Full wwPDB EM Validation Report ⓘ

Nov 8, 2022 – 09:18 AM JST

PDB ID	:	5Z57
EMDB ID	:	EMD-6890
Title	:	Cryo-EM structure of the human activated spliceosome (late Bact) at 6.5 angstrom
Authors	:	Zhang, X.; Yan, C.; Zhan, X.; Li, L.; Lei, J.; Shi, Y.
Deposited on	:	2018-01-17
Resolution	:	6.50 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

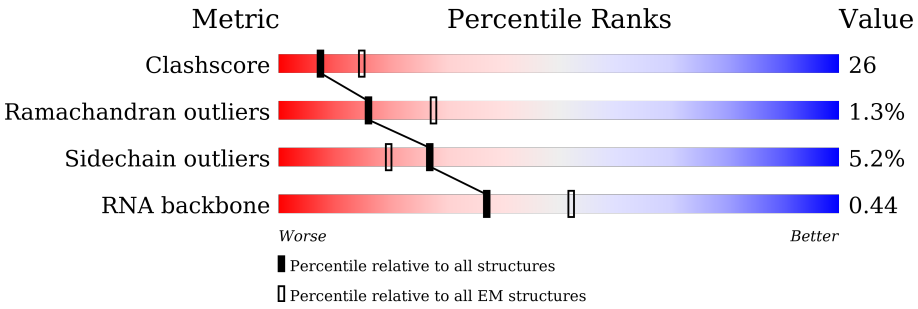
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 6.50 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	2335	18% 48% 33% · 15%
2	B	117	13% 29% 26% 14% · 28%
3	C	972	8% 49% 31% 7% · 12%
4	D	2136	78% 79% · 19%
5	E	357	22% 58% 22% · 16%
6	a	126	57% 64% 36%
6	h	126	60% 63% 37%

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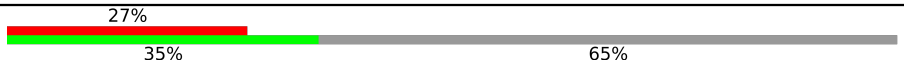
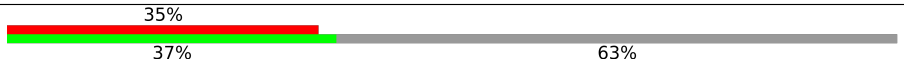
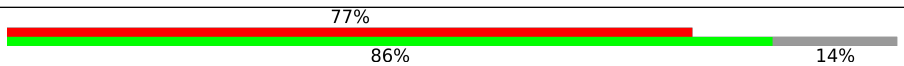
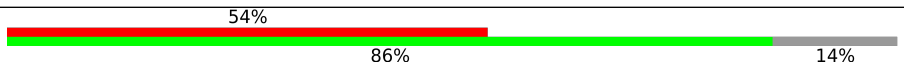
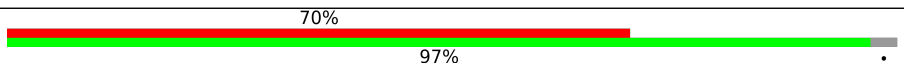
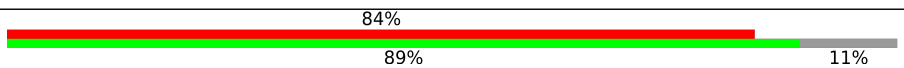
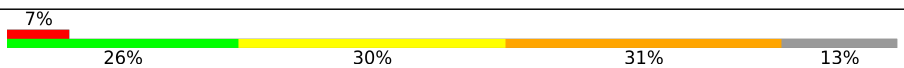
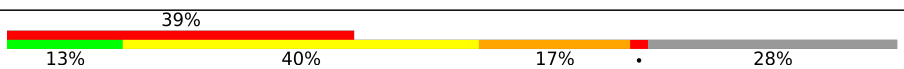
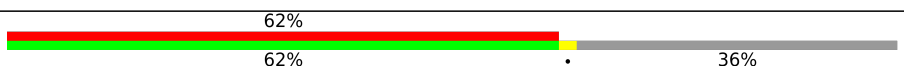
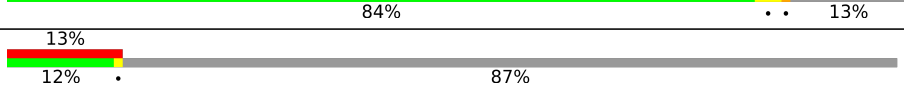
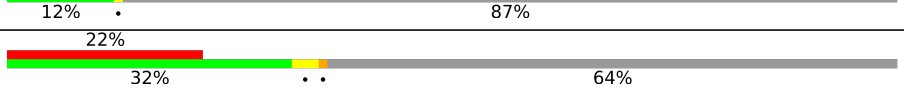
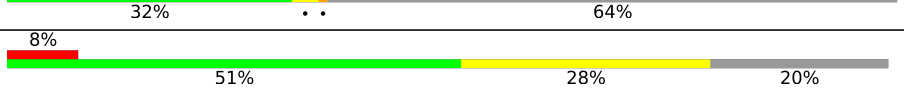
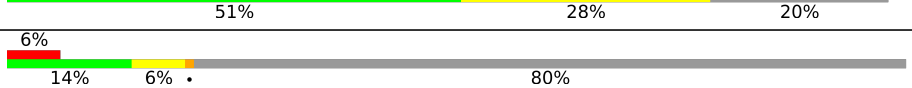
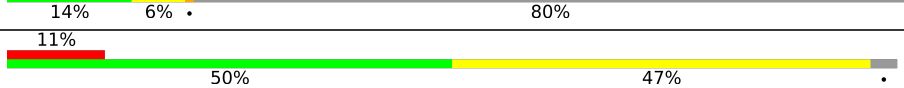
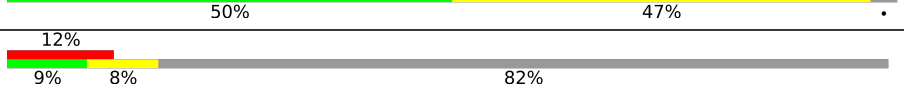
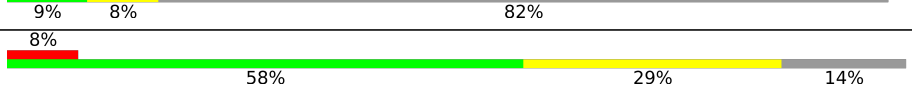
Mol	Chain	Length	Quality of chain
7	b	231	
7	i	231	
8	c	119	
8	j	119	
9	d	118	
9	k	118	
10	f	86	
10	m	86	
11	e	92	
11	l	92	
12	g	76	
12	n	76	
13	F	107	
14	G	274	
15	H	188	
16	o	255	
17	p	225	
18	w	501	
19	u	793	
20	v	464	
21	1	1304	
22	2	895	
23	3	1217	
24	4	424	
25	5	125	

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Mol	Chain	Length	Quality of chain
26	6	110	11% 55% 26% 19%
27	7	86	7% 43% 33% 23%
28	J	848	41% 54% 7% 38%
29	L	802	27% 35% 7% 57%
30	q	504	26% 25% 74%
30	r	504	25% 25% 74%
30	s	504	12% 13% 87%
30	t	504	13% 13% 87%
31	K	225	60% 54% 12% 32%
32	I	855	64% 60% 6% 34%
33	Q	1485	87% 89% 11%
34	N	144	6% 58% 36% 5%
35	O	420	28% 33% 31% 32%
36	P	229	25% 18% 18% 5% 58%
37	R	540	20% 25% 18% 9% 47%
38	S	166	40% 59% 30% 6%
39	T	514	36% 20% 39%
40	U	2752	99%
41	V	908	28% 44% 5% 50%
42	W	579	66% 64% 17% 17%
43	X	396	11% 31% 9% 60%
44	Y	322	16% 17% 67%
45	Z	619	8% 9% 7% 82%
46	x	1041	56% 55% 44%
47	y	301	68% 77% 23%

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
48	IHP	A	2401	-	-	X	-
50	GTP	C	1500	-	-	X	-
52	ZN	O	502	-	-	X	-

2 Entry composition (i)

There are 52 unique types of molecules in this entry. The entry contains 113433 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-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1978	16399	10552	2875	2897	75	0	0

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	84	1768	792	295	597	84	0	0

- Molecule 3 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	860	6716	4294	1120	1270	32	0	0

- Molecule 4 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	D	1722	8528	5084	1722	1722	0	0

- Molecule 5 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	299	2338	1470	410	445	13	0	0

- Molecule 6 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	a	81	399	237	81	81	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
6	h	80	Total 393	C 233	N 80	O 80	0	0

- Molecule 7 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	b	82	Total 405	C 241	N 82	O 82	0	0
7	i	86	Total 422	C 250	N 86	O 86	0	0

- Molecule 8 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	c	82	Total 406	C 242	N 82	O 82	0	0
8	j	82	Total 406	C 242	N 82	O 82	0	0

- Molecule 9 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	d	97	Total 480	C 286	N 97	O 97	0	0
9	k	85	Total 422	C 252	N 85	O 85	0	0

- Molecule 10 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	f	74	Total 361	C 213	N 74	O 74	0	0
10	m	74	Total 361	C 213	N 74	O 74	0	0

- Molecule 11 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	e	79	Total 391	C 233	N 79	O 79	0	0
11	l	79	Total 391	C 233	N 79	O 79	0	0

- Molecule 12 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	g	74	Total 363	C 215	N 74	O 74	0	0
12	n	68	Total 334	C 198	N 68	O 68	0	0

- Molecule 13 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	93	Total 1988	C 889	N 363	O 643	P 93	0	0

- Molecule 14 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	77	Total 1545	C 689	N 240	O 539	P 77	0	0

- Molecule 15 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	136	Total 2886	C 1289	N 499	O 962	P 136	0	0

- Molecule 16 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	o	162	Total 804	C 480	N 162	O 162	0	0

- Molecule 17 is a protein called U2 small nuclear ribonucleoprotein B".

Mol	Chain	Residues	Atoms				AltConf	Trace
17	p	165	Total 813	C 483	N 165	O 165	0	0

- Molecule 18 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	w	438	Total 2373	C 1450	N 461	O 459	S 3	0	0

- Molecule 19 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	u	104	Total	C	N	O	0	0
			520	312	104	104		

- Molecule 20 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	v	165	Total	C	N	O	S	0	0
			936	565	191	178	2		

- Molecule 21 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	1	1038	Total	C	N	O	S	0	0
			7702	4900	1347	1415	40		

- Molecule 22 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	2	183	Total	C	N	O	S	0	0
			1252	809	213	226	4		

- Molecule 23 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3	1177	Total	C	N	O	S	0	0
			9195	5834	1561	1755	45		

- Molecule 24 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	4	78	Total	C	N	O	0	0
			527	345	83	99		

- Molecule 25 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	5	108	Total	C	N	O	S	0	0
			807	512	142	150	3		

- Molecule 26 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	6	89	Total	C	N	O	S	0	0
			670	410	119	128	13		

- Molecule 27 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	7	66	Total	C	N	O	S	0	0
			540	343	94	98	5		

- Molecule 28 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	J	522	Total	C	N	O	S	0	0
			3463	2156	653	648	6		

- Molecule 29 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L	342	Total	C	N	O	S	0	0
			2260	1430	406	420	4		

- Molecule 30 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	q	132	Total	C	N	O	0	0
			659	395	132	132		
30	r	131	Total	C	N	O	0	0
			654	392	131	131		
30	s	67	Total	C	N	O	0	0
			335	201	67	67		
30	t	67	Total	C	N	O	0	0
			335	201	67	67		

- Molecule 31 is a protein called Pre-mRNA-splicing factor SPF27.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	K	152	Total	C	N	O	S	0	0
			979	611	177	189	2		

- Molecule 32 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	I	564	Total	C	N	O	0	0
			2778	1650	564	564		

- Molecule 33 is a protein called Intron-binding protein aquarius.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	Q	1317	Total	C	N	O	0	0
			6528	3894	1317	1317		

- Molecule 34 is a protein called Protein BUD31 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	N	143	Total	C	N	O	S	0	0
			1184	746	217	209	12		

- Molecule 35 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	O	285	Total	C	N	O	S	0	0
			2273	1428	401	424	20		

- Molecule 36 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	P	96	Total	C	N	O	S	0	0
			829	508	162	157	2		

- Molecule 37 is a protein called Skip.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	R	288	Total	C	N	O	S	0	0
			2188	1375	392	409	12		

- Molecule 38 is a protein called Peptidyl-prolyl cis-trans isomerase-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	S	159	Total	C	N	O	S	0	0
			1236	787	215	227	7		

- Molecule 39 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	T	313	Total	C	N	O	S	0	0
			2457	1552	447	450	8		

- Molecule 40 is a protein called Serine/arginine repetitive matrix protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	U	26	Total	C	N	O	S	0	0
			193	120	36	36	1		

- Molecule 41 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	V	452	Total	C	N	O	0	0
			2243	1339	452	452		

- Molecule 42 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	W	483	Total	C	N	O	0	0
			2384	1418	483	483		

- Molecule 43 is a protein called Smad nuclear-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	X	158	Total	C	N	O	S	0	0
			1012	645	172	194	1		

- Molecule 44 is a protein called RNA-binding motif protein, X-linked 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Y	105	Total	C	N	O	S	0	0
			743	470	127	144	2		

- Molecule 45 is a protein called BUD13 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	Z	113	Total	C	N	O	0	0
			755	474	147	134		

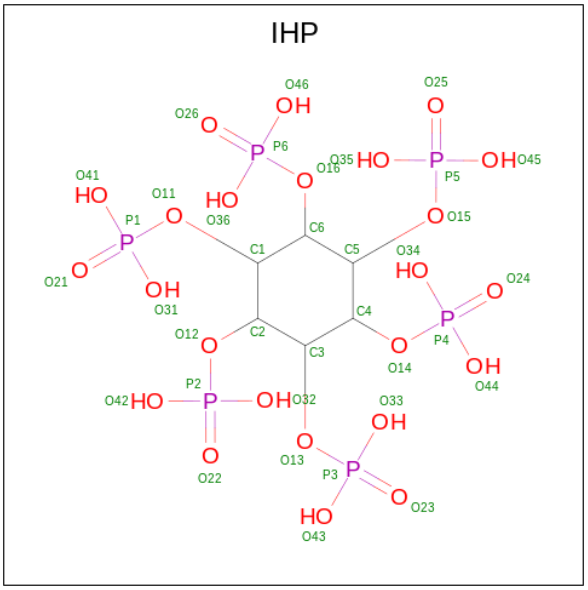
- Molecule 46 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	x	583	Total	C	N	O	0	0
			2882	1715	583	584		

- Molecule 47 is a protein called Peptidyl-prolyl cis-trans isomerase E.

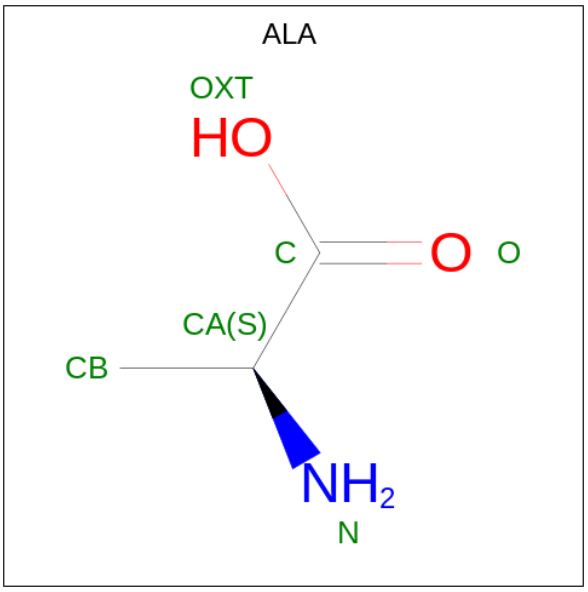
Mol	Chain	Residues	Atoms				AltConf	Trace
47	y	232	Total	C	N	O	0	0
			1133	669	232	232		

- Molecule 48 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: $C_6H_{18}O_{24}P_6$).



