



Full wwPDB EM Validation Report ⓘ

Jun 25, 2026 – 04:27 PM EDT

PDB ID : 8VVS / pdb_00008vvs
EMDB ID : EMD-43567
Title : Post-decoding post-hydrolysis state obtained from merged datasets of elongation inhibitor-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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

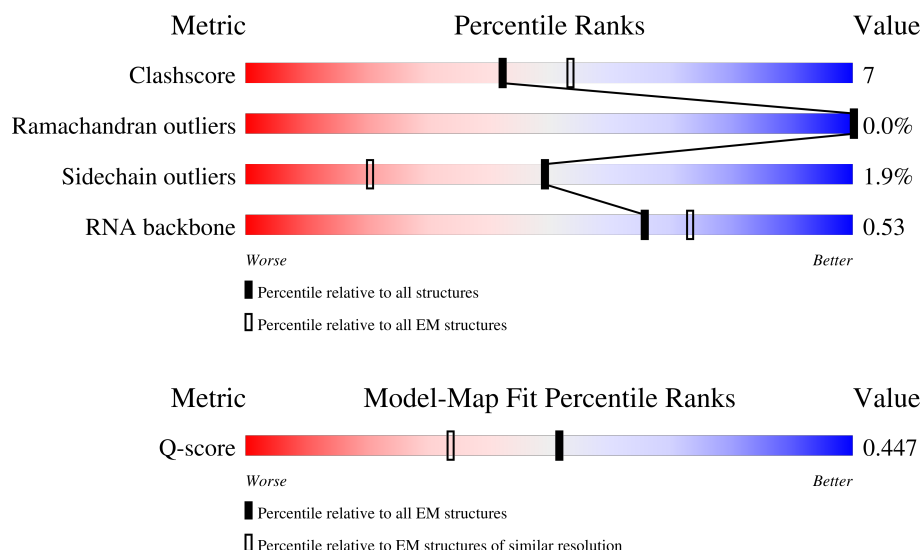
1 Overall quality at a glance

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	A	257	
2	B	403	
3	C	413	

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Mol	Chain	Length	Quality of chain
4	D	297	
5	E	291	
6	F	249	
7	G	319	
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	

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Mol	Chain	Length	Quality of chain
29	CA	125	
30	DA	135	
31	EA	110	
32	FA	129	
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	

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Mol	Chain	Length	Quality of chain
54	CB	293	
55	DB	281	
56	EB	263	
57	FB	204	
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	

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Mol	Chain	Length	Quality of chain
79	BC	84	
80	CC	69	
81	DC	56	
82	EC	133	
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 220703 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		

- 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 1 A.

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	2	Total	Mg	0
			2	2	
89	FA	1	Total	Mg	0
			1	1	
89	IA	1	Total	Mg	0
			1	1	
89	SA	1	Total	Mg	0
			1	1	
89	WA	158	Total	Mg	0
			158	158	
89	XA	3	Total	Mg	0
			3	3	
89	YA	2	Total	Mg	0
			2	2	
89	ZA	61	Total	Mg	0
			61	61	
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).

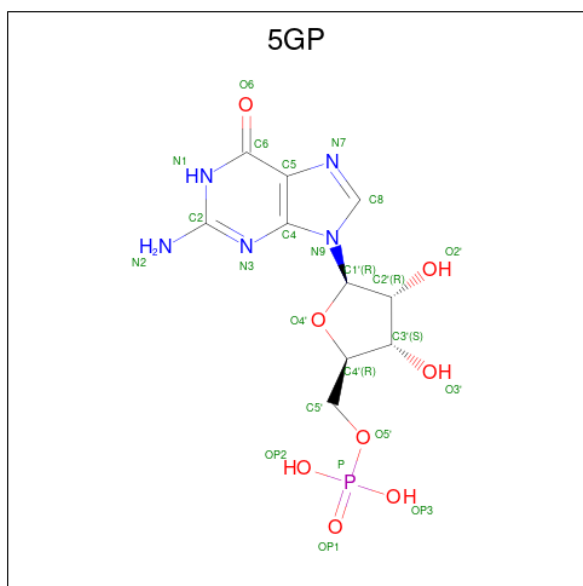
Mol	Chain	Residues	Atoms		AltConf
90	FA	1	Total	Zn	0
			1	1	
90	IA	1	Total	Zn	0
			1	1	

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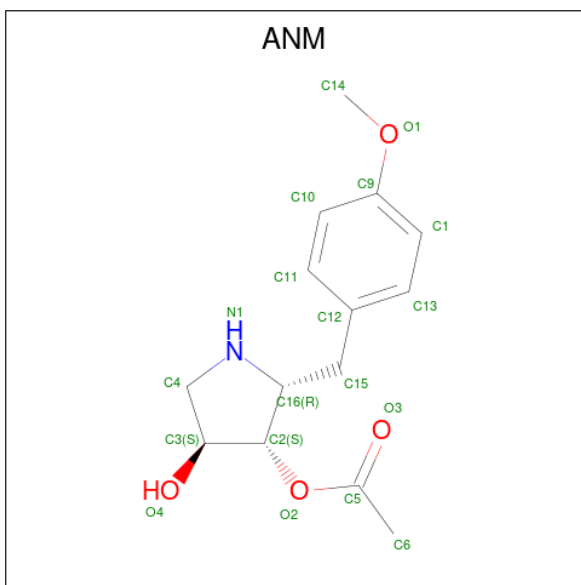
Mol	Chain	Residues	Atoms		AltConf
90	LA	1	Total	Zn	0
			1	1	
90	NA	1	Total	Zn	0
			1	1	
90	OA	1	Total	Zn	0
			1	1	
90	AC	1	Total	Zn	0
			1	1	
90	DC	1	Total	Zn	0
			1	1	
90	FC	1	Total	Zn	0
			1	1	

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



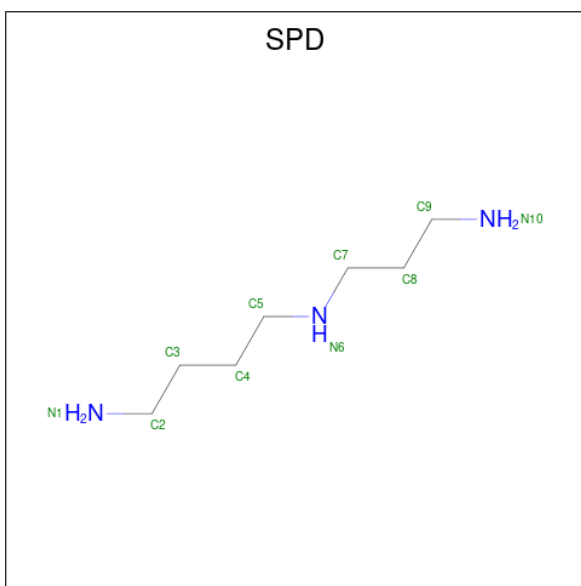
Mol	Chain	Residues	Atoms					AltConf
91	UA	1	Total	C	N	O	P	0
			24	10	5	8	1	

- 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	WA	1	Total	C	N	0
			10	7	3	

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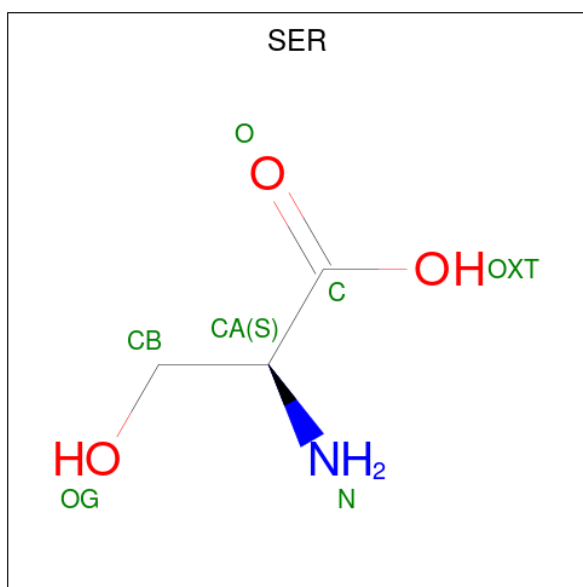
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Mol	Chain	Residues	Atoms			AltConf
93	ZA	1	Total	C	N	0
			10	7	3	

- 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: C₃H₇NO₃).



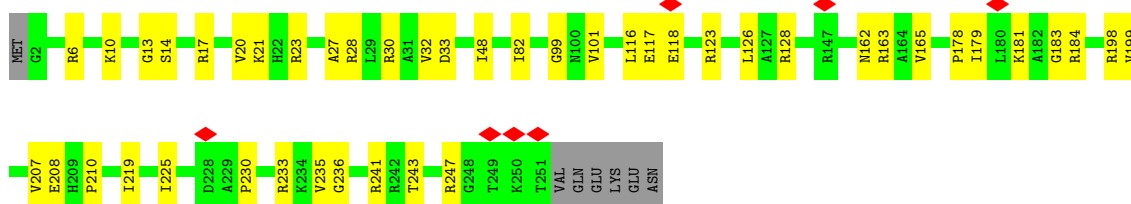
Mol	Chain	Residues	Atoms				AltConf
95	HC	1	Total	C	N	O	0
			6	3	1	2	

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.

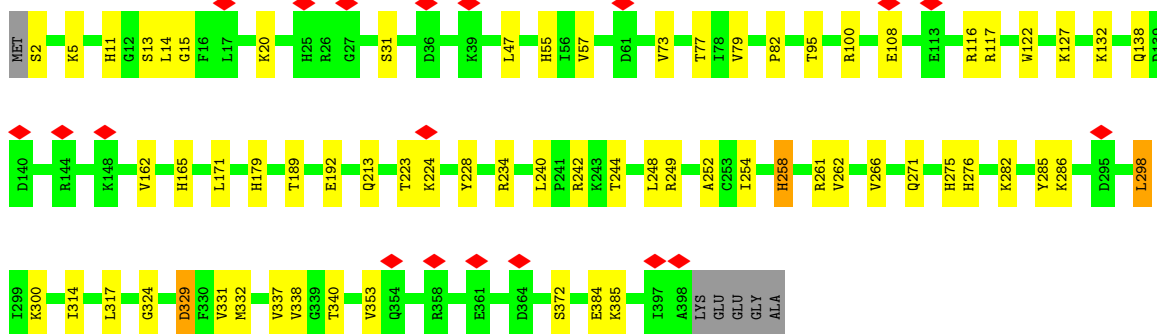
• Molecule 1: uL2

Chain A: 



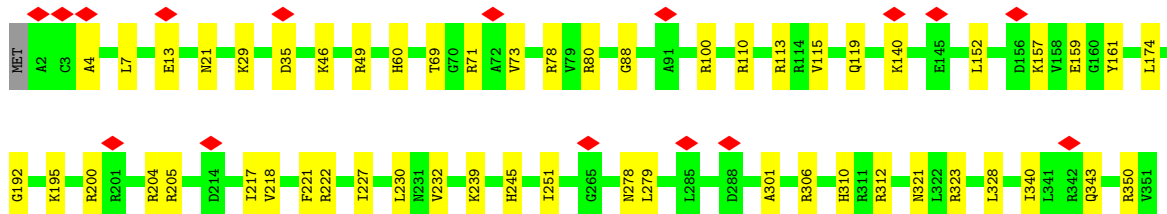
• Molecule 2: uL3

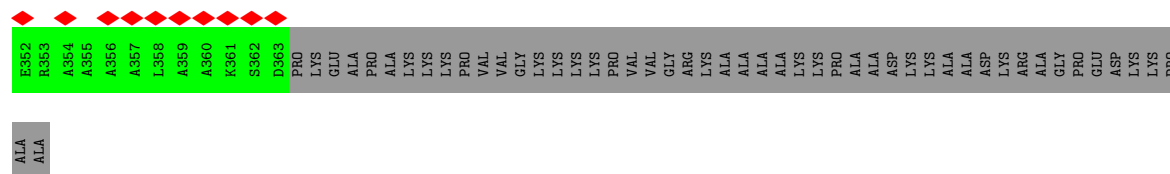
Chain B: 



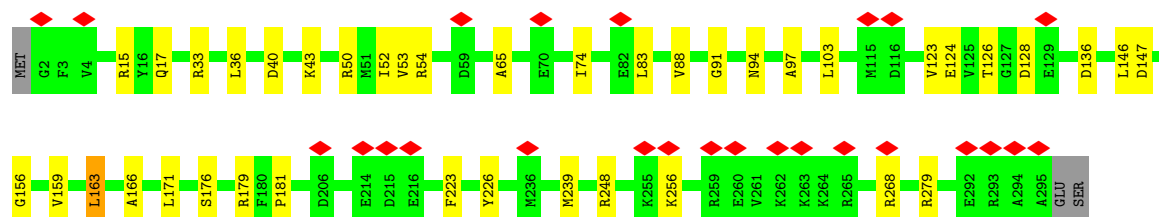
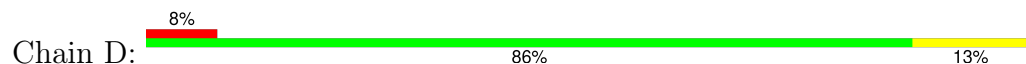
• Molecule 3: uL4

Chain C: 

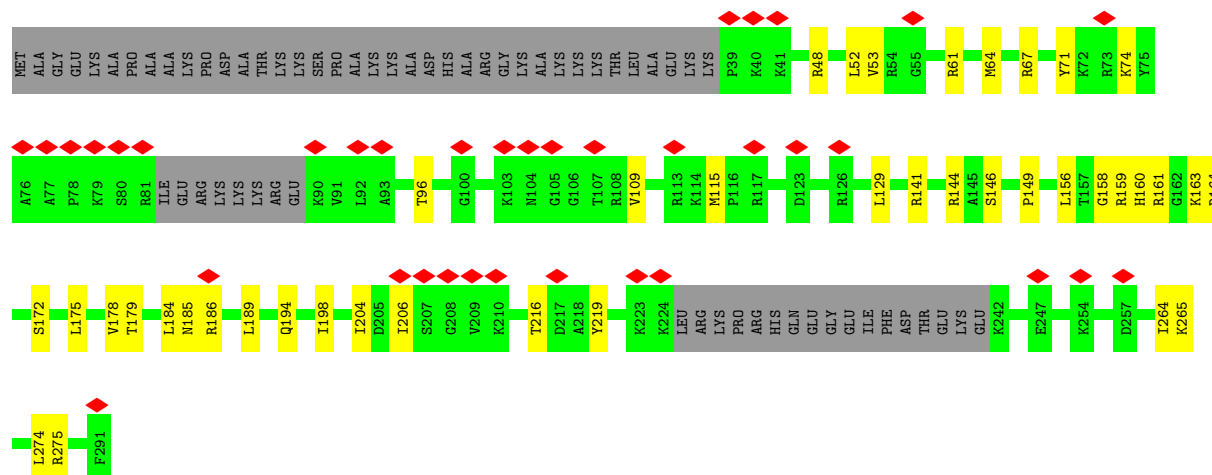




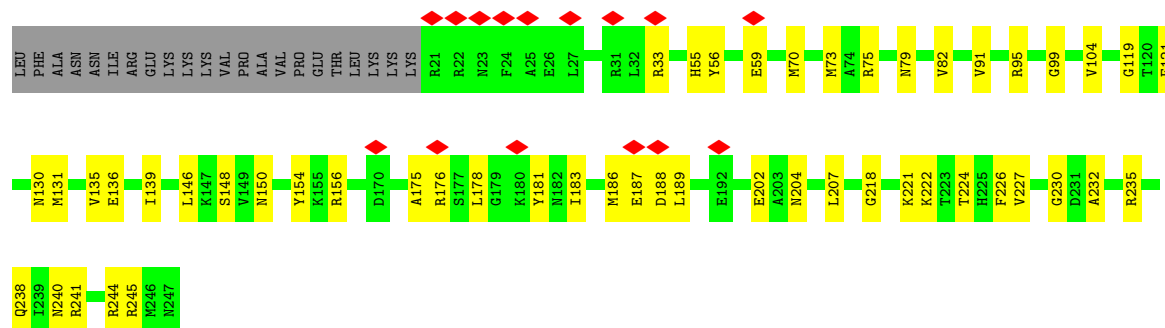
• Molecule 4: uL18



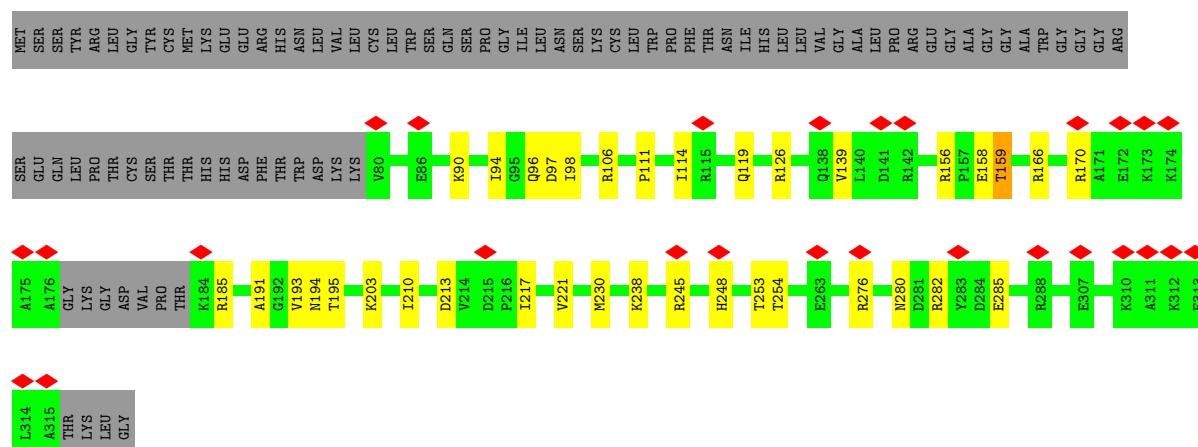
• Molecule 5: L6



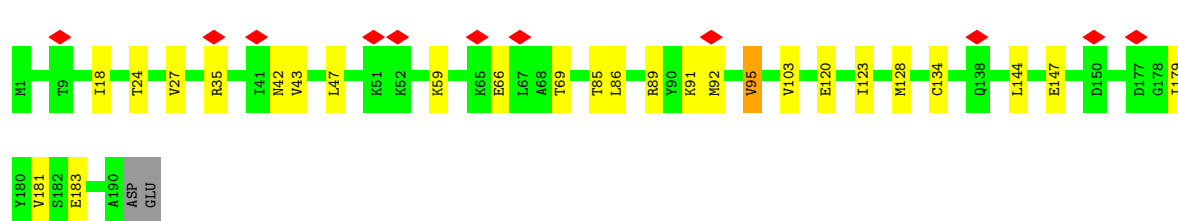
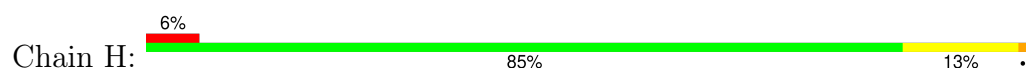
• Molecule 6: uL30



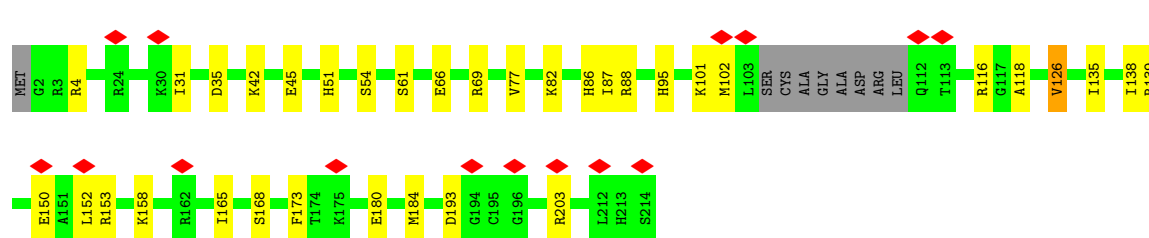
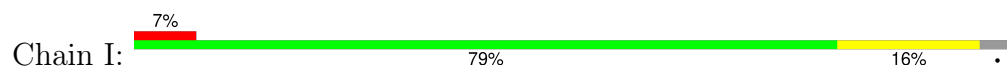
• Molecule 7: L7A



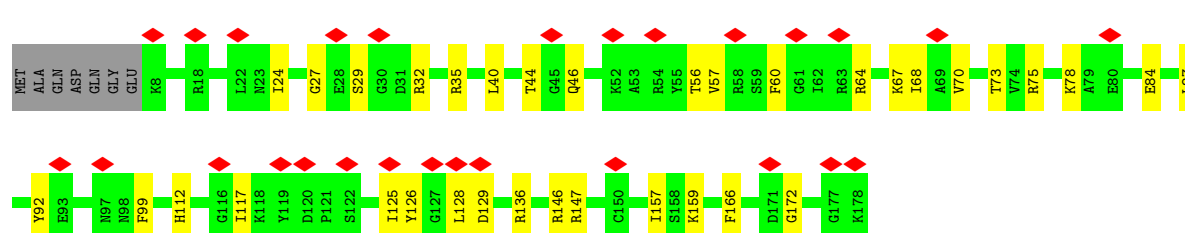
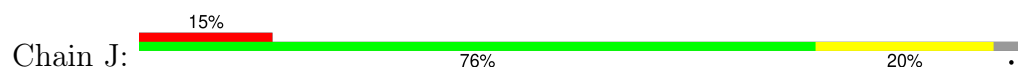
- Molecule 8: L9



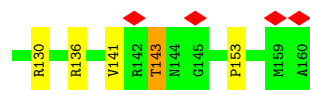
- Molecule 9: L10



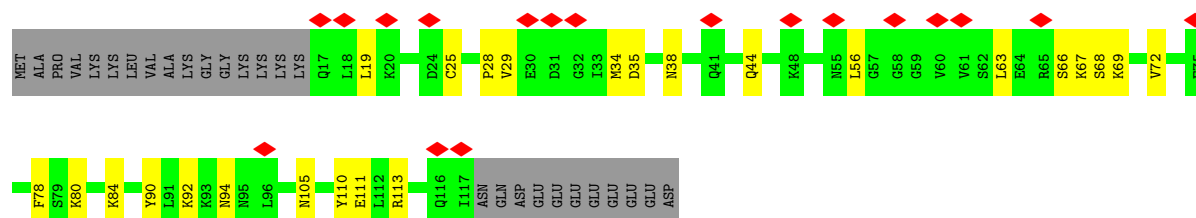
- Molecule 10: uL5



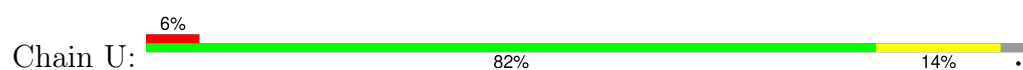
- Molecule 11: eL13



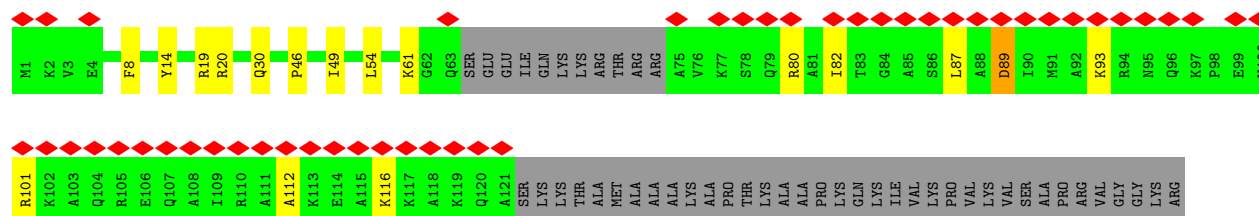
• Molecule 20: eL22



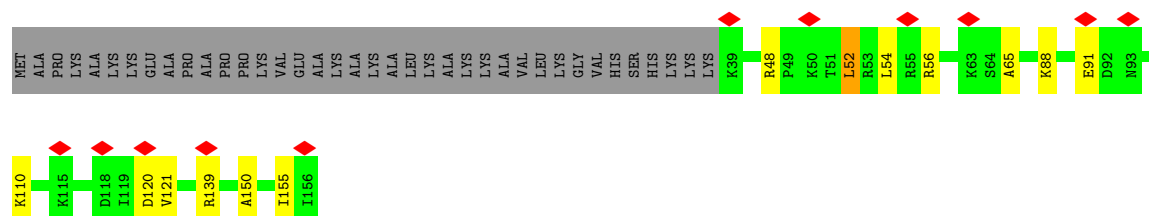
• Molecule 21: L23



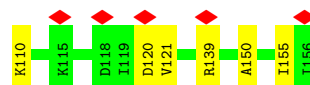
• Molecule 22: uL24



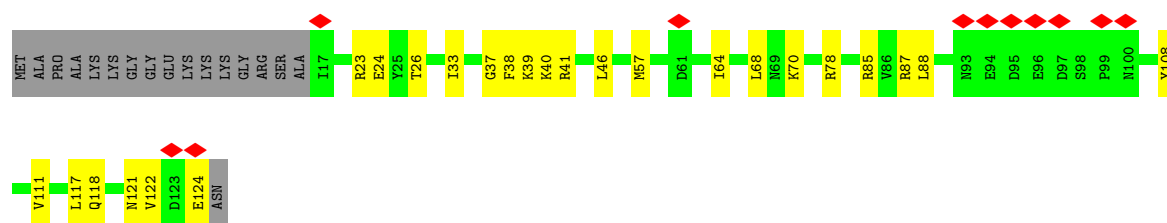
• Molecule 23: uL23



• Molecule 24: L26



Chain CA: 



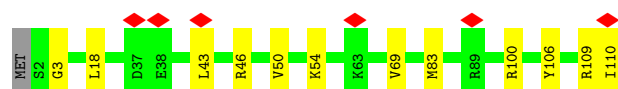
- Molecule 30: L32

Chain DA: 



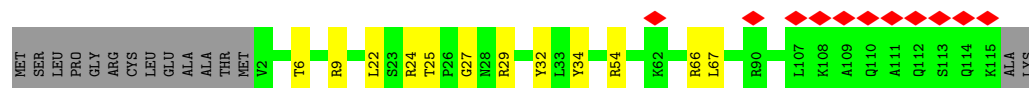
- Molecule 31: eL33

Chain EA: 



- Molecule 32: L34

Chain FA: 



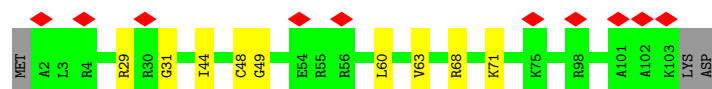
- Molecule 33: L35

Chain GA: 



- Molecule 34: L36

Chain HA: 

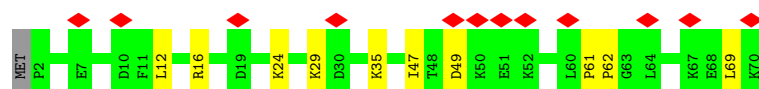
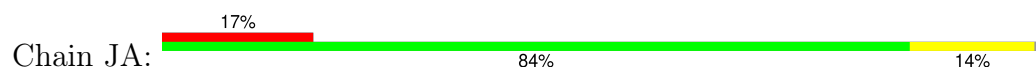


- Molecule 35: L37

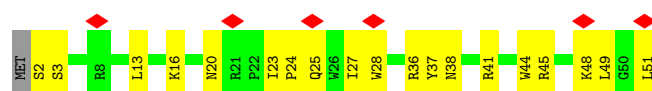
Chain IA: 



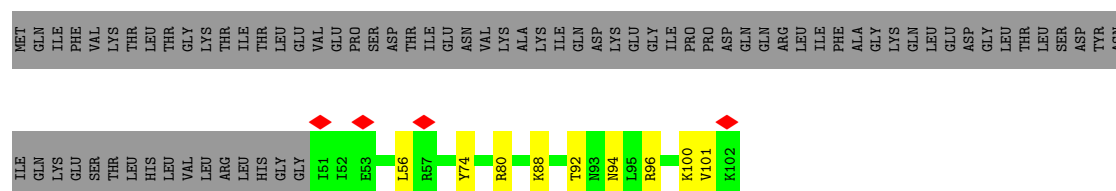
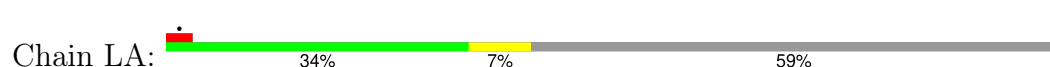
- Molecule 36: eL38



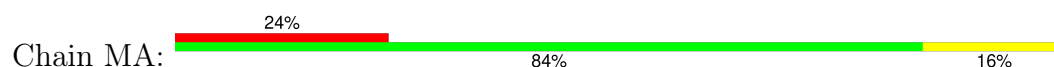
- Molecule 37: eL39



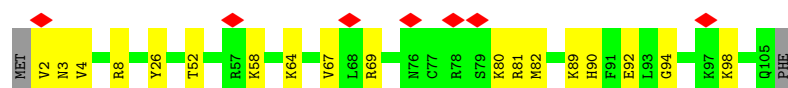
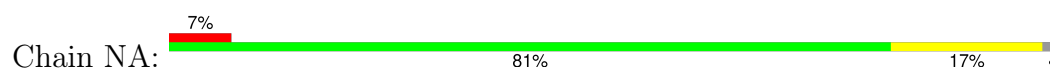
- Molecule 38: eL40



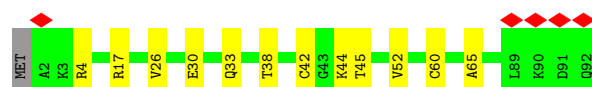
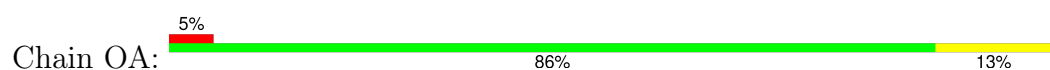
- Molecule 39: eL41



- Molecule 40: eL42

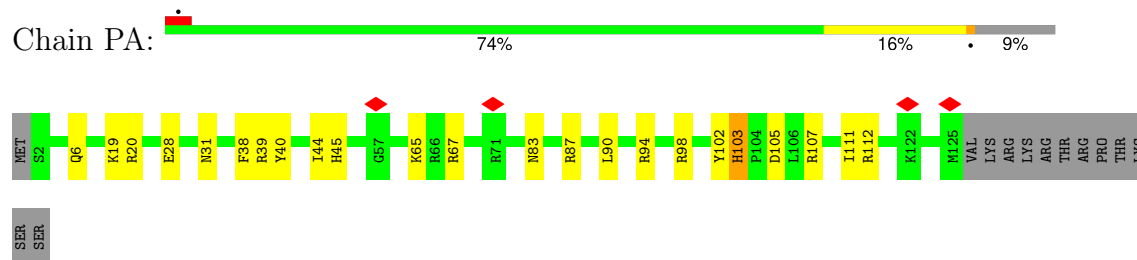


- Molecule 41: eL43



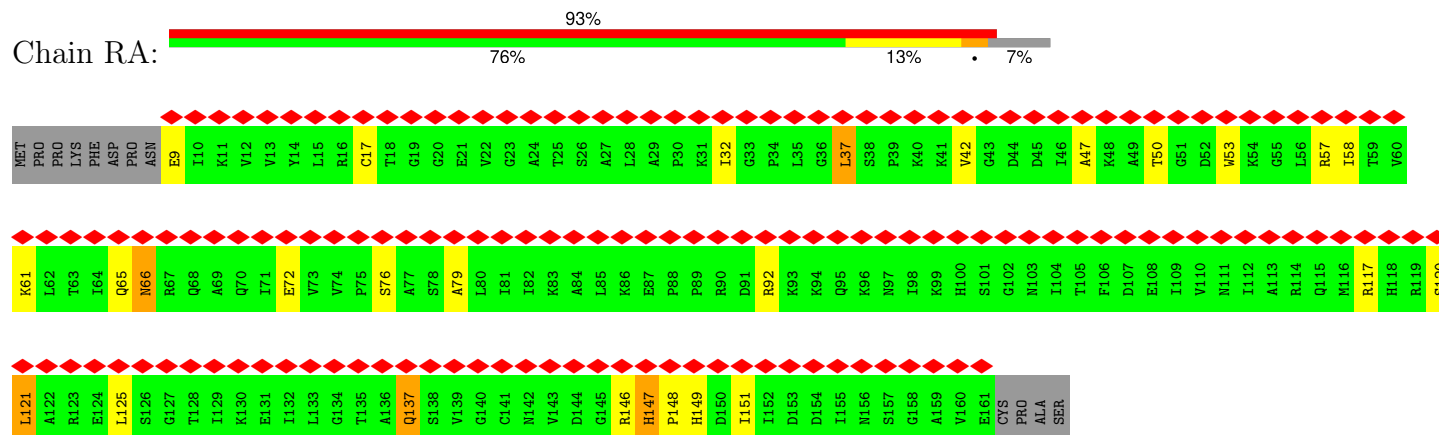
- Molecule 42: L28

Chain PA:



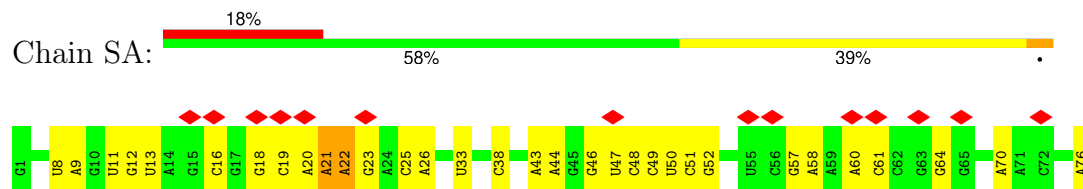
- Molecule 43: L12

Chain RA:



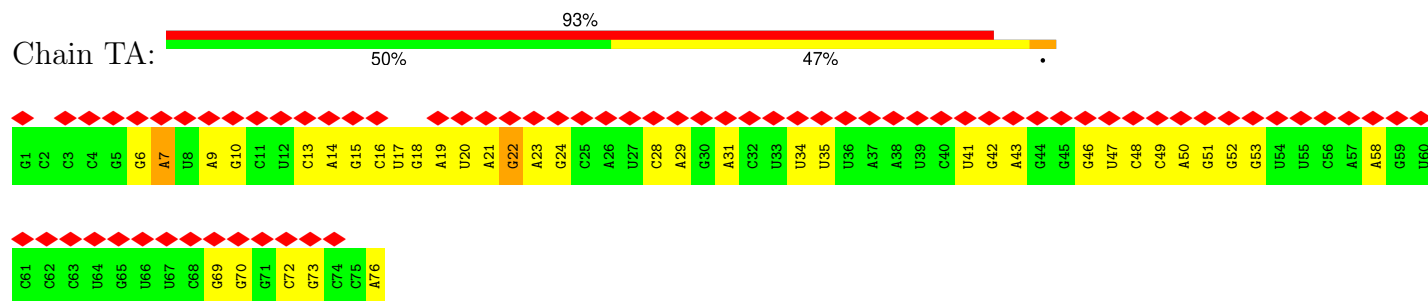
- Molecule 44: P-site tRNA

Chain SA:



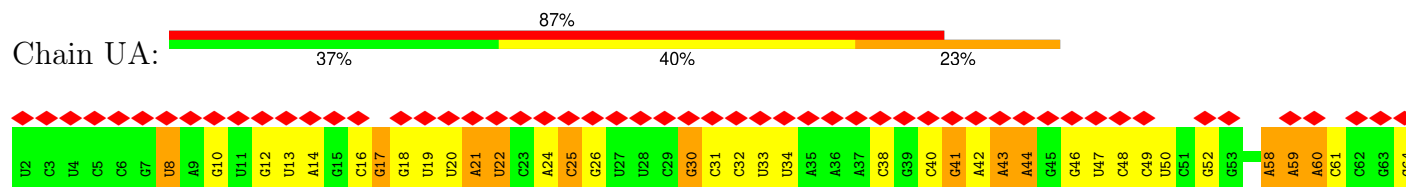
- Molecule 45: E-site tRNA

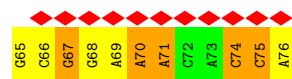
Chain TA:



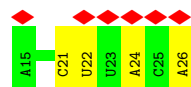
- Molecule 46: A-site tRNA

Chain UA:

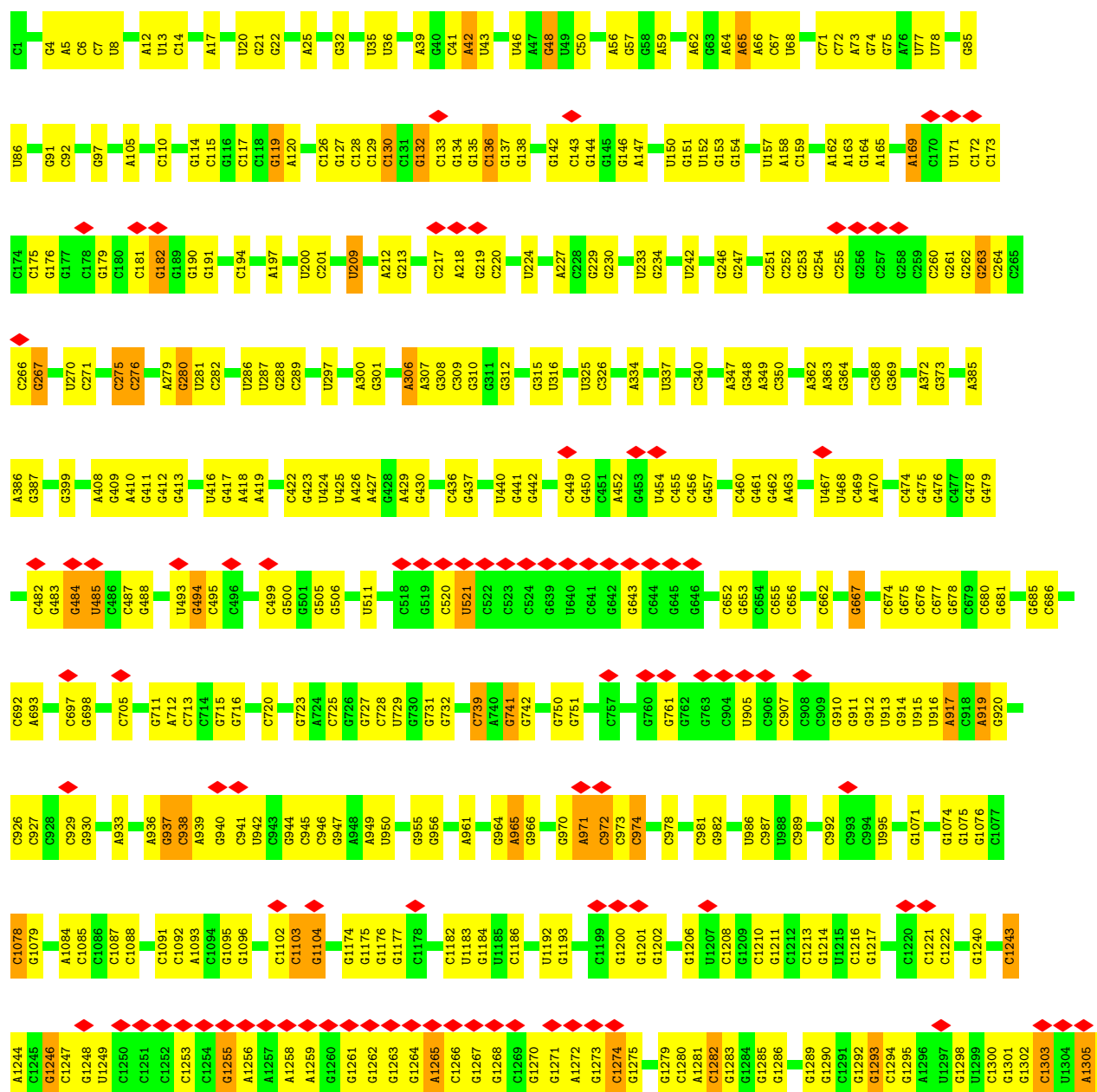




• Molecule 47: mRNA

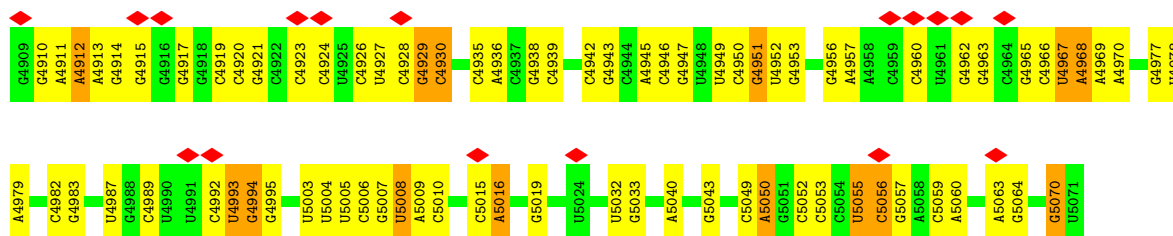


• Molecule 48: 28S rRNA



G2561	A2486	G2380	A2287	G1897	C1809	G1726	U1598	U1496	C1307
C2562	U2487	A2380	G2288	A1898	G1812	U1727	U1599	G1497	C1310
C2563	G2488	A2383	C2291	C1900	G1813	U1728	A1499	G1498	C1311
G2564	G2489	A2384	C2064	C1909	G1814	U1729	C1500	C1407	C1312
C2565	C2490	A2391	A2071	U1908	G1817	U1730	G1604	G	G
C2566	C2491	A2397	C2074	A1909	G1818	C1734	G1606	C	C1317
A2567	U2492	A2402	C2075	G1912	G1819	G1735	G1607	C	G1318
C2568	C2493	G2402	C2076	C1916	G1820	A1740	A1504	C	U1319
A2575	C2494	G2408	C2077	C1917	G1821	G1741	G1506	G	C1320
C2576	G2409	G2409	G2078	G1918	U1822	G1742	G1614	U1412	A1328
U2577	U2410	U2410	G2081	A1919	G1823	G1743	G1619	C1413	G1329
C2578	C2411	C2411	U2082	U1920	U1824	U1744	G1620	C1414	G1330
G	C2412	C2412	C2083	G1921	G1825	A1745	A1510	C1415	C1334
G	C2413	C2413	G2084	C1922	G1826	G1752	G1627	C1416	C1335
C2581	A2414	A2414	C2085	C1923	A1827	U1751	U1513	U1421	A1336
A2584	U2415	U2415	U2086	G1924	C1830	G1752	U1514	A1422	U1343
C2585	G2416	G2416	U2092	A1925	U1836	G1755	U1515	A1422	A1344
G	U2417	U2417	G2095	U1926	G1837	U1756	U1516	G1428	A1345
C2588	G2418	A2418	C2096	U1929	G1838	C1757	A1517	G1432	A1346
C2589	A2419	A2419	C2097	C1930	A1839	U1758	G1518	C1433	A1347
A2509	C2424	C2424	A2098	A1931	U1844	U1759	G1519	G1434	C1348
G	U2427	U2427	G2099	U1932	G1844	U1760	A1520	G1435	G1349
A2515	U2428	U2428	C2099	C1933	G1848	G1762	A1525	C1435	C1352
G2516	G2429	G2429	G2100	A1935	U1848	G1765	A1526	C1443	G1355
C2517	A2430	A2430	C2101	C1936	C1849	G1766	A1527	C1444	A1356
A2519	C2430	C2430	G2102	U1939	U1852	G1767	U1530	G1445	G1360
G2520	U2434	U2434	A2103	C1940	G1853	G1768	G1531	G1446	G1361
U2521	G2435	G2435	C2104	A1941	U1854	G1769	A1536	U1447	G1362
C2522	C2436	C2436	A2105	G1942	G1857	U1767	C1543	C1448	G1363
G2523	U2437	U2437	A2106	A1943	G1866	A1768	A1549	C1449	G1364
C2524	G2445	G2445	A2107	U1944	G1867	G1769	G1565	C1452	A1373
G2525	C2448	C2448	G2108	A1945	U1868	C1770	G1566	G1459	G1379
U2526	U2449	U2449	C2109	G1950	G1871	G1771	A1555	C1460	G1380
U2527	G2450	G2450	A2109	U1951	C1872	A1772	A1556	A1461	C1381
C2528	C2454	C2454	U2113	G1952	A1873	U1773	G1557	C1462	G1382
A2531	G2459	G2459	G2114	U1961	G1874	C1774	A1560	A1464	U1383
U2532	C2460	C2460	G2115	A1962	U1878	U1775	G1561	C1465	G1384
G2535	G2467	G2467	A2116	G1963	G1879	C1776	A1565	C1466	G1385
A2539	A2468	A2468	G2117	U1964	U1880	A1777	A1567	C1470	A1389
C2541	U2469	U2469	C2260	G1965	C1881	U1781	C1568	C1474	G1392
C2542	U2470	U2470	G2261	U1966	C1882	A1782	U1574	U1475	G1395
G2543	G2476	G2476	C2262	C1968	C1883	U1783	G1575	G1481	G1396
U2544	G2477	G2477	G2263	A1969	G1885	A1788	G1690	C1482	U1397
A2545	C2478	C2478	C2264	U1970	G1886	U1789	G1691	C1483	G1398
G2546	U2479	U2479	A2265	G1971	G1887	A1790	C1692	C1484	A1399
U2547	A2372	A2372	G2267	G1972	G1887	C1791	G1693	C1485	A1400
C2548	G2376	G2376	C2268	U1973	A1890	A1797	C1698	G1492	G1401
G2549	A2377	A2377	C2021	G1974	A1893	A1804	C1722	A1493	G1402
G2555	G2481	G2481	U2022	G1975	G1893	G1805		G1494	
C2556	C2482	C2482	G2023	U1976	A1893	A1806		G1495	
G2557	G2483	G2483	C2024	G1977		A1807			
C2558	C2484	C2484	C2025	G1978		G1808			
G2559	G2485	G2485	A2027	G1979					
C2560			A2028	G1979					
			G2036	G1979					
			G2048	G1979					
			A2049	G1979					
			U2050	G1979					
			G2054	G1979					

