



## Full wwPDB EM Validation Report ⓘ

Jul 21, 2025 – 08:19 PM EDT

PDB ID : 8VVR / pdb\_00008vvr  
EMDB ID : EMD-43566  
Title : Post-decoding/Post-hydrolysis state obtained from Anisomycin-treated mammalian ribosomes  
Authors : Loerch, S.; Petrossian, E.; Smith, P.R.; Campbell, Z.T.  
Deposited on : 2024-01-31  
Resolution : 3.10 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev118  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0rc1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.44

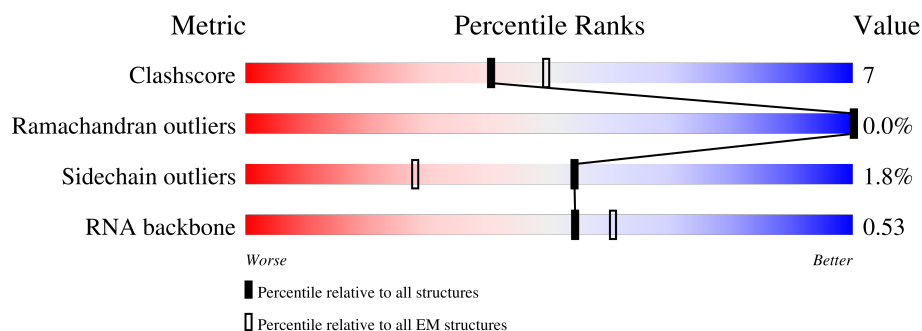
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	A	257	
2	B	403	
3	C	413	
4	D	297	
5	E	291	
6	F	249	
7	G	319	

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Mol	Chain	Length	Quality of chain
8	H	192	
9	I	214	
10	J	178	
11	K	211	
12	L	218	
13	M	204	
14	N	203	
15	O	213	
16	P	188	
17	Q	212	
18	R	224	
19	S	160	
20	T	128	
21	U	140	
22	V	157	
23	W	156	
24	X	145	
25	Y	136	
26	Z	148	
27	AA	245	
28	BA	115	
29	CA	125	
30	DA	135	
31	EA	110	
32	FA	129	

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Mol	Chain	Length	Quality of chain
33	GA	123	
34	HA	105	
35	IA	97	
36	JA	70	
37	KA	51	
38	LA	128	
39	MA	25	
40	NA	106	
41	OA	92	
42	PA	137	
43	RA	165	
44	SA	76	
45	TA	76	
46	UA	75	
47	VA	12	
48	WA	3584	
49	XA	120	
50	YA	156	
51	ZA	1869	
52	AB	295	
53	BB	264	
54	CB	293	
55	DB	281	
56	EB	263	
57	FB	204	

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Mol	Chain	Length	Quality of chain
58	GB	249	
59	HB	432	
60	IB	208	
61	JB	194	
62	KB	165	
63	LB	158	
64	MB	132	
65	NB	151	
66	OB	151	
67	PB	145	
68	QB	172	
69	RB	135	
70	SB	152	
71	TB	145	
72	UB	119	
73	VB	83	
74	WB	130	
75	XB	143	
76	YB	131	
77	ZB	124	
78	AC	115	
79	BC	84	
80	CC	69	
81	DC	56	
82	EC	133	

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Mol	Chain	Length	Quality of chain
83	FC	188	
84	GC	317	
85	IC	4	
86	b	318	
87	c	14	
88	HC	462	

## 2 Entry composition

There are 95 unique types of molecules in this entry. The entry contains 220661 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	250	Total	C	N	O	S	0	0
			1914	1199	392	317	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	397	Total	C	N	O	S	0	0
			3196	2035	603	545	13		

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 4 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	294	Total	C	N	O	S	0	0
			2395	1514	439	428	14		

- Molecule 5 is a protein called L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	228	Total	C	N	O	S	0	0
			1823	1173	349	298	3		

- Molecule 6 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	227	Total	C	N	O	S	0	0
			1897	1217	366	305	9		

- Molecule 7 is a protein called L7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	229	Total	C	N	O	S	0	0
			1850	1181	356	309	4		

- Molecule 8 is a protein called L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 9 is a protein called L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 10 is a protein called uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	171	Total	C	N	O	S	0	0
			1372	867	256	243	6		

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	46	ILE	-	insertion	UNP G1TPV0
K	47	ALA	-	insertion	UNP G1TPV0
K	48	PRO	-	insertion	UNP G1TPV0
K	49	ARG	-	insertion	UNP G1TPV0
K	50	PRO	-	insertion	UNP G1TPV0
K	51	ALA	-	insertion	UNP G1TPV0
K	52	ALA	-	insertion	UNP G1TPV0
K	53	GLY	-	insertion	UNP G1TPV0
K	54	PRO	-	insertion	UNP G1TPV0

- Molecule 12 is a protein called eL14.



Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 13 is a protein called eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	156	Total	C	N	O	S	0	0
			1266	793	245	219	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	43	SER	ALA	conflict	UNP G1TVT6

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	4	ASP	ASN	conflict	UNP G1TFE0
P	14	ARG	TRP	conflict	UNP G1TFE0
P	53	MET	LEU	conflict	UNP G1TFE0
P	58	ARG	TRP	conflict	UNP G1TFE0
P	75	ARG	GLN	conflict	UNP G1TFE0
P	80	ALA	PRO	conflict	UNP G1TFE0
P	86	VAL	ILE	conflict	UNP G1TFE0

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Chain	Residue	Modelled	Actual	Comment	Reference
P	104	ARG	HIS	conflict	UNP G1TFE0
P	110	ARG	CYS	conflict	UNP G1TFE0
P	137	VAL	GLY	conflict	UNP G1TFE0
P	157	GLY	ARG	conflict	UNP G1TFE0
P	181	ARG	TRP	conflict	UNP G1TFE0

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 19 is a protein called eL21.

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

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	101	Total	C	N	O	S	0	0
			826	530	144	150	2		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	18	LEU	VAL	conflict	UNP G1TSG1
T	32	GLY	ARG	conflict	UNP G1TSG1
T	36	ALA	GLU	conflict	UNP G1TSG1
T	39	PHE	SER	conflict	UNP G1TSG1
T	54	GLY	ARG	conflict	UNP G1TSG1
T	60	VAL	ALA	conflict	UNP G1TSG1
T	62	SER	THR	conflict	UNP G1TSG1
T	63	LEU	ILE	conflict	UNP G1TSG1

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Chain	Residue	Modelled	Actual	Comment	Reference
T	97	ARG	HIS	conflict	UNP G1TSG1
T	106	THR	SER	conflict	UNP G1TSG1
T	126	GLU	ASP	conflict	UNP G1TSG1

- Molecule 21 is a protein called L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	135	Total	C	N	O	S	0	0
			1004	631	191	177	5		

- Molecule 22 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	110	Total	C	N	O	S	0	0
			887	555	179	149	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	78	SER	PHE	conflict	UNP G1SE28

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 24 is a protein called L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 25 is a protein called L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 27 is a protein called L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AA	107	Total	C	N	O	S	0	0
			873	542	195	133	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BA	99	Total	C	N	O	S	0	0
			769	486	135	141	7		

- Molecule 29 is a protein called L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	CA	108	Total	C	N	O	S	0	0
			893	563	172	156	2		

- Molecule 30 is a protein called L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	DA	129	Total	C	N	O	S	0	0
			1064	673	220	166	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	EA	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 32 is a protein called L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	FA	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 33 is a protein called L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	GA	121	Total	C	N	O	S	0	0
			1008	637	203	167	1		

- Molecule 34 is a protein called L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	HA	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	IA	87	Total	C	N	O	S	0	0
			716	440	159	112	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	JA	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
JA	24	LYS	ASN	conflict	UNP G1U001

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	KA	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LA	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 39 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	MA	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	NA	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 41 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	OA	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	PA	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 43 is a protein called L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	RA	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 44 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	SA	76	Total	C	N	O	P	0	0
			1622	726	300	521	75		

- Molecule 45 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	TA	76	Total	C	N	O	P	0	0
			1615	722	286	532	75		

- Molecule 46 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	UA	75	Total	C	N	O	P	0	0
			1596	713	285	523	75		

- Molecule 47 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	VA	12	Total	C	N	O	P	0	0
			251	113	41	85	12		

- Molecule 48 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	WA	3578	Total	C	N	O	P	0	0
			76735	34173	14061	24923	3578		

- Molecule 49 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	XA	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
XA	2	U	N	conflict	GB X06789.1
XA	36	C	N	conflict	GB X06789.1
XA	102	U	N	conflict	GB X06789.1
XA	112	U	N	conflict	GB X06789.1
XA	114	U	N	conflict	GB X06789.1
XA	119	U	C	conflict	GB X06789.1
XA	120	U	N	conflict	GB X06789.1

- Molecule 50 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	YA	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 51 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	ZA	1716	Total	C	N	O	P	0	0
			36623	16347	6572	11989	1715		

- Molecule 52 is a protein called RPSA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AB	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 53 is a protein called S3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 54 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	CB	220	Total	C	N	O	S	0	0
			1707	1105	293	300	9		

- Molecule 55 is a protein called S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	DB	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 56 is a protein called S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	EB	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EB	25	GLY	SER	conflict	UNP G1TK17
EB	51	ARG	LYS	conflict	UNP G1TK17
EB	78	THR	ALA	conflict	UNP G1TK17
EB	156	VAL	MET	conflict	UNP G1TK17

- Molecule 57 is a protein called S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	FB	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		



- Molecule 58 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	GB	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 59 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	HB	185	Total	C	N	O	S	0	0
			1489	952	271	265	1		

- Molecule 60 is a protein called S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	IB	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
IB	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 61 is a protein called S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	JB	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 62 is a protein called S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	KB	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 63 is a protein called S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	LB	144	Total	C	N	O	S	0	0
			1180	752	223	199	6		

- Molecule 64 is a protein called S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	MB	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 65 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	NB	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 66 is a protein called S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	OB	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 67 is a protein called S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	PB	129	Total	C	N	O	S	0	0
			1058	670	201	180	7		

- Molecule 68 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	QB	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 69 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	RB	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 70 is a protein called S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SB	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 71 is a protein called S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	TB	142	Total	C	N	O	S	0	0
			1104	693	212	196	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
TB	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 72 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	UB	102	Total	C	N	O	S	0	0
			808	507	154	143	4		

- Molecule 73 is a protein called S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	VB	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
VB	3	ASN	SER	conflict	UNP G1TM82
VB	4	ASP	ASN	conflict	UNP G1TM82
VB	33	GLN	PRO	conflict	UNP G1TM82
VB	50	PHE	SER	conflict	UNP G1TM82
VB	75	ALA	SER	conflict	UNP G1TM82
VB	76	ASP	HIS	conflict	UNP G1TM82
VB	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 74 is a protein called S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	WB	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 75 is a protein called S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	XB	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 76 is a protein called S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	YB	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 77 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	ZB	85	Total	C	N	O	S	0	0
			683	439	128	115	1		

- Molecule 78 is a protein called S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	AC	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AC	28	ARG	CYS	conflict	UNP G1TFE8
AC	56	ALA	VAL	conflict	UNP G1TFE8
AC	109	ARG	PRO	conflict	UNP G1TFE8

- Molecule 79 is a protein called S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	BC	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 80 is a protein called S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	CC	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 81 is a protein called uS14.

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

- Molecule 82 is a protein called S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	EC	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 83 is a protein called S27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	FC	69	Total	C	N	O	S	0	0
			564	357	105	95	7		

- Molecule 84 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	GC	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 85 is a protein called peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
85	IC	4	Total	C	N	O	0	0
			20	12	4	4		

- Molecule 86 is a protein called RPLP0.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	b	167	Total	C	N	O	S	0	0
			1279	813	228	229	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	82	LEU	ILE	conflict	UNP G1SPK4

- Molecule 87 is a protein called RPLP peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	c	14	Total	C	N	O	S	0	0
			110	66	14	29	1		

- Molecule 88 is a protein called eukaryotic elongation factor 1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	HC	223	Total	C	N	O	S	0	0
			1664	1048	299	308	9		

- Molecule 89 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
89	A	1	Total	Mg	0
			1	1	
89	I	1	Total	Mg	0
			1	1	
89	O	1	Total	Mg	0
			1	1	
89	P	1	Total	Mg	0
			1	1	
89	U	1	Total	Mg	0
			1	1	
89	Z	1	Total	Mg	0
			1	1	
89	FA	1	Total	Mg	0
			1	1	
89	IA	1	Total	Mg	0
			1	1	
89	VA	1	Total	Mg	0
			1	1	
89	WA	142	Total	Mg	0
			142	142	
89	XA	4	Total	Mg	0
			4	4	
89	YA	2	Total	Mg	0
			2	2	
89	ZA	45	Total	Mg	0
			45	45	
89	AC	1	Total	Mg	0
			1	1	
89	HC	1	Total	Mg	0
			1	1	

- Molecule 90 is ZINC ION (CCD ID: ZN) (formula: Zn).

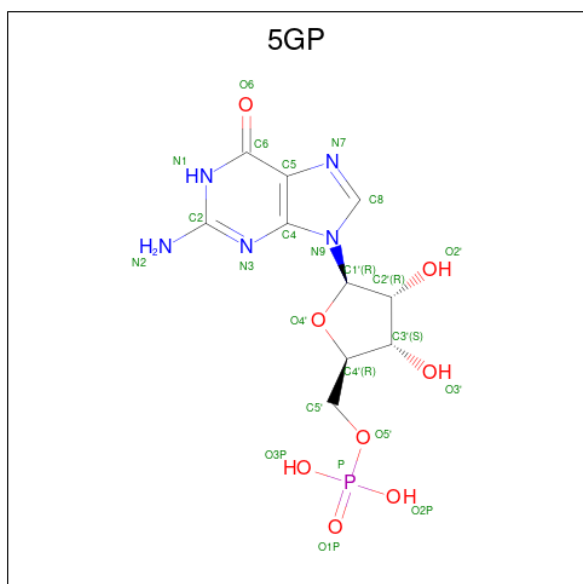
Mol	Chain	Residues	Atoms		AltConf
90	FA	1	Total	Zn	0
			1	1	
90	IA	1	Total	Zn	0
			1	1	

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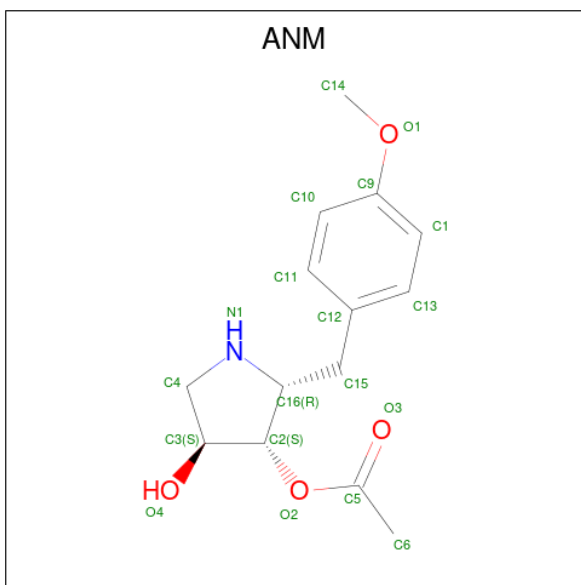
Mol	Chain	Residues	Atoms		AltConf
90	LA	1	Total	Zn	0
			1	1	
90	NA	1	Total	Zn	0
			1	1	
90	OA	1	Total	Zn	0
			1	1	
90	AC	1	Total	Zn	0
			1	1	
90	DC	1	Total	Zn	0
			1	1	
90	FC	1	Total	Zn	0
			1	1	

- Molecule 91 is GUANOSINE-5'-MONOPHOSPHATE (CCD ID: 5GP) (formula:  $C_{10}H_{14}N_5O_8P$ ).



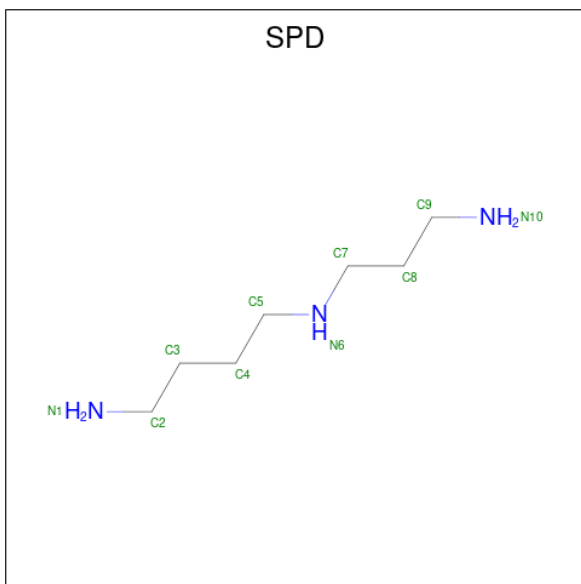
Mol	Chain	Residues	Atoms					AltConf
91	UA	1	Total	C	N	O	P	0
			24	10	5	8	1	

- Molecule 92 is ANISOMYCIN (CCD ID: ANM) (formula:  $C_{14}H_{19}NO_4$ ).



Mol	Chain	Residues	Atoms				AltConf
92	WA	1	Total	C	N	O	0
			19	14	1	4	

- Molecule 93 is SPERMIDINE (CCD ID: SPD) (formula:  $C_7H_{19}N_3$ ).



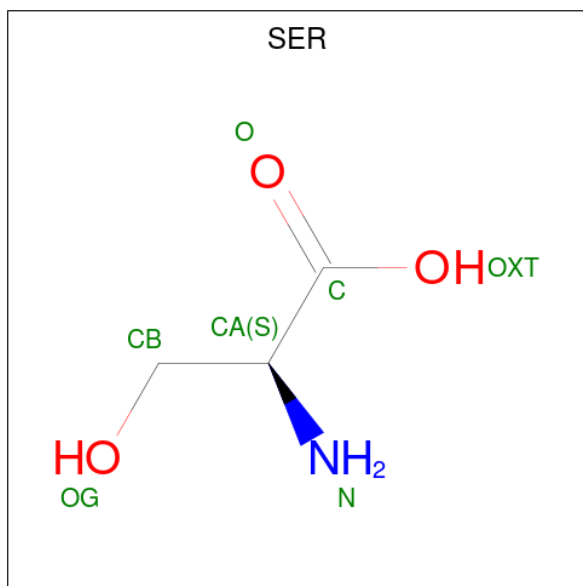
Mol	Chain	Residues	Atoms			AltConf
93	WA	1	Total	C	N	0
			10	7	3	
93	WA	1	Total	C	N	0
			10	7	3	
93	ZA	1	Total	C	N	0
			10	7	3	



- Molecule 94 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms			AltConf
94	WA	1	Total	K		0
			1	1		

- Molecule 95 is SERINE (CCD ID: SER) (formula: C<sub>3</sub>H<sub>7</sub>NO<sub>3</sub>).




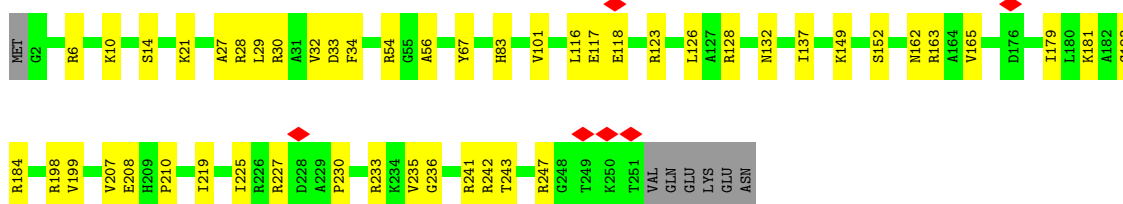
Mol	Chain	Residues	Atoms				AltConf
95	HC	1	Total	C	N	O	0
			6	3	1	2	

### 3 Residue-property plots [i](#)


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

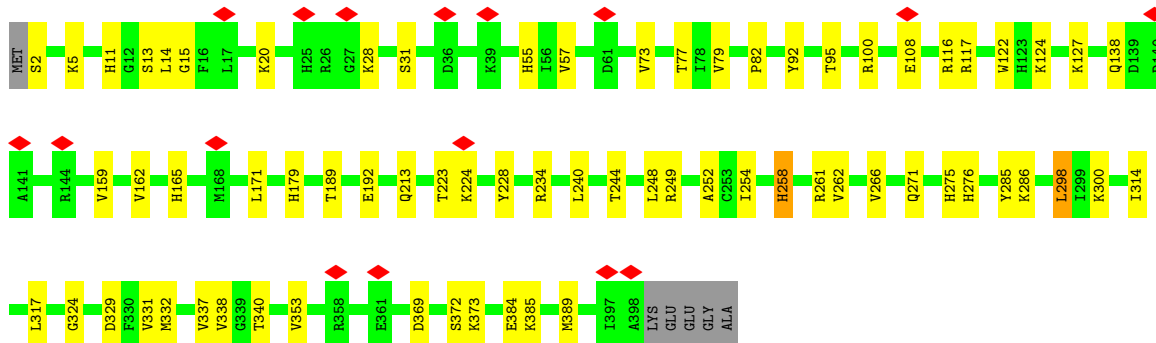
#### • Molecule 1: uL2

Chain A: 




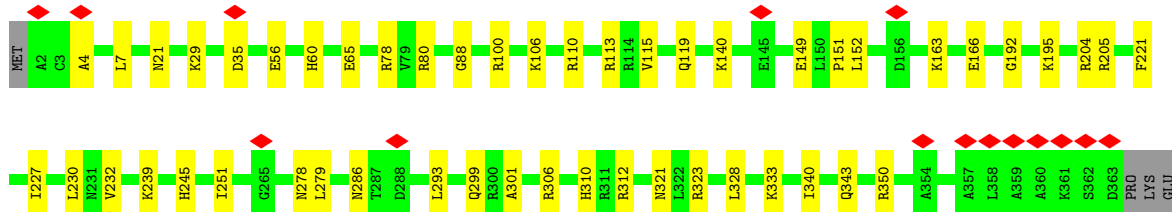
#### • Molecule 2: uL3

Chain B: 

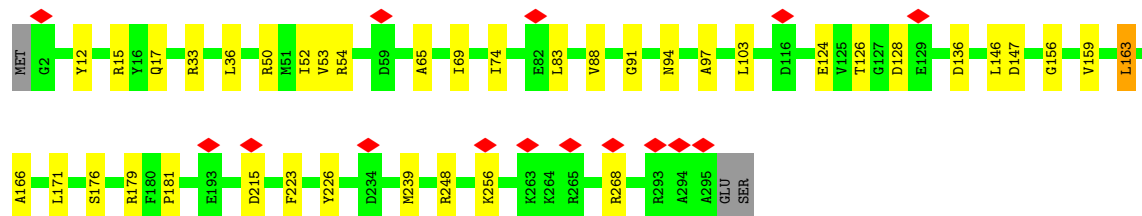
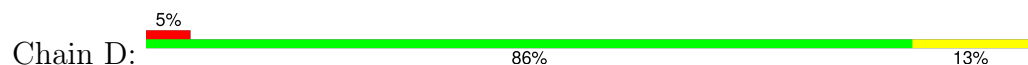


#### • Molecule 3: uL4

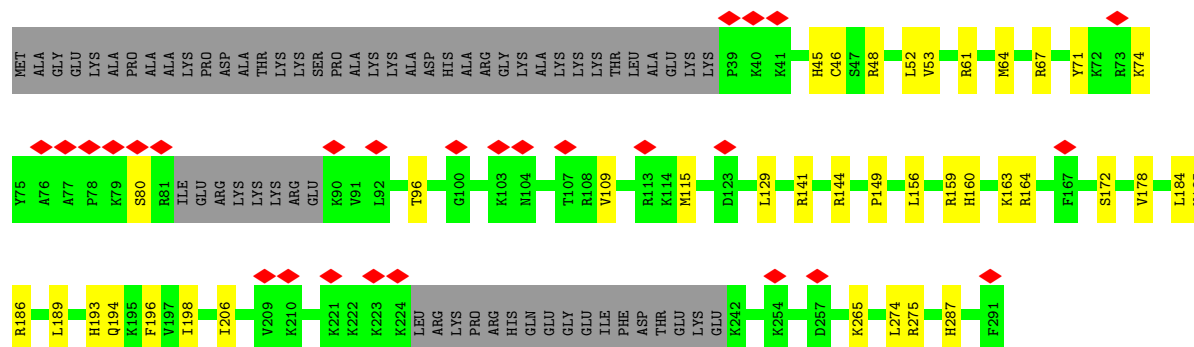
Chain C: 



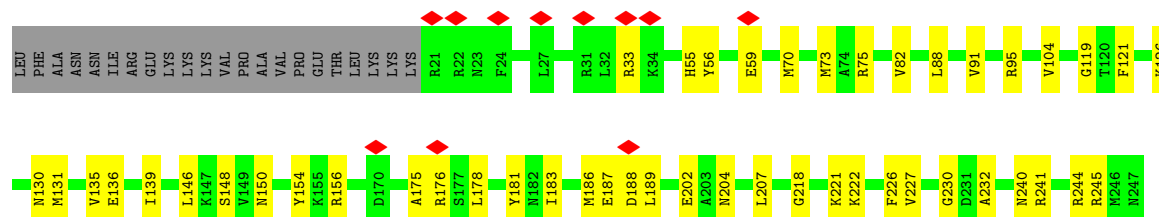
- Molecule 4: uL18



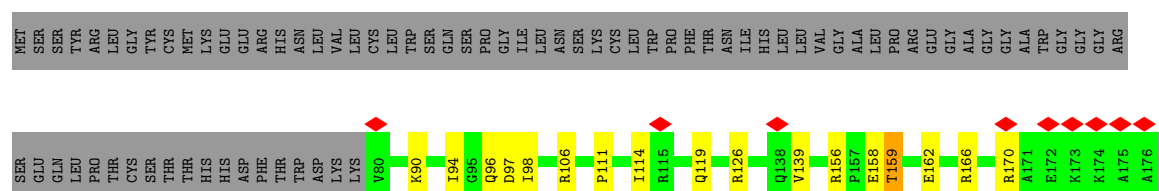
- Molecule 5: L6



- Molecule 6: uL30

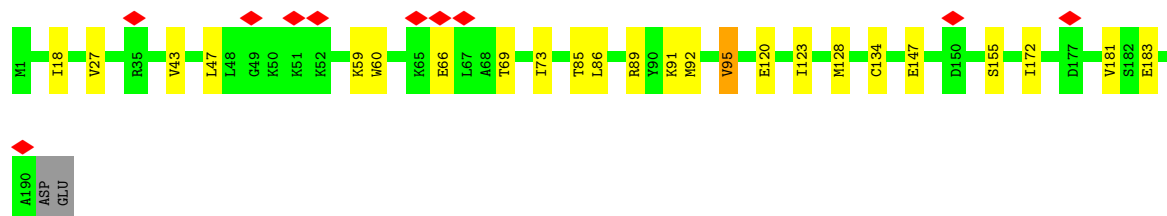
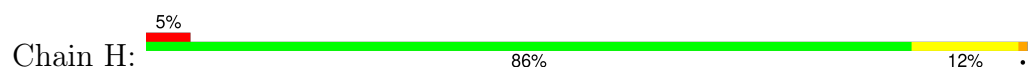


- Molecule 7: L7A

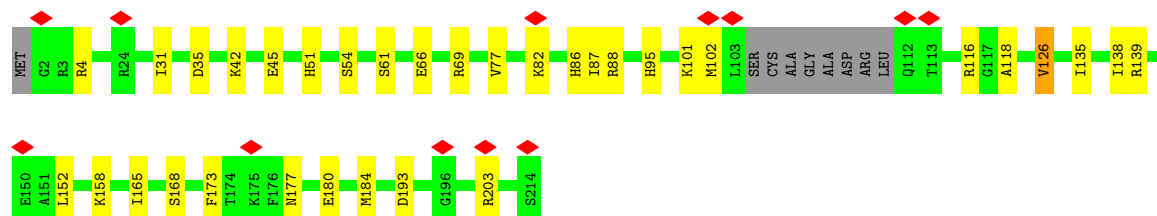
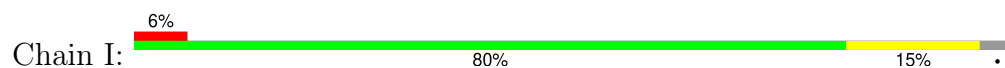




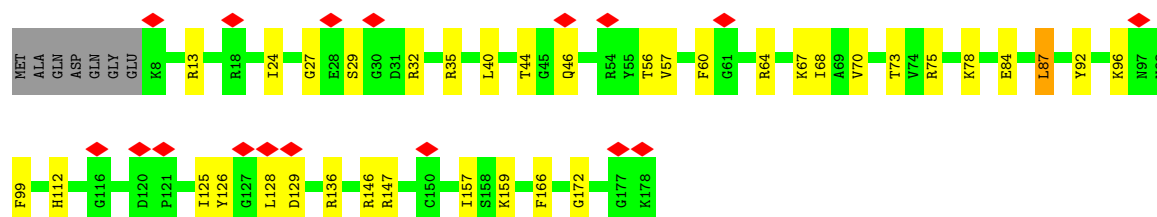
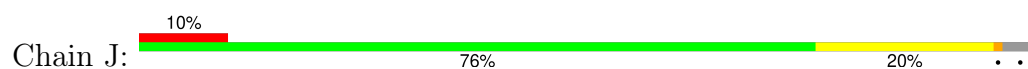
• Molecule 8: L9



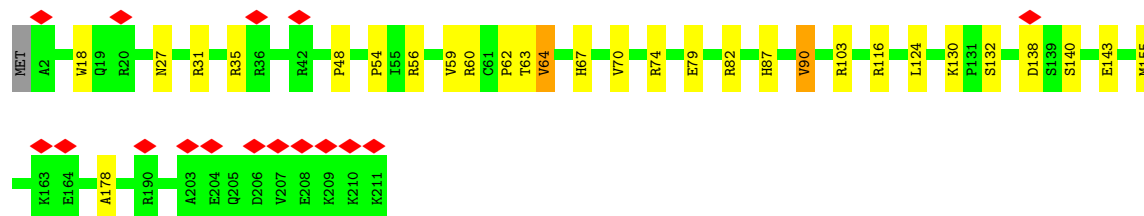
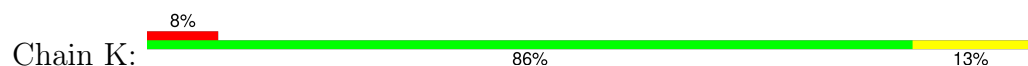
• Molecule 9: L10



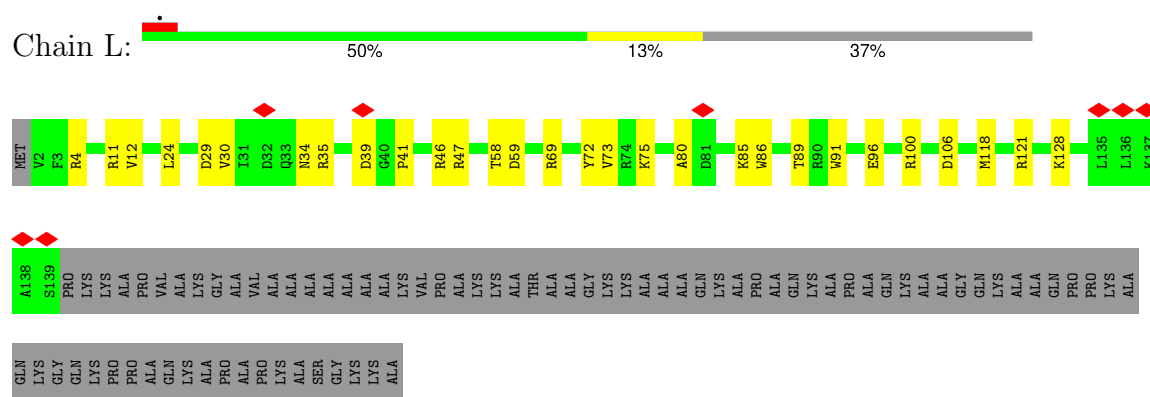
• Molecule 10: uL5



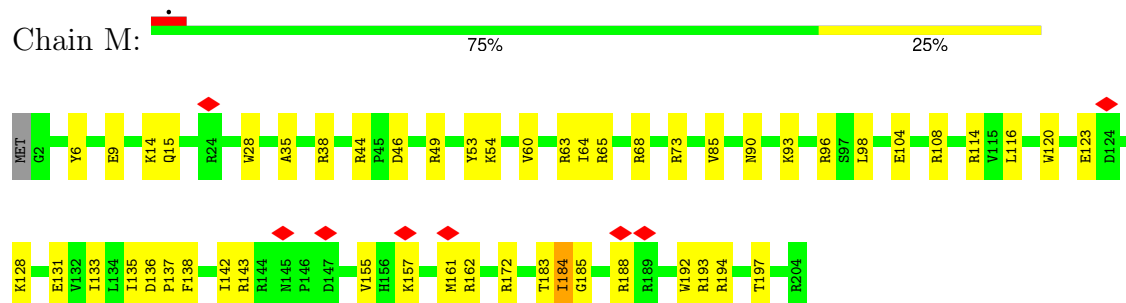
• Molecule 11: eL13



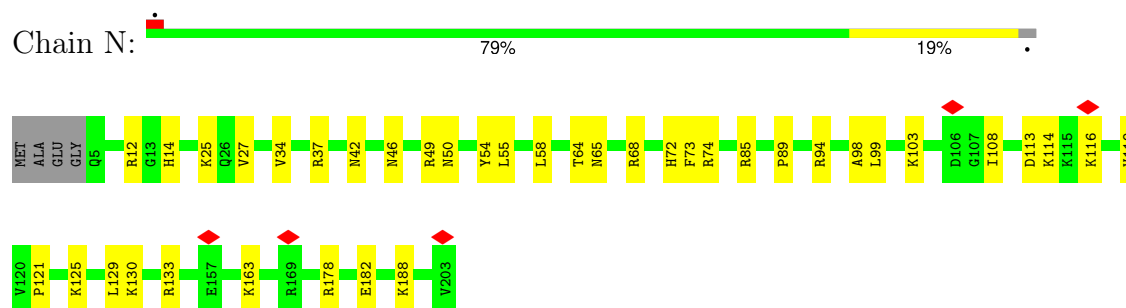
• Molecule 12: eL14



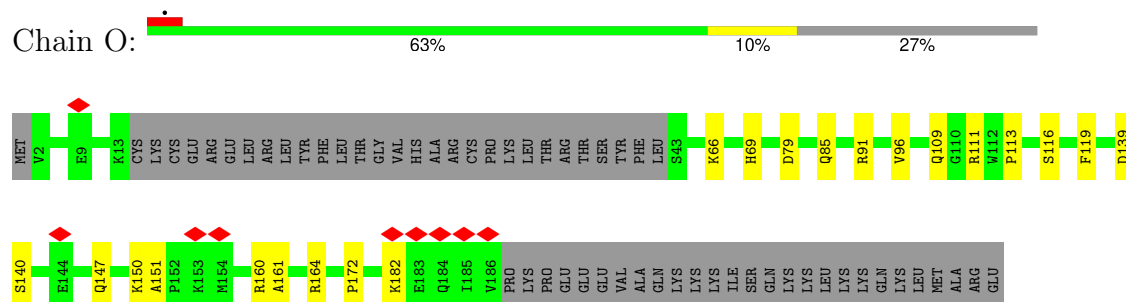
- Molecule 13: eL15



- Molecule 14: uL13

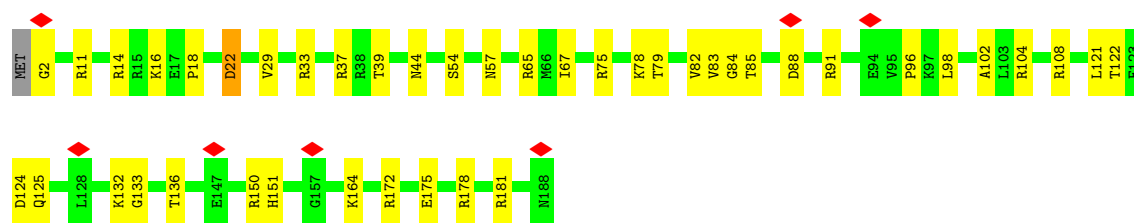


- Molecule 15: uL22

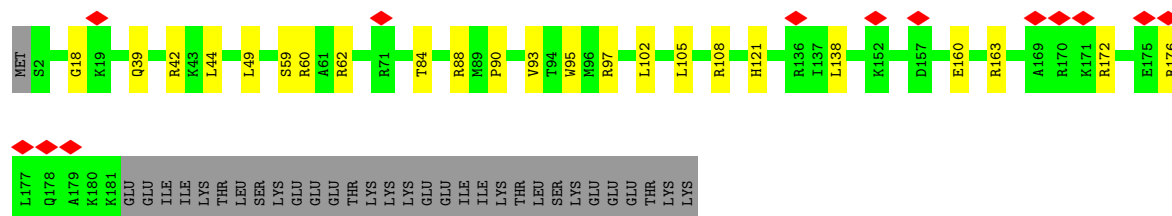
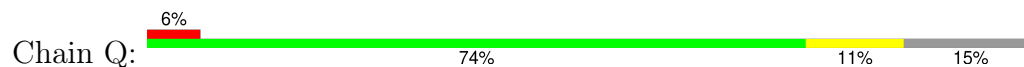


- Molecule 16: eL18

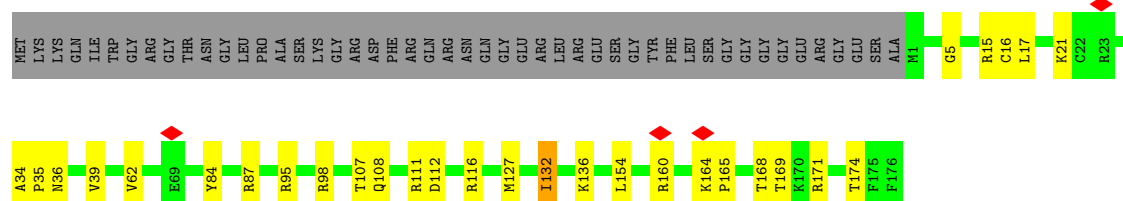




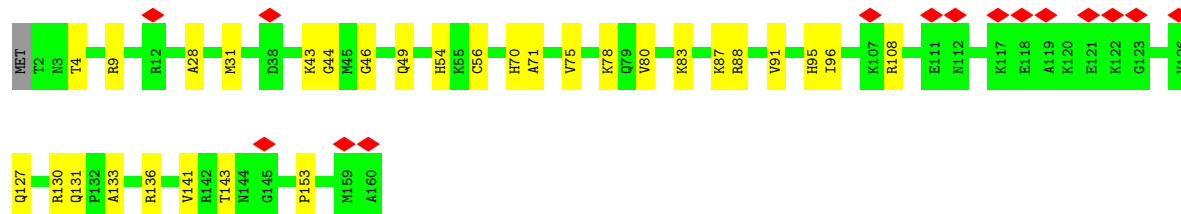
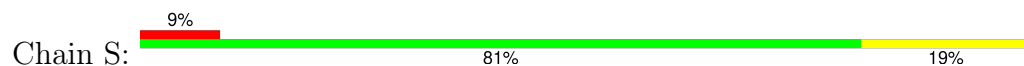
• Molecule 17: eL19



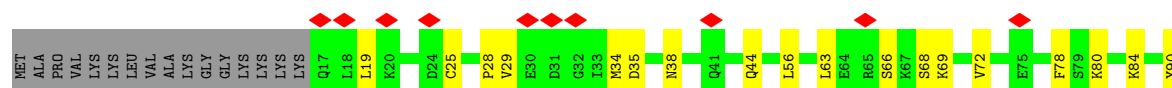
• Molecule 18: eL20



• Molecule 19: eL21

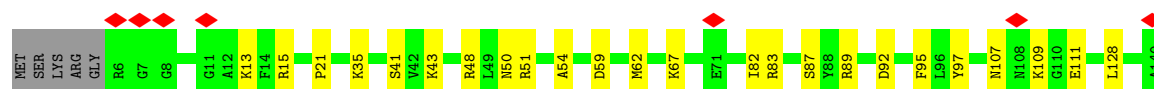
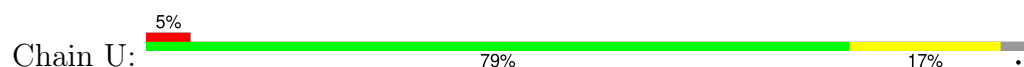


• Molecule 20: eL22

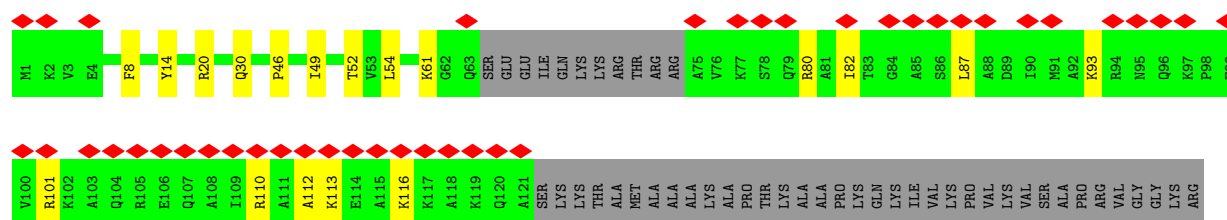




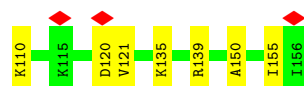
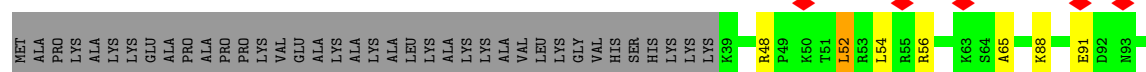
- Molecule 21: L23



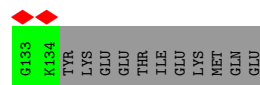
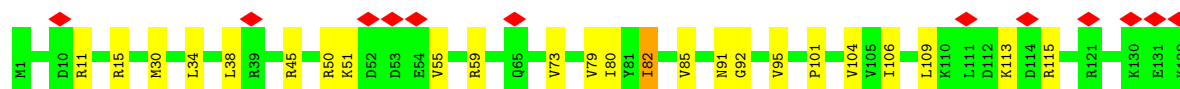
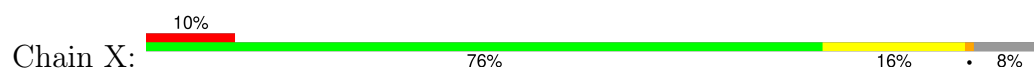
- Molecule 22: uL24



- Molecule 23: uL23

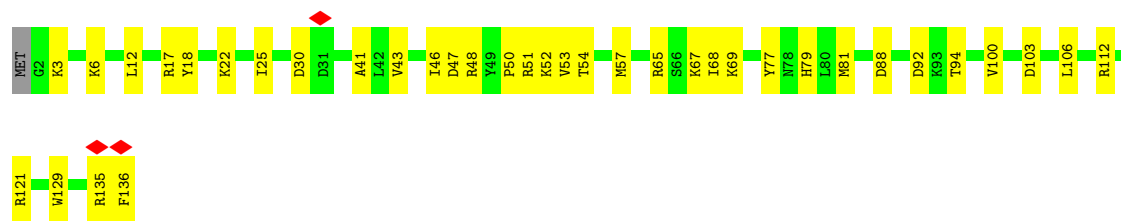


- Molecule 24: L26

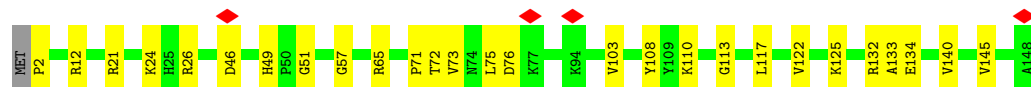
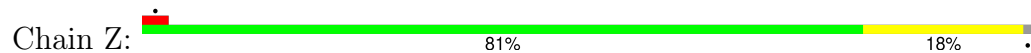


- Molecule 25: L27

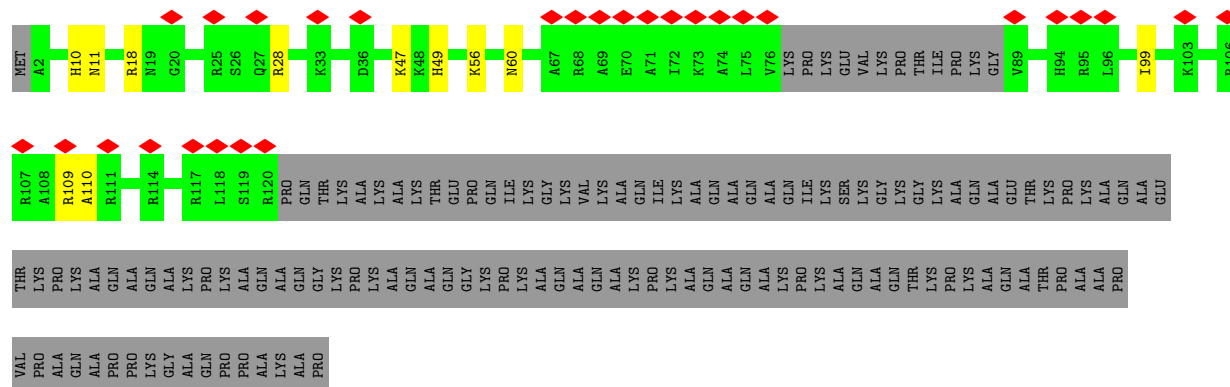
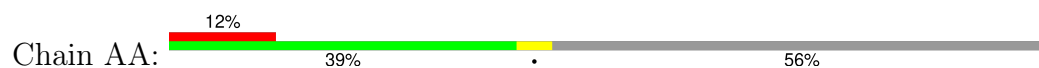




- Molecule 26: uL15



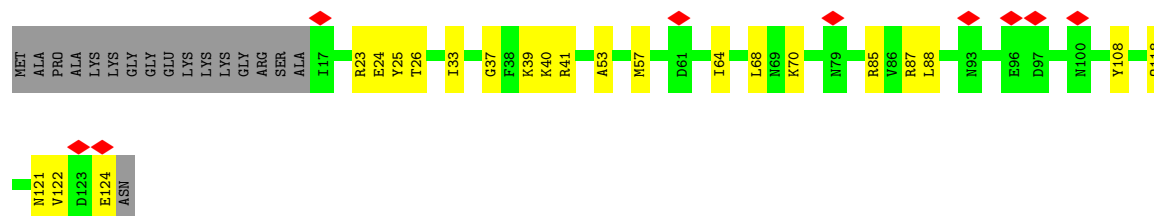
- Molecule 27: L29



- Molecule 28: eL30




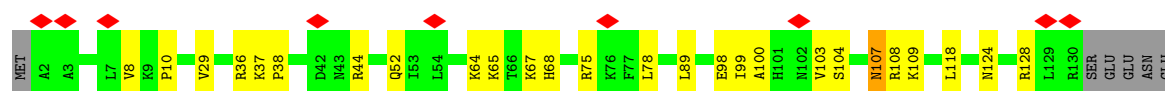
- Molecule 29: L31




- Molecule 30: L32



Chain DA: 




• Molecule 31: eL33

Chain EA: 




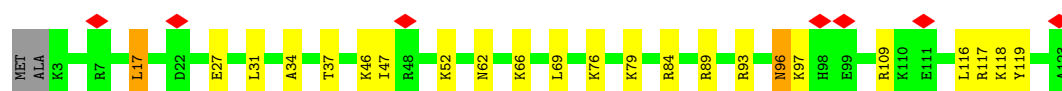
• Molecule 32: L34

Chain FA: 




• Molecule 33: L35

Chain GA: 



• Molecule 34: L36

Chain HA: 




• Molecule 35: L37

Chain IA: 

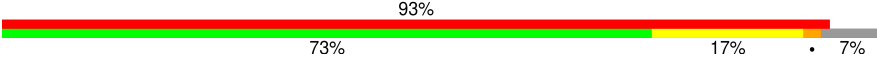


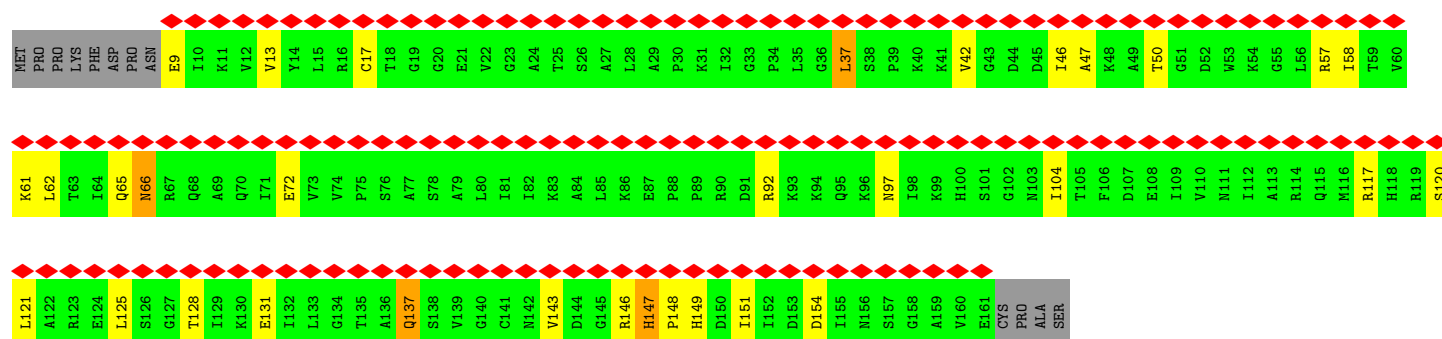
• Molecule 36: eL38

Chain JA: 



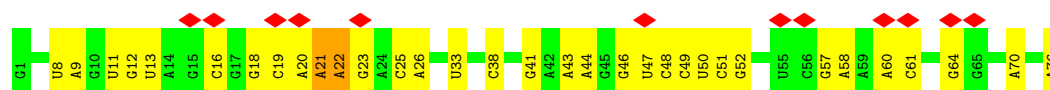


Chain RA: 




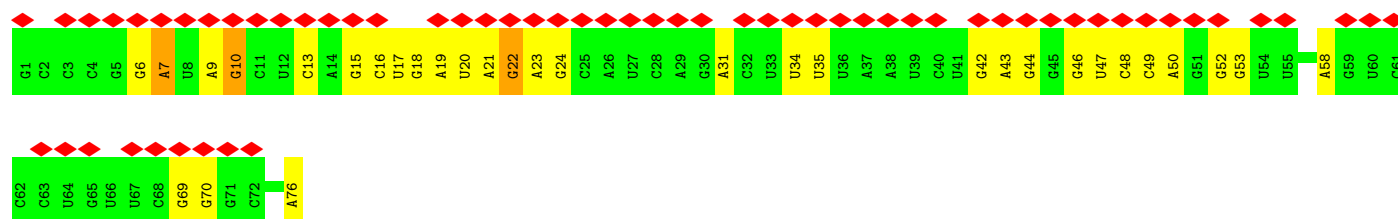
• Molecule 44: P-site tRNA

Chain SA: 




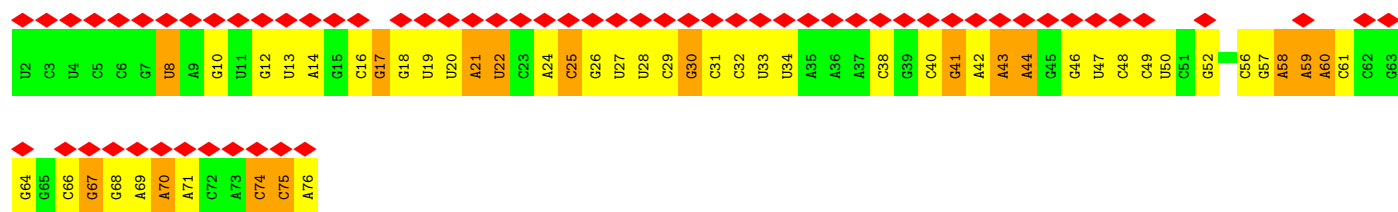
• Molecule 45: E-site tRNA

Chain TA: 




