66	-	80,80,80,80	0
56	MG	RA	3925	1/1	0.20	0.33	-	95,95,95,95	0
56	MG	RA	3600	1/1	0.11	0.94	-	94,94,94,94	0
56	MG	YA	3690	1/1	0.74	0.47	-	78,78,78,78	0
56	MG	RA	3016	1/1	0.60	0.86	-	109,109,109,109	0
56	MG	QA	1739	1/1	0.61	0.56	-	80,80,80,80	0
56	MG	QA	1765	1/1	0.40	0.93	-	80,80,80,80	0
56	MG	RA	3370	1/1	0.76	0.75	-	78,78,78,78	0
56	MG	YA	3081	1/1	0.84	0.41	-	81,81,81,81	0
56	MG	RA	3547	1/1	-0.09	0.61	-	99,99,99,99	0
56	MG	RA	3988	1/1	0.58	0.72	-	86,86,86,86	0
56	MG	XA	1749	1/1	0.09	1.00	-	98,98,98,98	0
56	MG	QA	1785	1/1	0.94	0.15	-	95,95,95,95	0
56	MG	QA	1766	1/1	0.89	0.10	-	96,96,96,96	0
56	MG	YA	3159	1/1	0.85	0.14	-	76,76,76,76	0
56	MG	RA	3692	1/1	0.82	0.59	-	84,84,84,84	0
56	MG	RA	3042	1/1	-0.06	0.75	-	92,92,92,92	0
56	MG	RA	3710	1/1	0.75	0.41	-	98,98,98,98	0
56	MG	YA	3034	1/1	0.86	0.28	-	74,74,74,74	0
56	MG	YA	3051	1/1	0.70	0.42	-	82,82,82,82	0
56	MG	YA	3394	1/1	0.23	0.93	-	75,75,75,75	0
56	MG	QA	1627	1/1	0.84	0.10	-	79,79,79,79	0
56	MG	YA	3508	1/1	0.52	0.39	-	83,83,83,83	0
56	MG	RA	3732	1/1	0.69	0.79	-	85,85,85,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3424	1/1	0.89	0.46	-	70,70,70,70	0
56	MG	RU	202	1/1	0.29	0.68	-	94,94,94,94	0
56	MG	QA	1679	1/1	0.46	0.80	-	87,87,87,87	0
56	MG	RA	3426	1/1	0.39	0.32	-	79,79,79,79	0
56	MG	XA	1718	1/1	0.88	0.59	-	78,78,78,78	0
56	MG	QA	1718	1/1	0.85	0.33	-	94,94,94,94	0
56	MG	RA	3940	1/1	0.56	0.79	-	90,90,90,90	0
56	MG	RA	3071	1/1	0.88	0.80	-	86,86,86,86	0
56	MG	RA	3363	1/1	0.87	0.15	-	91,91,91,91	0
56	MG	RA	3036	1/1	0.02	0.85	-	94,94,94,94	0
56	MG	XE	201	1/1	-0.13	1.00	-	93,93,93,93	0
56	MG	QA	1667	1/1	0.91	0.20	-	92,92,92,92	0
56	MG	YA	3617	1/1	0.83	0.51	-	74,74,74,74	0
56	MG	RA	3687	1/1	0.44	0.36	-	86,86,86,86	0
56	MG	RB	226	1/1	0.50	0.40	-	98,98,98,98	0
56	MG	QA	1693	1/1	0.86	0.60	-	87,87,87,87	0
56	MG	RA	3096	1/1	0.82	0.29	-	83,83,83,83	0
56	MG	YA	3188	1/1	0.31	0.28	-	92,92,92,92	0
56	MG	QA	1747	1/1	0.58	1.23	-	81,81,81,81	0
56	MG	YA	3677	1/1	0.89	1.45	-	79,79,79,79	0
56	MG	YA	3189	1/1	0.81	0.32	-	83,83,83,83	0
56	MG	YA	3057	1/1	0.40	0.69	-	90,90,90,90	0
56	MG	RA	3664	1/1	0.85	0.36	-	91,91,91,91	0
56	MG	RE	304	1/1	0.93	0.76	-	62,62,62,62	0
56	MG	RA	3888	1/1	0.52	0.74	-	89,89,89,89	0
56	MG	RA	3475	1/1	0.85	0.30	-	82,82,82,82	0
56	MG	QA	1695	1/1	0.83	0.46	-	93,93,93,93	0
56	MG	YA	3584	1/1	0.85	0.44	-	77,77,77,77	0
56	MG	RN	203	1/1	0.75	0.95	-	90,90,90,90	0
56	MG	YA	3228	1/1	0.40	1.01	-	73,73,73,73	0
56	MG	RA	3637	1/1	0.52	0.73	-	85,85,85,85	0
56	MG	QA	1864	1/1	0.72	0.40	-	97,97,97,97	0
56	MG	XA	1713	1/1	0.62	0.34	-	74,74,74,74	0
56	MG	YA	3490	1/1	0.95	0.24	-	67,67,67,67	0
56	MG	YA	3097	1/1	0.69	0.39	-	96,96,96,96	0
56	MG	YA	3544	1/1	0.58	0.47	-	63,63,63,63	0
56	MG	XA	1762	1/1	0.85	0.29	-	70,70,70,70	0
56	MG	QA	1809	1/1	0.57	0.47	-	86,86,86,86	0
56	MG	RA	3044	1/1	0.68	0.39	-	82,82,82,82	0
56	MG	YA	3244	1/1	0.16	1.19	-	97,97,97,97	0
56	MG	Y8	102	1/1	0.79	0.61	-	68,68,68,68	0
56	MG	XA	1655	1/1	0.61	0.49	-	82,82,82,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3059	1/1	-0.06	1.01	-	86,86,86,86	0
56	MG	YA	3095	1/1	0.77	0.54	-	64,64,64,64	0
56	MG	RA	3123	1/1	0.36	0.37	-	80,80,80,80	0
56	MG	QA	1719	1/1	0.54	1.13	-	73,73,73,73	0
56	MG	RA	3316	1/1	0.06	0.81	-	93,93,93,93	0
56	MG	RA	3049	1/1	0.85	0.17	-	80,80,80,80	0
56	MG	RA	3639	1/1	0.65	0.57	-	82,82,82,82	0
56	MG	YA	3158	1/1	0.82	0.43	-	84,84,84,84	0
56	MG	RA	3819	1/1	0.09	0.92	-	90,90,90,90	0
56	MG	RA	3555	1/1	0.61	0.52	-	80,80,80,80	0
56	MG	YA	3227	1/1	0.27	1.11	-	87,87,87,87	0
56	MG	RA	3005	1/1	0.66	0.74	-	91,91,91,91	0
56	MG	RA	3779	1/1	0.94	1.32	-	71,71,71,71	0
56	MG	RA	3108	1/1	0.71	0.85	-	89,89,89,89	0
56	MG	RA	3430	1/1	0.67	0.31	-	93,93,93,93	0
56	MG	RA	3028	1/1	0.87	0.15	-	84,84,84,84	0
56	MG	RA	3810	1/1	0.66	0.78	-	79,79,79,79	0
56	MG	QA	1831	1/1	0.23	0.82	-	99,99,99,99	0
56	MG	XA	1660	1/1	0.90	0.23	-	91,91,91,91	0
56	MG	YA	3655	1/1	0.82	0.53	-	62,62,62,62	0
56	MG	RA	4015	1/1	0.80	0.71	-	93,93,93,93	0
56	MG	RA	3202	1/1	0.77	0.40	-	87,87,87,87	0
56	MG	RR	204	1/1	0.54	0.51	-	75,75,75,75	0
56	MG	RA	3682	1/1	0.30	0.44	-	104,104,104,104	0
56	MG	RA	3749	1/1	0.72	0.21	-	70,70,70,70	0
56	MG	RA	3689	1/1	0.51	0.22	-	85,85,85,85	0
56	MG	RA	3329	1/1	0.86	0.29	-	94,94,94,94	0
56	MG	RA	3626	1/1	0.66	0.50	-	72,72,72,72	0
56	MG	YA	3628	1/1	0.47	0.34	-	87,87,87,87	0
56	MG	RA	3705	1/1	0.40	0.59	-	89,89,89,89	0
56	MG	YA	3581	1/1	0.34	0.58	-	80,80,80,80	0
56	MG	YA	3126	1/1	0.88	0.19	-	65,65,65,65	0
56	MG	RA	3282	1/1	0.79	0.98	-	102,102,102,102	0
56	MG	RA	4013	1/1	0.71	0.40	-	77,77,77,77	0
56	MG	RA	3228	1/1	0.42	0.56	-	104,104,104,104	0
56	MG	YA	3137	1/1	0.54	0.59	-	81,81,81,81	0
56	MG	RA	3576	1/1	0.61	0.51	-	92,92,92,92	0
56	MG	YA	3515	1/1	0.62	1.06	-	69,69,69,69	0
56	MG	RA	3103	1/1	0.55	0.48	-	101,101,101,101	0
56	MG	QA	1677	1/1	0.56	0.49	-	89,89,89,89	0
56	MG	YA	3526	1/1	0.83	0.68	-	65,65,65,65	0
56	MG	QA	1858	1/1	0.20	0.82	-	86,86,86,86	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
56	MG	RA	3229	1/1	0.52	0.82	-	104,104,104,104	0
56	MG	YA	3162	1/1	0.77	0.50	-	96,96,96,96	0
56	MG	YA	3292	1/1	0.49	0.50	-	74,74,74,74	0
56	MG	RA	4031	1/1	0.37	0.50	-	108,108,108,108	0
56	MG	RA	3520	1/1	0.53	0.53	-	91,91,91,91	0
56	MG	RA	3556	1/1	0.69	1.66	-	83,83,83,83	0
56	MG	YA	3555	1/1	0.83	0.39	-	64,64,64,64	0
56	MG	YA	3172	1/1	0.78	0.28	-	101,101,101,101	0
56	MG	QA	1673	1/1	0.59	0.71	-	75,75,75,75	0
56	MG	YA	3063	1/1	0.73	0.65	-	92,92,92,92	0
56	MG	YA	3369	1/1	0.85	0.32	-	72,72,72,72	0
56	MG	YA	3218	1/1	0.24	0.55	-	82,82,82,82	0
56	MG	QA	1774	1/1	0.58	1.10	-	84,84,84,84	0
56	MG	YA	3569	1/1	0.58	0.98	-	67,67,67,67	0
56	MG	RA	3019	1/1	0.85	0.40	-	108,108,108,108	0
56	MG	YB	212	1/1	0.75	0.54	-	79,79,79,79	0
56	MG	RA	3093	1/1	0.93	0.17	-	97,97,97,97	0
56	MG	RA	3276	1/1	0.69	0.77	-	95,95,95,95	0
56	MG	RA	3507	1/1	0.92	0.33	-	75,75,75,75	0
56	MG	RA	3832	1/1	0.91	0.33	-	84,84,84,84	0
56	MG	RA	3517	1/1	0.85	0.94	-	62,62,62,62	0
56	MG	RA	3053	1/1	0.47	0.54	-	98,98,98,98	0
56	MG	RA	3494	1/1	0.73	0.47	-	81,81,81,81	0
56	MG	RA	3095	1/1	0.87	0.49	-	92,92,92,92	0
56	MG	YA	3673	1/1	0.81	1.15	-	66,66,66,66	0
56	MG	RA	3685	1/1	0.60	0.57	-	80,80,80,80	0
56	MG	RA	3107	1/1	0.91	0.96	-	90,90,90,90	0
56	MG	YA	3042	1/1	0.81	0.24	-	76,76,76,76	0
56	MG	YA	3194	1/1	0.67	0.53	-	89,89,89,89	0
56	MG	RA	3886	1/1	0.03	0.56	-	97,97,97,97	0
56	MG	QA	1684	1/1	0.75	1.17	-	97,97,97,97	0
56	MG	YA	3105	1/1	0.57	0.60	-	81,81,81,81	0
56	MG	YA	3319	1/1	0.95	0.62	-	62,62,62,62	0
56	MG	QL	201	1/1	0.55	0.19	-	87,87,87,87	0
56	MG	RA	3905	1/1	0.98	0.63	-	63,63,63,63	0
56	MG	RA	3294	1/1	0.73	0.49	-	108,108,108,108	0
56	MG	QA	1812	1/1	0.77	0.37	-	69,69,69,69	0
56	MG	RA	3200	1/1	0.73	0.39	-	85,85,85,85	0
56	MG	RA	3792	1/1	0.87	0.48	-	87,87,87,87	0
56	MG	XA	1714	1/1	0.63	0.42	-	76,76,76,76	0
56	MG	RA	3929	1/1	0.81	0.44	-	85,85,85,85	0
56	MG	R5	104	1/1	0.39	1.34	-	97,97,97,97	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	Y5	101	1/1	0.59	0.57	-	91,91,91,91	0
56	MG	XA	1746	1/1	0.87	0.62	-	62,62,62,62	0
56	MG	RA	3515	1/1	0.76	0.38	-	90,90,90,90	0
56	MG	QA	1839	1/1	0.75	0.57	-	79,79,79,79	0
56	MG	RA	3403	1/1	0.82	1.01	-	87,87,87,87	0
56	MG	YA	3233	1/1	0.13	0.44	-	96,96,96,96	0
56	MG	YA	3055	1/1	0.27	0.37	-	88,88,88,88	0
56	MG	RA	3750	1/1	0.72	0.61	-	83,83,83,83	0
56	MG	YA	3594	1/1	0.77	0.70	-	70,70,70,70	0
56	MG	YA	3010	1/1	0.82	0.43	-	84,84,84,84	0
56	MG	RA	3270	1/1	0.97	0.57	-	95,95,95,95	0
56	MG	QA	1712	1/1	0.71	0.48	-	75,75,75,75	0
56	MG	RA	3936	1/1	0.67	0.36	-	82,82,82,82	0
56	MG	RA	3158	1/1	0.89	0.18	-	81,81,81,81	0
56	MG	QA	1767	1/1	0.83	0.38	-	88,88,88,88	0
56	MG	QA	1762	1/1	0.61	0.69	-	80,80,80,80	0
56	MG	YA	3130	1/1	0.64	0.86	-	90,90,90,90	0
56	MG	YA	3548	1/1	0.40	0.86	-	66,66,66,66	0
56	MG	RA	3765	1/1	0.83	0.28	-	91,91,91,91	0
56	MG	YA	3375	1/1	0.85	0.33	-	80,80,80,80	0
56	MG	RA	3156	1/1	0.32	0.59	-	105,105,105,105	0
56	MG	YA	3464	1/1	0.40	1.57	-	79,79,79,79	0
56	MG	RA	3322	1/1	0.40	0.79	-	93,93,93,93	0
56	MG	QA	1796	1/1	0.78	0.54	-	90,90,90,90	0
56	MG	RA	3407	1/1	0.63	0.60	-	95,95,95,95	0
56	MG	RA	3935	1/1	0.60	0.60	-	90,90,90,90	0
56	MG	RA	3806	1/1	0.30	0.73	-	90,90,90,90	0
56	MG	YA	3659	1/1	0.76	1.06	-	65,65,65,65	0
56	MG	RA	3802	1/1	0.64	0.48	-	85,85,85,85	0
56	MG	YA	3243	1/1	0.76	1.34	-	90,90,90,90	0
56	MG	RA	3881	1/1	0.86	0.29	-	80,80,80,80	0
56	MG	QA	1806	1/1	0.62	0.55	-	79,79,79,79	0
56	MG	YA	3711	1/1	0.84	0.30	-	83,83,83,83	0
56	MG	YA	3367	1/1	0.13	0.27	-	76,76,76,76	0
56	MG	XA	1705	1/1	0.71	0.27	-	84,84,84,84	0
56	MG	RA	3759	1/1	0.90	0.23	-	73,73,73,73	0
56	MG	YA	3720	1/1	0.55	0.44	-	75,75,75,75	0
56	MG	RA	3930	1/1	0.93	0.28	-	73,73,73,73	0
56	MG	YA	3619	1/1	0.64	0.59	-	65,65,65,65	0
56	MG	RA	3785	1/1	0.89	0.22	-	83,83,83,83	0
56	MG	RA	3180	1/1	0.58	1.07	-	80,80,80,80	0
56	MG	XA	1734	1/1	0.79	0.36	-	89,89,89,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3222	1/1	0.00	0.74	-	88,88,88,88	0
56	MG	RA	3239	1/1	0.73	0.64	-	106,106,106,106	0
56	MG	RA	3367	1/1	0.46	0.54	-	80,80,80,80	0
56	MG	YA	3047	1/1	0.70	0.41	-	86,86,86,86	0
56	MG	YA	3680	1/1	0.90	0.79	-	62,62,62,62	0
56	MG	RA	3578	1/1	-0.01	0.89	-	90,90,90,90	0
56	MG	RA	3554	1/1	0.78	0.56	-	74,74,74,74	0
56	MG	YA	3022	1/1	0.64	1.80	-	91,91,91,91	0
56	MG	YA	3376	1/1	0.67	0.41	-	84,84,84,84	0
56	MG	RA	3464	1/1	0.70	0.40	-	90,90,90,90	0
56	MG	YA	3245	1/1	0.53	0.41	-	88,88,88,88	0
56	MG	XA	1677	1/1	0.90	0.33	-	63,63,63,63	0
56	MG	RA	3337	1/1	0.48	0.69	-	92,92,92,92	0