G4654	U4653	A4451	A4327	C4127	G3948	A3863	C3767	A3655	U2845	G2744
U4654	U4654	U4454	G4328	A4128	A3949	A3864	C3763	A3655	A2846	A2745
U4557	U4557	C4455	G4329	A4129	C3950	A3870	C3763	G3661	A2847	A2746
C4562	C4562	U4459	G4332	A4130	A3951	C3871	G3767	A3664	G2850	A2747
U4565	U4565	C4460	G4333	A4131	U3952	C3872	C3767	A3665	A2851	A2748
A4566	A4566	U4461	G4334	C4136	G3953	A3873	U3772	A3666	C2751	U2749
U4568	U4568	C4463	A4338	G4137	A3954	A3874	C3773	G3666	C2857	C2750
G4569	G4569	U4466	C4343	A4138	A3954	G3875	U3772	A3667	C2858	G2752
G4572	G4572	U4467	C4348	C4139	A4064	G3876	U3773	C3672	G2864	G2758
G4575	G4575	C4468	U4349	C4140	U4065	A3877	A3777	G3673	G2865	A2759
U4576	U4576	A4469	G4350	C4141	C4066	A3878	G3778	G3674	A2866	G2760
G4577	G4577	C4351	A4352	C4142	G4067	C3880	G3779	C3675	G2761	G2762
U4578	U4578	C4352	G4256	C4143	U4068	G3881	A3785	G3683	U2871	U2763
U4579	U4579	U4355	C4262	C4144	U4069	A3786	A3787	G3686	A2883	G2764
U4580	U4580	U4356	C4263	C4145	U4070	A3787	U3788	C3687	G2886	U2765
U4581	U4581	A4368	G4264	C4146	U4071	A3788	U3788	G3688	A2887	A2766
A4586	A4586	G4372	C4265	C4147	U4072	A3797	A3797	A3689	C2892	U2771
U4587	U4587	G4375	G4266	C4148	U4073	U3798	A3798	G3691	G2896	C2772
G4588	G4588	A4376	U4267	C4149	U4074	C3799	A3799	A3694	A2897	G2773
G4589	G4589	U4502	G4268	C4150	U4075	U3800	U3800	U3699	G2898	U2889
A4592	A4592	A4503	G4269	C4151	G4078	U3804	U3804	U3699	A2899	G2779
U4596	U4596	C4509	G4270	C4152	A4079	U3807	U3807	G3700	G2899	G2780
G4597	G4597	C4510	A4273	C4153	C4082	G4083	A3787	C3700	C2901	C2781
U4701	U4701	U4511	G4274	C4154	G4083	A3903	A3819	G3700	C2901	G2782
A4702	A4702	A4512	A4275	C4155	U4084	A3909	U3820	U3709	U2902	G2783
G4706	G4706	U4513	A4276	C4156	A3908	G3909	G3821	C3710	C2903	U2703
A4707	A4707	G4514	G4277	C4157	G4088	G3910	G3811	A3713	G2904	U2703
G4872	G4872	A4515	A4283	C4158	G4089	A3910	G3812	A3714	A3598	C2704
C4873	C4873	A4520	G4293	C4159	C4090	C3912	G3813	U3715	G3599	G2705
A4874	A4874	C4521	A4294	C4171	G4091	C3913	U3816	A3715	C3600	G2706
G4875	G4875	U4523	G4295	C4172	G4092	U3914	G3817	A3719	A3601	G2707
C4876	C4876	U4524	U4295	A4174	G4095	G3915	A3818	A3719	G3602	G2708
G4877	G4877	C4524	U4397	G4175	G4096	U3916	A3819	A3720	U3609	U2709
A4878	A4878	U4525	U4398	U4176	G4097	G3918	U3820	G2797	A3610	U2710
G4879	G4879	G4526	G4403	C4177	C4098	G3919	G3821	G2798	C3599	C2711
C4722	C4722	C4526	C4402	C4178	C4099	G3920	G3825	A2800	A3612	C2712
U4823	U4823	A4529	G4403	C4179	G4099	G3920	G3825	A2808	A3613	G2713
G4824	G4824	C4529	U4406	A4180	A4100	A3925	U3840	A3726	G3617	C2721
U4825	U4825	G4530	U4407	C4185	G4101	C3926	G3841	A3726	A3626	C2722
C4826	C4826	U4531	G4407	G4186	G4101	C3926	U3842	A3729	G3627	G2723
G4827	G4827	U4532	U4408	C4187	C4102	U3929	C3845	A3729	C3627	G2723
A4828	A4828	C4533	C4415	U4190	C4103	A3930	U3846	A3730	G3628	A2727
C4829	C4829	U4534	U4415	U4191	C4109	A3930	U3846	A3730	G3628	G2728
U4830	U4830	A4546	U4421	U4192	G4109	U3934	A3847	A3734	G2824	G2728
G4831	G4831	U4541	C4422	C4193	G4110	G3935	A3847	U3736	C3635	U2732
C4832	C4832	C4423	A4424	G4194	G4111	G3936	U3850	G3737	G3636	C2733
A4833	A4833	G4542	A4424	C4195	C4112	G3936	A3851	A3738	A3637	G2734
U4834	U4834	U4543	C4321	C4201	U4113	G3940	A3857	A3739	U3643	U2736
C4835	C4835	A4546	G4322	C4201	U4113	G3941	C3857	A3750	A3644	G2737
G4836	G4836	U4547	U4323	C4205	C4114	A3945	A3858	A3750	A3648	U2738
A4837	A4837	C4446	G4324	A4205	U4115	A3945	C3857	A3750	A3649	G2739
C4838	C4838	A4550	A4325	A4205	C4116	A3946	A3858	A3750	A3649	G2739
U4839	U4839	G4552	A4326	A4214	C4117	G3946	G3861	C3754	A3650	U2742
G4840	G4840	A4553	G4326	A4214	C4118	A3947	A3862	C3755	A3650	U2743
A4841	A4841	C4450	G4326	A4214	C4118	A3947	A3862	C3755	A3650	U2743
C4842	C4842	G4450	G4326	A4214	C4118	A3947	A3862	C3755	A3650	U2743
U4843	U4843	G4450	G4326	A4214	C4118	A3947	A3862	C3755	A3650	U2743
G4844	G4844	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
A4845	A4845	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
C4846	C4846	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
U4847	U4847	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
G4848	G4848	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
A4849	A4849	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
C4850	C4850	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
U4851	U4851	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
G4852	G4852	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
A4853	A4853	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
C4854	C4854	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
U4855	U4855	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
G4856	G4856	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
A4857	A4857	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
C4858	C4858	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
U4859	U4859	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
G4860	G4860	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
A4861	A4861	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
C4862	C4862	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
U4863	U4863	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
G4864	G4864	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
A4865	A4865	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
C4866	C4866	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
U4867	U4867	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
G4868	G4868	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
A4869	A4869	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
C4870	C4870	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
U4871	U4871	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
G4872	G4872	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
A4873	A4873	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
C4874	C4874	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
U4875	U4875	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
G4876	G4876	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
A4877	A4877	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
C4878	C4878	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
U4879	U4879	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
G4880	G4880	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
A4881	A4881	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
C4882	C4882	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
U4883	U4883	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
G4884	G4884	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
A4885	A4885	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
C4886	C4886	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
U4887	U4887	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
G4888	G4888	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
A4889	A4889	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
C4890	C4890	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
U4891	U4891	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
G4892	G4892	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
A4893	A4893	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
C4894	C4894	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
U4895	U4895	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
G4896	G4896	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
A4897	A4897	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
C4898	C4898	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
U4899	U4899	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
G4900	G4900	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
A4901	A4901	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
C4902	C4902	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
U4903	U4903	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744
G4904	G4904	A4221	A4221	A4221	C4121	A4221	A4221	A4221	A4221	U2744



• Molecule 49: 5S rRNA

Chain XA: 71% 23% 5%



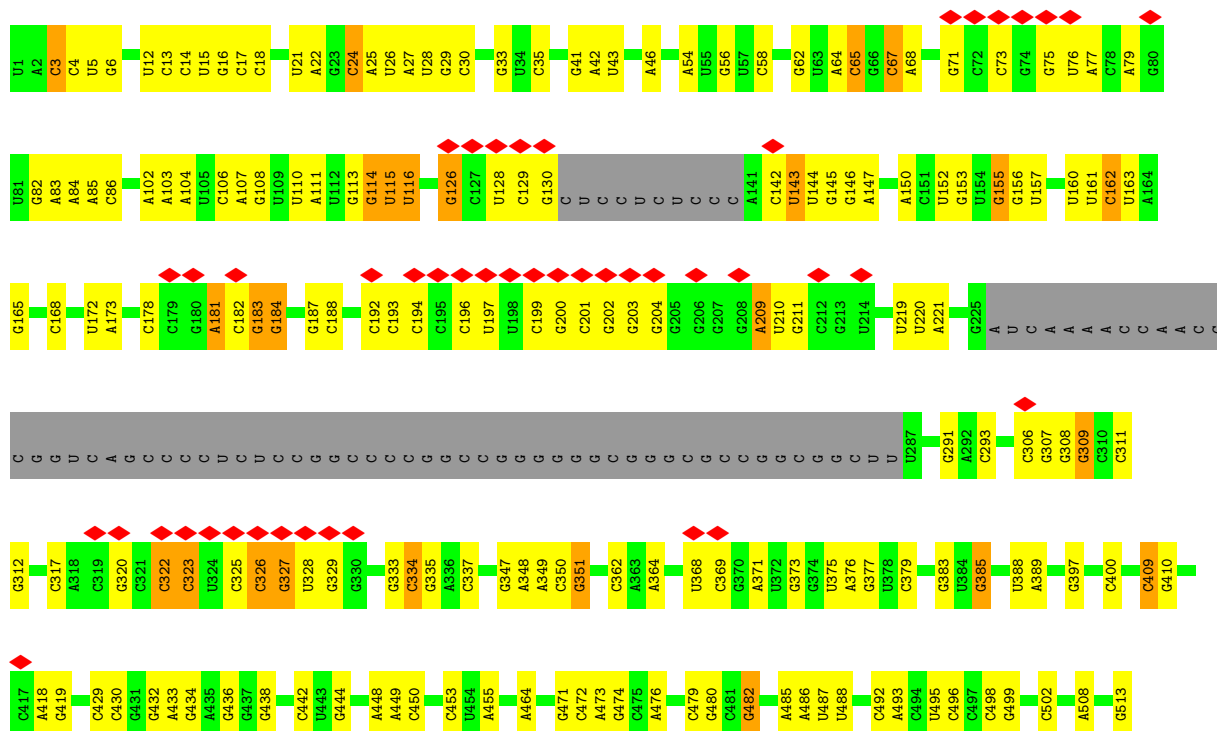
• Molecule 50: 5.8S rRNA

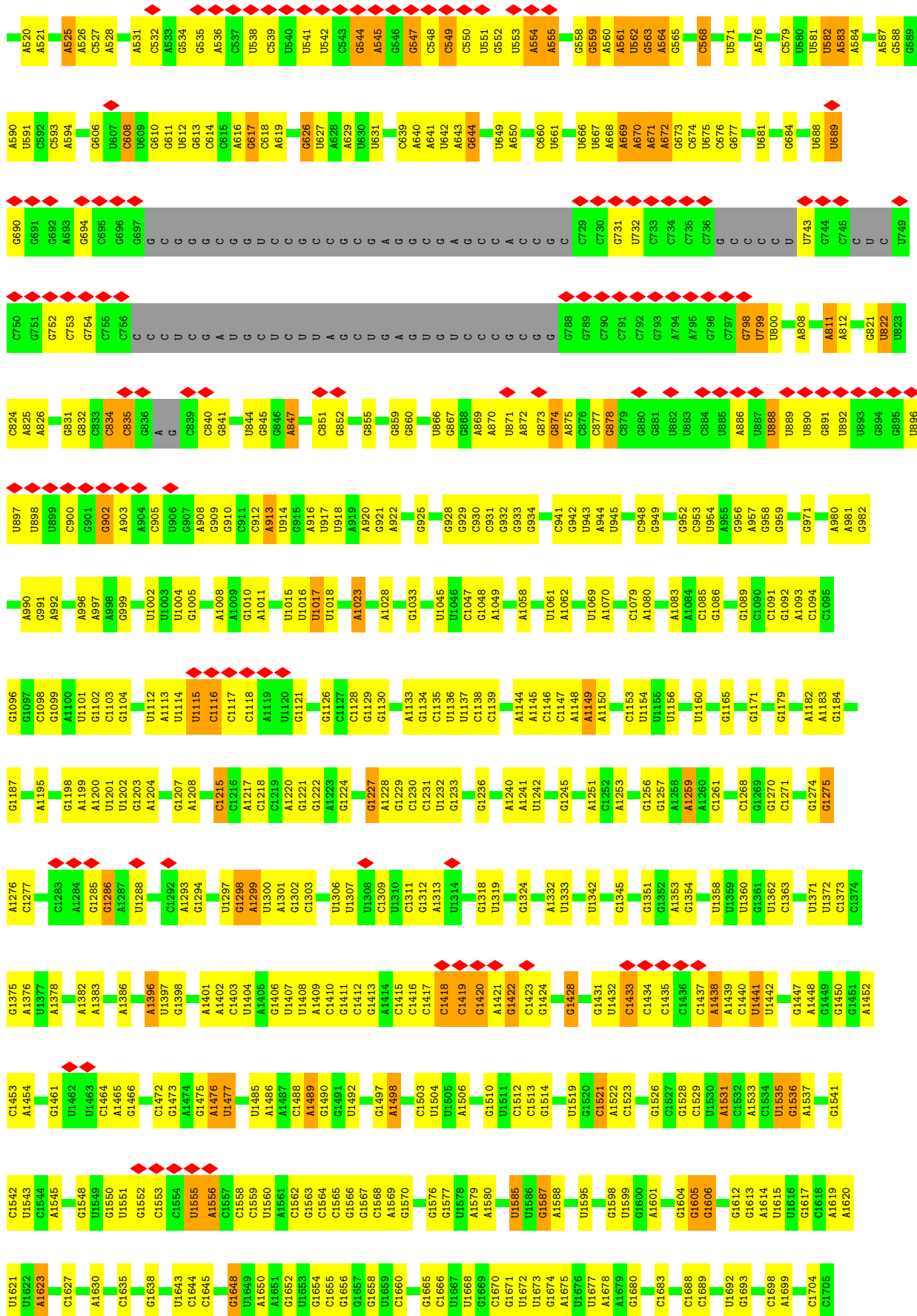
Chain YA: 10% 55% 38% 6%

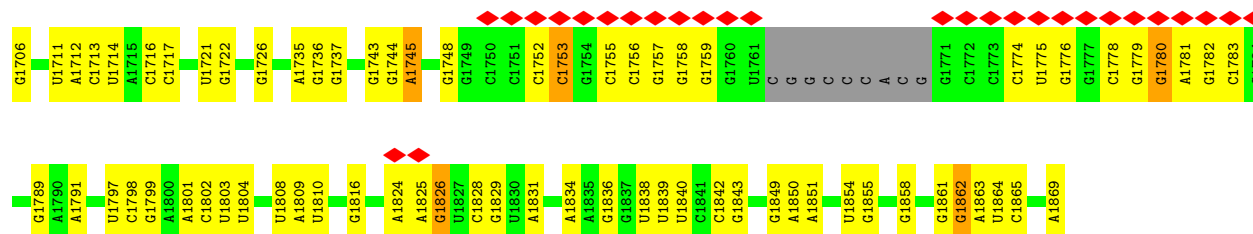


• Molecule 51: 18S rRNA

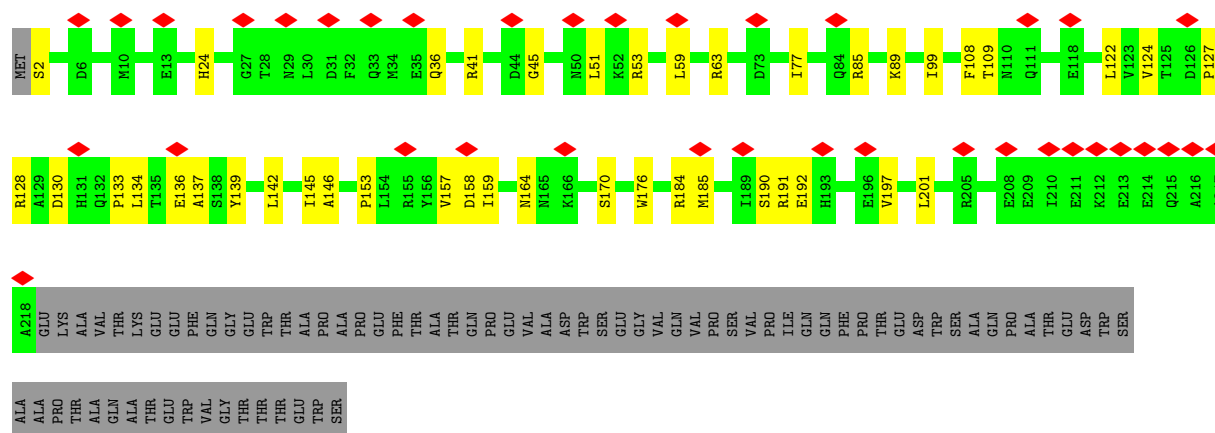
Chain ZA: 10% 51% 36% 6% 8%



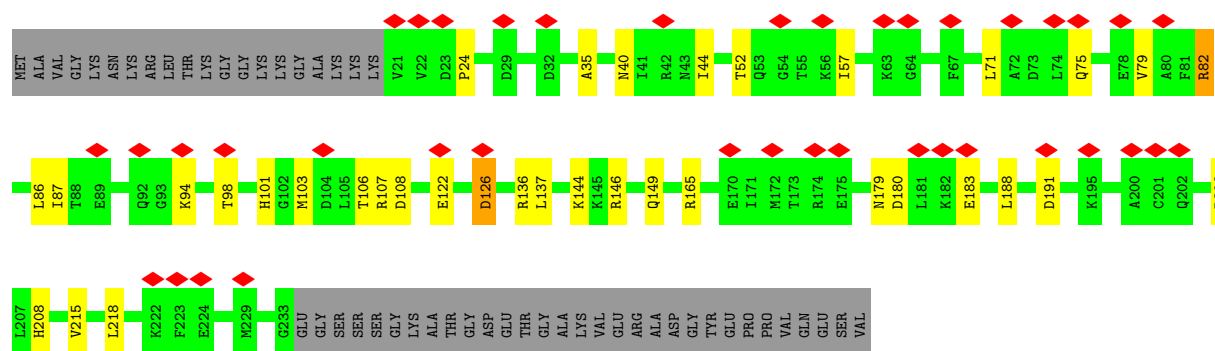




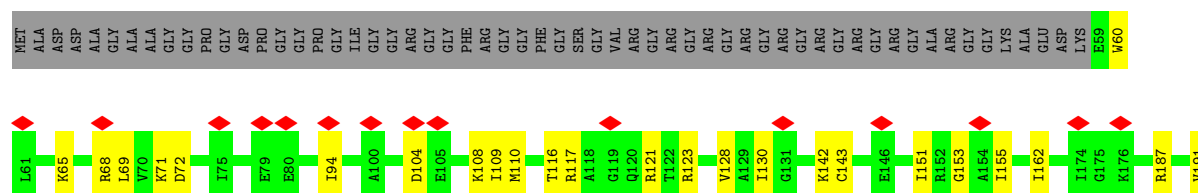
• Molecule 52: RPSA

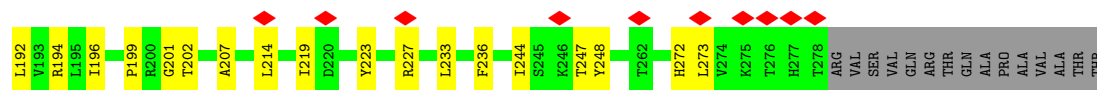


• Molecule 53: S3A

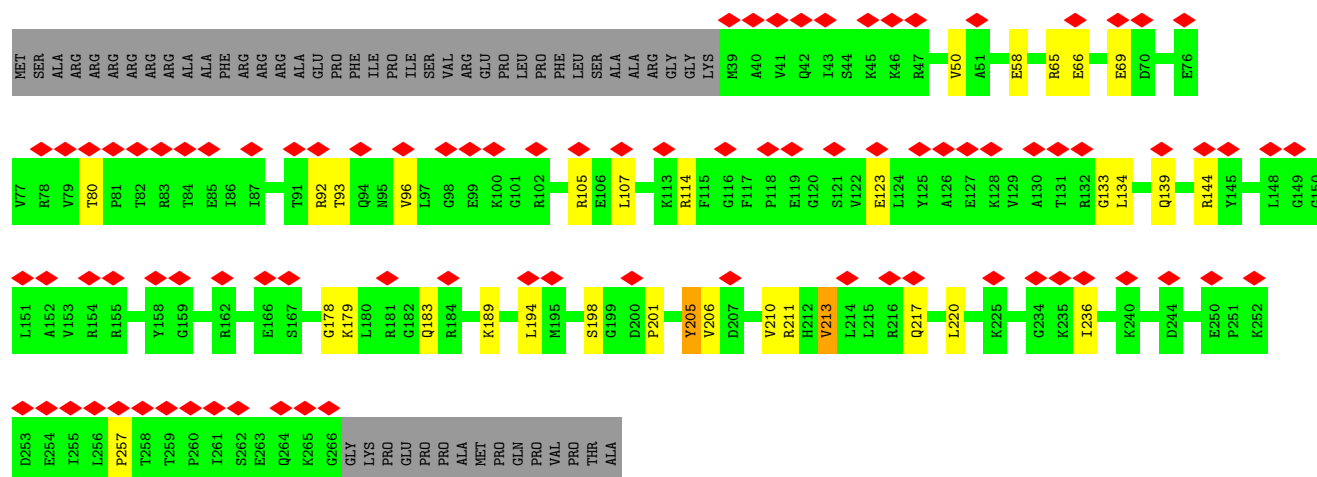


• Molecule 54: eS1

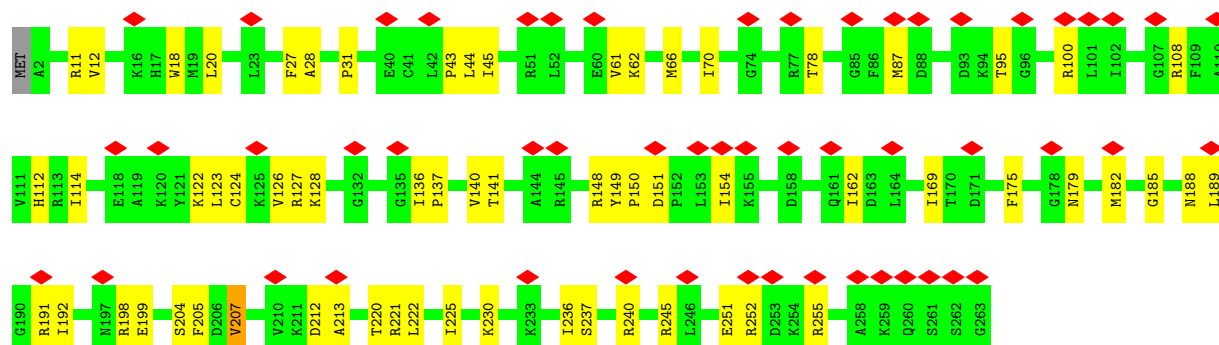
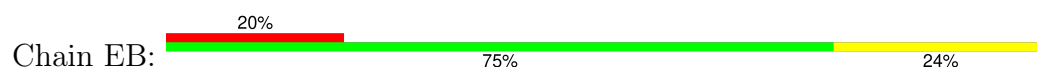




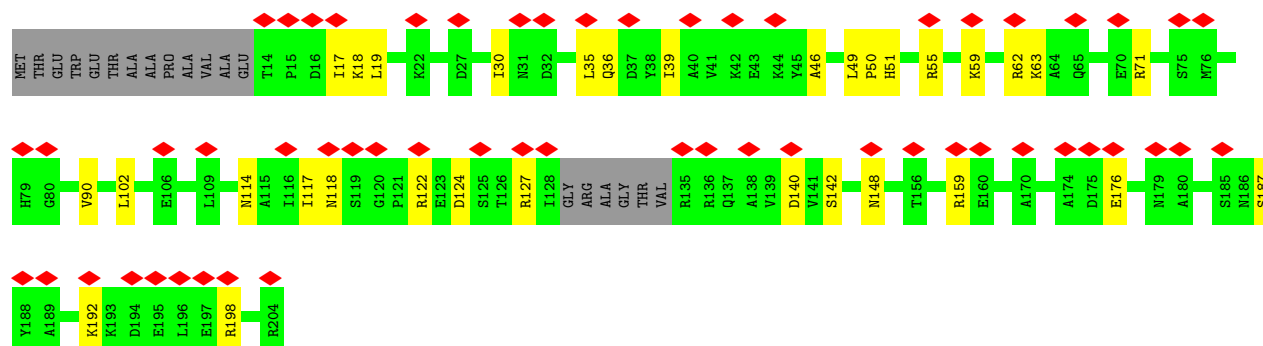
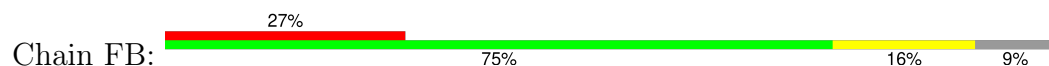
• Molecule 55: S3



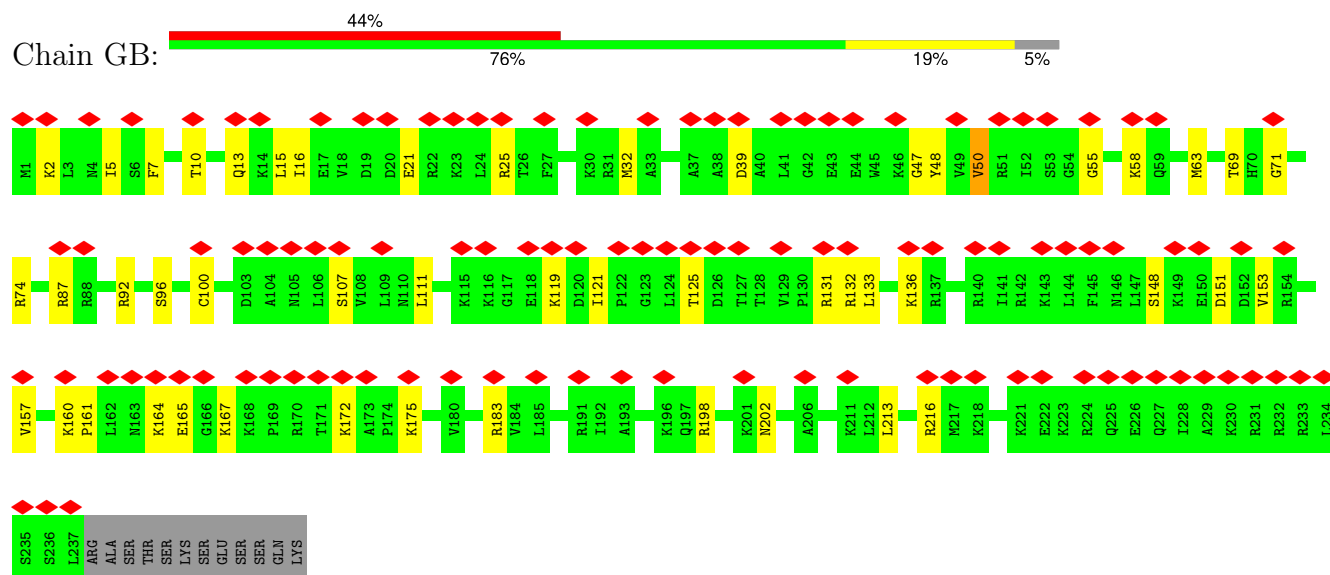
• Molecule 56: S4



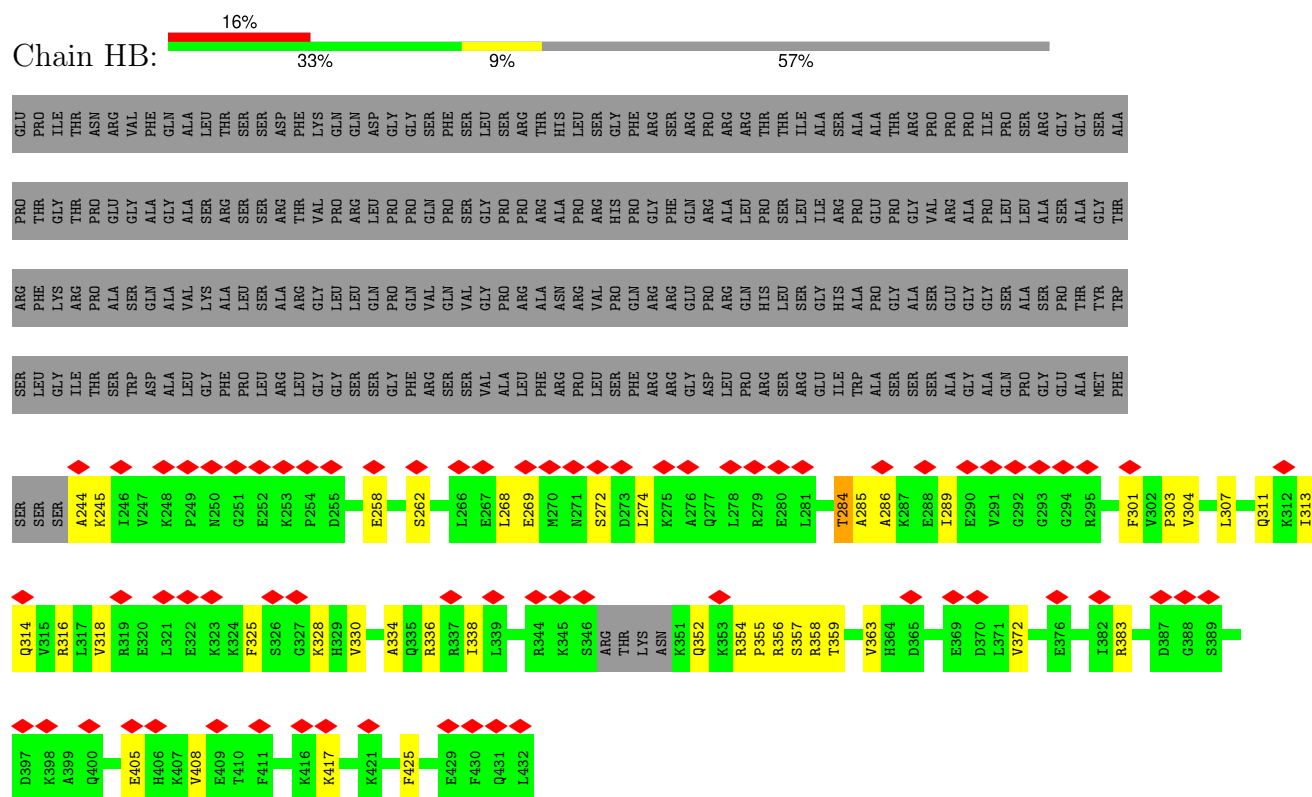
• Molecule 57: S5



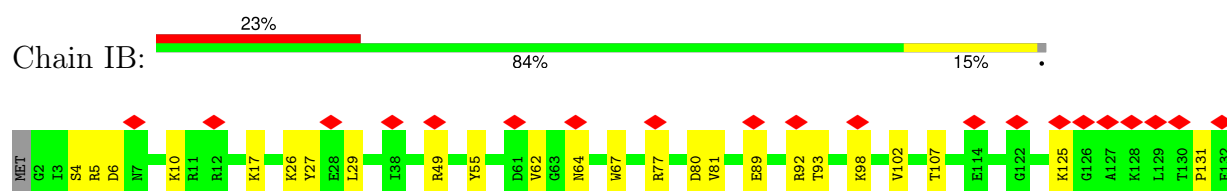
- Molecule 58: eS6

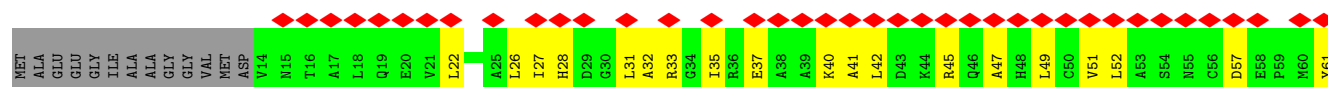


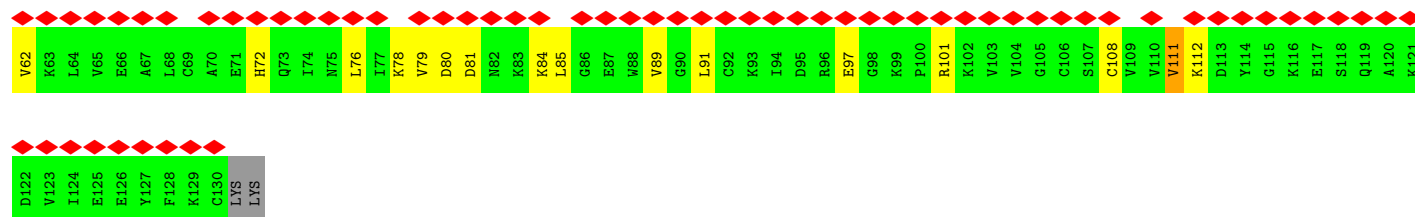
- Molecule 59: eS7



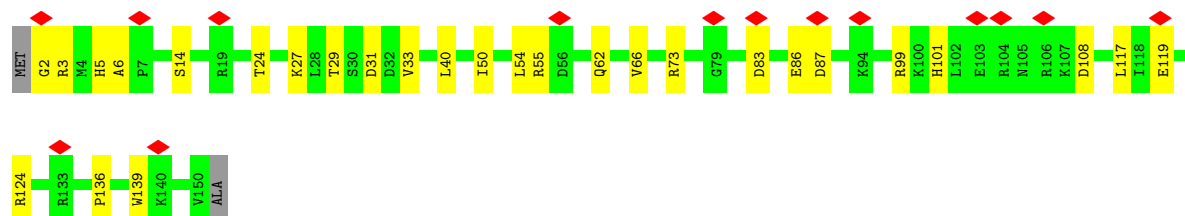
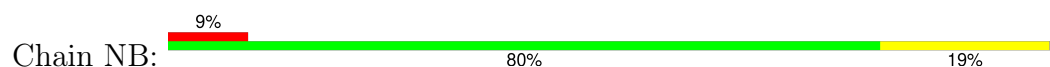
- Molecule 60: S8



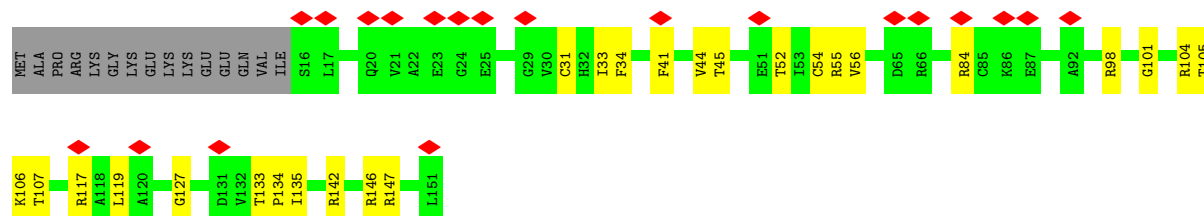
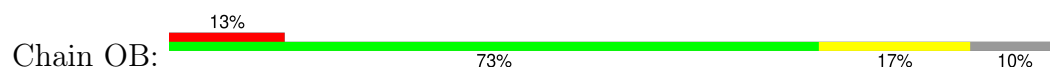




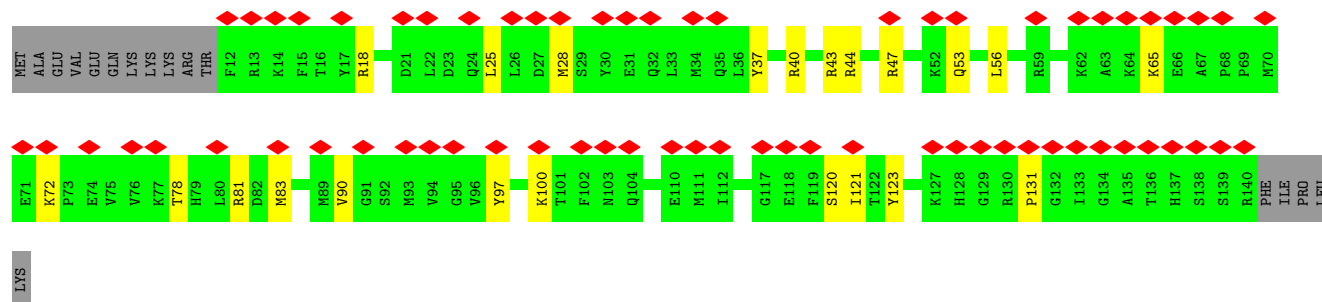
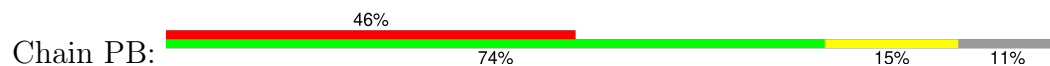
• Molecule 65: uS15



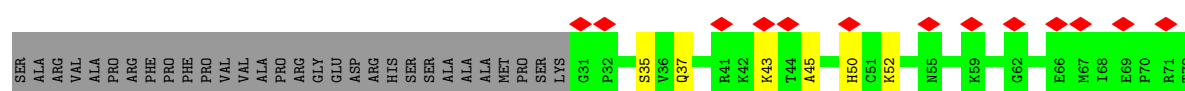
• Molecule 66: S14

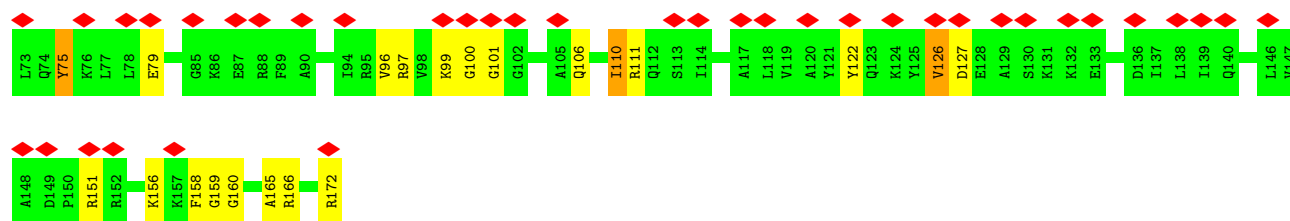


• Molecule 67: S15

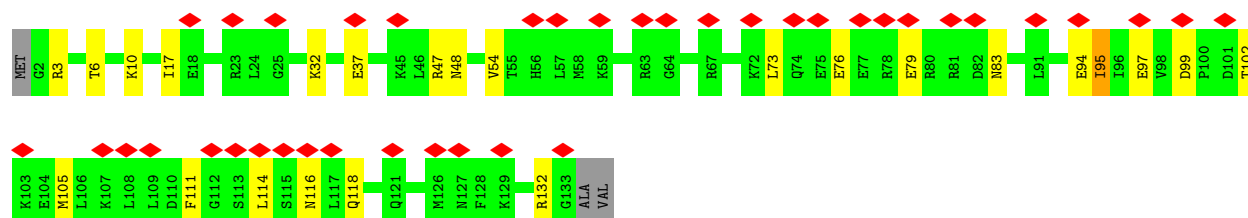
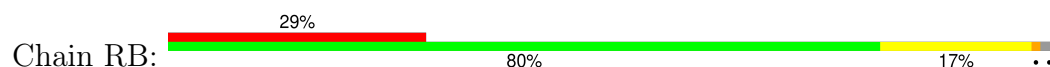


• Molecule 68: uS9

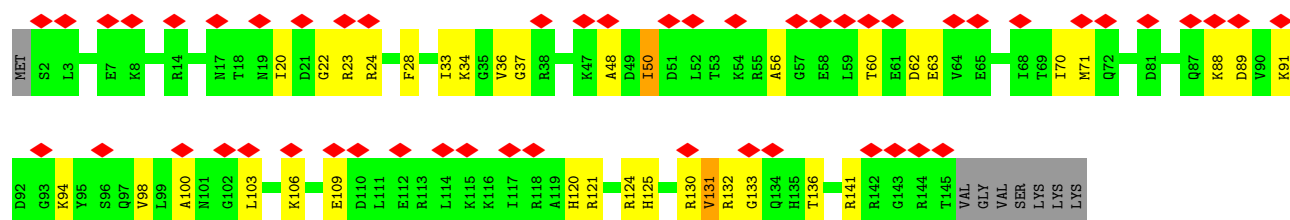




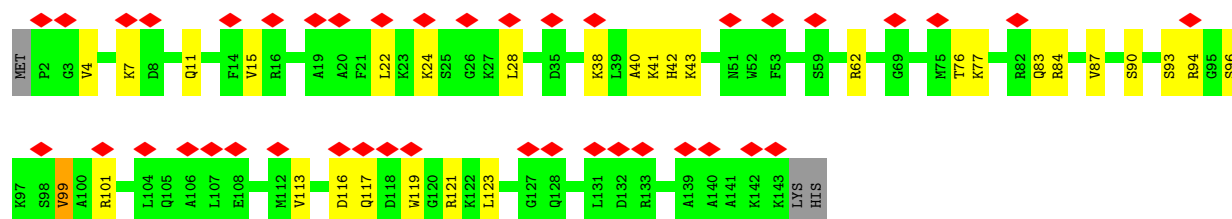
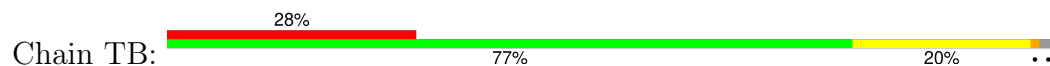
• Molecule 69: eS17



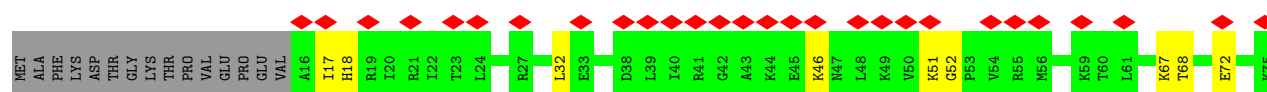
• Molecule 70: S18

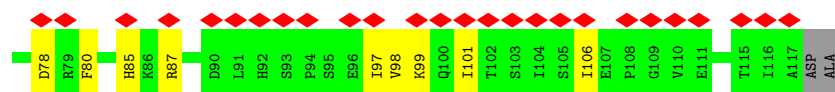


• Molecule 71: S19

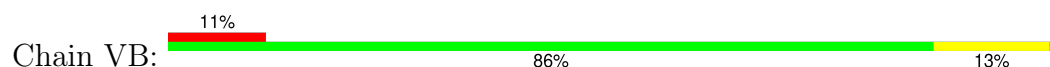


• Molecule 72: uS10

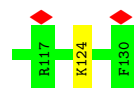
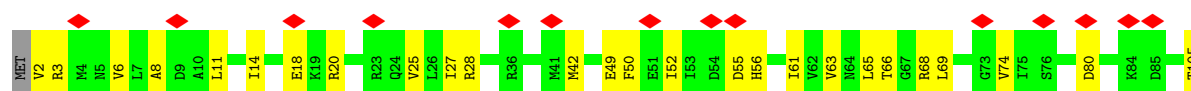
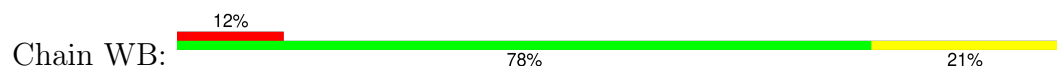




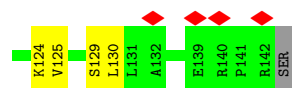
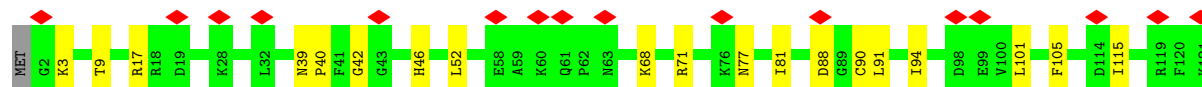
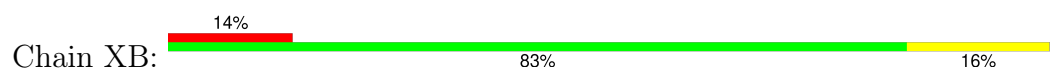
• Molecule 73: S21



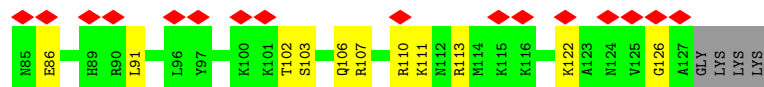
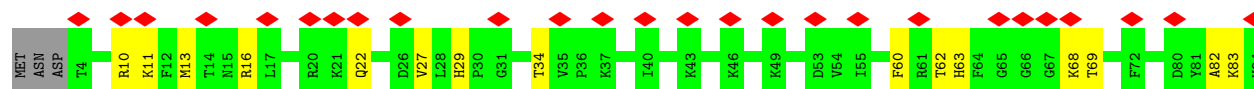
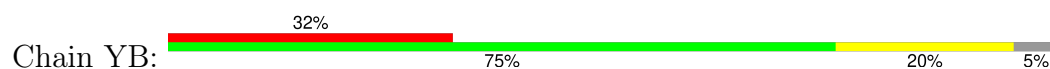
• Molecule 74: S15A



• Molecule 75: S23



• Molecule 76: S24



• Molecule 77: eS25





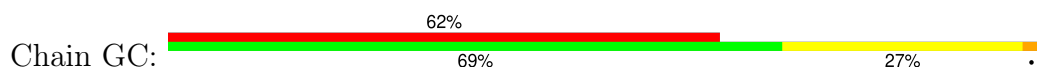
MET
 ALA
 ARG
 HIS
 PRO
 LEU
 TYR
 GLN
 GLY
 SER
 PRO
 ILE
 TRP
 CYS
 GLY
 ARG
 LEU
 ARG
 GLY
 GLY
 ALA
 GLY
 LEU
 PHE
 GLY
 GLY
 GLY
 ALA
 GLY
 LYS
 PRO
 ARG
 GLY
 PRO
 ASP
 PHE
 LEU
 PHE
 ASP
 PRO
 SER
 SER
 ALA
 ARG
 ARG
 TRP
 ALA
 ARG
 HIS
 GLN
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 ALA
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 LEU
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 GLU
 ASN
 PRO
 TYR
 GLY

GLU
 ASP
 HIS
 HIS
 ALA
 ARG
 GLY
 ILE
 PRO
 ASP
 ASP
 GLN
 ARG
 LEU
 PHE
 ILE
 ALA
 GLY
 LYS
 GLN
 LEU
 ASP
 GLY
 ARG
 THR
 LEU
 SER
 ASP
 TYR
 ASN
 ILE
 GLN
 LYS
 LEU
 SER
 THR
 LEU
 HIS
 VAL
 LEU
 LEU
 ARG
 LEU
 ARG
 GLY
 GLY
 ALA
 LYS
 LYS
 ASP
 LYS
 K82
 K83
 S84
 Y85
 T86
 T87
 P88

K89
 K90
 N91
 K92
 H93
 K94
 R95
 K96
 K97
 V98
 K99
 L100
 A101
 V102
 L103
 Y104
 Y105
 Y106
 K107
 Y108
 D109
 E110
 N111
 K112
 K113
 T114
 S115
 R116
 L117
 R118
 R119
 E120
 C121
 P122
 S123
 D124
 E125
 C126
 G127
 A128
 G129
 V130
 F131
 M132
 A133
 S134
 H135
 F136
 D137
 R138
 H139
 Y140
 C141
 G142
 K143
 C144
 C145
 L146
 T147
 Y148

C149
 F150
 ASN
 LYS
 PRO
 GLU
 ASP
 LYS

• Molecule 84: RACK1



MET
 T2
 E3
 Q4
 M5
 T6
 L7
 R8
 G9
 T10
 L11
 G13
 V18
 T19
 Q20
 I21
 A22
 Q26
 F27
 P28
 D29
 G95
 M30
 I31
 L32
 S33
 A34
 S35
 R36
 D37
 K38
 T39
 I40
 I41
 M42
 W43
 K44
 L45
 T46
 R47
 D48
 E49
 T50
 N51
 Y52
 G53
 I54
 R57
 R60
 G61
 H62
 S63
 S67
 D68
 V69

V70
 I71
 S72
 D73
 D74
 G75
 F76
 F77
 A78
 L79
 S82
 W83
 D84
 G85
 T86
 L87
 R88
 L89
 W90
 D91
 L92
 T93
 T94
 G95
 T96
 T97
 T98
 R99
 R100
 F101
 V102
 G103
 H104
 T105
 K106
 D107
 V108
 L109
 S110
 V111
 A112
 F113
 S114
 S115
 D116
 N117
 R118
 Q119
 I120
 V121
 S122
 G123
 S124
 R125
 D126
 K127
 T128
 I129
 K130

L131
 W132
 N133
 T134
 L135
 G136
 V137
 C138
 K139
 Y140
 T141
 V142
 Q143
 D144
 E145
 W150
 V151
 S152
 R155
 F156
 S157
 P158
 N159
 S160
 S161
 N162
 P163
 I164
 I165
 V166
 S167
 C168
 D171
 V174
 K175
 V176
 W177
 N178
 L179
 A180
 N181
 C182
 K183
 L184
 K185
 N186
 N187
 H188
 I189
 G190
 H191
 T192
 G193
 Y194
 L195
 N196

T197
 V198
 T199
 V200
 S201
 P202
 D203
 G204
 S205
 L206
 C207
 A208
 S209
 G210
 D213
 G214
 Q215
 A216
 W217
 L218
 W219
 D220
 L221
 N222
 E223
 G224
 K225
 H226
 L227
 Y228
 T229
 L230
 D231
 G232
 G233
 D234
 N237
 A238
 L239
 C240
 F241
 S242
 P243
 N244
 R245
 Y246
 W247
 L248
 A251
 T252
 G253
 P254
 S255
 I256
 K257
 I258
 W259

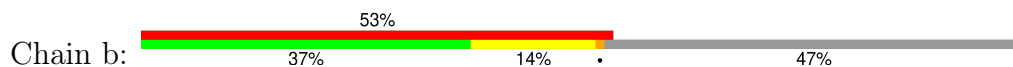
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 E262
 G263
 K264
 L265
 L266
 V267
 D268
 E269
 L270
 K271
 Q272
 E273
 V274
 L275
 S276
 T277
 S278
 S279
 K280
 A281
 E282
 C286
 T287
 S288
 L289
 A290
 W291
 S292
 A293
 D294
 G295
 Q296
 T297
 L298
 F299
 A300
 G301
 Y302
 T303
 D304
 N305
 L306
 V307
 R308
 V309
 W310
 Q311
 V312
 T313
 T314
 GLY
 THR
 ARG