• Molecule 46: A-site tRNA

Chain UA: 



• Molecule 47: mRNA

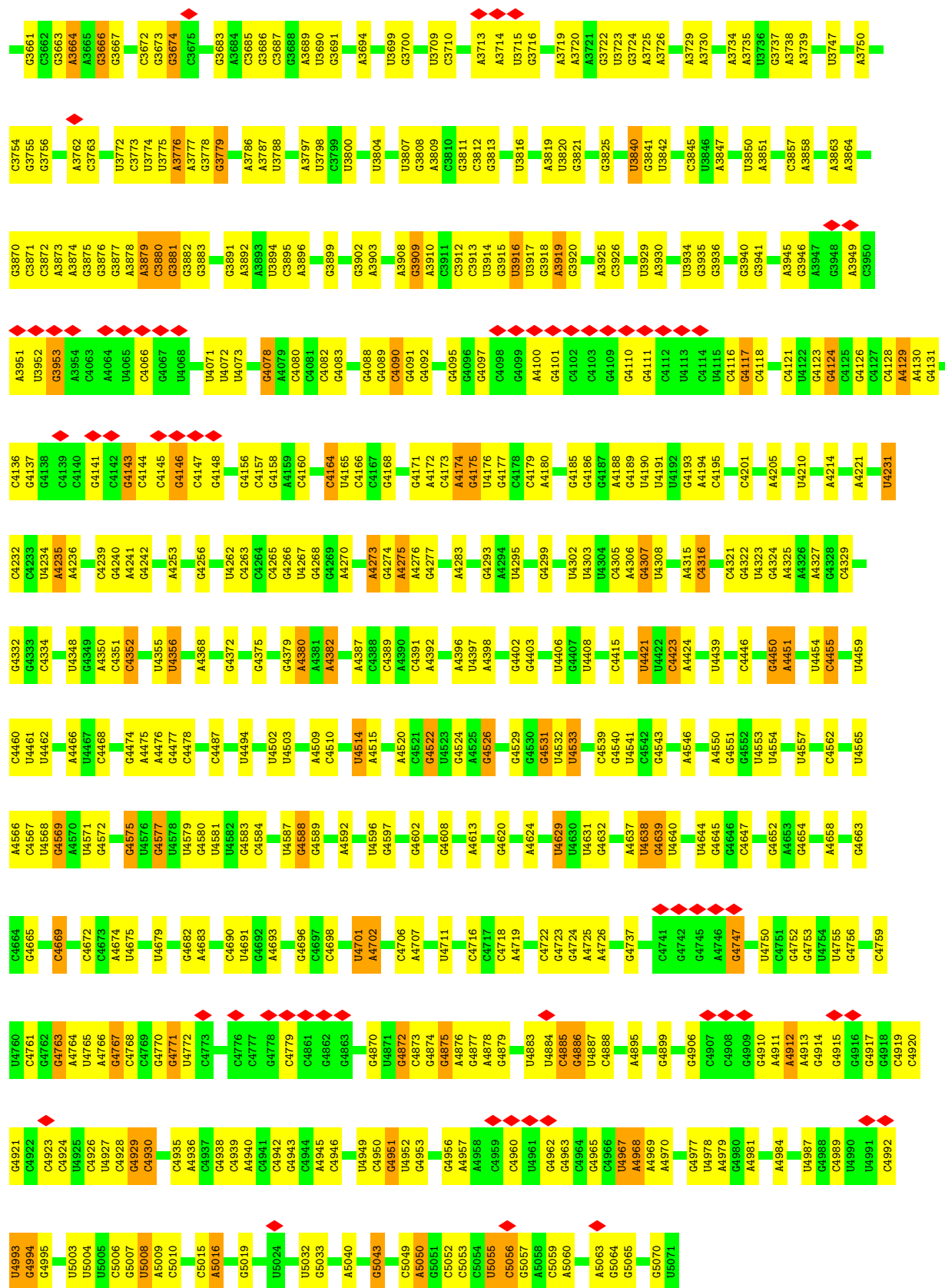
Chain VA: 



• Molecule 48: 28S rRNA







• Molecule 49: 5S rRNA

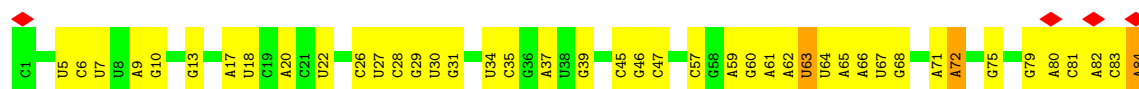
Chain XA: 



U

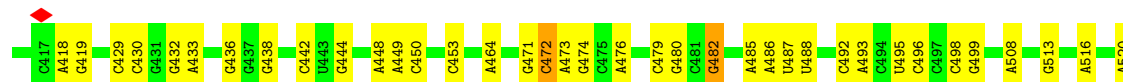
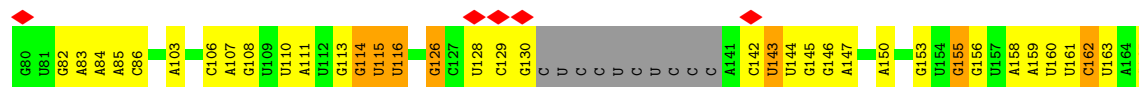
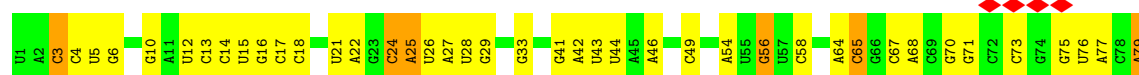
• Molecule 50: 5.8S rRNA

Chain YA: 



• Molecule 51: 18S rRNA

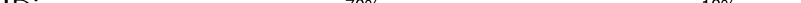
Chain ZA: 

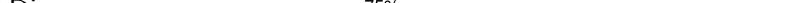


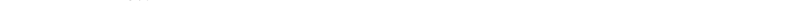








Chain DB: 

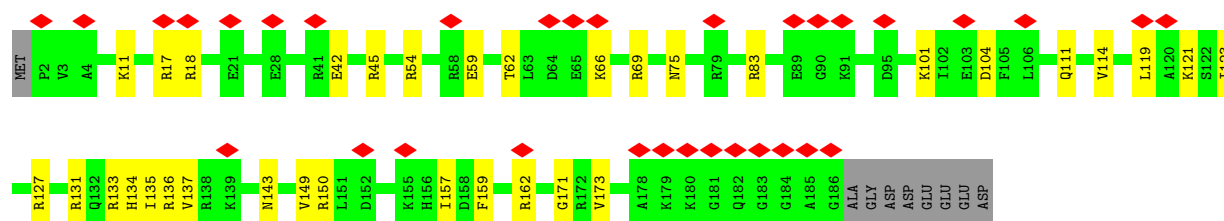
Chain EB: 

Chain FB: 

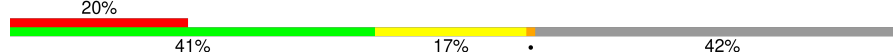
Chain GB: 

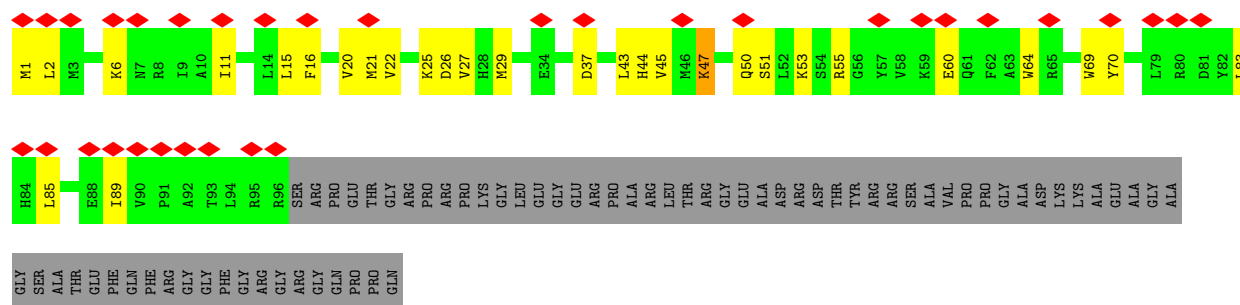


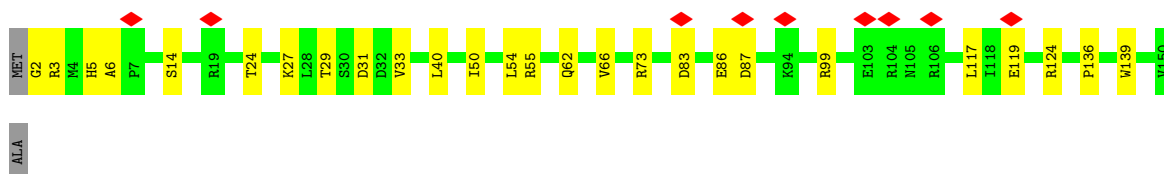
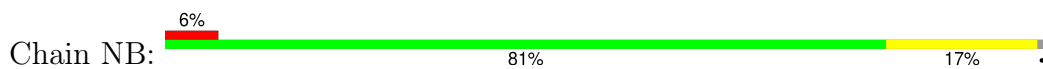
Chain JB: 



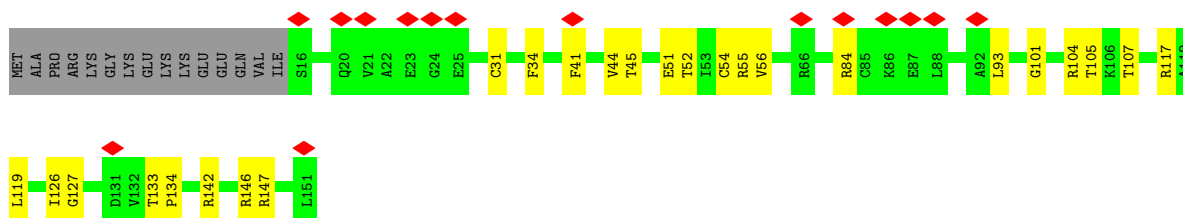
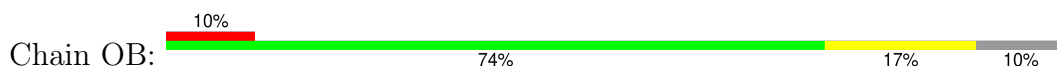
• Molecule 62: S10

Chain KB: 

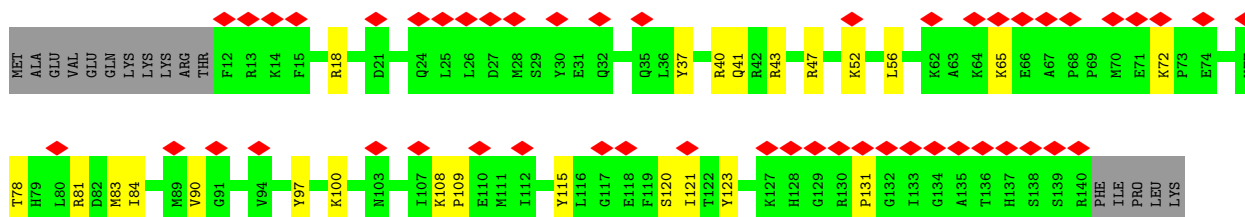
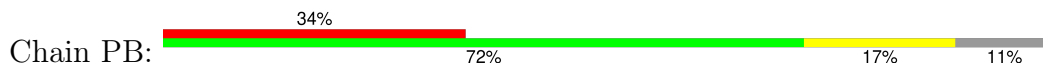




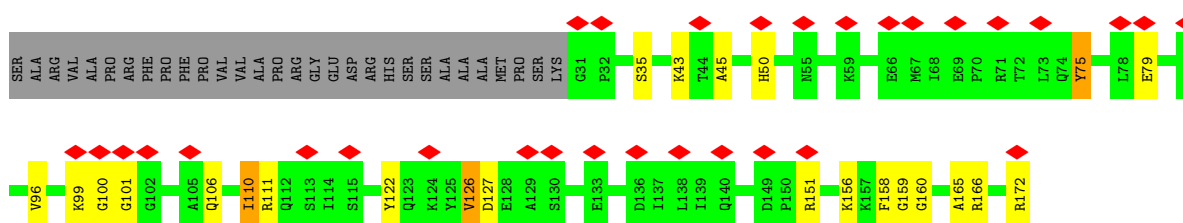
• Molecule 66: S14



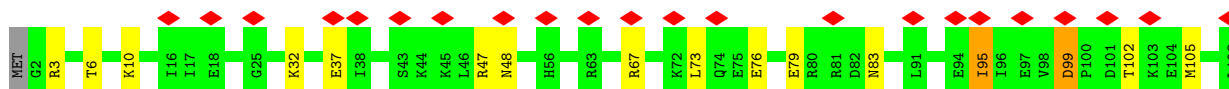
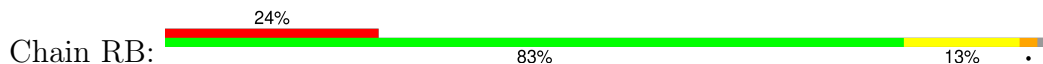
• Molecule 67: S15

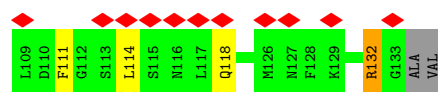


• Molecule 68: uS9

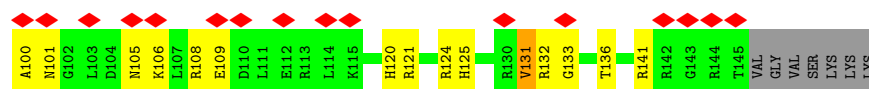
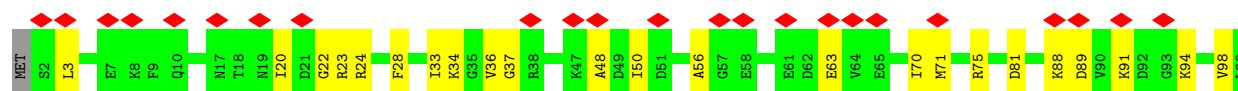


• Molecule 69: eS17

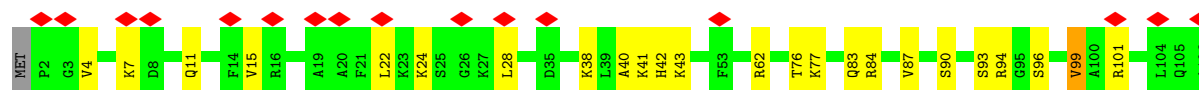
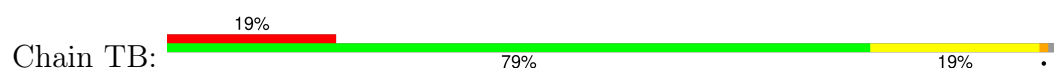




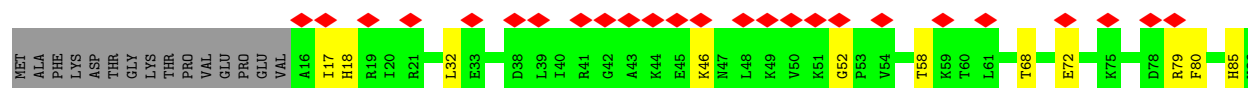
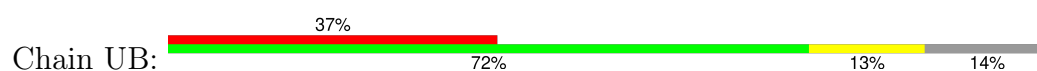
• Molecule 70: S18



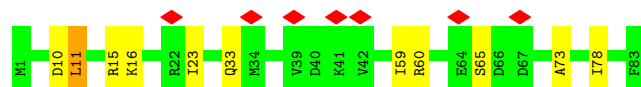
• Molecule 71: S19



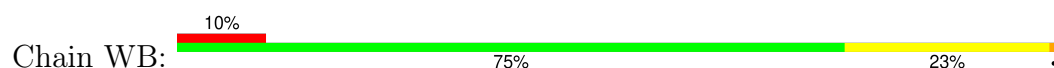
• Molecule 72: uS10

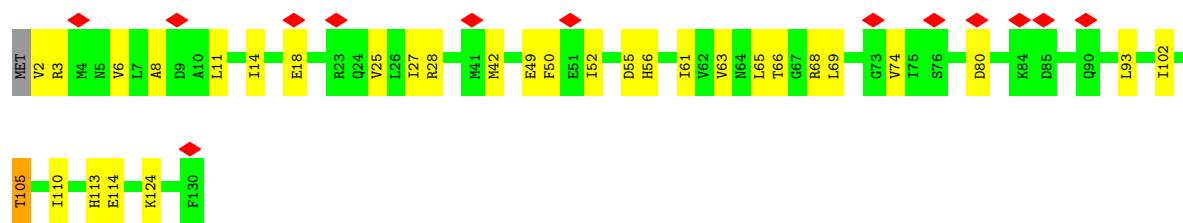


• Molecule 73: S21

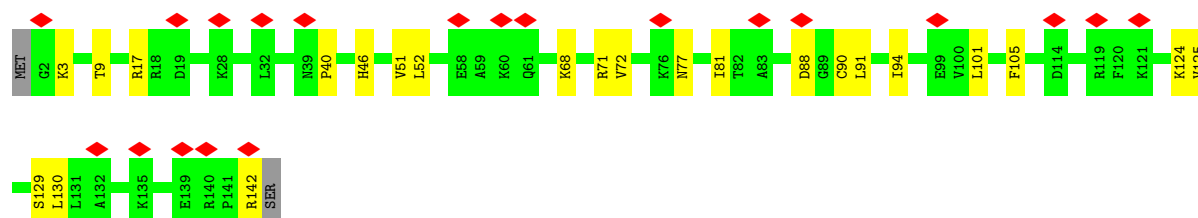
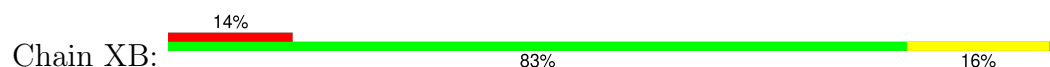


• Molecule 74: S15A

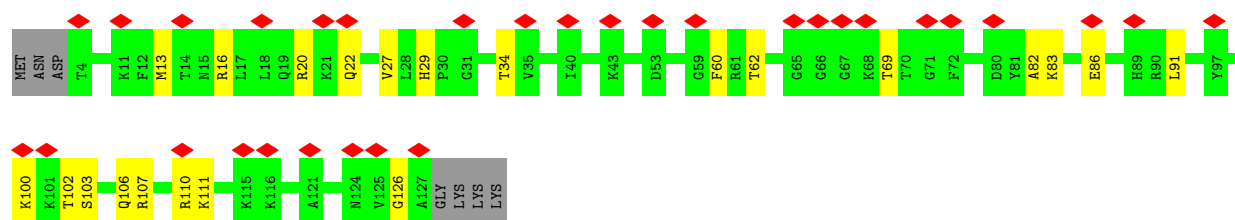
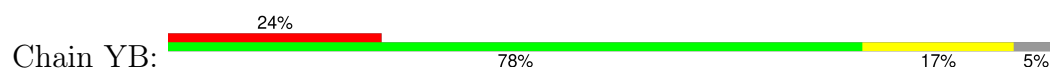




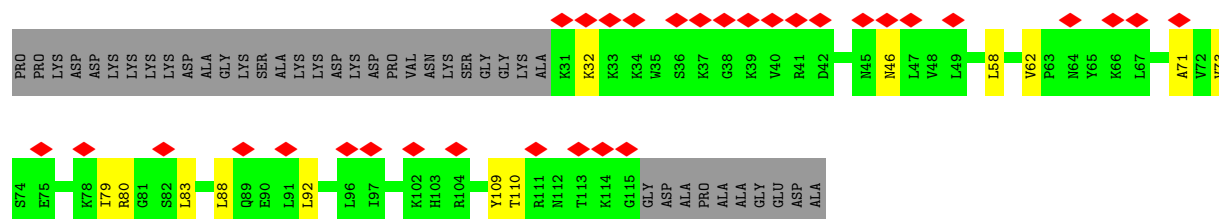
• Molecule 75: S23



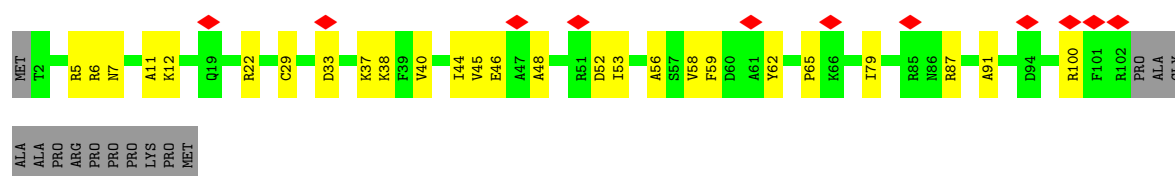
• Molecule 76: S24



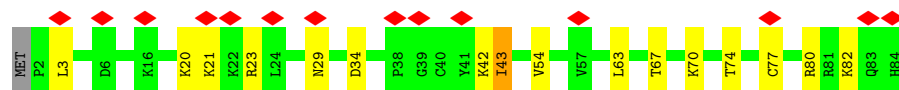
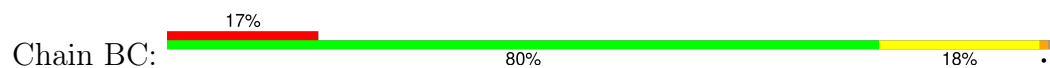
• Molecule 77: eS25



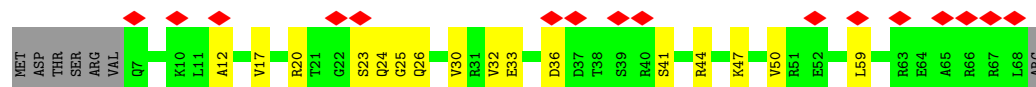
• Molecule 78: S26



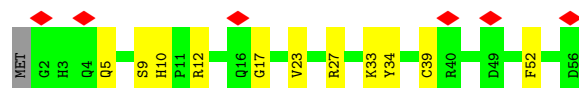
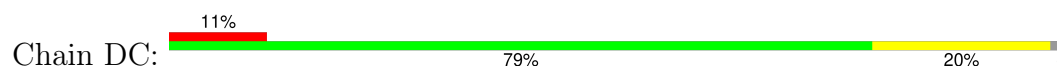
- Molecule 79: S27



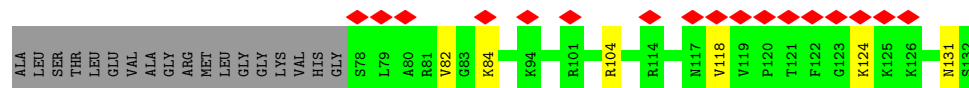
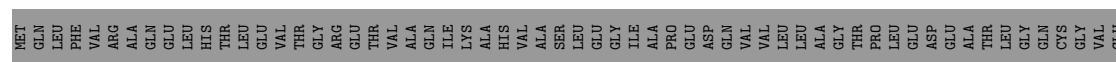
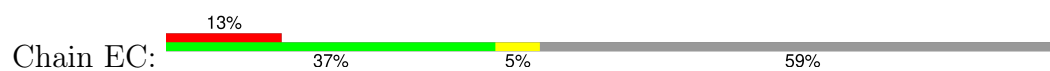
- Molecule 80: S28



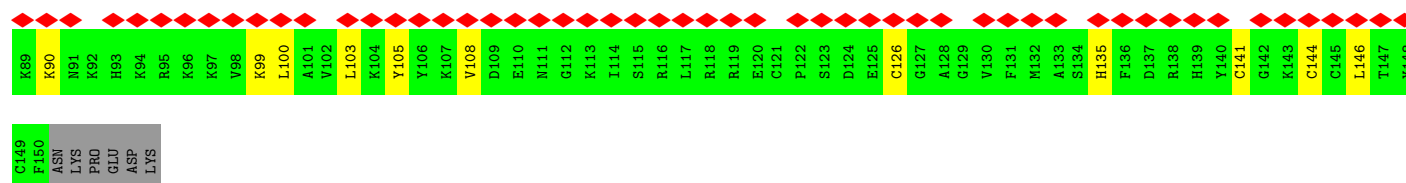
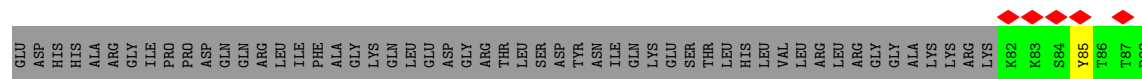
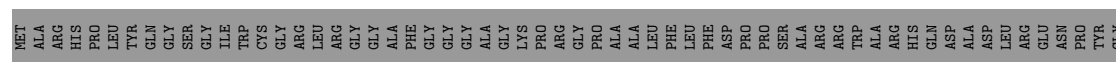
- Molecule 81: uS14



- Molecule 82: S30

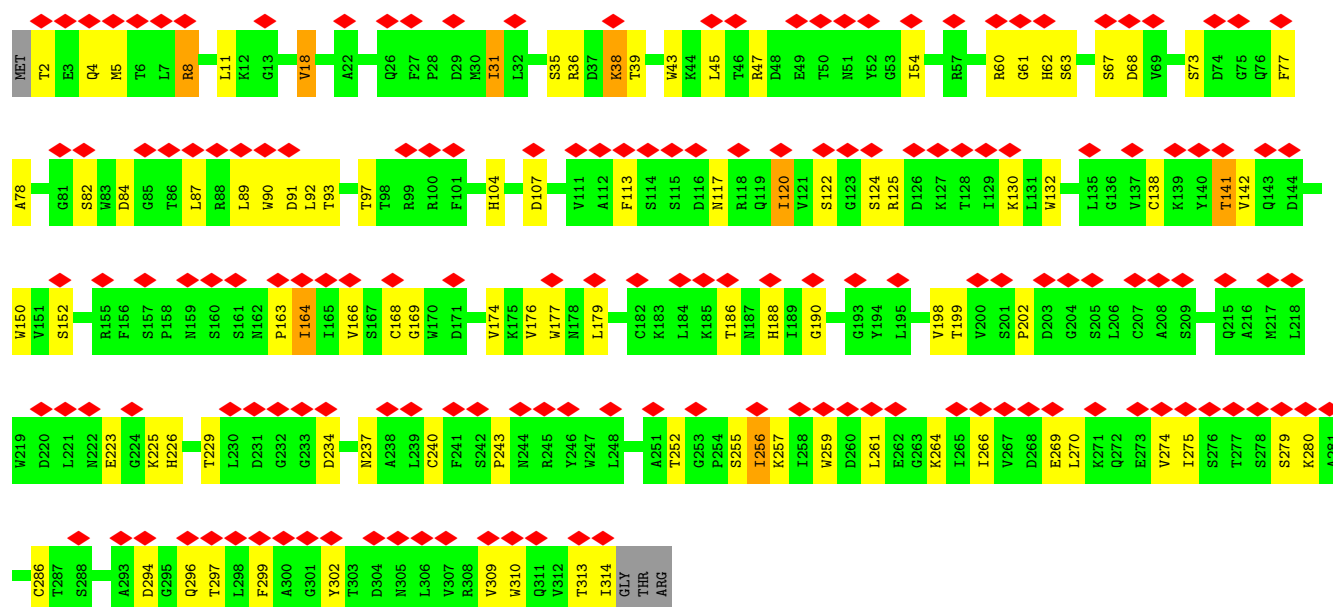


- Molecule 83: S27A

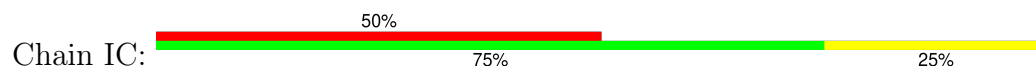


- Molecule 84: RACK1

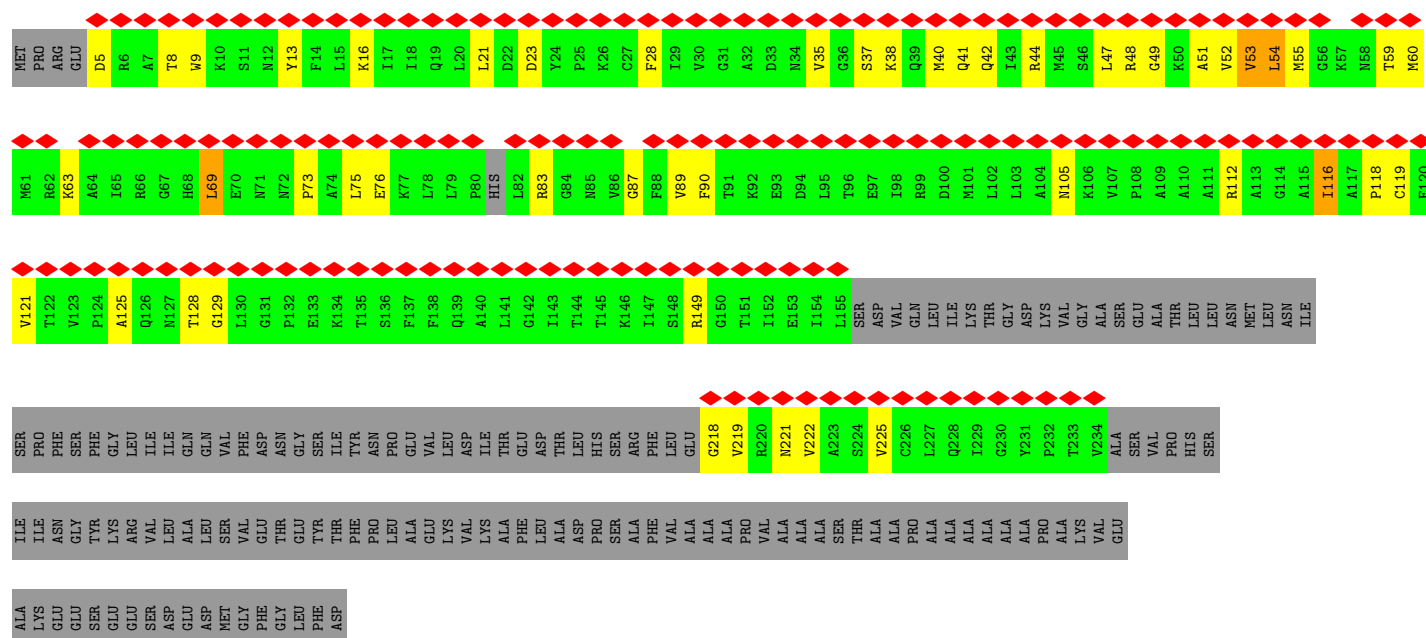
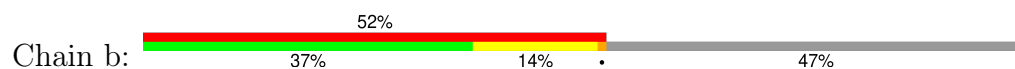




• Molecule 85: peptide



• Molecule 86: RPLP0

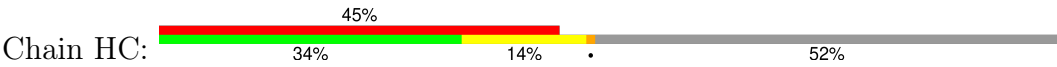


● Molecule 87: RPLP peptide



S241	E242	E243	S244	D245	E246	D247	W248	G249	F250	G251	L252	F253	D254
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● Molecule 88: eukaryotic elongation factor 1A



MET	GLY	LYS	GLU	LYS	THR	HIS	ILE	ASN	VAL	VAL	ILE	GLY	HIS	VAL	ASP	SER	GLY	LYS	SER	THR	THR	THR	GLY	HIS	LEU	ILE	TYR	ILE	LYS	CYS	GLY	GLY	ILE	ASP	LYS	ARG	THR	ILE	GLU	LYS	LYS	PHE	MET	LYS	ASP	ILE	GLY	THR	GLY	ALA	ALA	GLU	GLN	ALA	MET	GLY	ASP	LYS	GLY	VAL	PHE	SER	VAL	ILE	LYS	TYR	ALA	ALA	TRP	GLY	VAL	LEU
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ASP	LYS	LEU	LYS	ALA	GLU	ARG	GLU	ARG	GLY	ILE	THR	ILE	ASP	GLY	HIS	SER	LEU	TRP	LYS	PHE	LYS	GLU	THR	THR	VAL	GLN	LEU	THR	ILE	ILE	ASP	ALA	PRO	GLY	LYS	HIS	ASP	ARG	ASP	THR	PHE	ILE	LYS	ASN	LYS	MET	LYS	ASP	THR	THR	GLU	PRO	PRO	TYR	SER	ILE	GLY	THR	GLY	ALA	THR	THR	VAL	SER	VAL	ILE	ALA	ALA	TRP	GLY	VAL	LEU
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GLY	GLU	PHE	GLU	ALA	GLY	ILE	SER	ASN	LYS	GLY	GLN	THR	ARG	GLY	GLU	HIS	ALA	LEU	LEU	ALA	ALA	TYR	THR	THR	LEU	LEU	ILE	ILE	VAL	GLY	VAL	ASN	GLY	VAL	ASP	MET	LYS	THR	ASP	THR	THR	GLU	PRO	PRO	TYR	SER	GLN	LYS	ARG	THR	TYR	GLU	GLU	ILE	VAL	LYS	GLU	VAL	VAL	SER	THR	TYR	ILE	ALA	ALA	TRP	GLY	VAL	LEU
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ILE	GLY	TYR	ASN	PRO	THR	THR	VAL	PHE	VAL	PRO	THR	ILE	SER	GLY	TRP	GLY	ASP	ASN	MET	GLU	GLU	PRO	SER	ALA	ALA	MET	PRO	TRP	PHE	LYS	GLY	TRP	VAL	THR	THR	THR	ARG	ARG	LYS	ASP	GLY	ALA	SER	GLY	THR	THR	THR	LEU	GLU	ALA	ASP	CYS	ILE	LEU	PRO	PRO	THR	R240
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P241	T242	D243	K244	P245	L246	R247	L248	P249	L250	Q251	D252	V253	V254	K255	T256	G257	G258	T259	G260	T261	V262	P263	V264	G265	R266	V267	E268	T269	G270	V271	L272	K273	P274	G275	H276	V277	V278	T279	F280	A281	P282	V283	N284	V285	T286	T287	E288	V289	K290	S291	V292	E293	N294	H295	H296	E297	A298	L299	S300
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E301	A302	L303	P304	G305	D306	N307	V308	G309	F310	N311	V312	K313	N314	V315	S316	V317	K318	D319	V320	R321	R322	G323	N324	V325	A326	G327	D328	S329	K330	N331	D332	F333	P334	K335	E336	A337	A338	G339	F340	T341	A342	G343	V344	I345	I346	L347	N348	H349	P350	G351	Q352	I353	S354	A355	G356	Y357	A358	F359	V360
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L361	D362	C363	H364	T365	A366	H367	T368	A369	C370	K371	F372	A373	E374	L375	K376	E377	K378	I379	D380	R381	R382	S383	G384	K385	K386	L387	E388	D389	G390	P391	K392	F393	L394	K395	S396	G397	D398	A399	A400	I401	V402	D403	M404	V405	P406	G407	K408	P409	M410	C411	V412	E413	S414	F415	S416	D417	Y418	P419	P420
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L421	G422	R423	F424	A425	V426	R427	D428	M429	R430	Q431	T432	V433	A434	V435	G436	V437	T438	K439	A440	V441	D442	K443	K444	A445	A446	G447	A448	G449	K450	V451	T452	K453	S454	A455	Q456	K457	A458	Q459	K460	A461	K462
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## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	5498	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	75	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	33.748	Depositor
Minimum map value	-22.021	Depositor
Average map value	0.004	Depositor
Map value standard deviation	1.548	Depositor
Recommended contour level	6	Depositor
Map size (Å)	686.87994, 686.87994, 686.87994	wwPDB
Map dimensions	648, 648, 648	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, SPD, MG, 5GP, K, ANM

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	A	0.12	0/1952	0.28	0/2617
2	B	0.12	0/3264	0.28	0/4371
3	C	0.11	0/2937	0.25	0/3946
4	D	0.10	0/2441	0.24	0/3269
5	E	0.10	0/1859	0.26	0/2491
6	F	0.11	0/1933	0.27	0/2577
7	G	0.11	0/1881	0.26	0/2532
8	H	0.11	0/1535	0.28	0/2063
9	I	0.11	0/1702	0.24	0/2272
10	J	0.10	0/1395	0.28	0/1863
11	K	0.10	0/1733	0.25	0/2316
12	L	0.11	0/1158	0.26	0/1547
13	M	0.12	0/1746	0.27	0/2338
14	N	0.12	0/1662	0.28	0/2222
15	O	0.11	0/1292	0.29	0/1733
16	P	0.11	0/1539	0.28	0/2054
17	Q	0.10	0/1524	0.25	0/2013
18	R	0.11	0/1501	0.28	0/2012
19	S	0.10	0/1326	0.24	0/1770
20	T	0.11	0/840	0.31	0/1127
21	U	0.12	0/1018	0.27	0/1364
22	V	0.11	0/900	0.27	0/1194
23	W	0.10	0/984	0.25	0/1323
24	X	0.10	0/1132	0.23	0/1504
25	Y	0.11	0/1130	0.24	0/1507
26	Z	0.11	0/1191	0.26	0/1590
27	AA	0.08	0/886	0.20	0/1171
28	BA	0.10	0/779	0.23	0/1044
29	CA	0.11	0/908	0.27	0/1223
30	DA	0.11	0/1082	0.24	0/1443
31	EA	0.12	0/895	0.27	0/1198
32	FA	0.11	0/916	0.28	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	GA	0.09	0/1016	0.24	0/1341
34	HA	0.09	0/841	0.23	0/1112
35	IA	0.11	0/731	0.26	0/966
36	JA	0.09	0/575	0.26	0/761
37	KA	0.11	0/459	0.27	0/608
38	LA	0.10	0/435	0.26	0/575
39	MA	0.09	0/240	0.19	0/305
40	NA	0.10	0/864	0.23	0/1140
41	OA	0.12	0/718	0.32	0/953
42	PA	0.12	0/1010	0.30	0/1354
43	RA	0.12	0/1174	0.32	0/1582
44	SA	0.10	0/1815	0.23	0/2828
45	TA	0.09	0/1804	0.23	0/2810
46	UA	0.13	0/1783	0.32	0/2776
47	VA	0.08	0/279	0.21	0/431
48	WA	0.12	0/85839	0.25	0/133881
49	XA	0.11	0/2836	0.20	0/4421
50	YA	0.11	0/3701	0.24	0/5766
51	ZA	0.11	0/40949	0.25	0/63819
52	AB	0.11	0/1747	0.26	0/2374
53	BB	0.10	0/1756	0.26	0/2350
54	CB	0.12	0/1744	0.29	0/2358
55	DB	0.10	0/1796	0.25	0/2417
56	EB	0.11	0/2118	0.30	0/2849
57	FB	0.11	0/1492	0.29	0/2005
58	GB	0.10	0/1946	0.25	0/2590
59	HB	0.10	0/1511	0.27	0/2022
60	IB	0.11	0/1715	0.27	0/2287
61	JB	0.10	0/1550	0.27	0/2069
62	KB	0.10	0/834	0.28	0/1125
63	LB	0.10	0/1200	0.25	0/1604
64	MB	0.10	0/918	0.29	0/1233
65	NB	0.10	0/1226	0.23	0/1649
66	OB	0.11	0/1029	0.28	0/1380
67	PB	0.13	0/1079	0.29	0/1441
68	QB	0.12	0/1146	0.30	0/1534
69	RB	0.10	0/1082	0.26	0/1452
70	SB	0.10	0/1208	0.28	0/1618
71	TB	0.10	0/1123	0.25	0/1504
72	UB	0.10	0/818	0.28	0/1099
73	VB	0.10	0/643	0.27	0/860
74	WB	0.11	0/1051	0.31	0/1406
75	XB	0.10	0/1116	0.26	0/1490

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	YB	0.10	0/1028	0.28	0/1366
77	ZB	0.10	0/691	0.25	0/922
78	AC	0.11	0/828	0.27	0/1109
79	BC	0.08	0/665	0.23	0/891
80	CC	0.09	0/490	0.25	0/656
81	DC	0.09	0/470	0.24	0/623
82	EC	0.08	0/447	0.23	0/587
83	FC	0.10	0/576	0.27	0/764
84	GC	0.11	0/2493	0.31	0/3394
85	IC	0.05	0/19	0.15	0/25
86	b	0.14	0/1296	0.32	0/1745
87	c	0.12	0/111	0.30	0/145
88	HC	0.11	0/1694	0.29	0/2287
All	All	0.11	0/236766	0.25	0/347573