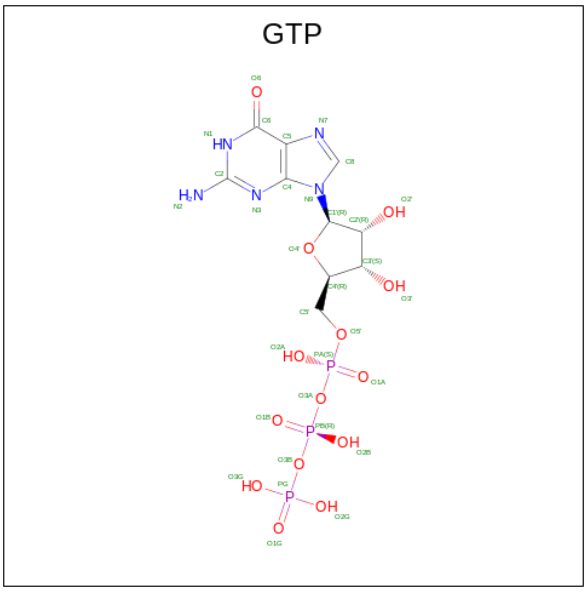
Mol	Chain	Residues	Atoms				AltConf
48	A	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 49 is ALANINE (three-letter code: ALA) (formula: $C_3H_7NO_2$).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
49	A	1	5	3	1	1	0

- Molecule 50 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

- Molecule 51 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
51	C	1	Total Mg 1 1	0
51	F	5	Total Mg 5 5	0

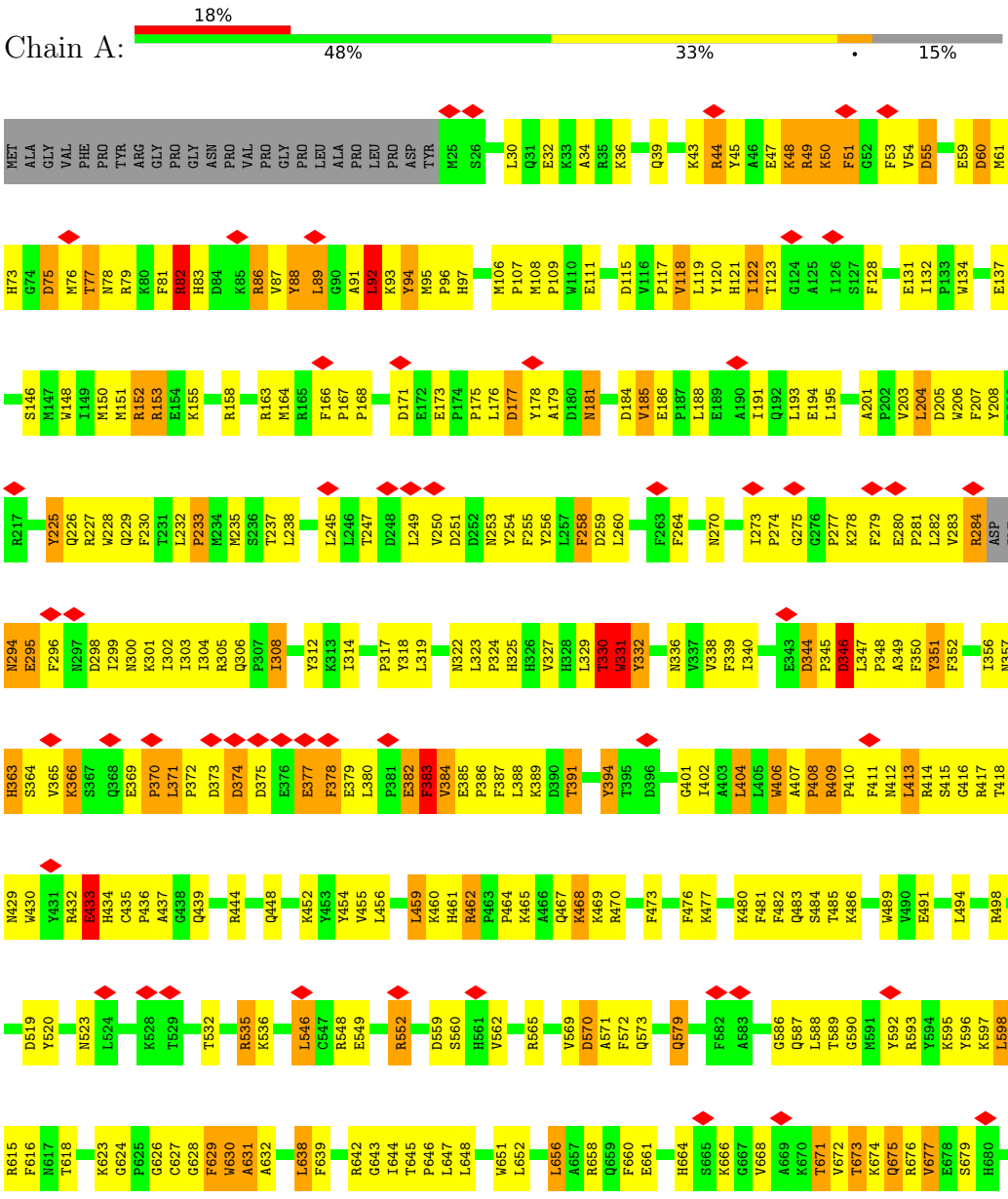
- Molecule 52 is ZINC ION (three-letter code: ZN) (formula: Zn).

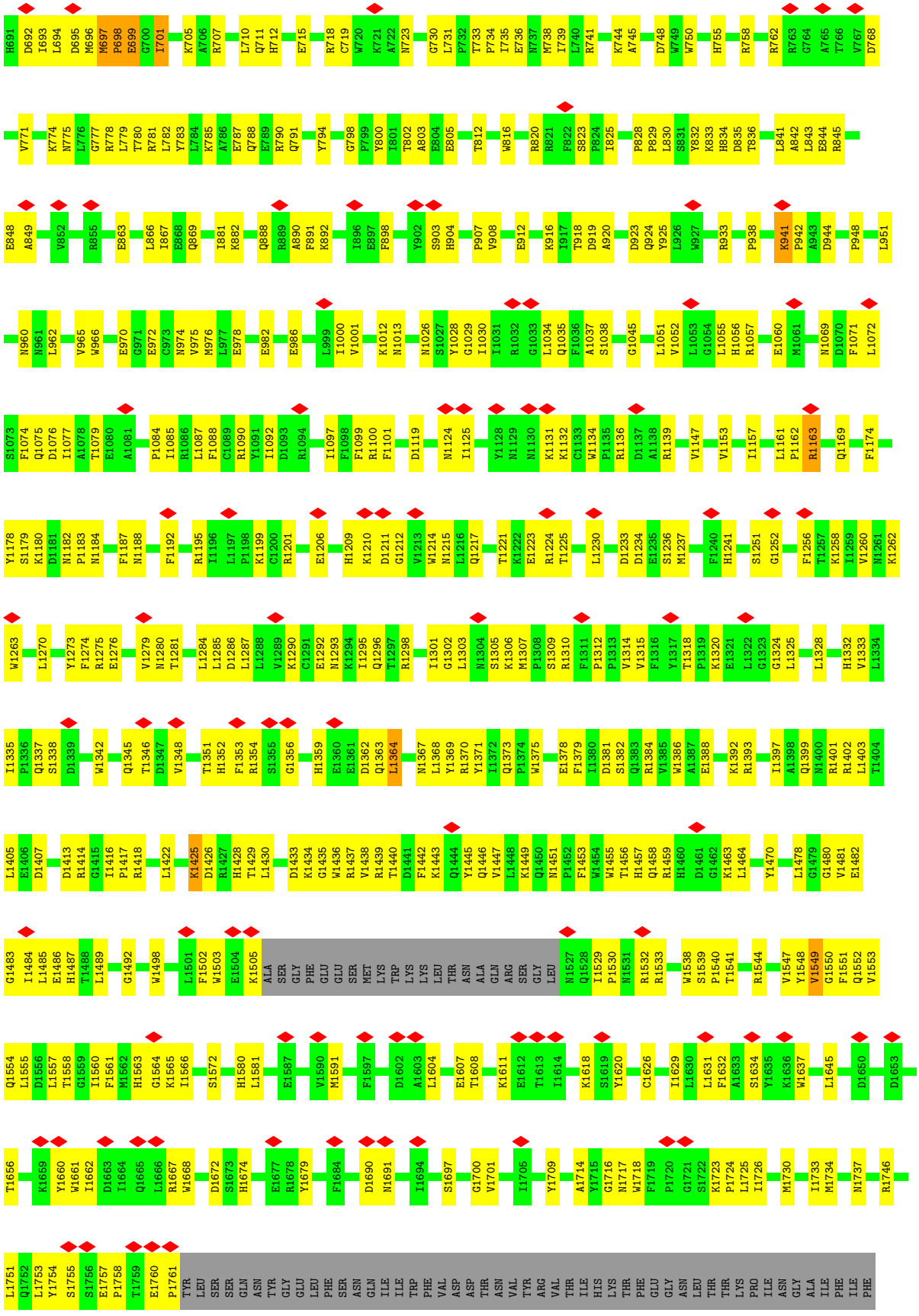
Mol	Chain	Residues	Atoms	AltConf
52	v	1	Total Zn 1 1	0
52	6	3	Total Zn 3 3	0
52	N	3	Total Zn 3 3	0
52	O	3	Total Zn 3 3	0

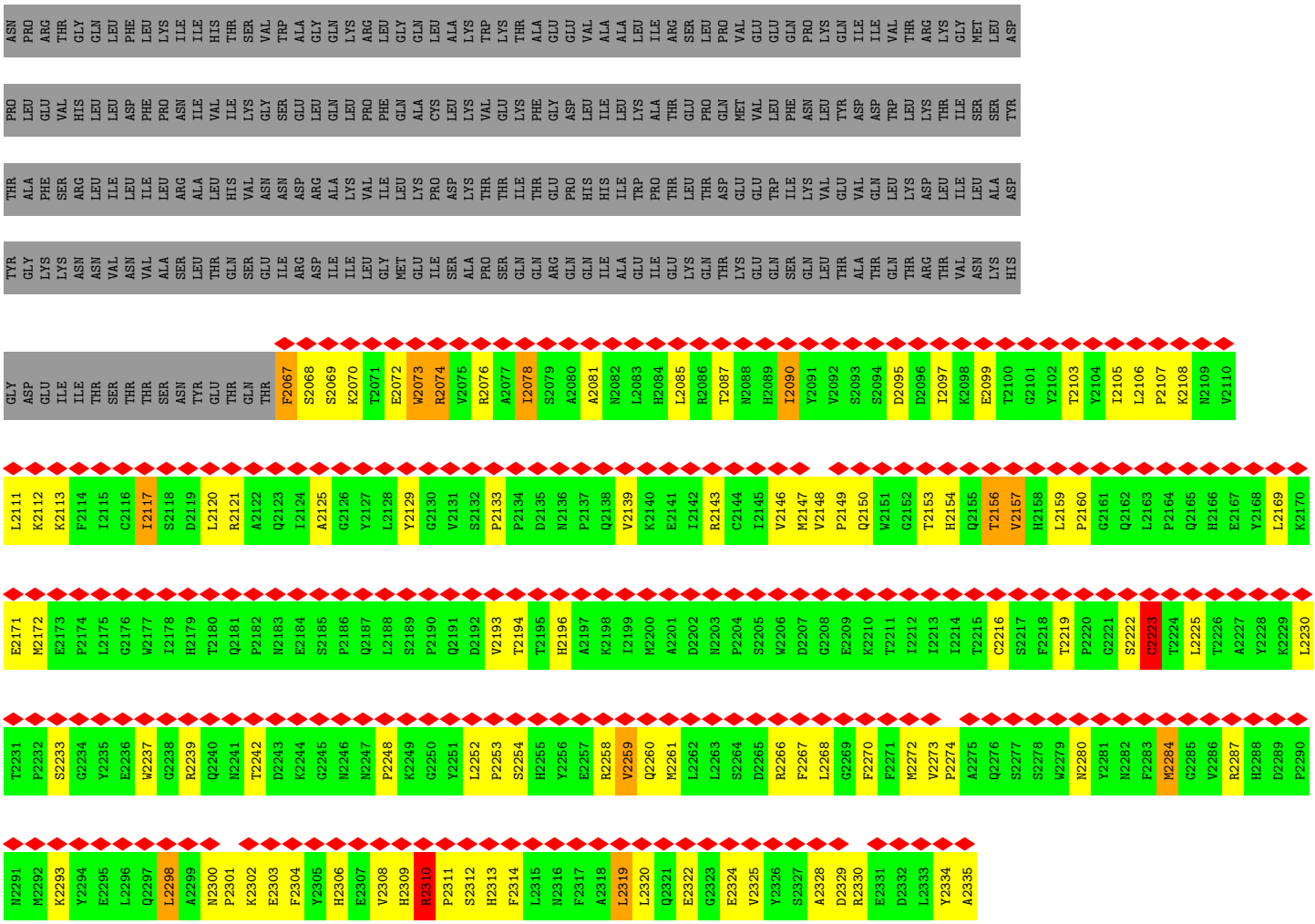
3 Residue-property plots (i)