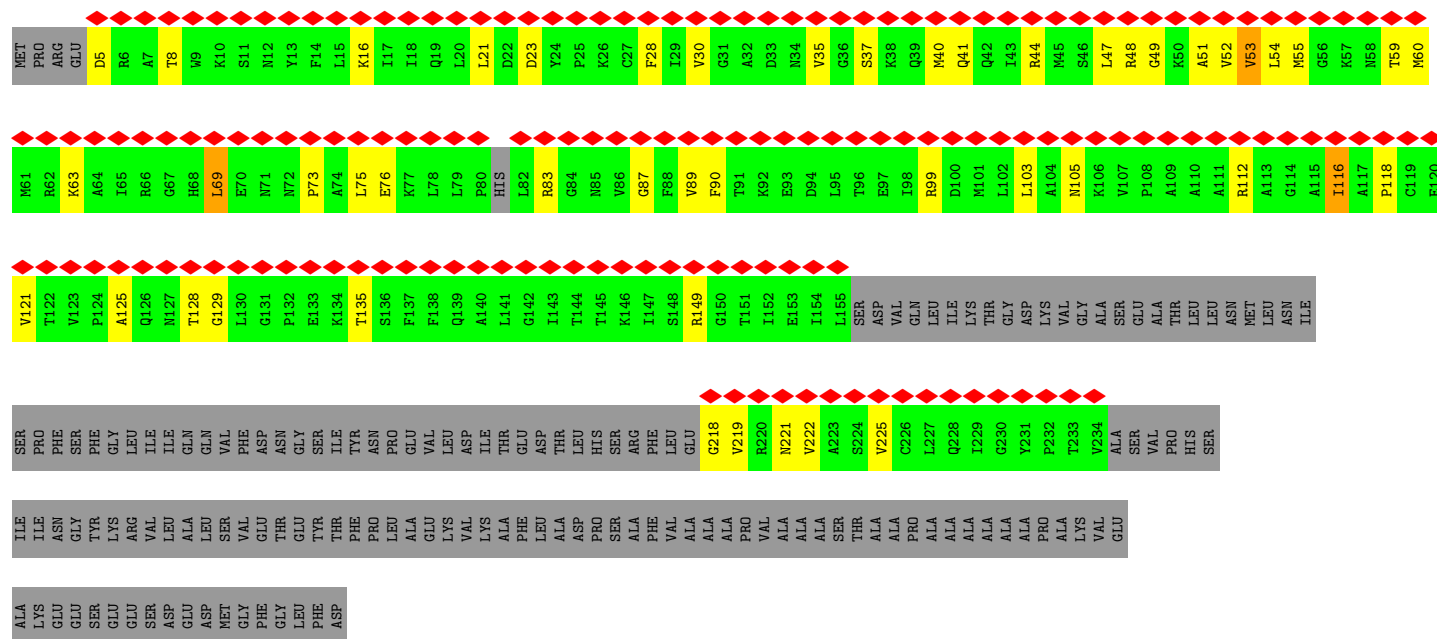
• Molecule 85: peptide



A195
 H196
 F197
 D198

• Molecule 86: RPLP0

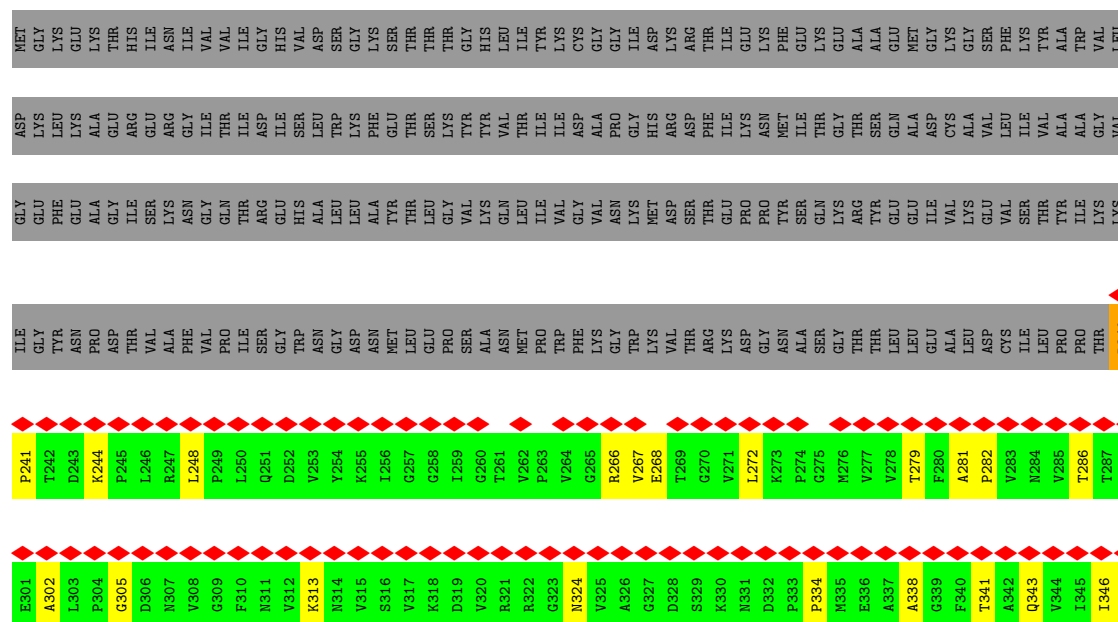
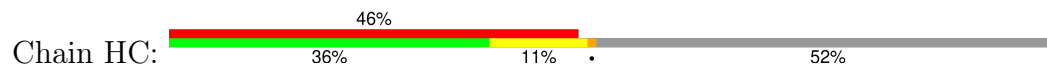




• Molecule 87: RPLP peptide



• Molecule 88: eukaryotic elongation factor 1 A



L421	G422	R423	F424	A425	V426	D427	D428	A429	R430	Q431	T432	V433	A434	V435	G436	V437	I438	K439	A440	V441	D442	K443	K444	A445	A446	G447	A448	G449	K450	V451	T452	K453	S454	A455	Q456	K457	A458	Q459	K460	A461	K462																		
L361	D362	C363	H364	T365	A366	H367	T368	A369	C370	K371	F372	A373	E374	L375	K376	E377	K378	L379	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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6359	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	33.575	Depositor
Minimum map value	-21.832	Depositor
Average map value	0.004	Depositor
Map value standard deviation	1.513	Depositor
Recommended contour level	6.5	Depositor
Map size ($\text{\AA}$)	686.87994, 686.87994, 686.87994	wwPDB
Map dimensions	648, 648, 648	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	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, MG, ANM, 5GP, SPD, K

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	0.11	0/1859	0.26	0/2491
6	F	0.12	0/1933	0.26	0/2577
7	G	0.11	0/1881	0.25	0/2532
8	H	0.11	0/1535	0.27	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	0.24	0/2316
12	L	0.11	0/1158	0.25	0/1547
13	M	0.12	0/1746	0.27	0/2338
14	N	0.13	0/1662	0.29	0/2222
15	O	0.12	0/1292	0.28	0/1733
16	P	0.11	0/1539	0.29	0/2054
17	Q	0.11	0/1524	0.25	0/2013
18	R	0.12	0/1501	0.29	0/2012
19	S	0.11	0/1326	0.24	0/1770
20	T	0.11	0/840	0.31	0/1127
21	U	0.12	0/1018	0.28	0/1364
22	V	0.11	0/900	0.26	0/1194
23	W	0.11	0/984	0.26	0/1323
24	X	0.10	0/1132	0.23	0/1504
25	Y	0.11	0/1130	0.23	0/1507
26	Z	0.11	0/1191	0.26	0/1590
27	AA	0.09	0/886	0.20	0/1171
28	BA	0.10	0/779	0.22	0/1044
29	CA	0.12	0/908	0.28	0/1223
30	DA	0.10	0/1082	0.24	0/1443
31	EA	0.12	0/895	0.27	0/1198
32	FA	0.11	0/916	0.26	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	GA	0.09	0/1016	0.23	0/1341
34	HA	0.09	0/841	0.23	0/1112
35	IA	0.12	0/731	0.27	0/966
36	JA	0.10	0/575	0.26	0/761
37	KA	0.11	0/459	0.27	0/608
38	LA	0.10	0/435	0.28	0/575
39	MA	0.10	0/240	0.19	0/305
40	NA	0.11	0/864	0.24	0/1140
41	OA	0.12	0/718	0.32	0/953
42	PA	0.12	0/1010	0.29	0/1354
43	RA	0.12	0/1174	0.32	0/1582
44	SA	0.10	0/1815	0.24	0/2828
45	TA	0.09	0/1804	0.22	0/2810
46	UA	0.13	0/1783	0.32	0/2776
47	VA	0.09	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	0.23	0/5766
51	ZA	0.11	0/40949	0.24	0/63819
52	AB	0.10	0/1747	0.25	0/2374
53	BB	0.10	0/1756	0.25	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	0.11	0/1511	0.28	0/2022
60	IB	0.11	0/1715	0.26	0/2287
61	JB	0.10	0/1550	0.27	0/2069
62	KB	0.11	0/834	0.28	0/1125
63	LB	0.11	0/1200	0.26	0/1604
64	MB	0.10	0/918	0.27	0/1233
65	NB	0.10	0/1226	0.23	0/1649
66	OB	0.11	0/1029	0.27	0/1380
67	PB	0.12	0/1079	0.28	0/1441
68	QB	0.12	0/1146	0.29	0/1534
69	RB	0.10	0/1082	0.25	0/1452
70	SB	0.10	0/1208	0.29	0/1618
71	TB	0.11	0/1123	0.25	0/1504
72	UB	0.11	0/818	0.28	0/1099
73	VB	0.10	0/643	0.25	0/860
74	WB	0.12	0/1051	0.30	0/1406
75	XB	0.10	0/1116	0.24	0/1490

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	YB	0.11	0/1028	0.28	0/1366
77	ZB	0.11	0/691	0.32	0/922
78	AC	0.10	0/828	0.27	0/1109
79	BC	0.09	0/665	0.23	0/891
80	CC	0.10	0/490	0.26	0/656
81	DC	0.10	0/470	0.25	0/623
82	EC	0.08	0/447	0.24	0/587
83	FC	0.09	0/576	0.23	0/764
84	GC	0.11	0/2493	0.32	0/3394
85	IC	0.06	0/19	0.14	0/25
86	b	0.14	0/1296	0.31	0/1745
87	c	0.12	0/111	0.29	0/145
88	HC	0.11	0/1694	0.30	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	35	0
2	B	3196	0	3339	51	0
3	C	2883	0	3053	37	0
4	D	2395	0	2427	30	0
5	E	1823	0	1995	31	0
6	F	1897	0	2021	36	0
7	G	1850	0	1991	23	0
8	H	1516	0	1597	15	0
9	I	1664	0	1712	23	0
10	J	1372	0	1412	21	0
11	K	1702	0	1820	26	0
12	L	1137	0	1211	24	0