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 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	A	1914	0	2013	40	0
2	B	3196	0	3339	53	0
3	C	2883	0	3053	32	0
4	D	2395	0	2427	29	0
5	E	1823	0	1995	29	0
6	F	1897	0	2021	33	0
7	G	1850	0	1991	25	0
8	H	1516	0	1597	13	0
9	I	1664	0	1712	22	0
10	J	1372	0	1412	23	0
11	K	1702	0	1820	25	0
12	L	1137	0	1211	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	M	1701	0	1749	37	0
14	N	1630	0	1778	30	0
15	O	1266	0	1302	15	0
16	P	1515	0	1634	35	0
17	Q	1508	0	1664	20	0
18	R	1462	0	1508	25	0
19	S	1298	0	1366	24	0
20	T	826	0	852	14	0
21	U	1004	0	1063	15	0
22	V	887	0	935	11	0
23	W	967	0	1040	11	0
24	X	1115	0	1205	16	0
25	Y	1107	0	1182	24	0
26	Z	1162	0	1209	24	0
27	AA	873	0	949	10	0
28	BA	769	0	803	11	0
29	CA	893	0	932	15	0
30	DA	1064	0	1160	20	0
31	EA	876	0	912	10	0
32	FA	906	0	998	5	0
33	GA	1008	0	1142	22	0
34	HA	830	0	916	6	0
35	IA	716	0	750	16	0
36	JA	569	0	637	9	0
37	KA	447	0	480	14	0
38	LA	429	0	465	7	0
39	MA	239	0	289	3	0
40	NA	851	0	920	15	0
41	OA	708	0	757	7	0
42	PA	994	0	1051	18	0
43	RA	1160	0	1218	18	0
44	SA	1622	0	825	15	0
45	TA	1615	0	820	14	0
46	UA	1596	0	810	19	0
47	VA	251	0	128	2	0
48	WA	76735	0	38762	941	0
49	XA	2538	0	1286	28	0
50	YA	3314	0	1683	40	0
51	ZA	36623	0	18504	475	0
52	AB	1710	0	1711	23	0
53	BB	1729	0	1803	23	0
54	CB	1707	0	1793	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	DB	1768	0	1863	21	0
56	EB	2076	0	2177	36	0
57	FB	1471	0	1522	24	0
58	GB	1923	0	2089	38	0
59	HB	1489	0	1582	25	0
60	IB	1686	0	1772	23	0
61	JB	1525	0	1640	27	0
62	KB	810	0	836	21	0
63	LB	1180	0	1254	14	0
64	MB	908	0	939	19	0
65	NB	1202	0	1289	18	0
66	OB	1016	0	1039	20	0
67	PB	1058	0	1104	17	0
68	QB	1128	0	1195	17	0
69	RB	1068	0	1121	15	0
70	SB	1190	0	1249	30	0
71	TB	1104	0	1140	20	0
72	UB	808	0	878	13	0
73	VB	636	0	637	8	0
74	WB	1034	0	1080	22	0
75	XB	1098	0	1167	15	0
76	YB	1011	0	1083	19	0
77	ZB	683	0	761	9	0
78	AC	814	0	864	19	0
79	BC	651	0	672	9	0
80	CC	488	0	514	12	0
81	DC	459	0	449	8	0
82	EC	443	0	492	7	0
83	FC	564	0	577	7	0
84	GC	2436	0	2393	49	0
85	IC	20	0	10	1	0
86	b	1279	0	1343	34	0
87	c	110	0	83	4	0
88	HC	1664	0	1721	31	0
89	A	1	0	0	0	0
89	AC	1	0	0	0	0
89	FA	1	0	0	0	0
89	HC	1	0	0	0	0
89	I	1	0	0	0	0
89	IA	1	0	0	0	0
89	O	1	0	0	0	0
89	P	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
89	U	1	0	0	0	0
89	VA	1	0	0	0	0
89	WA	142	0	0	0	0
89	XA	4	0	0	0	0
89	YA	2	0	0	0	0
89	Z	1	0	0	0	0
89	ZA	45	0	0	0	0
90	AC	1	0	0	0	0
90	DC	1	0	0	0	0
90	FA	1	0	0	0	0
90	FC	1	0	0	0	0
90	IA	1	0	0	0	0
90	LA	1	0	0	0	0
90	NA	1	0	0	0	0
90	OA	1	0	0	0	0
91	UA	24	0	11	0	0
92	WA	19	0	18	1	0
93	WA	20	0	38	1	0
93	ZA	10	0	19	0	0
94	WA	1	0	0	0	0
95	HC	6	0	4	0	0
All	All	220661	0	164207	2523	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (2523) 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)
48:WA:2847:A:H61	48:WA:3845:C:N4	1.54	1.04
48:WA:2847:A:N6	48:WA:3845:C:H42	1.58	1.00
51:ZA:197:U:H3	51:ZA:202:G:H1	1.04	1.00
48:WA:1249:U:H3	48:WA:1268:G:H1	1.03	0.96
51:ZA:1743:G:N2	51:ZA:1791:A:H62	1.64	0.95
48:WA:1446:G:H1	48:WA:2113:U:H3	1.08	0.92
51:ZA:1743:G:H21	51:ZA:1791:A:H62	0.95	0.92
46:UA:8:U:H3	46:UA:14:A:H62	1.13	0.91
44:SA:50:U:H3	44:SA:64:G:H1	0.97	0.90
51:ZA:1472:C:H42	51:ZA:1476:A:H62	1.18	0.90
55:DB:201:PRO:O	55:DB:205:TYR:HB2	1.72	0.90
51:ZA:1656:G:H1	51:ZA:1668:U:H3	1.16	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:1743:G:H21	51:ZA:1791:A:N6	1.69	0.87
48:WA:2487:U:H3	48:WA:2495:G:H1	1.19	0.85
51:ZA:1288:U:H3	51:ZA:1311:C:H42	1.24	0.82
48:WA:2575:A:H62	48:WA:2763:U:H3	1.27	0.81
48:WA:1761:G:H1	48:WA:1775:U:H3	1.25	0.80
51:ZA:677:G:H21	51:ZA:1028:A:H62	1.31	0.78
46:UA:8:U:H3	46:UA:14:A:N6	1.81	0.77
56:EB:185:GLY:H	56:EB:189:LEU:HD13	1.48	0.77
48:WA:4995:G:H1	48:WA:5060:A:H2	1.30	0.77
86:b:55:MET:HG3	86:b:87:GLY:HA3	1.67	0.76
74:WB:8:ALA:HA	74:WB:74:VAL:HG21	1.67	0.76
48:WA:2847:A:H61	48:WA:3845:C:H42	0.81	0.75
46:UA:10:G:H22	46:UA:25:C:H2'	1.51	0.75
48:WA:2522:C:O2	48:WA:2642:G:N2	2.20	0.74
35:IA:2:THR:N	48:WA:3644:A:HO2'	1.86	0.73
51:ZA:1472:C:N4	51:ZA:1476:A:H62	1.86	0.73
51:ZA:561:A:H5'	61:JB:171:GLY:HA3	1.71	0.72
48:WA:1452:C:HO2'	48:WA:2106:A:HO2'	1.36	0.72
86:b:5:ASP:N	86:b:8:THR:HG1	1.87	0.72
48:WA:1975:G:H2'	48:WA:1976:U:H2'	1.71	0.72
51:ZA:1396:A:O2'	51:ZA:1398:G:N7	2.20	0.72
48:WA:3699:U:H5''	48:WA:3700:G:H5'	1.72	0.72
48:WA:4770:G:H2'	48:WA:4771:G:C8	2.25	0.72
51:ZA:442:C:H42	51:ZA:449:A:H62	1.38	0.72
48:WA:4874:G:H4'	48:WA:4875:G:H5'	1.72	0.72
48:WA:4737:G:H1	48:WA:4967:U:H3	1.36	0.71
58:GB:69:THR:HG22	58:GB:71:GLY:H	1.54	0.71
5:E:48:ARG:HB2	5:E:64:MET:HE1	1.72	0.71
3:C:78:ARG:HB3	3:C:88:GLY:HA2	1.72	0.71
14:N:125:LYS:HG3	14:N:129:LEU:HD12	1.73	0.70
48:WA:995:U:H3	48:WA:1071:G:H1	1.38	0.70
10:J:75:ARG:NH1	49:XA:40:U:O2	2.25	0.70
72:UB:80:PHE:HB3	81:DC:52:PHE:HB3	1.71	0.70
69:RB:111:PHE:HB3	69:RB:114:LEU:HD11	1.73	0.69
51:ZA:15:U:O2'	51:ZA:669:A:N6	2.25	0.69
2:B:249:ARG:NH1	48:WA:2839:U:OP1	2.25	0.69
11:K:56:ARG:O	11:K:116:ARG:NH1	2.25	0.69
18:R:87:ARG:HH21	48:WA:2036:G:H5'	1.57	0.69
5:E:115:MET:O	42:PA:87:ARG:NH1	2.26	0.69
51:ZA:1298:G:HO2'	51:ZA:1299:A:H8	1.40	0.69
68:QB:96:VAL:HG11	68:QB:110:ILE:HG13	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:959:G:OP1	66:OB:104:ARG:NH2	2.27	0.68
51:ZA:1658:G:OP2	51:ZA:1660:C:N4	2.27	0.68
71:TB:76:THR:HB	71:TB:94:ARG:HB3	1.75	0.68
43:RA:121:LEU:HB2	86:b:49:GLY:HA2	1.76	0.68
48:WA:3946:G:H1	48:WA:4071:U:H3	1.42	0.68
51:ZA:1410:C:H2'	51:ZA:1411:G:H8	1.57	0.68
18:R:34:ALA:HB1	18:R:39:VAL:HG23	1.76	0.68
84:GC:256:ILE:HG23	84:GC:270:LEU:HB2	1.76	0.68
84:GC:199:THR:HG21	84:GC:240:CYS:HA	1.77	0.67
5:E:186:ARG:HH21	48:WA:4938:G:H2'	1.60	0.67
48:WA:1526:A:H62	48:WA:1653:G:H1	1.42	0.67
48:WA:2022:U:H2'	48:WA:2023:G:H8	1.59	0.67
48:WA:3643:U:OP2	48:WA:3648:A:N6	2.27	0.67
48:WA:4355:U:H5''	48:WA:4356:U:H5'	1.75	0.67
48:WA:4995:G:O6	48:WA:5060:A:N1	2.27	0.67
51:ZA:482:G:N1	51:ZA:485:A:OP2	2.27	0.67
51:ZA:888:U:H2'	51:ZA:900:C:H42	1.58	0.67
51:ZA:1674:G:OP1	57:FB:51:HIS:NE2	2.25	0.67
45:TA:15:G:N2	45:TA:48:C:C2	2.62	0.67
51:ZA:1091:C:HO2'	74:WB:2:VAL:N	1.93	0.67
51:ZA:957:A:H3'	51:ZA:958:G:H21	1.60	0.66
53:BB:107:ARG:NH1	66:OB:133:THR:O	2.27	0.66
54:CB:123:ARG:NH1	54:CB:143:CYS:SG	2.68	0.66
11:K:74:ARG:NH2	48:WA:109:G:OP2	2.29	0.66
48:WA:1766:G:OP2	48:WA:1766:G:N2	2.28	0.66
48:WA:3762:A:N6	51:ZA:1826:G:OP2	2.29	0.66
19:S:70:HIS:NE2	48:WA:4329:C:OP1	2.29	0.66
84:GC:31:ILE:HG23	84:GC:43:TRP:HB2	1.77	0.66
6:F:227:VAL:HA	18:R:39:VAL:HG12	1.76	0.66
48:WA:4696:G:OP1	48:WA:4696:G:N2	2.29	0.66
26:Z:21:ARG:NH2	48:WA:1319:U:OP1	2.28	0.66
51:ZA:1473:G:N2	51:ZA:1476:A:OP2	2.29	0.66
38:LA:74:TYR:O	48:WA:4474:G:O2'	2.14	0.65
51:ZA:377:G:H5'	60:IB:98:LYS:HB3	1.78	0.65
3:C:340:ILE:HD13	5:E:53:VAL:HG21	1.78	0.65
4:D:103:LEU:HD11	4:D:248:ARG:HE	1.61	0.65
11:K:31:ARG:HD3	11:K:35:ARG:HH21	1.61	0.65
48:WA:3694:A:H62	48:WA:3825:G:H21	1.43	0.65
2:B:249:ARG:NH2	48:WA:3847:A:OP2	2.30	0.65
51:ZA:1396:A:N7	51:ZA:1450:G:N2	2.45	0.65
88:HC:380:ASP:HB3	88:HC:383:SER:HB2	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:1092:C:H2'	48:WA:1093:A:H8	1.61	0.65
48:WA:4423:C:H42	48:WA:4477:G:H22	1.44	0.65
25:Y:103:ASP:HB3	25:Y:106:LEU:HB2	1.79	0.65
41:OA:4:ARG:NH2	48:WA:1557:G:O6	2.30	0.65
48:WA:102:G:HO2'	48:WA:1383:U:HO2'	1.44	0.65
48:WA:1929:U:OP1	48:WA:1951:U:O2'	2.13	0.65
51:ZA:114:G:N7	63:LB:69:ARG:NH2	2.45	0.65
51:ZA:1403:C:N4	51:ZA:1433:C:OP1	2.30	0.65
56:EB:122:LYS:NZ	56:EB:124:CYS:SG	2.68	0.65
51:ZA:1298:G:H4'	67:PB:78:THR:HA	1.79	0.64
37:KA:37:TYR:O	48:WA:362:A:N6	2.30	0.64
66:OB:142:ARG:HB3	78:AC:22:ARG:HD3	1.80	0.64
11:K:59:VAL:HB	48:WA:74:G:H5'	1.78	0.64
48:WA:1334:C:H2'	48:WA:1335:A:H8	1.63	0.64
8:H:85:THR:HG23	8:H:86:LEU:HG	1.78	0.64
48:WA:4539:C:H2'	48:WA:4540:G:H8	1.63	0.64
48:WA:4543:G:N2	48:WA:4546:A:OP2	2.28	0.64
48:WA:1726:G:N2	48:WA:1878:U:OP1	2.31	0.64
48:WA:1745:A:N1	48:WA:1791:C:O2'	2.29	0.64
84:GC:39:THR:HG22	84:GC:60:ARG:HG2	1.80	0.64
51:ZA:1130:G:N2	51:ZA:1130:G:OP2	2.31	0.64
31:EA:100:ARG:NH1	48:WA:4755:U:OP1	2.31	0.64
43:RA:17:CYS:O	43:RA:57:ARG:HA	1.98	0.64
4:D:256:LYS:HD2	49:XA:117:G:H5'	1.80	0.64
48:WA:970:G:N2	48:WA:2098:G:O2'	2.32	0.64
48:WA:961:A:H1'	48:WA:2078:G:H5''	1.79	0.63
74:WB:42:MET:HE2	74:WB:49:GLU:HA	1.80	0.63
86:b:121:VAL:HG13	86:b:221:ASN:HD21	1.64	0.63
19:S:43:LYS:NZ	48:WA:1735:G:OP1	2.31	0.63
48:WA:1554:G:O2'	48:WA:1576:G:N2	2.32	0.63
66:OB:105:THR:HG22	66:OB:107:THR:H	1.63	0.63
24:X:15:ARG:NH1	48:WA:230:G:OP1	2.32	0.63
35:IA:33:THR:HG22	35:IA:40:PRO:HG2	1.81	0.63
48:WA:916:U:H4'	48:WA:917:A:H5'	1.81	0.63
48:WA:1741:G:N3	48:WA:1744:A:N6	2.47	0.63
56:EB:87:MET:HE2	56:EB:123:LEU:HB2	1.80	0.63
51:ZA:649:U:H2'	51:ZA:650:A:H8	1.64	0.63
51:ZA:851:C:H5''	51:ZA:852:G:H5'	1.80	0.63
11:K:103:ARG:NH1	48:WA:73:A:N7	2.45	0.63
15:O:161:ALA:HB2	48:WA:1599:G:H5'	1.81	0.63
51:ZA:1521:C:OP2	70:SB:136:THR:OG1	2.16	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:65:ARG:NH1	48:WA:1504:G:OP1	2.32	0.63
51:ZA:925:G:H1	51:ZA:1017:U:H3	1.47	0.63
5:E:61:ARG:HB2	48:WA:1243:C:H5''	1.81	0.63
8:H:43:VAL:HG12	8:H:59:LYS:HD3	1.78	0.63
1:A:128:ARG:NH1	48:WA:3683:G:OP2	2.32	0.63
33:GA:66:LYS:HD3	50:YA:96:C:H5''	1.80	0.63
48:WA:2505:G:O2'	48:WA:2507:C:N4	2.32	0.63
58:GB:164:LYS:HG2	58:GB:165:GLU:HG3	1.80	0.63
50:YA:67:U:H2'	50:YA:68:G:H8	1.62	0.62
51:ZA:43:U:OP2	51:ZA:485:A:N6	2.30	0.62
7:G:111:PRO:HD2	7:G:114:ILE:HD12	1.81	0.62
21:U:43:LYS:HD3	21:U:62:MET:HE2	1.81	0.62
48:WA:67:C:OP2	48:WA:312:G:N2	2.31	0.62
48:WA:300:A:H2'	48:WA:301:G:H8	1.63	0.62
48:WA:2491:C:O2'	48:WA:2493:C:N3	2.32	0.62
53:BB:122:GLU:O	53:BB:165:ARG:NH1	2.32	0.62
16:P:82:VAL:HG12	16:P:84:GLY:H	1.63	0.62
48:WA:20:U:H3'	48:WA:21:G:H8	1.64	0.62
75:XB:68:LYS:HE2	82:EC:82:VAL:HG22	1.80	0.62
1:A:116:LEU:HB3	1:A:126:LEU:HB2	1.82	0.62
1:A:179:ILE:HG23	1:A:184:ARG:HB2	1.81	0.62
2:B:234:ARG:NH2	48:WA:4568:U:O2'	2.33	0.62
16:P:65:ARG:NH2	48:WA:1461:A:OP1	2.32	0.62
26:Z:72:THR:HG22	26:Z:110:LYS:HB3	1.81	0.62
48:WA:2460:C:H1'	48:WA:3673:G:H21	1.65	0.62
62:KB:27:VAL:HG13	62:KB:43:LEU:HD13	1.81	0.62
10:J:99:PHE:O	10:J:159:LYS:NZ	2.32	0.62
30:DA:36:ARG:NH1	48:WA:1663:C:OP1	2.33	0.62
51:ZA:1228:A:H2'	51:ZA:1229:G:C8	2.35	0.62
1:A:117:GLU:OE2	1:A:163:ARG:NH1	2.32	0.62
49:XA:28:C:H1'	49:XA:54:A:H61	1.64	0.62
51:ZA:1612:G:OP1	67:PB:18:ARG:NH2	2.33	0.62
48:WA:2603:A:N6	48:WA:2746:A:OP2	2.32	0.62
51:ZA:616:A:OP1	75:XB:68:LYS:NZ	2.31	0.62
38:LA:88:LYS:NZ	48:WA:4487:C:O2'	2.33	0.62
51:ZA:163:U:OP2	58:GB:87:ARG:NH2	2.30	0.62
14:N:49:ARG:NH1	48:WA:1932:U:OP2	2.31	0.61
5:E:164:ARG:NH1	12:L:106:ASP:OD2	2.32	0.61
51:ZA:429:C:O2'	51:ZA:811:A:N1	2.33	0.61
51:ZA:1259:A:N6	51:ZA:1519:U:OP1	2.33	0.61
51:ZA:1652:G:H1	51:ZA:1672:U:H3	1.47	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:GB:2:LYS:HB3	58:GB:15:LEU:HD11	1.82	0.61
61:JB:136:ARG:NH1	61:JB:159:PHE:O	2.32	0.61
6:F:176:ARG:NH1	48:WA:2103:A:N7	2.49	0.61
6:F:218:GLY:O	6:F:245:ARG:NH2	2.34	0.61
51:ZA:1286:G:N2	51:ZA:1312:G:O2'	2.31	0.61
30:DA:36:ARG:NH2	48:WA:2324:G:OP1	2.33	0.61
51:ZA:16:G:H5'	51:ZA:669:A:H61	1.64	0.61
81:DC:17:GLY:O	81:DC:27:ARG:NH1	2.33	0.61
51:ZA:165:G:N2	51:ZA:165:G:OP2	2.32	0.61
51:ZA:581:U:OP1	61:JB:133:ARG:NH2	2.33	0.61
51:ZA:954:U:O2	66:OB:55:ARG:NH2	2.33	0.61
51:ZA:1004:U:H2'	51:ZA:1005:G:H8	1.66	0.61
51:ZA:1227:G:N2	51:ZA:1635:C:O2'	2.33	0.61
65:NB:99:ARG:NH2	65:NB:119:GLU:OE2	2.34	0.61
17:Q:172:ARG:HH12	51:ZA:908:A:H5''	1.65	0.61
42:PA:67:ARG:NH1	48:WA:667:G:OP2	2.34	0.61
5:E:156:LEU:HD11	5:E:198:ILE:HG13	1.82	0.61
7:G:185:ARG:NH1	48:WA:119:G:OP1	2.34	0.61
9:I:203:ARG:NH1	49:XA:105:C:OP2	2.33	0.61
11:K:35:ARG:NH1	48:WA:105:A:O2'	2.34	0.61
42:PA:65:LYS:O	42:PA:102:TYR:OH	2.18	0.61
44:SA:33:U:OP2	68:QB:172:ARG:NH2	2.34	0.61
48:WA:35:U:O2'	48:WA:1527:A:N1	2.34	0.61
48:WA:2779:G:H5''	48:WA:2780:G:H5'	1.82	0.61
48:WA:3879:A:N3	48:WA:4403:G:O2'	2.30	0.61
51:ZA:1115:U:H1'	51:ZA:1116:C:H2'	1.83	0.61
80:CC:17:VAL:HA	80:CC:30:VAL:HG23	1.83	0.61
88:HC:426:VAL:HB	88:HC:434:ALA:HB3	1.82	0.61
20:T:113:ARG:NH2	48:WA:2704:C:O3'	2.33	0.61
29:CA:39:LYS:HG3	29:CA:40:LYS:HG2	1.83	0.61
14:N:116:LYS:HE3	18:R:169:THR:HG21	1.82	0.60
41:OA:4:ARG:NH1	48:WA:1556:A:OP2	2.33	0.60
68:QB:156:LYS:NZ	68:QB:160:GLY:O	2.33	0.60
11:K:54:PRO:HG2	11:K:56:ARG:HH12	1.66	0.60
16:P:16:LYS:O	16:P:33:ARG:NH2	2.34	0.60
48:WA:4747:G:H1	48:WA:4957:A:H61	1.47	0.60
70:SB:101:ASN:O	70:SB:105:ASN:ND2	2.32	0.60
25:Y:48:ARG:NH2	48:WA:2578:G:OP1	2.34	0.60
35:IA:52:LYS:NZ	48:WA:364:G:O6	2.33	0.60
48:WA:2337:C:H2'	48:WA:2338:G:H8	1.65	0.60
52:AB:36:GLN:O	52:AB:53:ARG:NH1	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:GC:4:GLN:HB3	84:GC:313:THR:HB	1.83	0.60
51:ZA:1418:C:H5'	51:ZA:1420:G:H21	1.65	0.60
48:WA:2522:C:H2'	48:WA:2523:G:H8	1.66	0.60
51:ZA:1228:A:H2'	51:ZA:1229:G:H8	1.66	0.60
5:E:159:ARG:NH1	48:WA:4942:C:OP1	2.33	0.60
33:GA:31:LEU:HB3	33:GA:47:ILE:HG22	1.82	0.60
61:JB:131:ARG:NH1	61:JB:143:ASN:OD1	2.35	0.60
13:M:192:TRP:NE1	48:WA:48:G:OP1	2.32	0.60
22:V:93:LYS:O	22:V:101:ARG:NH2	2.34	0.60
26:Z:65:ARG:NH2	48:WA:86:U:O2'	2.34	0.60
48:WA:262:G:H2'	48:WA:263:G:C8	2.37	0.60
51:ZA:1528:G:O2'	51:ZA:1666:C:OP1	2.20	0.60
51:ZA:1568:C:O2	51:ZA:1627:C:O2'	2.19	0.60
84:GC:174:VAL:HB	84:GC:188:HIS:HB2	1.83	0.60
51:ZA:1566:G:N7	71:TB:101:ARG:NH2	2.49	0.60
51:ZA:1677:U:OP1	57:FB:71:ARG:NH2	2.35	0.60
7:G:170:ARG:NH2	48:WA:119:G:O6	2.33	0.60
9:I:54:SER:HB2	9:I:135:ILE:HD11	1.84	0.60
30:DA:8:VAL:HG22	30:DA:10:PRO:HD3	1.82	0.60
48:WA:1973:U:O2	86:b:41:GLN:NE2	2.34	0.60
48:WA:2640:G:H1	48:WA:2699:A:H61	1.47	0.60
67:PB:121:ILE:HG22	70:SB:120:HIS:HD2	1.66	0.60
48:WA:1857:G:O6	48:WA:1882:G:N2	2.35	0.60
48:WA:4276:A:H2'	48:WA:4277:G:H8	1.66	0.60
70:SB:50:ILE:HD11	70:SB:63:GLU:HB3	1.84	0.60
51:ZA:1550:G:H3'	51:ZA:1579:A:H61	1.67	0.59
75:XB:91:LEU:HB3	82:EC:82:VAL:HG11	1.83	0.59
22:V:61:LYS:NZ	48:WA:5040:A:OP1	2.35	0.59
45:TA:15:G:N2	45:TA:48:C:O2	2.36	0.59
51:ZA:1261:C:O2	81:DC:10:HIS:NE2	2.29	0.59
51:ZA:1286:G:OP1	83:FC:99:LYS:NZ	2.35	0.59
51:ZA:1447:G:OP1	72:UB:85:HIS:ND1	2.35	0.59
51:ZA:197:U:O4	51:ZA:202:G:O6	2.19	0.59
51:ZA:1447:G:OP1	72:UB:87:ARG:NH2	2.35	0.59
2:B:385:LYS:NZ	48:WA:5004:U:OP2	2.35	0.59
7:G:210:ILE:HA	7:G:254:THR:HG22	1.84	0.59
48:WA:5055:U:OP1	48:WA:5056:C:N4	2.35	0.59
51:ZA:1015:U:O2'	65:NB:55:ARG:NH1	2.36	0.59
5:E:265:LYS:NZ	48:WA:4935:C:OP2	2.34	0.59
28:BA:36:LYS:NZ	48:WA:2659:G:OP2	2.35	0.59
48:WA:1392:G:N2	48:WA:1395:G:OP2	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:4476:A:OP2	48:WA:4478:C:N4	2.35	0.59
48:WA:4920:C:H2'	48:WA:4921:G:H8	1.68	0.59
51:ZA:1513:C:OP1	81:DC:12:ARG:NH1	2.35	0.59
57:FB:114:ASN:OD1	57:FB:118:ASN:ND2	2.35	0.59
3:C:110:ARG:O	3:C:113:ARG:NH1	2.35	0.59
7:G:282:ARG:NH2	7:G:285:GLU:OE1	2.36	0.59
24:X:55:VAL:HG12	24:X:106:ILE:HA	1.84	0.59
38:LA:92:THR:HG22	38:LA:94:ASN:H	1.67	0.59
59:HB:408:VAL:HG13	59:HB:425:PHE:HB2	1.83	0.59
84:GC:202:PRO:HG2	84:GC:243:PRO:HA	1.85	0.59
56:EB:87:MET:HE1	56:EB:236:ILE:HG21	1.84	0.59
24:X:34:LEU:HD23	24:X:38:LEU:HB3	1.85	0.59
49:XA:53:U:H4'	49:XA:54:A:H5'	1.85	0.59
51:ZA:24:C:OP1	61:JB:11:LYS:NZ	2.32	0.59
51:ZA:1092:G:OP1	65:NB:2:GLY:N	2.36	0.59
51:ZA:1373:C:O2'	69:RB:10:LYS:NZ	2.30	0.59
6:F:104:VAL:HG13	6:F:135:VAL:HG12	1.85	0.59
34:HA:48:CYS:SG	34:HA:49:GLY:N	2.76	0.59
48:WA:3863:A:H2'	48:WA:3864:A:H8	1.68	0.59
51:ZA:1758:G:H2'	51:ZA:1759:G:C8	2.38	0.59
65:NB:136:PRO:HG2	65:NB:139:TRP:HB2	1.83	0.59
70:SB:23:ARG:NH2	77:ZB:46:ASN:O	2.34	0.59
2:B:258:HIS:NE2	48:WA:3880:C:O2	2.36	0.59
11:K:116:ARG:NH2	11:K:155:MET:O	2.36	0.59
13:M:157:LYS:O	13:M:162:ARG:NH1	2.36	0.59
48:WA:1972:A:H5'	86:b:37:SER:HB3	1.84	0.59
48:WA:2555:A:N6	48:WA:2767:A:OP2	2.35	0.59
61:JB:127:ARG:HD3	82:EC:104:ARG:HD3	1.83	0.59
4:D:83:LEU:HB3	4:D:88:VAL:HB	1.84	0.58
9:I:4:ARG:NH1	48:WA:1868:U:OP1	2.32	0.58
14:N:54:TYR:OH	14:N:73:PHE:O	2.21	0.58
17:Q:105:LEU:HD23	17:Q:138:LEU:HD23	1.84	0.58
48:WA:4994:G:H2'	48:WA:4995:G:H8	1.68	0.58
51:ZA:106:C:H2'	51:ZA:107:A:H8	1.68	0.58
51:ZA:688:U:OP1	59:HB:354:ARG:NH2	2.36	0.58
51:ZA:1587:G:H21	71:TB:77:LYS:HD3	1.67	0.58
51:ZA:1617:G:N1	51:ZA:1620:A:OP2	2.34	0.58
16:P:22:ASP:OD1	16:P:22:ASP:N	2.35	0.58
55:DB:257:PRO:HB2	84:GC:190:GLY:HA2	1.85	0.58
59:HB:268:LEU:O	59:HB:272:SER:CB	2.51	0.58
84:GC:107:ASP:OD2	84:GC:125:ARG:NH1	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:89:PRO:HD3	48:WA:1916:C:H4'	1.85	0.58
17:Q:108:ARG:NH2	48:WA:2901:C:OP1	2.34	0.58
21:U:15:ARG:NH2	48:WA:4675:U:OP2	2.36	0.58
48:WA:2601:G:N2	48:WA:2749:U:O4	2.35	0.58
48:WA:2737:G:H2'	48:WA:2738:G:H8	1.67	0.58
48:WA:3850:U:H2'	48:WA:3851:A:H8	1.67	0.58
51:ZA:183:G:O2'	51:ZA:184:G:O4'	2.21	0.58
57:FB:35:LEU:HD22	57:FB:117:ILE:HD13	1.85	0.58
57:FB:50:PRO:HG2	57:FB:90:VAL:HG22	1.85	0.58
61:JB:137:VAL:HG22	61:JB:157:ILE:HG12	1.85	0.58
68:QB:158:PHE:O	68:QB:166:ARG:NH1	2.36	0.58
88:HC:352:GLN:HB2	88:HC:393:PHE:HB2	1.85	0.58
3:C:204:ARG:NH1	3:C:205:ARG:O	2.36	0.58
5:E:185:ASN:ND2	5:E:274:LEU:O	2.34	0.58
6:F:146:LEU:O	6:F:150:ASN:ND2	2.37	0.58
9:I:152:LEU:HB3	9:I:165:ILE:HD12	1.85	0.58
19:S:108:ARG:NH1	48:WA:1839:A:OP1	2.37	0.58
23:W:110:LYS:HG3	23:W:121:VAL:HB	1.86	0.58
40:NA:2:VAL:N	40:NA:90:HIS:O	2.36	0.58
74:WB:52:ILE:HG22	74:WB:61:ILE:HG12	1.84	0.58
15:O:160:ARG:NH2	48:WA:1599:G:OP1	2.37	0.58
48:WA:1797:A:N3	49:XA:79:U:O2'	2.37	0.58
56:EB:66:MET:SD	56:EB:78:THR:OG1	2.62	0.58
88:HC:378:LYS:HD2	88:HC:391:PRO:HB3	1.86	0.58
2:B:11:HIS:NE2	48:WA:4460:C:OP1	2.36	0.58
7:G:96:GLN:O	48:WA:4126:G:N2	2.37	0.58
7:G:276:ARG:HG3	7:G:280:ASN:HB2	1.85	0.58
24:X:30:MET:HB3	24:X:101:PRO:HG2	1.84	0.58
48:WA:2409:G:OP2	48:WA:2409:G:N2	2.34	0.58
48:WA:3892:A:N6	48:WA:4572:G:O2'	2.36	0.58
56:EB:112:HIS:NE2	56:EB:237:SER:O	2.37	0.58
2:B:20:LYS:HD3	48:WA:4719:A:H4'	1.86	0.58
16:P:67:ILE:HD12	16:P:96:PRO:HD2	1.85	0.58
31:EA:43:LEU:O	31:EA:109:ARG:NH1	2.37	0.58
32:FA:29:ARG:NH1	48:WA:2524:G:OP1	2.36	0.58
48:WA:2320:G:N2	48:WA:2323:G:OP2	2.29	0.58
48:WA:2577:U:O2	48:WA:2760:G:N2	2.35	0.58
67:PB:56:LEU:HD23	67:PB:83:MET:HE3	1.84	0.58
73:VB:16:LYS:HG2	73:VB:23:ILE:HG22	1.85	0.58
84:GC:18:VAL:HA	84:GC:35:SER:HA	1.85	0.58
48:WA:1255:G:H1	48:WA:1262:G:H22	1.52	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:4090:C:H2'	48:WA:4091:G:H8	1.69	0.58
51:ZA:1353:A:OP1	52:AB:139:TYR:OH	2.16	0.58
13:M:96:ARG:NH2	13:M:104:GLU:OE1	2.37	0.57
48:WA:4596:U:H2'	48:WA:4597:G:H8	1.69	0.57
51:ZA:1271:C:OP1	83:FC:90:LYS:NZ	2.37	0.57
51:ZA:1472:C:H42	51:ZA:1476:A:N6	1.97	0.57
70:SB:34:LYS:HB3	70:SB:100:ALA:HA	1.86	0.57
88:HC:360:VAL:HA	88:HC:369:ALA:HA	1.86	0.57
2:B:317:LEU:HB2	2:B:372:SER:HB2	1.86	0.57
48:WA:1446:G:N2	48:WA:2113:U:O2	2.30	0.57
48:WA:2772:C:H2'	48:WA:2773:G:H8	1.68	0.57
51:ZA:486:A:H1'	51:ZA:513:G:H22	1.69	0.57
51:ZA:1513:C:H2'	51:ZA:1514:G:H8	1.69	0.57
74:WB:11:LEU:HD12	74:WB:74:VAL:HG22	1.85	0.57
48:WA:2411:U:H4'	48:WA:2430:A:H4'	1.87	0.57
51:ZA:1562:C:H2'	51:ZA:1563:G:H8	1.69	0.57
56:EB:151:ASP:HB3	56:EB:154:ILE:HG12	1.86	0.57
5:E:129:LEU:O	48:WA:965:A:N6	2.37	0.57
27:AA:99:ILE:O	27:AA:109:ARG:NH1	2.37	0.57
30:DA:109:LYS:NZ	30:DA:128:ARG:O	2.34	0.57
48:WA:2377:A:H2'	48:WA:2378:A:H8	1.68	0.57
51:ZA:4:C:H4'	54:CB:207:ALA:HB2	1.86	0.57
51:ZA:453:C:O2'	58:GB:92:ARG:O	2.22	0.57
51:ZA:617:G:H4'	75:XB:88:ASP:HB2	1.85	0.57
63:LB:13:GLN:HE22	63:LB:35:ARG:HG3	1.70	0.57
16:P:14:ARG:NH2	48:WA:2085:C:OP2	2.37	0.57
49:XA:92:C:H2'	49:XA:93:G:H8	1.68	0.57
54:CB:69:LEU:HG	54:CB:273:LEU:HD21	1.87	0.57
79:BC:34:ASP:HB2	79:BC:82:LYS:HD2	1.85	0.57
4:D:33:ARG:NE	49:XA:7:G:OP1	2.36	0.57
48:WA:4910:G:O2'	48:WA:4915:G:N2	2.38	0.57
51:ZA:608:C:O4'	82:EC:131:ASN:ND2	2.37	0.57
48:WA:158:A:N1	48:WA:276:C:O2'	2.35	0.57
67:PB:123:TYR:OH	70:SB:124:ARG:NH1	2.36	0.57
42:PA:98:ARG:NH2	48:WA:2264:G:OP2	2.37	0.57
48:WA:4:G:H2'	48:WA:5:A:H8	1.69	0.57
48:WA:2649:A:H62	48:WA:2688:G:H8	1.51	0.57
51:ZA:1565:C:OP2	71:TB:101:ARG:NH1	2.37	0.57
59:HB:245:LYS:NZ	59:HB:269:GLU:OE2	2.35	0.57
88:HC:281:ALA:HB2	88:HC:334:PRO:HB2	1.87	0.57
10:J:87:LEU:HD12	10:J:92:TYR:HA	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:72:HIS:N	48:WA:4588:G:OP1	2.38	0.57
14:N:74:ARG:N	48:WA:4587:U:OP1	2.36	0.57
19:S:87:LYS:NZ	48:WA:4302:U:OP1	2.35	0.57
21:U:13:LYS:NZ	21:U:59:ASP:OD1	2.37	0.57
56:EB:162:ILE:HG22	56:EB:169:ILE:HA	1.87	0.57
70:SB:98:VAL:HG11	70:SB:106:LYS:HG3	1.86	0.57
37:KA:48:LYS:NZ	48:WA:2793:C:OP1	2.32	0.57
40:NA:98:LYS:HD2	48:WA:4235:A:H4'	1.86	0.57
51:ZA:612:U:O2'	82:EC:84:LYS:NZ	2.38	0.57
51:ZA:1477:U:OP2	69:RB:3:ARG:NH2	2.38	0.57
64:MB:52:LEU:HD23	64:MB:76:LEU:HD11	1.87	0.57
1:A:6:ARG:HH12	1:A:199:VAL:H	1.53	0.56
9:I:77:VAL:HG23	9:I:82:LYS:HA	1.87	0.56
48:WA:4956:G:H2'	48:WA:4957:A:H8	1.70	0.56
65:NB:24:THR:O	65:NB:27:LYS:NZ	2.35	0.56
65:NB:33:VAL:HG21	65:NB:66:VAL:HG11	1.87	0.56
2:B:5:LYS:NZ	48:WA:4503:U:OP1	2.38	0.56
31:EA:54:LYS:HE3	48:WA:4750:U:H5''	1.86	0.56
38:LA:96:ARG:NH2	48:WA:4475:A:O2'	2.38	0.56
48:WA:2899:G:H2'	48:WA:2900:G:H8	1.70	0.56
51:ZA:1419:C:OP2	51:ZA:1420:G:N2	2.37	0.56
51:ZA:1432:U:H2'	51:ZA:1438:A:H8	1.69	0.56
69:RB:95:ILE:HD11	69:RB:118:GLN:HB2	1.86	0.56
4:D:88:VAL:HA	4:D:239:MET:HE3	1.86	0.56
11:K:48:PRO:HG3	33:GA:118:LYS:HE3	1.87	0.56
12:L:11:ARG:NH1	12:L:58:THR:O	2.37	0.56
21:U:41:SER:HG	48:WA:4509:A:HO2'	1.44	0.56
36:JA:35:LYS:NZ	48:WA:2695:G:OP1	2.30	0.56
44:SA:38:C:O2'	51:ZA:1058:A:OP1	2.23	0.56
51:ZA:527:C:O2'	61:JB:121:LYS:NZ	2.37	0.56
51:ZA:1531:A:OP1	71:TB:84:ARG:NH2	2.37	0.56
51:ZA:1858:G:OP2	66:OB:146:ARG:NH2	2.33	0.56
54:CB:68:ARG:NH1	54:CB:72:ASP:OD1	2.39	0.56
56:EB:191:ARG:HH11	56:EB:245:ARG:HH21	1.52	0.56
70:SB:89:ASP:OD1	70:SB:94:LYS:N	2.38	0.56
70:SB:124:ARG:HB2	70:SB:131:VAL:HG13	1.88	0.56
78:AC:87:ARG:NH2	78:AC:91:ALA:O	2.38	0.56
83:FC:126:CYS:HB2	83:FC:144:CYS:HB2	1.86	0.56
2:B:276:HIS:ND1	48:WA:4718:C:OP1	2.37	0.56
26:Z:125:LYS:HG2	26:Z:145:VAL:HB	1.87	0.56
46:UA:59:A:N7	46:UA:60:A:N6	2.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:62:A:N3	48:WA:77:U:O2'	2.30	0.56
51:ZA:1745:A:H62	51:ZA:1789:G:H21	1.53	0.56
59:HB:355:PRO:HG2	59:HB:358:ARG:HG2	1.86	0.56
64:MB:51:VAL:O	64:MB:108:CYS:HA	2.06	0.56
13:M:90:ASN:ND2	48:WA:3930:A:OP1	2.38	0.56
19:S:71:ALA:HB3	48:WA:4315:A:H4'	1.88	0.56
21:U:13:LYS:HD2	21:U:128:LEU:HD11	1.88	0.56
46:UA:74:C:H3'	46:UA:75:C:H5''	1.87	0.56
48:WA:369:G:N2	48:WA:372:A:OP2	2.31	0.56
48:WA:992:C:O2	48:WA:1076:G:N2	2.38	0.56
48:WA:1095:G:H2'	48:WA:1096:G:H8	1.70	0.56
48:WA:4274:G:OP2	48:WA:4274:G:N2	2.39	0.56
51:ZA:677:G:N2	51:ZA:1028:A:H62	2.00	0.56
51:ZA:1147:C:OP1	78:AC:6:ARG:NH1	2.36	0.56
51:ZA:1156:U:O4	54:CB:194:ARG:NH1	2.38	0.56
51:ZA:1270:G:O2'	51:ZA:1299:A:N6	2.34	0.56
51:ZA:1613:G:OP1	70:SB:88:LYS:NZ	2.38	0.56
56:EB:100:ARG:HB2	56:EB:114:ILE:HD13	1.87	0.56
71:TB:22:LEU:HG	71:TB:28:LEU:HD21	1.87	0.56
76:YB:82:ALA:O	76:YB:86:GLU:HB2	2.05	0.56
86:b:53:VAL:HG12	86:b:89:VAL:HG12	1.88	0.56
37:KA:13:LEU:HD22	48:WA:2409:G:H2'	1.87	0.56
10:J:146:ARG:NH1	49:XA:27:G:OP1	2.39	0.56
11:K:140:SER:OG	11:K:143:GLU:OE1	2.22	0.56
12:L:80:ALA:O	12:L:85:LYS:NZ	2.35	0.56
13:M:114:ARG:HE	13:M:137:PRO:HG3	1.70	0.56
13:M:116:LEU:HD22	13:M:135:ILE:HD11	1.87	0.56
48:WA:1213:C:H2'	48:WA:1214:G:H8	1.69	0.56
51:ZA:126:G:H1'	51:ZA:181:A:H1'	1.87	0.56
68:QB:79:GLU:OE1	68:QB:111:ARG:NH1	2.38	0.56
8:H:128:MET:HE2	8:H:134:CYS:HB2	1.88	0.56
25:Y:3:LYS:O	25:Y:6:LYS:NZ	2.39	0.56
48:WA:1804:A:H5''	48:WA:1805:G:H5'	1.87	0.56
48:WA:1886:C:H2'	48:WA:1887:G:H8	1.71	0.56
48:WA:3809:A:HO2'	51:ZA:1816:G:HO2'	1.54	0.56
59:HB:244:ALA:HB3	59:HB:262:SER:HB2	1.87	0.56
20:T:25:CYS:HB2	20:T:28:PRO:HG2	1.88	0.56
25:Y:100:VAL:HG13	25:Y:106:LEU:HB3	1.88	0.56
32:FA:6:THR:HG22	48:WA:2402:G:H21	1.71	0.56
48:WA:4637:A:H2	48:WA:4665:G:H21	1.52	0.56
51:ZA:928:G:H2'	51:ZA:929:G:C8	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:1351:G:H1	51:ZA:1360:U:H3	1.54	0.56
53:BB:82:ARG:NH2	53:BB:191:ASP:OD1	2.39	0.56
57:FB:49:LEU:HD11	68:QB:75:TYR:HB3	1.87	0.56
76:YB:34:THR:HG23	76:YB:69:THR:HG21	1.88	0.56
1:A:117:GLU:O	1:A:162:ASN:ND2	2.38	0.56
26:Z:132:ARG:NH1	48:WA:1470:C:OP1	2.39	0.56
27:AA:56:LYS:O	27:AA:60:ASN:ND2	2.38	0.56
48:WA:1285:G:N1	48:WA:2078:G:OP1	2.35	0.56
48:WA:3918:G:H2'	48:WA:3919:A:C8	2.41	0.56
51:ZA:544:G:H2'	51:ZA:545:A:H8	1.70	0.56
3:C:321:ASN:OD1	48:WA:1282:C:O2'	2.23	0.55
15:O:79:ASP:OD2	15:O:85:GLN:NE2	2.39	0.55
48:WA:1334:C:H2'	48:WA:1335:A:C8	2.42	0.55
48:WA:1852:A:N3	48:WA:2285:G:O2'	2.38	0.55
48:WA:3719:A:N3	48:WA:4180:A:O2'	2.36	0.55
48:WA:4241:A:H2'	48:WA:4242:G:H8	1.71	0.55
48:WA:4701:U:H1'	48:WA:4702:A:H5''	1.88	0.55
51:ZA:64:A:H2	51:ZA:83:A:H62	1.55	0.55
51:ZA:1668:U:OP1	68:QB:159:GLY:N	2.39	0.55
55:DB:69:GLU:O	55:DB:92:ARG:NH2	2.39	0.55
13:M:183:THR:HG22	13:M:188:ARG:HB3	1.88	0.55
48:WA:1962:A:H1'	86:b:63:LYS:HG2	1.87	0.55
48:WA:4276:A:H2'	48:WA:4277:G:C8	2.41	0.55
51:ZA:3:C:O2	61:JB:18:ARG:NH1	2.39	0.55
54:CB:94:ILE:HD12	54:CB:162:ILE:HD11	1.88	0.55
66:OB:101:GLY:HA3	66:OB:134:PRO:HG2	1.88	0.55
1:A:241:ARG:NH1	48:WA:3661:G:OP1	2.39	0.55
2:B:329:ASP:OD1	2:B:329:ASP:N	2.36	0.55
14:N:130:LYS:HB2	14:N:133:ARG:HG2	1.88	0.55
15:O:147:GLN:OE1	48:WA:423:G:N2	2.33	0.55
21:U:35:LYS:HB2	21:U:67:LYS:HG3	1.88	0.55
29:CA:64:ILE:HG23	29:CA:68:LEU:HD23	1.88	0.55
48:WA:1560:A:H2'	48:WA:1561:G:H8	1.70	0.55
48:WA:4539:C:H2'	48:WA:4540:G:C8	2.41	0.55
66:OB:45:THR:HG22	66:OB:52:THR:HA	1.88	0.55
39:MA:23:ARG:NH2	48:WA:3809:A:OP1	2.38	0.55
46:UA:21:A:H2'	46:UA:22:U:H5''	1.88	0.55
50:YA:67:U:H2'	50:YA:68:G:C8	2.41	0.55
51:ZA:874:G:N3	59:HB:352:GLN:NE2	2.45	0.55
2:B:224:LYS:NZ	48:WA:4669:C:OP1	2.35	0.55
16:P:2:GLY:N	48:WA:1900:C:OP1	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:NA:81:ARG:NH2	48:WA:4295:U:O2'	2.40	0.55
42:PA:6:GLN:HG3	42:PA:44:ILE:HD12	1.88	0.55
51:ZA:1128:C:H2'	51:ZA:1129:G:C8	2.41	0.55
52:AB:145:ILE:HG12	52:AB:159:ILE:HB	1.89	0.55
7:G:203:LYS:NZ	7:G:230:MET:O	2.39	0.55
35:IA:49:TRP:O	48:WA:1648:A:O2'	2.24	0.55
48:WA:153:G:H2'	48:WA:154:G:H8	1.71	0.55
48:WA:181:C:H2'	48:WA:182:G:C8	2.42	0.55
48:WA:308:G:OP2	48:WA:308:G:N2	2.26	0.55
48:WA:4110:G:H2'	48:WA:4111:G:H8	1.70	0.55
51:ZA:210:U:H2'	51:ZA:211:G:H8	1.71	0.55
48:WA:1826:G:H2'	48:WA:1827:A:C8	2.41	0.55
48:WA:4176:U:H2'	48:WA:4177:G:H8	1.70	0.55
51:ZA:379:C:O2	60:IB:5:ARG:NH1	2.40	0.55
51:ZA:527:C:H2'	51:ZA:528:A:H8	1.71	0.55
76:YB:82:ALA:O	76:YB:86:GLU:CB	2.55	0.55
12:L:35:ARG:NH2	18:R:108:GLN:OE1	2.36	0.55
45:TA:49:C:H2'	45:TA:50:A:H8	1.72	0.55
48:WA:2507:C:H4'	48:WA:2508:G:H5'	1.89	0.55
48:WA:4637:A:OP1	48:WA:4638:U:O2'	2.24	0.55
54:CB:60:TRP:O	54:CB:71:LYS:NZ	2.38	0.55
1:A:101:VAL:HG22	1:A:165:VAL:HG22	1.87	0.55
9:I:101:LYS:NZ	9:I:102:MET:O	2.37	0.55
13:M:15:GLN:NE2	48:WA:280:G:O6	2.40	0.55
24:X:109:LEU:HD22	24:X:115:ARG:HH12	1.72	0.55
48:WA:1183:U:H2'	48:WA:1184:G:H8	1.72	0.55
48:WA:1935:G:H2'	48:WA:1936:A:C8	2.42	0.55
48:WA:1960:A:O2'	48:WA:2027:A:N6	2.39	0.55
48:WA:3601:A:H2'	48:WA:3602:G:C8	2.42	0.55
51:ZA:941:C:H2'	51:ZA:942:G:H8	1.72	0.55
51:ZA:1240:A:N7	67:PB:100:LYS:HB2	2.21	0.55
51:ZA:1529:C:O2'	71:TB:87:VAL:O	2.25	0.55
51:ZA:1808:U:H2'	51:ZA:1809:A:H8	1.71	0.55
73:VB:15:ARG:NH1	73:VB:33:GLN:OE1	2.37	0.55
33:GA:79:LYS:HE3	48:WA:136:C:H41	1.70	0.55
48:WA:4423:C:H42	48:WA:4477:G:N2	2.05	0.55
51:ZA:1453:C:OP1	69:RB:48:ASN:ND2	2.40	0.55
51:ZA:1599:U:OP2	77:ZB:46:ASN:ND2	2.39	0.55
74:WB:18:GLU:HG2	74:WB:65:LEU:HD13	1.89	0.55
83:FC:141:CYS:HB3	83:FC:146:LEU:H	1.71	0.55
4:D:268:ARG:NH1	48:WA:1182:C:OP1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:56:THR:HG22	10:J:64:ARG:H	1.72	0.54
15:O:150:LYS:O	50:YA:13:G:O2'	2.25	0.54
21:U:15:ARG:HB2	48:WA:4620:G:H5''	1.89	0.54
22:V:8:PHE:HZ	22:V:49:ILE:HD12	1.72	0.54
43:RA:9:GLU:O	43:RA:65:GLN:NE2	2.40	0.54
48:WA:261:G:H2'	48:WA:262:G:C8	2.42	0.54
48:WA:419:A:N3	48:WA:1334:C:O2'	2.38	0.54
48:WA:1247:C:H2'	48:WA:1248:G:H8	1.72	0.54
84:GC:67:SER:H	84:GC:82:SER:HA	1.72	0.54
6:F:75:ARG:NE	48:WA:731:G:OP2	2.39	0.54
13:M:65:ARG:NH2	48:WA:2459:G:OP1	2.39	0.54
13:M:68:ARG:HA	13:M:98:LEU:HD21	1.89	0.54
48:WA:4718:C:H2'	48:WA:4719:A:H8	1.70	0.54
51:ZA:168:C:OP1	58:GB:131:ARG:NH1	2.40	0.54
57:FB:140:ASP:OD2	80:CC:44:ARG:NH1	2.40	0.54
60:IB:178:ARG:HE	60:IB:181:GLN:HG3	1.72	0.54
81:DC:5:GLN:O	81:DC:9:SER:OG	2.25	0.54
42:PA:107:ARG:NH2	48:WA:2265:A:OP1	2.40	0.54
48:WA:85:G:O2'	48:WA:97:G:O6	2.25	0.54
48:WA:3719:A:OP2	48:WA:3737:G:N2	2.39	0.54
48:WA:3811:G:N2	48:WA:3811:G:OP2	2.39	0.54
48:WA:4240:G:H2'	48:WA:4241:A:H8	1.72	0.54
48:WA:4305:C:H2'	48:WA:4307:G:H8	1.73	0.54
51:ZA:912:C:H3'	51:ZA:913:A:H3'	1.89	0.54
52:AB:85:ARG:HH21	52:AB:201:LEU:HD12	1.71	0.54
53:BB:40:ASN:OD1	53:BB:75:GLN:NE2	2.41	0.54
58:GB:39:ASP:HB3	58:GB:47:GLY:H	1.72	0.54
1:A:225:ILE:HD11	1:A:233:ARG:HG3	1.90	0.54
2:B:57:VAL:HG22	2:B:73:VAL:HG22	1.89	0.54
16:P:88:ASP:OD2	16:P:108:ARG:NH1	2.39	0.54
17:Q:160:GLU:OE1	17:Q:163:ARG:NH2	2.39	0.54
23:W:48:ARG:NH2	48:WA:2476:G:OP2	2.38	0.54
41:OA:38:THR:HA	41:OA:45:THR:HA	1.89	0.54
42:PA:38:PHE:O	42:PA:45:HIS:NE2	2.32	0.54
51:ZA:1401:A:H4'	72:UB:52:GLY:HA3	1.90	0.54
65:NB:5:HIS:HB3	65:NB:117:LEU:HD13	1.90	0.54
79:BC:74:THR:OG1	79:BC:77:CYS:SG	2.66	0.54
4:D:124:GLU:OE1	4:D:126:THR:OG1	2.24	0.54
16:P:151:HIS:ND1	16:P:164:LYS:O	2.40	0.54
48:WA:484:G:H5'	48:WA:485:U:H5''	1.88	0.54
49:XA:110:G:H2'	49:XA:111:C:C6	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:562:U:H2'	51:ZA:563:G:C8	2.43	0.54
51:ZA:948:C:H2'	51:ZA:949:G:H8	1.73	0.54
51:ZA:1179:G:N2	51:ZA:1182:A:OP2	2.40	0.54
76:YB:102:THR:O	76:YB:107:ARG:NH2	2.41	0.54
84:GC:294:ASP:OD2	84:GC:296:GLN:NE2	2.37	0.54
3:C:301:ALA:HB1	16:P:132:LYS:HE3	1.89	0.54
18:R:127:MET:HA	19:S:153:PRO:HD2	1.90	0.54
51:ZA:155:G:H2'	51:ZA:156:G:H8	1.72	0.54
51:ZA:571:U:O2'	76:YB:60:PHE:O	2.25	0.54
51:ZA:866:U:H2'	51:ZA:867:G:C8	2.43	0.54
59:HB:268:LEU:O	59:HB:272:SER:HB3	2.07	0.54
2:B:117:ARG:NH2	48:WA:4987:U:OP1	2.34	0.54
11:K:178:ALA:N	26:Z:134:GLU:OE2	2.41	0.54
46:UA:17:G:H21	46:UA:58:A:H5'	1.72	0.54
48:WA:126:C:H2'	48:WA:127:G:H8	1.71	0.54
48:WA:2000:A:H2'	48:WA:2001:A:C8	2.43	0.54
48:WA:2523:G:H2'	48:WA:2524:G:H8	1.72	0.54
51:ZA:626:G:N2	51:ZA:626:G:OP2	2.41	0.54
52:AB:77:ILE:HG12	52:AB:99:ILE:HB	1.89	0.54
60:IB:4:SER:OG	60:IB:6:ASP:OD2	2.24	0.54
4:D:17:GLN:O	48:WA:4267:U:N3	2.34	0.54
13:M:184:ILE:O	13:M:194:ARG:NH2	2.40	0.54
22:V:80:ARG:HH21	58:GB:131:ARG:HG2	1.73	0.54
28:BA:50:ASN:ND2	28:BA:75:SER:O	2.40	0.54
48:WA:4763:G:N2	48:WA:4768:C:O3'	2.41	0.54
51:ZA:913:A:N6	59:HB:357:SER:O	2.41	0.54
56:EB:175:PHE:HE2	56:EB:198:ARG:HD2	1.72	0.54
58:GB:55:GLY:H	58:GB:63:MET:HE2	1.73	0.54
60:IB:80:ASP:OD1	60:IB:81:VAL:N	2.40	0.54
3:C:195:LYS:HE3	48:WA:2335:G:H5''	1.89	0.54
30:DA:98:GLU:OE1	48:WA:2326:C:O2'	2.25	0.54
48:WA:132:G:O6	48:WA:137:G:N1	2.41	0.54
48:WA:1335:A:H2'	48:WA:1336:A:H8	1.73	0.54
48:WA:2481:G:H2'	48:WA:2482:G:C8	2.43	0.54
51:ZA:1276:A:H1'	62:KB:50:GLN:HE22	1.72	0.54
51:ZA:1654:G:OP1	71:TB:90:SER:OG	2.21	0.54
56:EB:137:PRO:HB2	56:EB:150:PRO:HD2	1.90	0.54
70:SB:20:ILE:HD11	70:SB:33:ILE:HG13	1.89	0.54
14:N:65:ASN:ND2	48:WA:4567:C:OP1	2.34	0.54
37:KA:5:LYS:NZ	48:WA:2409:G:N7	2.56	0.54
48:WA:261:G:H2'	48:WA:262:G:H8	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:1727:U:H2'	48:WA:1728:U:H6	1.73	0.54
48:WA:1826:G:H2'	48:WA:1827:A:H8	1.72	0.54
59:HB:307:LEU:HD22	59:HB:334:ALA:HB2	1.89	0.54
59:HB:383:ARG:NH1	74:WB:49:GLU:OE2	2.40	0.54
6:F:91:VAL:O	6:F:119:GLY:HA2	2.08	0.53
48:WA:2747:A:H2'	48:WA:2748:A:H8	1.73	0.53
48:WA:3807:U:H2'	48:WA:3808:G:H8	1.73	0.53
48:WA:4239:C:O2'	48:WA:4323:U:O2	2.26	0.53
78:AC:59:PHE:HB2	78:AC:62:TYR:HB2	1.90	0.53
2:B:254:ILE:HG21	2:B:262:VAL:HG22	1.90	0.53
18:R:174:THR:OG1	48:WA:4765:U:O2'	2.23	0.53
46:UA:30:G:N7	46:UA:41:G:N2	2.55	0.53
47:VA:21:C:OP1	51:ZA:1704:C:N4	2.42	0.53
48:WA:1505:A:H4'	48:WA:1506:G:H5'	1.90	0.53
48:WA:3725:A:H2'	48:WA:3726:A:H8	1.73	0.53
51:ZA:981:A:H2'	51:ZA:982:G:C8	2.44	0.53
58:GB:165:GLU:OE1	58:GB:167:LYS:NZ	2.39	0.53
84:GC:255:SER:OG	84:GC:257:LYS:NZ	2.41	0.53
5:E:48:ARG:O	5:E:67:ARG:NH1	2.42	0.53
17:Q:60:ARG:HH12	48:WA:2617:C:H5''	1.73	0.53
37:KA:23:ILE:HG23	37:KA:38:ASN:HB2	1.90	0.53
51:ZA:111:A:O2'	63:LB:69:ARG:NH1	2.42	0.53
51:ZA:547:G:H2'	51:ZA:549:C:H6	1.74	0.53
51:ZA:844:U:OP1	56:EB:240:ARG:NH1	2.42	0.53
51:ZA:1293:A:N6	51:ZA:1294:G:O6	2.41	0.53
57:FB:124:ASP:OD2	80:CC:47:LYS:NZ	2.40	0.53
76:YB:13:MET:SD	76:YB:22:GLN:NE2	2.79	0.53
17:Q:44:LEU:HD22	17:Q:49:LEU:HD12	1.90	0.53
18:R:95:ARG:NH2	48:WA:1953:G:O2'	2.41	0.53
48:WA:1074:G:N2	48:WA:1075:G:O6	2.41	0.53
48:WA:2460:C:O2	48:WA:3673:G:N2	2.41	0.53
48:WA:4962:G:H2'	48:WA:4963:G:H8	1.73	0.53
51:ZA:375:U:OP2	63:LB:59:LYS:NZ	2.41	0.53
51:ZA:1711:U:H2'	51:ZA:1712:A:C8	2.43	0.53
79:BC:54:VAL:HG13	79:BC:63:LEU:HB2	1.90	0.53
9:I:118:ALA:O	48:WA:1866:G:O2'	2.23	0.53
14:N:12:ARG:O	18:R:171:ARG:NH2	2.39	0.53
15:O:164:ARG:NH2	48:WA:1598:U:O2'	2.41	0.53
18:R:132:ILE:HG23	18:R:136:LYS:HB2	1.91	0.53
48:WA:2000:A:N3	48:WA:2021:C:O2'	2.40	0.53
48:WA:2380:G:N2	48:WA:2383:A:OP2	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:4763:G:H2'	48:WA:4764:A:H8	1.72	0.53
2:B:261:ARG:HB2	14:N:64:THR:HG21	1.90	0.53
5:E:275:ARG:NH2	48:WA:4886:G:N7	2.57	0.53
14:N:188:LYS:NZ	48:WA:4895:A:OP1	2.42	0.53
48:WA:4969:A:H2'	48:WA:4970:A:H8	1.74	0.53
51:ZA:980:A:H2'	51:ZA:981:A:C8	2.44	0.53
56:EB:252:ARG:NH1	61:JB:75:ASN:OD1	2.42	0.53
2:B:189:THR:HG23	2:B:192:GLU:H	1.73	0.53
3:C:323:ARG:HB2	48:WA:1283:G:H5'	1.91	0.53
7:G:126:ARG:NH2	48:WA:4164:C:O2	2.35	0.53
48:WA:2460:C:O2'	48:WA:3673:G:N3	2.39	0.53
48:WA:3666:G:H2'	48:WA:3667:G:H8	1.74	0.53
48:WA:4241:A:H2'	48:WA:4242:G:C8	2.44	0.53
50:YA:64:U:H2'	50:YA:65:A:H8	1.73	0.53
51:ZA:1864:U:H5'	78:AC:79:ILE:HD11	1.90	0.53
87:c:241:SER:HB3	87:c:244:SER:HB3	1.89	0.53
6:F:121:PHE:O	6:F:204:ASN:ND2	2.41	0.53
34:HA:29:ARG:HH22	48:WA:276:C:H2'	1.73	0.53
40:NA:8:ARG:NH2	48:WA:4234:U:O4	2.38	0.53
48:WA:115:C:O2'	48:WA:276:C:OP1	2.26	0.53
48:WA:425:U:H2'	48:WA:426:A:H8	1.73	0.53
48:WA:2297:C:H2'	48:WA:2298:G:H8	1.73	0.53
48:WA:4770:G:H2'	48:WA:4771:G:H8	1.74	0.53
51:ZA:172:U:N3	51:ZA:337:C:O2'	2.41	0.53
51:ZA:1086:G:OP2	78:AC:12:LYS:NZ	2.37	0.53
51:ZA:1215:C:O2'	51:ZA:1645:C:OP2	2.26	0.53
56:EB:251:GLU:OE2	56:EB:255:ARG:NH2	2.41	0.53
84:GC:166:VAL:HG22	84:GC:176:VAL:HG22	1.90	0.53
84:GC:257:LYS:HG2	84:GC:269:GLU:HG3	1.89	0.53
5:E:52:LEU:HG	5:E:53:VAL:HG23	1.90	0.53
7:G:156:ARG:NH2	7:G:245:ARG:O	2.42	0.53
48:WA:417:G:OP1	48:WA:2331:U:O2'	2.25	0.53
48:WA:1183:U:H2'	48:WA:1184:G:C8	2.44	0.53
48:WA:1565:A:H2'	48:WA:1566:A:C8	2.44	0.53
51:ZA:107:A:H2'	51:ZA:108:G:C8	2.44	0.53
51:ZA:642:U:H4'	51:ZA:644:G:H4'	1.91	0.53
51:ZA:1418:C:OP2	51:ZA:1420:G:N2	2.41	0.53
51:ZA:1598:G:OP1	77:ZB:80:ARG:NH1	2.42	0.53
2:B:77:THR:HG21	2:B:337:VAL:HG22	1.90	0.53
3:C:312:ARG:NH2	48:WA:2077:G:OP1	2.41	0.53
13:M:155:VAL:O	13:M:162:ARG:NH2	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:46:GLY:O	19:S:49:GLN:NE2	2.42	0.53
48:WA:417:G:H1'	50:YA:17:A:H61	1.74	0.53
51:ZA:1808:U:H2'	51:ZA:1809:A:C8	2.44	0.53
84:GC:77:PHE:HB3	84:GC:89:LEU:HD11	1.91	0.53
84:GC:237:ASN:ND2	84:GC:286:CYS:O	2.38	0.53
6:F:95:ARG:NH2	48:WA:1897:G:OP1	2.41	0.52
48:WA:246:G:H2'	48:WA:247:G:H8	1.73	0.52
48:WA:4994:G:H2'	48:WA:4995:G:C8	2.43	0.52
51:ZA:1203:G:H2'	51:ZA:1204:A:C8	2.44	0.52
51:ZA:1623:A:H5''	70:SB:133:GLY:HA3	1.91	0.52
56:EB:199:GLU:HB3	56:EB:207:VAL:HG13	1.89	0.52
86:b:35:VAL:HG23	86:b:40:MET:HG2	1.91	0.52
20:T:63:LEU:HG	20:T:72:VAL:HG22	1.90	0.52
40:NA:80:LYS:O	48:WA:4348:U:O2'	2.25	0.52
48:WA:2871:U:O2'	48:WA:2883:A:N7	2.35	0.52
51:ZA:183:G:O2'	51:ZA:184:G:O5'	2.26	0.52
51:ZA:847:A:OP1	56:EB:108:ARG:NH2	2.42	0.52
51:ZA:941:C:H2'	51:ZA:942:G:C8	2.44	0.52
54:CB:244:ILE:O	54:CB:247:THR:OG1	2.25	0.52
88:HC:241:PRO:HB3	88:HC:244:LYS:HD2	1.90	0.52
42:PA:90:LEU:HG	42:PA:111:ILE:HG23	1.91	0.52
51:ZA:1428:G:O6	68:QB:99:LYS:NZ	2.42	0.52
51:ZA:1781:A:H2'	51:ZA:1782:G:C8	2.44	0.52
86:b:69:LEU:HD21	86:b:76:GLU:HB2	1.90	0.52
7:G:194:ASN:ND2	48:WA:151:G:N7	2.57	0.52
13:M:49:ARG:HH12	48:WA:152:U:P	2.32	0.52
16:P:172:ARG:HD2	26:Z:57:GLY:HA3	1.92	0.52
17:Q:97:ARG:NH2	48:WA:2727:A:OP2	2.43	0.52
23:W:110:LYS:NZ	23:W:121:VAL:O	2.42	0.52
30:DA:29:VAL:HB	48:WA:1334:C:H5''	1.91	0.52
48:WA:3909:G:N2	85:IC:197:PHE:O	2.41	0.52
48:WA:4706:C:H2'	48:WA:4707:A:H8	1.75	0.52
64:MB:47:ALA:HA	64:MB:112:LYS:HB3	1.91	0.52
2:B:95:THR:HG22	48:WA:4912:A:H4'	1.92	0.52
10:J:112:HIS:HE1	10:J:125:ILE:HA	1.74	0.52
25:Y:51:ARG:HB2	25:Y:65:ARG:HE	1.75	0.52
29:CA:70:LYS:HE2	48:WA:2391:A:H5'	1.92	0.52
33:GA:89:ARG:NH1	50:YA:37:A:OP2	2.41	0.52
48:WA:2413:C:O2'	48:WA:2528:C:O2	2.23	0.52
68:QB:45:ALA:HB2	68:QB:101:GLY:HA3	1.92	0.52
74:WB:66:THR:HG21	74:WB:68:ARG:HH11	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:223:THR:HB	2:B:275:HIS:H	1.75	0.52
2:B:324:GLY:HA2	48:WA:5053:C:H4'	1.91	0.52
3:C:4:ALA:O	3:C:29:LYS:NZ	2.40	0.52
11:K:79:GLU:OE1	11:K:82:ARG:NH1	2.42	0.52
17:Q:39:GLN:NE2	48:WA:2713:G:OP2	2.42	0.52
21:U:21:PRO:HA	21:U:54:ALA:HA	1.90	0.52
29:CA:24:GLU:OE2	29:CA:87:ARG:NH1	2.42	0.52
48:WA:2523:G:H2'	48:WA:2524:G:C8	2.44	0.52
48:WA:3724:G:H2'	48:WA:3725:A:H8	1.73	0.52
48:WA:3918:G:H2'	48:WA:3919:A:H8	1.75	0.52
51:ZA:145:G:H2'	51:ZA:146:G:C8	2.44	0.52
51:ZA:1245:G:N2	72:UB:72:GLU:OE2	2.42	0.52
2:B:13:SER:HB2	48:WA:4624:A:H4'	1.92	0.52
6:F:241:ARG:NH2	48:WA:945:C:OP1	2.39	0.52
10:J:32:ARG:HD2	10:J:35:ARG:HH22	1.75	0.52
11:K:87:HIS:HB3	11:K:90:VAL:HG23	1.92	0.52
17:Q:88:ARG:O	48:WA:2727:A:N6	2.43	0.52
20:T:105:ASN:HD21	20:T:111:GLU:HB2	1.74	0.52
25:Y:17:ARG:NH2	25:Y:18:TYR:OH	2.42	0.52
40:NA:26:TYR:HB3	40:NA:67:VAL:HB	1.92	0.52
48:WA:436:C:H2'	48:WA:437:G:H8	1.75	0.52
48:WA:2742:U:O2'	48:WA:2744:G:N2	2.43	0.52
62:KB:20:VAL:HG23	62:KB:70:TYR:HA	1.92	0.52
86:b:28:PHE:HB2	86:b:89:VAL:HG22	1.91	0.52
17:Q:62:ARG:NH1	48:WA:4647:C:OP2	2.42	0.52
25:Y:52:LYS:O	25:Y:65:ARG:NH2	2.43	0.52
48:WA:1776:C:H2'	48:WA:1777:A:H8	1.74	0.52
48:WA:1897:G:O2'	48:WA:1909:A:N3	2.37	0.52
48:WA:4095:G:H22	48:WA:4117:G:H1	1.58	0.52
51:ZA:1288:U:H3	51:ZA:1311:C:N4	1.99	0.52
51:ZA:1630:A:H5''	70:SB:37:GLY:N	2.24	0.52
3:C:343:GLN:HG2	48:WA:725:C:H1'	1.92	0.52
35:IA:27:TYR:HA	35:IA:34:CYS:HA	1.90	0.52
43:RA:61:LYS:HB2	43:RA:72:GLU:HG2	1.92	0.52
48:WA:2469:U:H4'	48:WA:2470:U:H5'	1.92	0.52
48:WA:3612:A:H2'	48:WA:3613:A:H8	1.74	0.52
48:WA:3691:G:O2'	48:WA:3820:U:OP2	2.26	0.52
48:WA:4232:C:H1'	48:WA:4273:A:N1	2.25	0.52
50:YA:71:A:H4'	50:YA:72:A:H5'	1.92	0.52
51:ZA:1016:U:H5''	65:NB:14:SER:HB2	1.91	0.52
51:ZA:1617:G:O6	67:PB:43:ARG:NH1	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:1630:A:H5''	70:SB:37:GLY:H	1.75	0.52
72:UB:46:LYS:NZ	72:UB:97:ILE:O	2.42	0.52
12:L:39:ASP:HB2	12:L:47:ARG:HE	1.75	0.52
31:EA:43:LEU:HB2	31:EA:109:ARG:HH12	1.75	0.52
48:WA:1249:U:O2	48:WA:1268:G:N2	2.36	0.52
48:WA:1384:G:H2'	48:WA:1385:G:H8	1.74	0.52
51:ZA:432:G:H2'	51:ZA:433:A:C8	2.44	0.52
51:ZA:521:A:OP1	61:JB:45:ARG:NH1	2.38	0.52
51:ZA:639:C:H2'	51:ZA:640:A:C8	2.46	0.52
86:b:116:ILE:HG22	86:b:118:PRO:HD2	1.91	0.52
1:A:30:ARG:O	1:A:163:ARG:NH2	2.42	0.51
18:R:15:ARG:HH21	19:S:141:VAL:HG22	1.75	0.51
21:U:43:LYS:HD2	48:WA:4510:C:H5''	1.92	0.51
26:Z:75:LEU:HG	26:Z:113:GLY:HA2	1.92	0.51
42:PA:31:ASN:ND2	42:PA:40:TYR:O	2.43	0.51
48:WA:1210:C:H2'	48:WA:1211:G:H8	1.74	0.51
48:WA:1335:A:H2'	48:WA:1336:A:C8	2.45	0.51
48:WA:1657:C:O2	48:WA:4392:A:O2'	2.28	0.51
51:ZA:432:G:H2'	51:ZA:433:A:H8	1.75	0.51
51:ZA:1692:U:H2'	51:ZA:1693:G:C8	2.45	0.51
57:FB:71:ARG:NH2	57:FB:148:ASN:OD1	2.33	0.51
66:OB:93:LEU:HD23	66:OB:119:LEU:HD13	1.92	0.51
2:B:254:ILE:HG23	2:B:266:VAL:HG11	1.93	0.51
10:J:44:THR:O	10:J:78:LYS:NZ	2.36	0.51
14:N:163:LYS:NZ	48:WA:4911:A:OP1	2.42	0.51
40:NA:64:LYS:HD2	48:WA:4372:G:H5''	1.91	0.51
51:ZA:1004:U:H2'	51:ZA:1005:G:C8	2.45	0.51
55:DB:144:ARG:HG3	55:DB:213:VAL:HG22	1.93	0.51
56:EB:127:ARG:N	56:EB:140:VAL:O	2.34	0.51
56:EB:128:LYS:HG2	56:EB:140:VAL:HB	1.92	0.51
20:T:44:GLN:HA	20:T:56:LEU:HD21	1.92	0.51
48:WA:1507:C:H2'	48:WA:1508:G:H8	1.76	0.51
48:WA:1997:G:O2'	86:b:48:ARG:NH1	2.43	0.51
48:WA:2445:G:OP2	48:WA:2518:G:N2	2.37	0.51
51:ZA:56:G:OP1	76:YB:111:LYS:NZ	2.42	0.51
60:IB:27:TYR:HB3	60:IB:49:ARG:HH12	1.75	0.51
60:IB:64:ASN:O	60:IB:186:ASP:HA	2.10	0.51
60:IB:162:LEU:HD11	60:IB:191:GLU:HG2	1.91	0.51
70:SB:24:ARG:HH21	70:SB:28:PHE:HB3	1.75	0.51
5:E:144:ARG:NH2	5:E:194:GLN:O	2.44	0.51
13:M:35:ALA:HA	13:M:65:ARG:HG2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:11:ARG:HG3	48:WA:229:G:H5''	1.91	0.51
40:NA:4:VAL:O	40:NA:94:GLY:N	2.39	0.51
42:PA:103:HIS:ND1	42:PA:105:ASP:OD1	2.40	0.51
48:WA:3882:G:H2'	48:WA:3883:G:C8	2.45	0.51
51:ZA:17:C:H2'	51:ZA:18:C:C6	2.46	0.51
56:EB:44:LEU:HD21	56:EB:70:ILE:HG21	1.93	0.51
3:C:306:ARG:HG2	48:WA:2101:C:H3'	1.92	0.51
13:M:9:GLU:HB2	34:HA:44:ILE:HG13	1.93	0.51
13:M:138:PHE:HA	13:M:143:ARG:HH21	1.76	0.51
19:S:83:LYS:NZ	48:WA:4307:G:O5'	2.43	0.51
48:WA:1343:U:H2'	48:WA:1344:A:H8	1.75	0.51
48:WA:1734:C:H2'	48:WA:1735:G:C8	2.46	0.51
48:WA:2519:A:N3	48:WA:2541:C:O2'	2.43	0.51
48:WA:2892:C:H42	48:WA:3613:A:H61	1.59	0.51
48:WA:3734:A:H2'	48:WA:3735:A:C8	2.45	0.51
48:WA:3872:C:H2'	48:WA:3873:A:H8	1.76	0.51
51:ZA:317:C:OP2	58:GB:183:ARG:NH2	2.42	0.51
84:GC:223:GLU:HB2	84:GC:225:LYS:HE3	1.91	0.51
8:H:155:SER:OG	48:WA:4690:C:O2'	2.28	0.51
13:M:73:ARG:NH1	48:WA:32:G:OP1	2.44	0.51
35:IA:19:CYS:HB3	35:IA:22:CYS:SG	2.50	0.51
45:TA:22:G:H2'	45:TA:23:A:H8	1.75	0.51
48:WA:1264:G:H2'	48:WA:1265:A:C8	2.46	0.51
48:WA:1373:A:N1	50:YA:28:C:O2'	2.40	0.51
48:WA:2761:G:O2'	48:WA:2762:G:O4'	2.25	0.51
48:WA:3920:G:OP2	93:WA:5229:SPD:N10	2.42	0.51
51:ZA:110:U:H3	51:ZA:351:G:H1	1.59	0.51
51:ZA:583:A:H3'	51:ZA:584:A:H8	1.75	0.51
51:ZA:640:A:H2'	51:ZA:641:A:C8	2.45	0.51
51:ZA:1375:G:H2'	51:ZA:1376:A:C8	2.45	0.51
52:AB:158:ASP:OD1	73:VB:60:ARG:NH1	2.39	0.51
79:BC:42:LYS:NZ	79:BC:43:ILE:O	2.44	0.51
84:GC:45:LEU:HB3	84:GC:47:ARG:HD3	1.92	0.51
84:GC:132:TRP:CD1	84:GC:138:CYS:HA	2.46	0.51
25:Y:92:ASP:OD2	25:Y:94:THR:OG1	2.21	0.51
48:WA:1525:A:N3	48:WA:4391:C:O2'	2.42	0.51
48:WA:1944:A:H2'	48:WA:1945:A:C8	2.46	0.51
48:WA:2416:G:H2'	48:WA:2417:U:H6	1.75	0.51
48:WA:2485:G:H2'	48:WA:2486:A:H8	1.76	0.51
48:WA:4577:G:N3	48:WA:5070:G:O2'	2.43	0.51
48:WA:4969:A:H2'	48:WA:4970:A:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:520:A:O2'	51:ZA:825:A:N3	2.36	0.51
79:BC:67:THR:OG1	79:BC:70:LYS:O	2.28	0.51
3:C:328:LEU:HD13	6:F:186:MET:HE2	1.93	0.51
37:KA:24:PRO:HG2	37:KA:27:ILE:HB	1.93	0.51
48:WA:1507:C:H2'	48:WA:1508:G:C8	2.46	0.51
48:WA:2467:C:H1'	48:WA:3674:G:H1	1.75	0.51
48:WA:2498:G:H2'	48:WA:2499:C:C6	2.45	0.51
48:WA:4090:C:H2'	48:WA:4091:G:C8	2.46	0.51
51:ZA:1670:C:H2'	51:ZA:1671:G:H8	1.76	0.51
54:CB:65:LYS:HG3	54:CB:273:LEU:HD22	1.93	0.51
88:HC:249:PRO:HB3	88:HC:364:HIS:HB2	1.92	0.51
2:B:15:GLY:O	48:WA:4589:G:N2	2.34	0.51
6:F:136:GLU:OE1	49:XA:96:U:O2'	2.24	0.51
12:L:128:LYS:NZ	48:WA:4899:G:OP1	2.43	0.51
42:PA:19:LYS:HB2	48:WA:2339:C:H4'	1.93	0.51
51:ZA:143:U:H4'	51:ZA:144:U:H5'	1.93	0.51
51:ZA:311:C:H5''	51:ZA:312:G:H5''	1.93	0.51
51:ZA:436:G:OP2	51:ZA:471:G:O2'	2.28	0.51
51:ZA:1758:G:H2'	51:ZA:1759:G:H8	1.74	0.51
52:AB:51:LEU:HD23	69:RB:105:MET:HE1	1.92	0.51
66:OB:117:ARG:NE	78:AC:52:ASP:OD2	2.44	0.51
68:QB:35:SER:OG	68:QB:50:HIS:NE2	2.41	0.51
70:SB:36:VAL:HG21	70:SB:71:MET:HE3	1.92	0.51
1:A:152:SER:OG	48:WA:3663:G:N7	2.41	0.51
12:L:121:ARG:NH2	48:WA:4883:U:OP1	2.38	0.51
14:N:55:LEU:HD23	14:N:58:LEU:HD12	1.93	0.51
17:Q:90:PRO:HG2	17:Q:93:VAL:HB	1.93	0.51
51:ZA:1220:A:N3	51:ZA:1677:U:O2'	2.37	0.51
77:ZB:58:LEU:HD12	77:ZB:62:VAL:HG21	1.93	0.51
17:Q:59:SER:HA	48:WA:2636:C:H5'	1.92	0.50
19:S:91:VAL:HB	19:S:96:ILE:HD11	1.93	0.50
45:TA:42:G:H2'	45:TA:43:A:H8	1.76	0.50
48:WA:1565:A:N6	51:ZA:1028:A:N1	2.58	0.50
48:WA:4637:A:H8	48:WA:5050:A:H61	1.60	0.50
48:WA:5059:C:H2'	48:WA:5060:A:C8	2.46	0.50
51:ZA:554:A:H1'	51:ZA:555:A:H2'	1.92	0.50
54:CB:187:ARG:HE	54:CB:192:LEU:HD12	1.75	0.50
55:DB:210:VAL:O	55:DB:211:ARG:NH1	2.40	0.50
3:C:35:ASP:OD1	3:C:35:ASP:N	2.44	0.50
17:Q:121:HIS:ND1	48:WA:2666:G:OP2	2.44	0.50
27:AA:49:HIS:NE2	48:WA:1817:G:O6	2.39	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:418:A:H4'	48:WA:2313:C:H5'	1.93	0.50
48:WA:456:C:H2'	48:WA:457:G:C8	2.46	0.50
48:WA:1998:C:H5'	86:b:48:ARG:HH11	1.75	0.50
50:YA:84:A:H1'	50:YA:85:U:H4'	1.93	0.50
53:BB:144:LYS:HE2	53:BB:206:PRO:HB2	1.93	0.50
55:DB:114:ARG:HB2	62:KB:22:VAL:HG11	1.94	0.50
61:JB:83:ARG:HD3	61:JB:150:ARG:HD3	1.92	0.50
6:F:135:VAL:HG23	6:F:139:ILE:HD13	1.92	0.50
9:I:95:HIS:HB3	9:I:126:VAL:HG12	1.92	0.50
10:J:29:SER:OG	10:J:67:LYS:O	2.26	0.50
27:AA:11:ASN:ND2	48:WA:1671:A:OP1	2.44	0.50
46:UA:64:G:OP2	46:UA:64:G:N2	2.34	0.50
48:WA:1413:C:N4	48:WA:1414:G:O6	2.44	0.50
51:ZA:84:A:N3	51:ZA:150:A:O2'	2.43	0.50
51:ZA:155:G:H2'	51:ZA:156:G:C8	2.47	0.50
57:FB:59:LYS:HB2	57:FB:62:ARG:HB2	1.94	0.50
10:J:84:GLU:OE2	10:J:92:TYR:OH	2.28	0.50
28:BA:17:ARG:HD2	28:BA:104:ILE:HA	1.93	0.50
51:ZA:5:U:H2'	51:ZA:6:G:H8	1.76	0.50
51:ZA:1362:U:H5''	51:ZA:1363:C:H5	1.76	0.50
76:YB:20:ARG:NH2	76:YB:22:GLN:OE1	2.44	0.50
1:A:132:ASN:ND2	48:WA:3685:C:OP1	2.43	0.50
1:A:247:ARG:HB3	51:ZA:1069:U:H4'	1.94	0.50
2:B:79:VAL:HB	2:B:331:VAL:HG23	1.93	0.50
44:SA:51:C:H2'	44:SA:52:G:H8	1.77	0.50
48:WA:1317:C:N4	48:WA:1318:G:O6	2.44	0.50
48:WA:1560:A:H2'	48:WA:1561:G:C8	2.47	0.50
48:WA:3850:U:H2'	48:WA:3851:A:C8	2.46	0.50
48:WA:4080:C:O2'	48:WA:4174:A:N6	2.44	0.50
51:ZA:1146:C:O2'	51:ZA:1150:A:N1	2.42	0.50
51:ZA:1541:G:H4'	71:TB:15:VAL:HG11	1.93	0.50
51:ZA:1711:U:H2'	51:ZA:1712:A:H8	1.77	0.50
48:WA:4323:U:H2'	48:WA:4324:G:C8	2.47	0.50
51:ZA:553:U:O2'	51:ZA:554:A:O5'	2.26	0.50
51:ZA:1018:U:O2'	65:NB:86:GLU:OE2	2.29	0.50
51:ZA:1048:G:H21	51:ZA:1070:A:H62	1.58	0.50
51:ZA:1245:G:O2'	51:ZA:1492:U:OP1	2.30	0.50
51:ZA:1332:A:O2'	55:DB:183:GLN:O	2.30	0.50
63:LB:59:LYS:HD3	63:LB:134:LEU:HB3	1.94	0.50
88:HC:279:THR:HB	88:HC:286:THR:HG23	1.92	0.50
12:L:59:ASP:OD1	12:L:59:ASP:N	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:172:ARG:NH1	48:WA:62:A:OP1	2.44	0.50
33:GA:27:GLU:OE2	33:GA:46:LYS:NZ	2.42	0.50
36:JA:12:LEU:HD21	36:JA:16:ARG:HH21	1.76	0.50
48:WA:4240:G:H2'	48:WA:4241:A:C8	2.45	0.50
48:WA:4406:U:O2'	48:WA:4408:U:O4	2.29	0.50
51:ZA:1406:G:H2'	51:ZA:1407:U:C6	2.47	0.50
79:BC:23:ARG:NH2	79:BC:29:ASN:OD1	2.43	0.50
10:J:27:GLY:HA2	10:J:68:ILE:HG23	1.93	0.50
26:Z:103:VAL:HG12	26:Z:108:TYR:HB2	1.93	0.50
32:FA:66:ARG:NH2	48:WA:2519:A:O2'	2.44	0.50
48:WA:1593:U:H3	48:WA:4557:U:H5''	1.77	0.50
48:WA:1944:A:OP2	48:WA:2042:A:N6	2.39	0.50
61:JB:59:GLU:O	61:JB:62:THR:OG1	2.30	0.50
3:C:56:GLU:OE1	3:C:106:LYS:NZ	2.44	0.50
48:WA:3612:A:H2'	48:WA:3613:A:C8	2.47	0.50
48:WA:3756:G:O6	48:WA:3773:C:N4	2.45	0.50
48:WA:4262:U:H2'	48:WA:4263:C:H6	1.75	0.50
48:WA:4977:G:O2'	48:WA:4979:A:N6	2.42	0.50
51:ZA:1605:G:H2'	51:ZA:1606:G:C4	2.47	0.50
70:SB:105:ASN:OD1	70:SB:108:ARG:NH2	2.41	0.50
74:WB:80:ASP:OD1	74:WB:124:LYS:NZ	2.45	0.50
6:F:33:ARG:NH1	48:WA:1274:C:OP2	2.45	0.49
30:DA:44:ARG:NH2	30:DA:52:GLN:OE1	2.45	0.49
43:RA:117:ARG:HG3	43:RA:125:LEU:HD11	1.94	0.49
45:TA:9:A:O2'	45:TA:10:G:N7	2.37	0.49
48:WA:4190:U:H2'	48:WA:4191:U:C6	2.47	0.49
50:YA:9:A:H2'	50:YA:10:G:H8	1.77	0.49
51:ZA:582:U:OP1	61:JB:162:ARG:NH1	2.45	0.49
51:ZA:1558:C:H2'	51:ZA:1559:C:C6	2.47	0.49
52:AB:176:TRP:NE1	52:AB:197:VAL:O	2.42	0.49
78:AC:44:ILE:HG23	78:AC:45:VAL:HG23	1.94	0.49
6:F:56:TYR:OH	6:F:188:ASP:OD1	2.28	0.49
23:W:139:ARG:HH12	48:WA:2535:C:H5''	1.76	0.49
25:Y:47:ASP:N	25:Y:69:LYS:O	2.43	0.49
25:Y:50:PRO:HD3	25:Y:68:ILE:HG13	1.93	0.49
28:BA:79:ILE:HG12	28:BA:90:ARG:HG2	1.94	0.49
45:TA:21:A:N1	45:TA:46:G:O2'	2.43	0.49
48:WA:2311:G:O2'	50:YA:18:U:O2	2.30	0.49
52:AB:190:SER:OG	52:AB:192:GLU:OE1	2.29	0.49
54:CB:192:LEU:HB3	54:CB:227:ARG:HB3	1.94	0.49
76:YB:27:VAL:HG12	76:YB:29:HIS:HD2	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:b:128:THR:OG1	86:b:129:GLY:N	2.40	0.49
1:A:236:GLY:N	48:WA:3689:A:O2'	2.45	0.49
12:L:41:PRO:HG3	12:L:73:VAL:HG12	1.95	0.49
30:DA:100:ALA:O	30:DA:108:ARG:NH2	2.45	0.49
37:KA:45:ARG:HH21	48:WA:2798:G:H5'	1.77	0.49
51:ZA:931:C:H2'	51:ZA:932:G:C8	2.47	0.49
54:CB:104:ASP:HB3	54:CB:130:ILE:HG13	1.93	0.49
59:HB:289:ILE:HD12	59:HB:417:LYS:HG2	1.93	0.49
86:b:52:VAL:HB	86:b:90:PHE:HB2	1.93	0.49
4:D:136:ASP:OD1	4:D:136:ASP:N	2.45	0.49
15:O:69:HIS:NE2	15:O:139:ASP:O	2.36	0.49
27:AA:28:ARG:HB3	48:WA:1807:A:C4	2.47	0.49
46:UA:69:A:H2'	46:UA:70:A:H8	1.77	0.49
49:XA:57:C:H2'	49:XA:58:A:H8	1.78	0.49
51:ZA:128:U:H3'	51:ZA:129:C:H6	1.76	0.49
51:ZA:1023:A:OP2	65:NB:124:ARG:NH1	2.39	0.49
51:ZA:1101:U:H2'	51:ZA:1102:G:C8	2.48	0.49
51:ZA:1139:C:H42	51:ZA:1149:A:H62	1.60	0.49
51:ZA:1277:C:OP1	62:KB:51:SER:OG	2.28	0.49
51:ZA:1615:U:O4	67:PB:40:ARG:NH2	2.45	0.49
52:AB:89:LYS:NZ	69:RB:83:ASN:OD1	2.43	0.49
59:HB:356:ARG:HD3	59:HB:359:THR:HG21	1.93	0.49
20:T:90:TYR:O	20:T:94:ASN:ND2	2.37	0.49
48:WA:3895:C:H2'	48:WA:3896:A:H8	1.77	0.49
51:ZA:822:U:H3	51:ZA:826:A:H62	1.61	0.49
56:EB:11:ARG:HA	56:EB:28:ALA:HB2	1.95	0.49
71:TB:41:LYS:NZ	71:TB:83:GLN:OE1	2.44	0.49
18:R:98:ARG:NH2	48:WA:750:G:O6	2.45	0.49
25:Y:25:ILE:HA	25:Y:43:VAL:HG12	1.93	0.49
26:Z:65:ARG:NH2	48:WA:86:U:HO2'	2.10	0.49
48:WA:2024:C:H5''	86:b:83:ARG:HD2	1.92	0.49
51:ZA:639:C:H2'	51:ZA:640:A:H8	1.77	0.49
51:ZA:1568:C:OP1	71:TB:96:SER:OG	2.28	0.49
51:ZA:1650:A:H5''	68:QB:165:ALA:HB2	1.95	0.49
51:ZA:1670:C:H2'	51:ZA:1671:G:C8	2.47	0.49
54:CB:72:ASP:OD2	54:CB:272:HIS:NE2	2.43	0.49
57:FB:122:ARG:HE	80:CC:59:LEU:HD21	1.77	0.49
58:GB:7:PHE:HB3	58:GB:10:THR:HG22	1.95	0.49
60:IB:81:VAL:HG22	60:IB:102:VAL:HG12	1.95	0.49
4:D:91:GLY:O	4:D:94:ASN:ND2	2.46	0.49
8:H:92:MET:HG2	8:H:181:VAL:HG22	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:64:VAL:HG12	48:WA:71:C:H4'	1.95	0.49
22:V:82:ILE:HG12	58:GB:131:ARG:HB2	1.94	0.49
35:IA:3:LYS:HB3	48:WA:3644:A:C4	2.48	0.49
35:IA:13:ASN:ND2	48:WA:1620:G:OP1	2.40	0.49
48:WA:1505:A:H1'	48:WA:1506:G:C8	2.48	0.49
48:WA:1751:A:H2'	48:WA:1752:G:C8	2.48	0.49
48:WA:1999:U:O2'	86:b:44:ARG:NH2	2.46	0.49
51:ZA:106:C:H2'	51:ZA:107:A:C8	2.46	0.49
51:ZA:1165:G:OP2	51:ZA:1165:G:N2	2.36	0.49
58:GB:48:TYR:OH	58:GB:119:LYS:O	2.27	0.49
61:JB:59:GLU:OE2	61:JB:69:ARG:NH2	2.45	0.49
64:MB:33:ARG:HD3	64:MB:91:LEU:HD22	1.94	0.49
2:B:122:TRP:CH2	2:B:127:LYS:HG2	2.48	0.49
2:B:252:ALA:HB1	48:WA:4526:G:N3	2.28	0.49
7:G:126:ARG:NE	48:WA:4078:G:OP1	2.36	0.49
14:N:94:ARG:HD2	48:WA:1311:C:H5''	1.94	0.49
20:T:66:SER:HB3	20:T:69:LYS:HB3	1.94	0.49
25:Y:112:ARG:NH2	48:WA:2574:C:O2'	2.46	0.49
37:KA:20:ASN:O	37:KA:41:ARG:NH1	2.45	0.49
39:MA:15:ARG:NH2	51:ZA:1183:A:OP1	2.46	0.49
41:OA:30:GLU:HA	41:OA:33:GLN:HG2	1.94	0.49
46:UA:69:A:H2'	46:UA:70:A:C8	2.47	0.49
48:WA:1639:A:OP1	48:WA:1642:C:N4	2.37	0.49
49:XA:28:C:O2'	49:XA:54:A:N1	2.46	0.49
51:ZA:1345:G:OP1	51:ZA:1688:C:O2'	2.31	0.49
55:DB:50:VAL:HG21	81:DC:34:TYR:HB3	1.94	0.49
58:GB:198:ARG:O	58:GB:202:ASN:ND2	2.33	0.49
78:AC:46:GLU:HG3	78:AC:48:ALA:H	1.78	0.49
10:J:136:ARG:HG3	10:J:157:ILE:HD11	1.94	0.49
13:M:44:ARG:NH1	48:WA:280:G:OP2	2.40	0.49
44:SA:22:A:H2'	44:SA:23:G:C8	2.48	0.49
48:WA:275:C:H2'	48:WA:276:C:C6	2.48	0.49
48:WA:2418:G:N2	48:WA:2428:U:O4	2.46	0.49
48:WA:4116:C:H2'	48:WA:4117:G:C8	2.48	0.49
48:WA:4652:G:H4'	48:WA:5010:C:H4'	1.95	0.49
48:WA:5008:U:H4'	48:WA:5009:A:H5'	1.93	0.49
51:ZA:65:C:H4'	58:GB:172:LYS:HD3	1.94	0.49
51:ZA:397:G:OP1	63:LB:106:HIS:NE2	2.46	0.49
62:KB:11:ILE:HD11	62:KB:45:VAL:HG22	1.94	0.49
5:E:67:ARG:NE	48:WA:1076:G:OP1	2.46	0.49
11:K:27:ASN:HB3	50:YA:29:G:H5''	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:50:ASN:ND2	48:WA:4459:U:OP1	2.45	0.49
25:Y:135:ARG:O	48:WA:4124:G:N2	2.42	0.49
28:BA:39:ARG:NH2	28:BA:63:TYR:OH	2.46	0.49
48:WA:164:G:H2'	48:WA:165:A:H8	1.78	0.49
48:WA:739:C:O2'	48:WA:742:G:OP1	2.29	0.49
48:WA:3934:U:H2'	48:WA:3935:G:H8	1.77	0.49
48:WA:4194:A:H2'	48:WA:4195:C:H6	1.78	0.49
51:ZA:1115:U:O2	51:ZA:1116:C:O2'	2.31	0.49
51:ZA:1854:U:OP2	66:OB:147:ARG:NH2	2.45	0.49
64:MB:26:LEU:HD22	64:MB:33:ARG:HH22	1.77	0.49
84:GC:91:ASP:OD2	84:GC:93:THR:OG1	2.26	0.49
88:HC:442:ASP:OD1	88:HC:443:LYS:N	2.44	0.49
20:T:56:LEU:HD13	20:T:63:LEU:HD13	1.93	0.48
30:DA:64:LYS:NZ	48:WA:2081:G:OP2	2.36	0.48
43:RA:37:LEU:HD12	43:RA:42:VAL:HB	1.95	0.48
48:WA:3601:A:H2'	48:WA:3602:G:H8	1.78	0.48
48:WA:4770:G:O2'	48:WA:4875:G:O6	2.30	0.48
51:ZA:1010:G:H2'	51:ZA:1011:A:H8	1.77	0.48
57:FB:30:ILE:HB	57:FB:36:GLN:HG2	1.94	0.48
58:GB:2:LYS:HD3	58:GB:15:LEU:HD21	1.94	0.48
59:HB:304:VAL:HG22	59:HB:334:ALA:HB1	1.95	0.48
3:C:192:GLY:O	3:C:195:LYS:NZ	2.45	0.48
5:E:96:THR:HG22	5:E:109:VAL:HG22	1.94	0.48
18:R:112:ASP:OD1	18:R:116:ARG:NH1	2.44	0.48
25:Y:67:LYS:NZ	48:WA:2575:A:OP1	2.37	0.48
42:PA:94:ARG:HG3	42:PA:107:ARG:HD2	1.94	0.48
48:WA:1176:G:H2'	48:WA:1177:G:C8	2.48	0.48
48:WA:1908:U:H2'	48:WA:1909:A:H8	1.78	0.48
51:ZA:582:U:H2'	51:ZA:583:A:H5''	1.95	0.48
51:ZA:1523:C:H3'	70:SB:141:ARG:HH21	1.78	0.48
51:ZA:1693:G:N2	51:ZA:1834:A:H8	2.11	0.48
52:AB:164:ASN:O	52:AB:170:SER:OG	2.22	0.48
63:LB:38:LYS:NZ	63:LB:61:PRO:O	2.46	0.48
83:FC:100:LEU:HD23	83:FC:103:LEU:HD23	1.96	0.48
84:GC:4:GLN:HG3	84:GC:314:ILE:HG22	1.96	0.48
19:S:70:HIS:N	48:WA:4316:C:OP1	2.46	0.48
48:WA:711:G:H2'	48:WA:712:A:H8	1.78	0.48
51:ZA:952:G:H2'	51:ZA:953:C:C6	2.48	0.48
52:AB:24:HIS:HB3	52:AB:51:LEU:HD21	1.95	0.48
61:JB:42:GLU:OE1	61:JB:45:ARG:NH2	2.45	0.48
88:HC:282:PRO:HG2	88:HC:324:ASN:HA	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
88:HC:287:THR:OG1	88:HC:288:GLU:N	2.46	0.48
1:A:21:LYS:HG2	48:WA:1543:C:H5''	1.95	0.48
14:N:42:ASN:HD22	14:N:125:LYS:HD3	1.79	0.48
14:N:46:ASN:O	14:N:50:ASN:ND2	2.43	0.48
48:WA:2560:C:H2'	48:WA:2561:G:C8	2.49	0.48
51:ZA:5:U:H2'	51:ZA:6:G:C8	2.48	0.48
51:ZA:333:G:H2'	51:ZA:334:C:O4'	2.14	0.48
51:ZA:498:C:H2'	51:ZA:499:G:C8	2.49	0.48
59:HB:258:GLU:N	59:HB:258:GLU:OE1	2.47	0.48
32:FA:24:ARG:NH2	48:WA:2615:C:OP1	2.46	0.48
48:WA:1671:A:N3	48:WA:1854:U:O2'	2.37	0.48
48:WA:1808:G:H2'	48:WA:1809:C:H6	1.79	0.48
48:WA:2575:A:N7	48:WA:2763:U:O4	2.46	0.48
51:ZA:1309:C:H5'	83:FC:105:TYR:CE1	2.49	0.48
51:ZA:1545:A:OP1	68:QB:100:GLY:N	2.43	0.48
6:F:178:LEU:HB3	6:F:183:ILE:HB	1.95	0.48
8:H:89:ARG:NH1	8:H:147:GLU:OE2	2.46	0.48
16:P:2:GLY:N	48:WA:2074:C:OP1	2.47	0.48
16:P:178:ARG:N	26:Z:51:GLY:HA2	2.29	0.48
24:X:45:ARG:NH2	48:WA:199:G:OP2	2.46	0.48
29:CA:118:GLN:OE1	48:WA:5057:G:N2	2.46	0.48
48:WA:711:G:H2'	48:WA:712:A:C8	2.49	0.48
48:WA:3879:A:O2'	48:WA:4402:G:N2	2.47	0.48
48:WA:4529:G:OP2	48:WA:4529:G:N2	2.46	0.48
48:WA:4644:U:H2'	48:WA:4645:G:H8	1.78	0.48
51:ZA:1271:C:N4	51:ZA:1512:C:N3	2.61	0.48
51:ZA:1656:G:O6	51:ZA:1668:U:O4	2.31	0.48
64:MB:32:ALA:HB1	64:MB:37:GLU:HB3	1.96	0.48
68:QB:126:VAL:HG12	68:QB:127:ASP:H	1.79	0.48
74:WB:11:LEU:HA	74:WB:14:ILE:HG12	1.95	0.48
75:XB:90:CYS:HB3	75:XB:130:LEU:HD11	1.95	0.48
86:b:60:MET:N	86:b:60:MET:SD	2.86	0.48
2:B:108:GLU:OE2	2:B:138:GLN:NE2	2.44	0.48
48:WA:287:U:H2'	48:WA:288:G:C8	2.48	0.48
48:WA:1874:G:O2'	48:WA:4221:A:N3	2.47	0.48
51:ZA:1829:G:H1'	51:ZA:1850:A:H2	1.79	0.48
53:BB:179:ASN:HB3	53:BB:183:GLU:HB2	1.95	0.48
58:GB:58:LYS:HA	58:GB:107:SER:HB2	1.95	0.48
1:A:118:GLU:OE2	48:WA:3664:A:O2'	2.31	0.48
6:F:82:VAL:HG22	18:R:62:VAL:HA	1.95	0.48
11:K:18:TRP:NE1	48:WA:1518:G:O2'	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:31:ARG:NH1	48:WA:337:U:OP1	2.42	0.48
15:O:111:ARG:NH2	48:WA:2364:U:OP1	2.46	0.48
33:GA:76:LYS:O	48:WA:136:C:N4	2.47	0.48
42:PA:28:GLU:HB2	42:PA:31:ASN:HB2	1.94	0.48
42:PA:39:ARG:NH1	48:WA:2268:C:O2'	2.46	0.48
46:UA:47:U:O2'	46:UA:50:U:OP1	2.25	0.48
48:WA:197:A:N1	48:WA:225:G:O2'	2.39	0.48
48:WA:655:C:H2'	48:WA:656:C:H6	1.79	0.48
48:WA:1095:G:H2'	48:WA:1096:G:C8	2.48	0.48
48:WA:2335:G:OP1	50:YA:20:A:O2'	2.32	0.48
48:WA:4350:A:O2'	48:WA:4352:C:OP2	2.29	0.48
51:ZA:373:G:OP1	63:LB:137:THR:OG1	2.28	0.48
51:ZA:1203:G:H2'	51:ZA:1204:A:H8	1.76	0.48
51:ZA:1485:U:OP1	55:DB:189:LYS:NZ	2.46	0.48
51:ZA:1536:G:H2'	51:ZA:1537:A:C8	2.49	0.48
80:CC:12:ALA:HB1	80:CC:32:VAL:HB	1.96	0.48
4:D:156:GLY:HA2	4:D:181:PRO:HD3	1.95	0.48
14:N:12:ARG:HD3	14:N:37:ARG:HH11	1.78	0.48
35:IA:54:LYS:O	35:IA:58:THR:HB	2.14	0.48
42:PA:12:ASN:OD1	42:PA:19:LYS:NZ	2.46	0.48
48:WA:1496:U:H2'	48:WA:1497:G:C8	2.49	0.48
48:WA:3612:A:O2'	60:IB:92:ARG:NH2	2.47	0.48
48:WA:4324:G:N2	48:WA:4327:A:OP2	2.40	0.48
48:WA:4706:C:H2'	48:WA:4707:A:C8	2.49	0.48
48:WA:4725:A:H2'	48:WA:4726:A:C8	2.49	0.48
51:ZA:544:G:H2'	51:ZA:545:A:C8	2.49	0.48
51:ZA:1712:A:H2'	51:ZA:1713:C:C6	2.49	0.48
53:BB:136:ARG:HB2	53:BB:218:LEU:HD11	1.96	0.48
64:MB:97:GLU:O	64:MB:101:ARG:NH2	2.45	0.48
71:TB:7:LYS:HA	71:TB:11:GLN:HE22	1.78	0.48
1:A:67:TYR:OH	48:WA:4089:G:N7	2.43	0.48
2:B:124:LYS:NZ	48:WA:5065:G:O6	2.45	0.48
5:E:71:TYR:HA	5:E:74:LYS:HE2	1.96	0.48
7:G:97:ASP:OD1	7:G:98:ILE:N	2.45	0.48
11:K:60:ARG:NH2	11:K:67:HIS:O	2.46	0.48
37:KA:3:SER:O	48:WA:2783:G:O2'	2.32	0.48
48:WA:2494:C:H2'	48:WA:2495:G:C8	2.49	0.48
48:WA:2557:G:H2'	48:WA:2558:G:H8	1.78	0.48
48:WA:2610:G:H2'	48:WA:2611:G:H8	1.78	0.48
48:WA:4275:A:H2'	48:WA:4276:A:C8	2.49	0.48
48:WA:4608:G:O2'	88:HC:430:ARG:NH2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:564:A:H2'	51:ZA:565:G:O4'	2.14	0.48
84:GC:226:HIS:NE2	84:GC:229:THR:OG1	2.45	0.48
1:A:243:THR:N	48:WA:3747:U:O2'	2.43	0.47
9:I:42:LYS:HB2	9:I:45:GLU:HG3	1.96	0.47
10:J:40:LEU:HD12	10:J:70:VAL:HG22	1.96	0.47
23:W:65:ALA:HB2	33:GA:69:LEU:HD11	1.96	0.47
43:RA:46:ILE:HD11	43:RA:62:LEU:HD21	1.96	0.47
51:ZA:1797:U:H2'	51:ZA:1798:C:C6	2.49	0.47
51:ZA:1854:U:H2'	51:ZA:1855:G:H8	1.79	0.47
69:RB:32:LYS:HD2	69:RB:47:ARG:HH11	1.78	0.47
76:YB:103:SER:HB3	76:YB:106:GLN:HG2	1.96	0.47
5:E:160:HIS:HB3	5:E:163:LYS:HD2	1.96	0.47
7:G:90:LYS:NZ	48:WA:4128:C:OP1	2.47	0.47
26:Z:2:PRO:HG3	48:WA:1511:C:H5''	1.96	0.47
36:JA:24:LYS:NZ	48:WA:2698:A:N1	2.44	0.47
40:NA:52:THR:HG22	48:WA:43:U:H4'	1.96	0.47
48:WA:164:G:H2'	48:WA:165:A:C8	2.49	0.47
48:WA:470:A:H62	48:WA:685:G:H21	1.62	0.47
48:WA:692:C:H2'	48:WA:693:A:C8	2.50	0.47
48:WA:2081:G:H2'	48:WA:2082:U:C6	2.49	0.47
48:WA:3719:A:H2'	48:WA:3720:A:C8	2.49	0.47
48:WA:4588:G:O6	48:WA:4719:A:N6	2.47	0.47
51:ZA:442:C:N4	51:ZA:449:A:H62	2.11	0.47
51:ZA:1358:U:OP2	54:CB:123:ARG:NH2	2.48	0.47
64:MB:49:LEU:HB3	64:MB:111:VAL:HG13	1.95	0.47
11:K:138:ASP:OD1	33:GA:117:ARG:NH2	2.43	0.47
28:BA:38:ILE:HG21	28:BA:63:TYR:HB3	1.95	0.47
35:IA:12:ARG:NH2	48:WA:1619:G:O3'	2.48	0.47
48:WA:162:A:H2'	48:WA:163:A:H8	1.79	0.47
48:WA:1872:C:H2'	48:WA:1873:A:H8	1.79	0.47
48:WA:4165:U:H5'	48:WA:4166:C:H5''	1.96	0.47
48:WA:4509:A:H2'	48:WA:4510:C:C6	2.49	0.47
48:WA:4950:C:OP2	48:WA:4951:G:O2'	2.25	0.47
49:XA:11:A:N1	49:XA:66:G:O2'	2.46	0.47
49:XA:62:U:O2'	49:XA:64:G:O4'	2.32	0.47
51:ZA:1528:G:H2'	51:ZA:1529:C:C6	2.50	0.47
51:ZA:1568:C:H2'	51:ZA:1569:A:C8	2.50	0.47
52:AB:2:SER:HB3	52:AB:59:LEU:HG	1.97	0.47
75:XB:91:LEU:HD23	82:EC:82:VAL:HG21	1.97	0.47
84:GC:62:HIS:ND1	84:GC:84:ASP:OD2	2.47	0.47
87:c:247:ASP:HB2	88:HC:383:SER:N	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:3:LYS:NZ	28:BA:40:GLN:O	2.40	0.47
40:NA:58:LYS:NZ	48:WA:4382:A:OP1	2.40	0.47
51:ZA:1113:A:H2'	51:ZA:1114:U:C6	2.49	0.47
52:AB:122:LEU:HB2	52:AB:142:LEU:HD21	1.96	0.47
59:HB:285:ALA:HB3	59:HB:301:PHE:HB2	1.97	0.47
64:MB:42:LEU:O	64:MB:72:HIS:ND1	2.47	0.47
77:ZB:73:VAL:HG21	77:ZB:88:LEU:HD11	1.97	0.47
25:Y:12:LEU:HB2	25:Y:81:MET:HB3	1.96	0.47
26:Z:71:PRO:HG2	26:Z:108:TYR:HA	1.96	0.47
36:JA:47:ILE:HG22	36:JA:49:ASP:H	1.79	0.47
44:SA:13:U:O2	44:SA:23:G:N2	2.44	0.47
48:WA:2413:C:H2'	48:WA:2414:A:C8	2.50	0.47
48:WA:2589:A:OP2	48:WA:2590:C:N4	2.47	0.47
51:ZA:153:G:N2	58:GB:13:GLN:OE1	2.38	0.47
51:ZA:1093:A:H2'	51:ZA:1094:C:C6	2.49	0.47
53:BB:86:LEU:HB3	53:BB:98:THR:HB	1.97	0.47
59:HB:338:ILE:HG12	59:HB:363:VAL:HG11	1.95	0.47
88:HC:266:ARG:NH1	88:HC:268:GLU:OE2	2.47	0.47
2:B:224:LYS:HG2	2:B:340:THR:HB	1.97	0.47
2:B:240:LEU:HB3	2:B:244:THR:HG21	1.96	0.47
4:D:146:LEU:HD21	4:D:159:VAL:HG22	1.96	0.47
7:G:106:ARG:NH1	48:WA:4165:U:OP1	2.46	0.47
14:N:113:ASP:OD1	14:N:114:LYS:N	2.48	0.47
45:TA:7:A:O2'	45:TA:49:C:OP2	2.32	0.47
48:WA:4494:U:O2'	48:WA:4514:U:O2	2.25	0.47
51:ZA:476:A:N3	51:ZA:488:U:O2'	2.41	0.47
51:ZA:551:U:H2'	51:ZA:552:G:C8	2.49	0.47
51:ZA:1401:A:H2'	51:ZA:1402:A:H8	1.79	0.47
52:AB:108:PHE:HB2	52:AB:136:GLU:HB3	1.97	0.47
57:FB:102:LEU:HG	77:ZB:110:THR:HG21	1.97	0.47
60:IB:67:TRP:NE1	60:IB:191:GLU:OE2	2.41	0.47
1:A:30:ARG:NH1	1:A:33:ASP:OD2	2.47	0.47
