



## Full wwPDB EM Validation Report ⓘ

Nov 5, 2024 – 03:13 AM JST

PDB ID : 5ZWM  
EMDB ID : EMD-6972  
Title : Cryo-EM structure of the yeast pre-B complex at an average resolution of 3.4 4.6 angstrom (tri-snRNP and U2 snRNP Part)  
Authors : Bai, R.; Wan, R.; Yan, C.; Lei, J.; Shi, Y.  
Deposited on : 2018-05-16  
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

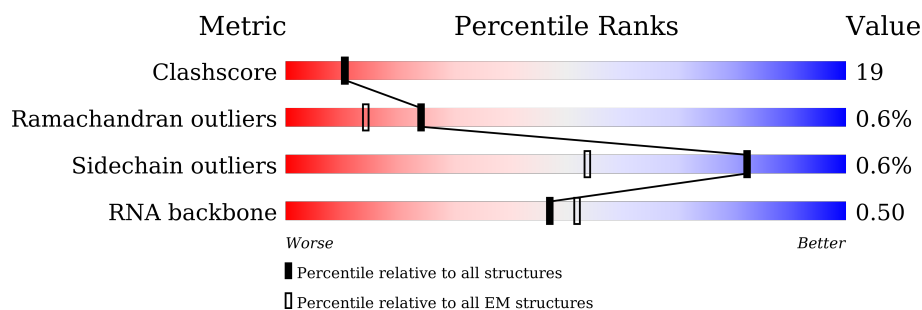
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.40 Å.

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





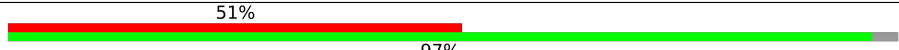
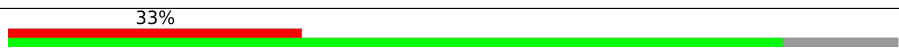

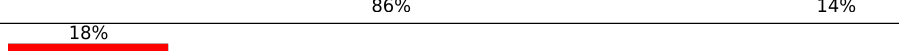
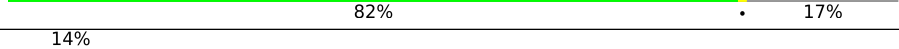


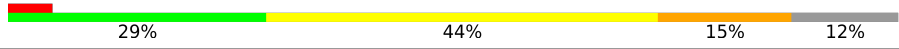

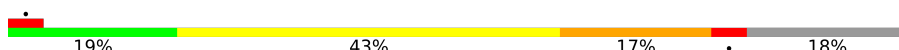
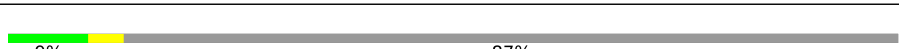







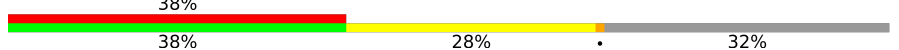

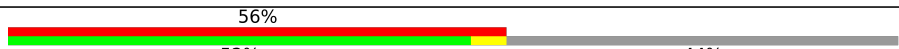
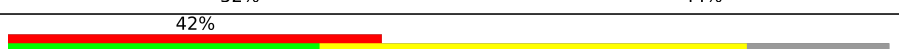
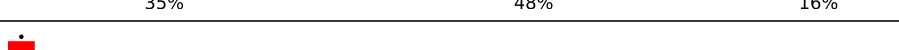
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	A	2413	 8% 60% 29% 10%
2	K	465	 53% 38% 8%
3	L	494	 58% 26% 16%
4	N	899	 65% 16% 19%
5	J	469	 50% 14% 35%
6	E	143	 71% 27% 2%
7	M	126	 75% 25%




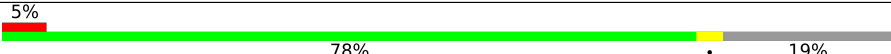


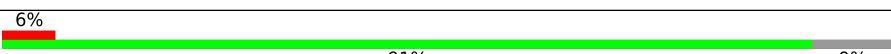
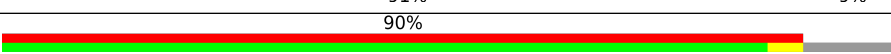

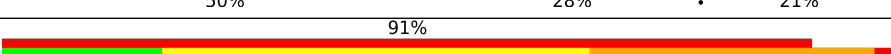


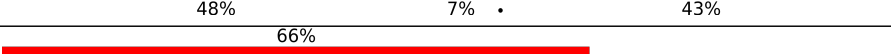



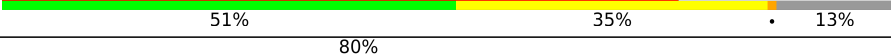





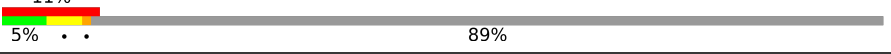


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Mol	Chain	Length	Quality of chain
8	C	1008	
9	z	109	
10	q	95	
11	r	89	
12	x	86	
13	t	93	
14	y	115	
15	s	187	
16	F	112	
17	I	160	
18	B	214	
19	O	587	
20	S	101	
20	d	101	
20	l	101	
21	P	196	
21	a	196	
21	h	196	
22	Q	146	
22	b	146	
22	m	146	
23	R	110	
23	c	110	
23	n	110	
24	T	94	

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Mol	Chain	Length	Quality of chain
24	e	94	
24	i	94	
25	U	86	
25	f	86	
25	j	86	
26	V	77	
26	g	77	
26	k	77	
27	D	2163	
28	G	44	
29	H	1175	
30	o	238	
31	p	111	
32	1	971	
33	2	436	
34	3	1361	
35	4	213	
36	5	107	
37	6	85	
38	X	148	
39	Y	266	
40	Z	204	
41	u	530	
42	w	280	
43	v	266	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
46	ZN	5	201	-	-	X	-

## 2 Entry composition

There are 46 unique types of molecules in this entry. The entry contains 111041 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 Pre-mRNA-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2177	Total	C	N	O	S	0	0
			17877	11496	3054	3263	64		

- Molecule 2 is a protein called U4/U6 small nuclear ribonucleoprotein PRP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	K	429	Total	C	N	O	S	0	0
			3375	2101	610	650	14		

- Molecule 3 is a protein called Pre-mRNA-processing factor 31.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	416	Total	C	N	O	S	0	0
			3171	2001	573	585	12		

- Molecule 4 is a protein called Pre-mRNA-splicing factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	728	Total	C	N	O	S	0	0
			4897	3045	905	933	14		

- Molecule 5 is a protein called U4/U6 small nuclear ribonucleoprotein PRP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	J	304	Total	C	N	O	S	0	0
			2439	1545	445	435	14		

- Molecule 6 is a protein called Spliceosomal protein DIB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	139	Total	C	N	O	S	0	0
			1146	725	199	211	11		

- Molecule 7 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	126	Total	C	N	O	S	0	0
			950	605	163	177	5		

- Molecule 8 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	843	Total	C	N	O	S	0	0
			6732	4350	1119	1235	28		

- Molecule 9 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	z	65	Total	C	N	O	0	0
			260	130	65	65		

- Molecule 10 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	q	92	Total	C	N	O	0	0
			368	184	92	92		

- Molecule 11 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	r	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 12 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	x	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 13 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	t	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 14 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	y	66	Total	C	N	O	0	0
			264	132	66	66		

- Molecule 15 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	s	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 16 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	F	99	Total	C	N	O	P	0	0
			2043	913	341	690	99		

- Molecule 17 is a RNA chain called U4 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	110	Total	C	N	O	P	0	0
			2334	1044	399	781	110		

- Molecule 18 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	B	175	Total	C	N	O	P	0	0
			3715	1663	651	1227	174		

- Molecule 19 is a protein called 66 kDa U4/U6.U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	74	Total	C	N	O	S	0	0
			574	350	103	120	1		

- Molecule 20 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	d	79	Total	C	N	O		0	0
			316	158	79	79			
20	S	82	Total	C	N	O	S	0	0
			632	402	109	119	2		
20	l	81	Total	C	N	O	S	0	0
			611	390	106	113	2		



- Molecule 21 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	a	73	Total	C	N	O		0	0
			292	146	73	73			
21	P	70	Total	C	N	O	S	0	0
			563	360	98	102	3		
21	h	78	Total	C	N	O	S	0	0
			610	389	110	108	3		

- Molecule 22 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	b	77	Total	C	N	O		0	0
			308	154	77	77			
22	Q	99	Total	C	N	O	S	0	0
			751	475	137	137	2		
22	m	82	Total	C	N	O	S	0	0
			644	409	110	123	2		

- Molecule 23 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	c	90	Total	C	N	O		0	0
			360	180	90	90			
23	R	92	Total	C	N	O	S	0	0
			752	481	136	131	4		
23	n	65	Total	C	N	O	S	0	0
			528	340	102	84	2		

- Molecule 24 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	e	72	Total	C	N	O		0	0
			288	144	72	72			
24	T	77	Total	C	N	O	S	0	0
			602	396	95	108	3		
24	i	75	Total	C	N	O	S	0	0
			575	379	92	101	3		

- Molecule 25 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	f	70	Total	C	N	O		0	0
			280	140	70	70			
25	U	73	Total	C	N	O	S	0	0
			585	376	102	106	1		
25	j	70	Total	C	N	O	S	0	0
			554	355	98	100	1		

- Molecule 26 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	g	70	Total	C	N	O		0	0
			280	140	70	70			
26	V	75	Total	C	N	O	S	0	0
			577	363	100	112	2		
26	k	69	Total	C	N	O	S	0	0
			529	337	93	97	2		

- Molecule 27 is a protein called Pre-mRNA-splicing helicase BRR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	D	1699	Total	C	N	O	S	1	0
			13601	8717	2266	2564	54		

- Molecule 28 is a RNA chain called Pre-mRNA-BPS.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	G	44	Total	C	N	O	P	0	0
			928	419	161	304	44		

- Molecule 29 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	H	206	Total	C	N	O	P	0	0
			4345	1940	722	1477	206		

- Molecule 30 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	o	135	Total	C	N	O	0	0
			841	538	142	161		

- Molecule 31 is a protein called U2 small nuclear ribonucleoprotein B''.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	p	73	Total	C	N	O	0	0
			466	304	81	81		

- Molecule 32 is a protein called U2 snRNP component HSH155.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	1	816	Total	C	N	O	S	0	0
			6472	4165	1101	1166	40		

- Molecule 33 is a protein called Cold sensitive U2 snRNA suppressor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	2	211	Total	C	N	O	S	0	0
			1726	1121	292	304	9		

- Molecule 34 is a protein called Pre-mRNA-splicing factor RSE1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	3	1180	Total	C	N	O	S	0	0
			9380	5996	1580	1753	51		

- Molecule 35 is a protein called Protein HSH49.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	4	173	Total	C	N	O	S	0	0
			1429	930	239	258	2		

- Molecule 36 is a protein called Pre-mRNA-splicing factor RDS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	5	103	Total	C	N	O	S	0	0
			814	503	154	143	14		

- Molecule 37 is a protein called RDS3 complex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	6	84	Total	C	N	O	S	0	0
			693	429	130	132	2		

- Molecule 38 is a protein called U2 snRNP component IST3.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	X	128	Total	C	N	O		
			1051	662	181	208	0	0

- Molecule 39 is a protein called Pre-mRNA-splicing factor CWC26.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Y	89	Total	C	N	O	S		
			730	458	130	140	2	0	0

- Molecule 40 is a protein called Pre-mRNA leakage protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Z	22	Total	C	N	O	S		
			173	110	25	37	1	0	0

- Molecule 41 is a protein called Pre-mRNA-splicing factor PRP9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	u	461	Total	C	N	O	S		
			3895	2475	675	730	15	0	0

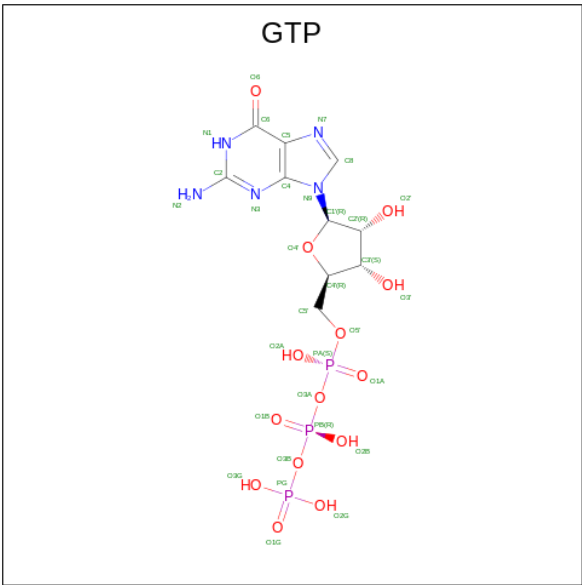
- Molecule 42 is a protein called Pre-mRNA-splicing factor PRP21.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	w	127	Total	C	N	O	S		
			1084	689	193	196	6	0	0

- Molecule 43 is a protein called Pre-mRNA-splicing factor PRP11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	v	174	Total	C	N	O	S		
			1372	862	235	269	6	0	0

- Molecule 44 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>14</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					AltConf
44	C	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 45 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
45	C	1	Total	Mg	0
			1	1	

- Molecule 46 is ZINC ION (three-letter code: ZN) (formula: Zn).

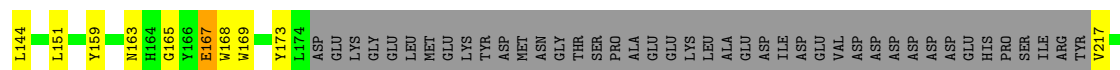
Mol	Chain	Residues	Atoms		AltConf
46	5	3	Total	Zn	0
			3	3	
46	u	2	Total	Zn	0
			2	2	
46	v	1	Total	Zn	0
			1	1	

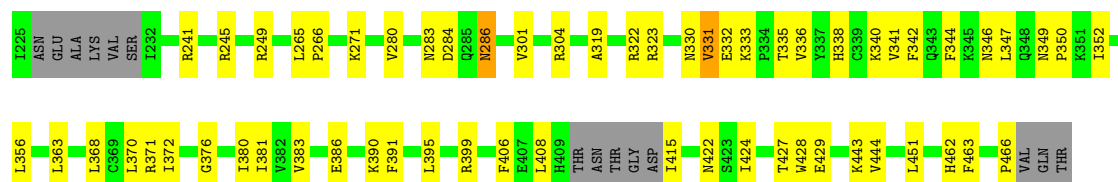




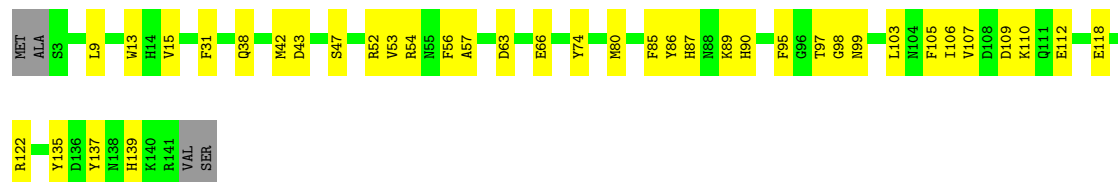




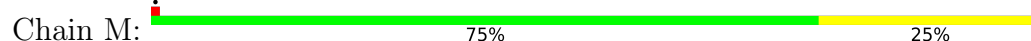




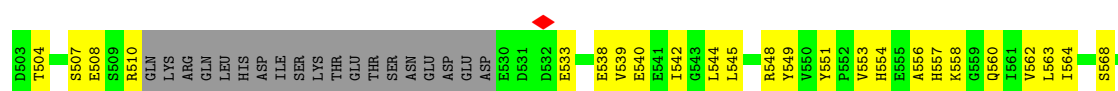
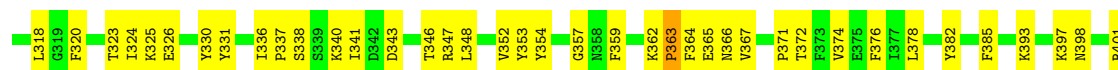
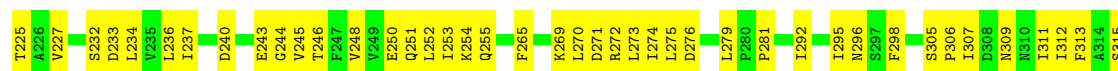
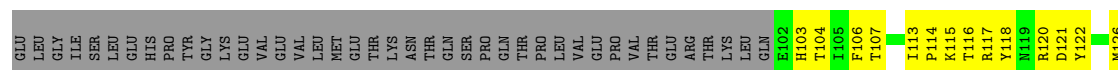
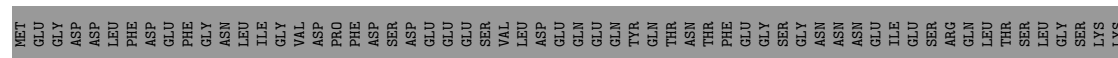
• Molecule 6: Spliceosomal protein DIB1

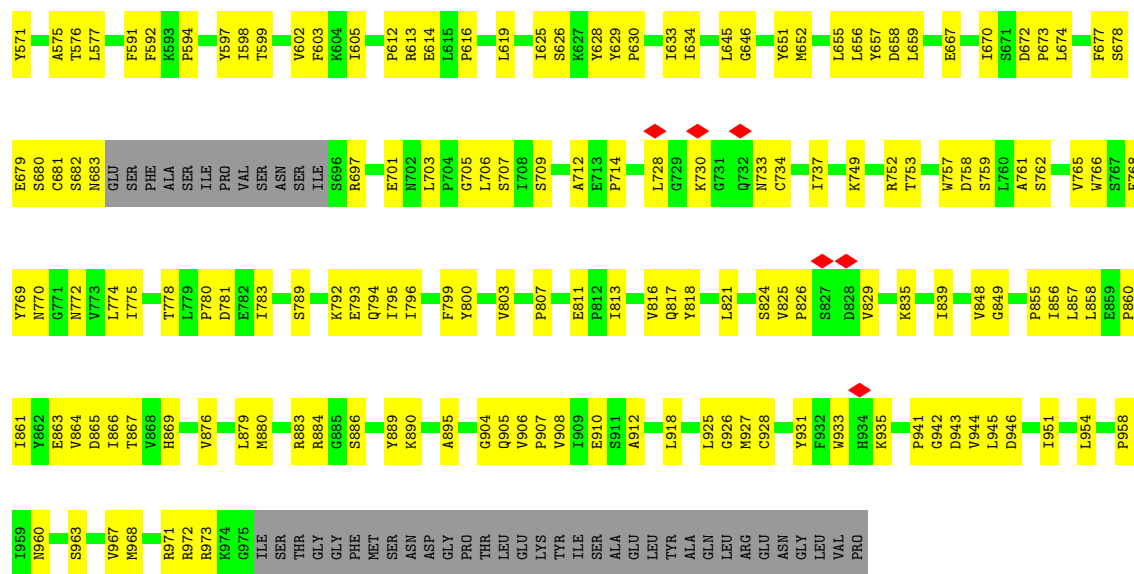


• Molecule 7: 13 kDa ribonucleoprotein-associated protein

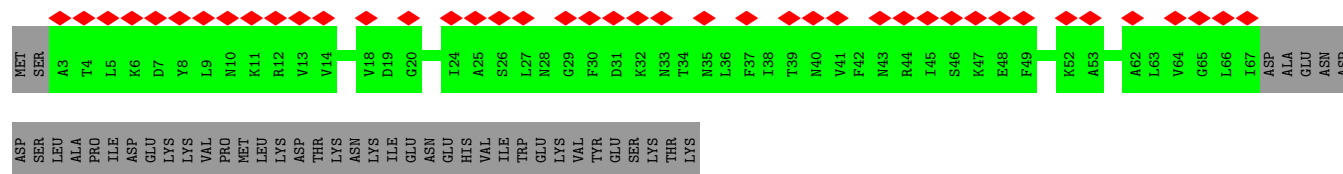
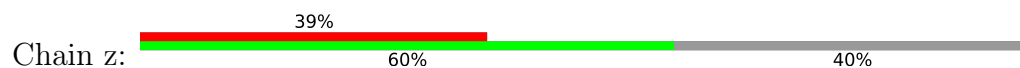


• Molecule 8: Pre-mRNA-splicing factor SNU114

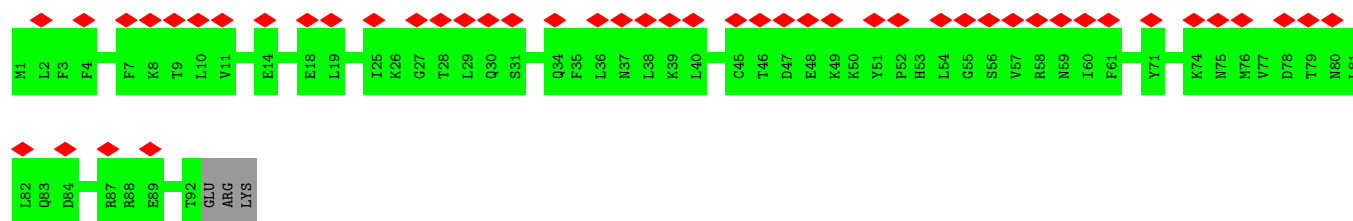




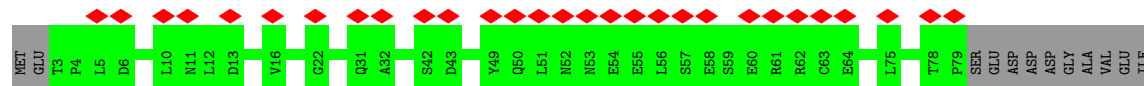
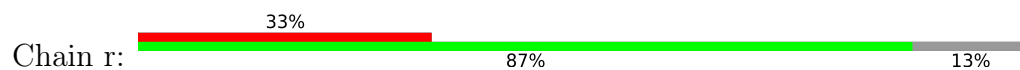
• Molecule 9: U6 snRNA-associated Sm-like protein LSm8



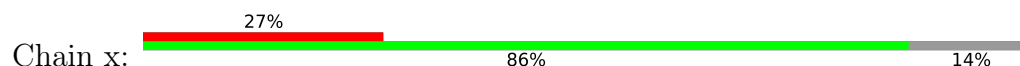
• Molecule 10: U6 snRNA-associated Sm-like protein LSm2

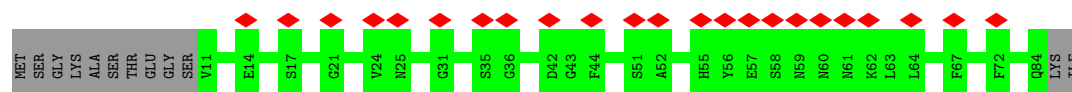


• Molecule 11: U6 snRNA-associated Sm-like protein LSm3

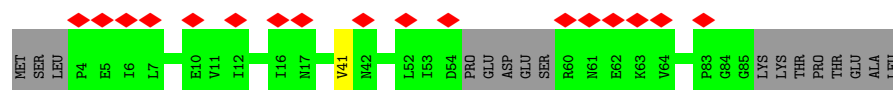
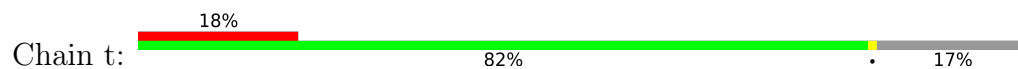


• Molecule 12: U6 snRNA-associated Sm-like protein LSm6

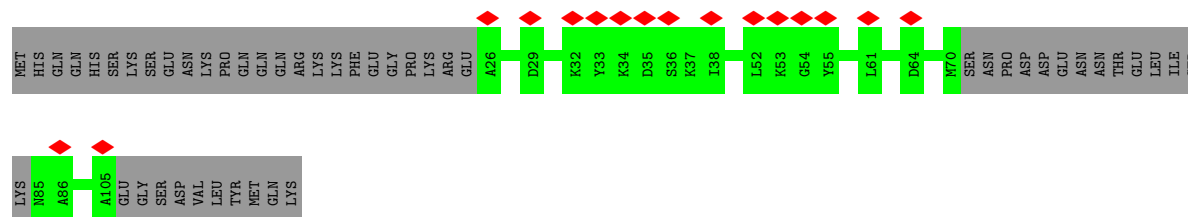




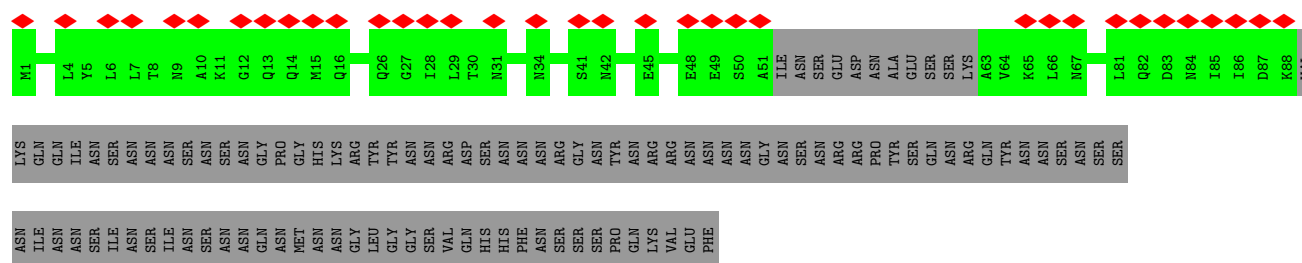
• Molecule 13: U6 snRNA-associated Sm-like protein LSm5



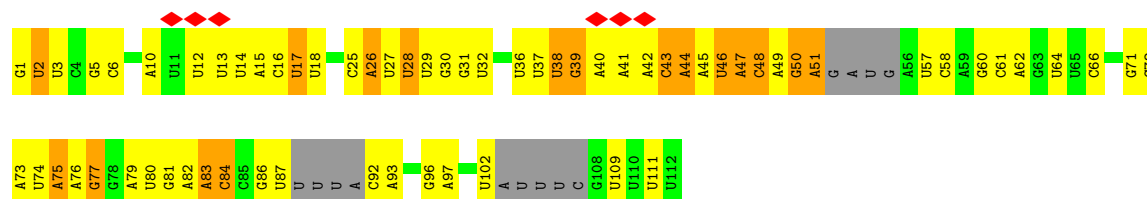
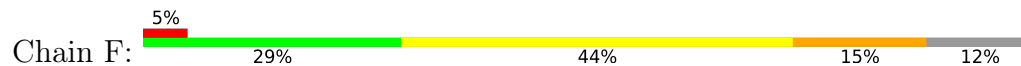
• Molecule 14: U6 snRNA-associated Sm-like protein LSm7



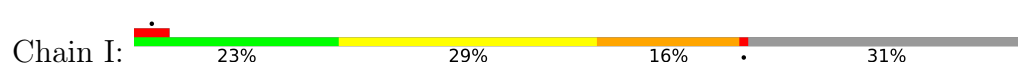
• Molecule 15: U6 snRNA-associated Sm-like protein LSm4



• Molecule 16: U6 snRNA

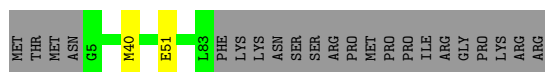
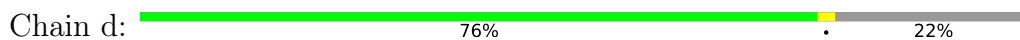


• Molecule 17: U4 snRNA

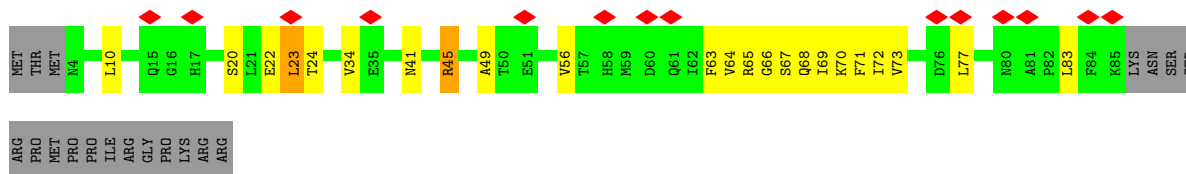




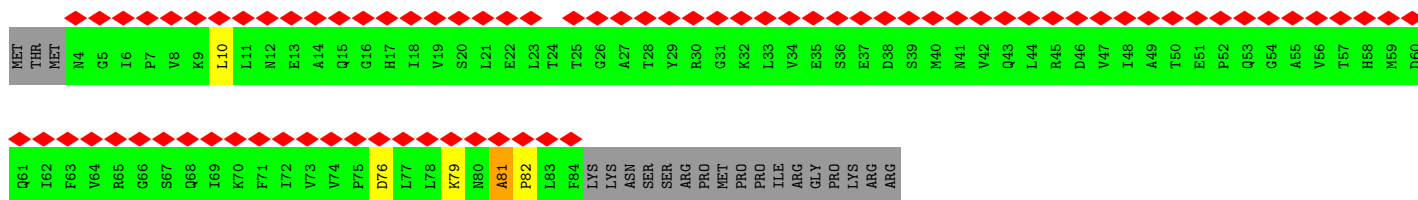
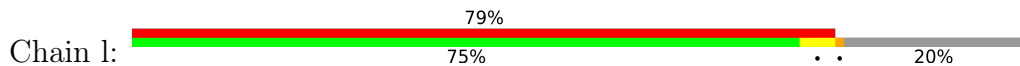
- Molecule 20: Small nuclear ribonucleoprotein Sm D3



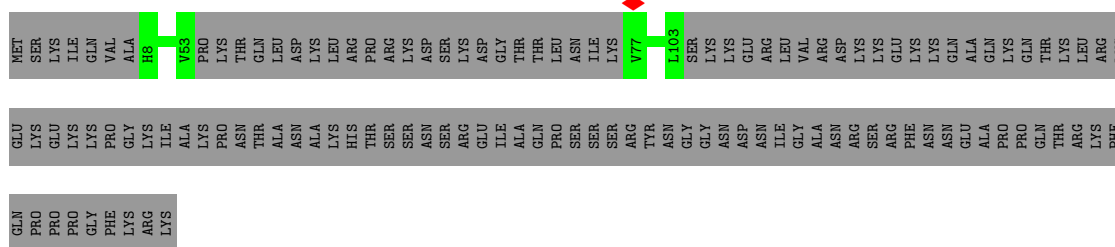
- Molecule 20: Small nuclear ribonucleoprotein Sm D3



- Molecule 20: Small nuclear ribonucleoprotein Sm D3

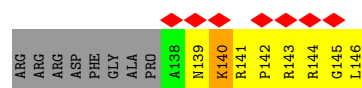


- Molecule 21: Small nuclear ribonucleoprotein-associated protein B

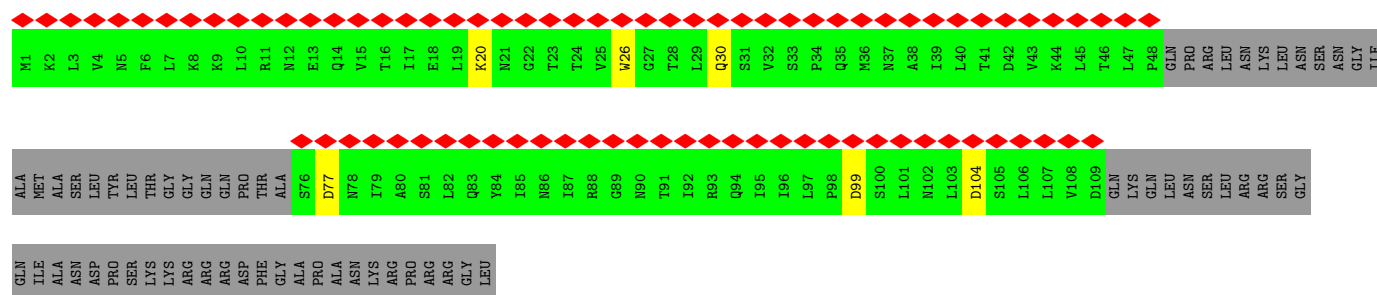


- Molecule 21: Small nuclear ribonucleoprotein-associated protein B

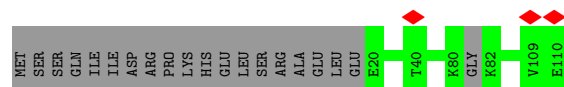
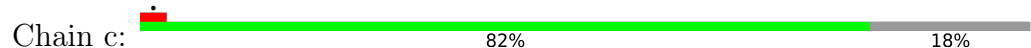




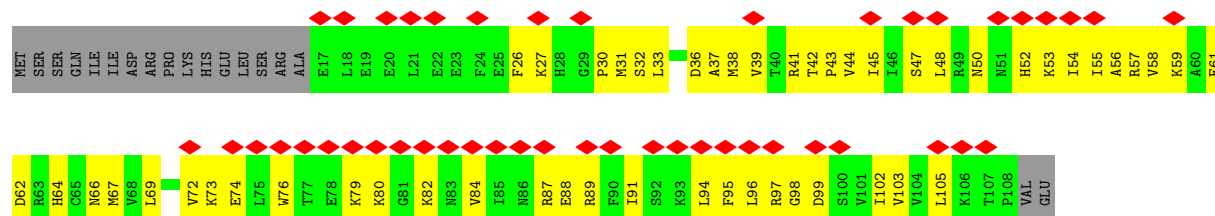
• Molecule 22: Small nuclear ribonucleoprotein Sm D1



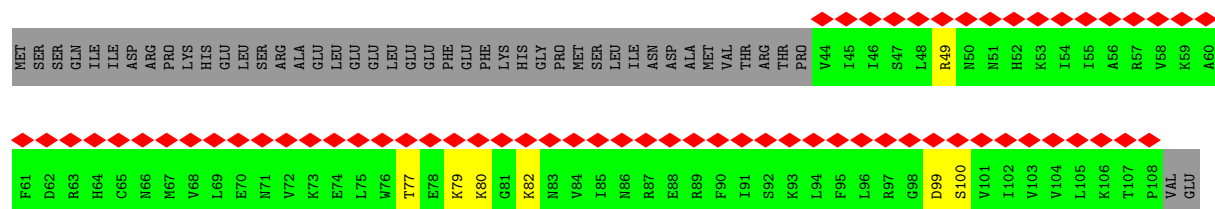
• Molecule 23: Small nuclear ribonucleoprotein Sm D2



• Molecule 23: Small nuclear ribonucleoprotein Sm D2



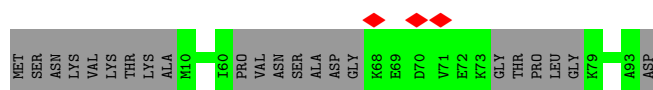
• Molecule 23: Small nuclear ribonucleoprotein Sm D2



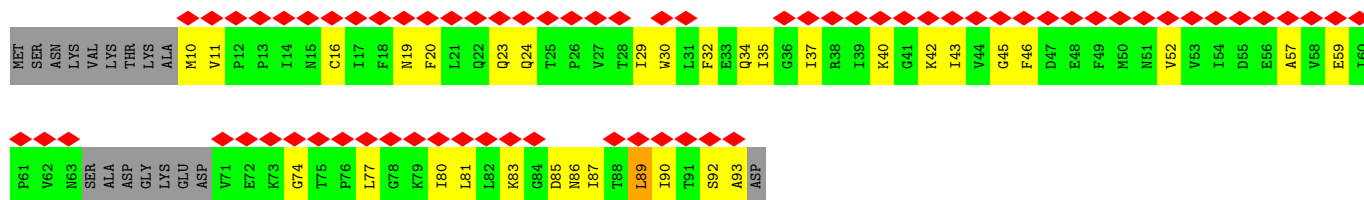
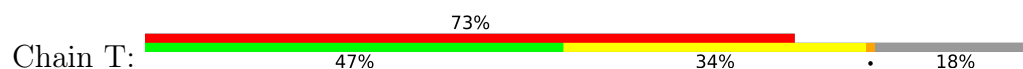
• Molecule 24: Small nuclear ribonucleoprotein E



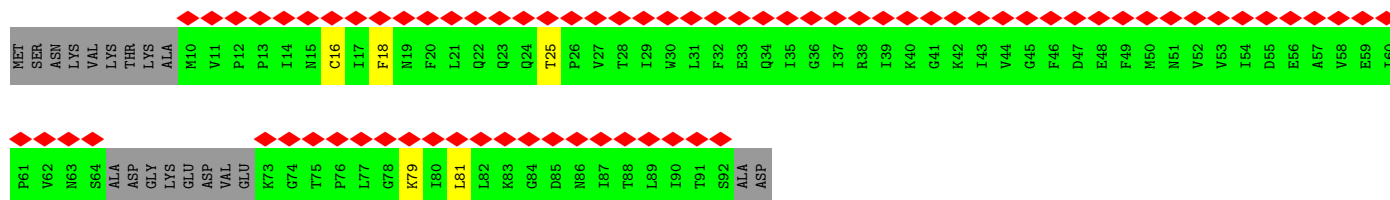
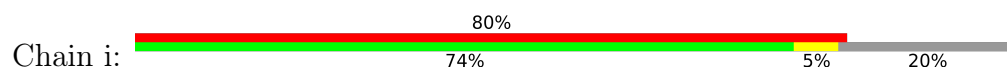




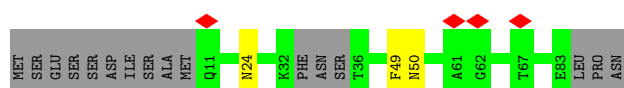
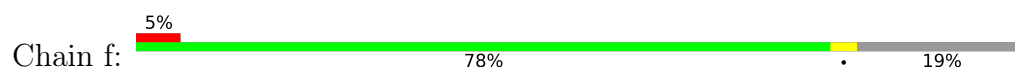
- Molecule 24: Small nuclear ribonucleoprotein E



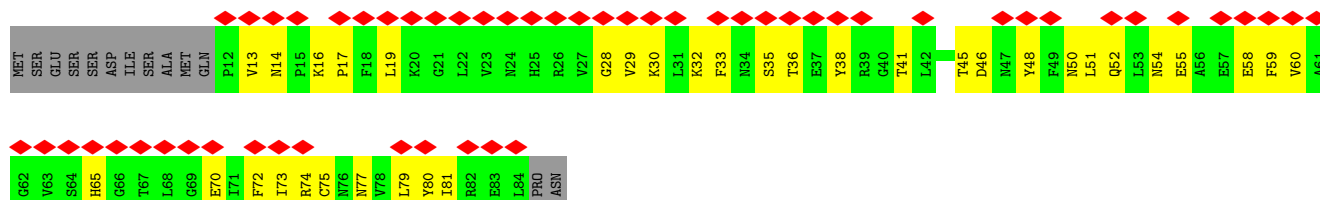
- Molecule 24: Small nuclear ribonucleoprotein E



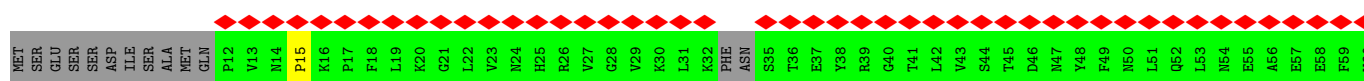
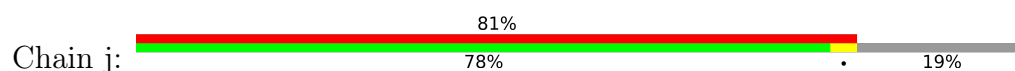
- Molecule 25: Small nuclear ribonucleoprotein F



- Molecule 25: Small nuclear ribonucleoprotein F

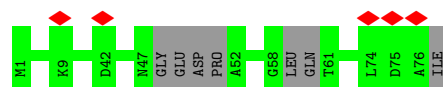
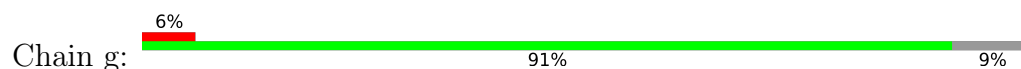


- Molecule 25: Small nuclear ribonucleoprotein F

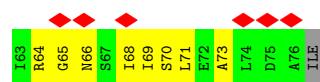




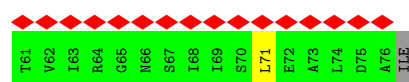
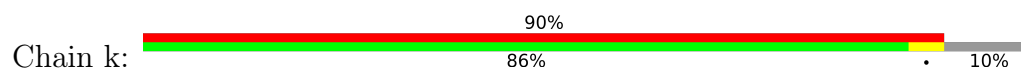
• Molecule 26: Small nuclear ribonucleoprotein G



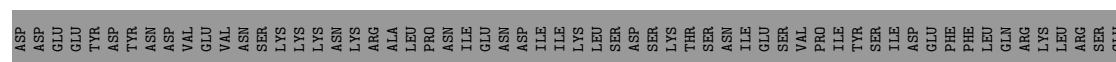
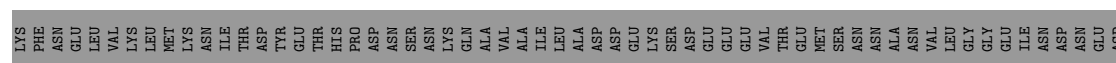
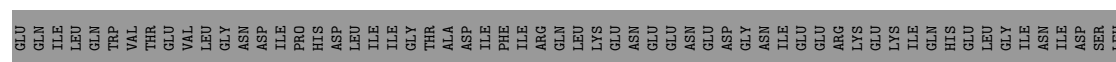
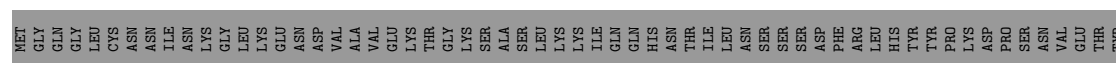
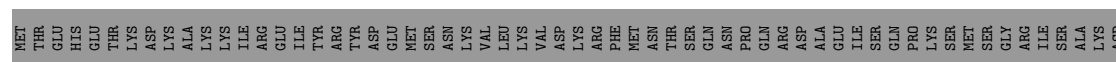
• Molecule 26: Small nuclear ribonucleoprotein G



• Molecule 26: Small nuclear ribonucleoprotein G

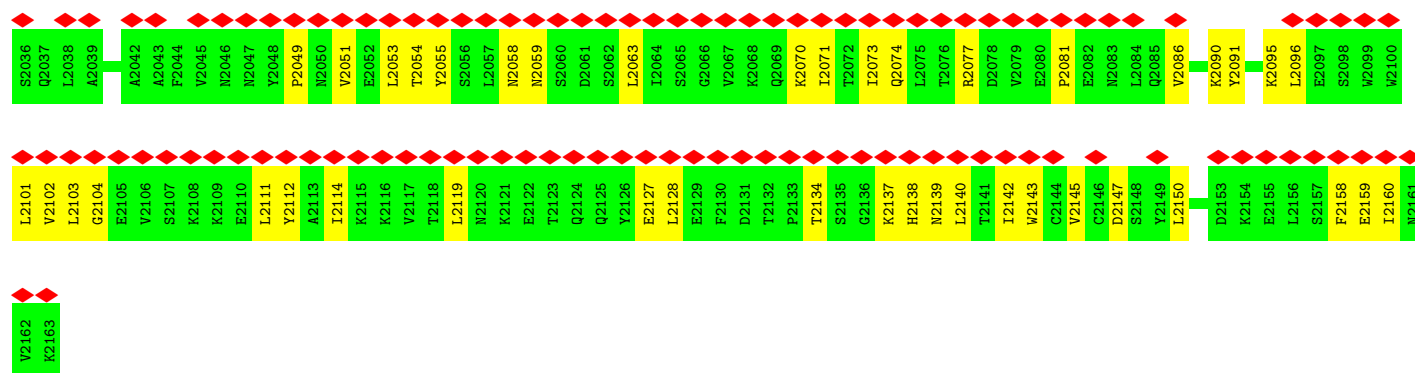


• Molecule 27: Pre-mRNA-splicing helicase BRR2

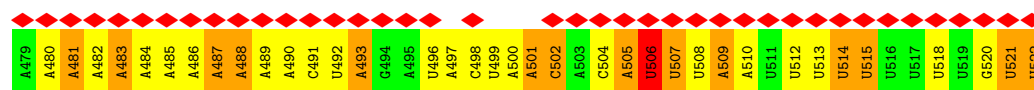
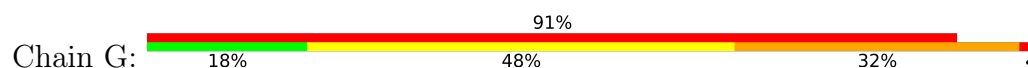




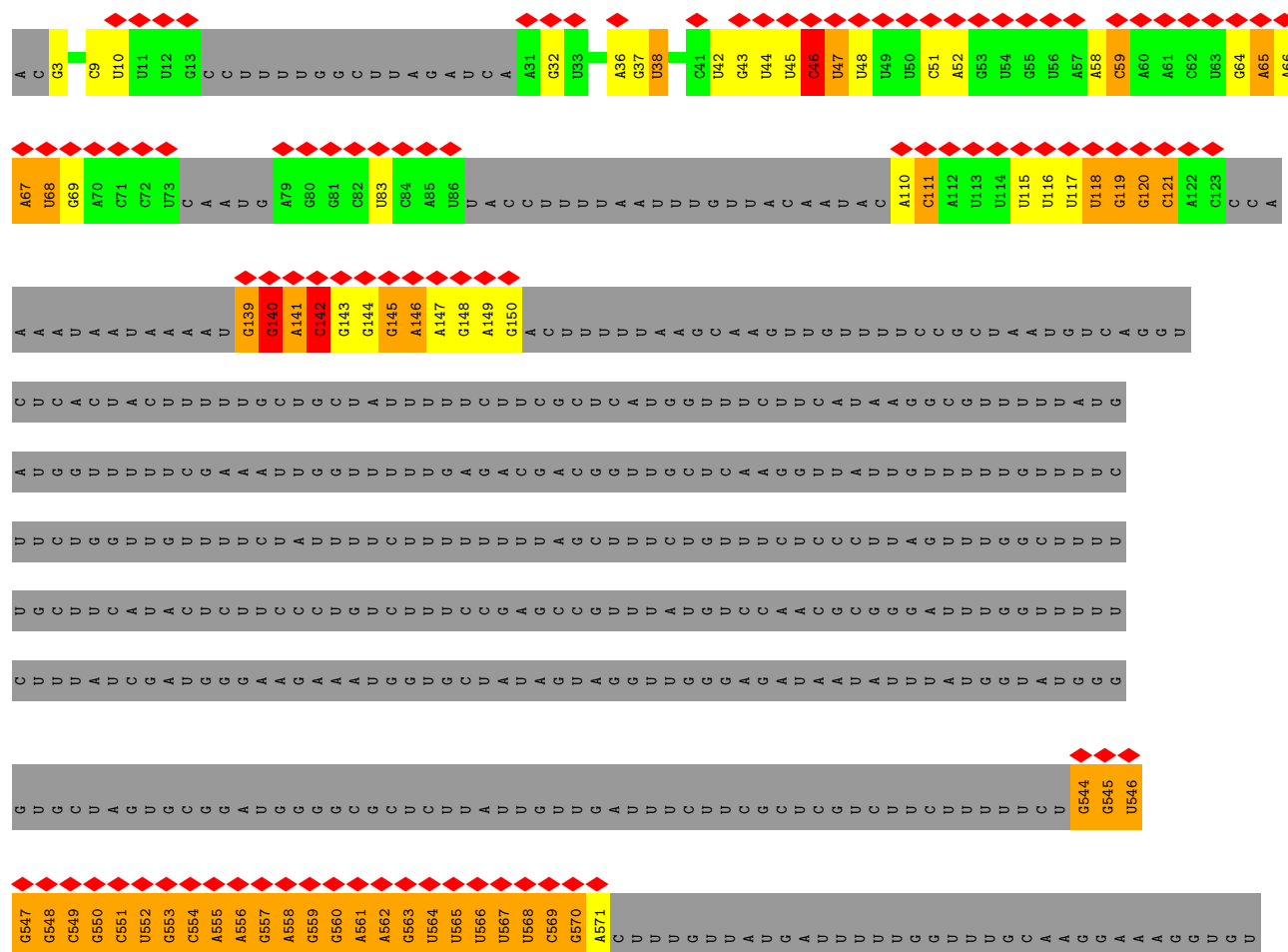


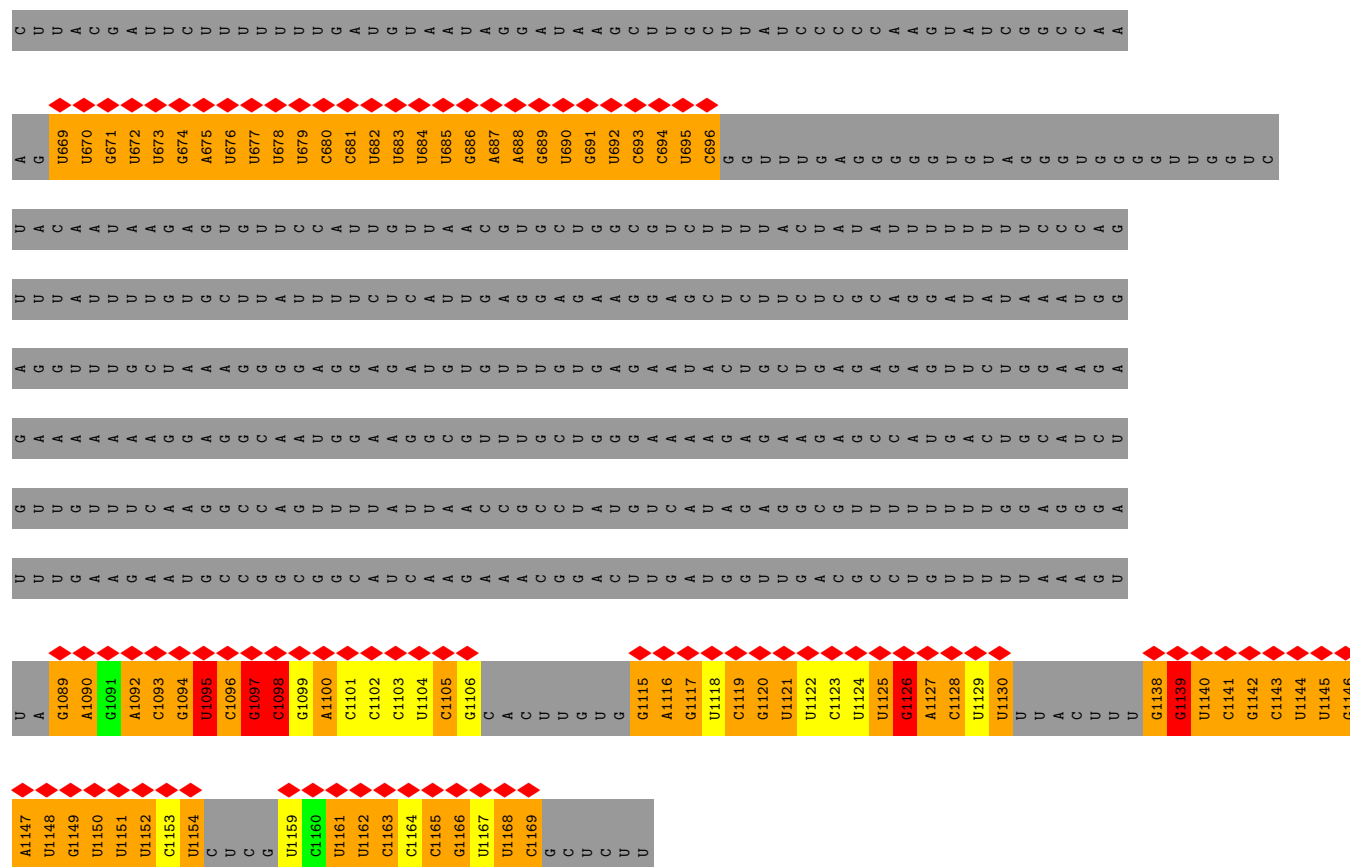


• Molecule 28: Pre-mRNA-BPS

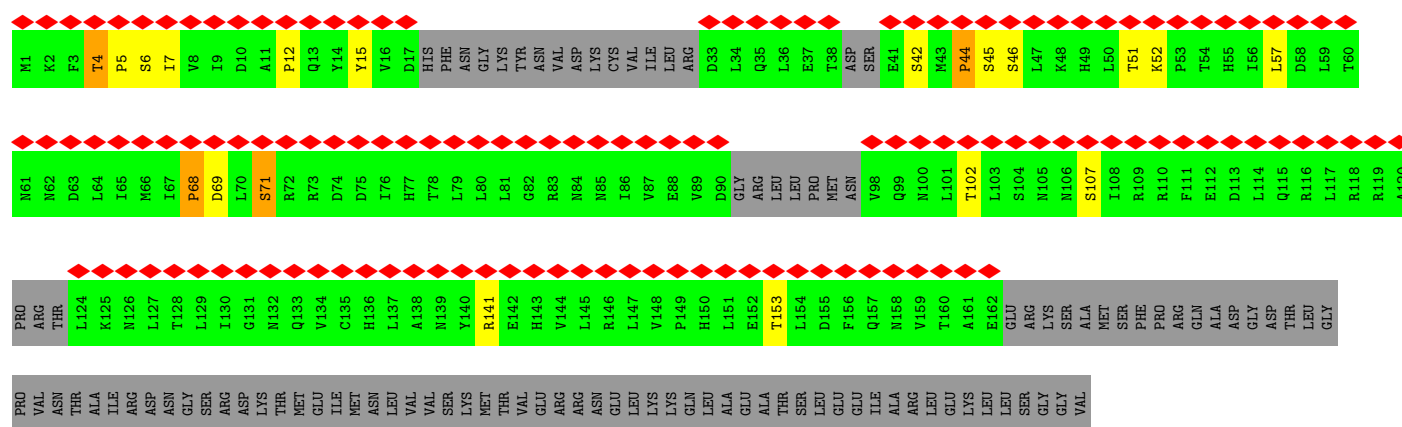


• Molecule 29: U2 snRNA



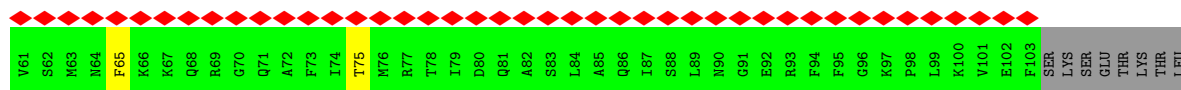


• Molecule 30: U2 small nuclear ribonucleoprotein A'