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Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	M	1701	0	1749	34	0
14	N	1630	0	1778	32	0
15	O	1266	0	1302	16	0
16	P	1515	0	1634	30	0
17	Q	1508	0	1664	24	0
18	R	1462	0	1508	24	0
19	S	1298	0	1366	21	0
20	T	826	0	852	17	0
21	U	1004	0	1063	15	0
22	V	887	0	935	11	0
23	W	967	0	1040	10	0
24	X	1115	0	1205	19	0
25	Y	1107	0	1182	22	0
26	Z	1162	0	1209	23	0
27	AA	873	0	949	8	0
28	BA	769	0	803	11	0
29	CA	893	0	932	16	0
30	DA	1064	0	1160	21	0
31	EA	876	0	912	12	0
32	FA	906	0	998	7	0
33	GA	1008	0	1142	18	0
34	HA	830	0	916	6	0
35	IA	716	0	750	17	0
36	JA	569	0	637	8	0
37	KA	447	0	480	13	0
38	LA	429	0	465	6	0
39	MA	239	0	289	4	0
40	NA	851	0	920	13	0
41	OA	708	0	757	9	0
42	PA	994	0	1051	16	0
43	RA	1160	0	1218	15	0
44	SA	1622	0	825	12	0
45	TA	1615	0	820	18	0
46	UA	1596	0	810	17	0
47	VA	251	0	128	1	0
48	WA	76735	0	38762	933	0
49	XA	2538	0	1286	27	0
50	YA	3314	0	1683	35	0
51	ZA	36623	0	18504	464	0
52	AB	1710	0	1711	26	0
53	BB	1729	0	1803	21	0
54	CB	1707	0	1793	29	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	37	0
57	FB	1471	0	1522	23	0
58	GB	1923	0	2089	38	0
59	HB	1489	0	1582	25	0
60	IB	1686	0	1772	21	0
61	JB	1525	0	1640	34	0
62	KB	810	0	836	20	0
63	LB	1180	0	1254	14	0
64	MB	908	0	939	19	0
65	NB	1202	0	1289	19	0
66	OB	1016	0	1039	20	0
67	PB	1058	0	1104	15	0
68	QB	1128	0	1195	20	0
69	RB	1068	0	1121	16	0
70	SB	1190	0	1249	28	0
71	TB	1104	0	1138	21	0
72	UB	808	0	878	14	0
73	VB	636	0	637	8	0
74	WB	1034	0	1080	20	0
75	XB	1098	0	1167	15	0
76	YB	1011	0	1083	18	0
77	ZB	683	0	761	8	0
78	AC	814	0	864	16	0
79	BC	651	0	672	8	0
80	CC	488	0	514	11	0
81	DC	459	0	449	9	0
82	EC	443	0	492	8	0
83	FC	564	0	577	7	0
84	GC	2436	0	2393	47	0
85	IC	20	0	10	0	0
86	b	1279	0	1343	29	0
87	c	110	0	83	4	0
88	HC	1664	0	1721	27	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	SA	1	0	0	0	0
89	U	1	0	0	0	0
89	WA	158	0	0	0	0
89	XA	3	0	0	0	0
89	YA	2	0	0	0	0
89	Z	2	0	0	0	0
89	ZA	61	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	0	0
93	WA	30	0	57	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	220703	0	164224	2507	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 (2507) 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)
46:UA:8:U:H3	46:UA:14:A:H62	1.07	1.03
48:WA:1446:G:H1	48:WA:2113:U:H3	1.02	1.00
48:WA:2847:A:H61	48:WA:3845:C:N4	1.57	1.00
48:WA:1249:U:H3	48:WA:1268:G:H1	1.07	0.99
51:ZA:197:U:H3	51:ZA:202:G:H1	0.98	0.97
51:ZA:1743:G:H21	51:ZA:1791:A:H62	1.03	0.96
48:WA:2847:A:N6	48:WA:3845:C:H42	1.62	0.95
44:SA:50:U:H3	44:SA:64:G:H1	1.01	0.92
55:DB:201:PRO:O	55:DB:205:TYR:HB2	1.72	0.89
51:ZA:1472:C:H42	51:ZA:1476:A:H62	1.21	0.88
46:UA:8:U:H3	46:UA:14:A:N6	1.70	0.88
48:WA:2487:U:H3	48:WA:2495:G:H1	1.22	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:1743:G:N2	51:ZA:1791:A:H62	1.72	0.88
48:WA:2847:A:H61	48:WA:3845:C:H42	0.88	0.85
51:ZA:1656:G:H1	51:ZA:1668:U:H3	1.21	0.84
48:WA:1761:G:H1	48:WA:1775:U:H3	1.26	0.81
51:ZA:1288:U:H3	51:ZA:1311:C:H42	1.24	0.80
51:ZA:1743:G:H21	51:ZA:1791:A:N6	1.78	0.79
56:EB:185:GLY:H	56:EB:189:LEU:HD13	1.46	0.78
48:WA:3694:A:H62	48:WA:3825:G:H21	1.31	0.77
74:WB:8:ALA:HA	74:WB:74:VAL:HG21	1.67	0.77
51:ZA:677:G:H21	51:ZA:1028:A:H62	1.33	0.75
86:b:55:MET:HG3	86:b:87:GLY:HA3	1.68	0.75
48:WA:2522:C:O2	48:WA:2642:G:N2	2.19	0.75
51:ZA:561:A:H5'	61:JB:171:GLY:HA3	1.69	0.75
48:WA:4995:G:H1	48:WA:5060:A:H2	1.33	0.73
46:UA:10:G:H22	46:UA:25:C:H2'	1.52	0.73
48:WA:4737:G:H1	48:WA:4967:U:H3	1.35	0.73
51:ZA:1396:A:O2'	51:ZA:1398:G:N7	2.21	0.73
35:IA:2:THR:N	48:WA:3644:A:HO2'	1.88	0.72
3:C:78:ARG:HB3	3:C:88:GLY:HA2	1.71	0.72
48:WA:3946:G:H1	48:WA:4071:U:H3	1.38	0.72
48:WA:1975:G:H2'	48:WA:1976:U:H2'	1.71	0.72
86:b:5:ASP:N	86:b:8:THR:HG1	1.87	0.72
48:WA:2575:A:H62	48:WA:2763:U:H3	1.37	0.71
48:WA:3699:U:H5''	48:WA:3700:G:H5'	1.72	0.71
51:ZA:1472:C:N4	51:ZA:1476:A:H62	1.87	0.71
10:J:75:ARG:NH1	49:XA:40:U:O2	2.24	0.71
72:UB:80:PHE:HB3	81:DC:52:PHE:HB3	1.71	0.71
48:WA:4770:G:H2'	48:WA:4771:G:C8	2.26	0.71
58:GB:69:THR:HG22	58:GB:71:GLY:H	1.55	0.71
51:ZA:15:U:O2'	51:ZA:669:A:N6	2.23	0.70
14:N:125:LYS:HG3	14:N:129:LEU:HD12	1.73	0.70
48:WA:1766:G:OP2	48:WA:1766:G:N2	2.24	0.70
48:WA:4355:U:H5''	48:WA:4356:U:H5'	1.73	0.70
51:ZA:1298:G:HO2'	51:ZA:1299:A:H8	1.40	0.69
5:E:48:ARG:HB2	5:E:64:MET:HE1	1.75	0.69
84:GC:256:ILE:HG23	84:GC:270:LEU:HB2	1.75	0.69
48:WA:4874:G:H4'	48:WA:4875:G:H5'	1.75	0.69
2:B:249:ARG:NH1	48:WA:2839:U:OP1	2.26	0.68
11:K:56:ARG:O	11:K:116:ARG:NH1	2.26	0.68
5:E:115:MET:O	42:PA:87:ARG:NH1	2.26	0.68
48:WA:995:U:H3	48:WA:1071:G:H1	1.40	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:1674:G:OP1	57:FB:51:HIS:NE2	2.25	0.68
11:K:31:ARG:HD3	11:K:35:ARG:HH21	1.59	0.67
58:GB:164:LYS:HG2	58:GB:165:GLU:HG3	1.75	0.67
54:CB:123:ARG:NH1	54:CB:143:CYS:SG	2.67	0.67
68:QB:96:VAL:HG11	68:QB:110:ILE:HG13	1.76	0.67
51:ZA:959:G:OP1	66:OB:104:ARG:NH2	2.28	0.67
51:ZA:1410:C:H2'	51:ZA:1411:G:H8	1.59	0.67
8:H:85:THR:HG23	8:H:86:LEU:HG	1.74	0.67
3:C:340:ILE:HD13	5:E:53:VAL:HG21	1.77	0.67
26:Z:21:ARG:NH2	48:WA:1319:U:OP1	2.28	0.67
48:WA:3643:U:OP2	48:WA:3648:A:N6	2.28	0.67
51:ZA:482:G:N1	51:ZA:485:A:OP2	2.26	0.67
48:WA:4995:G:O6	48:WA:5060:A:N1	2.28	0.66
51:ZA:1658:G:OP2	51:ZA:1660:C:N4	2.28	0.66
16:P:82:VAL:HG12	16:P:84:GLY:H	1.60	0.66
84:GC:31:ILE:HG23	84:GC:43:TRP:HB2	1.77	0.66
88:HC:378:LYS:HD2	88:HC:391:PRO:HB3	1.77	0.66
88:HC:380:ASP:HB3	88:HC:383:SER:HB2	1.78	0.66
53:BB:107:ARG:NH1	66:OB:133:THR:O	2.27	0.66
48:WA:4539:C:H2'	48:WA:4540:G:H8	1.61	0.66
19:S:70:HIS:NE2	48:WA:4329:C:OP1	2.29	0.66
48:WA:3762:A:N6	51:ZA:1826:G:OP2	2.29	0.66
5:E:186:ARG:HH21	48:WA:4938:G:H2'	1.61	0.65
48:WA:2022:U:H2'	48:WA:2023:G:H8	1.61	0.65
51:ZA:1324:G:H1	51:ZA:1504:U:H3	1.44	0.65
38:LA:74:TYR:O	48:WA:4474:G:O2'	2.14	0.65
48:WA:1526:A:H62	48:WA:1653:G:H1	1.44	0.65
48:WA:2460:C:H1'	48:WA:3673:G:H21	1.62	0.65
51:ZA:957:A:H3'	51:ZA:958:G:H21	1.60	0.65
51:ZA:1403:C:N4	51:ZA:1433:C:OP1	2.29	0.65
48:WA:1452:C:HO2'	48:WA:2106:A:HO2'	1.44	0.65
51:ZA:1130:G:N2	51:ZA:1130:G:OP2	2.29	0.65
51:ZA:442:C:H42	51:ZA:449:A:H62	1.44	0.65
51:ZA:888:U:H2'	51:ZA:900:C:H42	1.61	0.65
48:WA:4543:G:N2	48:WA:4546:A:OP2	2.28	0.65
17:Q:172:ARG:HH12	51:ZA:908:A:H5''	1.62	0.65
43:RA:121:LEU:HB2	86:b:49:GLY:HA2	1.79	0.65
51:ZA:1298:G:H4'	67:PB:78:THR:HA	1.79	0.65
6:F:227:VAL:HA	18:R:39:VAL:HG12	1.79	0.65
48:WA:4423:C:H42	48:WA:4477:G:H22	1.44	0.65
51:ZA:114:G:N7	63:LB:69:ARG:NH2	2.45	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:851:C:H5''	51:ZA:852:G:H5'	1.79	0.65
11:K:54:PRO:HG2	11:K:56:ARG:HH12	1.62	0.65
43:RA:17:CYS:O	43:RA:57:ARG:HA	1.96	0.65
48:WA:1092:C:H2'	48:WA:1093:A:H8	1.62	0.65
51:ZA:377:G:H5'	60:IB:98:LYS:HB3	1.79	0.64
51:ZA:1396:A:N7	51:ZA:1450:G:N2	2.45	0.64
69:RB:111:PHE:HB3	69:RB:114:LEU:HD11	1.78	0.64
1:A:128:ARG:NH1	48:WA:3683:G:OP2	2.30	0.64
11:K:59:VAL:HB	48:WA:74:G:H5'	1.78	0.64
48:WA:916:U:H4'	48:WA:917:A:H5'	1.79	0.64
24:X:15:ARG:NH1	48:WA:230:G:OP1	2.31	0.64
74:WB:42:MET:HE2	74:WB:49:GLU:HA	1.79	0.64
58:GB:2:LYS:HB3	58:GB:15:LEU:HD11	1.80	0.64
45:TA:15:G:N2	45:TA:48:C:C2	2.65	0.64
51:ZA:43:U:OP2	51:ZA:485:A:N6	2.29	0.64
51:ZA:616:A:OP1	75:XB:68:LYS:NZ	2.30	0.64
5:E:159:ARG:NH1	48:WA:4942:C:OP1	2.30	0.64
48:WA:308:G:OP2	48:WA:308:G:N2	2.27	0.64
74:WB:11:LEU:HD12	74:WB:74:VAL:HG22	1.77	0.64
1:A:116:LEU:HB3	1:A:126:LEU:HB2	1.80	0.63
56:EB:87:MET:HE2	56:EB:123:LEU:HB2	1.78	0.63
84:GC:199:THR:HG21	84:GC:240:CYS:HA	1.81	0.63
43:RA:117:ARG:HG3	43:RA:125:LEU:HD11	1.80	0.63
4:D:103:LEU:HD11	4:D:248:ARG:HE	1.63	0.63
35:IA:52:LYS:NZ	48:WA:364:G:O6	2.31	0.63
37:KA:37:TYR:O	48:WA:362:A:N6	2.30	0.63
41:OA:4:ARG:NH2	48:WA:1557:G:O6	2.31	0.63
66:OB:142:ARG:HB3	78:AC:22:ARG:HD3	1.80	0.63
84:GC:39:THR:HG22	84:GC:60:ARG:HG2	1.80	0.63
2:B:249:ARG:NH2	48:WA:3847:A:OP2	2.31	0.63
11:K:103:ARG:NH1	48:WA:73:A:N7	2.47	0.63
48:WA:1334:C:H2'	48:WA:1335:A:H8	1.64	0.63
71:TB:76:THR:HB	71:TB:94:ARG:HB3	1.79	0.63
80:CC:17:VAL:HA	80:CC:30:VAL:HG23	1.80	0.63
4:D:256:LYS:HD2	49:XA:117:G:H5'	1.81	0.63
7:G:185:ARG:NH1	48:WA:119:G:OP1	2.32	0.63
18:R:87:ARG:HH21	48:WA:2036:G:H5'	1.63	0.63
35:IA:33:THR:HG22	35:IA:40:PRO:HG2	1.81	0.63
70:SB:23:ARG:NH2	77:ZB:46:ASN:O	2.31	0.63
29:CA:39:LYS:HG3	29:CA:40:LYS:HG2	1.81	0.63
31:EA:100:ARG:NH1	48:WA:4755:U:OP1	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:300:A:H2'	48:WA:301:G:H8	1.62	0.63
48:WA:2467:C:H1'	48:WA:3674:G:H1	1.64	0.63
48:WA:1741:G:N3	48:WA:1744:A:N6	2.47	0.63
48:WA:4696:G:OP1	48:WA:4696:G:N2	2.29	0.63
75:XB:68:LYS:HE2	82:EC:82:VAL:HG22	1.79	0.63
15:O:161:ALA:HB2	48:WA:1599:G:H5'	1.81	0.62
48:WA:1554:G:O2'	48:WA:1576:G:N2	2.32	0.62
21:U:43:LYS:HD3	21:U:62:MET:HE2	1.79	0.62
42:PA:6:GLN:HG3	42:PA:44:ILE:HD12	1.81	0.62
48:WA:67:C:OP2	48:WA:312:G:N2	2.31	0.62
48:WA:3879:A:N3	48:WA:4403:G:O2'	2.29	0.62
56:EB:122:LYS:NZ	56:EB:124:CYS:SG	2.69	0.62
84:GC:107:ASP:OD2	84:GC:125:ARG:NH1	2.32	0.62
6:F:218:GLY:O	6:F:245:ARG:NH2	2.33	0.62
16:P:16:LYS:O	16:P:33:ARG:NH2	2.32	0.62
66:OB:105:THR:HG22	66:OB:107:THR:H	1.63	0.62
14:N:116:LYS:HE3	18:R:169:THR:HG21	1.81	0.62
18:R:34:ALA:HB1	18:R:39:VAL:HG23	1.80	0.62
51:ZA:1612:G:OP1	67:PB:18:ARG:NH2	2.32	0.62
7:G:276:ARG:HG3	7:G:280:ASN:HB2	1.81	0.62
51:ZA:581:U:OP1	61:JB:133:ARG:NH2	2.32	0.62
51:ZA:1473:G:N2	51:ZA:1476:A:OP2	2.32	0.62
51:ZA:1521:C:OP2	70:SB:136:THR:OG1	2.18	0.62
9:I:203:ARG:NH1	49:XA:105:C:OP2	2.32	0.62
43:RA:120:SER:HB3	86:b:48:ARG:HH21	1.65	0.62
49:XA:28:C:H1'	49:XA:54:A:H61	1.63	0.62
50:YA:67:U:H2'	50:YA:68:G:H8	1.63	0.62
53:BB:122:GLU:O	53:BB:165:ARG:NH1	2.32	0.62
19:S:87:LYS:NZ	48:WA:4302:U:OP1	2.32	0.62
1:A:179:ILE:HG23	1:A:184:ARG:HB2	1.82	0.62
48:WA:2603:A:N6	48:WA:2746:A:OP2	2.33	0.62
51:ZA:16:G:H5'	51:ZA:669:A:H61	1.63	0.62
61:JB:131:ARG:NH1	61:JB:143:ASN:OD1	2.33	0.62
10:J:99:PHE:O	10:J:159:LYS:NZ	2.32	0.61
28:BA:36:LYS:NZ	48:WA:2659:G:OP2	2.33	0.61
48:WA:970:G:N2	48:WA:2098:G:O2'	2.33	0.61
48:WA:5055:U:OP1	48:WA:5056:C:N4	2.32	0.61
51:ZA:925:G:H1	51:ZA:1017:U:H3	1.47	0.61
51:ZA:1228:A:H2'	51:ZA:1229:G:C8	2.35	0.61
51:ZA:24:C:OP1	61:JB:11:LYS:NZ	2.30	0.61
54:CB:69:LEU:HG	54:CB:273:LEU:HD21	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:113:ARG:NH2	48:WA:2704:C:O3'	2.32	0.61
26:Z:65:ARG:NH2	48:WA:86:U:O2'	2.33	0.61
33:GA:66:LYS:HD3	50:YA:96:C:H5''	1.81	0.61
41:OA:4:ARG:NH1	48:WA:1556:A:OP2	2.34	0.61
51:ZA:1270:G:O2'	51:ZA:1299:A:N6	2.34	0.61
51:ZA:1566:G:N7	71:TB:101:ARG:NH2	2.49	0.61
48:WA:961:A:H1'	48:WA:2078:G:H5''	1.81	0.61
48:WA:2505:G:O2'	48:WA:2507:C:N4	2.33	0.61
57:FB:114:ASN:OD1	57:FB:118:ASN:ND2	2.33	0.61
75:XB:91:LEU:HB3	82:EC:82:VAL:HG11	1.82	0.61
84:GC:4:GLN:HB3	84:GC:313:THR:HB	1.83	0.61
2:B:234:ARG:NH2	48:WA:4568:U:O2'	2.33	0.61
9:I:4:ARG:NH1	48:WA:1868:U:OP1	2.34	0.61
14:N:130:LYS:HB2	14:N:133:ARG:HG2	1.82	0.61
51:ZA:1259:A:N6	51:ZA:1519:U:OP1	2.33	0.61
61:JB:136:ARG:NH1	61:JB:159:PHE:O	2.32	0.61
25:Y:48:ARG:NH2	48:WA:2578:G:OP1	2.34	0.61
49:XA:53:U:H4'	49:XA:54:A:H5'	1.83	0.61
30:DA:36:ARG:NH2	48:WA:2324:G:OP1	2.33	0.61
81:DC:17:GLY:O	81:DC:27:ARG:NH1	2.33	0.61
24:X:55:VAL:HG12	24:X:106:ILE:HA	1.83	0.61
48:WA:4276:A:H2'	48:WA:4277:G:H8	1.65	0.61
51:ZA:1004:U:H2'	51:ZA:1005:G:H8	1.66	0.61
51:ZA:1286:G:N2	51:ZA:1312:G:O2'	2.30	0.61
26:Z:125:LYS:HG2	26:Z:145:VAL:HB	1.83	0.61
36:JA:24:LYS:NZ	48:WA:2698:A:N1	2.44	0.61
48:WA:1255:G:H1	48:WA:1262:G:H22	1.49	0.61
48:WA:2522:C:H2'	48:WA:2523:G:H8	1.65	0.61
51:ZA:165:G:N2	51:ZA:165:G:OP2	2.34	0.61
51:ZA:1015:U:O2'	65:NB:55:ARG:NH1	2.34	0.61
51:ZA:1227:G:N2	51:ZA:1635:C:O2'	2.34	0.61
51:ZA:1447:G:OP1	72:UB:85:HIS:ND1	2.34	0.61
25:Y:103:ASP:HB3	25:Y:106:LEU:HB2	1.83	0.60
8:H:43:VAL:HG12	8:H:59:LYS:HD3	1.82	0.60
16:P:65:ARG:NH2	48:WA:1461:A:OP1	2.33	0.60
22:V:61:LYS:NZ	48:WA:5040:A:OP1	2.34	0.60
48:WA:1726:G:N2	48:WA:1878:U:OP1	2.34	0.60
48:WA:2491:C:O2'	48:WA:2493:C:N3	2.34	0.60
51:ZA:649:U:H2'	51:ZA:650:A:H8	1.66	0.60
1:A:117:GLU:OE2	1:A:163:ARG:NH1	2.34	0.60
5:E:164:ARG:NH1	12:L:106:ASP:OD2	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:265:LYS:NZ	48:WA:4935:C:OP2	2.35	0.60
7:G:194:ASN:ND2	48:WA:151:G:N7	2.49	0.60
11:K:35:ARG:NH1	48:WA:105:A:O2'	2.35	0.60
51:ZA:163:U:OP2	58:GB:87:ARG:NH2	2.30	0.60
51:ZA:1654:G:OP1	71:TB:90:SER:OG	2.19	0.60
30:DA:8:VAL:HG22	30:DA:10:PRO:HD3	1.82	0.60
48:WA:35:U:O2'	48:WA:1527:A:N1	2.33	0.60
48:WA:1857:G:O6	48:WA:1882:G:N2	2.34	0.60
48:WA:4747:G:H1	48:WA:4957:A:H61	1.47	0.60
7:G:210:ILE:HA	7:G:254:THR:HG22	1.84	0.60
22:V:93:LYS:O	22:V:101:ARG:NH2	2.35	0.60
24:X:30:MET:HB3	24:X:101:PRO:HG2	1.83	0.60
48:WA:1745:A:N1	48:WA:1791:C:O2'	2.33	0.60
48:WA:1962:A:H1'	86:b:63:LYS:HG2	1.83	0.60
51:ZA:197:U:O4	51:ZA:202:G:O6	2.20	0.60
51:ZA:617:G:H4'	75:XB:88:ASP:HB2	1.83	0.60
5:E:185:ASN:ND2	5:E:274:LEU:O	2.35	0.60
48:WA:992:C:O2	48:WA:1076:G:N2	2.34	0.60
48:WA:4910:G:O2'	48:WA:4915:G:N2	2.35	0.60
48:WA:4994:G:H2'	48:WA:4995:G:H8	1.67	0.60
6:F:176:ARG:NH1	48:WA:2103:A:N7	2.50	0.60
30:DA:36:ARG:NH1	48:WA:1663:C:OP1	2.35	0.60
31:EA:43:LEU:O	31:EA:109:ARG:NH1	2.35	0.60
51:ZA:1228:A:H2'	51:ZA:1229:G:H8	1.67	0.60
51:ZA:1562:C:H2'	51:ZA:1563:G:H8	1.67	0.60
51:ZA:1587:G:H21	71:TB:77:LYS:HD3	1.66	0.60
70:SB:98:VAL:HG11	70:SB:106:LYS:HG3	1.83	0.60
51:ZA:1091:C:HO2'	74:WB:2:VAL:N	2.00	0.59
51:ZA:1447:G:OP1	72:UB:87:ARG:NH2	2.35	0.59
62:KB:27:VAL:HG13	62:KB:43:LEU:HD13	1.84	0.59
70:SB:50:ILE:HD11	70:SB:63:GLU:HB3	1.84	0.59
5:E:156:LEU:HD11	5:E:198:ILE:HG13	1.84	0.59
42:PA:67:ARG:NH1	48:WA:667:G:OP2	2.35	0.59
44:SA:33:U:OP2	68:QB:172:ARG:NH2	2.34	0.59
48:WA:262:G:H2'	48:WA:263:G:C8	2.37	0.59
51:ZA:1115:U:H1'	51:ZA:1116:C:H2'	1.84	0.59
51:ZA:1418:C:H5'	51:ZA:1420:G:H21	1.65	0.59
88:HC:426:VAL:HB	88:HC:434:ALA:HB3	1.83	0.59
48:WA:2337:C:H2'	48:WA:2338:G:H8	1.66	0.59
51:ZA:1568:C:O2	51:ZA:1627:C:O2'	2.20	0.59
60:IB:4:SER:OG	60:IB:6:ASP:OD2	2.21	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:486:A:H1'	51:ZA:513:G:H22	1.66	0.59
51:ZA:1240:A:N7	67:PB:100:LYS:HB2	2.18	0.59
51:ZA:1261:C:O2	81:DC:10:HIS:NE2	2.30	0.59
48:WA:20:U:H3'	48:WA:21:G:H8	1.67	0.59
48:WA:2555:A:N6	48:WA:2767:A:OP2	2.35	0.59
48:WA:2649:A:H62	48:WA:2688:G:H8	1.48	0.59
51:ZA:954:U:O2	66:OB:55:ARG:NH2	2.34	0.59
51:ZA:1528:G:O2'	51:ZA:1666:C:OP1	2.20	0.59
11:K:48:PRO:HG3	33:GA:118:LYS:HE3	1.85	0.59
48:WA:419:A:N3	48:WA:1334:C:O2'	2.34	0.59
51:ZA:1677:U:OP1	57:FB:71:ARG:NH2	2.35	0.59
15:O:160:ARG:NH2	48:WA:1599:G:OP1	2.36	0.59
16:P:65:ARG:NH1	48:WA:1504:G:OP1	2.35	0.59
48:WA:2000:A:OP2	86:b:16:LYS:NZ	2.30	0.59
48:WA:4274:G:OP2	48:WA:4274:G:N2	2.36	0.59
16:P:67:ILE:HD12	16:P:96:PRO:HD2	1.83	0.59
48:WA:1804:A:H5''	48:WA:1805:G:H5'	1.83	0.59
48:WA:2737:G:H2'	48:WA:2738:G:H8	1.67	0.59
48:WA:4920:C:H2'	48:WA:4921:G:H8	1.68	0.59
51:ZA:1286:G:OP1	83:FC:99:LYS:NZ	2.36	0.59
51:ZA:1373:C:O2'	69:RB:10:LYS:NZ	2.31	0.59
52:AB:36:GLN:O	52:AB:53:ARG:NH1	2.36	0.59
65:NB:136:PRO:HG2	65:NB:139:TRP:HB2	1.85	0.59
3:C:110:ARG:O	3:C:113:ARG:NH1	2.36	0.59
12:L:11:ARG:NH1	12:L:58:THR:O	2.35	0.59
48:WA:2377:A:H2'	48:WA:2378:A:H8	1.67	0.59
51:ZA:453:C:O2'	58:GB:92:ARG:O	2.20	0.59
51:ZA:1617:G:N1	51:ZA:1620:A:OP2	2.34	0.59
7:G:170:ARG:NH2	48:WA:119:G:O6	2.35	0.59
32:FA:6:THR:HG22	48:WA:2402:G:H21	1.68	0.59
45:TA:15:G:N2	45:TA:48:C:O2	2.36	0.59
51:ZA:106:C:H2'	51:ZA:107:A:H8	1.68	0.59
57:FB:35:LEU:HD22	57:FB:117:ILE:HD13	1.85	0.59
74:WB:52:ILE:HG22	74:WB:61:ILE:HG12	1.84	0.59
12:L:35:ARG:NH2	18:R:108:GLN:OE1	2.37	0.58
48:WA:2779:G:H5''	48:WA:2780:G:H5'	1.85	0.58
48:WA:4718:C:H2'	48:WA:4719:A:H8	1.68	0.58
51:ZA:1017:U:OP1	65:NB:62:GLN:NE2	2.36	0.58
54:CB:60:TRP:O	54:CB:71:LYS:NZ	2.36	0.58
7:G:282:ARG:NH2	7:G:285:GLU:OE1	2.35	0.58
21:U:15:ARG:NH2	48:WA:4675:U:OP2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:HA:48:CYS:SG	34:HA:49:GLY:N	2.76	0.58
48:WA:1095:G:H2'	48:WA:1096:G:H8	1.67	0.58
48:WA:2320:G:N2	48:WA:2323:G:OP2	2.29	0.58
51:ZA:1758:G:H2'	51:ZA:1759:G:C8	2.38	0.58
67:PB:121:ILE:HG22	70:SB:120:HIS:HD2	1.68	0.58
7:G:111:PRO:HD2	7:G:114:ILE:HD12	1.84	0.58
2:B:5:LYS:NZ	48:WA:4503:U:OP1	2.37	0.58
14:N:89:PRO:HD3	48:WA:1916:C:H4'	1.84	0.58
16:P:2:GLY:N	48:WA:1900:C:OP1	2.37	0.58
19:S:108:ARG:NH1	48:WA:1839:A:OP1	2.36	0.58
27:AA:99:ILE:O	27:AA:109:ARG:NH1	2.35	0.58
40:NA:2:VAL:N	40:NA:90:HIS:O	2.36	0.58
48:WA:1929:U:OP1	48:WA:1951:U:O2'	2.14	0.58
51:ZA:1513:C:OP1	81:DC:12:ARG:NH1	2.36	0.58
59:HB:268:LEU:O	59:HB:272:SER:CB	2.51	0.58
67:PB:56:LEU:HD23	67:PB:83:MET:HE3	1.84	0.58
26:Z:72:THR:HG22	26:Z:110:LYS:HB3	1.85	0.58
51:ZA:3:C:O2	61:JB:18:ARG:NH1	2.36	0.58
67:PB:123:TYR:OH	70:SB:124:ARG:NH1	2.36	0.58
33:GA:31:LEU:HB3	33:GA:47:ILE:HG22	1.84	0.58
38:LA:88:LYS:NZ	48:WA:4487:C:O2'	2.36	0.58
68:QB:158:PHE:O	68:QB:166:ARG:NH1	2.37	0.58
73:VB:16:LYS:HG2	73:VB:23:ILE:HG22	1.85	0.58
5:E:61:ARG:HB2	48:WA:1243:C:H5''	1.86	0.58
13:M:157:LYS:O	13:M:162:ARG:NH1	2.36	0.58
14:N:72:HIS:N	48:WA:4588:G:OP1	2.37	0.58
51:ZA:429:C:O2'	51:ZA:811:A:N1	2.37	0.58
51:ZA:1351:G:H1	51:ZA:1360:U:H3	1.52	0.58
56:EB:87:MET:HE1	56:EB:236:ILE:HG21	1.85	0.58
61:JB:127:ARG:HD3	82:EC:104:ARG:HD3	1.84	0.58
51:ZA:155:G:H2'	51:ZA:156:G:H8	1.69	0.58
51:ZA:1353:A:OP1	52:AB:139:TYR:OH	2.16	0.58
55:DB:257:PRO:HB2	84:GC:190:GLY:HA2	1.85	0.58
31:EA:54:LYS:HE3	48:WA:4750:U:H5''	1.84	0.58
51:ZA:1623:A:H5''	70:SB:133:GLY:HA3	1.85	0.58
29:CA:64:ILE:HG23	29:CA:68:LEU:HD23	1.86	0.57
32:FA:29:ARG:NH1	48:WA:2524:G:OP1	2.36	0.57
51:ZA:608:C:O4'	82:EC:131:ASN:ND2	2.36	0.57
51:ZA:1139:C:H42	51:ZA:1149:A:H62	1.52	0.57
56:EB:100:ARG:HB2	56:EB:114:ILE:HD13	1.85	0.57
68:QB:156:LYS:NZ	68:QB:160:GLY:O	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:20:LYS:HD3	48:WA:4719:A:H4'	1.87	0.57
6:F:104:VAL:HG13	6:F:135:VAL:HG12	1.86	0.57
46:UA:17:G:H21	46:UA:58:A:H5'	1.68	0.57
51:ZA:928:G:H2'	51:ZA:929:G:C8	2.39	0.57
9:I:152:LEU:HB3	9:I:165:ILE:HD12	1.84	0.57
17:Q:105:LEU:HD23	17:Q:138:LEU:HD23	1.84	0.57
48:WA:1797:A:N3	49:XA:79:U:O2'	2.37	0.57
48:WA:2411:U:H4'	48:WA:2430:A:H4'	1.86	0.57
51:ZA:544:G:H2'	51:ZA:545:A:H8	1.69	0.57
54:CB:94:ILE:HD12	54:CB:162:ILE:HD11	1.86	0.57
65:NB:99:ARG:NH2	65:NB:119:GLU:OE2	2.33	0.57
4:D:88:VAL:HA	4:D:239:MET:HE3	1.86	0.57
48:WA:3850:U:H2'	48:WA:3851:A:H8	1.67	0.57
48:WA:4596:U:H2'	48:WA:4597:G:H8	1.69	0.57
48:WA:4956:G:H2'	48:WA:4957:A:H8	1.69	0.57
51:ZA:1513:C:H2'	51:ZA:1514:G:H8	1.69	0.57
54:CB:187:ARG:HE	54:CB:192:LEU:HD12	1.68	0.57
84:GC:174:VAL:HB	84:GC:188:HIS:HB2	1.86	0.57
2:B:77:THR:HG21	2:B:337:VAL:HG22	1.86	0.57
13:M:96:ARG:NH2	13:M:104:GLU:OE1	2.38	0.57
23:W:110:LYS:HG3	23:W:121:VAL:HB	1.86	0.57
25:Y:3:LYS:O	25:Y:6:LYS:NZ	2.38	0.57
48:WA:1213:C:H2'	48:WA:1214:G:H8	1.68	0.57
51:ZA:1156:U:O4	54:CB:194:ARG:NH1	2.38	0.57
2:B:276:HIS:ND1	48:WA:4718:C:OP1	2.36	0.57
4:D:33:ARG:NE	49:XA:7:G:OP1	2.36	0.57
16:P:22:ASP:OD1	16:P:22:ASP:N	2.36	0.57
18:R:174:THR:HG1	48:WA:4765:U:HO2'	1.48	0.57
27:AA:56:LYS:O	27:AA:60:ASN:ND2	2.37	0.57
38:LA:92:THR:HG22	38:LA:94:ASN:H	1.70	0.57
51:ZA:64:A:H2	51:ZA:83:A:H62	1.52	0.57
51:ZA:1668:U:OP1	68:QB:159:GLY:N	2.38	0.57
9:I:77:VAL:HG23	9:I:82:LYS:HA	1.87	0.57
13:M:65:ARG:NH2	48:WA:2459:G:OP1	2.36	0.57
19:S:43:LYS:NZ	48:WA:1735:G:OP1	2.37	0.57
48:WA:1671:A:N3	48:WA:1854:U:O2'	2.37	0.57
48:WA:2577:U:O2	48:WA:2760:G:N2	2.37	0.57
48:WA:3918:G:H2'	48:WA:3919:A:C8	2.40	0.57
2:B:57:VAL:HG22	2:B:73:VAL:HG22	1.87	0.57
53:BB:82:ARG:NH2	53:BB:191:ASP:OD1	2.37	0.57
58:GB:55:GLY:H	58:GB:63:MET:HE2	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:MB:51:VAL:O	64:MB:108:CYS:HA	2.05	0.57
65:NB:24:THR:O	65:NB:27:LYS:NZ	2.36	0.57
18:R:127:MET:HA	19:S:153:PRO:HD2	1.87	0.57
51:ZA:183:G:O2'	51:ZA:184:G:O4'	2.23	0.57
51:ZA:941:C:H2'	51:ZA:942:G:H8	1.70	0.57
51:ZA:1245:G:N2	72:UB:72:GLU:OE2	2.37	0.57
51:ZA:1550:G:H3'	51:ZA:1579:A:H61	1.69	0.57
57:FB:49:LEU:HD11	68:QB:75:TYR:HB3	1.85	0.57
88:HC:352:GLN:HB2	88:HC:393:PHE:HB2	1.86	0.57
6:F:95:ARG:NH2	48:WA:1897:G:OP1	2.38	0.56
48:WA:2772:C:H2'	48:WA:2773:G:H8	1.69	0.56
49:XA:92:C:H2'	49:XA:93:G:H8	1.69	0.56
65:NB:33:VAL:HG21	65:NB:66:VAL:HG11	1.87	0.56
74:WB:66:THR:HG21	74:WB:68:ARG:HH11	1.70	0.56
1:A:117:GLU:O	1:A:162:ASN:ND2	2.38	0.56
2:B:317:LEU:HB2	2:B:372:SER:HB2	1.87	0.56
13:M:116:LEU:HD22	13:M:135:ILE:HD11	1.86	0.56
46:UA:30:G:N7	46:UA:41:G:N2	2.53	0.56
46:UA:74:C:H3'	46:UA:75:C:H5''	1.87	0.56
48:WA:62:A:N3	48:WA:77:U:O2'	2.31	0.56
48:WA:2409:G:OP2	48:WA:2409:G:N2	2.34	0.56
48:WA:3863:A:H2'	48:WA:3864:A:H8	1.70	0.56
48:WA:4539:C:H2'	48:WA:4540:G:C8	2.40	0.56
56:EB:66:MET:SD	56:EB:78:THR:OG1	2.63	0.56
3:C:46:LYS:HB3	3:C:49:ARG:HH21	1.70	0.56
3:C:321:ASN:OD1	48:WA:1282:C:O2'	2.23	0.56
8:H:128:MET:HE2	8:H:134:CYS:HB2	1.87	0.56
11:K:140:SER:OG	11:K:143:GLU:OE1	2.22	0.56
13:M:15:GLN:NE2	48:WA:280:G:O6	2.39	0.56
20:T:25:CYS:HB2	20:T:28:PRO:HG2	1.87	0.56
21:U:35:LYS:HB2	21:U:67:LYS:HG3	1.87	0.56
37:KA:13:LEU:HD22	48:WA:2409:G:H2'	1.87	0.56
46:UA:64:G:OP2	46:UA:64:G:N2	2.33	0.56
48:WA:4241:A:H2'	48:WA:4242:G:H8	1.70	0.56
48:WA:4476:A:OP2	48:WA:4478:C:N4	2.39	0.56
48:WA:4701:U:H1'	48:WA:4702:A:H5''	1.87	0.56
51:ZA:1089:G:O6	75:XB:3:LYS:NZ	2.38	0.56
51:ZA:1419:C:OP2	51:ZA:1420:G:N2	2.38	0.56
56:EB:112:HIS:NE2	56:EB:237:SER:O	2.39	0.56
56:EB:151:ASP:HB3	56:EB:154:ILE:HG12	1.87	0.56
70:SB:124:ARG:HB2	70:SB:131:VAL:HG13	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:b:53:VAL:HG12	86:b:89:VAL:HG12	1.87	0.56
3:C:204:ARG:NH1	3:C:205:ARG:O	2.39	0.56
5:E:275:ARG:NH2	48:WA:4886:G:N7	2.54	0.56
7:G:96:GLN:O	48:WA:4126:G:N2	2.38	0.56
24:X:34:LEU:HD23	24:X:38:LEU:HB3	1.86	0.56
48:WA:4090:C:H2'	48:WA:4091:G:H8	1.69	0.56
51:ZA:1565:C:OP2	71:TB:101:ARG:NH1	2.38	0.56
83:FC:141:CYS:HB3	83:FC:146:LEU:H	1.69	0.56
2:B:11:HIS:NE2	48:WA:4460:C:OP1	2.38	0.56
2:B:385:LYS:NZ	48:WA:5004:U:OP2	2.36	0.56
4:D:268:ARG:NH1	48:WA:1182:C:OP1	2.39	0.56
13:M:90:ASN:ND2	48:WA:3930:A:OP1	2.38	0.56
26:Z:132:ARG:NH1	48:WA:1470:C:OP1	2.38	0.56
48:WA:4637:A:H2	48:WA:4665:G:H21	1.51	0.56
59:HB:408:VAL:HG13	59:HB:425:PHE:HB2	1.86	0.56
70:SB:89:ASP:OD1	70:SB:94:LYS:N	2.38	0.56
9:I:54:SER:HB2	9:I:135:ILE:HD11	1.88	0.56
11:K:178:ALA:N	26:Z:134:GLU:OE2	2.39	0.56
17:Q:44:LEU:HD22	17:Q:49:LEU:HD12	1.87	0.56
21:U:13:LYS:NZ	21:U:59:ASP:OD1	2.38	0.56
30:DA:109:LYS:NZ	30:DA:128:ARG:O	2.34	0.56
48:WA:2601:G:N2	48:WA:2749:U:O4	2.39	0.56
48:WA:4276:A:H2'	48:WA:4277:G:C8	2.41	0.56
51:ZA:1023:A:OP2	65:NB:124:ARG:NH1	2.37	0.56
56:EB:162:ILE:HG22	56:EB:169:ILE:HA	1.88	0.56
59:HB:245:LYS:NZ	59:HB:269:GLU:OE2	2.33	0.56
77:ZB:58:LEU:HD12	77:ZB:62:VAL:HG21	1.87	0.56
4:D:83:LEU:HB3	4:D:88:VAL:HB	1.86	0.56
35:IA:49:TRP:O	48:WA:1648:A:O2'	2.22	0.56
42:PA:90:LEU:HG	42:PA:111:ILE:HG23	1.88	0.56
51:ZA:612:U:O2'	82:EC:84:LYS:NZ	2.39	0.56
61:JB:137:VAL:HG22	61:JB:157:ILE:HG12	1.87	0.56
76:YB:82:ALA:O	76:YB:86:GLU:HB2	2.06	0.56
81:DC:5:GLN:O	81:DC:9:SER:OG	2.23	0.56
48:WA:3601:A:H2'	48:WA:3602:G:C8	2.41	0.56
51:ZA:1016:U:H5''	65:NB:14:SER:HB2	1.87	0.56
51:ZA:1497:G:N7	62:KB:25:LYS:NZ	2.53	0.56
64:MB:52:LEU:HD23	64:MB:76:LEU:HD11	1.88	0.56
2:B:95:THR:HG22	48:WA:4912:A:H4'	1.88	0.56
13:M:120:TRP:HE1	13:M:123:GLU:HB3	1.71	0.56
48:WA:1935:G:H2'	48:WA:1936:A:C8	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:3811:G:N2	48:WA:3811:G:OP2	2.38	0.56
88:HC:281:ALA:HB2	88:HC:334:PRO:HB2	1.88	0.56
11:K:116:ARG:NH2	11:K:155:MET:O	2.38	0.56
13:M:183:THR:HG22	13:M:188:ARG:HB3	1.88	0.56
48:WA:181:C:H2'	48:WA:182:G:C8	2.41	0.56
51:ZA:1531:A:OP1	71:TB:84:ARG:NH2	2.38	0.56
84:GC:202:PRO:HG2	84:GC:243:PRO:HA	1.87	0.56
6:F:75:ARG:NE	48:WA:731:G:OP2	2.39	0.55
16:P:88:ASP:OD2	16:P:108:ARG:NH1	2.38	0.55
17:Q:39:GLN:NE2	48:WA:2713:G:OP2	2.39	0.55
48:WA:4110:G:H2'	48:WA:4111:G:H8	1.69	0.55
53:BB:40:ASN:OD1	53:BB:75:GLN:NE2	2.39	0.55
69:RB:95:ILE:HD11	69:RB:118:GLN:HB2	1.88	0.55
17:Q:97:ARG:NH2	48:WA:2727:A:OP2	2.39	0.55
44:SA:38:C:O2'	51:ZA:1058:A:OP1	2.25	0.55
48:WA:1247:C:H2'	48:WA:1248:G:H8	1.72	0.55
51:ZA:1401:A:H4'	72:UB:52:GLY:HA3	1.89	0.55
51:ZA:1432:U:H2'	51:ZA:1438:A:H8	1.71	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	1.70	0.55
52:AB:145:ILE:HG12	52:AB:159:ILE:HB	1.89	0.55
78:AC:87:ARG:NH2	78:AC:91:ALA:O	2.39	0.55
5:E:129:LEU:O	48:WA:965:A:N6	2.39	0.55
10:J:146:ARG:NH1	49:XA:27:G:OP1	2.39	0.55
20:T:105:ASN:HD21	20:T:111:GLU:HB2	1.70	0.55
23:W:48:ARG:NH2	48:WA:2476:G:OP2	2.38	0.55
37:KA:23:ILE:HG23	37:KA:38:ASN:HB2	1.88	0.55
51:ZA:4:C:H4'	54:CB:207:ALA:HB2	1.89	0.55
51:ZA:527:C:H2'	51:ZA:528:A:H8	1.71	0.55
51:ZA:562:U:H2'	51:ZA:563:G:C8	2.41	0.55
51:ZA:1128:C:H2'	51:ZA:1129:G:C8	2.41	0.55
55:DB:179:LYS:NZ	55:DB:217:GLN:O	2.36	0.55
79:BC:54:VAL:HG13	79:BC:63:LEU:HB2	1.87	0.55
14:N:54:TYR:OH	14:N:73:PHE:O	2.23	0.55
48:WA:115:C:O2'	48:WA:276:C:OP1	2.23	0.55
48:WA:1886:C:H2'	48:WA:1887:G:H8	1.72	0.55
48:WA:2397:A:HO2'	48:WA:2808:A:HO2'	1.55	0.55
48:WA:3892:A:N6	48:WA:4572:G:O2'	2.37	0.55
51:ZA:379:C:O2	60:IB:5:ARG:NH1	2.39	0.55
54:CB:68:ARG:NH1	54:CB:72:ASP:OD1	2.40	0.55
55:DB:69:GLU:O	55:DB:92:ARG:NH2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:FB:140:ASP:OD2	80:CC:44:ARG:NH1	2.39	0.55
76:YB:34:THR:HG23	76:YB:69:THR:HG21	1.89	0.55
86:b:116:ILE:HG22	86:b:118:PRO:HD2	1.88	0.55
10:J:56:THR:HG22	10:J:64:ARG:H	1.72	0.55
21:U:13:LYS:HD2	21:U:128:LEU:HD11	1.88	0.55
51:ZA:948:C:H2'	51:ZA:949:G:H8	1.72	0.55
68:QB:35:SER:OG	68:QB:50:HIS:NE2	2.37	0.55
2:B:189:THR:HG23	2:B:192:GLU:H	1.72	0.55
28:BA:50:ASN:ND2	28:BA:75:SER:O	2.39	0.55
45:TA:49:C:H2'	45:TA:50:A:H8	1.71	0.55
48:WA:3719:A:N3	48:WA:4180:A:O2'	2.39	0.55
3:C:301:ALA:HB1	16:P:132:LYS:HE3	1.87	0.55
19:S:46:GLY:O	19:S:49:GLN:NE2	2.40	0.55
23:W:110:LYS:NZ	23:W:121:VAL:O	2.39	0.55
44:SA:13:U:O2	44:SA:23:G:N2	2.40	0.55
46:UA:21:A:H2'	46:UA:22:U:H5''	1.87	0.55
48:WA:2000:A:N3	48:WA:2021:C:O2'	2.37	0.55
48:WA:4176:U:H2'	48:WA:4177:G:H8	1.71	0.55
7:G:203:LYS:NZ	7:G:230:MET:O	2.40	0.55
22:V:8:PHE:HZ	22:V:49:ILE:HD12	1.71	0.55
25:Y:100:VAL:HG13	25:Y:106:LEU:HB3	1.89	0.55
48:WA:153:G:H2'	48:WA:154:G:H8	1.72	0.55
51:ZA:1271:C:OP1	83:FC:90:LYS:NZ	2.37	0.55
6:F:91:VAL:O	6:F:119:GLY:HA2	2.07	0.55
6:F:146:LEU:O	6:F:150:ASN:ND2	2.37	0.55
16:P:14:ARG:NH2	48:WA:2085:C:OP2	2.40	0.55
17:Q:108:ARG:NH2	48:WA:2901:C:OP1	2.37	0.55
57:FB:124:ASP:OD2	80:CC:47:LYS:NZ	2.40	0.55
59:HB:355:PRO:HG2	59:HB:358:ARG:HG2	1.89	0.55
86:b:121:VAL:HG13	86:b:221:ASN:HD21	1.72	0.55
48:WA:369:G:N2	48:WA:372:A:OP2	2.33	0.55
48:WA:417:G:H1'	50:YA:17:A:H61	1.72	0.55
48:WA:4423:C:H42	48:WA:4477:G:N2	2.05	0.55
51:ZA:981:A:H2'	51:ZA:982:G:C8	2.42	0.55
51:ZA:1858:G:OP2	66:OB:146:ARG:NH2	2.34	0.55
48:WA:1392:G:N2	48:WA:1395:G:OP2	2.35	0.54
48:WA:3725:A:H2'	48:WA:3726:A:H8	1.72	0.54
49:XA:110:G:H2'	49:XA:111:C:C6	2.42	0.54
51:ZA:866:U:H2'	51:ZA:867:G:C8	2.42	0.54
51:ZA:1477:U:OP2	69:RB:3:ARG:NH2	2.40	0.54
56:EB:31:PRO:HG3	56:EB:43:PRO:HG3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:YB:13:MET:SD	76:YB:22:GLN:NE2	2.78	0.54
76:YB:82:ALA:O	76:YB:86:GLU:CB	2.55	0.54
5:E:144:ARG:NH1	31:EA:110:ILE:OXT	2.38	0.54
10:J:32:ARG:HD2	10:J:35:ARG:HH22	1.72	0.54
25:Y:135:ARG:O	48:WA:4124:G:N2	2.37	0.54
48:WA:1960:A:O2'	48:WA:2027:A:N6	2.39	0.54
50:YA:67:U:H2'	50:YA:68:G:C8	2.41	0.54
51:ZA:1203:G:H2'	51:ZA:1204:A:C8	2.42	0.54
51:ZA:1472:C:H42	51:ZA:1476:A:N6	1.99	0.54
72:UB:46:LYS:NZ	72:UB:97:ILE:O	2.39	0.54
88:HC:360:VAL:HA	88:HC:369:ALA:HA	1.90	0.54
6:F:156:ARG:NH2	48:WA:2075:C:O2'	2.40	0.54
7:G:156:ARG:NH2	7:G:245:ARG:O	2.40	0.54
20:T:66:SER:HB3	20:T:69:LYS:HB3	1.88	0.54
21:U:15:ARG:HB2	48:WA:4620:G:H5''	1.89	0.54
22:V:80:ARG:HH21	58:GB:131:ARG:HG2	1.71	0.54
48:WA:2899:G:H2'	48:WA:2900:G:H8	1.72	0.54
48:WA:4637:A:H8	48:WA:5050:A:H61	1.55	0.54
51:ZA:143:U:H4'	51:ZA:144:U:H5'	1.89	0.54
51:ZA:677:G:N2	51:ZA:1028:A:H62	2.03	0.54
51:ZA:1092:G:OP1	65:NB:2:GLY:N	2.40	0.54
4:D:94:ASN:OD1	4:D:97:ALA:N	2.36	0.54
16:P:121:LEU:HD22	16:P:125:GLN:HG2	1.89	0.54
48:WA:1334:C:H2'	48:WA:1335:A:C8	2.43	0.54
48:WA:2507:C:H4'	48:WA:2508:G:H5'	1.89	0.54
48:WA:4637:A:OP1	48:WA:4638:U:O2'	2.24	0.54
55:DB:144:ARG:HG3	55:DB:213:VAL:HG22	1.89	0.54
2:B:224:LYS:NZ	48:WA:4669:C:OP1	2.40	0.54
6:F:136:GLU:OE1	49:XA:96:U:O2'	2.23	0.54
10:J:87:LEU:HD12	10:J:92:TYR:HA	1.89	0.54
15:O:147:GLN:OE1	48:WA:423:G:N2	2.30	0.54
38:LA:80:ARG:HH21	48:WA:4698:C:H4'	1.72	0.54
40:NA:81:ARG:NH2	48:WA:4295:U:O2'	2.41	0.54
48:WA:126:C:H2'	48:WA:127:G:H8	1.71	0.54
48:WA:1565:A:N6	51:ZA:1028:A:N1	2.54	0.54
51:ZA:317:C:OP2	58:GB:183:ARG:NH2	2.39	0.54
51:ZA:1613:G:OP1	70:SB:88:LYS:NZ	2.40	0.54
59:HB:244:ALA:HB3	59:HB:262:SER:HB2	1.89	0.54
84:GC:18:VAL:HA	84:GC:35:SER:HA	1.90	0.54
86:b:69:LEU:HD21	86:b:76:GLU:HB2	1.89	0.54
7:G:90:LYS:NZ	48:WA:4128:C:OP1	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:52:LYS:O	25:Y:65:ARG:NH2	2.40	0.54
40:NA:4:VAL:O	40:NA:94:GLY:N	2.38	0.54
40:NA:98:LYS:HD2	48:WA:4235:A:H4'	1.88	0.54
41:OA:38:THR:HA	41:OA:45:THR:HA	1.89	0.54
46:UA:59:A:N7	46:UA:60:A:N6	2.55	0.54
48:WA:1852:A:N3	48:WA:2285:G:O2'	2.39	0.54
51:ZA:521:A:OP1	61:JB:45:ARG:NH1	2.37	0.54
51:ZA:688:U:OP1	59:HB:354:ARG:NH2	2.41	0.54
2:B:258:HIS:NE2	48:WA:3880:C:O2	2.41	0.54
39:MA:23:ARG:NH2	48:WA:3809:A:OP1	2.39	0.54
48:WA:1335:A:H2'	48:WA:1336:A:H8	1.73	0.54
48:WA:2000:A:H2'	48:WA:2001:A:C8	2.43	0.54
48:WA:3756:G:O6	48:WA:3773:C:N4	2.41	0.54
57:FB:59:LYS:HB2	57:FB:62:ARG:HB2	1.90	0.54
60:IB:80:ASP:OD1	60:IB:81:VAL:N	2.40	0.54
71:TB:22:LEU:HG	71:TB:28:LEU:HD21	1.90	0.54
79:BC:42:LYS:NZ	79:BC:43:ILE:O	2.41	0.54
1:A:30:ARG:NH1	1:A:33:ASP:OD2	2.41	0.54
9:I:101:LYS:NZ	9:I:102:MET:O	2.37	0.54
47:VA:21:C:OP1	51:ZA:1704:C:N4	2.41	0.54
48:WA:2481:G:H2'	48:WA:2482:G:C8	2.43	0.54
48:WA:4240:G:H2'	48:WA:4241:A:H8	1.73	0.54
51:ZA:1179:G:N2	51:ZA:1182:A:OP2	2.41	0.54
51:ZA:1293:A:N6	51:ZA:1294:G:O6	2.40	0.54
51:ZA:1630:A:H5''	70:SB:37:GLY:H	1.73	0.54
51:ZA:1808:U:H2'	51:ZA:1809:A:C8	2.43	0.54
53:BB:144:LYS:HE2	53:BB:206:PRO:HB2	1.90	0.54
56:EB:199:GLU:HB3	56:EB:207:VAL:HG13	1.88	0.54
83:FC:126:CYS:HB2	83:FC:144:CYS:HB2	1.89	0.54
4:D:123:VAL:HA	4:D:248:ARG:HH12	1.73	0.54
13:M:68:ARG:HA	13:M:98:LEU:HD21	1.90	0.54
13:M:184:ILE:O	13:M:194:ARG:NH2	2.41	0.54
16:P:151:HIS:ND1	16:P:164:LYS:O	2.41	0.54
19:S:71:ALA:HB3	48:WA:4315:A:H4'	1.90	0.54
21:U:21:PRO:HA	21:U:54:ALA:HA	1.89	0.54
48:WA:484:G:H5'	48:WA:485:U:H5''	1.89	0.54
48:WA:4469:A:O2'	48:WA:4512:A:N3	2.35	0.54
48:WA:4706:C:H2'	48:WA:4707:A:H8	1.73	0.54
48:WA:4994:G:H2'	48:WA:4995:G:C8	2.42	0.54
51:ZA:941:C:H2'	51:ZA:942:G:C8	2.42	0.54
61:JB:83:ARG:HD3	61:JB:150:ARG:HD3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
88:HC:241:PRO:HB3	88:HC:244:LYS:HD2	1.90	0.54
42:PA:98:ARG:NH2	48:WA:2264:G:OP2	2.39	0.54
48:WA:1560:A:H2'	48:WA:1561:G:H8	1.71	0.54
48:WA:4962:G:H2'	48:WA:4963:G:H8	1.73	0.54
51:ZA:980:A:H2'	51:ZA:981:A:C8	2.43	0.54
51:ZA:1711:U:H2'	51:ZA:1712:A:C8	2.43	0.54
57:FB:50:PRO:HG2	57:FB:90:VAL:HG22	1.89	0.54
12:L:128:LYS:NZ	48:WA:4899:G:OP1	2.40	0.53
48:WA:3918:G:H2'	48:WA:3919:A:H8	1.73	0.53
51:ZA:991:G:N7	78:AC:7:ASN:ND2	2.56	0.53
54:CB:65:LYS:HG3	54:CB:273:LEU:HD22	1.90	0.53
66:OB:101:GLY:HA3	66:OB:134:PRO:HG2	1.90	0.53
20:T:44:GLN:HA	20:T:56:LEU:HD21	1.89	0.53
45:TA:9:A:O2'	45:TA:10:G:N7	2.36	0.53
48:WA:1074:G:N2	48:WA:1075:G:O6	2.41	0.53
48:WA:1183:U:H2'	48:WA:1184:G:H8	1.73	0.53
48:WA:2871:U:O2'	48:WA:2883:A:N7	2.35	0.53
48:WA:3807:U:H2'	48:WA:3808:G:H8	1.73	0.53
48:WA:3920:G:OP2	93:WA:5244:SPD:N10	2.41	0.53
61:JB:59:GLU:OE2	61:JB:69:ARG:NH2	2.41	0.53
64:MB:47:ALA:HA	64:MB:112:LYS:HB3	1.89	0.53
13:M:114:ARG:HE	13:M:137:PRO:HG3	1.73	0.53
48:WA:85:G:O2'	48:WA:97:G:O6	2.26	0.53
48:WA:158:A:N1	48:WA:276:C:O2'	2.37	0.53
48:WA:2523:G:H2'	48:WA:2524:G:H8	1.73	0.53
51:ZA:1276:A:H1'	62:KB:50:GLN:HE22	1.74	0.53
59:HB:268:LEU:O	59:HB:272:SER:HB3	2.08	0.53
84:GC:255:SER:OG	84:GC:257:LYS:NZ	2.40	0.53
3:C:195:LYS:HE3	48:WA:2335:G:H5''	1.89	0.53
7:G:253:THR:OG1	48:WA:150:U:OP2	2.25	0.53
14:N:49:ARG:NH1	48:WA:1932:U:OP2	2.31	0.53
48:WA:261:G:H2'	48:WA:262:G:H8	1.72	0.53
48:WA:1973:U:O2	86:b:41:GLN:NE2	2.41	0.53
48:WA:4969:A:H2'	48:WA:4970:A:H8	1.73	0.53
51:ZA:183:G:O2'	51:ZA:184:G:O5'	2.26	0.53
51:ZA:912:C:H3'	51:ZA:913:A:H3'	1.90	0.53
51:ZA:1453:C:OP1	69:RB:48:ASN:ND2	2.42	0.53
52:AB:85:ARG:HH21	52:AB:201:LEU:HD12	1.73	0.53
59:HB:383:ARG:NH1	74:WB:49:GLU:OE2	2.41	0.53
70:SB:34:LYS:HB3	70:SB:100:ALA:HA	1.90	0.53
84:GC:67:SER:H	84:GC:82:SER:HA	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:52:LEU:HG	5:E:53:VAL:HG23	1.89	0.53
30:DA:104:SER:HB2	48:WA:2305:C:H5''	1.91	0.53
42:PA:19:LYS:HB2	48:WA:2339:C:H4'	1.90	0.53
42:PA:107:ARG:NH2	48:WA:2265:A:OP1	2.42	0.53
48:WA:2445:G:OP2	48:WA:2518:G:N2	2.36	0.53
48:WA:2747:A:H2'	48:WA:2748:A:H8	1.73	0.53
48:WA:4241:A:H2'	48:WA:4242:G:C8	2.43	0.53
48:WA:4421:U:OP1	48:WA:4423:C:N4	2.42	0.53
1:A:225:ILE:HD11	1:A:233:ARG:HG3	1.91	0.53
10:J:44:THR:O	10:J:78:LYS:NZ	2.36	0.53
14:N:188:LYS:NZ	48:WA:4895:A:OP1	2.42	0.53
15:O:164:ARG:NH2	48:WA:1598:U:O2'	2.42	0.53
38:LA:96:ARG:NH2	48:WA:4475:A:O2'	2.42	0.53
48:WA:261:G:H2'	48:WA:262:G:C8	2.44	0.53
48:WA:1727:U:H2'	48:WA:1728:U:H6	1.73	0.53
48:WA:2380:G:N2	48:WA:2383:A:OP2	2.38	0.53
51:ZA:107:A:H2'	51:ZA:108:G:C8	2.44	0.53
51:ZA:1652:G:H1	51:ZA:1672:U:H3	1.55	0.53
14:N:93:LYS:NZ	48:WA:1310:C:OP1	2.38	0.53
51:ZA:168:C:OP1	58:GB:131:ARG:NH1	2.41	0.53
51:ZA:375:U:OP2	63:LB:59:LYS:NZ	2.42	0.53
51:ZA:1215:C:O2'	51:ZA:1645:C:OP2	2.26	0.53
62:KB:83:LEU:HB3	62:KB:85:LEU:HD23	1.90	0.53
15:O:79:ASP:OD2	15:O:85:GLN:NE2	2.42	0.53
40:NA:80:LYS:O	48:WA:4348:U:O2'	2.24	0.53
48:WA:1373:A:N1	50:YA:28:C:O2'	2.38	0.53
48:WA:5008:U:H4'	48:WA:5009:A:H5'	1.90	0.53
54:CB:244:ILE:O	54:CB:247:THR:OG1	2.25	0.53
55:DB:210:VAL:O	55:DB:211:ARG:NH1	2.41	0.53
4:D:17:GLN:O	48:WA:4267:U:N3	2.36	0.53
25:Y:50:PRO:HD3	25:Y:68:ILE:HG13	1.91	0.53
48:WA:4:G:H2'	48:WA:5:A:H8	1.73	0.53
48:WA:1826:G:H2'	48:WA:1827:A:C8	2.43	0.53
48:WA:3691:G:O2'	48:WA:3820:U:OP2	2.25	0.53
51:ZA:874:G:N3	59:HB:352:GLN:NE2	2.46	0.53
51:ZA:1086:G:OP2	78:AC:12:LYS:NZ	2.38	0.53
51:ZA:1864:U:H5'	78:AC:79:ILE:HD11	1.90	0.53
16:P:172:ARG:HD2	26:Z:57:GLY:HA3	1.91	0.53
26:Z:75:LEU:HB3	26:Z:117:LEU:HD13	1.91	0.53
51:ZA:153:G:N2	58:GB:13:GLN:OE1	2.39	0.53
57:FB:71:ARG:NH2	57:FB:148:ASN:OD1	2.33	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:135:VAL:HG23	6:F:139:ILE:HD13	1.90	0.52
15:O:150:LYS:O	50:YA:13:G:O2'	2.26	0.52
29:CA:70:LYS:HE2	48:WA:2391:A:H5'	1.91	0.52
36:JA:12:LEU:HD21	36:JA:16:ARG:HH21	1.74	0.52
43:RA:61:LYS:HB2	43:RA:72:GLU:HG2	1.91	0.52
48:WA:2297:C:H2'	48:WA:2298:G:H8	1.73	0.52
48:WA:3724:G:H2'	48:WA:3725:A:H8	1.73	0.52
51:ZA:145:G:H2'	51:ZA:146:G:C8	2.44	0.52
52:AB:108:PHE:HB2	52:AB:136:GLU:HB3	1.92	0.52
70:SB:36:VAL:HG21	70:SB:71:MET:HE3	1.91	0.52
73:VB:15:ARG:NH1	73:VB:33:GLN:OE1	2.38	0.52
1:A:27:ALA:O	1:A:128:ARG:NH2	2.42	0.52
48:WA:1565:A:H2'	48:WA:1566:A:C8	2.45	0.52
48:WA:1897:G:O2'	48:WA:1909:A:N3	2.37	0.52
48:WA:4305:C:H2'	48:WA:4307:G:H8	1.74	0.52
48:WA:5059:C:H2'	48:WA:5060:A:C8	2.44	0.52
52:AB:77:ILE:HG12	52:AB:99:ILE:HB	1.91	0.52
53:BB:86:LEU:HB3	53:BB:98:THR:HB	1.92	0.52
56:EB:252:ARG:NH1	61:JB:75:ASN:OD1	2.42	0.52
60:IB:27:TYR:HB3	60:IB:49:ARG:HH12	1.74	0.52
66:OB:117:ARG:NE	78:AC:52:ASP:OD2	2.43	0.52
78:AC:44:ILE:HG23	78:AC:45:VAL:HG23	1.91	0.52
84:GC:4:GLN:HG3	84:GC:314:ILE:HG22	1.90	0.52
84:GC:77:PHE:HB3	84:GC:89:LEU:HD11	1.91	0.52
84:GC:166:VAL:HG22	84:GC:176:VAL:HG22	1.90	0.52
10:J:29:SER:OG	10:J:67:LYS:O	2.23	0.52
43:RA:37:LEU:HD12	43:RA:42:VAL:HB	1.91	0.52
51:ZA:639:C:H2'	51:ZA:640:A:C8	2.45	0.52
51:ZA:640:A:H2'	51:ZA:641:A:C8	2.44	0.52
71:TB:41:LYS:NZ	71:TB:83:GLN:OE1	2.42	0.52
79:BC:74:THR:OG1	79:BC:77:CYS:SG	2.68	0.52
2:B:261:ARG:HB2	14:N:64:THR:HG21	1.90	0.52
17:Q:60:ARG:HH12	48:WA:2617:C:H5''	1.73	0.52
40:NA:64:LYS:HD2	48:WA:4372:G:H5''	1.91	0.52
51:ZA:126:G:H1'	51:ZA:181:A:H1'	1.91	0.52
51:ZA:571:U:O2'	76:YB:60:PHE:O	2.28	0.52
53:BB:103:MET:HE2	53:BB:188:LEU:HD11	1.92	0.52
84:GC:259:TRP:HD1	84:GC:266:ILE:HA	1.75	0.52
84:GC:261:LEU:O	84:GC:264:LYS:NZ	2.36	0.52
5:E:141:ARG:NH1	5:E:172:SER:O	2.42	0.52
13:M:73:ARG:NH1	48:WA:32:G:OP1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:79:ILE:HG12	28:BA:90:ARG:HG2	1.92	0.52
48:WA:425:U:H2'	48:WA:426:A:H8	1.74	0.52
48:WA:3666:G:H2'	48:WA:3667:G:H8	1.75	0.52
50:YA:71:A:H4'	50:YA:72:A:H5'	1.92	0.52
51:ZA:1018:U:O2'	65:NB:86:GLU:OE2	2.28	0.52
51:ZA:1599:U:OP2	77:ZB:46:ASN:ND2	2.43	0.52
53:BB:179:ASN:HB3	53:BB:183:GLU:HB2	1.90	0.52
58:GB:48:TYR:OH	58:GB:119:LYS:O	2.27	0.52
3:C:4:ALA:O	3:C:29:LYS:NZ	2.42	0.52
13:M:49:ARG:HH12	48:WA:152:U:P	2.32	0.52
17:Q:62:ARG:NH1	48:WA:4647:C:OP2	2.41	0.52
42:PA:65:LYS:O	42:PA:102:TYR:OH	2.19	0.52
48:WA:1249:U:O2	48:WA:1268:G:N2	2.37	0.52
48:WA:1505:A:H4'	48:WA:1506:G:H5'	1.92	0.52
48:WA:2460:C:O2'	48:WA:3673:G:N3	2.40	0.52
51:ZA:65:C:OP1	58:GB:136:LYS:NZ	2.42	0.52
51:ZA:210:U:H2'	51:ZA:211:G:H8	1.74	0.52
51:ZA:1781:A:H2'	51:ZA:1782:G:C8	2.44	0.52
61:JB:42:GLU:OE1	61:JB:45:ARG:NH2	2.42	0.52
1:A:101:VAL:HG22	1:A:165:VAL:HG22	1.91	0.52
14:N:12:ARG:O	18:R:171:ARG:NH2	2.40	0.52
42:PA:28:GLU:HB2	42:PA:31:ASN:HB2	1.91	0.52
48:WA:1264:G:H2'	48:WA:1265:A:C8	2.44	0.52
48:WA:3882:G:H2'	48:WA:3883:G:C8	2.44	0.52
48:WA:4323:U:H2'	48:WA:4324:G:C8	2.45	0.52
51:ZA:1079:C:O2'	51:ZA:1182:A:N1	2.42	0.52
51:ZA:1358:U:OP2	54:CB:123:ARG:NH2	2.42	0.52
51:ZA:1617:G:O6	67:PB:43:ARG:NH1	2.42	0.52
80:CC:16:LYS:HD2	80:CC:31:ARG:HH12	1.75	0.52
2:B:13:SER:HB2	48:WA:4624:A:H4'	1.91	0.52
19:S:83:LYS:NZ	48:WA:4307:G:O5'	2.43	0.52
40:NA:26:TYR:HB3	40:NA:67:VAL:HB	1.91	0.52
48:WA:2519:A:N3	48:WA:2541:C:O2'	2.43	0.52
48:WA:3809:A:HO2'	51:ZA:1816:G:HO2'	1.58	0.52
48:WA:4239:C:O2'	48:WA:4323:U:O2	2.27	0.52
51:ZA:110:U:H3	51:ZA:351:G:H1	1.58	0.52
51:ZA:847:A:OP1	56:EB:108:ARG:NH2	2.43	0.52
51:ZA:1375:G:H2'	51:ZA:1376:A:C8	2.44	0.52
56:EB:191:ARG:HH11	56:EB:245:ARG:HH21	1.58	0.52
59:HB:325:PHE:O	59:HB:328:LYS:NZ	2.40	0.52
2:B:108:GLU:OE2	2:B:138:GLN:NE2	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:112:ASP:OD1	18:R:116:ARG:NH1	2.41	0.52
24:X:11:ARG:HG3	48:WA:229:G:H5''	1.91	0.52
48:WA:1507:C:H2'	48:WA:1508:G:H8	1.75	0.52
51:ZA:111:A:O2'	63:LB:69:ARG:NH1	2.43	0.52
51:ZA:1605:G:H2'	51:ZA:1606:G:C4	2.45	0.52
51:ZA:1630:A:H5''	70:SB:37:GLY:N	2.24	0.52
56:EB:251:GLU:OE2	56:EB:255:ARG:NH2	2.43	0.52
74:WB:18:GLU:HG3	74:WB:69:LEU:HD23	1.92	0.52
6:F:178:LEU:HB3	6:F:183:ILE:HB	1.91	0.52
26:Z:75:LEU:HG	26:Z:113:GLY:HA2	1.92	0.52
40:NA:8:ARG:NH2	48:WA:4234:U:O4	2.37	0.52
40:NA:58:LYS:NZ	48:WA:4382:A:OP1	2.39	0.52
48:WA:1183:U:H2'	48:WA:1184:G:C8	2.45	0.52
48:WA:3734:A:H2'	48:WA:3735:A:C8	2.45	0.52
51:ZA:5:U:H2'	51:ZA:6:G:H8	1.75	0.52
51:ZA:520:A:O2'	51:ZA:825:A:N3	2.37	0.52
79:BC:34:ASP:HB2	79:BC:82:LYS:HD2	1.91	0.52
86:b:28:PHE:HB2	86:b:89:VAL:HG22	1.92	0.52
2:B:234:ARG:NH1	2:B:271:GLN:O	2.35	0.51
3:C:312:ARG:NH2	48:WA:2077:G:OP1	2.43	0.51
14:N:94:ARG:HD2	48:WA:1311:C:H5''	1.91	0.51
30:DA:98:GLU:OE1	48:WA:2326:C:O2'	2.28	0.51
48:WA:417:G:OP1	48:WA:2331:U:O2'	2.26	0.51
51:ZA:583:A:H3'	51:ZA:584:A:H8	1.75	0.51
51:ZA:1523:C:H3'	70:SB:141:ARG:HH21	1.76	0.51
59:HB:304:VAL:HG22	59:HB:334:ALA:HB1	1.93	0.51
61:JB:59:GLU:O	61:JB:62:THR:OG1	2.28	0.51
62:KB:20:VAL:HG23	62:KB:70:TYR:HA	1.92	0.51
17:Q:160:GLU:OE1	17:Q:163:ARG:NH2	2.40	0.51
18:R:132:ILE:HG23	18:R:136:LYS:HB2	1.92	0.51
37:KA:48:LYS:NZ	48:WA:2793:C:OP1	2.37	0.51
45:TA:42:G:H2'	45:TA:43:A:H8	1.75	0.51
48:WA:4763:G:N2	48:WA:4768:C:O3'	2.44	0.51
51:ZA:1711:U:H2'	51:ZA:1712:A:H8	1.76	0.51
25:Y:47:ASP:N	25:Y:69:LYS:O	2.43	0.51
48:WA:1413:C:N4	48:WA:1414:G:O6	2.43	0.51
48:WA:1826:G:H2'	48:WA:1827:A:H8	1.74	0.51
48:WA:2761:G:O2'	48:WA:2762:G:O4'	2.24	0.51
48:WA:4969:A:H2'	48:WA:4970:A:C8	2.45	0.51
51:ZA:155:G:H2'	51:ZA:156:G:C8	2.46	0.51
9:I:118:ALA:O	48:WA:1866:G:O2'	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:GA:45:SER:OG	50:YA:78:G:O2'	2.25	0.51
51:ZA:476:A:N3	51:ZA:488:U:O2'	2.36	0.51
54:CB:65:LYS:HD2	54:CB:273:LEU:HD13	1.92	0.51
56:EB:127:ARG:N	56:EB:140:VAL:O	2.34	0.51
48:WA:1335:A:H2'	48:WA:1336:A:C8	2.45	0.51
48:WA:1639:A:OP1	48:WA:1642:C:N4	2.35	0.51
48:WA:2560:C:H2'	48:WA:2561:G:C8	2.46	0.51
48:WA:3612:A:H2'	48:WA:3613:A:H8	1.75	0.51
48:WA:3809:A:O2'	51:ZA:1816:G:O2'	2.28	0.51
50:YA:64:U:H2'	50:YA:65:A:H8	1.74	0.51
84:GC:237:ASN:ND2	84:GC:286:CYS:O	2.41	0.51
5:E:184:LEU:O	48:WA:4885:C:N4	2.43	0.51
13:M:35:ALA:HA	13:M:65:ARG:HG2	1.92	0.51
46:UA:47:U:O2'	46:UA:50:U:OP1	2.25	0.51
48:WA:1507:C:H2'	48:WA:1508:G:C8	2.45	0.51