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

• Molecule 1: Pre-mRNA-processing-splicing factor 8

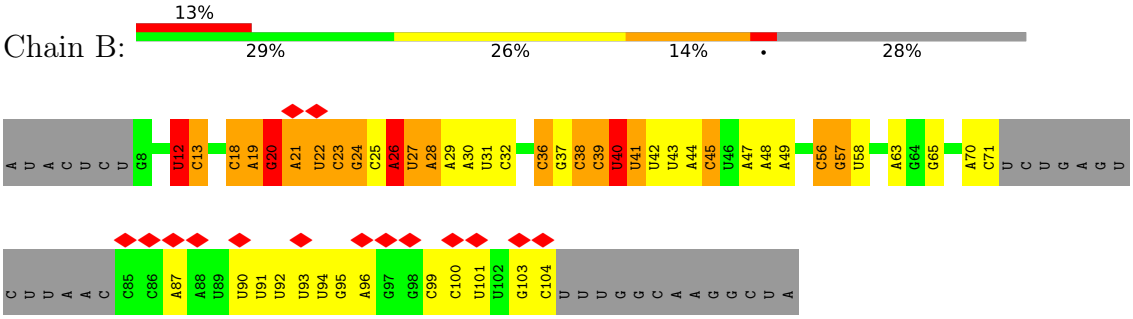






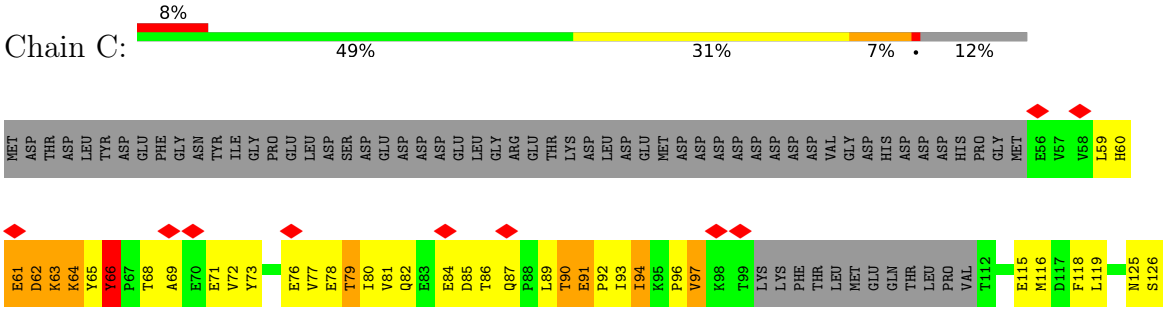
• Molecule 2: U5 snRNA

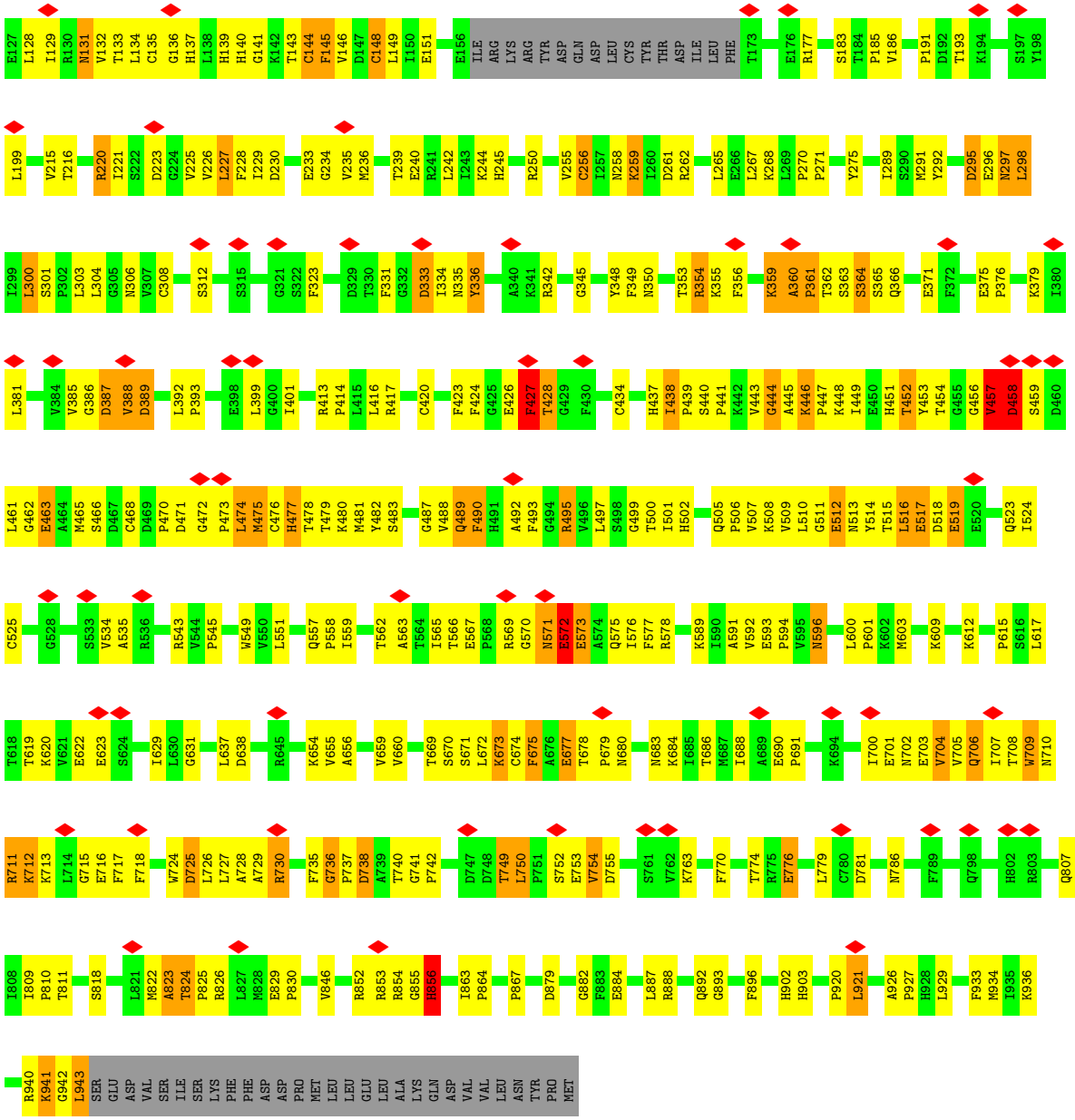
Chain B:



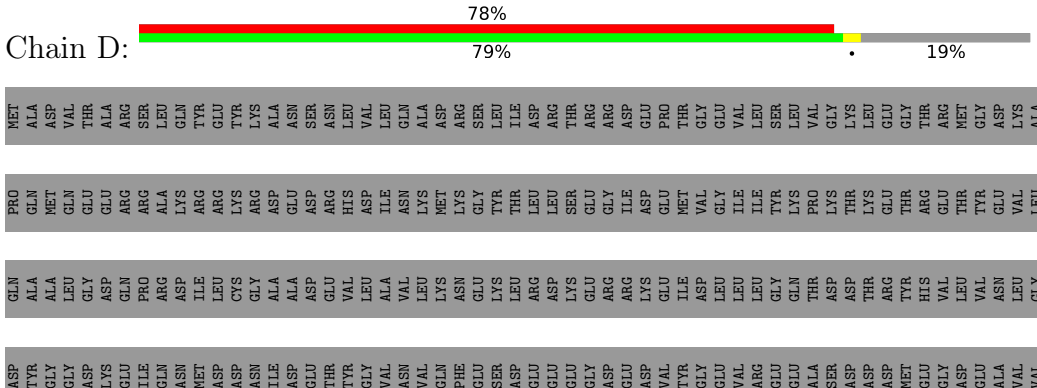
• Molecule 3: 116 kDa U5 small nuclear ribonucleoprotein component

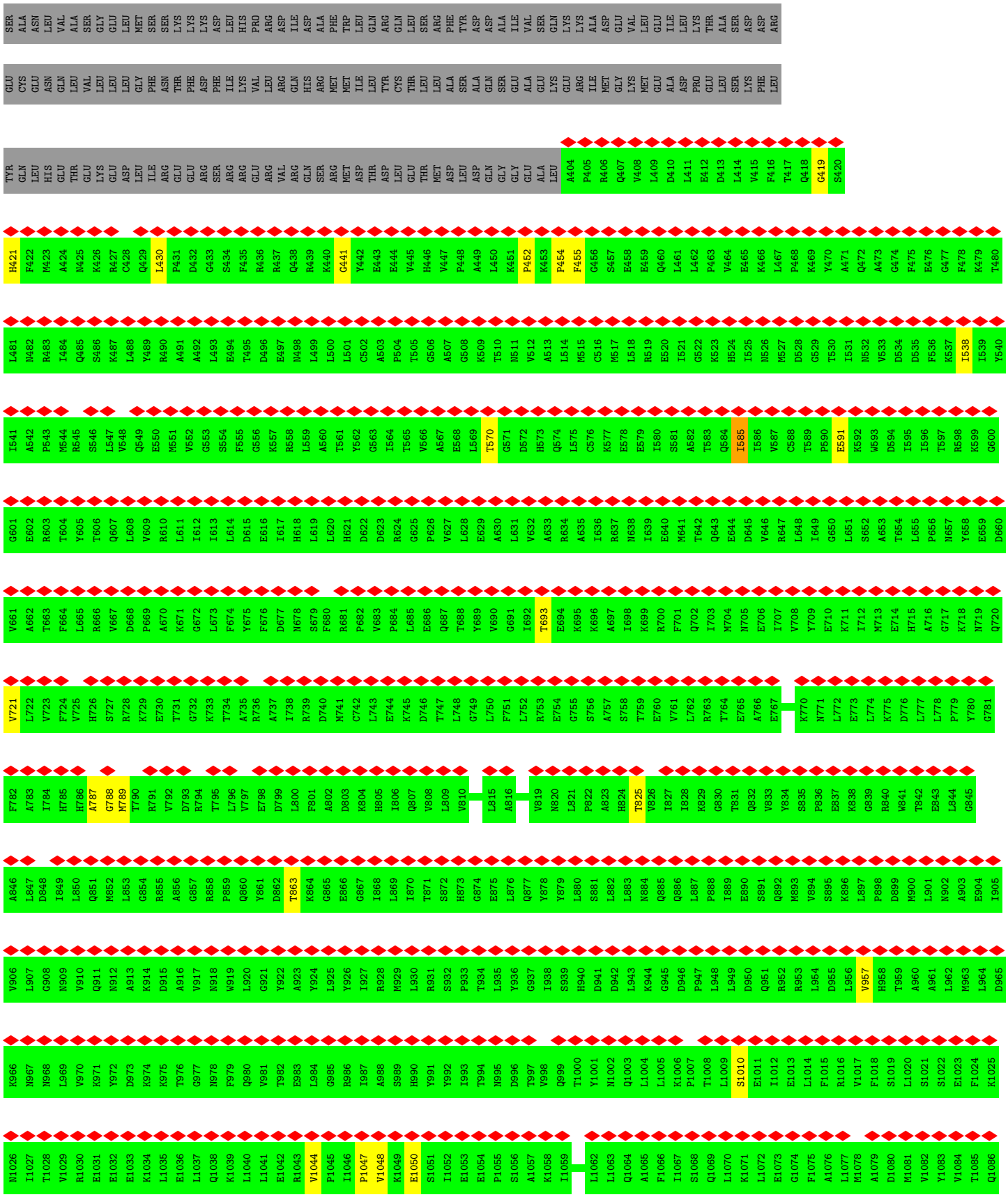
Chain C:





• Molecule 4: U5 small nuclear ribonucleoprotein 200 kDa helicase

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GLU CYS GLU ASN GLN LEU VAL LEU LEU LEU GLY PHE ASN THR PHE ASP PHE ILE LYS VAL LEU ARG GLU GLU ARG SER ARG ARG GLU ARG VAL ARG GLN HIS ARG MET MET ILE LEU TYR CYS THR LEU LEU ALA SER ALA GLN SER GLU ALA GLU LYS GLU ARG ILE MET GLY LYS MET GLU ALA ASP PRO GLU LEU SER LYS PHE LEU
TYR GLN LEU HIS GLU THR GLU LYS GLU ASP LEU ILE ARG GLU GLU ARG SER ARG ARG GLU ARG VAL ARG GLN SER ARG MET ASP THR ASP LEU GLU THR MET ASP LEU ASP GLN GLY GLY GLU ALA GLU LEU A404 P405 R406 Q407 V408 L409 D410 L411 E412 D413 L414 V415 F416 T417 Q418 G419 S420
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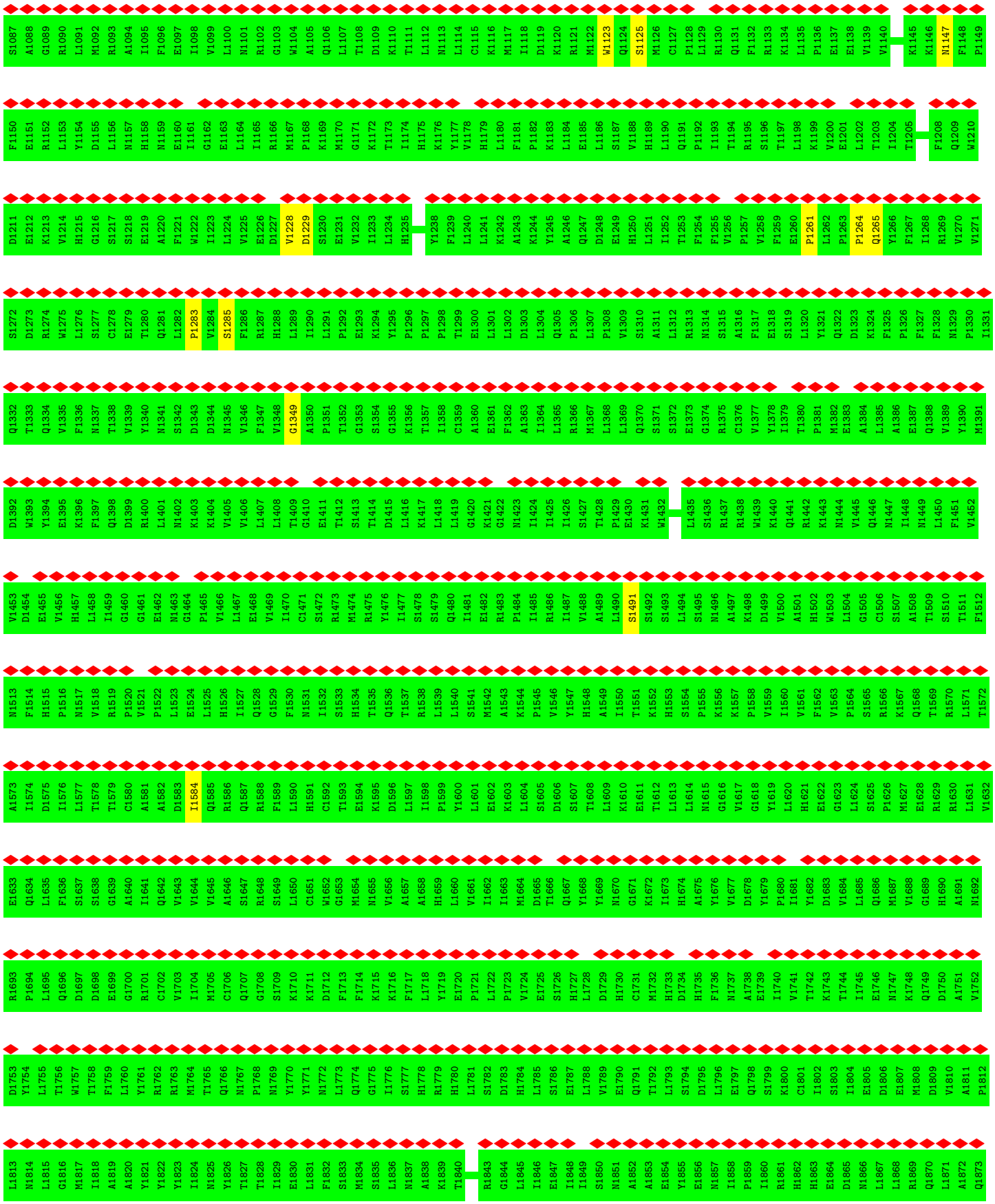
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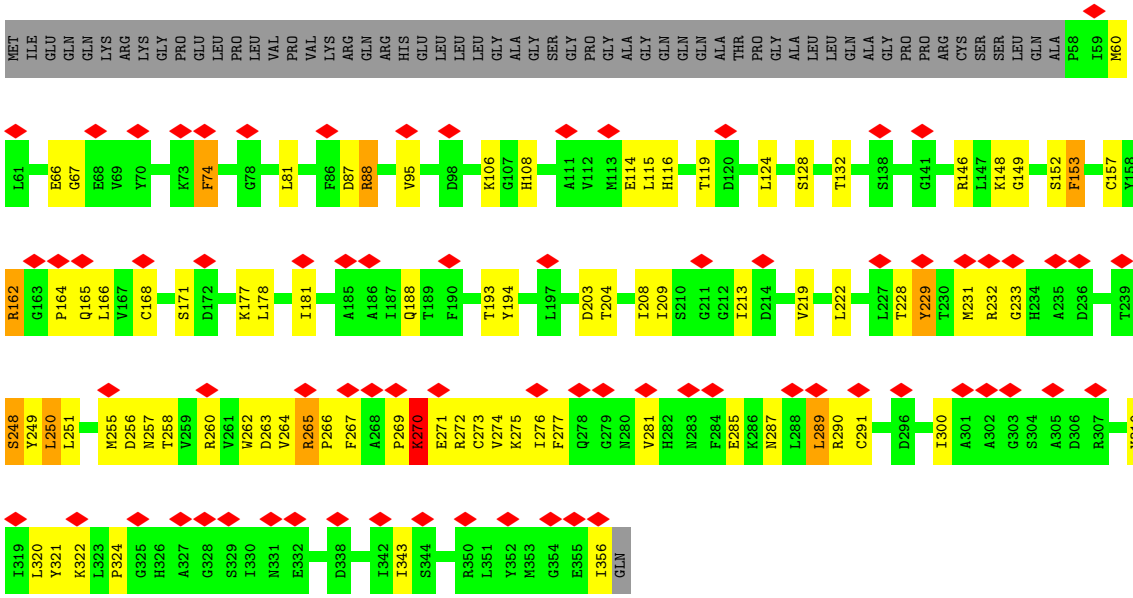
• Molecule 5: U5 small nuclear ribonucleoprotein 40 kDa protein