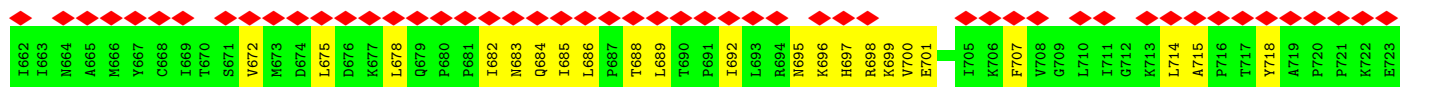
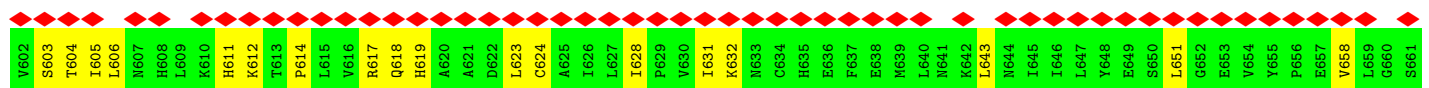
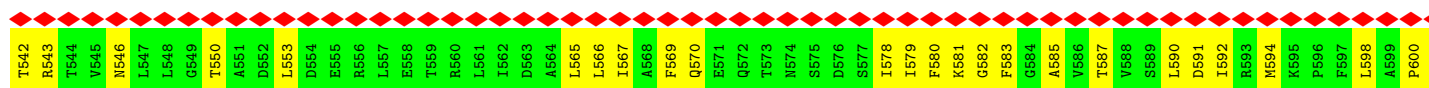
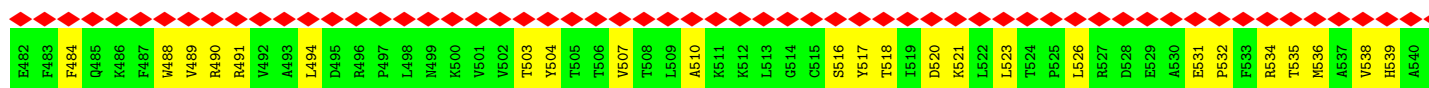
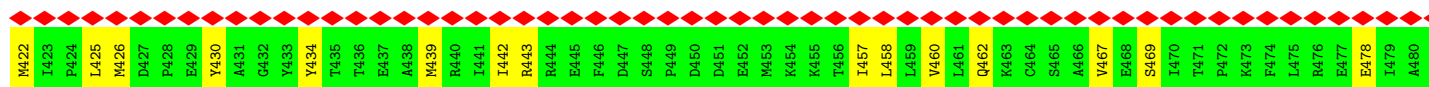
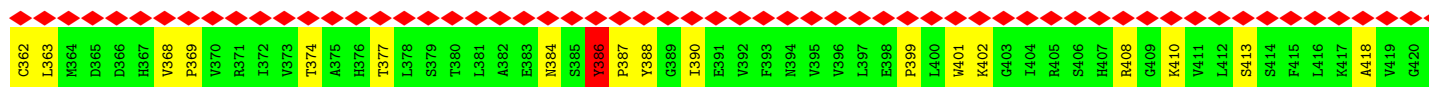
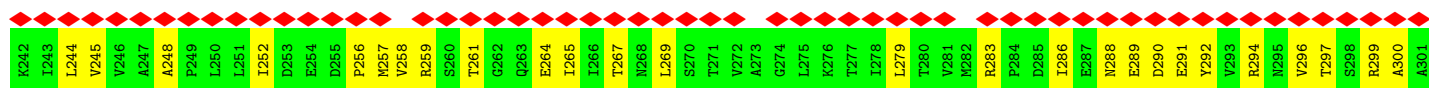
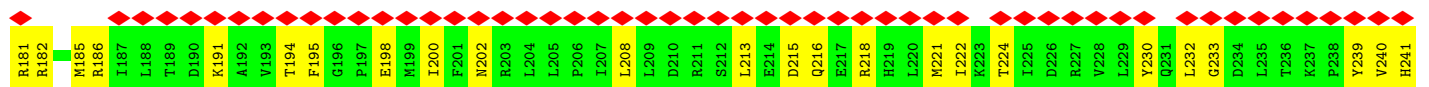
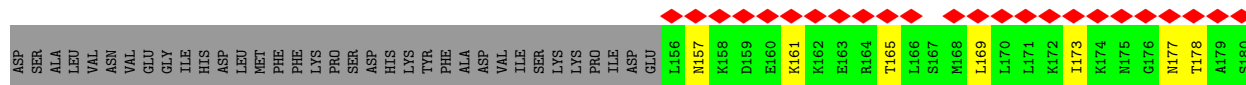
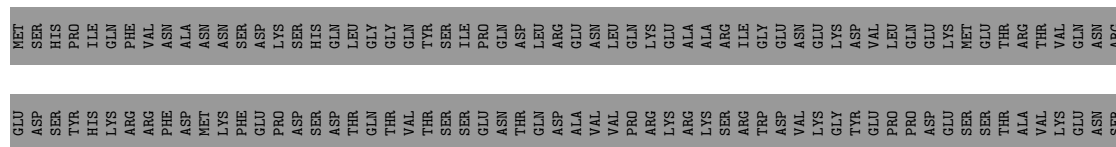
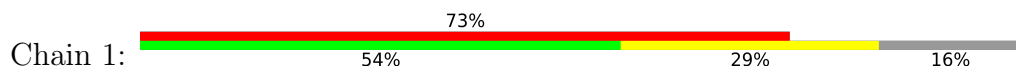


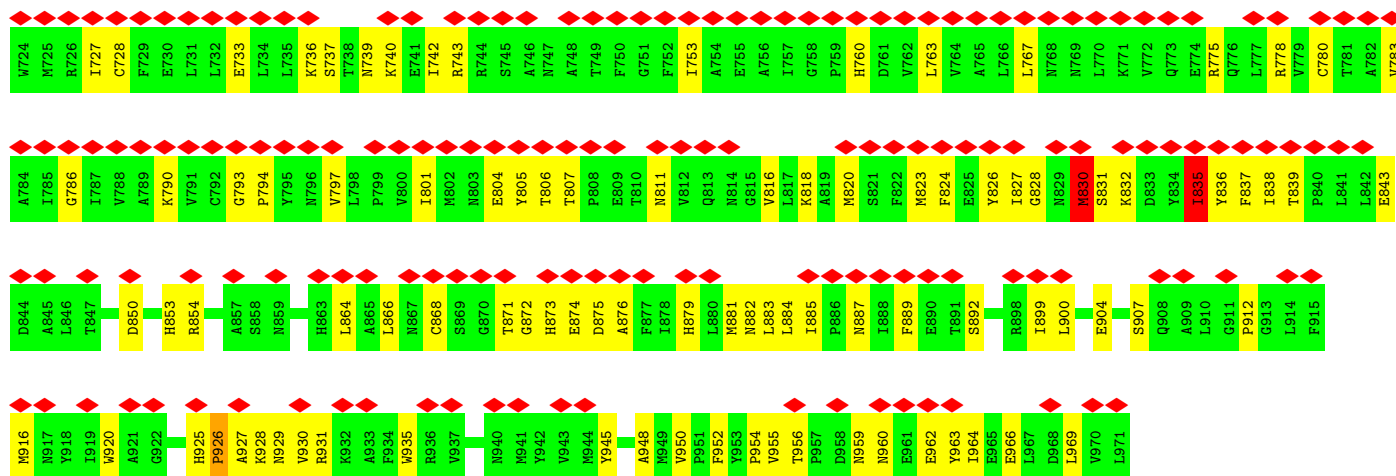
• Molecule 31: U2 small nuclear ribonucleoprotein B'



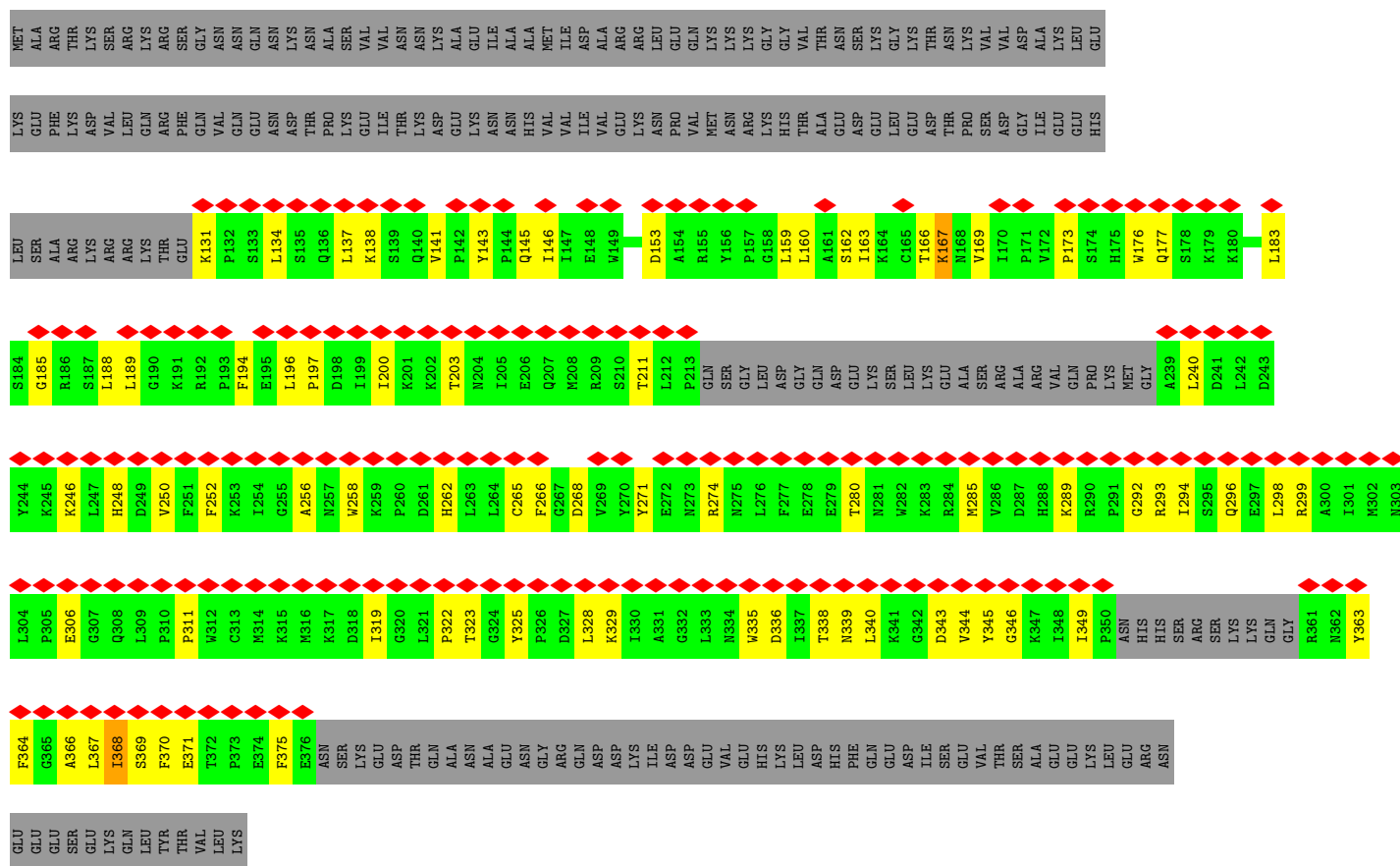
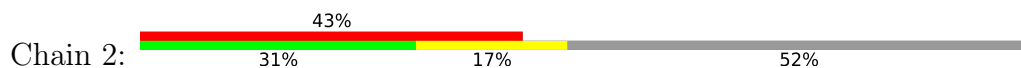


• Molecule 32: U2 snRNP component HSH155

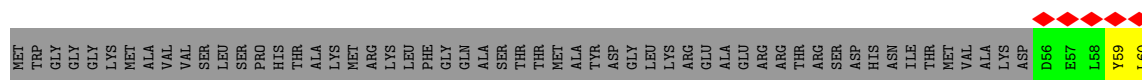
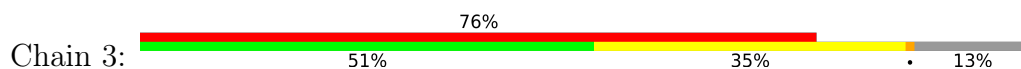




• Molecule 33: Cold sensitive U2 snRNA suppressor 1



• Molecule 34: Pre-mRNA-splicing factor RSE1

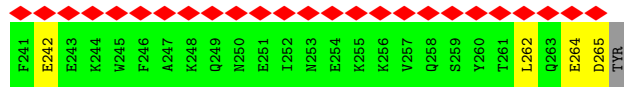




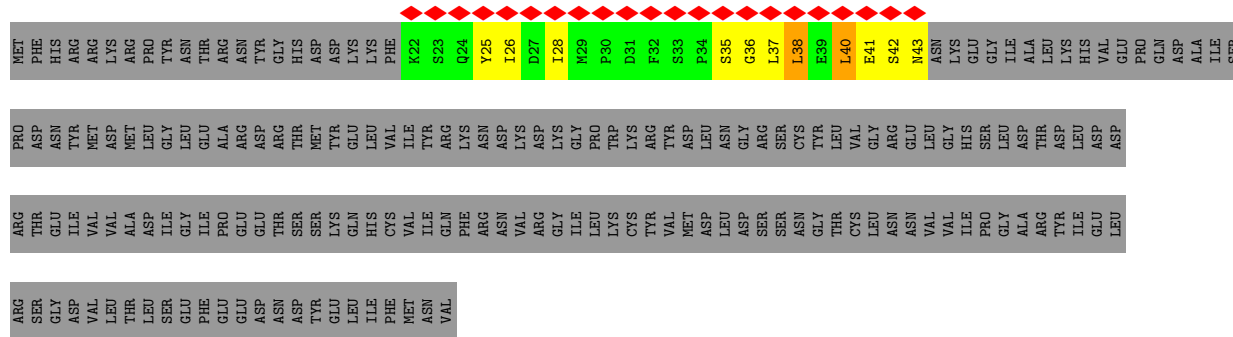




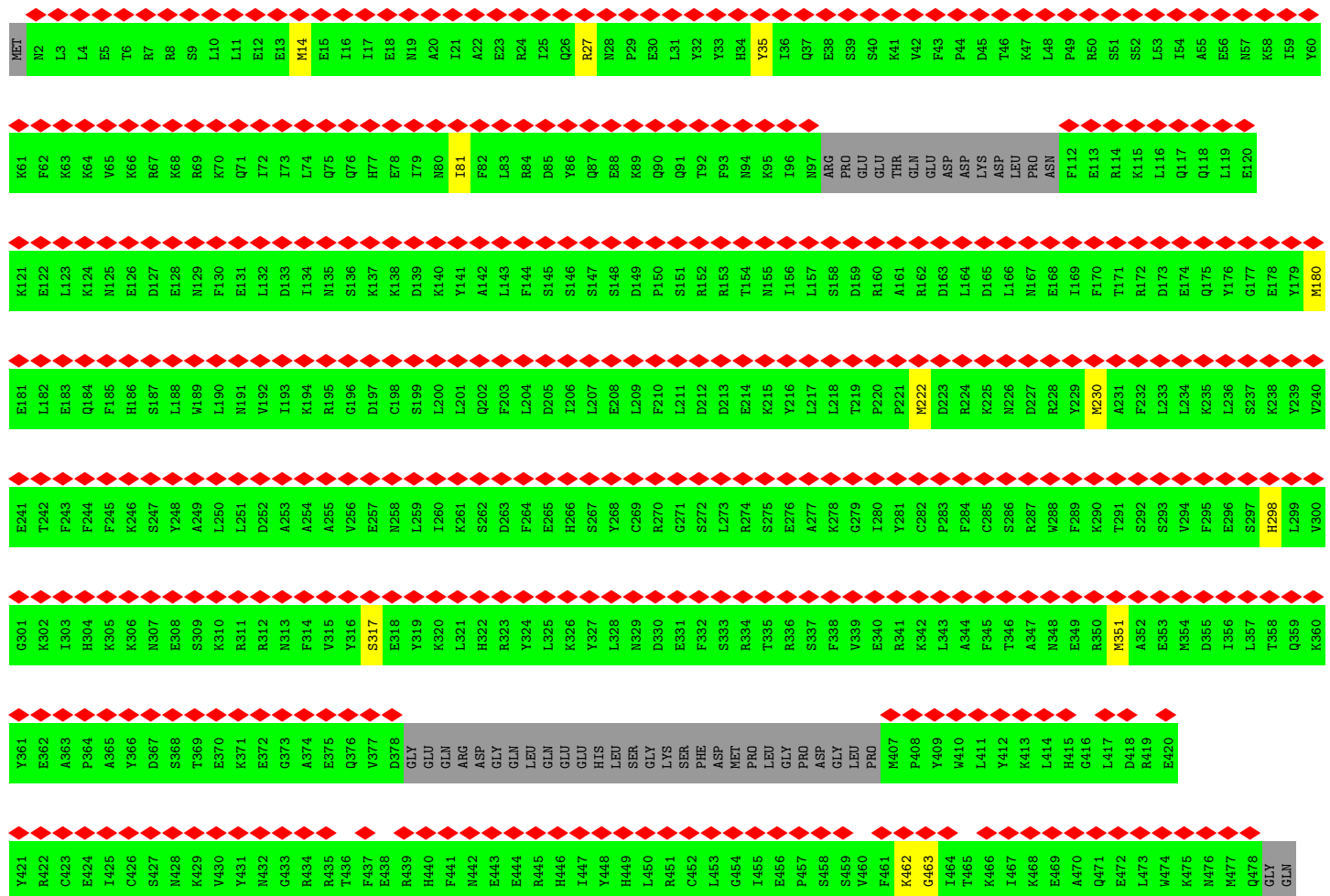
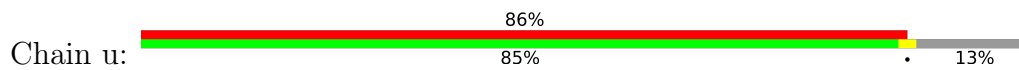


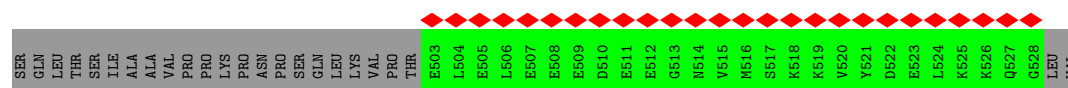


• Molecule 40: Pre-mRNA leakage protein 1

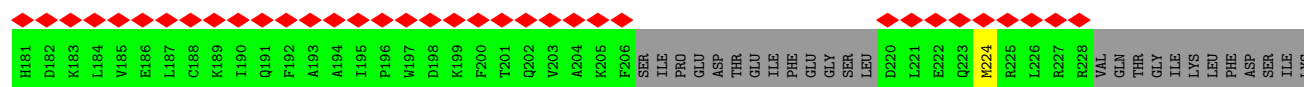
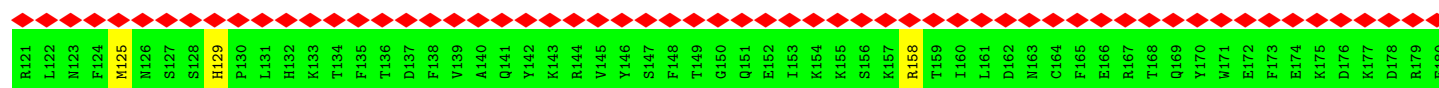
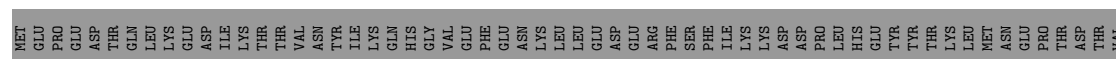
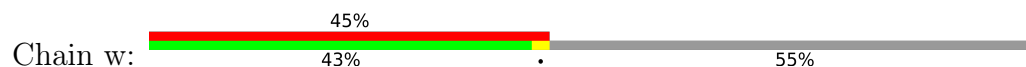


• Molecule 41: Pre-mRNA-splicing factor PRP9

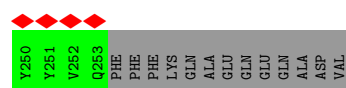
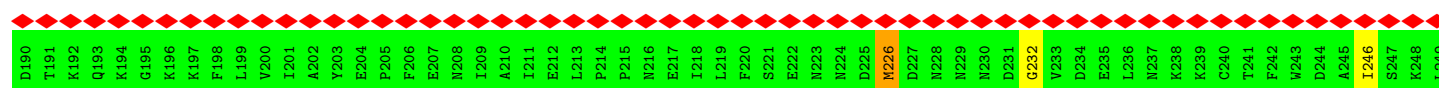
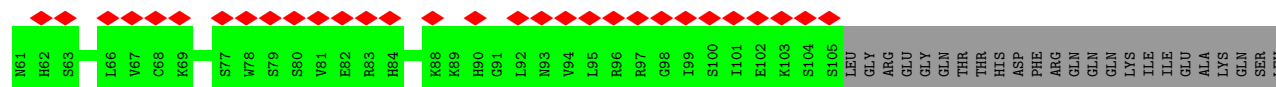
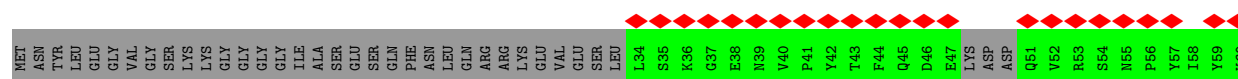




• Molecule 42: Pre-mRNA-splicing factor PRP21



• Molecule 43: Pre-mRNA-splicing factor PRP11



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	500657	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.386	Depositor
Minimum map value	-0.170	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.023	Depositor
Map size ( $\text{\AA}$ )	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.338, 1.338, 1.338	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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	0.33	2/18332 (0.0%)	0.51	1/24851 (0.0%)
2	K	0.33	0/3431	0.59	0/4631
3	L	0.31	0/3219	0.48	0/4332
4	N	0.28	0/4937	0.47	0/6704
5	J	0.30	0/2485	0.46	0/3333
6	E	0.34	0/1167	0.50	0/1571
7	M	0.31	0/963	0.51	0/1310
8	C	0.32	0/6874	0.52	0/9305
9	z	0.49	0/259	0.70	0/322
10	q	0.49	0/367	0.65	0/457
11	r	0.59	0/307	0.75	0/382
12	x	0.48	0/295	0.68	0/367
13	t	0.50	0/306	0.71	0/379
14	y	0.49	0/262	0.71	0/324
15	s	0.47	0/306	0.68	0/379
16	F	0.38	0/2277	0.90	0/3534
17	I	0.53	4/2604 (0.2%)	0.99	10/4046 (0.2%)
18	B	0.36	1/4151 (0.0%)	0.97	18/6462 (0.3%)
19	O	0.25	0/573	0.42	0/763
20	S	0.41	0/641	0.65	2/868 (0.2%)
20	d	0.29	0/315	0.46	0/392
20	l	0.45	1/620 (0.2%)	0.68	1/841 (0.1%)
21	P	0.41	0/567	0.61	0/762
21	a	0.28	0/290	0.46	0/359
21	h	0.37	0/615	0.61	0/829
22	Q	0.39	0/756	0.69	1/1023 (0.1%)
22	b	0.27	0/305	0.47	0/376
22	m	0.42	0/649	0.61	0/880
23	R	0.38	0/764	0.57	0/1026
23	c	0.25	0/358	0.45	0/444
23	n	0.41	0/535	0.57	0/717
24	T	0.38	0/612	0.59	1/830 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
24	e	0.29	0/285	0.43	0/351
24	i	0.43	0/585	0.62	0/795
25	U	0.39	0/597	0.62	0/807
25	f	0.30	0/278	0.45	0/344
25	j	0.44	0/564	0.66	2/761 (0.3%)
26	V	0.41	0/582	0.67	1/785 (0.1%)
26	g	0.25	0/277	0.46	0/341
26	k	0.37	0/532	0.60	0/715
27	D	0.40	1/13899 (0.0%)	0.62	6/18845 (0.0%)
28	G	0.26	0/1038	0.87	3/1611 (0.2%)
29	H	1.10	61/4835 (1.3%)	1.70	185/7502 (2.5%)
30	o	1.03	9/839 (1.1%)	1.65	11/1127 (1.0%)
31	p	0.81	3/467 (0.6%)	1.35	2/623 (0.3%)
32	1	0.28	0/6600	0.48	1/8962 (0.0%)
33	2	0.26	0/1775	0.45	0/2402
34	3	0.30	0/9564	0.57	1/12963 (0.0%)
35	4	0.26	0/1453	0.43	0/1954
36	5	0.28	0/827	0.46	0/1105
37	6	0.28	0/702	0.44	0/939
38	X	0.49	0/1071	0.65	0/1445
39	Y	0.52	0/743	0.70	0/994
40	Z	0.51	0/176	0.59	0/237
41	u	0.35	5/3972 (0.1%)	0.41	0/5322
42	w	0.45	4/1105 (0.4%)	0.37	0/1475
43	v	0.29	1/1396 (0.1%)	0.41	0/1881
All	All	0.42	92/114304 (0.1%)	0.71	246/157085 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	K	0	2
3	L	0	1
4	N	0	2
8	C	0	2
27	D	0	4
32	1	0	4
34	3	0	1
41	u	0	2
All	All	0	19



All (92) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	H	1161	U	O3'-P	-15.59	1.42	1.61
29	H	1092	A	O3'-P	-14.82	1.43	1.61
29	H	1116	A	O3'-P	-11.52	1.47	1.61
29	H	1163	C	O5'-C5'	9.10	1.59	1.44
29	H	1116	A	C3'-O3'	-8.99	1.29	1.42
29	H	1127	A	O3'-P	-8.68	1.50	1.61
29	H	1167	U	O3'-P	8.59	1.71	1.61
1	A	266	LEU	C-N	8.15	1.49	1.34
29	H	1164	C	O3'-P	-8.13	1.51	1.61
17	I	142	G	N7-C5	-7.95	1.34	1.39
29	H	1162	U	P-O5'	7.58	1.67	1.59
29	H	1163	C	P-O5'	7.54	1.67	1.59
30	o	46	SER	CB-OG	7.47	1.51	1.42
29	H	1117	G	P-O5'	7.21	1.67	1.59
30	o	45	SER	CB-OG	7.17	1.51	1.42
31	p	33	SER	CB-OG	7.11	1.51	1.42
30	o	69	ASP	CA-CB	-7.06	1.38	1.53
29	H	1154	U	C1'-N1	7.04	1.59	1.48
29	H	1128	C	C5'-C4'	-7.02	1.43	1.51
29	H	1096	C	O3'-P	7.00	1.69	1.61
30	o	6	SER	CB-OG	6.96	1.51	1.42
18	B	175	G	C1'-N9	-6.96	1.37	1.46
29	H	546	U	C1'-N1	6.93	1.59	1.48
29	H	1140	U	C1'-N1	6.91	1.59	1.48
29	H	564	U	C1'-N1	6.88	1.59	1.48
29	H	684	U	C1'-N1	6.86	1.59	1.48
29	H	679	U	C1'-N1	6.85	1.59	1.48
29	H	673	U	C1'-N1	6.84	1.59	1.48
29	H	566	U	C1'-N1	6.83	1.58	1.48
29	H	682	U	C1'-N1	6.82	1.58	1.48
29	H	685	U	C1'-N1	6.82	1.58	1.48
29	H	669	U	C1'-N1	6.81	1.58	1.48
29	H	567	U	C1'-N1	6.81	1.58	1.48
29	H	552	U	C1'-N1	6.81	1.58	1.48
29	H	678	U	C1'-N1	6.81	1.58	1.48
29	H	565	U	C1'-N1	6.80	1.58	1.48
29	H	672	U	C1'-N1	6.78	1.58	1.48
29	H	568	U	C1'-N1	6.78	1.58	1.48
29	H	676	U	C1'-N1	6.76	1.58	1.48
29	H	1095	U	O3'-P	6.51	1.69	1.61
29	H	1169	C	C1'-N1	6.51	1.58	1.48
29	H	696	C	C1'-N1	6.37	1.58	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	H	693	C	C1'-N1	6.34	1.58	1.48
29	H	554	C	C1'-N1	6.30	1.58	1.48
29	H	694	C	C1'-N1	6.30	1.58	1.48
29	H	1117	G	C5'-C4'	6.29	1.58	1.51
29	H	680	C	C1'-N1	6.29	1.58	1.48
29	H	549	C	C1'-N1	6.29	1.58	1.48
29	H	551	C	C1'-N1	6.27	1.58	1.48
29	H	681	C	C1'-N1	6.27	1.58	1.48
29	H	1168	U	C5'-C4'	-6.25	1.43	1.51
29	H	569	C	C1'-N1	6.24	1.58	1.48
29	H	1162	U	O3'-P	6.19	1.68	1.61
29	H	1162	U	O5'-C5'	6.09	1.54	1.44
17	I	142	G	C2-N2	-6.06	1.28	1.34
41	u	180	MET	CG-SD	6.00	1.96	1.81
17	I	73	A	C1'-N9	-5.99	1.38	1.46
29	H	1165	C	O5'-C5'	5.98	1.54	1.44
29	H	1151	U	O5'-C5'	-5.90	1.33	1.42
29	H	1163	C	O3'-P	5.87	1.68	1.61
29	H	1097	G	O3'-P	5.81	1.68	1.61
29	H	1162	U	C2-N3	5.79	1.41	1.37
30	o	42	SER	CB-OG	5.79	1.49	1.42
30	o	102	THR	CB-OG1	5.79	1.54	1.43
29	H	690	U	C1'-N1	5.75	1.57	1.48
29	H	1161	U	C3'-O3'	-5.74	1.34	1.42
29	H	695	U	C1'-N1	5.74	1.57	1.48
29	H	1162	U	C3'-C2'	-5.73	1.46	1.52
29	H	692	U	C1'-N1	5.71	1.57	1.48
29	H	683	U	C1'-N1	5.70	1.57	1.48
42	w	113	MET	CG-SD	5.70	1.96	1.81
29	H	121	C	C1'-N1	5.67	1.57	1.48
29	H	677	U	C1'-N1	5.62	1.57	1.48
29	H	670	U	C1'-N1	5.62	1.57	1.48
17	I	74	U	C1'-N1	5.59	1.57	1.48
30	o	15	TYR	CB-CG	-5.58	1.43	1.51
41	u	14	MET	CG-SD	5.55	1.95	1.81
43	v	226	MET	CG-SD	5.55	1.95	1.81
30	o	51	THR	CB-OG1	5.52	1.54	1.43
42	w	224	MET	CG-SD	5.51	1.95	1.81
42	w	93	MET	CG-SD	5.46	1.95	1.81
41	u	230	MET	CG-SD	5.45	1.95	1.81
41	u	351	MET	CG-SD	5.42	1.95	1.81
42	w	125	MET	CG-SD	5.40	1.95	1.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1014	LYS	C-N	-5.29	1.24	1.34
29	H	147	A	O3'-P	-5.22	1.54	1.61
31	p	75	THR	CB-OG1	5.20	1.53	1.43
41	u	222	MET	CG-SD	5.18	1.94	1.81
20	l	82	PRO	N-CD	5.16	1.55	1.47
30	o	153	THR	CB-OG1	5.09	1.53	1.43
31	p	65	PHE	CB-CG	-5.06	1.42	1.51
27	D	1695	TYR	CE1-CZ	-5.06	1.31	1.38

All (246) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	H	1162	U	C5'-C4'-O4'	14.85	126.92	109.10
29	H	1093	C	P-O5'-C5'	14.77	144.53	120.90
29	H	1147	A	C5'-C4'-C3'	-14.16	93.34	116.00
29	H	1092	A	C2'-C3'-O3'	14.09	140.49	109.50
29	H	1098	C	N1-C1'-C2'	-13.36	96.64	114.00
29	H	1151	U	C4'-C3'-O3'	-12.56	83.02	109.40
27	D	1213	ARG	NE-CZ-NH2	-12.13	114.23	120.30
18	B	96	U	O5'-P-OP1	-11.67	95.20	105.70
29	H	1151	U	P-O5'-C5'	11.65	139.54	120.90
29	H	1117	G	C5'-C4'-O4'	11.48	122.87	109.10
29	H	1117	G	C5'-C4'-C3'	-10.91	98.54	116.00
29	H	1163	C	C5'-C4'-O4'	10.55	121.77	109.10
29	H	1126	G	N9-C1'-C2'	-10.00	101.00	112.00
17	I	142	G	N1-C6-O6	-9.88	113.97	119.90
29	H	1139	G	N9-C1'-C2'	-9.75	101.27	112.00
29	H	1163	C	C5'-C4'-C3'	-9.72	100.44	116.00
29	H	1147	A	P-O5'-C5'	9.62	136.28	120.90
29	H	1162	U	C5'-C4'-C3'	-9.16	101.34	116.00
29	H	1168	U	C4'-C3'-O3'	-9.00	90.50	109.40
29	H	142	C	N1-C1'-C2'	-8.82	102.30	112.00
30	o	44	PRO	N-CA-CB	8.81	113.87	103.30
17	I	142	G	C5-C6-O6	8.75	133.85	128.60
29	H	1152	U	P-O5'-C5'	8.71	134.83	120.90
29	H	1151	U	O4'-C1'-N1	8.60	115.08	108.20
29	H	1092	A	P-O5'-C5'	8.56	134.60	120.90
29	H	1148	U	C4'-C3'-O3'	-8.53	91.50	109.40
29	H	148	G	C5'-C4'-C3'	-8.27	102.76	116.00
29	H	1165	C	C5'-C4'-C3'	-8.26	102.78	116.00
17	I	142	G	N1-C2-N3	8.21	128.83	123.90
29	H	1151	U	C5'-C4'-O4'	8.05	118.77	109.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	H	1168	U	P-O5'-C5'	-7.95	108.19	120.90
29	H	1167	U	C2'-C3'-O3'	7.88	126.85	109.50
29	H	1092	A	C4'-C3'-O3'	-7.86	92.90	109.40
17	I	71	U	C2-N1-C1'	7.82	127.09	117.70
29	H	1165	C	C5'-C4'-O4'	7.82	118.48	109.10
29	H	1147	A	C4'-C3'-O3'	7.75	128.51	113.00
29	H	1161	U	C5'-C4'-C3'	-7.75	103.60	116.00
29	H	1093	C	C5'-C4'-C3'	-7.73	103.63	116.00
29	H	1169	C	P-O5'-C5'	-7.65	108.67	120.90
18	B	33	U	P-O3'-C3'	7.63	128.86	119.70
29	H	1097	G	C3'-C2'-O2'	7.62	135.38	113.30
29	H	1165	C	C4'-C3'-O3'	7.56	128.12	113.00
18	B	40	C	C2-N3-C4	-7.45	116.18	119.90
29	H	1115	G	O5'-P-OP1	-7.29	99.14	105.70
29	H	1168	U	C2'-C3'-O3'	7.29	125.53	109.50
30	o	5	PRO	N-CA-CB	7.25	112.00	103.30
29	H	1089	G	C4'-C3'-O3'	7.24	127.49	113.00
30	o	42	SER	N-CA-CB	-7.24	99.64	110.50
29	H	1128	C	C5'-C4'-O4'	7.24	117.79	109.10
29	H	547	G	OP2-P-O3'	7.24	121.13	105.20
29	H	551	C	OP2-P-O3'	7.24	121.13	105.20
29	H	546	U	OP2-P-O3'	7.24	121.12	105.20
29	H	545	G	OP2-P-O3'	7.24	121.12	105.20
29	H	681	C	OP2-P-O3'	7.24	121.12	105.20
29	H	552	U	OP2-P-O3'	7.23	121.11	105.20
29	H	557	G	OP2-P-O3'	7.23	121.11	105.20
29	H	561	A	OP2-P-O3'	7.23	121.11	105.20
29	H	671	G	OP2-P-O3'	7.23	121.10	105.20
29	H	556	A	OP2-P-O3'	7.22	121.09	105.20
29	H	564	U	OP2-P-O3'	7.22	121.09	105.20
29	H	567	U	OP2-P-O3'	7.22	121.09	105.20
29	H	670	U	OP2-P-O3'	7.22	121.09	105.20
29	H	695	U	OP2-P-O3'	7.22	121.09	105.20
29	H	569	C	OP2-P-O3'	7.22	121.09	105.20
29	H	687	A	OP2-P-O3'	7.22	121.08	105.20
29	H	691	G	OP2-P-O3'	7.22	121.08	105.20
29	H	562	A	OP2-P-O3'	7.22	121.08	105.20
29	H	544	G	OP2-P-O3'	7.22	121.08	105.20
29	H	566	U	OP2-P-O3'	7.22	121.08	105.20
29	H	669	U	OP2-P-O3'	7.22	121.08	105.20
29	H	550	G	OP2-P-O3'	7.21	121.07	105.20
29	H	684	U	OP2-P-O3'	7.21	121.07	105.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	H	560	G	OP2-P-O3'	7.21	121.07	105.20
29	H	568	U	OP2-P-O3'	7.21	121.07	105.20
29	H	553	G	OP2-P-O3'	7.21	121.06	105.20
29	H	554	C	OP2-P-O3'	7.21	121.07	105.20
29	H	570	G	OP2-P-O3'	7.21	121.06	105.20
29	H	694	C	OP2-P-O3'	7.21	121.07	105.20
29	H	555	A	OP2-P-O3'	7.21	121.06	105.20
29	H	673	U	OP2-P-O3'	7.21	121.06	105.20
29	H	682	U	OP2-P-O3'	7.21	121.06	105.20
29	H	677	U	OP2-P-O3'	7.21	121.06	105.20
29	H	692	U	OP2-P-O3'	7.21	121.06	105.20
29	H	549	C	OP2-P-O3'	7.21	121.05	105.20
29	H	565	U	OP2-P-O3'	7.20	121.04	105.20
29	H	683	U	OP2-P-O3'	7.20	121.04	105.20
29	H	685	U	OP2-P-O3'	7.20	121.04	105.20
29	H	686	G	OP2-P-O3'	7.20	121.04	105.20
29	H	548	G	OP2-P-O3'	7.20	121.04	105.20
29	H	672	U	OP2-P-O3'	7.20	121.03	105.20
29	H	559	G	OP2-P-O3'	7.20	121.03	105.20
17	I	71	U	N1-C2-O2	7.19	127.83	122.80
29	H	680	C	OP2-P-O3'	7.19	121.02	105.20
29	H	693	C	OP2-P-O3'	7.19	121.02	105.20
29	H	689	G	OP2-P-O3'	7.19	121.02	105.20
29	H	558	A	OP2-P-O3'	7.19	121.01	105.20
29	H	674	G	OP2-P-O3'	7.19	121.01	105.20
29	H	676	U	OP2-P-O3'	7.19	121.01	105.20
29	H	679	U	OP2-P-O3'	7.19	121.01	105.20
29	H	690	U	OP2-P-O3'	7.19	121.01	105.20
29	H	563	G	OP2-P-O3'	7.19	121.01	105.20
29	H	678	U	OP2-P-O3'	7.18	121.01	105.20
29	H	675	A	OP2-P-O3'	7.18	121.00	105.20
29	H	1159	U	O5'-P-OP1	-7.18	99.24	105.70
29	H	688	A	OP2-P-O3'	7.18	120.99	105.20
29	H	1089	G	O5'-P-OP1	-7.13	99.28	105.70
29	H	1159	U	O5'-P-OP2	-7.12	99.30	105.70
29	H	139	G	O5'-P-OP2	-7.11	99.30	105.70
29	H	139	G	O5'-P-OP1	-7.09	99.32	105.70
29	H	1089	G	O5'-P-OP2	-7.08	99.33	105.70
29	H	1115	G	C4'-C3'-O3'	7.05	127.10	113.00
28	G	506	U	C2-N1-C1'	7.01	126.12	117.70
29	H	1115	G	O5'-P-OP2	-7.00	99.40	105.70
29	H	674	G	O3'-P-O5'	-6.82	91.04	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	H	558	A	O3'-P-O5'	-6.81	91.06	104.00
29	H	570	G	O3'-P-O5'	-6.81	91.06	104.00
29	H	683	U	O3'-P-O5'	-6.81	91.06	104.00
29	H	559	G	O3'-P-O5'	-6.80	91.08	104.00
29	H	567	U	O3'-P-O5'	-6.80	91.09	104.00
29	H	547	G	O3'-P-O5'	-6.79	91.09	104.00
29	H	679	U	O3'-P-O5'	-6.79	91.09	104.00
29	H	688	A	O3'-P-O5'	-6.79	91.10	104.00
29	H	545	G	O3'-P-O5'	-6.79	91.10	104.00
29	H	565	U	O3'-P-O5'	-6.79	91.10	104.00
29	H	686	G	O3'-P-O5'	-6.79	91.10	104.00
29	H	671	G	O3'-P-O5'	-6.79	91.10	104.00
29	H	684	U	O3'-P-O5'	-6.79	91.10	104.00
29	H	552	U	O3'-P-O5'	-6.79	91.11	104.00
29	H	563	G	O3'-P-O5'	-6.78	91.11	104.00
29	H	681	C	O3'-P-O5'	-6.78	91.11	104.00
29	H	693	C	O3'-P-O5'	-6.78	91.11	104.00
29	H	554	C	O3'-P-O5'	-6.78	91.12	104.00
29	H	560	G	O3'-P-O5'	-6.78	91.12	104.00
29	H	678	U	O3'-P-O5'	-6.78	91.12	104.00
29	H	676	U	O3'-P-O5'	-6.78	91.12	104.00
29	H	569	C	O3'-P-O5'	-6.78	91.12	104.00
29	H	675	A	O3'-P-O5'	-6.78	91.12	104.00
29	H	682	U	O3'-P-O5'	-6.78	91.13	104.00
29	H	548	G	O3'-P-O5'	-6.77	91.13	104.00
29	H	551	C	O3'-P-O5'	-6.77	91.13	104.00
29	H	553	G	O3'-P-O5'	-6.77	91.13	104.00
29	H	670	U	O3'-P-O5'	-6.77	91.13	104.00
29	H	550	G	O3'-P-O5'	-6.77	91.14	104.00
29	H	556	A	O3'-P-O5'	-6.77	91.14	104.00
29	H	672	U	O3'-P-O5'	-6.77	91.14	104.00
29	H	677	U	O3'-P-O5'	-6.77	91.14	104.00
29	H	692	U	O3'-P-O5'	-6.77	91.14	104.00
29	H	546	U	O3'-P-O5'	-6.77	91.14	104.00
29	H	564	U	O3'-P-O5'	-6.76	91.15	104.00
29	H	557	G	O3'-P-O5'	-6.76	91.15	104.00
29	H	561	A	O3'-P-O5'	-6.76	91.15	104.00
29	H	669	U	O3'-P-O5'	-6.76	91.15	104.00
29	H	691	G	O3'-P-O5'	-6.76	91.15	104.00
29	H	544	G	O3'-P-O5'	-6.76	91.15	104.00
29	H	566	U	O3'-P-O5'	-6.76	91.16	104.00
29	H	673	U	O3'-P-O5'	-6.76	91.16	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	H	562	A	O3'-P-O5'	-6.76	91.16	104.00
29	H	685	U	O3'-P-O5'	-6.76	91.16	104.00
29	H	694	C	O3'-P-O5'	-6.76	91.16	104.00
29	H	549	C	O3'-P-O5'	-6.75	91.17	104.00
29	H	689	G	O3'-P-O5'	-6.75	91.17	104.00
29	H	690	U	O3'-P-O5'	-6.75	91.17	104.00
29	H	695	U	O3'-P-O5'	-6.75	91.17	104.00
29	H	568	U	O3'-P-O5'	-6.75	91.18	104.00
18	B	114	G	N1-C6-O6	-6.75	115.85	119.90
29	H	680	C	O3'-P-O5'	-6.75	91.18	104.00
29	H	555	A	O3'-P-O5'	-6.74	91.19	104.00
29	H	687	A	O3'-P-O5'	-6.74	91.20	104.00
30	o	12	PRO	N-CA-CB	6.74	111.39	103.30
29	H	1096	C	C1'-C2'-O2'	-6.69	90.53	110.60
29	H	1129	U	C5'-C4'-O4'	6.66	117.09	109.10
22	Q	93	ARG	CG-CD-NE	-6.62	97.89	111.80
20	S	45	ARG	NE-CZ-NH1	-6.60	117.00	120.30
17	I	142	G	C6-N1-C2	-6.55	121.17	125.10
18	B	40	C	N1-C2-N3	6.52	123.76	119.20
29	H	140	G	N9-C1'-C2'	-6.50	104.86	112.00
29	H	148	G	C5'-C4'-O4'	6.49	116.89	109.10
30	o	57	LEU	N-CA-CB	6.35	123.10	110.40
30	o	4	THR	N-CA-CB	-6.32	98.30	110.30
29	H	1092	A	N9-C1'-C2'	6.29	122.18	114.00
17	I	71	U	N3-C2-O2	-6.27	117.81	122.20
18	B	79	C	C2-N1-C1'	6.25	125.68	118.80
18	B	96	U	C2-N1-C1'	6.22	125.17	117.70
29	H	1096	C	C4'-C3'-O3'	6.14	125.27	113.00
29	H	1152	U	C5'-C4'-C3'	-6.10	106.24	116.00
27	D	1213	ARG	NE-CZ-NH1	6.08	123.34	120.30
30	o	141	ARG	CD-NE-CZ	6.03	132.05	123.60
28	G	506	U	N1-C2-O2	6.03	127.02	122.80
29	H	1167	U	P-O3'-C3'	-6.03	112.47	119.70
28	G	506	U	N3-C2-O2	-6.01	117.99	122.20
29	H	1151	U	O3'-P-O5'	-5.99	92.61	104.00
34	3	962	LEU	CA-CB-CG	5.95	128.98	115.30
29	H	1162	U	C4'-C3'-O3'	5.93	124.87	113.00
18	B	115	G	N1-C2-N3	5.93	127.46	123.90
30	o	7	ILE	CA-CB-CG1	5.92	122.25	111.00
29	H	1167	U	C5'-C4'-O4'	-5.92	102.00	109.10
18	B	40	C	C6-N1-C1'	5.91	127.90	120.80
18	B	115	G	N3-C4-N9	-5.87	122.48	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	H	1148	U	C5'-C4'-O4'	5.86	116.13	109.10
26	V	50	ASP	C-N-CD	5.81	140.60	128.40
29	H	1115	G	P-O3'-C3'	5.80	126.66	119.70
18	B	32	G	OP2-P-O3'	5.76	117.87	105.20
29	H	1162	U	C2'-C3'-O3'	-5.74	96.88	109.50
30	o	68	PRO	N-CA-CB	5.70	110.14	103.30
24	T	89	LEU	CA-CB-CG	5.63	128.25	115.30
17	I	142	G	C8-N9-C4	-5.61	104.15	106.40
29	H	1162	U	P-O3'-C3'	5.60	126.42	119.70
29	H	1167	U	C5'-C4'-C3'	5.58	124.93	116.00
17	I	71	U	C6-N1-C1'	-5.58	113.39	121.20
25	j	74	ARG	NE-CZ-NH1	5.55	123.08	120.30
29	H	1097	G	C2'-C3'-O3'	-5.55	97.30	109.50
18	B	115	G	N3-C2-N2	-5.53	116.03	119.90
29	H	46	C	OP2-P-O3'	5.49	117.28	105.20
29	H	1162	U	C4'-C3'-C2'	5.48	108.08	102.60
29	H	1105	C	C4'-C3'-O3'	-5.47	97.90	109.40
27	D	789	LEU	CA-CB-CG	5.46	127.86	115.30
29	H	1168	U	C4'-C3'-C2'	-5.46	97.14	102.60
18	B	79	C	C2-N3-C4	5.46	122.63	119.90
20	S	23	LEU	CA-CB-CG	5.42	127.76	115.30
29	H	1151	U	N1-C1'-C2'	5.41	121.03	114.00
18	B	40	C	C2-N1-C1'	-5.40	112.86	118.80
29	H	1168	U	O3'-P-O5'	-5.36	93.81	104.00
29	H	1152	U	O4'-C4'-C3'	5.28	110.33	106.10
17	I	90	C	C2-N3-C4	5.26	122.53	119.90
1	A	615	LEU	CA-CB-CG	5.26	127.40	115.30
30	o	71	SER	N-CA-CB	-5.26	102.61	110.50
29	H	46	C	P-O3'-C3'	5.22	125.96	119.70
27	D	813	ARG	CG-CD-NE	5.21	122.74	111.80
18	B	79	C	C5-C6-N1	5.20	123.60	121.00
20	l	81	ALA	C-N-CD	5.20	139.31	128.40
32	1	321	CYS	CA-CB-SG	5.18	123.32	114.00
18	B	95	C	OP1-P-O3'	5.16	116.54	105.20
18	B	94	C	P-O3'-C3'	5.15	125.88	119.70
29	H	1148	U	P-O5'-C5'	5.14	129.13	120.90
29	H	1163	C	C4'-C3'-O3'	5.14	123.27	113.00
27	D	793	LEU	CA-CB-CG	5.12	127.07	115.30
29	H	1161	U	C5'-C4'-O4'	5.11	115.24	109.10
30	o	107	SER	N-CA-CB	-5.11	102.83	110.50
18	B	115	G	N9-C4-C5	5.11	107.44	105.40
31	p	33	SER	N-CA-CB	5.10	118.16	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	D	1894	LEU	CA-CB-CG	5.10	127.03	115.30
25	j	74	ARG	NE-CZ-NH2	-5.10	117.75	120.30
29	H	1169	C	O5'-C5'-C4'	-5.06	102.09	111.70
29	H	1147	A	O5'-C5'-C4'	5.05	121.29	111.70
31	p	46	VAL	CA-CB-CG2	5.05	118.47	110.90
29	H	146	A	C5'-C4'-C3'	-5.03	107.95	116.00

There are no chirality outliers.

All (19) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
32	1	386	TYR	Peptide
32	1	830	MET	Peptide
32	1	835	ILE	Peptide
32	1	926	PRO	Peptide
34	3	208	GLU	Peptide
1	A	239	PHE	Peptide
8	C	363	PRO	Peptide
8	C	770	ASN	Peptide
27	D	1369	GLY	Peptide
27	D	684	LEU	Peptide
27	D	685	ARG	Peptide
27	D	790	ASP	Peptide
2	K	208	GLN	Peptide
2	K	383	GLU	Peptide
3	L	397	GLU	Peptide
4	N	11	PRO	Peptide
4	N	802	GLN	Peptide
41	u	462	LYS	Peptide
41	u	463	GLY	Peptide

## 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	17877	0	17800	639	0
2	K	3375	0	3343	176	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	L	3171	0	3140	127	0
4	N	4897	0	3994	115	0
5	J	2439	0	2341	62	0
6	E	1146	0	1133	29	0
7	M	950	0	1004	24	0
8	C	6732	0	6904	274	0
9	z	260	0	72	0	0
10	q	368	0	99	0	0
11	r	308	0	80	0	0
12	x	296	0	83	0	0
13	t	308	0	85	0	0
14	y	264	0	76	0	0
15	s	308	0	85	0	0
16	F	2043	0	1033	49	0
17	I	2334	0	1173	108	0
18	B	3715	0	1878	150	0
19	O	574	0	552	31	0
20	S	632	0	653	26	0
20	d	316	0	86	0	0
20	l	611	0	627	0	0
21	P	563	0	600	40	0
21	a	292	0	78	0	0
21	h	610	0	640	0	0
22	Q	751	0	776	65	0
22	b	308	0	78	0	0
22	m	644	0	686	0	0
23	R	752	0	786	50	0
23	c	360	0	89	0	0
23	n	528	0	573	0	0
24	T	602	0	631	37	0
24	e	288	0	74	0	0
24	i	575	0	597	0	0
25	U	585	0	587	39	0
25	f	280	0	77	0	0
25	j	554	0	556	0	0
26	V	577	0	595	37	0
26	g	280	0	79	0	0
26	k	529	0	557	0	0
27	D	13601	0	13596	641	0
28	G	928	0	468	48	0
29	H	4345	0	2199	249	0
30	o	841	0	614	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	p	466	0	373	0	0
32	1	6472	0	6702	243	0
33	2	1726	0	1734	62	0
34	3	9380	0	9482	399	0
35	4	1429	0	1458	44	0
36	5	814	0	811	30	0
37	6	693	0	705	25	0
38	X	1051	0	1015	100	0
39	Y	730	0	710	52	0
40	Z	173	0	165	7	0
41	u	3895	0	3824	0	0
42	w	1084	0	1081	0	0
43	v	1372	0	1345	0	0
44	C	32	0	12	6	0
45	C	1	0	0	0	0
46	5	3	0	0	3	0
46	u	2	0	0	0	0
46	v	1	0	0	0	0
All	All	111041	0	100594	3508	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 19.