48:WA:2523:G:H2'	48:WA:2524:G:C8	2.45	0.51
48:WA:3895:C:H2'	48:WA:3896:A:H8	1.75	0.51
13:M:138:PHE:HA	13:M:143:ARG:HH21	1.75	0.51
35:IA:19:CYS:HB3	35:IA:22:CYS:SG	2.50	0.51
42:PA:39:ARG:NH1	48:WA:2268:C:O2'	2.43	0.51
48:WA:2460:C:O2	48:WA:3673:G:N2	2.43	0.51
51:ZA:432:G:H2'	51:ZA:433:A:C8	2.45	0.51
51:ZA:1004:U:H2'	51:ZA:1005:G:C8	2.46	0.51
56:EB:44:LEU:HD21	56:EB:70:ILE:HG21	1.92	0.51
58:GB:39:ASP:HB3	58:GB:47:GLY:H	1.74	0.51
59:HB:258:GLU:HG3	59:HB:286:ALA:HB3	1.91	0.51
78:AC:59:PHE:HB2	78:AC:62:TYR:HB2	1.93	0.51
84:GC:45:LEU:HB3	84:GC:47:ARG:HD3	1.92	0.51
84:GC:223:GLU:HB2	84:GC:225:LYS:HE3	1.92	0.51
1:A:179:ILE:O	48:WA:3655:A:O2'	2.18	0.51
15:O:66:LYS:NZ	48:WA:425:U:OP1	2.37	0.51
16:P:150:ARG:NH2	48:WA:1501:C:OP1	2.44	0.51
30:DA:29:VAL:HB	48:WA:1334:C:H5''	1.92	0.51
33:GA:27:GLU:OE2	33:GA:46:LYS:NZ	2.41	0.51
34:HA:29:ARG:HH22	48:WA:276:C:H2'	1.75	0.51
48:WA:3850:U:H2'	48:WA:3851:A:C8	2.45	0.51
51:ZA:1288:U:H3	51:ZA:1311:C:N4	2.02	0.51
54:CB:104:ASP:HB3	54:CB:130:ILE:HG13	1.92	0.51
66:OB:45:THR:HG22	66:OB:52:THR:HA	1.92	0.51
88:HC:282:PRO:HG2	88:HC:324:ASN:HA	1.91	0.51
5:E:160:HIS:HB3	5:E:163:LYS:HD2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:192:TRP:NE1	48:WA:48:G:OP1	2.31	0.51
48:WA:4232:C:H1'	48:WA:4273:A:N1	2.26	0.51
51:ZA:17:C:H2'	51:ZA:18:C:C6	2.46	0.51
51:ZA:1146:C:O2'	51:ZA:1150:A:N1	2.40	0.51
51:ZA:1245:G:O2'	51:ZA:1492:U:OP1	2.29	0.51
51:ZA:1428:G:O6	68:QB:99:LYS:NZ	2.44	0.51
1:A:207:VAL:HG13	1:A:208:GLU:HG3	1.93	0.51
4:D:124:GLU:OE1	4:D:126:THR:OG1	2.27	0.51
33:GA:79:LYS:HE3	48:WA:136:C:H41	1.76	0.51
37:KA:3:SER:O	48:WA:2783:G:O2'	2.29	0.51
48:WA:1944:A:H2'	48:WA:1945:A:C8	2.46	0.51
51:ZA:1406:G:H2'	51:ZA:1407:U:C6	2.46	0.51
51:ZA:1692:U:H2'	51:ZA:1693:G:C8	2.46	0.51
59:HB:289:ILE:HD12	59:HB:417:LYS:HG2	1.93	0.51
70:SB:24:ARG:HH21	70:SB:28:PHE:HB3	1.76	0.51
86:b:35:VAL:HG23	86:b:40:MET:HG2	1.93	0.51
7:G:158:GLU:OE2	7:G:166:ARG:NH2	2.34	0.50
17:Q:88:ARG:O	48:WA:2727:A:N6	2.43	0.50
33:GA:107:GLN:NE2	33:GA:111:GLU:OE2	2.43	0.50
44:SA:22:A:H2'	44:SA:23:G:C8	2.46	0.50
48:WA:181:C:H2'	48:WA:182:G:H8	1.74	0.50
48:WA:1210:C:H2'	48:WA:1211:G:H8	1.75	0.50
51:ZA:432:G:H2'	51:ZA:433:A:H8	1.76	0.50
74:WB:18:GLU:HG2	74:WB:65:LEU:HD13	1.92	0.50
75:XB:40:PRO:O	75:XB:77:ASN:ND2	2.44	0.50
15:O:111:ARG:NH2	48:WA:2364:U:OP1	2.44	0.50
28:BA:17:ARG:HD2	28:BA:104:ILE:HA	1.93	0.50
48:WA:418:A:H4'	48:WA:2313:C:H5'	1.93	0.50
56:EB:95:THR:HG22	76:YB:16:ARG:HB2	1.92	0.50
59:HB:307:LEU:HD22	59:HB:334:ALA:HB2	1.91	0.50
71:TB:38:LYS:NZ	71:TB:40:ALA:O	2.42	0.50
76:YB:27:VAL:HG12	76:YB:29:HIS:HD2	1.76	0.50
84:GC:132:TRP:CD1	84:GC:138:CYS:HA	2.46	0.50
1:A:6:ARG:HH12	1:A:199:VAL:H	1.59	0.50
4:D:52:ILE:HD13	49:XA:6:C:H4'	1.93	0.50
42:PA:94:ARG:HG3	42:PA:107:ARG:HD2	1.92	0.50
48:WA:456:C:H2'	48:WA:457:G:C8	2.47	0.50
48:WA:1317:C:N4	48:WA:1318:G:O6	2.44	0.50
51:ZA:311:C:H5''	51:ZA:312:G:H5''	1.93	0.50
51:ZA:554:A:H1'	51:ZA:555:A:H2'	1.92	0.50
51:ZA:1418:C:OP2	51:ZA:1420:G:N2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:1829:G:H1'	51:ZA:1850:A:H2	1.76	0.50
59:HB:338:ILE:HG12	59:HB:363:VAL:HG11	1.93	0.50
60:IB:178:ARG:HE	60:IB:181:GLN:HG3	1.76	0.50
75:XB:91:LEU:HD23	82:EC:82:VAL:HG21	1.94	0.50
84:GC:286:CYS:HA	84:GC:302:TYR:HA	1.92	0.50
3:C:323:ARG:HB2	48:WA:1283:G:H5'	1.93	0.50
7:G:126:ARG:NE	48:WA:4078:G:OP1	2.35	0.50
9:I:193:ASP:OD2	48:WA:1752:G:N2	2.44	0.50
10:J:40:LEU:HD12	10:J:70:VAL:HG22	1.93	0.50
48:WA:1657:C:O2	48:WA:4392:A:O2'	2.29	0.50
48:WA:2498:G:H2'	48:WA:2499:C:C6	2.46	0.50
48:WA:2813:G:N1	48:WA:2816:C:OP2	2.34	0.50
51:ZA:639:C:H2'	51:ZA:640:A:H8	1.76	0.50
51:ZA:642:U:H4'	51:ZA:644:G:H4'	1.93	0.50
16:P:122:THR:OG1	16:P:124:ASP:OD1	2.27	0.50
48:WA:1525:A:N3	48:WA:4391:C:O2'	2.42	0.50
48:WA:2024:C:H5''	86:b:83:ARG:HD2	1.92	0.50
48:WA:3934:U:H2'	48:WA:3935:G:H8	1.76	0.50
88:HC:442:ASP:OD1	88:HC:443:LYS:N	2.44	0.50
48:WA:2416:G:H2'	48:WA:2417:U:H6	1.76	0.50
48:WA:2469:U:H4'	48:WA:2470:U:H5'	1.94	0.50
51:ZA:1147:C:OP1	78:AC:6:ARG:NH1	2.36	0.50
64:MB:97:GLU:O	64:MB:101:ARG:NH2	2.43	0.50
77:ZB:73:VAL:HG21	77:ZB:88:LEU:HD11	1.93	0.50
2:B:329:ASP:OD1	2:B:329:ASP:N	2.34	0.50
5:E:67:ARG:NE	48:WA:1076:G:OP1	2.45	0.50
6:F:241:ARG:NH2	48:WA:945:C:OP1	2.40	0.50
14:N:46:ASN:O	14:N:50:ASN:ND2	2.41	0.50
42:PA:112:ARG:NH1	48:WA:2266:C:OP1	2.44	0.50
48:WA:1776:C:H2'	48:WA:1777:A:H8	1.75	0.50
1:A:118:GLU:OE2	48:WA:3664:A:O2'	2.29	0.50
3:C:343:GLN:HG2	48:WA:725:C:H1'	1.94	0.50
6:F:121:PHE:O	6:F:204:ASN:ND2	2.45	0.50
12:L:41:PRO:HG3	12:L:73:VAL:HG12	1.93	0.50
17:Q:90:PRO:HG2	17:Q:93:VAL:HB	1.93	0.50
48:WA:1095:G:H2'	48:WA:1096:G:C8	2.47	0.50
48:WA:1285:G:N1	48:WA:2078:G:OP1	2.34	0.50
48:WA:1908:U:H2'	48:WA:1909:A:H8	1.77	0.50
51:ZA:1407:U:O2'	68:QB:37:GLN:NE2	2.44	0.50
59:HB:268:LEU:O	59:HB:272:SER:OG	2.24	0.50
63:LB:80:MET:HE2	63:LB:122:ILE:HG13	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:MB:32:ALA:HB1	64:MB:37:GLU:HB3	1.93	0.50
68:QB:45:ALA:HB2	68:QB:101:GLY:HA3	1.94	0.50
5:E:48:ARG:O	5:E:67:ARG:NH1	2.45	0.50
13:M:14:LYS:HE2	48:WA:280:G:H5''	1.93	0.50
33:GA:89:ARG:NH1	50:YA:37:A:OP2	2.39	0.50
35:IA:12:ARG:NH2	48:WA:1619:G:O3'	2.45	0.50
37:KA:45:ARG:HH21	48:WA:2798:G:H5'	1.77	0.50
48:WA:32:G:H21	48:WA:50:C:H5	1.59	0.50
50:YA:47:C:H1'	50:YA:61:A:H2'	1.93	0.50
51:ZA:1010:G:H2'	51:ZA:1011:A:H8	1.75	0.50
51:ZA:1362:U:H5''	51:ZA:1363:C:H5	1.76	0.50
51:ZA:1670:C:H2'	51:ZA:1671:G:H8	1.77	0.50
52:AB:176:TRP:NE1	52:AB:197:VAL:O	2.43	0.50
64:MB:33:ARG:HD3	64:MB:91:LEU:HD22	1.94	0.50
18:R:164:LYS:HB2	18:R:165:PRO:HD3	1.95	0.49
20:T:63:LEU:HG	20:T:72:VAL:HG22	1.93	0.49
23:W:139:ARG:HH12	48:WA:2535:C:H5''	1.77	0.49
31:EA:46:ARG:HD3	31:EA:106:TYR:HD2	1.77	0.49
36:JA:12:LEU:HG	36:JA:16:ARG:HE	1.77	0.49
45:TA:22:G:H2'	45:TA:23:A:H8	1.76	0.49
51:ZA:5:U:H2'	51:ZA:6:G:C8	2.47	0.49
51:ZA:65:C:O2'	51:ZA:67:C:OP2	2.28	0.49
51:ZA:106:C:H2'	51:ZA:107:A:C8	2.45	0.49
51:ZA:553:U:O2'	51:ZA:554:A:O5'	2.26	0.49
51:ZA:1693:G:N2	51:ZA:1834:A:H8	2.10	0.49
55:DB:50:VAL:HG21	81:DC:34:TYR:HB3	1.93	0.49
2:B:324:GLY:HA2	48:WA:5053:C:H4'	1.94	0.49
13:M:9:GLU:HB2	34:HA:44:ILE:HG13	1.94	0.49
14:N:42:ASN:HD22	14:N:125:LYS:HD3	1.77	0.49
46:UA:69:A:H2'	46:UA:70:A:H8	1.78	0.49
48:WA:436:C:H2'	48:WA:437:G:H8	1.77	0.49
48:WA:3719:A:OP2	48:WA:3737:G:N2	2.44	0.49
51:ZA:844:U:OP1	56:EB:240:ARG:NH1	2.40	0.49
51:ZA:1165:G:OP2	51:ZA:1165:G:N2	2.36	0.49
51:ZA:1232:U:H3	51:ZA:1526:G:H1	1.60	0.49
52:AB:2:SER:HB3	52:AB:59:LEU:HG	1.95	0.49
64:MB:26:LEU:HD22	64:MB:33:ARG:HH22	1.77	0.49
79:BC:67:THR:OG1	79:BC:70:LYS:O	2.30	0.49
1:A:21:LYS:HG2	48:WA:1543:C:H5''	1.95	0.49
1:A:28:ARG:HE	1:A:123:ARG:HD3	1.77	0.49
2:B:213:GLN:NE2	2:B:285:TYR:O	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:146:ARG:HG2	10:J:147:ARG:HG3	1.93	0.49
27:AA:11:ASN:ND2	48:WA:1671:A:OP1	2.46	0.49
42:PA:103:HIS:ND1	42:PA:105:ASP:OD1	2.43	0.49
48:WA:1560:A:H2'	48:WA:1561:G:C8	2.47	0.49
48:WA:4090:C:H2'	48:WA:4091:G:C8	2.47	0.49
51:ZA:1332:A:O2'	55:DB:183:GLN:O	2.30	0.49
51:ZA:1401:A:H2'	51:ZA:1402:A:H8	1.77	0.49
51:ZA:1568:C:H2'	51:ZA:1569:A:C8	2.48	0.49
52:AB:51:LEU:HD23	69:RB:105:MET:HE1	1.93	0.49
56:EB:11:ARG:HA	56:EB:28:ALA:HB2	1.95	0.49
84:GC:62:HIS:ND1	84:GC:84:ASP:OD2	2.45	0.49
2:B:15:GLY:O	48:WA:4589:G:N2	2.35	0.49
7:G:97:ASP:OD1	7:G:98:ILE:N	2.45	0.49
11:K:27:ASN:HB3	50:YA:29:G:H5''	1.94	0.49
18:R:15:ARG:HH21	19:S:141:VAL:HG22	1.78	0.49
20:T:56:LEU:HD13	20:T:63:LEU:HD13	1.93	0.49
28:BA:38:ILE:HG21	28:BA:63:TYR:HB3	1.93	0.49
29:CA:24:GLU:OE2	29:CA:87:ARG:NH1	2.45	0.49
35:IA:3:LYS:HB3	48:WA:3644:A:C4	2.48	0.49
35:IA:27:TYR:HA	35:IA:34:CYS:HA	1.93	0.49
48:WA:1808:G:H2'	48:WA:1809:C:H6	1.78	0.49
48:WA:2742:U:O2'	48:WA:2744:G:N2	2.45	0.49
48:WA:4080:C:O2'	48:WA:4174:A:N6	2.45	0.49
51:ZA:65:C:H4'	58:GB:172:LYS:HD3	1.93	0.49
51:ZA:1558:C:H2'	51:ZA:1559:C:C6	2.47	0.49
4:D:91:GLY:O	4:D:94:ASN:ND2	2.45	0.49
11:K:79:GLU:OE1	11:K:82:ARG:NH1	2.45	0.49
13:M:172:ARG:NH1	48:WA:62:A:OP1	2.45	0.49
14:N:74:ARG:N	48:WA:4587:U:OP1	2.38	0.49
24:X:132:LYS:NZ	48:WA:246:G:O3'	2.44	0.49
27:AA:28:ARG:HB3	48:WA:1807:A:C4	2.48	0.49
51:ZA:172:U:N3	51:ZA:337:C:O2'	2.45	0.49
51:ZA:1854:U:H2'	51:ZA:1855:G:H8	1.77	0.49
56:EB:137:PRO:HB2	56:EB:150:PRO:HD2	1.95	0.49
16:P:175:GLU:OE2	26:Z:49:HIS:ND1	2.42	0.49
48:WA:982:G:OP2	48:WA:982:G:N2	2.40	0.49
48:WA:1505:A:H1'	48:WA:1506:G:C8	2.48	0.49
48:WA:2000:A:H62	86:b:55:MET:HE2	1.78	0.49
48:WA:4350:A:O2'	48:WA:4352:C:OP2	2.28	0.49
51:ZA:1485:U:OP1	55:DB:189:LYS:NZ	2.44	0.49
53:BB:137:LEU:HG	53:BB:215:VAL:HG22	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:223:THR:HB	2:B:275:HIS:H	1.78	0.49
5:E:144:ARG:NH2	5:E:194:GLN:O	2.46	0.49
48:WA:275:C:H2'	48:WA:276:C:C6	2.47	0.49
48:WA:4240:G:H2'	48:WA:4241:A:C8	2.46	0.49
48:WA:4262:U:H2'	48:WA:4263:C:H6	1.76	0.49
51:ZA:84:A:N3	51:ZA:150:A:O2'	2.45	0.49
51:ZA:161:U:O2'	58:GB:87:ARG:NH1	2.46	0.49
51:ZA:397:G:OP1	63:LB:106:HIS:NE2	2.46	0.49
51:ZA:931:C:H2'	51:ZA:932:G:C8	2.47	0.49
59:HB:356:ARG:HD3	59:HB:359:THR:HG21	1.94	0.49
2:B:117:ARG:NH2	48:WA:4987:U:OP1	2.36	0.49
21:U:50:ASN:ND2	48:WA:4459:U:OP1	2.45	0.49
48:WA:711:G:H2'	48:WA:712:A:H8	1.78	0.49
48:WA:1256:A:N1	48:WA:1261:G:O6	2.45	0.49
48:WA:1343:U:H2'	48:WA:1344:A:H8	1.77	0.49
51:ZA:1615:U:O4	67:PB:40:ARG:NH2	2.45	0.49
51:ZA:1650:A:H5''	68:QB:165:ALA:HB2	1.95	0.49
60:IB:64:ASN:O	60:IB:186:ASP:HA	2.12	0.49
67:PB:44:ARG:NH2	67:PB:53:GLN:OE1	2.39	0.49
6:F:55:HIS:NE2	6:F:59:GLU:OE2	2.45	0.49
6:F:82:VAL:HG22	18:R:62:VAL:HA	1.95	0.49
48:WA:162:A:H2'	48:WA:163:A:H8	1.77	0.49
48:WA:246:G:H2'	48:WA:247:G:H8	1.77	0.49
48:WA:1751:A:H2'	48:WA:1752:G:C8	2.48	0.49
51:ZA:1745:A:H62	51:ZA:1789:G:H21	1.61	0.49
52:AB:190:SER:OG	52:AB:192:GLU:OE1	2.29	0.49
60:IB:81:VAL:HG22	60:IB:102:VAL:HG12	1.95	0.49
84:GC:294:ASP:OD2	84:GC:296:GLN:NE2	2.41	0.49
2:B:79:VAL:HB	2:B:331:VAL:HG23	1.94	0.49
3:C:328:LEU:HD13	6:F:186:MET:HE2	1.95	0.49
8:H:92:MET:HG2	8:H:181:VAL:HG22	1.95	0.49
12:L:121:ARG:NH2	48:WA:4883:U:OP1	2.38	0.49
36:JA:35:LYS:NZ	48:WA:2695:G:OP1	2.30	0.49
48:WA:3612:A:H2'	48:WA:3613:A:C8	2.48	0.49
68:QB:79:GLU:OE1	68:QB:111:ARG:NH1	2.46	0.49
3:C:35:ASP:OD1	3:C:35:ASP:N	2.46	0.48
20:T:35:ASP:HB2	20:T:38:ASN:HB3	1.95	0.48
42:PA:31:ASN:ND2	42:PA:40:TYR:O	2.46	0.48
48:WA:132:G:O6	48:WA:137:G:N1	2.41	0.48
48:WA:2418:G:N2	48:WA:2428:U:O4	2.46	0.48
48:WA:3598:A:H61	63:LB:2:ALA:HA	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:4190:U:H2'	48:WA:4191:U:C6	2.48	0.48
48:WA:4763:G:H2'	48:WA:4764:A:H8	1.77	0.48
51:ZA:436:G:OP2	51:ZA:471:G:O2'	2.30	0.48
51:ZA:498:C:H2'	51:ZA:499:G:C8	2.48	0.48
51:ZA:1101:U:H2'	51:ZA:1102:G:C8	2.48	0.48
60:IB:67:TRP:NE1	60:IB:191:GLU:OE2	2.40	0.48
74:WB:80:ASP:OD1	74:WB:124:LYS:NZ	2.41	0.48
1:A:247:ARG:HB3	51:ZA:1069:U:H4'	1.95	0.48
6:F:244:ARG:NH1	48:WA:947:G:OP1	2.40	0.48
9:I:158:LYS:NZ	48:WA:4415:C:O2	2.45	0.48
25:Y:17:ARG:NH2	25:Y:18:TYR:OH	2.46	0.48
51:ZA:333:G:H2'	51:ZA:334:C:O4'	2.13	0.48
51:ZA:1115:U:O2	51:ZA:1116:C:O2'	2.30	0.48
51:ZA:1271:C:N4	51:ZA:1512:C:N3	2.60	0.48
51:ZA:1545:A:OP1	68:QB:100:GLY:N	2.42	0.48
51:ZA:1758:G:H2'	51:ZA:1759:G:H8	1.76	0.48
69:RB:32:LYS:HG3	69:RB:47:ARG:HD3	1.95	0.48
84:GC:38:LYS:NZ	84:GC:63:SER:O	2.46	0.48
15:O:118:GLU:O	15:O:122:HIS:ND1	2.36	0.48
45:TA:23:A:H2'	45:TA:24:G:C8	2.47	0.48
51:ZA:1309:C:H5'	83:FC:105:TYR:HE1	1.79	0.48
51:ZA:1536:G:H2'	51:ZA:1537:A:C8	2.48	0.48
67:PB:43:ARG:HH12	67:PB:47:ARG:HH11	1.61	0.48
74:WB:11:LEU:HA	74:WB:14:ILE:HG12	1.94	0.48
12:L:24:LEU:HD11	12:L:86:TRP:CG	2.48	0.48
13:M:93:LYS:NZ	48:WA:4179:C:OP1	2.37	0.48
20:T:19:LEU:HD22	20:T:78:PHE:H	1.78	0.48
24:X:59:ARG:HD2	48:WA:209:U:H5'	1.94	0.48
48:WA:164:G:H2'	48:WA:165:A:H8	1.79	0.48
48:WA:3601:A:H2'	48:WA:3602:G:H8	1.78	0.48
48:WA:3872:C:H2'	48:WA:3873:A:H8	1.79	0.48
48:WA:3952:U:H2'	48:WA:3953:G:C8	2.48	0.48
48:WA:4950:C:OP2	48:WA:4951:G:O2'	2.24	0.48
51:ZA:564:A:H2'	51:ZA:565:G:O4'	2.13	0.48
51:ZA:1203:G:H2'	51:ZA:1204:A:H8	1.74	0.48
51:ZA:1275:G:N2	51:ZA:1506:A:OP2	2.46	0.48
52:AB:41:ARG:HE	52:AB:45:GLY:HA2	1.78	0.48
62:KB:16:PHE:HE2	62:KB:89:ILE:HG22	1.79	0.48
84:GC:234:ASP:HB2	84:GC:252:THR:HB	1.94	0.48
4:D:53:VAL:HG11	4:D:159:VAL:HA	1.96	0.48
10:J:35:ARG:NH1	10:J:126:TYR:OH	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:163:LYS:NZ	48:WA:4911:A:OP1	2.42	0.48
26:Z:103:VAL:HG12	26:Z:108:TYR:HB2	1.95	0.48
32:FA:66:ARG:NH2	48:WA:2519:A:O2'	2.46	0.48
48:WA:1974:G:H2'	48:WA:1975:G:O4'	2.13	0.48
48:WA:2485:G:H2'	48:WA:2486:A:H8	1.79	0.48
48:WA:4631:U:H2'	48:WA:4632:G:H8	1.79	0.48
48:WA:4706:C:H2'	48:WA:4707:A:C8	2.49	0.48
51:ZA:373:G:OP1	63:LB:137:THR:OG1	2.27	0.48
51:ZA:582:U:H2'	51:ZA:583:A:H5''	1.95	0.48
51:ZA:1220:A:N3	51:ZA:1677:U:O2'	2.38	0.48
51:ZA:1277:C:OP1	62:KB:51:SER:OG	2.28	0.48
54:CB:201:GLY:O	61:JB:54:ARG:NH1	2.47	0.48
56:EB:18:TRP:HB3	56:EB:20:LEU:HD13	1.94	0.48
88:HC:266:ARG:NH1	88:HC:268:GLU:OE2	2.46	0.48
8:H:24:THR:HG21	8:H:35:ARG:HE	1.79	0.48
39:MA:15:ARG:NH2	51:ZA:1183:A:OP1	2.46	0.48
40:NA:69:ARG:HG3	40:NA:82:MET:HE1	1.95	0.48
46:UA:69:A:H2'	46:UA:70:A:C8	2.48	0.48
48:WA:1263:G:H2'	48:WA:1264:G:C8	2.48	0.48
48:WA:2896:A:H2'	48:WA:2897:A:C8	2.49	0.48
48:WA:3635:C:H2'	48:WA:3636:G:C8	2.49	0.48
49:XA:57:C:H2'	49:XA:58:A:H8	1.78	0.48
51:ZA:128:U:H3'	51:ZA:129:C:H6	1.78	0.48
51:ZA:916:A:C5	65:NB:73:ARG:HD3	2.48	0.48
54:CB:192:LEU:HB3	54:CB:227:ARG:HB3	1.96	0.48
4:D:15:ARG:HH11	48:WA:1745:A:H1'	1.77	0.48
7:G:191:ALA:O	7:G:195:THR:OG1	2.28	0.48
10:J:46:GLN:NE2	10:J:73:THR:O	2.43	0.48
18:R:98:ARG:NH2	48:WA:750:G:O6	2.46	0.48
25:Y:51:ARG:HB2	25:Y:65:ARG:HE	1.78	0.48
44:SA:51:C:H2'	44:SA:52:G:H8	1.79	0.48
48:WA:739:C:O2'	48:WA:742:G:OP1	2.29	0.48
48:WA:4116:C:H2'	48:WA:4117:G:C8	2.49	0.48
48:WA:4529:G:OP2	48:WA:4529:G:N2	2.44	0.48
51:ZA:326:C:O2	51:ZA:327:G:N1	2.47	0.48
51:ZA:1798:C:H2'	51:ZA:1799:G:O4'	2.14	0.48
2:B:14:LEU:O	48:WA:4589:G:O2'	2.26	0.48
13:M:44:ARG:NH1	48:WA:280:G:OP2	2.42	0.48
19:S:130:ARG:HH21	48:WA:1730:U:H1'	1.78	0.48
35:IA:52:LYS:HG2	35:IA:55:ARG:HH22	1.78	0.48
48:WA:408:A:O2'	48:WA:411:G:OP2	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:2081:G:H2'	48:WA:2082:U:C6	2.49	0.48
48:WA:2541:C:H2'	48:WA:2542:C:C6	2.48	0.48
48:WA:3719:A:H2'	48:WA:3720:A:C8	2.49	0.48
48:WA:4275:A:H2'	48:WA:4276:A:C8	2.49	0.48
50:YA:9:A:H2'	50:YA:10:G:H8	1.78	0.48
51:ZA:562:U:OP1	61:JB:134:HIS:NE2	2.46	0.48
51:ZA:1670:C:H2'	51:ZA:1671:G:C8	2.49	0.48
64:MB:49:LEU:HB3	64:MB:111:VAL:HG13	1.95	0.48
79:BC:23:ARG:NH2	79:BC:29:ASN:OD1	2.40	0.48
15:O:71:ARG:HH21	15:O:138:VAL:HG23	1.78	0.48
19:S:91:VAL:HB	19:S:96:ILE:HD11	1.96	0.48
21:U:43:LYS:HD2	48:WA:4510:C:H5''	1.96	0.48
35:IA:13:ASN:ND2	48:WA:1620:G:OP1	2.42	0.48
48:WA:287:U:H2'	48:WA:288:G:C8	2.48	0.48
48:WA:4194:A:H2'	48:WA:4195:C:H6	1.79	0.48
51:ZA:1528:G:H2'	51:ZA:1529:C:C6	2.49	0.48
51:ZA:1541:G:H4'	71:TB:15:VAL:HG11	1.96	0.48
64:MB:42:LEU:O	64:MB:72:HIS:ND1	2.47	0.48
4:D:166:ALA:HB1	4:D:171:LEU:HD12	1.96	0.48
5:E:71:TYR:HA	5:E:74:LYS:HE2	1.96	0.48
6:F:154:TYR:OH	6:F:187:GLU:OE2	2.32	0.48
7:G:106:ARG:NH1	48:WA:4165:U:OP1	2.45	0.48
7:G:126:ARG:NH2	48:WA:4164:C:O2	2.38	0.48
9:I:95:HIS:HB3	9:I:126:VAL:HG12	1.95	0.48
11:K:54:PRO:HG2	11:K:56:ARG:NH1	2.29	0.48
13:M:38:ARG:NH2	50:YA:142:U:OP1	2.43	0.48
20:T:90:TYR:O	20:T:94:ASN:ND2	2.39	0.48
26:Z:71:PRO:HG2	26:Z:108:TYR:HA	1.96	0.48
48:WA:711:G:H2'	48:WA:712:A:C8	2.49	0.48
48:WA:1516:U:H2'	48:WA:1517:A:C8	2.49	0.48
48:WA:1944:A:H2'	48:WA:1945:A:H8	1.79	0.48
51:ZA:1139:C:O2'	74:WB:20:ARG:NH1	2.46	0.48
51:ZA:1781:A:H2'	51:ZA:1782:G:H8	1.79	0.48
52:AB:164:ASN:O	52:AB:170:SER:OG	2.22	0.48
74:WB:27:ILE:HG13	74:WB:61:ILE:HB	1.96	0.48
15:O:96:VAL:HB	15:O:109:GLN:HE21	1.78	0.47
48:WA:1606:G:H2'	48:WA:1607:G:C8	2.49	0.47
48:WA:3699:U:O2'	48:WA:3819:A:OP2	2.28	0.47
48:WA:4406:U:O2'	48:WA:4408:U:O4	2.31	0.47
51:ZA:952:G:H2'	51:ZA:953:C:C6	2.49	0.47
71:TB:96:SER:HB3	71:TB:99:VAL:HG22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:136:ARG:HG3	10:J:157:ILE:HD11	1.95	0.47
14:N:130:LYS:NZ	48:WA:2057:G:O5'	2.48	0.47
17:Q:42:ARG:NH2	48:WA:2526:U:OP1	2.47	0.47
17:Q:59:SER:HA	48:WA:2636:C:H5'	1.94	0.47
17:Q:121:HIS:ND1	48:WA:2666:G:OP2	2.47	0.47
37:KA:20:ASN:O	37:KA:41:ARG:NH1	2.46	0.47
37:KA:25:GLN:O	37:KA:28:TRP:NE1	2.46	0.47
48:WA:1872:C:H2'	48:WA:1873:A:H8	1.79	0.47
49:XA:64:G:H2'	49:XA:65:G:H8	1.79	0.47
51:ZA:1309:C:H5'	83:FC:105:TYR:CE1	2.49	0.47
53:BB:87:ILE:HG22	53:BB:101:HIS:HB2	1.96	0.47
80:CC:20:ARG:NH2	80:CC:25:GLY:O	2.46	0.47
86:b:60:MET:N	86:b:60:MET:SD	2.87	0.47
87:c:248:MET:HB3	87:c:250:PHE:HD2	1.79	0.47
2:B:228:TYR:O	48:WA:2837:A:O2'	2.31	0.47
5:E:96:THR:HG22	5:E:109:VAL:HG22	1.95	0.47
13:M:155:VAL:O	13:M:162:ARG:NH2	2.47	0.47
13:M:178:HIS:ND1	48:WA:68:U:OP1	2.38	0.47
14:N:85:ARG:HG3	14:N:99:LEU:HD11	1.95	0.47
48:WA:146:G:H2'	48:WA:147:A:H8	1.79	0.47
48:WA:955:G:H2'	48:WA:956:G:H8	1.79	0.47
48:WA:1292:G:H2'	48:WA:1293:G:H8	1.79	0.47
51:ZA:4:C:O2'	61:JB:18:ARG:NH2	2.46	0.47
51:ZA:1447:G:H2'	51:ZA:1448:A:C8	2.49	0.47
58:GB:198:ARG:O	58:GB:202:ASN:ND2	2.35	0.47
63:LB:59:LYS:HD3	63:LB:134:LEU:HB3	1.96	0.47
66:OB:146:ARG:HG3	78:AC:29:CYS:HB2	1.96	0.47
76:YB:102:THR:OG1	76:YB:107:ARG:NH2	2.47	0.47
2:B:254:ILE:HG21	2:B:262:VAL:HG22	1.96	0.47
3:C:306:ARG:HG2	48:WA:2101:C:H3'	1.95	0.47
48:WA:128:C:H2'	48:WA:129:C:C6	2.49	0.47
48:WA:1452:C:O2'	48:WA:2106:A:O2'	2.19	0.47
48:WA:1881:C:O2'	48:WA:1893:A:N3	2.43	0.47
48:WA:2745:A:H2'	48:WA:2746:A:C8	2.50	0.47
48:WA:3879:A:O2'	48:WA:4402:G:N2	2.47	0.47
48:WA:4423:C:N4	48:WA:4477:G:H22	2.09	0.47
56:EB:188:ASN:OD1	56:EB:245:ARG:NH2	2.48	0.47
58:GB:32:MET:HB2	58:GB:100:CYS:HB2	1.95	0.47
84:GC:91:ASP:OD2	84:GC:93:THR:OG1	2.25	0.47
1:A:236:GLY:N	48:WA:3689:A:O2'	2.47	0.47
13:M:184:ILE:HG23	13:M:194:ARG:HH22	1.77	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:12:LEU:HB2	25:Y:81:MET:HB3	1.95	0.47
25:Y:88:ASP:O	25:Y:121:ARG:NH1	2.40	0.47
28:BA:39:ARG:NH2	28:BA:63:TYR:OH	2.47	0.47
30:DA:100:ALA:O	30:DA:108:ARG:NH2	2.48	0.47
44:SA:21:A:O2'	44:SA:22:A:O5'	2.25	0.47
48:WA:692:C:H2'	48:WA:693:A:C8	2.50	0.47
48:WA:2542:C:H2'	48:WA:2543:G:H8	1.80	0.47
48:WA:2557:G:H2'	48:WA:2558:G:H8	1.79	0.47
48:WA:2591:C:N3	48:WA:2759:A:N6	2.62	0.47
48:WA:2892:C:H42	48:WA:3613:A:H61	1.62	0.47
48:WA:4968:A:H2'	48:WA:4969:A:C8	2.50	0.47
50:YA:84:A:H1'	50:YA:85:U:H4'	1.97	0.47
51:ZA:547:G:H2'	51:ZA:549:C:H6	1.79	0.47
51:ZA:1275:G:H22	51:ZA:1506:A:P	2.38	0.47
52:AB:122:LEU:HB2	52:AB:142:LEU:HD21	1.96	0.47
64:MB:33:ARG:NH2	64:MB:89:VAL:O	2.47	0.47
87:c:250:PHE:HA	87:c:253:PHE:HD2	1.80	0.47
4:D:156:GLY:HA2	4:D:181:PRO:HD3	1.95	0.47
14:N:65:ASN:ND2	48:WA:4567:C:OP1	2.38	0.47
23:W:150:ALA:HB1	23:W:155:ILE:HG13	1.97	0.47
41:OA:17:ARG:NH2	48:WA:1579:G:OP1	2.42	0.47
48:WA:1176:G:H2'	48:WA:1177:G:C8	2.50	0.47
48:WA:1384:G:H2'	48:WA:1385:G:H8	1.79	0.47
51:ZA:107:A:H2'	51:ZA:108:G:H8	1.79	0.47
51:ZA:1418:C:N4	51:ZA:1422:G:OP1	2.48	0.47
72:UB:67:LYS:NZ	72:UB:78:ASP:OD1	2.35	0.47
76:YB:102:THR:O	76:YB:107:ARG:NH2	2.48	0.47
84:GC:257:LYS:HG2	84:GC:269:GLU:HG3	1.96	0.47
1:A:241:ARG:NH1	48:WA:3661:G:OP1	2.48	0.47
4:D:33:ARG:HH21	49:XA:7:G:H4'	1.80	0.47
4:D:126:THR:HG22	4:D:128:ASP:H	1.79	0.47
6:F:33:ARG:NH1	48:WA:1274:C:OP2	2.48	0.47
6:F:222:LYS:HE3	48:WA:1909:A:H4'	1.97	0.47
9:I:61:SER:HA	9:I:126:VAL:HG23	1.96	0.47
10:J:112:HIS:HE1	10:J:125:ILE:HA	1.79	0.47
11:K:31:ARG:NH1	48:WA:337:U:OP1	2.42	0.47
11:K:35:ARG:NH2	48:WA:337:U:OP1	2.48	0.47
23:W:120:ASP:OD1	23:W:120:ASP:N	2.46	0.47
24:X:82:ILE:HD12	24:X:85:VAL:HG21	1.95	0.47
29:CA:118:GLN:OE1	48:WA:5057:G:N2	2.47	0.47
30:DA:64:LYS:NZ	48:WA:2081:G:OP2	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:1496:U:H2'	48:WA:1497:G:C8	2.50	0.47
48:WA:1813:G:H2'	48:WA:1814:C:H6	1.80	0.47
48:WA:2082:U:H2'	48:WA:2083:C:C6	2.50	0.47
48:WA:2260:C:H5''	48:WA:2261:G:C8	2.50	0.47
48:WA:2363:G:O2'	48:WA:3861:G:O6	2.28	0.47
48:WA:2377:A:H2'	48:WA:2378:A:C8	2.47	0.47
48:WA:3719:A:H2'	48:WA:3720:A:H8	1.79	0.47
48:WA:3725:A:H2'	48:WA:3726:A:C8	2.50	0.47
51:ZA:322:C:H2'	51:ZA:323:C:H5''	1.96	0.47
51:ZA:918:U:O2'	74:WB:56:HIS:O	2.33	0.47
51:ZA:1098:C:H2'	51:ZA:1099:G:C8	2.49	0.47
51:ZA:1139:C:N4	51:ZA:1149:A:H62	2.13	0.47
51:ZA:1217:A:H2'	51:ZA:1218:C:C6	2.50	0.47
54:CB:191:VAL:HG11	54:CB:236:PHE:HA	1.96	0.47
61:JB:133:ARG:HB3	61:JB:143:ASN:HD22	1.80	0.47
68:QB:126:VAL:HG12	68:QB:127:ASP:H	1.79	0.47
71:TB:42:HIS:HB3	71:TB:93:SER:HB3	1.97	0.47
1:A:14:SER:OG	48:WA:1630:C:OP1	2.33	0.47
4:D:17:GLN:NE2	19:S:22:HIS:O	2.45	0.47
4:D:223:PHE:HB3	4:D:226:TYR:HB2	1.96	0.47
8:H:95:VAL:HB	38:LA:56:LEU:HB3	1.96	0.47
9:I:31:ILE:HB	9:I:66:GLU:HB2	1.97	0.47
24:X:83:GLU:HG3	24:X:84:ARG:HG3	1.96	0.47
39:MA:11:ARG:NH2	51:ZA:1184:G:OP1	2.48	0.47
48:WA:2522:C:H2'	48:WA:2523:G:C8	2.48	0.47
51:ZA:544:G:H2'	51:ZA:545:A:C8	2.50	0.47
51:ZA:1755:C:H2'	51:ZA:1756:C:C6	2.49	0.47
52:AB:24:HIS:HB3	52:AB:51:LEU:HD21	1.97	0.47
55:DB:114:ARG:HB2	62:KB:22:VAL:HG11	1.97	0.47
2:B:252:ALA:HB1	48:WA:4526:G:N3	2.30	0.47
8:H:91:LYS:HB2	8:H:183:GLU:HB3	1.97	0.47
23:W:65:ALA:HB2	33:GA:69:LEU:HD11	1.97	0.47
25:Y:46:ILE:HG23	25:Y:68:ILE:HG23	1.96	0.47
29:CA:33:ILE:HD11	29:CA:41:ARG:HB3	1.97	0.47
36:JA:47:ILE:HG22	36:JA:49:ASP:H	1.79	0.47
48:WA:4450:G:H5''	48:WA:4451:A:H5'	1.96	0.47
50:YA:153:C:H2'	50:YA:154:G:C8	2.50	0.47
51:ZA:613:G:N1	51:ZA:629:A:OP2	2.48	0.47
51:ZA:1345:G:OP1	51:ZA:1688:C:O2'	2.32	0.47
52:AB:128:ARG:HG2	52:AB:153:PRO:HD2	1.96	0.47
73:VB:11:LEU:HD23	73:VB:11:LEU:H	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:59:ASP:OD1	12:L:59:ASP:N	2.47	0.47
29:CA:26:THR:OG1	29:CA:85:ARG:NH1	2.42	0.47
30:DA:89:LEU:HD13	30:DA:118:LEU:HD22	1.96	0.47
45:TA:7:A:O2'	45:TA:49:C:OP2	2.32	0.47
48:WA:1446:G:N2	48:WA:2113:U:O2	2.31	0.47
48:WA:1972:A:H5'	86:b:37:SER:HB3	1.97	0.47
48:WA:2002:G:O2'	48:WA:2003:G:N7	2.46	0.47
48:WA:3723:U:H2'	48:WA:3724:G:H8	1.80	0.47
48:WA:3788:U:OP1	48:WA:4552:G:O2'	2.26	0.47
51:ZA:348:A:H2'	51:ZA:349:A:C8	2.50	0.47
55:DB:66:GLU:HG2	55:DB:107:LEU:HD21	1.97	0.47
60:IB:162:LEU:HD11	60:IB:191:GLU:HG2	1.97	0.47
62:KB:11:ILE:HD11	62:KB:45:VAL:HG22	1.96	0.47
66:OB:106:LYS:HD2	66:OB:135:ILE:HG22	1.97	0.47
2:B:55:HIS:CD2	48:WA:4629:U:HO2'	2.32	0.46
5:E:216:THR:HG23	5:E:219:TYR:H	1.80	0.46
14:N:55:LEU:HD23	14:N:58:LEU:HD12	1.97	0.46
25:Y:67:LYS:NZ	48:WA:2575:A:OP1	2.42	0.46
48:WA:164:G:H2'	48:WA:165:A:C8	2.50	0.46
48:WA:169:A:N1	48:WA:267:G:C6	2.83	0.46
48:WA:1819:U:H2'	48:WA:1820:G:O4'	2.15	0.46
48:WA:2581:G:N2	48:WA:2584:A:OP2	2.31	0.46
50:YA:45:C:H2'	50:YA:46:G:H8	1.80	0.46
51:ZA:626:G:N2	51:ZA:626:G:OP2	2.48	0.46
51:ZA:694:G:N1	51:ZA:732:U:O4	2.48	0.46
51:ZA:1113:A:H2'	51:ZA:1114:U:C6	2.50	0.46
57:FB:127:ARG:O	80:CC:26:GLN:NE2	2.49	0.46
84:GC:61:GLY:HA3	84:GC:90:TRP:HZ2	1.80	0.46
2:B:254:ILE:HG23	2:B:266:VAL:HG11	1.97	0.46
12:L:29:ASP:OD1	12:L:30:VAL:N	2.47	0.46
14:N:68:ARG:NH2	48:WA:4566:A:OP1	2.48	0.46
41:OA:30:GLU:HA	41:OA:33:GLN:HG2	1.96	0.46
45:TA:49:C:H2'	45:TA:50:A:C8	2.49	0.46
48:WA:478:G:H2'	48:WA:479:G:H8	1.80	0.46
48:WA:2449:U:H1'	48:WA:2746:A:H2	1.80	0.46
51:ZA:1386:A:OP2	55:DB:198:SER:OG	2.30	0.46
58:GB:165:GLU:OE1	58:GB:167:LYS:NZ	2.39	0.46
2:B:298:LEU:HD13	2:B:300:LYS:HE3	1.97	0.46
3:C:49:ARG:HD3	48:WA:349:A:C8	2.50	0.46
14:N:178:ARG:NH1	14:N:182:GLU:OE2	2.48	0.46
15:O:93:ASN:O	15:O:109:GLN:NE2	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:92:ASP:OD2	25:Y:94:THR:OG1	2.23	0.46
30:DA:46:ARG:NH1	48:WA:1884:U:OP2	2.48	0.46
48:WA:262:G:H2'	48:WA:263:G:H8	1.77	0.46
48:WA:270:U:H2'	48:WA:271:C:C6	2.50	0.46
48:WA:3913:C:H2'	48:WA:3914:U:H6	1.80	0.46
48:WA:4460:C:H2'	48:WA:4461:U:C6	2.51	0.46
50:YA:60:G:O6	50:YA:96:C:O2'	2.32	0.46
55:DB:58:GLU:OE2	55:DB:114:ARG:NE	2.48	0.46
75:XB:46:HIS:HB3	75:XB:101:LEU:HD11	1.97	0.46
76:YB:103:SER:HB3	76:YB:106:GLN:HG2	1.97	0.46
11:K:18:TRP:NE1	48:WA:1518:G:O2'	2.48	0.46
11:K:60:ARG:NH2	11:K:67:HIS:O	2.47	0.46
31:EA:43:LEU:HB2	31:EA:109:ARG:HH12	1.81	0.46
48:WA:1330:G:O2'	48:WA:2351:A:OP1	2.34	0.46
48:WA:2413:C:H2'	48:WA:2414:A:C8	2.51	0.46
48:WA:2850:G:O2'	48:WA:3840:U:O4	2.30	0.46
48:WA:3895:C:H2'	48:WA:3896:A:C8	2.51	0.46
48:WA:4509:A:H2'	48:WA:4510:C:C6	2.51	0.46
55:DB:133:GLY:HA2	55:DB:139:GLN:HE21	1.79	0.46
65:NB:5:HIS:HB3	65:NB:117:LEU:HD13	1.98	0.46
65:NB:87:ASP:OD1	65:NB:87:ASP:N	2.48	0.46
71:TB:116:ASP:OD1	71:TB:117:GLN:N	2.49	0.46
14:N:113:ASP:OD1	14:N:114:LYS:N	2.49	0.46
27:AA:47:LYS:NZ	48:WA:1466:C:O3'	2.48	0.46
48:WA:2626:G:H2'	48:WA:2627:U:C6	2.51	0.46
48:WA:4262:U:H2'	48:WA:4263:C:C6	2.50	0.46
48:WA:4690:C:H2'	48:WA:4691:U:C6	2.51	0.46
49:XA:62:U:O2'	49:XA:64:G:O4'	2.33	0.46
51:ZA:1797:U:H2'	51:ZA:1798:C:C6	2.50	0.46
58:GB:74:ARG:HG2	58:GB:96:SER:HB3	1.98	0.46
84:GC:107:ASP:N	84:GC:107:ASP:OD1	2.48	0.46
4:D:40:ASP:HB2	4:D:43:LYS:HG2	1.96	0.46
4:D:146:LEU:HD21	4:D:159:VAL:HG22	1.98	0.46
17:Q:84:THR:HG22	48:WA:2866:A:H5''	1.97	0.46
18:R:1:MET:HE2	18:R:43:ARG:HG3	1.97	0.46
33:GA:96:ASN:N	33:GA:96:ASN:OD1	2.47	0.46
34:HA:60:LEU:HA	34:HA:63:VAL:HG22	1.97	0.46
48:WA:1292:G:H2'	48:WA:1293:G:C8	2.51	0.46
48:WA:1405:G:H2'	48:WA:1406:G:C8	2.50	0.46
48:WA:2599:G:H2'	48:WA:2600:A:C8	2.51	0.46
48:WA:4929:G:H5''	48:WA:4930:C:H5	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:527:C:H2'	51:ZA:528:A:C8	2.49	0.46
51:ZA:1324:G:O2'	51:ZA:1510:G:O2'	2.31	0.46
80:CC:36:ASP:OD1	80:CC:36:ASP:N	2.46	0.46
4:D:54:ARG:NH2	4:D:147:ASP:OD2	2.47	0.46
7:G:139:VAL:HG11	7:G:238:LYS:HG3	1.98	0.46
10:J:57:VAL:HG12	10:J:60:PHE:H	1.81	0.46
12:L:39:ASP:HB2	12:L:47:ARG:HE	1.80	0.46
14:N:12:ARG:HD3	14:N:37:ARG:HH11	1.79	0.46
14:N:34:VAL:HG22	14:N:103:LYS:HB3	1.97	0.46
18:R:111:ARG:NH2	48:WA:2064:C:O2'	2.49	0.46
48:WA:715:G:H2'	48:WA:716:G:H8	1.80	0.46
48:WA:2575:A:N7	48:WA:2763:U:O4	2.49	0.46
48:WA:2745:A:H2'	48:WA:2746:A:H8	1.80	0.46
48:WA:4110:G:H2'	48:WA:4111:G:C8	2.48	0.46
56:EB:204:SER:OG	56:EB:205:PHE:N	2.48	0.46
64:MB:22:LEU:HD13	64:MB:89:VAL:HA	1.98	0.46
88:HC:272:LEU:HB3	88:HC:302:ALA:HB3	1.98	0.46
3:C:110:ARG:NH1	48:WA:1510:A:OP1	2.46	0.46
4:D:146:LEU:HD22	4:D:163:LEU:HD13	1.97	0.46
22:V:82:ILE:HG12	58:GB:131:ARG:HB2	1.97	0.46
45:TA:23:A:H2'	45:TA:24:G:H8	1.81	0.46
48:WA:655:C:H2'	48:WA:656:C:H6	1.81	0.46
48:WA:1825:G:H2'	48:WA:1826:G:C8	2.51	0.46
48:WA:1881:C:H2'	48:WA:1882:G:O4'	2.16	0.46
48:WA:2413:C:O2'	48:WA:2528:C:O2	2.24	0.46
48:WA:2494:C:H2'	48:WA:2495:G:C8	2.51	0.46
51:ZA:196:C:H2'	51:ZA:197:U:C6	2.51	0.46
51:ZA:209:A:H2'	51:ZA:210:U:O4'	2.16	0.46
51:ZA:293:C:H5''	63:LB:38:LYS:HD2	1.98	0.46
61:JB:114:VAL:HG21	61:JB:135:ILE:HD13	1.97	0.46
86:b:52:VAL:HB	86:b:90:PHE:HB2	1.98	0.46
9:I:42:LYS:HB2	9:I:45:GLU:HG3	1.98	0.46
9:I:51:HIS:CD2	9:I:168:SER:HB2	2.51	0.46
13:M:49:ARG:HH21	48:WA:114:G:P	2.39	0.46
25:Y:54:THR:H	25:Y:57:MET:HE2	1.81	0.46
35:IA:82:THR:OG1	50:YA:94:G:N2	2.44	0.46
48:WA:169:A:C2	48:WA:267:G:C2	3.04	0.46
48:WA:1300:C:H2'	48:WA:1301:G:H8	1.81	0.46
48:WA:4143:G:N2	48:WA:4146:G:OP2	2.34	0.46
48:WA:4725:A:H2'	48:WA:4726:A:C8	2.51	0.46
51:ZA:551:U:H2'	51:ZA:552:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:582:U:OP1	61:JB:162:ARG:NH1	2.48	0.46
51:ZA:1535:U:O4	57:FB:159:ARG:NE	2.49	0.46
68:QB:122:TYR:HA	68:QB:126:VAL:HG23	1.97	0.46
76:YB:62:THR:HA	76:YB:69:THR:HG22	1.98	0.46
84:GC:104:HIS:NE2	84:GC:122:SER:OG	2.47	0.46
88:HC:364:HIS:CD2	88:HC:421:LEU:HG	2.51	0.46
16:P:178:ARG:N	26:Z:51:GLY:HA2	2.31	0.46
32:FA:24:ARG:NH2	48:WA:2615:C:OP1	2.49	0.46
48:WA:1543:C:H1'	48:WA:2450:G:H21	1.81	0.46
48:WA:1593:U:H3	48:WA:4557:U:H5''	1.81	0.46
48:WA:3609:U:H2'	48:WA:3610:A:C8	2.51	0.46
48:WA:4165:U:H5'	48:WA:4166:C:H5''	1.97	0.46
51:ZA:1406:G:H2'	51:ZA:1407:U:H6	1.81	0.46
51:ZA:1828:C:H2'	51:ZA:1829:G:C8	2.50	0.46
56:EB:151:ASP:OD1	58:GB:216:ARG:NH1	2.49	0.46
80:CC:12:ALA:HB1	80:CC:32:VAL:HB	1.98	0.46
2:B:116:ARG:NH2	48:WA:4989:C:OP1	2.49	0.45
10:J:24:ILE:HG12	10:J:128:LEU:HB3	1.98	0.45
48:WA:674:C:H2'	48:WA:675:G:H8	1.81	0.45
48:WA:986:U:H2'	48:WA:987:C:C6	2.51	0.45
48:WA:1307:C:OP1	50:YA:7:U:O2'	2.34	0.45
48:WA:1448:C:H2'	48:WA:1449:C:C6	2.51	0.45
48:WA:2027:A:H8	48:WA:2028:A:H1'	1.81	0.45
48:WA:4588:G:O6	48:WA:4719:A:N6	2.49	0.45
48:WA:4929:G:H5''	48:WA:4930:C:C5	2.51	0.45
51:ZA:1431:G:H2'	51:ZA:1432:U:C6	2.50	0.45
57:FB:122:ARG:HE	80:CC:59:LEU:HD21	1.81	0.45
14:N:27:VAL:HG13	14:N:98:ALA:HB1	1.98	0.45
16:P:133:GLY:O	16:P:136:THR:OG1	2.25	0.45
48:WA:462:G:H2'	48:WA:463:A:C8	2.52	0.45
48:WA:2642:G:H2'	48:WA:2643:A:C8	2.51	0.45
48:WA:3925:A:H2'	48:WA:3926:C:C6	2.51	0.45
48:WA:4321:C:H2'	48:WA:4322:G:H8	1.81	0.45
51:ZA:996:A:H2'	51:ZA:997:A:C8	2.51	0.45
51:ZA:1010:G:H2'	51:ZA:1011:A:C8	2.51	0.45
51:ZA:1801:A:H2'	51:ZA:1802:C:C6	2.51	0.45
53:BB:136:ARG:HB2	53:BB:218:LEU:HD11	1.99	0.45
63:LB:13:GLN:HB2	63:LB:16:ILE:HG12	1.97	0.45
72:UB:46:LYS:HD2	72:UB:101:ILE:HD13	1.98	0.45
87:c:247:ASP:HB2	88:HC:383:SER:N	2.32	0.45
88:HC:346:ILE:O	88:HC:397:GLY:N	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:65:ALA:HB2	4:D:74:ILE:HD13	1.98	0.45
8:H:120:GLU:HG2	48:WA:4613:A:H2	1.81	0.45
15:O:69:HIS:NE2	15:O:139:ASP:O	2.38	0.45
48:WA:36:U:OP1	48:WA:1653:G:N2	2.42	0.45
48:WA:1806:A:H4'	48:WA:1807:A:O5'	2.16	0.45
48:WA:4147:C:H2'	48:WA:4148:G:H8	1.81	0.45
51:ZA:1221:G:H2'	51:ZA:1222:G:H8	1.81	0.45
65:NB:29:THR:OG1	65:NB:31:ASP:OD1	2.31	0.45
66:OB:54:CYS:HB2	66:OB:84:ARG:HG2	1.98	0.45
69:RB:102:THR:O	69:RB:105:MET:HG3	2.17	0.45
86:b:16:LYS:HB3	86:b:16:LYS:HE2	1.66	0.45
6:F:235:ARG:HB2	6:F:238:GLN:HB2	1.98	0.45
14:N:37:ARG:HH21	14:N:108:ILE:HD11	1.82	0.45
30:DA:99:ILE:HG21	30:DA:108:ARG:HG2	1.98	0.45
37:KA:24:PRO:HG2	37:KA:27:ILE:HB	1.99	0.45
48:WA:162:A:H2'	48:WA:163:A:C8	2.52	0.45
48:WA:1247:C:H2'	48:WA:1248:G:C8	2.50	0.45
48:WA:1295:G:OP2	48:WA:1295:G:N2	2.36	0.45
48:WA:2413:C:H2'	48:WA:2414:A:H8	1.80	0.45
50:YA:110:U:O2'	50:YA:111:U:O4'	2.34	0.45
51:ZA:1093:A:H2'	51:ZA:1094:C:C6	2.51	0.45
58:GB:7:PHE:HB3	58:GB:10:THR:HG22	1.99	0.45
63:LB:45:LYS:HE2	63:LB:45:LYS:HB2	1.79	0.45
73:VB:59:ILE:HD12	79:BC:3:LEU:HD11	1.97	0.45
1:A:183:GLY:HA2	48:WA:1615:A:H5'	1.99	0.45
3:C:7:LEU:HB3	3:C:21:ASN:HB3	1.98	0.45
3:C:152:LEU:HD23	3:C:251:ILE:HG12	1.98	0.45
10:J:27:GLY:HA2	10:J:68:ILE:HG23	1.97	0.45
29:CA:23:ARG:HG2	29:CA:121:ASN:HA	1.99	0.45
30:DA:78:LEU:HD11	48:WA:2326:C:H4'	1.98	0.45
42:PA:38:PHE:O	42:PA:45:HIS:NE2	2.31	0.45
43:RA:66:ASN:OD1	43:RA:66:ASN:N	2.50	0.45
45:TA:21:A:N1	45:TA:46:G:O2'	2.47	0.45
48:WA:1306:C:H2'	48:WA:1307:C:C6	2.52	0.45
48:WA:2083:C:H2'	48:WA:2084:G:C8	2.51	0.45
51:ZA:671:A:H4'	51:ZA:672:A:H5''	1.99	0.45
51:ZA:917:U:H2'	51:ZA:918:U:C6	2.51	0.45
51:ZA:1486:A:O3'	54:CB:121:ARG:NH2	2.50	0.45
58:GB:39:ASP:N	58:GB:39:ASP:OD1	2.49	0.45
81:DC:33:LYS:HE2	81:DC:34:TYR:CZ	2.51	0.45
83:FC:100:LEU:HD23	83:FC:103:LEU:HD23	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:GC:152:SER:N	84:GC:168:CYS:O	2.49	0.45
84:GC:226:HIS:NE2	84:GC:229:THR:OG1	2.48	0.45
2:B:224:LYS:HG2	2:B:340:THR:HB	1.99	0.45
6:F:130:ASN:ND2	48:WA:1729:U:OP1	2.49	0.45
9:I:87:ILE:HG12	9:I:138:ILE:HG12	1.98	0.45
12:L:47:ARG:HH22	12:L:69:ARG:HA	1.81	0.45
19:S:44:GLY:HA2	19:S:95:HIS:HB3	1.99	0.45
48:WA:1685:U:H2'	48:WA:1686:A:C8	2.52	0.45
48:WA:2516:G:O2'	48:WA:2745:A:N6	2.49	0.45
48:WA:3912:C:H2'	48:WA:3913:C:C6	2.52	0.45
48:WA:4637:A:O2'	48:WA:4639:G:OP1	2.33	0.45
64:MB:40:LYS:HG2	64:MB:45:ARG:HD2	1.99	0.45
72:UB:32:LEU:HD21	72:UB:87:ARG:HG2	1.98	0.45
1:A:13:GLY:O	1:A:17:ARG:NE	2.35	0.45
48:WA:229:G:H2'	48:WA:230:G:H8	1.82	0.45
48:WA:680:C:H2'	48:WA:681:G:C8	2.51	0.45
48:WA:910:G:H2'	48:WA:911:G:H8	1.82	0.45
48:WA:1474:C:H2'	48:WA:1475:U:C6	2.52	0.45
48:WA:4682:G:H2'	48:WA:4683:A:C8	2.51	0.45
51:ZA:991:G:C6	51:ZA:1134:G:H4'	2.52	0.45
51:ZA:1103:C:H2'	51:ZA:1104:G:C8	2.51	0.45
51:ZA:1716:C:H2'	51:ZA:1717:C:H6	1.81	0.45
69:RB:132:ARG:H	69:RB:132:ARG:HD2	1.81	0.45
74:WB:55:ASP:OD1	74:WB:56:HIS:N	2.47	0.45
84:GC:87:LEU:HD22	84:GC:120:ILE:HD11	1.98	0.45
84:GC:163:PRO:HB2	84:GC:179:LEU:HB3	1.98	0.45
1:A:28:ARG:HB3	1:A:123:ARG:HB3	1.99	0.45
1:A:181:LYS:HB2	48:WA:1579:G:C5	2.52	0.45
1:A:198:ARG:NH2	48:WA:3690:U:OP2	2.50	0.45
48:WA:65:A:N6	48:WA:75:G:H1'	2.32	0.45
48:WA:254:G:H2'	48:WA:255:C:C6	2.51	0.45
48:WA:422:C:H2'	48:WA:423:G:H8	1.81	0.45
48:WA:727:G:H2'	48:WA:728:C:C6	2.52	0.45
48:WA:1848:G:H2'	48:WA:1849:C:H6	1.82	0.45
48:WA:1999:U:O2'	86:b:44:ARG:NH2	2.50	0.45
48:WA:3612:A:O2'	60:IB:92:ARG:NH2	2.50	0.45
48:WA:3875:G:H2'	48:WA:3876:G:C8	2.52	0.45
48:WA:3912:C:H2'	48:WA:3913:C:H6	1.81	0.45
48:WA:4461:U:H2'	48:WA:4462:U:C6	2.52	0.45
48:WA:4663:G:N2	48:WA:5006:C:O3'	2.50	0.45
48:WA:4747:G:H1	48:WA:4957:A:N6	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:XA:63:C:H5'	49:XA:64:G:H5''	1.98	0.45
51:ZA:1144:A:H2'	51:ZA:1145:A:C8	2.52	0.45
51:ZA:1712:A:H2'	51:ZA:1713:C:C6	2.52	0.45
59:HB:258:GLU:N	59:HB:258:GLU:OE1	2.46	0.45
74:WB:50:PHE:HB3	74:WB:63:VAL:HG13	1.98	0.45
78:AC:11:ALA:HB3	78:AC:33:ASP:HB2	1.98	0.45
3:C:230:LEU:HD21	3:C:239:LYS:HD2	1.99	0.45
11:K:124:LEU:HD11	33:GA:119:TYR:HB2	1.98	0.45
13:M:4:TYR:OH	48:WA:151:G:OP2	2.27	0.45
14:N:65:ASN:OD1	14:N:67:SER:OG	2.25	0.45
19:S:4:THR:O	19:S:9:ARG:NE	2.50	0.45
23:W:52:LEU:HD22	23:W:54:LEU:HD12	1.99	0.45
27:AA:110:ALA:HB1	48:WA:1273:G:H5'	1.98	0.45
30:DA:124:ASN:OD1	30:DA:124:ASN:N	2.49	0.45
43:RA:47:ALA:O	43:RA:50:THR:OG1	2.35	0.45
48:WA:212:A:H2'	48:WA:213:G:H8	1.82	0.45
48:WA:260:C:H2'	48:WA:261:G:C8	2.52	0.45
48:WA:1808:G:H2'	48:WA:1809:C:C6	2.52	0.45
48:WA:3709:U:H2'	48:WA:3710:C:C6	2.52	0.45
51:ZA:128:U:H3'	51:ZA:129:C:C6	2.51	0.45
51:ZA:155:G:H4'	58:GB:15:LEU:HD22	1.98	0.45
53:BB:106:THR:HG22	53:BB:108:ASP:H	1.80	0.45
54:CB:199:PRO:O	54:CB:202:THR:OG1	2.34	0.45
70:SB:120:HIS:CE1	70:SB:124:ARG:HD2	2.52	0.45
88:HC:267:VAL:O	88:HC:305:GLY:N	2.37	0.45
5:E:161:ARG:NH2	48:WA:4947:G:O2'	2.50	0.45
5:E:179:THR:O	5:E:179:THR:OG1	2.35	0.45
13:M:53:TYR:HB2	13:M:133:ILE:HD13	1.99	0.45
13:M:185:GLY:HA2	48:WA:78:U:H5''	1.99	0.45
14:N:121:PRO:HD3	18:R:168:THR:HG22	1.99	0.45
18:R:17:LEU:HD11	19:S:136:ARG:HH21	1.83	0.45
26:Z:117:LEU:HB3	26:Z:140:VAL:HG21	1.99	0.45
44:SA:11:U:H2'	44:SA:12:G:C8	2.52	0.45
48:WA:129:C:H2'	48:WA:130:C:C6	2.52	0.45
48:WA:652:C:H2'	48:WA:653:G:C8	2.52	0.45
48:WA:2001:A:H2'	48:WA:2002:G:C5	2.52	0.45
48:WA:2902:U:H2'	48:WA:2903:G:C8	2.52	0.45
49:XA:11:A:N1	49:XA:66:G:O2'	2.47	0.45
51:ZA:15:U:H2'	51:ZA:16:G:O4'	2.17	0.45
51:ZA:1595:U:OP1	77:ZB:102:LYS:NZ	2.45	0.45
51:ZA:1614:A:H2'	51:ZA:1615:U:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:MB:41:ALA:HA	64:MB:45:ARG:HB2	1.99	0.45
69:RB:73:LEU:O	69:RB:76:GLU:HG3	2.16	0.45
75:XB:52:LEU:HD11	75:XB:71:ARG:HD3	1.99	0.45
84:GC:124:SER:OG	84:GC:125:ARG:N	2.50	0.45
3:C:192:GLY:O	3:C:195:LYS:NZ	2.50	0.44
7:G:159:THR:HG22	7:G:248:HIS:NE2	2.33	0.44
24:X:91:ASN:OD1	24:X:92:GLY:N	2.50	0.44
46:UA:12:G:H2'	46:UA:13:U:O4'	2.16	0.44
46:UA:43:A:H3'	46:UA:44:A:C8	2.52	0.44
48:WA:251:C:H2'	48:WA:252:C:C6	2.52	0.44
48:WA:520:C:H2'	48:WA:521:U:C5	2.52	0.44
48:WA:2609:C:H2'	48:WA:2610:G:H8	1.83	0.44
48:WA:3857:C:H2'	48:WA:3858:A:H8	1.81	0.44
48:WA:4962:G:H2'	48:WA:4963:G:C8	2.51	0.44
49:XA:12:U:OP2	49:XA:67:C:O2'	2.35	0.44
51:ZA:568:C:H42	51:ZA:582:U:H3	1.63	0.44
51:ZA:743:U:H3	51:ZA:798:G:N2	2.14	0.44
52:AB:157:VAL:O	73:VB:65:SER:OG	2.33	0.44
52:AB:158:ASP:OD1	73:VB:60:ARG:NH1	2.43	0.44
54:CB:108:LYS:HB2	54:CB:233:LEU:HD22	1.98	0.44
56:EB:175:PHE:HE1	56:EB:198:ARG:HD2	1.82	0.44
69:RB:17:ILE:HD11	69:RB:54:VAL:HA	1.99	0.44
86:b:128:THR:OG1	86:b:129:GLY:N	2.44	0.44
48:WA:2610:G:H2'	48:WA:2611:G:H8	1.82	0.44
48:WA:2760:G:H2'	48:WA:2761:G:C8	2.52	0.44
48:WA:4565:U:C2	48:WA:4566:A:C8	3.05	0.44
48:WA:4752:G:H2'	48:WA:4753:G:H8	1.81	0.44
50:YA:153:C:H2'	50:YA:154:G:H8	1.83	0.44
51:ZA:1230:C:H2'	51:ZA:1231:C:H6	1.82	0.44
51:ZA:1440:C:O2'	51:ZA:1441:U:O4'	2.35	0.44
51:ZA:1576:G:H2'	51:ZA:1577:G:C8	2.53	0.44
53:BB:180:ASP:OD1	53:BB:180:ASP:N	2.49	0.44
57:FB:142:SER:HB2	80:CC:50:VAL:HG22	1.98	0.44
60:IB:26:LYS:O	60:IB:29:LEU:HB2	2.17	0.44
2:B:282:LYS:NZ	48:WA:4676:C:O2'	2.49	0.44
48:WA:1174:G:H2'	48:WA:1175:G:C8	2.53	0.44
48:WA:3724:G:H2'	48:WA:3725:A:C8	2.52	0.44
48:WA:3870:G:H22	48:WA:3902:G:H1'	1.83	0.44
51:ZA:1198:G:H2'	51:ZA:1199:A:C8	2.52	0.44
51:ZA:1383:A:H4'	55:DB:194:LEU:HG	1.99	0.44
51:ZA:1419:C:H4'	51:ZA:1420:G:C2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:1780:G:H2'	51:ZA:1781:A:C8	2.52	0.44
51:ZA:1802:C:H2'	51:ZA:1803:U:C6	2.53	0.44
62:KB:60:GLU:OE1	62:KB:69:TRP:NE1	2.42	0.44
68:QB:106:GLN:O	68:QB:110:ILE:HG22	2.17	0.44
70:SB:125:HIS:CE1	70:SB:131:VAL:HG21	2.52	0.44
15:O:151:ALA:HB3	15:O:172:PRO:HG2	2.00	0.44
35:IA:44:LYS:N	48:WA:22:G:OP1	2.42	0.44
48:WA:1781:U:H2'	48:WA:1782:A:C8	2.53	0.44
48:WA:2851:A:O2'	48:WA:2857:G:N7	2.46	0.44
51:ZA:495:U:O2'	56:EB:27:PHE:O	2.32	0.44
51:ZA:1643:U:H2'	51:ZA:1644:C:C6	2.52	0.44
51:ZA:1778:C:H2'	51:ZA:1779:G:C8	2.52	0.44
54:CB:196:ILE:HB	54:CB:223:TYR:HB2	2.00	0.44
54:CB:214:LEU:HD22	54:CB:219:ILE:HD12	1.99	0.44
56:EB:128:LYS:HG2	56:EB:140:VAL:HB	1.99	0.44
59:HB:274:LEU:HD21	59:HB:316:ARG:HD2	1.99	0.44
66:OB:34:PHE:HB3	66:OB:41:PHE:HB2	1.99	0.44
86:b:59:THR:OG1	86:b:60:MET:SD	2.75	0.44
88:HC:286:THR:O	88:HC:452:THR:OG1	2.33	0.44
88:HC:363:CYS:HB3	88:HC:424:PHE:HB3	1.98	0.44
2:B:286:LYS:HB3	2:B:332:MET:HB3	2.00	0.44
11:K:64:VAL:HG12	48:WA:71:C:H4'	1.99	0.44
13:M:8:GLN:NE2	48:WA:279:A:OP2	2.49	0.44
25:Y:22:LYS:NZ	25:Y:129:TRP:O	2.49	0.44
25:Y:41:ALA:HB2	25:Y:77:TYR:HE1	1.83	0.44
30:DA:82:VAL:HG13	30:DA:114:ARG:HG2	1.99	0.44
37:KA:36:ARG:NH2	48:WA:413:G:O4'	2.51	0.44
43:RA:137:GLN:HE21	43:RA:137:GLN:HB3	1.59	0.44
48:WA:56:A:H2'	48:WA:57:G:C8	2.53	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:3738:A:H2'	48:WA:3739:A:C8	2.52	0.44
48:WA:3877:G:N1	48:WA:3881:G:OP1	2.45	0.44
48:WA:4230:G:O2'	48:WA:4375:G:O6	2.33	0.44
48:WA:4644:U:H2'	48:WA:4645:G:H8	1.82	0.44
51:ZA:152:U:O4'	58:GB:132:ARG:NH1	2.51	0.44
51:ZA:527:C:H4'	61:JB:121:LYS:HD2	1.98	0.44
51:ZA:1656:G:O6	51:ZA:1668:U:O4	2.35	0.44
62:KB:37:ASP:OD1	62:KB:37:ASP:N	2.51	0.44
72:UB:46:LYS:HD3	72:UB:97:ILE:HG22	1.99	0.44
21:U:107:ASN:HD21	21:U:111:GLU:HB2	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:109:LEU:HD22	24:X:115:ARG:HH12	1.83	0.44
25:Y:25:ILE:HA	25:Y:43:VAL:HG12	1.98	0.44
33:GA:109:ARG:HH22	48:WA:267:G:P	2.41	0.44
34:HA:68:ARG:NH2	34:HA:71:LYS:HD2	2.33	0.44
48:WA:7:C:H2'	48:WA:8:U:C6	2.53	0.44
48:WA:190:G:H2'	48:WA:191:G:H8	1.82	0.44
48:WA:971:A:H5'	48:WA:972:C:H2'	1.98	0.44
48:WA:1263:G:H2'	48:WA:1264:G:H8	1.83	0.44
48:WA:1311:C:H2'	48:WA:1312:C:C6	2.52	0.44
48:WA:1444:C:N3	48:WA:1445:A:N6	2.65	0.44
48:WA:1506:G:H2'	48:WA:1507:C:C6	2.52	0.44
48:WA:1848:G:H2'	48:WA:1849:C:C6	2.53	0.44
48:WA:4942:C:H5'	48:WA:4943:G:H5''	1.99	0.44
49:XA:92:C:H2'	49:XA:93:G:C8	2.50	0.44
50:YA:102:G:OP2	50:YA:104:A:O2'	2.26	0.44
51:ZA:219:U:H2'	51:ZA:220:U:C6	2.53	0.44
51:ZA:1112:U:H2'	51:ZA:1113:A:C8	2.53	0.44
51:ZA:1688:C:H2'	51:ZA:1689:C:H6	1.83	0.44
57:FB:55:ARG:HG2	68:QB:151:ARG:HD3	1.99	0.44
58:GB:2:LYS:HD3	58:GB:15:LEU:HD21	1.99	0.44
61:JB:29:LEU:HB3	82:EC:115:PHE:HE2	1.83	0.44
5:E:48:ARG:HG2	48:WA:986:U:OP1	2.17	0.44
6:F:148:SER:OG	6:F:244:ARG:NH2	2.46	0.44
6:F:221:LYS:HB3	6:F:230:GLY:HA2	1.99	0.44
9:I:88:ARG:HH21	9:I:173:PHE:HD2	1.64	0.44
12:L:12:VAL:O	12:L:58:THR:OG1	2.25	0.44
29:CA:68:LEU:HA	29:CA:108:TYR:HB2	2.00	0.44
48:WA:6:C:H2'	48:WA:7:C:H6	1.83	0.44
48:WA:65:A:H61	48:WA:75:G:H1'	1.82	0.44
48:WA:424:U:H2'	48:WA:425:U:C6	2.53	0.44
48:WA:1300:C:H2'	48:WA:1301:G:C8	2.53	0.44
48:WA:1678:C:N4	48:WA:4380:A:H2'	2.32	0.44
48:WA:1874:G:O2'	48:WA:4221:A:N3	2.48	0.44
48:WA:2092:U:OP1	48:WA:2268:C:N4	2.51	0.44
48:WA:3873:A:H2'	48:WA:3874:A:C8	2.52	0.44
48:WA:4738:C:H42	48:WA:4966:C:H42	1.66	0.44
48:WA:4977:G:O2'	48:WA:4979:A:N6	2.47	0.44
51:ZA:12:U:H2'	51:ZA:13:C:H6	1.83	0.44
56:EB:126:VAL:HA	56:EB:141:THR:HA	1.99	0.44
73:VB:73:ALA:HB1	73:VB:78:ILE:HB	1.99	0.44
1:A:230:PRO:HG2	1:A:233:ARG:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:82:PRO:HG3	2:B:171:LEU:HD21	2.00	0.44
9:I:66:GLU:OE1	9:I:69:ARG:NH1	2.50	0.44
9:I:116:ARG:HH12	48:WA:4201:C:H42	1.66	0.44
16:P:181:ARG:NH2	48:WA:4368:A:OP1	2.50	0.44
46:UA:64:G:H2'	46:UA:65:G:H8	1.82	0.44
48:WA:1302:G:H2'	48:WA:1303:C:C6	2.52	0.44
48:WA:1496:U:H2'	48:WA:1497:G:H8	1.83	0.44
48:WA:1727:U:H2'	48:WA:1728:U:C6	2.52	0.44
48:WA:2560:C:H2'	48:WA:2561:G:H8	1.81	0.44
48:WA:2589:A:O2'	48:WA:2590:C:O4'	2.33	0.44
48:WA:2640:G:H1	48:WA:2699:A:H61	1.66	0.44
48:WA:5032:U:H2'	48:WA:5033:G:H8	1.83	0.44