4:D:65:ALA:HB2	4:D:74:ILE:HD13	1.97	0.47
5:E:141:ARG:NH1	5:E:172:SER:O	2.47	0.47
14:N:130:LYS:NZ	48:WA:2057:G:O5'	2.48	0.47
15:O:96:VAL:HB	15:O:109:GLN:HE21	1.78	0.47
20:T:35:ASP:HB2	20:T:38:ASN:HB3	1.97	0.47
48:WA:652:C:H2'	48:WA:653:G:C8	2.49	0.47
48:WA:1606:G:H2'	48:WA:1607:G:C8	2.50	0.47
48:WA:2896:A:H2'	48:WA:2897:A:C8	2.50	0.47
48:WA:3635:C:H2'	48:WA:3636:G:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:3723:U:H2'	48:WA:3724:G:H8	1.80	0.47
48:WA:4575:G:N2	48:WA:4724:G:OP2	2.48	0.47
51:ZA:610:G:H2'	51:ZA:611:G:H8	1.79	0.47
51:ZA:991:G:N7	78:AC:7:ASN:ND2	2.62	0.47
51:ZA:1049:A:O2'	51:ZA:1854:U:O2	2.33	0.47
51:ZA:1755:C:H2'	51:ZA:1756:C:C6	2.50	0.47
86:b:59:THR:OG1	86:b:60:MET:SD	2.73	0.47
1:A:183:GLY:HA2	48:WA:1615:A:H5'	1.97	0.47
1:A:207:VAL:HG13	1:A:208:GLU:HG3	1.96	0.47
2:B:228:TYR:O	48:WA:2837:A:O2'	2.31	0.47
4:D:126:THR:HG22	4:D:128:ASP:H	1.79	0.47
45:TA:23:A:H2'	45:TA:24:G:C8	2.50	0.47
48:WA:1428:G:N1	48:WA:1460:C:OP2	2.35	0.47
48:WA:1813:G:H2'	48:WA:1814:C:H6	1.80	0.47
48:WA:2813:G:N1	48:WA:2816:C:OP2	2.36	0.47
48:WA:3598:A:H61	63:LB:2:ALA:HA	1.79	0.47
51:ZA:1093:A:O3'	74:WB:28:ARG:NH2	2.47	0.47
51:ZA:1745:A:H62	51:ZA:1789:G:N2	2.13	0.47
52:AB:109:THR:OG1	52:AB:136:GLU:OE1	2.25	0.47
53:BB:144:LYS:HD3	53:BB:208:HIS:HB3	1.96	0.47
59:HB:258:GLU:HG3	59:HB:286:ALA:HB3	1.95	0.47
62:KB:83:LEU:HB3	62:KB:85:LEU:HD23	1.97	0.47
67:PB:81:ARG:NH1	67:PB:120:SER:OG	2.45	0.47
7:G:191:ALA:O	7:G:195:THR:OG1	2.29	0.47
10:J:46:GLN:NE2	10:J:73:THR:O	2.44	0.47
13:M:185:GLY:HA2	48:WA:78:U:H5''	1.97	0.47
48:WA:2522:C:H2'	48:WA:2523:G:C8	2.48	0.47
48:WA:4631:U:H2'	48:WA:4632:G:H8	1.80	0.47
51:ZA:77:A:H2	58:GB:175:LYS:HG3	1.80	0.47
51:ZA:155:G:H4'	58:GB:15:LEU:HD22	1.97	0.47
51:ZA:348:A:H2'	51:ZA:349:A:C8	2.50	0.47
51:ZA:917:U:H2'	51:ZA:918:U:C6	2.49	0.47
57:FB:122:ARG:N	57:FB:197:GLU:OE2	2.41	0.47
66:OB:146:ARG:HG3	78:AC:29:CYS:HB2	1.97	0.47
74:WB:18:GLU:HG3	74:WB:69:LEU:HD23	1.97	0.47
76:YB:102:THR:OG1	76:YB:107:ARG:NH2	2.47	0.47
3:C:152:LEU:HD23	3:C:251:ILE:HG12	1.97	0.47
4:D:54:ARG:NH2	4:D:147:ASP:OD2	2.47	0.47
6:F:55:HIS:NE2	6:F:59:GLU:OE2	2.47	0.47
14:N:85:ARG:HG3	14:N:99:LEU:HD11	1.97	0.47
16:P:133:GLY:O	16:P:136:THR:OG1	2.26	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:1516:U:H2'	48:WA:1517:A:C8	2.50	0.47
48:WA:2542:C:H2'	48:WA:2543:G:H8	1.80	0.47
48:WA:4262:U:H2'	48:WA:4263:C:C6	2.50	0.47
48:WA:4423:C:N4	48:WA:4477:G:H22	2.10	0.47
48:WA:4929:G:H5''	48:WA:4930:C:H5	1.80	0.47
51:ZA:128:U:H3'	51:ZA:129:C:C6	2.49	0.47
51:ZA:322:C:H2'	51:ZA:323:C:H5''	1.96	0.47
51:ZA:1781:A:H2'	51:ZA:1782:G:H8	1.80	0.47
54:CB:196:ILE:HB	54:CB:223:TYR:HB2	1.97	0.47
59:HB:268:LEU:O	59:HB:272:SER:OG	2.26	0.47
4:D:53:VAL:HG11	4:D:159:VAL:HA	1.97	0.46
5:E:144:ARG:NH1	31:EA:110:ILE:OXT	2.39	0.46
5:E:184:LEU:O	48:WA:4885:C:N4	2.47	0.46
16:P:175:GLU:OE2	26:Z:49:HIS:ND1	2.45	0.46
25:Y:136:PHE:OXT	48:WA:4124:G:O2'	2.30	0.46
31:EA:50:VAL:HG22	31:EA:69:VAL:HG22	1.96	0.46
48:WA:1825:G:H2'	48:WA:1826:G:C8	2.50	0.46
48:WA:2751:C:H2'	48:WA:2752:G:H8	1.79	0.46
51:ZA:196:C:H2'	51:ZA:197:U:C6	2.51	0.46
51:ZA:1309:C:H5'	83:FC:105:TYR:HE1	1.80	0.46
53:BB:146:ARG:HB2	53:BB:149:GLN:HB2	1.97	0.46
55:DB:66:GLU:HG2	55:DB:107:LEU:HD21	1.98	0.46
7:G:213:ASP:OD1	7:G:213:ASP:N	2.48	0.46
15:O:151:ALA:HB3	15:O:172:PRO:HG2	1.98	0.46
16:P:121:LEU:HD22	16:P:125:GLN:HG2	1.96	0.46
28:BA:103:ASP:HB3	28:BA:106:ARG:HH21	1.80	0.46
48:WA:1306:C:H2'	48:WA:1307:C:C6	2.51	0.46
48:WA:2599:G:H2'	48:WA:2600:A:C8	2.50	0.46
49:XA:12:U:OP2	49:XA:67:C:O2'	2.33	0.46
51:ZA:65:C:OP1	58:GB:136:LYS:NZ	2.46	0.46
51:ZA:527:C:H2'	51:ZA:528:A:C8	2.49	0.46
51:ZA:694:G:N1	51:ZA:732:U:O4	2.48	0.46
63:LB:50:ALA:HA	63:LB:55:TYR:HE1	1.80	0.46
65:NB:29:THR:OG1	65:NB:31:ASP:OD1	2.30	0.46
3:C:7:LEU:HB3	3:C:21:ASN:HB3	1.98	0.46
10:J:146:ARG:HG2	10:J:147:ARG:HG3	1.96	0.46
18:R:164:LYS:HB2	18:R:165:PRO:HD3	1.97	0.46
19:S:44:GLY:HA2	19:S:95:HIS:HB3	1.97	0.46
23:W:120:ASP:N	23:W:120:ASP:OD1	2.47	0.46
48:WA:2082:U:H2'	48:WA:2083:C:C6	2.50	0.46
48:WA:2581:G:N2	48:WA:2584:A:OP2	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:3719:A:H2'	48:WA:3720:A:H8	1.80	0.46
51:ZA:671:A:H4'	51:ZA:672:A:H5''	1.98	0.46
51:ZA:1217:A:H2'	51:ZA:1218:C:C6	2.50	0.46
51:ZA:1828:C:H2'	51:ZA:1829:G:C8	2.50	0.46
71:TB:116:ASP:OD1	71:TB:117:GLN:N	2.49	0.46
88:HC:272:LEU:HB3	88:HC:302:ALA:HB3	1.98	0.46
16:P:37:ARG:NH1	48:WA:2089:C:OP2	2.47	0.46
31:EA:46:ARG:HD3	31:EA:106:TYR:HD2	1.78	0.46
39:MA:11:ARG:NH2	51:ZA:1844:U:OP1	2.41	0.46
48:WA:181:C:H2'	48:WA:182:G:H8	1.78	0.46
48:WA:2745:A:H2'	48:WA:2746:A:C8	2.51	0.46
48:WA:3912:C:H2'	48:WA:3913:C:H6	1.80	0.46
48:WA:4128:C:H5''	48:WA:4129:A:H5''	1.97	0.46
48:WA:4929:G:H5''	48:WA:4930:C:C5	2.50	0.46
50:YA:47:C:H1'	50:YA:61:A:H2'	1.97	0.46
51:ZA:10:G:O2'	54:CB:113:GLN:OE1	2.32	0.46
51:ZA:1103:C:H2'	51:ZA:1104:G:C8	2.50	0.46
51:ZA:1447:G:H2'	51:ZA:1448:A:C8	2.51	0.46
86:b:47:LEU:HD13	86:b:51:ALA:HB3	1.98	0.46
2:B:213:GLN:NE2	2:B:285:TYR:O	2.49	0.46
8:H:18:ILE:HG12	8:H:27:VAL:HG22	1.96	0.46
12:L:29:ASP:OD1	12:L:30:VAL:N	2.48	0.46
31:EA:21:GLN:NE2	48:WA:1311:C:O2	2.49	0.46
40:NA:3:ASN:HA	40:NA:92:GLU:HG3	1.96	0.46
48:WA:478:G:H2'	48:WA:479:G:H8	1.80	0.46
48:WA:1330:G:O2'	48:WA:2351:A:OP1	2.34	0.46
48:WA:2377:A:H2'	48:WA:2378:A:C8	2.48	0.46
48:WA:3725:A:H2'	48:WA:3726:A:C8	2.51	0.46
64:MB:33:ARG:HH11	64:MB:91:LEU:HD13	1.80	0.46
6:F:156:ARG:NH2	48:WA:2075:C:O2'	2.49	0.46
8:H:95:VAL:HB	38:LA:56:LEU:HB3	1.96	0.46
9:I:31:ILE:HB	9:I:66:GLU:HB2	1.98	0.46
17:Q:84:THR:HG22	48:WA:2866:A:H5''	1.97	0.46
20:T:19:LEU:HD22	20:T:78:PHE:H	1.80	0.46
30:DA:89:LEU:HD13	30:DA:118:LEU:HD22	1.96	0.46
30:DA:104:SER:HB2	48:WA:2305:C:H5''	1.98	0.46
34:HA:70:LEU:HD13	34:HA:87:ARG:HE	1.81	0.46
46:UA:17:G:HO2'	46:UA:57:G:H22	1.60	0.46
48:WA:1295:G:OP2	48:WA:1295:G:N2	2.34	0.46
48:WA:2541:C:H2'	48:WA:2542:C:C6	2.51	0.46
48:WA:4690:C:H2'	48:WA:4691:U:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:1798:C:H2'	51:ZA:1799:G:O4'	2.16	0.46
54:CB:201:GLY:O	61:JB:54:ARG:NH1	2.49	0.46
60:IB:131:PRO:HD2	60:IB:134:GLU:HB2	1.97	0.46
71:TB:96:SER:HB3	71:TB:99:VAL:HG22	1.97	0.46
84:GC:124:SER:OG	84:GC:125:ARG:N	2.49	0.46
15:O:66:LYS:NZ	48:WA:425:U:OP1	2.42	0.46
48:WA:128:C:H2'	48:WA:129:C:C6	2.51	0.46
48:WA:262:G:H2'	48:WA:263:G:H8	1.78	0.46
48:WA:306:A:H2'	48:WA:307:A:C8	2.51	0.46
48:WA:1263:G:H2'	48:WA:1264:G:C8	2.50	0.46
48:WA:2745:A:H2'	48:WA:2746:A:H8	1.80	0.46
48:WA:3952:U:H2'	48:WA:3953:G:C8	2.51	0.46
48:WA:4110:G:H2'	48:WA:4111:G:C8	2.49	0.46
50:YA:45:C:H2'	50:YA:46:G:H8	1.81	0.46
51:ZA:326:C:O2	51:ZA:327:G:N1	2.49	0.46
58:GB:5:ILE:HD12	58:GB:16:ILE:HD13	1.97	0.46
62:KB:16:PHE:HE2	62:KB:89:ILE:HG22	1.80	0.46
64:MB:22:LEU:HD13	64:MB:89:VAL:HA	1.97	0.46
2:B:234:ARG:NH1	2:B:271:GLN:O	2.37	0.46
6:F:130:ASN:ND2	48:WA:1729:U:OP1	2.48	0.46
9:I:51:HIS:HD2	9:I:168:SER:HB2	1.81	0.46
11:K:54:PRO:HG2	11:K:56:ARG:NH1	2.30	0.46
12:L:24:LEU:HD11	12:L:86:TRP:CG	2.51	0.46
14:N:37:ARG:HH21	14:N:108:ILE:HD11	1.81	0.46
33:GA:62:ASN:ND2	50:YA:60:G:O6	2.39	0.46
36:JA:24:LYS:HE2	36:JA:69:LEU:HD11	1.98	0.46
48:WA:2701:C:H2'	48:WA:2702:G:H8	1.80	0.46
48:WA:4571:U:OP1	48:WA:4984:A:O2'	2.30	0.46
51:ZA:12:U:H5''	54:CB:110:MET:HE2	1.98	0.46
51:ZA:1406:G:H2'	51:ZA:1407:U:H6	1.81	0.46
51:ZA:1431:G:H2'	51:ZA:1432:U:C6	2.50	0.46
51:ZA:1524:G:OP2	70:SB:141:ARG:NE	2.46	0.46
54:CB:65:LYS:HD2	54:CB:273:LEU:HD13	1.96	0.46
72:UB:98:VAL:HG23	72:UB:101:ILE:HD11	1.98	0.46
73:VB:59:ILE:HD12	79:BC:3:LEU:HD11	1.97	0.46
1:A:27:ALA:O	1:A:128:ARG:NH2	2.45	0.46
4:D:94:ASN:OD1	4:D:97:ALA:N	2.36	0.46
30:DA:99:ILE:HG21	30:DA:108:ARG:HG2	1.98	0.46
30:DA:103:VAL:O	30:DA:128:ARG:NH1	2.49	0.46
48:WA:352:G:O2'	50:YA:22:U:O4	2.30	0.46
48:WA:2851:A:O2'	48:WA:2857:G:N7	2.43	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:4391:C:H2'	48:WA:4392:A:C8	2.51	0.46
51:ZA:1198:G:H2'	51:ZA:1199:A:C8	2.51	0.46
52:AB:157:VAL:O	73:VB:65:SER:OG	2.33	0.46
69:RB:102:THR:O	69:RB:105:MET:HG3	2.16	0.46
1:A:198:ARG:NH2	48:WA:3690:U:OP2	2.49	0.46
3:C:119:GLN:NE2	48:WA:1352:C:O2	2.45	0.46
11:K:35:ARG:NH2	48:WA:337:U:OP1	2.49	0.46
27:AA:110:ALA:HB1	48:WA:1273:G:H5'	1.98	0.46
46:UA:17:G:O2'	46:UA:57:G:N2	2.34	0.46
48:WA:270:U:H2'	48:WA:271:C:C6	2.51	0.46
48:WA:2413:C:H2'	48:WA:2414:A:H8	1.80	0.46
48:WA:2626:G:H2'	48:WA:2627:U:C6	2.52	0.46
50:YA:153:C:H2'	50:YA:154:G:C8	2.51	0.46
51:ZA:516:A:N1	51:ZA:643:A:O2'	2.46	0.46
51:ZA:1202:U:H2'	51:ZA:1203:G:H8	1.81	0.46
51:ZA:1617:G:N2	51:ZA:1619:A:H3'	2.31	0.46
53:BB:103:MET:HE2	53:BB:188:LEU:HD11	1.98	0.46
60:IB:26:LYS:O	60:IB:29:LEU:HB2	2.16	0.46
88:HC:285:VAL:HG22	88:HC:450:LYS:HB3	1.97	0.46
1:A:219:ILE:HD11	48:WA:3691:G:H5'	1.98	0.45
2:B:14:LEU:O	48:WA:4589:G:O2'	2.25	0.45
46:UA:12:G:H2'	46:UA:13:U:O4'	2.15	0.45
48:WA:715:G:H2'	48:WA:716:G:H8	1.80	0.45
48:WA:1247:C:H2'	48:WA:1248:G:C8	2.50	0.45
48:WA:1292:G:H2'	48:WA:1293:G:H8	1.81	0.45
48:WA:1974:G:H2'	48:WA:1975:G:O4'	2.16	0.45
48:WA:2310:A:H4'	48:WA:2336:C:H4'	1.98	0.45
48:WA:3913:C:H2'	48:WA:3914:U:H6	1.81	0.45
48:WA:4321:C:H2'	48:WA:4322:G:H8	1.81	0.45
48:WA:4450:G:H5''	48:WA:4451:A:H5'	1.97	0.45
48:WA:4460:C:H2'	48:WA:4461:U:C6	2.51	0.45
51:ZA:743:U:H3	51:ZA:798:G:N2	2.14	0.45
51:ZA:916:A:C5	65:NB:73:ARG:HD3	2.51	0.45
74:WB:27:ILE:HG13	74:WB:61:ILE:HB	1.98	0.45
4:D:33:ARG:HH21	49:XA:7:G:H4'	1.81	0.45
5:E:186:ARG:HG3	48:WA:4940:A:H5'	1.99	0.45
9:I:116:ARG:HH12	48:WA:4201:C:H42	1.63	0.45
23:W:150:ALA:HB1	23:W:155:ILE:HG13	1.98	0.45
29:CA:33:ILE:HD11	29:CA:41:ARG:HB3	1.98	0.45
43:RA:137:GLN:HE21	43:RA:137:GLN:HB3	1.53	0.45
48:WA:462:G:H2'	48:WA:463:A:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:1543:C:H1'	48:WA:2450:G:H21	1.81	0.45
48:WA:4147:C:H2'	48:WA:4148:G:H8	1.81	0.45
51:ZA:618:C:H2'	51:ZA:619:A:O4'	2.17	0.45
51:ZA:918:U:O2'	74:WB:56:HIS:O	2.35	0.45
72:UB:32:LEU:HD21	72:UB:87:ARG:HG2	1.98	0.45
75:XB:51:VAL:HG22	75:XB:72:VAL:HG22	1.97	0.45
88:HC:344:VAL:HG12	88:HC:436:GLY:HA3	1.98	0.45
4:D:223:PHE:HB3	4:D:226:TYR:HB2	1.97	0.45
7:G:253:THR:OG1	48:WA:150:U:OP2	2.27	0.45
12:L:47:ARG:HH22	12:L:69:ARG:HA	1.81	0.45
16:P:122:THR:OG1	16:P:124:ASP:OD1	2.27	0.45
26:Z:75:LEU:HB3	26:Z:117:LEU:HD13	1.97	0.45
43:RA:131:GLU:HB2	48:WA:1975:G:N2	2.31	0.45
44:SA:43:A:H2'	44:SA:44:A:C8	2.51	0.45
48:WA:175:C:H2'	48:WA:176:G:H8	1.81	0.45
48:WA:674:C:H2'	48:WA:675:G:H8	1.81	0.45
48:WA:910:G:H2'	48:WA:911:G:H8	1.82	0.45
51:ZA:107:A:H2'	51:ZA:108:G:H8	1.80	0.45
51:ZA:649:U:H2'	51:ZA:650:A:C8	2.49	0.45
51:ZA:1778:C:H2'	51:ZA:1779:G:C8	2.51	0.45
55:DB:58:GLU:OE2	55:DB:114:ARG:NE	2.49	0.45
70:SB:125:HIS:CE1	70:SB:131:VAL:HG21	2.51	0.45
10:J:35:ARG:NH1	10:J:126:TYR:OH	2.49	0.45
34:HA:60:LEU:HA	34:HA:63:VAL:HG22	1.97	0.45
48:WA:1292:G:H2'	48:WA:1293:G:C8	2.52	0.45
48:WA:1806:A:H4'	48:WA:1807:A:O5'	2.15	0.45
48:WA:1848:G:H2'	48:WA:1849:C:C6	2.52	0.45
48:WA:4747:G:H1	48:WA:4957:A:N6	2.14	0.45
51:ZA:209:A:H2'	51:ZA:210:U:O4'	2.16	0.45
51:ZA:220:U:H2'	51:ZA:221:A:H8	1.81	0.45
51:ZA:1716:C:H2'	51:ZA:1717:C:H6	1.81	0.45
56:EB:18:TRP:HB3	56:EB:20:LEU:HD13	1.97	0.45
56:EB:126:VAL:HA	56:EB:141:THR:HA	1.98	0.45
62:KB:26:ASP:HB3	62:KB:29:MET:HE3	1.98	0.45
84:GC:107:ASP:N	84:GC:107:ASP:OD1	2.49	0.45
1:A:137:ILE:HD11	1:A:149:LYS:HB2	1.98	0.45
4:D:146:LEU:HD22	4:D:163:LEU:HD13	1.97	0.45
9:I:88:ARG:HH21	9:I:173:PHE:HD2	1.64	0.45
16:P:181:ARG:NH2	48:WA:4368:A:OP1	2.49	0.45
48:WA:422:C:H2'	48:WA:423:G:H8	1.81	0.45
48:WA:425:U:H2'	48:WA:426:A:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:3609:U:H2'	48:WA:3610:A:C8	2.51	0.45
48:WA:4421:U:OP1	48:WA:4423:C:N4	2.49	0.45
48:WA:4968:A:H2'	48:WA:4969:A:C8	2.52	0.45
51:ZA:527:C:H4'	61:JB:121:LYS:HD2	1.97	0.45
51:ZA:562:U:OP1	61:JB:134:HIS:NE2	2.49	0.45
51:ZA:613:G:N1	51:ZA:629:A:OP2	2.50	0.45
51:ZA:1418:C:N4	51:ZA:1422:G:OP1	2.50	0.45
53:BB:137:LEU:HG	53:BB:215:VAL:HG22	1.97	0.45
61:JB:114:VAL:HG21	61:JB:135:ILE:HD13	1.97	0.45
64:MB:33:ARG:NH2	64:MB:89:VAL:O	2.49	0.45
67:PB:43:ARG:HH12	67:PB:47:ARG:HH11	1.65	0.45
70:SB:75:ARG:NE	70:SB:81:ASP:OD1	2.38	0.45
84:GC:5:MET:HE3	84:GC:310:TRP:HB3	1.98	0.45
88:HC:346:ILE:O	88:HC:397:GLY:N	2.47	0.45
9:I:61:SER:HA	9:I:126:VAL:HG23	1.97	0.45
13:M:53:TYR:HB2	13:M:133:ILE:HD13	1.99	0.45
24:X:82:ILE:HD12	24:X:85:VAL:HG21	1.98	0.45
30:DA:78:LEU:HB2	42:PA:20:ARG:HD2	1.99	0.45
48:WA:146:G:H2'	48:WA:147:A:H8	1.81	0.45
48:WA:1343:U:H2'	48:WA:1344:A:C8	2.51	0.45
48:WA:1848:G:H2'	48:WA:1849:C:H6	1.82	0.45
48:WA:2002:G:O2'	48:WA:2003:G:N7	2.47	0.45
48:WA:2609:C:H2'	48:WA:2610:G:H8	1.82	0.45
48:WA:2751:C:H2'	48:WA:2752:G:C8	2.52	0.45
48:WA:4143:G:N2	48:WA:4146:G:OP2	2.35	0.45
51:ZA:1275:G:H22	51:ZA:1506:A:P	2.39	0.45
51:ZA:1458:G:OP1	84:GC:279:SER:OG	2.26	0.45
62:KB:60:GLU:OE1	62:KB:69:TRP:NE1	2.41	0.45
66:OB:31:CYS:HB3	66:OB:44:VAL:HG22	1.98	0.45
70:SB:22:GLY:HA2	70:SB:56:ALA:HB3	1.98	0.45
84:GC:234:ASP:HB2	84:GC:252:THR:HB	1.98	0.45
3:C:333:LYS:NZ	48:WA:983:G:O2'	2.41	0.45
9:I:66:GLU:OE1	9:I:69:ARG:NH1	2.49	0.45
13:M:184:ILE:HG23	13:M:194:ARG:HH22	1.82	0.45
20:T:28:PRO:HB2	20:T:34:MET:HG2	1.98	0.45
20:T:84:LYS:HB2	20:T:110:TYR:CE2	2.51	0.45
25:Y:54:THR:H	25:Y:57:MET:HE2	1.82	0.45
44:SA:21:A:O2'	44:SA:22:A:O5'	2.25	0.45
45:TA:49:C:H2'	45:TA:50:A:C8	2.50	0.45
48:WA:212:A:H2'	48:WA:213:G:H8	1.81	0.45
48:WA:251:C:H2'	48:WA:252:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:986:U:H2'	48:WA:987:C:C6	2.52	0.45
48:WA:1944:A:H2'	48:WA:1945:A:H8	1.81	0.45
48:WA:2516:G:O2'	48:WA:2745:A:N6	2.49	0.45
48:WA:3738:A:H2'	48:WA:3739:A:C8	2.51	0.45
51:ZA:1480:A:O2'	72:UB:79:ARG:NH2	2.49	0.45
52:AB:127:PRO:HG3	52:AB:146:ALA:HB1	1.98	0.45
52:AB:128:ARG:HG2	52:AB:153:PRO:HD2	1.99	0.45
59:HB:336:ARG:HD2	59:HB:363:VAL:HG23	1.99	0.45
62:KB:37:ASP:N	62:KB:37:ASP:OD1	2.50	0.45
84:GC:286:CYS:HA	84:GC:302:TYR:HA	1.97	0.45
6:F:222:LYS:HE3	48:WA:1909:A:H4'	1.99	0.45
14:N:12:ARG:HB2	14:N:37:ARG:HD2	1.99	0.45
16:P:54:SER:OG	16:P:57:ASN:OD1	2.27	0.45
17:Q:176:ARG:NH1	51:ZA:909:G:OP1	2.50	0.45
48:WA:260:C:H2'	48:WA:261:G:C8	2.52	0.45
51:ZA:54:A:OP1	76:YB:111:LYS:NZ	2.44	0.45
53:BB:106:THR:HG22	53:BB:108:ASP:H	1.80	0.45
58:GB:74:ARG:HG2	58:GB:96:SER:HB3	1.99	0.45
63:LB:13:GLN:HB2	63:LB:16:ILE:HG12	1.97	0.45
63:LB:45:LYS:HE2	63:LB:45:LYS:HB2	1.79	0.45
86:b:16:LYS:HE2	86:b:16:LYS:HB3	1.64	0.45
3:C:293:LEU:O	3:C:299:GLN:NE2	2.46	0.45
48:WA:36:U:OP1	48:WA:1653:G:N2	2.40	0.45
48:WA:677:C:H2'	48:WA:678:G:C8	2.51	0.45
48:WA:723:G:OP1	48:WA:938:C:N4	2.49	0.45
48:WA:1398:G:O2'	48:WA:1470:C:O2'	2.31	0.45
48:WA:1448:C:H2'	48:WA:1449:C:C6	2.52	0.45
48:WA:3895:C:H2'	48:WA:3896:A:C8	2.52	0.45
48:WA:3925:A:H2'	48:WA:3926:C:C6	2.51	0.45
51:ZA:1801:A:H2'	51:ZA:1802:C:C6	2.51	0.45
53:BB:99:ASN:OD1	53:BB:100:PHE:N	2.50	0.45
54:CB:109:ILE:HD11	54:CB:151:ILE:HD11	1.99	0.45
1:A:10:LYS:NZ	48:WA:3689:A:OP2	2.48	0.45
3:C:140:LYS:HE3	3:C:245:HIS:HB2	1.99	0.45
16:P:79:THR:HB	16:P:136:THR:HG22	1.98	0.45
43:RA:47:ALA:O	43:RA:50:THR:OG1	2.35	0.45
48:WA:520:C:H2'	48:WA:521:U:C5	2.52	0.45
48:WA:2000:A:OP2	86:b:16:LYS:NZ	2.35	0.45
48:WA:3873:A:H2'	48:WA:3874:A:C8	2.51	0.45
48:WA:4072:U:H2'	48:WA:4073:U:C6	2.52	0.45
49:XA:92:C:H2'	49:XA:93:G:C8	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:YA:106:G:H4'	50:YA:137:A:H5'	1.99	0.45
51:ZA:1440:C:O2'	51:ZA:1441:U:O4'	2.35	0.45
51:ZA:1535:U:O4	57:FB:159:ARG:NE	2.50	0.45
51:ZA:1614:A:H2'	51:ZA:1615:U:C6	2.52	0.45
55:DB:133:GLY:HA2	55:DB:139:GLN:HE21	1.82	0.45
55:DB:234:GLY:HA3	55:DB:239:LYS:HG2	1.97	0.45
56:EB:95:THR:HG22	76:YB:16:ARG:HB2	1.99	0.45
58:GB:39:ASP:N	58:GB:39:ASP:OD1	2.50	0.45
70:SB:48:ALA:HB2	70:SB:70:ILE:HG13	1.98	0.45
73:VB:11:LEU:HD23	73:VB:11:LEU:H	1.82	0.45
75:XB:40:PRO:O	75:XB:77:ASN:ND2	2.49	0.45
77:ZB:92:LEU:HD22	77:ZB:109:TYR:HE1	1.82	0.45
1:A:227:ARG:NH1	48:WA:3667:G:O3'	2.50	0.44
4:D:52:ILE:HD13	49:XA:6:C:H4'	1.99	0.44
13:M:14:LYS:HE2	48:WA:280:G:H5''	1.99	0.44
19:S:127:GLN:HE21	19:S:131:GLN:HE21	1.65	0.44
22:V:20:ARG:HD3	22:V:30:GLN:HG3	1.99	0.44
45:TA:52:G:H2'	45:TA:53:G:H8	1.82	0.44
48:WA:1307:C:OP1	50:YA:7:U:O2'	2.35	0.44
51:ZA:381:C:H41	60:IB:27:TYR:HB2	1.82	0.44
51:ZA:570:C:O2'	76:YB:34:THR:O	2.34	0.44
51:ZA:1017:U:OP1	65:NB:62:GLN:NE2	2.41	0.44
51:ZA:1315:U:H4'	62:KB:2:LEU:HB3	1.99	0.44
51:ZA:1643:U:H2'	51:ZA:1644:C:C6	2.52	0.44
53:BB:52:THR:HG23	53:BB:57:ILE:HG22	1.98	0.44
53:BB:126:ASP:N	53:BB:126:ASP:OD1	2.50	0.44
88:HC:363:CYS:HB3	88:HC:424:PHE:HB3	1.98	0.44
9:I:87:ILE:HG12	9:I:138:ILE:HG12	1.99	0.44
18:R:17:LEU:HD11	19:S:136:ARG:HH21	1.82	0.44
19:S:28:ALA:HA	19:S:31:MET:HG2	1.99	0.44
19:S:130:ARG:HH21	48:WA:1730:U:H1'	1.82	0.44
21:U:82:ILE:HG22	21:U:83:ARG:HG3	1.99	0.44
30:DA:124:ASN:N	30:DA:124:ASN:OD1	2.49	0.44
37:KA:25:GLN:O	37:KA:28:TRP:NE1	2.50	0.44
48:WA:457:G:H1	48:WA:700:C:H42	1.65	0.44
48:WA:677:C:H2'	48:WA:678:G:H8	1.83	0.44
48:WA:961:A:N6	48:WA:1285:G:H1'	2.33	0.44
48:WA:1300:C:H2'	48:WA:1301:G:C8	2.53	0.44
48:WA:1492:G:H2'	48:WA:1493:A:H8	1.82	0.44
48:WA:1619:G:H1'	48:WA:2515:A:N6	2.31	0.44
48:WA:2449:U:H1'	48:WA:2746:A:H2	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:2564:G:N2	48:WA:2567:A:OP2	2.36	0.44
48:WA:2589:A:O2'	48:WA:2590:C:O4'	2.32	0.44
48:WA:3672:C:H2'	48:WA:3673:G:C8	2.53	0.44
48:WA:3912:C:H2'	48:WA:3913:C:C6	2.52	0.44
48:WA:4663:G:N2	48:WA:5006:C:O3'	2.51	0.44
51:ZA:1010:G:H2'	51:ZA:1011:A:C8	2.52	0.44
51:ZA:1408:U:H2'	51:ZA:1409:A:C8	2.53	0.44
59:HB:384:VAL:HG22	59:HB:390:ARG:HG2	1.99	0.44
72:UB:46:LYS:HD3	72:UB:97:ILE:HG22	2.00	0.44
74:WB:14:ILE:HG22	74:WB:25:VAL:HG11	1.98	0.44
74:WB:50:PHE:HB3	74:WB:63:VAL:HG13	1.98	0.44
2:B:252:ALA:HB1	48:WA:4526:G:C2	2.52	0.44
7:G:158:GLU:OE2	7:G:166:ARG:NH2	2.34	0.44
14:N:27:VAL:HG13	14:N:98:ALA:HB1	1.98	0.44
14:N:178:ARG:NH1	14:N:182:GLU:OE2	2.50	0.44
40:NA:69:ARG:HG3	40:NA:82:MET:HE1	1.98	0.44
46:UA:67:G:H2'	46:UA:68:G:H8	1.82	0.44
48:WA:955:G:H2'	48:WA:956:G:H8	1.82	0.44
48:WA:1405:G:H2'	48:WA:1406:G:C8	2.52	0.44
48:WA:1414:G:H2'	48:WA:1415:C:C6	2.53	0.44
48:WA:1444:C:N3	48:WA:1445:A:N6	2.65	0.44
48:WA:1727:U:H2'	48:WA:1728:U:C6	2.52	0.44
48:WA:2612:G:H2'	48:WA:2613:A:H8	1.83	0.44
51:ZA:375:U:H2'	51:ZA:376:A:C8	2.53	0.44
51:ZA:419:G:N2	51:ZA:661:U:O2	2.51	0.44
53:BB:87:ILE:HG22	53:BB:101:HIS:HB2	2.00	0.44
68:QB:106:GLN:O	68:QB:110:ILE:HG22	2.17	0.44
71:TB:42:HIS:HB3	71:TB:93:SER:HB3	1.99	0.44
88:HC:364:HIS:CD2	88:HC:421:LEU:HG	2.53	0.44
2:B:384:GLU:OE2	22:V:14:TYR:OH	2.32	0.44
24:X:50:ARG:HB2	24:X:115:ARG:HH21	1.82	0.44
35:IA:34:CYS:HB3	35:IA:39:TYR:H	1.82	0.44
48:WA:6:C:H2'	48:WA:7:C:H6	1.82	0.44
48:WA:1819:U:H2'	48:WA:1820:G:O4'	2.18	0.44
48:WA:1935:G:H8	48:WA:1935:G:O5'	2.00	0.44
51:ZA:65:C:C2	58:GB:133:LEU:HD22	2.53	0.44
51:ZA:1376:A:OP1	69:RB:67:ARG:NH1	2.41	0.44
51:ZA:1802:C:H2'	51:ZA:1803:U:C6	2.53	0.44
10:J:57:VAL:HG12	10:J:60:PHE:H	1.83	0.44
25:Y:88:ASP:O	25:Y:121:ARG:NH1	2.44	0.44
29:CA:23:ARG:NE	29:CA:25:TYR:OH	2.36	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:JA:12:LEU:HG	36:JA:16:ARG:HE	1.82	0.44
37:KA:2:SER:N	48:WA:2408:G:N7	2.65	0.44
48:WA:4:G:H2'	48:WA:5:A:C8	2.52	0.44
48:WA:169:A:C2	48:WA:267:G:C2	3.05	0.44
48:WA:325:U:H2'	48:WA:326:C:C6	2.52	0.44
48:WA:2297:C:H2'	48:WA:2298:G:C8	2.52	0.44
48:WA:2650:G:H2'	48:WA:2651:G:H8	1.83	0.44
48:WA:3738:A:H2'	48:WA:3739:A:H8	1.83	0.44
51:ZA:1098:C:H2'	51:ZA:1099:G:C8	2.52	0.44
51:ZA:1324:G:O2'	51:ZA:1510:G:O2'	2.29	0.44
51:ZA:1858:G:N7	66:OB:146:ARG:NH1	2.66	0.44
56:EB:112:HIS:NE2	56:EB:237:SER:OG	2.45	0.44
73:VB:73:ALA:HB1	73:VB:78:ILE:HB	1.99	0.44
1:A:34:PHE:HE2	7:G:94:ILE:HD11	1.83	0.44
2:B:55:HIS:CE1	48:WA:4629:U:HO2'	2.34	0.44
5:E:149:PRO:HB2	5:E:206:ILE:HG21	2.00	0.44
13:M:120:TRP:HE1	13:M:123:GLU:HB3	1.82	0.44
18:R:5:GLY:O	18:R:111:ARG:NH2	2.50	0.44
28:BA:50:ASN:OD1	28:BA:51:ASN:N	2.50	0.44
30:DA:107:ASN:OD1	30:DA:107:ASN:N	2.50	0.44
33:GA:89:ARG:O	33:GA:93:ARG:HG2	2.17	0.44
48:WA:254:G:H2'	48:WA:255:C:C6	2.52	0.44
51:ZA:1585:U:O2'	51:ZA:1587:G:OP2	2.31	0.44
51:ZA:1855:G:OP2	66:OB:147:ARG:NH1	2.50	0.44
86:b:69:LEU:HD22	86:b:73:PRO:HA	1.99	0.44
6:F:226:PHE:N	6:F:232:ALA:O	2.46	0.44
24:X:73:VAL:HG13	24:X:80:ILE:HG22	2.00	0.44
48:WA:1820:G:O2'	48:WA:1821:G:OP1	2.33	0.44
48:WA:2260:C:H5''	48:WA:2261:G:C8	2.53	0.44
48:WA:2760:G:H2'	48:WA:2761:G:C8	2.53	0.44
51:ZA:675:U:H2'	51:ZA:676:C:H6	1.81	0.44
51:ZA:1096:G:H1	51:ZA:1136:U:H3	1.66	0.44
51:ZA:1671:G:H2'	51:ZA:1672:U:C6	2.53	0.44
58:GB:32:MET:HB2	58:GB:100:CYS:HB2	1.99	0.44
69:RB:132:ARG:H	69:RB:132:ARG:HD2	1.82	0.44
84:GC:87:LEU:HD22	84:GC:120:ILE:HD11	1.98	0.44
84:GC:259:TRP:HD1	84:GC:266:ILE:HA	1.82	0.44
29:CA:122:VAL:HG12	29:CA:124:GLU:H	1.83	0.44
48:WA:2287:A:H2'	48:WA:2288:G:H8	1.83	0.44
48:WA:3724:G:H2'	48:WA:3725:A:C8	2.52	0.44
48:WA:4920:C:H2'	48:WA:4921:G:C8	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:XA:63:C:H5'	49:XA:64:G:H5''	1.99	0.44
51:ZA:1232:U:H2'	51:ZA:1233:G:C8	2.52	0.44
51:ZA:1486:A:O3'	54:CB:121:ARG:NH2	2.51	0.44
51:ZA:1543:U:P	71:TB:62:ARG:HH22	2.41	0.44
51:ZA:1606:G:O2'	51:ZA:1632:G:N2	2.50	0.44
54:CB:191:VAL:HG11	54:CB:236:PHE:HA	1.99	0.44
86:b:23:ASP:HB2	86:b:90:PHE:HB3	1.99	0.44
4:D:166:ALA:HB1	4:D:171:LEU:HD12	2.00	0.44
13:M:49:ARG:HH21	48:WA:114:G:P	2.41	0.44
15:O:119:PHE:HE1	48:WA:397:G:H22	1.66	0.44
24:X:113:LYS:NZ	50:YA:84:A:N1	2.66	0.44
25:Y:41:ALA:HB2	25:Y:77:TYR:HE1	1.83	0.44
48:WA:712:A:H2'	48:WA:713:C:C6	2.53	0.44
48:WA:1266:C:H2'	48:WA:1267:G:C8	2.53	0.44
48:WA:1881:C:H2'	48:WA:1882:G:O4'	2.17	0.44
48:WA:2001:A:H2'	48:WA:2002:G:C5	2.53	0.44
49:XA:77:A:H62	49:XA:99:G:H21	1.66	0.44
51:ZA:921:G:C5	74:WB:28:ARG:HD3	2.53	0.44
51:ZA:945:U:O2	51:ZA:1045:U:O2'	2.35	0.44
51:ZA:1497:G:N7	62:KB:25:LYS:NZ	2.62	0.44
64:MB:41:ALA:HA	64:MB:45:ARG:HB2	1.99	0.44
78:AC:11:ALA:HB3	78:AC:33:ASP:HB2	1.99	0.44
16:P:178:ARG:NH2	26:Z:46:ASP:OD1	2.50	0.43
19:S:78:LYS:NZ	48:WA:4303:U:OP1	2.51	0.43
32:FA:9:ARG:HG2	32:FA:34:TYR:CZ	2.53	0.43
33:GA:66:LYS:NZ	50:YA:97:A:OP2	2.43	0.43
44:SA:50:U:O4	44:SA:64:G:O6	2.35	0.43
48:WA:162:A:H2'	48:WA:163:A:C8	2.53	0.43
48:WA:460:C:H2'	48:WA:461:G:H8	1.83	0.43
48:WA:470:A:H62	48:WA:685:G:N2	2.16	0.43
48:WA:1808:G:H2'	48:WA:1809:C:C6	2.53	0.43
48:WA:2850:G:O2'	48:WA:3840:U:O4	2.32	0.43
48:WA:4461:U:H2'	48:WA:4462:U:C6	2.53	0.43
51:ZA:1688:C:H2'	51:ZA:1689:C:H6	1.83	0.43
56:EB:204:SER:OG	56:EB:205:PHE:N	2.51	0.43
75:XB:94:ILE:HG12	75:XB:125:VAL:HG21	1.99	0.43
77:ZB:79:ILE:HB	77:ZB:83:LEU:HD23	2.00	0.43
81:DC:33:LYS:HE2	81:DC:34:TYR:CZ	2.53	0.43
2:B:92:TYR:HB2	2:B:159:VAL:HB	1.99	0.43
8:H:66:GLU:O	8:H:69:THR:OG1	2.34	0.43
12:L:12:VAL:O	12:L:58:THR:OG1	2.24	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:135:LYS:NZ	48:WA:2438:U:OP2	2.51	0.43
48:WA:408:A:O2'	48:WA:411:G:OP2	2.26	0.43
48:WA:1249:U:O4	48:WA:1268:G:O6	2.36	0.43
48:WA:3875:G:H2'	48:WA:3876:G:C8	2.53	0.43
48:WA:4682:G:H2'	48:WA:4683:A:C8	2.52	0.43
50:YA:110:U:O2'	50:YA:111:U:O4'	2.36	0.43
54:CB:199:PRO:O	54:CB:202:THR:OG1	2.35	0.43
56:EB:45:ILE:HA	56:EB:61:VAL:HG11	2.01	0.43
62:KB:1:MET:HG3	62:KB:47:LYS:HG3	2.00	0.43
64:MB:79:VAL:HG21	64:MB:85:LEU:HD13	2.01	0.43
66:OB:54:CYS:HB2	66:OB:84:ARG:HG2	1.99	0.43
76:YB:110:ARG:NH1	76:YB:126:GLY:O	2.51	0.43
84:GC:38:LYS:NZ	84:GC:63:SER:O	2.51	0.43
87:c:250:PHE:HA	87:c:253:PHE:HD2	1.82	0.43
6:F:240:ASN:O	6:F:244:ARG:HG2	2.18	0.43
13:M:38:ARG:NH2	50:YA:142:U:OP1	2.46	0.43
17:Q:102:LEU:HD22	17:Q:138:LEU:HD22	2.00	0.43
23:W:52:LEU:HD22	23:W:54:LEU:HD12	2.00	0.43
35:IA:76:HIS:NE2	50:YA:93:C:OP1	2.43	0.43
44:SA:25:C:H2'	44:SA:26:A:H8	1.84	0.43
48:WA:129:C:H2'	48:WA:130:C:C6	2.52	0.43
48:WA:1256:A:N1	48:WA:1261:G:O6	2.51	0.43
48:WA:1311:C:H2'	48:WA:1312:C:C6	2.53	0.43
48:WA:1685:U:H2'	48:WA:1686:A:C8	2.53	0.43
48:WA:2609:C:H2'	48:WA:2610:G:C8	2.53	0.43
48:WA:3870:G:H22	48:WA:3902:G:H1'	1.84	0.43
48:WA:5032:U:H2'	48:WA:5033:G:H8	1.84	0.43
51:ZA:15:U:H2'	51:ZA:16:G:O4'	2.17	0.43
51:ZA:219:U:H2'	51:ZA:220:U:C6	2.53	0.43
51:ZA:996:A:H2'	51:ZA:997:A:C8	2.53	0.43
51:ZA:1648:G:H22	51:ZA:1675:A:P	2.40	0.43
6:F:189:LEU:HD21	6:F:207:LEU:HD21	2.00	0.43
7:G:139:VAL:HG11	7:G:238:LYS:HG3	2.01	0.43
8:H:172:ILE:HD11	38:LA:98:LYS:HZ1	1.84	0.43
12:L:34:ASN:ND2	48:WA:1926:C:OP1	2.51	0.43
13:M:193:ARG:O	13:M:197:THR:OG1	2.27	0.43
19:S:4:THR:OG1	48:WA:4210:U:OP2	2.29	0.43
33:GA:52:LYS:NZ	50:YA:63:U:O2'	2.36	0.43
35:IA:12:ARG:O	48:WA:2406:A:O2'	2.32	0.43
43:RA:66:ASN:OD1	43:RA:66:ASN:N	2.51	0.43
48:WA:229:G:H2'	48:WA:230:G:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:1690:G:H2'	48:WA:1691:G:C8	2.53	0.43
48:WA:2000:A:O2'	48:WA:2001:A:O4'	2.31	0.43
48:WA:2000:A:H1'	48:WA:2021:C:O2'	2.18	0.43
48:WA:4910:G:H1'	48:WA:4915:G:H22	1.83	0.43
51:ZA:547:G:H2'	51:ZA:549:C:C6	2.53	0.43
51:ZA:1503:C:H2'	51:ZA:1504:U:C6	2.53	0.43
57:FB:176:GLU:OE2	57:FB:187:SER:OG	2.36	0.43
84:GC:163:PRO:HB2	84:GC:179:LEU:HB3	2.00	0.43
88:HC:250:LEU:HD22	88:HC:324:ASN:HB2	2.00	0.43
1:A:14:SER:OG	48:WA:1630:C:OP1	2.36	0.43
2:B:298:LEU:HD13	2:B:300:LYS:HE3	2.00	0.43
3:C:221:PHE:HB3	3:C:227:ILE:HG21	1.99	0.43
13:M:93:LYS:NZ	48:WA:4179:C:OP1	2.38	0.43
16:P:67:ILE:HD13	16:P:98:LEU:HD11	2.01	0.43
18:R:16:CYS:SG	18:R:17:LEU:N	2.92	0.43
21:U:107:ASN:HD21	21:U:111:GLU:HB2	1.83	0.43
24:X:59:ARG:HD2	48:WA:209:U:H5'	1.99	0.43
34:HA:31:GLY:HA3	48:WA:310:G:C4	2.53	0.43
40:NA:77:CYS:SG	40:NA:79:SER:OG	2.65	0.43
43:RA:147:HIS:CD2	43:RA:148:PRO:HD3	2.53	0.43
45:TA:69:G:H2'	45:TA:70:G:H8	1.84	0.43
48:WA:474:C:H2'	48:WA:475:G:C8	2.53	0.43
48:WA:1678:C:N4	48:WA:4380:A:H2'	2.33	0.43
48:WA:1781:U:H2'	48:WA:1782:A:C8	2.54	0.43
48:WA:2641:U:H2'	48:WA:2696:G:C6	2.53	0.43
48:WA:4188:A:H2'	48:WA:4189:G:H8	1.83	0.43
48:WA:4580:G:H2'	48:WA:4581:U:C6	2.53	0.43
50:YA:57:C:O2	50:YA:61:A:O2'	2.36	0.43
51:ZA:70:G:H21	51:ZA:79:A:H62	1.65	0.43
51:ZA:1513:C:H2'	51:ZA:1514:G:C8	2.52	0.43
57:FB:40:ALA:HB1	57:FB:45:TYR:CD1	2.54	0.43
63:LB:12:LYS:HA	63:LB:56:ILE:HD13	1.99	0.43
67:PB:41:GLN:HG3	67:PB:84:ILE:HD13	2.00	0.43
68:QB:122:TYR:HA	68:QB:126:VAL:HG23	1.99	0.43
70:SB:33:ILE:HD13	70:SB:71:MET:HE1	2.01	0.43
78:AC:44:ILE:HG21	78:AC:65:PRO:HG2	2.00	0.43
88:HC:372:PHE:HE1	88:HC:402:VAL:HG21	1.83	0.43
2:B:55:HIS:CD2	48:WA:4629:U:HO2'	2.36	0.43
2:B:100:ARG:NE	48:WA:4913:A:OP2	2.52	0.43
2:B:317:LEU:HB3	48:WA:5003:U:H4'	2.00	0.43
18:R:111:ARG:NH2	48:WA:2064:C:O2'	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:29:VAL:HG21	20:T:68:SER:HB2	2.01	0.43
27:AA:47:LYS:NZ	48:WA:1466:C:O3'	2.50	0.43
29:CA:68:LEU:HA	29:CA:108:TYR:HB2	2.01	0.43
38:LA:80:ARG:HH21	48:WA:4698:C:H4'	1.82	0.43
45:TA:23:A:H2'	45:TA:24:G:H8	1.84	0.43
48:WA:1087:C:H2'	48:WA:1088:C:C6	2.54	0.43
48:WA:1474:C:H2'	48:WA:1475:U:C6	2.54	0.43
48:WA:1755:G:H2'	48:WA:1756:U:C2	2.53	0.43
48:WA:2027:A:H8	48:WA:2028:A:H1'	1.83	0.43
48:WA:3666:G:H2'	48:WA:3667:G:C8	2.52	0.43
48:WA:3713:A:O2'	48:WA:3715:U:OP2	2.27	0.43
48:WA:3729:A:H2'	48:WA:3730:A:C8	2.54	0.43
51:ZA:1230:C:H2'	51:ZA:1231:C:H6	1.83	0.43
51:ZA:1386:A:OP2	55:DB:198:SER:OG	2.33	0.43
51:ZA:1419:C:H4'	51:ZA:1420:G:C2	2.54	0.43
51:ZA:1461:G:O2'	51:ZA:1465:A:N6	2.51	0.43
51:ZA:1576:G:H2'	51:ZA:1577:G:C8	2.54	0.43
56:EB:179:ASN:HD22	56:EB:230:LYS:HA	1.82	0.43
60:IB:62:VAL:HG12	60:IB:77:ARG:HA	2.01	0.43
62:KB:51:SER:O	62:KB:55:ARG:HG2	2.18	0.43
69:RB:73:LEU:O	69:RB:76:GLU:HG3	2.17	0.43
84:GC:8:ARG:HB3	84:GC:309:VAL:HG23	2.00	0.43
2:B:28:LYS:NZ	48:WA:4584:C:OP2	2.49	0.43
2:B:31:SER:OG	48:WA:4716:C:OP1	2.31	0.43
4:D:176:SER:HB3	48:WA:4325:A:H4'	2.00	0.43
6:F:154:TYR:OH	6:F:187:GLU:OE2	2.36	0.43
10:J:112:HIS:HD1	10:J:126:TYR:H	1.67	0.43
12:L:72:TYR:HD1	12:L:75:LYS:HE2	1.82	0.43
26:Z:117:LEU:HB3	26:Z:140:VAL:HG21	2.01	0.43
48:WA:2732:U:H2'	48:WA:2733:C:C6	2.54	0.43
51:ZA:24:C:O2'	51:ZA:25:A:OP1	2.35	0.43
51:ZA:193:C:H2'	51:ZA:194:C:H6	1.84	0.43
51:ZA:943:U:H2'	51:ZA:944:A:H8	1.83	0.43
51:ZA:1144:A:H2'	51:ZA:1145:A:C8	2.54	0.43
72:UB:46:LYS:HD2	72:UB:101:ILE:HD13	2.01	0.43
82:EC:84:LYS:HE3	82:EC:84:LYS:HB3	1.90	0.43
13:M:54:LYS:NZ	48:WA:153:G:OP2	2.47	0.43
15:O:140:SER:OG	15:O:182:LYS:O	2.25	0.43
25:Y:22:LYS:NZ	25:Y:129:TRP:O	2.50	0.43
27:AA:18:ARG:NH1	48:WA:1670:A:O3'	2.44	0.43
48:WA:1506:G:H2'	48:WA:1507:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:2626:G:H2'	48:WA:2627:U:H6	1.82	0.43
48:WA:3857:C:H2'	48:WA:3858:A:H8	1.83	0.43
50:YA:102:G:OP2	50:YA:104:A:O2'	2.27	0.43
51:ZA:202:G:H2'	51:ZA:203:G:C8	2.54	0.43
51:ZA:388:U:H2'	51:ZA:389:A:C8	2.54	0.43
51:ZA:1016:U:OP2	79:BC:20:LYS:NZ	2.52	0.43
51:ZA:1103:C:H2'	51:ZA:1104:G:H8	1.84	0.43
61:JB:111:GLN:HE21	61:JB:123:ILE:HG22	1.83	0.43
65:NB:3:ARG:HB2	65:NB:6:ALA:HB3	2.01	0.43
74:WB:113:HIS:NE2	74:WB:114:GLU:OE2	2.51	0.43
80:CC:33:GLU:HG2	80:CC:41:SER:HB3	2.01	0.43
88:HC:273:LYS:NZ	88:HC:300:SER:O	2.51	0.43
3:C:278:ASN:OD1	3:C:279:LEU:N	2.52	0.43
4:D:69:ILE:HG12	19:S:31:MET:HG3	2.01	0.43
5:E:48:ARG:HG2	48:WA:986:U:OP1	2.19	0.43
6:F:181:TYR:CZ	6:F:202:GLU:HG2	2.54	0.43
16:P:75:ARG:HA	16:P:78:LYS:HD3	2.00	0.43
20:T:80:LYS:HG2	20:T:110:TYR:CE2	2.54	0.43
27:AA:10:HIS:NE2	48:WA:1879:G:O6	2.44	0.43
48:WA:4451:A:H8	92:WA:5228:ANM:H61	1.83	0.43
48:WA:4637:A:O2'	48:WA:4639:G:OP1	2.31	0.43
48:WA:4718:C:H2'	48:WA:4719:A:C8	2.52	0.43
48:WA:4962:G:H2'	48:WA:4963:G:C8	2.52	0.43
50:YA:66:A:H2'	50:YA:67:U:C6	2.54	0.43
51:ZA:12:U:H2'	51:ZA:13:C:H6	1.84	0.43
51:ZA:14:C:H2'	51:ZA:15:U:C6	2.53	0.43
51:ZA:929:G:H2'	51:ZA:930:C:O4'	2.18	0.43
51:ZA:1563:G:H5''	71:TB:121:ARG:NH1	2.34	0.43
51:ZA:1654:G:H2'	51:ZA:1655:C:C6	2.54	0.43
76:YB:83:LYS:HD2	76:YB:91:LEU:HD22	2.01	0.43
1:A:230:PRO:HG2	1:A:233:ARG:HB3	2.01	0.43
12:L:86:TRP:O	12:L:89:THR:OG1	2.35	0.43
30:DA:65:LYS:O	30:DA:75:ARG:NH2	2.49	0.43
48:WA:971:A:H5'	48:WA:972:C:H2'	2.00	0.43
48:WA:1881:C:O2'	48:WA:1893:A:N3	2.48	0.43
48:WA:2376:A:H2'	48:WA:2377:A:C8	2.54	0.43
48:WA:3863:A:H2'	48:WA:3864:A:C8	2.52	0.43
48:WA:4239:C:OP1	48:WA:4329:C:O2'	2.31	0.43
48:WA:4568:U:H2'	48:WA:4569:G:O4'	2.19	0.43
51:ZA:12:U:H2'	51:ZA:13:C:C6	2.54	0.43
51:ZA:479:C:H4'	88:HC:255:LYS:HD2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:959:G:H1'	51:ZA:964:A:H61	1.83	0.43
51:ZA:1407:U:H2'	51:ZA:1408:U:C6	2.54	0.43
58:GB:21:GLU:O	58:GB:25:ARG:HG3	2.19	0.43
64:MB:52:LEU:HD11	64:MB:78:LYS:HE3	2.00	0.43
76:YB:62:THR:HA	76:YB:69:THR:HG22	2.01	0.43
76:YB:100:LYS:HE2	76:YB:107:ARG:HH21	1.84	0.43
29:CA:53:ALA:HA	29:CA:88:LEU:HD21	2.01	0.42
29:CA:57:MET:HG2	29:CA:88:LEU:HD23	2.01	0.42
37:KA:36:ARG:NH2	48:WA:413:G:O4'	2.53	0.42
48:WA:281:U:H2'	48:WA:282:C:H6	1.83	0.42
48:WA:1302:G:H2'	48:WA:1303:C:C6	2.54	0.42
48:WA:1664:C:H2'	48:WA:1665:C:H6	1.83	0.42
48:WA:1939:C:OP2	48:WA:1940:C:O2'	2.25	0.42
48:WA:2092:U:OP1	48:WA:2268:C:N4	2.52	0.42
48:WA:2665:G:N2	48:WA:2678:A:O2'	2.52	0.42
48:WA:2899:G:H2'	48:WA:2900:G:C8	2.51	0.42
48:WA:3709:U:H2'	48:WA:3710:C:C6	2.54	0.42
48:WA:4993:U:H2'	48:WA:4994:G:C8	2.53	0.42
49:XA:4:U:H2'	49:XA:5:A:C8	2.54	0.42
50:YA:5:U:H2'	50:YA:6:C:H6	1.84	0.42
50:YA:153:C:H2'	50:YA:154:G:H8	1.84	0.42
51:ZA:1809:A:H2'	51:ZA:1810:U:C6	2.54	0.42
62:KB:1:MET:HE1	62:KB:44:HIS:CE1	2.54	0.42
84:GC:2:THR:O	84:GC:2:THR:OG1	2.34	0.42
3:C:163:LYS:HB2	3:C:166:GLU:HG3	2.01	0.42
12:L:118:MET:HE1	48:WA:4930:C:O2	2.19	0.42
16:P:150:ARG:NH2	48:WA:1501:C:OP1	2.52	0.42
22:V:112:ALA:O	22:V:116:LYS:HG2	2.20	0.42
48:WA:190:G:H2'	48:WA:191:G:H8	1.83	0.42
48:WA:2083:C:H2'	48:WA:2084:G:C8	2.53	0.42
48:WA:4156:G:H2'	48:WA:4157:C:C6	2.54	0.42
48:WA:4639:G:H2'	48:WA:4640:U:C6	2.54	0.42
51:ZA:479:C:H2'	51:ZA:480:G:C8	2.54	0.42
51:ZA:1079:C:O2'	51:ZA:1182:A:N1	2.49	0.42
51:ZA:1232:U:H2'	51:ZA:1233:G:H8	1.84	0.42
51:ZA:1294:G:H2'	51:ZA:1295:A:H8	1.83	0.42
51:ZA:1318:G:H2'	51:ZA:1319:U:C6	2.54	0.42
51:ZA:1671:G:H2'	51:ZA:1672:U:H6	1.83	0.42
51:ZA:1780:G:H2'	51:ZA:1781:A:C8	2.54	0.42
51:ZA:1842:C:H2'	51:ZA:1843:G:C8	2.54	0.42
74:WB:55:ASP:OD1	74:WB:56:HIS:N	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:CC:36:ASP:OD1	80:CC:36:ASP:N	2.52	0.42
1:A:21:LYS:HE3	48:WA:2745:A:H1'	2.00	0.42
6:F:148:SER:OG	6:F:244:ARG:NH2	2.49	0.42
10:J:24:ILE:HG12	10:J:128:LEU:HB3	2.00	0.42
16:P:39:THR:OG1	16:P:44:ASN:ND2	2.47	0.42
33:GA:109:ARG:HH22	48:WA:267:G:P	2.42	0.42
35:IA:44:LYS:N	48:WA:22:G:OP1	2.40	0.42
44:SA:26:A:H61	44:SA:44:A:H61	1.66	0.42
48:WA:727:G:H2'	48:WA:728:C:C6	2.54	0.42
48:WA:741:G:H2'	48:WA:742:G:H8	1.85	0.42
48:WA:1492:G:H2'	48:WA:1493:A:C8	2.53	0.42
48:WA:1647:C:H2'	48:WA:1648:A:C8	2.53	0.42
48:WA:2391:A:H2'	48:WA:2392:G:C8	2.54	0.42
48:WA:2448:C:H2'	48:WA:2449:U:C6	2.53	0.42
48:WA:4387:A:H61	48:WA:4533:U:H5'	1.83	0.42
51:ZA:920:A:O2'	51:ZA:922:A:O5'	2.37	0.42
51:ZA:1093:A:H2'	51:ZA:1094:C:H6	1.84	0.42
51:ZA:1112:U:H2'	51:ZA:1113:A:C8	2.54	0.42
51:ZA:1199:A:H2'	51:ZA:1200:A:C8	2.54	0.42
51:ZA:1488:C:H3'	51:ZA:1489:A:H4'	2.00	0.42
58:GB:2:LYS:HB2	58:GB:108:VAL:HG22	2.00	0.42
75:XB:46:HIS:HB3	75:XB:101:LEU:HD11	2.01	0.42
2:B:55:HIS:HB2	2:B:369:ASP:HB2	2.01	0.42
9:I:35:ASP:HA	9:I:87:ILE:O	2.19	0.42
10:J:87:LEU:HD13	10:J:87:LEU:HA	1.88	0.42
14:N:34:VAL:HG22	14:N:103:LYS:HB3	2.02	0.42
14:N:68:ARG:NH2	48:WA:4566:A:OP1	2.52	0.42
33:GA:97:LYS:HD3	48:WA:135:G:C6	2.55	0.42
37:KA:15:LYS:HD3	50:YA:45:C:P	2.59	0.42
48:WA:66:A:O2'	48:WA:326:C:O2	2.33	0.42
48:WA:478:G:H2'	48:WA:479:G:C8	2.54	0.42
48:WA:1346:C:H2'	48:WA:1347:A:C8	2.54	0.42
48:WA:2000:A:H4'	86:b:9:TRP:HZ2	1.85	0.42
48:WA:2628:U:H1'	48:WA:2631:C:H41	1.84	0.42
48:WA:2642:G:H2'	48:WA:2643:A:C8	2.55	0.42
51:ZA:409:C:H2'	51:ZA:410:G:C8	2.54	0.42
51:ZA:536:A:H61	51:ZA:549:C:N4	2.17	0.42
62:KB:15:LEU:HD13	62:KB:21:MET:HB2	2.01	0.42
70:SB:89:ASP:OD1	70:SB:89:ASP:N	2.50	0.42
1:A:242:ARG:NH2	1:A:243:THR:O	2.52	0.42
3:C:350:ARG:HD2	48:WA:725:C:OP1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:13:ARG:O	10:J:136:ARG:NH1	2.52	0.42
12:L:96:GLU:OE2	12:L:100:ARG:NH2	2.52	0.42
19:S:87:LYS:HZ2	48:WA:4307:G:N2	2.17	0.42
23:W:88:LYS:HA	23:W:91:GLU:HG2	2.02	0.42
29:CA:39:LYS:HE3	48:WA:2372:A:H5'	2.01	0.42
48:WA:32:G:H21	48:WA:50:C:H5	1.66	0.42
48:WA:655:C:H2'	48:WA:656:C:C6	2.55	0.42
48:WA:912:G:H2'	48:WA:913:U:H6	1.84	0.42
48:WA:1463:C:H2'	48:WA:1464:A:H8	1.84	0.42
48:WA:1463:C:H2'	48:WA:1464:A:C8	2.54	0.42
48:WA:2001:A:H2'	48:WA:2002:G:C4	2.55	0.42
48:WA:2680:A:H2'	48:WA:2681:G:H8	1.85	0.42
48:WA:3872:C:H2'	48:WA:3873:A:C8	2.54	0.42
51:ZA:1171:G:O2'	51:ZA:1187:G:O6	2.38	0.42
51:ZA:1577:G:O2'	51:ZA:1579:A:N3	2.51	0.42
51:ZA:1736:G:H2'	51:ZA:1737:G:C8	2.55	0.42
61:JB:101:LYS:N	61:JB:104:ASP:OD2	2.47	0.42
62:KB:6:LYS:HE3	62:KB:6:LYS:HB3	1.83	0.42
70:SB:120:HIS:CE1	70:SB:124:ARG:HD2	2.54	0.42
80:CC:23:SER:OG	80:CC:24:GLN:OE1	2.31	0.42
1:A:54:ARG:HG2	1:A:56:ALA:H	1.85	0.42
2:B:116:ARG:NH2	48:WA:4989:C:OP1	2.52	0.42
5:E:45:HIS:ND1	5:E:46:CYS:O	2.50	0.42
9:I:86:HIS:HB3	9:I:139:ARG:HG2	2.02	0.42
11:K:130:LYS:HE3	11:K:132:SER:HB2	2.00	0.42
33:GA:34:ALA:HA	33:GA:37:THR:HG22	2.01	0.42
46:UA:43:A:H3'	46:UA:44:A:C8	2.54	0.42
48:WA:1300:C:H2'	48:WA:1301:G:H8	1.85	0.42
48:WA:2081:G:H2'	48:WA:2082:U:H6	1.84	0.42
48:WA:2295:U:H2'	48:WA:2296:G:C8	2.55	0.42
51:ZA:495:U:O2'	56:EB:27:PHE:O	2.34	0.42
51:ZA:681:U:H4'	75:XB:9:THR:HG22	2.00	0.42
51:ZA:694:G:H22	51:ZA:732:U:H3	1.67	0.42
51:ZA:1383:A:H4'	55:DB:194:LEU:HG	2.01	0.42
58:GB:148:SER:N	58:GB:151:ASP:OD2	2.52	0.42
84:GC:104:HIS:NE2	84:GC:122:SER:OG	2.50	0.42
1:A:28:ARG:HE	1:A:123:ARG:HD3	1.84	0.42
1:A:179:ILE:O	48:WA:3655:A:O2'	2.19	0.42
2:B:2:SER:N	48:WA:4522:G:H5'	2.34	0.42
4:D:12:TYR:OH	48:WA:4267:U:OP1	2.38	0.42
17:Q:108:ARG:NH1	48:WA:2901:C:OP2	2.41	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:75:VAL:HG22	19:S:88:ARG:HG2	2.01	0.42
22:V:49:ILE:O	22:V:52:THR:OG1	2.29	0.42
25:Y:79:HIS:ND1	48:WA:2582:U:O2'	2.43	0.42
30:DA:67:LYS:HG2	30:DA:68:HIS:CD2	2.55	0.42
33:GA:96:ASN:N	33:GA:96:ASN:OD1	2.50	0.42
48:WA:325:U:H2'	48:WA:326:C:H6	1.84	0.42
48:WA:1263:G:H2'	48:WA:1264:G:H8	1.85	0.42
48:WA:1513:U:H2'	48:WA:1514:G:H8	1.85	0.42
48:WA:2545:A:H5'	50:YA:127:U:H1'	2.02	0.42
48:WA:2734:G:H2'	48:WA:2735:C:C6	2.55	0.42
48:WA:3935:G:H2'	48:WA:3936:G:H8	1.84	0.42
48:WA:4131:G:O6	48:WA:4158:G:N2	2.53	0.42
48:WA:4194:A:H2'	48:WA:4195:C:C6	2.55	0.42
48:WA:4565:U:C2	48:WA:4566:A:C8	3.08	0.42
48:WA:4956:G:H2'	48:WA:4957:A:C8	2.52	0.42
51:ZA:161:U:O2'	58:GB:87:ARG:NH1	2.53	0.42
51:ZA:674:C:H2'	51:ZA:675:U:C6	2.55	0.42
51:ZA:909:G:H2'	51:ZA:910:G:H8	1.84	0.42
53:BB:43:ASN:OD1	53:BB:43:ASN:N	2.52	0.42
64:MB:79:VAL:HG11	64:MB:85:LEU:HB2	2.01	0.42
66:OB:126:ILE:N	78:AC:56:ALA:O	2.51	0.42
84:GC:152:SER:N	84:GC:168:CYS:O	2.52	0.42
1:A:83:HIS:HB3	41:OA:64:VAL:HG13	2.01	0.42
2:B:82:PRO:HG3	2:B:171:LEU:HD21	2.02	0.42
27:AA:18:ARG:HH12	48:WA:1671:A:P	2.43	0.42
48:WA:1192:U:H2'	48:WA:1193:G:N3	2.34	0.42
48:WA:1246:G:H2'	48:WA:1247:C:C6	2.55	0.42
48:WA:1348:C:H2'	48:WA:1349:G:C8	2.54	0.42
48:WA:1788:A:H2'	48:WA:1791:C:C5	2.55	0.42
48:WA:2495:G:O2'	50:YA:127:U:OP1	2.29	0.42
48:WA:2664:G:H2'	48:WA:2665:G:C8	2.55	0.42
48:WA:2737:G:H2'	48:WA:2738:G:C8	2.53	0.42
50:YA:141:C:H2'	50:YA:142:U:C6	2.55	0.42
51:ZA:323:C:N4	51:ZA:328:U:OP1	2.37	0.42
51:ZA:1803:U:H2'	51:ZA:1804:U:C6	2.55	0.42
51:ZA:1839:U:H2'	51:ZA:1840:U:C6	2.55	0.42
55:DB:80:THR:HG21	72:UB:106:ILE:HD12	2.02	0.42
56:EB:129:ILE:HD13	56:EB:139:LEU:HB3	2.01	0.42
57:FB:127:ARG:O	80:CC:26:GLN:NE2	2.53	0.42
57:FB:167:LYS:HA	77:ZB:71:ALA:HB1	2.00	0.42
62:KB:53:LYS:HE2	62:KB:53:LYS:HB3	1.95	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:OB:34:PHE:HB3	66:OB:41:PHE:HB2	2.01	0.42
2:B:286:LYS:HB3	2:B:332:MET:HB3	2.02	0.42
4:D:36:LEU:HG	4:D:50:ARG:HD2	2.02	0.42
7:G:201:GLU:OE2	13:M:6:TYR:OH	2.30	0.42
13:M:136:ASP:OD2	50:YA:141:C:O2'	2.32	0.42
36:JA:37:ARG:NE	36:JA:38:CYS:O	2.53	0.42
41:OA:42:CYS:HB3	41:OA:60:CYS:HB2	2.02	0.42
48:WA:7:C:H2'	48:WA:8:U:C6	2.55	0.42
48:WA:169:A:N1	48:WA:267:G:C6	2.88	0.42
48:WA:4171:G:H4'	48:WA:4173:C:C2	2.55	0.42
49:XA:3:C:H2'	49:XA:4:U:H6	1.85	0.42
50:YA:30:U:H2'	50:YA:31:G:C8	2.54	0.42
51:ZA:85:A:H2'	51:ZA:86:C:H6	1.85	0.42
51:ZA:385:G:O2'	60:IB:10:LYS:NZ	2.51	0.42
51:ZA:444:G:O6	60:IB:26:LYS:HE3	2.20	0.42
51:ZA:1221:G:H2'	51:ZA:1222:G:H8	1.85	0.42
51:ZA:1662:U:O4	51:ZA:1663:A:N6	2.50	0.42
53:BB:65:ARG:HH12	66:OB:51:GLU:HG2	1.84	0.42
57:FB:142:SER:HB2	80:CC:50:VAL:HG22	2.01	0.42
60:IB:106:SER:HB3	60:IB:171:LEU:HG	2.02	0.42
61:JB:149:VAL:HG11	61:JB:157:ILE:HD11	2.02	0.42
73:VB:10:ASP:OD1	73:VB:10:ASP:N	2.52	0.42
5:E:80:SER:OG	48:WA:1272:A:N1	2.53	0.42
8:H:120:GLU:HG2	48:WA:4613:A:H2	1.85	0.42
9:I:51:HIS:CD2	9:I:168:SER:HB2	2.54	0.42
12:L:4:ARG:NH2	48:WA:4767:G:O6	2.33	0.42
22:V:46:PRO:HB2	22:V:54:LEU:HD12	2.00	0.42
29:CA:37:GLY:O	29:CA:41:ARG:HG3	2.20	0.42
37:KA:8:ARG:H	37:KA:8:ARG:HG3	1.65	0.42
48:WA:127:G:H2'	48:WA:128:C:C6	2.55	0.42
48:WA:424:U:H2'	48:WA:425:U:C6	2.55	0.42
48:WA:494:G:H2'	48:WA:495:C:C6	2.54	0.42
48:WA:3722:G:H22	48:WA:3735:A:H2	1.66	0.42
48:WA:3913:C:H2'	48:WA:3914:U:C6	2.54	0.42
48:WA:4455:C:O2	48:WA:4531:G:N2	2.53	0.42
48:WA:4752:G:H2'	48:WA:4753:G:H8	1.84	0.42
51:ZA:21:U:H2'	51:ZA:22:A:C8	2.55	0.42
51:ZA:28:U:H2'	51:ZA:29:G:H8	1.85	0.42
51:ZA:349:A:H2'	51:ZA:350:C:C6	2.55	0.42
51:ZA:991:G:C6	51:ZA:1134:G:H4'	2.55	0.42
51:ZA:1620:A:OP1	67:PB:115:TYR:OH	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:PB:108:LYS:HG3	67:PB:109:PRO:HD2	2.01	0.42
3:C:310:HIS:NE2	48:WA:2102:G:H2'	2.35	0.41
14:N:25:LYS:HD2	14:N:25:LYS:HA	1.90	0.41
24:X:91:ASN:OD1	24:X:92:GLY:N	2.53	0.41
48:WA:469:C:H2'	48:WA:470:A:C8	2.55	0.41
48:WA:2416:G:H2'	48:WA:2417:U:C6	2.54	0.41
48:WA:2449:U:H2'	48:WA:2450:G:H8	1.84	0.41
48:WA:2542:C:H2'	48:WA:2543:G:C8	2.55	0.41
48:WA:3877:G:N1	48:WA:3881:G:OP1	2.46	0.41
48:WA:4540:G:H2'	48:WA:4541:U:C6	2.55	0.41
49:XA:64:G:H2'	49:XA:65:G:H8	1.84	0.41
51:ZA:902:G:H2'	51:ZA:903:A:H8	1.85	0.41
54:CB:128:VAL:HG11	54:CB:155:ILE:HG12	2.01	0.41
54:CB:253:PRO:HA	54:CB:256:TRP:CD1	2.55	0.41
58:GB:50:VAL:HG13	58:GB:111:LEU:HB3	2.01	0.41
58:GB:50:VAL:HG11	58:GB:111:LEU:HD13	2.02	0.41
64:MB:81:ASP:HB3	64:MB:84:LYS:HB2	2.02	0.41
69:RB:37:GLU:HG3	84:GC:150:TRP:HE1	1.85	0.41
70:SB:121:ARG:HG3	70:SB:131:VAL:HG11	2.01	0.41
84:GC:61:GLY:HA3	84:GC:90:TRP:HZ2	1.83	0.41
11:K:60:ARG:NH2	48:WA:72:C:N3	2.67	0.41
26:Z:73:VAL:HB	26:Z:108:TYR:CG	2.55	0.41
33:GA:17:LEU:HD12	33:GA:17:LEU:HA	1.77	0.41
35:IA:52:LYS:HG2	35:IA:55:ARG:NH2	2.35	0.41
48:WA:288:G:H2'	48:WA:289:C:C6	2.55	0.41
48:WA:481:G:O2'	48:WA:483:G:OP2	2.33	0.41
48:WA:675:G:H2'	48:WA:676:C:C6	2.55	0.41
48:WA:1496:U:H2'	48:WA:1497:G:H8	1.85	0.41
48:WA:1664:C:H2'	48:WA:1665:C:C6	2.55	0.41
48:WA:2766:A:H2'	48:WA:2767:A:H8	1.85	0.41
48:WA:3873:A:H2'	48:WA:3874:A:H8	1.86	0.41
48:WA:4596:U:H2'	48:WA:4597:G:C8	2.52	0.41
48:WA:5015:C:H4'	48:WA:5016:A:H5''	2.02	0.41
51:ZA:799:U:H2'	51:ZA:800:U:C6	2.55	0.41
51:ZA:834:C:H2'	51:ZA:835:C:C5	2.55	0.41
51:ZA:921:G:OP2	79:BC:21:LYS:NZ	2.45	0.41
51:ZA:1047:C:H2'	51:ZA:1048:G:O4'	2.21	0.41
51:ZA:1236:G:O2'	67:PB:131:PRO:O	2.28	0.41
54:CB:116:THR:OG1	54:CB:117:ARG:N	2.53	0.41
55:DB:178:GLY:HA3	55:DB:220:LEU:HD12	2.03	0.41
60:IB:89:GLU:O	60:IB:93:THR:HG22	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:KB:11:ILE:HD13	62:KB:11:ILE:HA	1.89	0.41
70:SB:91:LYS:NZ	70:SB:109:GLU:OE1	2.53	0.41
86:b:112:ARG:NH1	86:b:119:CYS:SG	2.93	0.41
86:b:112:ARG:NE	86:b:121:VAL:HG11	2.35	0.41
88:HC:338:ALA:HB2	88:HC:444:LYS:HD3	2.02	0.41
9:I:158:LYS:NZ	48:WA:4415:C:O2	2.43	0.41
12:L:46:ARG:HH11	48:WA:942:U:H5	1.68	0.41
15:O:113:PRO:HB2	15:O:116:SER:HB2	2.02	0.41
16:P:65:ARG:HH21	48:WA:1461:A:H5''	1.86	0.41
17:Q:42:ARG:NH2	48:WA:2526:U:OP1	2.53	0.41
17:Q:95:TRP:CE2	48:WA:1574:U:H4'	2.55	0.41
18:R:87:ARG:HH11	49:XA:87:G:H5'	1.85	0.41
24:X:59:ARG:NH2	48:WA:210:C:OP1	2.45	0.41
25:Y:46:ILE:HG23	25:Y:68:ILE:HG23	2.02	0.41
28:BA:10:SER:OG	28:BA:11:LEU:N	2.51	0.41
36:JA:49:ASP:HB2	36:JA:52:LYS:HE2	2.02	0.41
47:VA:26:A:O2'	55:DB:184:ARG:NH1	2.53	0.41
48:WA:441:G:H2'	48:WA:442:G:H8	1.85	0.41
48:WA:1174:G:H2'	48:WA:1175:G:C8	2.55	0.41
48:WA:2592:G:H1'	48:WA:2758:G:N2	2.35	0.41
48:WA:2618:C:H2'	48:WA:2619:G:H8	1.85	0.41
48:WA:2872:A:H2'	48:WA:2873:A:C8	2.55	0.41
48:WA:3772:U:H2'	48:WA:3773:C:C6	2.54	0.41
51:ZA:1201:U:H2'	51:ZA:1202:U:C6	2.55	0.41
51:ZA:1415:C:O2'	71:TB:132:ASP:OD2	2.25	0.41
51:ZA:1862:G:O2'	78:AC:5:ARG:NH2	2.54	0.41
57:FB:18:LYS:HE3	57:FB:46:ALA:HB3	2.02	0.41
69:RB:99:ASP:OD1	69:RB:102:THR:N	2.41	0.41
74:WB:105:THR:HG22	74:WB:110:ILE:HG12	2.03	0.41
75:XB:124:LYS:HG2	75:XB:129:SER:HA	2.02	0.41
88:HC:370:CYS:HA	88:HC:406:PRO:HA	2.02	0.41
4:D:15:ARG:HH11	48:WA:1745:A:H1'	1.86	0.41
4:D:179:ARG:HD3	4:D:179:ARG:HA	1.79	0.41
19:S:4:THR:O	19:S:9:ARG:NE	2.53	0.41
21:U:87:SER:HA	21:U:97:TYR:HB3	2.02	0.41
41:OA:17:ARG:NH2	48:WA:1579:G:OP1	2.48	0.41
48:WA:229:G:H2'	48:WA:230:G:C8	2.55	0.41
48:WA:680:C:H2'	48:WA:681:G:C8	2.55	0.41
48:WA:2902:U:H2'	48:WA:2903:G:C8	2.55	0.41
48:WA:4995:G:C6	48:WA:5060:A:N1	2.89	0.41
49:XA:3:C:H2'	49:XA:4:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:371:A:OP2	60:IB:10:LYS:HB2	2.20	0.41
51:ZA:1415:C:H2'	51:ZA:1416:C:C6	2.55	0.41
51:ZA:1713:C:H2'	51:ZA:1714:U:C6	2.55	0.41
53:BB:35:ALA:HB2	53:BB:44:ILE:HD11	2.01	0.41
56:EB:31:PRO:HG3	56:EB:43:PRO:HG3	2.02	0.41
57:FB:192:LYS:HD3	57:FB:192:LYS:HA	1.84	0.41
67:PB:52:LYS:HE3	67:PB:52:LYS:HB2	1.88	0.41
88:HC:410:MET:HE2	88:HC:410:MET:HB3	1.96	0.41
2:B:165:HIS:HA	2:B:179:HIS:O	2.21	0.41
10:J:166:PHE:CE2	10:J:172:GLY:HA3	2.55	0.41
13:M:85:VAL:HG23	48:WA:43:U:OP1	2.21	0.41
26:Z:21:ARG:HB2	48:WA:1320:C:OP1	2.20	0.41
42:PA:112:ARG:NH1	48:WA:2266:C:OP1	2.54	0.41
43:RA:120:SER:HB3	86:b:48:ARG:HH21	1.85	0.41
43:RA:146:ARG:HD3	43:RA:146:ARG:HA	1.82	0.41
44:SA:8:U:O2'	44:SA:21:A:N1	2.44	0.41
48:WA:126:C:H2'	48:WA:127:G:C8	2.52	0.41
48:WA:1078:C:H2'	48:WA:1079:G:O4'	2.20	0.41
48:WA:1347:A:H2'	48:WA:1348:C:C6	2.55	0.41
48:WA:4082:C:H2'	48:WA:4083:G:H8	1.84	0.41
48:WA:4265:C:H2'	48:WA:4266:G:O4'	2.21	0.41
51:ZA:666:U:H2'	51:ZA:667:U:C6	2.55	0.41
51:ZA:1579:A:H4'	51:ZA:1581:C:C5	2.56	0.41
51:ZA:1673:U:H2'	51:ZA:1674:G:O4'	2.20	0.41
56:EB:136:ILE:HG23	56:EB:149:TYR:CE1	2.56	0.41
58:GB:216:ARG:HA	58:GB:216:ARG:HD3	1.91	0.41
59:HB:284:THR:HG23	59:HB:303:PRO:HG3	2.02	0.41
61:JB:119:LEU:HB2	61:JB:159:PHE:CZ	2.54	0.41
63:LB:55:TYR:CD2	63:LB:115:PRO:HG2	2.55	0.41
84:GC:90:TRP:NE1	84:GC:97:THR:OG1	2.53	0.41
1:A:29:LEU:O	1:A:123:ARG:NH1	2.54	0.41
3:C:60:HIS:NE2	3:C:100:ARG:HD3	2.36	0.41
6:F:131:MET:O	6:F:135:VAL:HG22	2.21	0.41
18:R:36:ASN:OD1	18:R:36:ASN:N	2.54	0.41
42:PA:6:GLN:NE2	42:PA:44:ILE:O	2.53	0.41
44:SA:41:G:O2'	51:ZA:1639:G:N3	2.53	0.41
48:WA:65:A:N6	48:WA:75:G:H1'	2.36	0.41
48:WA:2561:G:H2'	48:WA:2562:C:C6	2.55	0.41
48:WA:2591:C:H2'	48:WA:2592:G:O4'	2.20	0.41
48:WA:3600:C:H2'	48:WA:3601:A:H8	1.84	0.41
48:WA:3686:G:H2'	48:WA:3687:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:3754:C:H2'	48:WA:3779:G:H5''	2.03	0.41
48:WA:3797:A:H2'	48:WA:3798:U:C6	2.56	0.41
48:WA:4091:G:H2'	48:WA:4092:G:C8	2.55	0.41
51:ZA:675:U:H2'	51:ZA:676:C:C6	2.56	0.41
51:ZA:953:C:H5''	53:BB:24:PRO:HB2	2.02	0.41
51:ZA:1268:C:O2	67:PB:97:TYR:OH	2.38	0.41
51:ZA:1446:A:H5''	72:UB:58:THR:HG23	2.02	0.41
59:HB:274:LEU:HD21	59:HB:316:ARG:HD2	2.02	0.41
59:HB:318:VAL:HG23	59:HB:330:VAL:HG13	2.03	0.41
60:IB:114:GLU:OE2	60:IB:123:ARG:NH1	2.54	0.41
84:GC:73:SER:OG	84:GC:117:ASN:ND2	2.38	0.41
86:b:38:LYS:O	86:b:42:GLN:HG2	2.20	0.41
6:F:126:LYS:HB2	19:S:133:ALA:HB3	2.03	0.41
8:H:60:TRP:O	48:WA:4766:A:N6	2.38	0.41
12:L:91:TRP:CZ2	48:WA:4872:G:H2'	2.55	0.41
16:P:82:VAL:O	16:P:102:ALA:HA	2.20	0.41
29:CA:26:THR:OG1	29:CA:85:ARG:NH1	2.49	0.41
36:JA:41:TYR:OH	48:WA:2540:U:OP1	2.28	0.41
40:NA:89:LYS:HE3	48:WA:4231:U:H4'	2.02	0.41
48:WA:221:C:H2'	48:WA:222:C:C6	2.55	0.41
48:WA:2664:G:H2'	48:WA:2665:G:H8	1.86	0.41
48:WA:3650:A:H1'	48:WA:3787:A:H61	1.85	0.41
48:WA:3915:G:H3'	48:WA:3916:U:H4'	2.02	0.41
48:WA:4322:G:H2'	48:WA:4323:U:C6	2.56	0.41
48:WA:4993:U:O2'	48:WA:4994:G:H5'	2.21	0.41
51:ZA:21:U:O2'	61:JB:17:ARG:O	2.39	0.41
51:ZA:115:U:H2'	51:ZA:116:U:C6	2.56	0.41
51:ZA:304:C:OP1	60:IB:75:LYS:NZ	2.52	0.41
51:ZA:388:U:H2'	51:ZA:389:A:H8	1.86	0.41
51:ZA:409:C:H2'	51:ZA:410:G:H8	1.84	0.41
51:ZA:832:G:N1	51:ZA:843:C:N3	2.68	0.41
51:ZA:1183:A:H2'	51:ZA:1184:G:H8	1.85	0.41
51:ZA:1390:U:H2'	51:ZA:1391:C:C6	2.56	0.41
51:ZA:1555:U:H2'	51:ZA:1556:A:C8	2.56	0.41
51:ZA:1648:G:N7	68:QB:43:LYS:HE2	2.36	0.41
52:AB:124:VAL:HG21	52:AB:134:LEU:HD21	2.01	0.41
52:AB:130:ASP:C	52:AB:133:PRO:HD2	2.45	0.41
56:EB:212:ASP:OD1	56:EB:213:ALA:N	2.52	0.41
58:GB:54:GLY:O	58:GB:110:ASN:ND2	2.54	0.41
84:GC:164:ILE:HG23	84:GC:176:VAL:HG13	2.03	0.41
1:A:28:ARG:HB3	1:A:123:ARG:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:389:MET:O	48:WA:5043:G:N1	2.51	0.41
5:E:287:HIS:CE1	31:EA:33:VAL:HG22	2.56	0.41
7:G:119:GLN:HG3	13:M:28:TRP:CH2	2.55	0.41
13:M:108:ARG:HB2	13:M:161:MET:HE1	2.03	0.41
24:X:51:LYS:HB2	50:YA:72:A:OP2	2.21	0.41
25:Y:30:ASP:OD1	25:Y:30:ASP:N	2.51	0.41
33:GA:84:ARG:NH2	48:WA:17:A:OP1	2.37	0.41
48:WA:269:G:H2'	48:WA:270:U:C6	2.56	0.41
48:WA:440:U:H2'	48:WA:441:G:H8	1.85	0.41
48:WA:1648:A:H2'	48:WA:1649:U:C6	2.56	0.41
48:WA:1872:C:H2'	48:WA:1873:A:C8	2.56	0.41
48:WA:2266:C:H2'	48:WA:2267:G:O4'	2.20	0.41
48:WA:2599:G:H2'	48:WA:2600:A:H8	1.85	0.41
48:WA:3650:A:H1'	48:WA:3787:A:N6	2.36	0.41
48:WA:3776:A:H2'	48:WA:3777:A:C8	2.54	0.41
51:ZA:158:A:H2'	51:ZA:159:A:O4'	2.20	0.41
51:ZA:429:C:H2'	51:ZA:430:C:C6	2.56	0.41
51:ZA:1683:C:N3	80:CC:24:GLN:HG3	2.36	0.41
51:ZA:1688:C:H2'	51:ZA:1689:C:C6	2.56	0.41
55:DB:144:ARG:HG3	55:DB:213:VAL:HG13	2.03	0.41
56:EB:221:ARG:O	56:EB:225:ILE:HG12	2.20	0.41
57:FB:35:LEU:HD23	57:FB:39:ILE:HD11	2.03	0.41
88:HC:342:ALA:HB3	88:HC:404:MET:HE1	2.03	0.41
7:G:159:THR:HG22	7:G:248:HIS:NE2	2.35	0.41
10:J:96:LYS:O	10:J:159:LYS:NZ	2.41	0.41
11:K:62:PRO:HG3	48:WA:74:G:H1'	2.03	0.41
11:K:124:LEU:HD11	33:GA:119:TYR:HB2	2.01	0.41
14:N:14:HIS:CE1	14:N:119:VAL:HG13	2.56	0.41
15:O:91:ARG:NH1	48:WA:423:G:OP1	2.48	0.41
17:Q:18:GLY:HA3	48:WA:2824:G:H5''	2.02	0.41
18:R:21:LYS:HE2	18:R:21:LYS:HB2	1.87	0.41
18:R:107:THR:O	18:R:111:ARG:HG2	2.20	0.41
26:Z:12:ARG:NH1	48:WA:2347:G:OP2	2.54	0.41
26:Z:24:LYS:HD3	26:Z:26:ARG:HH21	1.86	0.41
43:RA:104:ILE:HB	43:RA:143:VAL:HG22	2.03	0.41
43:RA:146:ARG:O	43:RA:149:HIS:ND1	2.38	0.41
44:SA:11:U:H2'	44:SA:12:G:C8	2.55	0.41
46:UA:28:U:H2'	46:UA:29:C:C6	2.55	0.41
48:WA:221:C:H2'	48:WA:222:C:H6	1.85	0.41
48:WA:368:C:H2'	48:WA:369:G:C8	2.56	0.41
48:WA:475:G:H2'	48:WA:476:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:1444:C:H2'	48:WA:1445:A:C8	2.56	0.41
48:WA:1481:G:H2'	48:WA:1482:C:C6	2.55	0.41
48:WA:1506:G:H2'	48:WA:1507:C:H6	1.85	0.41
48:WA:2287:A:H2'	48:WA:2288:G:C8	2.55	0.41
48:WA:4455:C:H1'	48:WA:4531:G:H22	1.85	0.41
51:ZA:65:C:P	58:GB:175:LYS:H	2.43	0.41
51:ZA:162:C:H2'	51:ZA:163:U:O4'	2.21	0.41
51:ZA:220:U:H2'	51:ZA:221:A:C8	2.56	0.41
51:ZA:495:U:H2'	51:ZA:496:C:O4'	2.21	0.41
51:ZA:877:C:H2'	51:ZA:878:G:C8	2.56	0.41
51:ZA:916:A:C6	65:NB:73:ARG:HD3	2.56	0.41
51:ZA:944:A:H2'	51:ZA:945:U:H6	1.86	0.41
51:ZA:1005:G:OP2	53:BB:162:ARG:NH1	2.54	0.41
51:ZA:1284:A:C5	64:MB:91:LEU:HD11	2.56	0.41
51:ZA:1403:C:H42	51:ZA:1432:U:P	2.43	0.41
52:AB:102:ARG:HA	52:AB:102:ARG:HD2	1.83	0.41
53:BB:180:ASP:OD1	53:BB:180:ASP:N	2.52	0.41
55:DB:134:LEU:HD12	55:DB:236:ILE:HG12	2.02	0.41
57:FB:55:ARG:HG2	68:QB:151:ARG:HD3	2.01	0.41
58:GB:121:ILE:HG22	58:GB:123:GLY:H	1.86	0.41
59:HB:248:LYS:HD2	59:HB:248:LYS:HA	1.92	0.41
65:NB:83:ASP:OD1	65:NB:83:ASP:N	2.54	0.41
65:NB:87:ASP:OD1	65:NB:87:ASP:N	2.54	0.41
66:OB:127:GLY:HA2	78:AC:58:VAL:HG22	2.02	0.41
75:XB:52:LEU:HD11	75:XB:71:ARG:HD3	2.03	0.41
80:CC:20:ARG:NH2	80:CC:25:GLY:O	2.54	0.41
84:GC:130:LYS:HG2	84:GC:141:THR:HB	2.02	0.41
86:b:125:ALA:HA	86:b:218:GLY:HA2	2.02	0.41
1:A:181:LYS:HB2	48:WA:1579:G:C5	2.56	0.41
3:C:149:GLU:HG2	3:C:151:PRO:HD2	2.03	0.41
4:D:215:ASP:OD1	4:D:215:ASP:N	2.54	0.41
6:F:70:MET:HA	6:F:73:MET:HG2	2.03	0.41
8:H:91:LYS:HB2	8:H:183:GLU:HB3	2.03	0.41
9:I:177:ASN:HB2	9:I:180:GLU:HG3	2.01	0.41
19:S:54:HIS:ND1	19:S:56:CYS:SG	2.82	0.41
21:U:48:ARG:HB3	21:U:51:ARG:HE	1.86	0.41
40:NA:9:ARG:HA	40:NA:20:PRO:HA	2.02	0.41
43:RA:97:ASN:ND2	48:WA:1981:A:OP1	2.54	0.41
44:SA:50:U:H2'	44:SA:51:C:C6	2.56	0.41
48:WA:440:U:H2'	48:WA:441:G:C8	2.56	0.41
48:WA:1255:G:H1	48:WA:1262:G:N2	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:1310:C:H2'	48:WA:1311:C:C6	2.56	0.41
48:WA:1346:C:H2'	48:WA:1347:A:H8	1.86	0.41
48:WA:2540:U:H2'	48:WA:2541:C:C6	2.56	0.41
48:WA:4091:G:H2'	48:WA:4092:G:H8	1.86	0.41
51:ZA:26:U:H2'	51:ZA:27:A:C8	2.55	0.41
51:ZA:1617:G:N7	67:PB:47:ARG:NH1	2.69	0.41
84:GC:152:SER:H	84:GC:169:GLY:HA2	1.85	0.41
88:HC:341:THR:HB	88:HC:440:ALA:HB3	2.03	0.41
13:M:63:ARG:NH1	13:M:131:GLU:OE2	2.54	0.40
16:P:18:PRO:HG3	16:P:29:VAL:HG21	2.04	0.40
16:P:178:ARG:H	26:Z:51:GLY:HA2	1.84	0.40
29:CA:23:ARG:HG2	29:CA:121:ASN:HA	2.03	0.40
48:WA:913:U:H2'	48:WA:914:G:O4'	2.21	0.40
48:WA:1293:G:H2'	48:WA:1294:C:C6	2.56	0.40
48:WA:1336:A:H2'	48:WA:1337:G:H8	1.86	0.40
48:WA:2786:C:H2'	48:WA:2787:C:C6	2.57	0.40
48:WA:3929:U:H2'	48:WA:3930:A:C8	2.56	0.40
48:WA:5007:G:H22	48:WA:5043:G:H1'	1.86	0.40
51:ZA:199:C:O2'	51:ZA:200:G:H5'	2.21	0.40
51:ZA:561:A:H5''	61:JB:173:VAL:HG12	2.03	0.40
51:ZA:1143:A:O3'	51:ZA:1355:C:N4	2.54	0.40
51:ZA:1338:G:H2'	51:ZA:1339:U:C6	2.56	0.40
58:GB:160:LYS:HD2	58:GB:161:PRO:HD2	2.03	0.40
86:b:13:TYR:HA	86:b:16:LYS:HE2	2.03	0.40
88:HC:335:MET:HE3	88:HC:443:LYS:HD2	2.03	0.40
1:A:210:PRO:HG2	1:A:235:VAL:HG11	2.03	0.40
6:F:221:LYS:HB3	6:F:230:GLY:HA2	2.03	0.40
22:V:110:ARG:HA	22:V:113:LYS:HG2	2.03	0.40
30:DA:44:ARG:NH2	48:WA:1314:A:O2'	2.55	0.40
35:IA:2:THR:O	35:IA:7:SER:OG	2.29	0.40
45:TA:43:A:H2'	45:TA:44:G:C8	2.56	0.40
48:WA:926:C:H2'	48:WA:927:C:C6	2.56	0.40
48:WA:1658:U:H2'	48:WA:1659:G:H8	1.86	0.40
48:WA:2731:C:H2'	48:WA:2732:U:C6	2.56	0.40
48:WA:3709:U:H2'	48:WA:3710:C:H6	1.86	0.40
49:XA:15:C:H2'	49:XA:16:A:C8	2.56	0.40
49:XA:58:A:H2'	49:XA:59:G:H8	1.86	0.40
51:ZA:569:A:H2'	51:ZA:570:C:H6	1.86	0.40
51:ZA:1139:C:N4	51:ZA:1149:A:H62	2.20	0.40
51:ZA:1198:G:H2'	51:ZA:1199:A:H8	1.85	0.40
51:ZA:1579:A:H4'	51:ZA:1581:C:H5	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:CB:142:LYS:HG2	54:CB:153:GLY:HA3	2.02	0.40
54:CB:166:ARG:HB2	54:CB:248:TYR:CG	2.56	0.40
55:DB:93:THR:HA	55:DB:96:VAL:HG12	2.03	0.40
61:JB:133:ARG:HB3	61:JB:143:ASN:HD22	1.86	0.40
69:RB:76:GLU:HA	69:RB:79:GLU:HG3	2.03	0.40
71:TB:42:HIS:NE2	71:TB:43:LYS:HE3	2.36	0.40
74:WB:3:ARG:HD3	74:WB:6:VAL:HG12	2.02	0.40
78:AC:38:LYS:HG2	78:AC:40:VAL:HG23	2.04	0.40
84:GC:78:ALA:HB2	84:GC:92:LEU:HD11	2.03	0.40
3:C:230:LEU:HD21	3:C:239:LYS:HD2	2.03	0.40
6:F:88:LEU:HD11	6:F:121:PHE:HB3	2.03	0.40
16:P:85:THR:HG22	16:P:104:ARG:HB2	2.03	0.40
16:P:91:ARG:HB3	26:Z:76:ASP:HB3	2.03	0.40
28:BA:22:MET:HE1	28:BA:29:LEU:HD21	2.03	0.40
30:DA:37:LYS:HD2	30:DA:38:PRO:HD2	2.03	0.40
46:UA:27:U:H2'	46:UA:28:U:C6	2.57	0.40
48:WA:263:G:H2'	48:WA:264:C:C6	2.57	0.40
48:WA:312:G:H1	48:WA:325:U:H3	1.69	0.40
48:WA:1363:G:H2'	48:WA:1364:G:H8	1.85	0.40
48:WA:1741:G:H2'	48:WA:1742:C:C6	2.56	0.40
48:WA:4870:G:O2'	48:WA:4874:G:OP1	2.37	0.40
51:ZA:1623:A:C6	70:SB:132:ARG:HD3	2.56	0.40
51:ZA:1627:C:H2'	51:ZA:1628:C:H6	1.86	0.40
60:IB:157:LYS:NZ	60:IB:158:ILE:O	2.51	0.40
62:KB:64:TRP:CD2	81:DC:23:VAL:HG22	2.56	0.40
64:MB:19:GLN:OE1	64:MB:88:TRP:HB3	2.21	0.40
84:GC:35:SER:OG	84:GC:36:ARG:N	2.54	0.40
7:G:158:GLU:HB2	7:G:162:GLU:HB2	2.02	0.40
13:M:46:ASP:OD1	13:M:46:ASP:N	2.54	0.40
13:M:123:GLU:OE1	13:M:128:LYS:NZ	2.54	0.40
14:N:121:PRO:HD3	18:R:168:THR:HG22	2.03	0.40
16:P:11:ARG:HG3	48:WA:2083:C:H5''	2.03	0.40
23:W:56:ARG:HE	48:WA:14:C:P	2.44	0.40
24:X:106:ILE:HG21	24:X:109:LEU:HD23	2.03	0.40
26:Z:113:GLY:N	26:Z:133:ALA:HB2	2.36	0.40
31:EA:100:ARG:HG2	48:WA:4755:U:OP2	2.22	0.40
33:GA:109:ARG:NH2	48:WA:267:G:OP1	2.45	0.40
43:RA:128:THR:O	43:RA:131:GLU:HG2	2.22	0.40
48:WA:751:G:O2'	48:WA:914:G:N1	2.51	0.40
48:WA:753:G:H3'	48:WA:754:G:H8	1.86	0.40
48:WA:1859:C:H2'	48:WA:1860:A:C8	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:2685:C:H2'	48:WA:2686:C:C6	2.57	0.40
48:WA:2762:G:H4'	48:WA:2763:U:H5'	2.03	0.40
48:WA:2782:C:H2'	48:WA:2783:G:H8	1.85	0.40
48:WA:3600:C:H2'	48:WA:3601:A:C8	2.56	0.40
48:WA:4175:G:H2'	48:WA:4176:U:C6	2.56	0.40
48:WA:4942:C:H5'	48:WA:4943:G:H5''	2.03	0.40
50:YA:26:C:H2'	50:YA:27:U:C6	2.57	0.40
51:ZA:316:G:H2'	51:ZA:317:C:C6	2.56	0.40
51:ZA:568:C:H42	51:ZA:582:U:H3	1.69	0.40
51:ZA:1033:G:N1	51:ZA:1080:A:O2'	2.43	0.40
51:ZA:1221:G:H2'	51:ZA:1222:G:C8	2.56	0.40
51:ZA:1380:C:H2'	51:ZA:1381:G:C8	2.56	0.40
52:AB:137:ALA:HA	52:AB:142:LEU:HB3	2.02	0.40
56:EB:59:ASP:O	56:EB:63:LYS:HG2	2.22	0.40
56:EB:155:LYS:HA	56:EB:155:LYS:HD3	1.88	0.40
65:NB:40:LEU:HD12	65:NB:50:ILE:HG23	2.04	0.40
74:WB:93:LEU:HB2	74:WB:102:ILE:HD11	2.04	0.40
75:XB:142:ARG:HA	75:XB:142:ARG:HH11	1.86	0.40
78:AC:37:LYS:HB2	78:AC:37:LYS:HE3	1.84	0.40
78:AC:45:VAL:HG11	78:AC:53:ILE:HG13	2.03	0.40
84:GC:261:LEU:O	84:GC:264:LYS:NZ	2.38	0.40
87:c:242:GLU:O	87:c:246:GLU:HB2	2.21	0.40
2:B:373:LYS:HD2	48:WA:4629:U:H4'	2.04	0.40
3:C:65:GLU:HB3	3:C:80:ARG:HD3	2.03	0.40
3:C:286:ASN:N	16:P:124:ASP:OD2	2.55	0.40
5:E:193:HIS:HB3	5:E:196:PHE:HD2	1.87	0.40
6:F:175:ALA:HB1	48:WA:2104:G:C8	2.57	0.40
9:I:193:ASP:OD2	48:WA:1752:G:N2	2.53	0.40
18:R:35:PRO:HD2	18:R:39:VAL:HG21	2.03	0.40
21:U:89:ARG:HB2	21:U:95:PHE:CE2	2.56	0.40
33:GA:89:ARG:CZ	33:GA:93:ARG:HH12	2.34	0.40
48:WA:227:A:N6	48:WA:242:U:O4'	2.54	0.40
48:WA:273:U:H2'	48:WA:274:C:C6	2.56	0.40
48:WA:441:G:H2'	48:WA:442:G:C8	2.57	0.40
48:WA:456:C:H2'	48:WA:457:G:H8	1.84	0.40
48:WA:457:G:H2'	48:WA:458:C:C6	2.55	0.40
48:WA:1380:C:H4'	48:WA:1381:C:H5'	2.04	0.40
48:WA:1867:G:N2	48:WA:1870:A:OP2	2.43	0.40
48:WA:2001:A:N6	86:b:44:ARG:HH21	2.20	0.40
48:WA:2294:C:H2'	48:WA:2295:U:C6	2.57	0.40
48:WA:2635:U:H2'	48:WA:2636:C:C6	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:4553:U:H2'	48:WA:4554:U:C6	2.56	0.40
51:ZA:49:C:H2'	51:ZA:472:C:H41	1.86	0.40
51:ZA:651:U:H2'	51:ZA:652:U:C6	2.57	0.40
51:ZA:842:C:H2'	51:ZA:843:C:C6	2.56	0.40
51:ZA:1089:G:O6	75:XB:3:LYS:NZ	2.37	0.40
51:ZA:1202:U:H2'	51:ZA:1203:G:C8	2.56	0.40
71:TB:38:LYS:NZ	71:TB:40:ALA:O	2.43	0.40
76:YB:29:HIS:O	76:YB:29:HIS:ND1	2.55	0.40
84:GC:31:ILE:HD12	84:GC:299:PHE:CD2	2.57	0.40
86:b:54:LEU:HD22	86:b:54:LEU:HA	1.91	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	248/257 (96%)	236 (95%)	12 (5%)	0	100	100
2	B	395/403 (98%)	383 (97%)	12 (3%)	0	100	100
3	C	360/413 (87%)	348 (97%)	12 (3%)	0	100	100
4	D	292/297 (98%)	286 (98%)	6 (2%)	0	100	100
5	E	222/291 (76%)	217 (98%)	5 (2%)	0	100	100
6	F	225/249 (90%)	219 (97%)	6 (3%)	0	100	100
7	G	225/319 (70%)	220 (98%)	5 (2%)	0	100	100
8	H	188/192 (98%)	182 (97%)	6 (3%)	0	100	100
9	I	201/214 (94%)	196 (98%)	5 (2%)	0	100	100
10	J	169/178 (95%)	167 (99%)	2 (1%)	0	100	100
11	K	208/211 (99%)	202 (97%)	6 (3%)	0	100	100
12	L	136/218 (62%)	132 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	M	201/204 (98%)	198 (98%)	3 (2%)	0	100	100
14	N	197/203 (97%)	195 (99%)	2 (1%)	0	100	100
15	O	154/213 (72%)	151 (98%)	3 (2%)	0	100	100
16	P	185/188 (98%)	181 (98%)	4 (2%)	0	100	100
17	Q	178/212 (84%)	174 (98%)	4 (2%)	0	100	100
18	R	174/224 (78%)	166 (95%)	8 (5%)	0	100	100
19	S	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
20	T	99/128 (77%)	96 (97%)	3 (3%)	0	100	100
21	U	133/140 (95%)	129 (97%)	4 (3%)	0	100	100
22	V	106/157 (68%)	104 (98%)	2 (2%)	0	100	100
23	W	116/156 (74%)	115 (99%)	1 (1%)	0	100	100
24	X	132/145 (91%)	128 (97%)	4 (3%)	0	100	100
25	Y	133/136 (98%)	131 (98%)	2 (2%)	0	100	100
26	Z	145/148 (98%)	141 (97%)	4 (3%)	0	100	100
27	AA	103/245 (42%)	101 (98%)	2 (2%)	0	100	100
28	BA	97/115 (84%)	95 (98%)	2 (2%)	0	100	100
29	CA	106/125 (85%)	104 (98%)	2 (2%)	0	100	100
30	DA	127/135 (94%)	124 (98%)	3 (2%)	0	100	100
31	EA	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
32	FA	112/129 (87%)	111 (99%)	1 (1%)	0	100	100
33	GA	119/123 (97%)	117 (98%)	2 (2%)	0	100	100
34	HA	100/105 (95%)	93 (93%)	7 (7%)	0	100	100
35	IA	85/97 (88%)	84 (99%)	1 (1%)	0	100	100
36	JA	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
37	KA	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
38	LA	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
39	MA	23/25 (92%)	23 (100%)	0	0	100	100
40	NA	102/106 (96%)	98 (96%)	4 (4%)	0	100	100
41	OA	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
42	PA	122/137 (89%)	119 (98%)	3 (2%)	0	100	100
43	RA	151/165 (92%)	140 (93%)	11 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	AB	215/295 (73%)	213 (99%)	2 (1%)	0	100	100
53	BB	211/264 (80%)	207 (98%)	4 (2%)	0	100	100
54	CB	218/293 (74%)	213 (98%)	5 (2%)	0	100	100
55	DB	226/281 (80%)	225 (100%)	1 (0%)	0	100	100
56	EB	260/263 (99%)	251 (96%)	9 (4%)	0	100	100
57	FB	181/204 (89%)	175 (97%)	6 (3%)	0	100	100
58	GB	235/249 (94%)	231 (98%)	4 (2%)	0	100	100
59	HB	181/432 (42%)	176 (97%)	5 (3%)	0	100	100
60	IB	204/208 (98%)	201 (98%)	3 (2%)	0	100	100
61	JB	183/194 (94%)	179 (98%)	4 (2%)	0	100	100
62	KB	94/165 (57%)	92 (98%)	2 (2%)	0	100	100
63	LB	140/158 (89%)	136 (97%)	4 (3%)	0	100	100
64	MB	115/132 (87%)	109 (95%)	6 (5%)	0	100	100
65	NB	147/151 (97%)	146 (99%)	1 (1%)	0	100	100
66	OB	134/151 (89%)	130 (97%)	4 (3%)	0	100	100
67	PB	127/145 (88%)	125 (98%)	2 (2%)	0	100	100
68	QB	140/172 (81%)	136 (97%)	4 (3%)	0	100	100
69	RB	130/135 (96%)	127 (98%)	3 (2%)	0	100	100
70	SB	142/152 (93%)	139 (98%)	3 (2%)	0	100	100
71	TB	140/145 (97%)	135 (96%)	5 (4%)	0	100	100
72	UB	100/119 (84%)	97 (97%)	3 (3%)	0	100	100
73	VB	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
74	WB	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
75	XB	139/143 (97%)	135 (97%)	4 (3%)	0	100	100
76	YB	122/131 (93%)	120 (98%)	2 (2%)	0	100	100
77	ZB	83/124 (67%)	82 (99%)	1 (1%)	0	100	100
78	AC	99/115 (86%)	96 (97%)	3 (3%)	0	100	100
79	BC	81/84 (96%)	79 (98%)	2 (2%)	0	100	100
80	CC	60/69 (87%)	60 (100%)	0	0	100	100
81	DC	53/56 (95%)	53 (100%)	0	0	100	100
82	EC	53/133 (40%)	51 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
83	FC	67/188 (36%)	63 (94%)	4 (6%)	0	100	100
84	GC	311/317 (98%)	301 (97%)	10 (3%)	0	100	100
85	IC	2/4 (50%)	2 (100%)	0	0	100	100
86	b	162/318 (51%)	152 (94%)	9 (6%)	1 (1%)	22	53
87	c	12/14 (86%)	12 (100%)	0	0	100	100
88	HC	221/462 (48%)	209 (95%)	12 (5%)	0	100	100
All	All	11783/14293 (82%)	11469 (97%)	313 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
86	b	225	VAL