All (3508) 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)
1:A:2310:GLU:CB	1:A:2333:PHE:CZ	1.85	1.52
1:A:2398:LEU:HD13	27:D:1060:LYS:CD	1.36	1.51
1:A:2310:GLU:CB	1:A:2333:PHE:HZ	1.19	1.44
1:A:2398:LEU:HD13	27:D:1060:LYS:CE	1.48	1.42
1:A:2310:GLU:HB2	1:A:2333:PHE:CZ	0.89	1.41
32:1:494:LEU:HD13	38:X:7:ILE:CG2	1.49	1.41
1:A:2398:LEU:CD1	27:D:1060:LYS:HD2	1.53	1.38
1:A:2310:GLU:HB2	1:A:2333:PHE:CE1	1.58	1.38
1:A:2152:TRP:CH2	27:D:1061:ALA:O	1.83	1.31
39:Y:207:THR:O	39:Y:214:LEU:CD1	1.79	1.28
38:X:63:SER:CB	38:X:74:PHE:CE1	2.16	1.27
1:A:2395:PHE:CD1	27:D:1062:PRO:HD3	1.72	1.23
1:A:2398:LEU:CG	27:D:1060:LYS:HD2	1.72	1.17
29:H:1099:G:O2'	29:H:1100:A:H5'	1.42	1.16
32:1:494:LEU:HD13	38:X:7:ILE:HG21	1.18	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:539:LEU:O	27:D:543:TYR:HB3	1.44	1.14
32:1:494:LEU:HD11	38:X:23:TRP:CD1	1.83	1.13
32:1:494:LEU:CD1	38:X:7:ILE:HG21	1.79	1.12
1:A:547:LEU:O	1:A:551:LEU:HB2	1.51	1.08
27:D:804:HIS:CE1	27:D:813:ARG:HG3	1.89	1.07
1:A:2398:LEU:CD1	27:D:1060:LYS:CE	2.33	1.06
17:I:99:G:H4'	27:D:1186:GLU:HB3	1.31	1.06
8:C:867:THR:O	8:C:926:GLY:HA2	1.55	1.06
32:1:494:LEU:CD1	38:X:7:ILE:CG2	2.34	1.05
38:X:63:SER:HB2	38:X:74:PHE:CE1	1.84	1.05
17:I:75:U:C5	27:D:1100:PHE:HE1	1.73	1.05
1:A:1667:GLN:NE2	19:O:211:ASN:OD1	1.90	1.04
2:K:446:SER:OG	2:K:451:PHE:CE1	2.11	1.03
24:T:59:GLU:HG3	24:T:77:LEU:HD11	1.40	1.03
1:A:2183:TYR:HE2	1:A:2289:ILE:HG12	1.20	1.03
18:B:162:G:H3'	18:B:163:C:H4'	1.41	1.03
1:A:2398:LEU:HD13	27:D:1060:LYS:HD2	1.03	1.02
19:O:206:LYS:HD3	27:D:1051:LYS:HE3	1.39	1.02
39:Y:207:THR:O	39:Y:214:LEU:HD13	0.85	1.02
1:A:2395:PHE:CD1	27:D:1061:ALA:HA	1.95	1.01
24:T:83:LYS:NZ	25:U:75:CYS:O	1.93	1.01
29:H:110:A:H4'	29:H:111:C:C5'	1.89	1.01
17:I:91:U:O2	17:I:142:G:N2	1.95	1.00
27:D:757:LEU:O	27:D:761:PHE:HB3	1.62	0.99
1:A:2398:LEU:HD22	27:D:1060:LYS:HB2	1.41	0.99
1:A:2395:PHE:CE1	27:D:1061:ALA:HA	1.96	0.99
29:H:110:A:C4'	29:H:111:C:H5'	1.91	0.99
21:P:88:ARG:NH2	20:S:66:GLY:O	1.97	0.98
1:A:2395:PHE:CG	27:D:1062:PRO:HD3	1.97	0.98
1:A:1674:ASP:OD2	1:A:2200:LYS:HD3	1.62	0.97
1:A:2067:TYR:CB	19:O:194:LEU:HD22	1.94	0.97
1:A:2398:LEU:CD1	27:D:1060:LYS:NZ	2.28	0.96
1:A:2311:GLY:N	1:A:2333:PHE:HE1	1.64	0.96
32:1:494:LEU:HD13	38:X:7:ILE:HG23	1.44	0.96
2:K:187:ASP:HB3	2:K:451:PHE:HZ	1.28	0.95
29:H:1099:G:C2'	29:H:1100:A:H5'	1.97	0.95
27:D:556:LYS:NZ	27:D:602:THR:O	1.98	0.95
36:5:49:CYS:HG	46:5:201:ZN:ZN	0.64	0.95
1:A:2152:TRP:HH2	27:D:1061:ALA:O	1.32	0.95
27:D:527:LYS:HE3	27:D:670:LEU:HB3	1.46	0.95
1:A:1962:ARG:HD3	19:O:186:GLU:OE2	1.66	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:G:520:G:C6	38:X:34:TYR:CE2	2.56	0.94
1:A:2152:TRP:CZ2	27:D:1061:ALA:O	2.21	0.94
27:D:912:PHE:HB3	27:D:944:LEU:HD23	1.47	0.94
27:D:869:LEU:HD13	27:D:904:GLN:HE21	1.32	0.93
24:T:87:ILE:O	26:V:64:ARG:NE	2.02	0.93
32:1:494:LEU:HB2	38:X:7:ILE:HG12	1.50	0.93
17:I:150:G:OP2	25:U:74:ARG:NH2	2.00	0.93
17:I:91:U:H3	17:I:142:G:H1	0.94	0.93
29:H:1165:C:H2'	29:H:1166:G:H8	1.32	0.93
1:A:2311:GLY:N	1:A:2333:PHE:CE1	2.36	0.93
1:A:2310:GLU:CG	1:A:2333:PHE:HZ	1.81	0.93
32:1:494:LEU:CD1	38:X:23:TRP:CD1	2.51	0.93
39:Y:208:SER:HB2	39:Y:212:ARG:O	1.68	0.93
18:B:175:G:N2	18:B:176:A:N6	2.16	0.92
16:F:102:U:H3	29:H:3:G:H1	1.17	0.92
18:B:175:G:N2	18:B:176:A:H62	1.65	0.92
22:Q:144:ARG:NH1	22:Q:145:GLY:O	2.03	0.92
32:1:490:ARG:NH2	38:X:25:ASN:HB3	1.86	0.91
21:P:88:ARG:NH1	20:S:67:SER:O	2.02	0.91
17:I:78:A:C2	27:D:1110:ARG:NE	2.38	0.91
27:D:781:LEU:HD21	27:D:798:GLU:HA	1.52	0.91
27:D:1086:GLN:NE2	27:D:1138:LYS:O	2.03	0.91
18:B:32:G:H1	18:B:121:U:H3	1.16	0.91
1:A:2398:LEU:HD12	27:D:1060:LYS:NZ	1.84	0.90
18:B:22:G:H1	18:B:149:U:H3	0.95	0.90
29:H:1165:C:H2'	29:H:1166:G:C8	2.06	0.90
16:F:30:G:H1	18:B:96:U:H3	1.15	0.90
29:H:110:A:H4'	29:H:111:C:H5'	0.95	0.90
2:K:446:SER:OG	2:K:451:PHE:CZ	2.24	0.90
2:K:232:ASN:HB3	2:K:247:GLN:HE22	1.34	0.90
2:K:395:ILE:HG22	2:K:396:VAL:H	1.35	0.90
27:D:1387:HIS:HB2	27:D:1470:LEU:HD13	1.52	0.90
1:A:2398:LEU:HB2	27:D:1060:LYS:CD	2.02	0.90
18:B:1:A:H61	18:B:164:C:H42	1.11	0.89
17:I:72:A:OP2	27:D:1047:ARG:NH1	2.05	0.89
18:B:114:G:H2'	18:B:115:G:C8	2.08	0.89
39:Y:213:LYS:HB3	39:Y:230:SER:OG	1.72	0.89
1:A:1861:THR:HG22	19:O:161:ILE:HG12	1.55	0.88
1:A:2398:LEU:CD1	27:D:1060:LYS:CD	2.22	0.88
22:Q:35:GLN:OE1	22:Q:37:ASN:ND2	2.06	0.88
1:A:609:GLU:O	1:A:613:SER:HB2	1.73	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2310:GLU:CB	1:A:2333:PHE:CE1	2.32	0.88
17:I:145:U:H3	26:V:35:PHE:HB3	1.39	0.88
27:D:1687:LEU:HB2	27:D:1698:TYR:HE1	1.36	0.88
17:I:75:U:C5	27:D:1100:PHE:CE1	2.62	0.87
17:I:146:U:H5''	17:I:147:U:H5'	1.56	0.87
8:C:542:ILE:O	8:C:553:VAL:HB	1.72	0.87
27:D:1085:SER:HG	27:D:1140:TRP:HE1	1.17	0.87
1:A:2398:LEU:CB	27:D:1060:LYS:HD2	2.04	0.87
27:D:2049:PRO:HB2	27:D:2051:VAL:HG13	1.55	0.87
1:A:1087:ASN:HD21	3:L:272:LEU:HG	1.40	0.86
27:D:804:HIS:HE1	27:D:813:ARG:HG3	1.38	0.86
22:Q:36:MET:SD	23:R:97:ARG:NH1	2.48	0.86
1:A:617:ASN:ND2	18:B:99:U:O2'	2.09	0.86
1:A:2310:GLU:C	1:A:2333:PHE:HE1	1.80	0.86
1:A:716:ARG:HE	18:B:112:C:H1'	1.42	0.85
27:D:636:ILE:HG22	27:D:671:SER:HB2	1.58	0.85
1:A:2183:TYR:CE2	1:A:2289:ILE:HG12	2.11	0.85
39:Y:207:THR:C	39:Y:214:LEU:HD13	1.94	0.85
39:Y:214:LEU:HD21	39:Y:227:MET:HB2	1.58	0.85
1:A:976:GLN:HE22	1:A:1310:LYS:HB3	1.41	0.85
1:A:1565:THR:O	1:A:1820:ARG:NH2	2.10	0.85
27:D:1524:TRP:HD1	27:D:1780:ARG:CZ	1.89	0.85
27:D:1524:TRP:HB2	27:D:1780:ARG:HG3	1.58	0.85
27:D:1609:MET:HG2	27:D:1611:ASN:H	1.42	0.85
29:H:1099:G:O2'	29:H:1100:A:C5'	2.24	0.85
32:1:390:ILE:HD12	32:1:426:MET:HA	1.59	0.85
1:A:1088:VAL:HG12	1:A:1089:VAL:H	1.42	0.84
2:K:167:LEU:O	4:N:728:ARG:NH2	2.10	0.84
34:3:393:VAL:HA	34:3:404:LEU:O	1.76	0.84
27:D:1213:ARG:HH22	27:D:1316:LYS:CG	1.90	0.84
1:A:2067:TYR:O	19:O:194:LEU:HD21	1.78	0.84
38:X:63:SER:HB3	38:X:74:PHE:CE1	2.11	0.84
38:X:48:LEU:O	39:Y:231:ARG:NH1	2.11	0.84
1:A:1862:VAL:O	19:O:159:ASP:N	2.10	0.83
27:D:784:GLU:HG3	27:D:819:LEU:HD21	1.58	0.83
38:X:63:SER:OG	38:X:74:PHE:CZ	2.31	0.83
4:N:746:MET:HG2	4:N:749:ARG:HH12	1.44	0.83
8:C:603:PHE:HB3	8:C:646:GLY:O	1.78	0.83
27:D:1216:MET:HG3	27:D:1218:PHE:HE1	1.42	0.83
17:I:97:U:H3	17:I:135:A:H61	1.22	0.83
1:A:1575:TRP:HB2	3:L:391:MET:HB3	1.60	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:B:8:U:H3	18:B:157:G:H1	1.27	0.83
32:1:494:LEU:CB	38:X:7:ILE:HG12	2.09	0.83
34:3:363:VAL:HG12	34:3:364:THR:H	1.42	0.82
1:A:2152:TRP:CZ3	27:D:1064:PRO:HG3	2.14	0.82
34:3:130:LEU:HB3	34:3:195:ILE:HD13	1.61	0.82
3:L:120:TYR:HE2	3:L:141:ILE:HG12	1.45	0.82
18:B:166:U:O2'	18:B:167:A:OP1	1.97	0.82
2:K:169:GLY:HA2	4:N:724:SER:HB3	1.59	0.82
17:I:145:U:H1'	26:V:66:ASN:HB2	1.62	0.82
28:G:520:G:N1	38:X:34:TYR:CD2	2.48	0.82
32:1:830:MET:O	32:1:832:LYS:N	2.11	0.82
38:X:63:SER:HB2	38:X:74:PHE:HE1	1.38	0.82
1:A:165:LEU:HD22	1:A:730:ILE:HD11	1.62	0.82
32:1:494:LEU:HB3	38:X:7:ILE:HG23	1.61	0.81
1:A:547:LEU:O	1:A:551:LEU:CB	2.27	0.81
2:K:410:LEU:HB2	2:K:422:TYR:HB2	1.62	0.81
18:B:175:G:H21	18:B:176:A:H62	1.23	0.81
27:D:462:GLU:OE1	27:D:729:LYS:NZ	2.13	0.81
27:D:2134:THR:O	27:D:2138:HIS:NE2	2.13	0.81
34:3:105:ASP:HB2	34:3:114:ILE:HD11	1.61	0.81
27:D:1213:ARG:HH22	27:D:1316:LYS:HG2	1.43	0.81
17:I:134:U:H2'	17:I:135:A:H8	1.46	0.81
27:D:589:THR:HA	27:D:611:LYS:HG2	1.62	0.81
25:U:19:LEU:HD21	25:U:45:THR:HG21	1.63	0.81
34:3:71:PHE:HA	34:3:97:THR:HG22	1.63	0.81
38:X:63:SER:OG	38:X:74:PHE:CE1	2.32	0.81
1:A:1910:LYS:HD2	19:O:169:ILE:HG12	1.63	0.81
8:C:133:ILE:HA	8:C:209:MET:O	1.79	0.80
1:A:2398:LEU:HD13	27:D:1060:LYS:HE3	1.61	0.80
27:D:2103:LEU:HD11	27:D:2140:LEU:HB3	1.64	0.80
29:H:1149:G:H5''	29:H:1149:G:C8	2.16	0.80
17:I:142:G:N2	21:P:39:LYS:NZ	2.29	0.80
27:D:563:LEU:HD21	27:D:836:TRP:CD1	2.16	0.80
1:A:287:GLU:HG2	1:A:288:GLU:H	1.46	0.80
1:A:690:LYS:O	1:A:694:ASN:ND2	2.15	0.80
27:D:1277:LYS:O	27:D:1281:GLN:HB2	1.81	0.80
27:D:766:ILE:O	27:D:769:LYS:NZ	2.14	0.80
23:R:74:GLU:OE2	23:R:89:ARG:NE	2.15	0.80
34:3:157:LEU:O	34:3:176:ASN:HA	1.81	0.80
2:K:177:PRO:HB3	2:K:457:TRP:HA	1.64	0.80
8:C:133:ILE:HG22	8:C:209:MET:HB3	1.62	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1688:TYR:HD1	27:D:1695:TYR:CD1	2.00	0.79
1:A:880:THR:O	3:L:180:LYS:NZ	2.16	0.79
1:A:1851:PHE:O	1:A:1881:THR:HA	1.83	0.79
2:K:135:ARG:NH2	5:J:167:GLU:OE2	2.15	0.79
18:B:162:G:H3'	18:B:163:C:C4'	2.12	0.79
32:1:294:ARG:HB3	32:1:332:THR:HG21	1.64	0.79
24:T:30:TRP:HB3	26:V:23:ARG:HH12	1.47	0.79
17:I:98:G:H1	17:I:134:U:H3	1.31	0.79
3:L:327:THR:HG22	3:L:328:VAL:H	1.47	0.79
1:A:2398:LEU:HD12	27:D:1060:LYS:HZ1	1.45	0.79
22:Q:3:LEU:HD23	23:R:95:PHE:HE1	1.48	0.79
1:A:2398:LEU:CD2	27:D:1060:LYS:HD2	2.13	0.78
18:B:126:A:H5'	18:B:127:U:OP2	1.83	0.78
27:D:1887:VAL:HG21	22:Q:140:LYS:HD2	1.65	0.78
2:K:452:LEU:HB3	2:K:464:TRP:HB2	1.64	0.78
27:D:1557:ILE:HA	27:D:1695:TYR:HE2	1.46	0.78
8:C:706:LEU:HA	8:C:824:SER:O	1.82	0.78
34:3:365:ILE:HG21	34:3:381:LEU:HG	1.63	0.78
8:C:315:SER:OG	44:C:1500:GTP:O6	2.00	0.78
1:A:1014:LYS:O	1:A:1016:SER:N	2.15	0.78
34:3:364:THR:OG1	34:3:384:ASN:ND2	2.16	0.78
18:B:158:G:N2	18:B:160:U:O4	2.17	0.78
1:A:789:ALA:HB1	1:A:816:ILE:HD11	1.64	0.77
27:D:1895:ARG:O	27:D:1897:GLY:N	2.16	0.77
3:L:376:LYS:NZ	17:I:55:U:O2'	2.17	0.77
27:D:1515:LEU:HB2	27:D:1518:ALA:HB2	1.65	0.77
32:1:222:ILE:HG23	32:1:265:ILE:HD11	1.65	0.77
25:U:32:LYS:HA	25:U:79:LEU:HD12	1.66	0.77
1:A:2398:LEU:HB2	27:D:1060:LYS:HD3	1.62	0.77
34:3:118:GLN:HE22	34:3:171:LEU:HB3	1.49	0.77
27:D:677:TYR:HD2	27:D:691:LEU:HD21	1.47	0.77
21:P:88:ARG:HG2	21:P:90:GLU:H	1.47	0.77
32:1:490:ARG:HH22	38:X:25:ASN:HD22	1.33	0.77
8:C:605:ILE:HG13	8:C:652:MET:HE1	1.66	0.77
2:K:230:SER:HB2	2:K:232:ASN:HD22	1.50	0.77
1:A:2249:ASP:OD1	27:D:1309:ASN:ND2	2.18	0.76
27:D:1777:TYR:OH	27:D:1781:ARG:NH1	2.17	0.76
32:1:386:TYR:CD2	32:1:387:PRO:HD3	2.20	0.76
1:A:2398:LEU:HD22	27:D:1060:LYS:CB	2.15	0.76
4:N:21:ARG:NH2	6:E:74:TYR:OH	2.17	0.76
27:D:1772:TRP:HZ3	27:D:1773:PHE:CE1	2.02	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:446:SER:OG	2:K:451:PHE:CD1	2.38	0.76
4:N:743:LYS:O	4:N:747:GLU:HB2	1.85	0.76
17:I:76:A:N7	27:D:1107:ARG:NH2	2.33	0.76
18:B:1:A:H61	18:B:164:C:N4	1.82	0.76
18:B:32:G:H4'	18:B:33:U:OP2	1.83	0.76
27:D:708:CYS:SG	27:D:889:ILE:HA	2.25	0.76
24:T:37:ILE:HD11	24:T:59:GLU:HB3	1.66	0.76
39:Y:209:LEU:O	39:Y:209:LEU:HD12	1.85	0.76
17:I:78:A:C2	27:D:1110:ARG:NH2	2.54	0.76
27:D:841:PRO:HG2	27:D:877:ARG:HG2	1.68	0.76
28:G:520:G:C2	38:X:34:TYR:CG	2.74	0.76
1:A:261:LEU:HD22	1:A:642:GLY:HA2	1.67	0.75
17:I:142:G:N2	21:P:39:LYS:HZ3	1.82	0.75
1:A:687:ILE:HD11	1:A:706:PRO:HG2	1.67	0.75
32:1:835:ILE:O	32:1:837:PHE:N	2.19	0.75
1:A:796:ASN:HD21	1:A:858:LYS:HG2	1.51	0.75
1:A:181:HIS:HA	1:A:704:TRP:HZ2	1.51	0.75
32:1:348:VAL:HG13	32:1:349:LEU:H	1.52	0.75
34:3:639:LYS:HB3	34:3:686:GLN:HA	1.66	0.75
2:K:438:ASP:OD2	4:N:762:GLN:NE2	2.20	0.75
27:D:1620:TYR:HD2	27:D:1655:LEU:HD21	1.50	0.75
32:1:490:ARG:HH22	38:X:25:ASN:HB3	1.51	0.75
2:K:187:ASP:HB3	2:K:451:PHE:CZ	2.19	0.75
17:I:78:A:C2	27:D:1110:ARG:CZ	2.69	0.75
34:3:783:ILE:HG13	34:3:784:SER:H	1.51	0.75
1:A:2157:ILE:HG23	27:D:1066:ARG:HG2	1.67	0.75
8:C:769:TYR:HE1	8:C:774:LEU:HB2	1.52	0.75
1:A:1252:SER:O	1:A:1274:ARG:NH1	2.20	0.75
1:A:1320:LEU:HD21	1:A:1367:ILE:HG12	1.67	0.75
18:B:29:G:H2'	18:B:30:A:H8	1.52	0.75
27:D:515:SER:HB2	27:D:687:PRO:HG3	1.68	0.75
26:V:64:ARG:HH11	26:V:66:ASN:HB3	1.49	0.75
18:B:48:G:H1	18:B:67:U:H3	1.32	0.74
32:1:566:LEU:HD21	32:1:601:ILE:HG12	1.69	0.74
8:C:493:LEU:HB2	8:C:556:ALA:HB3	1.67	0.74
39:Y:214:LEU:HD21	39:Y:227:MET:CB	2.17	0.74
27:D:1524:TRP:HD1	27:D:1780:ARG:NE	1.85	0.74
27:D:761:PHE:HE2	27:D:769:LYS:HD3	1.53	0.74
26:V:56:GLN:NE2	26:V:60:GLN:O	2.20	0.74
29:H:142:C:H2'	29:H:143:G:H8	1.52	0.74
34:3:239:ASP:OD2	34:3:295:VAL:N	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1962:ARG:HD3	19:O:186:GLU:CD	2.07	0.74
1:A:2398:LEU:HD21	27:D:1056:GLN:O	1.88	0.74
27:D:1688:TYR:HD1	27:D:1695:TYR:HD1	1.34	0.74
3:L:112:MET:HB2	3:L:204:LEU:HD21	1.69	0.74
17:I:79:A:H61	27:D:593:ARG:HG3	1.50	0.74
34:3:179:LEU:HD23	34:3:189:PRO:HG2	1.69	0.74
1:A:1674:ASP:OD2	1:A:2200:LYS:CD	2.35	0.74
1:A:1458:TRP:HZ2	1:A:1489:PRO:HB2	1.53	0.74
1:A:1673:LEU:HD12	1:A:2150:ASN:OD1	1.86	0.74
2:K:159:LEU:HD22	2:K:430:MET:HG3	1.68	0.74
17:I:134:U:H2'	17:I:135:A:C8	2.23	0.74
29:H:1138:G:P	29:H:1138:G:O4'	2.45	0.74
8:C:951:ILE:HG12	8:C:958:PRO:HD3	1.70	0.73
40:Z:36:GLY:O	40:Z:40:LEU:HB2	1.87	0.73
1:A:923:TYR:OH	1:A:936:GLU:OE1	2.04	0.73
34:3:384:ASN:O	34:3:415:ASN:ND2	2.18	0.73
37:6:57:ARG:NH1	37:6:59:ASP:OD2	2.20	0.73
1:A:1309:ILE:HG12	1:A:1356:LEU:HD12	1.70	0.73
27:D:516:ASN:HD22	27:D:685:ARG:HB3	1.53	0.73
8:C:884:ARG:HB2	8:C:910:GLU:HG3	1.70	0.73
32:1:790:LYS:HD2	32:1:826:TYR:HB3	1.70	0.73
34:3:822:HIS:ND1	34:3:846:MET:O	2.21	0.73
3:L:401:LEU:H	4:N:214:SER:HB3	1.54	0.73
28:G:513:U:OP2	32:1:259:ARG:NH1	2.21	0.73
27:D:539:LEU:O	27:D:543:TYR:CB	2.31	0.73
1:A:1964:PRO:HA	1:A:2016:LYS:HE3	1.71	0.73
32:1:198:GLU:O	32:1:202:ASN:HB2	1.88	0.73
8:C:765:VAL:HA	8:C:775:ILE:HG12	1.69	0.73
24:T:20:PHE:HE1	24:T:92:SER:HB2	1.52	0.73
32:1:542:THR:HG22	32:1:582:GLY:HA3	1.68	0.73
34:3:186:ARG:NH2	37:6:38:ASP:OD1	2.22	0.73
2:K:321:LEU:HD11	5:J:169:TRP:HE1	1.52	0.73
18:B:162:G:O3'	18:B:164:C:OP1	2.07	0.73
29:H:140:G:H1	29:H:1168:U:H3	1.37	0.73
34:3:927:ARG:HG3	34:3:928:THR:HG23	1.69	0.73
1:A:1943:PRO:HD3	19:O:169:ILE:CD1	2.19	0.72
17:I:76:A:OP2	27:D:590:GLY:HA3	1.89	0.72
27:D:511:PHE:CE1	27:D:537:LYS:HB2	2.23	0.72
32:1:581:LYS:O	32:1:585:ALA:N	2.20	0.72
27:D:1680:VAL:HG23	27:D:1710:ALA:HB2	1.72	0.72
32:1:778:ARG:NH1	32:1:811:ASN:OD1	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:397:THR:OG1	2:K:413:CYS:O	2.07	0.72
32:1:213:LEU:HD13	32:1:218:ARG:HB2	1.69	0.72
8:C:160:ARG:NH1	8:C:161:ILE:O	2.23	0.72
27:D:523:THR:HG23	27:D:527:LYS:HD3	1.70	0.72
34:3:157:LEU:HD12	34:3:204:LEU:HD11	1.72	0.72
34:3:732:ARG:NH1	34:3:757:ASP:OD1	2.22	0.72
27:D:1392:LYS:HD2	27:D:1469:GLU:OE1	1.90	0.72
27:D:1822:ILE:HG12	27:D:1844:ILE:HG12	1.70	0.72
29:H:119:G:H4'	29:H:119:G:OP1	1.90	0.72
27:D:535:VAL:HG13	27:D:557:ILE:HD13	1.72	0.72
32:1:686:LEU:HD21	32:1:727:ILE:HD11	1.72	0.72
34:3:396:ASP:HB2	34:3:404:LEU:HG	1.72	0.72
34:3:1096:LEU:HD13	34:3:1187:PHE:HZ	1.54	0.72
1:A:2067:TYR:O	19:O:194:LEU:CD2	2.38	0.71
8:C:219:VAL:HG21	8:C:931:TYR:HB3	1.70	0.71
29:H:142:C:H2'	29:H:143:G:C8	2.24	0.71
32:1:443:ARG:NH1	32:1:478:GLU:OE2	2.23	0.71
34:3:250:PRO:HG2	34:3:273:LEU:HB3	1.71	0.71
32:1:490:ARG:HH22	38:X:25:ASN:ND2	1.87	0.71
4:N:803:ASN:OD1	4:N:834:LYS:NZ	2.23	0.71
18:B:163:C:H4'	18:B:164:C:OP1	1.88	0.71
27:D:589:THR:HG21	27:D:608:THR:HG23	1.71	0.71
34:3:102:GLU:OE2	34:3:116:LYS:NZ	2.23	0.71
34:3:641:GLN:HE21	34:3:653:TYR:HE1	1.38	0.71
27:D:1396:VAL:HG13	27:D:1445:LEU:HD11	1.73	0.71
34:3:65:LEU:HB2	34:3:1225:VAL:HG23	1.71	0.71
1:A:975:TYR:HB2	1:A:1314:SER:HB3	1.70	0.71
1:A:1015:PRO:HB2	1:A:1510:ILE:HG12	1.72	0.71
1:A:1020:ILE:HG22	1:A:1022:PRO:HD2	1.72	0.71
34:3:369:ILE:HD13	34:3:421:ILE:HD11	1.72	0.71
1:A:244:ASP:OD1	1:A:596:ASN:ND2	2.22	0.71
5:J:340:LYS:NZ	5:J:429:GLU:OE1	2.22	0.71
21:P:88:ARG:HH12	20:S:67:SER:C	1.93	0.71
1:A:2398:LEU:HB2	27:D:1060:LYS:HD2	1.67	0.71
17:I:91:U:O2'	17:I:92:C:OP1	2.08	0.71
8:C:968:MET:HB3	8:C:972:ARG:HH12	1.54	0.71
27:D:1367:PHE:HD2	27:D:1532:ILE:HG23	1.53	0.71
32:1:805:TYR:HB2	32:1:816:VAL:HG11	1.73	0.71
34:3:153:ASP:OD2	34:3:1302:ARG:NH1	2.24	0.71
1:A:1201:TYR:OH	1:A:1248:VAL:O	2.08	0.70
1:A:341:ALA:HA	1:A:355:LEU:HD23	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:44:ILE:HG12	2:K:76:LEU:HD13	1.73	0.70
27:D:454:LYS:HG3	27:D:463:ILE:HG22	1.73	0.70
27:D:2051:VAL:HG12	27:D:2077:ARG:HA	1.71	0.70
29:H:1093:C:H2'	29:H:1094:G:O4'	1.90	0.70
32:1:835:ILE:HG12	32:1:864:LEU:HD11	1.73	0.70
1:A:956:LYS:O	1:A:960:THR:OG1	2.04	0.70
1:A:2398:LEU:CD1	27:D:1060:LYS:HZ1	2.01	0.70
2:K:411:VAL:HG11	2:K:452:LEU:HD11	1.73	0.70
17:I:97:U:H2'	17:I:98:G:C8	2.26	0.70
34:3:291:SER:OG	37:6:80:TYR:OH	2.09	0.70
34:3:886:PHE:HE2	34:3:1225:VAL:HG21	1.56	0.70
1:A:2395:PHE:HD1	27:D:1060:LYS:O	1.74	0.70
18:B:29:G:H2'	18:B:30:A:C8	2.26	0.70
32:1:618:GLN:HG3	32:1:658:VAL:HG22	1.73	0.70
3:L:441:MET:SD	3:L:444:ARG:NH2	2.64	0.70
34:3:611:VAL:HG21	34:3:621:LYS:HE2	1.74	0.70
18:B:147:C:H2'	18:B:148:G:H8	1.54	0.70
39:Y:215:TYR:CE2	39:Y:232:TRP:CE3	2.79	0.70
1:A:2152:TRP:CE3	27:D:1064:PRO:HG3	2.26	0.70
8:C:232:SER:OG	8:C:234:LEU:O	2.08	0.70
32:1:489:VAL:HG11	38:X:26:GLU:HG2	1.74	0.70
18:B:74:U:O2'	18:B:77:A:OP2	2.07	0.70
27:D:1456:SER:HA	27:D:1465:ILE:HD13	1.73	0.70
27:D:1629:LEU:HD13	27:D:1639:ILE:HB	1.73	0.70
27:D:639:LEU:HA	27:D:644:GLY:HA3	1.74	0.70
29:H:1149:G:H5''	29:H:1149:G:H8	1.56	0.70
34:3:638:SER:HB3	34:3:641:GLN:HB3	1.74	0.70
38:X:63:SER:CB	38:X:74:PHE:CD1	2.75	0.70
1:A:864:GLN:NE2	1:A:1099:ASN:OD1	2.24	0.70
8:C:857:LEU:HD22	8:C:967:VAL:HG23	1.71	0.70
34:3:104:TYR:OH	34:3:481:GLN:NE2	2.25	0.70
2:K:171:GLN:HG2	2:K:172:LEU:H	1.57	0.69
17:I:145:U:N3	26:V:35:PHE:HB3	2.05	0.69
27:D:626:GLU:OE2	27:D:658:SER:OG	2.06	0.69
27:D:1101:ILE:O	27:D:1105:ALA:HB2	1.92	0.69
27:D:1517:ASN:HB3	27:D:1781:ARG:HH12	1.55	0.69
38:X:46:ASP:OD1	40:Z:38:LEU:HD22	1.92	0.69
1:A:1347:ARG:NH1	1:A:1450:GLU:OE2	2.26	0.69
18:B:116:U:H2'	18:B:117:G:H8	1.56	0.69
34:3:181:ARG:NH1	36:5:84:ASP:OD1	2.25	0.69
39:Y:215:TYR:CE2	39:Y:232:TRP:HE3	2.09	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:1198:ILE:HG13	37:6:48:ALA:HB1	1.72	0.69
1:A:1624:LEU:HD22	1:A:1633:PHE:HB3	1.74	0.69
27:D:450:GLU:O	27:D:466:PRO:HD2	1.93	0.69
27:D:667:ILE:HG21	27:D:684:LEU:HD11	1.73	0.69
38:X:57:PRO:HG2	39:Y:231:ARG:HH21	1.58	0.69
24:T:40:LYS:O	24:T:57:ALA:HA	1.93	0.69
1:A:1952:PRO:HB2	3:L:426:GLY:H	1.58	0.69
2:K:400:ARG:NH2	2:K:444:ASP:OD1	2.25	0.69
5:J:159:TYR:O	5:J:163:ASN:ND2	2.26	0.69
8:C:126:MET:SD	8:C:132:ARG:NH1	2.66	0.69
16:F:30:G:N2	18:B:96:U:O2	2.22	0.69
29:H:557:G:H1	29:H:683:U:H3	1.41	0.69
35:4:17:ASP:HB3	35:4:20:ILE:HG12	1.74	0.69
6:E:95:PHE:HB3	6:E:137:TYR:CE2	2.28	0.69
8:C:397:LYS:HE3	8:C:413:LEU:HD11	1.74	0.69
27:D:578:LEU:HB3	27:D:583:ILE:HD12	1.74	0.69
23:R:72:VAL:HB	23:R:91:ILE:O	1.93	0.69
1:A:2152:TRP:CZ3	27:D:1062:PRO:O	2.46	0.69
2:K:395:ILE:HD11	7:M:123:THR:HA	1.75	0.69
39:Y:170:LEU:O	39:Y:172:ILE:HG12	1.92	0.68
1:A:1733:TRP:CE2	1:A:1772:GLY:HA3	2.29	0.68
17:I:150:G:C8	23:R:99:ASP:HB3	2.29	0.68
27:D:589:THR:OG1	27:D:608:THR:OG1	2.06	0.68
3:L:124:PHE:CE2	3:L:127:LEU:HB2	2.28	0.68
3:L:261:SER:OG	3:L:281:GLN:OE1	2.10	0.68
8:C:393:LYS:HB3	8:C:413:LEU:HD22	1.75	0.68
27:D:765:ASN:HB3	27:D:768:HIS:HD2	1.57	0.68
21:P:39:LYS:HE3	22:Q:35:GLN:HE21	1.59	0.68
20:S:65:ARG:HE	20:S:67:SER:HB3	1.58	0.68
17:I:77:U:C2	27:D:1107:ARG:HA	2.29	0.68
29:H:545:G:H1	29:H:695:U:H3	1.41	0.68
29:H:118:U:H4'	29:H:119:G:OP1	1.92	0.68
32:1:458:LEU:O	32:1:462:GLN:HB2	1.93	0.68
1:A:216:GLN:NE2	1:A:280:LEU:O	2.24	0.68
8:C:398:ASN:OD1	8:C:401:ARG:NH2	2.26	0.68
18:B:27:G:C2	18:B:131:A:N3	2.61	0.68
32:1:489:VAL:HG13	38:X:26:GLU:CD	2.14	0.68
22:Q:7:LEU:HB3	22:Q:32:VAL:HG11	1.76	0.68
33:2:371:GLU:H	34:3:1234:LYS:HB3	1.56	0.68
1:A:1197:ASN:ND2	1:A:1221:ASN:OD1	2.26	0.68
8:C:867:THR:O	8:C:926:GLY:CA	2.38	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:R:33:LEU:HD12	25:U:72:PHE:HB2	1.75	0.68
24:T:30:TRP:HB3	26:V:23:ARG:NH1	2.09	0.68
34:3:594:MET:O	34:3:598:SER:OG	2.11	0.68
37:6:54:SER:HA	37:6:65:THR:HG21	1.76	0.68
34:3:704:SER:OG	34:3:712:PHE:O	2.10	0.68
1:A:956:LYS:HD3	3:L:452:ALA:HA	1.74	0.68
27:D:1213:ARG:NH2	27:D:1316:LYS:HG2	2.08	0.68
29:H:550:G:H1	29:H:690:U:H3	1.41	0.68
34:3:126:SER:HB2	34:3:151:THR:HG22	1.75	0.68
34:3:630:ILE:HG21	34:3:646:LEU:HB2	1.76	0.68
34:3:1124:LEU:HB2	34:3:1130:ILE:HD12	1.76	0.68
8:C:269:LYS:HG2	44:C:1500:GTP:C5	2.28	0.67
8:C:445:PRO:O	8:C:449:PHE:HB3	1.94	0.67
27:D:1640:LEU:HD23	27:D:1666:ILE:HG12	1.76	0.67
29:H:563:G:H1	29:H:677:U:H3	1.41	0.67
1:A:2380:LEU:HB3	1:A:2384:ASN:HD22	1.59	0.67
2:K:369:GLY:HA2	2:K:395:ILE:HG23	1.76	0.67
17:I:141:G:C2'	17:I:142:G:H5'	2.25	0.67
29:H:1092:A:H3'	29:H:1093:C:H6	1.58	0.67
1:A:963:VAL:HG21	3:L:280:ARG:HH12	1.59	0.67
1:A:1286:TRP:NE1	1:A:1348:GLU:OE1	2.27	0.67
8:C:307:ILE:HA	8:C:324:ILE:HD11	1.76	0.67
27:D:1890:GLU:HB3	22:Q:143:ARG:HE	1.59	0.67
24:T:24:GLN:HB3	24:T:42:LYS:HD2	1.75	0.67
1:A:1063:PHE:HE1	1:A:1086:ASN:HD22	1.40	0.67
8:C:633:ILE:HB	8:C:645:LEU:HB2	1.77	0.67
16:F:28:U:H3	18:B:98:U:H3	1.42	0.67
18:B:147:C:H2'	18:B:148:G:C8	2.29	0.67
29:H:1149:G:H2'	29:H:1150:U:H6	1.58	0.67
40:Z:40:LEU:O	40:Z:43:ASN:O	2.12	0.67
5:J:395:LEU:HA	5:J:399:ARG:HD3	1.77	0.67
8:C:598:ILE:HG23	8:C:933:TRP:CZ2	2.29	0.67
18:B:40:C:O2	18:B:115:G:N2	2.27	0.67
29:H:566:U:H3	29:H:674:G:H1	1.40	0.67
32:1:494:LEU:CD1	38:X:7:ILE:HG23	2.14	0.67
33:2:176:TRP:O	33:2:177:GLN:HG2	1.93	0.67
34:3:369:ILE:HD11	34:3:380:LEU:HB2	1.77	0.67
1:A:1943:PRO:HD3	19:O:169:ILE:HD11	1.77	0.67
2:K:446:SER:CB	2:K:451:PHE:CE1	2.76	0.67
27:D:556:LYS:HB2	27:D:628:VAL:HA	1.77	0.67
27:D:1756:ASN:HA	27:D:1854:SER:OG	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:570:G:H1	29:H:670:U:H3	1.41	0.67
33:2:293:ARG:HG2	33:2:344:VAL:HG22	1.76	0.67
34:3:211:LYS:HD2	34:3:230:ILE:HD11	1.76	0.67
1:A:2018:ASN:HD22	1:A:2058:LEU:HD22	1.58	0.67
2:K:439:LYS:NZ	7:M:122:GLU:OE1	2.23	0.67
3:L:424:THR:HG22	3:L:425:SER:H	1.59	0.67
17:I:75:U:H5	27:D:1100:PHE:CE1	2.12	0.67
27:D:677:TYR:CD2	27:D:691:LEU:HD21	2.30	0.67
27:D:1971:LEU:HA	27:D:2111:LEU:HB2	1.77	0.67
8:C:865:ASP:HB2	8:C:931:TYR:HE2	1.60	0.66
2:K:292:TRP:CD1	2:K:299:GLU:HA	2.30	0.66
27:D:1890:GLU:O	22:Q:143:ARG:NE	2.28	0.66
34:3:363:VAL:O	34:3:364:THR:HG23	1.95	0.66
34:3:886:PHE:CE2	34:3:1225:VAL:HG21	2.30	0.66
36:5:73:CYS:SG	46:5:203:ZN:ZN	1.84	0.66
1:A:967:VAL:HG23	1:A:1088:VAL:HG11	1.77	0.66
17:I:143:A:C6	25:U:48:TYR:HD2	2.13	0.66
27:D:2077:ARG:NH1	27:D:2119:LEU:O	2.28	0.66
29:H:548:G:H1	29:H:692:U:H3	1.41	0.66
34:3:153:ASP:OD1	34:3:154:SER:N	2.28	0.66
37:6:50:LEU:HD21	37:6:62:ILE:HG23	1.77	0.66
4:N:304:PRO:O	4:N:308:LEU:N	2.28	0.66
34:3:380:LEU:HD23	34:3:388:LEU:HD21	1.76	0.66
1:A:1490:ARG:NH1	1:A:1535:LYS:O	2.27	0.66
8:C:274:ILE:HD13	8:C:385:PHE:HD2	1.60	0.66
8:C:354:TYR:HA	8:C:359:PHE:HA	1.76	0.66
18:B:127:U:H1'	18:B:128:A:C8	2.31	0.66
27:D:542:HIS:CD2	27:D:555:PHE:HB3	2.31	0.66
27:D:757:LEU:O	27:D:761:PHE:CB	2.41	0.66
23:R:102:ILE:HG22	23:R:103:VAL:HG23	1.77	0.66
35:4:184:PHE:HA	35:4:188:GLY:HA2	1.77	0.66
38:X:63:SER:HB3	38:X:74:PHE:CD1	2.30	0.66
1:A:920:LYS:HD3	1:A:940:ILE:HG21	1.78	0.66
2:K:171:GLN:HA	4:N:723:ARG:HH21	1.58	0.66
8:C:942:GLY:HA3	8:C:963:SER:H	1.61	0.66
19:O:149:TYR:HD2	19:O:178:VAL:HG12	1.60	0.66
27:D:1077:ASN:O	27:D:1081:GLN:HG3	1.96	0.66
27:D:1620:TYR:CD2	27:D:1655:LEU:HD21	2.30	0.66
27:D:2137:LYS:HB2	27:D:2159:GLU:OE2	1.94	0.66
1:A:928:ARG:NH1	1:A:1586:GLN:OE1	2.29	0.66
22:Q:107:LEU:HD11	23:R:59:LYS:HG3	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1:198:GLU:O	32:1:202:ASN:CB	2.43	0.66
32:1:386:TYR:O	32:1:388:TYR:N	2.29	0.66
33:2:146:ILE:HD11	34:3:1178:PRO:HG2	1.78	0.66
1:A:1050:LEU:HD23	1:A:1248:VAL:HG22	1.77	0.66
28:G:522:U:H3	39:Y:155:ARG:NH2	1.94	0.66
27:D:1493:SER:HA	27:D:1524:TRP:HH2	1.60	0.66
34:3:493:VAL:HA	34:3:937:LYS:HG2	1.77	0.66
1:A:1756:PHE:HD1	1:A:1774:MET:HG2	1.60	0.66
34:3:77:GLY:HA3	34:3:146:THR:HG21	1.77	0.66
1:A:2259:ILE:HD11	1:A:2293:ILE:HD11	1.77	0.65
27:D:571:VAL:HG21	27:D:587:GLU:HG2	1.78	0.65
32:1:491:ARG:NH1	38:X:27:TYR:OH	2.29	0.65
32:1:695:ASN:HD22	32:1:700:VAL:HG11	1.60	0.65
32:1:966:GLU:HA	32:1:969:LEU:HD13	1.78	0.65
34:3:527:LEU:HD12	34:3:528:PRO:HD2	1.78	0.65
1:A:2310:GLU:C	1:A:2333:PHE:CE1	2.67	0.65
32:1:678:LEU:HD12	32:1:682:ILE:HD11	1.78	0.65
32:1:489:VAL:CG1	38:X:26:GLU:HG2	2.26	0.65
28:G:520:G:N2	38:X:34:TYR:CG	2.65	0.65
33:2:336:ASP:OD2	33:2:338:THR:OG1	2.14	0.65
16:F:92:C:H2'	16:F:93:A:H8	1.61	0.65
21:P:21:ARG:HH11	21:P:29:VAL:HG11	1.62	0.65
21:P:21:ARG:NH1	21:P:51:GLU:OE2	2.30	0.65
22:Q:26:TRP:CE3	22:Q:44:LYS:HG2	2.31	0.65
33:2:323:THR:OG1	35:4:62:ASP:OD1	2.14	0.65
18:B:50:G:H1	18:B:65:U:H3	1.45	0.65
29:H:1115:G:H1	29:H:1130:U:H3	1.43	0.65
32:1:337:VAL:HG11	32:1:359:ILE:HD11	1.79	0.65
32:1:494:LEU:CB	38:X:7:ILE:HG23	2.26	0.65
1:A:404:ASN:ND2	8:C:142:LEU:HD13	2.11	0.65
1:A:2018:ASN:HB3	1:A:2021:SER:OG	1.97	0.65
1:A:2067:TYR:CB	19:O:194:LEU:CD2	2.73	0.65
18:B:95:C:H1'	18:B:96:U:H4'	1.79	0.65
19:O:194:LEU:HD13	19:O:197:ARG:NH1	2.12	0.65
32:1:507:VAL:HG21	32:1:543:ARG:HD2	1.77	0.65
1:A:394:ARG:HB2	8:C:667:GLU:OE2	1.97	0.65
1:A:2398:LEU:CB	27:D:1060:LYS:CD	2.69	0.65
27:D:1585:LEU:HD21	27:D:1683:LEU:HD23	1.79	0.65
33:2:200:ILE:O	33:2:203:THR:OG1	2.12	0.65
8:C:222:MET:O	8:C:225:THR:OG1	2.13	0.65
18:B:1:A:N6	18:B:164:C:H42	1.90	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1704:GLU:HG2	1:A:1731:LYS:HD3	1.77	0.64
1:A:1832:GLU:OE1	3:L:428:ARG:NH1	2.26	0.64
2:K:415:TYR:CD1	2:K:439:LYS:HB3	2.32	0.64
8:C:318:LEU:HA	8:C:422:LYS:HG2	1.80	0.64
8:C:860:PRO:HG2	8:C:908:VAL:HG11	1.79	0.64
27:D:1487:VAL:O	27:D:1490:THR:OG1	2.13	0.64
27:D:1489:GLU:OE2	27:D:1744:SER:OG	2.11	0.64
28:G:520:G:N1	38:X:34:TYR:CE2	2.65	0.64
8:C:510:ARG:NH2	8:C:533:GLU:OE1	2.30	0.64
17:I:151:G:H4'	17:I:152:A:O4'	1.97	0.64
18:B:36:A:H61	18:B:118:U:H3	1.45	0.64
23:R:54:ILE:HG23	23:R:72:VAL:HG13	1.78	0.64
29:H:1098:C:H2'	29:H:1099:G:H8	1.63	0.64
32:1:651:LEU:HD21	32:1:692:ILE:HD11	1.79	0.64
32:1:881:MET:HG2	32:1:885:ILE:HD11	1.77	0.64
34:3:994:LEU:HB3	34:3:1006:TYR:HB2	1.79	0.64
39:Y:171:GLY:C	39:Y:172:ILE:HG12	2.16	0.64
1:A:1400:ILE:HG22	1:A:1401:SER:H	1.63	0.64
1:A:1563:LYS:O	1:A:1782:ASN:ND2	2.30	0.64
1:A:2310:GLU:OE1	1:A:2333:PHE:CZ	2.49	0.64
7:M:113:GLN:HE21	16:F:77:G:H4'	1.62	0.64
8:C:705:GLY:HA3	8:C:826:PRO:HG3	1.79	0.64
27:D:453:PHE:HE2	27:D:455:ARG:HE	1.45	0.64
27:D:1216:MET:HG3	27:D:1218:PHE:CE1	2.30	0.64
3:L:136:GLN:NE2	3:L:166:LYS:O	2.31	0.64
8:C:539:VAL:HG13	8:C:564:ILE:HG23	1.79	0.64
8:C:780:PRO:HA	8:C:783:ILE:HB	1.78	0.64
27:D:747:ARG:NH1	27:D:1047:ARG:HG3	2.12	0.64
27:D:804:HIS:CD2	27:D:834:LEU:HD11	2.33	0.64
1:A:140:ARG:HH21	1:A:252:GLU:HB2	1.61	0.64
1:A:1805:ILE:HG23	1:A:1809:ASN:HD21	1.62	0.64
18:B:95:C:H4'	18:B:96:U:OP1	1.96	0.64
18:B:162:G:C3'	18:B:163:C:H4'	2.22	0.64
29:H:1138:G:O2'	29:H:1139:G:C8	2.50	0.64
27:D:1688:TYR:HD2	27:D:1895:ARG:HA	1.63	0.64
21:P:86:ILE:HG22	20:S:72:ILE:HG22	1.77	0.64
29:H:37:G:OP1	32:1:186:ARG:NH2	2.31	0.64
29:H:1097:G:C2	29:H:1146:G:C4	2.86	0.64
1:A:1624:LEU:HD21	1:A:1635:HIS:CE1	2.32	0.64
3:L:98:PHE:HA	3:L:101:ILE:HG22	1.80	0.64
3:L:124:PHE:HB2	3:L:183:PHE:HD1	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1524:TRP:CD1	27:D:1780:ARG:CZ	2.79	0.64
24:T:85:ASP:OD2	25:U:32:LYS:NZ	2.27	0.64
29:H:1099:G:H2'	29:H:1100:A:H5'	1.80	0.64
29:H:1138:G:O2'	29:H:1139:G:H8	1.79	0.64
2:K:179:SER:H	2:K:194:SER:HA	1.63	0.64
3:L:298:VAL:HG12	3:L:302:MET:HG2	1.80	0.64
27:D:677:TYR:HB2	27:D:691:LEU:HD11	1.78	0.64
29:H:1120:G:H2'	29:H:1121:U:H6	1.62	0.64
32:1:494:LEU:HD11	38:X:23:TRP:CG	2.31	0.64
33:2:145:GLN:HE21	34:3:1178:PRO:HG3	1.62	0.64
34:3:130:LEU:HD23	34:3:149:ALA:HB2	1.77	0.64
1:A:243:ASP:HB3	1:A:246:GLU:HB2	1.79	0.64
1:A:1258:LEU:HD22	1:A:1269:ILE:HD12	1.79	0.64
3:L:120:TYR:HD1	3:L:123:ARG:HB3	1.61	0.64
3:L:227:PRO:HG3	3:L:325:ARG:HB3	1.80	0.64
21:P:39:LYS:HE3	22:Q:35:GLN:NE2	2.13	0.64
33:2:336:ASP:HB3	33:2:339:ASN:HD22	1.62	0.64
34:3:156:ASN:HD22	34:3:178:PRO:HA	1.63	0.64
8:C:182:LYS:NZ	8:C:186:ASP:OD2	2.24	0.64
8:C:236:LEU:HD21	8:C:435:LEU:HD11	1.80	0.64
1:A:1365:THR:O	1:A:1369:ASN:ND2	2.31	0.63
2:K:316:GLN:OE1	2:K:320:SER:OG	2.17	0.63
3:L:328:VAL:HA	3:L:331:HIS:HD2	1.62	0.63
5:J:344:PHE:CE1	5:J:347:LEU:HB2	2.33	0.63
27:D:1700:ILE:O	27:D:1704:LEU:HG	1.98	0.63
34:3:1036:LYS:NZ	34:3:1082:TYR:OH	2.31	0.63
1:A:1267:VAL:HG22	1:A:1302:LEU:HD23	1.81	0.63
34:3:884:ASN:OD1	34:3:885:TRP:N	2.23	0.63
35:4:114:ASN:ND2	35:4:177:ARG:O	2.32	0.63
1:A:976:GLN:NE2	1:A:1310:LYS:HB3	2.12	0.63
8:C:757:TRP:HD1	8:C:762:SER:HB3	1.64	0.63
27:D:610:GLU:HG2	27:D:643:ARG:NH2	2.14	0.63
1:A:681:LYS:O	1:A:684:LYS:HB3	1.99	0.63
8:C:445:PRO:O	8:C:449:PHE:CB	2.47	0.63
18:B:27:G:H8	18:B:27:G:OP2	1.81	0.63
27:D:1372:LYS:HD3	27:D:1708:GLY:HA3	1.80	0.63
1:A:408:SER:HB3	1:A:410:ILE:HD12	1.80	0.63
8:C:405:ARG:HH22	18:B:1:A:H8	1.47	0.63
27:D:1688:TYR:CD1	27:D:1695:TYR:CD1	2.85	0.63
27:D:1917:THR:HG22	27:D:1918:SER:H	1.64	0.63
32:1:945:TYR:HB3	32:1:948:ALA:HB3	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:4:43:ASP:HB2	35:4:50:GLN:HE21	1.63	0.63
1:A:1632:ILE:HG21	1:A:1645:LEU:HD13	1.81	0.63
8:C:603:PHE:CB	8:C:646:GLY:O	2.46	0.63
17:I:141:G:O2'	17:I:142:G:H5'	1.99	0.63
27:D:520:CYS:HB3	27:D:673:THR:HA	1.78	0.63
27:D:568:GLN:HA	27:D:587:GLU:OE2	1.99	0.63
34:3:128:LYS:NZ	34:3:193:MET:O	2.32	0.63
1:A:456:GLU:HG3	8:C:357:GLY:HA3	1.80	0.63
1:A:992:ASP:OD2	1:A:1085:LYS:NZ	2.30	0.63
1:A:1058:ALA:HB3	1:A:1105:ARG:HH21	1.63	0.63
3:L:357:PRO:O	3:L:358:ILE:HG13	1.99	0.63
28:G:520:G:C2	38:X:34:TYR:CD1	2.86	0.63
32:1:510:ALA:HA	32:1:518:THR:HG21	1.80	0.63
17:I:142:G:H5''	17:I:143:A:OP2	1.99	0.63
22:Q:44:LYS:HB2	22:Q:79:ILE:HG21	1.81	0.63
32:1:484:PHE:HA	32:1:488:TRP:HD1	1.64	0.63
34:3:961:CYS:O	34:3:962:LEU:HD12	1.99	0.63
1:A:1790:TRP:HZ3	1:A:1798:ILE:HD12	1.63	0.62
8:C:274:ILE:HD12	8:C:382:TYR:CD1	2.34	0.62
32:1:542:THR:O	32:1:546:ASN:ND2	2.31	0.62
1:A:1481:GLU:HA	1:A:1484:TRP:NE1	2.14	0.62
34:3:97:THR:OG1	34:3:97:THR:O	2.17	0.62
1:A:656:ILE:O	1:A:660:ILE:HG13	2.00	0.62
8:C:652:MET:HG3	8:C:655:LEU:HD12	1.80	0.62
27:D:1668:LYS:HE3	27:D:1702:GLU:HG3	1.80	0.62
22:Q:3:LEU:HD13	23:R:62:ASP:HB2	1.81	0.62
32:1:334:ILE:HD11	32:1:362:CYS:HB3	1.80	0.62
1:A:1073:ILE:HG23	1:A:1074:VAL:HG23	1.79	0.62
1:A:1208:PRO:O	1:A:1212:ARG:HG3	1.98	0.62
1:A:1376:ASN:OD1	1:A:1377:SER:N	2.32	0.62
1:A:2398:LEU:HD22	27:D:1060:LYS:HD2	1.81	0.62
16:F:43:C:O2'	16:F:44:A:O5'	2.14	0.62
32:1:494:LEU:HD12	38:X:7:ILE:HG21	1.77	0.62
1:A:1172:PHE:HZ	1:A:1230:ILE:HD11	1.64	0.62
34:3:394:SER:HB3	34:3:404:LEU:HB2	1.80	0.62
34:3:1124:LEU:HB3	34:3:1128:THR:HG23	1.82	0.62
36:5:49:CYS:SG	46:5:201:ZN:ZN	1.78	0.62
3:L:401:LEU:N	4:N:214:SER:HB3	2.15	0.62
8:C:130:PRO:HB3	8:C:558:LYS:NZ	2.15	0.62
8:C:703:LEU:O	8:C:705:GLY:N	2.33	0.62
38:X:72:GLN:HA	38:X:72:GLN:OE1	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:175:LEU:O	3:L:179:MET:HB2	2.00	0.62
27:D:781:LEU:HD21	27:D:798:GLU:HG2	1.80	0.62
27:D:1541:ILE:HD12	27:D:1542:GLU:HG2	1.82	0.62
27:D:1996:GLN:NE2	27:D:2150:LEU:H	1.97	0.62
24:T:35:ILE:HA	26:V:23:ARG:HH21	1.64	0.62
32:1:494:LEU:HB3	38:X:7:ILE:CG2	2.29	0.62
34:3:629:GLY:O	34:3:630:ILE:HG13	1.99	0.62
34:3:987:PHE:CD2	34:3:1054:LEU:HB2	2.34	0.62
4:N:849:TYR:O	4:N:853:GLY:N	2.20	0.62
27:D:1148:GLN:HE22	27:D:1297:TRP:HA	1.64	0.62
1:A:2189:LEU:HD13	1:A:2224:VAL:HG23	1.81	0.62
27:D:1772:TRP:CZ3	27:D:1773:PHE:CE1	2.86	0.62
29:H:1098:C:O5'	29:H:1098:C:H6	1.82	0.62
33:2:167:LYS:NZ	34:3:1111:ASP:OD2	2.21	0.62
34:3:253:VAL:HG21	34:3:327:VAL:HG11	1.82	0.62
37:6:23:ASP:OD1	37:6:24:GLU:N	2.29	0.62
1:A:1014:LYS:HE2	1:A:1024:LEU:HD13	1.82	0.62
3:L:239:ALA:O	3:L:243:ALA:HB2	2.00	0.62
24:T:90:ILE:HB	26:V:62:VAL:HG13	1.81	0.62
29:H:143:G:H2'	29:H:144:G:H8	1.65	0.62
34:3:379:VAL:O	34:3:390:LYS:HA	1.99	0.62
34:3:699:MET:HA	34:3:719:GLN:O	1.99	0.62
1:A:1145:MET:SD	1:A:1160:LEU:HD22	2.40	0.61
1:A:2349:PHE:CD2	1:A:2379:PRO:HG3	2.35	0.61
1:A:2395:PHE:CD1	27:D:1062:PRO:CD	2.67	0.61
2:K:392:HIS:HD2	2:K:396:VAL:HG22	1.65	0.61
8:C:220:ASN:HB3	8:C:651:TYR:HB2	1.80	0.61
1:A:1501:THR:HG21	4:N:163:THR:HG21	1.82	0.61
8:C:468:LEU:HD11	8:C:493:LEU:HD23	1.81	0.61
16:F:74:U:H2'	16:F:75:A:C8	2.35	0.61
26:V:30:ARG:HE	26:V:41:ASP:HB3	1.65	0.61
32:1:531:GLU:OE1	32:1:534:ARG:NH2	2.33	0.61
32:1:763:LEU:HD11	32:1:797:VAL:HG22	1.81	0.61
3:L:222:ILE:HA	3:L:225:ILE:HG12	1.82	0.61
27:D:1731:TYR:OH	22:Q:146:LEU:O	2.15	0.61
27:D:1925:LYS:NZ	27:D:1946:ASP:OD2	2.25	0.61
1:A:304:ASP:OD1	1:A:305:LEU:N	2.32	0.61
27:D:1220:ILE:HD11	27:D:1272:PHE:HE2	1.65	0.61
32:1:820:MET:HA	32:1:823:MET:HG2	1.81	0.61
34:3:768:ARG:NH2	34:3:1359:ASN:O	2.32	0.61
2:K:179:SER:HA	2:K:441:ILE:HG21	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:271:ASP:O	8:C:275:LEU:HB2	1.99	0.61
27:D:1370:SER:OG	27:D:1535:PHE:HB2	2.00	0.61
34:3:128:LYS:NZ	34:3:194:GLU:OE1	2.29	0.61
34:3:154:SER:HB3	34:3:1302:ARG:HD2	1.83	0.61
2:K:395:ILE:HG22	2:K:396:VAL:N	2.12	0.61
4:N:261:LYS:HB3	4:N:285:HIS:CD2	2.35	0.61
5:J:443:LYS:HG2	5:J:444:VAL:H	1.65	0.61
27:D:571:VAL:HG21	27:D:587:GLU:CG	2.31	0.61
21:P:49:ILE:HG22	21:P:81:VAL:HA	1.82	0.61
29:H:1161:U:O2'	29:H:1162:U:H5'	2.01	0.61
32:1:739:ASN:OD1	32:1:740:LYS:N	2.32	0.61
2:K:286:ASP:O	2:K:287:MET:HG2	1.99	0.61
18:B:136:G:O2'	18:B:137:U:O4'	2.19	0.61
27:D:1367:PHE:HE2	27:D:1518:ALA:HB1	1.64	0.61
27:D:1550:SER:C	27:D:1551:PHE:HD1	2.03	0.61
34:3:638:SER:HA	34:3:683:GLN:HA	1.83	0.61
34:3:642:LEU:HD21	34:3:644:ILE:HG23	1.81	0.61
8:C:598:ILE:HG22	8:C:599:THR:HG23	1.82	0.61
18:B:19:A:N6	18:B:151:A:N1	2.47	0.61
27:D:960:ILE:HG23	27:D:961:SER:H	1.65	0.61
29:H:1149:G:H2'	29:H:1150:U:C6	2.34	0.61
34:3:205:SER:HB2	34:3:211:LYS:HG2	1.82	0.61
38:X:78:LYS:NZ	39:Y:162:LEU:O	2.34	0.61
1:A:406:PRO:HG2	44:C:1500:GTP:O2'	2.01	0.61
1:A:609:GLU:O	1:A:613:SER:CB	2.47	0.61
1:A:2157:ILE:CG2	27:D:1066:ARG:HG2	2.31	0.61
4:N:101:LYS:O	4:N:105:ALA:HB2	2.00	0.61
7:M:93:VAL:HG12	7:M:95:ARG:H	1.64	0.61
8:C:176:ARG:NH1	8:C:184:GLU:O	2.34	0.61
8:C:415:TYR:HB3	8:C:419:PRO:HG2	1.83	0.61
22:Q:7:LEU:HD11	23:R:95:PHE:CE2	2.36	0.61
32:1:494:LEU:HB3	38:X:7:ILE:CG1	2.31	0.61
1:A:768:GLU:OE1	4:N:108:LYS:NZ	2.34	0.60
1:A:1313:ASP:OD1	1:A:1359:ILE:HG21	2.01	0.60
2:K:292:TRP:HE1	2:K:299:GLU:HG3	1.66	0.60
2:K:312:SER:HB2	2:K:353:TYR:O	2.01	0.60
17:I:146:U:O4'	20:S:67:SER:HB2	2.01	0.60
28:G:520:G:C5	38:X:34:TYR:CZ	2.88	0.60
29:H:1126:G:HO2'	29:H:1127:A:H8	1.50	0.60
34:3:640:THR:OG1	34:3:686:GLN:O	2.20	0.60
34:3:1216:CYS:SG	34:3:1228:PHE:HB2	2.41	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:51:PHE:HE2	7:M:114:ILE:HG23	1.66	0.60
8:C:504:THR:O	8:C:507:SER:OG	2.15	0.60
8:C:918:LEU:HD23	8:C:928:CYS:HB2	1.83	0.60
27:D:1524:TRP:CD1	27:D:1780:ARG:NE	2.69	0.60
27:D:1688:TYR:CZ	27:D:1896:LYS:HE2	2.36	0.60
34:3:994:LEU:HB2	34:3:1008:ILE:HD11	1.83	0.60
1:A:1161:TYR:HD1	1:A:1170:MET:HG2	1.67	0.60
2:K:261:LEU:HB3	2:K:292:TRP:CZ3	2.37	0.60
29:H:1139:G:H2'	29:H:1140:U:C6	2.36	0.60
32:1:516:SER:O	32:1:520:ASP:HB2	2.01	0.60
32:1:767:LEU:HD22	32:1:804:GLU:HG2	1.82	0.60
1:A:683:LEU:HD13	1:A:706:PRO:HB2	1.82	0.60
16:F:2:U:H2'	16:F:3:U:C6	2.36	0.60
17:I:77:U:H1'	27:D:1107:ARG:HG3	1.84	0.60
28:G:514:U:H4'	28:G:515:U:H5'	1.83	0.60
32:1:177:ASN:OD1	32:1:178:THR:N	2.34	0.60
34:3:493:VAL:O	34:3:499:SER:OG	2.13	0.60
34:3:1037:PHE:HB2	34:3:1042:LEU:HB2	1.82	0.60
6:E:42:MET:HE1	6:E:107:VAL:H	1.65	0.60
18:B:27:G:OP1	18:B:141:G:O5'	2.19	0.60
18:B:27:G:N2	18:B:131:A:N3	2.48	0.60
34:3:184:LEU:HD21	37:6:45:GLY:HA3	1.83	0.60
34:3:379:VAL:HG22	34:3:391:LEU:HB2	1.83	0.60
39:Y:173:ASN:O	39:Y:174:VAL:HG12	2.02	0.60
1:A:1147:PHE:CD2	1:A:1153:GLU:HG2	2.37	0.60
1:A:1682:THR:OG1	1:A:1702:THR:OG1	2.20	0.60
1:A:2310:GLU:CA	1:A:2333:PHE:CE1	2.85	0.60
5:J:167:GLU:HB3	5:J:169:TRP:HE3	1.66	0.60
8:C:737:ILE:HG12	8:C:768:PHE:HB3	1.83	0.60
17:I:62:G:OP1	27:D:714:ASN:HB3	2.02	0.60
27:D:1409:LEU:HD22	27:D:1427:LYS:HB2	1.84	0.60
27:D:2104:GLY:HA2	27:D:2112:TYR:HD2	1.66	0.60
34:3:335:ILE:HD12	34:3:407:LEU:HD11	1.83	0.60
34:3:547:ASN:HA	34:3:563:ILE:O	2.00	0.60
1:A:1213:MET:HG2	1:A:1259:LEU:HD12	1.82	0.60
1:A:1777:ILE:HG12	1:A:1784:TYR:HB3	1.82	0.60
1:A:1910:LYS:CD	19:O:169:ILE:HG12	2.30	0.60
2:K:65:GLU:HG3	2:K:66:ASN:H	1.66	0.60
8:C:116:THR:OG1	8:C:120:ARG:NH1	2.34	0.60
27:D:707:PHE:HD2	27:D:895:VAL:HG13	1.67	0.60
1:A:902:PRO:HG2	1:A:905:TYR:HB2	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1154:VAL:O	27:D:1157:ILE:HG13	2.02	0.60
27:D:1772:TRP:HZ3	27:D:1773:PHE:CZ	2.20	0.60
27:D:2013:VAL:HG13	27:D:2018:ASP:HB2	1.83	0.60
1:A:431:ILE:HA	8:C:895:ALA:HB1	1.84	0.60
1:A:982:TYR:HB2	1:A:1106:GLY:HA3	1.82	0.60
1:A:2310:GLU:CG	1:A:2333:PHE:CZ	2.66	0.60
7:M:34:LYS:HB3	7:M:39:GLU:HG2	1.83	0.60
27:D:683:PHE:HA	27:D:946:VAL:HG21	1.83	0.60
32:1:494:LEU:CB	38:X:7:ILE:CG1	2.78	0.60
34:3:854:ASN:OD1	34:3:855:ALA:N	2.35	0.60
1:A:976:GLN:HE22	1:A:1310:LYS:CB	2.13	0.59
2:K:135:ARG:NH1	2:K:360:ASN:O	2.33	0.59
4:N:842:TRP:HA	4:N:845:LEU:HD12	1.82	0.59
16:F:36:U:H3	16:F:45:A:H61	1.50	0.59
17:I:96:A:H2'	17:I:97:U:O4'	2.02	0.59
27:D:490:ALA:C	27:D:491:PHE:HD1	2.05	0.59
27:D:781:LEU:CD2	27:D:798:GLU:HA	2.29	0.59
27:D:2008:CYS:SG	27:D:2013:VAL:HB	2.42	0.59
25:U:28:GLY:HA2	25:U:38:TYR:O	2.02	0.59
29:H:1149:G:H8	29:H:1149:G:C5'	2.15	0.59
34:3:236:VAL:HG13	34:3:257:ILE:HG23	1.84	0.59
5:J:346:ASN:O	5:J:422:ASN:ND2	2.35	0.59
34:3:412:THR:O	34:3:413:ILE:HG23	2.03	0.59
34:3:831:THR:HA	34:3:836:TRP:HA	1.83	0.59
34:3:924:PHE:CD2	34:3:952:ARG:HD2	2.37	0.59
38:X:90:ASP:OD2	39:Y:223:ARG:NH2	2.35	0.59
1:A:161:PHE:O	1:A:165:LEU:HB2	2.02	0.59
1:A:430:PRO:O	1:A:431:ILE:HG22	2.03	0.59
2:K:355:VAL:HG22	2:K:366:THR:HG22	1.84	0.59
3:L:225:ILE:O	3:L:325:ARG:NH1	2.35	0.59
20:S:65:ARG:NH1	26:V:65:GLY:O	2.35	0.59
1:A:675:HIS:NE2	18:B:102:C:OP1	2.36	0.59
2:K:165:LEU:HD22	2:K:465:ASN:HB3	1.83	0.59
27:D:1428:LEU:HD11	27:D:1445:LEU:HB2	1.85	0.59
27:D:1779:TYR:CE1	27:D:1783:HIS:HE1	2.21	0.59
33:2:296:GLN:NE2	33:2:306:GLU:OE2	2.35	0.59
38:X:48:LEU:O	39:Y:231:ARG:CZ	2.49	0.59
38:X:89:VAL:HG22	38:X:104:ILE:HG22	1.85	0.59
1:A:794:LYS:HB3	1:A:854:ARG:NH1	2.16	0.59
2:K:285:HIS:O	2:K:309:GLY:HA2	2.03	0.59
4:N:241:PRO:HB3	4:N:277:ILE:HD11	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:I:90:C:N3	22:Q:34:PRO:HD2	2.17	0.59
27:D:563:LEU:HD11	27:D:836:TRP:CE2	2.38	0.59
29:H:1149:G:C8	29:H:1149:G:C5'	2.85	0.59
29:H:1152:U:H2'	29:H:1153:C:C6	2.38	0.59
34:3:433:MET:O	34:3:485:ASN:HB3	2.02	0.59
34:3:1090:ILE:O	34:3:1117:HIS:HA	2.01	0.59
1:A:1202:ASN:ND2	1:A:1246:ALA:O	2.34	0.59
1:A:1308:GLU:HG2	1:A:1311:LYS:HD2	1.84	0.59
2:K:66:ASN:ND2	16:F:74:U:O2	2.35	0.59
8:C:803:VAL:HG13	8:C:813:ILE:HB	1.84	0.59
28:G:521:U:OP2	32:1:408:ARG:NH2	2.34	0.59
28:G:522:U:H3	39:Y:155:ARG:CZ	2.16	0.59
38:X:11:GLU:HG2	38:X:16:ILE:HG21	1.84	0.59
1:A:1414:TRP:CD1	1:A:1555:THR:HG22	2.37	0.59
1:A:2310:GLU:CA	1:A:2333:PHE:CZ	2.82	0.59
4:N:809:LEU:HD12	4:N:841:THR:HG22	1.85	0.59
27:D:568:GLN:NE2	27:D:587:GLU:OE1	2.36	0.59
32:1:696:LYS:HG2	32:1:697:HIS:H	1.68	0.59
38:X:123:LYS:O	38:X:127:ASP:N	2.34	0.59
1:A:897:PRO:O	1:A:1006:ARG:NH1	2.36	0.59
5:J:265:LEU:HD12	5:J:266:PRO:HD2	1.85	0.59
19:O:183:LYS:O	19:O:187:GLU:HB2	2.02	0.59
32:1:698:ARG:HE	32:1:739:ASN:HD22	1.51	0.59
34:3:1199:ILE:HA	34:3:1220:GLY:HA2	1.84	0.59
8:C:968:MET:HB3	8:C:972:ARG:NH1	2.18	0.59
18:B:161:U:H2'	18:B:162:G:C8	2.38	0.59
29:H:1140:U:C2	29:H:1141:C:C5	2.91	0.59
29:H:1146:G:O2'	29:H:1147:A:O5'	2.15	0.59
32:1:327:TRP:HZ2	32:1:369:PRO:HG2	1.68	0.59
34:3:599:ILE:HB	34:3:610:ILE:HB	1.85	0.59
1:A:1755:LYS:HE3	1:A:1759:TYR:CE2	2.38	0.59
18:B:43:G:H2'	18:B:44:A:C8	2.38	0.59
27:D:765:ASN:CB	27:D:768:HIS:HD2	2.16	0.59
23:R:27:LYS:O	23:R:32:SER:OG	2.20	0.59
34:3:180:THR:O	36:5:83:LYS:HB3	2.03	0.59
34:3:736:ILE:HG23	34:3:738:GLN:H	1.68	0.59
1:A:1674:ASP:OD2	1:A:2200:LYS:NZ	2.33	0.58
27:D:1372:LYS:HA	27:D:1376:LYS:NZ	2.18	0.58
21:P:18:TYR:HD1	21:P:101:PRO:HG3	1.67	0.58
32:1:442:ILE:HG23	32:1:457:ILE:HG23	1.83	0.58
32:1:632:LYS:HD2	32:1:672:VAL:HG13	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:208:GLU:HG3	34:3:209:GLN:H	1.67	0.58
38:X:40:ARG:NH1	38:X:72:GLN:O	2.36	0.58
1:A:867:ILE:HD13	1:A:1101:TYR:CG	2.38	0.58
1:A:927:VAL:HG13	3:L:385:ARG:HD2	1.83	0.58
27:D:1779:TYR:CE1	27:D:1783:HIS:CE1	2.91	0.58
27:D:1781:ARG:HG3	27:D:1789:TYR:HE2	1.66	0.58
33:2:292:GLY:N	35:4:31:GLN:OE1	2.30	0.58
34:3:382:GLN:NE2	34:3:416:SER:OG	2.36	0.58
1:A:365:ASN:OD1	1:A:366:GLU:N	2.36	0.58
1:A:1207:TRP:HB3	1:A:1211:SER:OG	2.03	0.58
1:A:1391:PRO:HD2	1:A:1394:LEU:HD12	1.85	0.58
4:N:401:ILE:O	4:N:405:SER:N	2.34	0.58
8:C:597:TYR:CE1	8:C:630:PRO:HB2	2.38	0.58
8:C:794:GLN:HG2	8:C:835:LYS:HG2	1.84	0.58
18:B:67:U:H2'	18:B:68:A:H8	1.68	0.58
32:1:538:VAL:O	32:1:542:THR:HG23	2.03	0.58
1:A:551:LEU:HG	1:A:557:PHE:HE2	1.69	0.58
8:C:348:LEU:HD12	8:C:372:THR:HG22	1.84	0.58
27:D:789:LEU:O	27:D:794:ARG:NE	2.32	0.58
34:3:232:ARG:HE	34:3:235:MET:HG3	1.68	0.58
34:3:387:ASP:HA	34:3:412:THR:HG22	1.84	0.58
34:3:1191:ASN:ND2	34:3:1316:LYS:HB2	2.18	0.58
2:K:197:GLY:HA2	2:K:221:ILE:HG13	1.85	0.58
6:E:137:TYR:O	6:E:139:HIS:N	2.37	0.58
8:C:706:LEU:HD23	8:C:825:VAL:HA	1.85	0.58
27:D:645:PRO:HA	27:D:648:GLU:OE2	2.03	0.58
27:D:1367:PHE:CE2	27:D:1518:ALA:HB1	2.39	0.58
23:R:72:VAL:HG21	23:R:94:LEU:HB3	1.85	0.58
1:A:325:LYS:HB2	1:A:405:ASN:HD22	1.68	0.58
2:K:171:GLN:NE2	2:K:209:PRO:O	2.36	0.58
8:C:138:VAL:HG12	8:C:146:LYS:HG2	1.85	0.58
18:B:32:G:O2'	18:B:34:C:H5''	2.03	0.58
27:D:1898:ASP:O	27:D:1902:LEU:HG	2.03	0.58
24:T:59:GLU:OE2	25:U:30:LYS:NZ	2.20	0.58
34:3:328:VAL:HG22	34:3:337:VAL:HG12	1.86	0.58
34:3:515:ASN:HB2	34:3:886:PHE:HE1	1.68	0.58
1:A:874:ILE:O	1:A:875:THR:OG1	2.21	0.58
1:A:956:LYS:NZ	3:L:451:GLN:HG3	2.19	0.58
27:D:794:ARG:O	27:D:798:GLU:HG3	2.04	0.58
27:D:1748:TYR:CE2	22:Q:142:PRO:HD2	2.39	0.58
26:V:8:LYS:HA	26:V:11:MET:HG2	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:1116:ARG:HH22	34:3:1141:LEU:HD21	1.69	0.58
36:5:74:TRP:HZ2	36:5:78:ARG:HH21	1.50	0.58
1:A:377:VAL:HG12	1:A:379:ILE:H	1.68	0.58
5:J:319:ALA:O	5:J:323:ARG:HG2	2.03	0.58
16:F:38:U:O2'	16:F:39:G:OP2	2.20	0.58
27:D:2053:LEU:HD21	27:D:2142:ILE:HG22	1.86	0.58
25:U:46:ASP:OD1	25:U:50:ASN:N	2.33	0.58
1:A:2159:ASN:HA	1:A:2162:LEU:HD13	1.86	0.58
27:D:978:LEU:HD23	27:D:981:LEU:HD12	1.86	0.58
27:D:1700:ILE:HD11	27:D:1740:LEU:HD13	1.84	0.58
22:Q:3:LEU:HD23	23:R:95:PHE:CE1	2.35	0.58
32:1:601:ILE:O	32:1:604:THR:OG1	2.16	0.58
34:3:766:LYS:HD3	34:3:836:TRP:CE2	2.38	0.58
2:K:175:THR:O	2:K:176:LYS:HG2	2.04	0.57
4:N:286:GLU:HG3	4:N:287:SER:H	1.68	0.57
4:N:760:VAL:O	4:N:764:LEU:CB	2.52	0.57
18:B:77:A:H4'	18:B:78:A:OP1	2.03	0.57
27:D:1488:TYR:O	27:D:1492:ILE:HG12	2.03	0.57
34:3:1222:GLN:HE22	37:6:48:ALA:HB2	1.68	0.57
1:A:585:ARG:HD3	1:A:733:GLN:HG2	1.86	0.57
1:A:1253:LYS:O	1:A:1274:ARG:NH2	2.36	0.57
1:A:1694:MET:O	1:A:1759:TYR:OH	2.22	0.57
8:C:869:HIS:HD2	8:C:925:LEU:HB3	1.69	0.57
17:I:149:U:O4	23:R:66:ASN:ND2	2.32	0.57
27:D:848:LYS:HA	27:D:889:ILE:HB	1.86	0.57
27:D:1246:THR:O	27:D:1289:PHE:HE2	1.87	0.57
27:D:1434:LEU:HB2	27:D:2096:LEU:HG	1.84	0.57
29:H:1141:C:H2'	29:H:1142:G:H8	1.68	0.57
32:1:257:MET:HG3	36:5:100:HIS:ND1	2.18	0.57
34:3:367:SER:HB2	34:3:382:GLN:HG2	1.84	0.57
1:A:181:HIS:HA	1:A:704:TRP:CZ2	2.36	0.57
1:A:194:HIS:HB3	1:A:198:ALA:H	1.68	0.57
3:L:184:LYS:HE2	3:L:186:LYS:HB2	1.86	0.57
3:L:462:ASN:HA	4:N:830:ARG:HD2	1.87	0.57
8:C:625:ILE:HD11	8:C:659:LEU:HD13	1.86	0.57
32:1:882:ASN:ND2	33:2:268:ASP:O	2.37	0.57
34:3:432:GLU:O	34:3:485:ASN:ND2	2.37	0.57
35:4:136:ARG:HB2	35:4:154:TYR:HD2	1.69	0.57
1:A:1704:GLU:HA	1:A:1731:LYS:HG2	1.86	0.57
2:K:285:HIS:C	2:K:287:MET:H	2.06	0.57
8:C:709:SER:O	8:C:821:LEU:N	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:752:ARG:HA	8:C:757:TRP:H	1.70	0.57
28:G:505:A:H1'	28:G:506:U:H6	1.68	0.57
29:H:1097:G:H1'	29:H:1146:G:N2	2.20	0.57
34:3:189:PRO:HA	34:3:206:SER:HB3	1.86	0.57
34:3:783:ILE:HG13	34:3:784:SER:N	2.18	0.57
1:A:662:GLN:NE2	16:F:1:G:N3	2.52	0.57
8:C:562:VAL:HG23	8:C:564:ILE:HD11	1.86	0.57
27:D:1216:MET:CG	27:D:1218:PHE:HE1	2.14	0.57
27:D:1396:VAL:HG11	27:D:1452:PHE:CE2	2.38	0.57
29:H:36:A:N7	32:1:182:ARG:NH2	2.52	0.57
34:3:365:ILE:HD13	34:3:381:LEU:HG	1.87	0.57
1:A:2064:GLY:O	1:A:2068:ASN:N	2.37	0.57
18:B:10:U:H2'	18:B:11:A:N7	2.20	0.57
27:D:505:LYS:HA	27:D:508:HIS:NE2	2.19	0.57
27:D:1217:ARG:NH2	27:D:1788:TYR:OH	2.37	0.57
27:D:2102:VAL:O	27:D:2142:ILE:HA	2.03	0.57
21:P:21:ARG:NH1	21:P:29:VAL:HG11	2.19	0.57
25:U:74:ARG:HB3	25:U:77:ASN:HD22	1.70	0.57
33:2:183:LEU:HD22	33:2:188:LEU:HD11	1.87	0.57
40:Z:37:LEU:O	40:Z:41:GLU:HG2	2.05	0.57
1:A:1277:GLU:O	1:A:1279:VAL:HG23	2.05	0.57
2:K:451:PHE:CD1	2:K:451:PHE:N	2.73	0.57
8:C:143:HIS:HA	44:C:1500:GTP:O3B	2.04	0.57
8:C:245:VAL:HG11	8:C:295:ILE:HG22	1.86	0.57
34:3:159:ILE:HD12	34:3:224:ILE:HD11	1.87	0.57
34:3:390:LYS:HD2	34:3:410:PHE:CZ	2.39	0.57
27:D:648:GLU:OE1	27:D:943:TYR:HB3	2.04	0.57
27:D:801:ILE:HG22	27:D:827:VAL:HB	1.86	0.57
22:Q:43:VAL:HG11	22:Q:85:ILE:HD12	1.87	0.57
20:S:68:GLN:HG3	26:V:69:ILE:HA	1.86	0.57
24:T:10:MET:HG3	26:V:30:ARG:O	2.04	0.57
33:2:265:CYS:SG	33:2:266:PHE:N	2.78	0.57
35:4:139:GLU:O	35:4:151:ALA:HA	2.04	0.57
2:K:32:LEU:HD23	2:K:34:HIS:H	1.70	0.57
27:D:1415:ARG:HA	27:D:1418:HIS:CE1	2.40	0.57
22:Q:30:GLN:HE22	22:Q:84:TYR:HE1	1.53	0.57
1:A:1865:THR:HG22	1:A:1866:PHE:H	1.69	0.57
4:N:285:HIS:ND1	4:N:285:HIS:O	2.38	0.57
8:C:240:ASP:HB2	8:C:243:GLU:HB3	1.87	0.57
8:C:472:VAL:HB	8:C:575:ALA:HB3	1.87	0.57
8:C:883:ARG:NH2	8:C:912:ALA:O	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1008:PHE:N	27:D:1008:PHE:HD1	2.02	0.57
27:D:1370:SER:HB2	27:D:1514:CYS:SG	2.45	0.57
27:D:1513:ASN:OD1	27:D:1514:CYS:N	2.31	0.57
29:H:677:U:H2'	29:H:678:U:H6	1.70	0.57
29:H:678:U:H2'	29:H:679:U:H6	1.70	0.57
32:1:256:PRO:HA	32:1:259:ARG:HD2	1.86	0.57
34:3:190:ILE:O	34:3:191:SER:OG	2.20	0.57
34:3:269:ILE:HD11	34:3:282:LYS:HG3	1.86	0.57
34:3:540:PRO:HB2	34:3:612:PRO:HG3	1.86	0.57
1:A:1836:ASN:H	1:A:1839:ASN:HB3	1.70	0.56
8:C:701:GLU:HB2	8:C:706:LEU:HB2	1.87	0.56
16:F:72:C:H2'	16:F:73:A:H8	1.70	0.56
27:D:1101:ILE:O	27:D:1105:ALA:CB	2.53	0.56
29:H:669:U:H2'	29:H:670:U:H6	1.70	0.56
29:H:671:G:H2'	29:H:672:U:H6	1.70	0.56
29:H:689:G:H2'	29:H:690:U:H6	1.71	0.56
32:1:675:LEU:HD11	32:1:714:LEU:HB3	1.86	0.56
32:1:874:GLU:HB3	34:3:1315:ARG:HH22	1.70	0.56
33:2:329:LYS:HG3	33:2:349:ILE:HD12	1.86	0.56
34:3:162:ILE:HG22	34:3:171:LEU:HD12	1.87	0.56
34:3:600:ILE:HD13	34:3:642:LEU:HD13	1.86	0.56
1:A:358:ARG:NE	1:A:361:GLU:OE2	2.34	0.56
1:A:1231:GLN:NE2	1:A:1241:ILE:O	2.35	0.56
1:A:1668:ILE:HD13	1:A:1801:SER:HB2	1.85	0.56
1:A:1883:ASN:ND2	1:A:1886:THR:OG1	2.35	0.56
3:L:367:ARG:NH1	17:I:58:G:N7	2.53	0.56
21:P:40:HIS:O	21:P:89:GLY:HA3	2.05	0.56
25:U:16:LYS:HB2	25:U:17:PRO:HD3	1.87	0.56
29:H:682:U:H2'	29:H:683:U:H6	1.70	0.56
34:3:147:PHE:CD1	34:3:147:PHE:N	2.73	0.56
1:A:535:HIS:HE2	18:B:105:A:P	2.28	0.56
1:A:1498:ASP:HB2	4:N:159:LEU:HD12	1.86	0.56
1:A:1512:ARG:NH1	1:A:1529:ASN:OD1	2.38	0.56
1:A:2310:GLU:CD	1:A:2333:PHE:HZ	2.08	0.56
2:K:410:LEU:O	2:K:421:VAL:HA	2.04	0.56
2:K:439:LYS:HB2	2:K:457:TRP:CD1	2.39	0.56
3:L:400:VAL:HG21	4:N:154:PRO:HG2	1.85	0.56
5:J:330:ASN:OD1	5:J:331:VAL:HG23	2.04	0.56
8:C:106:PHE:HE2	8:C:554:HIS:CE1	2.23	0.56
8:C:133:ILE:CA	8:C:209:MET:O	2.52	0.56
27:D:1688:TYR:CD1	27:D:1695:TYR:CE1	2.93	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:565:U:H2'	29:H:566:U:H6	1.70	0.56
29:H:672:U:H2'	29:H:673:U:H6	1.70	0.56
29:H:684:U:H2'	29:H:685:U:H6	1.70	0.56
29:H:691:G:H2'	29:H:692:U:H6	1.71	0.56
29:H:694:C:H2'	29:H:695:U:H6	1.70	0.56
32:1:598:LEU:HD11	32:1:631:ILE:HG12	1.87	0.56
36:5:22:LEU:HG	36:5:70:ALA:HB2	1.87	0.56
39:Y:229:GLY:O	39:Y:231:ARG:N	2.38	0.56
1:A:579:LEU:HD22	1:A:619:PHE:CE1	2.40	0.56
1:A:1711:VAL:HG13	1:A:1789:ASN:HB3	1.86	0.56
2:K:192:THR:O	2:K:199:LEU:HA	2.05	0.56
2:K:230:SER:OG	2:K:233:GLN:OE1	2.22	0.56
18:B:114:G:H2'	18:B:115:G:H8	1.68	0.56
18:B:149:U:H2'	18:B:150:U:O4'	2.06	0.56
27:D:562:PRO:HG3	27:D:635:GLU:OE1	2.05	0.56
27:D:790:ASP:OD1	27:D:794:ARG:NH2	2.38	0.56
29:H:680:C:H2'	29:H:681:C:H6	1.71	0.56
29:H:683:U:H2'	29:H:684:U:H6	1.71	0.56
29:H:693:C:H2'	29:H:694:C:H6	1.71	0.56
29:H:693:C:C2	29:H:694:C:C5	2.93	0.56
34:3:1122:LYS:NZ	34:3:1202:PHE:O	2.38	0.56
1:A:1810:PRO:O	1:A:1814:VAL:HG23	2.05	0.56
3:L:359:PRO:HB3	6:E:118:GLU:HG2	1.88	0.56
5:J:363:LEU:HD11	5:J:391:PHE:HD2	1.70	0.56
8:C:884:ARG:HB3	8:C:907:PRO:HG2	1.85	0.56
27:D:1008:PHE:N	27:D:1008:PHE:CD1	2.72	0.56
29:H:143:G:H2'	29:H:144:G:C8	2.41	0.56
29:H:568:U:H2'	29:H:569:C:H6	1.71	0.56
34:3:207:VAL:HB	34:3:236:VAL:HG23	1.88	0.56
34:3:517:VAL:HG21	34:3:828:VAL:HG21	1.87	0.56
1:A:1060:LYS:HA	1:A:1101:TYR:CE2	2.41	0.56
1:A:1335:TRP:CD1	1:A:1367:ILE:HD12	2.41	0.56
1:A:1473:ARG:HH11	1:A:1474:ARG:H	1.52	0.56
4:N:144:LYS:NZ	17:I:55:U:O5'	2.39	0.56
4:N:668:HIS:CE1	4:N:669:LYS:HG3	2.41	0.56
27:D:1213:ARG:HE	27:D:1281:GLN:NE2	2.03	0.56
27:D:1779:TYR:O	27:D:1782:ILE:HG22	2.06	0.56
27:D:2058:ASN:ND2	27:D:2070:LYS:O	2.38	0.56
20:S:23:LEU:HD21	26:V:69:ILE:HG23	1.87	0.56
29:H:551:C:H2'	29:H:552:U:H6	1.70	0.56
29:H:694:C:C2	29:H:695:U:C5	2.94	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1739:ARG:NH2	1:A:1745:SER:OG	2.39	0.56
1:A:2177:VAL:HG12	1:A:2179:GLU:H	1.70	0.56
2:K:314:SER:OG	2:K:355:VAL:O	2.23	0.56
2:K:441:ILE:H	2:K:456:GLY:HA2	1.71	0.56
27:D:478:LYS:HB2	27:D:504:SER:HB2	1.88	0.56
27:D:901:VAL:HA	27:D:906:LEU:HD13	1.87	0.56
27:D:1771:ASP:O	27:D:1774:THR:OG1	2.18	0.56
29:H:681:C:H2'	29:H:682:U:H6	1.70	0.56
34:3:187:VAL:HG23	34:3:209:GLN:HG2	1.86	0.56
3:L:123:ARG:NH1	3:L:184:LYS:O	2.39	0.56
17:I:77:U:H2'	17:I:78:A:C8	2.41	0.56
18:B:14:G:C2	18:B:15:A:C8	2.93	0.56
27:D:1125:THR:HG21	27:D:1251:ILE:HD11	1.87	0.56
28:G:509:A:H2	32:1:503:THR:HG21	1.71	0.56
29:H:681:C:C2	29:H:682:U:C5	2.94	0.56
29:H:695:U:C2	29:H:696:C:C5	2.94	0.56
29:H:695:U:H2'	29:H:696:C:H6	1.71	0.56
29:H:1126:G:O2'	29:H:1127:A:C5'	2.54	0.56
33:2:194:PHE:HE2	33:2:196:LEU:HD23	1.71	0.56
34:3:545:ASP:OD1	34:3:546:ASN:N	2.37	0.56
38:X:27:TYR:HD2	38:X:30:ASN:HD22	1.54	0.56
3:L:124:PHE:CD1	3:L:183:PHE:HB2	2.41	0.56
8:C:626:SER:HB2	8:C:634:ILE:HD13	1.88	0.56
17:I:5:U:H2'	17:I:6:U:H6	1.71	0.56
27:D:617:ARG:HH12	27:D:1009:TYR:HD1	1.53	0.56
29:H:551:C:C2	29:H:552:U:C5	2.94	0.56
29:H:676:U:H2'	29:H:677:U:H6	1.70	0.56
29:H:684:U:C2	29:H:685:U:C5	2.94	0.56
29:H:1139:G:C5	29:H:1140:U:C5	2.94	0.56
34:3:699:MET:HB3	34:3:720:LEU:HD23	1.88	0.56
35:4:40:TYR:HD1	35:4:53:ALA:HB2	1.71	0.56
1:A:520:VAL:O	1:A:524:LYS:HG2	2.06	0.56
1:A:551:LEU:HG	1:A:557:PHE:CE2	2.41	0.56
1:A:1899:TRP:HE3	1:A:1905:LEU:HD22	1.71	0.56
4:N:237:ASP:OD2	4:N:240:ASN:ND2	2.35	0.56
4:N:832:LEU:HD21	4:N:845:LEU:HD11	1.87	0.56
7:M:79:VAL:HG13	7:M:121:ILE:HG23	1.87	0.56
27:D:1497:PHE:HD1	27:D:1775:TYR:CD2	2.24	0.56
27:D:1740:LEU:HD11	22:Q:146:LEU:HD12	1.88	0.56
27:D:1996:GLN:HE22	27:D:2150:LEU:N	2.03	0.56
29:H:565:U:C2	29:H:566:U:C5	2.94	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:680:C:C2	29:H:681:C:C5	2.94	0.56
29:H:1126:G:O2'	29:H:1127:A:O5'	2.24	0.56
29:H:1139:G:C4	29:H:1140:U:C5	2.94	0.56
29:H:1139:G:HO2'	29:H:1140:U:H6	1.53	0.56
27:D:898:TYR:HA	27:D:901:VAL:HG22	1.88	0.55
27:D:1579:ASN:OD1	27:D:1678:ASP:HB3	2.06	0.55
29:H:567:U:H2'	29:H:568:U:H6	1.70	0.55
29:H:567:U:C2	29:H:568:U:C5	2.94	0.55
29:H:682:U:C2	29:H:683:U:C5	2.94	0.55
29:H:692:U:H2'	29:H:693:C:H6	1.71	0.55
1:A:1125:LEU:HD22	1:A:1230:ILE:HG23	1.88	0.55
2:K:389:ILE:HD11	2:K:427:TRP:HB3	1.86	0.55
3:L:402:ASP:OD1	3:L:403:SER:N	2.40	0.55
16:F:2:U:H2'	16:F:3:U:H6	1.70	0.55
27:D:1165:VAL:HG11	27:D:1170:TYR:CE1	2.40	0.55
27:D:1213:ARG:HH22	27:D:1316:LYS:HG3	1.71	0.55
27:D:1902:LEU:HD22	27:D:1928:LEU:HD12	1.87	0.55
29:H:672:U:C2	29:H:673:U:C5	2.94	0.55
29:H:692:U:C2	29:H:693:C:C5	2.94	0.55
29:H:1125:U:O2'	29:H:1126:G:C8	2.57	0.55
32:1:494:LEU:CG	38:X:7:ILE:HG23	2.36	0.55
34:3:975:ASP:O	34:3:977:ILE:HD12	2.07	0.55
34:3:1097:PHE:HE1	34:3:1108:PRO:HB3	1.70	0.55
2:K:316:GLN:HG2	2:K:318:ASP:H	1.70	0.55
2:K:458:ASP:OD2	2:K:462:LYS:NZ	2.39	0.55
3:L:160:HIS:O	3:L:164:LYS:HB3	2.06	0.55
17:I:147:U:H3	21:P:42:ASN:HD21	1.54	0.55
18:B:116:U:H2'	18:B:117:G:C8	2.39	0.55
29:H:545:G:H2'	29:H:546:U:H6	1.70	0.55
29:H:553:G:C4	29:H:554:C:C5	2.94	0.55
29:H:564:U:H2'	29:H:565:U:H6	1.70	0.55
29:H:1098:C:H2'	29:H:1099:G:C8	2.41	0.55
1:A:363:ASP:O	1:A:368:ASN:ND2	2.39	0.55
2:K:177:PRO:O	2:K:194:SER:OG	2.15	0.55
4:N:695:THR:HG22	4:N:704:LEU:HB3	1.89	0.55
5:J:301:VAL:HG22	5:J:304:ARG:HH21	1.70	0.55
17:I:73:A:H3'	27:D:833:THR:HG22	1.88	0.55
27:D:809:THR:HA	27:D:1092:PHE:CD1	2.41	0.55
27:D:1208:ALA:O	27:D:1209:GLN:HG3	2.06	0.55
29:H:545:G:C4	29:H:546:U:C5	2.95	0.55
29:H:564:U:C2	29:H:565:U:C5	2.94	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:679:U:C2	29:H:680:C:C5	2.94	0.55
29:H:683:U:C2	29:H:684:U:C5	2.95	0.55
34:3:351:PRO:HD3	34:3:407:LEU:HD13	1.89	0.55
34:3:839:ARG:HG3	34:3:880:PRO:HG2	1.87	0.55
35:4:119:ILE:O	35:4:149:LYS:NZ	2.38	0.55
1:A:2308:THR:OG1	1:A:2333:PHE:CE2	2.60	0.55
2:K:167:LEU:HA	2:K:464:TRP:HA	1.89	0.55
2:K:395:ILE:CG2	2:K:396:VAL:H	2.12	0.55
2:K:413:CYS:SG	2:K:443:LEU:HD13	2.47	0.55
27:D:1458:ARG:HH22	27:D:1462:ARG:NH1	2.03	0.55
27:D:1781:ARG:HG3	27:D:1789:TYR:CE2	2.40	0.55
29:H:691:G:C4	29:H:692:U:C5	2.95	0.55
1:A:342:LEU:HD22	1:A:392:ASN:ND2	2.21	0.55
4:N:720:VAL:HG12	4:N:722:ALA:H	1.72	0.55
8:C:889:TYR:CD2	8:C:890:LYS:HG2	2.41	0.55
29:H:548:G:C4	29:H:549:C:C5	2.94	0.55
29:H:550:G:H2'	29:H:551:C:H6	1.71	0.55
29:H:566:U:C2	29:H:567:U:C5	2.94	0.55
29:H:675:A:H2'	29:H:676:U:H6	1.70	0.55
1:A:884:SER:HB3	3:L:180:LYS:HZ3	1.72	0.55
1:A:1303:LYS:HG3	1:A:1353:THR:HG22	1.89	0.55
2:K:239:GLU:HA	2:K:267:ARG:HB2	1.89	0.55
8:C:185:ILE:HG21	18:B:75:A:OP2	2.07	0.55
26:V:64:ARG:NH1	26:V:66:ASN:HB3	2.21	0.55