Chain E:



• Molecule 6: Small nuclear ribonucleoprotein Sm D3

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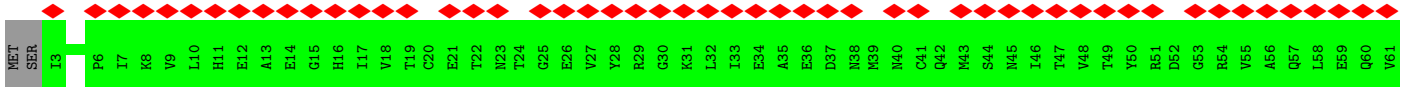
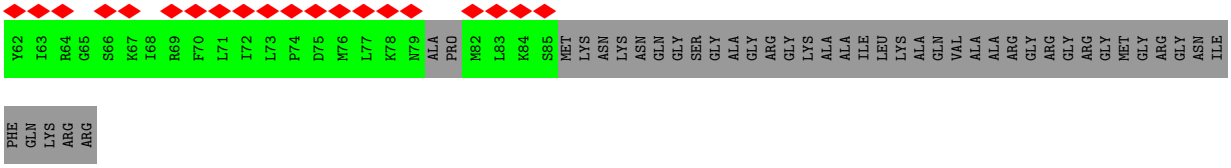
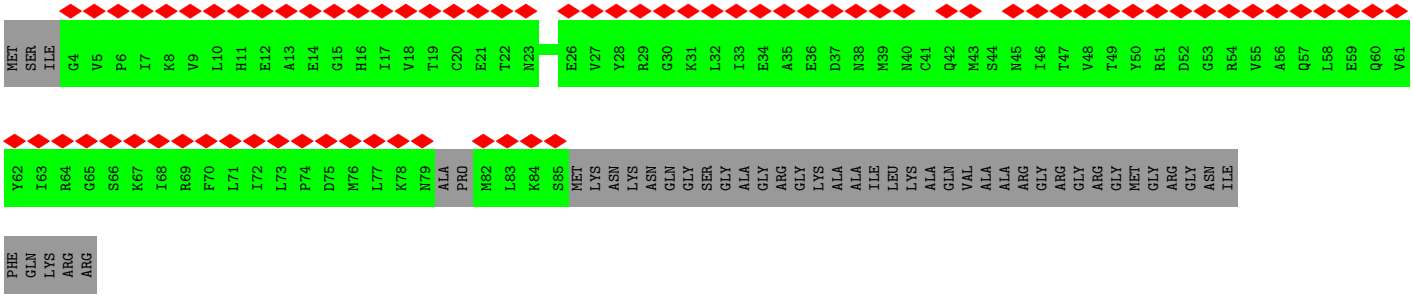
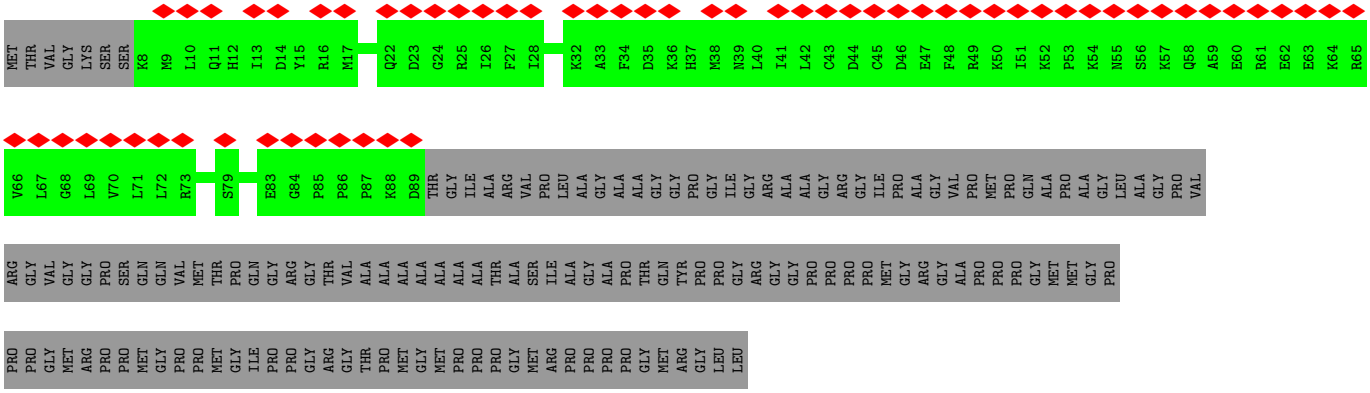




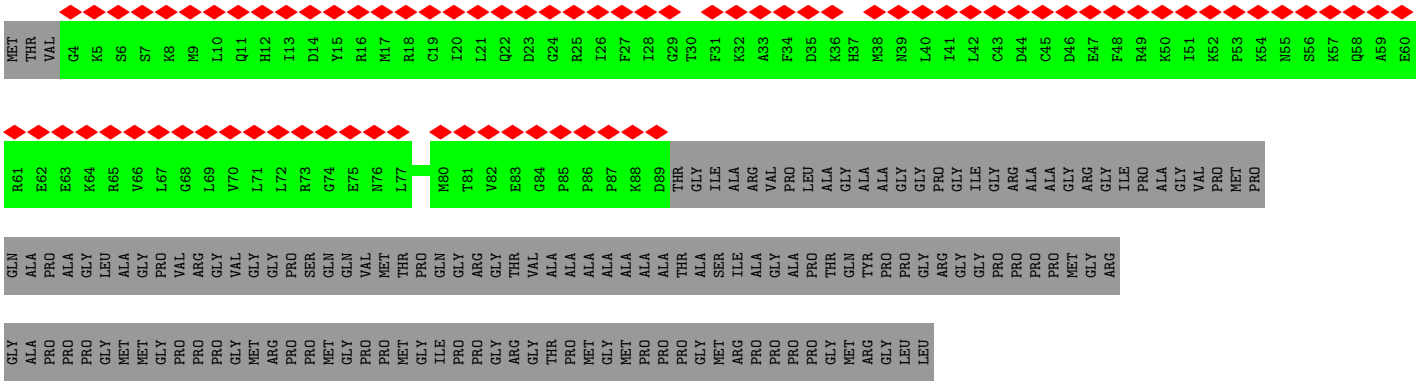
• Molecule 6: Small nuclear ribonucleoprotein Sm D3



• Molecule 7: Small nuclear ribonucleoprotein-associated proteins B and B'



• Molecule 7: Small nuclear ribonucleoprotein-associated proteins B and B'



• Molecule 8: Small nuclear ribonucleoprotein Sm D1

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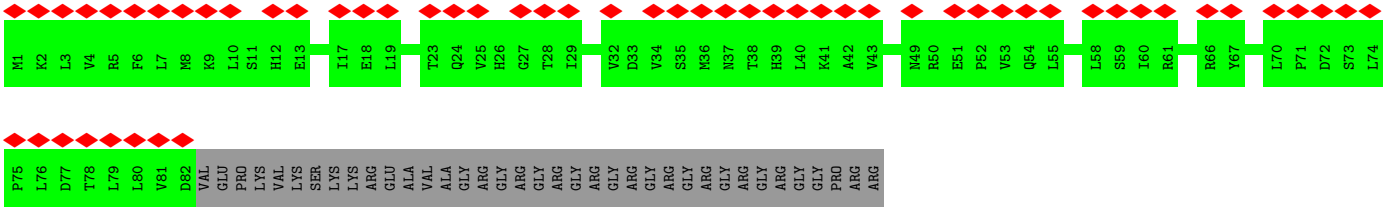
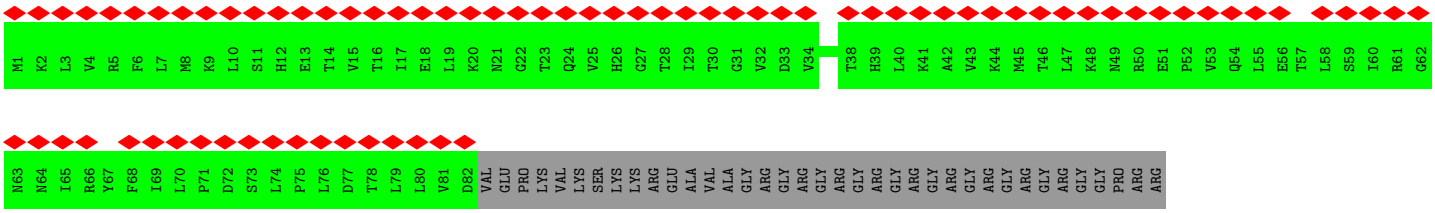


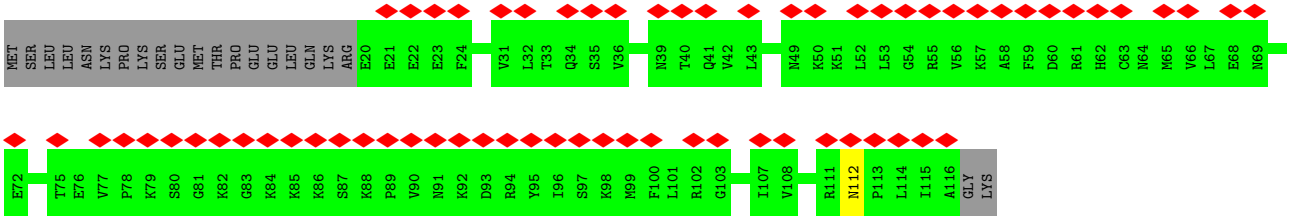
• Molecule 8: Small nuclear ribonucleoprotein Sm D1

Chain j:



• Molecule 9: Small nuclear ribonucleoprotein Sm D2

Chain d:

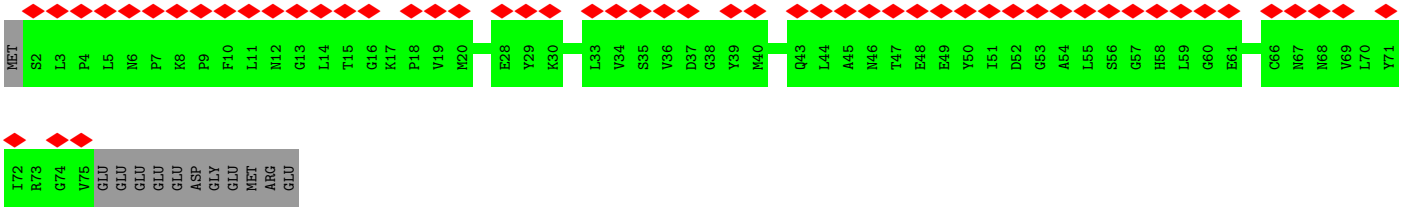


• Molecule 9: Small nuclear ribonucleoprotein Sm D2

Chain k:

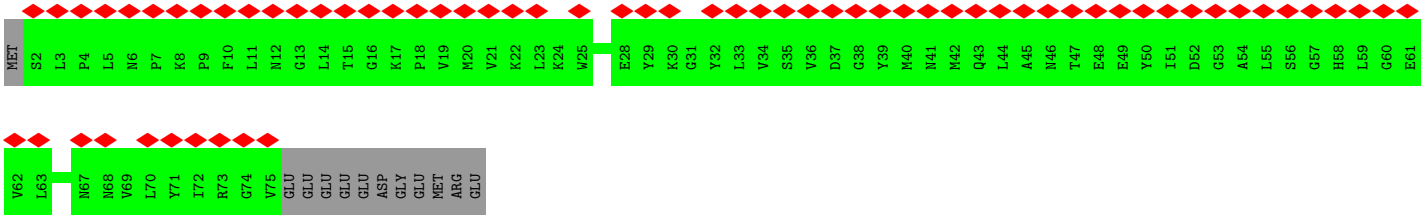
• Molecule 10: Small nuclear ribonucleoprotein F

Chain f:



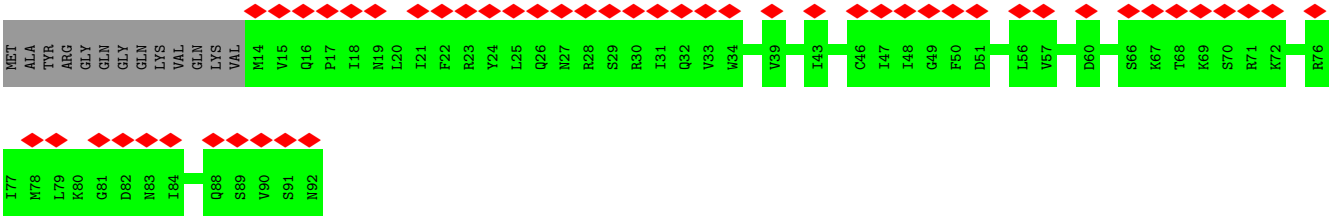
• Molecule 10: Small nuclear ribonucleoprotein F

Chain m:



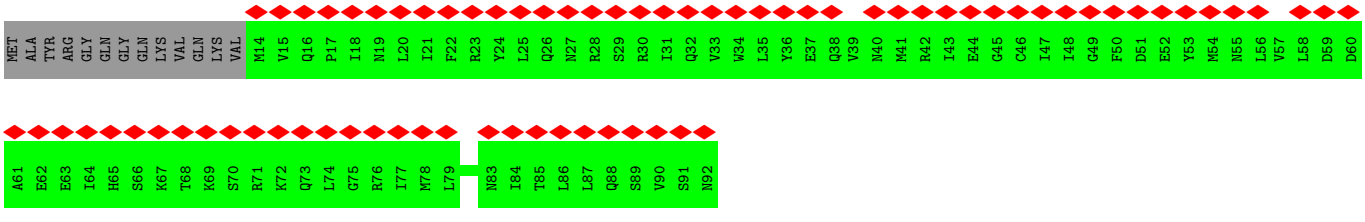
• Molecule 11: Small nuclear ribonucleoprotein E

Chain e:



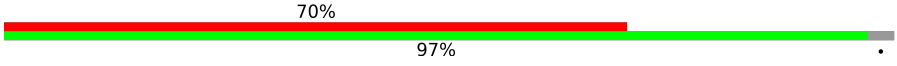
• Molecule 11: Small nuclear ribonucleoprotein E