### 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 PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	192/199 (96%)	191 (100%)	1 (0%)	86	92
2	B	344/348 (99%)	337 (98%)	7 (2%)	50	74
3	C	302/337 (90%)	300 (99%)	2 (1%)	81	90
4	D	247/250 (99%)	246 (100%)	1 (0%)	89	94
5	E	201/251 (80%)	199 (99%)	2 (1%)	73	86
6	F	198/218 (91%)	198 (100%)	0	100	100
7	G	197/273 (72%)	194 (98%)	3 (2%)	60	80
8	H	169/171 (99%)	165 (98%)	4 (2%)	44	70
9	I	175/181 (97%)	173 (99%)	2 (1%)	70	84
10	J	144/149 (97%)	142 (99%)	2 (1%)	62	81
11	K	175/176 (99%)	171 (98%)	4 (2%)	45	70
12	L	117/161 (73%)	117 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	M	171/172 (99%)	167 (98%)	4 (2%)	45	70
14	N	171/173 (99%)	171 (100%)	0	100	100
15	O	137/190 (72%)	137 (100%)	0	100	100
16	P	164/165 (99%)	162 (99%)	2 (1%)	67	83
17	Q	159/191 (83%)	159 (100%)	0	100	100
18	R	157/192 (82%)	153 (98%)	4 (2%)	42	69
19	S	139/140 (99%)	137 (99%)	2 (1%)	62	81
20	T	91/114 (80%)	91 (100%)	0	100	100
21	U	103/107 (96%)	101 (98%)	2 (2%)	52	75
22	V	89/126 (71%)	88 (99%)	1 (1%)	70	84
23	W	106/134 (79%)	105 (99%)	1 (1%)	75	88
24	X	124/135 (92%)	120 (97%)	4 (3%)	34	63
25	Y	117/118 (99%)	116 (99%)	1 (1%)	75	88
26	Z	119/120 (99%)	118 (99%)	1 (1%)	79	89
27	AA	87/184 (47%)	87 (100%)	0	100	100
28	BA	85/98 (87%)	83 (98%)	2 (2%)	44	70
29	CA	98/110 (89%)	98 (100%)	0	100	100
30	DA	115/121 (95%)	114 (99%)	1 (1%)	75	88
31	EA	88/89 (99%)	88 (100%)	0	100	100
32	FA	98/109 (90%)	95 (97%)	3 (3%)	35	63
33	GA	109/110 (99%)	106 (97%)	3 (3%)	38	66
34	HA	86/89 (97%)	86 (100%)	0	100	100
35	IA	74/80 (92%)	73 (99%)	1 (1%)	62	81
36	JA	64/65 (98%)	64 (100%)	0	100	100
37	KA	47/48 (98%)	46 (98%)	1 (2%)	48	72
38	LA	48/116 (41%)	47 (98%)	1 (2%)	48	72
39	MA	24/24 (100%)	24 (100%)	0	100	100
40	NA	92/94 (98%)	92 (100%)	0	100	100
41	OA	74/75 (99%)	73 (99%)	1 (1%)	62	81
42	PA	108/121 (89%)	107 (99%)	1 (1%)	75	88
43	RA	126/137 (92%)	117 (93%)	9 (7%)	12	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	AB	180/244 (74%)	179 (99%)	1 (1%)	84	91
53	BB	194/231 (84%)	192 (99%)	2 (1%)	73	86
54	CB	186/225 (83%)	185 (100%)	1 (0%)	86	92
55	DB	190/232 (82%)	189 (100%)	1 (0%)	86	92
56	EB	224/225 (100%)	219 (98%)	5 (2%)	47	71
57	FB	158/170 (93%)	156 (99%)	2 (1%)	65	82
58	GB	207/218 (95%)	203 (98%)	4 (2%)	52	75
59	HB	165/360 (46%)	161 (98%)	4 (2%)	44	70
60	IB	178/180 (99%)	176 (99%)	2 (1%)	70	84
61	JB	161/168 (96%)	160 (99%)	1 (1%)	84	91
62	KB	87/136 (64%)	86 (99%)	1 (1%)	70	84
63	LB	130/142 (92%)	128 (98%)	2 (2%)	60	80
64	MB	99/108 (92%)	93 (94%)	6 (6%)	15	43
65	NB	130/131 (99%)	129 (99%)	1 (1%)	79	89
66	OB	106/119 (89%)	105 (99%)	1 (1%)	75	88
67	PB	115/130 (88%)	111 (96%)	4 (4%)	31	61
68	QB	117/140 (84%)	114 (97%)	3 (3%)	41	68
69	RB	119/121 (98%)	115 (97%)	4 (3%)	32	62
70	SB	125/132 (95%)	123 (98%)	2 (2%)	58	79
71	TB	112/115 (97%)	109 (97%)	3 (3%)	40	67
72	UB	93/107 (87%)	90 (97%)	3 (3%)	34	63
73	VB	67/67 (100%)	66 (98%)	1 (2%)	60	80
74	WB	112/113 (99%)	111 (99%)	1 (1%)	75	88
75	XB	113/115 (98%)	110 (97%)	3 (3%)	40	67
76	YB	107/113 (95%)	107 (100%)	0	100	100
77	ZB	75/102 (74%)	74 (99%)	1 (1%)	65	82
78	AC	88/98 (90%)	87 (99%)	1 (1%)	70	84
79	BC	75/76 (99%)	73 (97%)	2 (3%)	40	67
80	CC	55/62 (89%)	55 (100%)	0	100	100
81	DC	48/49 (98%)	47 (98%)	1 (2%)	48	72
82	EC	46/106 (43%)	44 (96%)	2 (4%)	25	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
83	FC	62/154 (40%)	59 (95%)	3 (5%)	21	51
84	GC	272/275 (99%)	252 (93%)	20 (7%)	11	36
86	b	138/258 (54%)	128 (93%)	10 (7%)	12	38
87	c	12/12 (100%)	12 (100%)	0	100	100
88	HC	179/379 (47%)	163 (91%)	16 (9%)	8	29
All	All	10256/12074 (85%)	10069 (98%)	187 (2%)	54	76