29:H:553:G:H2'	29:H:554:C:H6	1.71	0.55
29:H:563:G:H2'	29:H:564:U:H6	1.70	0.55
29:H:568:U:C2	29:H:569:C:C5	2.94	0.55
29:H:671:G:C4	29:H:672:U:C5	2.95	0.55
29:H:676:U:C2	29:H:677:U:C5	2.94	0.55
32:1:386:TYR:CG	32:1:387:PRO:HD3	2.42	0.55
32:1:916:MET:HB3	32:1:920:TRP:NE1	2.21	0.55
34:3:182:THR:O	34:3:183:THR:HG23	2.06	0.55
1:A:963:VAL:HG21	3:L:280:ARG:NH1	2.20	0.55
1:A:1393:GLU:HG2	3:L:395:LYS:O	2.06	0.55
2:K:115:SER:HA	2:K:118:ILE:HD12	1.89	0.55
4:N:105:ALA:HA	4:N:108:LYS:HG2	1.89	0.55
8:C:292:ILE:O	8:C:296:ASN:ND2	2.38	0.55
27:D:535:VAL:HG13	27:D:557:ILE:CD1	2.37	0.55
27:D:766:ILE:HG23	27:D:767:THR:HG23	1.89	0.55
27:D:1628:HIS:O	27:D:1632:PRO:HD2	2.06	0.55
32:1:864:LEU:O	32:1:868:CYS:HB2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:416:SER:HA	34:3:431:SER:HA	1.89	0.55
34:3:432:GLU:HB2	37:6:62:ILE:HD12	1.88	0.55
34:3:650:GLU:HA	34:3:671:GLU:HA	1.87	0.55
39:Y:264:GLU:HG3	39:Y:265:ASP:H	1.72	0.55
1:A:1586:GLN:HE21	1:A:1595:ARG:HD2	1.72	0.55
3:L:218:ILE:O	3:L:222:ILE:HB	2.07	0.55
8:C:133:ILE:O	8:C:134:ILE:HG23	2.07	0.55
8:C:158:HIS:CE1	8:C:549:TYR:HE2	2.25	0.55
27:D:516:ASN:HD22	27:D:685:ARG:CB	2.18	0.55
27:D:1431:ASP:HB2	27:D:1434:LEU:HB3	1.89	0.55
27:D:1583:VAL:HG22	27:D:1681:ILE:HB	1.89	0.55
27:D:1609:MET:SD	27:D:1611:ASN:ND2	2.79	0.55
29:H:566:U:H2'	29:H:567:U:H6	1.70	0.55
32:1:252:ILE:HD13	32:1:296:VAL:HG22	1.89	0.55
32:1:490:ARG:HH22	38:X:25:ASN:CB	2.19	0.55
34:3:770:LEU:HB2	34:3:827:TRP:NE1	2.22	0.55
34:3:957:ILE:HG22	34:3:962:LEU:HD11	1.89	0.55
1:A:794:LYS:HB3	1:A:854:ARG:HH12	1.70	0.55
1:A:1509:ARG:NH2	1:A:1533:ASP:OD1	2.40	0.55
1:A:1714:PRO:HB2	1:A:1787:TYR:CE2	2.42	0.55
1:A:1790:TRP:CZ3	1:A:1798:ILE:HD12	2.42	0.55
1:A:1889:LEU:HD12	1:A:1989:PHE:HB2	1.89	0.55
27:D:1220:ILE:HG22	27:D:1222:ILE:HG13	1.88	0.55
27:D:1245:ASP:HA	27:D:1288:PHE:HD1	1.71	0.55
27:D:1779:TYR:CZ	27:D:1783:HIS:CE1	2.95	0.55
29:H:679:U:H2'	29:H:680:C:H6	1.70	0.55
32:1:824:PHE:HZ	32:1:838:ILE:HD13	1.72	0.55
33:2:329:LYS:HB3	33:2:335:TRP:HB2	1.88	0.55
34:3:1096:LEU:HD13	34:3:1187:PHE:CZ	2.39	0.55
34:3:1117:HIS:O	34:3:1133:ASP:HA	2.07	0.55
34:3:1243:ILE:HG21	34:3:1353:ILE:HD11	1.87	0.55
38:X:63:SER:HB2	38:X:74:PHE:CD1	2.40	0.55
1:A:2189:LEU:HD21	1:A:2347:GLY:C	2.28	0.54
3:L:268:LEU:HD13	3:L:270:HIS:CE1	2.41	0.54
8:C:656:LEU:HD13	8:C:670:ILE:HD13	1.89	0.54
18:B:114:G:N2	18:B:115:G:C2	2.75	0.54
27:D:465:ILE:HB	27:D:705:GLN:HB2	1.89	0.54
27:D:1489:GLU:OE2	27:D:1746:LEU:HG	2.06	0.54
20:S:49:ALA:O	20:S:56:VAL:HA	2.07	0.54
29:H:669:U:C2	29:H:670:U:C5	2.94	0.54
29:H:689:G:C4	29:H:690:U:C5	2.95	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1458:TRP:CZ2	1:A:1489:PRO:HB2	2.40	0.54
8:C:273:LEU:HD11	8:C:279:LEU:HD22	1.88	0.54
27:D:639:LEU:HD23	27:D:943:TYR:CD2	2.42	0.54
27:D:1194:ASP:HB3	27:D:1198:ARG:HH12	1.72	0.54
27:D:2138:HIS:O	27:D:2159:GLU:HG3	2.08	0.54
24:T:43:ILE:HD12	24:T:52:VAL:HG11	1.90	0.54
28:G:513:U:O3'	32:1:299:ARG:NH2	2.40	0.54
29:H:675:A:C4	29:H:676:U:C5	2.95	0.54
29:H:678:U:C2	29:H:679:U:C5	2.94	0.54
34:3:125:THR:HG22	34:3:191:SER:HA	1.89	0.54
39:Y:213:LYS:HB3	39:Y:230:SER:CB	2.38	0.54
1:A:570:GLN:O	1:A:574:GLN:HG2	2.08	0.54
1:A:1458:TRP:HE1	1:A:1489:PRO:HD2	1.71	0.54
1:A:2157:ILE:CG1	27:D:1064:PRO:HB2	2.37	0.54
1:A:2398:LEU:HD22	27:D:1060:LYS:CG	2.38	0.54
2:K:125:ILE:HG12	2:K:337:ARG:HD3	1.90	0.54
27:D:642:ASP:O	27:D:645:PRO:HG2	2.06	0.54
27:D:1368:VAL:HB	27:D:1511:LEU:HD23	1.90	0.54
29:H:548:G:H2'	29:H:549:C:H6	1.71	0.54
29:H:550:G:C4	29:H:551:C:C5	2.94	0.54
29:H:677:U:C2	29:H:678:U:C5	2.95	0.54
29:H:1097:G:C5	29:H:1146:G:C6	2.96	0.54
34:3:165:HIS:HB3	34:3:170:ARG:HD3	1.89	0.54
27:D:1757:GLU:HB3	27:D:1763:ILE:HD12	1.90	0.54
29:H:563:G:C4	29:H:564:U:C5	2.95	0.54
2:K:139:GLU:OE1	2:K:379:ARG:NH2	2.35	0.54
3:L:279:VAL:HG21	3:L:286:PHE:CE1	2.43	0.54
3:L:417:LEU:HD21	4:N:229:ILE:HD12	1.90	0.54
27:D:614:ILE:HD11	27:D:1009:TYR:CG	2.42	0.54
24:T:30:TRP:CE2	24:T:89:LEU:HD22	2.42	0.54
34:3:381:LEU:O	34:3:389:PHE:HB2	2.08	0.54
27:D:789:LEU:HD11	27:D:797:ILE:HG13	1.88	0.54
27:D:1624:LEU:HD12	27:D:1630:ARG:HD2	1.88	0.54
23:R:80:LYS:HE3	23:R:82:LYS:HG3	1.90	0.54
34:3:96:ALA:HB2	34:3:101:LEU:HD13	1.90	0.54
1:A:1268:ARG:HD3	1:A:1301:TYR:HD2	1.73	0.54
2:K:317:CYS:SG	2:K:359:PRO:HA	2.48	0.54
3:L:113:HIS:CD2	3:L:134:PRO:HA	2.42	0.54
27:D:1489:GLU:CD	27:D:1746:LEU:HG	2.28	0.54
27:D:1629:LEU:HD23	27:D:1648:ASP:OD2	2.08	0.54
29:H:67:A:O2'	29:H:68:U:OP2	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:1127:A:O2'	29:H:1128:C:H5'	2.08	0.54
29:H:1148:U:H2'	29:H:1149:G:C8	2.43	0.54
32:1:605:ILE:HG21	32:1:624:CYS:SG	2.47	0.54
34:3:632:ILE:HA	34:3:646:LEU:HA	1.88	0.54
34:3:839:ARG:NH1	34:3:1357:ARG:O	2.41	0.54
1:A:579:LEU:HD11	1:A:626:LEU:HD12	1.90	0.54
1:A:2189:LEU:HD22	1:A:2349:PHE:CE1	2.42	0.54
3:L:175:LEU:O	3:L:179:MET:CB	2.55	0.54
3:L:371:LYS:HD3	17:I:18:A:H61	1.72	0.54
3:L:398:GLN:OE1	3:L:414:ASN:ND2	2.34	0.54
4:N:140:GLN:NE2	17:I:19:U:O2	2.41	0.54
4:N:286:GLU:HB2	4:N:292:CYS:SG	2.47	0.54
8:C:769:TYR:CE1	8:C:774:LEU:HB2	2.37	0.54
17:I:18:A:H5''	17:I:19:U:O5'	2.08	0.54
27:D:491:PHE:HE1	27:D:533:LEU:HD21	1.73	0.54
27:D:516:ASN:O	27:D:687:PRO:HD2	2.08	0.54
27:D:793:LEU:HD13	27:D:808:LEU:HD13	1.88	0.54
28:G:520:G:H4'	38:X:74:PHE:CE2	2.43	0.54
29:H:46:C:H4'	29:H:47:U:H5''	1.89	0.54
34:3:76:ILE:HD11	34:3:422:PHE:CE1	2.43	0.54
34:3:1223:GLY:O	34:3:1224:THR:OG1	2.24	0.54
1:A:2041:PRO:HG2	1:A:2043:PHE:CE2	2.43	0.54
18:B:111:C:H2'	18:B:112:C:C6	2.43	0.54
27:D:455:ARG:HB2	27:D:462:GLU:HG3	1.90	0.54
27:D:706:GLN:C	27:D:707:PHE:HD1	2.10	0.54
27:D:1814:LEU:HB3	27:D:1820:ILE:HG12	1.90	0.54
24:T:59:GLU:O	24:T:74:GLY:HA2	2.08	0.54
1:A:480:TYR:CE2	8:C:275:LEU:HD23	2.43	0.54
1:A:933:GLU:OE1	1:A:933:GLU:N	2.38	0.54
1:A:1696:SER:HA	1:A:1759:TYR:HE1	1.73	0.54
1:A:1732:MET:HG3	1:A:1791:PHE:HE2	1.72	0.54
2:K:220:LYS:HB3	2:K:239:GLU:HB3	1.90	0.54
3:L:125:PRO:HD2	3:L:182:SER:HB2	1.89	0.54
4:N:708:LEU:HD22	4:N:725:ILE:HG21	1.90	0.54
5:J:406:PHE:HE1	5:J:408:LEU:HB2	1.73	0.54
17:I:6:U:H2'	17:I:7:A:H8	1.71	0.54
18:B:127:U:O2'	18:B:128:A:N7	2.23	0.54
34:3:208:GLU:H	34:3:236:VAL:HA	1.72	0.54
2:K:207:LEU:HD11	2:K:463:LEU:HB2	1.88	0.53
5:J:341:VAL:HG22	5:J:381:ILE:HG12	1.91	0.53
8:C:161:ILE:HD12	8:C:162:PRO:HD2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:338:SER:O	8:C:341:ILE:HG12	2.08	0.53
27:D:1748:TYR:HB3	22:Q:140:LYS:N	2.23	0.53
33:2:248:HIS:CE1	33:2:375:PHE:HB2	2.43	0.53
33:2:367:LEU:HB2	33:2:370:PHE:HE1	1.71	0.53
34:3:764:ASP:OD2	34:3:766:LYS:HE2	2.08	0.53
38:X:64:ARG:NH2	38:X:69:GLY:O	2.41	0.53
1:A:2189:LEU:HD22	1:A:2349:PHE:HE1	1.73	0.53
8:C:347:ARG:O	8:C:352:VAL:HG11	2.08	0.53
18:B:130:A:H4'	18:B:131:A:O5'	2.08	0.53
19:O:151:ILE:HB	19:O:180:GLU:HG2	1.90	0.53
27:D:614:ILE:HD11	27:D:1009:TYR:CD1	2.43	0.53
27:D:945:TYR:CE2	27:D:949:LEU:HD11	2.43	0.53
27:D:1312:LYS:N	27:D:1787:SER:OG	2.39	0.53
23:R:56:ALA:HB2	23:R:72:VAL:HA	1.90	0.53
20:S:34:VAL:CG2	20:S:45:ARG:HG3	2.39	0.53
34:3:943:ASP:HB2	34:3:952:ARG:HG2	1.91	0.53
1:A:1888:HIS:HE1	1:A:1988:LEU:HD22	1.74	0.53
1:A:2165:ARG:HB3	1:A:2300:VAL:HG13	1.89	0.53
2:K:270:ASP:OD1	2:K:271:VAL:N	2.40	0.53
3:L:102:ILE:HD11	3:L:214:ILE:HG21	1.89	0.53
3:L:139:LYS:O	3:L:142:SER:OG	2.17	0.53
18:B:128:A:H2'	18:B:129:G:H2'	1.90	0.53
22:Q:7:LEU:HD11	23:R:95:PHE:CZ	2.44	0.53
32:1:689:LEU:HA	32:1:692:ILE:HD12	1.89	0.53
34:3:299:PRO:HD2	34:3:377:PHE:CE1	2.44	0.53
34:3:547:ASN:ND2	34:3:564:ASP:HB2	2.24	0.53
34:3:655:LYS:HE2	34:3:664:ILE:HD11	1.89	0.53
1:A:1350:ILE:HG23	1:A:1356:LEU:HD22	1.90	0.53
1:A:2310:GLU:CD	1:A:2333:PHE:CZ	2.82	0.53
8:C:292:ILE:HG12	8:C:311:ILE:HD13	1.91	0.53
8:C:855:PRO:O	8:C:944:VAL:HG11	2.09	0.53
18:B:84:A:H2'	18:B:85:U:H6	1.73	0.53
18:B:111:C:H2'	18:B:112:C:H6	1.73	0.53
34:3:712:PHE:CE2	34:3:713:LEU:HD23	2.43	0.53
1:A:259:GLU:HG3	1:A:260:PRO:HD2	1.89	0.53
1:A:1156:HIS:ND1	1:A:1157:PRO:HD2	2.24	0.53
2:K:176:LYS:HZ2	7:M:72:GLU:HB2	1.74	0.53
8:C:474:LYS:NZ	8:C:628:TYR:O	2.40	0.53
16:F:74:U:H2'	16:F:75:A:H8	1.72	0.53
27:D:563:LEU:HD11	27:D:836:TRP:NE1	2.24	0.53
27:D:1380:ALA:HB2	27:D:1511:LEU:HD11	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1:904:GLU:O	32:1:907:SER:OG	2.22	0.53
33:2:162:SER:O	33:2:166:THR:OG1	2.24	0.53
34:3:211:LYS:HB2	34:3:230:ILE:HG13	1.91	0.53
34:3:441:PHE:HB3	34:3:475:LEU:HD23	1.88	0.53
36:5:41:ARG:HH12	36:5:83:LYS:NZ	2.05	0.53
1:A:1257:ASN:OD1	1:A:1268:ARG:NH2	2.41	0.53
1:A:1943:PRO:HD3	19:O:169:ILE:HD12	1.91	0.53
1:A:2070:ASN:HB3	27:D:858:GLY:O	2.08	0.53
1:A:2183:TYR:CD1	1:A:2219:LYS:HB2	2.44	0.53
3:L:434:GLN:HA	4:N:149:PRO:HB3	1.90	0.53
4:N:757:GLU:HG2	4:N:780:LEU:HD11	1.90	0.53
27:D:759:ASN:O	27:D:763:GLU:HG3	2.09	0.53
27:D:1213:ARG:NH2	27:D:1316:LYS:CG	2.67	0.53
27:D:1476:ALA:HB3	27:D:1512:SER:HB2	1.91	0.53
33:2:366:ALA:O	34:3:1232:LEU:HD22	2.09	0.53
39:Y:214:LEU:N	39:Y:230:SER:OG	2.42	0.53
1:A:620:HIS:HB3	1:A:669:TYR:CE2	2.44	0.53
1:A:1834:PHE:CD1	1:A:1958:PRO:HG2	2.43	0.53
2:K:171:GLN:HG2	2:K:172:LEU:N	2.22	0.53
5:J:370:LEU:HD13	5:J:451:LEU:HG	1.89	0.53
8:C:163:ASP:OD2	8:C:548:ARG:NH1	2.41	0.53
27:D:1436:LEU:HD22	27:D:1462:ARG:CZ	2.37	0.53
1:A:1674:ASP:OD2	1:A:2200:LYS:CE	2.56	0.53
17:I:72:A:OP2	27:D:1047:ARG:CZ	2.56	0.53
27:D:924:VAL:HG12	27:D:998:ALA:HB2	1.90	0.53
27:D:1679:GLU:HG2	27:D:1719:LYS:HB3	1.91	0.53
32:1:536:MET:HA	32:1:539:HIS:HD2	1.74	0.53
34:3:65:LEU:HD11	34:3:1227:CYS:SG	2.48	0.53
34:3:612:PRO:HA	34:3:618:TYR:HD1	1.74	0.53
38:X:35:ILE:HD13	38:X:51:PHE:CE2	2.43	0.53
1:A:1268:ARG:CG	1:A:1301:TYR:HB2	2.39	0.53
4:N:742:ALA:O	4:N:746:MET:HB2	2.09	0.53
27:D:567:VAL:HG13	27:D:606:VAL:HG12	1.89	0.53
27:D:781:LEU:HD21	27:D:798:GLU:CA	2.33	0.53
27:D:1457:ARG:NH1	27:D:1854:SER:O	2.42	0.53
24:T:20:PHE:CE1	24:T:92:SER:HB2	2.40	0.53
29:H:1089:G:H2'	29:H:1090:A:O5'	2.09	0.53
32:1:361:ASP:OD1	32:1:362:CYS:N	2.42	0.53
32:1:614:PRO:HA	32:1:617:ARG:HE	1.74	0.53
34:3:1023:HIS:HB3	34:3:1058:GLN:HA	1.91	0.53
1:A:297:SER:HB3	18:B:32:G:OP1	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1804:THR:HG21	19:O:218:GLU:OE1	2.10	0.53
1:A:2046:GLU:HA	1:A:2049:ILE:HD12	1.91	0.53
1:A:2208:TYR:HE1	1:A:2255:LEU:HD13	1.74	0.53
2:K:376:TRP:CH2	2:K:386:LEU:HD23	2.44	0.53
2:K:390:LEU:HD13	5:J:428:TRP:CD1	2.43	0.53
2:K:459:ARG:NH2	7:M:72:GLU:O	2.42	0.53
3:L:239:ALA:O	3:L:243:ALA:CB	2.57	0.53
5:J:372:ILE:O	5:J:376:GLY:HA3	2.08	0.53
8:C:274:ILE:HD12	8:C:382:TYR:HD1	1.73	0.53
27:D:1399:ASN:O	27:D:1405:ILE:HD11	2.09	0.53
22:Q:95:ILE:HG23	23:R:95:PHE:HB3	1.90	0.53
32:1:580:PHE:HZ	32:1:619:HIS:HD1	1.57	0.53
39:Y:208:SER:HA	39:Y:214:LEU:CD1	2.39	0.53
1:A:1335:TRP:CZ2	1:A:1339:LEU:HD13	2.44	0.52
8:C:880:MET:HB3	8:C:886:SER:HA	1.91	0.52
32:1:208:LEU:HD21	32:1:221:MET:HB2	1.91	0.52
1:A:701:CYS:SG	1:A:702:GLY:N	2.81	0.52
1:A:1633:PHE:HZ	1:A:1694:MET:HG3	1.74	0.52
4:N:760:VAL:O	4:N:764:LEU:HB2	2.08	0.52
8:C:682:SER:HA	8:C:714:PRO:HG3	1.92	0.52
17:I:140:G:H2'	17:I:141:G:O4'	2.09	0.52
27:D:781:LEU:HD11	27:D:798:GLU:HA	1.90	0.52
27:D:1898:ASP:HA	27:D:1943:PHE:CZ	2.45	0.52
26:V:30:ARG:HE	26:V:41:ASP:CB	2.21	0.52
32:1:569:PHE:HD1	32:1:579:ILE:HG21	1.72	0.52
34:3:257:ILE:HD11	34:3:264:LEU:HD11	1.91	0.52
34:3:1112:ASP:OD1	34:3:1113:SER:N	2.41	0.52
1:A:394:ARG:HE	1:A:396:ARG:HH12	1.57	0.52
1:A:1775:ILE:HG12	1:A:1786:ALA:HB2	1.91	0.52
2:K:288:THR:HA	2:K:303:GLN:O	2.09	0.52
4:N:746:MET:HG2	4:N:749:ARG:NH1	2.20	0.52
8:C:458:ILE:HG23	8:C:459:PRO:HD2	1.91	0.52
17:I:143:A:N7	25:U:48:TYR:HE2	2.08	0.52
27:D:1783:HIS:CE1	27:D:1799:ILE:HG21	2.44	0.52
23:R:37:ALA:HA	23:R:42:THR:HG22	1.92	0.52
28:G:498:C:H2'	28:G:499:U:H6	1.75	0.52
36:5:67:VAL:HG23	36:5:68:ASN:H	1.74	0.52
1:A:1490:ARG:NH1	1:A:1536:LEU:HA	2.25	0.52
1:A:2174:ASP:OD1	1:A:2175:ASP:N	2.42	0.52
4:N:849:TYR:CD1	4:N:855:ASP:HB2	2.45	0.52
28:G:500:A:OP1	32:1:818:LYS:NZ	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:G:520:G:C2	38:X:34:TYR:CD2	2.95	0.52
32:1:532:PRO:O	32:1:535:THR:OG1	2.26	0.52
36:5:42:LYS:HG2	36:5:71:PHE:HE1	1.75	0.52
1:A:921:ASP:HB3	3:L:403:SER:HB2	1.91	0.52
1:A:1161:TYR:CD1	1:A:1170:MET:HG2	2.44	0.52
3:L:379:PHE:CZ	4:N:144:LYS:HD3	2.43	0.52
4:N:269:GLN:O	4:N:272:PRO:HG3	2.10	0.52
4:N:691:TYR:HB3	4:N:708:LEU:HD12	1.90	0.52
18:B:75:A:O2'	18:B:76:U:H3'	2.09	0.52
27:D:645:PRO:HG3	27:D:911:GLN:O	2.10	0.52
27:D:851:ASP:HA	27:D:861:GLU:O	2.10	0.52
27:D:2077:ARG:HH12	27:D:2081:PRO:HG3	1.73	0.52
34:3:1178:PRO:O	34:3:1182:ASP:HB2	2.10	0.52
1:A:1562:PHE:O	1:A:1565:THR:OG1	2.17	0.52
6:E:98:GLY:HA3	16:F:30:G:H4'	1.92	0.52
8:C:942:GLY:HA2	8:C:960:ASN:O	2.09	0.52
27:D:1763:ILE:HG21	27:D:1769:CYS:HB3	1.91	0.52
23:R:26:PHE:CE1	23:R:31:MET:HB3	2.45	0.52
20:S:10:LEU:HB2	20:S:83:LEU:HD11	1.90	0.52
25:U:14:ASN:HB2	25:U:17:PRO:HD2	1.92	0.52
32:1:338:GLN:HG3	32:1:377:THR:HG22	1.91	0.52
1:A:1817:GLU:HA	1:A:1820:ARG:HG2	1.91	0.52
3:L:120:TYR:CE2	3:L:141:ILE:HG12	2.34	0.52
3:L:343:LYS:HD3	17:I:27:U:O2'	2.09	0.52
8:C:933:TRP:C	8:C:935:LYS:H	2.13	0.52
32:1:410:LYS:O	32:1:413:SER:OG	2.27	0.52
34:3:104:TYR:HD1	34:3:113:LEU:HA	1.75	0.52
34:3:691:LEU:HB3	34:3:703:MET:HB2	1.92	0.52
1:A:185:GLN:HG2	1:A:263:PRO:HD3	1.91	0.52
3:L:98:PHE:O	3:L:102:ILE:HG12	2.09	0.52
8:C:616:PRO:O	8:C:619:LEU:HB2	2.10	0.52
16:F:17:U:H2'	16:F:18:U:C6	2.44	0.52
17:I:6:U:H2'	17:I:7:A:C8	2.44	0.52
17:I:91:U:H2'	17:I:92:C:C6	2.45	0.52
18:B:27:G:N3	18:B:131:A:N3	2.58	0.52
27:D:656:TRP:HH2	27:D:929:ILE:HG13	1.73	0.52
27:D:1557:ILE:HA	27:D:1695:TYR:CE2	2.36	0.52
27:D:1924:PHE:CZ	27:D:1928:LEU:HD11	2.45	0.52
27:D:1933:TYR:HE1	27:D:2090:LYS:O	1.93	0.52
34:3:332:GLU:HG2	34:3:333:ASN:N	2.24	0.52
34:3:511:ILE:HG23	34:3:888:VAL:HG13	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:1006:TYR:HD1	34:3:1021:LEU:HA	1.73	0.52
34:3:1159:LEU:HD23	34:3:1164:ILE:HD13	1.92	0.52
1:A:1320:LEU:HD22	1:A:1370:ARG:HD2	1.92	0.52
1:A:1494:LEU:O	1:A:1499:ARG:NH2	2.43	0.52
2:K:172:LEU:HD23	4:N:752:ASN:HD22	1.75	0.52
2:K:213:LYS:NZ	2:K:215:ASP:OD1	2.41	0.52
4:N:256:LYS:HG2	4:N:257:PHE:H	1.75	0.52
16:F:96:G:H2'	16:F:97:A:H8	1.75	0.52
17:I:75:U:O2	27:D:643:ARG:NH1	2.42	0.52
18:B:164:C:O2	18:B:164:C:H2'	2.09	0.52
27:D:765:ASN:CB	27:D:768:HIS:CD2	2.93	0.52
27:D:1513:ASN:ND2	27:D:1704:LEU:HD13	2.25	0.52
27:D:1938:GLU:OE1	27:D:1938:GLU:N	2.40	0.52
34:3:125:THR:H	34:3:152:SER:HA	1.75	0.52
36:5:40:LYS:HG3	36:5:41:ARG:HG3	1.91	0.52
4:N:212:VAL:HG12	4:N:215:LEU:HD23	1.92	0.52
18:B:127:U:H1'	18:B:128:A:N7	2.25	0.52
27:D:1426:ASN:HD22	27:D:1442:SER:HB2	1.73	0.52
24:T:35:ILE:HG22	26:V:23:ARG:HE	1.74	0.52
26:V:10:TYR:CE2	26:V:71:LEU:HD11	2.45	0.52
34:3:294:PHE:HZ	34:3:381:LEU:HD11	1.74	0.52
34:3:983:ALA:O	34:3:995:ILE:HB	2.10	0.52
8:C:423:HIS:O	8:C:427:LEU:HB2	2.09	0.51
8:C:616:PRO:HA	8:C:619:LEU:HD12	1.92	0.51
8:C:869:HIS:NE2	8:C:925:LEU:HD22	2.24	0.51
19:O:210:LEU:HB3	19:O:212:VAL:HG13	1.92	0.51
27:D:804:HIS:HE1	27:D:813:ARG:CG	2.18	0.51
27:D:1387:HIS:CE1	27:D:1392:LYS:HB3	2.46	0.51
23:R:50:ASN:ND2	23:R:52:HIS:CD2	2.78	0.51
23:R:50:ASN:ND2	23:R:52:HIS:HD2	2.09	0.51
29:H:1097:G:C2	29:H:1146:G:C5	2.98	0.51
32:1:244:LEU:O	32:1:248:ALA:CB	2.58	0.51
32:1:580:PHE:CZ	32:1:619:HIS:HA	2.46	0.51
34:3:486:PRO:HG2	34:3:505:PHE:HB2	1.91	0.51
1:A:1488:ILE:HB	1:A:1489:PRO:HD3	1.93	0.51
1:A:1850:LEU:HD23	1:A:1883:ASN:HB3	1.92	0.51
3:L:359:PRO:O	6:E:122:ARG:NH2	2.43	0.51
5:J:283:ASN:OD1	5:J:284:ASP:N	2.43	0.51
8:C:697:ARG:HH21	8:C:849:GLY:HA2	1.75	0.51
16:F:10:A:H61	16:F:16:C:H42	1.57	0.51
18:B:16:U:O2'	18:B:18:A:N7	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1115:ILE:O	27:D:1119:ARG:HG2	2.11	0.51
27:D:1853:ALA:HB1	27:D:1863:ILE:HG13	1.93	0.51
29:H:139:G:H2'	29:H:140:G:O5'	2.09	0.51
29:H:1140:U:H2'	29:H:1141:C:H6	1.75	0.51
32:1:927:ALA:O	32:1:929:ASN:N	2.43	0.51
34:3:607:LEU:HB2	34:3:624:TRP:HB3	1.92	0.51
39:Y:224:PHE:O	39:Y:225:ALA:HB3	2.11	0.51
1:A:1045:GLN:HG2	1:A:1175:GLU:HG2	1.92	0.51
1:A:1855:THR:HA	1:A:1937:ARG:NH2	2.25	0.51
2:K:46:GLU:HB2	2:K:73:ARG:NH1	2.26	0.51
2:K:177:PRO:HB2	2:K:195:TRP:NE1	2.25	0.51
3:L:358:ILE:HG22	3:L:360:GLU:H	1.74	0.51
8:C:269:LYS:HG2	44:C:1500:GTP:C4	2.46	0.51
27:D:1751:HIS:HA	27:D:1810:CYS:SG	2.50	0.51
29:H:1139:G:HO2'	29:H:1140:U:C5'	2.24	0.51
32:1:539:HIS:ND1	32:1:578:ILE:HG12	2.25	0.51
33:2:131:LYS:NZ	33:2:153:ASP:OD1	2.44	0.51
34:3:102:GLU:HG2	34:3:116:LYS:HG2	1.92	0.51
34:3:294:PHE:HE2	34:3:365:ILE:HB	1.76	0.51
1:A:165:LEU:HG	1:A:578:MET:SD	2.50	0.51
1:A:1051:GLU:O	1:A:1246:ALA:HA	2.09	0.51
1:A:1578:ALA:HB1	1:A:1602:PRO:HB3	1.92	0.51
8:C:883:ARG:NH2	8:C:910:GLU:O	2.41	0.51
8:C:889:TYR:H	8:C:904:GLY:HA2	1.76	0.51
16:F:61:C:H2'	16:F:62:A:O4'	2.10	0.51
18:B:114:G:N2	18:B:115:G:N3	2.58	0.51
27:D:505:LYS:HA	27:D:508:HIS:CD2	2.45	0.51
27:D:724:ASP:HA	27:D:760:LYS:NZ	2.25	0.51
27:D:1936:ARG:HD3	27:D:2090:LYS:HE3	1.92	0.51
22:Q:141:ARG:HB2	22:Q:142:PRO:HD3	1.92	0.51
32:1:539:HIS:O	32:1:542:THR:OG1	2.23	0.51
34:3:217:ASP:OD1	34:3:218:TYR:N	2.43	0.51
34:3:242:VAL:HG22	34:3:252:PHE:HB2	1.92	0.51
1:A:849:LEU:HD12	1:A:973:GLU:HB3	1.91	0.51
2:K:287:MET:HA	2:K:310:VAL:HG23	1.92	0.51
4:N:789:LEU:HD11	7:M:45:ASN:HB3	1.91	0.51
8:C:176:ARG:HH22	8:C:188:GLY:HA2	1.75	0.51
8:C:253:ILE:HD11	8:C:298:PHE:HB2	1.93	0.51
8:C:470:ALA:HB3	8:C:577:LEU:HD22	1.93	0.51
27:D:648:GLU:OE2	27:D:912:PHE:HD1	1.93	0.51
27:D:1395:ALA:HB3	27:D:1444:VAL:HG22	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1563:MET:HE1	27:D:1684:GLY:HA2	1.92	0.51
26:V:56:GLN:HG3	26:V:61:THR:HB	1.93	0.51
33:2:325:TYR:HB3	33:2:328:LEU:HB2	1.92	0.51
1:A:1585:MET:HB3	1:A:1598:LEU:HD13	1.92	0.51
5:J:381:ILE:HD13	5:J:463:PHE:HD2	1.75	0.51
8:C:701:GLU:HG2	8:C:703:LEU:H	1.75	0.51
27:D:1217:ARG:C	27:D:1218:PHE:HD1	2.14	0.51
32:1:955:VAL:HA	32:1:959:ASN:HD22	1.75	0.51
34:3:59:TYR:CE1	34:3:1316:LYS:HD2	2.46	0.51
34:3:105:ASP:OD1	34:3:106:THR:N	2.41	0.51
34:3:292:ALA:HA	34:3:331:PHE:CD1	2.45	0.51
34:3:1073:LYS:HD2	34:3:1090:ILE:HD11	1.92	0.51
34:3:1298:SER:C	34:3:1300:LEU:H	2.14	0.51
35:4:164:ALA:O	35:4:168:LEU:HB2	2.11	0.51
38:X:49:THR:HG23	39:Y:233:ASP:HB2	1.92	0.51
1:A:287:GLU:HG2	1:A:288:GLU:N	2.22	0.51
1:A:1835:LEU:HD21	1:A:1843:LEU:HD21	1.93	0.51
8:C:326:GLU:HG2	8:C:330:TYR:HE2	1.75	0.51
18:B:27:G:OP1	18:B:141:G:C5'	2.58	0.51
27:D:683:PHE:CD1	27:D:943:TYR:HA	2.46	0.51
27:D:1032:PHE:HB3	27:D:1077:ASN:HB2	1.92	0.51
27:D:1890:GLU:HB3	22:Q:143:ARG:NE	2.26	0.51
27:D:1913:PHE:HE2	27:D:1917:THR:HB	1.76	0.51
28:G:487:A:H2'	28:G:488:A:H5'	1.92	0.51
32:1:579:ILE:O	32:1:583:PHE:N	2.38	0.51
33:2:329:LYS:O	33:2:346:GLY:HA2	2.10	0.51
38:X:105:ASP:OD1	38:X:106:HIS:N	2.43	0.51
2:K:64:VAL:HG12	2:K:65:GLU:H	1.76	0.51
2:K:177:PRO:HB2	2:K:195:TRP:CD1	2.44	0.51
3:L:356:LEU:HD13	6:E:52:ARG:HB3	1.91	0.51
4:N:148:ALA:HB1	4:N:152:LEU:HD12	1.92	0.51
8:C:270:LEU:HD11	8:C:313:PHE:HB3	1.93	0.51
8:C:326:GLU:HG2	8:C:330:TYR:CE2	2.45	0.51
16:F:79:A:H2'	16:F:80:U:C6	2.46	0.51
27:D:1213:ARG:HE	27:D:1281:GLN:HE21	1.58	0.51
27:D:1748:TYR:CE2	22:Q:142:PRO:CD	2.94	0.51
27:D:2071:ILE:O	27:D:2127:GLU:HA	2.11	0.51
27:D:2071:ILE:HG22	27:D:2128:LEU:HB2	1.92	0.51
29:H:1139:G:H2'	29:H:1140:U:H6	1.76	0.51
32:1:363:LEU:HA	32:1:374:THR:HG21	1.93	0.51
32:1:399:PRO:HA	32:1:402:LYS:HG2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2:203:THR:HG22	33:2:250:VAL:HG21	1.91	0.51
34:3:293:ASN:HD22	34:3:364:THR:HB	1.76	0.51
1:A:1791:PHE:H	1:A:1794:LEU:HD12	1.76	0.51
1:A:2207:ILE:HD12	1:A:2256:LEU:HB2	1.93	0.51
8:C:542:ILE:HA	8:C:563:LEU:O	2.11	0.51
8:C:680:SER:HB2	8:C:858:LEU:HD11	1.92	0.51
27:D:536:LEU:HD21	27:D:578:LEU:CD2	2.41	0.51
27:D:1457:ARG:O	27:D:1760:ASN:ND2	2.44	0.51
27:D:1687:LEU:HB2	27:D:1698:TYR:CE1	2.29	0.51
27:D:1750:ILE:HD13	27:D:1806:LEU:HG	1.93	0.51
27:D:1996:GLN:HE22	27:D:2150:LEU:H	1.59	0.51
32:1:685:ILE:O	32:1:688:THR:OG1	2.25	0.51
32:1:689:LEU:HD21	32:1:707:PHE:CD2	2.45	0.51
32:1:887:ASN:HB3	32:1:899:ILE:HD13	1.92	0.51
34:3:410:PHE:HE1	34:3:445:GLY:HA3	1.76	0.51
34:3:496:SER:HB3	34:3:497:PRO:HD3	1.92	0.51
34:3:1048:THR:OG1	34:3:1065:THR:O	2.26	0.51
1:A:2183:TYR:HE1	1:A:2219:LYS:HG3	1.76	0.51
3:L:315:ARG:HD3	7:M:66:HIS:CE1	2.46	0.51
8:C:353:TYR:HD1	8:C:371:PRO:HA	1.74	0.51
27:D:789:LEU:HB2	27:D:794:ARG:HG2	1.93	0.51
27:D:1424:ILE:H	27:D:1443:HIS:CD2	2.29	0.51
20:S:10:LEU:HD12	20:S:83:LEU:HD12	1.93	0.51
32:1:264:GLU:HA	32:1:267:THR:HG22	1.93	0.51
32:1:418:ALA:O	32:1:422:MET:HG2	2.11	0.51
34:3:332:GLU:HG2	34:3:333:ASN:H	1.76	0.51
35:4:67:ILE:HD13	35:4:85:GLN:HB3	1.92	0.51
1:A:487:ASN:OD1	1:A:488:ARG:HG3	2.11	0.50
2:K:218:VAL:HG21	2:K:238:ALA:HB3	1.92	0.50
3:L:355:ALA:HB2	6:E:54:ARG:NH1	2.27	0.50
5:J:338:HIS:O	5:J:383:VAL:HA	2.11	0.50
8:C:115:LYS:O	8:C:116:THR:OG1	2.24	0.50
8:C:121:ASP:OD1	8:C:122:TYR:N	2.44	0.50
18:B:94:C:H5'	18:B:95:C:OP2	2.11	0.50
27:D:682:ARG:NH2	27:D:946:VAL:HG13	2.26	0.50
29:H:1120:G:H2'	29:H:1121:U:C6	2.45	0.50
32:1:832:LYS:HB2	32:1:871:THR:HG21	1.93	0.50
34:3:1002:ARG:NH2	34:3:1004:LEU:HD11	2.26	0.50
34:3:1166:TYR:CZ	34:3:1184:LYS:HE3	2.46	0.50
35:4:170:ASN:ND2	35:4:179:THR:HG22	2.25	0.50
1:A:138:HIS:O	1:A:142:ILE:HG12	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:301:TRP:HD1	1:A:493:MET:SD	2.34	0.50
1:A:1647:GLN:O	1:A:1650:ARG:NH1	2.44	0.50
1:A:1840:TYR:HH	1:A:2005:PHE:HE2	1.60	0.50
1:A:2051:ILE:O	1:A:2055:MET:HG2	2.11	0.50
2:K:177:PRO:HB2	2:K:195:TRP:HE1	1.75	0.50
5:J:245:ARG:O	5:J:249:ARG:HG2	2.11	0.50
8:C:281:PRO:HG3	8:C:382:TYR:CD2	2.46	0.50
18:B:123:U:H2'	18:B:124:C:C6	2.46	0.50
27:D:639:LEU:HD23	27:D:943:TYR:CE2	2.46	0.50
27:D:810:ARG:HH11	27:D:813:ARG:HE	1.57	0.50
28:G:520:G:N2	38:X:34:TYR:CB	2.73	0.50
32:1:288:ASN:OD1	32:1:289:GLU:N	2.43	0.50
37:6:22:GLY:HA2	37:6:26:THR:HG21	1.94	0.50
1:A:1888:HIS:CE1	1:A:1988:LEU:HD22	2.46	0.50
3:L:399:THR:HB	3:L:407:GLU:HB3	1.93	0.50
27:D:1493:SER:HA	27:D:1524:TRP:CH2	2.43	0.50
27:D:1861:PHE:CD2	22:Q:140:LYS:HD3	2.46	0.50
21:P:86:ILE:O	20:S:71:PHE:HB2	2.12	0.50
22:Q:139:ASN:O	22:Q:140:LYS:HB3	2.10	0.50
23:R:76:TRP:NE1	23:R:87:ARG:HB2	2.27	0.50
24:T:59:GLU:O	24:T:74:GLY:CA	2.59	0.50
33:2:159:LEU:O	33:2:162:SER:OG	2.29	0.50
34:3:63:LEU:HB2	34:3:1227:CYS:SG	2.51	0.50
1:A:863:ARG:HH12	1:A:1059:GLU:HB3	1.76	0.50
2:K:60:LYS:HB3	2:K:61:PRO:HD2	1.94	0.50
27:D:2073:ILE:HD11	27:D:2142:ILE:HD13	1.92	0.50
29:H:64:G:H2'	29:H:65:A:C8	2.46	0.50
32:1:739:ASN:HB3	32:1:742:ILE:HD12	1.94	0.50
34:3:936:PRO:O	34:3:937:LYS:HD2	2.12	0.50
34:3:994:LEU:HD22	34:3:1006:TYR:HD2	1.77	0.50
34:3:1087:VAL:O	34:3:1094:VAL:HA	2.12	0.50
1:A:175:LEU:HD22	1:A:571:LEU:HD23	1.93	0.50
1:A:905:TYR:CE2	1:A:907:ASN:HB2	2.47	0.50
2:K:69:VAL:HB	5:J:322:ARG:NH1	2.26	0.50
2:K:243:ILE:HB	2:K:261:LEU:HB2	1.93	0.50
4:N:678:TYR:O	4:N:682:GLY:N	2.26	0.50
4:N:706:VAL:HA	4:N:746:MET:HE1	1.93	0.50
6:E:85:PHE:HD1	6:E:90:HIS:HA	1.76	0.50
17:I:151:G:N7	25:U:32:LYS:HD3	2.27	0.50
18:B:166:U:O2'	18:B:167:A:P	2.70	0.50
27:D:1387:HIS:CB	27:D:1470:LEU:HD13	2.32	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:U:41:THR:HG23	25:U:55:GLU:OE2	2.12	0.50
28:G:505:A:H1'	28:G:506:U:C6	2.46	0.50
34:3:432:GLU:OE1	37:6:62:ILE:HB	2.11	0.50
36:5:51:PHE:HD1	36:5:52:GLY:H	1.59	0.50
1:A:169:PRO:HA	1:A:172:ILE:HD12	1.93	0.50
1:A:1011:ASN:ND2	1:A:1143:GLU:O	2.45	0.50
1:A:1512:ARG:HD2	1:A:1529:ASN:OD1	2.12	0.50
1:A:1863:HIS:HA	19:O:159:ASP:N	2.26	0.50
2:K:283:ALA:HB1	2:K:310:VAL:HG12	1.93	0.50
3:L:361:ASP:OD1	3:L:362:GLN:N	2.45	0.50
6:E:97:THR:HG23	6:E:99:ASN:H	1.77	0.50
17:I:92:C:H2'	17:I:93:C:H6	1.75	0.50
27:D:453:PHE:CE2	27:D:455:ARG:HG3	2.46	0.50
27:D:1168:GLY:O	27:D:1172:GLN:HG3	2.11	0.50
27:D:1913:PHE:CE2	27:D:1917:THR:HB	2.47	0.50
24:T:40:LYS:NZ	24:T:93:ALA:HB3	2.26	0.50
29:H:44:U:C2	29:H:45:U:C5	3.00	0.50
29:H:145:G:H2'	29:H:146:A:H8	1.77	0.50
32:1:580:PHE:HZ	32:1:619:HIS:HA	1.76	0.50
33:2:367:LEU:O	33:2:368:ILE:HG22	2.12	0.50
34:3:766:LYS:HD3	34:3:836:TRP:CZ2	2.47	0.50
34:3:1097:PHE:HB3	34:3:1106:PHE:HB3	1.93	0.50
1:A:2206:PHE:HE2	1:A:2241:ILE:HA	1.76	0.50
8:C:130:PRO:HB3	8:C:558:LYS:HZ2	1.75	0.50
27:D:1252:LEU:HD11	27:D:1288:PHE:CE1	2.46	0.50
26:V:20:ASN:ND2	26:V:69:ILE:HD11	2.27	0.50
28:G:492:U:H2'	28:G:493:A:C8	2.47	0.50
32:1:252:ILE:HD11	32:1:296:VAL:HA	1.93	0.50
34:3:493:VAL:HG13	34:3:499:SER:OG	2.11	0.50
34:3:503:LYS:HD3	34:3:941:PHE:CD1	2.46	0.50
4:N:161:LYS:O	4:N:165:GLU:CB	2.60	0.50
8:C:789:SER:HA	8:C:792:LYS:HG2	1.92	0.50
27:D:464:HIS:CE1	27:D:706:GLN:NE2	2.80	0.50
27:D:985:GLU:HG3	27:D:1001:LEU:HD22	1.93	0.50
27:D:1320:PRO:HB2	27:D:1534:ASN:O	2.12	0.50
21:P:19:LYS:HD2	21:P:99:ASP:HB2	1.93	0.50
32:1:927:ALA:C	32:1:929:ASN:H	2.14	0.50
34:3:630:ILE:HD13	34:3:646:LEU:HD13	1.94	0.50
1:A:1156:HIS:CG	1:A:1157:PRO:HD2	2.47	0.50
1:A:1400:ILE:HG22	1:A:1401:SER:N	2.25	0.50
1:A:1705:SER:HB3	1:A:1709:TRP:NE1	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2255:LEU:HD11	1:A:2281:PHE:HE1	1.77	0.50
2:K:178:ILE:HD13	2:K:461:ILE:HG13	1.94	0.50
4:N:251:GLU:OE2	4:N:255:ARG:HB3	2.12	0.50
4:N:890:GLU:O	4:N:894:ARG:HG2	2.12	0.50
27:D:1209:GLN:NE2	27:D:1788:TYR:O	2.45	0.50
27:D:1387:HIS:CE1	27:D:1470:LEU:HB2	2.47	0.50
27:D:1624:LEU:O	27:D:1624:LEU:HD23	2.12	0.50
27:D:1629:LEU:HD23	27:D:1648:ASP:CG	2.32	0.50
28:G:491:C:H2'	28:G:492:U:C6	2.47	0.50
34:3:643:ILE:HG21	34:3:691:LEU:HD11	1.94	0.50
39:Y:170:LEU:HD22	39:Y:170:LEU:N	2.27	0.50
1:A:837:GLY:O	1:A:1317:ARG:NH1	2.30	0.49
5:J:335:THR:HG23	5:J:336:VAL:HG22	1.94	0.49
8:C:104:THR:O	8:C:107:THR:OG1	2.20	0.49
18:B:113:G:C2	18:B:114:G:C8	3.00	0.49
27:D:1461:GLN:OE1	27:D:1461:GLN:N	2.44	0.49
29:H:142:C:O2'	29:H:143:G:O4'	2.29	0.49
32:1:743:ARG:HD2	32:1:780:CYS:SG	2.52	0.49
33:2:294:ILE:HG23	33:2:298:LEU:HD23	1.93	0.49
34:3:215:LEU:HB3	34:3:225:SER:HB3	1.94	0.49
34:3:673:ASP:OD1	34:3:674:THR:N	2.45	0.49
1:A:653:ILE:HA	1:A:656:ILE:HD12	1.95	0.49
1:A:1285:VAL:HG22	1:A:1301:TYR:CE1	2.47	0.49
1:A:1447:TRP:HB3	1:A:1451:PHE:CE2	2.47	0.49
1:A:1578:ALA:HA	1:A:1581:PHE:HB3	1.94	0.49
1:A:1751:TYR:O	1:A:1755:LYS:HG2	2.11	0.49
1:A:2075:THR:O	1:A:2079:ILE:HD12	2.12	0.49
5:J:331:VAL:HG12	5:J:333:LYS:N	2.27	0.49
27:D:656:TRP:CH2	27:D:929:ILE:HG13	2.47	0.49
27:D:1035:PHE:CD2	27:D:1080:LEU:HD22	2.47	0.49
34:3:106:THR:HG21	34:3:422:PHE:CE2	2.47	0.49
34:3:339:ASP:OD1	34:3:340:MET:N	2.45	0.49
35:4:165:ILE:HG12	35:4:180:VAL:HG12	1.94	0.49
1:A:285:PRO:HD2	1:A:298:TYR:OH	2.12	0.49
1:A:1070:LEU:HA	1:A:1073:ILE:HG22	1.94	0.49
1:A:1089:VAL:HG22	1:A:1098:VAL:HG22	1.94	0.49
1:A:1882:LEU:HB3	1:A:1889:LEU:HD23	1.93	0.49
1:A:2381:GLU:HB3	1:A:2384:ASN:HB2	1.94	0.49
2:K:233:GLN:HA	2:K:246:PHE:O	2.13	0.49
27:D:467:ALA:HB1	27:D:702:PRO:HB2	1.95	0.49
27:D:747:ARG:HH12	27:D:1047:ARG:HG3	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1584:PHE:HZ	27:D:1709:LEU:HD22	1.77	0.49
24:T:43:ILE:HG23	24:T:52:VAL:HG13	1.94	0.49
32:1:931:ARG:NE	37:6:24:GLU:OE2	2.44	0.49
34:3:59:TYR:HE1	34:3:1316:LYS:HD2	1.76	0.49
34:3:353:ARG:NH2	34:3:387:ASP:OD1	2.44	0.49
34:3:712:PHE:HE2	34:3:713:LEU:HD23	1.76	0.49
34:3:1192:HIS:CE1	34:3:1312:ALA:HB3	2.47	0.49
1:A:1286:TRP:HA	1:A:1448:GLU:OE2	2.12	0.49
1:A:1586:GLN:HG2	1:A:1595:ARG:HH11	1.77	0.49
1:A:2157:ILE:HG13	27:D:1064:PRO:HB2	1.94	0.49
1:A:2306:ASN:HB2	1:A:2335:THR:OG1	2.12	0.49
2:K:225:ASP:OD1	2:K:226:TRP:N	2.45	0.49
2:K:285:HIS:O	2:K:287:MET:N	2.45	0.49
3:L:398:GLN:NE2	3:L:419:GLN:HG3	2.28	0.49
4:N:846:PHE:HE1	4:N:859:LEU:HD23	1.77	0.49
8:C:183:GLN:HE21	8:C:657:TYR:HD2	1.60	0.49
16:F:38:U:H4'	16:F:39:G:O5'	2.12	0.49
27:D:820:PHE:CD2	27:D:828:LEU:HD22	2.48	0.49
27:D:2007:LYS:HB3	27:D:2030:ILE:HD12	1.93	0.49
28:G:520:G:C6	38:X:34:TYR:CZ	3.00	0.49
29:H:1151:U:H2'	29:H:1152:U:C6	2.46	0.49
32:1:517:TYR:OH	32:1:521:LYS:NZ	2.42	0.49
32:1:872:GLY:HA2	34:3:1315:ARG:HG3	1.95	0.49
33:2:299:ARG:NH2	33:2:343:ASP:O	2.40	0.49
34:3:379:VAL:CG2	34:3:391:LEU:HB2	2.41	0.49
36:5:20:GLY:H	36:5:43:VAL:HG23	1.77	0.49
1:A:1717:LEU:HG	1:A:1786:ALA:HB3	1.93	0.49
1:A:1739:ARG:HD2	1:A:1751:TYR:CE2	2.47	0.49
1:A:2177:VAL:H	1:A:2338:GLN:HE22	1.58	0.49
3:L:273:HIS:ND1	3:L:273:HIS:O	2.45	0.49
4:N:161:LYS:O	4:N:165:GLU:HB2	2.11	0.49
8:C:343:ASP:O	8:C:346:THR:OG1	2.28	0.49
8:C:544:LEU:HG	8:C:553:VAL:HG21	1.94	0.49
8:C:864:VAL:HG12	8:C:866:ILE:HG13	1.95	0.49
17:I:78:A:H2	27:D:1110:ARG:NH2	2.08	0.49
27:D:835:ALA:HA	27:D:874:ARG:HD3	1.94	0.49
27:D:1431:ASP:OD2	27:D:2095:LYS:HD2	2.13	0.49
21:P:96:VAL:HG12	22:Q:85:ILE:HG12	1.95	0.49
22:Q:96:ILE:HG13	23:R:94:LEU:HD13	1.94	0.49
29:H:1089:G:C2'	29:H:1090:A:O5'	2.60	0.49
32:1:925:HIS:CG	32:1:926:PRO:HD2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:98:GLU:OE2	37:6:47:SER:OG	2.27	0.49
1:A:1400:ILE:HG21	1:A:1440:ILE:HD11	1.94	0.49
1:A:1709:TRP:HB3	1:A:1791:PHE:CE1	2.47	0.49
2:K:77:ALA:O	2:K:81:MET:HG2	2.13	0.49
3:L:127:LEU:HD11	3:L:131:ILE:HD12	1.93	0.49
6:E:53:VAL:HG12	6:E:57:ALA:HB3	1.93	0.49
17:I:150:G:N2	17:I:152:A:H5'	2.28	0.49
27:D:588:LEU:HD11	27:D:599:ILE:HD11	1.94	0.49
27:D:1095:ASN:O	27:D:1099:VAL:HG23	2.12	0.49
27:D:1852:ILE:O	27:D:1856:TYR:HD2	1.96	0.49
29:H:1097:G:C2	29:H:1098:C:C4	3.00	0.49
32:1:715:ALA:HB1	32:1:718:TYR:CD2	2.47	0.49
32:1:827:ILE:HG13	32:1:827:ILE:O	2.12	0.49
34:3:266:VAL:HG12	34:3:290:PRO:HA	1.94	0.49
34:3:455:LEU:HD11	34:3:464:LEU:HB3	1.93	0.49
34:3:636:THR:HB	34:3:679:VAL:HG23	1.93	0.49
1:A:139:LEU:HD13	1:A:193:TYR:CG	2.48	0.49
1:A:388:PRO:HB2	1:A:398:VAL:HG11	1.94	0.49
1:A:1578:ALA:CB	1:A:1602:PRO:HB3	2.43	0.49
2:K:435:GLY:N	2:K:464:TRP:HH2	2.11	0.49
2:K:438:ASP:HB3	2:K:457:TRP:HB2	1.95	0.49
6:E:38:GLN:HA	6:E:106:ILE:HD11	1.93	0.49
8:C:775:ILE:HD12	8:C:817:GLN:HE21	1.76	0.49
18:B:8:U:O4	18:B:157:G:O6	2.31	0.49
18:B:74:U:H3'	18:B:75:A:H5''	1.94	0.49
27:D:1524:TRP:CD1	27:D:1780:ARG:NH2	2.80	0.49
27:D:2051:VAL:CG1	27:D:2077:ARG:HG2	2.43	0.49
26:V:65:GLY:HA2	26:V:68:ILE:HD12	1.95	0.49
32:1:600:PRO:O	32:1:603:SER:OG	2.19	0.49
34:3:324:ASN:OD1	34:3:341:ASN:ND2	2.43	0.49
1:A:286:LEU:HD21	1:A:289:ASP:HB2	1.93	0.49
1:A:852:LEU:HD23	1:A:855:LEU:HD12	1.94	0.49
1:A:1481:GLU:HA	1:A:1484:TRP:HE1	1.75	0.49
4:N:13:ALA:HB3	4:N:15:TYR:CE2	2.47	0.49
4:N:772:LEU:O	4:N:775:VAL:N	2.46	0.49
5:J:349:ASN:HB3	5:J:352:ILE:HD12	1.95	0.49
17:I:101:C:H2'	17:I:102:A:H8	1.77	0.49
17:I:151:G:H21	17:I:152:A:N6	2.10	0.49
18:B:78:A:H3'	18:B:78:A:OP2	2.13	0.49
19:O:150:ASN:OD1	19:O:151:ILE:N	2.45	0.49
21:P:29:VAL:HB	21:P:51:GLU:HG3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:U:51:LEU:HB2	25:U:73:ILE:HB	1.94	0.49
28:G:481:A:H5'	35:4:52:TYR:CD2	2.48	0.49
32:1:494:LEU:CD1	38:X:23:TRP:CG	2.93	0.49
32:1:583:PHE:O	32:1:587:THR:HG23	2.12	0.49
33:2:262:HIS:HB2	33:2:280:THR:HG22	1.95	0.49
38:X:19:PRO:HA	38:X:22:SER:OG	2.13	0.49
1:A:481:HIS:NE2	8:C:276:ASP:OD1	2.46	0.49
7:M:44:LEU:O	7:M:74:LYS:NZ	2.43	0.49
8:C:967:VAL:O	8:C:971:ARG:HG2	2.13	0.49
17:I:91:U:C2	17:I:142:G:N2	2.78	0.49
27:D:1740:LEU:HD11	22:Q:146:LEU:CD1	2.42	0.49
27:D:1950:ILE:O	27:D:1954:VAL:HG13	2.12	0.49
32:1:733:GLU:HG2	32:1:736:LYS:HZ1	1.78	0.49
1:A:395:PRO:HB2	1:A:398:VAL:HG21	1.95	0.49
1:A:2183:TYR:HE2	1:A:2289:ILE:CG1	2.08	0.49
2:K:382:ASP:OD1	2:K:383:GLU:N	2.46	0.49
8:C:353:TYR:CD1	8:C:371:PRO:HA	2.48	0.49
18:B:10:U:O2	18:B:156:G:N1	2.46	0.49
27:D:945:TYR:O	27:D:949:LEU:HG	2.13	0.49
27:D:1016:ASP:OD1	27:D:1017:VAL:N	2.46	0.49
27:D:1095:ASN:O	27:D:1098:ILE:HG22	2.12	0.49
22:Q:4:VAL:HG11	22:Q:34:PRO:HA	1.95	0.49
34:3:118:GLN:HE21	34:3:1299:ILE:HD13	1.78	0.49
1:A:255:ILE:HD11	1:A:637:VAL:HG13	1.94	0.48
1:A:503:LYS:HA	1:A:506:PHE:CE2	2.47	0.48
1:A:688:TYR:HA	1:A:691:PHE:CE2	2.47	0.48
1:A:884:SER:HB3	3:L:180:LYS:NZ	2.27	0.48
1:A:1952:PRO:HB2	3:L:426:GLY:N	2.26	0.48
4:N:9:GLN:HB3	4:N:11:PRO:HD3	1.95	0.48
4:N:464:ILE:O	4:N:467:ALA:HB3	2.14	0.48
8:C:793:GLU:HA	8:C:796:ILE:HG22	1.95	0.48
27:D:1228:TRP:CE2	27:D:1261:PRO:HG3	2.48	0.48
27:D:1241:LEU:HA	27:D:1292:LEU:HD23	1.95	0.48
23:R:47:SER:OG	23:R:103:VAL:HB	2.12	0.48
25:U:60:VAL:HG12	25:U:65:HIS:HB2	1.95	0.48
26:V:47:ASN:HD21	26:V:51:PRO:HB2	1.78	0.48
29:H:1099:G:HO2'	29:H:1100:A:H5'	1.66	0.48
32:1:341:GLY:O	32:1:384:ASN:ND2	2.46	0.48
32:1:950:VAL:HG13	37:6:39:THR:HG22	1.95	0.48
34:3:607:LEU:HD13	34:3:624:TRP:HD1	1.78	0.48
39:Y:167:VAL:O	39:Y:171:GLY:N	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:209:ILE:HG21	1:A:303:PHE:HE2	1.78	0.48
1:A:219:ALA:HB1	1:A:266:LEU:HD13	1.94	0.48
1:A:1525:PHE:HD2	3:L:405:GLY:HA3	1.78	0.48
2:K:73:ARG:O	2:K:76:LEU:HB2	2.13	0.48
8:C:406:VAL:HG11	8:C:427:LEU:HD21	1.95	0.48
27:D:1320:PRO:HB2	27:D:1535:PHE:HA	1.94	0.48
25:U:33:PHE:C	25:U:35:SER:H	2.16	0.48
32:1:161:LYS:O	32:1:165:THR:HG23	2.12	0.48
32:1:491:ARG:HD2	38:X:27:TYR:OH	2.13	0.48
32:1:960:ASN:HD21	32:1:963:TYR:HA	1.78	0.48
34:3:1133:ASP:OD2	34:3:1137:ASN:HB2	2.13	0.48
1:A:220:THR:O	1:A:224:MET:HG2	2.12	0.48
1:A:400:ILE:HB	8:C:186:ASP:HB3	1.95	0.48
1:A:972:MET:HG2	1:A:981:VAL:HG21	1.95	0.48
1:A:1033:ASN:HD21	1:A:1298:ALA:HB3	1.78	0.48
1:A:1087:ASN:ND2	3:L:272:LEU:HG	2.19	0.48
1:A:1963:LEU:HD13	1:A:1965:PHE:HE2	1.77	0.48
2:K:378:ILE:HG22	5:J:168:TRP:HE1	1.78	0.48
3:L:280:ARG:NH2	17:I:37:U:OP2	2.46	0.48
4:N:721:ARG:O	4:N:725:ILE:HD12	2.12	0.48
8:C:856:ILE:HA	8:C:944:VAL:HG11	1.94	0.48
16:F:47:A:H3'	16:F:48:C:H5'	1.94	0.48
18:B:86:G:H2'	18:B:87:G:H8	1.76	0.48
27:D:1908:ARG:HD3	23:R:39:VAL:HG23	1.95	0.48
22:Q:88:ARG:NH1	22:Q:90:ASN:HB3	2.28	0.48
32:1:494:LEU:CB	38:X:7:ILE:CG2	2.89	0.48
32:1:801:ILE:HG22	32:1:816:VAL:HG13	1.95	0.48
39:Y:217:LYS:HB3	39:Y:218:PRO:HD2	1.95	0.48
1:A:645:ASP:OD1	1:A:646:ALA:N	2.46	0.48
1:A:842:LYS:HE2	1:A:1322:ALA:HA	1.94	0.48
1:A:1090:ILE:O	1:A:1096:SER:HA	2.13	0.48
1:A:1211:SER:HA	1:A:1257:ASN:ND2	2.28	0.48
1:A:2152:TRP:HZ3	27:D:1064:PRO:HG3	1.75	0.48
4:N:655:PHE:O	4:N:659:ARG:CB	2.62	0.48
7:M:33:LEU:HD11	7:M:100:ALA:HB1	1.95	0.48
8:C:143:HIS:HA	44:C:1500:GTP:PB	2.54	0.48
8:C:362:LYS:CG	8:C:363:PRO:HD2	2.43	0.48
8:C:652:MET:HA	8:C:655:LEU:HD12	1.96	0.48
8:C:678:SER:HB2	8:C:858:LEU:HB2	1.94	0.48
17:I:136:U:O2'	27:D:1194:ASP:OD2	2.26	0.48
27:D:675:PRO:HG3	27:D:905:GLN:C	2.34	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1459:TRP:NE1	27:D:1762:ILE:HD11	2.28	0.48
21:P:50:GLU:O	21:P:79:LYS:HA	2.14	0.48
33:2:367:LEU:C	33:2:369:SER:H	2.16	0.48
1:A:299:LYS:HA	1:A:493:MET:HG3	1.95	0.48
1:A:930:ASN:HB3	1:A:933:GLU:OE1	2.14	0.48
1:A:995:LEU:HD11	1:A:1078:ILE:HG23	1.95	0.48
1:A:2166:LEU:HD11	1:A:2194:ILE:HG13	1.95	0.48
1:A:2395:PHE:CG	27:D:1062:PRO:CD	2.82	0.48
3:L:282:GLU:HG3	3:L:286:PHE:CD2	2.49	0.48
8:C:707:SER:HB3	8:C:824:SER:HB3	1.96	0.48
18:B:76:U:O2'	18:B:78:A:OP1	2.30	0.48
18:B:143:U:H2'	18:B:144:G:H8	1.78	0.48
27:D:828:LEU:HG	27:D:830:CYS:SG	2.53	0.48
27:D:1804:SER:HA	27:D:1807:VAL:HG22	1.96	0.48
22:Q:29:LEU:HD23	22:Q:40:LEU:HG	1.94	0.48
28:G:504:C:OP1	36:5:25:LYS:NZ	2.21	0.48
29:H:1116:A:O2'	29:H:1117:G:H5'	2.13	0.48
32:1:327:TRP:HD1	32:1:330:ARG:HH21	1.61	0.48
32:1:830:MET:O	32:1:832:LYS:HG2	2.13	0.48
34:3:74:SER:OG	34:3:95:VAL:HG22	2.13	0.48
34:3:586:ASP:OD1	34:3:587:THR:N	2.47	0.48
34:3:1136:GLY:HA2	34:3:1197:ASP:O	2.14	0.48
35:4:136:ARG:HB2	35:4:154:TYR:CD2	2.49	0.48
1:A:772:GLU:HA	1:A:775:ARG:HB2	1.96	0.48
1:A:1964:PRO:HB3	1:A:2013:ARG:HD2	1.95	0.48
2:K:195:TRP:CZ3	2:K:220:LYS:HE3	2.49	0.48
4:N:212:VAL:HG13	4:N:215:LEU:H	1.78	0.48
27:D:2011:ILE:HD12	27:D:2030:ILE:HD11	1.96	0.48
22:Q:31:SER:HB2	22:Q:39:ILE:HD11	1.95	0.48
23:R:38:MET:SD	23:R:61:PHE:HE2	2.36	0.48
28:G:499:U:H2'	28:G:500:A:C8	2.49	0.48
29:H:45:U:H2'	29:H:46:C:C6	2.49	0.48
33:2:322:PRO:HA	35:4:65:TYR:CE2	2.49	0.48
34:3:414:GLN:NE2	34:3:434:ASN:O	2.47	0.48
34:3:533:LYS:HA	34:3:848:SER:OG	2.14	0.48
34:3:1043:THR:HG21	34:3:1052:TYR:HE2	1.79	0.48
35:4:110:LEU:HD12	35:4:155:PHE:HE2	1.77	0.48
37:6:50:LEU:CD2	37:6:62:ILE:HG23	2.43	0.48
1:A:1169:TYR:OH	1:A:1262:MET:HA	2.14	0.48
1:A:1414:TRP:HB2	1:A:1558:GLU:HG3	1.94	0.48
1:A:1748:ILE:HG22	1:A:1785:ASP:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:205:GLU:O	3:L:209:LYS:HG2	2.13	0.48
4:N:787:SER:O	17:I:40:G:O2'	2.31	0.48
8:C:152:LEU:O	8:C:155:ILE:HG13	2.13	0.48
8:C:227:VAL:HG11	8:C:474:LYS:HB2	1.94	0.48
27:D:1688:TYR:CD2	27:D:1895:ARG:HA	2.44	0.48
27:D:1847:LEU:O	27:D:1851:LEU:HD13	2.13	0.48
23:R:79:LYS:HD3	23:R:84:VAL:HG22	1.95	0.48
32:1:401:TRP:CZ2	32:1:434:TYR:HD1	2.31	0.48
32:1:550:THR:HG23	32:1:553:LEU:HD22	1.96	0.48
33:2:134:LEU:HD13	33:2:138:LYS:HE2	1.96	0.48
34:3:1037:PHE:CE2	34:3:1038:LYS:HG2	2.49	0.48
35:4:108:ALA:HA	35:4:194:TYR:OH	2.14	0.48
1:A:717:GLY:HA3	18:B:84:A:O2'	2.14	0.48
2:K:200:GLN:HB3	2:K:213:LYS:HG3	1.96	0.48
2:K:267:ARG:HG3	2:K:285:HIS:CD2	2.49	0.48
3:L:120:TYR:CD1	3:L:123:ARG:HB3	2.46	0.48
3:L:367:ARG:NH2	17:I:57:U:C4	2.81	0.48
4:N:261:LYS:HE2	4:N:285:HIS:HA	1.94	0.48
8:C:250:GLU:HG2	8:C:298:PHE:CE2	2.48	0.48
8:C:766:TRP:CZ2	8:C:792:LYS:HB3	2.49	0.48
27:D:836:TRP:HE3	27:D:870:GLN:HE22	1.62	0.48
27:D:1515:LEU:O	27:D:1534:ASN:ND2	2.44	0.48
27:D:1682:ILE:HD12	27:D:1722:ILE:HG12	1.95	0.48
27:D:2103:LEU:HD13	27:D:2142:ILE:HG13	1.96	0.48
34:3:71:PHE:O	34:3:430:LEU:HD21	2.13	0.48
1:A:644:VAL:O	1:A:645:ASP:HB2	2.14	0.48
1:A:1447:TRP:HB3	1:A:1451:PHE:HE2	1.78	0.48
1:A:1673:LEU:HD21	1:A:1681:VAL:HG23	1.96	0.48
4:N:726:LEU:HD21	4:N:746:MET:HE1	1.96	0.48
8:C:237:ILE:HD12	8:C:265:PHE:HE1	1.78	0.48
8:C:769:TYR:N	8:C:772:ASN:O	2.45	0.48
21:P:15:LEU:HB3	21:P:20:LEU:HD11	1.95	0.48
22:Q:8:LYS:HE3	22:Q:34:PRO:HG3	1.96	0.48
29:H:42:U:C2	29:H:43:G:C8	3.02	0.48
29:H:1093:C:C2	29:H:1094:G:C8	3.02	0.48
29:H:1162:U:O2'	29:H:1163:C:H5'	2.14	0.48
29:H:1166:G:H8	29:H:1166:G:O5'	1.96	0.48
32:1:606:LEU:HD21	32:1:643:LEU:HD23	1.96	0.48
32:1:928:LYS:HD2	37:6:24:GLU:OE2	2.14	0.48
34:3:551:PHE:HD2	34:3:591:THR:HG21	1.79	0.48
34:3:1193:PHE:CE1	34:3:1308:ARG:HD2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:543:ASN:OD1	1:A:544:LYS:N	2.47	0.48
1:A:635:THR:HG21	1:A:656:ILE:HD11	1.96	0.48
1:A:966:PRO:HA	1:A:1088:VAL:HG12	1.95	0.48
4:N:692:LEU:HD23	4:N:708:LEU:HD11	1.96	0.48
8:C:292:ILE:HD13	8:C:306:PRO:HD3	1.95	0.48
27:D:1032:PHE:HE2	27:D:1081:GLN:HG2	1.79	0.48
27:D:1255:ASP:N	27:D:1255:ASP:OD1	2.47	0.48
21:P:53:VAL:HB	21:P:54:PRO:HD3	1.96	0.48
29:H:1097:G:H2'	29:H:1098:C:H5	1.78	0.48
34:3:60:LEU:HB2	34:3:1317:VAL:HG22	1.94	0.48
1:A:863:ARG:NH1	1:A:1059:GLU:HB3	2.29	0.47
2:K:290:ARG:HA	2:K:301:LEU:O	2.13	0.47
5:J:342:PHE:HB2	5:J:380:ILE:HB	1.95	0.47
17:I:143:A:C5	25:U:48:TYR:HD2	2.31	0.47
27:D:542:HIS:O	27:D:551:ASN:HB3	2.14	0.47
27:D:1621:ILE:HD12	27:D:1630:ARG:HG3	1.96	0.47
21:P:28:ARG:HD3	21:P:50:GLU:OE2	2.14	0.47
29:H:142:C:C2'	29:H:143:G:H8	2.23	0.47
29:H:679:U:H2'	29:H:680:C:C6	2.49	0.47
32:1:954:PRO:O	32:1:959:ASN:ND2	2.47	0.47
34:3:294:PHE:CE2	34:3:330:GLY:HA3	2.49	0.47
1:A:460:PRO:HG3	8:C:376:PHE:CD1	2.49	0.47
1:A:691:PHE:CZ	1:A:701:CYS:HB2	2.49	0.47
1:A:1451:PHE:O	1:A:1454:SER:N	2.45	0.47
1:A:1649:PHE:CE1	1:A:1815:LEU:HD21	2.49	0.47
6:E:53:VAL:HG13	6:E:56:PHE:CZ	2.49	0.47
8:C:835:LYS:HB3	8:C:839:ILE:HD12	1.95	0.47
8:C:879:LEU:O	8:C:883:ARG:HG2	2.14	0.47
27:D:843:HIS:HA	27:D:876:GLY:HA2	1.96	0.47
27:D:1987:VAL:HG23	27:D:2150:LEU:HD22	1.95	0.47
24:T:46:PHE:O	25:U:14:ASN:ND2	2.47	0.47
29:H:1094:G:C6	29:H:1149:G:C6	3.03	0.47
34:3:208:GLU:HG3	34:3:209:GLN:N	2.29	0.47
34:3:380:LEU:HB3	34:3:388:LEU:HD11	1.96	0.47
38:X:49:THR:CG2	39:Y:233:ASP:HB2	2.45	0.47
1:A:1268:ARG:HG2	1:A:1301:TYR:HB2	1.95	0.47
1:A:2398:LEU:HD12	27:D:1060:LYS:HZ2	1.72	0.47
2:K:446:SER:OG	2:K:451:PHE:CE2	2.60	0.47
17:I:143:A:C5	25:U:48:TYR:CD2	3.02	0.47
27:D:585:VAL:HG22	27:D:604:VAL:HB	1.97	0.47
24:T:85:ASP:OD1	24:T:86:ASN:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:U:58:GLU:C	25:U:59:PHE:HD1	2.17	0.47
34:3:94:CYS:SG	34:3:101:LEU:HD11	2.54	0.47
34:3:211:LYS:NZ	34:3:256:GLU:OE2	2.38	0.47
34:3:750:TYR:HE1	34:3:777:LEU:HD21	1.79	0.47
34:3:1107:ILE:HD12	34:3:1108:PRO:HD2	1.96	0.47
35:4:138:PRO:HA	35:4:152:TYR:O	2.14	0.47
1:A:713:ASN:HB3	18:B:84:A:H5'	1.96	0.47
1:A:796:ASN:OD1	1:A:858:LYS:HE2	2.14	0.47
2:K:428:LEU:HD11	5:J:466:PRO:HD2	1.96	0.47
18:B:67:U:H2'	18:B:68:A:C8	2.47	0.47
21:P:76:LYS:HD3	21:P:79:LYS:HD3	1.96	0.47
24:T:90:ILE:HB	26:V:62:VAL:CG1	2.44	0.47
32:1:850:ASP:OD1	32:1:853:HIS:HD2	1.98	0.47
33:2:363:TYR:HA	34:3:1125:ASP:OD2	2.14	0.47
34:3:503:LYS:HG2	34:3:929:ILE:HD11	1.97	0.47
1:A:228:LYS:HD2	1:A:701:CYS:H	1.77	0.47
1:A:374:ILE:HD12	8:C:674:LEU:HD22	1.97	0.47
1:A:1863:HIS:HB2	1:A:1871:ALA:HB3	1.95	0.47
3:L:113:HIS:HD2	3:L:134:PRO:HA	1.80	0.47
8:C:835:LYS:O	8:C:839:ILE:HB	2.15	0.47
17:I:141:G:H2'	17:I:142:G:H5'	1.97	0.47
27:D:587:GLU:O	27:D:594:LEU:HG	2.15	0.47
27:D:1252:LEU:HD11	27:D:1288:PHE:CD1	2.49	0.47
29:H:1143:C:H4'	29:H:1144:U:H2'	1.96	0.47
32:1:169:LEU:O	32:1:173:ILE:HD12	2.13	0.47
32:1:935:TRP:CE3	37:6:22:GLY:HA3	2.49	0.47
38:X:33:ILE:HG22	38:X:85:THR:HG23	1.95	0.47
1:A:984:VAL:HG12	1:A:985:ASP:N	2.30	0.47
1:A:1169:TYR:CZ	1:A:1262:MET:HG2	2.50	0.47
1:A:1616:ARG:HH21	1:A:1618:ASN:HD22	1.63	0.47
1:A:2017:THR:HB	1:A:2062:GLU:OE1	2.13	0.47
1:A:2177:VAL:N	1:A:2338:GLN:HE22	2.12	0.47
2:K:353:TYR:CE1	7:M:126:ILE:HG12	2.48	0.47
2:K:362:TYR:HB2	2:K:379:ARG:HG3	1.95	0.47
16:F:50:G:H4'	16:F:51:A:OP2	2.15	0.47
17:I:138:U:H5	27:D:1227:ILE:HG12	1.79	0.47
18:B:32:G:HO2'	18:B:34:C:H6	1.59	0.47
27:D:491:PHE:N	27:D:491:PHE:CD1	2.82	0.47
27:D:574:PHE:HB2	27:D:585:VAL:HG11	1.97	0.47
27:D:1685:THR:O	27:D:1697:PRO:HA	2.15	0.47
27:D:1724:THR:HG22	27:D:1725:SER:N	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:2051:VAL:HG12	27:D:2077:ARG:HG2	1.97	0.47
22:Q:23:THR:HA	22:Q:48:PRO:HD3	1.96	0.47
26:V:31:GLY:H	26:V:39:VAL:HB	1.78	0.47
28:G:506:U:O2	28:G:507:U:H5''	2.14	0.47
38:X:52:SER:HB3	39:Y:231:ARG:CZ	2.44	0.47
1:A:364:TYR:CE2	1:A:1209:LYS:HB3	2.50	0.47
1:A:676:GLN:HG2	1:A:714:PHE:HB2	1.96	0.47
1:A:688:TYR:HD1	1:A:691:PHE:CZ	2.32	0.47
1:A:876:PRO:HB3	3:L:172:ILE:HG22	1.95	0.47
1:A:1054:LEU:O	1:A:1239:THR:HB	2.14	0.47
1:A:1126:LEU:HD11	1:A:1161:TYR:CD2	2.50	0.47
1:A:1286:TRP:CZ2	1:A:1302:LEU:HD11	2.50	0.47
1:A:1562:PHE:CZ	1:A:1570:TRP:HB3	2.50	0.47
1:A:1777:ILE:HG12	1:A:1784:TYR:CB	2.45	0.47
1:A:2398:LEU:HD22	27:D:1060:LYS:CD	2.43	0.47
2:K:244:LYS:HE3	2:K:257:LEU:HD22	1.96	0.47
3:L:137:TYR:O	3:L:141:ILE:HG13	2.15	0.47
3:L:222:ILE:HD11	3:L:242:ILE:HD12	1.97	0.47
3:L:410:LEU:O	3:L:410:LEU:HD12	2.15	0.47
5:J:335:THR:HG23	5:J:336:VAL:H	1.79	0.47
6:E:9:LEU:HD13	6:E:15:VAL:HA	1.97	0.47
8:C:116:THR:HG22	8:C:118:TYR:H	1.80	0.47
8:C:233:ASP:OD1	8:C:487:ARG:NH2	2.47	0.47
8:C:423:HIS:O	8:C:427:LEU:CB	2.63	0.47
17:I:137:G:H5''	27:D:1198:ARG:NH2	2.29	0.47
18:B:166:U:H4'	18:B:167:A:OP1	2.14	0.47
27:D:686:VAL:HG12	27:D:687:PRO:O	2.14	0.47
27:D:781:LEU:HD23	27:D:781:LEU:C	2.35	0.47
27:D:1640:LEU:HB2	27:D:1664:LEU:HD11	1.97	0.47
23:R:53:LYS:O	23:R:74:GLU:HA	2.15	0.47
24:T:24:GLN:CB	24:T:42:LYS:HD2	2.44	0.47
28:G:501:A:C6	32:1:783:VAL:HG11	2.49	0.47
29:H:565:U:H2'	29:H:566:U:C6	2.50	0.47
29:H:566:U:H2'	29:H:567:U:C6	2.50	0.47
29:H:689:G:H2'	29:H:690:U:C6	2.50	0.47
32:1:611:HIS:CD2	32:1:612:LYS:H	2.31	0.47
32:1:683:ASN:OD1	32:1:684:GLN:N	2.46	0.47
33:2:311:PRO:HG2	35:4:74:VAL:HG22	1.96	0.47
33:2:322:PRO:HB3	35:4:32:ILE:O	2.14	0.47
34:3:832:TRP:HB3	34:3:835:VAL:HG23	1.97	0.47
34:3:1003:LEU:HD23	34:3:1059:LEU:HD11	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:1193:PHE:CZ	34:3:1308:ARG:HD2	2.49	0.47
2:K:171:GLN:O	2:K:172:LEU:HD12	2.15	0.47
7:M:61:ILE:O	7:M:65:LEU:HG	2.15	0.47
8:C:132:ARG:O	8:C:133:ILE:HG12	2.14	0.47
27:D:635:GLU:N	27:D:670:LEU:O	2.47	0.47
29:H:139:G:C2'	29:H:140:G:O5'	2.62	0.47
29:H:551:C:H2'	29:H:552:U:C6	2.50	0.47
29:H:678:U:H2'	29:H:679:U:C6	2.50	0.47
29:H:693:C:H2'	29:H:694:C:C6	2.50	0.47
29:H:1140:U:H2'	29:H:1141:C:C6	2.50	0.47
34:3:337:VAL:HG22	34:3:346:LEU:HB2	1.97	0.47
1:A:227:GLU:OE2	1:A:231:ARG:NH1	2.28	0.47
1:A:325:LYS:HB2	1:A:405:ASN:ND2	2.28	0.47
1:A:2032:ILE:HD13	1:A:2043:PHE:CE1	2.50	0.47
1:A:2393:LEU:O	1:A:2397:GLU:CB	2.63	0.47
4:N:887:THR:HB	4:N:890:GLU:HB3	1.96	0.47
8:C:943:ASP:OD2	8:C:946:ASP:HB2	2.15	0.47
16:F:29:U:H2'	16:F:30:G:C8	2.50	0.47
17:I:151:G:HO2'	24:T:32:PHE:HE2	1.60	0.47
22:Q:34:PRO:C	22:Q:36:MET:H	2.17	0.47
28:G:514:U:C4'	28:G:515:U:H5'	2.45	0.47
29:H:671:G:H2'	29:H:672:U:C6	2.50	0.47
29:H:682:U:H2'	29:H:683:U:C6	2.50	0.47
29:H:695:U:H2'	29:H:696:C:C6	2.50	0.47
29:H:1097:G:C6	29:H:1146:G:C6	3.02	0.47
32:1:258:VAL:HA	32:1:261:THR:HG22	1.97	0.47
32:1:963:TYR:CG	32:1:964:ILE:N	2.83	0.47
35:4:108:ALA:HB3	35:4:155:PHE:O	2.15	0.47
1:A:2395:PHE:CD1	27:D:1061:ALA:CA	2.84	0.47
2:K:388:GLN:HE21	5:J:462:HIS:CE1	2.32	0.47
2:K:408:LYS:O	2:K:424:SER:HB3	2.15	0.47
2:K:443:LEU:HG	2:K:444:ASP:N	2.30	0.47
5:J:280:VAL:O	5:J:286:ASN:ND2	2.48	0.47
8:C:148:SER:O	8:C:151:ASP:HB3	2.15	0.47
8:C:465:GLU:CD	8:C:466:GLY:H	2.19	0.47
8:C:697:ARG:HG3	8:C:709:SER:HA	1.97	0.47
17:I:150:G:O2'	17:I:152:A:OP1	2.32	0.47
18:B:21:G:H2'	18:B:22:G:C8	2.50	0.47
24:T:11:VAL:O	26:V:31:GLY:HA3	2.15	0.47
33:2:185:GLY:O	33:2:189:LEU:HG	2.14	0.47
34:3:259:ASN:O	37:6:75:PRO:HD3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:300:LYS:H	1:A:493:MET:HG2	1.80	0.46
1:A:1213:MET:HE1	1:A:1250:VAL:HB	1.97	0.46
1:A:1313:ASP:OD1	1:A:1359:ILE:HD13	2.15	0.46
1:A:1498:ASP:HB2	4:N:159:LEU:HB2	1.96	0.46
1:A:1527:TRP:CE3	1:A:1528:THR:HG23	2.49	0.46
1:A:2395:PHE:CD1	27:D:1060:LYS:O	2.63	0.46
4:N:13:ALA:HB3	4:N:15:TYR:CD2	2.50	0.46
4:N:652:ALA:O	4:N:656:LEU:CB	2.63	0.46
16:F:5:G:H2'	16:F:6:C:C6	2.49	0.46
17:I:5:U:H2'	17:I:6:U:C6	2.50	0.46
17:I:150:G:H2'	17:I:151:G:H5''	1.97	0.46
27:D:783:THR:O	27:D:787:ASN:ND2	2.48	0.46
27:D:1372:LYS:CD	27:D:1708:GLY:HA3	2.45	0.46
20:S:23:LEU:HD23	20:S:24:THR:H	1.80	0.46
32:1:823:MET:O	32:1:827:ILE:HG12	2.15	0.46
34:3:370:VAL:HG23	34:3:379:VAL:HG12	1.98	0.46
34:3:964:PHE:CZ	34:3:972:LYS:HD3	2.50	0.46
1:A:364:TYR:CB	1:A:1214:ARG:HG2	2.45	0.46
1:A:1889:LEU:HB2	1:A:1989:PHE:HB2	1.97	0.46
2:K:366:THR:O	2:K:373:ILE:HA	2.16	0.46
5:J:406:PHE:CE1	5:J:408:LEU:HB2	2.50	0.46
6:E:53:VAL:CG1	6:E:57:ALA:HB3	2.46	0.46
8:C:139:ILE:HD12	8:C:252:LEU:HD22	1.96	0.46
27:D:699:ARG:HH21	27:D:875:ALA:HB3	1.81	0.46
27:D:1213:ARG:HG3	27:D:1313:LEU:HB3	1.96	0.46
27:D:1629:LEU:HD21	27:D:1652:VAL:CG2	2.45	0.46
22:Q:43:VAL:CG1	22:Q:85:ILE:HD12	2.44	0.46
29:H:677:U:H2'	29:H:678:U:C6	2.50	0.46
32:1:523:LEU:HD23	32:1:526:LEU:HD12	1.97	0.46
34:3:411:ASP:OD2	34:3:472:LEU:HG	2.14	0.46
34:3:952:ARG:HA	34:3:972:LYS:O	2.14	0.46
34:3:1306:GLU:HG3	36:5:78:ARG:NH1	2.30	0.46
39:Y:160:LYS:HB2	39:Y:160:LYS:NZ	2.30	0.46
3:L:232:LEU:HD23	3:L:334:LYS:HG3	1.97	0.46
8:C:197:THR:HG23	8:C:545:LEU:HD12	1.97	0.46
8:C:468:LEU:HA	8:C:491:GLY:HA3	1.97	0.46
8:C:576:THR:HG21	8:C:591:PHE:HB3	1.96	0.46
32:1:232:LEU:HD12	32:1:233:GLY:N	2.30	0.46
38:X:124:GLU:O	38:X:128:ARG:HG2	2.16	0.46
1:A:1545:ASP:HA	1:A:1548:GLN:HG2	1.97	0.46
2:K:180:ALA:O	2:K:192:THR:HA	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:219:THR:HG22	4:N:221:GLU:HG2	1.97	0.46
6:E:85:PHE:CD1	6:E:90:HIS:HA	2.50	0.46
16:F:83:A:H1'	16:F:84:C:H5'	1.97	0.46
27:D:986:LEU:HD21	27:D:1015:MET:HG2	1.97	0.46
20:S:23:LEU:HD23	20:S:24:THR:N	2.30	0.46
33:2:252:PHE:O	33:2:256:ALA:HB2	2.15	0.46
34:3:88:ARG:HH12	34:3:144:TRP:N	2.14	0.46
34:3:1046:GLY:O	34:3:1073:LYS:HA	2.16	0.46
34:3:1171:ILE:O	34:3:1174:GLN:N	2.48	0.46
36:5:41:ARG:HH12	36:5:83:LYS:HZ2	1.62	0.46
1:A:774:ILE:HG23	1:A:777:LYS:HD3	1.97	0.46
2:K:290:ARG:HB3	2:K:292:TRP:NE1	2.29	0.46
18:B:114:G:C2	18:B:115:G:C4	3.03	0.46
27:D:633:ILE:HG21	27:D:636:ILE:HD13	1.98	0.46
27:D:1351:ILE:HB	27:D:1374:THR:HG21	1.97	0.46
27:D:1459:TRP:HE1	27:D:1762:ILE:HD11	1.81	0.46
27:D:1902:LEU:HB3	27:D:1928:LEU:HD12	1.98	0.46
28:G:490:A:H2'	28:G:491:C:C6	2.51	0.46
29:H:120:G:H4'	29:H:121:C:O4'	2.15	0.46
29:H:680:C:H2'	29:H:681:C:C6	2.49	0.46
29:H:690:U:H2'	29:H:691:G:H8	1.81	0.46
32:1:565:LEU:O	32:1:569:PHE:CB	2.63	0.46
32:1:624:CYS:O	32:1:628:ILE:HG12	2.15	0.46
32:1:935:TRP:CZ3	37:6:22:GLY:HA3	2.51	0.46
33:2:163:ILE:O	33:2:169:VAL:HG21	2.14	0.46
34:3:186:ARG:HB2	34:3:207:VAL:HG23	1.97	0.46
34:3:678:LYS:H	34:3:694:ALA:HB3	1.80	0.46
34:3:1116:ARG:HH12	34:3:1189:LEU:HD13	1.79	0.46
1:A:354:PRO:O	1:A:355:LEU:HB3	2.16	0.46
1:A:1014:LYS:HD3	1:A:1144:PHE:CE1	2.51	0.46
3:L:131:ILE:HD11	3:L:175:LEU:HD11	1.98	0.46
5:J:408:LEU:O	5:J:415:ILE:N	2.48	0.46
17:I:90:C:N3	22:Q:34:PRO:CD	2.78	0.46
27:D:496:THR:O	27:D:497:THR:OG1	2.30	0.46
27:D:809:THR:HA	27:D:1092:PHE:CG	2.50	0.46
27:D:1194:ASP:HB3	27:D:1198:ARG:NH1	2.30	0.46
27:D:1496:ILE:HD12	27:D:1524:TRP:CZ3	2.50	0.46
21:P:33:GLN:O	21:P:45:LEU:HA	2.16	0.46
22:Q:18:GLU:O	22:Q:93:ARG:HB3	2.15	0.46
28:G:488:A:H2'	28:G:489:A:H8	1.80	0.46
29:H:544:G:H2'	29:H:545:G:H8	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:559:G:H2'	29:H:560:G:H8	1.81	0.46
29:H:567:U:H2'	29:H:568:U:C6	2.50	0.46
29:H:669:U:H2'	29:H:670:U:C6	2.49	0.46
29:H:691:G:H2'	29:H:692:U:C6	2.50	0.46
34:3:68:GLN:HE21	34:3:1222:GLN:HG2	1.79	0.46
34:3:1118:VAL:HG12	34:3:1139:TRP:HZ2	1.81	0.46
34:3:1124:LEU:HB2	34:3:1130:ILE:CD1	2.45	0.46
38:X:32:TYR:CE1	38:X:78:LYS:HD3	2.50	0.46
1:A:563:ASP:OD1	1:A:564:TRP:N	2.49	0.46
1:A:928:ARG:NH2	4:N:145:THR:OG1	2.44	0.46
1:A:2319:LYS:HG3	1:A:2320:ASP:H	1.79	0.46
7:M:51:PHE:CE1	7:M:53:ILE:HD11	2.51	0.46
8:C:292:ILE:HA	8:C:295:ILE:HG12	1.97	0.46
8:C:331:TYR:CE1	8:C:404:PHE:HD1	2.34	0.46
16:F:15:A:H2'	16:F:16:C:H6	1.81	0.46
27:D:1631:ALA:HB3	27:D:1632:PRO:HD3	1.98	0.46
29:H:562:A:H2'	29:H:563:G:H8	1.81	0.46
29:H:688:A:H2'	29:H:689:G:H8	1.81	0.46
29:H:1152:U:H2'	29:H:1153:C:H6	1.80	0.46
32:1:327:TRP:CZ2	32:1:369:PRO:HG2	2.49	0.46
32:1:565:LEU:O	32:1:569:PHE:HB2	2.16	0.46
32:1:806:THR:HB	33:2:211:THR:HG21	1.98	0.46
33:2:271:TYR:CZ	33:2:274:ARG:HB2	2.51	0.46
34:3:71:PHE:HD1	34:3:97:THR:CG2	2.28	0.46
1:A:318:LEU:HD23	1:A:501:LEU:HD23	1.98	0.46
1:A:616:GLY:O	1:A:619:PHE:HB3	2.15	0.46
2:K:322:VAL:HB	2:K:336:ILE:HD11	1.98	0.46
4:N:778:ILE:HG23	4:N:794:PHE:HE1	1.81	0.46
8:C:605:ILE:HD11	8:C:673:PRO:HA	1.98	0.46
28:G:481:A:H61	35:4:86:VAL:HB	1.80	0.46
32:1:195:PHE:HB2	32:1:200:ILE:HD11	1.98	0.46
32:1:286:ILE:HG23	32:1:332:THR:OG1	2.16	0.46
32:1:439:MET:HA	32:1:442:ILE:HD12	1.98	0.46
32:1:698:ARG:HG3	32:1:699:LYS:N	2.31	0.46
34:3:78:HIS:O	34:3:146:THR:HG22	2.16	0.46
38:X:82:GLN:HB3	39:Y:168:GLN:NE2	2.31	0.46
39:Y:223:ARG:HG3	39:Y:242:GLU:OE2	2.16	0.46
2:K:64:VAL:HG12	2:K:65:GLU:N	2.31	0.46
2:K:395:ILE:HD11	7:M:123:THR:HG23	1.98	0.46
8:C:272:ARG:HG3	8:C:276:ASP:OD2	2.16	0.46
8:C:471:HIS:HB2	8:C:592:PHE:CE2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:772:ASN:ND2	8:C:816:VAL:H	2.14	0.46
19:O:212:VAL:HG23	19:O:213:SER:H	1.80	0.46
27:D:1217:ARG:HH12	22:Q:146:LEU:HD23	1.80	0.46
27:D:1564:LEU:HD21	27:D:1597:ALA:HB1	1.98	0.46
27:D:1587:SER:HB3	27:D:1895:ARG:CZ	2.45	0.46
26:V:15:ILE:HG22	26:V:73:ALA:HA	1.97	0.46
29:H:1139:G:C6	29:H:1140:U:C4	3.04	0.46
32:1:484:PHE:HA	32:1:488:TRP:CD1	2.48	0.46
34:3:732:ARG:NH2	34:3:737:GLY:O	2.49	0.46
39:Y:209:LEU:HD12	39:Y:209:LEU:C	2.36	0.46
1:A:248:PRO:HD3	1:A:595:TYR:CE1	2.50	0.46
1:A:460:PRO:HD3	8:C:354:TYR:OH	2.16	0.46
1:A:1711:VAL:HG12	1:A:1712:SER:N	2.30	0.46
1:A:1762:ASP:OD1	1:A:1763:ASN:N	2.49	0.46
2:K:291:LEU:HB3	2:K:301:LEU:HB3	1.97	0.46
3:L:289:ASP:HB3	3:L:293:LYS:HE3	1.98	0.46
8:C:315:SER:HB3	8:C:320:PHE:CE2	2.51	0.46
8:C:474:LYS:HZ3	8:C:630:PRO:HD3	1.81	0.46
16:F:26:A:H2'	16:F:27:U:H6	1.80	0.46
17:I:99:G:H4'	27:D:1186:GLU:CB	2.23	0.46
27:D:1999:HIS:ND1	27:D:1999:HIS:O	2.49	0.46
27:D:2055:TYR:CE2	27:D:2158:PHE:CD2	3.04	0.46
22:Q:46:THR:OG1	22:Q:79:ILE:HG12	2.16	0.46
29:H:545:G:H2'	29:H:546:U:C6	2.50	0.46
29:H:553:G:H2'	29:H:554:C:C6	2.50	0.46
29:H:673:U:H2'	29:H:674:G:H8	1.81	0.46
29:H:1165:C:C2	29:H:1166:G:N7	2.83	0.46
32:1:430:TYR:HB3	32:1:434:TYR:CE2	2.50	0.46
34:3:156:ASN:ND2	34:3:178:PRO:HA	2.29	0.46
34:3:369:ILE:HG23	34:3:419:LEU:HB2	1.98	0.46
1:A:171:ALA:HB2	1:A:201:PHE:CD1	2.51	0.45
1:A:867:ILE:HD13	1:A:1101:TYR:CD1	2.51	0.45
1:A:1050:LEU:CD2	1:A:1248:VAL:HG22	2.44	0.45
1:A:1733:TRP:CZ2	1:A:1772:GLY:HA3	2.51	0.45
2:K:393:ARG:HB2	5:J:429:GLU:HG2	1.98	0.45
7:M:113:GLN:NE2	16:F:77:G:H4'	2.29	0.45
8:C:331:TYR:OH	8:C:428:ILE:O	2.34	0.45
8:C:613:ARG:NH1	8:C:614:GLU:OE2	2.49	0.45
16:F:15:A:H2'	16:F:16:C:C6	2.51	0.45
16:F:92:C:H2'	16:F:93:A:C8	2.45	0.45
17:I:78:A:N1	27:D:1110:ARG:NE	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:B:22:G:O6	18:B:149:U:O4	2.34	0.45
18:B:75:A:N6	18:B:77:A:N1	2.65	0.45
18:B:135:G:N1	18:B:136:G:N2	2.64	0.45
27:D:929:ILE:HD13	27:D:935:ALA:HA	1.99	0.45
27:D:1371:GLY:O	27:D:1376:LYS:NZ	2.40	0.45
27:D:1888:GLU:HB3	27:D:1953:LYS:HG2	1.97	0.45
28:G:502:C:OP2	32:1:775:ARG:NH1	2.31	0.45
29:H:555:A:H2'	29:H:556:A:H8	1.82	0.45
29:H:1126:G:O2'	29:H:1127:A:H8	1.97	0.45
32:1:760:HIS:HB3	33:2:240:LEU:HD12	1.97	0.45
32:1:866:LEU:HD21	36:5:79:LEU:HD21	1.98	0.45
34:3:1097:PHE:CE1	34:3:1108:PRO:HB3	2.48	0.45
34:3:1356:VAL:HA	34:3:1360:TYR:CD2	2.51	0.45
39:Y:208:SER:CB	39:Y:214:LEU:HD12	2.45	0.45
1:A:2199:VAL:HG23	1:A:2200:LYS:HG3	1.98	0.45
8:C:866:ILE:HG23	8:C:918:LEU:HD21	1.98	0.45
27:D:610:GLU:OE2	27:D:646:VAL:HG21	2.17	0.45
27:D:765:ASN:HB2	27:D:768:HIS:CD2	2.51	0.45
27:D:1482:GLY:HA3	22:Q:143:ARG:O	2.15	0.45
27:D:1677:THR:O	27:D:1710:ALA:HA	2.15	0.45
27:D:1722:ILE:HG22	27:D:1724:THR:OG1	2.16	0.45
27:D:1757:GLU:CB	27:D:1763:ILE:HD12	2.46	0.45
27:D:1772:TRP:CZ3	27:D:1773:PHE:CZ	3.03	0.45