56	MG	YA	3353	1/1	0.79	0.54	-	68,68,68,68	0
56	MG	QA	1837	1/1	0.48	0.75	-	87,87,87,87	0
56	MG	QA	1738	1/1	0.05	0.78	-	101,101,101,101	0
56	MG	RD	314	1/1	0.39	0.81	-	80,80,80,80	0
56	MG	RW	202	1/1	0.62	0.47	-	99,99,99,99	0
56	MG	RA	3769	1/1	0.47	0.51	-	85,85,85,85	0
56	MG	RA	3662	1/1	0.41	0.55	-	94,94,94,94	0
56	MG	RA	3513	1/1	0.04	1.32	-	87,87,87,87	0
56	MG	QA	1696	1/1	0.34	0.82	-	71,71,71,71	0
56	MG	RA	3368	1/1	-0.01	0.68	-	90,90,90,90	0
56	MG	RA	3063	1/1	0.91	0.31	-	83,83,83,83	0
56	MG	XA	1719	1/1	0.77	0.45	-	78,78,78,78	0
56	MG	QA	1817	1/1	0.63	0.47	-	85,85,85,85	0
56	MG	RA	3523	1/1	0.73	0.43	-	94,94,94,94	0
56	MG	YA	3688	1/1	0.68	0.41	-	72,72,72,72	0
56	MG	RA	3245	1/1	0.73	0.11	-	86,86,86,86	0
56	MG	YA	3545	1/1	0.87	0.56	-	82,82,82,82	0
56	MG	RA	3155	1/1	0.67	0.55	-	95,95,95,95	0
56	MG	QA	1810	1/1	0.81	0.68	-	81,81,81,81	0
56	MG	YA	3333	1/1	0.53	0.45	-	85,85,85,85	0
56	MG	RA	3914	1/1	0.91	0.56	-	70,70,70,70	0
56	MG	RA	3860	1/1	0.72	1.50	-	85,85,85,85	0
56	MG	RA	3970	1/1	0.66	0.56	-	96,96,96,96	0
56	MG	RA	3393	1/1	0.94	0.35	-	64,64,64,64	0
56	MG	YA	3106	1/1	0.60	0.44	-	92,92,92,92	0
56	MG	YA	3214	1/1	0.88	0.41	-	76,76,76,76	0
56	MG	RA	3395	1/1	0.95	0.60	-	62,62,62,62	0
56	MG	XA	1769	1/1	0.97	0.57	-	77,77,77,77	0
56	MG	QA	1733	1/1	-0.47	0.76	-	94,94,94,94	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3190	1/1	0.91	0.31	-	69,69,69,69	0
56	MG	RA	3188	1/1	0.79	0.56	-	104,104,104,104	0
56	MG	QA	1652	1/1	0.64	0.27	-	83,83,83,83	0
56	MG	YA	3500	1/1	0.80	1.03	-	84,84,84,84	0
56	MG	YA	3254	1/1	0.88	0.40	-	87,87,87,87	0
56	MG	XA	1791	1/1	0.90	0.11	-	74,74,74,74	0
56	MG	YA	3231	1/1	0.40	0.85	-	93,93,93,93	0
56	MG	QA	1607	1/1	0.88	0.28	-	91,91,91,91	0
56	MG	XA	1703	1/1	0.69	0.47	-	82,82,82,82	0
56	MG	XA	1678	1/1	0.86	0.30	-	72,72,72,72	0
56	MG	YA	3414	1/1	0.33	0.71	-	92,92,92,92	0
56	MG	YA	3177	1/1	0.11	0.61	-	95,95,95,95	0
56	MG	RA	3438	1/1	0.15	0.83	-	91,91,91,91	0
56	MG	QA	1613	1/1	0.92	0.15	-	98,98,98,98	0
56	MG	YB	205	1/1	-0.13	0.92	-	93,93,93,93	0
56	MG	YA	3667	1/1	0.91	0.67	-	65,65,65,65	0
56	MG	QA	1772	1/1	0.72	0.37	-	96,96,96,96	0
56	MG	RA	3435	1/1	0.13	0.69	-	75,75,75,75	0
56	MG	QA	1642	1/1	0.25	1.32	-	101,101,101,101	0
56	MG	QA	1683	1/1	0.77	0.28	-	95,95,95,95	0
56	MG	QA	1842	1/1	0.34	0.78	-	95,95,95,95	0
56	MG	XA	1785	1/1	0.83	0.89	-	82,82,82,82	0
56	MG	YA	3497	1/1	0.32	0.58	-	95,95,95,95	0
56	MG	XA	1684	1/1	0.72	1.05	-	70,70,70,70	0
56	MG	RA	3589	1/1	0.79	0.35	-	94,94,94,94	0
56	MG	RA	3548	1/1	-0.37	0.94	-	109,109,109,109	0
56	MG	QA	1867	1/1	0.34	0.74	-	96,96,96,96	0
56	MG	RA	3350	1/1	0.69	0.26	-	74,74,74,74	0
56	MG	RA	3962	1/1	0.25	1.20	-	95,95,95,95	0
56	MG	YB	210	1/1	0.66	0.82	-	88,88,88,88	0
56	MG	YA	3437	1/1	0.75	0.50	-	62,62,62,62	0
56	MG	RA	3463	1/1	0.84	0.55	-	69,69,69,69	0
56	MG	QA	1869	1/1	0.01	1.39	-	105,105,105,105	0
56	MG	XA	1676	1/1	0.43	0.83	-	98,98,98,98	0
56	MG	YA	3340	1/1	0.93	0.56	-	62,62,62,62	0
56	MG	YA	3686	1/1	0.83	0.46	-	77,77,77,77	0
56	MG	RA	3285	1/1	0.84	0.69	-	108,108,108,108	0
56	MG	YB	218	1/1	0.43	0.31	-	85,85,85,85	0
56	MG	RA	3311	1/1	0.71	0.51	-	83,83,83,83	0
56	MG	YA	3410	1/1	0.94	0.59	-	68,68,68,68	0
56	MG	XA	1626	1/1	0.76	0.66	-	78,78,78,78	0
56	MG	RA	3176	1/1	0.36	1.02	-	102,102,102,102	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3423	1/1	0.54	0.59	-	92,92,92,92	0
56	MG	RB	227	1/1	-0.20	0.37	-	88,88,88,88	0
56	MG	RA	3956	1/1	0.94	0.29	-	80,80,80,80	0
56	MG	YA	3213	1/1	0.94	0.52	-	63,63,63,63	0
56	MG	RA	3345	1/1	0.89	0.66	-	62,62,62,62	0
56	MG	YA	3678	1/1	0.76	0.51	-	62,62,62,62	0
56	MG	RA	3124	1/1	0.59	0.47	-	73,73,73,73	0
56	MG	YA	3298	1/1	0.80	0.24	-	82,82,82,82	0
56	MG	XA	1687	1/1	0.52	0.34	-	90,90,90,90	0
56	MG	QA	1676	1/1	0.54	0.88	-	97,97,97,97	0
56	MG	YA	3096	1/1	0.49	0.19	-	87,87,87,87	0
56	MG	RA	3972	1/1	0.95	0.74	-	62,62,62,62	0
56	MG	RA	3261	1/1	0.77	1.23	-	87,87,87,87	0
56	MG	YA	3381	1/1	0.48	0.67	-	70,70,70,70	0
56	MG	RA	3811	1/1	0.78	0.88	-	85,85,85,85	0
56	MG	RA	3024	1/1	0.71	0.68	-	105,105,105,105	0
56	MG	RA	3909	1/1	0.82	0.67	-	62,62,62,62	0
56	MG	RA	3263	1/1	0.82	0.64	-	93,93,93,93	0
56	MG	RA	3193	1/1	0.39	0.69	-	103,103,103,103	0
56	MG	YA	3248	1/1	0.57	0.54	-	88,88,88,88	0
56	MG	YA	3732	1/1	0.83	0.26	-	86,86,86,86	0
56	MG	YA	3257	1/1	0.71	0.49	-	89,89,89,89	0
56	MG	YD	301	1/1	0.63	0.43	-	66,66,66,66	0
56	MG	RA	3371	1/1	-0.32	1.55	-	97,97,97,97	0
56	MG	QA	1611	1/1	0.24	1.17	-	80,80,80,80	0
56	MG	RA	3897	1/1	0.71	0.60	-	72,72,72,72	0
56	MG	RA	3058	1/1	0.34	0.77	-	89,89,89,89	0
56	MG	RA	3688	1/1	0.64	0.71	-	79,79,79,79	0
56	MG	YA	3198	1/1	0.41	0.35	-	88,88,88,88	0
56	MG	YA	3741	1/1	0.59	0.60	-	96,96,96,96	0
56	MG	YA	3114	1/1	0.61	0.76	-	90,90,90,90	0
56	MG	QO	101	1/1	0.82	0.29	-	86,86,86,86	0
56	MG	RA	3327	1/1	0.72	0.56	-	69,69,69,69	0
56	MG	RA	3233	1/1	0.92	0.80	-	96,96,96,96	0
56	MG	YA	3024	1/1	0.70	0.24	-	91,91,91,91	0
56	MG	YB	213	1/1	0.76	0.53	-	81,81,81,81	0
56	MG	RA	3652	1/1	0.83	0.16	-	81,81,81,81	0
56	MG	YA	3602	1/1	0.82	1.45	-	75,75,75,75	0
56	MG	RA	3847	1/1	0.66	0.62	-	103,103,103,103	0
56	MG	YA	3529	1/1	0.48	0.61	-	72,72,72,72	0
56	MG	XA	1656	1/1	0.48	0.55	-	85,85,85,85	0
56	MG	YA	3483	1/1	0.74	0.62	-	88,88,88,88	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	QA	1850	1/1	0.88	0.37	-	78,78,78,78	0
56	MG	YA	3547	1/1	0.41	0.65	-	88,88,88,88	0
56	MG	YA	3286	1/1	0.81	0.28	-	80,80,80,80	0
56	MG	QV	103	1/1	0.72	0.48	-	86,86,86,86	0
56	MG	YA	3731	1/1	0.80	1.43	-	78,78,78,78	0
56	MG	RA	3798	1/1	0.22	0.74	-	93,93,93,93	0
56	MG	YA	3645	1/1	0.78	0.39	-	88,88,88,88	0
56	MG	RA	3199	1/1	0.66	0.64	-	81,81,81,81	0
56	MG	XA	1693	1/1	0.74	0.54	-	95,95,95,95	0
56	MG	RA	3216	1/1	0.74	0.74	-	104,104,104,104	0
56	MG	RA	3954	1/1	0.79	0.26	-	82,82,82,82	0
56	MG	RA	3636	1/1	0.39	0.19	-	94,94,94,94	0
56	MG	RA	3737	1/1	-0.24	1.18	-	84,84,84,84	0
56	MG	YA	3041	1/1	0.07	0.89	-	96,96,96,96	0
56	MG	RA	3090	1/1	0.28	0.71	-	84,84,84,84	0
56	MG	QA	1685	1/1	0.38	0.30	-	89,89,89,89	0
56	MG	RA	3663	1/1	0.43	1.20	-	103,103,103,103	0
56	MG	RA	3800	1/1	0.61	0.40	-	93,93,93,93	0
56	MG	QA	1863	1/1	0.84	0.50	-	81,81,81,81	0
56	MG	YA	3400	1/1	0.88	0.40	-	75,75,75,75	0
56	MG	RH	202	1/1	0.71	0.22	-	95,95,95,95	0
56	MG	YA	3603	1/1	0.16	1.23	-	82,82,82,82	0
56	MG	RA	3111	1/1	0.27	0.43	-	100,100,100,100	0
56	MG	RA	3782	1/1	0.63	0.90	-	99,99,99,99	0
56	MG	QA	1692	1/1	0.83	0.57	-	98,98,98,98	0
56	MG	RA	3859	1/1	0.51	1.25	-	89,89,89,89	0
56	MG	YA	3206	1/1	0.67	0.56	-	73,73,73,73	0
56	MG	RA	3133	1/1	0.75	0.57	-	85,85,85,85	0
56	MG	YA	3165	1/1	0.85	0.46	-	100,100,100,100	0
56	MG	QA	1628	1/1	0.47	0.38	-	77,77,77,77	0
56	MG	QA	1749	1/1	0.58	0.50	-	83,83,83,83	0
56	MG	YA	3179	1/1	0.51	0.59	-	102,102,102,102	0
56	MG	YA	3366	1/1	0.83	0.12	-	95,95,95,95	0
56	MG	RA	3052	1/1	0.70	0.44	-	95,95,95,95	0
56	MG	RA	3853	1/1	0.83	0.56	-	90,90,90,90	0
56	MG	QA	1674	1/1	0.53	0.35	-	94,94,94,94	0
56	MG	RA	3540	1/1	0.65	0.53	-	68,68,68,68	0
56	MG	RA	3619	1/1	0.90	0.43	-	67,67,67,67	0
56	MG	RV	204	1/1	0.49	0.34	-	79,79,79,79	0
56	MG	QG	201	1/1	0.08	0.87	-	101,101,101,101	0
56	MG	RA	3908	1/1	0.76	0.74	-	92,92,92,92	0
56	MG	YA	3642	1/1	0.55	0.74	-	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3533	1/1	0.86	0.45	-	76,76,76,76	0
56	MG	YA	3652	1/1	0.89	0.49	-	79,79,79,79	0
56	MG	RA	3319	1/1	0.90	0.80	-	69,69,69,69	0
56	MG	QA	1853	1/1	0.21	0.76	-	89,89,89,89	0
56	MG	YA	3498	1/1	0.64	0.22	-	89,89,89,89	0
56	MG	QH	201	1/1	0.13	0.51	-	87,87,87,87	0
56	MG	YA	3644	1/1	0.70	0.50	-	75,75,75,75	0
56	MG	QA	1669	1/1	0.61	0.78	-	81,81,81,81	0
56	MG	YA	3140	1/1	0.84	0.36	-	79,79,79,79	0
56	MG	RB	212	1/1	0.59	0.67	-	85,85,85,85	0
56	MG	RA	4022	1/1	0.83	0.47	-	77,77,77,77	0
56	MG	RA	3059	1/1	0.85	0.16	-	84,84,84,84	0
56	MG	QA	1640	1/1	0.20	0.71	-	99,99,99,99	0
56	MG	RA	3120	1/1	0.47	0.54	-	83,83,83,83	0
56	MG	RA	3831	1/1	0.86	0.23	-	90,90,90,90	0
56	MG	RA	3668	1/1	0.80	0.48	-	80,80,80,80	0
56	MG	RA	3985	1/1	0.89	0.53	-	70,70,70,70	0
56	MG	RA	3910	1/1	0.67	0.50	-	83,83,83,83	0
56	MG	RA	3196	1/1	0.00	0.51	-	114,114,114,114	0
56	MG	YA	3181	1/1	0.62	0.54	-	93,93,93,93	0
56	MG	R0	102	1/1	0.31	0.57	-	88,88,88,88	0
56	MG	YA	3624	1/1	0.60	0.45	-	92,92,92,92	0
56	MG	YA	3363	1/1	0.86	0.60	-	75,75,75,75	0
56	MG	RA	3799	1/1	0.75	1.02	-	82,82,82,82	0
56	MG	YA	3304	1/1	0.73	0.34	-	82,82,82,82	0
56	MG	QA	1688	1/1	0.77	1.07	-	81,81,81,81	0
56	MG	RA	3851	1/1	0.96	0.39	-	73,73,73,73	0
56	MG	YA	3726	1/1	0.95	0.74	-	85,85,85,85	0
56	MG	YA	3017	1/1	0.18	0.63	-	91,91,91,91	0
56	MG	YA	3344	1/1	0.22	0.20	-	90,90,90,90	0
56	MG	YA	3455	1/1	0.56	0.45	-	86,86,86,86	0
56	MG	RA	3641	1/1	0.77	0.33	-	79,79,79,79	0
56	MG	RA	3978	1/1	0.50	0.85	-	75,75,75,75	0
56	MG	YA	3408	1/1	0.25	0.81	-	90,90,90,90	0
56	MG	XA	1773	1/1	0.76	0.90	-	79,79,79,79	0
56	MG	YB	202	1/1	0.92	0.14	-	72,72,72,72	0
56	MG	YP	201	1/1	0.62	0.29	-	89,89,89,89	0
56	MG	RA	3793	1/1	0.84	0.57	-	71,71,71,71	0
56	MG	YA	3433	1/1	-0.37	0.75	-	97,97,97,97	0
56	MG	RA	3529	1/1	0.52	0.54	-	90,90,90,90	0
56	MG	QD	301	1/1	0.33	1.26	-	94,94,94,94	0
56	MG	YA	3637	1/1	0.65	0.55	-	85,85,85,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	QA	1848	1/1	0.51	0.81	-	81,81,81,81	0
56	MG	QA	1723	1/1	0.66	0.68	-	86,86,86,86	0
56	MG	RA	3703	1/1	0.30	0.49	-	95,95,95,95	0
56	MG	RA	3926	1/1	0.64	0.46	-	78,78,78,78	0
56	MG	YA	3635	1/1	0.48	0.85	-	83,83,83,83	0
56	MG	YA	3674	1/1	0.89	0.70	-	77,77,77,77	0
56	MG	RA	3219	1/1	0.37	1.35	-	88,88,88,88	0