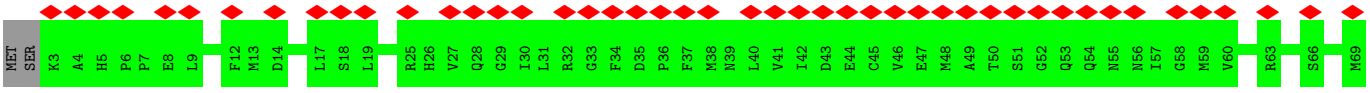
Chain l:

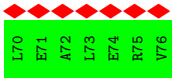


• Molecule 12: Small nuclear ribonucleoprotein G

Chain g:

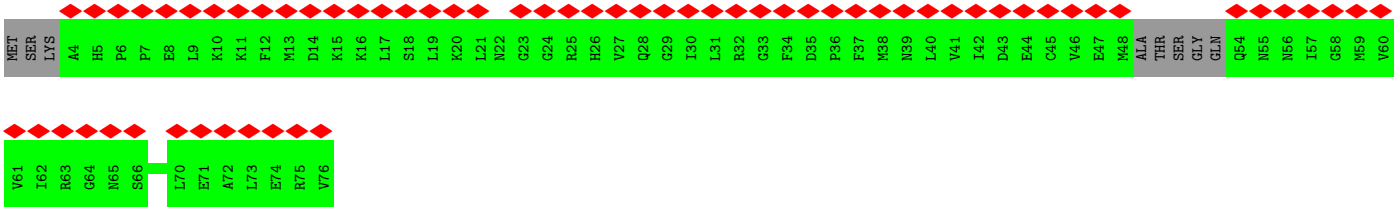






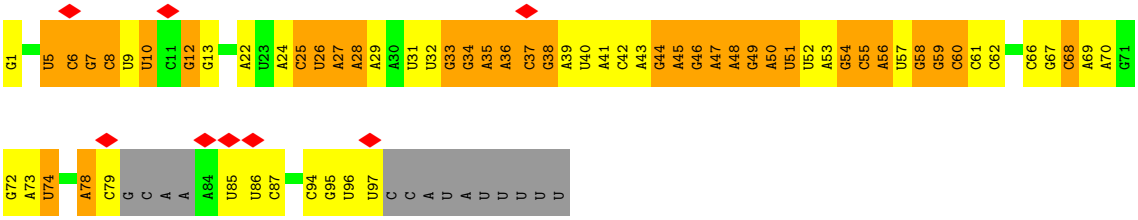
• Molecule 12: Small nuclear ribonucleoprotein G

Chain n:



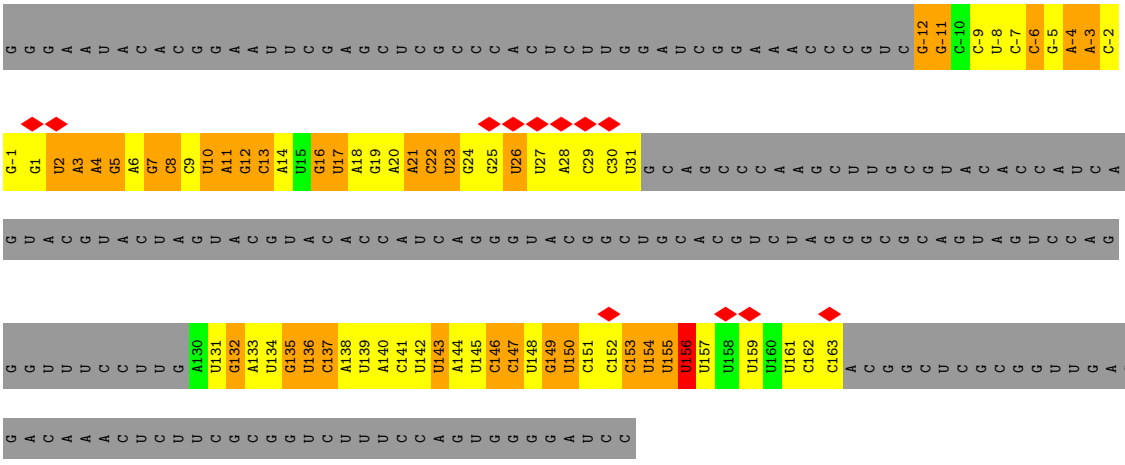
• Molecule 13: U6 snRNA

Chain F:



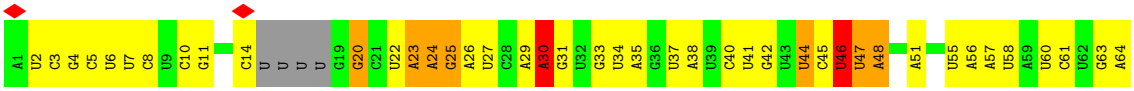
• Molecule 14: pre-mRNA

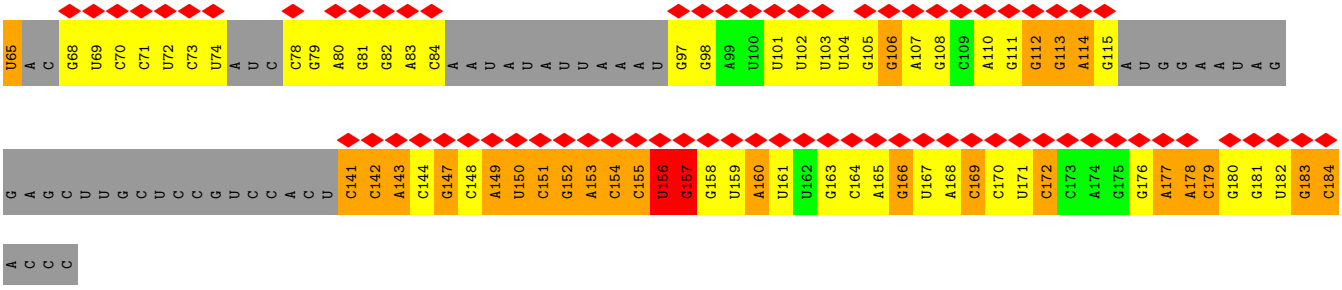
Chain G:



• Molecule 15: U2 snRNA

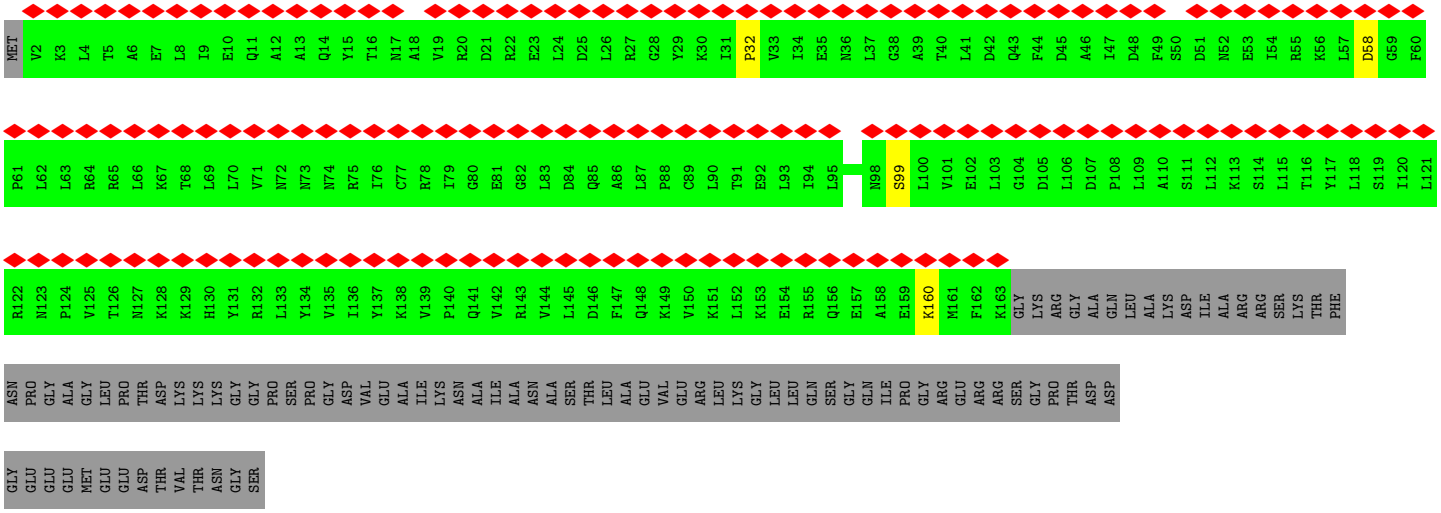
Chain H:





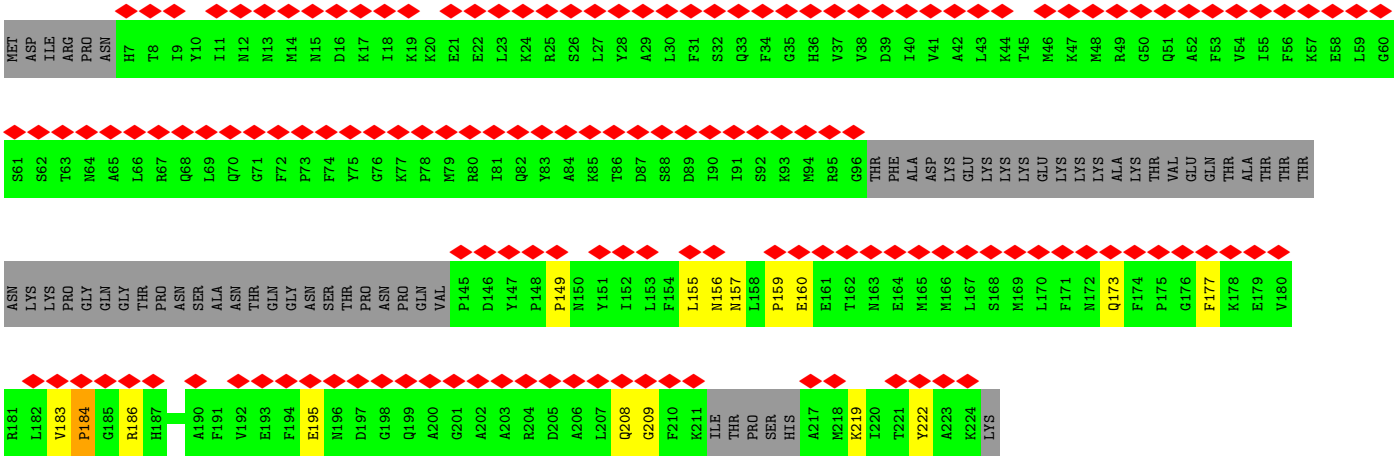
• Molecule 16: U2 small nuclear ribonucleoprotein A'

Chain o:



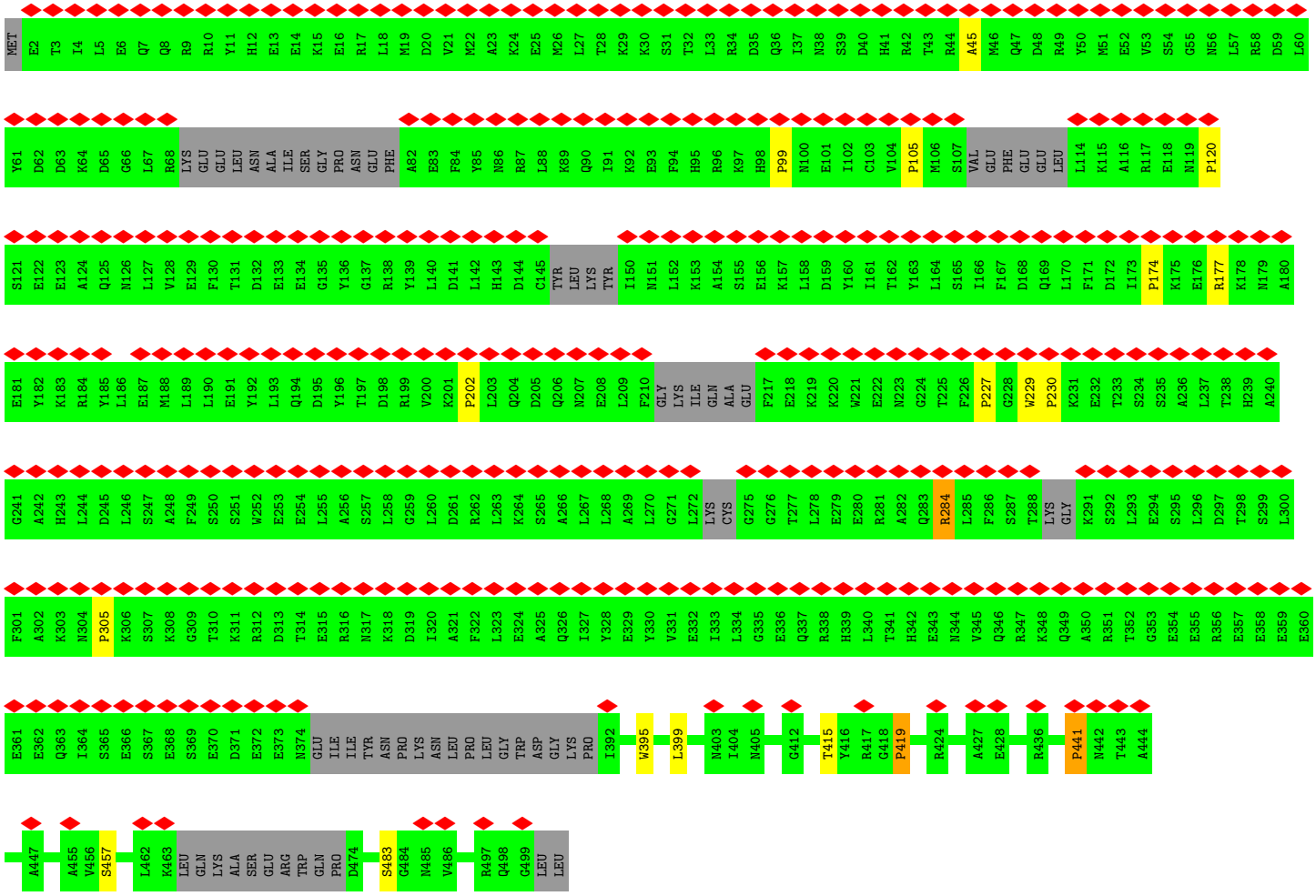
• Molecule 17: U2 small nuclear ribonucleoprotein B"

Chain p:

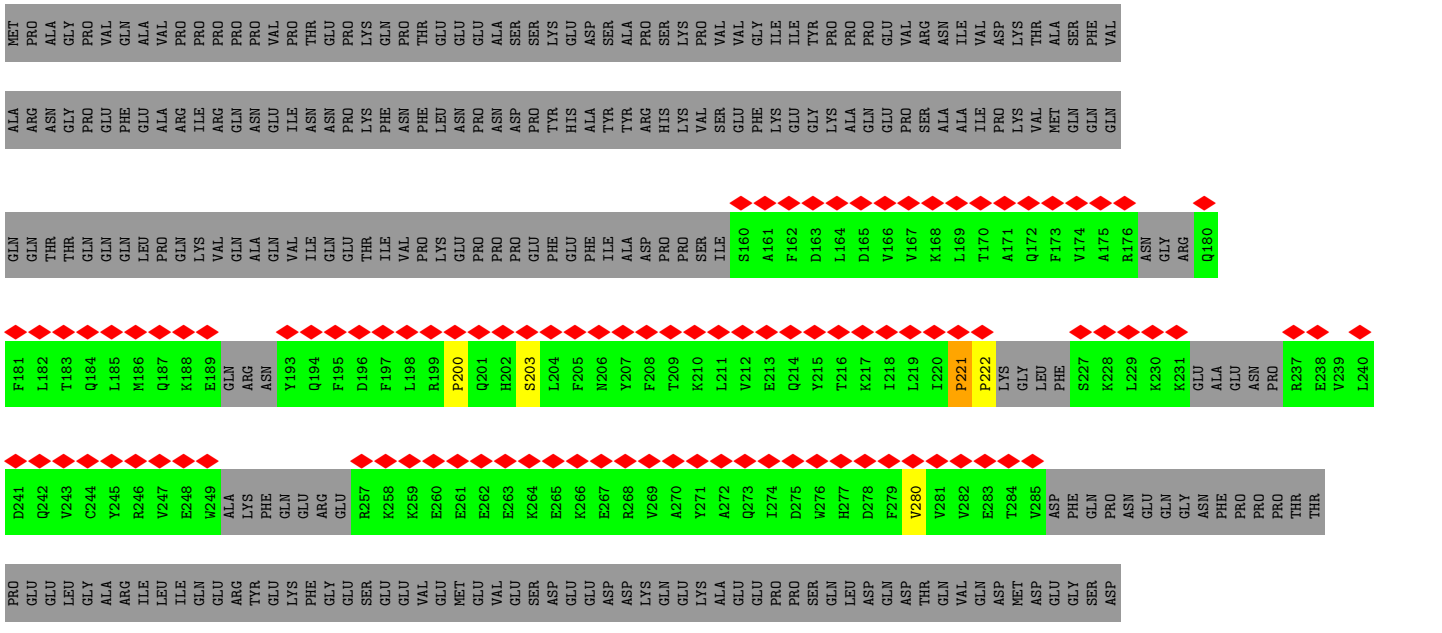


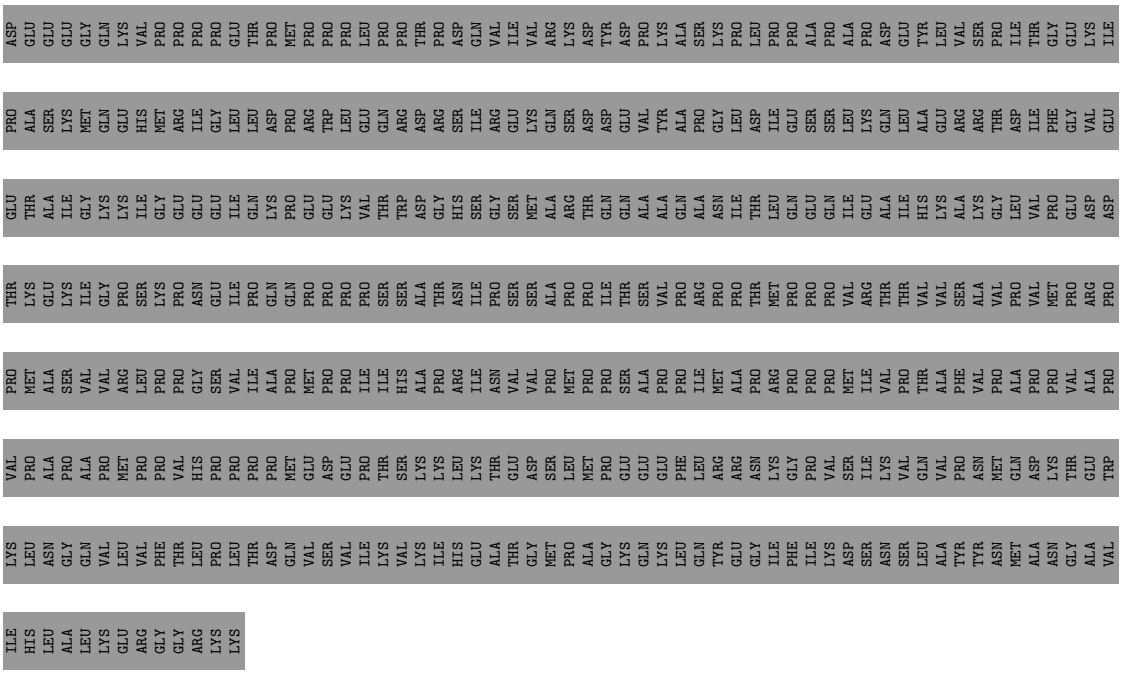
• Molecule 18: Splicing factor 3A subunit 3

Chain w:

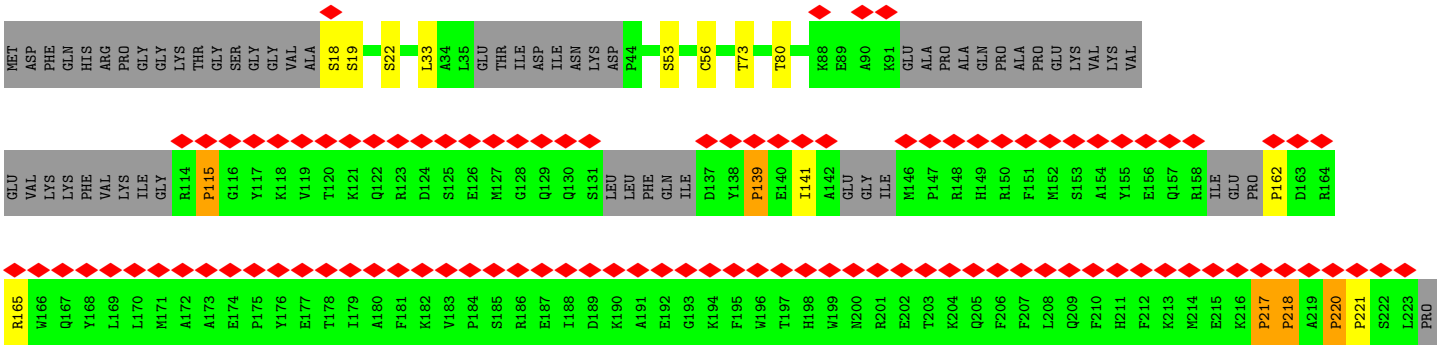


• Molecule 19: Splicing factor 3A subunit 1

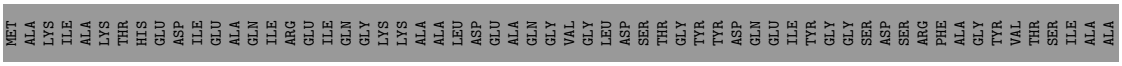


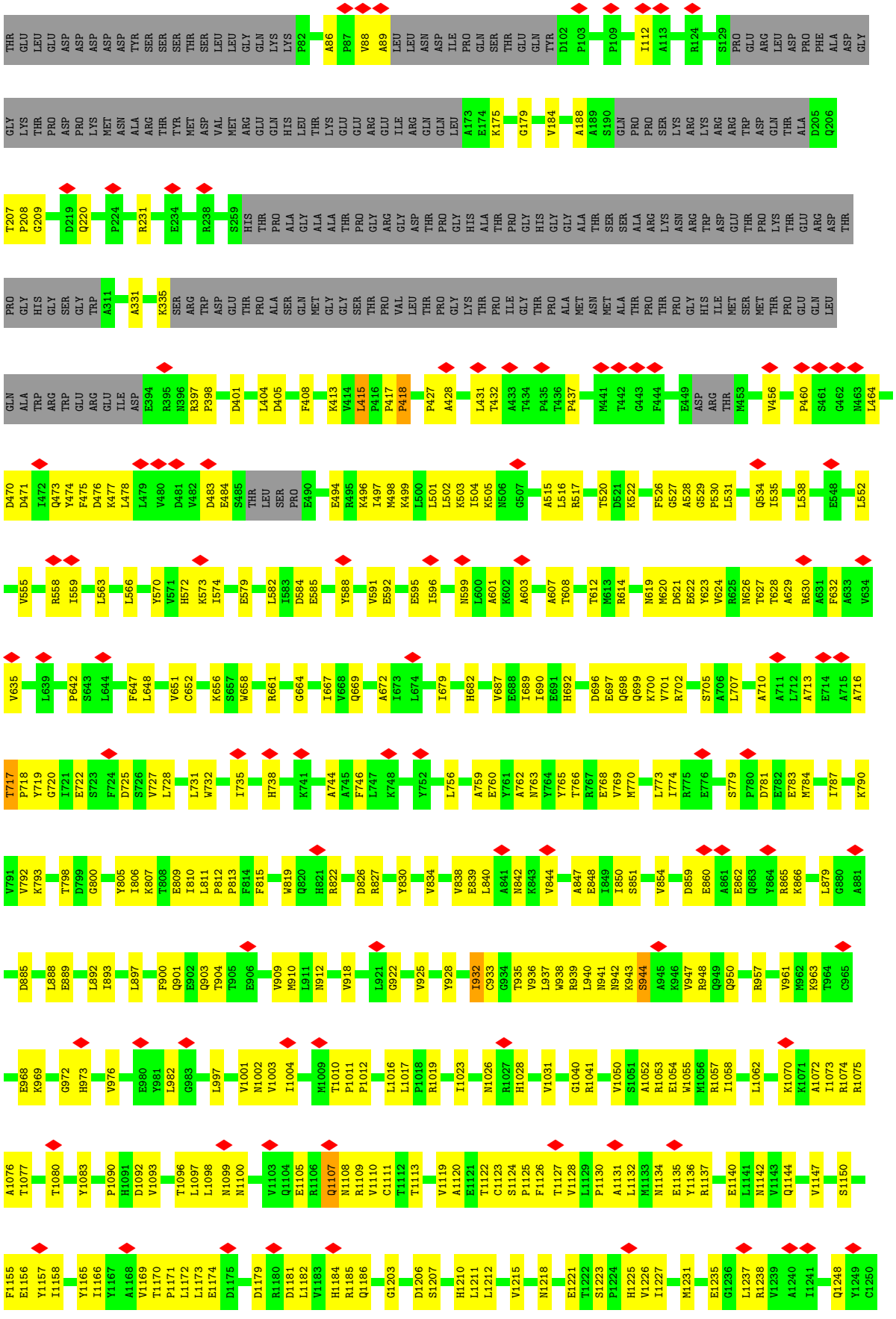


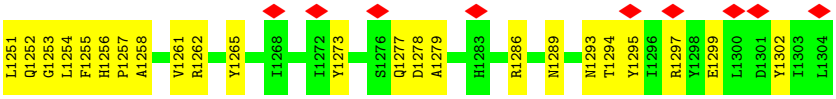
• Molecule 20: Splicing factor 3A subunit 2



• Molecule 21: Splicing factor 3B subunit 1

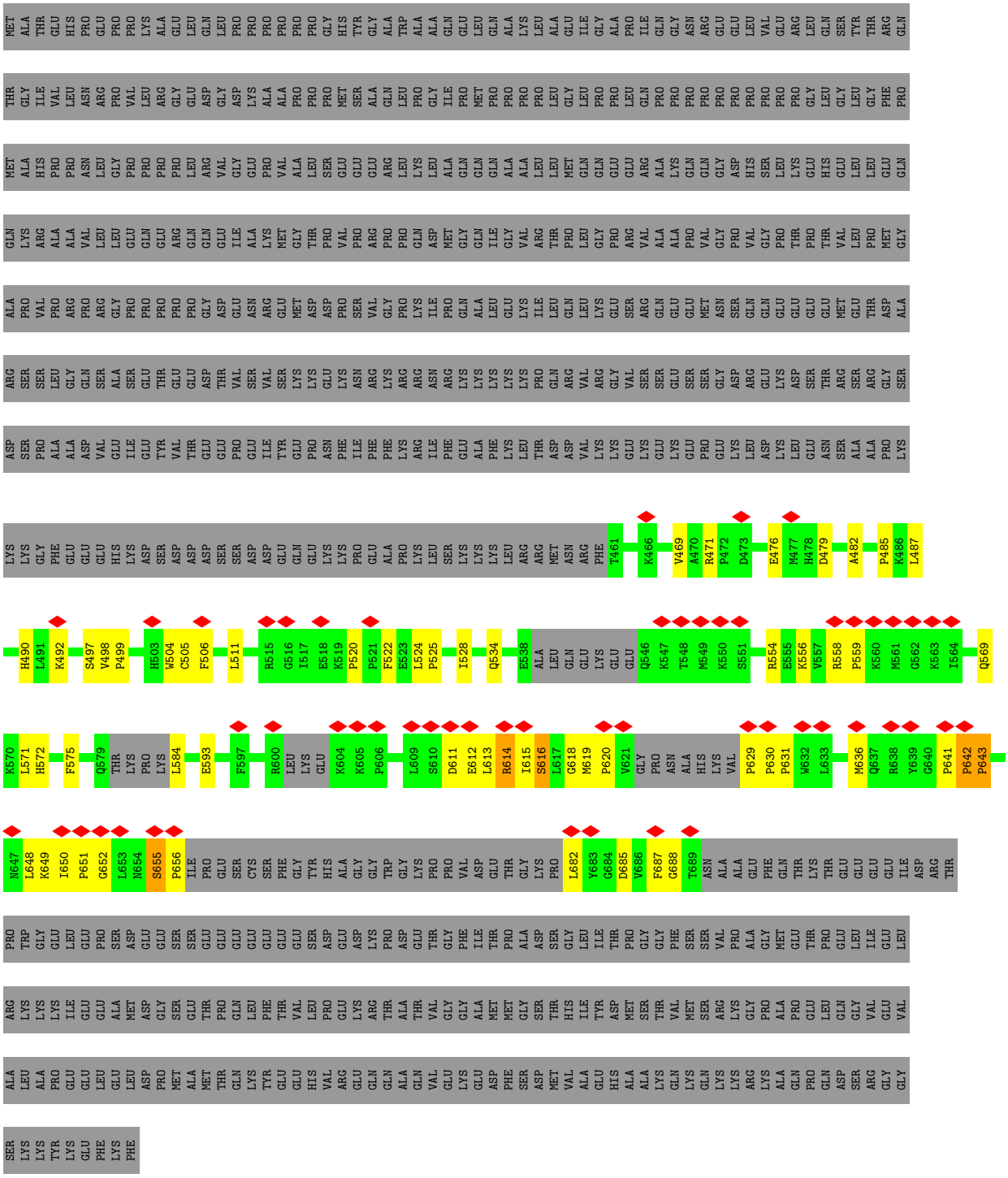






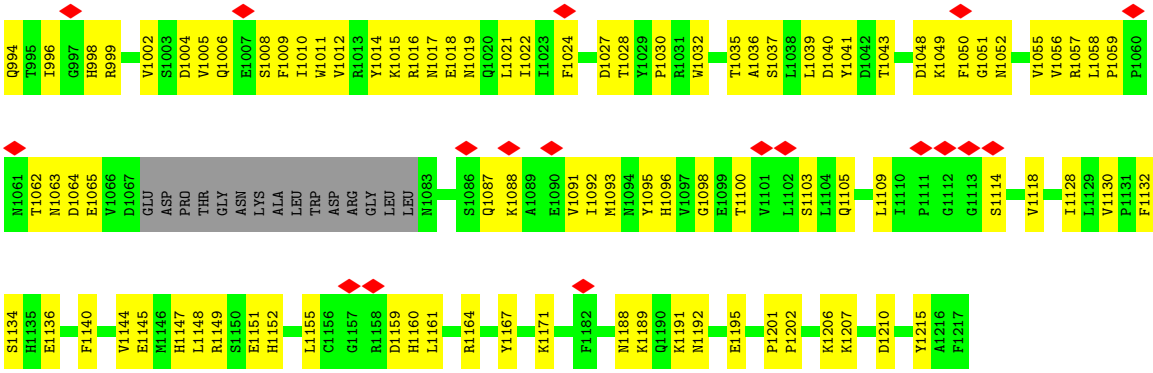
• Molecule 22: Splicing factor 3B subunit 2