All (187) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	VAL
2	B	162	VAL
2	B	248	LEU
2	B	258	HIS
2	B	298	LEU
2	B	314	ILE
2	B	338	VAL
2	B	353	VAL
3	C	115	VAL
3	C	232	VAL
4	D	163	LEU
5	E	178	VAL
5	E	189	LEU
7	G	159	THR
7	G	193	VAL
7	G	221	VAL
8	H	47	LEU
8	H	73	ILE
8	H	95	VAL
8	H	123	ILE
9	I	126	VAL
9	I	184	MET
10	J	87	LEU
10	J	129	ASP
11	K	63	THR
11	K	64	VAL
11	K	70	VAL
11	K	90	VAL
13	M	60	VAL
13	M	64	ILE

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Mol	Chain	Res	Type
13	M	142	ILE
13	M	184	ILE
16	P	22	ASP
16	P	83	VAL
18	R	84	TYR
18	R	132	ILE
18	R	154	LEU
18	R	160	ARG
19	S	80	VAL
19	S	143	THR
21	U	92	ASP
21	U	109	LYS
22	V	87	LEU
23	W	52	LEU
24	X	79	VAL
24	X	82	ILE
24	X	95	VAL
24	X	104	VAL
25	Y	53	VAL
26	Z	122	VAL
28	BA	14	ILE
28	BA	71	VAL
30	DA	107	ASN
32	FA	22	LEU
32	FA	32	TYR
32	FA	67	LEU
33	GA	17	LEU
33	GA	96	ASN
33	GA	116	LEU
35	IA	59	THR
37	KA	51	LEU
38	LA	100	LYS
41	OA	52	VAL
42	PA	103	HIS
43	RA	13	VAL
43	RA	37	LEU
43	RA	58	ILE
43	RA	66	ASN
43	RA	92	ARG
43	RA	137	GLN
43	RA	147	HIS
43	RA	151	ILE