23:R:66:ASN:OD1	23:R:98:GLY:N	2.50	0.45
20:S:22:GLU:HG2	20:S:70:LYS:HD2	1.97	0.45
29:H:548:G:H2'	29:H:549:C:C6	2.50	0.45
29:H:564:U:H2'	29:H:565:U:C6	2.50	0.45
29:H:570:G:H2'	29:H:571:A:H8	1.82	0.45
29:H:670:U:H2'	29:H:671:G:H8	1.81	0.45
29:H:685:U:H2'	29:H:686:G:H8	1.81	0.45
32:1:221:MET:O	32:1:224:THR:OG1	2.24	0.45
32:1:843:GLU:OE1	32:1:879:HIS:NE2	2.49	0.45
34:3:153:ASP:O	34:3:154:SER:OG	2.21	0.45
34:3:333:ASN:O	34:3:350:ILE:HG22	2.17	0.45
38:X:11:GLU:HG2	38:X:16:ILE:CG2	2.46	0.45
1:A:2162:LEU:HD23	1:A:2194:ILE:O	2.16	0.45
4:N:771:ALA:HB3	4:N:806:ARG:HH21	1.81	0.45
5:J:443:LYS:HG2	5:J:444:VAL:N	2.30	0.45
6:E:112:GLU:HG2	6:E:135:TYR:CE2	2.51	0.45
8:C:869:HIS:CD2	8:C:925:LEU:HB3	2.51	0.45
18:B:94:C:H3'	18:B:95:C:H4'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1165:VAL:HG13	27:D:1166:PRO:HD2	1.98	0.45
27:D:1625:THR:OG1	27:D:1648:ASP:HB2	2.17	0.45
27:D:2011:ILE:CD1	27:D:2030:ILE:HD11	2.46	0.45
21:P:21:ARG:HB2	21:P:98:GLU:OE1	2.16	0.45
20:S:20:SER:OG	20:S:73:VAL:HB	2.16	0.45
29:H:554:C:H2'	29:H:555:A:H8	1.82	0.45
29:H:672:U:H2'	29:H:673:U:C6	2.50	0.45
29:H:694:C:H2'	29:H:695:U:C6	2.50	0.45
32:1:489:VAL:CG1	38:X:26:GLU:CG	2.94	0.45
34:3:294:PHE:CE2	34:3:365:ILE:HB	2.51	0.45
34:3:932:PHE:HA	34:3:984:ILE:HD11	1.98	0.45
34:3:977:ILE:HG12	34:3:1004:LEU:HD22	1.99	0.45
1:A:620:HIS:HB3	1:A:669:TYR:CD2	2.51	0.45
1:A:1014:LYS:HD2	1:A:1014:LYS:HA	1.58	0.45
1:A:1049:LEU:HB2	1:A:1249:SER:OG	2.16	0.45
1:A:1105:ARG:HD2	1:A:1517:TYR:CE1	2.51	0.45
1:A:1169:TYR:CE2	1:A:1262:MET:HG2	2.52	0.45
4:N:144:LYS:O	4:N:145:THR:OG1	2.30	0.45
8:C:251:GLN:HE22	8:C:254:LYS:HD3	1.81	0.45
8:C:605:ILE:HG13	8:C:652:MET:CE	2.42	0.45
8:C:769:TYR:HA	8:C:800:TYR:HE1	1.80	0.45
16:F:16:C:O2'	16:F:17:U:O5'	2.35	0.45
23:R:38:MET:HG3	23:R:39:VAL:N	2.30	0.45
29:H:568:U:H2'	29:H:569:C:C6	2.50	0.45
29:H:683:U:H2'	29:H:684:U:C6	2.50	0.45
29:H:692:U:H2'	29:H:693:C:C6	2.50	0.45
32:1:591:ASP:OD1	32:1:592:ILE:HD12	2.17	0.45
33:2:166:THR:HG22	33:2:167:LYS:H	1.82	0.45
1:A:234:PHE:HD2	1:A:699:PRO:HB2	1.81	0.45
1:A:454:LEU:HD11	8:C:340:LYS:HG3	1.98	0.45
1:A:537:THR:HG21	18:B:84:A:H62	1.82	0.45
1:A:939:LEU:HD21	3:L:441:MET:HE2	1.98	0.45
1:A:1317:ARG:HE	1:A:1366:ARG:NH1	2.15	0.45
18:B:75:A:N6	18:B:77:A:C6	2.85	0.45
27:D:1436:LEU:HD22	27:D:1462:ARG:NH2	2.31	0.45
27:D:1453:GLU:OE2	27:D:1494:ARG:NH2	2.42	0.45
21:P:28:ARG:NH1	20:S:22:GLU:OE2	2.48	0.45
22:Q:4:VAL:HG12	22:Q:8:LYS:HZ2	1.80	0.45
26:V:47:ASN:OD1	26:V:51:PRO:HD2	2.17	0.45
26:V:59:LEU:O	26:V:60:GLN:HG2	2.16	0.45
28:G:520:G:C4	38:X:34:TYR:CZ	3.03	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:1139:G:H2'	29:H:1140:U:C5	2.51	0.45
32:1:835:ILE:O	32:1:838:ILE:N	2.32	0.45
34:3:641:GLN:NE2	34:3:705:LEU:HD23	2.31	0.45
34:3:1198:ILE:O	34:3:1221:LEU:N	2.50	0.45
35:4:171:GLN:O	35:4:178:ILE:HG12	2.17	0.45
1:A:221:TRP:CB	1:A:318:LEU:HD11	2.46	0.45
1:A:283:SER:O	1:A:285:PRO:HD3	2.17	0.45
1:A:2183:TYR:CE1	1:A:2219:LYS:HG3	2.51	0.45
1:A:2189:LEU:HD11	1:A:2347:GLY:HA3	1.99	0.45
4:N:256:LYS:HG2	4:N:257:PHE:N	2.32	0.45
4:N:760:VAL:O	4:N:764:LEU:HB3	2.16	0.45
8:C:183:GLN:HE21	8:C:657:TYR:HB3	1.80	0.45
27:D:766:ILE:HD12	27:D:769:LYS:HZ1	1.81	0.45
27:D:1880:LEU:HD21	27:D:1931:GLN:HE21	1.81	0.45
27:D:2101:LEU:O	27:D:2114:ILE:HA	2.16	0.45
24:T:80:ILE:HG23	25:U:80:TYR:HB2	1.98	0.45
32:1:590:LEU:HD11	32:1:594:MET:HE1	1.97	0.45
34:3:487:SER:O	34:3:1200:THR:HG21	2.16	0.45
34:3:600:ILE:HG13	34:3:608:ARG:O	2.16	0.45
34:3:1302:ARG:NH2	34:3:1307:TYR:HA	2.32	0.45
35:4:13:VAL:HG21	35:4:55:ILE:HD12	1.98	0.45
37:6:47:SER:O	37:6:51:GLU:HG2	2.17	0.45
38:X:89:VAL:HG21	38:X:106:HIS:CD2	2.51	0.45
1:A:140:ARG:NH2	1:A:252:GLU:HB2	2.29	0.45
1:A:364:TYR:HB2	1:A:1214:ARG:HG2	1.99	0.45
1:A:518:VAL:HG12	1:A:685:HIS:HB3	1.99	0.45
1:A:660:ILE:HD12	1:A:711:TRP:CE2	2.52	0.45
1:A:1047:ALA:HA	1:A:1172:PHE:O	2.17	0.45
1:A:1667:GLN:CD	19:O:211:ASN:OD1	2.52	0.45
1:A:2003:THR:HA	1:A:2006:SER:OG	2.16	0.45
4:N:124:ASP:OD1	4:N:125:ALA:N	2.48	0.45
8:C:193:LEU:HD23	8:C:224:GLU:HB3	1.98	0.45
16:F:96:G:H2'	16:F:97:A:C8	2.51	0.45
18:B:73:U:H2'	18:B:74:U:C6	2.51	0.45
27:D:452:SER:HB2	27:D:466:PRO:HG3	1.99	0.45
27:D:766:ILE:HD12	27:D:769:LYS:NZ	2.31	0.45
27:D:1933:TYR:OH	27:D:2091:TYR:HB2	2.16	0.45
22:Q:107:LEU:HD12	23:R:59:LYS:HE3	1.99	0.45
29:H:546:U:H2'	29:H:547:G:H8	1.81	0.45
29:H:549:C:H2'	29:H:550:G:H8	1.81	0.45
29:H:681:C:H2'	29:H:682:U:C6	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1:835:ILE:HG23	32:1:864:LEU:HD21	1.99	0.45
1:A:796:ASN:ND2	1:A:858:LYS:HG2	2.26	0.45
1:A:1575:TRP:N	3:L:391:MET:O	2.28	0.45
1:A:2192:LYS:HE3	1:A:2379:PRO:HG2	1.97	0.45
4:N:277:ILE:H	4:N:277:ILE:HD12	1.82	0.45
4:N:815:PHE:HB2	4:N:824:SER:HB3	1.99	0.45
8:C:452:LYS:HZ2	8:C:487:ARG:HH12	1.65	0.45
8:C:778:THR:OG1	8:C:780:PRO:HD2	2.16	0.45
17:I:33:A:H2'	17:I:34:G:O4'	2.17	0.45
18:B:65:U:H2'	18:B:66:A:H8	1.81	0.45
18:B:83:C:H4'	18:B:84:A:OP1	2.16	0.45
18:B:164:C:OP2	18:B:165:A:OP1	2.34	0.45
27:D:820:PHE:HB2	27:D:825:LEU:HD12	1.99	0.45
27:D:1163:SER:HB2	27:D:1184:ARG:HH22	1.82	0.45
22:Q:9:LYS:HD3	22:Q:106:LEU:HD22	1.99	0.45
22:Q:16:THR:HA	22:Q:25:VAL:O	2.16	0.45
29:H:563:G:H2'	29:H:564:U:C6	2.50	0.45
29:H:569:C:H2'	29:H:570:G:H8	1.81	0.45
29:H:674:G:H2'	29:H:675:A:H8	1.81	0.45
32:1:346:ILE:O	32:1:349:LEU:HG	2.16	0.45
32:1:462:GLN:HE21	32:1:504:TYR:HE2	1.63	0.45
39:Y:167:VAL:O	39:Y:171:GLY:HA2	2.17	0.45
39:Y:213:LYS:C	39:Y:230:SER:OG	2.55	0.45
39:Y:220:PRO:HG3	39:Y:236:HIS:CE1	2.51	0.45
1:A:218:SER:HA	1:A:318:LEU:HD13	1.99	0.45
1:A:700:GLY:O	1:A:701:CYS:HB3	2.17	0.45
1:A:939:LEU:HD11	3:L:441:MET:HE2	1.97	0.45
1:A:984:VAL:HG12	1:A:985:ASP:H	1.82	0.45
1:A:1126:LEU:HD13	1:A:1134:LEU:HD12	1.98	0.45
1:A:1345:TYR:HD2	1:A:1346:PHE:CE1	2.34	0.45
1:A:1699:ALA:HB1	1:A:1733:TRP:HB2	1.98	0.45
1:A:1715:SER:O	1:A:1787:TYR:HA	2.16	0.45
1:A:1962:ARG:CD	19:O:186:GLU:CD	2.82	0.45
2:K:128:SER:CB	2:K:337:ARG:HH21	2.29	0.45
2:K:373:ILE:HB	2:K:389:ILE:HB	1.99	0.45
5:J:347:LEU:HD23	5:J:371:ARG:NH2	2.31	0.45
8:C:171:GLY:HA3	8:C:422:LYS:NZ	2.32	0.45
8:C:866:ILE:HA	8:C:927:MET:O	2.16	0.45
8:C:876:VAL:HA	8:C:879:LEU:HD12	1.99	0.45
18:B:10:U:H1'	18:B:156:G:H22	1.82	0.45
27:D:508:HIS:O	27:D:512:GLU:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1014:SER:OG	27:D:1039:GLU:HB3	2.16	0.45
22:Q:44:LYS:HB2	22:Q:79:ILE:CG2	2.46	0.45
29:H:558:A:H2'	29:H:559:G:H8	1.81	0.45
29:H:675:A:H2'	29:H:676:U:C6	2.50	0.45
34:3:162:ILE:HG22	34:3:171:LEU:CD1	2.46	0.45
34:3:582:LYS:N	34:3:601:GLN:OE1	2.50	0.45
1:A:416:GLU:HG2	1:A:418:ASP:H	1.82	0.45
1:A:535:HIS:NE2	18:B:105:A:OP1	2.43	0.45
1:A:1098:VAL:HG23	3:L:276:GLU:OE1	2.17	0.45
1:A:1833:PRO:HD3	3:L:383:HIS:CE1	2.52	0.45
1:A:2310:GLU:OE1	1:A:2333:PHE:HZ	1.94	0.45
1:A:2398:LEU:CD2	27:D:1060:LYS:HB2	2.28	0.45
3:L:124:PHE:CD2	3:L:127:LEU:HB2	2.51	0.45
4:N:244:TRP:CE3	4:N:267:GLY:HA3	2.52	0.45
4:N:762:GLN:O	4:N:765:GLN:HG2	2.17	0.45
6:E:95:PHE:HB3	6:E:137:TYR:HE2	1.80	0.45
6:E:103:LEU:HD11	6:E:105:PHE:CE2	2.52	0.45
8:C:681:CYS:HA	8:C:855:PRO:HA	1.99	0.45
8:C:856:ILE:HA	8:C:944:VAL:CG1	2.47	0.45
17:I:143:A:N7	25:U:48:TYR:CE2	2.85	0.45
18:B:93:G:H5'	18:B:94:C:OP2	2.17	0.45
27:D:1403:GLU:HG2	27:D:1642:LYS:NZ	2.32	0.45
27:D:1411:ASP:O	27:D:1415:ARG:HG2	2.17	0.45
27:D:2063:LEU:HD13	27:D:2160:ILE:HB	1.99	0.45
23:R:48:LEU:HD11	23:R:54:ILE:HD12	1.98	0.45
23:R:67:MET:HE2	23:R:69:LEU:HD21	1.98	0.45
29:H:547:G:H2'	29:H:548:G:H8	1.81	0.45
29:H:550:G:H2'	29:H:551:C:C6	2.50	0.45
29:H:556:A:H2'	29:H:557:G:H8	1.81	0.45
29:H:1150:U:C6	29:H:1150:U:OP2	2.70	0.45
34:3:119:ASN:HB2	34:3:1325:ASN:HD21	1.82	0.45
34:3:854:ASN:HB3	34:3:857:VAL:H	1.82	0.45
34:3:1294:GLU:HG3	36:5:41:ARG:HG2	1.98	0.45
38:X:16:ILE:CG2	38:X:17:LEU:N	2.80	0.45
38:X:57:PRO:HG2	39:Y:231:ARG:NH2	2.27	0.45
1:A:1088:VAL:HG12	1:A:1089:VAL:N	2.22	0.44
1:A:1657:ILE:HG12	1:A:1811:ALA:HB1	1.99	0.44
3:L:447:GLU:O	3:L:450:GLN:HG2	2.17	0.44
4:N:241:PRO:HA	4:N:244:TRP:HD1	1.81	0.44
5:J:249:ARG:HD3	17:I:10:C:OP1	2.17	0.44
7:M:54:MET:HB2	7:M:80:PHE:CD1	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:402:SER:O	8:C:405:ARG:NH1	2.50	0.44
18:B:79:C:N4	18:B:114:G:O6	2.50	0.44
18:B:162:G:OP1	18:B:163:C:C6	2.70	0.44
18:B:166:U:C6	18:B:166:U:OP1	2.70	0.44
27:D:981:LEU:HD23	27:D:986:LEU:HD12	1.99	0.44
27:D:1000:ASP:N	27:D:1000:ASP:OD1	2.50	0.44
21:P:39:LYS:HD2	21:P:39:LYS:HA	1.48	0.44
23:R:44:VAL:O	23:R:55:ILE:HD12	2.17	0.44
24:T:29:ILE:HD11	24:T:87:ILE:HA	1.98	0.44
29:H:676:U:H2'	29:H:677:U:C6	2.50	0.44
32:1:244:LEU:O	32:1:248:ALA:HB2	2.18	0.44
34:3:508:ASN:ND2	34:3:924:PHE:O	2.48	0.44
34:3:528:PRO:HG2	34:3:554:PHE:CZ	2.51	0.44
1:A:208:VAL:HB	1:A:213:TYR:HB2	1.99	0.44
1:A:209:ILE:HG21	1:A:303:PHE:CE2	2.53	0.44
1:A:1774:MET:O	1:A:1786:ALA:HA	2.16	0.44
1:A:1794:LEU:O	1:A:1798:ILE:N	2.36	0.44
1:A:2010:LEU:HD21	1:A:2083:ILE:HD13	1.98	0.44
1:A:2395:PHE:HD1	27:D:1060:LYS:C	2.20	0.44
2:K:393:ARG:O	2:K:416:ASP:HB2	2.16	0.44
3:L:343:LYS:NZ	17:I:28:C:OP1	2.50	0.44
8:C:861:ILE:HG23	8:C:906:VAL:O	2.17	0.44
17:I:76:A:C8	27:D:1107:ARG:CZ	3.00	0.44
27:D:491:PHE:HD1	27:D:491:PHE:N	2.16	0.44
27:D:529:ASN:O	27:D:533:LEU:HG	2.17	0.44
27:D:676:ASN:HD22	27:D:907:PRO:HB3	1.82	0.44
27:D:1218:PHE:N	27:D:1218:PHE:CD1	2.85	0.44
27:D:1610:LEU:HD23	27:D:1612:VAL:HB	1.99	0.44
24:T:34:GLN:O	26:V:23:ARG:NH2	2.51	0.44
28:G:489:A:H2'	28:G:490:A:C8	2.52	0.44
32:1:567:ILE:O	32:1:570:GLN:HG2	2.17	0.44
34:3:61:TYR:CE2	34:3:63:LEU:HD11	2.52	0.44
34:3:177:GLN:HE22	36:5:44:ARG:HD3	1.83	0.44
34:3:523:ILE:HD11	34:3:873:ILE:HG13	1.98	0.44
34:3:564:ASP:OD1	34:3:565:ASN:N	2.48	0.44
1:A:326:ASN:ND2	1:A:407:VAL:HG22	2.32	0.44
1:A:802:PRO:O	1:A:804:MET:HG2	2.17	0.44
1:A:1336:ASN:HD21	1:A:1399:MET:HA	1.82	0.44
1:A:1859:ARG:NH2	19:O:161:ILE:HD13	2.32	0.44
1:A:2241:ILE:HD12	1:A:2284:LYS:HD3	1.98	0.44
1:A:2398:LEU:CD1	27:D:1060:LYS:HZ2	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:182:SER:HA	2:K:444:ASP:OD2	2.18	0.44
2:K:220:LYS:O	2:K:239:GLU:N	2.51	0.44
2:K:393:ARG:NH1	5:J:427:THR:O	2.50	0.44
3:L:120:TYR:OH	3:L:141:ILE:HG23	2.18	0.44
3:L:143:ILE:HD11	3:L:164:LYS:HD2	1.99	0.44
4:N:286:GLU:CG	4:N:287:SER:H	2.30	0.44
8:C:507:SER:HB2	8:C:591:PHE:HB2	2.00	0.44
8:C:697:ARG:HH22	8:C:848:VAL:HG12	1.83	0.44
18:B:97:U:H2'	18:B:98:U:H6	1.82	0.44
27:D:602:THR:HG22	27:D:603:GLN:N	2.33	0.44
27:D:1120:GLY:HA2	27:D:1251:ILE:HB	1.98	0.44
27:D:1537:PRO:O	27:D:1540:ARG:NH1	2.50	0.44
23:R:30:PRO:HA	25:U:52:GLN:HB2	1.99	0.44
29:H:51:C:H2'	29:H:52:A:H8	1.83	0.44
29:H:149:A:H2'	29:H:150:G:H8	1.82	0.44
29:H:557:G:H2'	29:H:558:A:H8	1.82	0.44
29:H:560:G:H2'	29:H:561:A:H8	1.82	0.44
29:H:561:A:H2'	29:H:562:A:H8	1.81	0.44
29:H:687:A:H2'	29:H:688:A:H8	1.82	0.44
34:3:1085:LEU:HB2	34:3:1097:PHE:HB2	1.99	0.44
1:A:372:ARG:O	8:C:973:ARG:NH2	2.50	0.44
1:A:553:ASN:OD1	1:A:554:THR:N	2.47	0.44
1:A:632:ILE:O	1:A:635:THR:OG1	2.26	0.44
1:A:1393:GLU:HG3	3:L:391:MET:SD	2.57	0.44
4:N:290:HIS:O	4:N:294:THR:HG23	2.18	0.44
8:C:318:LEU:HB3	8:C:425:LEU:HD12	1.98	0.44
8:C:508:GLU:OE2	8:C:594:PRO:HG2	2.18	0.44
18:B:10:U:H1'	18:B:156:G:N2	2.33	0.44
19:O:194:LEU:HD13	19:O:197:ARG:HH11	1.78	0.44
27:D:499:LEU:HD23	27:D:503:GLN:HB3	2.00	0.44
27:D:644:GLY:N	27:D:645:PRO:HD2	2.33	0.44
27:D:845:VAL:HG21	27:D:874:ARG:O	2.16	0.44
27:D:1377:THR:O	27:D:1381:GLU:HG3	2.17	0.44
21:P:89:GLY:O	21:P:92:ILE:HG22	2.17	0.44
34:3:75:CYS:SG	34:3:94:CYS:HB3	2.57	0.44
34:3:704:SER:HB3	34:3:716:ILE:HD11	2.00	0.44
38:X:110:ARG:HE	38:X:110:ARG:HB3	1.61	0.44
1:A:342:LEU:HD22	1:A:392:ASN:HD21	1.83	0.44
1:A:2318:ASN:HB3	1:A:2322:MET:HG3	1.99	0.44
3:L:113:HIS:CE1	3:L:117:ILE:HD11	2.52	0.44
8:C:218:HIS:HB3	8:C:221:PHE:HD2	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:251:GLN:NE2	8:C:254:LYS:HD3	2.32	0.44
18:B:17:C:O2'	18:B:18:A:OP2	2.29	0.44
27:D:536:LEU:HD23	27:D:536:LEU:HA	1.69	0.44
27:D:617:ARG:HD3	27:D:1006:SER:OG	2.18	0.44
27:D:723:ASN:HB3	27:D:756:TRP:NE1	2.33	0.44
27:D:1541:ILE:H	27:D:1541:ILE:HG13	1.65	0.44
28:G:506:U:P	32:1:698:ARG:HD3	2.58	0.44
29:H:141:A:H2'	29:H:142:C:C6	2.52	0.44
32:1:489:VAL:HG13	38:X:26:GLU:CG	2.48	0.44
32:1:531:GLU:HA	32:1:534:ARG:HE	1.82	0.44
34:3:75:CYS:HB2	34:3:129:SER:OG	2.18	0.44
34:3:175:VAL:HG11	34:3:224:ILE:HD12	1.99	0.44
1:A:591:LEU:HB3	1:A:599:LEU:HD11	2.00	0.44
1:A:953:ARG:HG2	1:A:957:TYR:CE2	2.52	0.44
1:A:1414:TRP:CB	1:A:1558:GLU:HG3	2.48	0.44
1:A:1490:ARG:HA	1:A:1490:ARG:HD3	1.83	0.44
2:K:304:GLU:HG2	2:K:305:GLY:H	1.83	0.44
8:C:683:ASN:ND2	8:C:712:ALA:O	2.39	0.44
17:I:23:C:H2'	17:I:24:A:C8	2.53	0.44
27:D:1751:HIS:NE2	27:D:1813:ASP:OD2	2.50	0.44
27:D:2054:THR:OG1	27:D:2074:GLN:HB3	2.16	0.44
28:G:488:A:H2'	28:G:489:A:C8	2.52	0.44
32:1:198:GLU:HG2	32:1:239:TYR:OH	2.18	0.44
32:1:728:CYS:SG	32:1:753:ILE:HG21	2.57	0.44
34:3:477:ILE:O	34:3:479:SER:N	2.50	0.44
1:A:670:LYS:O	1:A:673:VAL:HG12	2.18	0.44
1:A:1317:ARG:HE	1:A:1366:ARG:HH12	1.65	0.44
1:A:1440:ILE:O	1:A:1443:TYR:N	2.45	0.44
1:A:1477:PHE:O	1:A:1481:GLU:N	2.51	0.44
1:A:1603:ASN:O	1:A:1607:THR:HG23	2.17	0.44
1:A:2349:PHE:CE2	1:A:2379:PRO:HG3	2.52	0.44
2:K:433:LEU:HB3	2:K:464:TRP:CZ3	2.52	0.44
8:C:385:PHE:HE1	8:C:425:LEU:HD11	1.83	0.44
8:C:497:ASP:O	8:C:538:GLU:HA	2.18	0.44
18:B:84:A:H2'	18:B:85:U:C6	2.51	0.44
27:D:758:LYS:O	27:D:762:ALA:HB3	2.18	0.44
27:D:1163:SER:HB3	27:D:1184:ARG:HH12	1.83	0.44
27:D:1912:ARG:HA	27:D:1912:ARG:HD2	1.67	0.44
28:G:514:U:H4'	28:G:515:U:OP2	2.18	0.44
29:H:9:C:H2'	29:H:10:U:H6	1.83	0.44
32:1:442:ILE:HD11	32:1:460:VAL:CG1	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1:873:HIS:O	32:1:875:ASP:N	2.46	0.44
32:1:889:PHE:CE2	33:2:176:TRP:HB3	2.53	0.44
32:1:962:GLU:HG3	37:6:36:ARG:HD2	1.99	0.44
35:4:171:GLN:HA	35:4:177:ARG:HH11	1.83	0.44
1:A:770:MET:HG2	4:N:119:TRP:CZ3	2.53	0.44
1:A:889:TRP:HA	1:A:1128:GLN:HE22	1.83	0.44
1:A:1678:ILE:HG23	1:A:1704:GLU:O	2.17	0.44
2:K:48:ASP:OD1	2:K:69:VAL:HG21	2.18	0.44
2:K:167:LEU:HD23	2:K:435:GLY:HA3	1.99	0.44
2:K:345:LEU:HD13	2:K:376:TRP:CG	2.53	0.44
5:J:368:LEU:HD13	5:J:370:LEU:HG	1.99	0.44
6:E:43:ASP:O	6:E:47:SER:HB3	2.18	0.44
8:C:312:ILE:HG12	8:C:323:THR:HG22	1.99	0.44
8:C:336:ILE:HB	8:C:337:PRO:HD2	2.00	0.44
16:F:43:C:O2'	16:F:44:A:H8	2.00	0.44
16:F:79:A:H2'	16:F:80:U:H6	1.82	0.44
17:I:76:A:OP1	27:D:608:THR:OG1	2.27	0.44
27:D:1008:PHE:HE2	27:D:1110:ARG:HG3	1.83	0.44
27:D:1473:TYR:CE2	27:D:1492:ILE:HD12	2.52	0.44
27:D:1763:ILE:HD13	27:D:1769:CYS:HA	2.00	0.44
27:D:2007:LYS:O	27:D:2010:GLU:HB3	2.18	0.44
29:H:1099:G:H2'	29:H:1100:A:H8	1.83	0.44
34:3:1258:TYR:CZ	34:3:1262:LYS:HD2	2.53	0.44
1:A:628:MET:SD	1:A:660:ILE:HD13	2.58	0.44
1:A:1023:LEU:HD13	1:A:1451:PHE:CE1	2.53	0.44
1:A:1655:GLN:NE2	1:A:1688:PRO:O	2.50	0.44
1:A:1857:VAL:HG21	1:A:1913:THR:HG21	1.99	0.44
2:K:41:LEU:HD11	2:K:74:ILE:HG12	2.00	0.44
2:K:345:LEU:HD22	2:K:376:TRP:CE3	2.52	0.44
3:L:382:SER:O	3:L:386:GLN:HG3	2.18	0.44
4:N:98:SER:OG	4:N:99:ASN:N	2.48	0.44
8:C:246:THR:HG23	8:C:248:VAL:HG12	1.99	0.44
8:C:799:PHE:HZ	8:C:818:TYR:HD2	1.66	0.44
18:B:43:G:H2'	18:B:44:A:H8	1.81	0.44
27:D:1263:ILE:HD11	27:D:1693:HIS:O	2.18	0.44
27:D:1431:ASP:OD2	27:D:2096:LEU:N	2.37	0.44
22:Q:26:TRP:HE3	22:Q:44:LYS:HG2	1.82	0.44
24:T:10:MET:HA	26:V:30:ARG:C	2.38	0.44
24:T:45:GLY:HA3	25:U:13:VAL:O	2.18	0.44
29:H:684:U:H2'	29:H:685:U:C6	2.50	0.44
29:H:1146:G:HO2'	29:H:1147:A:P	2.37	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:331:PHE:HD2	34:3:334:HIS:NE2	2.15	0.44
34:3:387:ASP:HA	34:3:412:THR:CG2	2.48	0.44
1:A:850:GLY:O	1:A:854:ARG:HG2	2.19	0.43
1:A:909:THR:HG21	4:N:167:GLU:HB3	1.99	0.43
1:A:2398:LEU:HA	27:D:1060:LYS:HZ2	1.82	0.43
2:K:52:ARG:HG3	2:K:62:GLU:HG3	2.00	0.43
3:L:237:ILE:O	3:L:240:GLN:N	2.51	0.43
18:B:14:G:N3	18:B:14:G:H2'	2.33	0.43
18:B:34:C:OP1	18:B:34:C:H4'	2.18	0.43
27:D:578:LEU:HD23	27:D:578:LEU:HA	1.71	0.43
27:D:1220:ILE:HD13	27:D:1241:LEU:HD11	2.00	0.43
27:D:1224:ALA:HB1	27:D:1226:TRP:CZ3	2.53	0.43
27:D:1459:TRP:CZ3	27:D:1502:LEU:HD11	2.53	0.43
27:D:1887:VAL:HG21	22:Q:140:LYS:CD	2.43	0.43
27:D:1897:GLY:O	27:D:1901:LEU:HB2	2.18	0.43
22:Q:30:GLN:NE2	22:Q:84:TYR:HE1	2.16	0.43
20:S:64:VAL:HG23	26:V:70:SER:HB2	2.00	0.43
24:T:81:LEU:HB3	25:U:81:ILE:HG22	1.99	0.43
28:G:483:A:N1	35:4:10:THR:HG21	2.32	0.43
28:G:489:A:H2'	28:G:490:A:H8	1.82	0.43
29:H:68:U:H2'	29:H:69:G:H8	1.82	0.43
34:3:1071:ILE:HG12	34:3:1089:ASP:OD2	2.18	0.43
38:X:33:ILE:CG2	38:X:85:THR:HG23	2.48	0.43
38:X:46:ASP:OD2	40:Z:35:SER:OG	2.34	0.43
38:X:51:PHE:CE1	38:X:92:LEU:HD23	2.53	0.43
38:X:87:LEU:HD21	39:Y:222:ASN:HD21	1.82	0.43
1:A:807:PRO:HB2	4:N:111:LEU:HD23	2.00	0.43
1:A:1169:TYR:CE2	1:A:1262:MET:HE3	2.52	0.43
1:A:1791:PHE:HD2	1:A:1794:LEU:HD11	1.82	0.43
1:A:2029:ASP:HB2	1:A:2032:ILE:HD12	2.00	0.43
3:L:445:ILE:O	3:L:449:ASN:ND2	2.51	0.43
4:N:251:GLU:OE1	4:N:260:ALA:HB2	2.17	0.43
18:B:16:U:H2'	18:B:17:C:O4'	2.18	0.43
27:D:457:LYS:HE3	27:D:462:GLU:OE2	2.17	0.43
29:H:552:U:H2'	29:H:553:G:H8	1.81	0.43
32:1:157:ASN:O	32:1:161:LYS:HG3	2.18	0.43
33:2:141:VAL:HG12	33:2:143:TYR:H	1.83	0.43
34:3:180:THR:HG21	34:3:188:SER:HB2	2.00	0.43
34:3:365:ILE:HG23	34:3:382:GLN:O	2.18	0.43
34:3:770:LEU:HD12	34:3:770:LEU:O	2.18	0.43
39:Y:232:TRP:CZ3	39:Y:234:GLY:HA2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:364:VAL:O	2:K:375:VAL:HA	2.19	0.43
5:J:335:THR:HG23	5:J:336:VAL:N	2.33	0.43
8:C:495:ARG:HG3	8:C:540:GLU:O	2.19	0.43
8:C:677:PHE:HB2	8:C:811:GLU:OE1	2.18	0.43
17:I:51:U:H2'	17:I:52:G:H8	1.83	0.43
18:B:10:U:H2'	18:B:11:A:C8	2.53	0.43
18:B:159:C:O2'	18:B:161:U:OP2	2.19	0.43
27:D:683:PHE:CA	27:D:946:VAL:HG21	2.48	0.43
27:D:707:PHE:CD2	27:D:895:VAL:HG13	2.50	0.43
27:D:1396:VAL:HG12	27:D:1398:ILE:HG13	2.00	0.43
27:D:1917:THR:HG22	27:D:1918:SER:N	2.32	0.43
27:D:1951:LEU:HA	27:D:1954:VAL:HG22	1.99	0.43
32:1:181:ARG:O	32:1:185:MET:HG2	2.19	0.43
32:1:241:HIS:O	32:1:245:VAL:HG23	2.18	0.43
32:1:786:GLY:HA2	32:1:823:MET:HB3	2.00	0.43
34:3:434:ASN:HD21	34:3:504:HIS:CE1	2.36	0.43
1:A:1206:CYS:SG	1:A:1306:GLU:HG3	2.58	0.43
1:A:1935:VAL:HG11	1:A:1940:MET:HB2	2.00	0.43
1:A:1962:ARG:HG3	1:A:2013:ARG:HH12	1.83	0.43
2:K:40:VAL:O	2:K:43:LYS:HG2	2.18	0.43
5:J:163:ASN:C	5:J:165:GLY:H	2.22	0.43
8:C:240:ASP:O	8:C:244:GLY:N	2.45	0.43
18:B:10:U:O2	18:B:11:A:N6	2.51	0.43
18:B:118:U:H2'	18:B:119:U:C6	2.53	0.43
27:D:521:ALA:O	27:D:672:ALA:HA	2.17	0.43
27:D:703:LEU:HD21	27:D:872:LEU:HD23	2.00	0.43
27:D:758:LYS:O	27:D:762:ALA:CB	2.67	0.43
27:D:1204:VAL:O	27:D:1304:ILE:HG21	2.18	0.43
27:D:1621:ILE:HG21	27:D:1633:LEU:HD22	2.01	0.43
27:D:1675:CYS:O	27:D:1677:THR:HG23	2.18	0.43
25:U:33:PHE:N	25:U:33:PHE:CD1	2.86	0.43
29:H:1094:G:H2'	29:H:1095:U:C6	2.54	0.43
32:1:279:LEU:O	32:1:283:ARG:HG3	2.18	0.43
32:1:292:TYR:O	32:1:296:VAL:HG23	2.18	0.43
32:1:698:ARG:HG3	32:1:699:LYS:H	1.82	0.43
32:1:881:MET:O	32:1:884:LEU:N	2.50	0.43
34:3:192:TYR:HB2	34:3:205:SER:OG	2.18	0.43
34:3:542:THR:OG1	34:3:547:ASN:HB2	2.18	0.43
34:3:551:PHE:CD1	34:3:560:ILE:HG12	2.54	0.43
39:Y:222:ASN:OD1	39:Y:223:ARG:N	2.51	0.43
1:A:1343:PHE:HD1	1:A:1350:ILE:HD13	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:218:VAL:HG23	2:K:240:ASP:CG	2.39	0.43
3:L:113:HIS:O	3:L:117:ILE:HD12	2.18	0.43
4:N:803:ASN:O	4:N:834:LYS:NZ	2.45	0.43
8:C:227:VAL:HG13	8:C:473:LEU:HB3	1.99	0.43
8:C:471:HIS:HB2	8:C:592:PHE:CZ	2.54	0.43
8:C:504:THR:HB	8:C:594:PRO:HG3	2.01	0.43
8:C:672:ASP:OD1	8:C:673:PRO:HD2	2.18	0.43
18:B:175:G:H4'	18:B:176:A:O4'	2.18	0.43
27:D:1392:LYS:HB3	27:D:1469:GLU:OE1	2.19	0.43
27:D:1519:ARG:O	27:D:1523:GLU:HG3	2.18	0.43
27:D:1633:LEU:CD1	27:D:1652:VAL:HG22	2.48	0.43
27:D:1694:LYS:HG2	27:D:1695:TYR:N	2.33	0.43
27:D:1992:ASN:HD21	27:D:1994:LEU:HB2	1.82	0.43
26:V:18:ASN:O	26:V:69:ILE:HB	2.19	0.43
29:H:1138:G:C6	29:H:1139:G:O6	2.71	0.43
32:1:191:LYS:HE3	32:1:194:THR:HG21	2.00	0.43
32:1:793:GLY:HA2	32:1:794:PRO:HD3	1.88	0.43
1:A:1063:PHE:O	1:A:1066:LEU:N	2.51	0.43
1:A:2006:SER:O	1:A:2009:THR:OG1	2.35	0.43
1:A:2050:THR:O	1:A:2053:SER:OG	2.31	0.43
4:N:826:LYS:O	4:N:830:ARG:HB2	2.19	0.43
8:C:103:HIS:O	8:C:107:THR:HG23	2.19	0.43
8:C:861:ILE:HG21	8:C:905:GLN:HB3	1.99	0.43
18:B:9:U:H2'	18:B:10:U:O4'	2.19	0.43
18:B:13:A:C2	18:B:14:G:H1'	2.53	0.43
18:B:175:G:C2	18:B:176:A:N6	2.84	0.43
27:D:468:PRO:HD2	27:D:702:PRO:HB2	2.01	0.43
27:D:682:ARG:CZ	27:D:946:VAL:HG13	2.49	0.43
27:D:1402:GLY:HA2	27:D:1405:ILE:HD12	2.00	0.43
27:D:1497:PHE:HD1	27:D:1775:TYR:CE2	2.36	0.43
27:D:2077:ARG:NH1	27:D:2081:PRO:HG3	2.34	0.43
20:S:34:VAL:HG23	20:S:45:ARG:HG3	2.01	0.43
29:H:1094:G:H2'	29:H:1095:U:H6	1.83	0.43
33:2:364:PHE:CE2	34:3:1124:LEU:HD11	2.54	0.43
34:3:519:TYR:CE1	34:3:874:GLY:HA3	2.53	0.43
34:3:945:HIS:CE1	34:3:947:GLY:HA3	2.54	0.43
34:3:1125:ASP:HB3	34:3:1128:THR:HG22	2.00	0.43
38:X:24:HIS:HB3	38:X:86:ILE:HG12	2.00	0.43
1:A:936:GLU:HG2	1:A:986:PRO:HB3	2.00	0.43
3:L:123:ARG:HD3	3:L:189:LEU:HD11	2.00	0.43
3:L:302:MET:O	3:L:306:LEU:N	2.41	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:31:PHE:O	6:E:80:MET:HA	2.18	0.43
7:M:37:ALA:HB2	7:M:98:ILE:HD11	2.00	0.43
7:M:58:CYS:SG	7:M:63:ILE:HD11	2.59	0.43
8:C:679:GLU:OE1	8:C:807:PRO:HD2	2.17	0.43
8:C:884:ARG:NH2	8:C:941:PRO:HD2	2.34	0.43
27:D:539:LEU:HG	27:D:555:PHE:CZ	2.54	0.43
27:D:1584:PHE:CD2	27:D:1706:MET:HG2	2.54	0.43
27:D:1668:LYS:HD3	27:D:1687:LEU:HD13	2.01	0.43
27:D:2143:TRP:HB3	27:D:2145:VAL:HG23	2.01	0.43
29:H:142:C:C2'	29:H:143:G:C8	3.00	0.43
33:2:367:LEU:O	33:2:369:SER:N	2.50	0.43
34:3:693:ILE:HG23	34:3:701:LYS:HB2	2.01	0.43
35:4:172:LEU:HD21	35:4:175:ASN:HA	2.01	0.43
38:X:117:LYS:HG2	40:Z:25:TYR:HB3	2.01	0.43
39:Y:167:VAL:HG11	39:Y:209:LEU:HD23	2.00	0.43
1:A:1014:LYS:HE2	1:A:1024:LEU:CD1	2.47	0.43
3:L:367:ARG:NH2	17:I:58:G:O6	2.52	0.43
5:J:331:VAL:HG12	5:J:332:GLU:N	2.33	0.43
8:C:863:GLU:HB3	8:C:931:TYR:CE1	2.54	0.43
17:I:143:A:C6	25:U:48:TYR:CD2	3.01	0.43
27:D:617:ARG:NH1	27:D:1009:TYR:HD1	2.16	0.43
27:D:1557:ILE:CA	27:D:1695:TYR:HE2	2.24	0.43
27:D:1748:TYR:HE2	22:Q:142:PRO:CD	2.32	0.43
29:H:43:G:C4	29:H:44:U:C5	3.06	0.43
38:X:28:LYS:HA	38:X:82:GLN:HE22	1.82	0.43
38:X:50:VAL:HG12	39:Y:237:ARG:CD	2.49	0.43
1:A:569:LEU:HD21	1:A:637:VAL:HG21	2.00	0.43
1:A:681:LYS:NZ	16:F:1:G:O6	2.41	0.43
1:A:1575:TRP:NE1	3:L:393:PHE:HD1	2.17	0.43
1:A:2333:PHE:HD2	1:A:2333:PHE:HA	1.72	0.43
2:K:69:VAL:HG22	2:K:72:ARG:HH12	1.84	0.43
8:C:374:VAL:HG22	8:C:378:LEU:HD12	2.00	0.43
8:C:488:ILE:CD1	8:C:556:ALA:HB1	2.49	0.43
8:C:869:HIS:CD2	8:C:925:LEU:HD13	2.54	0.43
16:F:1:G:C2	16:F:2:U:C5	3.06	0.43
17:I:77:U:C2	17:I:78:A:N7	2.87	0.43
17:I:148:U:O4	21:P:41:MET:HG3	2.19	0.43
18:B:174:G:C2	18:B:176:A:H4'	2.54	0.43
27:D:804:HIS:CG	27:D:834:LEU:HD11	2.54	0.43
27:D:1224:ALA:HB3	27:D:1264:VAL:HA	2.00	0.43
27:D:1355:VAL:HG11	27:D:1368:VAL:HG13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1458:ARG:HB3	27:D:1461:GLN:HB2	2.01	0.43
27:D:1550:SER:HA	27:D:1724:THR:O	2.18	0.43
21:P:88:ARG:HH22	20:S:69:ILE:H	1.66	0.43
29:H:1098:C:HO2'	29:H:1099:G:C5'	2.31	0.43
29:H:1148:U:H2'	29:H:1149:G:H8	1.83	0.43
32:1:534:ARG:O	32:1:538:VAL:HG23	2.18	0.43
32:1:925:HIS:ND1	32:1:926:PRO:HD2	2.34	0.43
33:2:173:PRO:O	33:2:176:TRP:HD1	2.00	0.43
34:3:61:TYR:HB2	34:3:1231:LEU:HD11	2.00	0.43
34:3:770:LEU:HB2	34:3:827:TRP:CD1	2.54	0.43
34:3:1109:TYR:CD1	34:3:1110:VAL:HG23	2.54	0.43
34:3:1299:ILE:O	34:3:1300:LEU:HD12	2.19	0.43
38:X:35:ILE:O	38:X:74:PHE:HA	2.18	0.43
1:A:880:THR:HG23	3:L:180:LYS:HE3	2.00	0.43
1:A:1834:PHE:CE1	1:A:1958:PRO:HG2	2.54	0.43
3:L:300:LYS:NZ	3:L:304:ARG:HH22	2.17	0.43
4:N:25:GLY:O	4:N:26:PHE:HB2	2.18	0.43
4:N:264:ILE:O	4:N:268:CYS:HB2	2.19	0.43
18:B:23:C:N4	18:B:24:G:O6	2.52	0.43
18:B:154:G:H2'	18:B:155:U:C6	2.54	0.43
27:D:1688:TYR:CD1	27:D:1695:TYR:HD1	2.23	0.43
27:D:1689:ASP:N	27:D:1689:ASP:OD1	2.52	0.43
25:U:50:ASN:HB3	25:U:72:PHE:CE1	2.54	0.43
29:H:52:A:N6	29:H:64:G:O6	2.52	0.43
32:1:698:ARG:O	32:1:701:GLU:N	2.52	0.43
32:1:839:THR:HG21	32:1:876:ALA:HB1	2.00	0.43
32:1:912:PRO:HG2	32:1:952:PHE:HE2	1.84	0.43
33:2:319:ILE:HD13	35:4:68:LYS:HE2	2.00	0.43
34:3:649:TYR:O	34:3:672:LEU:N	2.51	0.43
34:3:950:GLN:HE21	34:3:973:ILE:CG2	2.32	0.43
35:4:111:PHE:HE2	35:4:113:LYS:HE3	1.84	0.43
36:5:103:LYS:HG3	36:5:104:LYS:H	1.84	0.43
38:X:19:PRO:O	38:X:25:ASN:HB2	2.19	0.43
1:A:1400:ILE:HG23	1:A:1542:TYR:CZ	2.54	0.42
1:A:1865:THR:HG22	1:A:1866:PHE:N	2.33	0.42
1:A:1880:PHE:HD1	1:A:1891:LEU:HD21	1.84	0.42
1:A:1920:LEU:O	1:A:1923:SER:OG	2.27	0.42
2:K:382:ASP:CG	2:K:383:GLU:H	2.22	0.42
2:K:402:SER:OG	2:K:407:GLY:HA2	2.19	0.42
2:K:415:TYR:HB3	2:K:439:LYS:HD3	2.00	0.42
2:K:416:ASP:O	2:K:417:ASN:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:B:124:C:H2'	18:B:125:C:O4'	2.18	0.42
23:R:58:VAL:HA	23:R:69:LEU:HD23	2.01	0.42
29:H:1153:C:H2'	29:H:1154:U:H6	1.84	0.42
34:3:930:LEU:HD13	34:3:984:ILE:HG23	2.01	0.42
39:Y:223:ARG:CG	39:Y:242:GLU:OE2	2.67	0.42
1:A:2041:PRO:HG2	1:A:2043:PHE:CZ	2.54	0.42
2:K:143:HIS:HA	5:J:151:LEU:HD13	2.01	0.42
3:L:245:ALA:HB3	3:L:251:PHE:HB2	2.01	0.42
3:L:447:GLU:O	3:L:451:GLN:HG2	2.19	0.42
4:N:864:ASP:CG	4:N:889:ARG:HH21	2.22	0.42
8:C:457:SER:O	8:C:458:ILE:HB	2.19	0.42
17:I:92:C:H1'	21:P:39:LYS:HD3	2.01	0.42
27:D:558:VAL:HB	27:D:631:LEU:HD12	2.01	0.42
27:D:766:ILE:CD1	27:D:769:LYS:HZ1	2.32	0.42
27:D:1700:ILE:CD1	27:D:1740:LEU:HD13	2.49	0.42
32:1:550:THR:HG21	32:1:590:LEU:HD23	2.01	0.42
34:3:60:LEU:HD12	34:3:1317:VAL:HG22	2.01	0.42
1:A:400:ILE:HG23	8:C:187:ARG:HE	1.85	0.42
1:A:850:GLY:HA2	1:A:853:THR:HG22	2.01	0.42
1:A:1342:LEU:HD21	1:A:1356:LEU:HD21	2.01	0.42
1:A:1566:GLY:HA3	1:A:1816:ARG:HD3	2.02	0.42
1:A:1633:PHE:CZ	1:A:1694:MET:HG3	2.54	0.42
2:K:390:LEU:HD13	5:J:428:TRP:HD1	1.82	0.42
17:I:92:C:C1'	21:P:39:LYS:HD3	2.50	0.42
18:B:22:G:N2	18:B:149:U:O2	2.34	0.42
18:B:26:A:N6	18:B:141:G:H8	2.16	0.42
23:R:73:LYS:HE3	23:R:88:GLU:HG3	2.01	0.42
20:S:24:THR:HA	20:S:70:LYS:HE3	2.00	0.42
32:1:213:LEU:HD12	32:1:213:LEU:O	2.19	0.42
32:1:240:VAL:HG13	32:1:269:LEU:HD21	2.01	0.42
32:1:353:THR:HG23	34:3:277:LEU:HD21	2.01	0.42
32:1:916:MET:HB3	32:1:920:TRP:HE1	1.82	0.42
32:1:956:THR:H	32:1:959:ASN:HB3	1.84	0.42
34:3:61:TYR:HB2	34:3:1231:LEU:CD1	2.49	0.42
34:3:228:LEU:HD12	34:3:273:LEU:HD11	2.01	0.42
34:3:1305:GLN:O	34:3:1309:SER:CB	2.67	0.42
39:Y:170:LEU:N	39:Y:170:LEU:CD2	2.82	0.42
39:Y:215:TYR:CE2	39:Y:232:TRP:CZ3	3.08	0.42
1:A:299:LYS:HA	1:A:493:MET:CG	2.49	0.42
1:A:1030:GLN:HG3	1:A:1034:ASN:ND2	2.34	0.42
1:A:2043:PHE:HB2	1:A:2048:TRP:CD1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:127:TYR:CE2	2:K:276:SER:HB2	2.54	0.42
2:K:262:VAL:HG12	2:K:263:GLY:N	2.34	0.42
4:N:770:ASN:ND2	4:N:772:LEU:HB2	2.34	0.42
17:I:145:U:O4	26:V:37:ASN:ND2	2.47	0.42
19:O:149:TYR:CD2	19:O:178:VAL:HG12	2.47	0.42
27:D:561:ALA:HB1	27:D:566:LEU:HD22	2.01	0.42
27:D:1095:ASN:HA	27:D:1098:ILE:HG22	2.01	0.42
27:D:1875:THR:O	27:D:1879:MET:HG3	2.20	0.42
27:D:2095:LYS:NZ	27:D:2147:ASP:OD2	2.46	0.42
23:R:41:ARG:O	23:R:57:ARG:HD2	2.20	0.42
20:S:41:ASN:HB3	20:S:63:PHE:CZ	2.55	0.42
34:3:927:ARG:HG2	34:3:979:CYS:SG	2.60	0.42
1:A:149:MET:HG2	1:A:154:TYR:CZ	2.54	0.42
1:A:919:LEU:HD21	1:A:1108:LYS:HE3	2.01	0.42
1:A:1656:LYS:O	1:A:1660:SER:HB2	2.20	0.42
1:A:1714:PRO:HA	1:A:1788:GLY:O	2.20	0.42
1:A:2060:LEU:HD21	1:A:2079:ILE:HG23	2.01	0.42
1:A:2395:PHE:HB2	27:D:1062:PRO:HG3	2.01	0.42
2:K:451:PHE:N	2:K:451:PHE:HD1	2.15	0.42
5:J:167:GLU:HB3	5:J:169:TRP:CE3	2.51	0.42
5:J:301:VAL:HG22	5:J:304:ARG:NH2	2.32	0.42
8:C:116:THR:HG22	8:C:117:ARG:N	2.35	0.42
18:B:166:U:C6	18:B:166:U:C3'	3.02	0.42
19:O:168:SER:O	19:O:172:ASP:CB	2.67	0.42
27:D:580:PHE:CE2	27:D:581:LEU:HG	2.54	0.42
27:D:907:PRO:HG2	27:D:947:ARG:NH2	2.34	0.42
27:D:2030:ILE:HG22	27:D:2031:LEU:HD12	2.02	0.42
27:D:2137:LYS:HE3	27:D:2159:GLU:OE2	2.20	0.42
22:Q:33:SER:HB3	22:Q:37:ASN:HB2	2.02	0.42
29:H:38:U:H4'	32:1:892:SER:OG	2.20	0.42
34:3:154:SER:HB3	34:3:1302:ARG:CD	2.48	0.42
34:3:155:GLY:O	34:3:179:LEU:N	2.44	0.42
34:3:419:LEU:HD23	34:3:429:ALA:HA	2.01	0.42
34:3:455:LEU:HD11	34:3:464:LEU:CB	2.49	0.42
1:A:805:PRO:HG2	1:A:808:ILE:HD12	2.00	0.42
1:A:1345:TYR:CD2	1:A:1346:PHE:CE1	3.07	0.42
1:A:1466:GLN:O	1:A:1470:GLN:HB2	2.20	0.42
4:N:257:PHE:CD2	4:N:258:SER:N	2.88	0.42
4:N:770:ASN:HD21	4:N:772:LEU:HB2	1.83	0.42
8:C:219:VAL:HA	8:C:222:MET:HG2	2.00	0.42
27:D:695:ASP:OD1	27:D:696:SER:N	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:956:LYS:O	27:D:958:PRO:HD3	2.20	0.42
27:D:1113:PHE:HZ	27:D:1240:LEU:HD13	1.84	0.42
27:D:1381:GLU:HG2	27:D:1416:PHE:CZ	2.54	0.42
27:D:1938:GLU:HG2	27:D:1938:GLU:O	2.20	0.42
28:G:496:U:H2'	28:G:497:A:H8	1.83	0.42
32:1:605:ILE:HD11	32:1:623:LEU:HD22	2.01	0.42
33:2:285:MET:HE2	35:4:23:GLU:HG3	2.00	0.42
34:3:542:THR:HB	34:3:545:ASP:HB3	2.01	0.42
34:3:642:LEU:HD22	34:3:654:PHE:HD2	1.84	0.42
34:3:738:GLN:NE2	34:3:740:ASN:OD1	2.53	0.42
39:Y:231:ARG:HG3	39:Y:231:ARG:HH11	1.85	0.42
1:A:680:CYS:HG	1:A:711:TRP:HE1	1.65	0.42
1:A:939:LEU:HD21	3:L:445:ILE:HD11	2.01	0.42
1:A:1199:ILE:HD11	8:C:612:PRO:HG2	2.01	0.42
1:A:1308:GLU:OE1	1:A:1346:PHE:HZ	2.03	0.42
1:A:1699:ALA:HA	1:A:1735:ASP:OD1	2.19	0.42
1:A:1964:PRO:O	1:A:2012:LEU:HB3	2.20	0.42
2:K:395:ILE:HD12	2:K:415:TYR:CD2	2.55	0.42
6:E:109:ASP:OD1	6:E:110:LYS:N	2.52	0.42
8:C:568:SER:HA	8:C:571:TYR:CE2	2.55	0.42
19:O:206:LYS:HB2	19:O:208:LYS:NZ	2.34	0.42
27:D:524:GLY:O	27:D:525:SER:HB3	2.19	0.42
27:D:557:ILE:HD12	27:D:604:VAL:HG22	2.00	0.42
27:D:708:CYS:SG	27:D:889:ILE:HG12	2.60	0.42
27:D:981:LEU:HB3	27:D:987:VAL:HG22	2.01	0.42
27:D:1412:TRP:CE2	27:D:1416:PHE:HE2	2.38	0.42
29:H:1097:G:C4	29:H:1146:G:C2	3.07	0.42
34:3:486:PRO:HG2	34:3:505:PHE:CB	2.50	0.42
34:3:542:THR:HG22	34:3:615:LYS:NZ	2.35	0.42
34:3:1065:THR:HG22	34:3:1105:VAL:HA	2.01	0.42
35:4:108:ALA:O	35:4:154:TYR:HA	2.19	0.42
35:4:125:VAL:HG12	35:4:129:ASN:HD21	1.84	0.42
1:A:1122:ASP:OD1	1:A:1161:TYR:OH	2.29	0.42
1:A:2152:TRP:CZ3	27:D:1064:PRO:CG	2.95	0.42
2:K:261:LEU:HD13	2:K:292:TRP:HE3	1.84	0.42
8:C:251:GLN:HG2	8:C:933:TRP:CE2	2.55	0.42
16:F:46:U:C4	16:F:47:A:C2	3.07	0.42
17:I:142:G:N2	21:P:39:LYS:CE	2.82	0.42
18:B:118:U:H2'	18:B:119:U:H6	1.84	0.42
27:D:830:CYS:SG	27:D:834:LEU:HD22	2.59	0.42
27:D:929:ILE:CD1	27:D:935:ALA:HA	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1415:ARG:HA	27:D:1418:HIS:HE1	1.83	0.42
27:D:2059:ASN:OD1	27:D:2059:ASN:N	2.53	0.42
28:G:520:G:N2	38:X:34:TYR:HB2	2.34	0.42
29:H:1098:C:O5'	29:H:1098:C:C6	2.69	0.42
32:1:368:VAL:N	32:1:369:PRO:HD2	2.35	0.42
32:1:889:PHE:CZ	32:1:930:VAL:HG22	2.54	0.42
32:1:955:VAL:HG12	32:1:963:TYR:HD1	1.83	0.42
34:3:61:TYR:HD1	34:3:1318:ILE:HD11	1.83	0.42
34:3:337:VAL:CG2	34:3:346:LEU:HB2	2.50	0.42
34:3:421:ILE:HG22	34:3:422:PHE:O	2.20	0.42
34:3:561:LEU:HG	34:3:569:GLU:O	2.20	0.42
34:3:929:ILE:HG12	34:3:941:PHE:CD1	2.55	0.42
1:A:1814:VAL:CG1	1:A:1818:ARG:HE	2.32	0.42
1:A:1892:LYS:HD2	1:A:1985:GLN:O	2.20	0.42
3:L:368:ALA:O	16:F:60:G:C8	2.73	0.42
6:E:86:TYR:CE2	6:E:87:HIS:HD2	2.38	0.42
7:M:23:VAL:HG21	7:M:117:VAL:HG21	2.01	0.42
8:C:200:CYS:HB3	8:C:436:VAL:HG21	2.02	0.42
8:C:251:GLN:HE21	8:C:255:GLN:HE21	1.67	0.42
8:C:305:SER:OG	8:C:307:ILE:HG22	2.20	0.42
17:I:135:A:C6	17:I:136:U:C4	3.07	0.42
27:D:1183:ILE:O	27:D:1183:ILE:HG22	2.19	0.42
27:D:1587:SER:HB3	27:D:1895:ARG:NE	2.35	0.42
27:D:1699:THR:HG22	22:Q:144:ARG:HD2	2.01	0.42
27:D:1781:ARG:HG2	27:D:1789:TYR:OH	2.20	0.42
27:D:1978:ASP:O	27:D:1982:MET:HG3	2.20	0.42
25:U:30:LYS:HE2	25:U:80:TYR:CE2	2.55	0.42
32:1:387:PRO:HA	32:1:425:LEU:HB3	2.02	0.42
32:1:900:LEU:O	32:1:904:GLU:HG2	2.20	0.42
33:2:340:LEU:HD13	33:2:345:TYR:HA	2.02	0.42
34:3:1043:THR:HG21	34:3:1052:TYR:CE2	2.55	0.42
34:3:1345:GLN:O	34:3:1349:ILE:HG12	2.20	0.42
38:X:89:VAL:O	38:X:93:ASN:HB2	2.20	0.42
1:A:617:ASN:HD21	18:B:99:U:HO2'	1.65	0.42
1:A:630:LYS:NZ	1:A:634:ASP:OD2	2.43	0.42
1:A:1033:ASN:HD22	1:A:1288:LEU:HB3	1.85	0.42
1:A:1057:MET:O	1:A:1061:ILE:HG13	2.19	0.42
1:A:1925:PRO:O	1:A:1929:GLN:HG3	2.19	0.42
1:A:1941:LEU:HD23	1:A:1941:LEU:HA	1.91	0.42
2:K:65:GLU:OE1	5:J:241:ARG:NH2	2.53	0.42
2:K:112:PRO:HA	5:J:217:VAL:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:232:ASN:O	2:K:247:GLN:NE2	2.53	0.42
2:K:390:LEU:HB2	5:J:428:TRP:CD1	2.55	0.42
4:N:150:ASP:O	4:N:153:ILE:HG12	2.19	0.42
5:J:342:PHE:HB3	5:J:424:ILE:HD11	2.01	0.42
8:C:234:LEU:HD23	8:C:443:TYR:HB2	2.00	0.42
16:F:5:G:H2'	16:F:6:C:H6	1.85	0.42
17:I:91:U:O2	21:P:39:LYS:NZ	2.37	0.42
17:I:135:A:C4	17:I:136:U:C5	3.08	0.42
17:I:152:A:H2'	17:I:153:A:C8	2.54	0.42
18:B:150:U:H4'	18:B:151:A:OP1	2.19	0.42
27:D:486:TRP:NE1	27:D:487:CYS:SG	2.90	0.42
27:D:589:THR:HB	27:D:608:THR:H	1.85	0.42
27:D:730:VAL:HG22	27:D:740:ILE:HD13	2.01	0.42
27:D:912:PHE:CD2	27:D:944:LEU:HD23	2.55	0.42
27:D:1412:TRP:CD1	27:D:1416:PHE:CE2	3.07	0.42
23:R:55:ILE:HG23	23:R:73:LYS:HB3	2.01	0.42
29:H:51:C:H2'	29:H:52:A:C8	2.55	0.42
32:1:290:ASP:OD1	32:1:291:GLU:N	2.53	0.42
34:3:493:VAL:HG23	34:3:937:LYS:HB3	2.02	0.42
34:3:1116:ARG:NH2	34:3:1141:LEU:HD21	2.35	0.42
34:3:1190:LEU:O	34:3:1315:ARG:HD3	2.19	0.42
34:3:1217:ILE:HA	34:3:1226:GLY:O	2.19	0.42
38:X:43:THR:OG1	38:X:44:GLU:OE1	2.38	0.42
40:Z:26:ILE:HG22	40:Z:28:ILE:H	1.84	0.42
1:A:266:LEU:HG	1:A:267:PRO:HD2	2.02	0.41
1:A:1372:LYS:HE2	1:A:1383:PHE:CB	2.50	0.41
2:K:350:LYS:HB3	2:K:351:PRO:HD2	2.01	0.41
3:L:138:SER:HA	3:L:141:ILE:HD12	2.01	0.41
3:L:173:LEU:O	3:L:176:THR:OG1	2.26	0.41
3:L:204:LEU:HD23	3:L:204:LEU:HA	1.82	0.41
5:J:346:ASN:N	5:J:422:ASN:OD1	2.46	0.41
5:J:386:GLU:HG2	5:J:390:LYS:HE2	2.01	0.41
8:C:120:ARG:NH2	8:C:549:TYR:OH	2.53	0.41
8:C:408:LEU:HD21	8:C:427:LEU:HD22	2.01	0.41
8:C:749:LYS:O	8:C:753:THR:OG1	2.25	0.41
27:D:484:PRO:O	27:D:488:GLN:HG3	2.20	0.41
27:D:945:TYR:CE1	27:D:970:ARG:HD3	2.55	0.41
27:D:1183:ILE:O	27:D:1184:ARG:HG2	2.20	0.41
21:P:39:LYS:CE	22:Q:35:GLN:NE2	2.83	0.41
28:G:509:A:O3'	32:1:543:ARG:NH2	2.53	0.41
28:G:520:G:C4	38:X:34:TYR:CE1	3.07	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:68:U:H2'	29:H:69:G:C8	2.54	0.41
32:1:807:THR:HG22	33:2:211:THR:HG23	2.02	0.41
34:3:188:SER:O	34:3:190:ILE:N	2.49	0.41
34:3:197:PRO:HG2	34:3:244:ASP:HB3	2.02	0.41
34:3:411:ASP:OD1	34:3:472:LEU:HA	2.19	0.41
34:3:1073:LYS:HD2	34:3:1090:ILE:CD1	2.48	0.41
35:4:197:ASP:OD1	35:4:198:VAL:N	2.53	0.41
4:N:741:ILE:O	4:N:745:GLN:HB3	2.20	0.41
7:M:97:VAL:HG22	17:I:30:G:H2'	2.02	0.41
8:C:195:GLY:C	8:C:545:LEU:HD13	2.39	0.41
8:C:557:HIS:O	8:C:560:GLN:HG2	2.20	0.41
17:I:149:U:C2	23:R:64:HIS:HB3	2.55	0.41
18:B:87:G:H2'	18:B:88:U:H6	1.85	0.41
27:D:1493:SER:CA	27:D:1524:TRP:HH2	2.28	0.41
21:P:18:TYR:CD1	21:P:101:PRO:HG3	2.53	0.41
21:P:31:ILE:O	21:P:48:CYS:HA	2.20	0.41
23:R:76:TRP:CZ3	23:R:89:ARG:HG2	2.56	0.41
25:U:36:THR:HG21	25:U:38:TYR:CZ	2.55	0.41
32:1:689:LEU:HD21	32:1:707:PHE:HD2	1.85	0.41
32:1:925:HIS:HA	33:2:160:LEU:HD11	2.02	0.41
1:A:644:VAL:HG12	1:A:648:GLN:HB2	2.03	0.41
1:A:939:LEU:HD23	1:A:939:LEU:HA	1.81	0.41
1:A:1341:SER:HB3	1:A:1524:PRO:HB2	2.02	0.41
5:J:271:LYS:HD3	16:F:62:A:H5''	2.02	0.41
18:B:103:A:O2'	18:B:104:G:O5'	2.30	0.41
18:B:114:G:C2	18:B:115:G:C5	3.08	0.41
27:D:648:GLU:CD	27:D:912:PHE:CD1	2.94	0.41
27:D:1141:PRO:HG3	27:D:1298:TRP:CZ3	2.55	0.41
27:D:1486:ALA:HA	27:D:1489:GLU:HG2	2.02	0.41
27:D:1933:TYR:CE1	27:D:2090:LYS:O	2.73	0.41
23:R:36:ASP:HA	23:R:39:VAL:HG12	2.02	0.41
29:H:1139:G:C2'	29:H:1140:U:H6	2.34	0.41
29:H:1146:G:H2'	29:H:1147:A:H8	1.84	0.41
29:H:1149:G:C4	29:H:1150:U:C5	3.08	0.41
32:1:828:GLY:HA3	36:5:38:ARG:NH2	2.36	0.41
33:2:246:LYS:O	33:2:250:VAL:HG23	2.21	0.41
34:3:118:GLN:HB2	34:3:1325:ASN:OD1	2.20	0.41
34:3:224:ILE:O	36:5:17:VAL:HG11	2.20	0.41
34:3:327:VAL:O	34:3:337:VAL:HA	2.21	0.41
34:3:759:ASP:OD1	34:3:760:GLY:N	2.53	0.41
34:3:1308:ARG:HD3	34:3:1308:ARG:HA	1.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:LEU:HA	1:A:199:ILE:HD11	2.03	0.41
1:A:268:LEU:HD13	1:A:273:ASP:HB2	2.01	0.41
1:A:297:SER:HB2	18:B:32:G:H5'	2.03	0.41
1:A:659:HIS:O	1:A:662:GLN:N	2.54	0.41
1:A:1144:PHE:CD2	1:A:1145:MET:HG2	2.56	0.41
1:A:1375:LEU:CD2	1:A:1607:THR:HG22	2.50	0.41
1:A:1477:PHE:O	1:A:1481:GLU:HG3	2.21	0.41
1:A:2152:TRP:HZ3	27:D:1064:PRO:CG	2.32	0.41
1:A:2307:LEU:HD11	1:A:2311:GLY:HA3	2.02	0.41
2:K:167:LEU:HD13	4:N:724:SER:HB2	2.01	0.41
2:K:235:ILE:HA	2:K:244:LYS:O	2.20	0.41
2:K:264:HIS:CE1	2:K:290:ARG:HH11	2.38	0.41
2:K:269:SER:OG	2:K:311:PHE:HA	2.20	0.41
2:K:279:PHE:HB3	2:K:291:LEU:HD11	2.02	0.41
4:N:144:LYS:HE3	17:I:19:U:OP1	2.20	0.41
4:N:863:PHE:CE2	4:N:888:PRO:HB2	2.55	0.41
5:J:350:PRO:HB2	16:F:83:A:N7	2.35	0.41
8:C:113:ILE:HD13	8:C:551:TYR:HD1	1.85	0.41
8:C:274:ILE:HD13	8:C:385:PHE:CD2	2.48	0.41
8:C:385:PHE:CE1	8:C:425:LEU:HD11	2.55	0.41
18:B:69:G:H2'	18:B:70:A:C8	2.55	0.41
18:B:70:A:H2'	18:B:71:A:C8	2.56	0.41
27:D:1312:LYS:H	27:D:1787:SER:HG	1.65	0.41
27:D:1439:LEU:HD21	27:D:1465:ILE:HG13	2.01	0.41
25:U:54:ASN:OD1	25:U:55:GLU:N	2.51	0.41
33:2:293:ARG:O	35:4:31:GLN:NE2	2.53	0.41
34:3:326:PHE:CD1	34:3:339:ASP:HA	2.55	0.41
34:3:453:ASN:HA	34:3:464:LEU:HD11	2.03	0.41
34:3:488:ILE:HG22	34:3:489:LYS:HG2	2.02	0.41
34:3:526:SER:HA	34:3:870:ARG:HG3	2.02	0.41
1:A:1814:VAL:HG12	1:A:1818:ARG:HE	1.85	0.41
1:A:2032:ILE:HG22	1:A:2041:PRO:HB2	2.02	0.41
2:K:306:HIS:CD2	2:K:310:VAL:HG22	2.55	0.41
2:K:337:ARG:HD2	5:J:173:TYR:CE2	2.55	0.41
8:C:309:ASN:HD21	8:C:325:LYS:HG3	1.85	0.41
8:C:502:LEU:HB3	8:C:576:THR:OG1	2.20	0.41
8:C:758:ASP:HB3	8:C:761:ALA:HB3	2.02	0.41
27:D:593:ARG:O	27:D:593:ARG:HG2	2.20	0.41
27:D:1668:LYS:CE	27:D:1702:GLU:HG3	2.47	0.41
27:D:1862:THR:OG1	27:D:1887:VAL:HG12	2.20	0.41
27:D:1905:LEU:HD11	27:D:1937:LEU:HD13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:R:76:TRP:HZ3	23:R:89:ARG:HG2	1.85	0.41
29:H:58:A:H2'	29:H:59:C:O4'	2.19	0.41
32:1:230:TYR:HE2	37:6:5:GLN:HG3	1.85	0.41
32:1:430:TYR:HB3	32:1:434:TYR:HE2	1.85	0.41
33:2:134:LEU:HA	33:2:137:LEU:HB3	2.02	0.41
34:3:157:LEU:HD11	34:3:202:ILE:HG21	2.01	0.41
34:3:180:THR:HG21	34:3:188:SER:CB	2.51	0.41
34:3:676:PRO:CB	34:3:693:ILE:HD11	2.50	0.41
34:3:1089:ASP:HB2	34:3:1092:GLU:O	2.20	0.41
34:3:1291:ILE:HA	34:3:1296:SER:HB2	2.03	0.41
36:5:72:TYR:OH	36:5:87:PRO:HG3	2.20	0.41
1:A:370:ILE:HB	1:A:375:PHE:HZ	1.85	0.41
1:A:375:PHE:CE2	8:C:954:LEU:HD23	2.56	0.41
1:A:1409:ALA:HB1	1:A:1428:GLY:HA3	2.03	0.41
1:A:1658:HIS:HE1	1:A:1690:LYS:NZ	2.19	0.41
2:K:51:VAL:HG13	2:K:76:LEU:HD11	2.01	0.41
3:L:358:ILE:CG2	3:L:360:GLU:H	2.33	0.41
4:N:273:ARG:O	4:N:303:ASN:ND2	2.47	0.41
4:N:666:ILE:HG22	4:N:667:CYS:N	2.36	0.41
4:N:674:LEU:O	4:N:678:TYR:HD2	2.03	0.41
6:E:105:PHE:CE2	6:E:137:TYR:CZ	3.09	0.41
8:C:366:ASN:OD1	8:C:367:VAL:HG23	2.20	0.41
8:C:778:THR:HG23	8:C:781:ASP:H	1.85	0.41
18:B:27:G:OP1	18:B:141:G:H5''	2.19	0.41
27:D:453:PHE:HE2	27:D:455:ARG:NE	2.14	0.41
27:D:587:GLU:O	27:D:592:SER:HB3	2.21	0.41
22:Q:4:VAL:HG11	22:Q:34:PRO:O	2.21	0.41
22:Q:4:VAL:CG1	22:Q:34:PRO:HA	2.50	0.41
25:U:59:PHE:N	25:U:59:PHE:CD1	2.88	0.41
29:H:1097:G:N1	29:H:1146:G:C5	2.88	0.41
29:H:1143:C:H4'	29:H:1144:U:H3'	2.01	0.41
32:1:843:GLU:OE1	32:1:883:LEU:HD11	2.21	0.41
33:2:248:HIS:ND1	33:2:375:PHE:HB2	2.35	0.41
34:3:187:VAL:HG21	37:6:17:LYS:O	2.20	0.41
34:3:333:ASN:OD1	34:3:334:HIS:ND1	2.44	0.41
34:3:951:CYS:SG	34:3:952:ARG:N	2.93	0.41
35:4:43:ASP:HB2	35:4:50:GLN:NE2	2.32	0.41
36:5:67:VAL:HG23	36:5:68:ASN:N	2.35	0.41
38:X:27:TYR:O	38:X:29:ASP:N	2.48	0.41
1:A:929:LEU:HG	4:N:148:ALA:HB2	2.03	0.41
1:A:1317:ARG:O	1:A:1321:MET:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:350:LYS:HB3	2:K:351:PRO:CD	2.49	0.41
2:K:390:LEU:HD22	5:J:428:TRP:NE1	2.35	0.41
3:L:328:VAL:HA	3:L:331:HIS:CD2	2.48	0.41
5:J:352:ILE:O	5:J:356:LEU:HG	2.20	0.41
8:C:175:LEU:HD23	8:C:176:ARG:N	2.35	0.41
8:C:629:TYR:OH	8:C:658:ASP:OD2	2.37	0.41
8:C:733:ASN:OD1	8:C:734:CYS:N	2.54	0.41
18:B:163:C:P	18:B:164:C:OP1	2.79	0.41
27:D:491:PHE:CE1	27:D:533:LEU:HD21	2.54	0.41
27:D:727:TYR:CD2	27:D:760:LYS:HE2	2.55	0.41
27:D:1821:GLU:CG	27:D:1845:SER:HB2	2.51	0.41
22:Q:26:TRP:O	22:Q:43:VAL:HA	2.21	0.41
29:H:142:C:HO2'	29:H:143:G:H8	1.66	0.41
32:1:874:GLU:HB3	34:3:1315:ARG:NH2	2.35	0.41
34:3:527:LEU:HD21	34:3:552:ILE:HG21	2.03	0.41
35:4:42:LYS:HB2	35:4:49:TYR:CE1	2.56	0.41
1:A:576:HIS:HE1	1:A:593:LEU:O	2.04	0.41
1:A:631:LEU:HD21	1:A:663:LEU:HD13	2.03	0.41
1:A:766:ILE:O	1:A:770:MET:HG3	2.20	0.41
1:A:1521:ARG:HD3	3:L:404:TYR:CE2	2.55	0.41
1:A:2152:TRP:HZ3	27:D:1064:PRO:CD	2.33	0.41
1:A:2326:SER:O	1:A:2329:PHE:HB3	2.21	0.41
2:K:422:TYR:HD1	2:K:429:LYS:HA	1.85	0.41
3:L:398:GLN:CD	3:L:419:GLN:HG3	2.41	0.41
18:B:30:A:H2'	18:B:31:G:H8	1.86	0.41
18:B:38:A:N1	18:B:117:G:C6	2.88	0.41
27:D:912:PHE:CB	27:D:944:LEU:HD23	2.33	0.41
27:D:1583:VAL:HB	27:D:1665:LEU:HD23	2.03	0.41
27:D:1640:LEU:CD1	27:D:1649:GLU:HG3	2.51	0.41
27:D:1890:GLU:C	22:Q:143:ARG:HE	2.23	0.41
23:R:80:LYS:HE3	23:R:82:LYS:CG	2.50	0.41
25:U:29:VAL:HG22	25:U:81:ILE:HG13	2.02	0.41
25:U:45:THR:HG23	25:U:50:ASN:O	2.20	0.41
32:1:173:ILE:HG12	32:1:185:MET:SD	2.61	0.41
34:3:97:THR:OG1	34:3:100:HIS:HB3	2.21	0.41
34:3:426:TYR:HA	34:3:439:PHE:O	2.20	0.41
34:3:690:LEU:HA	34:3:703:MET:O	2.21	0.41
38:X:3:LYS:O	38:X:7:ILE:HD12	2.21	0.41
38:X:68:THR:HG23	38:X:70:GLU:HG2	2.03	0.41
1:A:167:TYR:CD1	1:A:547:LEU:HD21	2.56	0.41
1:A:380:ARG:HB3	1:A:382:GLU:OE1	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:408:SER:HA	8:C:272:ARG:NH2	2.36	0.41
1:A:522:TYR:CE1	1:A:686:ILE:HD12	2.55	0.41
1:A:1043:ARG:O	1:A:1045:GLN:HG3	2.21	0.41
1:A:1048:VAL:HA	1:A:1249:SER:O	2.20	0.41
1:A:1417:GLN:HB2	1:A:1783:MET:CE	2.51	0.41
1:A:2193:PHE:HA	1:A:2196:ILE:HG12	2.03	0.41
1:A:2249:ASP:OD1	27:D:1307:SER:OG	2.34	0.41
1:A:2319:LYS:HG3	1:A:2320:ASP:N	2.36	0.41
2:K:235:ILE:HD13	2:K:280:ILE:HG21	2.03	0.41
2:K:235:ILE:CD1	2:K:280:ILE:HD13	2.51	0.41
2:K:390:LEU:HD12	2:K:390:LEU:O	2.21	0.41
3:L:359:PRO:HD3	6:E:56:PHE:CD2	2.56	0.41
5:J:163:ASN:HB3	5:J:167:GLU:O	2.20	0.41
5:J:271:LYS:HE3	5:J:304:ARG:HH11	1.85	0.41
8:C:161:ILE:HG12	8:C:177:TYR:OH	2.21	0.41
8:C:365:GLU:HG3	8:C:366:ASN:H	1.86	0.41
8:C:625:ILE:HG23	8:C:629:TYR:HD2	1.85	0.41
8:C:728:LEU:HD12	8:C:730:LYS:HE3	2.02	0.41
8:C:752:ARG:HD3	8:C:759:SER:HA	2.01	0.41
8:C:884:ARG:CB	8:C:910:GLU:HG3	2.44	0.41
16:F:47:A:C3'	16:F:48:C:H5'	2.50	0.41
18:B:26:A:O4'	18:B:131:A:H5'	2.21	0.41
18:B:150:U:HO2'	18:B:151:A:P	2.44	0.41
27:D:594:LEU:HD22	27:D:598:GLN:OE1	2.21	0.41
27:D:707:PHE:N	27:D:707:PHE:CD1	2.89	0.41
27:D:778:LYS:O	27:D:782:LYS:HG2	2.21	0.41
27:D:944:LEU:O	27:D:948:MET:HG2	2.20	0.41
27:D:1647:ASN:O	27:D:1651:ILE:HG12	2.21	0.41
27:D:1861:PHE:CB	22:Q:140:LYS:HZ3	2.34	0.41
27:D:1898:ASP:HA	27:D:1943:PHE:HZ	1.86	0.41
27:D:1973:ALA:O	27:D:1977:MET:HG3	2.21	0.41
27:D:2139:ASN:ND2	27:D:2159:GLU:OE1	2.53	0.41
23:R:45:ILE:HG23	23:R:105:LEU:HB3	2.02	0.41
23:R:48:LEU:HD21	23:R:96:LEU:HD21	2.02	0.41
23:R:105:LEU:HD12	25:U:70:GLU:O	2.21	0.41
20:S:77:LEU:HD23	20:S:77:LEU:O	2.20	0.41
28:G:522:U:H5	38:X:111:PRO:O	2.04	0.41
29:H:548:G:C6	29:H:549:C:N4	2.89	0.41
29:H:1118:U:H2'	29:H:1119:C:H6	1.86	0.41
29:H:1139:G:O2'	29:H:1140:U:O5'	2.33	0.41
29:H:1144:U:O2	29:H:1144:U:C2'	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1:198:GLU:O	32:1:202:ASN:HB3	2.20	0.41
32:1:467:VAL:HG12	32:1:469:SER:H	1.86	0.41
34:3:380:LEU:HA	34:3:389:PHE:O	2.21	0.41
34:3:390:LYS:O	34:3:407:LEU:HA	2.20	0.41
34:3:626:PRO:HB3	34:3:630:ILE:HB	2.02	0.41
34:3:643:ILE:HG23	34:3:651:LEU:HD21	2.02	0.41
34:3:643:ILE:HD11	34:3:653:TYR:HD1	1.85	0.41
34:3:693:ILE:CG2	34:3:701:LYS:HB2	2.51	0.41
34:3:832:TRP:CG	34:3:833:LYS:N	2.89	0.41
34:3:1129:VAL:O	34:3:1140:THR:HA	2.20	0.41
34:3:1135:TYR:HB3	34:3:1311:TYR:CE2	2.56	0.41
34:3:1189:LEU:HD21	34:3:1192:HIS:HB2	2.03	0.41
35:4:10:THR:HA	35:4:56:GLU:HA	2.03	0.41
36:5:41:ARG:NH1	36:5:83:LYS:HZ2	2.18	0.41
38:X:32:TYR:OH	39:Y:162:LEU:HD11	2.20	0.41
39:Y:208:SER:HB3	39:Y:212:ARG:N	2.36	0.41
1:A:293:VAL:HG22	1:A:294:ASN:N	2.36	0.41
1:A:499:VAL:HG12	1:A:501:LEU:HD12	2.02	0.41
1:A:507:LEU:O	1:A:508:GLN:HB2	2.21	0.41
1:A:615:LEU:HD21	1:A:619:PHE:CE2	2.56	0.41
1:A:1996:LEU:HA	1:A:1999:ILE:O	2.21	0.41
2:K:274:HIS:HD2	2:K:276:SER:HB3	1.86	0.41
4:N:771:ALA:O	4:N:775:VAL:HG23	2.21	0.41
8:C:133:ILE:HG13	8:C:134:ILE:N	2.36	0.41
18:B:24:G:H2'	18:B:25:G:C8	2.56	0.41
18:B:65:U:H2'	18:B:66:A:C8	2.57	0.41
27:D:777:SER:O	27:D:781:LEU:HB2	2.21	0.41
27:D:1699:THR:HG22	22:Q:144:ARG:CZ	2.50	0.41
24:T:86:ASN:HD21	25:U:79:LEU:HA	1.86	0.41
29:H:1092:A:H3'	29:H:1093:C:C6	2.47	0.41
32:1:297:THR:HA	32:1:300:ALA:HB3	2.03	0.41
32:1:348:VAL:HG13	32:1:349:LEU:N	2.29	0.41
34:3:76:ILE:HD11	34:3:422:PHE:CD1	2.56	0.41
34:3:242:VAL:HG22	34:3:252:PHE:CB	2.51	0.41
34:3:270:PHE:HD2	34:3:284:ALA:HB3	1.85	0.41
34:3:555:PRO:O	34:3:587:THR:HB	2.21	0.41
34:3:612:PRO:HA	34:3:618:TYR:CD1	2.54	0.41
34:3:1007:LYS:HE3	34:3:1009:LEU:HD21	2.03	0.41
1:A:194:HIS:CE1	1:A:196:SER:HG	2.38	0.40
1:A:1054:LEU:HD21	1:A:1168:ILE:HD11	2.03	0.40
1:A:1234:VAL:HG12	1:A:1235:PRO:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2043:PHE:HB3	1:A:2047:GLN:HB2	2.02	0.40
2:K:67:GLU:OE1	2:K:75:ARG:NE	2.45	0.40
2:K:183:LEU:HD23	2:K:190:VAL:HG22	2.02	0.40
4:N:793:ILE:HA	4:N:796:ASP:HB3	2.02	0.40
5:J:141:ASN:HD22	5:J:144:LEU:HG	1.85	0.40
8:C:795:ILE:O	8:C:799:PHE:HB2	2.21	0.40
18:B:117:G:H2'	18:B:118:U:C6	2.56	0.40
18:B:148:G:H2'	18:B:149:U:C6	2.56	0.40
27:D:1326:ASN:OD1	27:D:1326:ASN:N	2.54	0.40
27:D:1651:ILE:O	27:D:1655:LEU:HG	2.21	0.40
27:D:2104:GLY:HA2	27:D:2112:TYR:CD2	2.53	0.40
24:T:16:CYS:HA	24:T:19:ASN:ND2	2.36	0.40
28:G:499:U:H2'	28:G:500:A:H8	1.85	0.40
29:H:43:G:H2'	29:H:44:U:C6	2.56	0.40
32:1:335:LYS:O	32:1:338:GLN:HB2	2.21	0.40
34:3:542:THR:HG21	34:3:547:ASN:OD1	2.21	0.40
34:3:742:HIS:HE2	34:3:752:LYS:HE2	1.85	0.40
34:3:1179:ASN:OD1	34:3:1180:THR:N	2.54	0.40
36:5:37:VAL:C	36:5:38:ARG:HG2	2.42	0.40
36:5:43:VAL:HA	36:5:72:TYR:CE2	2.56	0.40
1:A:457:ASP:OD1	1:A:458:PHE:N	2.54	0.40
1:A:697:LYS:HA	1:A:697:LYS:HD2	1.90	0.40
1:A:1125:LEU:O	1:A:1233:ARG:NH1	2.54	0.40
1:A:1601:ILE:N	1:A:1602:PRO:HD2	2.36	0.40
1:A:1673:LEU:HA	1:A:1678:ILE:HB	2.02	0.40
1:A:1879:ILE:HG12	1:A:1913:THR:HG22	2.03	0.40
1:A:2395:PHE:HE1	27:D:1061:ALA:HA	1.74	0.40
3:L:340:LYS:O	3:L:344:LEU:HG	2.21	0.40
8:C:104:THR:O	8:C:107:THR:N	2.55	0.40
8:C:114:PRO:HB2	8:C:160:ARG:O	2.20	0.40
8:C:362:LYS:HG3	8:C:363:PRO:HD2	2.03	0.40
8:C:405:ARG:NH2	18:B:1:A:C8	2.86	0.40
8:C:869:HIS:CD2	8:C:925:LEU:HD22	2.56	0.40
8:C:945:LEU:HD12	8:C:945:LEU:O	2.22	0.40
16:F:80:U:H2'	16:F:81:G:H8	1.86	0.40
17:I:94:U:C4	17:I:95:C:C4	3.09	0.40
17:I:133:C:H2'	17:I:134:U:C6	2.56	0.40
27:D:502:ILE:HD11	27:D:522:PRO:HD2	2.02	0.40
27:D:610:GLU:OE1	27:D:1009:TYR:CE2	2.73	0.40
27:D:1092:PHE:CD1	27:D:1095:ASN:HB3	2.56	0.40
27:D:1331:THR:HG23	27:D:1346:LYS:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1367:PHE:HB2	27:D:1527:MET:SD	2.62	0.40
27:D:1689:ASP:OD1	27:D:1692:GLU:HB3	2.21	0.40
27:D:1853:ALA:CB	27:D:1863:ILE:HG13	2.52	0.40
21:P:88:ARG:HG2	21:P:90:GLU:N	2.24	0.40
32:1:854:ARG:NH1	33:2:183:LEU:HD12	2.35	0.40
34:3:131:ASP:OD1	34:3:146:THR:OG1	2.34	0.40
34:3:270:PHE:CD2	34:3:284:ALA:HB3	2.56	0.40
34:3:820:VAL:HG12	34:3:828:VAL:HG12	2.03	0.40
34:3:1336:PHE:O	34:3:1339:LYS:HG2	2.21	0.40
1:A:156:THR:OG1	1:A:157:ASP:N	2.54	0.40
1:A:913:VAL:HG21	4:N:163:THR:HG22	2.03	0.40
1:A:1087:ASN:HA	1:A:1099:ASN:O	2.22	0.40
1:A:2177:VAL:HB	1:A:2338:GLN:HE22	1.87	0.40
1:A:2264:GLU:HG2	1:A:2266:LEU:HG	2.03	0.40
2:K:51:VAL:HG13	2:K:76:LEU:CD1	2.51	0.40
2:K:269:SER:H	2:K:284:SER:HA	1.85	0.40
3:L:172:ILE:O	3:L:176:THR:HG23	2.21	0.40
3:L:305:MET:HG2	3:L:337:LEU:CD2	2.52	0.40
4:N:832:LEU:HD11	4:N:845:LEU:HD11	2.03	0.40
17:I:96:A:C6	17:I:137:G:C6	3.09	0.40
18:B:85:U:C2	18:B:86:G:C8	3.09	0.40
27:D:619:SER:O	27:D:622:LEU:HG	2.21	0.40
27:D:1245:ASP:HA	27:D:1288:PHE:CD1	2.55	0.40
27:D:1387:HIS:CE1	27:D:1392:LYS:CB	3.04	0.40
27:D:1448:THR:HB	27:D:1449:PRO:HD2	2.02	0.40
27:D:1497:PHE:CE2	27:D:1762:ILE:HG21	2.55	0.40
22:Q:139:ASN:O	22:Q:140:LYS:CB	2.69	0.40
23:R:43:PRO:HA	23:R:56:ALA:O	2.22	0.40
34:3:118:GLN:HE21	34:3:1299:ILE:CD1	2.33	0.40
34:3:507:ASN:ND2	34:3:509:LYS:HE2	2.36	0.40
35:4:135:ILE:HB	35:4:156:GLU:HG2	2.04	0.40
1:A:264:ILE:HD12	1:A:647:PHE:CE1	2.57	0.40
1:A:2152:TRP:CD1	1:A:2391:HIS:CD2	3.09	0.40
2:K:362:TYR:CD1	2:K:363:GLN:HG3	2.56	0.40
2:K:380:LYS:O	2:K:382:ASP:N	2.53	0.40
3:L:441:MET:CE	3:L:444:ARG:HH21	2.34	0.40
6:E:63:ASP:HB2	6:E:66:GLU:HB2	2.01	0.40
7:M:8:ALA:HA	7:M:80:PHE:CE2	2.56	0.40
16:F:61:C:C2	16:F:62:A:C8	3.09	0.40
17:I:24:A:C2	17:I:50:G:C2	3.09	0.40
17:I:91:U:O2'	17:I:92:C:P	2.79	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:502:ILE:CD1	27:D:522:PRO:HD2	2.51	0.40
27:D:557:ILE:HG23	27:D:630:LEU:HD23	2.04	0.40
27:D:725:ALA:O	27:D:729:LYS:HG2	2.21	0.40
27:D:1486:ALA:HB1	27:D:1746:LEU:HD23	2.03	0.40
27:D:1585:LEU:CD1	27:D:1591:CYS:HA	2.52	0.40
27:D:1641:TYR:CZ	27:D:1644:MET:HG2	2.57	0.40
27:D:1895:ARG:O	27:D:1895:ARG:HG3	2.21	0.40
27:D:2086:VAL:HB	27:D:2095:LYS:HB3	2.03	0.40
24:T:19:ASN:O	24:T:23:GLN:HG3	2.22	0.40
29:H:43:G:H2'	29:H:44:U:H6	1.87	0.40
29:H:1145:U:O2	29:H:1145:U:C2'	2.69	0.40
32:1:215:ASP:OD1	32:1:216:GLN:N	2.53	0.40
32:1:737:SER:O	32:1:743:ARG:NH1	2.54	0.40
33:2:289:LYS:HB3	35:4:30:ILE:HD13	2.02	0.40
34:3:71:PHE:CD2	34:3:95:VAL:HG11	2.57	0.40
34:3:99:THR:O	34:3:120:LEU:HD12	2.21	0.40
34:3:115:ALA:HB2	34:3:169:LEU:HD12	2.02	0.40
34:3:513:LEU:HD21	34:3:886:PHE:CD2	2.56	0.40
34:3:782:GLU:O	34:3:816:MET:N	2.54	0.40
34:3:1029:SER:OG	34:3:1045:MET:HA	2.20	0.40
35:4:107:ILE:HD13	35:4:154:TYR:HB3	2.03	0.40
35:4:110:LEU:O	35:4:152:TYR:HA	2.22	0.40
36:5:2:SER:OG	36:5:3:ARG:N	2.54	0.40
37:6:20:GLY:O	37:6:21:LEU:HD12	2.22	0.40
1:A:1046:SER:O	1:A:1173:HIS:HD2	2.04	0.40
3:L:126:GLU:O	3:L:130:LEU:HG	2.21	0.40
4:N:15:TYR:OH	6:E:13:TRP:CD1	2.69	0.40
6:E:87:HIS:C	6:E:89:LYS:H	2.24	0.40
8:C:473:LEU:HD23	8:C:473:LEU:HA	1.95	0.40
8:C:775:ILE:HD12	8:C:817:GLN:NE2	2.37	0.40
16:F:26:A:H2'	16:F:27:U:C6	2.56	0.40
16:F:42:A:O2'	16:F:43:C:H5'	2.21	0.40
27:D:464:HIS:CE1	27:D:706:GLN:HE21	2.40	0.40
27:D:562:PRO:HA	27:D:609:PRO:CD	2.51	0.40
27:D:781:LEU:HD21	27:D:798:GLU:CG	2.49	0.40
27:D:1580:SER:H	27:D:1678:ASP:HB2	1.85	0.40
27:D:1688:TYR:CE1	27:D:1896:LYS:HE2	2.57	0.40
20:S:34:VAL:HG22	20:S:45:ARG:HD2	2.02	0.40
26:V:8:LYS:HD2	26:V:11:MET:HG3	2.02	0.40
26:V:36:LEU:O	26:V:38:VAL:HG23	2.21	0.40
29:H:145:G:O2'	29:H:146:A:H5'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:1161:U:H2'	29:H:1162:U:H6	1.86	0.40
29:H:1168:U:H2'	29:H:1169:C:C6	2.56	0.40
33:2:197:PRO:HB3	33:2:258:TRP:CH2	2.56	0.40
33:2:364:PHE:CD2	34:3:1124:LEU:HD21	2.57	0.40
34:3:1035:LEU:HD11	34:3:1042:LEU:HD23	2.03	0.40
34:3:1299:ILE:C	34:3:1300:LEU:HD12	2.42	0.40
35:4:13:VAL:HG12	35:4:16:ILE:HD11	2.03	0.40
36:5:37:VAL:O	36:5:38:ARG:HG2	2.22	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	2169/2413 (90%)	2040 (94%)	115 (5%)	14 (1%)	22	50
2	K	425/465 (91%)	388 (91%)	34 (8%)	3 (1%)	19	47
3	L	410/494 (83%)	392 (96%)	15 (4%)	3 (1%)	19	47
4	N	678/899 (75%)	626 (92%)	51 (8%)	1 (0%)	48	78
5	J	294/469 (63%)	281 (96%)	10 (3%)	3 (1%)	13	39
6	E	137/143 (96%)	128 (93%)	9 (7%)	0	100	100
7	M	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
8	C	837/1008 (83%)	779 (93%)	53 (6%)	5 (1%)	22	50
9	z	63/109 (58%)	61 (97%)	2 (3%)	0	100	100
10	q	90/95 (95%)	83 (92%)	7 (8%)	0	100	100
11	r	75/89 (84%)	70 (93%)	5 (7%)	0	100	100
12	x	72/86 (84%)	70 (97%)	2 (3%)	0	100	100
13	t	73/93 (78%)	69 (94%)	3 (4%)	1 (1%)	9	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	y	62/115 (54%)	62 (100%)	0	0	100	100
15	s	73/187 (39%)	72 (99%)	1 (1%)	0	100	100
19	O	68/587 (12%)	64 (94%)	3 (4%)	1 (2%)	8	30
20	S	80/101 (79%)	77 (96%)	3 (4%)	0	100	100
20	d	77/101 (76%)	69 (90%)	6 (8%)	2 (3%)	4	22
20	l	79/101 (78%)	70 (89%)	8 (10%)	1 (1%)	10	33
21	P	66/196 (34%)	62 (94%)	4 (6%)	0	100	100
21	a	69/196 (35%)	63 (91%)	6 (9%)	0	100	100
21	h	74/196 (38%)	67 (90%)	7 (10%)	0	100	100
22	Q	93/146 (64%)	89 (96%)	3 (3%)	1 (1%)	12	37
22	b	71/146 (49%)	66 (93%)	4 (6%)	1 (1%)	9	31
22	m	78/146 (53%)	74 (95%)	4 (5%)	0	100	100
23	R	90/110 (82%)	89 (99%)	1 (1%)	0	100	100
23	c	86/110 (78%)	83 (96%)	3 (4%)	0	100	100
23	n	63/110 (57%)	60 (95%)	3 (5%)	0	100	100
24	T	73/94 (78%)	72 (99%)	1 (1%)	0	100	100
24	e	66/94 (70%)	62 (94%)	4 (6%)	0	100	100
24	i	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
25	U	71/86 (83%)	68 (96%)	3 (4%)	0	100	100
25	f	66/86 (77%)	59 (89%)	4 (6%)	3 (4%)	2	13
25	j	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	8	30
26	V	73/77 (95%)	66 (90%)	6 (8%)	1 (1%)	9	31
26	g	64/77 (83%)	58 (91%)	6 (9%)	0	100	100
26	k	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
27	D	1694/2163 (78%)	1631 (96%)	60 (4%)	3 (0%)	44	72
30	o	125/238 (52%)	111 (89%)	12 (10%)	2 (2%)	8	29
31	p	69/111 (62%)	67 (97%)	2 (3%)	0	100	100
32	1	814/971 (84%)	762 (94%)	46 (6%)	6 (1%)	19	47
33	2	205/436 (47%)	192 (94%)	11 (5%)	2 (1%)	13	39
34	3	1164/1361 (86%)	1046 (90%)	109 (9%)	9 (1%)	16	44
35	4	165/213 (78%)	164 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	5	101/107 (94%)	87 (86%)	13 (13%)	1 (1%)	13	39
37	6	82/85 (96%)	78 (95%)	3 (4%)	1 (1%)	11	35
38	X	126/148 (85%)	117 (93%)	7 (6%)	2 (2%)	8	29
39	Y	85/266 (32%)	80 (94%)	3 (4%)	2 (2%)	5	23
40	Z	20/204 (10%)	14 (70%)	6 (30%)	0	100	100
41	u	453/530 (86%)	415 (92%)	38 (8%)	0	100	100
42	w	123/280 (44%)	112 (91%)	11 (9%)	0	100	100
43	v	168/266 (63%)	142 (84%)	25 (15%)	1 (1%)	22	50
All	All	12585/17187 (73%)	11769 (94%)	746 (6%)	70 (1%)	24	50