51:ZA:77:A:H2	58:GB:175:LYS:HG3	1.83	0.44
51:ZA:929:G:H2'	51:ZA:930:C:O4'	2.18	0.44
52:AB:124:VAL:HG21	52:AB:134:LEU:HD21	1.99	0.44
53:BB:126:ASP:N	53:BB:126:ASP:OD1	2.51	0.44
54:CB:128:VAL:HG11	54:CB:155:ILE:HG12	1.99	0.44
55:DB:134:LEU:HD12	55:DB:236:ILE:HG12	2.00	0.44
59:HB:318:VAL:HG23	59:HB:330:VAL:HG13	2.00	0.44
67:PB:81:ARG:NH1	67:PB:120:SER:OG	2.51	0.44
75:XB:39:ASN:OD1	75:XB:42:GLY:N	2.50	0.44
88:HC:382:ARG:HD3	88:HC:382:ARG:HA	1.76	0.44
1:A:82:ILE:HD11	1:A:99:GLY:HA3	2.00	0.44
2:B:384:GLU:OE2	22:V:14:TYR:OH	2.30	0.44
12:L:86:TRP:O	12:L:89:THR:OG1	2.34	0.44
16:P:79:THR:HB	16:P:136:THR:HG22	1.99	0.44
19:S:5:LYS:HD2	48:WA:4304:U:H4'	2.00	0.44
48:WA:325:U:H2'	48:WA:326:C:C6	2.53	0.44
48:WA:460:C:H2'	48:WA:461:G:H8	1.83	0.44
48:WA:677:C:H2'	48:WA:678:G:C8	2.52	0.44
48:WA:1678:C:H41	48:WA:4380:A:H2'	1.82	0.44
48:WA:2664:G:H2'	48:WA:2665:G:H8	1.83	0.44
51:ZA:375:U:H2'	51:ZA:376:A:C8	2.53	0.44
51:ZA:1236:G:O2'	67:PB:131:PRO:O	2.26	0.44
54:CB:199:PRO:HG3	61:JB:58:ARG:HD3	1.99	0.44
4:D:176:SER:HB3	48:WA:4325:A:H4'	2.00	0.43
22:V:46:PRO:HB2	22:V:54:LEU:HD12	1.99	0.43
28:BA:50:ASN:OD1	28:BA:51:ASN:N	2.51	0.43
45:TA:41:U:H4'	57:FB:198:ARG:HD3	2.00	0.43
48:WA:1414:G:H2'	48:WA:1415:C:C6	2.53	0.43
48:WA:2297:C:H2'	48:WA:2298:G:C8	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:4391:C:H2'	48:WA:4392:A:C8	2.53	0.43
48:WA:4920:C:H2'	48:WA:4921:G:C8	2.50	0.43
51:ZA:921:G:C5	74:WB:28:ARG:HD3	2.53	0.43
60:IB:89:GLU:O	60:IB:93:THR:HG22	2.18	0.43
77:ZB:79:ILE:HB	77:ZB:83:LEU:HD23	2.00	0.43
88:HC:392:LYS:HG3	88:HC:393:PHE:CD2	2.53	0.43
6:F:189:LEU:HD21	6:F:207:LEU:HD21	2.00	0.43
6:F:240:ASN:O	6:F:244:ARG:HG2	2.17	0.43
8:H:103:VAL:HG11	8:H:144:LEU:HD21	1.99	0.43
10:J:84:GLU:OE2	10:J:92:TYR:OH	2.27	0.43
11:K:87:HIS:HB3	11:K:90:VAL:HG23	2.00	0.43
20:T:80:LYS:HG2	20:T:110:TYR:CE2	2.53	0.43
20:T:84:LYS:HB2	20:T:110:TYR:CE2	2.53	0.43
30:DA:67:LYS:HG2	30:DA:68:HIS:CD2	2.54	0.43
40:NA:52:THR:HG22	48:WA:43:U:H4'	2.00	0.43
48:WA:475:G:H2'	48:WA:476:G:C8	2.53	0.43
48:WA:1087:C:H2'	48:WA:1088:C:C6	2.54	0.43
48:WA:4072:U:H2'	48:WA:4073:U:C6	2.53	0.43
51:ZA:3:C:O2	61:JB:17:ARG:NH2	2.49	0.43
51:ZA:202:G:H2'	51:ZA:203:G:C8	2.53	0.43
59:HB:336:ARG:HD2	59:HB:363:VAL:HG23	2.00	0.43
2:B:252:ALA:HB1	48:WA:4526:G:C2	2.52	0.43
3:C:13:GLU:OE1	3:C:161:TYR:OH	2.27	0.43
4:D:136:ASP:OD1	4:D:136:ASP:N	2.47	0.43
9:I:86:HIS:HB3	9:I:139:ARG:HG2	2.00	0.43
10:J:112:HIS:HD1	10:J:126:TYR:H	1.66	0.43
17:Q:99:MET:HB3	17:Q:103:ARG:NH1	2.33	0.43
18:R:95:ARG:NH2	48:WA:1953:G:O2'	2.51	0.43
34:HA:31:GLY:HA3	48:WA:310:G:C4	2.53	0.43
48:WA:2628:U:H1'	48:WA:2631:C:H41	1.83	0.43
48:WA:2650:G:H2'	48:WA:2651:G:H8	1.83	0.43
48:WA:4128:C:H5''	48:WA:4129:A:H5''	2.00	0.43
48:WA:4652:G:H4'	48:WA:5010:C:H4'	2.00	0.43
51:ZA:65:C:C2	58:GB:133:LEU:HD22	2.53	0.43
51:ZA:1093:A:O3'	74:WB:28:ARG:NH2	2.51	0.43
51:ZA:1671:G:H2'	51:ZA:1672:U:C6	2.53	0.43
51:ZA:1803:U:H2'	51:ZA:1804:U:C6	2.54	0.43
57:FB:18:LYS:HE3	57:FB:46:ALA:HB3	2.01	0.43
59:HB:285:ALA:HB3	59:HB:301:PHE:HB2	2.01	0.43
66:OB:142:ARG:O	78:AC:22:ARG:NH1	2.51	0.43
75:XB:94:ILE:HG12	75:XB:125:VAL:HG21	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:GC:164:ILE:HG23	84:GC:176:VAL:HG13	2.00	0.43
6:F:181:TYR:CZ	6:F:202:GLU:HG2	2.52	0.43
9:I:51:HIS:HD2	9:I:168:SER:HB2	1.84	0.43
17:Q:95:TRP:CE2	48:WA:1574:U:H4'	2.54	0.43
22:V:20:ARG:HD3	22:V:30:GLN:HG3	2.01	0.43
30:DA:33:ARG:NE	48:WA:1305:A:N3	2.67	0.43
36:JA:29:LYS:HB2	36:JA:29:LYS:HE3	1.85	0.43
45:TA:50:A:H2'	45:TA:51:G:H8	1.83	0.43
48:WA:425:U:H2'	48:WA:426:A:C8	2.53	0.43
48:WA:469:C:H2'	48:WA:470:A:C8	2.54	0.43
48:WA:1266:C:H2'	48:WA:1267:G:C8	2.53	0.43
48:WA:1398:G:O2'	48:WA:1470:C:O2'	2.31	0.43
48:WA:2287:A:H2'	48:WA:2288:G:H8	1.83	0.43
48:WA:4580:G:H2'	48:WA:4581:U:C6	2.53	0.43
51:ZA:419:G:N2	51:ZA:661:U:O2	2.51	0.43
51:ZA:1408:U:H2'	51:ZA:1409:A:C8	2.54	0.43
73:VB:10:ASP:N	73:VB:10:ASP:OD1	2.51	0.43
86:b:69:LEU:HD22	86:b:73:PRO:HA	1.99	0.43
2:B:31:SER:OG	48:WA:4716:C:OP1	2.30	0.43
3:C:140:LYS:HE3	3:C:245:HIS:HB2	2.00	0.43
16:P:75:ARG:HA	16:P:78:LYS:HD3	2.00	0.43
20:T:29:VAL:HG21	20:T:68:SER:HB2	1.99	0.43
48:WA:416:U:H4'	48:WA:2332:G:H4'	2.01	0.43
48:WA:1734:C:H2'	48:WA:1735:G:C8	2.54	0.43
48:WA:1812:G:H1	48:WA:1830:C:H42	1.65	0.43
48:WA:2664:G:H2'	48:WA:2665:G:C8	2.54	0.43
51:ZA:610:G:H2'	51:ZA:611:G:H8	1.82	0.43
51:ZA:1809:A:H2'	51:ZA:1810:U:C6	2.54	0.43
51:ZA:1855:G:OP2	66:OB:147:ARG:NH1	2.51	0.43
53:BB:146:ARG:HB2	53:BB:149:GLN:HB2	2.01	0.43
55:DB:178:GLY:HA3	55:DB:220:LEU:HD12	2.01	0.43
57:FB:30:ILE:HB	57:FB:36:GLN:HG2	2.01	0.43
64:MB:81:ASP:HB3	64:MB:84:LYS:HB2	2.01	0.43
74:WB:14:ILE:HG22	74:WB:25:VAL:HG11	1.99	0.43
77:ZB:92:LEU:HD22	77:ZB:109:TYR:HE1	1.84	0.43
8:H:59:LYS:HE2	8:H:66:GLU:HB3	2.00	0.43
12:L:46:ARG:HH11	48:WA:942:U:H5	1.66	0.43
14:N:14:HIS:CE1	14:N:119:VAL:HG13	2.53	0.43
14:N:51:LYS:NZ	14:N:144:GLU:OE1	2.37	0.43
16:P:54:SER:OG	16:P:57:ASN:OD1	2.28	0.43
16:P:104:ARG:NH2	48:WA:1355:G:N7	2.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:179:GLY:H	26:Z:51:GLY:HA2	1.84	0.43
17:Q:102:LEU:HD22	17:Q:138:LEU:HD22	2.00	0.43
30:DA:107:ASN:OD1	30:DA:107:ASN:N	2.52	0.43
31:EA:3:GLY:O	48:WA:4947:G:N1	2.50	0.43
48:WA:1346:C:H2'	48:WA:1347:A:C8	2.53	0.43
48:WA:1619:G:H1'	48:WA:2515:A:N6	2.33	0.43
48:WA:4171:G:H4'	48:WA:4173:C:C2	2.53	0.43
48:WA:4770:G:H2'	48:WA:4771:G:H8	1.75	0.43
51:ZA:14:C:H2'	51:ZA:15:U:C6	2.53	0.43
51:ZA:618:C:H2'	51:ZA:619:A:O4'	2.19	0.43
51:ZA:649:U:H2'	51:ZA:650:A:C8	2.50	0.43
51:ZA:1221:G:H2'	51:ZA:1222:G:C8	2.53	0.43
52:AB:127:PRO:HG3	52:AB:146:ALA:HB1	1.99	0.43
58:GB:50:VAL:HG11	58:GB:111:LEU:HD13	2.01	0.43
80:CC:33:GLU:HG2	80:CC:41:SER:HB3	2.01	0.43
1:A:243:THR:HB	48:WA:3750:A:H5''	2.00	0.43
2:B:240:LEU:HB3	2:B:244:THR:HG21	2.00	0.43
12:L:10:GLY:O	12:L:62:LEU:N	2.39	0.43
25:Y:25:ILE:HG12	25:Y:43:VAL:HG12	2.00	0.43
35:IA:34:CYS:HB3	35:IA:39:TYR:H	1.84	0.43
44:SA:25:C:H2'	44:SA:26:A:H8	1.84	0.43
48:WA:325:U:H2'	48:WA:326:C:H6	1.84	0.43
48:WA:2732:U:H2'	48:WA:2733:C:C6	2.54	0.43
48:WA:3913:C:H2'	48:WA:3914:U:C6	2.53	0.43
49:XA:3:C:H2'	49:XA:4:U:C6	2.54	0.43
49:XA:3:C:H2'	49:XA:4:U:H6	1.84	0.43
50:YA:141:C:H2'	50:YA:142:U:C6	2.54	0.43
51:ZA:674:C:H2'	51:ZA:675:U:C6	2.54	0.43
51:ZA:909:G:H2'	51:ZA:910:G:H8	1.83	0.43
51:ZA:1617:G:N2	51:ZA:1619:A:H3'	2.34	0.43
51:ZA:1862:G:N2	78:AC:76:SER:OG	2.52	0.43
54:CB:116:THR:OG1	54:CB:117:ARG:N	2.52	0.43
60:IB:157:LYS:NZ	60:IB:158:ILE:O	2.48	0.43
61:JB:111:GLN:HE21	61:JB:123:ILE:HG22	1.84	0.43
62:KB:22:VAL:HG22	62:KB:68:TYR:HD1	1.83	0.43
70:SB:60:THR:OG1	70:SB:62:ASP:OD1	2.30	0.43
71:TB:113:VAL:HG12	71:TB:123:LEU:HD23	2.01	0.43
86:b:47:LEU:HD13	86:b:51:ALA:HB3	2.01	0.43
1:A:30:ARG:O	1:A:163:ARG:NH2	2.50	0.43
41:OA:44:LYS:NZ	48:WA:2674:C:OP1	2.38	0.43
48:WA:1492:G:H2'	48:WA:1493:A:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:2097:A:H2'	48:WA:2098:G:C8	2.54	0.43
48:WA:2449:U:H2'	48:WA:2450:G:H8	1.83	0.43
48:WA:2609:C:H2'	48:WA:2610:G:C8	2.54	0.43
48:WA:3935:G:H2'	48:WA:3936:G:H8	1.83	0.43
48:WA:4265:C:H2'	48:WA:4266:G:O4'	2.19	0.43
51:ZA:28:U:H2'	51:ZA:29:G:H8	1.84	0.43
51:ZA:54:A:OP1	76:YB:111:LYS:NZ	2.34	0.43
51:ZA:681:U:H4'	75:XB:9:THR:HG22	1.99	0.43
51:ZA:1048:G:H21	51:ZA:1070:A:H62	1.66	0.43
51:ZA:1201:U:H2'	51:ZA:1202:U:C6	2.54	0.43
51:ZA:1513:C:H2'	51:ZA:1514:G:C8	2.52	0.43
51:ZA:1654:G:H2'	51:ZA:1655:C:C6	2.54	0.43
54:CB:72:ASP:OD2	54:CB:272:HIS:NE2	2.48	0.43
58:GB:58:LYS:HA	58:GB:107:SER:HB2	2.00	0.43
78:AC:44:ILE:HG21	78:AC:65:PRO:HG2	2.01	0.43
11:K:169:ILE:HG12	26:Z:123:ILE:HD11	2.01	0.43
15:O:91:ARG:NH1	48:WA:423:G:OP1	2.49	0.43
32:FA:9:ARG:HG2	32:FA:34:TYR:CZ	2.54	0.43
33:GA:89:ARG:O	33:GA:93:ARG:HG2	2.18	0.43
35:IA:55:ARG:NH2	48:WA:364:G:O6	2.48	0.43
40:NA:3:ASN:HA	40:NA:92:GLU:HG3	1.99	0.43
48:WA:92:C:OP2	48:WA:4343:C:O2'	2.33	0.43
48:WA:229:G:H2'	48:WA:230:G:C8	2.53	0.43
48:WA:1249:U:O4	48:WA:1268:G:O6	2.37	0.43
48:WA:1255:G:H1	48:WA:1262:G:N2	2.17	0.43
48:WA:2310:A:H4'	48:WA:2336:C:H4'	2.01	0.43
48:WA:2618:C:H2'	48:WA:2619:G:H8	1.84	0.43
48:WA:4993:U:H2'	48:WA:4994:G:C8	2.53	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:C6	2.54	0.43
51:ZA:495:U:H2'	51:ZA:496:C:O4'	2.19	0.43
51:ZA:527:C:O2'	61:JB:121:LYS:NZ	2.40	0.43
51:ZA:1461:G:O2'	51:ZA:1465:A:N6	2.51	0.43
51:ZA:1488:C:H3'	51:ZA:1489:A:H4'	2.00	0.43
51:ZA:1498:A:OP2	55:DB:65:ARG:NH2	2.47	0.43
51:ZA:1563:G:H5''	71:TB:121:ARG:NH1	2.34	0.43
55:DB:80:THR:HG21	72:UB:106:ILE:HD12	2.01	0.43
62:KB:1:MET:HG3	62:KB:47:LYS:HG3	2.01	0.43
64:MB:33:ARG:HH11	64:MB:91:LEU:HD13	1.82	0.43
72:UB:98:VAL:HG23	72:UB:101:ILE:HD11	2.00	0.43
1:A:10:LYS:NZ	48:WA:3689:A:OP2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:132:LYS:NZ	48:WA:4730:U:OP1	2.44	0.43
7:G:119:GLN:HG3	13:M:28:TRP:CH2	2.54	0.43
23:W:88:LYS:HA	23:W:91:GLU:HG2	2.01	0.43
25:Y:73:LYS:HD3	25:Y:75:TYR:CZ	2.54	0.43
28:BA:38:ILE:HD11	28:BA:46:VAL:HG21	2.00	0.43
28:BA:103:ASP:HB3	28:BA:106:ARG:HH21	1.83	0.43
43:RA:146:ARG:O	43:RA:149:HIS:ND1	2.36	0.43
48:WA:478:G:H2'	48:WA:479:G:C8	2.54	0.43
48:WA:1246:G:H2'	48:WA:1247:C:C6	2.54	0.43
48:WA:1428:G:N1	48:WA:1460:C:OP2	2.35	0.43
48:WA:2751:C:H2'	48:WA:2752:G:H8	1.83	0.43
48:WA:3738:A:H2'	48:WA:3739:A:H8	1.84	0.43
48:WA:3863:A:H2'	48:WA:3864:A:C8	2.53	0.43
48:WA:4577:G:N3	48:WA:5070:G:O2'	2.52	0.43
51:ZA:877:C:H2'	51:ZA:878:G:C8	2.54	0.43
58:GB:160:LYS:HD2	58:GB:161:PRO:HD2	2.01	0.43
61:JB:119:LEU:HB2	61:JB:159:PHE:CZ	2.54	0.43
66:OB:31:CYS:HB3	66:OB:44:VAL:HG22	2.01	0.43
13:M:108:ARG:HB2	13:M:161:MET:HE1	2.01	0.42
16:P:67:ILE:HD13	16:P:98:LEU:HD11	2.01	0.42
19:S:28:ALA:HA	19:S:31:MET:HG2	2.00	0.42
26:Z:2:PRO:HG3	48:WA:1511:C:H5''	2.01	0.42
29:CA:39:LYS:HE2	29:CA:40:LYS:HD3	2.01	0.42
48:WA:1343:U:H2'	48:WA:1344:A:C8	2.54	0.42
48:WA:1939:C:OP2	48:WA:1940:C:O2'	2.26	0.42
48:WA:2081:G:H2'	48:WA:2082:U:H6	1.83	0.42
48:WA:2592:G:H1'	48:WA:2758:G:N2	2.34	0.42
48:WA:2665:G:N2	48:WA:2678:A:O2'	2.48	0.42
48:WA:4956:G:H2'	48:WA:4957:A:C8	2.53	0.42
51:ZA:35:C:H5''	51:ZA:579:C:H5''	2.01	0.42
51:ZA:916:A:C6	65:NB:73:ARG:HD3	2.54	0.42
51:ZA:1556:A:H61	81:DC:14:PHE:HB3	1.84	0.42
51:ZA:1585:U:O2'	51:ZA:1587:G:OP2	2.30	0.42
54:CB:109:ILE:HD11	54:CB:151:ILE:HD11	2.01	0.42
56:EB:112:HIS:NE2	56:EB:237:SER:OG	2.46	0.42
57:FB:17:ILE:HG23	57:FB:19:LEU:HD11	2.00	0.42
61:JB:97:ILE:HA	61:JB:100:LEU:HD13	2.01	0.42
75:XB:124:LYS:HG2	75:XB:129:SER:HA	2.01	0.42
2:B:100:ARG:NE	48:WA:4913:A:OP2	2.49	0.42
3:C:71:ARG:HB2	3:C:73:VAL:HG22	2.01	0.42
6:F:99:GLY:HA2	48:WA:1879:G:H4'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:224:THR:HB	6:F:230:GLY:HA3	2.02	0.42
8:H:66:GLU:O	8:H:69:THR:OG1	2.35	0.42
18:R:35:PRO:HD2	18:R:39:VAL:HG21	2.01	0.42
24:X:2:LYS:HE3	24:X:2:LYS:HB3	1.89	0.42
41:OA:42:CYS:HB3	41:OA:60:CYS:HB2	2.01	0.42
48:WA:741:G:H2'	48:WA:742:G:H8	1.84	0.42
48:WA:2612:G:H2'	48:WA:2613:A:H8	1.84	0.42
48:WA:2626:G:H2'	48:WA:2627:U:H6	1.82	0.42
48:WA:4095:G:H22	48:WA:4117:G:H1	1.66	0.42
49:XA:4:U:H2'	49:XA:5:A:C8	2.54	0.42
51:ZA:1103:C:H2'	51:ZA:1104:G:H8	1.84	0.42
51:ZA:1617:G:N7	67:PB:47:ARG:NH1	2.67	0.42
65:NB:3:ARG:HB2	65:NB:6:ALA:HB3	2.01	0.42
86:b:112:ARG:NE	86:b:121:VAL:HG11	2.34	0.42
1:A:210:PRO:HG2	1:A:235:VAL:HG11	2.01	0.42
2:B:2:SER:N	48:WA:4522:G:H5'	2.33	0.42
5:E:146:SER:OG	31:EA:110:ILE:O	2.30	0.42
24:X:57:VAL:HB	24:X:63:LYS:HA	2.00	0.42
48:WA:127:G:H2'	48:WA:128:C:C6	2.55	0.42
48:WA:306:A:H2'	48:WA:307:A:C8	2.54	0.42
48:WA:1310:C:H2'	48:WA:1311:C:C6	2.54	0.42
48:WA:1647:C:H2'	48:WA:1648:A:C8	2.53	0.42
48:WA:2000:A:H1'	48:WA:2021:C:O2'	2.20	0.42
48:WA:2266:C:H2'	48:WA:2267:G:O4'	2.18	0.42
48:WA:2376:A:H2'	48:WA:2377:A:C8	2.55	0.42
48:WA:3709:U:H2'	48:WA:3710:C:H6	1.84	0.42
48:WA:4063:C:H2'	48:WA:4064:A:C8	2.54	0.42
48:WA:4091:G:H2'	48:WA:4092:G:H8	1.84	0.42
48:WA:4322:G:H2'	48:WA:4323:U:C6	2.55	0.42
48:WA:4454:U:H3	48:WA:4533:U:H3	1.67	0.42
51:ZA:1407:U:H2'	51:ZA:1408:U:C6	2.54	0.42
51:ZA:1842:C:H2'	51:ZA:1843:G:C8	2.54	0.42
52:AB:130:ASP:C	52:AB:133:PRO:HD2	2.44	0.42
53:BB:144:LYS:HD3	53:BB:208:HIS:HB3	2.01	0.42
55:DB:93:THR:HA	55:DB:96:VAL:HG12	2.01	0.42
84:GC:5:MET:HE3	84:GC:310:TRP:HB3	2.00	0.42
2:B:317:LEU:HB3	48:WA:5003:U:H4'	2.01	0.42
3:C:13:GLU:OE2	3:C:157:LYS:NZ	2.45	0.42
10:J:166:PHE:CE2	10:J:172:GLY:HA3	2.54	0.42
18:R:15:ARG:HH12	18:R:18:PRO:HG3	1.84	0.42
22:V:89:ASP:N	22:V:89:ASP:OD1	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:121:ARG:NH1	48:WA:194:C:O2'	2.41	0.42
32:FA:25:THR:HG23	32:FA:27:GLY:H	1.84	0.42
48:WA:913:U:H2'	48:WA:914:G:O4'	2.19	0.42
48:WA:2000:A:O2'	48:WA:2001:A:O4'	2.32	0.42
48:WA:2311:G:O2'	50:YA:18:U:O2	2.37	0.42
48:WA:2751:C:H2'	48:WA:2752:G:C8	2.55	0.42
48:WA:3672:C:H2'	48:WA:3673:G:C8	2.55	0.42
48:WA:4568:U:H2'	48:WA:4569:G:O4'	2.20	0.42
51:ZA:21:U:O2'	61:JB:17:ARG:O	2.37	0.42
51:ZA:162:C:H5''	58:GB:87:ARG:HH22	1.84	0.42
51:ZA:309:G:OP2	60:IB:55:TYR:OH	2.36	0.42
51:ZA:1202:U:H2'	51:ZA:1203:G:H8	1.84	0.42
51:ZA:1268:C:O2	67:PB:97:TYR:OH	2.37	0.42
51:ZA:1403:C:H42	51:ZA:1432:U:P	2.41	0.42
52:AB:89:LYS:NZ	69:RB:83:ASN:OD1	2.44	0.42
52:AB:109:THR:OG1	52:AB:136:GLU:OE1	2.31	0.42
54:CB:108:LYS:HD2	54:CB:233:LEU:HD13	2.01	0.42
71:TB:42:HIS:NE2	71:TB:43:LYS:HE3	2.35	0.42
1:A:219:ILE:HD11	48:WA:3691:G:H5'	2.01	0.42
3:C:159:GLU:HA	3:C:217:ILE:HB	2.02	0.42
4:D:36:LEU:HG	4:D:50:ARG:HD2	2.01	0.42
7:G:213:ASP:OD1	7:G:213:ASP:N	2.48	0.42
12:L:80:ALA:O	12:L:85:LYS:NZ	2.37	0.42
22:V:112:ALA:O	22:V:116:LYS:HG2	2.20	0.42
33:GA:84:ARG:NH2	48:WA:17:A:OP1	2.34	0.42
48:WA:2335:G:OP1	50:YA:20:A:O2'	2.38	0.42
51:ZA:85:A:H2'	51:ZA:86:C:H6	1.84	0.42
51:ZA:525:A:H2'	51:ZA:526:A:H8	1.85	0.42
52:AB:137:ALA:HA	52:AB:142:LEU:HB3	2.00	0.42
70:SB:22:GLY:HA2	70:SB:56:ALA:HB3	2.01	0.42
71:TB:7:LYS:HA	71:TB:11:GLN:HE22	1.85	0.42
84:GC:300:ALA:HB3	84:GC:310:TRP:HZ3	1.84	0.42
88:HC:240:ARG:HA	88:HC:241:PRO:HD3	1.91	0.42
88:HC:410:MET:HE2	88:HC:410:MET:HB3	1.93	0.42
3:C:218:VAL:O	3:C:222:ARG:HB3	2.19	0.42
5:E:175:LEU:HD21	48:WA:4943:G:C5	2.55	0.42
8:H:18:ILE:HG12	8:H:27:VAL:HG22	2.01	0.42
19:S:75:VAL:HG22	19:S:88:ARG:HG2	2.01	0.42
24:X:27:ARG:HB2	24:X:75:ARG:CZ	2.48	0.42
36:JA:24:LYS:HE2	36:JA:69:LEU:HD11	2.02	0.42
43:RA:76:SER:OG	48:WA:1976:U:OP1	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:494:G:H2'	48:WA:495:C:C6	2.54	0.42
48:WA:712:A:H2'	48:WA:713:C:C6	2.55	0.42
48:WA:1348:C:H2'	48:WA:1349:G:C8	2.54	0.42
48:WA:1664:C:H2'	48:WA:1665:C:H6	1.84	0.42
48:WA:2561:G:H2'	48:WA:2562:C:C6	2.54	0.42
48:WA:3767:G:OP1	48:WA:3812:C:N4	2.53	0.42
48:WA:4156:G:H2'	48:WA:4157:C:C6	2.54	0.42
48:WA:4910:G:H1'	48:WA:4915:G:H22	1.85	0.42
48:WA:5015:C:H4'	48:WA:5016:A:H5''	2.01	0.42
51:ZA:21:U:H2'	51:ZA:22:A:C8	2.55	0.42
51:ZA:388:U:H2'	51:ZA:389:A:C8	2.55	0.42
51:ZA:1318:G:H2'	51:ZA:1319:U:C6	2.54	0.42
66:OB:33:ILE:HD11	66:OB:119:LEU:HD21	2.02	0.42
69:RB:37:GLU:HG3	84:GC:150:TRP:HE1	1.83	0.42
70:SB:20:ILE:HD11	70:SB:33:ILE:HG13	2.01	0.42
2:B:122:TRP:CH2	2:B:127:LYS:HG2	2.54	0.42
8:H:89:ARG:NH1	8:H:147:GLU:OE2	2.53	0.42
11:K:60:ARG:NH2	48:WA:72:C:N3	2.67	0.42
43:RA:9:GLU:O	43:RA:65:GLN:NE2	2.53	0.42
46:UA:70:A:H2'	46:UA:71:A:O4'	2.20	0.42
48:WA:281:U:H2'	48:WA:282:C:H6	1.84	0.42
48:WA:1690:G:H2'	48:WA:1691:G:C8	2.54	0.42
48:WA:2701:C:H2'	48:WA:2702:G:H8	1.83	0.42
51:ZA:193:C:H2'	51:ZA:194:C:H6	1.85	0.42
51:ZA:1648:G:H22	51:ZA:1675:A:P	2.42	0.42
53:BB:94:LYS:HD2	53:BB:94:LYS:HA	1.90	0.42
58:GB:148:SER:OG	58:GB:151:ASP:OD2	2.33	0.42
70:SB:89:ASP:OD1	70:SB:89:ASP:N	2.51	0.42
75:XB:90:CYS:HB3	75:XB:130:LEU:HD11	2.02	0.42
84:GC:73:SER:OG	84:GC:117:ASN:ND2	2.39	0.42
86:b:112:ARG:HE	86:b:121:VAL:HG11	1.84	0.42
86:b:125:ALA:HA	86:b:218:GLY:HA2	2.02	0.42
2:B:252:ALA:HB3	48:WA:4459:U:O2	2.20	0.42
9:I:150:GLU:OE2	9:I:153:ARG:NH2	2.45	0.42
12:L:34:ASN:ND2	48:WA:1926:C:OP1	2.53	0.42
13:M:11:TRP:O	13:M:14:LYS:NZ	2.42	0.42
17:Q:165:LYS:HE2	17:Q:165:LYS:HB3	1.94	0.42
31:EA:83:MET:HE3	31:EA:83:MET:HB3	1.95	0.42
33:GA:34:ALA:HA	33:GA:37:THR:HG22	2.01	0.42
37:KA:2:SER:N	48:WA:2408:G:N7	2.68	0.42
39:MA:1:MET:HB2	51:ZA:1706:G:H5'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:475:G:H2'	48:WA:476:G:H8	1.83	0.42
48:WA:1755:G:H2'	48:WA:1756:U:C2	2.54	0.42
48:WA:3666:G:H2'	48:WA:3667:G:C8	2.53	0.42
51:ZA:1402:A:H5'	72:UB:51:LYS:HD2	2.00	0.42
51:ZA:1536:G:H2'	51:ZA:1537:A:H8	1.83	0.42
53:BB:35:ALA:HB2	53:BB:44:ILE:HD11	2.02	0.42
58:GB:5:ILE:HD12	58:GB:16:ILE:HD13	2.02	0.42
62:KB:53:LYS:HE2	62:KB:53:LYS:HB3	1.94	0.42
86:b:23:ASP:HB2	86:b:90:PHE:HB3	2.00	0.42
3:C:60:HIS:NE2	3:C:100:ARG:HD3	2.35	0.42
14:N:12:ARG:HB2	14:N:37:ARG:HD2	2.01	0.42
20:T:28:PRO:HB2	20:T:34:MET:HG2	2.01	0.42
23:W:56:ARG:HE	48:WA:14:C:P	2.43	0.42
29:CA:39:LYS:HE3	48:WA:2372:A:H5'	2.00	0.42
35:IA:2:THR:O	35:IA:7:SER:OG	2.27	0.42
48:WA:312:G:H1	48:WA:325:U:H3	1.68	0.42
48:WA:440:U:H2'	48:WA:441:G:C8	2.55	0.42
48:WA:1506:G:H2'	48:WA:1507:C:H6	1.84	0.42
48:WA:1788:A:H2'	48:WA:1791:C:C5	2.55	0.42
48:WA:2521:U:O2'	48:WA:2532:U:O2	2.34	0.42
48:WA:4194:A:H2'	48:WA:4195:C:C6	2.55	0.42
51:ZA:444:G:O6	60:IB:26:LYS:HE3	2.20	0.42
51:ZA:479:C:H2'	51:ZA:480:G:C8	2.55	0.42
51:ZA:561:A:H5''	61:JB:173:VAL:HG12	2.02	0.42
51:ZA:913:A:N6	59:HB:357:SER:O	2.53	0.42
51:ZA:1160:U:O4	75:XB:3:LYS:NZ	2.53	0.42
61:JB:149:VAL:HG11	61:JB:157:ILE:HD11	2.02	0.42
62:KB:64:TRP:CD2	81:DC:23:VAL:HG22	2.55	0.42
66:OB:127:GLY:HA2	78:AC:58:VAL:HG22	2.01	0.42
3:C:221:PHE:HB3	3:C:227:ILE:HG21	2.01	0.42
3:C:310:HIS:NE2	48:WA:2102:G:H2'	2.35	0.42
5:E:204:ILE:HD12	5:E:264:ILE:HG22	2.02	0.42
6:F:56:TYR:OH	6:F:188:ASP:OD1	2.29	0.42
6:F:70:MET:HA	6:F:73:MET:HG2	2.02	0.42
12:L:96:GLU:OE2	12:L:100:ARG:NH2	2.52	0.42
18:R:127:MET:HG2	19:S:153:PRO:HB2	2.02	0.42
21:U:87:SER:HA	21:U:97:TYR:HB3	2.02	0.42
30:DA:78:LEU:HB2	42:PA:20:ARG:HD2	2.02	0.42
43:RA:147:HIS:CD2	43:RA:148:PRO:HD3	2.55	0.42
50:YA:5:U:H2'	50:YA:6:C:H6	1.85	0.42
51:ZA:385:G:O2'	60:IB:10:LYS:NZ	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:442:C:N4	51:ZA:449:A:H62	2.16	0.42
51:ZA:666:U:H2'	51:ZA:667:U:C6	2.54	0.42
51:ZA:799:U:H2'	51:ZA:800:U:C6	2.55	0.42
51:ZA:808:A:H2	51:ZA:855:G:H22	1.67	0.42
51:ZA:1398:G:O3'	84:GC:88:ARG:NH2	2.53	0.42
51:ZA:1568:C:OP1	71:TB:96:SER:OG	2.33	0.42
56:EB:45:ILE:HA	56:EB:61:VAL:HG11	2.02	0.42
65:NB:83:ASP:OD1	65:NB:83:ASP:N	2.53	0.42
70:SB:48:ALA:HB2	70:SB:70:ILE:HG13	2.02	0.42
84:GC:90:TRP:NE1	84:GC:97:THR:OG1	2.53	0.42
87:c:245:ASP:HA	88:HC:382:ARG:HD2	2.02	0.42
4:D:279:ARG:HD2	48:WA:1183:U:H4'	2.01	0.41
12:L:4:ARG:NH2	48:WA:4767:G:O6	2.35	0.41
24:X:106:ILE:HG21	24:X:109:LEU:HD23	2.02	0.41
48:WA:175:C:H2'	48:WA:176:G:H8	1.85	0.41
48:WA:912:G:H2'	48:WA:913:U:H6	1.84	0.41
48:WA:981:C:H41	48:WA:1283:G:H21	1.68	0.41
48:WA:1192:U:H2'	48:WA:1193:G:N3	2.35	0.41
48:WA:1346:C:H2'	48:WA:1347:A:H8	1.85	0.41
48:WA:1481:G:H2'	48:WA:1482:C:C6	2.54	0.41
48:WA:1492:G:H2'	48:WA:1493:A:C8	2.54	0.41
48:WA:2635:U:H2'	48:WA:2636:C:C6	2.55	0.41
48:WA:2737:G:H2'	48:WA:2738:G:C8	2.52	0.41
48:WA:3713:A:O2'	48:WA:3715:U:OP2	2.27	0.41
48:WA:4993:U:O2'	48:WA:4994:G:H5'	2.20	0.41
51:ZA:388:U:H2'	51:ZA:389:A:H8	1.85	0.41
51:ZA:1673:U:H2'	51:ZA:1674:G:O4'	2.20	0.41
51:ZA:1736:G:H2'	51:ZA:1737:G:C8	2.55	0.41
51:ZA:1839:U:H2'	51:ZA:1840:U:C6	2.55	0.41
63:LB:12:LYS:HA	63:LB:56:ILE:HD13	2.01	0.41
76:YB:63:HIS:CE1	76:YB:68:LYS:HD2	2.55	0.41
3:C:278:ASN:OD1	3:C:279:LEU:N	2.54	0.41
5:E:149:PRO:HB2	5:E:206:ILE:HG21	2.02	0.41
12:L:31:ILE:H	12:L:36:ALA:HA	1.85	0.41
12:L:118:MET:HE1	48:WA:4930:C:O2	2.20	0.41
16:P:2:GLY:N	48:WA:2074:C:OP1	2.53	0.41
16:P:178:ARG:NH2	26:Z:46:ASP:OD1	2.52	0.41
21:U:87:SER:HB3	22:V:19:ARG:HH21	1.85	0.41
48:WA:2319:C:H2'	48:WA:2320:G:C8	2.55	0.41
48:WA:2561:G:H2'	48:WA:2562:C:H6	1.85	0.41
48:WA:2589:A:OP2	48:WA:2590:C:N4	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:3722:G:H22	48:WA:3735:A:H2	1.66	0.41
51:ZA:1858:G:N7	66:OB:146:ARG:NH1	2.68	0.41
54:CB:142:LYS:HG2	54:CB:153:GLY:HA3	2.01	0.41
55:DB:105:ARG:NE	62:KB:93:THR:O	2.43	0.41
76:YB:83:LYS:HD2	76:YB:91:LEU:HD22	2.02	0.41
76:YB:110:ARG:HA	76:YB:113:ARG:HD2	2.02	0.41
88:HC:338:ALA:HB2	88:HC:444:LYS:HD3	2.01	0.41
2:B:165:HIS:HA	2:B:179:HIS:O	2.21	0.41
2:B:242:ARG:NH2	48:WA:2858:C:O2	2.46	0.41
3:C:350:ARG:HD2	48:WA:725:C:OP1	2.20	0.41
5:E:158:GLY:O	5:E:161:ARG:HG3	2.19	0.41
11:K:91:ALA:HB1	11:K:96:ILE:HB	2.01	0.41
24:X:52:ASP:OD2	24:X:110:LYS:NZ	2.52	0.41
31:EA:50:VAL:HG22	31:EA:69:VAL:HG22	2.01	0.41
33:GA:109:ARG:NH2	48:WA:267:G:OP1	2.48	0.41
37:KA:44:TRP:CZ3	37:KA:45:ARG:HD3	2.54	0.41
45:TA:28:C:H2'	45:TA:29:A:C8	2.55	0.41
48:WA:440:U:H2'	48:WA:441:G:H8	1.84	0.41
48:WA:2540:U:H2'	48:WA:2541:C:C6	2.55	0.41
48:WA:2734:G:H2'	48:WA:2735:C:C6	2.55	0.41
48:WA:3779:G:O2'	48:WA:3817:G:O6	2.34	0.41
49:XA:58:A:H2'	49:XA:59:G:H8	1.85	0.41
51:ZA:558:G:H2'	51:ZA:559:G:C8	2.55	0.41
51:ZA:1096:G:H1	51:ZA:1136:U:H3	1.68	0.41
53:BB:71:LEU:HD23	53:BB:79:VAL:HG22	2.02	0.41
84:GC:79:LEU:HD11	84:GC:87:LEU:HD23	2.02	0.41
9:I:180:GLU:H	9:I:180:GLU:HG3	1.75	0.41
29:CA:37:GLY:O	29:CA:41:ARG:HG3	2.20	0.41
33:GA:87:LYS:HD3	33:GA:91:MET:HB3	2.02	0.41
44:SA:8:U:O2'	44:SA:21:A:N1	2.47	0.41
48:WA:675:G:H2'	48:WA:676:C:C6	2.55	0.41
48:WA:926:C:H2'	48:WA:927:C:C6	2.55	0.41
48:WA:4091:G:H2'	48:WA:4092:G:C8	2.55	0.41
48:WA:4131:G:O6	48:WA:4158:G:N2	2.53	0.41
48:WA:4239:C:OP1	48:WA:4329:C:O2'	2.35	0.41
51:ZA:1199:A:H2'	51:ZA:1200:A:C8	2.55	0.41
51:ZA:1406:G:N2	51:ZA:1441:U:O2	2.53	0.41
52:AB:184:ARG:HD3	52:AB:191:ARG:HG2	2.03	0.41
61:JB:124:HIS:CD2	82:EC:108:ARG:HE	2.38	0.41
63:LB:144:LYS:HB2	63:LB:144:LYS:HE3	1.84	0.41
67:PB:25:LEU:O	67:PB:28:MET:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:YB:110:ARG:NH1	76:YB:126:GLY:O	2.53	0.41
16:P:82:VAL:O	16:P:102:ALA:HA	2.20	0.41
28:BA:10:SER:OG	28:BA:11:LEU:N	2.53	0.41
29:CA:122:VAL:HG12	29:CA:124:GLU:H	1.84	0.41
36:JA:61:PRO:HA	36:JA:62:PRO:HD3	1.97	0.41
48:WA:474:C:H2'	48:WA:475:G:C8	2.56	0.41
48:WA:2564:G:N2	48:WA:2567:A:OP2	2.38	0.41
48:WA:2762:G:H4'	48:WA:2763:U:H5'	2.02	0.41
48:WA:3873:A:H2'	48:WA:3874:A:H8	1.86	0.41
48:WA:3929:U:H2'	48:WA:3930:A:C8	2.54	0.41
48:WA:4175:G:H2'	48:WA:4176:U:C6	2.55	0.41
49:XA:15:C:H2'	49:XA:16:A:C8	2.55	0.41
51:ZA:1543:U:P	71:TB:62:ARG:HH22	2.43	0.41
56:EB:221:ARG:O	56:EB:225:ILE:HG12	2.19	0.41
58:GB:167:LYS:HE2	58:GB:167:LYS:HB2	1.88	0.41
74:WB:3:ARG:HD3	74:WB:6:VAL:HG12	2.01	0.41
84:GC:265:ILE:HD12	84:GC:265:ILE:HA	1.97	0.41
3:C:119:GLN:NE2	48:WA:1352:C:O2	2.48	0.41
8:H:92:MET:HE2	8:H:179:ILE:HG22	2.03	0.41
17:Q:108:ARG:NH1	48:WA:2901:C:OP2	2.46	0.41
20:T:92:LYS:HD2	20:T:92:LYS:HA	1.87	0.41
24:X:113:LYS:NZ	50:YA:84:A:N1	2.68	0.41
48:WA:368:C:H2'	48:WA:369:G:C8	2.55	0.41
48:WA:441:G:H2'	48:WA:442:G:H8	1.85	0.41
48:WA:655:C:H2'	48:WA:656:C:C6	2.55	0.41
48:WA:1664:C:H2'	48:WA:1665:C:C6	2.55	0.41
48:WA:1740:A:H2'	48:WA:1741:G:H8	1.86	0.41
48:WA:2448:C:H2'	48:WA:2449:U:C6	2.55	0.41
48:WA:2591:C:H2'	48:WA:2592:G:O4'	2.20	0.41
48:WA:4143:G:N2	48:WA:4145:C:O2'	2.53	0.41
48:WA:4639:G:H2'	48:WA:4640:U:C6	2.56	0.41
48:WA:4889:C:H2'	48:WA:4890:C:C6	2.55	0.41
51:ZA:156:G:H2'	51:ZA:157:U:C6	2.55	0.41
51:ZA:220:U:H2'	51:ZA:221:A:H8	1.85	0.41
51:ZA:902:G:H2'	51:ZA:903:A:H8	1.86	0.41
51:ZA:953:C:H5''	53:BB:24:PRO:HB2	2.02	0.41
51:ZA:1049:A:O2'	51:ZA:1854:U:O2	2.35	0.41
51:ZA:1415:C:H2'	51:ZA:1416:C:C6	2.55	0.41
51:ZA:1745:A:H62	51:ZA:1789:G:N2	2.18	0.41
58:GB:121:ILE:N	58:GB:125:THR:OG1	2.51	0.41
63:LB:55:TYR:CD1	63:LB:115:PRO:HG2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:152:LEU:HD21	3:C:174:LEU:HD13	2.02	0.41
6:F:131:MET:O	6:F:135:VAL:HG22	2.21	0.41
21:U:82:ILE:HG22	21:U:83:ARG:HG3	2.02	0.41
30:DA:103:VAL:O	30:DA:128:ARG:NH1	2.54	0.41
33:GA:52:LYS:NZ	50:YA:63:U:O2'	2.36	0.41
37:KA:16:LYS:HG3	37:KA:49:LEU:HD21	2.02	0.41
46:UA:67:G:H2'	46:UA:68:G:H8	1.86	0.41
48:WA:288:G:H2'	48:WA:289:C:C6	2.56	0.41
48:WA:1363:G:H2'	48:WA:1364:G:H8	1.84	0.41
48:WA:1648:A:H2'	48:WA:1649:U:C6	2.56	0.41
48:WA:2545:A:H5'	50:YA:127:U:H1'	2.03	0.41
48:WA:3686:G:H2'	48:WA:3687:C:C6	2.56	0.41
50:YA:30:U:H2'	50:YA:31:G:C8	2.56	0.41
50:YA:106:G:H4'	50:YA:137:A:H5'	2.01	0.41
51:ZA:16:G:H5'	51:ZA:669:A:N6	2.34	0.41
51:ZA:520:A:H5''	61:JB:12:THR:HG23	2.03	0.41
51:ZA:1407:U:H4'	68:QB:97:ARG:NH2	2.36	0.41
57:FB:176:GLU:OE2	57:FB:187:SER:OG	2.38	0.41
62:KB:15:LEU:HD13	62:KB:21:MET:HB2	2.03	0.41
84:GC:5:MET:HB2	84:GC:270:LEU:HD21	2.03	0.41
12:L:91:TRP:CZ2	48:WA:4872:G:H2'	2.55	0.41
17:Q:12:SER:OG	17:Q:17:CYS:O	2.29	0.41
26:Z:21:ARG:HB2	48:WA:1320:C:OP1	2.21	0.41
27:AA:43:MET:HG2	27:AA:47:LYS:HE2	2.03	0.41
29:CA:111:VAL:HG21	29:CA:117:LEU:HD21	2.03	0.41
48:WA:1280:C:H2'	48:WA:1281:A:O4'	2.20	0.41
48:WA:1347:A:H2'	48:WA:1348:C:C6	2.56	0.41
48:WA:2599:G:H2'	48:WA:2600:A:H8	1.86	0.41
48:WA:2846:A:N6	48:WA:3841:G:O2'	2.54	0.41
51:ZA:669:A:H2'	51:ZA:670:A:C4	2.56	0.41
51:ZA:834:C:H2'	51:ZA:835:C:C5	2.55	0.41
51:ZA:943:U:H2'	51:ZA:944:A:H8	1.85	0.41
51:ZA:1678:A:OP2	57:FB:63:LYS:NZ	2.54	0.41
53:BB:52:THR:HG23	53:BB:57:ILE:HG22	2.03	0.41
59:HB:311:GLN:HA	59:HB:314:GLN:HB2	2.03	0.41
60:IB:131:PRO:HD2	60:IB:134:GLU:HB2	2.03	0.41
62:KB:11:ILE:HD13	62:KB:11:ILE:HA	1.88	0.41
64:MB:35:ILE:HG12	64:MB:61:TYR:CZ	2.55	0.41
66:OB:98:ARG:HH21	66:OB:134:PRO:HG3	1.86	0.41
70:SB:121:ARG:HG3	70:SB:131:VAL:HG11	2.03	0.41
86:b:99:ARG:HD2	86:b:103:LEU:HD23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:47:LEU:HD12	2:B:47:LEU:HA	1.87	0.41
3:C:80:ARG:NH2	48:WA:1647:C:OP1	2.37	0.41
6:F:79:ASN:HA	19:S:143:THR:HG22	2.02	0.41
6:F:226:PHE:N	6:F:232:ALA:O	2.49	0.41
8:H:42:ASN:O	8:H:59:LYS:NZ	2.39	0.41
16:P:85:THR:HG22	16:P:104:ARG:HB2	2.01	0.41
18:R:16:CYS:SG	18:R:17:LEU:N	2.94	0.41
19:S:87:LYS:HE3	48:WA:4302:U:H5''	2.03	0.41
26:Z:73:VAL:HB	26:Z:108:TYR:CG	2.56	0.41
35:IA:52:LYS:HG2	35:IA:55:ARG:NH2	2.36	0.41
43:RA:53:TRP:HZ3	43:RA:79:ALA:HB1	1.86	0.41
44:SA:43:A:H2'	44:SA:44:A:C8	2.56	0.41
48:WA:126:C:H2'	48:WA:127:G:C8	2.53	0.41
48:WA:227:A:N6	48:WA:242:U:O4'	2.53	0.41
48:WA:470:A:H62	48:WA:685:G:H21	1.68	0.41
48:WA:1078:C:H2'	48:WA:1079:G:O4'	2.20	0.41
48:WA:1348:C:H2'	48:WA:1349:G:H8	1.86	0.41
48:WA:1463:C:H2'	48:WA:1464:A:C8	2.55	0.41
48:WA:1482:C:O2'	48:WA:1484:G:OP2	2.39	0.41
48:WA:1872:C:H2'	48:WA:1873:A:C8	2.56	0.41
48:WA:2416:G:H2'	48:WA:2417:U:C6	2.55	0.41
48:WA:2467:C:H2'	48:WA:2468:G:O4'	2.21	0.41
48:WA:2864:G:N3	48:WA:3626:A:H2'	2.36	0.41
48:WA:4462:U:H2'	48:WA:4463:C:C6	2.56	0.41
51:ZA:26:U:H2'	51:ZA:27:A:H8	1.85	0.41
51:ZA:29:G:H2'	51:ZA:30:C:C6	2.56	0.41
51:ZA:84:A:H5''	76:YB:122:LYS:HD2	2.01	0.41
51:ZA:115:U:H2'	51:ZA:116:U:C6	2.56	0.41
51:ZA:675:U:H2'	51:ZA:676:C:H6	1.84	0.41
51:ZA:689:U:H2'	51:ZA:690:G:C8	2.56	0.41
51:ZA:822:U:H3	51:ZA:826:A:H62	1.69	0.41
51:ZA:1047:C:H2'	51:ZA:1048:G:O4'	2.21	0.41
51:ZA:1542:C:H5''	71:TB:62:ARG:NH1	2.36	0.41
51:ZA:1555:U:H2'	51:ZA:1556:A:C8	2.55	0.41
51:ZA:1648:G:N7	68:QB:43:LYS:HE2	2.36	0.41
56:EB:148:ARG:NH2	58:GB:202:ASN:OD1	2.47	0.41
56:EB:182:MET:HE2	56:EB:192:ILE:HD11	2.03	0.41
57:FB:35:LEU:HD23	57:FB:39:ILE:HD11	2.03	0.41
57:FB:192:LYS:HA	57:FB:192:LYS:HD3	1.87	0.41
58:GB:21:GLU:O	58:GB:25:ARG:HG3	2.21	0.41
59:HB:284:THR:HG23	59:HB:303:PRO:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:IB:62:VAL:HG12	60:IB:77:ARG:HA	2.03	0.41
62:KB:6:LYS:HE3	62:KB:6:LYS:HB3	1.81	0.41
65:NB:40:LEU:HD12	65:NB:50:ILE:HG23	2.03	0.41
69:RB:76:GLU:HA	69:RB:79:GLU:HG3	2.03	0.41
88:HC:341:THR:HB	88:HC:440:ALA:HB3	2.02	0.41
88:HC:343:GLN:HA	88:HC:401:ILE:HA	2.02	0.41
1:A:48:ILE:HD13	41:OA:65:ALA:HB2	2.01	0.41
12:L:46:ARG:NH2	48:WA:937:G:O2'	2.50	0.41
20:T:105:ASN:ND2	20:T:111:GLU:HB2	2.35	0.41
29:CA:38:PHE:HB3	29:CA:78:ARG:HG2	2.02	0.41
45:TA:69:G:H2'	45:TA:70:G:H8	1.86	0.41
48:WA:347:A:H2'	48:WA:348:G:C8	2.56	0.41
48:WA:973:C:O2'	48:WA:974:C:H5''	2.21	0.41
48:WA:1474:C:N4	48:WA:1495:G:O6	2.54	0.41
48:WA:2542:C:H2'	48:WA:2543:G:C8	2.55	0.41
48:WA:3797:A:H2'	48:WA:3798:U:C6	2.56	0.41
48:WA:4553:U:H2'	48:WA:4554:U:C6	2.56	0.41
48:WA:4608:G:O2'	88:HC:430:ARG:NH2	2.53	0.41
49:XA:28:C:O2'	49:XA:54:A:N1	2.51	0.41
51:ZA:102:A:H4'	51:ZA:104:A:C8	2.56	0.41
51:ZA:944:A:H2'	51:ZA:945:U:H6	1.86	0.41
51:ZA:1298:G:O2'	51:ZA:1299:A:H8	2.02	0.41
51:ZA:1598:G:H3'	77:ZB:80:ARG:HD2	2.02	0.41
51:ZA:1752:C:H2'	51:ZA:1753:C:C6	2.56	0.41
56:EB:136:ILE:HG23	56:EB:149:TYR:CE1	2.56	0.41
56:EB:212:ASP:OD1	56:EB:213:ALA:N	2.54	0.41
62:KB:26:ASP:HB3	62:KB:29:MET:HE3	2.01	0.41
64:MB:79:VAL:HG21	64:MB:85:LEU:HD13	2.03	0.41
65:NB:101:HIS:NE2	65:NB:108:ASP:OD2	2.46	0.41
70:SB:124:ARG:NE	70:SB:130:ARG:O	2.38	0.41
10:J:112:HIS:HD2	10:J:117:ILE:HD11	1.86	0.40
17:Q:27:ASN:OD1	17:Q:27:ASN:N	2.54	0.40
25:Y:3:LYS:NZ	28:BA:40:GLN:O	2.44	0.40
32:FA:54:ARG:H	32:FA:54:ARG:HG2	1.75	0.40
40:NA:89:LYS:HE3	48:WA:4231:U:H4'	2.03	0.40
45:TA:14:A:H3'	45:TA:15:G:H8	1.86	0.40
48:WA:260:C:N4	48:WA:261:G:O6	2.54	0.40
48:WA:680:C:H2'	48:WA:681:G:H8	1.86	0.40
48:WA:727:G:H2'	48:WA:728:C:H6	1.85	0.40
48:WA:728:C:H2'	48:WA:729:U:C6	2.56	0.40
48:WA:1103:C:H2'	48:WA:1104:G:C8	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:WA:1432:C:H2'	48:WA:1433:C:H6	1.86	0.40
48:WA:2886:G:H2'	48:WA:2887:A:H8	1.86	0.40
48:WA:4084:G:H2'	48:WA:4085:U:C6	2.55	0.40
48:WA:4324:G:N2	48:WA:4327:A:OP2	2.38	0.40
48:WA:4770:G:O2'	48:WA:4875:G:O6	2.39	0.40
50:YA:26:C:H2'	50:YA:27:U:C6	2.56	0.40
50:YA:79:G:H3'	50:YA:80:A:H4'	2.03	0.40
51:ZA:433:A:H2'	51:ZA:434:G:C8	2.56	0.40
51:ZA:824:C:C2	61:JB:144:ILE:HG12	2.56	0.40
51:ZA:1135:C:H2'	51:ZA:1136:U:C6	2.56	0.40
51:ZA:1183:A:H2'	51:ZA:1184:G:H8	1.85	0.40
51:ZA:1688:C:H2'	51:ZA:1689:C:C6	2.57	0.40
52:AB:51:LEU:HD13	52:AB:51:LEU:HA	1.89	0.40
52:AB:63:ARG:HG3	52:AB:185:MET:HE1	2.02	0.40
70:SB:34:LYS:HE2	70:SB:103:LEU:HD22	2.01	0.40
78:AC:37:LYS:HB2	78:AC:37:LYS:HE3	1.83	0.40
1:A:20:VAL:HA	1:A:23:ARG:HG3	2.04	0.40
3:C:195:LYS:HA	3:C:200:ARG:HA	2.03	0.40
9:I:35:ASP:HA	9:I:87:ILE:O	2.21	0.40
11:K:109:SER:O	11:K:113:ASN:ND2	2.53	0.40
15:O:61:THR:HG21	15:O:116:SER:HB3	2.03	0.40
31:EA:100:ARG:HG2	48:WA:4755:U:OP2	2.22	0.40
43:RA:32:ILE:H	43:RA:32:ILE:HG13	1.75	0.40
45:TA:72:C:H2'	45:TA:73:G:C8	2.56	0.40
48:WA:429:A:H2'	48:WA:430:G:C8	2.56	0.40
48:WA:1513:U:H2'	48:WA:1514:G:H8	1.87	0.40
48:WA:1813:G:H2'	48:WA:1814:C:C6	2.56	0.40
48:WA:2454:G:H21	48:WA:2509:A:H62	1.68	0.40
48:WA:3729:A:H2'	48:WA:3730:A:C8	2.57	0.40
48:WA:4982:C:H3'	48:WA:4983:G:H21	1.85	0.40
51:ZA:429:C:H2'	51:ZA:430:C:C6	2.56	0.40
51:ZA:1671:G:H2'	51:ZA:1672:U:H6	1.85	0.40
51:ZA:1713:C:H2'	51:ZA:1714:U:C6	2.56	0.40
64:MB:80:ASP:N	64:MB:80:ASP:OD1	2.52	0.40
1:A:21:LYS:HE3	48:WA:2745:A:H1'	2.04	0.40
3:C:69:THR:HG21	48:WA:3908:A:H2'	2.03	0.40
11:K:16:LYS:HG2	48:WA:46:U:H5''	2.03	0.40
12:L:65:PRO:HG3	48:WA:919:A:N3	2.37	0.40
13:M:46:ASP:OD1	13:M:46:ASP:N	2.54	0.40
16:P:39:THR:OG1	16:P:44:ASN:ND2	2.48	0.40
21:U:89:ARG:HB2	21:U:95:PHE:CE1	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:EA:18:LEU:HB2	48:WA:1918:G:O6	2.22	0.40
35:IA:54:LYS:O	35:IA:58:THR:HB	2.21	0.40
48:WA:723:G:OP1	48:WA:938:C:N4	2.54	0.40
48:WA:2260:C:H5''	48:WA:2261:G:H8	1.86	0.40
48:WA:2295:U:H2'	48:WA:2296:G:C8	2.57	0.40
48:WA:2541:C:H2'	48:WA:2542:C:H6	1.86	0.40
48:WA:2782:C:H2'	48:WA:2783:G:H8	1.85	0.40
48:WA:3754:C:H2'	48:WA:3779:G:H5''	2.03	0.40
48:WA:3915:G:H3'	48:WA:3916:U:H4'	2.02	0.40
48:WA:4301:U:H2'	48:WA:4302:U:H6	1.86	0.40
48:WA:4540:G:H2'	48:WA:4541:U:C6	2.56	0.40
48:WA:5004:U:H2'	48:WA:5005:U:H6	1.86	0.40
48:WA:5006:C:H2'	48:WA:5007:G:O4'	2.21	0.40
51:ZA:409:C:H2'	51:ZA:410:G:C8	2.56	0.40
51:ZA:455:A:O2'	51:ZA:1735:A:N3	2.45	0.40
51:ZA:1033:G:N1	51:ZA:1080:A:O2'	2.43	0.40
51:ZA:1503:C:H2'	51:ZA:1504:U:C6	2.57	0.40
51:ZA:1623:A:C6	70:SB:132:ARG:HD3	2.57	0.40
56:EB:179:ASN:HD22	56:EB:230:LYS:HA	1.85	0.40
76:YB:10:ARG:HG2	76:YB:11:LYS:HG3	2.03	0.40
84:GC:35:SER:OG	84:GC:36:ARG:N	2.54	0.40
88:HC:279:THR:HB	88:HC:286:THR:HG23	2.02	0.40
4:D:179:ARG:HD3	4:D:179:ARG:HA	1.82	0.40
6:F:175:ALA:HB1	48:WA:2104:G:C8	2.56	0.40
7:G:217:ILE:O	7:G:221:VAL:HG23	2.22	0.40
20:T:66:SER:OG	20:T:67:LYS:N	2.54	0.40
24:X:73:VAL:HG13	24:X:80:ILE:HG22	2.04	0.40
26:Z:76:ASP:OD1	26:Z:115:GLY:HA3	2.22	0.40
45:TA:52:G:H2'	45:TA:53:G:H8	1.87	0.40
48:WA:41:C:O2'	48:WA:42:A:H5'	2.21	0.40
48:WA:287:U:H2'	48:WA:288:G:H8	1.86	0.40
48:WA:426:A:H2'	48:WA:427:A:C8	2.57	0.40
48:WA:426:A:H2'	48:WA:427:A:H8	1.87	0.40
48:WA:1444:C:H2'	48:WA:1445:A:C8	2.57	0.40
48:WA:1530:U:H2'	48:WA:1531:G:C8	2.57	0.40
48:WA:2287:A:H2'	48:WA:2288:G:C8	2.56	0.40
48:WA:3772:U:H2'	48:WA:3773:C:C6	2.56	0.40
49:XA:58:A:H2'	49:XA:59:G:C8	2.57	0.40
51:ZA:26:U:H2'	51:ZA:27:A:C8	2.55	0.40
51:ZA:371:A:OP2	60:IB:10:LYS:HB2	2.21	0.40
51:ZA:1134:G:H2'	51:ZA:1135:C:C6	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:1306:U:H2'	51:ZA:1307:U:O4'	2.21	0.40
51:ZA:1412:C:H2'	51:ZA:1413:G:C8	2.56	0.40
64:MB:52:LEU:HD11	64:MB:78:LYS:HE3	2.02	0.40
69:RB:94:GLU:O	69:RB:116:ASN:ND2	2.52	0.40
72:UB:99:LYS:HE3	72:UB:99:LYS:HB3	1.93	0.40
79:BC:56:CYS:HB3	79:BC:59:CYS:HB3	2.04	0.40
1:A:178:PRO:HD2	41:OA:26:VAL:HG22	2.02	0.40
11:K:39:ARG:NH2	48:WA:1364:G:OP1	2.54	0.40
17:Q:18:GLY:HA3	48:WA:2824:G:H5''	2.03	0.40
17:Q:93:VAL:HG21	48:WA:2727:A:H1'	2.04	0.40
18:R:107:THR:O	18:R:111:ARG:HG2	2.21	0.40
21:U:43:LYS:HE3	21:U:43:LYS:HB3	1.93	0.40
26:Z:12:ARG:NH1	48:WA:2347:G:OP2	2.55	0.40
26:Z:12:ARG:HD3	26:Z:12:ARG:HA	1.88	0.40
27:AA:49:HIS:HB3	27:AA:52:LYS:HE2	2.04	0.40
29:CA:57:MET:HG2	29:CA:88:LEU:HD23	2.02	0.40
30:DA:44:ARG:NH2	30:DA:52:GLN:OE1	2.52	0.40
44:SA:50:U:O4	44:SA:64:G:O6	2.39	0.40
48:WA:263:G:H2'	48:WA:264:C:C6	2.57	0.40
48:WA:286:U:H2'	48:WA:287:U:C6	2.56	0.40
48:WA:1091:C:H2'	48:WA:1092:C:C6	2.57	0.40
48:WA:2006:U:H2'	48:WA:2007:G:H8	1.86	0.40
48:WA:2902:U:H2'	48:WA:2903:G:H8	1.85	0.40
48:WA:4082:C:H2'	48:WA:4083:G:H8	1.86	0.40
48:WA:4718:C:H2'	48:WA:4719:A:C8	2.53	0.40
51:ZA:12:U:H5''	54:CB:110:MET:HE2	2.03	0.40
51:ZA:349:A:H2'	51:ZA:350:C:C6	2.57	0.40
51:ZA:375:U:H2'	51:ZA:376:A:H8	1.87	0.40
51:ZA:831:G:H2'	51:ZA:832:G:C8	2.55	0.40
51:ZA:945:U:O2	51:ZA:1045:U:O2'	2.39	0.40
51:ZA:1171:G:O2'	51:ZA:1187:G:O6	2.35	0.40
60:IB:17:LYS:HD3	60:IB:17:LYS:HA	1.95	0.40
68:QB:50:HIS:HE1	68:QB:52:LYS:HD3	1.86	0.40
69:RB:97:GLU:HG2	69:RB:118:GLN:HB3	2.04	0.40
70:SB:91:LYS:NZ	70:SB:109:GLU:OE1	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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%)	385 (98%)	10 (2%)	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%)	183 (97%)	5 (3%)	0	100	100
9	I	201/214 (94%)	196 (98%)	5 (2%)	0	100	100
10	J	169/178 (95%)	168 (99%)	1 (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
13	M	201/204 (98%)	196 (98%)	5 (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%)	180 (97%)	5 (3%)	0	100	100
17	Q	178/212 (84%)	175 (98%)	3 (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%)	95 (96%)	4 (4%)	0	100	100
21	U	133/140 (95%)	128 (96%)	5 (4%)	0	100	100
22	V	106/157 (68%)	103 (97%)	3 (3%)	0	100	100
23	W	116/156 (74%)	114 (98%)	2 (2%)	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	Z	145/148 (98%)	143 (99%)	2 (1%)	0	100	100
27	AA	103/245 (42%)	101 (98%)	2 (2%)	0	100	100
28	BA	97/115 (84%)	96 (99%)	1 (1%)	0	100	100
29	CA	106/125 (85%)	104 (98%)	2 (2%)	0	100	100
30	DA	127/135 (94%)	122 (96%)	5 (4%)	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%)	95 (95%)	5 (5%)	0	100	100
35	IA	85/97 (88%)	83 (98%)	2 (2%)	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%)	50 (100%)	0	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%)	85 (96%)	4 (4%)	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
52	AB	215/295 (73%)	211 (98%)	4 (2%)	0	100	100
53	BB	211/264 (80%)	207 (98%)	4 (2%)	0	100	100
54	CB	218/293 (74%)	214 (98%)	4 (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%)	174 (96%)	7 (4%)	0	100	100
58	GB	235/249 (94%)	233 (99%)	2 (1%)	0	100	100
59	HB	181/432 (42%)	175 (97%)	6 (3%)	0	100	100
60	IB	204/208 (98%)	201 (98%)	3 (2%)	0	100	100
61	JB	183/194 (94%)	180 (98%)	3 (2%)	0	100	100
62	KB	94/165 (57%)	92 (98%)	2 (2%)	0	100	100
63	LB	140/158 (89%)	138 (99%)	2 (1%)	0	100	100
64	MB	115/132 (87%)	109 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
65	NB	147/151 (97%)	146 (99%)	1 (1%)	0	100	100
66	OB	134/151 (89%)	128 (96%)	6 (4%)	0	100	100
67	PB	127/145 (88%)	123 (97%)	4 (3%)	0	100	100
68	QB	140/172 (81%)	135 (96%)	5 (4%)	0	100	100
69	RB	130/135 (96%)	126 (97%)	4 (3%)	0	100	100
70	SB	142/152 (93%)	139 (98%)	3 (2%)	0	100	100
71	TB	140/145 (97%)	135 (96%)	4 (3%)	1 (1%)	18	49
72	UB	100/119 (84%)	96 (96%)	4 (4%)	0	100	100
73	VB	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
74	WB	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
75	XB	139/143 (97%)	136 (98%)	3 (2%)	0	100	100
76	YB	122/131 (93%)	119 (98%)	3 (2%)	0	100	100
77	ZB	83/124 (67%)	83 (100%)	0	0	100	100
78	AC	99/115 (86%)	96 (97%)	3 (3%)	0	100	100
79	BC	81/84 (96%)	80 (99%)	1 (1%)	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
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%)	150 (93%)	11 (7%)	1 (1%)	21	52
87	c	12/14 (86%)	11 (92%)	1 (8%)	0	100	100
88	HC	221/462 (48%)	209 (95%)	12 (5%)	0	100	100
All	All	11783/14293 (82%)	11464 (97%)	317 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
71	TB	119	TRP
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%)	81	85
2	B	344/348 (99%)	336 (98%)	8 (2%)	44	70
3	C	302/337 (90%)	300 (99%)	2 (1%)	76	82
4	D	247/250 (99%)	246 (100%)	1 (0%)	84	86
5	E	201/251 (80%)	199 (99%)	2 (1%)	68	79
6	F	198/218 (91%)	198 (100%)	0	100	100
7	G	197/273 (72%)	194 (98%)	3 (2%)	57	75
8	H	169/171 (99%)	166 (98%)	3 (2%)	51	73
9	I	175/181 (97%)	173 (99%)	2 (1%)	65	78
10	J	144/149 (97%)	143 (99%)	1 (1%)	76	82
11	K	175/176 (99%)	171 (98%)	4 (2%)	44	70
12	L	117/161 (73%)	117 (100%)	0	100	100
13	M	171/172 (99%)	167 (98%)	4 (2%)	44	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%)	63	78
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%)	59	76
20	T	91/114 (80%)	91 (100%)	0	100	100
21	U	103/107 (96%)	102 (99%)	1 (1%)	68	79
22	V	89/126 (71%)	87 (98%)	2 (2%)	45	71
23	W	106/134 (79%)	105 (99%)	1 (1%)	70	80
24	X	124/135 (92%)	120 (97%)	4 (3%)	34	64
25	Y	117/118 (99%)	116 (99%)	1 (1%)	70	80
26	Z	119/120 (99%)	118 (99%)	1 (1%)	73	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	AA	87/184 (47%)	86 (99%)	1 (1%)	65	78
28	BA	85/98 (87%)	83 (98%)	2 (2%)	43	69
29	CA	98/110 (89%)	97 (99%)	1 (1%)	68	79
30	DA	115/121 (95%)	115 (100%)	0	100	100
31	EA	88/89 (99%)	88 (100%)	0	100	100
32	FA	98/109 (90%)	95 (97%)	3 (3%)	35	64
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%)	59	76
36	JA	64/65 (98%)	64 (100%)	0	100	100
37	KA	47/48 (98%)	46 (98%)	1 (2%)	47	71
38	LA	48/116 (41%)	46 (96%)	2 (4%)	26	58
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%)	59	76
42	PA	108/121 (89%)	106 (98%)	2 (2%)	50	73
43	RA	126/137 (92%)	118 (94%)	8 (6%)	16	45
52	AB	180/244 (74%)	180 (100%)	0	100	100
53	BB	194/231 (84%)	192 (99%)	2 (1%)	68	79
54	CB	186/225 (83%)	185 (100%)	1 (0%)	81	85
55	DB	190/232 (82%)	186 (98%)	4 (2%)	47	71
56	EB	224/225 (100%)	219 (98%)	5 (2%)	45	71
57	FB	158/170 (93%)	157 (99%)	1 (1%)	78	83
58	GB	207/218 (95%)	203 (98%)	4 (2%)	50	73
59	HB	165/360 (46%)	161 (98%)	4 (2%)	43	69
60	IB	178/180 (99%)	176 (99%)	2 (1%)	65	78
61	JB	161/168 (96%)	159 (99%)	2 (1%)	63	78
62	KB	87/136 (64%)	86 (99%)	1 (1%)	65	78
63	LB	130/142 (92%)	128 (98%)	2 (2%)	57	75
64	MB	99/108 (92%)	93 (94%)	6 (6%)	17	46
65	NB	130/131 (99%)	129 (99%)	1 (1%)	73	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	OB	106/119 (89%)	105 (99%)	1 (1%)	70	80
67	PB	115/130 (88%)	111 (96%)	4 (4%)	32	62
68	QB	117/140 (84%)	114 (97%)	3 (3%)	40	68
69	RB	119/121 (98%)	116 (98%)	3 (2%)	42	69
70	SB	125/132 (95%)	123 (98%)	2 (2%)	55	75
71	TB	112/116 (97%)	109 (97%)	3 (3%)	39	67
72	UB	93/107 (87%)	90 (97%)	3 (3%)	34	64
73	VB	67/67 (100%)	65 (97%)	2 (3%)	36	65
74	WB	112/113 (99%)	111 (99%)	1 (1%)	70	80
75	XB	113/115 (98%)	109 (96%)	4 (4%)	32	62
76	YB	107/113 (95%)	107 (100%)	0	100	100
77	ZB	75/102 (74%)	74 (99%)	1 (1%)	61	77
78	AC	88/98 (90%)	87 (99%)	1 (1%)	65	78
79	BC	75/76 (99%)	73 (97%)	2 (3%)	39	67
80	CC	55/62 (89%)	55 (100%)	0	100	100
81	DC	48/49 (98%)	47 (98%)	1 (2%)	47	71
82	EC	46/106 (43%)	45 (98%)	1 (2%)	45	71
83	FC	62/154 (40%)	59 (95%)	3 (5%)	23	54
84	GC	272/275 (99%)	250 (92%)	22 (8%)	11	36
86	b	138/258 (54%)	126 (91%)	12 (9%)	9	34
87	c	12/12 (100%)	12 (100%)	0	100	100
88	HC	179/379 (47%)	164 (92%)	15 (8%)	10	35
All	All	10256/12075 (85%)	10063 (98%)	193 (2%)	49	73