56	MG	RE	305	1/1	0.42	0.55	-	92,92,92,92	0
56	MG	RA	3983	1/1	0.80	0.39	-	91,91,91,91	0
56	MG	RA	3418	1/1	0.96	0.17	-	64,64,64,64	0
56	MG	YD	307	1/1	0.73	0.52	-	79,79,79,79	0
56	MG	RA	3745	1/1	0.74	0.61	-	73,73,73,73	0
56	MG	YA	3359	1/1	0.92	1.02	-	62,62,62,62	0
56	MG	RA	3686	1/1	0.34	0.74	-	97,97,97,97	0
56	MG	YA	3649	1/1	0.51	0.82	-	79,79,79,79	0
56	MG	YA	3075	1/1	0.29	1.78	-	89,89,89,89	0
56	MG	RB	207	1/1	0.72	0.23	-	93,93,93,93	0
56	MG	RA	3873	1/1	0.57	0.40	-	77,77,77,77	0
56	MG	RA	3621	1/1	0.66	0.54	-	95,95,95,95	0
56	MG	YA	3467	1/1	0.71	0.79	-	76,76,76,76	0
56	MG	YA	3352	1/1	0.29	0.13	-	88,88,88,88	0
56	MG	RA	3747	1/1	0.38	1.50	-	93,93,93,93	0
56	MG	RA	3522	1/1	0.33	0.35	-	84,84,84,84	0
56	MG	YA	3250	1/1	0.29	0.37	-	103,103,103,103	0
56	MG	RA	3927	1/1	0.10	0.96	-	91,91,91,91	0
56	MG	QA	1787	1/1	0.59	0.40	-	89,89,89,89	0
56	MG	YA	3643	1/1	0.82	0.30	-	79,79,79,79	0
56	MG	YA	3441	1/1	0.60	0.58	-	80,80,80,80	0
56	MG	RA	3415	1/1	0.81	0.42	-	62,62,62,62	0
56	MG	QA	1736	1/1	-0.11	1.42	-	82,82,82,82	0
56	MG	RA	3289	1/1	0.81	0.40	-	99,99,99,99	0
56	MG	RA	3919	1/1	0.62	0.85	-	83,83,83,83	0
56	MG	RA	3127	1/1	0.93	0.50	-	81,81,81,81	0
56	MG	RA	3726	1/1	0.82	0.50	-	74,74,74,74	0
56	MG	YA	3512	1/1	0.90	0.26	-	74,74,74,74	0
56	MG	RA	3447	1/1	0.51	0.62	-	78,78,78,78	0
56	MG	QA	1697	1/1	0.17	0.69	-	88,88,88,88	0
56	MG	RA	3844	1/1	0.46	0.47	-	100,100,100,100	0
56	MG	RA	3674	1/1	0.84	0.84	-	70,70,70,70	0
56	MG	QA	1833	1/1	0.55	0.38	-	106,106,106,106	0
56	MG	YA	3253	1/1	0.86	0.62	-	87,87,87,87	0
56	MG	RA	3336	1/1	0.62	0.46	-	86,86,86,86	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3898	1/1	0.70	0.44	-	85,85,85,85	0
56	MG	RB	204	1/1	0.34	0.25	-	85,85,85,85	0
56	MG	RA	3360	1/1	0.92	0.54	-	68,68,68,68	0
56	MG	XA	1701	1/1	0.36	0.45	-	74,74,74,74	0
56	MG	RA	3591	1/1	0.88	0.70	-	92,92,92,92	0
56	MG	RA	4007	1/1	0.71	0.44	-	76,76,76,76	0
56	MG	XA	1765	1/1	0.63	1.09	-	77,77,77,77	0
56	MG	QA	1740	1/1	0.78	0.65	-	69,69,69,69	0
56	MG	RA	3086	1/1	0.61	1.22	-	111,111,111,111	0
56	MG	RB	203	1/1	-0.22	0.93	-	102,102,102,102	0
56	MG	RN	202	1/1	-0.27	2.06	-	102,102,102,102	0
56	MG	YA	3373	1/1	0.72	0.19	-	71,71,71,71	0
56	MG	RA	3632	1/1	0.65	0.90	-	88,88,88,88	0
56	MG	YA	3305	1/1	0.63	0.25	-	69,69,69,69	0
56	MG	YA	3531	1/1	0.25	1.31	-	80,80,80,80	0
56	MG	YA	3267	1/1	-0.52	1.71	-	102,102,102,102	0
56	MG	YA	3207	1/1	0.95	0.29	-	87,87,87,87	0
56	MG	QA	1748	1/1	-0.14	1.50	-	98,98,98,98	0
56	MG	RA	3999	1/1	0.18	0.43	-	98,98,98,98	0
56	MG	RA	3660	1/1	0.67	0.82	-	77,77,77,77	0
56	MG	RA	3247	1/1	0.18	0.86	-	89,89,89,89	0
56	MG	YA	3157	1/1	0.38	0.79	-	66,66,66,66	0
56	MG	RA	3429	1/1	0.79	0.25	-	98,98,98,98	0
56	MG	R1	101	1/1	0.42	0.65	-	89,89,89,89	0
56	MG	RA	3140	1/1	0.85	1.04	-	97,97,97,97	0
56	MG	RA	3828	1/1	0.13	0.49	-	84,84,84,84	0
56	MG	RA	3015	1/1	0.82	0.53	-	84,84,84,84	0
56	MG	YT	201	1/1	0.78	0.74	-	85,85,85,85	0
56	MG	RA	3171	1/1	-0.40	0.93	-	92,92,92,92	0
56	MG	QA	1838	1/1	0.24	0.51	-	87,87,87,87	0
56	MG	RA	3209	1/1	0.72	0.38	-	88,88,88,88	0
56	MG	RA	3787	1/1	0.16	0.79	-	88,88,88,88	0
56	MG	XA	1650	1/1	0.62	0.30	-	87,87,87,87	0
56	MG	RA	3398	1/1	0.23	0.73	-	80,80,80,80	0
56	MG	YE	307	1/1	0.90	0.35	-	85,85,85,85	0
56	MG	YA	3438	1/1	0.73	0.55	-	80,80,80,80	0
56	MG	YA	3713	1/1	0.50	0.63	-	83,83,83,83	0
56	MG	RA	3763	1/1	0.65	0.27	-	77,77,77,77	0
56	MG	RA	3943	1/1	0.35	0.63	-	91,91,91,91	0
56	MG	RA	3287	1/1	0.91	0.60	-	102,102,102,102	0
56	MG	RA	3720	1/1	0.84	0.44	-	73,73,73,73	0
56	MG	RA	3734	1/1	0.43	0.59	-	85,85,85,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	QA	1868	1/1	0.52	1.40	-	82,82,82,82	0
56	MG	YA	3023	1/1	0.92	0.17	-	80,80,80,80	0
56	MG	RA	3461	1/1	0.78	1.48	-	84,84,84,84	0
56	MG	RA	3478	1/1	0.77	0.68	-	78,78,78,78	0
56	MG	RA	4069	1/1	-0.29	1.52	-	86,86,86,86	0
56	MG	RA	3355	1/1	0.97	0.07	-	88,88,88,88	0
56	MG	QA	1797	1/1	0.82	0.51	-	75,75,75,75	0
56	MG	YA	3136	1/1	0.94	0.33	-	65,65,65,65	0
56	MG	RA	3268	1/1	0.96	0.32	-	79,79,79,79	0
56	MG	YA	3454	1/1	0.79	0.36	-	94,94,94,94	0
56	MG	YA	3117	1/1	0.79	0.45	-	87,87,87,87	0
56	MG	RA	3573	1/1	0.71	0.53	-	88,88,88,88	0
56	MG	XA	1708	1/1	0.85	0.82	-	75,75,75,75	0
56	MG	YA	3638	1/1	0.62	0.85	-	64,64,64,64	0
56	MG	YA	3255	1/1	0.65	0.46	-	81,81,81,81	0
56	MG	YA	3682	1/1	0.90	0.41	-	62,62,62,62	0
56	MG	YA	3501	1/1	0.55	1.03	-	74,74,74,74	0
56	MG	RA	3582	1/1	0.39	0.77	-	87,87,87,87	0
56	MG	QA	1710	1/1	0.70	0.64	-	74,74,74,74	0
56	MG	YA	3196	1/1	0.54	0.70	-	91,91,91,91	0
56	MG	QA	1699	1/1	0.84	0.20	-	89,89,89,89	0
56	MG	RA	3946	1/1	0.90	0.86	-	67,67,67,67	0
56	MG	QA	1859	1/1	0.37	0.81	-	85,85,85,85	0
56	MG	YA	3661	1/1	0.91	0.62	-	73,73,73,73	0
56	MG	XA	1751	1/1	0.87	0.23	-	87,87,87,87	0
56	MG	XA	1754	1/1	-0.15	1.24	-	88,88,88,88	0
56	MG	YA	3494	1/1	0.94	0.41	-	64,64,64,64	0
56	MG	XF	203	1/1	0.21	2.52	-	103,103,103,103	0
56	MG	YA	3543	1/1	0.80	0.34	-	80,80,80,80	0
56	MG	RA	3262	1/1	0.76	0.18	-	83,83,83,83	0
56	MG	YA	3651	1/1	0.70	0.64	-	78,78,78,78	0
56	MG	YA	3167	1/1	0.10	1.03	-	87,87,87,87	0
56	MG	RA	3039	1/1	-0.09	1.09	-	97,97,97,97	0
56	MG	QA	1745	1/1	-0.04	0.89	-	82,82,82,82	0
56	MG	RA	3481	1/1	0.73	0.67	-	71,71,71,71	0
56	MG	RA	3516	1/1	0.94	0.49	-	84,84,84,84	0
56	MG	XA	1771	1/1	0.80	0.95	-	72,72,72,72	0
56	MG	QA	1789	1/1	0.77	0.37	-	85,85,85,85	0
56	MG	RA	3752	1/1	0.71	0.58	-	85,85,85,85	0
56	MG	RA	3249	1/1	0.81	0.46	-	99,99,99,99	0
56	MG	RA	4010	1/1	0.31	1.61	-	79,79,79,79	0
56	MG	RA	3388	1/1	0.73	0.75	-	96,96,96,96	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3552	1/1	0.47	0.73	-	93,93,93,93	0
56	MG	YA	3459	1/1	0.85	0.29	-	63,63,63,63	0
56	MG	RA	3657	1/1	0.83	1.07	-	70,70,70,70	0
56	MG	YA	3211	1/1	0.04	1.03	-	98,98,98,98	0
56	MG	RA	3825	1/1	0.23	0.83	-	85,85,85,85	0
56	MG	RA	3320	1/1	0.92	0.57	-	62,62,62,62	0
56	MG	RA	3149	1/1	0.62	0.59	-	73,73,73,73	0
56	MG	QA	1820	1/1	0.67	0.41	-	76,76,76,76	0
56	MG	QA	1663	1/1	0.87	0.23	-	90,90,90,90	0
56	MG	YA	3418	1/1	0.72	0.69	-	90,90,90,90	0
56	MG	RA	3698	1/1	0.69	0.53	-	87,87,87,87	0
56	MG	RA	3383	1/1	0.90	0.35	-	63,63,63,63	0
56	MG	RQ	203	1/1	0.29	0.84	-	96,96,96,96	0
56	MG	XA	1674	1/1	-0.17	1.36	-	94,94,94,94	0
56	MG	QA	1603	1/1	0.74	0.46	-	86,86,86,86	0
56	MG	YB	206	1/1	0.13	0.86	-	89,89,89,89	0
56	MG	XA	1706	1/1	0.81	0.14	-	78,78,78,78	0
56	MG	RA	3162	1/1	0.92	0.70	-	83,83,83,83	0
56	MG	QA	1856	1/1	0.65	0.57	-	94,94,94,94	0
56	MG	YA	3521	1/1	0.54	0.53	-	97,97,97,97	0
56	MG	QA	1873	1/1	-0.34	1.75	-	91,91,91,91	0
56	MG	XA	1682	1/1	0.57	0.71	-	83,83,83,83	0
56	MG	YA	3076	1/1	0.67	0.52	-	92,92,92,92	0
56	MG	XA	1607	1/1	0.81	0.28	-	95,95,95,95	0
56	MG	YA	3180	1/1	0.71	0.28	-	73,73,73,73	0
56	MG	RA	3605	1/1	0.80	0.58	-	90,90,90,90	0
56	MG	QA	1728	1/1	0.20	0.35	-	80,80,80,80	0
56	MG	YA	3357	1/1	0.79	1.26	-	78,78,78,78	0
56	MG	YA	3123	1/1	0.63	0.70	-	105,105,105,105	0
56	MG	QA	1753	1/1	0.39	0.61	-	87,87,87,87	0
56	MG	YA	3026	1/1	0.57	0.54	-	84,84,84,84	0
56	MG	YA	3238	1/1	0.74	0.45	-	100,100,100,100	0
56	MG	RA	3013	1/1	0.42	0.68	-	83,83,83,83	0
56	MG	RA	3106	1/1	0.16	0.56	-	107,107,107,107	0
56	MG	RA	3002	1/1	0.83	0.34	-	67,67,67,67	0
56	MG	RA	3139	1/1	0.81	0.45	-	89,89,89,89	0
56	MG	RA	3160	1/1	0.81	0.94	-	102,102,102,102	0
56	MG	YA	3239	1/1	0.80	0.53	-	98,98,98,98	0
56	MG	YA	3109	1/1	0.28	0.62	-	85,85,85,85	0
56	MG	RA	3776	1/1	0.62	0.69	-	86,86,86,86	0
56	MG	RA	3723	1/1	0.50	0.38	-	79,79,79,79	0
56	MG	RA	3973	1/1	0.88	0.82	-	99,99,99,99	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3346	1/1	0.74	0.52	-	79,79,79,79	0
56	MG	YA	3640	1/1	0.62	1.02	-	70,70,70,70	0
56	MG	QA	1726	1/1	0.84	0.53	-	88,88,88,88	0
56	MG	RA	3731	1/1	0.97	0.31	-	74,74,74,74	0
56	MG	RA	3976	1/1	0.83	0.34	-	76,76,76,76	0
56	MG	YA	3426	1/1	0.85	0.33	-	72,72,72,72	0
56	MG	RA	3365	1/1	0.15	0.61	-	88,88,88,88	0
56	MG	YA	3700	1/1	0.96	0.43	-	64,64,64,64	0
56	MG	YA	3492	1/1	0.97	0.81	-	62,62,62,62	0
56	MG	YA	3205	1/1	0.01	2.40	-	86,86,86,86	0
56	MG	RA	3277	1/1	0.89	0.34	-	85,85,85,85	0
56	MG	R5	102	1/1	-0.15	0.53	-	97,97,97,97	0
56	MG	R9	103	1/1	0.70	0.47	-	93,93,93,93	0
56	MG	YA	3312	1/1	0.14	1.26	-	80,80,80,80	0
56	MG	YA	3014	1/1	0.95	0.19	-	82,82,82,82	0
56	MG	RA	3762	1/1	0.98	0.58	-	65,65,65,65	0
56	MG	RA	3425	1/1	0.08	1.09	-	91,91,91,91	0
56	MG	RA	3099	1/1	0.28	0.66	-	94,94,94,94	0
56	MG	RB	224	1/1	0.42	0.86	-	86,86,86,86	0
56	MG	RA	3545	1/1	0.84	0.34	-	85,85,85,85	0
56	MG	XA	1651	1/1	0.31	1.56	-	96,96,96,96	0
56	MG	RA	4000	1/1	0.48	0.64	-	95,95,95,95	0
56	MG	RA	3428	1/1	0.24	0.81	-	92,92,92,92	0
56	MG	YG	201	1/1	-0.61	2.04	-	103,103,103,103	0
56	MG	QA	1778	1/1	0.38	0.67	-	88,88,88,88	0
56	MG	YA	3460	1/1	0.69	0.38	-	85,85,85,85	0
56	MG	QA	1790	1/1	0.77	0.40	-	81,81,81,81	0
56	MG	YA	3329	1/1	0.93	0.46	-	62,62,62,62	0
56	MG	XA	1743	1/1	0.52	0.54	-	89,89,89,89	0
56	MG	YA	3164	1/1	0.04	1.20	-	98,98,98,98	0
56	MG	RA	4054	1/1	0.17	1.94	-	91,91,91,91	0
56	MG	RA	3173	1/1	0.65	0.54	-	90,90,90,90	0
56	MG	YI	201	1/1	0.07	0.36	-	94,94,94,94	0
56	MG	YA	3308	1/1	-0.13	1.09	-	92,92,92,92	0
56	MG	RA	3201	1/1	0.84	0.54	-	96,96,96,96	0
56	MG	RA	3215	1/1	0.47	0.75	-	90,90,90,90	0
56	MG	YA	3537	1/1	0.94	0.50	-	62,62,62,62	0
56	MG	YA	3083	1/1	0.39	0.32	-	90,90,90,90	0
56	MG	YA	3002	1/1	0.93	0.19	-	75,75,75,75	0
56	MG	QA	1678	1/1	0.81	0.32	-	93,93,93,93	0
56	MG	YA	3356	1/1	0.00	0.28	-	85,85,85,85	0
56	MG	RA	3546	1/1	0.37	0.56	-	95,95,95,95	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3413	1/1	0.74	0.52	-	83,83,83,83	0