All (70) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	240	PRO
2	K	395	ILE
3	L	328	VAL
8	C	364	PHE
8	C	602	VAL
30	o	68	PRO
32	1	831	SER
32	1	836	TYR
33	2	368	ILE
34	3	363	VAL
34	3	413	ILE
34	3	1299	ILE
38	X	17	LEU
1	A	156	THR
1	A	1088	VAL
5	J	167	GLU
8	C	133	ILE
8	C	134	ILE
20	d	40	MET
22	b	12	ASN
25	f	24	ASN
25	f	49	PHE
22	Q	140	LYS
32	1	830	MET
32	1	835	ILE
39	Y	172	ILE

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Mol	Chain	Res	Type
39	Y	230	SER
5	J	331	VAL
27	D	791	PRO
27	D	1896	LYS
26	V	60	GLN
34	3	364	THR
1	A	508	GLN
1	A	1621	VAL
1	A	1869	ASN
1	A	2321	ILE
3	L	151	LYS
4	N	736	ASP
5	J	286	ASN
19	O	212	VAL
27	D	960	ILE
34	3	961	CYS
34	3	1233	SER
37	6	19	ILE
1	A	239	PHE
1	A	645	ASP
25	f	50	ASN
20	l	81	ALA
33	2	167	LYS
38	X	18	SER
43	v	232	GLY
2	K	286	ASP
20	d	51	GLU
36	5	38	ARG
1	A	1870	VAL
25	j	15	PRO
30	o	52	LYS
32	1	348	VAL
8	C	829	VAL
34	3	859	ILE
1	A	407	VAL
13	t	41	VAL
1	A	699	PRO
1	A	2330	GLU
2	K	176	LYS
3	L	358	ILE
32	1	386	TYR
34	3	523	ILE