All (193) 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	329	ASP

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Mol	Chain	Res	Type
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	94	ILE
7	G	159	THR
7	G	193	VAL
8	H	47	LEU
8	H	95	VAL
8	H	123	ILE
9	I	126	VAL
9	I	184	MET
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
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	109	LYS
22	V	87	LEU
22	V	89	ASP
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

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Mol	Chain	Res	Type
27	AA	50	ASN
28	BA	14	ILE
28	BA	71	VAL
29	CA	46	LEU
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
38	LA	101	VAL
41	OA	52	VAL
42	PA	83	ASN
42	PA	103	HIS
43	RA	37	LEU
43	RA	58	ILE
43	RA	66	ASN
43	RA	92	ARG
43	RA	121	LEU
43	RA	137	GLN
43	RA	147	HIS
43	RA	151	ILE
53	BB	82	ARG
53	BB	126	ASP
54	CB	248	TYR
55	DB	123	GLU
55	DB	205	TYR
55	DB	206	VAL
55	DB	213	VAL
56	EB	12	VAL
56	EB	62	LYS
56	EB	207	VAL
56	EB	220	THR
56	EB	222	LEU
57	FB	102	LEU
58	GB	50	VAL
58	GB	153	VAL
58	GB	157	VAL
58	GB	213	LEU

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Mol	Chain	Res	Type
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
61	JB	117	LEU
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
69	RB	6	THR
69	RB	95	ILE
69	RB	99	ASP
70	SB	50	ILE
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
73	VB	52	THR
74	WB	105	THR
75	XB	17	ARG
75	XB	81	ILE

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Mol	Chain	Res	Type
75	XB	105	PHE
75	XB	115	ILE
77	ZB	32	LYS
78	AC	100	ARG
79	BC	43	ILE
79	BC	80	ARG
81	DC	39	CYS
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	37	ASP
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	185	LYS
84	GC	186	THR
84	GC	198	VAL
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	30	VAL
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	135	THR

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Mol	Chain	Res	Type
86	b	149	ARG
86	b	219	VAL
86	b	222	VAL
88	HC	240	ARG
88	HC	248	LEU
88	HC	290	LYS
88	HC	313	LYS
88	HC	347	LEU
88	HC	360	VAL
88	HC	368	ILE
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 (80) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	205	ASN
2	B	175	GLN
2	B	179	HIS
3	C	21	ASN
3	C	41	HIS
3	C	329	ASN
3	C	347	HIS
4	D	131	ASN
4	D	282	GLN
6	F	98	ASN
9	I	59	GLN
9	I	73	ASN
9	I	166	HIS
10	J	23	ASN
11	K	159	ASN
12	L	48	GLN
13	M	86	HIS
13	M	182	HIS
15	O	63	GLN
15	O	93	ASN

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Mol	Chain	Res	Type
15	O	149	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
23	W	107	HIS
27	AA	6	ASN
28	BA	15	ASN
28	BA	72	HIS
29	CA	116	ASN
31	EA	55	ASN
40	NA	25	GLN
42	PA	21	ASN
42	PA	31	ASN
43	RA	137	GLN
52	AB	141	ASN
53	BB	101	HIS
53	BB	186	ASN
54	CB	136	HIS
54	CB	172	ASN
55	DB	95	ASN
55	DB	245	HIS
56	EB	50	ASN
56	EB	142	HIS
57	FB	83	ASN
58	GB	110	ASN
59	HB	271	ASN
60	IB	22	HIS
60	IB	35	ASN
61	JB	124	HIS
61	JB	140	GLN
63	LB	11	GLN
64	MB	46	GLN
64	MB	75	ASN
66	OB	32	HIS
68	QB	37	GLN
68	QB	55	ASN
69	RB	116	ASN

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Mol	Chain	Res	Type
71	TB	51	ASN
71	TB	126	GLN
74	WB	91	ASN
75	XB	61	GLN
75	XB	77	ASN
76	YB	29	HIS
76	YB	63	HIS
76	YB	112	ASN
78	AC	7	ASN
78	AC	72	HIS
80	CC	29	GLN
80	CC	45	ASN
81	DC	16	GLN
84	GC	222	ASN
84	GC	305	ASN
86	b	42	GLN
88	HC	348	ASN
88	HC	352	GLN

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%)	15 (20%)	0
46	UA	74/75 (98%)	37 (50%)	1 (1%)
47	VA	11/12 (91%)	3 (27%)	0
48	WA	3556/3584 (99%)	603 (16%)	20 (0%)
49	XA	118/120 (98%)	9 (7%)	0
50	YA	155/156 (99%)	33 (21%)	0
51	ZA	1707/1869 (91%)	326 (19%)	8 (0%)
All	All	5771/5968 (96%)	1042 (18%)	32 (0%)

All (1042) 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

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Mol	Chain	Res	Type
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	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
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

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Mol	Chain	Res	Type
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	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
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	59	A
48	WA	64	A
48	WA	65	A
48	WA	66	A
48	WA	91	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

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Mol	Chain	Res	Type
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	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
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	309	C
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	386	A

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Mol	Chain	Res	Type
48	WA	387	G
48	WA	399	G
48	WA	409	G
48	WA	410	A
48	WA	412	G
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
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	643	G
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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	1279	G
48	WA	1282	C
48	WA	1286	G
48	WA	1289	G
48	WA	1290	G
48	WA	1294	C
48	WA	1298	G
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

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Mol	Chain	Res	Type
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
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	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

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Mol	Chain	Res	Type
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	1883	C
48	WA	1890	A
48	WA	1899	A
48	WA	1912	G
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	1935	G
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

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Mol	Chain	Res	Type
48	WA	2004	A
48	WA	2005	G
48	WA	2006	U
48	WA	2023	G
48	WA	2027	A
48	WA	2028	A
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
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

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Mol	Chain	Res	Type
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	2477	G
48	WA	2485	G
48	WA	2491	C
48	WA	2492	U
48	WA	2493	C
48	WA	2505	G
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	2577	U
48	WA	2585	C
48	WA	2588	G
48	WA	2591	C
48	WA	2603	A
48	WA	2622	G
48	WA	2625	A
48	WA	2629	C
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

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Mol	Chain	Res	Type
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	2760	G
48	WA	2766	A
48	WA	2771	U
48	WA	2789	A
48	WA	2790	U
48	WA	2792	U
48	WA	2796	C
48	WA	2798	G
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	2844	G
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	3750	A

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Mol	Chain	Res	Type
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	3785	A
48	WA	3786	A
48	WA	3788	U
48	WA	3800	U
48	WA	3804	U
48	WA	3810	C
48	WA	3812	C
48	WA	3813	G
48	WA	3816	U
48	WA	3819	A
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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	4338	A
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
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	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	4550	A
48	WA	4551	G
48	WA	4562	C
48	WA	4569	G

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Mol	Chain	Res	Type
48	WA	4575	G
48	WA	4577	G
48	WA	4579	U
48	WA	4586	A
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	4672	C
48	WA	4674	A
48	WA	4679	U
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

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Mol	Chain	Res	Type
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
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	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
48	WA	5070	G
49	XA	7	G
49	XA	11	A
49	XA	33	U
49	XA	41	G

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Mol	Chain	Res	Type
49	XA	54	A
49	XA	63	C
49	XA	64	G
49	XA	100	A
49	XA	110	G
50	YA	16	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
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	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
50	YA	155	C
51	ZA	3	C
51	ZA	25	A
51	ZA	33	G
51	ZA	41	G

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Mol	Chain	Res	Type
51	ZA	42	A
51	ZA	46	A
51	ZA	56	G
51	ZA	58	C
51	ZA	62	G
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
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

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Mol	Chain	Res	Type
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
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	383	G
51	ZA	385	G
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	502	C
51	ZA	508	A
51	ZA	525	A
51	ZA	531	A
51	ZA	532	C
51	ZA	534	G

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Mol	Chain	Res	Type
51	ZA	535	G
51	ZA	536	A
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
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	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

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Mol	Chain	Res	Type
51	ZA	670	A
51	ZA	671	A
51	ZA	672	A
51	ZA	673	G
51	ZA	684	G
51	ZA	689	U
51	ZA	731	G
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
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	896	U
51	ZA	897	U
51	ZA	898	U
51	ZA	902	G

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Mol	Chain	Res	Type
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	990	A
51	ZA	992	A
51	ZA	999	G
51	ZA	1002	U
51	ZA	1008	A
51	ZA	1017	U
51	ZA	1023	A
51	ZA	1061	U
51	ZA	1062	A
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

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Mol	Chain	Res	Type
51	ZA	1253	A
51	ZA	1256	G
51	ZA	1257	G
51	ZA	1259	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
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

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Mol	Chain	Res	Type
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
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	1570	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	1648	G
51	ZA	1665	G
51	ZA	1680	G
51	ZA	1683	C

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Mol	Chain	Res	Type
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
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 (32) 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

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Mol	Chain	Res	Type
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
51	ZA	24	C
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 252 ligands modelled in this entry, 245 are monoatomic - leaving 7 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	$\# Z > 2$
91	5GP	UA	101	46	26,26,26	0.98	1 (3%)	39,40,40	1.78	7 (17%)
93	SPD	WA	5244	-	9,9,9	0.27	0	8,8,8	0.34	0
93	SPD	WA	5245	-	9,9,9	0.28	0	8,8,8	0.30	0
92	ANM	WA	5243	94	20,20,20	4.07	7 (35%)	24,27,27	1.40	2 (8%)
95	SER	HC	502	-	4,5,6	0.59	0	1,5,7	0.54	0
93	SPD	ZA	1944	-	9,9,9	0.26	0	8,8,8	0.29	0
93	SPD	WA	5246	-	9,9,9	0.26	0	8,8,8	0.29	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
91	5GP	UA	101	46	-	5/10/26/26	0/3/3/3
93	SPD	WA	5244	-	-	1/7/7/7	-
93	SPD	WA	5245	-	-	1/7/7/7	-
92	ANM	WA	5243	94	-	6/10/23/23	0/2/2/2
95	SER	HC	502	-	-	1/2/4/6	-
93	SPD	ZA	1944	-	-	1/7/7/7	-
93	SPD	WA	5246	-	-	1/7/7/7	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
92	WA	5243	ANM	C3-C2	-11.79	1.32	1.53
92	WA	5243	ANM	C16-N1	-8.84	1.30	1.47
92	WA	5243	ANM	C2-C16	7.40	1.68	1.53
92	WA	5243	ANM	C4-C3	4.00	1.58	1.53
92	WA	5243	ANM	C4-N1	3.87	1.60	1.47
92	WA	5243	ANM	O2-C5	3.52	1.43	1.35
91	UA	101	5GP	C6-N1	-2.50	1.34	1.38
92	WA	5243	ANM	C6-C5	2.44	1.57	1.49

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
91	UA	101	5GP	C5-C4-N3	-6.07	118.72	128.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
92	WA	5243	ANM	O2-C5-C6	5.19	120.35	111.09
91	UA	101	5GP	C2-N3-C4	4.77	120.51	112.30
91	UA	101	5GP	N9-C4-N3	3.89	133.73	125.95
91	UA	101	5GP	C5-C6-N1	2.48	119.57	113.25
91	UA	101	5GP	C2-N1-C6	-2.36	120.83	125.11
91	UA	101	5GP	O6-C6-C5	-2.35	120.33	126.53
91	UA	101	5GP	N9-C8-N7	-2.19	109.35	113.40
92	WA	5243	ANM	C2-O2-C5	-2.12	114.42	117.72

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
91	UA	101	5GP	C5'-O5'-P-OP1
92	WA	5243	ANM	C6-C5-O2-C2
92	WA	5243	ANM	O3-C5-O2-C2
92	WA	5243	ANM	C10-C9-O1-C14
92	WA	5243	ANM	C1-C9-O1-C14
91	UA	101	5GP	O4'-C4'-C5'-O5'
91	UA	101	5GP	C3'-C4'-C5'-O5'
93	WA	5245	SPD	C8-C7-N6-C5
93	ZA	1944	SPD	C2-C3-C4-C5
93	WA	5244	SPD	C2-C3-C4-C5
92	WA	5243	ANM	C11-C12-C15-C16
92	WA	5243	ANM	C13-C12-C15-C16
91	UA	101	5GP	C4'-C5'-O5'-P
95	HC	502	SER	N-CA-CB-OG
91	UA	101	5GP	C5'-O5'-P-OP2
93	WA	5246	SPD	C8-C7-N6-C5

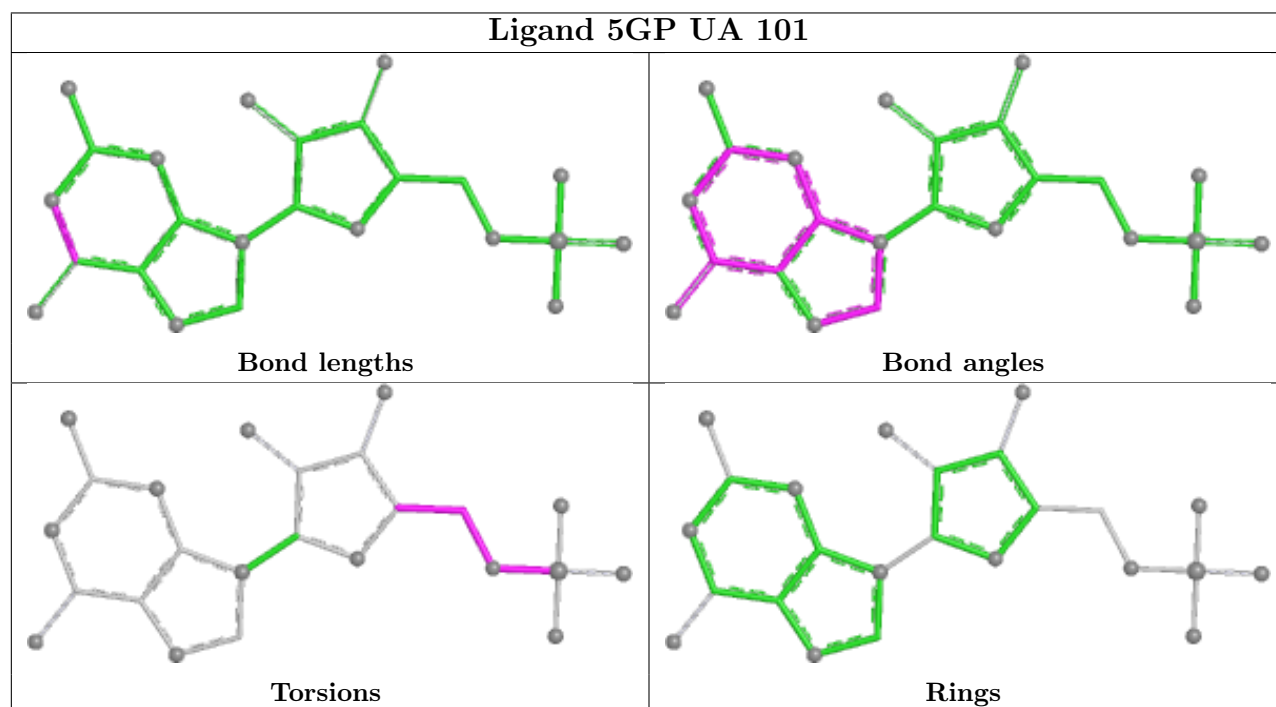
There are no ring outliers.