56	MG	RA	3397	1/1	0.37	0.69	-	76,76,76,76	0
56	MG	XA	1735	1/1	0.78	0.24	-	83,83,83,83	0
56	MG	YA	3557	1/1	0.74	0.58	-	66,66,66,66	0
56	MG	RA	3739	1/1	0.90	0.40	-	69,69,69,69	0
56	MG	QA	1878	1/1	0.92	0.21	-	98,98,98,98	0
56	MG	RA	3838	1/1	0.73	0.54	-	77,77,77,77	0
56	MG	QA	1722	1/1	-0.51	0.98	-	93,93,93,93	0
56	MG	QI	201	1/1	0.38	1.13	-	100,100,100,100	0
56	MG	YA	3568	1/1	0.93	0.45	-	63,63,63,63	0
56	MG	RB	221	1/1	0.83	0.23	-	84,84,84,84	0
56	MG	QA	1841	1/1	0.46	0.37	-	94,94,94,94	0
56	MG	RA	3933	1/1	0.76	0.61	-	84,84,84,84	0
56	MG	RA	3878	1/1	0.94	0.37	-	62,62,62,62	0
56	MG	YA	3567	1/1	0.94	0.65	-	62,62,62,62	0
56	MG	RA	3543	1/1	0.61	0.41	-	83,83,83,83	0
56	MG	QA	1757	1/1	-0.10	0.58	-	102,102,102,102	0
56	MG	RA	3912	1/1	0.89	0.27	-	78,78,78,78	0
56	MG	RA	3789	1/1	0.70	0.23	-	80,80,80,80	0
56	MG	YA	3362	1/1	0.84	0.64	-	70,70,70,70	0
56	MG	QA	1807	1/1	0.26	0.56	-	95,95,95,95	0
56	MG	YA	3108	1/1	0.29	0.62	-	90,90,90,90	0
56	MG	RA	3620	1/1	0.97	0.81	-	81,81,81,81	0
56	MG	RA	3214	1/1	0.95	0.33	-	86,86,86,86	0
56	MG	RA	3204	1/1	0.68	0.61	-	103,103,103,103	0
56	MG	Y1	102	1/1	0.67	0.36	-	87,87,87,87	0
56	MG	RA	3989	1/1	0.70	0.75	-	84,84,84,84	0
56	MG	RA	3417	1/1	0.61	0.30	-	89,89,89,89	0
56	MG	RA	3078	1/1	0.85	0.85	-	90,90,90,90	0
56	MG	RA	3097	1/1	0.67	1.29	-	90,90,90,90	0
56	MG	QA	1756	1/1	0.72	0.75	-	80,80,80,80	0
56	MG	QA	1617	1/1	0.81	0.34	-	98,98,98,98	0
56	MG	RA	3068	1/1	0.80	0.48	-	91,91,91,91	0
56	MG	RA	3775	1/1	0.37	1.33	-	94,94,94,94	0
56	MG	RA	3594	1/1	0.95	0.50	-	80,80,80,80	0
56	MG	RA	3459	1/1	0.66	0.38	-	88,88,88,88	0
56	MG	YA	3235	1/1	0.79	0.45	-	93,93,93,93	0
56	MG	QA	1630	1/1	0.38	1.44	-	79,79,79,79	0
56	MG	QA	1720	1/1	0.70	0.87	-	85,85,85,85	0
56	MG	YA	3190	1/1	0.48	0.69	-	92,92,92,92	0
56	MG	RA	3456	1/1	0.46	0.45	-	71,71,71,71	0
56	MG	RA	3410	1/1	0.90	0.69	-	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3006	1/1	0.50	0.62	-	82,82,82,82	0
56	MG	YA	3195	1/1	0.68	0.31	-	89,89,89,89	0
56	MG	YA	3313	1/1	0.49	0.67	-	89,89,89,89	0
56	MG	RA	3741	1/1	0.39	0.80	-	92,92,92,92	0
56	MG	XA	1614	1/1	0.81	0.19	-	77,77,77,77	0
56	MG	YA	3590	1/1	0.90	0.38	-	65,65,65,65	0
56	MG	RA	3509	1/1	0.81	0.46	-	81,81,81,81	0
56	MG	RA	3955	1/1	0.39	0.88	-	90,90,90,90	0
56	MG	YA	3541	1/1	0.25	0.43	-	94,94,94,94	0
56	MG	YA	3154	1/1	0.79	0.52	-	81,81,81,81	0
56	MG	XA	1691	1/1	0.25	0.40	-	84,84,84,84	0
56	MG	RA	3284	1/1	0.66	0.69	-	87,87,87,87	0
56	MG	RA	3586	1/1	0.41	0.68	-	76,76,76,76	0
56	MG	XA	1782	1/1	0.39	1.41	-	79,79,79,79	0
56	MG	RA	3167	1/1	0.74	0.26	-	84,84,84,84	0
56	MG	RA	3597	1/1	0.57	0.74	-	89,89,89,89	0
56	MG	RA	3503	1/1	0.95	0.47	-	65,65,65,65	0
56	MG	YA	3489	1/1	0.56	0.40	-	77,77,77,77	0
56	MG	QA	1826	1/1	0.88	0.98	-	110,110,110,110	0
56	MG	YA	3618	1/1	0.79	0.80	-	82,82,82,82	0
56	MG	RA	3339	1/1	0.76	0.74	-	86,86,86,86	0
56	MG	YA	3251	1/1	0.71	0.49	-	93,93,93,93	0
56	MG	RA	3549	1/1	0.94	0.44	-	76,76,76,76	0
56	MG	YA	3458	1/1	-0.04	1.00	-	88,88,88,88	0
56	MG	YA	3009	1/1	0.93	0.22	-	70,70,70,70	0
56	MG	YA	3739	1/1	0.25	0.77	-	75,75,75,75	0
56	MG	YA	3722	1/1	0.28	0.89	-	93,93,93,93	0
56	MG	XA	1722	1/1	0.56	0.68	-	88,88,88,88	0
56	MG	RA	3913	1/1	0.71	0.73	-	94,94,94,94	0
56	MG	RA	3259	1/1	0.56	0.74	-	86,86,86,86	0
56	MG	QA	1725	1/1	0.84	0.40	-	76,76,76,76	0
56	MG	YW	202	1/1	0.65	0.41	-	81,81,81,81	0
56	MG	YA	3743	1/1	0.87	0.42	-	63,63,63,63	0
56	MG	RA	3313	1/1	0.91	0.72	-	63,63,63,63	0
56	MG	YA	3038	1/1	0.92	0.48	-	77,77,77,77	0
56	MG	RF	310	1/1	0.66	0.68	-	78,78,78,78	0
56	MG	YA	3574	1/1	0.31	0.82	-	86,86,86,86	0
56	MG	YA	3223	1/1	0.59	0.44	-	65,65,65,65	0
56	MG	RA	3690	1/1	0.07	0.84	-	90,90,90,90	0
56	MG	YA	3276	1/1	0.51	0.32	-	77,77,77,77	0
56	MG	YA	3639	1/1	0.89	0.77	-	65,65,65,65	0
56	MG	QA	1709	1/1	0.80	0.22	-	90,90,90,90	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3884	1/1	0.87	0.29	-	96,96,96,96	0
56	MG	RA	3876	1/1	0.19	0.90	-	92,92,92,92	0
56	MG	YA	3592	1/1	0.81	0.32	-	78,78,78,78	0
56	MG	YA	3119	1/1	0.53	0.74	-	68,68,68,68	0
56	MG	RA	3633	1/1	0.64	0.45	-	93,93,93,93	0
56	MG	YA	3502	1/1	0.84	0.29	-	71,71,71,71	0
56	MG	QA	1794	1/1	0.29	0.79	-	72,72,72,72	0
56	MG	RA	3836	1/1	0.68	0.50	-	73,73,73,73	0
56	MG	RA	4014	1/1	0.87	0.32	-	79,79,79,79	0
56	MG	YA	3260	1/1	0.88	0.56	-	95,95,95,95	0
56	MG	R3	101	1/1	-0.07	1.30	-	87,87,87,87	0
56	MG	XA	1710	1/1	0.39	0.33	-	78,78,78,78	0
56	MG	RZ	301	1/1	0.56	0.73	-	87,87,87,87	0
56	MG	YA	3482	1/1	0.94	0.85	-	62,62,62,62	0
56	MG	RV	201	1/1	0.36	0.30	-	100,100,100,100	0
56	MG	XA	1755	1/1	0.60	0.75	-	87,87,87,87	0
56	MG	YA	3505	1/1	0.24	0.76	-	88,88,88,88	0
56	MG	QA	1729	1/1	0.58	0.68	-	87,87,87,87	0
56	MG	YA	3068	1/1	0.82	0.40	-	79,79,79,79	0
56	MG	YA	3436	1/1	0.84	0.50	-	65,65,65,65	0
56	MG	RA	3067	1/1	-0.21	1.47	-	100,100,100,100	0
56	MG	YA	3434	1/1	0.93	0.45	-	72,72,72,72	0
56	MG	YA	3525	1/1	0.02	1.06	-	88,88,88,88	0
56	MG	RA	3683	1/1	0.69	0.32	-	85,85,85,85	0
56	MG	YA	3100	1/1	0.90	0.33	-	78,78,78,78	0
56	MG	RA	3445	1/1	0.45	0.95	-	81,81,81,81	0
56	MG	RA	3796	1/1	0.65	0.57	-	90,90,90,90	0
56	MG	QA	1846	1/1	0.65	0.28	-	92,92,92,92	0
56	MG	RA	3066	1/1	0.12	0.78	-	104,104,104,104	0
56	MG	YA	3315	1/1	0.97	0.41	-	64,64,64,64	0
56	MG	YA	3191	1/1	0.78	0.46	-	86,86,86,86	0
56	MG	YA	3626	1/1	0.93	0.70	-	62,62,62,62	0
56	MG	RB	218	1/1	0.67	0.49	-	86,86,86,86	0
56	MG	QA	1844	1/1	0.82	0.32	-	100,100,100,100	0
56	MG	YA	3695	1/1	-0.31	1.27	-	88,88,88,88	0
56	MG	QM	201	1/1	0.53	0.29	-	91,91,91,91	0
56	MG	RA	3676	1/1	0.33	0.29	-	84,84,84,84	0
56	MG	YA	3462	1/1	0.31	0.86	-	97,97,97,97	0
56	MG	XA	1698	1/1	-0.09	1.09	-	87,87,87,87	0
56	MG	YA	3301	1/1	0.70	0.83	-	74,74,74,74	0
56	MG	YN	201	1/1	0.38	1.56	-	90,90,90,90	0
56	MG	QA	1775	1/1	0.71	0.44	-	91,91,91,91	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3174	1/1	0.28	1.00	-	85,85,85,85	0
56	MG	YA	3103	1/1	0.90	0.32	-	67,67,67,67	0
56	MG	YA	3395	1/1	0.90	0.29	-	63,63,63,63	0
56	MG	RA	3007	1/1	0.59	0.39	-	75,75,75,75	0
56	MG	YA	3563	1/1	0.73	0.27	-	72,72,72,72	0
56	MG	YA	3372	1/1	0.84	0.46	-	69,69,69,69	0
56	MG	XA	1606	1/1	0.81	0.32	-	90,90,90,90	0
56	MG	RA	3495	1/1	0.20	0.84	-	83,83,83,83	0
56	MG	XA	1783	1/1	0.50	0.47	-	97,97,97,97	0
56	MG	RB	202	1/1	0.93	0.26	-	80,80,80,80	0
56	MG	YA	3045	1/1	0.84	0.26	-	64,64,64,64	0
56	MG	YA	3428	1/1	0.47	0.56	-	104,104,104,104	0
56	MG	QA	1862	1/1	0.13	0.67	-	82,82,82,82	0
56	MG	RA	3369	1/1	0.68	1.87	-	79,79,79,79	0
56	MG	RA	3711	1/1	0.57	0.89	-	88,88,88,88	0
56	MG	RA	3453	1/1	0.46	0.30	-	82,82,82,82	0
56	MG	YA	3698	1/1	0.76	0.80	-	76,76,76,76	0
56	MG	QA	1821	1/1	0.39	0.78	-	89,89,89,89	0
56	MG	RB	211	1/1	0.24	0.45	-	89,89,89,89	0
56	MG	RA	3583	1/1	0.59	0.95	-	79,79,79,79	0
56	MG	YA	3469	1/1	0.19	0.62	-	91,91,91,91	0
56	MG	YA	3634	1/1	0.84	0.40	-	86,86,86,86	0
56	MG	YA	3264	1/1	0.65	0.34	-	93,93,93,93	0
56	MG	XA	1667	1/1	0.66	1.22	-	83,83,83,83	0
56	MG	XA	1778	1/1	0.75	0.85	-	70,70,70,70	0
56	MG	YA	3282	1/1	0.90	0.64	-	62,62,62,62	0
56	MG	RB	228	1/1	0.74	0.70	-	92,92,92,92	0
56	MG	YA	3093	1/1	0.70	0.37	-	86,86,86,86	0
56	MG	RA	3065	1/1	0.66	0.45	-	92,92,92,92	0
56	MG	YB	215	1/1	0.77	0.23	-	79,79,79,79	0
56	MG	YA	3101	1/1	0.62	0.38	-	92,92,92,92	0
56	MG	RA	3304	1/1	0.82	0.68	-	76,76,76,76	0
56	MG	RA	3968	1/1	-0.01	0.98	-	84,84,84,84	0
56	MG	RA	3296	1/1	0.13	0.69	-	91,91,91,91	0
56	MG	YA	3523	1/1	0.66	0.69	-	72,72,72,72	0
56	MG	RA	3074	1/1	0.65	0.44	-	69,69,69,69	0
56	MG	RA	3627	1/1	0.72	0.37	-	81,81,81,81	0
56	MG	YA	3539	1/1	0.91	0.75	-	72,72,72,72	0
56	MG	RA	3375	1/1	0.46	0.53	-	98,98,98,98	0
56	MG	XA	1702	1/1	0.51	0.54	-	75,75,75,75	0
56	MG	YA	3132	1/1	0.70	0.38	-	93,93,93,93	0
56	MG	RA	3653	1/1	-0.03	1.12	-	100,100,100,100	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3161	1/1	-0.10	1.02	-	91,91,91,91	0
56	MG	YA	3265	1/1	0.55	0.54	-	77,77,77,77	0
56	MG	XA	1732	1/1	0.94	0.53	-	87,87,87,87	0
56	MG	YA	3354	1/1	0.66	0.52	-	84,84,84,84	0
56	MG	XA	1642	1/1	0.88	0.61	-	84,84,84,84	0
56	MG	RA	3089	1/1	0.87	0.14	-	91,91,91,91	0
56	MG	QA	1609	1/1	0.72	0.20	-	95,95,95,95	0
56	MG	YA	3263	1/1	0.74	0.52	-	70,70,70,70	0
56	MG	YA	3149	1/1	0.91	0.86	-	95,95,95,95	0
56	MG	RA	3493	1/1	0.91	0.59	-	70,70,70,70	0
56	MG	YA	3735	1/1	0.56	0.59	-	85,85,85,85	0
56	MG	RA	3977	1/1	0.45	0.43	-	89,89,89,89	0
56	MG	R4	102	1/1	-0.26	0.53	-	97,97,97,97	0
56	MG	YA	3675	1/1	0.79	0.64	-	68,68,68,68	0
56	MG	RA	3778	1/1	0.16	0.48	-	105,105,105,105	0
56	MG	RA	3184	1/1	0.43	0.32	-	92,92,92,92	0
56	MG	QA	1633	1/1	0.82	0.15	-	84,84,84,84	0
56	MG	RA	3669	1/1	0.75	0.56	-	68,68,68,68	0
56	MG	RA	3840	1/1	0.21	1.97	-	97,97,97,97	0
56	MG	QA	1601	1/1	0.65	0.39	-	101,101,101,101	0
56	MG	YA	3723	1/1	0.12	1.35	-	89,89,89,89	0
56	MG	YA	3178	1/1	0.58	0.61	-	78,78,78,78	0
56	MG	QA	1784	1/1	0.52	0.36	-	96,96,96,96	0
56	MG	RA	3693	1/1	0.19	1.00	-	102,102,102,102	0
56	MG	QA	1750	1/1	0.84	0.24	-	69,69,69,69	0
56	MG	QA	1836	1/1	0.78	0.42	-	77,77,77,77	0
56	MG	YA	3370	1/1	0.84	0.41	-	66,66,66,66	0
56	MG	YA	3310	1/1	0.63	2.02	-	80,80,80,80	0
56	MG	QA	1761	1/1	0.93	0.14	-	88,88,88,88	0
56	MG	QA	1660	1/1	0.49	0.16	-	81,81,81,81	0
56	MG	YA	3072	1/1	0.89	0.52	-	100,100,100,100	0
56	MG	QA	1791	1/1	0.80	0.27	-	89,89,89,89	0
56	MG	RA	3112	1/1	0.49	0.76	-	96,96,96,96	0
56	MG	RA	3175	1/1	0.94	0.68	-	78,78,78,78	0
56	MG	YA	3416	1/1	0.75	0.46	-	75,75,75,75	0
56	MG	RA	3115	1/1	0.24	0.41	-	78,78,78,78	0
56	MG	RA	3110	1/1	0.84	0.75	-	94,94,94,94	0
56	MG	QA	1643	1/1	0.57	0.70	-	86,86,86,86	0
56	MG	YA	3379	1/1	0.94	0.27	-	73,73,73,73	0