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Mol	Chain	Res	Type
34	3	1031	ILE
1	A	264	ILE

### 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	1964/2182 (90%)	1962 (100%)	2 (0%)	92	97
2	K	373/410 (91%)	371 (100%)	2 (0%)	86	91
3	L	327/445 (74%)	327 (100%)	0	100	100
4	N	361/813 (44%)	361 (100%)	0	100	100
5	J	248/436 (57%)	248 (100%)	0	100	100
6	E	129/132 (98%)	129 (100%)	0	100	100
7	M	104/104 (100%)	104 (100%)	0	100	100
8	C	757/910 (83%)	757 (100%)	0	100	100
19	O	60/534 (11%)	60 (100%)	0	100	100
20	S	71/89 (80%)	71 (100%)	0	100	100
20	l	67/89 (75%)	64 (96%)	3 (4%)	23	50
21	P	64/176 (36%)	64 (100%)	0	100	100
21	h	67/176 (38%)	67 (100%)	0	100	100
22	Q	81/129 (63%)	81 (100%)	0	100	100
22	m	77/129 (60%)	71 (92%)	6 (8%)	10	33
23	R	85/103 (82%)	85 (100%)	0	100	100
23	n	59/103 (57%)	52 (88%)	7 (12%)	4	16
24	T	69/83 (83%)	69 (100%)	0	100	100
24	i	65/83 (78%)	60 (92%)	5 (8%)	10	33
25	U	65/77 (84%)	65 (100%)	0	100	100
25	j	61/77 (79%)	60 (98%)	1 (2%)	58	75
26	V	64/66 (97%)	64 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	k	58/66 (88%)	55 (95%)	3 (5%)	19	45
27	D	1524/1955 (78%)	1522 (100%)	2 (0%)	92	97
30	o	46/219 (21%)	43 (94%)	3 (6%)	14	39
31	p	23/100 (23%)	22 (96%)	1 (4%)	25	50
32	1	724/867 (84%)	724 (100%)	0	100	100
33	2	190/392 (48%)	190 (100%)	0	100	100
34	3	1088/1244 (88%)	1087 (100%)	1 (0%)	92	97
35	4	154/189 (82%)	154 (100%)	0	100	100
36	5	93/97 (96%)	92 (99%)	1 (1%)	70	81
37	6	76/77 (99%)	76 (100%)	0	100	100
38	X	114/132 (86%)	112 (98%)	2 (2%)	54	73
39	Y	77/240 (32%)	67 (87%)	10 (13%)	3	13
40	Z	21/186 (11%)	18 (86%)	3 (14%)	2	10
41	u	425/492 (86%)	420 (99%)	5 (1%)	67	80
42	w	118/259 (46%)	115 (98%)	3 (2%)	42	65
43	v	156/236 (66%)	154 (99%)	2 (1%)	65	78
All	All	10105/14097 (72%)	10043 (99%)	62 (1%)	82	90