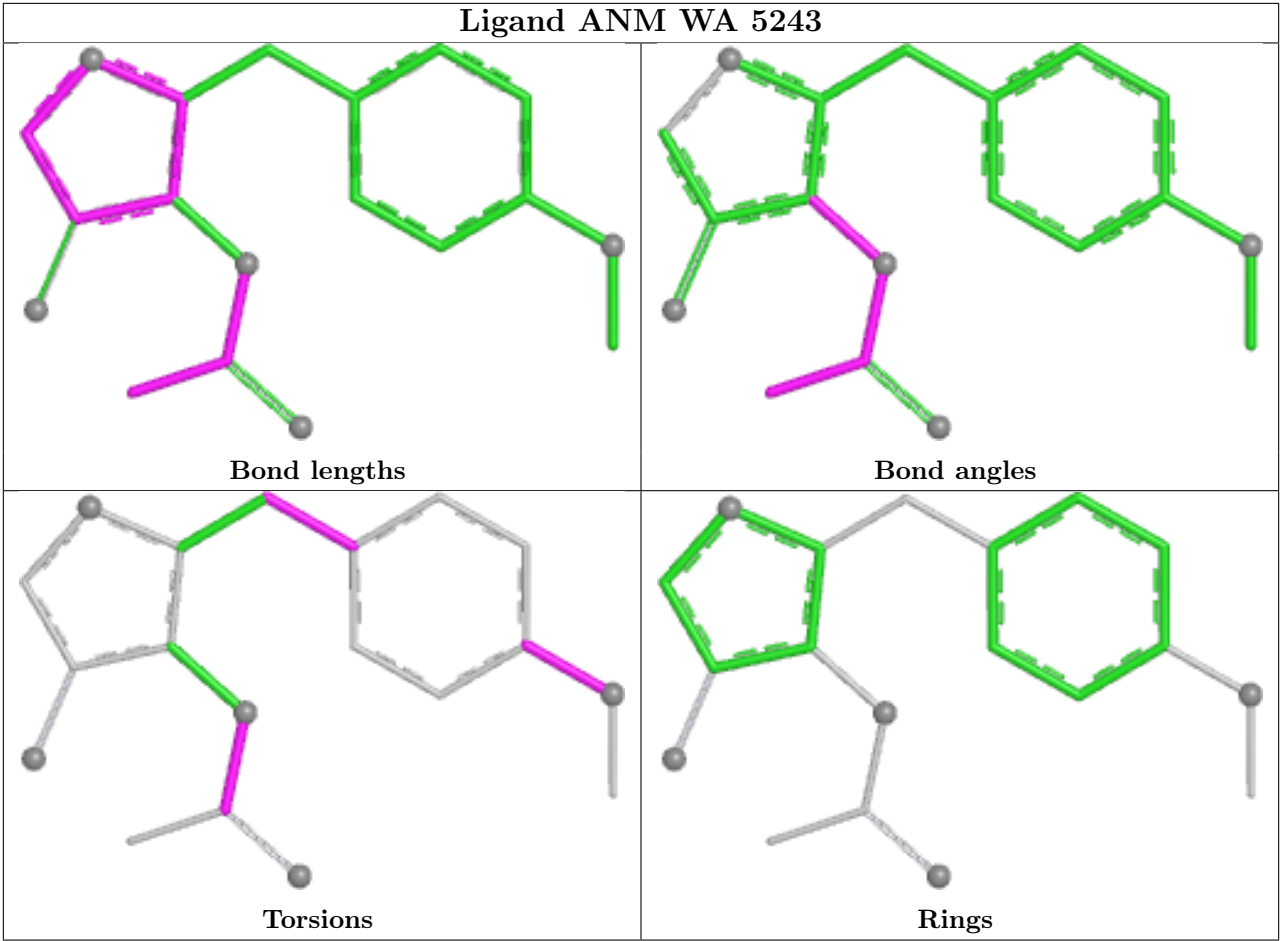
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
93	WA	5244	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.





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
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	37.06
1	WA	1225:G	O3'	1239:G	P	20.73
1	WA	996:C	O3'	1070:G	P	17.80
1	WA	4779:C	O3'	4861:C	P	17.50

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	WA	763:G	O3'	904:C	P	16.92
1	WA	524:C	O3'	639:G	P	16.84
1	WA	4103:C	O3'	4109:G	P	16.47
1	WA	1698:C	O3'	1722:C	P	14.93
1	WA	5024:U	O3'	5030:G	P	13.96
1	WA	1366:U	O3'	1370:A	P	13.55
1	WA	2904:G	O3'	3598:A	P	12.94
1	b	106:LYS	C	107:VAL	N	11.94
1	WA	4731:A	O3'	4737:G	P	10.50
1	WA	3954:A	O3'	4063:C	P	9.86
1	WA	1186:C	O3'	1189:C	P	9.83
1	WA	182:G	O3'	189:G	P	9.44
1	b	107:VAL	C	108:PRO	N	8.69
1	WA	4742:G	O3'	4745:G	P	5.84
1	WA	513:U	O3'	516:C	P	5.54
1	WA	501:G	O3'	505:G	P	4.87
1	WA	1106:U	O3'	1174:G	P	4.49
1	WA	4901:G	O3'	4904:C	P	4.35
1	WA	2030:C	O3'	2031:A	P	3.57

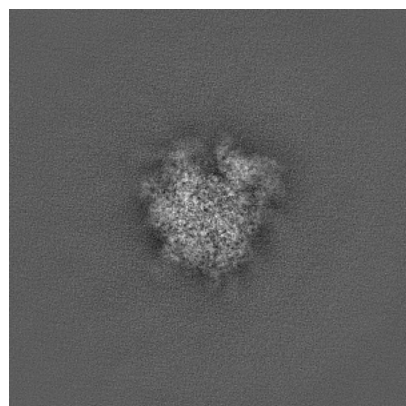
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43567. These allow visual inspection of the internal detail of the map and identification of artifacts.

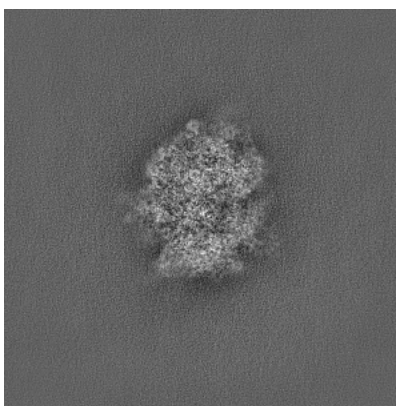
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

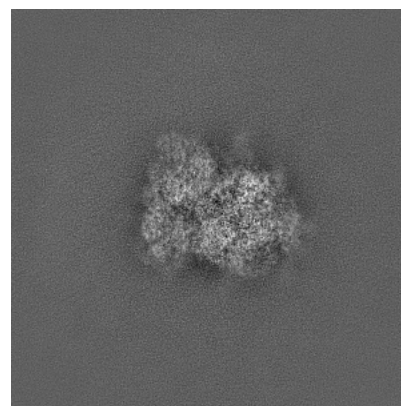
6.1.1 Primary map



X

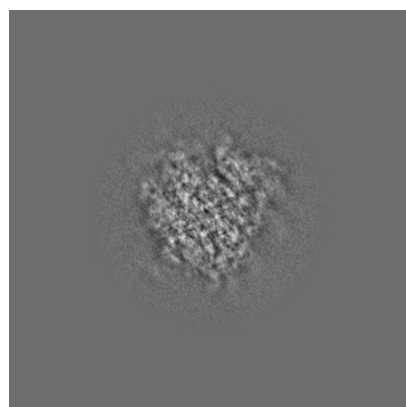


Y

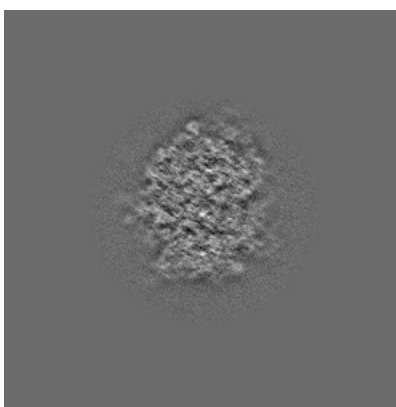


Z

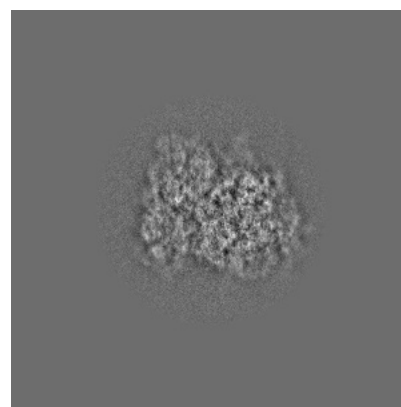
6.1.2 Raw map



X



Y

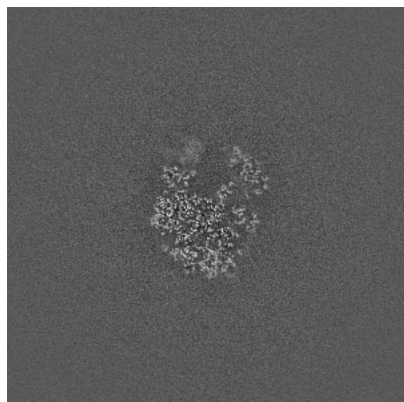


Z

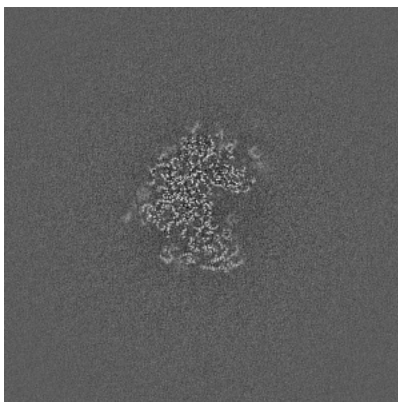
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

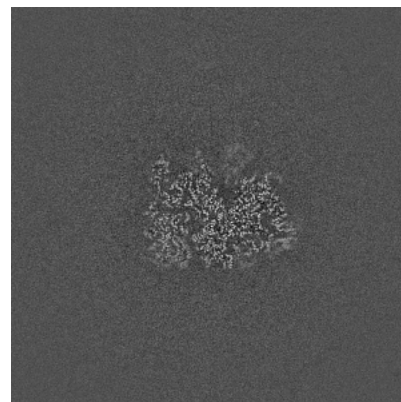
6.2.1 Primary map



X Index: 324

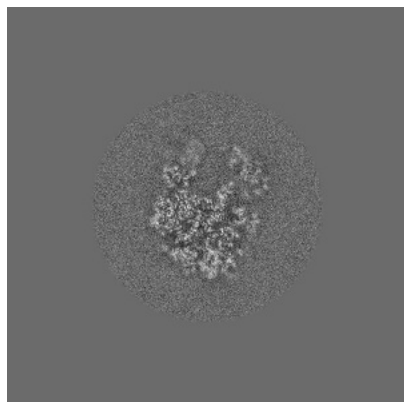


Y Index: 324

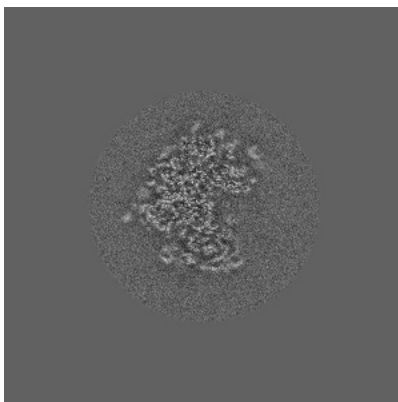


Z Index: 324

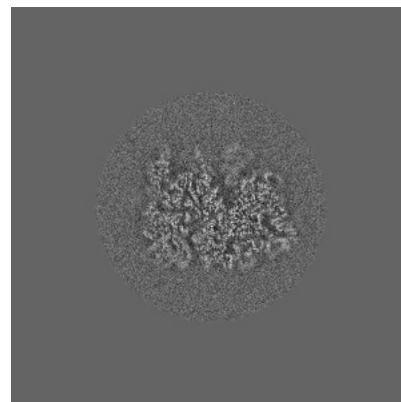
6.2.2 Raw map



X Index: 324



Y Index: 324

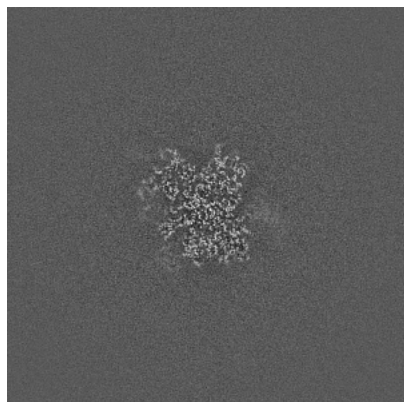


Z Index: 324

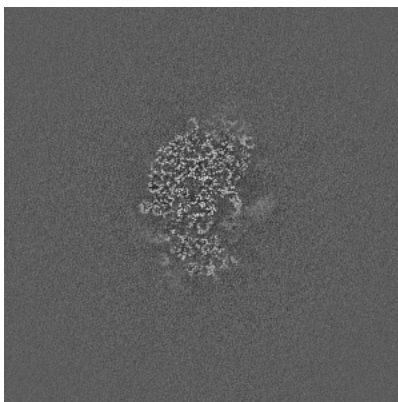
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

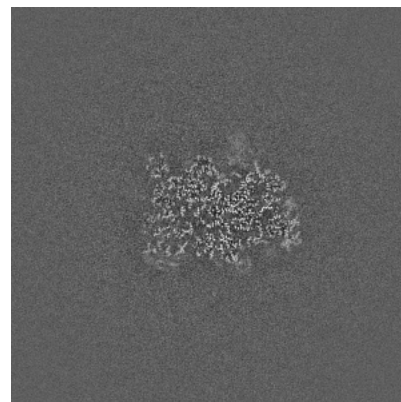
6.3.1 Primary map



X Index: 377

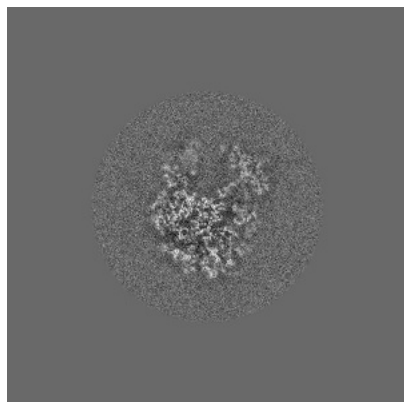


Y Index: 301

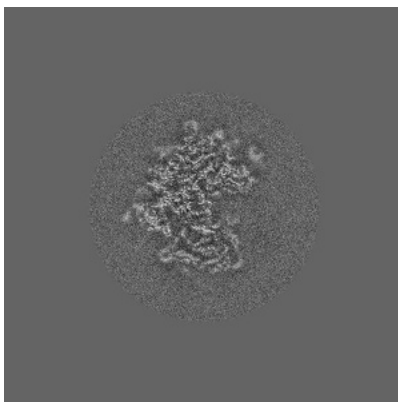


Z Index: 311

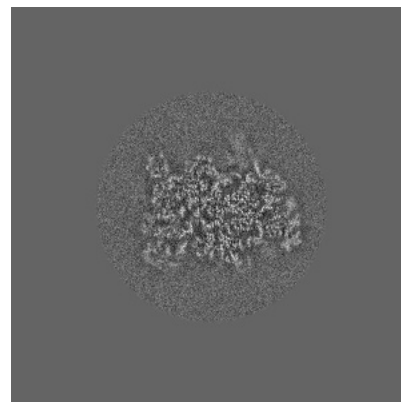
6.3.2 Raw map



X Index: 322



Y Index: 327

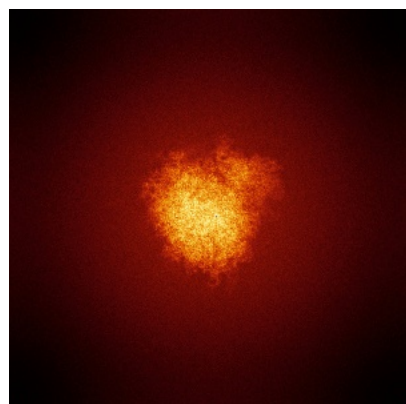


Z Index: 311

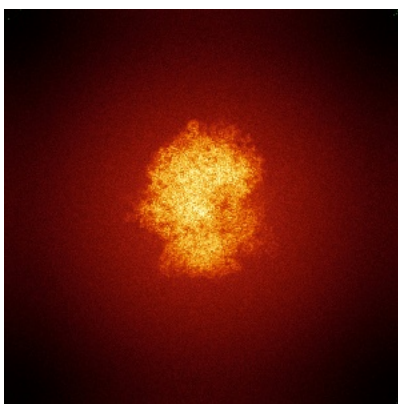
The images above show the largest variance slices of the map in three orthogonal directions.

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

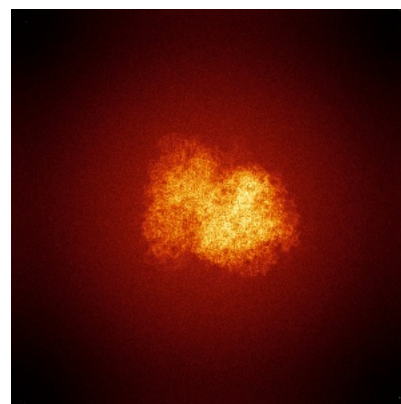
6.4.1 Primary map



X

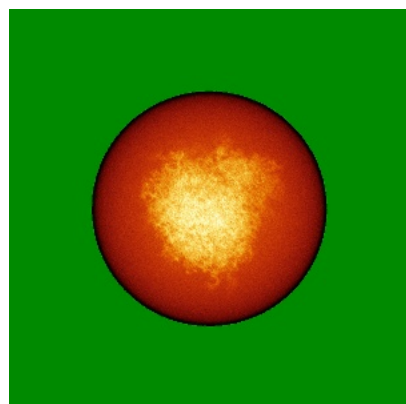


Y

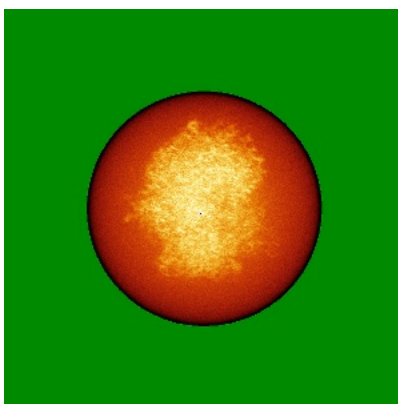


Z

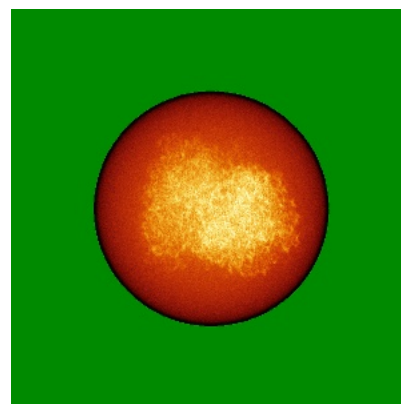
6.4.2 Raw map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 6.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

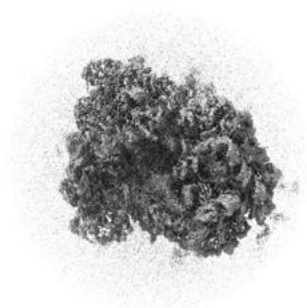
6.5.2 Raw map



X



Y



Z

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.

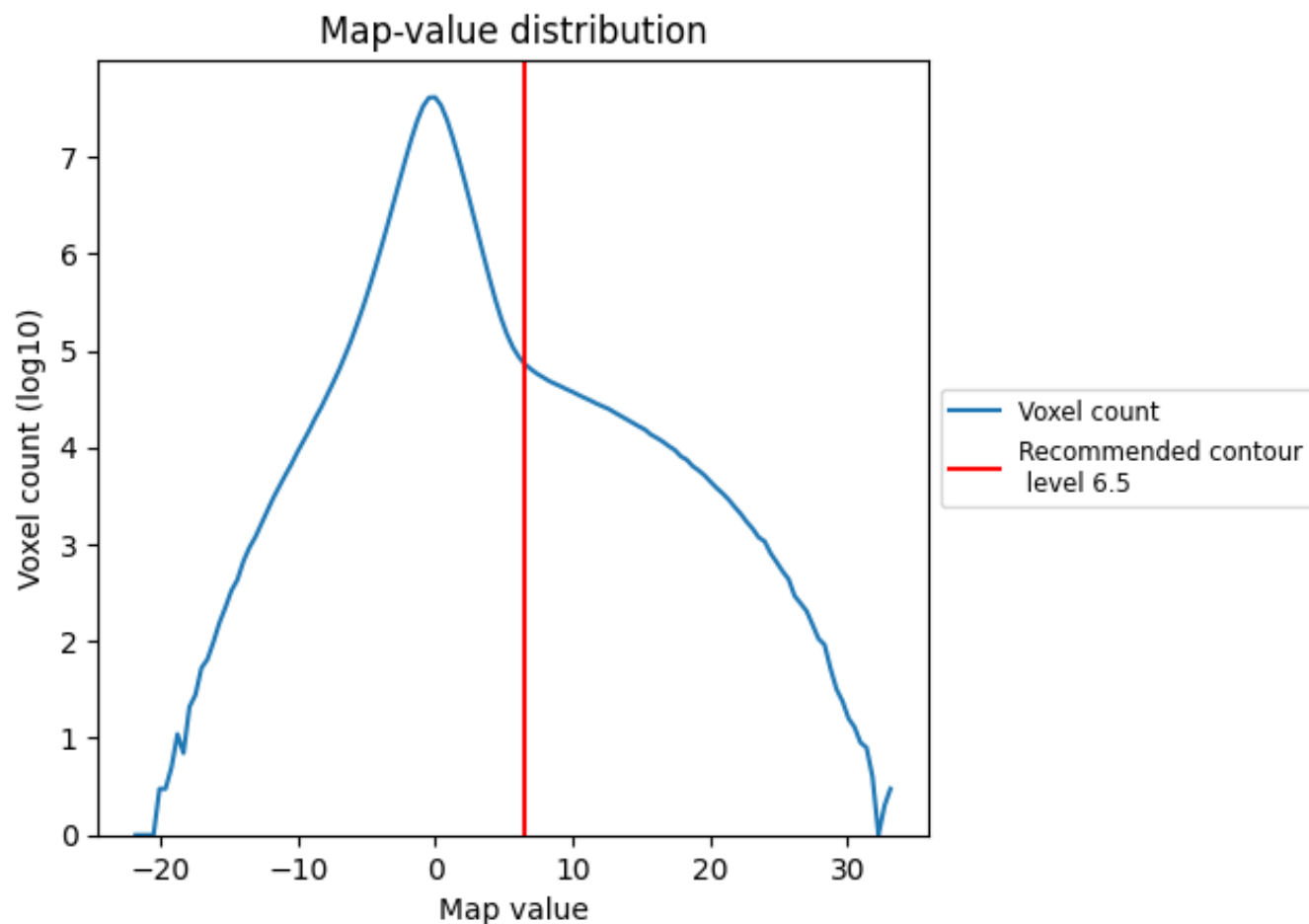
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

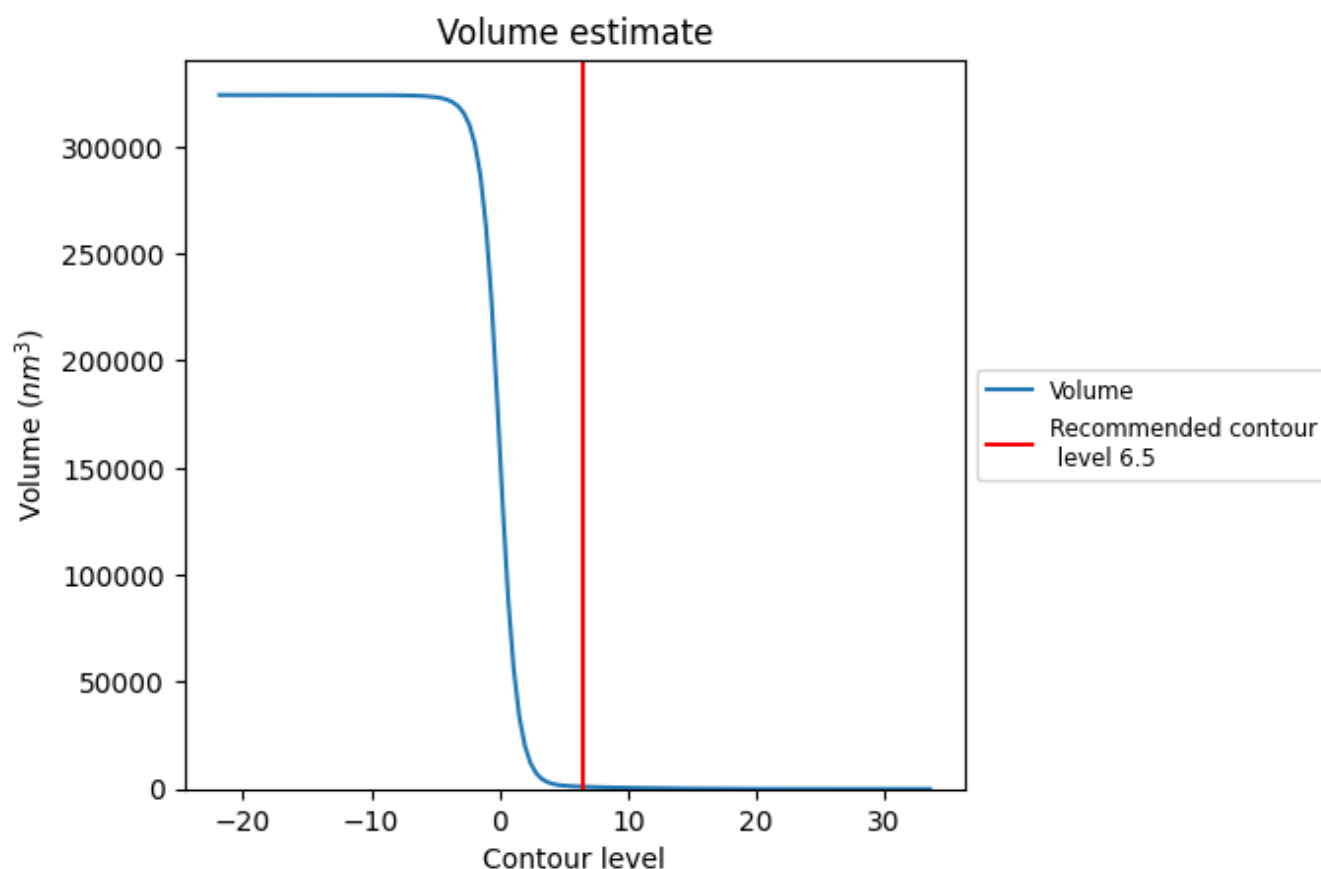
This section contains the results of statistical analysis of the map.

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.

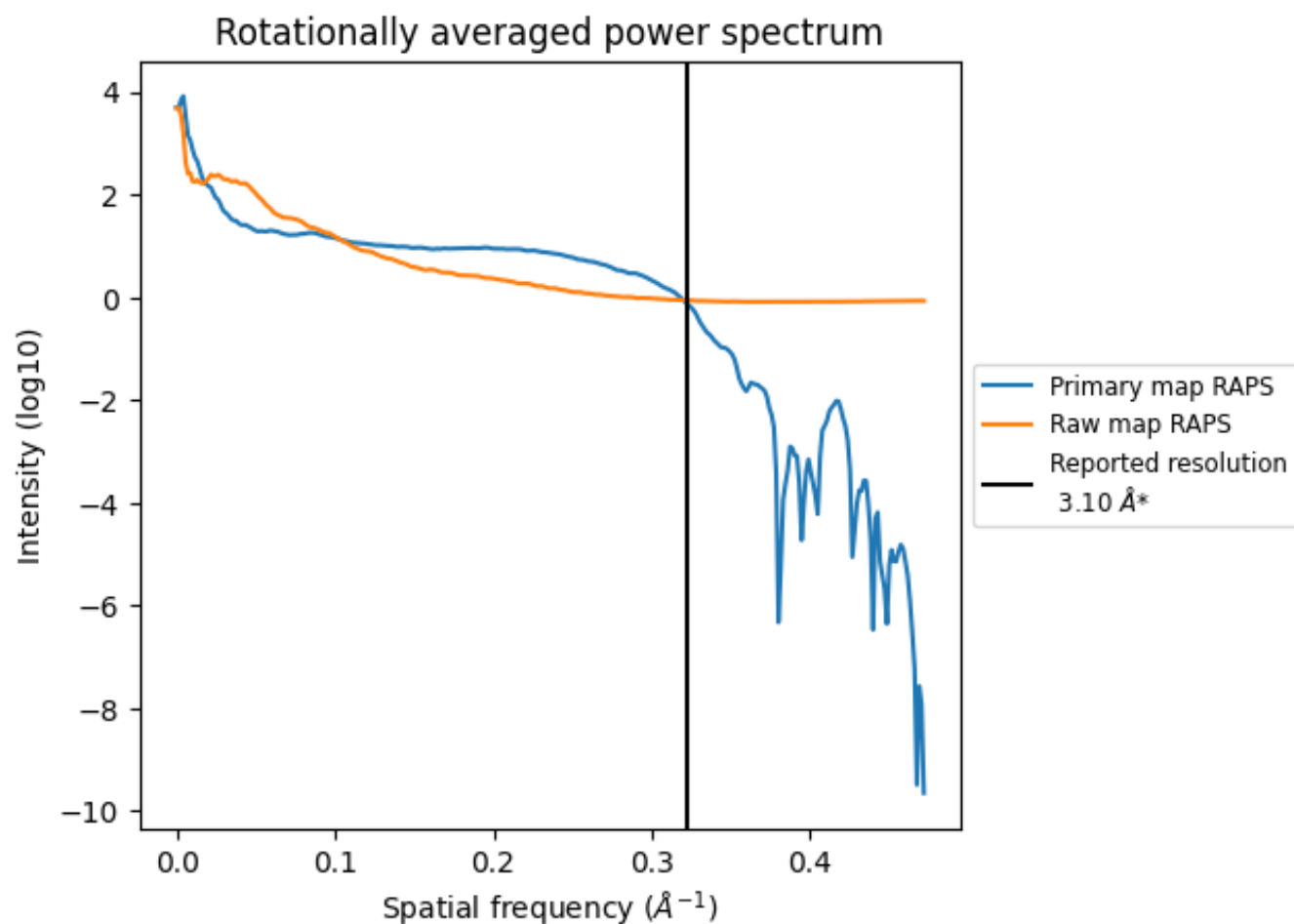
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1042 nm^3 ; this corresponds to an approximate mass of 941 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 ⓘ

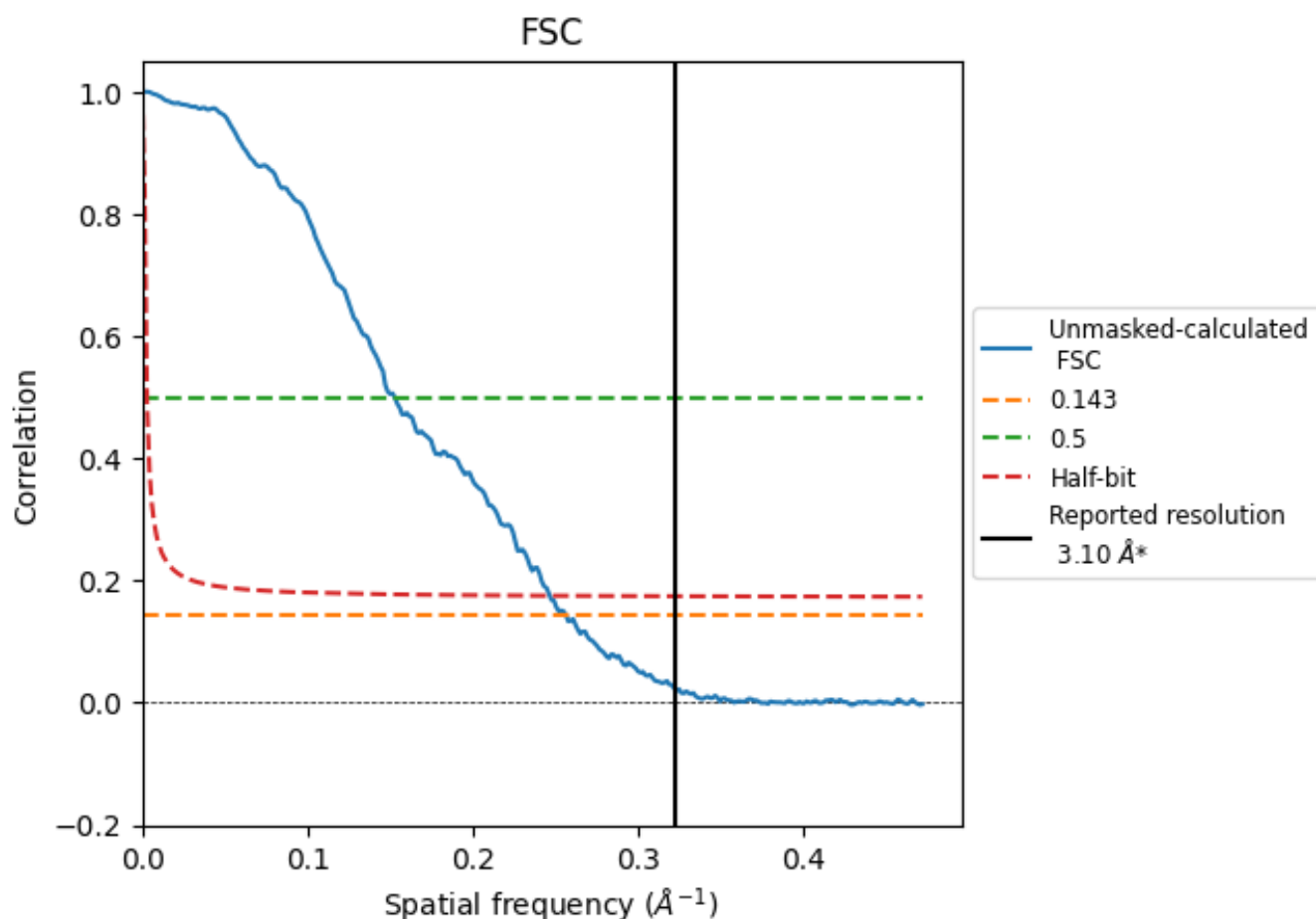


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

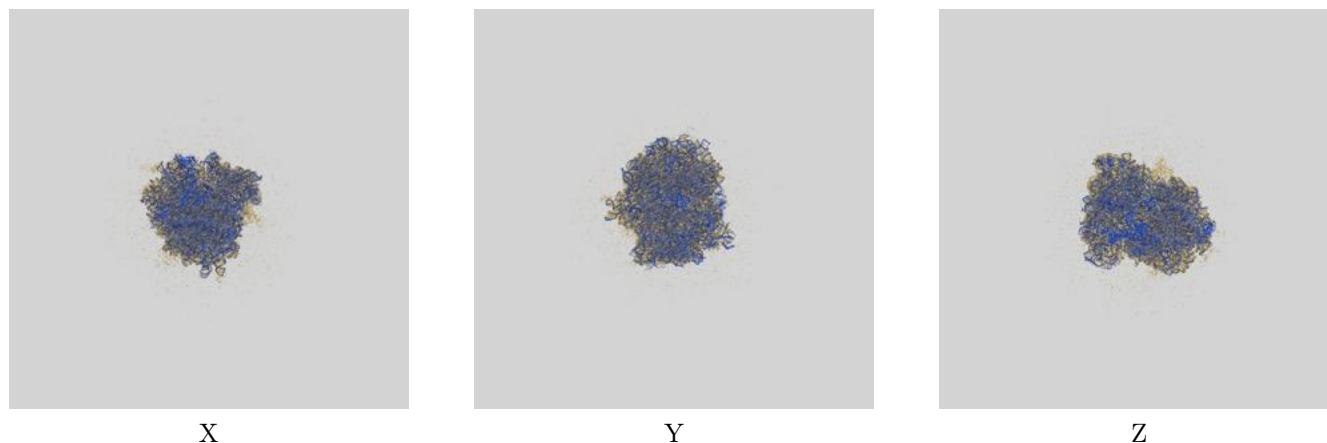
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.90	6.55	4.06

*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 3.90 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

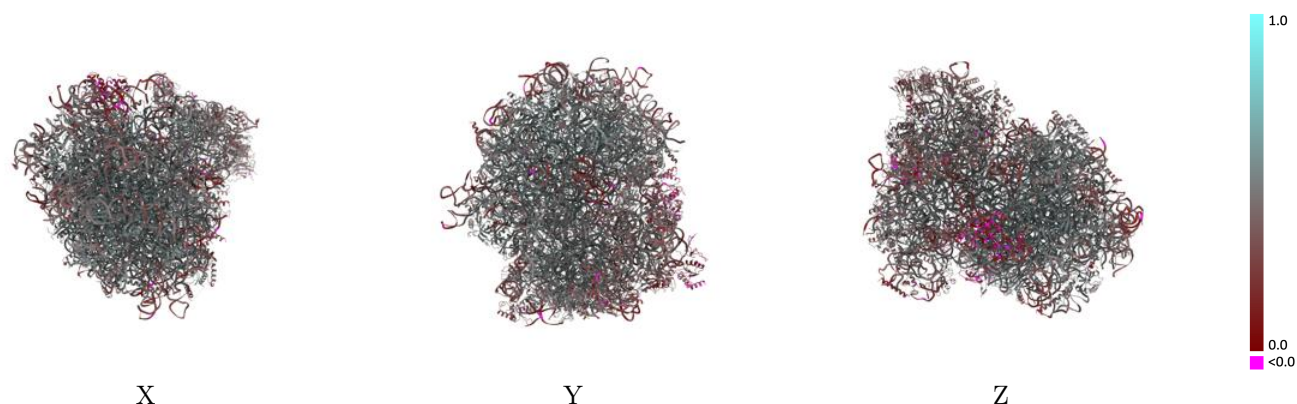
This section contains information regarding the fit between EMDB map EMD-43567 and PDB model 8VVS. Per-residue inclusion information can be found in section 3 on page 26.

9.1 Map-model overlay [i](#)



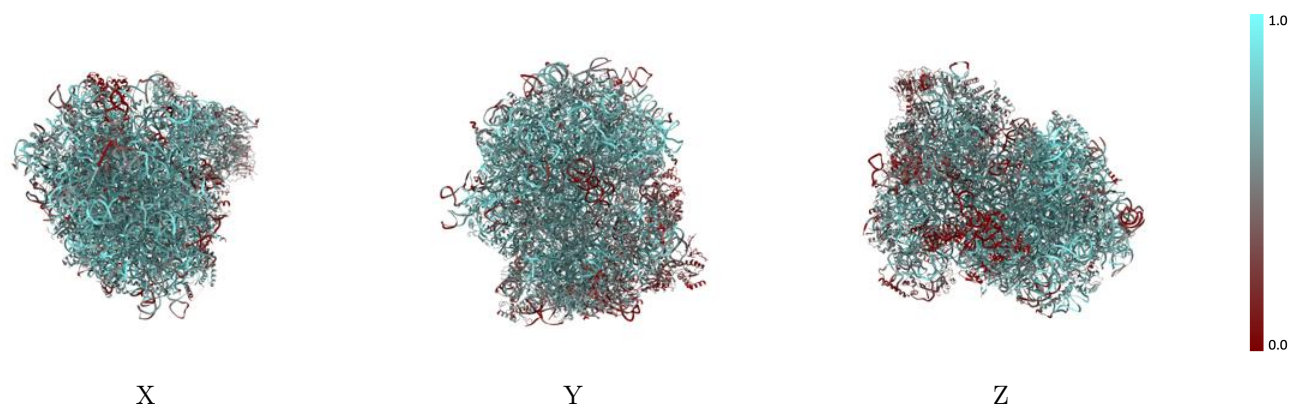
The images above show the 3D surface view of the map at the recommended contour level 6.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



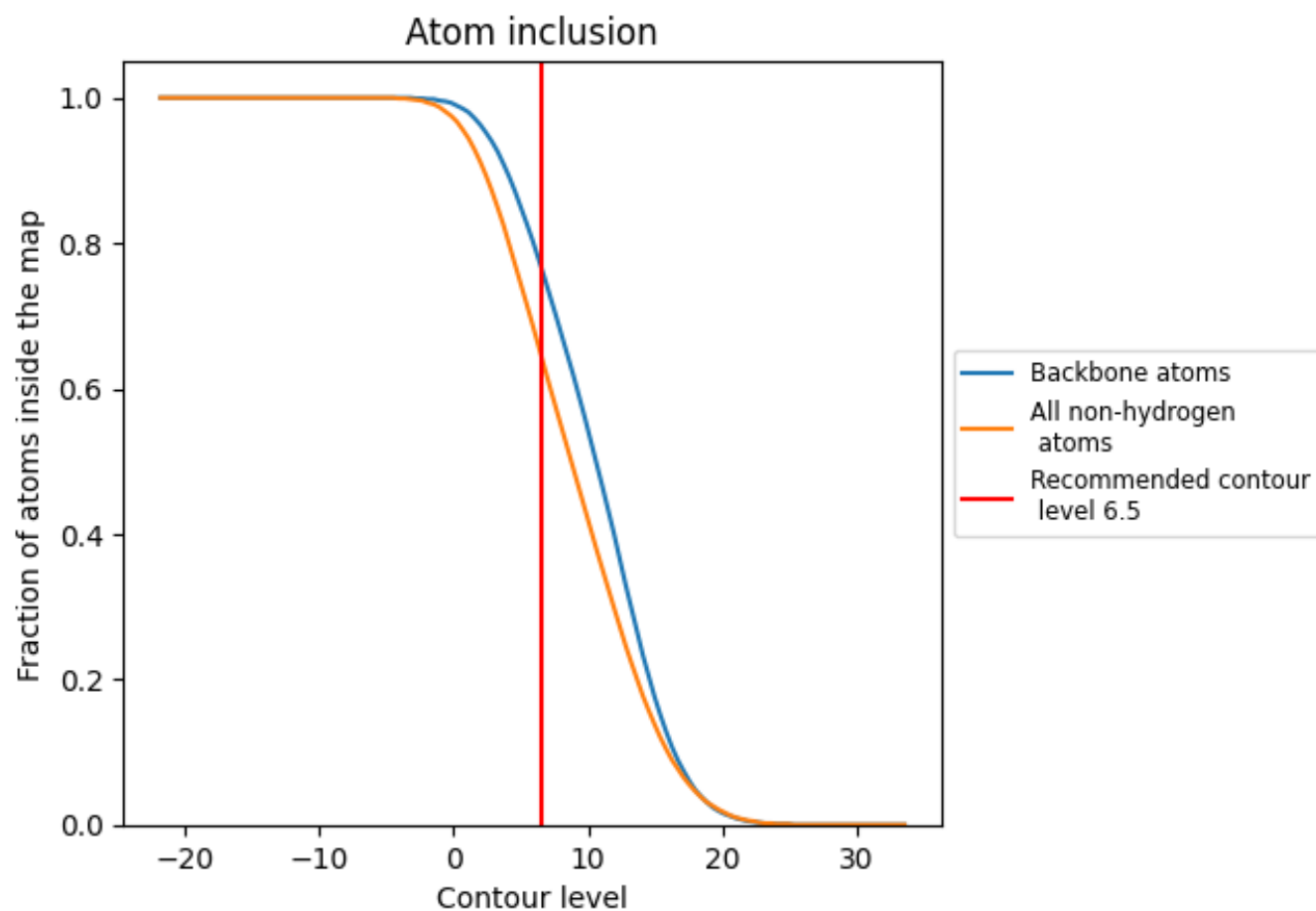
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (6.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 65% 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 (6.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6460	 0.4470
A	 0.6850	 0.5250
AA	 0.5240	 0.4290
AB	 0.5640	 0.4480
AC	 0.5950	 0.4800
B	 0.6640	 0.5000
BA	 0.6370	 0.4740
BB	 0.5470	 0.4620
BC	 0.4960	 0.4430
C	 0.6580	 0.5050
CA	 0.6370	 0.4870
CB	 0.5790	 0.4700
CC	 0.4830	 0.4270
D	 0.6490	 0.4570
DA	 0.6690	 0.5140
DB	 0.4440	 0.4000
DC	 0.5360	 0.4510
E	 0.5860	 0.4560
EA	 0.6590	 0.5230
EB	 0.5430	 0.4600
EC	 0.4440	 0.3890
F	 0.6400	 0.4970
FA	 0.6370	 0.4940
FB	 0.4920	 0.4150
FC	 0.1510	 0.2610
G	 0.5960	 0.4450
GA	 0.6280	 0.4750
GB	 0.4160	 0.3710
GC	 0.3270	 0.3460
H	 0.6140	 0.4700
HA	 0.6240	 0.4600
HB	 0.4550	 0.3990
HC	 0.0940	 0.2990
I	 0.6600	 0.5050
IA	 0.6960	 0.5230



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Chain	Atom inclusion	Q-score
IB	 0.5400	 0.4470
IC	 0.4500	 0.4450
J	 0.5850	 0.4410
JA	 0.5550	 0.4330
JB	 0.5490	 0.4390
K	 0.6270	 0.4870
KA	 0.6230	 0.4920
KB	 0.4160	 0.3740
L	 0.6270	 0.4650
LA	 0.6710	 0.5040
LB	 0.5980	 0.4910
M	 0.6990	 0.5240
MA	 0.6190	 0.4880
MB	 0.1710	 0.2180
N	 0.6630	 0.4960
NA	 0.6490	 0.5150
NB	 0.6130	 0.4650
O	 0.6530	 0.5080
OA	 0.6490	 0.5070
OB	 0.5720	 0.4590
P	 0.6760	 0.5120
PA	 0.6630	 0.5020
PB	 0.4030	 0.3730
Q	 0.6320	 0.4700
QB	 0.4780	 0.4160
R	 0.6550	 0.4970
RA	 0.0190	 0.1040
RB	 0.4910	 0.4190
S	 0.6370	 0.4920
SA	 0.5680	 0.4020
SB	 0.4790	 0.4040
T	 0.5610	 0.4300
TA	 0.1550	 0.2340
TB	 0.4980	 0.4050
U	 0.6480	 0.5110
UA	 0.1610	 0.2630
UB	 0.4050	 0.3770
V	 0.4820	 0.3960
VA	 0.4820	 0.4170
VB	 0.5850	 0.4520
W	 0.6310	 0.4740
WA	 0.7500	 0.4610

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Chain	Atom inclusion	Q-score
WB	 0.6060	 0.4800
X	 0.6350	 0.4820
XA	 0.8460	 0.4940
XB	 0.5810	 0.4850
Y	 0.6570	 0.4800
YA	 0.7580	 0.4690
YB	 0.4740	 0.4100
Z	 0.7070	 0.5150
ZA	 0.6920	 0.4370
ZB	 0.3880	 0.3790
b	 0.0410	 0.1270
c	 0.0090	 0.1480