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Mol	Chain	Res	Type
43	RA	154	ASP
52	AB	124	VAL
53	BB	82	ARG
53	BB	126	ASP
54	CB	248	TYR
55	DB	205	TYR
56	EB	12	VAL
56	EB	62	LYS
56	EB	207	VAL
56	EB	220	THR
56	EB	222	LEU
57	FB	102	LEU
57	FB	109	LEU
58	GB	50	VAL
58	GB	153	VAL
58	GB	157	VAL
58	GB	213	LEU
59	HB	284	THR
59	HB	313	ILE
59	HB	372	VAL
59	HB	405	GLU
60	IB	107	THR
60	IB	125	LYS
61	JB	66	LYS
62	KB	47	LYS
63	LB	48	LYS
63	LB	52	GLU
64	MB	27	ILE
64	MB	28	HIS
64	MB	31	LEU
64	MB	57	ASP
64	MB	62	VAL
64	MB	111	VAL
65	NB	54	LEU
66	OB	56	VAL
67	PB	37	TYR
67	PB	65	LYS
67	PB	72	LYS
67	PB	90	VAL
68	QB	75	TYR
68	QB	110	ILE
68	QB	126	VAL

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Mol	Chain	Res	Type
69	RB	6	THR
69	RB	95	ILE
69	RB	99	ASP
69	RB	132	ARG
70	SB	3	LEU
70	SB	131	VAL
71	TB	4	VAL
71	TB	24	LYS
71	TB	99	VAL
72	UB	17	ILE
72	UB	18	HIS
72	UB	68	THR
73	VB	11	LEU
74	WB	105	THR
75	XB	17	ARG
75	XB	81	ILE
75	XB	105	PHE
77	ZB	32	LYS
78	AC	100	ARG
79	BC	43	ILE
79	BC	80	ARG
81	DC	39	CYS
82	EC	118	VAL
82	EC	124	LYS
83	FC	85	TYR
83	FC	108	VAL
83	FC	135	HIS
84	GC	8	ARG
84	GC	11	LEU
84	GC	18	VAL
84	GC	31	ILE
84	GC	38	LYS
84	GC	54	ILE
84	GC	68	ASP
84	GC	113	PHE
84	GC	120	ILE
84	GC	141	THR
84	GC	142	VAL
84	GC	164	ILE
84	GC	177	TRP
84	GC	186	THR
84	GC	198	VAL

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Mol	Chain	Res	Type
84	GC	256	ILE
84	GC	274	VAL
84	GC	275	ILE
84	GC	280	LYS
84	GC	297	THR
86	b	21	LEU
86	b	53	VAL
86	b	54	LEU
86	b	69	LEU
86	b	75	LEU
86	b	105	ASN
86	b	116	ILE
86	b	149	ARG
86	b	219	VAL
86	b	222	VAL
88	HC	240	ARG
88	HC	248	LEU
88	HC	287	THR
88	HC	290	LYS
88	HC	312	VAL
88	HC	313	LYS
88	HC	347	LEU
88	HC	360	VAL
88	HC	371	LYS
88	HC	387	LEU
88	HC	408	LYS
88	HC	429	MET
88	HC	432	THR
88	HC	438	ILE
88	HC	439	LYS
88	HC	444	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (88) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	205	ASN
3	C	21	ASN
3	C	41	HIS
3	C	187	GLN
3	C	203	GLN
3	C	329	ASN
3	C	347	HIS

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Mol	Chain	Res	Type
4	D	131	ASN
4	D	275	GLN
4	D	282	GLN
6	F	98	ASN
8	H	63	ASN
9	I	59	GLN
9	I	73	ASN
10	J	23	ASN
11	K	159	ASN
12	L	48	GLN
12	L	125	ASN
13	M	182	HIS
15	O	10	ASN
15	O	93	ASN
17	Q	34	ASN
17	Q	58	HIS
17	Q	118	HIS
18	R	163	HIS
19	S	127	GLN
19	S	139	HIS
20	T	38	ASN
20	T	105	ASN
21	U	108	ASN
22	V	48	GLN
27	AA	6	ASN
28	BA	33	GLN
28	BA	72	HIS
29	CA	18	ASN
29	CA	116	ASN
31	EA	55	ASN
32	FA	14	ASN
34	HA	15	HIS
35	IA	48	ASN
37	KA	33	ASN
42	PA	21	ASN
42	PA	31	ASN
42	PA	100	ASN
43	RA	137	GLN
53	BB	158	HIS
53	BB	186	ASN
53	BB	202	GLN
54	CB	136	HIS

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Mol	Chain	Res	Type
54	CB	172	ASN
54	CB	178	HIS
55	DB	95	ASN
56	EB	50	ASN
57	FB	79	HIS
58	GB	110	ASN
59	HB	271	ASN
60	IB	7	ASN
60	IB	22	HIS
60	IB	35	ASN
60	IB	155	ASN
61	JB	124	HIS
61	JB	140	GLN
63	LB	19	ASN
64	MB	46	GLN
64	MB	75	ASN
65	NB	49	GLN
65	NB	58	HIS
66	OB	32	HIS
68	QB	37	GLN
68	QB	55	ASN
69	RB	116	ASN
70	SB	10	GLN
71	TB	126	GLN
73	VB	21	ASN
74	WB	15	ASN
75	XB	61	GLN
76	YB	29	HIS
76	YB	63	HIS
76	YB	112	ASN
77	ZB	112	ASN
78	AC	7	ASN
80	CC	29	GLN
80	CC	45	ASN
81	DC	16	GLN
84	GC	222	ASN
86	b	42	GLN
88	HC	348	ASN
88	HC	367	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
44	SA	75/76 (98%)	16 (21%)	3 (4%)
45	TA	75/76 (98%)	16 (21%)	0
46	UA	74/75 (98%)	38 (51%)	1 (1%)
47	VA	11/12 (91%)	3 (27%)	0
48	WA	3556/3584 (99%)	610 (17%)	20 (0%)
49	XA	118/120 (98%)	10 (8%)	0
50	YA	155/156 (99%)	32 (20%)	0
51	ZA	1707/1869 (91%)	327 (19%)	9 (0%)
All	All	5771/5968 (96%)	1052 (18%)	33 (0%)

All (1052) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
44	SA	9	A
44	SA	16	C
44	SA	18	G
44	SA	19	C
44	SA	20	A
44	SA	21	A
44	SA	22	A
44	SA	46	G
44	SA	47	U
44	SA	48	C
44	SA	49	C
44	SA	58	A
44	SA	60	A
44	SA	61	C
44	SA	70	A
44	SA	76	A
45	TA	6	G
45	TA	7	A
45	TA	10	G
45	TA	13	C
45	TA	16	C
45	TA	17	U
45	TA	18	G
45	TA	19	A
45	TA	20	U
45	TA	22	G
45	TA	31	A
45	TA	34	U
45	TA	35	U
45	TA	47	U

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Mol	Chain	Res	Type
45	TA	58	A
45	TA	76	A
46	UA	8	U
46	UA	16	C
46	UA	17	G
46	UA	18	G
46	UA	19	U
46	UA	20	U
46	UA	21	A
46	UA	22	U
46	UA	24	A
46	UA	25	C
46	UA	26	G
46	UA	30	G
46	UA	31	C
46	UA	32	C
46	UA	33	U
46	UA	34	U
46	UA	38	C
46	UA	40	C
46	UA	41	G
46	UA	42	A
46	UA	43	A
46	UA	44	A
46	UA	46	G
46	UA	48	C
46	UA	49	C
46	UA	52	G
46	UA	56	C
46	UA	58	A
46	UA	59	A
46	UA	60	A
46	UA	61	C
46	UA	66	C
46	UA	67	G
46	UA	70	A
46	UA	71	A
46	UA	74	C
46	UA	75	C
46	UA	76	A
47	VA	22	U
47	VA	24	A

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Mol	Chain	Res	Type
47	VA	26	A
48	WA	12	A
48	WA	13	U
48	WA	25	A
48	WA	39	A
48	WA	42	A
48	WA	48	G
48	WA	56	A
48	WA	59	A
48	WA	64	A
48	WA	65	A
48	WA	66	A
48	WA	91	G
48	WA	109	G
48	WA	110	C
48	WA	117	C
48	WA	119	G
48	WA	120	A
48	WA	130	C
48	WA	132	G
48	WA	133	C
48	WA	134	G
48	WA	135	G
48	WA	136	C
48	WA	138	G
48	WA	142	G
48	WA	143	C
48	WA	144	G
48	WA	151	G
48	WA	157	U
48	WA	159	C
48	WA	169	A
48	WA	171	U
48	WA	172	C
48	WA	173	C
48	WA	179	G
48	WA	182	G
48	WA	197	A
48	WA	200	U
48	WA	201	C
48	WA	209	U
48	WA	217	C

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Mol	Chain	Res	Type
48	WA	218	A
48	WA	219	G
48	WA	220	C
48	WA	224	U
48	WA	233	U
48	WA	234	G
48	WA	253	G
48	WA	263	G
48	WA	266	C
48	WA	267	G
48	WA	276	C
48	WA	280	G
48	WA	297	U
48	WA	306	A
48	WA	315	G
48	WA	316	U
48	WA	334	A
48	WA	340	C
48	WA	350	C
48	WA	363	A
48	WA	373	G
48	WA	379	G
48	WA	386	A
48	WA	387	G
48	WA	399	G
48	WA	409	G
48	WA	410	A
48	WA	412	G
48	WA	414	C
48	WA	449	C
48	WA	450	G
48	WA	452	A
48	WA	454	U
48	WA	455	C
48	WA	467	U
48	WA	468	U
48	WA	482	C
48	WA	483	G
48	WA	484	G
48	WA	485	U
48	WA	487	C
48	WA	488	G

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Mol	Chain	Res	Type
48	WA	489	G
48	WA	493	U
48	WA	494	G
48	WA	499	C
48	WA	500	G
48	WA	506	G
48	WA	511	U
48	WA	521	U
48	WA	662	C
48	WA	667	G
48	WA	686	C
48	WA	697	C
48	WA	698	G
48	WA	705	C
48	WA	720	C
48	WA	732	G
48	WA	739	C
48	WA	741	G
48	WA	751	G
48	WA	761	G
48	WA	905	U
48	WA	907	C
48	WA	915	U
48	WA	917	A
48	WA	919	A
48	WA	920	G
48	WA	929	C
48	WA	930	G
48	WA	933	A
48	WA	936	A
48	WA	937	G
48	WA	938	C
48	WA	939	A
48	WA	940	G
48	WA	941	C
48	WA	944	G
48	WA	946	C
48	WA	949	A
48	WA	950	U
48	WA	964	G
48	WA	965	A
48	WA	966	G

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Mol	Chain	Res	Type
48	WA	971	A
48	WA	972	C
48	WA	974	C
48	WA	978	C
48	WA	989	C
48	WA	1078	C
48	WA	1084	A
48	WA	1085	C
48	WA	1102	C
48	WA	1103	C
48	WA	1104	G
48	WA	1186	C
48	WA	1200	G
48	WA	1201	G
48	WA	1202	G
48	WA	1206	G
48	WA	1208	C
48	WA	1216	C
48	WA	1217	G
48	WA	1221	C
48	WA	1222	C
48	WA	1240	G
48	WA	1243	C
48	WA	1244	A
48	WA	1246	G
48	WA	1253	C
48	WA	1255	G
48	WA	1258	A
48	WA	1259	A
48	WA	1265	A
48	WA	1270	G
48	WA	1271	G
48	WA	1272	A
48	WA	1274	C
48	WA	1275	G
48	WA	1282	C
48	WA	1286	G
48	WA	1287	U
48	WA	1289	G
48	WA	1290	G
48	WA	1294	C
48	WA	1298	G

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Mol	Chain	Res	Type
48	WA	1303	C
48	WA	1305	A
48	WA	1328	A
48	WA	1356	A
48	WA	1360	G
48	WA	1361	G
48	WA	1379	G
48	WA	1381	C
48	WA	1382	G
48	WA	1383	U
48	WA	1389	A
48	WA	1396	G
48	WA	1399	A
48	WA	1400	A
48	WA	1421	G
48	WA	1422	A
48	WA	1435	A
48	WA	1447	U
48	WA	1448	C
48	WA	1459	G
48	WA	1485	C
48	WA	1499	A
48	WA	1500	G
48	WA	1503	C
48	WA	1504	G
48	WA	1520	A
48	WA	1525	A
48	WA	1527	A
48	WA	1536	A
48	WA	1549	A
48	WA	1566	A
48	WA	1568	C
48	WA	1580	U
48	WA	1593	U
48	WA	1598	U
48	WA	1599	G
48	WA	1604	U
48	WA	1614	G
48	WA	1626	G
48	WA	1627	G
48	WA	1633	A
48	WA	1635	G

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Mol	Chain	Res	Type
48	WA	1636	A
48	WA	1640	A
48	WA	1643	G
48	WA	1656	G
48	WA	1663	C
48	WA	1678	C
48	WA	1679	U
48	WA	1686	A
48	WA	1693	G
48	WA	1743	G
48	WA	1744	A
48	WA	1748	A
48	WA	1756	U
48	WA	1757	C
48	WA	1763	G
48	WA	1765	C
48	WA	1768	A
48	WA	1769	A
48	WA	1770	C
48	WA	1771	G
48	WA	1772	A
48	WA	1774	C
48	WA	1782	A
48	WA	1783	U
48	WA	1789	A
48	WA	1806	A
48	WA	1807	A
48	WA	1817	G
48	WA	1821	G
48	WA	1823	G
48	WA	1824	U
48	WA	1830	C
48	WA	1836	U
48	WA	1838	G
48	WA	1839	A
48	WA	1844	G
48	WA	1857	G
48	WA	1871	G
48	WA	1880	G
48	WA	1890	A
48	WA	1899	A
48	WA	1912	G

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Mol	Chain	Res	Type
48	WA	1920	U
48	WA	1922	C
48	WA	1923	C
48	WA	1924	G
48	WA	1931	A
48	WA	1933	C
48	WA	1950	G
48	WA	1963	G
48	WA	1964	A
48	WA	1975	G
48	WA	1976	U
48	WA	1977	G
48	WA	1984	G
48	WA	1985	A
48	WA	1986	A
48	WA	1987	G
48	WA	1988	U
48	WA	1989	C
48	WA	1990	G
48	WA	1992	A
48	WA	1993	A
48	WA	1999	U
48	WA	2000	A
48	WA	2003	G
48	WA	2004	A
48	WA	2005	G
48	WA	2010	U
48	WA	2023	G
48	WA	2027	A
48	WA	2028	A
48	WA	2046	U
48	WA	2048	G
48	WA	2049	A
48	WA	2050	U
48	WA	2054	G
48	WA	2057	G
48	WA	2058	G
48	WA	2064	C
48	WA	2071	A
48	WA	2086	U
48	WA	2095	G
48	WA	2096	C

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Mol	Chain	Res	Type
48	WA	2097	A
48	WA	2099	A
48	WA	2102	G
48	WA	2104	G
48	WA	2106	A
48	WA	2107	A
48	WA	2108	G
48	WA	2109	A
48	WA	2114	G
48	WA	2118	C
48	WA	2261	G
48	WA	2262	C
48	WA	2269	U
48	WA	2270	A
48	WA	2277	G
48	WA	2291	C
48	WA	2302	A
48	WA	2303	G
48	WA	2308	G
48	WA	2315	A
48	WA	2316	G
48	WA	2333	G
48	WA	2335	G
48	WA	2350	G
48	WA	2353	C
48	WA	2362	A
48	WA	2384	A
48	WA	2397	A
48	WA	2412	C
48	WA	2419	A
48	WA	2424	C
48	WA	2427	U
48	WA	2434	U
48	WA	2435	G
48	WA	2436	G
48	WA	2473	G
48	WA	2477	G
48	WA	2485	G
48	WA	2491	C
48	WA	2492	U
48	WA	2493	C
48	WA	2505	G

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Mol	Chain	Res	Type
48	WA	2506	C
48	WA	2507	C
48	WA	2509	A
48	WA	2515	A
48	WA	2531	A
48	WA	2539	A
48	WA	2546	G
48	WA	2547	U
48	WA	2548	G
48	WA	2549	G
48	WA	2555	A
48	WA	2585	C
48	WA	2588	G
48	WA	2591	C
48	WA	2603	A
48	WA	2620	G
48	WA	2622	G
48	WA	2629	C
48	WA	2640	G
48	WA	2655	C
48	WA	2664	G
48	WA	2672	C
48	WA	2677	G
48	WA	2688	G
48	WA	2689	U
48	WA	2697	A
48	WA	2698	A
48	WA	2705	G
48	WA	2707	G
48	WA	2709	U
48	WA	2710	U
48	WA	2711	C
48	WA	2712	C
48	WA	2713	G
48	WA	2721	C
48	WA	2723	G
48	WA	2727	A
48	WA	2728	G
48	WA	2742	U
48	WA	2756	G
48	WA	2760	G
48	WA	2766	A

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Mol	Chain	Res	Type
48	WA	2771	U
48	WA	2789	A
48	WA	2790	U
48	WA	2792	U
48	WA	2796	C
48	WA	2800	A
48	WA	2808	A
48	WA	2816	C
48	WA	2828	U
48	WA	2829	G
48	WA	2830	U
48	WA	2845	U
48	WA	2857	G
48	WA	2899	G
48	WA	3599	G
48	WA	3600	C
48	WA	3617	G
48	WA	3627	G
48	WA	3628	G
48	WA	3637	A
48	WA	3650	A
48	WA	3664	A
48	WA	3666	G
48	WA	3674	G
48	WA	3714	A
48	WA	3716	G
48	WA	3750	A
48	WA	3755	G
48	WA	3763	C
48	WA	3774	U
48	WA	3775	U
48	WA	3776	A
48	WA	3778	G
48	WA	3779	G
48	WA	3786	A
48	WA	3788	U
48	WA	3800	U
48	WA	3804	U
48	WA	3812	C
48	WA	3813	G
48	WA	3816	U
48	WA	3819	A

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Mol	Chain	Res	Type
48	WA	3821	G
48	WA	3840	U
48	WA	3841	G
48	WA	3842	U
48	WA	3871	C
48	WA	3878	A
48	WA	3879	A
48	WA	3880	C
48	WA	3881	G
48	WA	3891	G
48	WA	3894	U
48	WA	3899	G
48	WA	3903	A
48	WA	3908	A
48	WA	3909	G
48	WA	3910	A
48	WA	3916	U
48	WA	3917	U
48	WA	3919	A
48	WA	3940	G
48	WA	3941	G
48	WA	3945	A
48	WA	3949	A
48	WA	3951	A
48	WA	3953	G
48	WA	4066	C
48	WA	4078	G
48	WA	4088	G
48	WA	4090	C
48	WA	4097	G
48	WA	4100	A
48	WA	4101	G
48	WA	4118	C
48	WA	4121	C
48	WA	4123	G
48	WA	4124	G
48	WA	4129	A
48	WA	4130	A
48	WA	4136	C
48	WA	4137	G
48	WA	4141	G
48	WA	4143	G

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Mol	Chain	Res	Type
48	WA	4144	C
48	WA	4145	C
48	WA	4146	G
48	WA	4160	C
48	WA	4164	C
48	WA	4168	G
48	WA	4172	A
48	WA	4174	A
48	WA	4175	G
48	WA	4185	G
48	WA	4186	G
48	WA	4193	G
48	WA	4205	A
48	WA	4214	A
48	WA	4231	U
48	WA	4235	A
48	WA	4236	A
48	WA	4253	A
48	WA	4256	G
48	WA	4268	G
48	WA	4270	A
48	WA	4273	A
48	WA	4275	A
48	WA	4283	A
48	WA	4293	G
48	WA	4299	G
48	WA	4306	A
48	WA	4307	G
48	WA	4308	U
48	WA	4316	C
48	WA	4332	G
48	WA	4334	C
48	WA	4351	C
48	WA	4352	C
48	WA	4356	U
48	WA	4375	G
48	WA	4379	G
48	WA	4380	A
48	WA	4382	A
48	WA	4389	C
48	WA	4396	A
48	WA	4397	U

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Mol	Chain	Res	Type
48	WA	4398	A
48	WA	4421	U
48	WA	4423	C
48	WA	4424	A
48	WA	4439	U
48	WA	4446	C
48	WA	4450	G
48	WA	4451	A
48	WA	4454	U
48	WA	4455	C
48	WA	4466	A
48	WA	4468	C
48	WA	4502	U
48	WA	4514	U
48	WA	4515	A
48	WA	4520	A
48	WA	4522	G
48	WA	4524	G
48	WA	4526	G
48	WA	4531	G
48	WA	4532	U
48	WA	4533	U
48	WA	4550	A
48	WA	4551	G
48	WA	4562	C
48	WA	4569	G
48	WA	4575	G
48	WA	4577	G
48	WA	4579	U
48	WA	4583	G
48	WA	4588	G
48	WA	4592	A
48	WA	4602	G
48	WA	4629	U
48	WA	4638	U
48	WA	4639	G
48	WA	4654	G
48	WA	4658	A
48	WA	4669	C
48	WA	4672	C
48	WA	4674	A
48	WA	4679	U

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Mol	Chain	Res	Type
48	WA	4693	A
48	WA	4702	A
48	WA	4711	U
48	WA	4722	C
48	WA	4723	G
48	WA	4747	G
48	WA	4756	G
48	WA	4759	C
48	WA	4761	C
48	WA	4763	G
48	WA	4767	G
48	WA	4771	G
48	WA	4772	U
48	WA	4779	C
48	WA	4872	G
48	WA	4873	C
48	WA	4875	G
48	WA	4876	A
48	WA	4877	G
48	WA	4878	A
48	WA	4879	G
48	WA	4884	U
48	WA	4885	C
48	WA	4887	U
48	WA	4888	C
48	WA	4906	G
48	WA	4912	A
48	WA	4914	G
48	WA	4917	G
48	WA	4919	C
48	WA	4923	C
48	WA	4924	C
48	WA	4926	C
48	WA	4927	U
48	WA	4928	C
48	WA	4929	G
48	WA	4930	C
48	WA	4936	A
48	WA	4939	C
48	WA	4945	A
48	WA	4946	C
48	WA	4949	U

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Mol	Chain	Res	Type
48	WA	4951	G
48	WA	4952	U
48	WA	4953	G
48	WA	4960	C
48	WA	4965	G
48	WA	4967	U
48	WA	4968	A
48	WA	4978	U
48	WA	4981	A
48	WA	4992	C
48	WA	4993	U
48	WA	4994	G
48	WA	5008	U
48	WA	5016	A
48	WA	5019	G
48	WA	5043	G
48	WA	5049	C
48	WA	5050	A
48	WA	5052	C
48	WA	5055	U
48	WA	5056	C
48	WA	5063	A
48	WA	5064	G
49	XA	7	G
49	XA	11	A
49	XA	33	U
49	XA	41	G
49	XA	50	A
49	XA	54	A
49	XA	63	C
49	XA	64	G
49	XA	100	A
49	XA	110	G
50	YA	34	U
50	YA	35	C
50	YA	39	G
50	YA	59	A
50	YA	62	A
50	YA	63	U
50	YA	72	A
50	YA	75	G
50	YA	79	G

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Mol	Chain	Res	Type
50	YA	80	A
50	YA	81	C
50	YA	82	A
50	YA	83	C
50	YA	84	A
50	YA	85	U
50	YA	86	U
50	YA	87	G
50	YA	90	C
50	YA	94	G
50	YA	95	A
50	YA	103	A
50	YA	105	C
50	YA	110	U
50	YA	111	U
50	YA	112	G
50	YA	114	G
50	YA	123	U
50	YA	124	U
50	YA	125	C
50	YA	126	C
50	YA	127	U
50	YA	150	C
51	ZA	3	C
51	ZA	25	A
51	ZA	33	G
51	ZA	41	G
51	ZA	42	A
51	ZA	44	U
51	ZA	46	A
51	ZA	56	G
51	ZA	58	C
51	ZA	65	C
51	ZA	67	C
51	ZA	68	A
51	ZA	71	G
51	ZA	73	C
51	ZA	75	G
51	ZA	76	U
51	ZA	79	A
51	ZA	82	G
51	ZA	103	A

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Mol	Chain	Res	Type
51	ZA	113	G
51	ZA	114	G
51	ZA	115	U
51	ZA	116	U
51	ZA	126	G
51	ZA	130	G
51	ZA	142	C
51	ZA	143	U
51	ZA	147	A
51	ZA	155	G
51	ZA	160	U
51	ZA	162	C
51	ZA	173	A
51	ZA	178	C
51	ZA	181	A
51	ZA	182	C
51	ZA	183	G
51	ZA	184	G
51	ZA	187	G
51	ZA	188	C
51	ZA	192	C
51	ZA	199	C
51	ZA	200	G
51	ZA	201	C
51	ZA	204	G
51	ZA	209	A
51	ZA	291	G
51	ZA	292	A
51	ZA	306	C
51	ZA	307	G
51	ZA	308	G
51	ZA	309	G
51	ZA	320	G
51	ZA	322	C
51	ZA	323	C
51	ZA	325	C
51	ZA	326	C
51	ZA	327	G
51	ZA	328	U
51	ZA	329	G
51	ZA	334	C
51	ZA	335	G

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Mol	Chain	Res	Type
51	ZA	347	G
51	ZA	351	G
51	ZA	362	C
51	ZA	364	A
51	ZA	368	U
51	ZA	369	C
51	ZA	371	A
51	ZA	383	G
51	ZA	385	G
51	ZA	386	C
51	ZA	400	C
51	ZA	409	C
51	ZA	418	A
51	ZA	438	G
51	ZA	448	A
51	ZA	450	C
51	ZA	464	A
51	ZA	472	C
51	ZA	473	A
51	ZA	474	G
51	ZA	482	G
51	ZA	487	U
51	ZA	492	C
51	ZA	493	A
51	ZA	508	A
51	ZA	525	A
51	ZA	531	A
51	ZA	532	C
51	ZA	534	G
51	ZA	535	G
51	ZA	538	U
51	ZA	539	C
51	ZA	541	U
51	ZA	542	U
51	ZA	544	G
51	ZA	545	A
51	ZA	547	G
51	ZA	548	C
51	ZA	549	C
51	ZA	550	C
51	ZA	554	A
51	ZA	555	A

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Mol	Chain	Res	Type
51	ZA	559	G
51	ZA	560	A
51	ZA	561	A
51	ZA	562	U
51	ZA	563	G
51	ZA	564	A
51	ZA	568	C
51	ZA	574	A
51	ZA	576	A
51	ZA	582	U
51	ZA	583	A
51	ZA	587	A
51	ZA	588	G
51	ZA	590	A
51	ZA	591	U
51	ZA	593	C
51	ZA	594	A
51	ZA	606	G
51	ZA	608	C
51	ZA	614	C
51	ZA	617	G
51	ZA	626	G
51	ZA	627	U
51	ZA	631	U
51	ZA	643	A
51	ZA	644	G
51	ZA	660	C
51	ZA	668	A
51	ZA	669	A
51	ZA	671	A
51	ZA	672	A
51	ZA	673	G
51	ZA	684	G
51	ZA	689	U
51	ZA	752	G
51	ZA	753	C
51	ZA	754	G
51	ZA	798	G
51	ZA	799	U
51	ZA	811	A
51	ZA	812	A
51	ZA	821	G

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Mol	Chain	Res	Type
51	ZA	822	U
51	ZA	834	C
51	ZA	835	C
51	ZA	840	C
51	ZA	841	G
51	ZA	845	G
51	ZA	847	A
51	ZA	859	G
51	ZA	860	G
51	ZA	869	A
51	ZA	870	A
51	ZA	871	U
51	ZA	872	A
51	ZA	873	G
51	ZA	874	G
51	ZA	875	A
51	ZA	878	G
51	ZA	886	A
51	ZA	888	U
51	ZA	889	U
51	ZA	890	U
51	ZA	891	G
51	ZA	892	U
51	ZA	897	U
51	ZA	898	U
51	ZA	902	G
51	ZA	905	C
51	ZA	913	A
51	ZA	914	U
51	ZA	920	A
51	ZA	922	A
51	ZA	933	G
51	ZA	934	G
51	ZA	956	G
51	ZA	971	G
51	ZA	985	G
51	ZA	990	A
51	ZA	992	A
51	ZA	999	G
51	ZA	1002	U
51	ZA	1008	A
51	ZA	1023	A

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Mol	Chain	Res	Type
51	ZA	1061	U
51	ZA	1062	A
51	ZA	1078	C
51	ZA	1083	A
51	ZA	1085	C
51	ZA	1115	U
51	ZA	1116	C
51	ZA	1117	C
51	ZA	1118	C
51	ZA	1121	G
51	ZA	1126	G
51	ZA	1133	A
51	ZA	1138	C
51	ZA	1148	A
51	ZA	1149	A
51	ZA	1153	C
51	ZA	1154	U
51	ZA	1195	A
51	ZA	1207	G
51	ZA	1208	A
51	ZA	1215	C
51	ZA	1224	G
51	ZA	1227	G
51	ZA	1233	G
51	ZA	1241	A
51	ZA	1242	U
51	ZA	1251	A
51	ZA	1253	A
51	ZA	1256	G
51	ZA	1257	G
51	ZA	1259	A
51	ZA	1260	A
51	ZA	1274	G
51	ZA	1275	G
51	ZA	1285	G
51	ZA	1286	G
51	ZA	1297	U
51	ZA	1298	G
51	ZA	1299	A
51	ZA	1300	U
51	ZA	1301	A
51	ZA	1302	G

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Mol	Chain	Res	Type
51	ZA	1303	C
51	ZA	1313	A
51	ZA	1333	U
51	ZA	1342	U
51	ZA	1354	G
51	ZA	1371	U
51	ZA	1372	U
51	ZA	1378	A
51	ZA	1382	A
51	ZA	1396	A
51	ZA	1397	U
51	ZA	1404	U
51	ZA	1417	C
51	ZA	1418	C
51	ZA	1419	C
51	ZA	1420	G
51	ZA	1421	A
51	ZA	1422	G
51	ZA	1423	C
51	ZA	1424	G
51	ZA	1428	G
51	ZA	1433	C
51	ZA	1434	C
51	ZA	1435	C
51	ZA	1437	C
51	ZA	1438	A
51	ZA	1439	A
51	ZA	1441	U
51	ZA	1442	U
51	ZA	1452	A
51	ZA	1454	A
51	ZA	1464	C
51	ZA	1466	G
51	ZA	1475	G
51	ZA	1476	A
51	ZA	1477	U
51	ZA	1489	A
51	ZA	1490	G
51	ZA	1498	A
51	ZA	1521	C
51	ZA	1522	A
51	ZA	1531	A

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
51	ZA	1533	A
51	ZA	1535	U
51	ZA	1536	G
51	ZA	1548	G
51	ZA	1551	U
51	ZA	1552	G
51	ZA	1553	C
51	ZA	1555	U
51	ZA	1556	A
51	ZA	1560	U
51	ZA	1564	C
51	ZA	1567	G
51	ZA	1580	A
51	ZA	1585	U
51	ZA	1587	G
51	ZA	1588	A
51	ZA	1601	A
51	ZA	1604	G
51	ZA	1605	G
51	ZA	1606	G
51	ZA	1621	U
51	ZA	1623	A
51	ZA	1638	G
51	ZA	1646	C
51	ZA	1648	G
51	ZA	1665	G
51	ZA	1680	G
51	ZA	1683	C
51	ZA	1698	C
51	ZA	1699	A
51	ZA	1721	U
51	ZA	1722	G
51	ZA	1726	G
51	ZA	1744	G
51	ZA	1745	A
51	ZA	1748	G
51	ZA	1753	C
51	ZA	1757	G
51	ZA	1774	C
51	ZA	1775	U
51	ZA	1776	G
51	ZA	1780	G

*Continued on next page...*

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Mol	Chain	Res	Type
51	ZA	1783	C
51	ZA	1824	A
51	ZA	1825	A
51	ZA	1826	G
51	ZA	1831	A
51	ZA	1836	G
51	ZA	1838	U
51	ZA	1849	G
51	ZA	1851	A
51	ZA	1861	G
51	ZA	1862	G
51	ZA	1863	A
51	ZA	1865	C
51	ZA	1869	A

All (33) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
44	SA	20	A
44	SA	21	A
44	SA	57	G
46	UA	19	U
48	WA	12	A
48	WA	275	C
48	WA	385	A
48	WA	505	G
48	WA	971	A
48	WA	1293	G
48	WA	1635	G
48	WA	1677	C
48	WA	1806	A
48	WA	1820	G
48	WA	2048	G
48	WA	2095	G
48	WA	2268	C
48	WA	2697	A
48	WA	3627	G
48	WA	4117	G
48	WA	4450	G
48	WA	4701	U
48	WA	4886	G
48	WA	4951	G

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
51	ZA	24	C
51	ZA	370	G
51	ZA	541	U
51	ZA	561	A
51	ZA	752	G
51	ZA	870	A
51	ZA	890	U
51	ZA	1137	U
51	ZA	1433	C

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 219 ligands modelled in this entry, 213 are monoatomic - leaving 6 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
92	ANM	WA	5228	94	20,20,20	4.08	7 (35%)	24,27,27	1.38	2 (8%)
91	5GP	UA	101	46	22,26,26	1.23	2 (9%)	24,40,40	1.28	4 (16%)
95	SER	HC	502	-	4,5,6	0.57	0	1,5,7	0.58	0
93	SPD	WA	5230	-	9,9,9	0.28	0	8,8,8	0.29	0
93	SPD	WA	5229	-	9,9,9	0.28	0	8,8,8	0.33	0
93	SPD	ZA	1933	-	9,9,9	0.26	0	8,8,8	0.30	0

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
92	ANM	WA	5228	94	-	6/10/23/23	0/2/2/2
91	5GP	UA	101	46	-	5/6/26/26	0/3/3/3
95	SER	HC	502	-	-	0/2/4/6	-
93	SPD	WA	5230	-	-	1/7/7/7	-
93	SPD	WA	5229	-	-	0/7/7/7	-
93	SPD	ZA	1933	-	-	1/7/7/7	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
92	WA	5228	ANM	C3-C2	-11.79	1.32	1.53
92	WA	5228	ANM	C16-N1	-8.89	1.30	1.47
92	WA	5228	ANM	C2-C16	7.41	1.68	1.53
91	UA	101	5GP	C5-C6	-4.13	1.39	1.47
92	WA	5228	ANM	C4-C3	3.97	1.58	1.53
92	WA	5228	ANM	C4-N1	3.86	1.60	1.47
92	WA	5228	ANM	O2-C5	3.52	1.43	1.35
92	WA	5228	ANM	C6-C5	2.44	1.57	1.49
91	UA	101	5GP	C6-N1	-2.34	1.34	1.37

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
92	WA	5228	ANM	O2-C5-C6	5.04	120.08	111.09
91	UA	101	5GP	C8-N7-C5	2.91	107.50	102.55
91	UA	101	5GP	C5-C6-N1	2.88	119.57	114.07
91	UA	101	5GP	C2-N1-C6	-2.31	120.88	125.11
92	WA	5228	ANM	C2-O2-C5	-2.28	114.17	117.72
91	UA	101	5GP	O6-C6-C5	-2.03	120.30	124.32

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
92	WA	5228	ANM	C6-C5-O2-C2
92	WA	5228	ANM	O3-C5-O2-C2
92	WA	5228	ANM	C1-C9-O1-C14
92	WA	5228	ANM	C10-C9-O1-C14
91	UA	101	5GP	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
91	UA	101	5GP	C3'-C4'-C5'-O5'
93	WA	5230	SPD	C8-C7-N6-C5
91	UA	101	5GP	C5'-O5'-P-O1P
93	ZA	1933	SPD	C2-C3-C4-C5
92	WA	5228	ANM	C11-C12-C15-C16
92	WA	5228	ANM	C13-C12-C15-C16
91	UA	101	5GP	C4'-C5'-O5'-P
91	UA	101	5GP	C5'-O5'-P-O3P

There are no ring outliers.