56	MG	QA	1798	1/1	0.89	0.20	-	89,89,89,89	0
56	MG	YA	3524	1/1	0.14	0.84	-	85,85,85,85	0
56	MG	RA	3544	1/1	0.84	0.39	-	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3781	1/1	0.64	0.71	-	90,90,90,90	0
56	MG	QA	1876	1/1	0.88	0.28	-	80,80,80,80	0
56	MG	YA	3546	1/1	0.84	0.77	-	75,75,75,75	0
56	MG	YO	202	1/1	0.48	0.20	-	81,81,81,81	0
56	MG	RA	3666	1/1	0.65	0.56	-	80,80,80,80	0
56	MG	QA	1852	1/1	-0.10	1.02	-	84,84,84,84	0
56	MG	YA	3258	1/1	0.27	0.71	-	86,86,86,86	0
56	MG	RR	203	1/1	0.09	0.46	-	81,81,81,81	0
56	MG	XA	1712	1/1	-0.11	0.72	-	96,96,96,96	0
56	MG	YA	3050	1/1	0.05	0.68	-	92,92,92,92	0
56	MG	QA	1865	1/1	0.68	0.81	-	98,98,98,98	0
56	MG	RA	3694	1/1	0.45	0.50	-	93,93,93,93	0
56	MG	XA	1775	1/1	0.33	0.72	-	98,98,98,98	0
56	MG	RA	3341	1/1	0.76	0.82	-	73,73,73,73	0
56	MG	YA	3393	1/1	0.52	0.60	-	89,89,89,89	0
56	MG	YA	3256	1/1	0.88	0.21	-	85,85,85,85	0
56	MG	RA	3835	1/1	0.61	0.53	-	89,89,89,89	0
56	MG	RB	223	1/1	0.62	1.10	-	96,96,96,96	0
56	MG	RA	3994	1/1	0.45	0.17	-	91,91,91,91	0
56	MG	RA	3137	1/1	0.32	1.17	-	102,102,102,102	0
56	MG	RA	3343	1/1	0.80	0.29	-	80,80,80,80	0
56	MG	RA	3246	1/1	0.34	0.75	-	84,84,84,84	0
56	MG	YA	3070	1/1	0.06	0.72	-	99,99,99,99	0
56	MG	XA	1788	1/1	0.37	0.67	-	95,95,95,95	0
56	MG	RA	3841	1/1	0.20	0.95	-	91,91,91,91	0
56	MG	RA	3877	1/1	0.87	0.88	-	74,74,74,74	0
56	MG	YA	3078	1/1	-0.24	0.65	-	97,97,97,97	0
56	MG	RA	3834	1/1	0.87	0.91	-	63,63,63,63	0
56	MG	RA	3964	1/1	0.40	2.04	-	104,104,104,104	0
56	MG	YA	3087	1/1	0.98	0.36	-	100,100,100,100	0
56	MG	RA	3210	1/1	0.77	2.13	-	110,110,110,110	0
56	MG	XA	1752	1/1	0.87	0.59	-	81,81,81,81	0
56	MG	YA	3046	1/1	0.87	0.32	-	82,82,82,82	0
56	MG	RA	3490	1/1	0.87	0.52	-	67,67,67,67	0
56	MG	RA	3060	1/1	0.96	0.22	-	83,83,83,83	0
56	MG	RA	3991	1/1	0.49	0.63	-	75,75,75,75	0
56	MG	RA	3291	1/1	0.73	0.38	-	81,81,81,81	0
56	MG	QA	1636	1/1	0.16	0.55	-	90,90,90,90	0
56	MG	XA	1649	1/1	0.62	0.46	-	94,94,94,94	0
56	MG	YA	3452	1/1	0.19	0.88	-	84,84,84,84	0
56	MG	QA	1735	1/1	0.37	0.58	-	93,93,93,93	0
56	MG	YA	3734	1/1	0.70	0.42	-	83,83,83,83	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3145	1/1	0.86	0.25	-	88,88,88,88	0
56	MG	RA	3916	1/1	0.93	0.32	-	71,71,71,71	0
56	MG	YA	3185	1/1	0.23	0.67	-	99,99,99,99	0
56	MG	YA	3342	1/1	0.86	0.68	-	62,62,62,62	0
56	MG	YA	3029	1/1	0.87	0.62	-	62,62,62,62	0
56	MG	YA	3271	1/1	0.90	0.90	-	67,67,67,67	0
56	MG	XA	1686	1/1	0.32	0.65	-	96,96,96,96	0
56	MG	RA	3768	1/1	0.83	0.53	-	74,74,74,74	0
56	MG	RA	3434	1/1	0.28	0.60	-	85,85,85,85	0
56	MG	RA	3317	1/1	0.67	0.46	-	82,82,82,82	0
56	MG	RA	3254	1/1	0.58	0.44	-	105,105,105,105	0
56	MG	YA	3048	1/1	0.79	0.32	-	98,98,98,98	0
56	MG	XA	1630	1/1	0.89	0.20	-	64,64,64,64	0
56	MG	QA	1668	1/1	-0.01	0.85	-	92,92,92,92	0
56	MG	YA	3703	1/1	0.86	0.44	-	90,90,90,90	0
56	MG	YA	3300	1/1	0.65	0.47	-	91,91,91,91	0
56	MG	YA	3593	1/1	0.81	0.60	-	87,87,87,87	0
56	MG	RB	214	1/1	0.60	0.64	-	67,67,67,67	0
56	MG	RA	3560	1/1	0.48	0.56	-	97,97,97,97	0
56	MG	RA	3756	1/1	0.70	0.53	-	73,73,73,73	0
56	MG	RA	3017	1/1	0.96	0.90	-	82,82,82,82	0
56	MG	XA	1704	1/1	0.57	0.51	-	90,90,90,90	0
56	MG	RA	3303	1/1	0.39	0.56	-	92,92,92,92	0
56	MG	YB	201	1/1	0.44	0.63	-	103,103,103,103	0
56	MG	YA	3506	1/1	0.06	1.07	-	95,95,95,95	0
56	MG	RG	202	1/1	0.86	0.07	-	86,86,86,86	0
56	MG	QA	1795	1/1	-0.18	1.27	-	97,97,97,97	0
56	MG	RA	3306	1/1	0.68	1.03	-	97,97,97,97	0
56	MG	RA	3080	1/1	0.92	0.83	-	98,98,98,98	0
56	MG	RA	3922	1/1	0.64	0.64	-	80,80,80,80	0
56	MG	RA	3718	1/1	0.83	0.84	-	65,65,65,65	0
56	MG	YA	3405	1/1	0.87	0.52	-	71,71,71,71	0
56	MG	RA	3047	1/1	0.38	0.34	-	66,66,66,66	0
56	MG	RA	3446	1/1	0.48	1.01	-	77,77,77,77	0
56	MG	RA	3244	1/1	0.08	1.24	-	98,98,98,98	0
56	MG	RA	3557	1/1	0.49	0.40	-	94,94,94,94	0
56	MG	RA	3777	1/1	0.80	0.34	-	84,84,84,84	0
56	MG	YA	3163	1/1	-0.24	2.13	-	99,99,99,99	0
56	MG	RA	3592	1/1	0.47	0.67	-	93,93,93,93	0
56	MG	RA	3987	1/1	0.85	0.79	-	79,79,79,79	0
56	MG	YA	3585	1/1	0.92	0.64	-	64,64,64,64	0
56	MG	RA	3448	1/1	0.08	1.18	-	87,87,87,87	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3296	1/1	0.87	0.63	-	62,62,62,62	0
56	MG	QA	1666	1/1	0.65	0.42	-	96,96,96,96	0
56	MG	YA	3496	1/1	0.34	1.39	-	85,85,85,85	0
56	MG	YA	3018	1/1	0.67	0.41	-	97,97,97,97	0
56	MG	RA	3755	1/1	0.79	1.16	-	100,100,100,100	0
56	MG	YA	3559	1/1	0.88	0.33	-	80,80,80,80	0
56	MG	RA	3372	1/1	0.91	0.23	-	87,87,87,87	0
56	MG	QA	1714	1/1	0.63	0.57	-	82,82,82,82	0
56	MG	RA	3260	1/1	0.93	0.16	-	99,99,99,99	0
56	MG	YA	3171	1/1	0.52	0.55	-	90,90,90,90	0
56	MG	YA	3065	1/1	0.94	0.85	-	86,86,86,86	0
56	MG	RA	3189	1/1	0.43	1.91	-	109,109,109,109	0
56	MG	RA	3338	1/1	0.79	0.74	-	62,62,62,62	0
56	MG	YA	3380	1/1	0.82	0.47	-	83,83,83,83	0
56	MG	R0	104	1/1	0.76	0.49	-	86,86,86,86	0
56	MG	XA	1739	1/1	0.86	0.73	-	82,82,82,82	0
56	MG	RA	3325	1/1	0.93	0.33	-	77,77,77,77	0
56	MG	XE	202	1/1	0.71	0.14	-	94,94,94,94	0
56	MG	RA	3843	1/1	0.43	0.67	-	88,88,88,88	0
56	MG	YA	3015	1/1	0.73	0.80	-	89,89,89,89	0
56	MG	YA	3142	1/1	0.88	0.64	-	76,76,76,76	0
56	MG	YA	3203	1/1	0.57	0.63	-	93,93,93,93	0
56	MG	RA	3258	1/1	0.84	0.49	-	102,102,102,102	0
56	MG	YA	3493	1/1	0.14	0.84	-	86,86,86,86	0
56	MG	XA	1789	1/1	0.83	0.69	-	81,81,81,81	0
56	MG	YA	3510	1/1	0.83	0.46	-	77,77,77,77	0
56	MG	XA	1641	1/1	0.90	0.24	-	77,77,77,77	0
56	MG	RA	3213	1/1	0.03	0.73	-	112,112,112,112	0
56	MG	RA	3485	1/1	0.90	0.56	-	70,70,70,70	0
56	MG	QA	1847	1/1	0.09	1.28	-	94,94,94,94	0
56	MG	YA	3098	1/1	0.78	0.36	-	95,95,95,95	0
56	MG	YA	3080	1/1	0.92	0.33	-	84,84,84,84	0
56	MG	RA	3154	1/1	0.57	0.34	-	85,85,85,85	0
56	MG	RA	3487	1/1	0.37	0.74	-	83,83,83,83	0
56	MG	YA	3406	1/1	0.72	0.42	-	95,95,95,95	0
56	MG	RA	3629	1/1	-0.13	0.85	-	88,88,88,88	0
56	MG	YA	3718	1/1	0.68	0.42	-	94,94,94,94	0
56	MG	YA	3480	1/1	0.84	0.47	-	62,62,62,62	0
56	MG	RA	3012	1/1	0.73	0.52	-	84,84,84,84	0
56	MG	YA	3236	1/1	0.64	0.49	-	80,80,80,80	0
56	MG	RA	3885	1/1	-0.09	0.46	-	98,98,98,98	0
56	MG	YA	3629	1/1	0.43	0.81	-	80,80,80,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3427	1/1	0.20	0.58	-	88,88,88,88	0
56	MG	QA	1602	1/1	0.86	0.17	-	88,88,88,88	0
56	MG	RA	3541	1/1	0.74	0.40	-	87,87,87,87	0
56	MG	RA	3700	1/1	0.26	0.89	-	104,104,104,104	0
56	MG	RA	3048	1/1	0.72	0.25	-	88,88,88,88	0
56	MG	YA	3066	1/1	0.92	0.60	-	78,78,78,78	0
56	MG	RA	3272	1/1	0.68	0.65	-	90,90,90,90	0
56	MG	RA	3577	1/1	0.93	0.32	-	69,69,69,69	0
56	MG	RA	3599	1/1	0.71	0.62	-	99,99,99,99	0
56	MG	YA	3471	1/1	0.03	0.98	-	99,99,99,99	0
56	MG	QA	1800	1/1	0.68	0.56	-	85,85,85,85	0
56	MG	QA	1702	1/1	0.44	0.90	-	86,86,86,86	0
56	MG	RA	3203	1/1	0.47	0.99	-	98,98,98,98	0
56	MG	RA	3243	1/1	0.84	0.84	-	103,103,103,103	0
56	MG	XA	1695	1/1	0.94	0.54	-	73,73,73,73	0
56	MG	QA	1870	1/1	0.79	0.90	-	81,81,81,81	0
56	MG	RA	3433	1/1	0.32	0.91	-	90,90,90,90	0
56	MG	RA	3145	1/1	0.67	0.46	-	71,71,71,71	0
56	MG	RA	3310	1/1	0.54	0.56	-	93,93,93,93	0
56	MG	YA	3573	1/1	0.85	0.83	-	64,64,64,64	0
56	MG	XA	1750	1/1	0.71	0.91	-	85,85,85,85	0
56	MG	RA	3238	1/1	0.43	0.46	-	109,109,109,109	0
56	MG	QA	1763	1/1	0.84	0.35	-	84,84,84,84	0
56	MG	YA	3025	1/1	0.25	0.88	-	74,74,74,74	0
56	MG	QA	1615	1/1	0.57	0.34	-	93,93,93,93	0
56	MG	YA	3082	1/1	0.66	1.12	-	108,108,108,108	0
56	MG	RA	3820	1/1	0.85	0.42	-	76,76,76,76	0
56	MG	RA	3957	1/1	0.31	0.51	-	79,79,79,79	0
56	MG	R5	105	1/1	-0.23	1.68	-	95,95,95,95	0
56	MG	YA	3676	1/1	0.95	0.94	-	63,63,63,63	0
56	MG	QL	202	1/1	0.12	0.45	-	82,82,82,82	0
56	MG	RA	3525	1/1	0.06	0.98	-	92,92,92,92	0
56	MG	RA	3992	1/1	0.88	0.50	-	101,101,101,101	0
56	MG	XA	1639	1/1	0.84	0.21	-	86,86,86,86	0
56	MG	YA	3625	1/1	0.76	0.53	-	86,86,86,86	0
56	MG	YA	3266	1/1	0.91	0.36	-	91,91,91,91	0
56	MG	RA	3575	1/1	0.82	0.43	-	70,70,70,70	0
56	MG	YA	3589	1/1	0.87	0.40	-	62,62,62,62	0
56	MG	RA	3442	1/1	0.74	0.89	-	82,82,82,82	0
56	MG	XA	1652	1/1	0.09	0.67	-	92,92,92,92	0
56	MG	QA	1700	1/1	-0.14	0.99	-	94,94,94,94	0
56	MG	RA	3896	1/1	0.80	1.22	-	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3714	1/1	0.84	0.57	-	63,63,63,63	0
56	MG	YA	3064	1/1	0.28	0.52	-	86,86,86,86	0
56	MG	YA	3043	1/1	0.50	0.57	-	63,63,63,63	0
56	MG	YA	3212	1/1	0.93	0.24	-	87,87,87,87	0
56	MG	RA	3649	1/1	0.31	0.48	-	94,94,94,94	0
56	MG	QA	1760	1/1	0.65	0.59	-	97,97,97,97	0
56	MG	RH	201	1/1	-0.49	0.82	-	89,89,89,89	0
56	MG	RA	3083	1/1	0.87	0.70	-	95,95,95,95	0
56	MG	RA	3963	1/1	0.30	0.71	-	88,88,88,88	0
56	MG	RA	3923	1/1	0.89	0.31	-	74,74,74,74	0
56	MG	QA	1608	1/1	0.79	0.33	-	107,107,107,107	0
56	MG	RA	3757	1/1	0.72	0.33	-	98,98,98,98	0
56	MG	XA	1664	1/1	0.67	0.50	-	102,102,102,102	0
56	MG	YA	3327	1/1	0.01	1.00	-	85,85,85,85	0
56	MG	QA	1698	1/1	0.33	0.73	-	97,97,97,97	0
56	MG	YA	3423	1/1	0.78	0.34	-	83,83,83,83	0
56	MG	RA	3308	1/1	0.86	0.83	-	94,94,94,94	0
56	MG	RA	3297	1/1	0.82	0.33	-	102,102,102,102	0
56	MG	RU	201	1/1	0.76	0.34	-	85,85,85,85	0
56	MG	RA	3286	1/1	0.59	0.79	-	100,100,100,100	0
56	MG	RA	3595	1/1	0.65	0.54	-	91,91,91,91	0
56	MG	YA	3138	1/1	0.89	0.27	-	72,72,72,72	0
56	MG	RA	3129	1/1	0.79	0.38	-	91,91,91,91	0
56	MG	YA	3598	1/1	0.92	0.53	-	62,62,62,62	0
56	MG	XA	1699	1/1	0.55	0.55	-	82,82,82,82	0
56	MG	RA	3331	1/1	0.92	0.92	-	75,75,75,75	0
56	MG	YA	3479	1/1	0.94	0.48	-	62,62,62,62	0
56	MG	YA	3215	1/1	0.86	0.32	-	86,86,86,86	0
56	MG	RA	3069	1/1	0.84	0.37	-	70,70,70,70	0
56	MG	RA	3617	1/1	0.93	0.52	-	62,62,62,62	0
56	MG	RA	3482	1/1	-0.27	0.33	-	100,100,100,100	0
56	MG	XA	1745	1/1	0.45	0.91	-	71,71,71,71	0
56	MG	RA	3194	1/1	0.58	0.67	-	99,99,99,99	0