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2332	THR
1	A	2333	PHE
2	K	443	LEU
2	K	451	PHE
27	D	491	PHE
27	D	1008	PHE
24	i	16	CYS
24	i	18	PHE
24	i	25	THR
24	i	79	LYS
24	i	81	LEU
25	j	79	LEU
26	k	18	ASN
26	k	41	ASP
26	k	71	LEU

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Mol	Chain	Res	Type
20	l	10	LEU
20	l	76	ASP
20	l	79	LYS
22	m	20	LYS
22	m	26	TRP
22	m	30	GLN
22	m	77	ASP
22	m	99	ASP
22	m	104	ASP
23	n	49	ARG
23	n	77	THR
23	n	79	LYS
23	n	80	LYS
23	n	82	LYS
23	n	99	ASP
23	n	100	SER
30	o	4	THR
30	o	44	PRO
30	o	71	SER
31	p	38	LYS
34	3	147	PHE
36	5	38	ARG
38	X	6	GLN
38	X	110	ARG
39	Y	160	LYS
39	Y	168	GLN
39	Y	169	LYS
39	Y	174	VAL
39	Y	207	THR
39	Y	208	SER
39	Y	209	LEU
39	Y	213	LYS
39	Y	214	LEU
39	Y	262	LEU
40	Z	38	LEU
40	Z	40	LEU
40	Z	42	SER
41	u	27	ARG
41	u	35	TYR
41	u	81	ILE
41	u	298	HIS
41	u	317	SER

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Mol	Chain	Res	Type
42	w	113	MET
42	w	129	HIS
42	w	158	ARG
43	v	226	MET
43	v	246	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (141) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	326	ASN
1	A	392	ASN
1	A	429	ASN
1	A	617	ASN
1	A	692	ASN
1	A	848	ASN
1	A	864	GLN
1	A	868	GLN
1	A	976	GLN
1	A	997	GLN
1	A	1033	ASN
1	A	1045	GLN
1	A	1087	ASN
1	A	1097	HIS
1	A	1099	ASN
1	A	1369	ASN
1	A	1532	HIS
1	A	1603	ASN
1	A	1618	ASN
1	A	1635	HIS
1	A	1809	ASN
1	A	1839	ASN
1	A	1947	HIS
1	A	2018	ASN
1	A	2306	ASN
1	A	2338	GLN
2	K	232	ASN
2	K	247	GLN
2	K	374	ASN
2	K	450	HIS
3	L	113	HIS
3	L	160	HIS
3	L	185	ASN

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Mol	Chain	Res	Type
3	L	201	ASN
3	L	331	HIS
4	N	213	ASN
4	N	770	ASN
5	J	141	ASN
5	J	276	ASN
5	J	409	HIS
6	E	14	HIS
6	E	87	HIS
8	C	158	HIS
8	C	183	GLN
8	C	251	GLN
8	C	554	HIS
8	C	721	GLN
8	C	776	ASN
8	C	817	GLN
8	C	869	HIS
8	C	929	GLN
27	D	516	ASN
27	D	568	GLN
27	D	621	ASN
27	D	676	ASN
27	D	706	GLN
27	D	739	GLN
27	D	768	HIS
27	D	804	HIS
27	D	894	ASN
27	D	904	GLN
27	D	921	ASN
27	D	1103	GLN
27	D	1148	GLN
27	D	1281	GLN
27	D	1349	ASN
27	D	1418	HIS
27	D	1443	HIS
27	D	1611	ASN
27	D	1726	HIS
27	D	1931	GLN
27	D	1968	ASN
27	D	1996	GLN
27	D	2069	GLN
27	D	2139	ASN

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Mol	Chain	Res	Type
21	P	33	GLN
22	Q	30	GLN
23	R	52	HIS
20	S	4	ASN
25	U	76	ASN
25	U	77	ASN
26	V	54	ASN
24	i	34	GLN
24	i	86	ASN
25	j	52	GLN
26	k	66	ASN
20	l	41	ASN
22	m	30	GLN
22	m	102	ASN
23	n	71	ASN
32	1	175	ASN
32	1	311	ASN
32	1	367	HIS
32	1	407	HIS
32	1	539	HIS
32	1	695	ASN
32	1	803	ASN
32	1	853	HIS
32	1	887	ASN
32	1	925	HIS
33	2	145	GLN
33	2	204	ASN
33	2	262	HIS
33	2	273	ASN
33	2	339	ASN
34	3	156	ASN
34	3	177	GLN
34	3	209	GLN
34	3	248	ASN
34	3	259	ASN
34	3	382	GLN
34	3	481	GLN
34	3	507	ASN
34	3	590	HIS
34	3	609	HIS
34	3	641	GLN
34	3	669	HIS

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Mol	Chain	Res	Type
34	3	719	GLN
34	3	738	GLN
34	3	920	GLN
34	3	945	HIS
34	3	950	GLN
34	3	1154	HIS
34	3	1192	HIS
34	3	1203	HIS
34	3	1359	ASN
35	4	50	GLN
35	4	170	ASN
35	4	187	ASN
36	5	14	GLN
38	X	25	ASN
38	X	106	HIS
39	Y	168	GLN
39	Y	173	ASN
39	Y	236	HIS
39	Y	239	ASN
41	u	34	HIS
41	u	91	GLN
41	u	167	ASN
41	u	202	GLN
43	v	93	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	F	95/112 (84%)	38 (40%)	1 (1%)
17	I	106/160 (66%)	31 (29%)	6 (5%)
18	B	173/214 (80%)	64 (36%)	13 (7%)
28	G	43/44 (97%)	22 (51%)	2 (4%)
29	H	196/1175 (16%)	52 (26%)	23 (11%)
All	All	613/1705 (35%)	207 (33%)	45 (7%)

All (207) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
16	F	2	U
16	F	12	U
16	F	13	U

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Mol	Chain	Res	Type
16	F	14	U
16	F	17	U
16	F	25	C
16	F	26	A
16	F	28	U
16	F	31	G
16	F	32	U
16	F	37	U
16	F	38	U
16	F	39	G
16	F	40	A
16	F	41	A
16	F	43	C
16	F	44	A
16	F	46	U
16	F	47	A
16	F	48	C
16	F	49	A
16	F	50	G
16	F	51	A
16	F	57	U
16	F	58	C
16	F	64	U
16	F	66	C
16	F	71	G
16	F	75	A
16	F	76	A
16	F	77	G
16	F	82	A
16	F	83	A
16	F	84	C
16	F	86	G
16	F	87	U
16	F	109	U
16	F	111	U
17	I	2	U
17	I	15	G
17	I	19	U
17	I	20	A
17	I	25	U
17	I	27	U
17	I	28	C

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Mol	Chain	Res	Type
17	I	29	A
17	I	30	G
17	I	39	C
17	I	40	G
17	I	41	U
17	I	48	U
17	I	55	U
17	I	60	U
17	I	74	U
17	I	75	U
17	I	76	A
17	I	77	U
17	I	78	A
17	I	79	A
17	I	92	C
17	I	98	G
17	I	134	U
17	I	135	A
17	I	138	U
17	I	139	A
17	I	143	A
17	I	144	A
17	I	145	U
17	I	151	G
18	B	12	C
18	B	13	A
18	B	18	A
18	B	20	U
18	B	24	G
18	B	27	G
18	B	28	G
18	B	32	G
18	B	33	U
18	B	34	C
18	B	35	A
18	B	39	U
18	B	40	C
18	B	41	A
18	B	75	A
18	B	76	U
18	B	77	A
18	B	78	A

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Mol	Chain	Res	Type
18	B	79	C
18	B	80	G
18	B	81	A
18	B	82	A
18	B	83	C
18	B	84	A
18	B	90	C
18	B	92	U
18	B	94	C
18	B	95	C
18	B	96	U
18	B	97	U
18	B	100	A
18	B	101	C
18	B	103	A
18	B	104	G
18	B	108	C
18	B	109	A
18	B	113	G
18	B	121	U
18	B	126	A
18	B	127	U
18	B	128	A
18	B	129	G
18	B	131	A
18	B	132	A
18	B	139	A
18	B	140	A
18	B	141	G
18	B	142	C
18	B	151	A
18	B	160	U
18	B	162	G
18	B	163	C
18	B	164	C
18	B	165	A
18	B	166	U
18	B	167	A
18	B	168	U
18	B	169	U
18	B	170	U
18	B	171	U

*Continued on next page...*

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Mol	Chain	Res	Type
18	B	172	U
18	B	173	U
18	B	174	G
18	B	175	G
28	G	481	A
28	G	482	A
28	G	483	A
28	G	484	A
28	G	485	A
28	G	486	A
28	G	487	A
28	G	488	A
28	G	493	A
28	G	501	A
28	G	502	C
28	G	505	A
28	G	506	U
28	G	507	U
28	G	508	U
28	G	509	A
28	G	510	A
28	G	512	U
28	G	515	U
28	G	518	U
28	G	521	U
28	G	522	U
29	H	32	G
29	H	38	U
29	H	47	U
29	H	48	U
29	H	59	C
29	H	65	A
29	H	66	A
29	H	67	A
29	H	68	U
29	H	83	U
29	H	111	C
29	H	115	U
29	H	116	U
29	H	117	U
29	H	118	U
29	H	119	G

*Continued on next page...*

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Mol	Chain	Res	Type
29	H	120	G
29	H	140	G
29	H	141	A
29	H	142	C
29	H	145	G
29	H	1090	A
29	H	1094	G
29	H	1095	U
29	H	1096	C
29	H	1097	G
29	H	1098	C
29	H	1100	A
29	H	1101	C
29	H	1102	C
29	H	1103	C
29	H	1104	U
29	H	1105	C
29	H	1106	G
29	H	1119	C
29	H	1120	G
29	H	1121	U
29	H	1122	U
29	H	1123	C
29	H	1124	U
29	H	1125	U
29	H	1126	G
29	H	1130	U
29	H	1139	G
29	H	1141	C
29	H	1142	G
29	H	1143	C
29	H	1144	U
29	H	1145	U
29	H	1146	G
29	H	1150	U
29	H	1166	G

All (45) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	F	50	G
17	I	18	A

*Continued on next page...*



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Mol	Chain	Res	Type
17	I	19	U
17	I	24	A
17	I	91	U
17	I	134	U
17	I	142	G
18	B	17	C
18	B	32	G
18	B	33	U
18	B	77	A
18	B	83	C
18	B	94	C
18	B	95	C
18	B	128	A
18	B	130	A
18	B	150	U
18	B	166	U
18	B	168	U
18	B	172	U
28	G	480	A
28	G	514	U
29	H	46	C
29	H	66	A
29	H	117	U
29	H	1095	U
29	H	1096	C
29	H	1097	G
29	H	1100	A
29	H	1101	C
29	H	1102	C
29	H	1105	C
29	H	1119	C
29	H	1120	G
29	H	1121	U
29	H	1122	U
29	H	1123	C
29	H	1124	U
29	H	1125	U
29	H	1138	G
29	H	1141	C
29	H	1142	G
29	H	1144	U
29	H	1145	U

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Mol	Chain	Res	Type
29	H	1149	G

## 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 8 ligands modelled in this entry, 7 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
44	GTP	C	1500	45	26,34,34	0.94	1 (3%)	32,54,54	1.61	4 (12%)

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
44	GTP	C	1500	45	-	4/18/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	C	1500	GTP	C6-N1	-2.42	1.34	1.37

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C	1500	GTP	PB-O3B-PG	-4.54	117.24	132.83
44	C	1500	GTP	PA-O3A-PB	-4.03	119.00	132.83
44	C	1500	GTP	C3'-C2'-C1'	3.35	106.02	100.98
44	C	1500	GTP	C8-N7-C5	2.49	107.74	102.99

There are no chirality outliers.

All (4) torsion outliers are listed below:

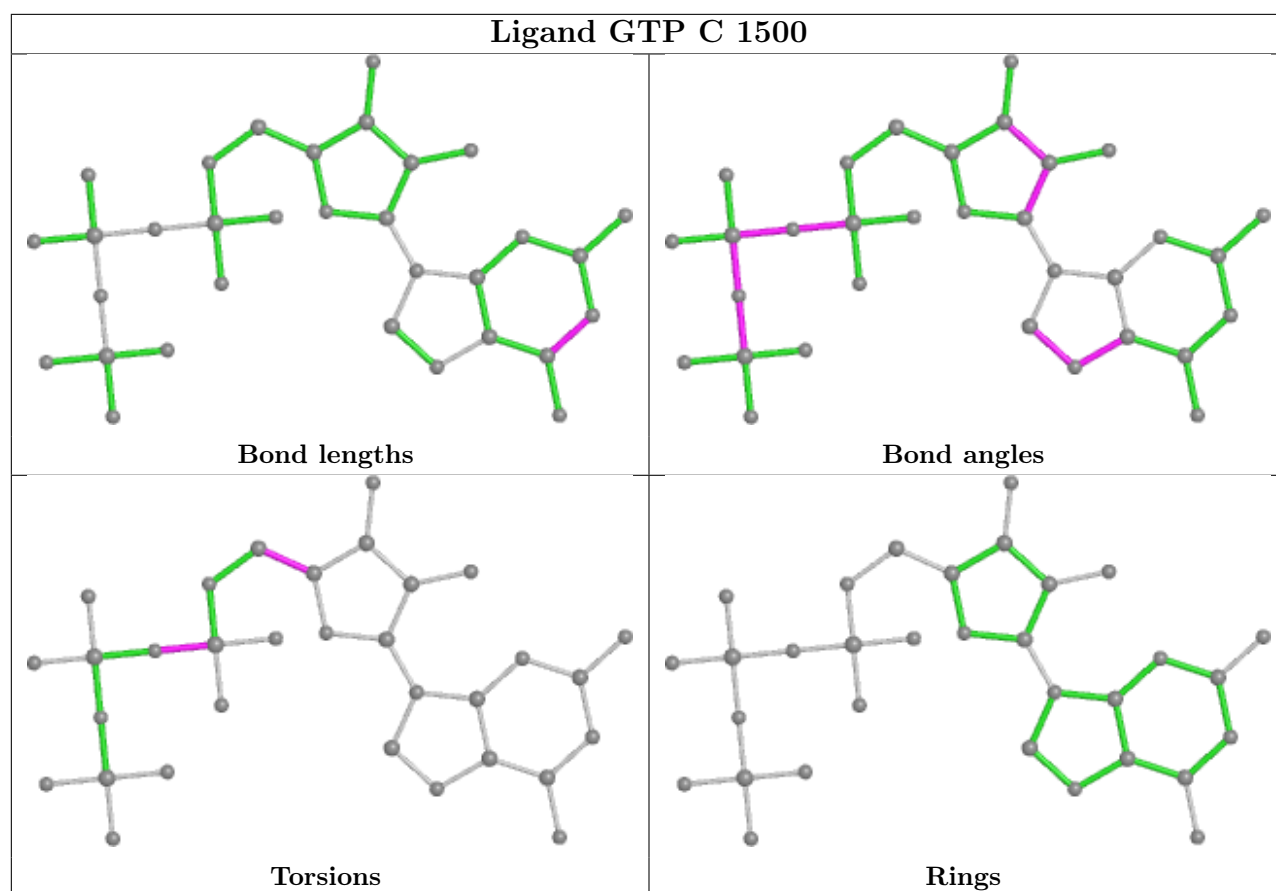
Mol	Chain	Res	Type	Atoms
44	C	1500	GTP	O4'-C4'-C5'-O5'
44	C	1500	GTP	C3'-C4'-C5'-O5'
44	C	1500	GTP	PB-O3A-PA-O2A
44	C	1500	GTP	PB-O3A-PA-O1A

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
44	C	1500	GTP	6	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 [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

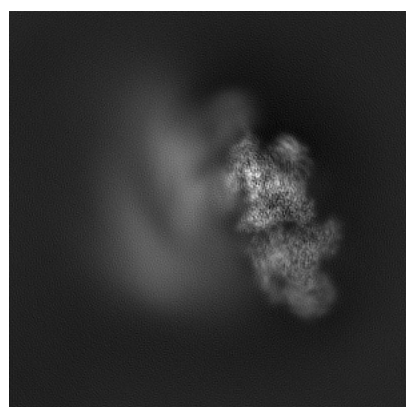
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6972. These allow visual inspection of the internal detail of the map and identification of artifacts.

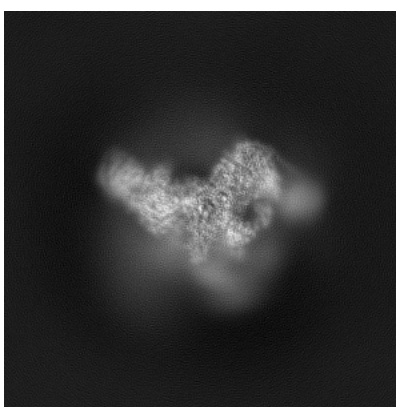
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

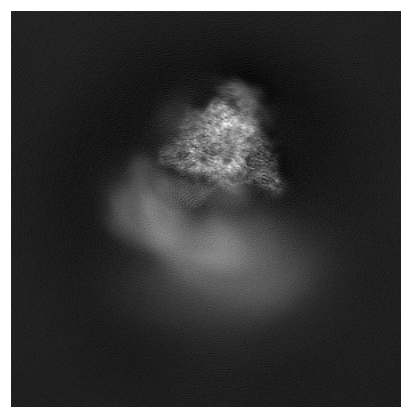
#### 6.1.1 Primary map



X



Y

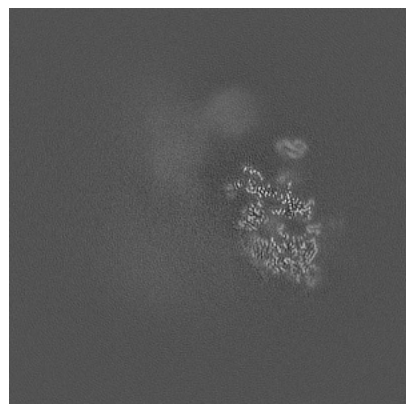


Z

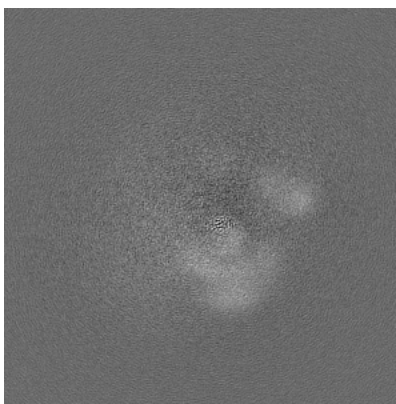
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

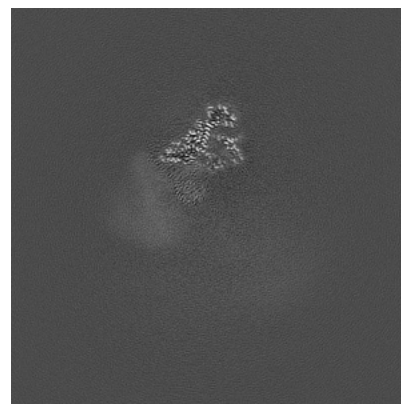
#### 6.2.1 Primary map



X Index: 200



Y Index: 200

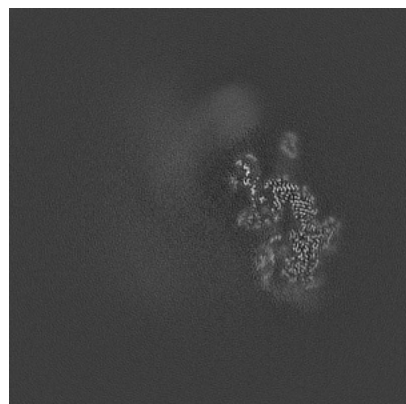


Z Index: 200

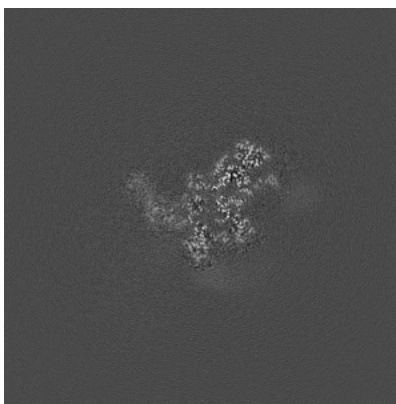
The images above show central slices of the map in three orthogonal directions.

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

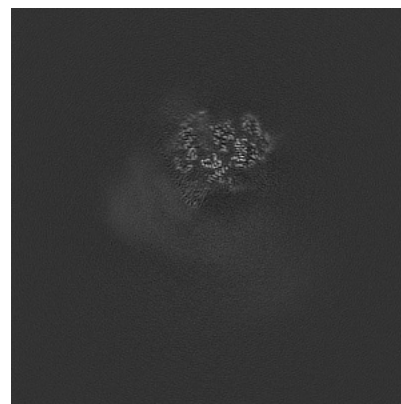
### 6.3.1 Primary map



X Index: 212



Y Index: 247

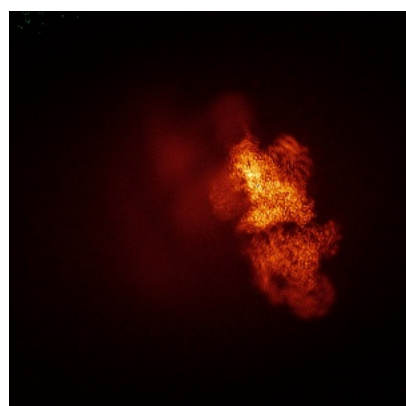


Z Index: 224

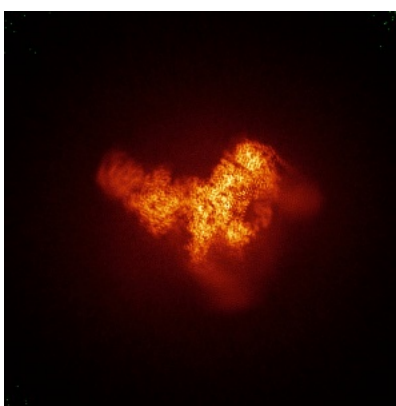
The images above show the largest variance slices of the map in three orthogonal directions.

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

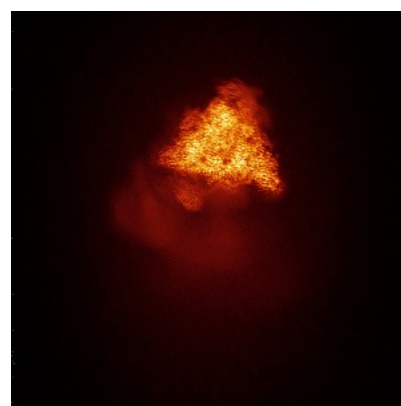
### 6.4.1 Primary map



X



Y



Z

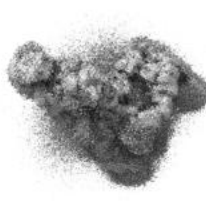
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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

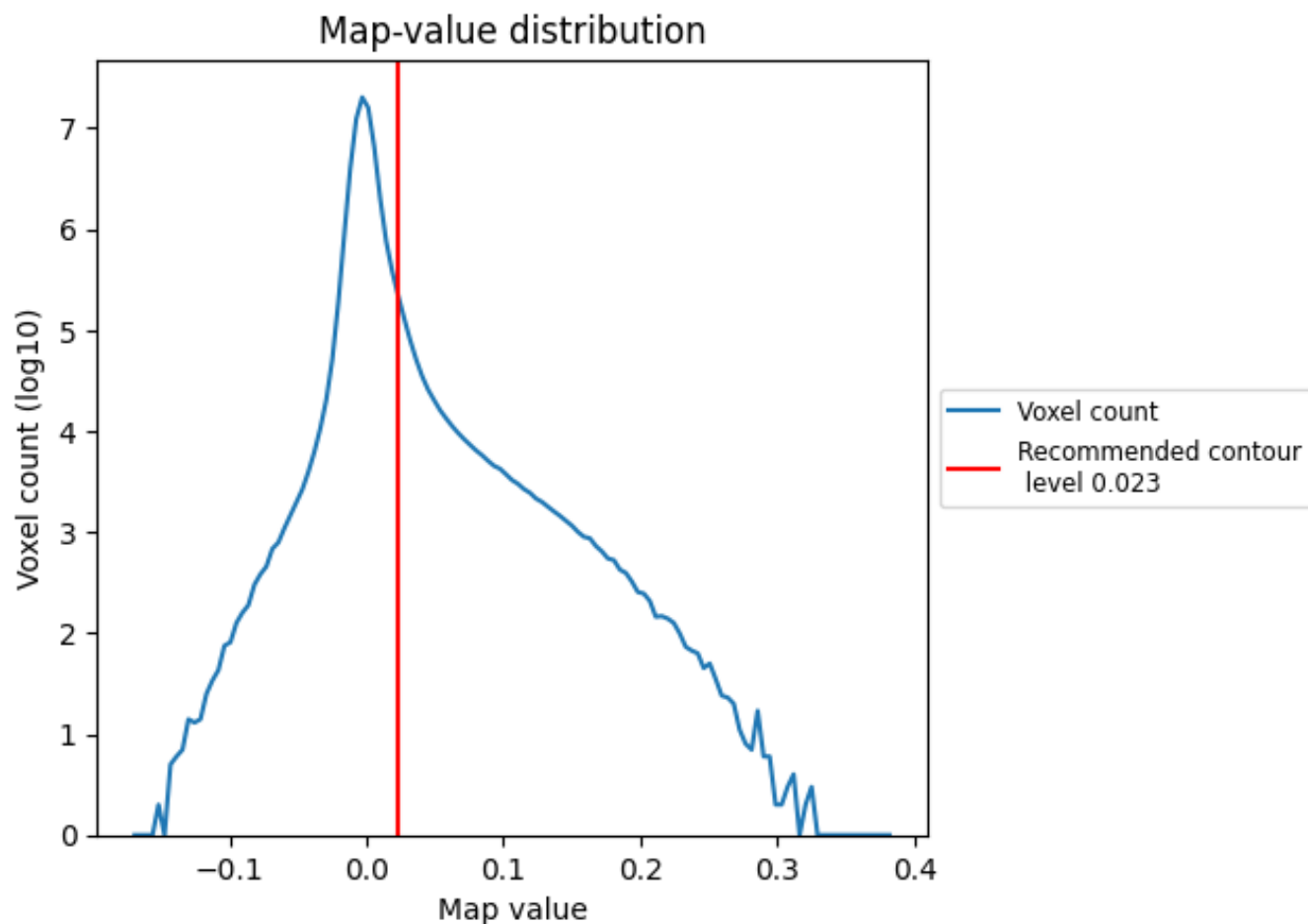
## 6.6 Mask visualisation [i](#)

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.

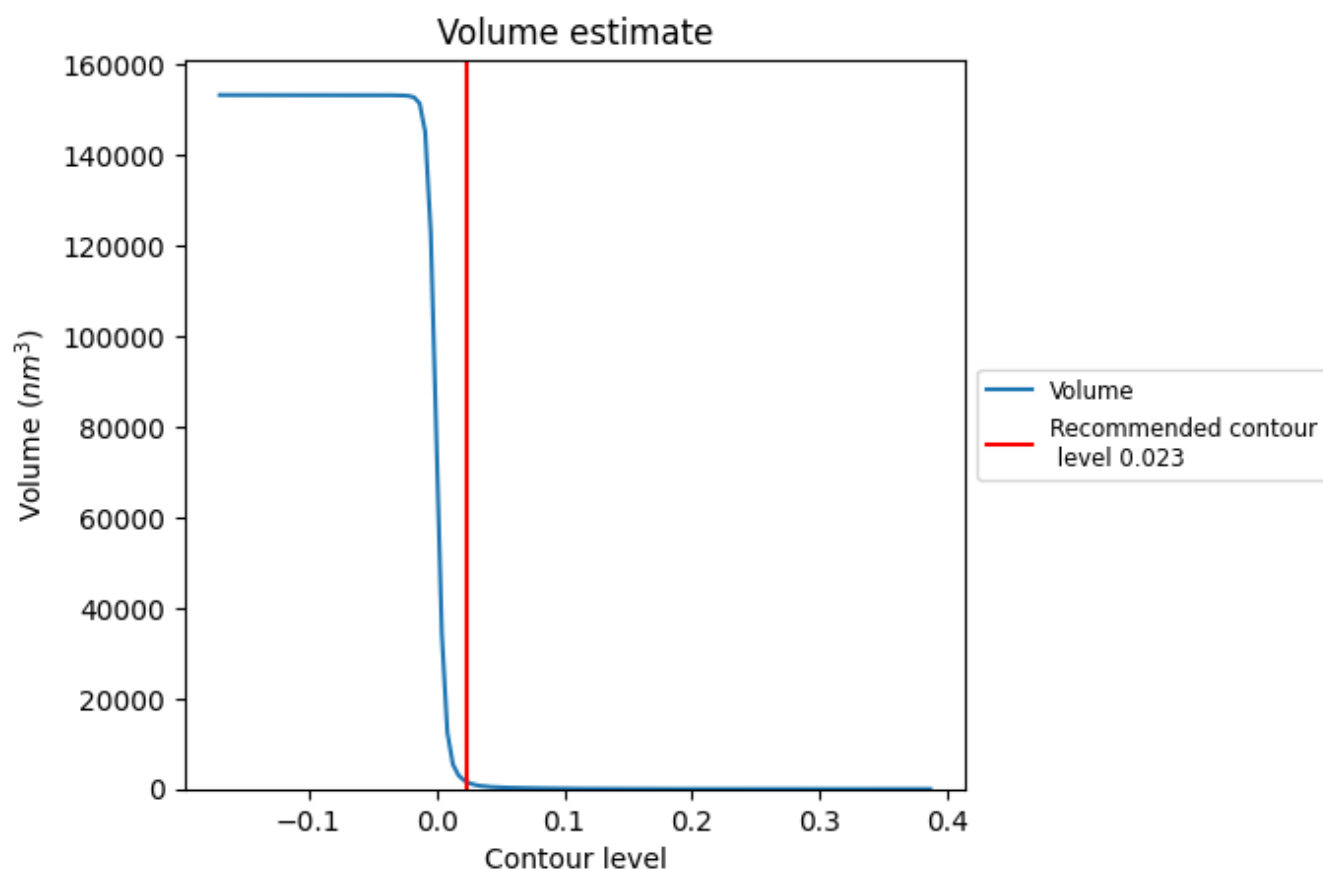
### 7.1 Map-value distribution [i](#)



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.



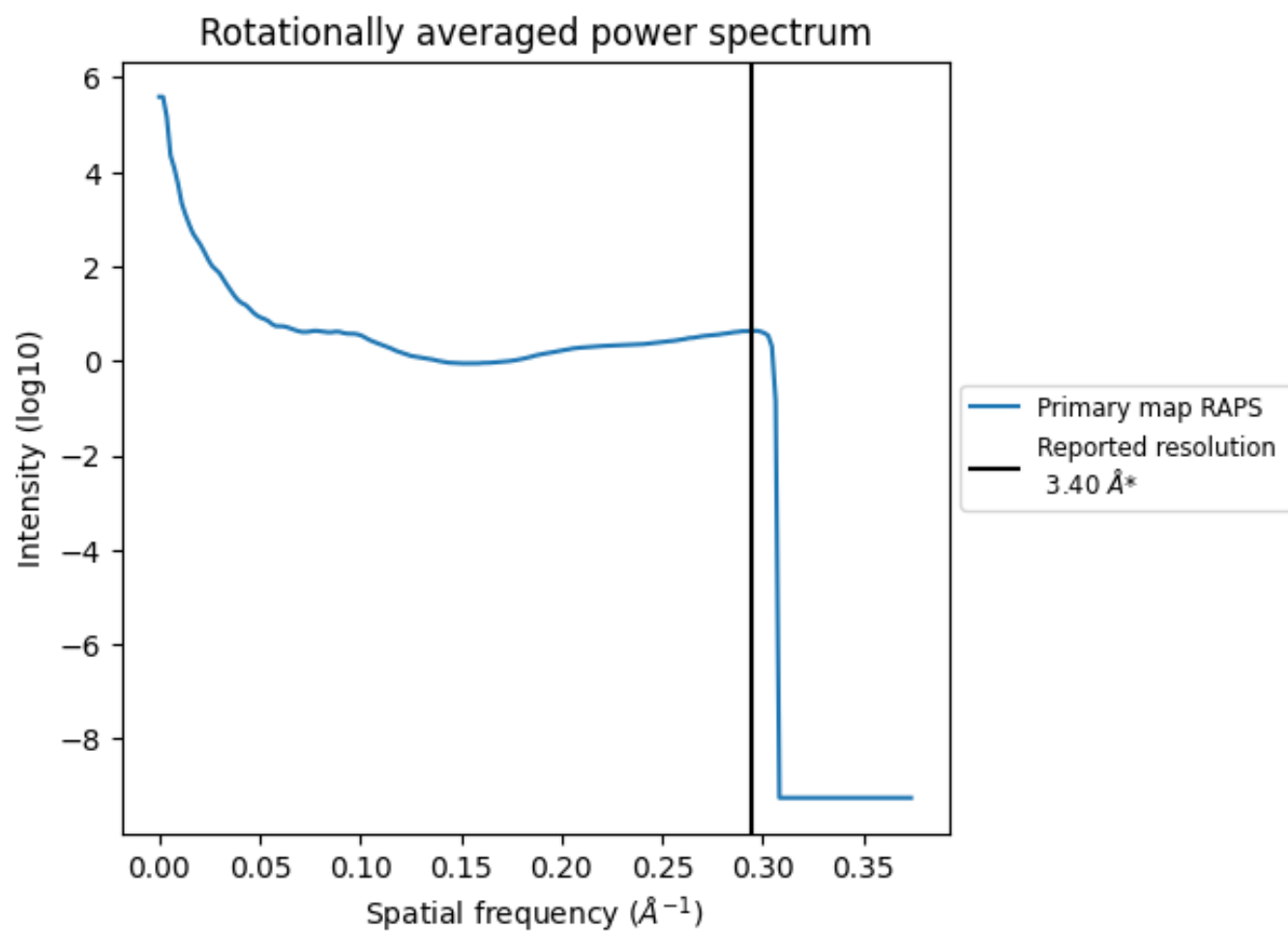
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1701  $\text{nm}^3$ ; this corresponds to an approximate mass of 1536 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 0.294 Å<sup>-1</sup>

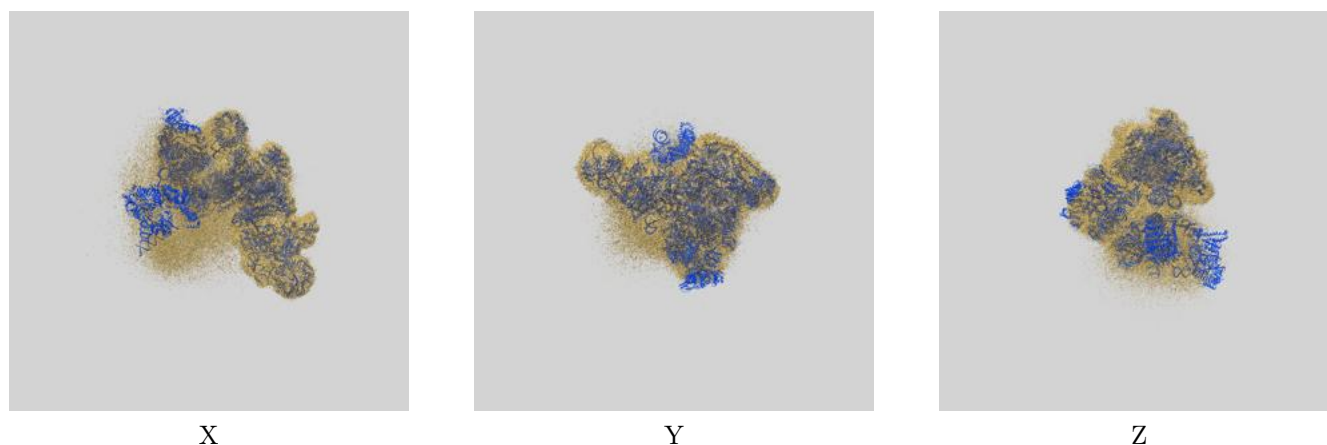
## 8 Fourier-Shell correlation

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

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

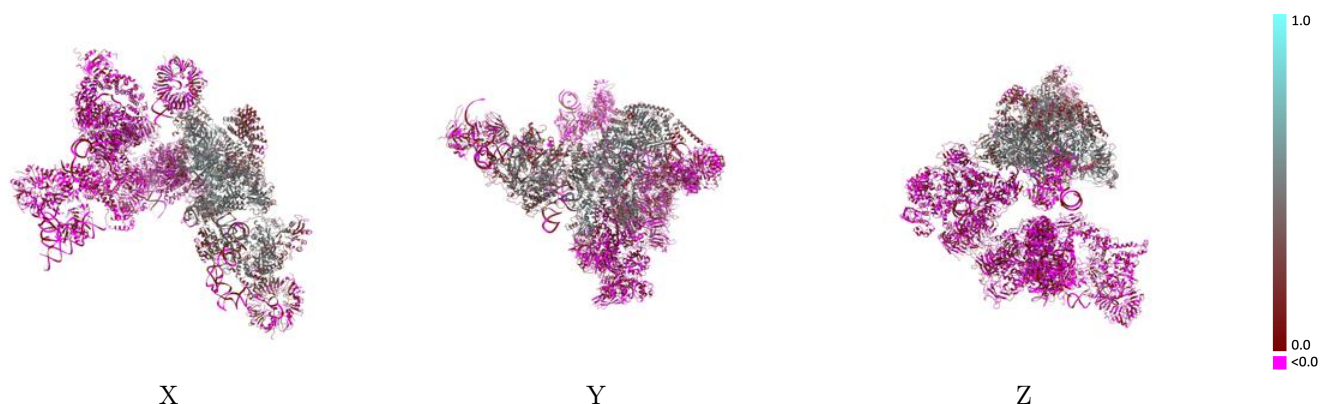
This section contains information regarding the fit between EMDB map EMD-6972 and PDB model 5ZWM. Per-residue inclusion information can be found in section 3 on page 14.

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



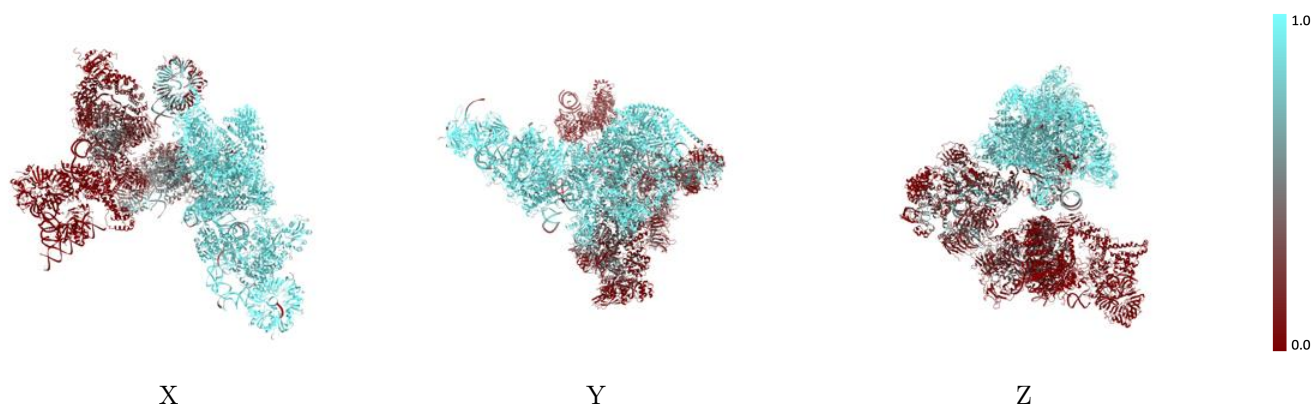
The images above show the 3D surface view of the map at the recommended contour level 0.023 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



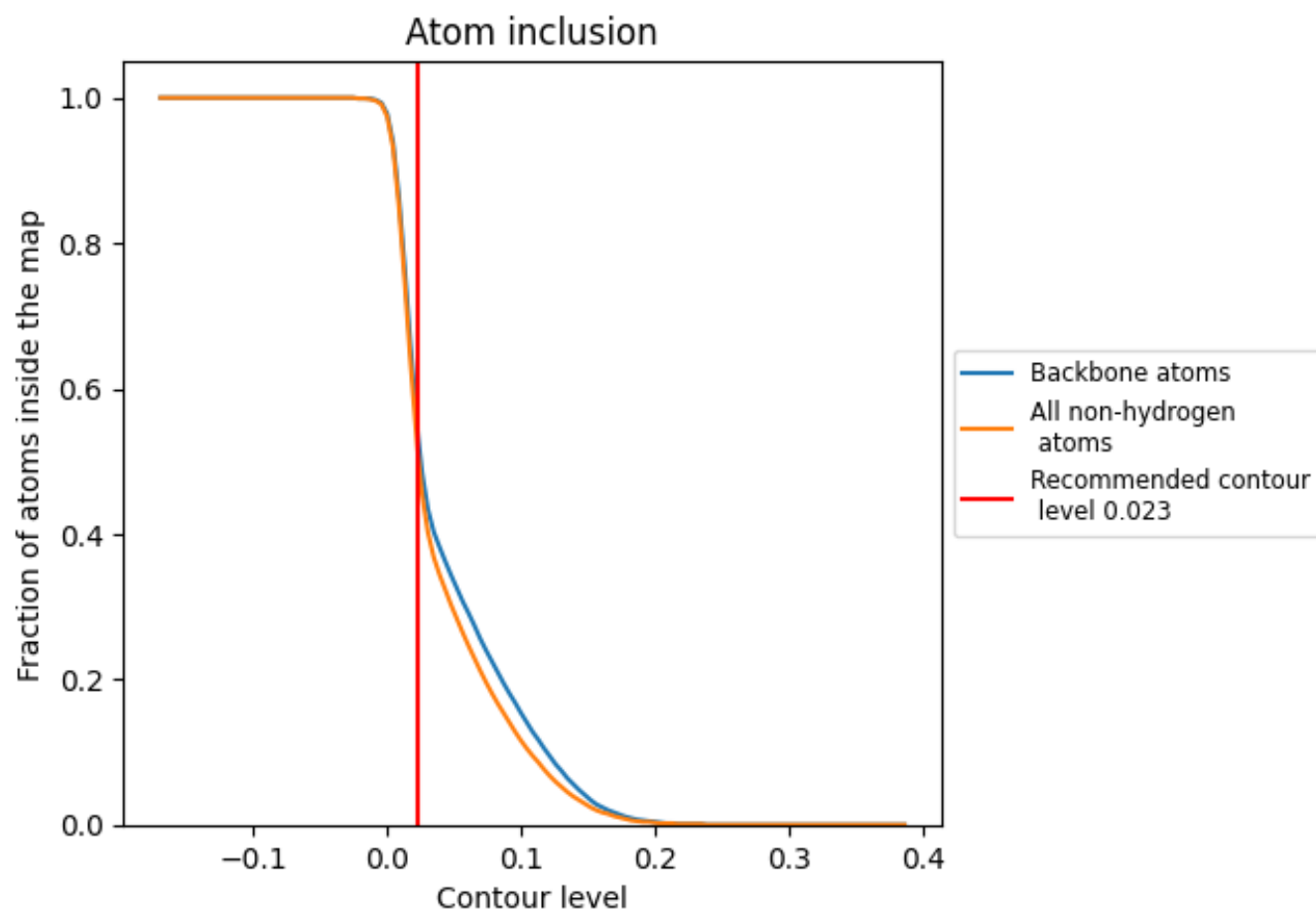
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.023).







































































## 9.4 Atom inclusion ⓘ



At the recommended contour level, 53% of all backbone atoms, 50% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ















































The table lists the average atom inclusion at the recommended contour level (0.023) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5050	 0.1620
1	 0.1700	 0.0010
2	 0.1600	 0.0170
3	 0.1710	 0.0070
4	 0.0560	 -0.0180
5	 0.2770	 0.0070
6	 0.3170	 -0.0020
A	 0.8430	 0.3780
B	 0.8820	 0.1520
C	 0.9060	 0.3540
D	 0.2770	 -0.0020
E	 0.9180	 0.4420
F	 0.8230	 0.2670
G	 0.2000	 -0.0050
H	 0.0740	 0.0020
I	 0.8240	 0.3140
J	 0.9240	 0.4150
K	 0.9220	 0.4350
L	 0.9290	 0.4290
M	 0.9550	 0.5200
N	 0.9200	 0.3230
O	 0.7580	 0.2720
P	 0.5390	 -0.0080
Q	 0.3850	 -0.0020
R	 0.4290	 -0.0110
S	 0.5940	 0.0110
T	 0.1550	 -0.0060
U	 0.2720	 -0.0290
V	 0.2620	 0.0160
X	 0.0050	 0.0070
Y	 0.0010	 -0.0100
Z	 0.0060	 -0.0350
a	 0.9490	 0.2050
b	 0.9380	 0.1490
c	 0.9310	 0.0690



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Chain	Atom inclusion	Q-score
d	 0.9810	 0.2910
e	 0.9510	 0.0850
f	 0.9210	 0.1000
g	 0.8570	 0.0540
h	 0.0070	 0.0250
i	 0.0020	 0.0280
j	 0.0040	 -0.0190
k	 0.0040	 -0.0070
l	 0.0150	 0.0050
m	 0.0080	 0.0080
n	 0.0020	 0.0010
o	 0.0080	 0.0140
p	 0.0060	 0.0150
q	 0.4430	 0.0150
r	 0.5030	 0.0150
s	 0.4160	 0.0280
t	 0.6400	 0.0210
u	 0.0320	 -0.0030
v	 0.0980	 -0.0010
w	 0.0060	 -0.0230
x	 0.5510	 0.0480
y	 0.6170	 0.0200
z	 0.2920	 -0.0110