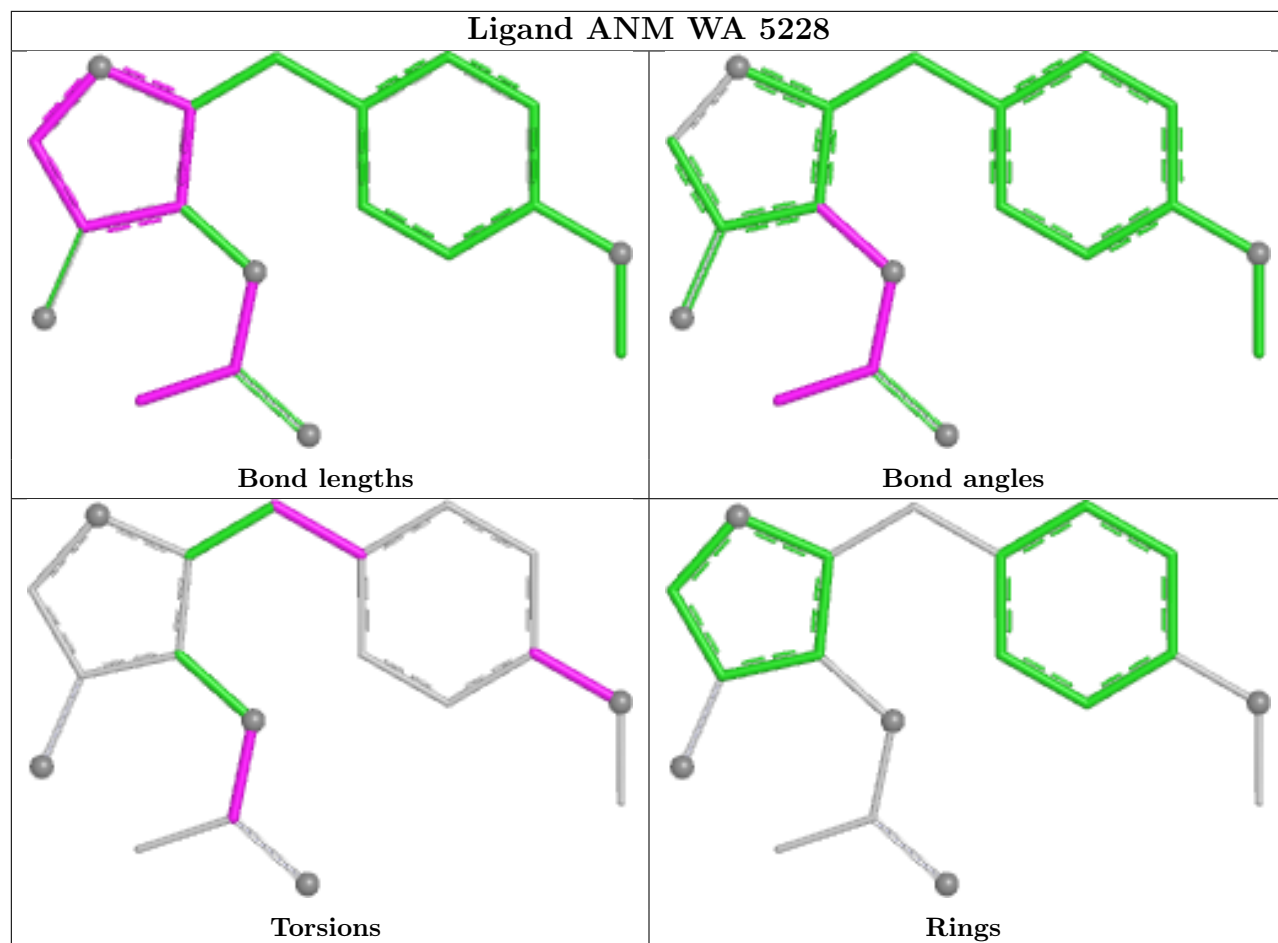
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
92	WA	5228	ANM	1	0
93	WA	5229	SPD	1	0

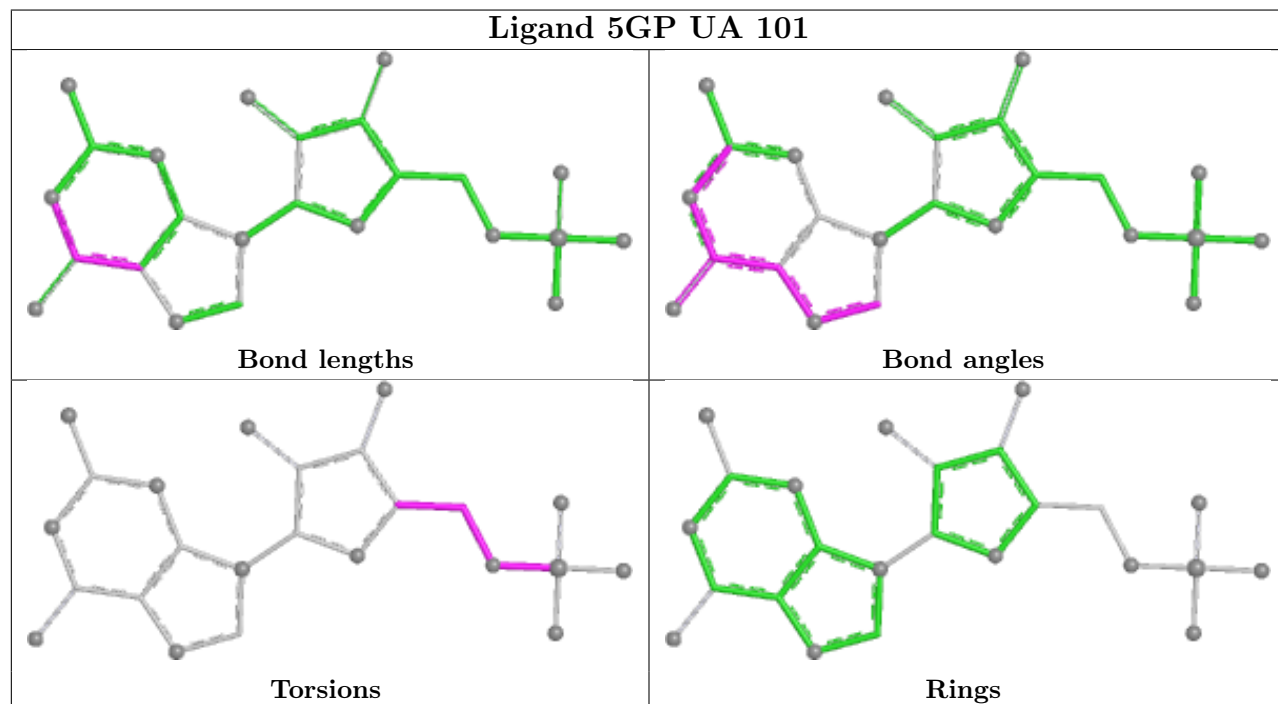
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



## Ligand ANM WA 5228



## Ligand 5GP UA 101



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
48	WA	21
86	b	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	WA	2118:C	O3'	2260:C	P	37.14
1	WA	1225:G	O3'	1239:G	P	20.72
1	WA	996:C	O3'	1070:G	P	17.81
1	WA	4779:C	O3'	4861:C	P	17.44
1	WA	524:C	O3'	639:G	P	16.85
1	WA	763:G	O3'	904:C	P	16.83
1	WA	4103:C	O3'	4109:G	P	16.58
1	WA	1698:C	O3'	1722:C	P	14.92
1	WA	5024:U	O3'	5030:G	P	13.93
1	WA	1366:U	O3'	1370:A	P	13.62
1	WA	2904:G	O3'	3598:A	P	12.69
1	b	106:LYS	C	107:VAL	N	11.91
1	WA	4731:A	O3'	4737:G	P	10.44
1	WA	3954:A	O3'	4063:C	P	10.11
1	WA	1186:C	O3'	1189:C	P	9.75
1	WA	182:G	O3'	189:G	P	9.42
1	b	107:VAL	C	108:PRO	N	8.67
1	WA	513:U	O3'	516:C	P	5.66
1	WA	4742:G	O3'	4745:G	P	5.66
1	WA	501:G	O3'	505:G	P	4.99
1	WA	1106:U	O3'	1174:G	P	4.39
1	WA	4901:G	O3'	4904:C	P	4.35
1	WA	2030:C	O3'	2031:A	P	3.62

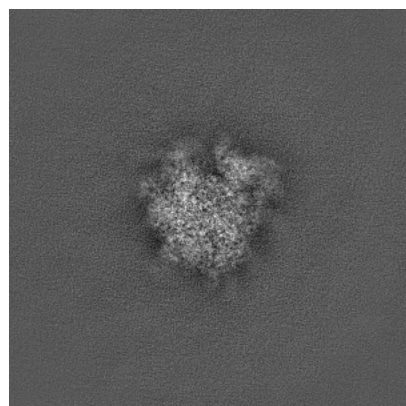
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43566. These allow visual inspection of the internal detail of the map and identification of artifacts.

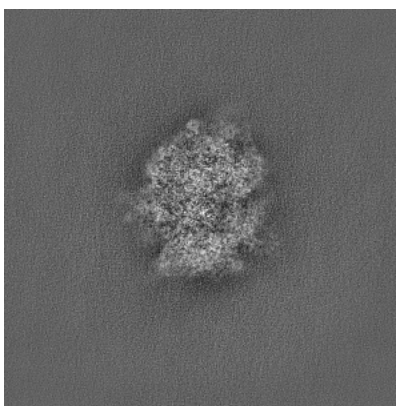
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

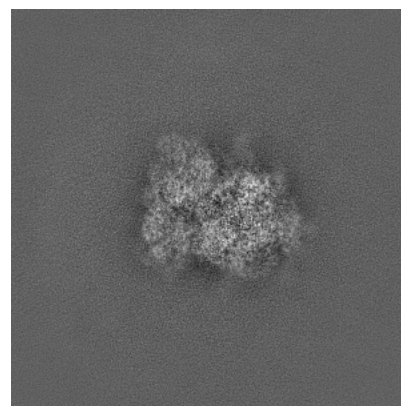
#### 6.1.1 Primary map



X

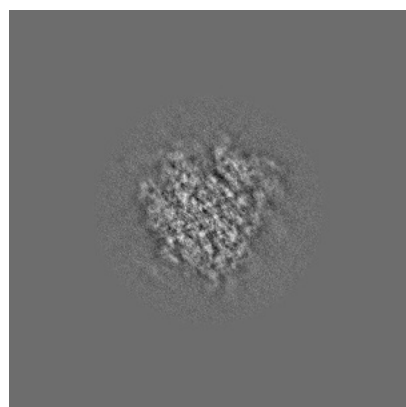


Y

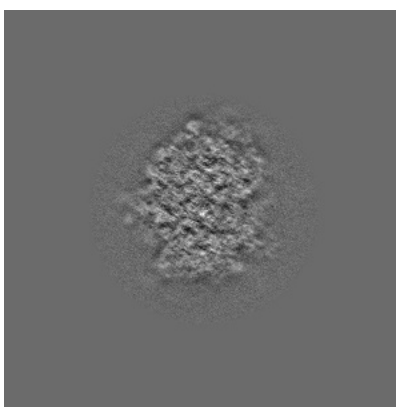


Z

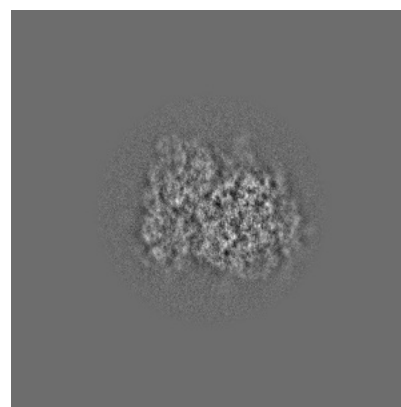
#### 6.1.2 Raw map



X



Y

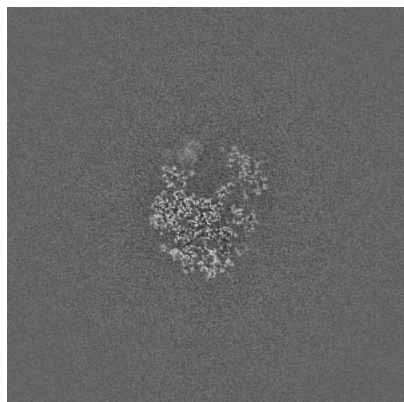


Z

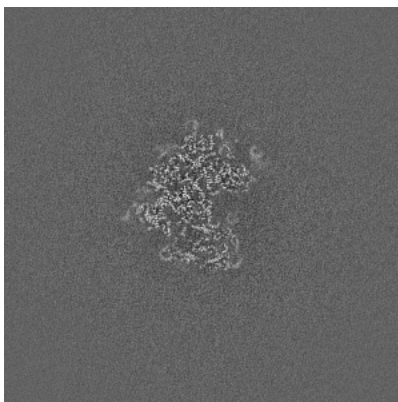
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

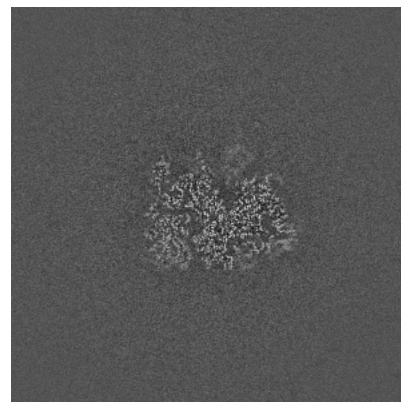
### 6.2.1 Primary map



X Index: 324

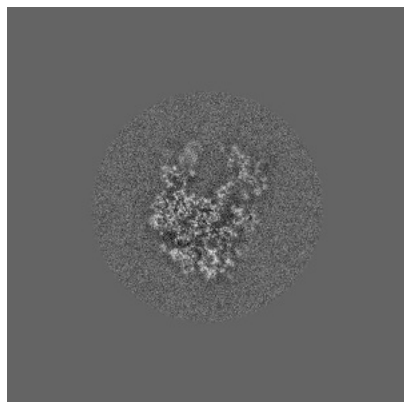


Y Index: 324

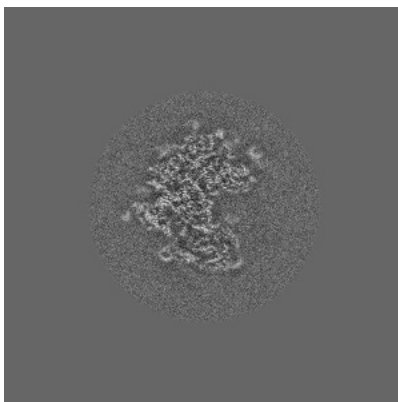


Z Index: 324

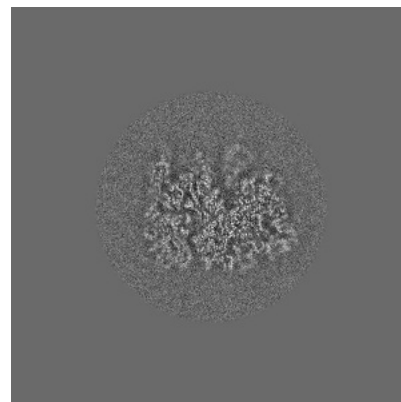
### 6.2.2 Raw map



X Index: 324



Y Index: 324

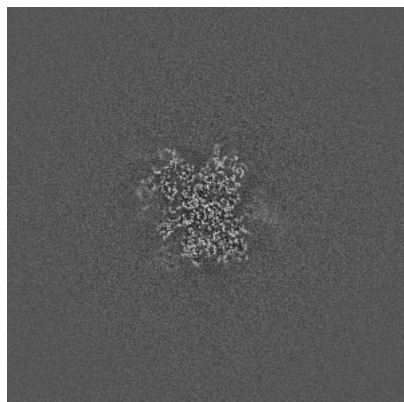


Z Index: 324

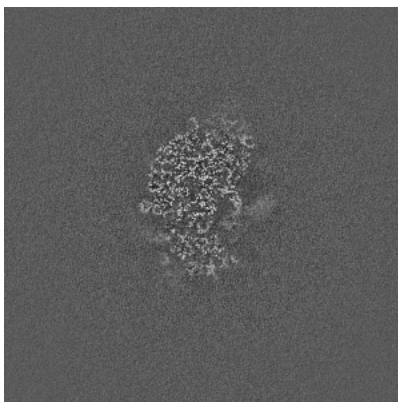
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

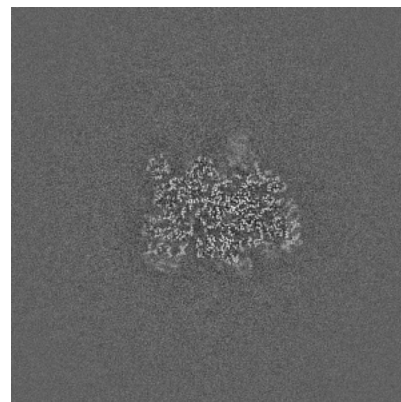
### 6.3.1 Primary map



X Index: 378

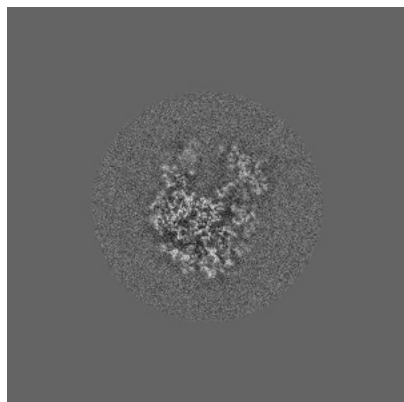


Y Index: 299

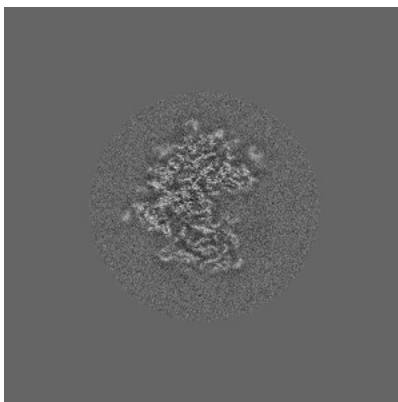


Z Index: 312

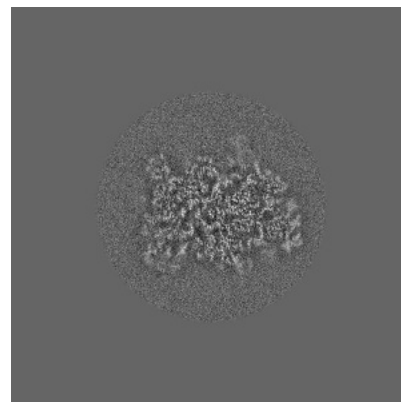
### 6.3.2 Raw map



X Index: 323



Y Index: 325



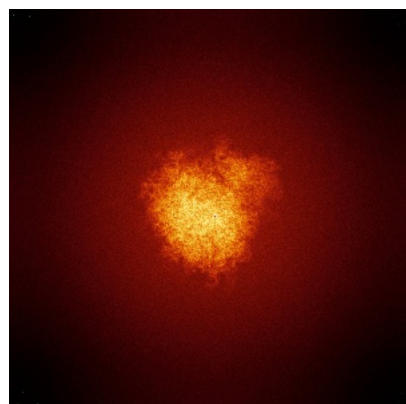
Z Index: 311

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

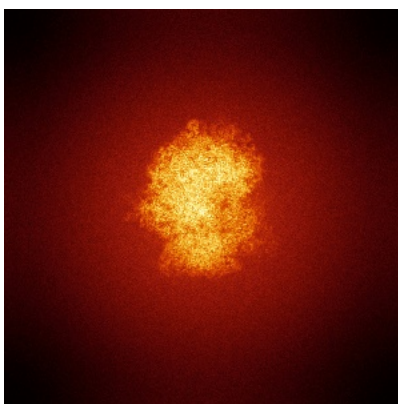


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

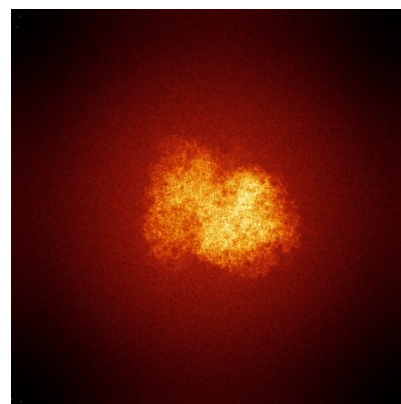
### 6.4.1 Primary map



X

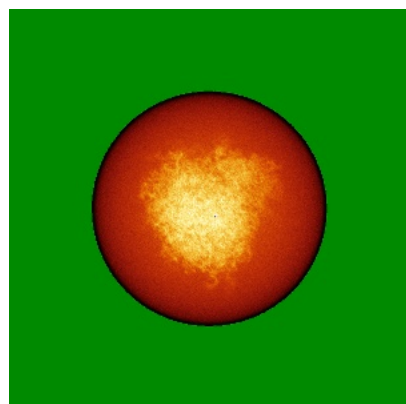


Y

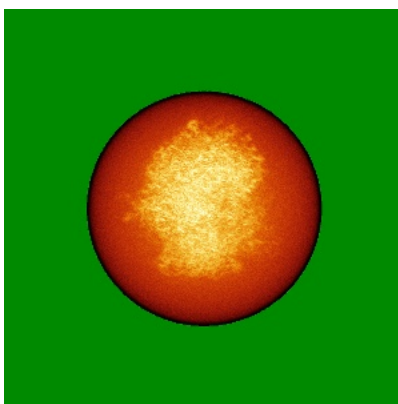


Z

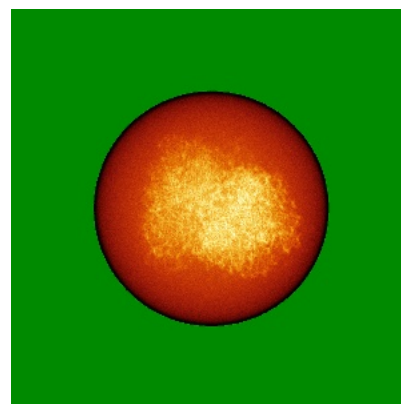
### 6.4.2 Raw map



X



Y

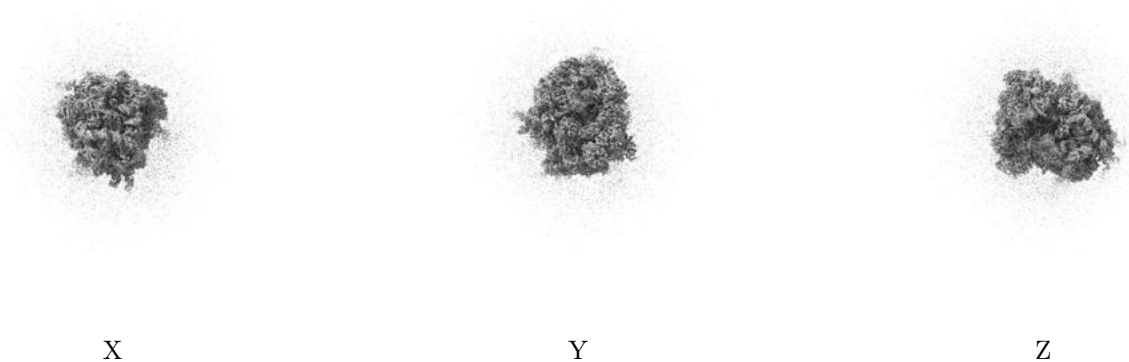


Z

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

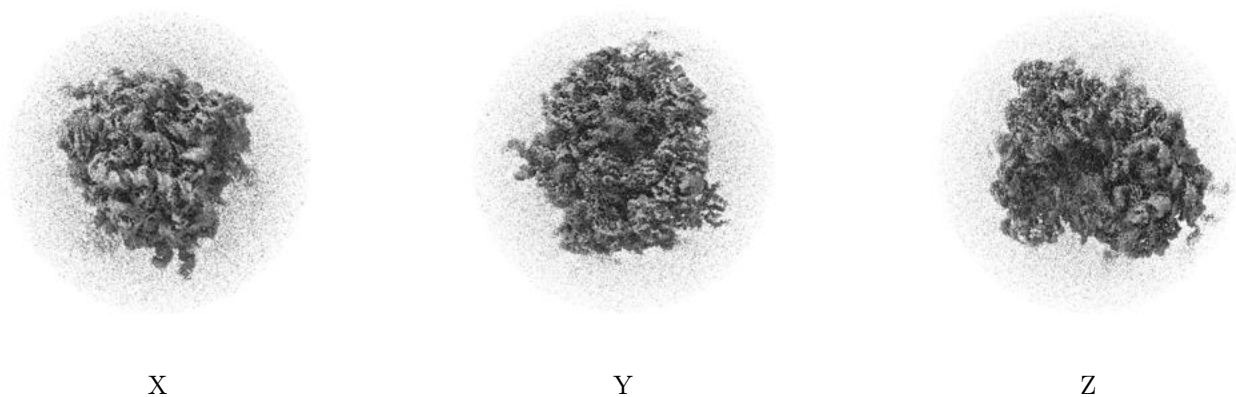
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 6.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

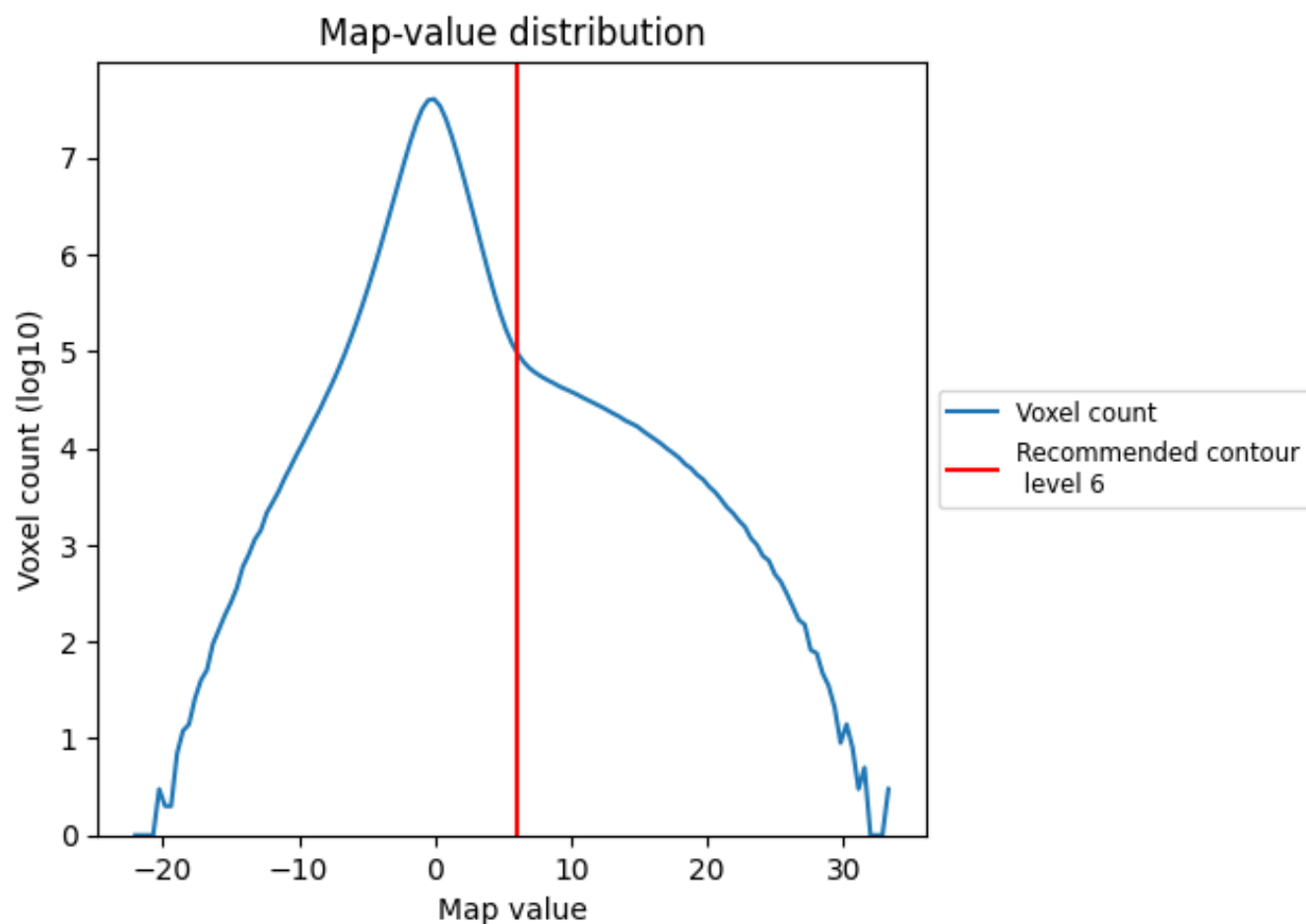
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

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

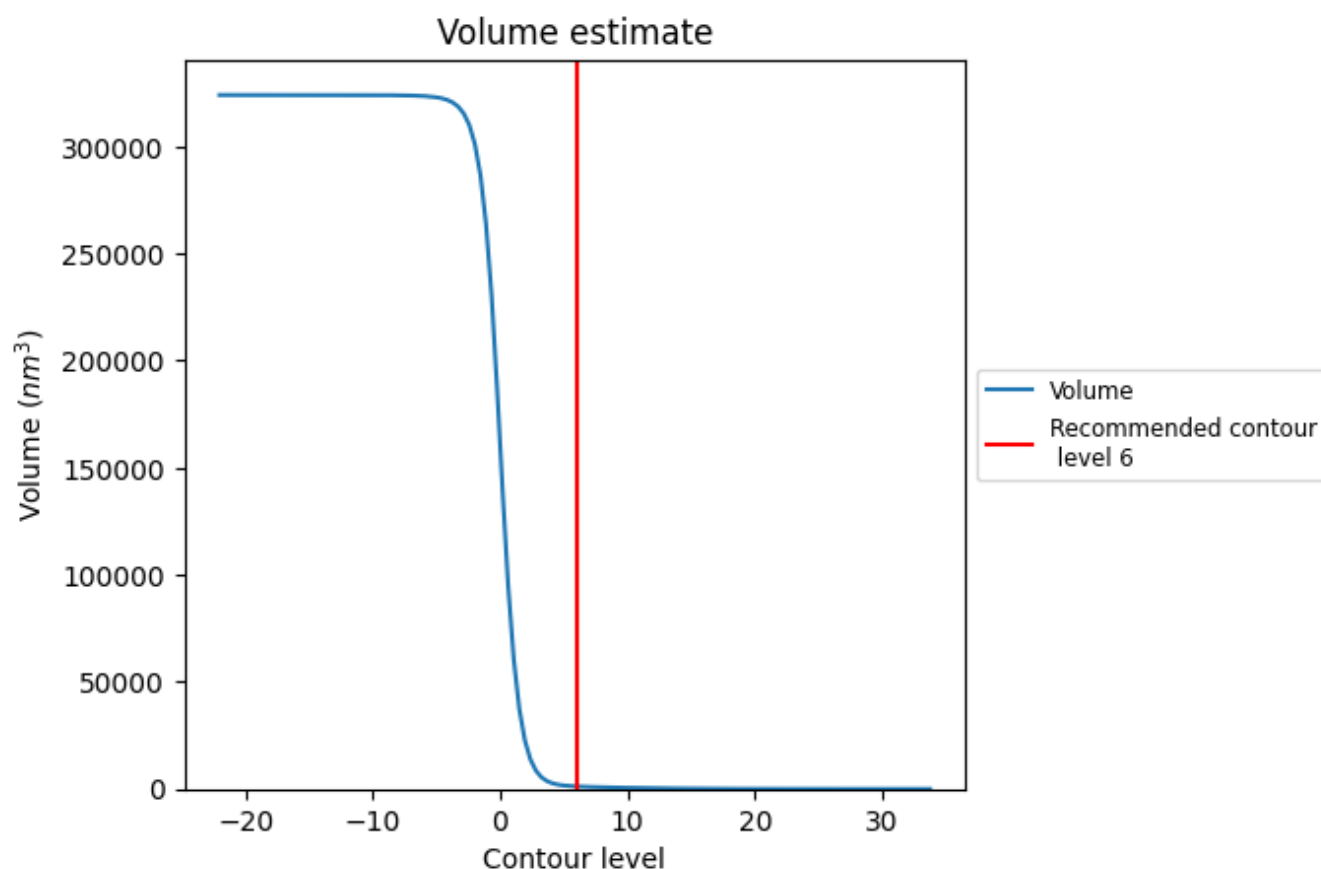
### 7.1 Map-value distribution [i](#)



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



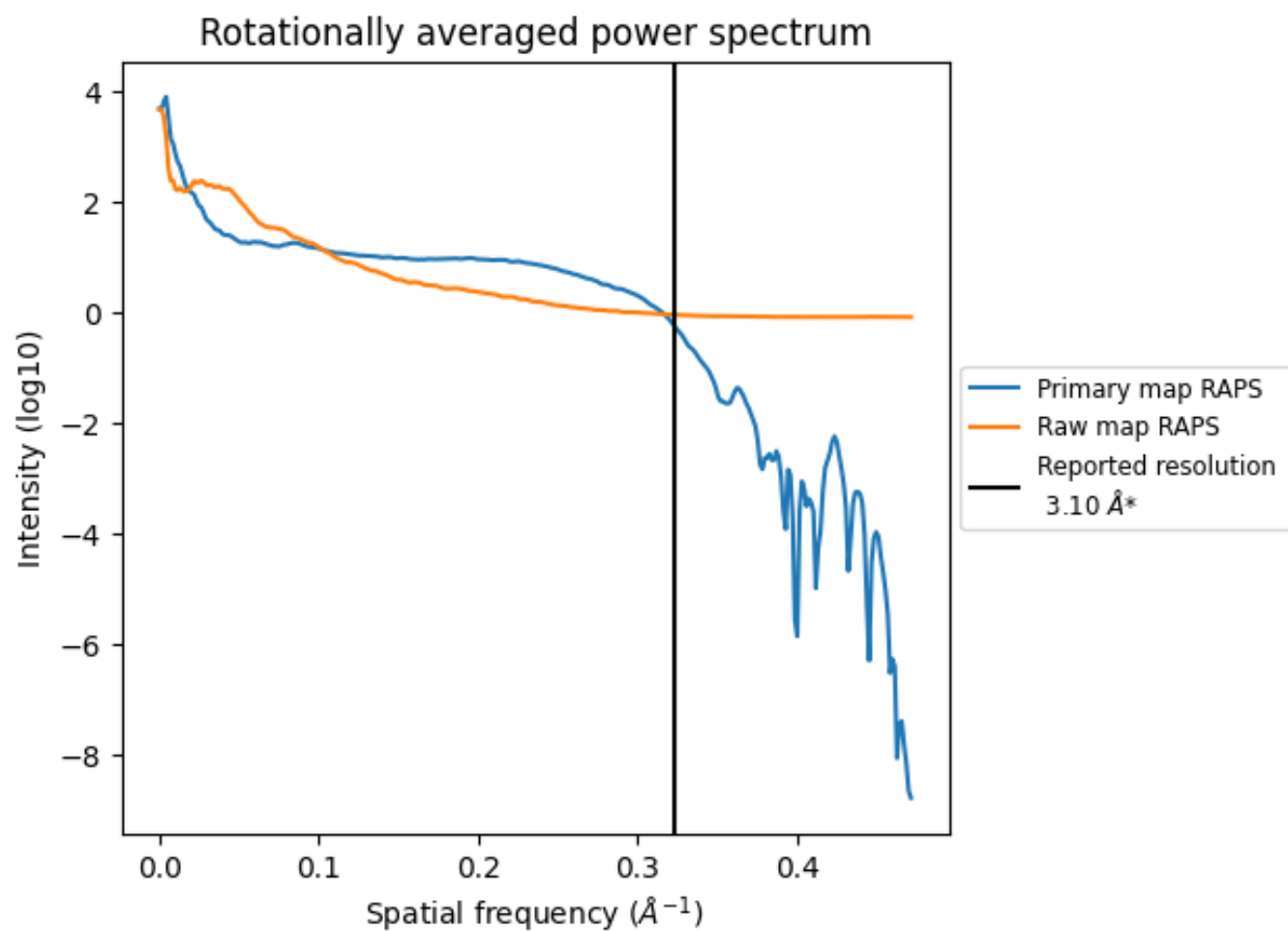
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1186  $\text{nm}^3$ ; this corresponds to an approximate mass of 1072 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum ⓘ

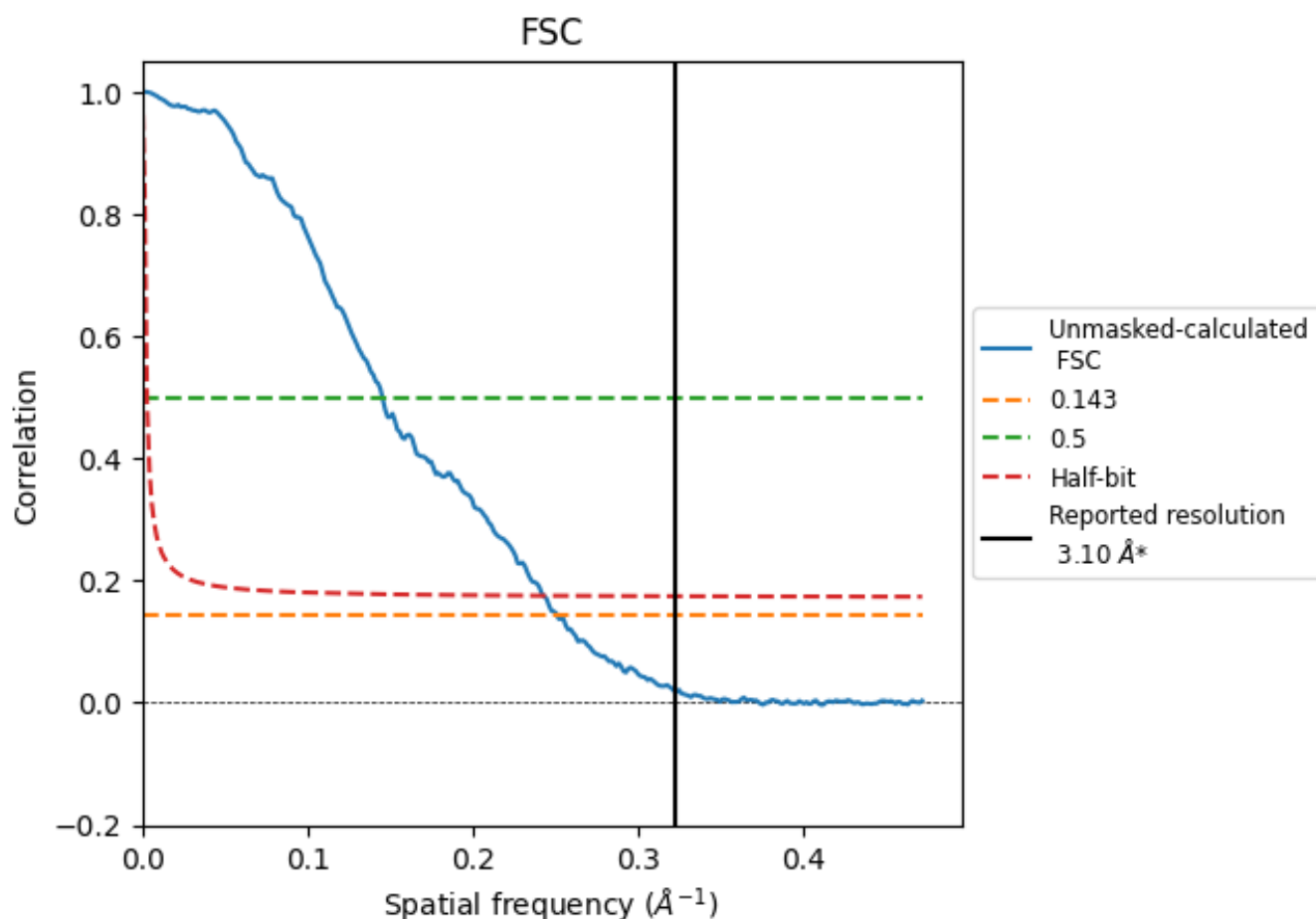


\*Reported resolution corresponds to spatial frequency of 0.323 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.323  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

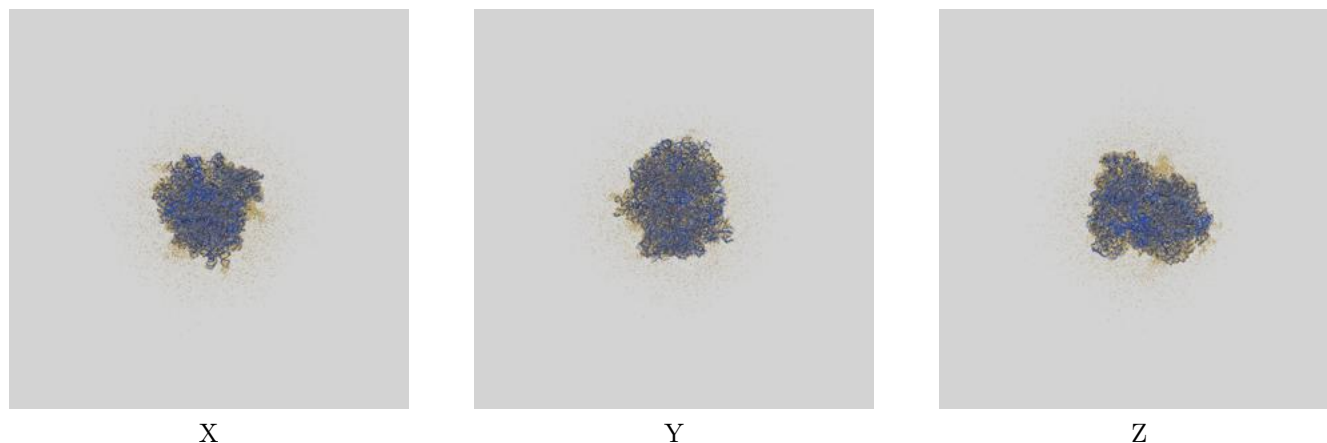
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.99	6.89	4.12

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.99 differs from the reported value 3.1 by more than 10 %

## 9 Map-model fit [i](#)

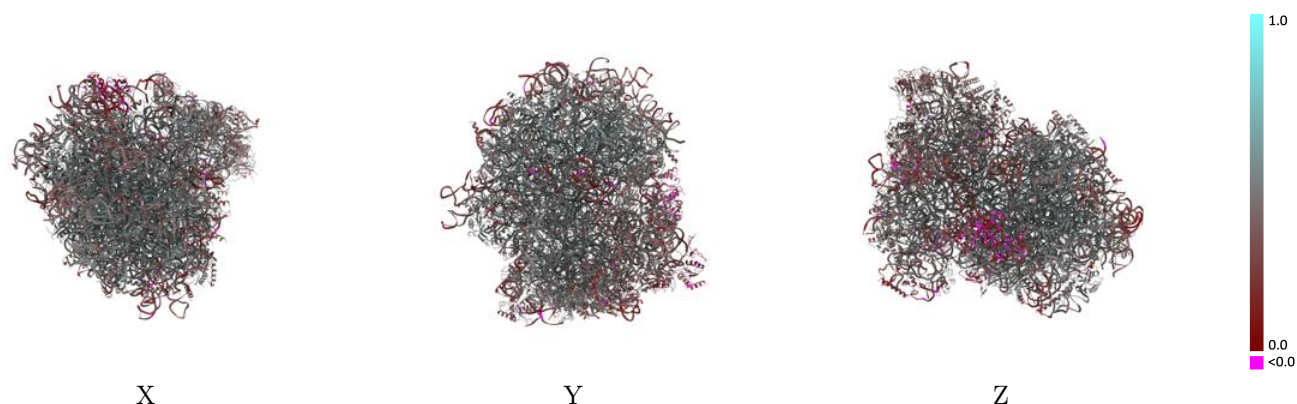
This section contains information regarding the fit between EMDB map EMD-43566 and PDB model 8VVR. Per-residue inclusion information can be found in section [3](#) on page [26](#).

### 9.1 Map-model overlay [i](#)



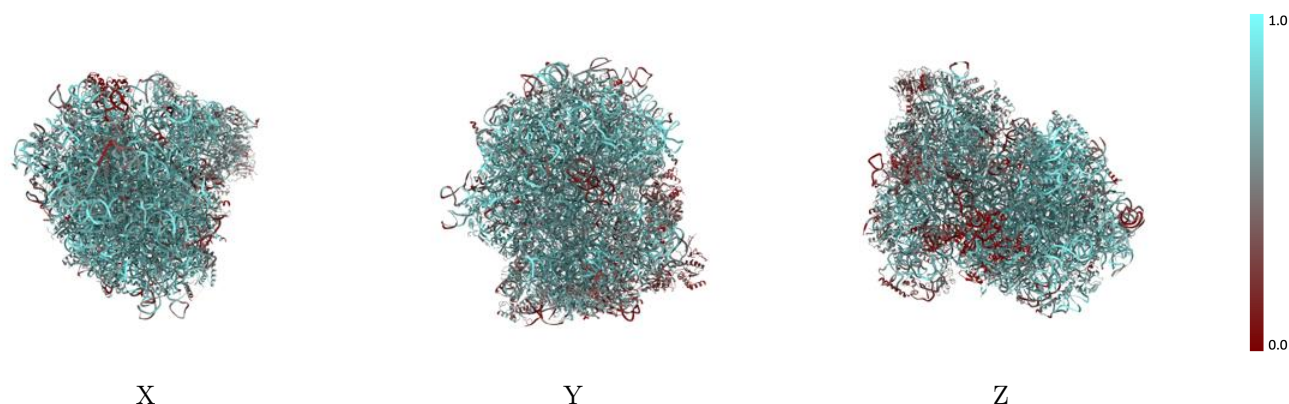
The images above show the 3D surface view of the map at the recommended contour level 6.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



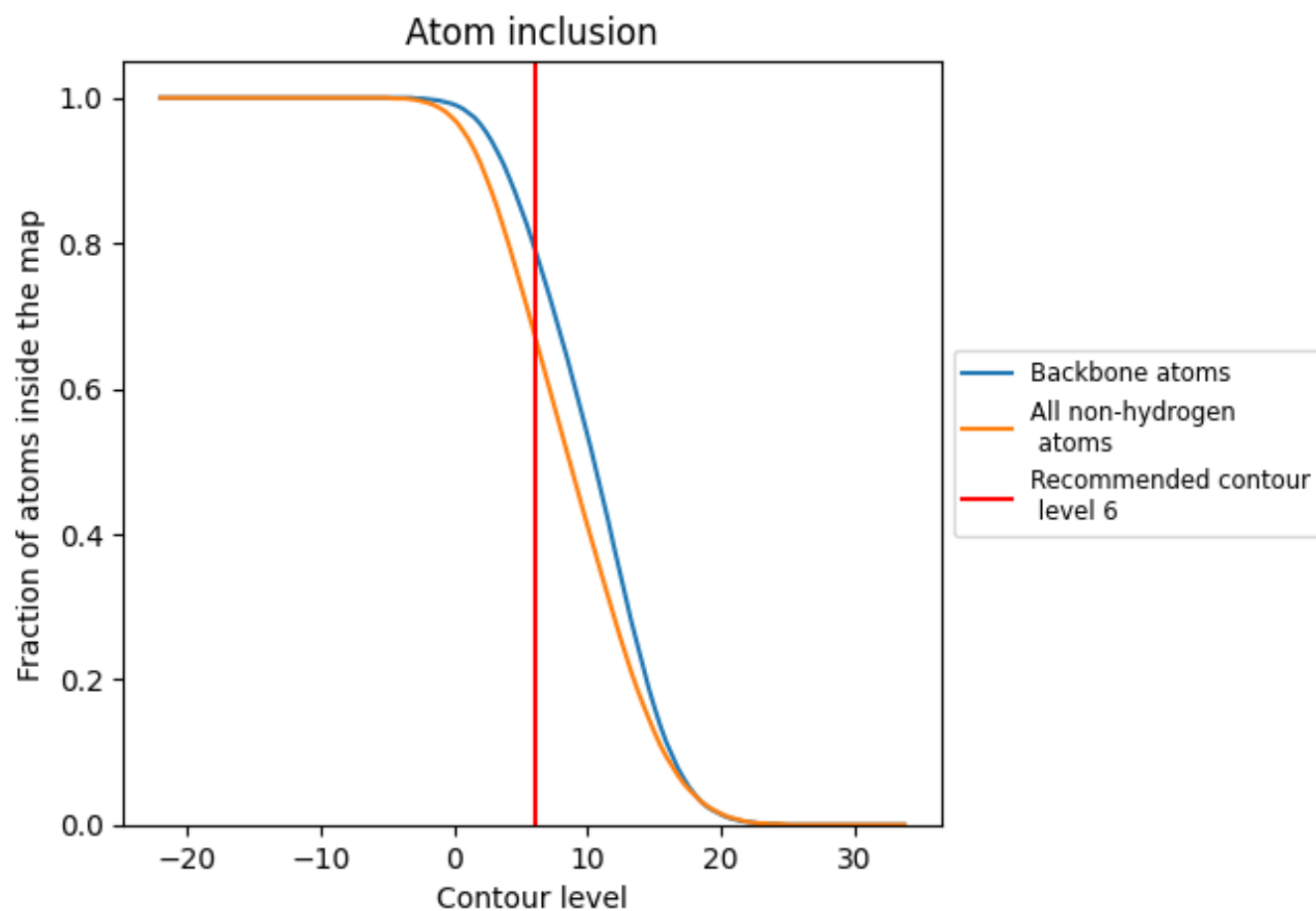
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (6).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 68% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (6) and Q-score for the entire model and for each chain.





















































































Chain	Atom inclusion	Q-score
All	 0.6750	 0.4410
A	 0.7060	 0.5200
AA	 0.5450	 0.4210
AB	 0.5990	 0.4410
AC	 0.6220	 0.4750
B	 0.6880	 0.4930
BA	 0.6640	 0.4640
BB	 0.5780	 0.4560
BC	 0.5540	 0.4340
C	 0.6780	 0.4980
CA	 0.6660	 0.4830
CB	 0.6130	 0.4630
CC	 0.5080	 0.4150
D	 0.6790	 0.4540
DA	 0.6810	 0.5090
DB	 0.4850	 0.3960
DC	 0.5910	 0.4400
E	 0.6230	 0.4470
EA	 0.6760	 0.5190
EB	 0.5700	 0.4510
EC	 0.4860	 0.3880
F	 0.6670	 0.4910
FA	 0.6590	 0.4870
FB	 0.5380	 0.4110
FC	 0.2160	 0.2470
G	 0.6390	 0.4380
GA	 0.6530	 0.4700
GB	 0.4720	 0.3630
GC	 0.3960	 0.3440
H	 0.6500	 0.4630
HA	 0.6510	 0.4520
HB	 0.5010	 0.3870
HC	 0.1340	 0.2910
I	 0.6900	 0.4970
IA	 0.7070	 0.5150



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



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Chain	Atom inclusion	Q-score
IB	 0.5690	 0.4410
IC	 0.4500	 0.4380
J	 0.6210	 0.4360
JA	 0.5730	 0.4280
JB	 0.5880	 0.4320
K	 0.6560	 0.4800
KA	 0.6350	 0.4850
KB	 0.4820	 0.3660
L	 0.6510	 0.4610
LA	 0.7090	 0.4940
LB	 0.6240	 0.4810
M	 0.7110	 0.5170
MA	 0.6470	 0.4830
MB	 0.2220	 0.2090
N	 0.6930	 0.4880
NA	 0.6740	 0.5080
NB	 0.6420	 0.4630
O	 0.6750	 0.4990
OA	 0.6700	 0.5030
OB	 0.6030	 0.4530
P	 0.6930	 0.5050
PA	 0.6880	 0.4970
PB	 0.4600	 0.3640
Q	 0.6680	 0.4640
QB	 0.5400	 0.4130
R	 0.6790	 0.4910
RA	 0.0400	 0.0950
RB	 0.5420	 0.4090
S	 0.6650	 0.4890
SA	 0.6200	 0.3980
SB	 0.5400	 0.3980
T	 0.6020	 0.4290
TA	 0.2320	 0.2320
TB	 0.5440	 0.4010
U	 0.6690	 0.5050
UA	 0.2220	 0.2550
UB	 0.4550	 0.3760
V	 0.5090	 0.3860
VA	 0.5440	 0.4210
VB	 0.6220	 0.4440
W	 0.6510	 0.4700
WA	 0.7710	 0.4530

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Chain	Atom inclusion	Q-score
WB	 0.6230	 0.4740
X	 0.6600	 0.4770
XA	 0.8620	 0.4890
XB	 0.6020	 0.4740
Y	 0.6940	 0.4730
YA	 0.7790	 0.4620
YB	 0.5050	 0.3960
Z	 0.7280	 0.5100
ZA	 0.7230	 0.4300
ZB	 0.4480	 0.3710
b	 0.0650	 0.1310
c	 0.0180	 0.1630