56	MG	YA	3444	1/1	0.63	0.35	-	97,97,97,97	0
56	MG	XA	1617	1/1	-0.45	1.67	-	100,100,100,100	0
56	MG	RA	3915	1/1	0.69	0.74	-	73,73,73,73	0
56	MG	RT	202	1/1	0.18	0.81	-	87,87,87,87	0
56	MG	YA	3542	1/1	0.61	0.81	-	71,71,71,71	0
56	MG	YA	3653	1/1	0.82	0.84	-	64,64,64,64	0
56	MG	RA	3550	1/1	0.59	0.48	-	88,88,88,88	0
56	MG	XA	1613	1/1	0.92	0.09	-	73,73,73,73	0
56	MG	XA	1730	1/1	0.75	0.46	-	88,88,88,88	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	XA	1670	1/1	0.80	0.34	-	89,89,89,89	0
56	MG	RA	3736	1/1	0.72	0.70	-	85,85,85,85	0
56	MG	YA	3182	1/1	0.58	0.63	-	103,103,103,103	0
56	MG	YA	3736	1/1	0.64	0.76	-	115,115,115,115	0
56	MG	YA	3470	1/1	0.67	0.51	-	74,74,74,74	0
56	MG	YA	3528	1/1	0.79	1.36	-	72,72,72,72	0
56	MG	R1	103	1/1	0.70	0.69	-	76,76,76,76	0
56	MG	QA	1783	1/1	0.88	0.51	-	63,63,63,63	0
56	MG	YA	3461	1/1	-0.20	0.91	-	87,87,87,87	0
56	MG	RA	4055	1/1	0.79	0.60	-	95,95,95,95	0
56	MG	XA	1680	1/1	0.79	0.76	-	80,80,80,80	0
56	MG	QA	1705	1/1	-0.02	1.00	-	95,95,95,95	0
56	MG	RA	3432	1/1	0.29	0.74	-	77,77,77,77	0
56	MG	YA	3193	1/1	0.37	0.47	-	85,85,85,85	0
56	MG	RD	310	1/1	0.24	0.92	-	86,86,86,86	0
56	MG	YA	3322	1/1	0.89	0.42	-	64,64,64,64	0
56	MG	RA	3153	1/1	0.83	0.48	-	90,90,90,90	0
56	MG	XA	1602	1/1	0.25	1.02	-	88,88,88,88	0
56	MG	YA	3473	1/1	0.40	0.44	-	82,82,82,82	0
56	MG	YA	3349	1/1	0.74	0.58	-	62,62,62,62	0
56	MG	RA	3740	1/1	0.91	0.46	-	85,85,85,85	0
56	MG	RA	3813	1/1	0.28	1.07	-	107,107,107,107	0
56	MG	RA	3504	1/1	0.94	0.40	-	62,62,62,62	0
56	MG	RB	217	1/1	0.38	0.48	-	87,87,87,87	0
56	MG	YA	3728	1/1	0.70	0.51	-	89,89,89,89	0
56	MG	YA	3556	1/1	0.35	0.55	-	73,73,73,73	0
56	MG	YA	3487	1/1	0.74	0.36	-	84,84,84,84	0
56	MG	YA	3230	1/1	0.15	0.50	-	92,92,92,92	0
56	MG	YA	3116	1/1	0.72	0.67	-	95,95,95,95	0
56	MG	XA	1624	1/1	0.29	0.89	-	85,85,85,85	0
56	MG	RA	3748	1/1	-0.26	0.49	-	86,86,86,86	0
56	MG	QA	1716	1/1	0.84	0.55	-	75,75,75,75	0
56	MG	RA	3406	1/1	0.91	0.75	-	68,68,68,68	0
56	MG	RA	3701	1/1	0.75	0.42	-	64,64,64,64	0
56	MG	QA	1816	1/1	-0.09	0.56	-	98,98,98,98	0
56	MG	RA	3236	1/1	0.46	1.08	-	97,97,97,97	0
56	MG	RA	3997	1/1	0.39	0.52	-	106,106,106,106	0
56	MG	RA	3427	1/1	0.18	0.46	-	90,90,90,90	0
56	MG	QA	1776	1/1	0.81	0.42	-	83,83,83,83	0
56	MG	RA	3680	1/1	0.82	1.04	-	69,69,69,69	0
56	MG	RA	3460	1/1	0.87	0.49	-	79,79,79,79	0
56	MG	RA	3861	1/1	0.95	0.92	-	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3758	1/1	0.46	0.69	-	93,93,93,93	0
56	MG	RA	3506	1/1	0.71	0.35	-	70,70,70,70	0
56	MG	RA	3895	1/1	0.92	0.84	-	63,63,63,63	0
56	MG	RA	3138	1/1	0.12	0.50	-	79,79,79,79	0
56	MG	RA	3561	1/1	0.91	1.16	-	62,62,62,62	0
56	MG	RA	3815	1/1	0.85	1.16	-	99,99,99,99	0
56	MG	YA	3306	1/1	-0.05	0.99	-	87,87,87,87	0
56	MG	QY	402	1/1	-0.12	1.12	-	92,92,92,92	0
56	MG	YA	3604	1/1	0.78	0.86	-	66,66,66,66	0
56	MG	RA	3658	1/1	0.43	0.45	-	90,90,90,90	0
56	MG	RA	3918	1/1	0.34	0.95	-	93,93,93,93	0
56	MG	RA	3269	1/1	0.86	0.32	-	90,90,90,90	0
56	MG	YA	3186	1/1	0.09	0.40	-	106,106,106,106	0
56	MG	YA	3597	1/1	0.89	0.95	-	71,71,71,71	0
56	MG	XA	1661	1/1	0.72	0.55	-	95,95,95,95	0
56	MG	RA	3808	1/1	0.21	0.75	-	85,85,85,85	0
56	MG	YA	3445	1/1	0.67	0.58	-	94,94,94,94	0
56	MG	RA	3974	1/1	0.83	0.31	-	88,88,88,88	0
56	MG	XA	1721	1/1	0.80	1.30	-	78,78,78,78	0
56	MG	XA	1646	1/1	0.55	0.58	-	104,104,104,104	0
56	MG	RA	3818	1/1	0.65	0.96	-	92,92,92,92	0
56	MG	YB	216	1/1	0.44	0.39	-	66,66,66,66	0
56	MG	YA	3290	1/1	0.73	0.88	-	91,91,91,91	0
56	MG	RA	3223	1/1	0.93	0.06	-	77,77,77,77	0
56	MG	YA	3128	1/1	0.71	0.57	-	82,82,82,82	0
56	MG	RA	3009	1/1	0.96	0.20	-	73,73,73,73	0
56	MG	YA	3457	1/1	0.12	0.63	-	87,87,87,87	0
56	MG	RA	3932	1/1	0.76	0.75	-	88,88,88,88	0
56	MG	QA	1866	1/1	0.41	0.77	-	90,90,90,90	0
56	MG	RA	3650	1/1	0.84	0.29	-	76,76,76,76	0
56	MG	YA	3037	1/1	0.89	0.29	-	84,84,84,84	0
56	MG	QA	1741	1/1	0.59	0.59	-	97,97,97,97	0
56	MG	RA	3606	1/1	0.20	0.64	-	87,87,87,87	0
56	MG	QA	1777	1/1	0.88	0.53	-	83,83,83,83	0
56	MG	RA	3665	1/1	0.86	0.28	-	62,62,62,62	0
56	MG	XA	1635	1/1	0.81	0.33	-	70,70,70,70	0
56	MG	YA	3293	1/1	0.71	1.28	-	65,65,65,65	0
56	MG	RA	3278	1/1	0.34	0.97	-	89,89,89,89	0
56	MG	YA	3627	1/1	0.86	0.31	-	82,82,82,82	0
56	MG	RA	3979	1/1	0.80	0.78	-	70,70,70,70	0
56	MG	RB	210	1/1	0.88	0.75	-	96,96,96,96	0
56	MG	YB	209	1/1	0.47	0.53	-	102,102,102,102	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	QA	1779	1/1	0.99	0.07	-	91,91,91,91	0
56	MG	QA	1751	1/1	0.36	1.18	-	78,78,78,78	0
56	MG	RA	4019	1/1	0.22	1.37	-	103,103,103,103	0
56	MG	RA	3899	1/1	0.29	0.87	-	93,93,93,93	0
56	MG	QA	1662	1/1	0.80	0.32	-	90,90,90,90	0
56	MG	RA	3449	1/1	0.72	0.51	-	83,83,83,83	0
56	MG	YA	3478	1/1	0.73	0.57	-	62,62,62,62	0
56	MG	YA	3062	1/1	0.67	0.40	-	84,84,84,84	0
56	MG	YA	3412	1/1	0.65	0.43	-	90,90,90,90	0
56	MG	QA	1686	1/1	0.46	0.73	-	89,89,89,89	0
56	MG	YA	3004	1/1	0.91	0.24	-	63,63,63,63	0
56	MG	RA	3947	1/1	0.83	0.40	-	63,63,63,63	0
56	MG	YA	3358	1/1	0.76	0.85	-	90,90,90,90	0
56	MG	YA	3442	1/1	0.70	0.56	-	90,90,90,90	0
56	MG	YB	203	1/1	0.57	0.25	-	72,72,72,72	0
56	MG	YA	3229	1/1	0.81	0.30	-	83,83,83,83	0
56	MG	YA	3566	1/1	0.76	0.42	-	73,73,73,73	0
56	MG	RA	4016	1/1	0.72	0.45	-	87,87,87,87	0
56	MG	XA	1790	1/1	0.62	0.84	-	87,87,87,87	0
56	MG	RA	3519	1/1	0.70	0.94	-	86,86,86,86	0
56	MG	YA	3520	1/1	0.74	0.22	-	100,100,100,100	0
56	MG	YA	3654	1/1	0.48	0.38	-	91,91,91,91	0
56	MG	XA	1761	1/1	0.95	0.66	-	80,80,80,80	0
56	MG	QA	1875	1/1	0.74	0.32	-	78,78,78,78	0
56	MG	RA	3579	1/1	0.65	0.62	-	63,63,63,63	0
56	MG	YA	3113	1/1	0.43	0.63	-	79,79,79,79	0
56	MG	RA	3569	1/1	0.95	0.45	-	62,62,62,62	0
56	MG	RA	3264	1/1	0.89	0.37	-	84,84,84,84	0
56	MG	QA	1605	1/1	0.81	0.17	-	90,90,90,90	0
56	MG	RP	202	1/1	-0.23	0.48	-	98,98,98,98	0
56	MG	QG	203	1/1	-0.15	1.46	-	97,97,97,97	0
56	MG	RA	3961	1/1	0.62	0.49	-	87,87,87,87	0
56	MG	RA	3081	1/1	0.43	0.52	-	92,92,92,92	0
56	MG	YA	3553	1/1	0.77	0.71	-	73,73,73,73	0
56	MG	RA	3414	1/1	0.94	0.42	-	62,62,62,62	0
56	MG	RB	213	1/1	0.83	0.81	-	71,71,71,71	0
56	MG	QA	1707	1/1	0.88	0.51	-	66,66,66,66	0
56	MG	RA	3719	1/1	0.88	0.30	-	79,79,79,79	0
56	MG	YA	3696	1/1	0.47	0.82	-	91,91,91,91	0
56	MG	QA	1730	1/1	0.55	0.32	-	73,73,73,73	0
56	MG	QE	202	1/1	0.58	0.69	-	88,88,88,88	0
56	MG	XA	1679	1/1	0.91	0.67	-	102,102,102,102	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	QA	1834	1/1	-0.18	0.92	-	97,97,97,97	0
56	MG	YA	3562	1/1	0.37	0.53	-	82,82,82,82	0
56	MG	YA	3262	1/1	0.79	0.56	-	88,88,88,88	0
56	MG	RA	3880	1/1	0.98	0.62	-	62,62,62,62	0
56	MG	QA	1824	1/1	0.78	0.58	-	69,69,69,69	0
56	MG	YA	3288	1/1	0.90	0.65	-	62,62,62,62	0
56	MG	RA	3725	1/1	0.68	0.45	-	86,86,86,86	0
56	MG	RA	3849	1/1	0.54	0.86	-	85,85,85,85	0
56	MG	RA	3183	1/1	0.61	0.50	-	97,97,97,97	0
56	MG	RA	3764	1/1	0.30	0.47	-	77,77,77,77	0
56	MG	RA	3488	1/1	0.91	0.19	-	67,67,67,67	0
56	MG	QA	1604	1/1	0.46	0.66	-	96,96,96,96	0
56	MG	RA	3031	1/1	0.65	0.49	-	96,96,96,96	0
56	MG	QA	1813	1/1	0.83	0.46	-	90,90,90,90	0
56	MG	YA	3519	1/1	0.73	0.36	-	72,72,72,72	0
56	MG	XA	1622	1/1	0.71	0.59	-	78,78,78,78	0
56	MG	RT	203	1/1	-0.29	2.40	-	100,100,100,100	0
56	MG	RA	3362	1/1	0.55	0.60	-	91,91,91,91	0
56	MG	RA	3206	1/1	0.84	0.31	-	86,86,86,86	0
56	MG	XA	1756	1/1	0.73	1.16	-	81,81,81,81	0
56	MG	RA	3172	1/1	0.04	0.71	-	105,105,105,105	0
56	MG	XA	1672	1/1	-0.05	0.99	-	95,95,95,95	0
56	MG	QA	1632	1/1	0.67	0.50	-	91,91,91,91	0
56	MG	RA	3587	1/1	0.68	0.48	-	78,78,78,78	0
56	MG	RA	3934	1/1	0.93	0.54	-	81,81,81,81	0
56	MG	QA	1764	1/1	0.33	1.28	-	83,83,83,83	0
56	MG	YA	3717	1/1	0.62	0.72	-	100,100,100,100	0
56	MG	RA	3441	1/1	0.54	0.77	-	67,67,67,67	0
56	MG	RA	3011	1/1	0.39	0.69	-	93,93,93,93	0
56	MG	RA	3531	1/1	-0.06	0.58	-	90,90,90,90	0
56	MG	RA	3984	1/1	0.62	0.57	-	87,87,87,87	0
56	MG	QE	201	1/1	0.47	0.33	-	95,95,95,95	0
56	MG	QV	102	1/1	0.90	0.22	-	94,94,94,94	0
56	MG	RA	3753	1/1	0.50	0.70	-	92,92,92,92	0
56	MG	RA	3826	1/1	0.72	0.30	-	95,95,95,95	0
56	MG	YR	201	1/1	0.78	0.46	-	82,82,82,82	0
56	MG	QA	1819	1/1	0.06	0.82	-	83,83,83,83	0
56	MG	RA	3422	1/1	0.65	0.55	-	73,73,73,73	0
56	MG	RA	3267	1/1	0.77	0.71	-	85,85,85,85	0
56	MG	XV	103	1/1	0.58	0.59	-	84,84,84,84	0
56	MG	RA	3004	1/1	0.85	0.17	-	63,63,63,63	0
56	MG	RA	3944	1/1	0.57	0.60	-	97,97,97,97	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3192	1/1	0.31	0.37	-	83,83,83,83	0
56	MG	YA	3697	1/1	0.61	0.41	-	78,78,78,78	0
56	MG	YA	3631	1/1	0.67	0.44	-	76,76,76,76	0
56	MG	RA	3883	1/1	0.53	0.88	-	88,88,88,88	0
56	MG	RD	311	1/1	0.56	0.84	-	101,101,101,101	0
56	MG	RA	3960	1/1	0.18	0.72	-	92,92,92,92	0
56	MG	YA	3662	1/1	0.80	0.51	-	68,68,68,68	0
56	MG	YT	203	1/1	0.73	0.55	-	91,91,91,91	0
56	MG	RA	3565	1/1	0.49	0.56	-	103,103,103,103	0
56	MG	XA	1729	1/1	0.22	0.74	-	83,83,83,83	0
56	MG	RA	3942	1/1	0.68	0.43	-	95,95,95,95	0
56	MG	RA	3937	1/1	0.77	0.81	-	80,80,80,80	0
56	MG	YA	3463	1/1	0.15	0.92	-	86,86,86,86	0
56	MG	RA	3198	1/1	0.14	3.01	-	98,98,98,98	0
56	MG	QA	1675	1/1	0.81	0.49	-	91,91,91,91	0
56	MG	RA	3794	1/1	0.80	0.36	-	72,72,72,72	0
56	MG	QA	1732	1/1	0.72	0.57	-	72,72,72,72	0
56	MG	XA	1681	1/1	0.79	0.17	-	100,100,100,100	0
56	MG	RA	3347	1/1	0.94	0.74	-	62,62,62,62	0
56	MG	QA	1755	1/1	0.49	0.89	-	81,81,81,81	0
56	MG	YA	3422	1/1	0.82	0.32	-	90,90,90,90	0
56	MG	RA	3833	1/1	0.24	0.53	-	92,92,92,92	0
56	MG	RA	3864	1/1	0.51	0.82	-	93,93,93,93	0
56	MG	RA	3309	1/1	0.18	0.90	-	93,93,93,93	0
56	MG	YA	3432	1/1	0.80	0.36	-	76,76,76,76	0
56	MG	XA	1603	1/1	0.81	0.33	-	83,83,83,83	0
56	MG	XA	1608	1/1	0.62	0.71	-	76,76,76,76	0
56	MG	RA	3182	1/1	0.72	0.99	-	97,97,97,97	0
56	MG	QG	202	1/1	0.59	0.71	-	87,87,87,87	0
56	MG	XA	1787	1/1	0.59	0.65	-	78,78,78,78	0
56	MG	RA	3855	1/1	0.96	0.33	-	71,71,71,71	0
56	MG	RA	3033	1/1	-0.07	0.48	-	100,100,100,100	0
56	MG	YA	3527	1/1	0.67	0.38	-	74,74,74,74	0
56	MG	QA	1752	1/1	0.81	0.37	-	94,94,94,94	0
56	MG	XA	1757	1/1	0.95	0.61	-	76,76,76,76	0
56	MG	QA	1758	1/1	0.74	0.35	-	93,93,93,93	0
56	MG	RA	3846	1/1	0.65	0.53	-	98,98,98,98	0
56	MG	YA	3309	1/1	0.07	1.03	-	90,90,90,90	0
56	MG	RA	3038	1/1	0.90	0.15	-	86,86,86,86	0
56	MG	RA	3169	1/1	0.64	0.23	-	90,90,90,90	0
56	MG	RA	3830	1/1	0.75	1.56	-	78,78,78,78	0
56	MG	YQ	202	1/1	0.20	0.69	-	89,89,89,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3663	1/1	0.33	1.33	-	98,98,98,98	0
56	MG	XA	1634	1/1	0.98	0.48	-	69,69,69,69	0
56	MG	RA	3743	1/1	0.63	0.78	-	89,89,89,89	0
56	MG	RA	3100	1/1	0.57	0.53	-	102,102,102,102	0
56	MG	XA	1711	1/1	0.42	0.69	-	94,94,94,94	0
56	MG	YB	219	1/1	0.88	0.47	-	63,63,63,63	0
56	MG	YA	3099	1/1	0.48	0.38	-	82,82,82,82	0
56	MG	XA	1668	1/1	0.92	0.52	-	92,92,92,92	0
56	MG	QA	1701	1/1	0.61	0.50	-	77,77,77,77	0
56	MG	RA	3126	1/1	0.65	0.91	-	89,89,89,89	0
56	MG	RA	3281	1/1	0.76	0.24	-	90,90,90,90	0
56	MG	QA	1754	1/1	0.90	0.27	-	85,85,85,85	0
56	MG	RA	3612	1/1	0.63	0.20	-	80,80,80,80	0
56	MG	YA	3141	1/1	0.68	0.44	-	79,79,79,79	0
56	MG	YA	3721	1/1	0.55	0.69	-	74,74,74,74	0
56	MG	RA	3865	1/1	0.90	0.33	-	93,93,93,93	0
56	MG	RA	3879	1/1	0.11	0.96	-	93,93,93,93	0
56	MG	RA	3559	1/1	0.34	0.73	-	84,84,84,84	0
56	MG	QA	1861	1/1	0.86	0.38	-	72,72,72,72	0
56	MG	RA	3499	1/1	0.22	1.30	-	80,80,80,80	0
56	MG	RA	3152	1/1	0.81	0.26	-	93,93,93,93	0
56	MG	YA	3371	1/1	0.84	1.01	-	68,68,68,68	0
56	MG	RA	3280	1/1	0.56	0.84	-	95,95,95,95	0
56	MG	RA	3728	1/1	0.14	0.76	-	99,99,99,99	0
56	MG	RA	3380	1/1	0.91	0.68	-	64,64,64,64	0
56	MG	RA	3151	1/1	0.81	0.52	-	84,84,84,84	0
56	MG	XA	1717	1/1	0.84	0.38	-	82,82,82,82	0
56	MG	XA	1784	1/1	0.93	0.34	-	80,80,80,80	0
56	MG	RA	3890	1/1	0.77	0.99	-	77,77,77,77	0
56	MG	YA	3259	1/1	0.75	0.78	-	98,98,98,98	0
56	MG	YA	3147	1/1	-0.08	1.01	-	86,86,86,86	0
56	MG	YA	3073	1/1	0.83	0.31	-	86,86,86,86	0
56	MG	YA	3716	1/1	0.32	0.89	-	87,87,87,87	0
56	MG	YA	3125	1/1	0.42	0.34	-	81,81,81,81	0
56	MG	YB	208	1/1	0.72	0.47	-	93,93,93,93	0
56	MG	YA	3641	1/1	0.83	0.94	-	83,83,83,83	0
56	MG	RA	3061	1/1	0.57	0.25	-	89,89,89,89	0
56	MG	YA	3069	1/1	0.77	0.58	-	98,98,98,98	0
56	MG	YA	3390	1/1	0.47	0.33	-	88,88,88,88	0
56	MG	YA	3220	1/1	0.74	0.56	-	105,105,105,105	0
56	MG	XA	1643	1/1	0.94	0.31	-	81,81,81,81	0
56	MG	YA	3261	1/1	0.75	0.59	-	85,85,85,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3780	1/1	0.66	0.48	-	89,89,89,89	0
56	MG	QA	1694	1/1	0.18	0.77	-	91,91,91,91	0
56	MG	YA	3168	1/1	0.29	0.90	-	100,100,100,100	0
56	MG	RA	3411	1/1	0.73	0.52	-	93,93,93,93	0
56	MG	YA	3226	1/1	0.59	0.56	-	87,87,87,87	0
56	MG	YA	3330	1/1	0.91	1.11	-	62,62,62,62	0
56	MG	QA	1804	1/1	0.86	0.40	-	85,85,85,85	0
56	MG	RA	3558	1/1	0.74	0.36	-	76,76,76,76	0
56	MG	QA	1801	1/1	0.59	0.33	-	76,76,76,76	0
56	MG	XA	1620	1/1	0.17	0.17	-	93,93,93,93	0
56	MG	YA	3208	1/1	-0.55	1.38	-	102,102,102,102	0
56	MG	RA	3716	1/1	0.03	0.37	-	91,91,91,91	0
56	MG	YA	3564	1/1	0.96	0.29	-	63,63,63,63	0
56	MG	RA	3766	1/1	0.93	1.11	-	71,71,71,71	0
56	MG	RA	3691	1/1	0.69	1.05	-	93,93,93,93	0
56	MG	RA	3253	1/1	0.57	0.52	-	81,81,81,81	0
56	MG	RA	3642	1/1	0.49	0.55	-	92,92,92,92	0
56	MG	RA	3057	1/1	0.36	0.58	-	96,96,96,96	0
56	MG	RA	3469	1/1	0.95	0.39	-	68,68,68,68	0
56	MG	QA	1687	1/1	0.72	0.62	-	94,94,94,94	0
56	MG	RA	3351	1/1	0.93	0.19	-	89,89,89,89	0
56	MG	QA	1811	1/1	0.77	0.23	-	78,78,78,78	0
56	MG	YA	3693	1/1	0.75	0.64	-	70,70,70,70	0
56	MG	RA	3288	1/1	0.56	0.53	-	96,96,96,96	0
56	MG	RA	3242	1/1	0.47	0.43	-	99,99,99,99	0
56	MG	YA	3143	1/1	0.54	0.45	-	106,106,106,106	0
56	MG	RA	3907	1/1	0.96	0.45	-	70,70,70,70	0
56	MG	QA	1792	1/1	0.88	0.82	-	84,84,84,84	0
56	MG	RA	3651	1/1	0.79	0.40	-	80,80,80,80	0
56	MG	QA	1670	1/1	0.67	0.42	-	84,84,84,84	0
56	MG	YA	3622	1/1	0.88	0.37	-	66,66,66,66	0
56	MG	YB	204	1/1	0.77	0.52	-	95,95,95,95	0
56	MG	YA	3031	1/1	0.71	0.32	-	63,63,63,63	0
56	MG	RA	3695	1/1	0.59	0.83	-	107,107,107,107	0
56	MG	RA	3791	1/1	0.37	0.47	-	84,84,84,84	0
56	MG	YB	211	1/1	0.51	0.30	-	80,80,80,80	0
56	MG	YA	3067	1/1	0.77	0.32	-	76,76,76,76	0
56	MG	YA	3411	1/1	0.37	0.64	-	90,90,90,90	0
56	MG	RA	3804	1/1	0.17	0.52	-	92,92,92,92	0
56	MG	XA	1767	1/1	0.63	0.81	-	78,78,78,78	0
56	MG	RA	3998	1/1	0.89	0.46	-	84,84,84,84	0
56	MG	YA	3144	1/1	0.90	0.10	-	82,82,82,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3530	1/1	-0.14	0.59	-	102,102,102,102	0
56	MG	RA	3498	1/1	-0.14	0.57	-	83,83,83,83	0
56	MG	YA	3451	1/1	0.63	0.64	-	94,94,94,94	0
56	MG	XA	1692	1/1	0.82	0.55	-	69,69,69,69	0
56	MG	YA	3061	1/1	0.65	0.48	-	65,65,65,65	0
56	MG	YA	3079	1/1	0.51	0.67	-	97,97,97,97	0
56	MG	YA	3596	1/1	0.63	0.57	-	66,66,66,66	0
56	MG	RQ	202	1/1	0.78	0.69	-	73,73,73,73	0
56	MG	QA	1713	1/1	0.04	0.73	-	95,95,95,95	0
56	MG	RA	3105	1/1	0.37	1.08	-	92,92,92,92	0
56	MG	YA	3481	1/1	0.65	0.60	-	79,79,79,79	0
56	MG	RA	3951	1/1	0.31	0.77	-	85,85,85,85	0
56	MG	RA	3354	1/1	0.73	0.67	-	70,70,70,70	0
56	MG	YA	3672	1/1	0.56	0.67	-	76,76,76,76	0
56	MG	RA	3661	1/1	0.77	0.34	-	73,73,73,73	0
56	MG	RA	3866	1/1	0.64	0.38	-	76,76,76,76	0
56	MG	YA	3160	1/1	0.78	0.30	-	88,88,88,88	0
56	MG	XA	1748	1/1	0.55	0.73	-	79,79,79,79	0
56	MG	YA	3708	1/1	0.74	1.08	-	66,66,66,66	0
56	MG	RA	3159	1/1	0.49	0.67	-	94,94,94,94	0
56	MG	XA	1675	1/1	0.56	0.43	-	90,90,90,90	0
56	MG	RA	3542	1/1	0.77	0.72	-	79,79,79,79	0
56	MG	XA	1601	1/1	0.11	0.89	-	93,93,93,93	0
56	MG	RA	3340	1/1	0.61	0.56	-	82,82,82,82	0
56	MG	RA	3298	1/1	0.65	0.16	-	79,79,79,79	0
56	MG	RA	3863	1/1	0.86	0.29	-	86,86,86,86	0
56	MG	YA	3035	1/1	-0.27	1.00	-	93,93,93,93	0
56	MG	YA	3551	1/1	0.31	0.50	-	73,73,73,73	0
56	MG	RA	3608	1/1	0.62	0.62	-	83,83,83,83	0
56	MG	QA	1646	1/1	0.46	0.74	-	71,71,71,71	0
56	MG	YA	3599	1/1	-0.13	0.96	-	83,83,83,83	0
56	MG	XA	1689	1/1	0.94	0.44	-	75,75,75,75	0
56	MG	RA	3344	1/1	0.97	0.25	-	67,67,67,67	0
56	MG	RA	3457	1/1	0.70	0.17	-	89,89,89,89	0
56	MG	RA	3980	1/1	0.90	0.36	-	77,77,77,77	0
56	MG	XA	1665	1/1	0.72	0.28	-	72,72,72,72	0
56	MG	YA	3278	1/1	0.60	0.96	-	72,72,72,72	0
56	MG	RA	3091	1/1	0.70	1.15	-	102,102,102,102	0
56	MG	RA	3975	1/1	0.46	0.34	-	98,98,98,98	0
56	MG	YA	3224	1/1	0.93	0.35	-	71,71,71,71	0
56	MG	RA	3950	1/1	0.71	1.05	-	86,86,86,86	0
56	MG	RA	3672	1/1	0.61	0.47	-	89,89,89,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3334	1/1	0.88	0.43	-	82,82,82,82	0
56	MG	QA	1815	1/1	0.84	0.32	-	87,87,87,87	0
56	MG	RA	3783	1/1	-0.35	0.71	-	96,96,96,96	0
56	MG	RA	3730	1/1	0.76	0.70	-	89,89,89,89	0
56	MG	RA	3079	1/1	0.24	0.80	-	111,111,111,111	0
56	MG	YA	3719	1/1	0.33	0.25	-	89,89,89,89	0
56	MG	YA	3001	1/1	0.39	0.75	-	96,96,96,96	0
56	MG	RA	3416	1/1	0.93	0.36	-	75,75,75,75	0
56	MG	YA	3197	1/1	0.73	0.45	-	93,93,93,93	0
56	MG	QA	1648	1/1	0.86	0.17	-	87,87,87,87	0
56	MG	QA	1855	1/1	-0.48	0.73	-	106,106,106,106	0
56	MG	QV	104	1/1	0.69	0.60	-	79,79,79,79	0
56	MG	YA	3200	1/1	0.66	0.47	-	77,77,77,77	0
56	MG	RA	3673	1/1	0.65	0.38	-	86,86,86,86	0
56	MG	RA	3035	1/1	0.58	0.35	-	95,95,95,95	0
56	MG	XA	1638	1/1	0.25	0.82	-	98,98,98,98	0
56	MG	YA	3586	1/1	0.63	1.11	-	76,76,76,76	0
56	MG	RA	3255	1/1	0.77	0.57	-	97,97,97,97	0
56	MG	XA	1653	1/1	0.63	0.58	-	89,89,89,89	0
56	MG	YA	3365	1/1	0.57	0.38	-	86,86,86,86	0
56	MG	QA	1664	1/1	-0.25	1.44	-	91,91,91,91	0
56	MG	QA	1793	1/1	0.28	0.79	-	93,93,93,93	0
56	MG	RA	3921	1/1	0.93	0.88	-	63,63,63,63	0
56	MG	RA	3996	1/1	0.48	0.59	-	89,89,89,89	0
56	MG	RA	3143	1/1	0.83	0.28	-	77,77,77,77	0
56	MG	YA	3608	1/1	0.90	0.30	-	66,66,66,66	0
56	MG	YA	3121	1/1	0.94	0.09	-	77,77,77,77	0
56	MG	RA	3615	1/1	0.75	0.51	-	62,62,62,62	0
56	MG	RA	3054	1/1	-0.05	0.86	-	94,94,94,94	0
56	MG	QA	1805	1/1	0.66	0.94	-	76,76,76,76	0
56	MG	RA	3191	1/1	0.77	0.28	-	90,90,90,90	0
56	MG	RA	3824	1/1	0.24	0.61	-	92,92,92,92	0
56	MG	RA	3604	1/1	0.40	0.77	-	107,107,107,107	0
56	MG	QD	304	1/1	0.67	0.52	-	97,97,97,97	0
56	MG	XA	1605	1/1	0.21	1.09	-	96,96,96,96	0
56	MG	XA	1740	1/1	0.75	0.59	-	70,70,70,70	0
56	MG	R7	101	1/1	0.26	0.54	-	88,88,88,88	0
56	MG	R9	101	1/1	0.12	0.47	-	100,100,100,100	0
56	MG	XA	1709	1/1	0.84	0.26	-	88,88,88,88	0
56	MG	RA	3584	1/1	0.63	0.57	-	76,76,76,76	0
56	MG	RA	3439	1/1	0.52	0.24	-	84,84,84,84	0
56	MG	RA	3237	1/1	0.49	0.96	-	96,96,96,96	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3026	1/1	0.93	1.22	-	100,100,100,100	0
56	MG	YA	3242	1/1	0.55	0.85	-	107,107,107,107	0
56	MG	RA	3318	1/1	0.93	0.73	-	71,71,71,71	0
56	MG	RA	3920	1/1	0.69	0.46	-	80,80,80,80	0
56	MG	QA	1657	1/1	0.76	0.42	-	101,101,101,101	0
56	MG	XA	1733	1/1	0.77	0.98	-	69,69,69,69	0
56	MG	YA	3155	1/1	0.90	0.65	-	85,85,85,85	0
56	MG	YA	3738	1/1	0.80	0.93	-	99,99,99,99	0
56	MG	YA	3571	1/1	0.94	0.69	-	64,64,64,64	0
56	MG	YA	3225	1/1	0.47	0.96	-	96,96,96,96	0
56	MG	RA	3134	1/1	0.16	0.99	-	96,96,96,96	0
56	MG	QA	1830	1/1	0.95	0.37	-	69,69,69,69	0
56	MG	RA	3580	1/1	0.92	0.41	-	64,64,64,64	0
56	MG	XA	1610	1/1	0.53	1.06	-	88,88,88,88	0
56	MG	RA	3250	1/1	0.24	0.93	-	84,84,84,84	0
56	MG	YA	3575	1/1	0.93	0.75	-	67,67,67,67	0
56	MG	RA	3087	1/1	0.76	1.00	-	113,113,113,113	0
56	MG	YA	3591	1/1	0.92	0.79	-	62,62,62,62	0
56	MG	YA	3431	1/1	0.78	0.97	-	84,84,84,84	0
56	MG	RA	3114	1/1	0.71	0.52	-	95,95,95,95	0
56	MG	XA	1766	1/1	0.55	1.07	-	88,88,88,88	0
56	MG	XA	1648	1/1	0.49	0.29	-	89,89,89,89	0
56	MG	RA	3358	1/1	0.70	0.26	-	81,81,81,81	0
56	MG	RA	3207	1/1	0.72	0.62	-	96,96,96,96	0
56	MG	RA	3816	1/1	0.75	0.29	-	79,79,79,79	0
56	MG	RA	3761	1/1	0.83	0.26	-	70,70,70,70	0
56	MG	YE	306	1/1	0.65	0.81	-	62,62,62,62	0
56	MG	YA	3302	1/1	0.71	0.27	-	89,89,89,89	0
56	MG	YA	3583	1/1	0.80	0.52	-	74,74,74,74	0
56	MG	RA	3150	1/1	0.33	0.27	-	84,84,84,84	0
56	MG	QA	1659	1/1	0.83	0.97	-	92,92,92,92	0
56	MG	RA	3534	1/1	0.85	0.38	-	75,75,75,75	0
56	MG	QA	1803	1/1	0.58	0.37	-	81,81,81,81	0
56	MG	YA	3484	1/1	-0.11	0.63	-	99,99,99,99	0
56	MG	RA	3857	1/1	0.86	0.69	-	76,76,76,76	0
56	MG	RB	216	1/1	0.81	0.55	-	88,88,88,88	0
56	MG	YA	3706	1/1	0.74	0.88	-	75,75,75,75	0
56	MG	QA	1641	1/1	0.94	0.31	-	95,95,95,95	0
56	MG	QA	1651	1/1	0.70	0.47	-	90,90,90,90	0
56	MG	XA	1726	1/1	0.46	0.53	-	96,96,96,96	0
56	MG	RA	3474	1/1	0.95	0.38	-	70,70,70,70	0
56	MG	XA	1615	1/1	0.90	0.19	-	89,89,89,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	XV	102	1/1	0.48	0.13	-	84,84,84,84	0
56	MG	YA	3127	1/1	0.93	0.36	-	70,70,70,70	0
56	MG	YA	3294	1/1	0.96	0.69	-	62,62,62,62	0
56	MG	RA	3982	1/1	0.91	0.14	-	79,79,79,79	0
56	MG	RA	3667	1/1	0.87	0.63	-	88,88,88,88	0
56	MG	QA	1879	1/1	-0.07	1.40	-	105,105,105,105	0
56	MG	RA	3212	1/1	0.88	0.60	-	80,80,80,80	0
56	MG	RA	3450	1/1	0.54	0.28	-	79,79,79,79	0
56	MG	XA	1647	1/1	0.96	0.88	-	70,70,70,70	0
56	MG	QA	1689	1/1	0.91	0.49	-	81,81,81,81	0
56	MG	RA	3675	1/1	0.68	0.60	-	84,84,84,84	0
56	MG	RA	3010	1/1	0.91	0.50	-	79,79,79,79	0
56	MG	YA	3513	1/1	0.60	0.85	-	81,81,81,81	0
56	MG	YA	3289	1/1	-0.12	1.36	-	92,92,92,92	0
56	MG	YA	3086	1/1	-0.10	0.76	-	92,92,92,92	0
56	MG	RA	3037	1/1	0.68	0.48	-	100,100,100,100	0
56	MG	YA	3118	1/1	0.80	0.44	-	74,74,74,74	0
56	MG	YA	3609	1/1	0.88	0.59	-	75,75,75,75	0
56	MG	RA	3640	1/1	0.56	0.49	-	84,84,84,84	0
56	MG	YA	3572	1/1	0.88	0.43	-	72,72,72,72	0
56	MG	RA	3567	1/1	0.55	0.44	-	90,90,90,90	0
56	MG	RA	3376	1/1	0.68	0.78	-	78,78,78,78	0
56	MG	RB	222	1/1	0.62	0.48	-	79,79,79,79	0
56	MG	RA	3894	1/1	0.82	0.78	-	69,69,69,69	0
56	MG	RA	4011	1/1	-0.10	0.38	-	102,102,102,102	0
56	MG	RA	3648	1/1	0.24	0.29	-	97,97,97,97	0
56	MG	RA	3001	1/1	0.61	0.47	-	91,91,91,91	0
56	MG	YO	201	1/1	0.45	0.64	-	86,86,86,86	0
56	MG	RA	3056	1/1	0.83	0.84	-	87,87,87,87	0
56	MG	RA	3195	1/1	0.95	0.61	-	97,97,97,97	0
56	MG	RA	3147	1/1	0.99	0.17	-	84,84,84,84	0
56	MG	RA	3706	1/1	0.91	0.47	-	78,78,78,78	0
56	MG	RA	3610	1/1	0.81	0.49	-	91,91,91,91	0
56	MG	XA	1671	1/1	0.92	0.25	-	84,84,84,84	0
56	MG	YA	3234	1/1	0.93	0.35	-	92,92,92,92	0
56	MG	RA	3500	1/1	0.78	0.63	-	94,94,94,94	0
56	MG	YA	3279	1/1	0.93	0.81	-	62,62,62,62	0
56	MG	YA	3364	1/1	0.65	0.23	-	81,81,81,81	0
56	MG	RA	3646	1/1	0.74	0.35	-	92,92,92,92	0
56	MG	QA	1703	1/1	0.56	0.41	-	63,63,63,63	0
56	MG	RA	3135	1/1	0.93	0.37	-	91,91,91,91	0
56	MG	YA	3522	1/1	0.79	0.60	-	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3593	1/1	0.86	1.02	-	84,84,84,84	0
56	MG	RA	3721	1/1	0.66	0.86	-	67,67,67,67	0
56	MG	RA	3240	1/1	0.82	0.52	-	106,106,106,106	0
56	MG	YA	3040	1/1	0.56	0.48	-	88,88,88,88	0
56	MG	XA	1779	1/1	0.71	0.43	-	92,92,92,92	0
56	MG	YA	3173	1/1	0.25	0.58	-	99,99,99,99	0
56	MG	RA	3076	1/1	0.25	1.20	-	96,96,96,96	0
56	MG	RA	3735	1/1	0.53	0.59	-	77,77,77,77	0
56	MG	YA	3338	1/1	0.61	1.04	-	85,85,85,85	0
56	MG	QA	1624	1/1	0.79	0.51	-	74,74,74,74	0
56	MG	YA	3389	1/1	0.68	0.62	-	71,71,71,71	0
56	MG	YA	3486	1/1	-0.02	1.11	-	105,105,105,105	0
56	MG	RA	3801	1/1	0.75	0.32	-	92,92,92,92	0
56	MG	YA	3124	1/1	0.94	0.17	-	93,93,93,93	0
56	MG	RA	3161	1/1	0.91	0.28	-	83,83,83,83	0
56	MG	RA	3760	1/1	0.36	0.80	-	98,98,98,98	0
56	MG	RA	3480	1/1	0.91	0.50	-	62,62,62,62	0
56	MG	YA	3120	1/1	0.72	0.61	-	86,86,86,86	0
56	MG	YA	3331	1/1	0.88	0.73	-	62,62,62,62	0
56	MG	RA	3995	1/1	0.24	0.46	-	91,91,91,91	0
56	MG	RA	3373	1/1	0.44	0.77	-	82,82,82,82	0
56	MG	RA	3492	1/1	0.46	0.56	-	78,78,78,78	0
56	MG	RA	3729	1/1	0.44	0.69	-	82,82,82,82	0
56	MG	QA	1612	1/1	0.44	0.56	-	89,89,89,89	0
56	MG	R7	102	1/1	0.47	0.66	-	75,75,75,75	0
56	MG	RA	3293	1/1	0.85	0.26	-	87,87,87,87	0
56	MG	RA	3314	1/1	0.71	0.55	-	77,77,77,77	0
56	MG	RA	3772	1/1	0.52	0.56	-	69,69,69,69	0
56	MG	RA	3274	1/1	0.79	0.37	-	88,88,88,88	0
56	MG	YA	3636	1/1	0.79	0.93	-	72,72,72,72	0
56	MG	RA	3018	1/1	0.84	0.48	-	95,95,95,95	0
56	MG	RA	3590	1/1	0.38	0.73	-	100,100,100,100	0
56	MG	RO	201	1/1	0.89	0.26	-	72,72,72,72	0
56	MG	XA	1640	1/1	0.74	0.47	-	92,92,92,92	0
56	MG	RA	3822	1/1	0.95	0.55	-	73,73,73,73	0
56	MG	XA	1662	1/1	-0.18	0.37	-	97,97,97,97	0
56	MG	YA	3692	1/1	0.57	0.53	-	84,84,84,84	0
56	MG	XA	1715	1/1	0.23	0.96	-	94,94,94,94	0
56	MG	QA	1639	1/1	0.78	0.18	-	93,93,93,93	0
56	MG	RA	3628	1/1	0.04	1.22	-	89,89,89,89	0
56	MG	RA	3003	1/1	0.49	0.56	-	91,91,91,91	0
56	MG	XJ	201	1/1	0.40	0.38	-	97,97,97,97	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3491	1/1	0.88	0.54	-	91,91,91,91	0
56	MG	RA	3511	1/1	0.87	0.16	-	71,71,71,71	0
56	MG	YA	3712	1/1	0.56	0.77	-	80,80,80,80	0
56	MG	QA	1768	1/1	0.24	0.54	-	89,89,89,89	0
56	MG	RA	3596	1/1	0.67	0.38	-	98,98,98,98	0
56	MG	YA	3169	1/1	0.80	0.40	-	85,85,85,85	0
56	MG	RA	3467	1/1	0.02	0.66	-	89,89,89,89	0
56	MG	QA	1827	1/1	0.81	0.40	-	74,74,74,74	0
56	MG	RA	4053	1/1	0.26	1.73	-	103,103,103,103	0
56	MG	RA	3218	1/1	0.07	0.46	-	88,88,88,88	0
56	MG	RA	3817	1/1	0.57	0.80	-	92,92,92,92	0
56	MG	XA	1663	1/1	0.73	0.23	-	83,83,83,83	0
56	MG	YA	3504	1/1	0.12	0.54	-	93,93,93,93	0
56	MG	RA	3837	1/1	0.53	0.63	-	90,90,90,90	0
56	MG	RA	3104	1/1	0.94	0.32	-	77,77,77,77	0
56	MG	QQ	201	1/1	0.79	0.24	-	91,91,91,91	0
56	MG	YA	3620	1/1	0.53	0.34	-	75,75,75,75	0
56	MG	RA	3389	1/1	0.90	0.82	-	69,69,69,69	0
56	MG	YA	3396	1/1	0.42	0.89	-	67,67,67,67	0
56	MG	RA	3655	1/1	0.52	0.27	-	94,94,94,94	0
56	MG	RA	3085	1/1	0.31	0.86	-	91,91,91,91	0
56	MG	XA	1685	1/1	0.40	0.77	-	62,62,62,62	0
56	MG	RT	201	1/1	0.82	1.45	-	78,78,78,78	0
56	MG	QA	1721	1/1	0.92	0.69	-	62,62,62,62	0
56	MG	RA	3870	1/1	0.92	1.64	-	86,86,86,86	0
56	MG	RA	3790	1/1	0.62	0.58	-	102,102,102,102	0
56	MG	YA	3054	1/1	0.82	0.45	-	102,102,102,102	0
56	MG	YA	3615	1/1	0.91	0.26	-	65,65,65,65	0
56	MG	YA	3135	1/1	0.82	0.40	-	63,63,63,63	0
56	MG	RA	3949	1/1	0.71	0.77	-	95,95,95,95	0
56	MG	RA	3225	1/1	0.14	0.97	-	111,111,111,111	0
56	MG	RA	3699	1/1	0.76	0.50	-	107,107,107,107	0
56	MG	QA	1822	1/1	0.88	0.33	-	97,97,97,97	0
56	MG	QH	202	1/1	0.52	0.47	-	91,91,91,91	0
56	MG	RA	3051	1/1	0.81	0.75	-	97,97,97,97	0
56	MG	YA	3683	1/1	0.74	0.27	-	82,82,82,82	0
56	MG	YA	3646	1/1	0.83	0.43	-	68,68,68,68	0
56	MG	YA	3277	1/1	0.92	0.52	-	62,62,62,62	0
56	MG	YA	3450	1/1	0.48	0.94	-	79,79,79,79	0
56	MG	Y7	101	1/1	0.90	0.93	-	99,99,99,99	0
56	MG	YA	3032	1/1	0.35	0.72	-	93,93,93,93	0
56	MG	RA	3602	1/1	0.74	1.58	-	97,97,97,97	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3891	1/1	0.87	0.92	-	69,69,69,69	0
56	MG	QA	1799	1/1	0.23	0.66	-	99,99,99,99	0
56	MG	RA	3405	1/1	0.74	0.19	-	85,85,85,85	0
56	MG	RA	3451	1/1	0.71	1.35	-	74,74,74,74	0
56	MG	YA	3435	1/1	0.11	1.10	-	87,87,87,87	0
56	MG	YA	3443	1/1	0.87	0.27	-	83,83,83,83	0
56	MG	YA	3175	1/1	-0.01	1.24	-	101,101,101,101	0
56	MG	RA	3224	1/1	0.44	0.73	-	93,93,93,93	0
56	MG	RA	3166	1/1	0.60	0.82	-	83,83,83,83	0
56	MG	YA	3202	1/1	0.52	0.42	-	82,82,82,82	0
56	MG	QA	1653	1/1	0.76	0.55	-	84,84,84,84	0
56	MG	RA	3046	1/1	0.94	0.80	-	99,99,99,99	0
56	MG	RA	3958	1/1	0.45	0.48	-	80,80,80,80	0
56	MG	RE	301	1/1	0.91	0.57	-	107,107,107,107	0
56	MG	RA	3945	1/1	0.83	0.21	-	63,63,63,63	0
56	MG	YA	3084	1/1	0.03	1.21	-	101,101,101,101	0
56	MG	QA	1825	1/1	0.62	0.59	-	86,86,86,86	0
56	MG	YA	3595	1/1	0.77	0.48	-	83,83,83,83	0
56	MG	YA	3561	1/1	0.27	1.18	-	89,89,89,89	0
56	MG	YA	3558	1/1	0.54	0.70	-	87,87,87,87	0
56	MG	YA	3466	1/1	0.72	0.56	-	79,79,79,79	0
56	MG	RA	3353	1/1	0.72	0.65	-	84,84,84,84	0
56	MG	XA	1768	1/1	0.96	0.89	-	62,62,62,62	0
56	MG	YA	3671	1/1	0.97	0.53	-	62,62,62,62	0
56	MG	RA	3489	1/1	0.65	0.38	-	67,67,67,67	0
56	MG	XA	1724	1/1	0.81	0.36	-	75,75,75,75	0
56	MG	YA	3056	1/1	0.77	0.46	-	86,86,86,86	0
56	MG	RA	3283	1/1	0.88	0.57	-	88,88,88,88	0
56	MG	YA	3232	1/1	0.87	0.25	-	84,84,84,84	0
56	MG	YA	3402	1/1	0.83	0.27	-	86,86,86,86	0
56	MG	YA	3280	1/1	0.90	0.33	-	64,64,64,64	0
56	MG	RG	203	1/1	0.27	0.81	-	83,83,83,83	0
56	MG	YA	3385	1/1	0.79	0.49	-	69,69,69,69	0
56	MG	RA	3872	1/1	0.12	0.60	-	83,83,83,83	0
56	MG	RA	3440	1/1	-0.17	1.18	-	89,89,89,89	0
56	MG	RA	3164	1/1	0.33	0.79	-	100,100,100,100	0
56	MG	RA	3643	1/1	0.78	0.48	-	88,88,88,88	0
56	MG	RA	3527	1/1	0.44	1.07	-	73,73,73,73	0
56	MG	YA	3425	1/1	0.16	0.55	-	88,88,88,88	0
56	MG	RA	3454	1/1	0.76	0.41	-	87,87,87,87	0
56	MG	QA	1788	1/1	0.93	0.58	-	93,93,93,93	0
56	MG	QA	1629	1/1	0.84	0.89	-	83,83,83,83	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RB	220	1/1	0.90	0.71	-	75,75,75,75	0
56	MG	RF	307	1/1	0.82	0.66	-	74,74,74,74	0
56	MG	RF	302	1/1	0.39	0.76	-	80,80,80,80	0
56	MG	RA	3295	1/1	0.47	0.44	-	92,92,92,92	0
56	MG	RA	3301	1/1	0.45	1.69	-	93,93,93,93	0
56	MG	RA	3931	1/1	0.70	0.47	-	78,78,78,78	0
56	MG	YA	3275	1/1	0.85	0.51	-	89,89,89,89	0
56	MG	YA	3204	1/1	0.67	0.38	-	89,89,89,89	0
56	MG	QA	1734	1/1	0.49	0.77	-	84,84,84,84	0
56	MG	XA	1604	1/1	0.71	1.05	-	98,98,98,98	0
56	MG	RA	3845	1/1	0.57	0.73	-	97,97,97,97	0
56	MG	QA	1649	1/1	0.93	0.27	-	73,73,73,73	0
56	MG	RA	3181	1/1	0.16	0.82	-	86,86,86,86	0
56	MG	YA	3044	1/1	0.87	0.30	-	68,68,68,68	0

6.5 Other polymers [i](#)

There are no such residues in this entry.