Chain 2:



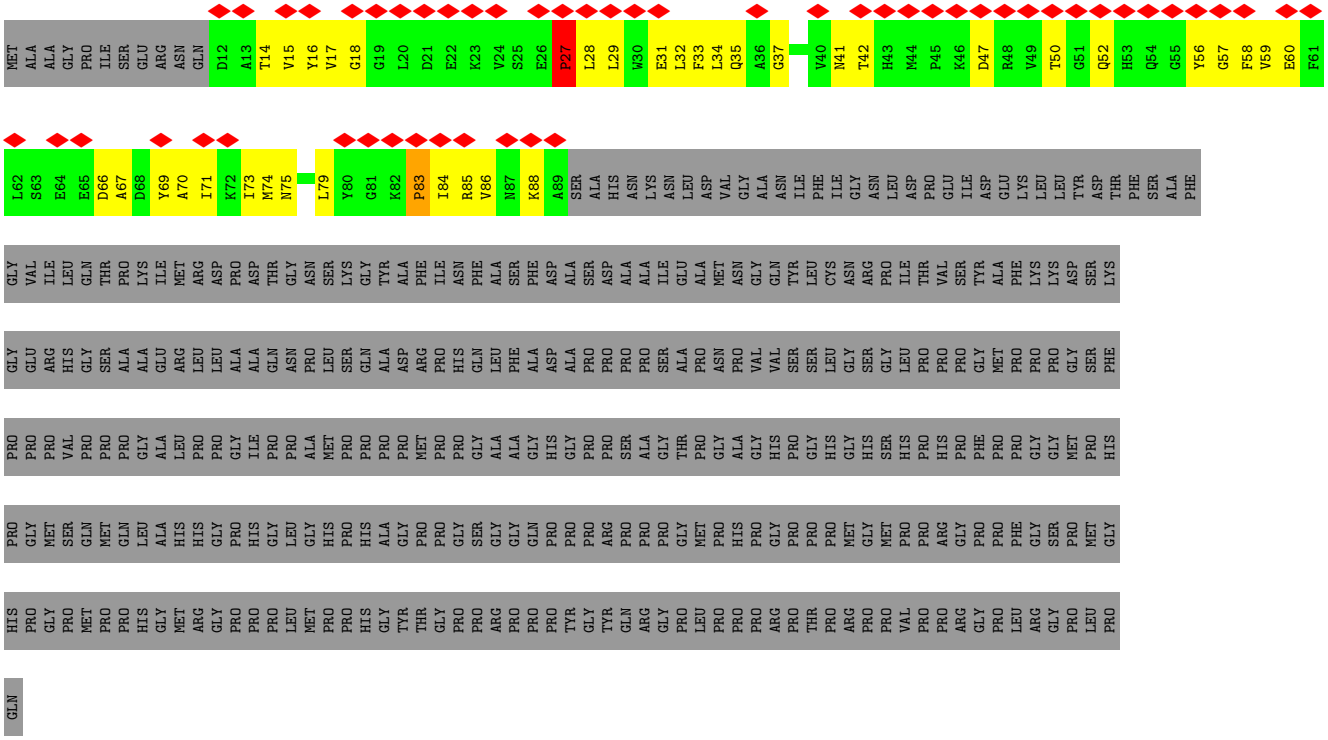
• Molecule 23: Splicing factor 3B subunit 3

Chain 3:



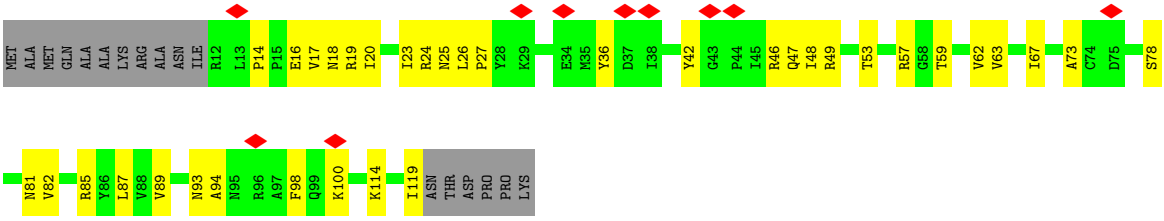
• Molecule 24: Splicing factor 3B subunit 4

Chain 4:



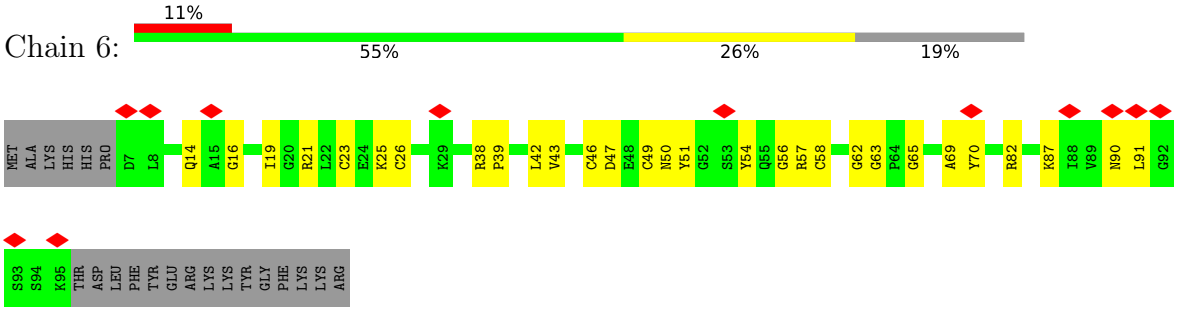
• Molecule 25: Splicing factor 3B subunit 6

Chain 5:



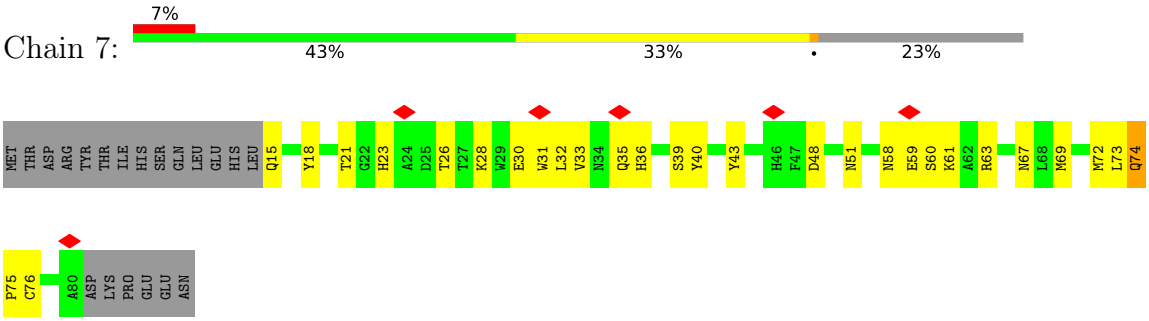
• Molecule 26: PHD finger-like domain-containing protein 5A

Chain 6:



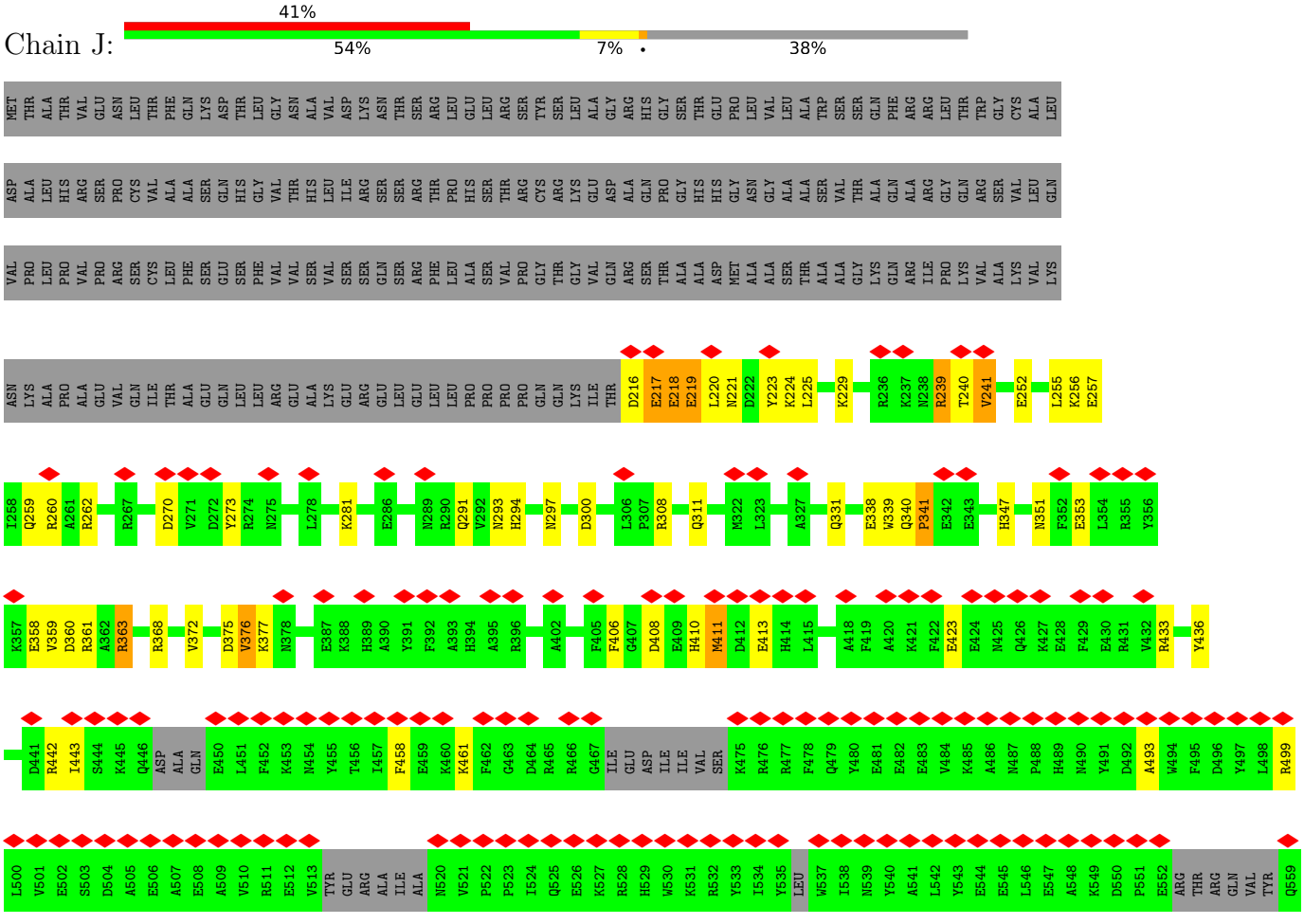
• Molecule 27: Splicing factor 3B subunit 5

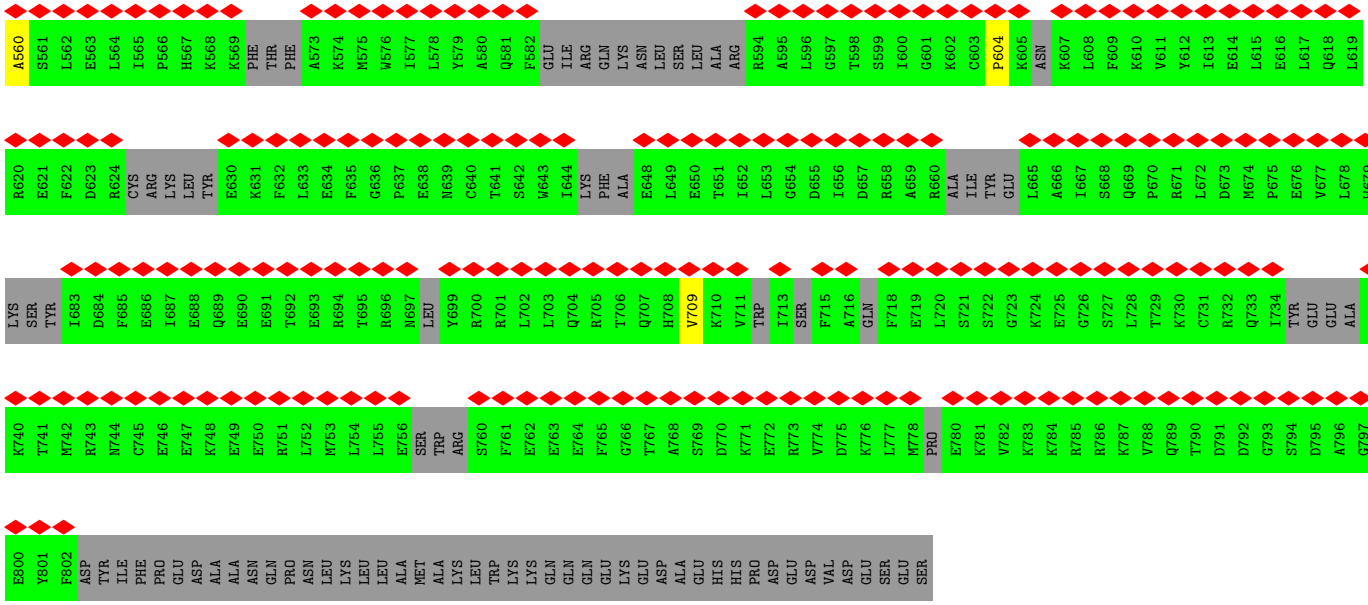
Chain 7:



• Molecule 28: Crooked neck-like protein 1

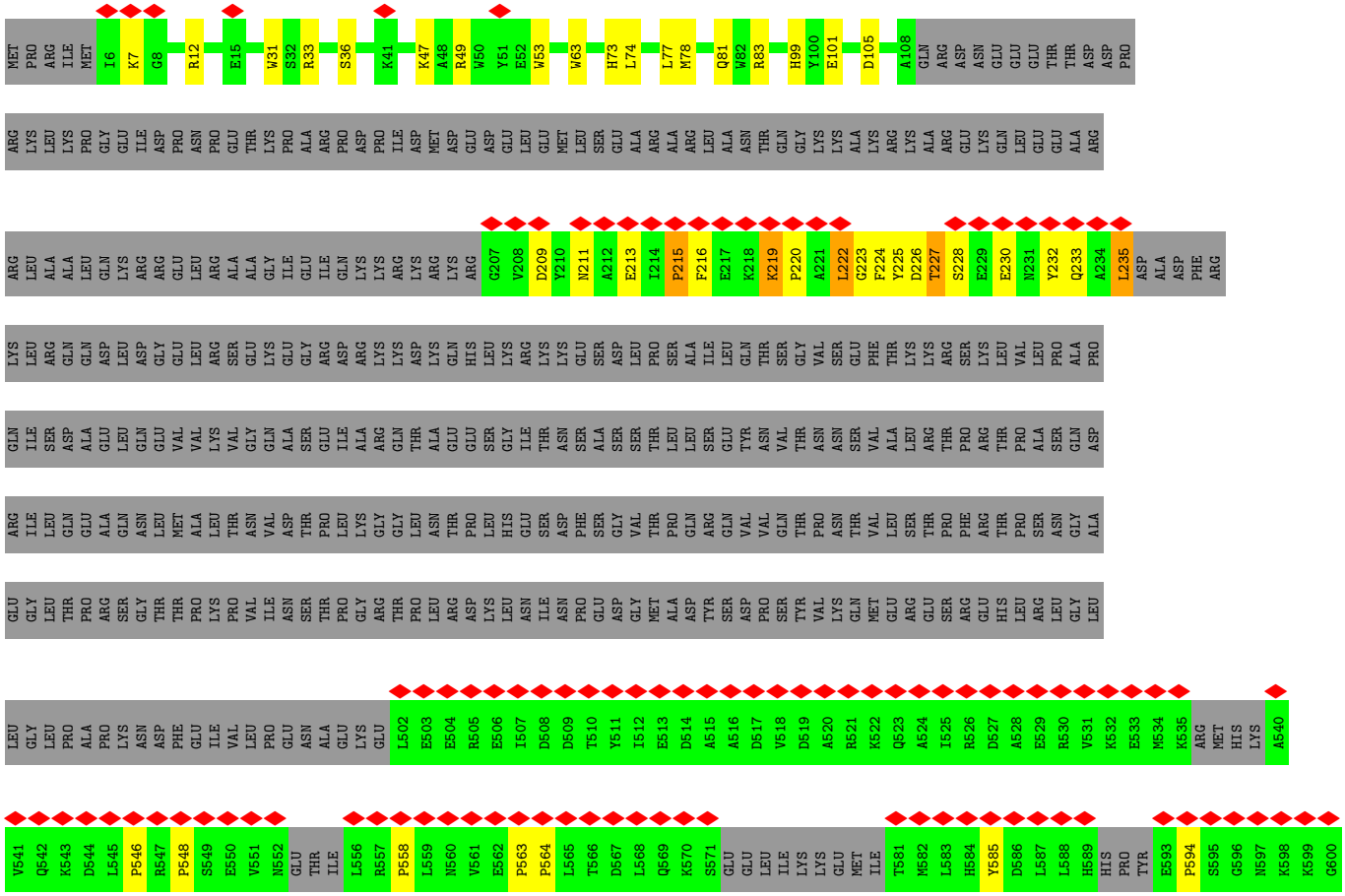
Chain J:

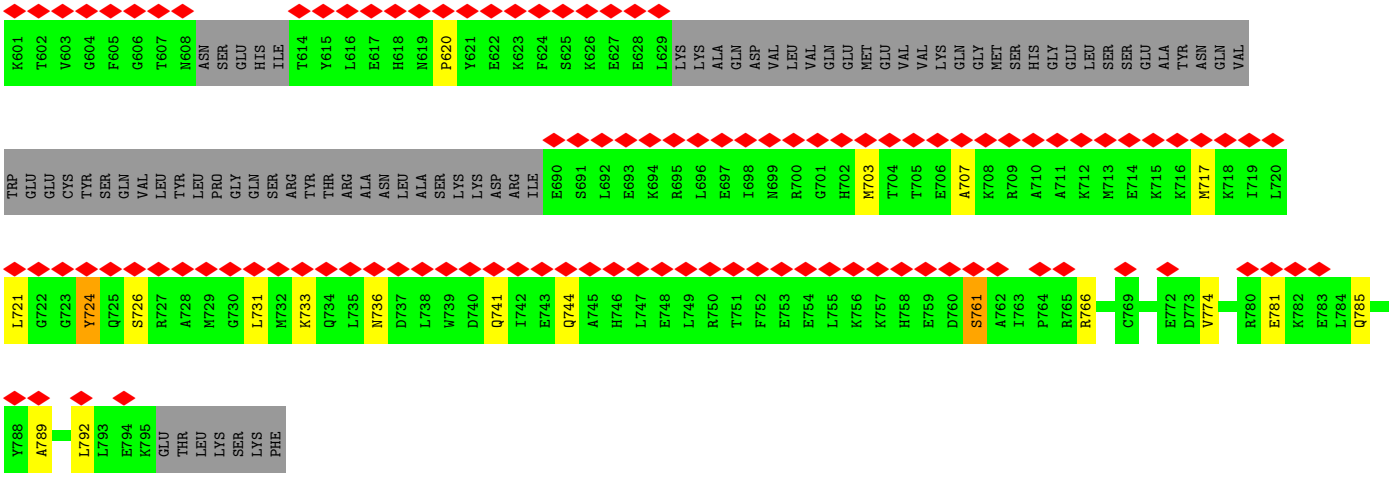




• Molecule 29: Cell division cycle 5-like protein

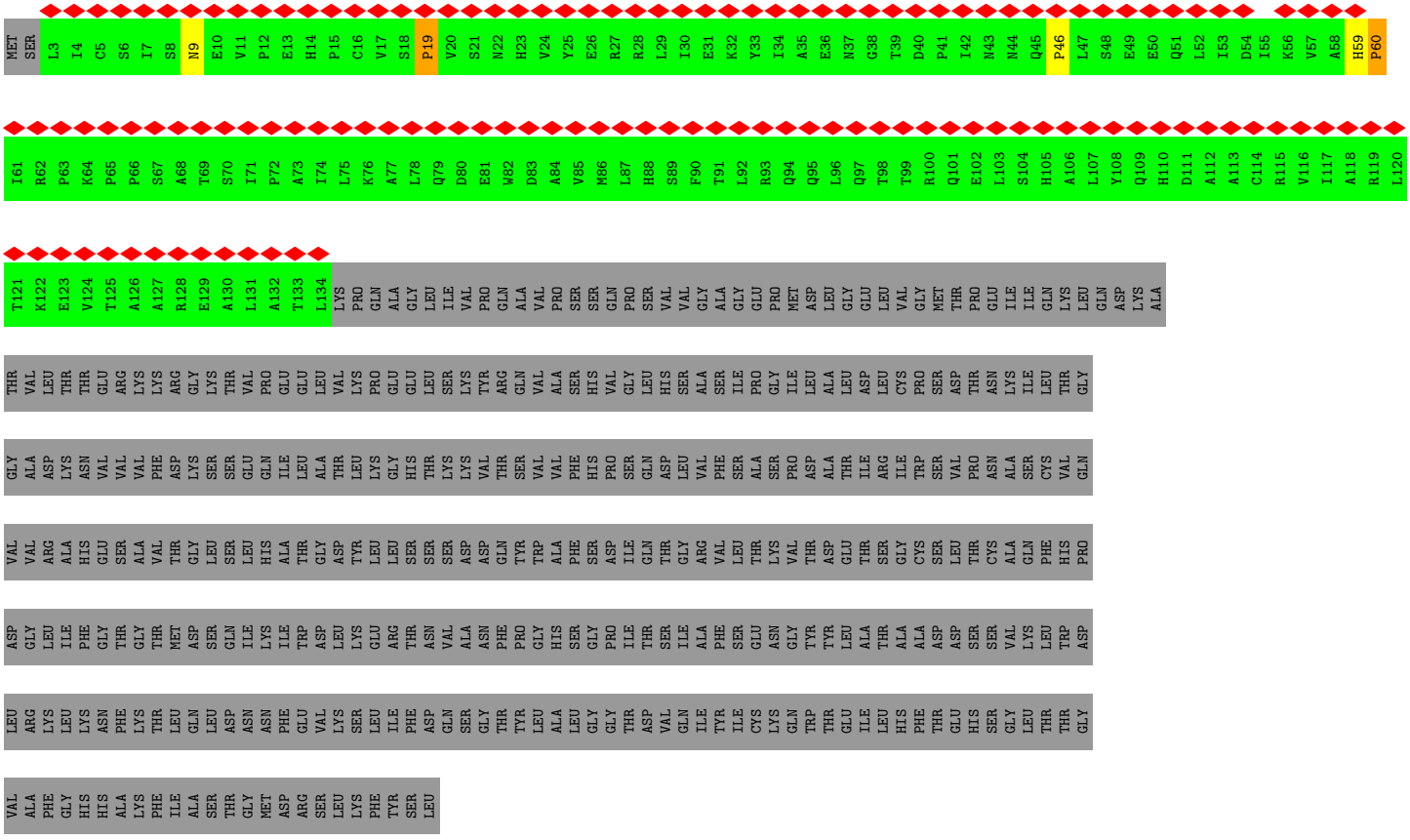
Chain L:





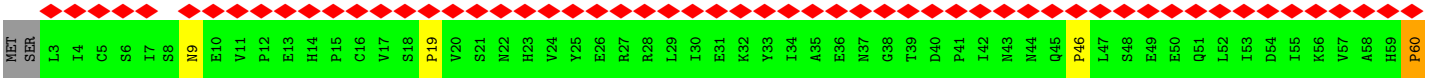
• Molecule 30: Pre-mRNA-processing factor 19

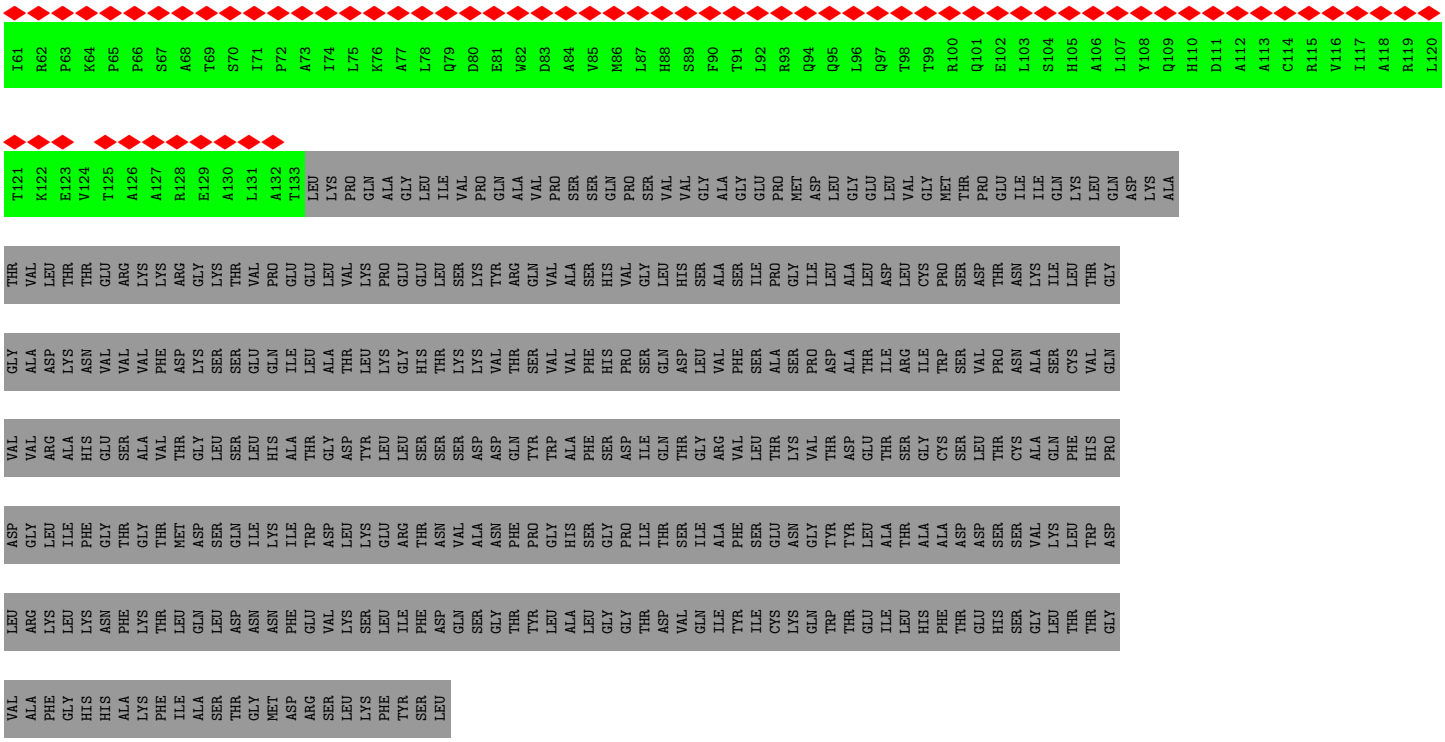
Chain q:



• Molecule 30: Pre-mRNA-processing factor 19

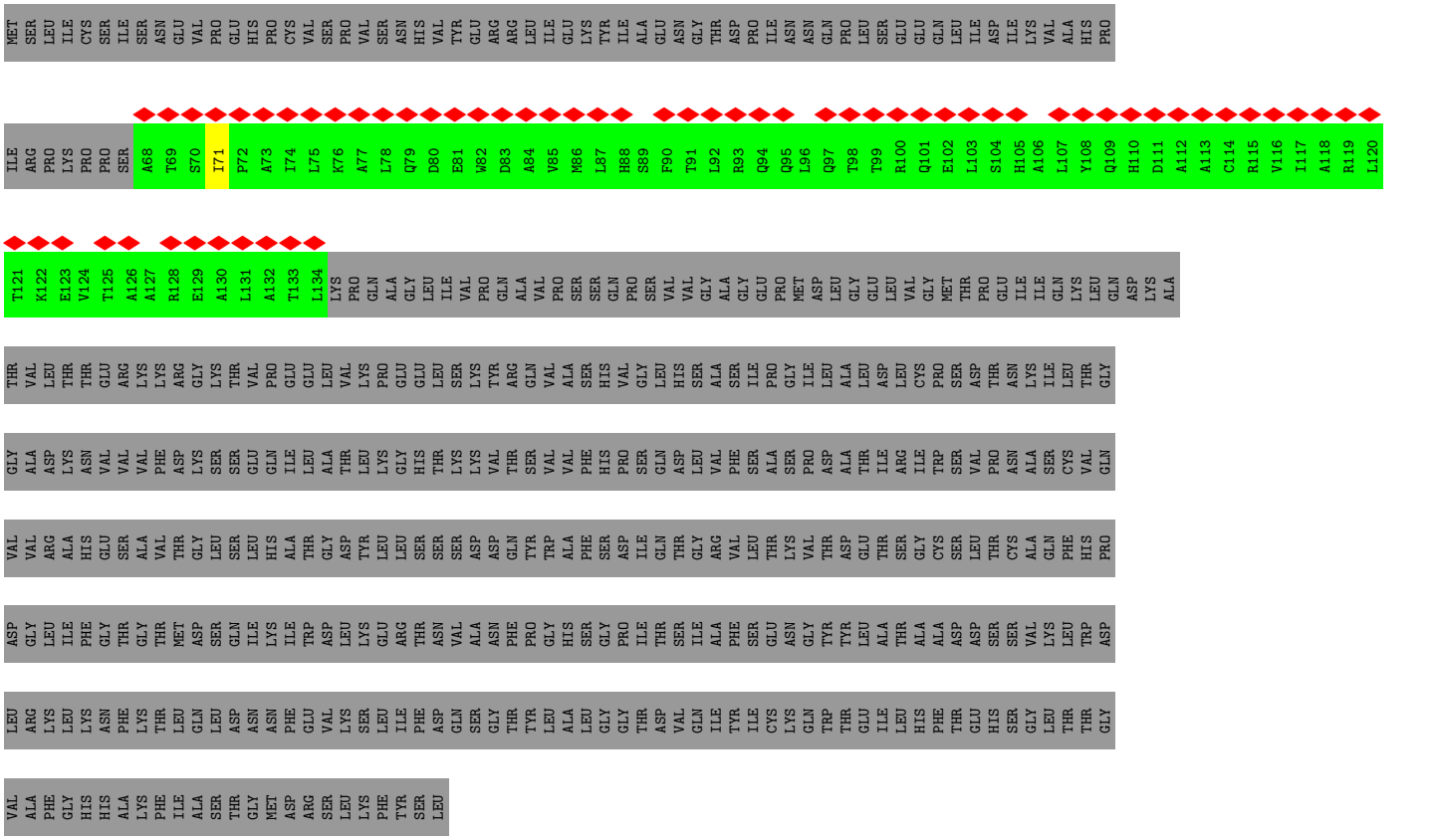
Chain r:





- Molecule 30: Pre-mRNA-processing factor 19

Chain s:

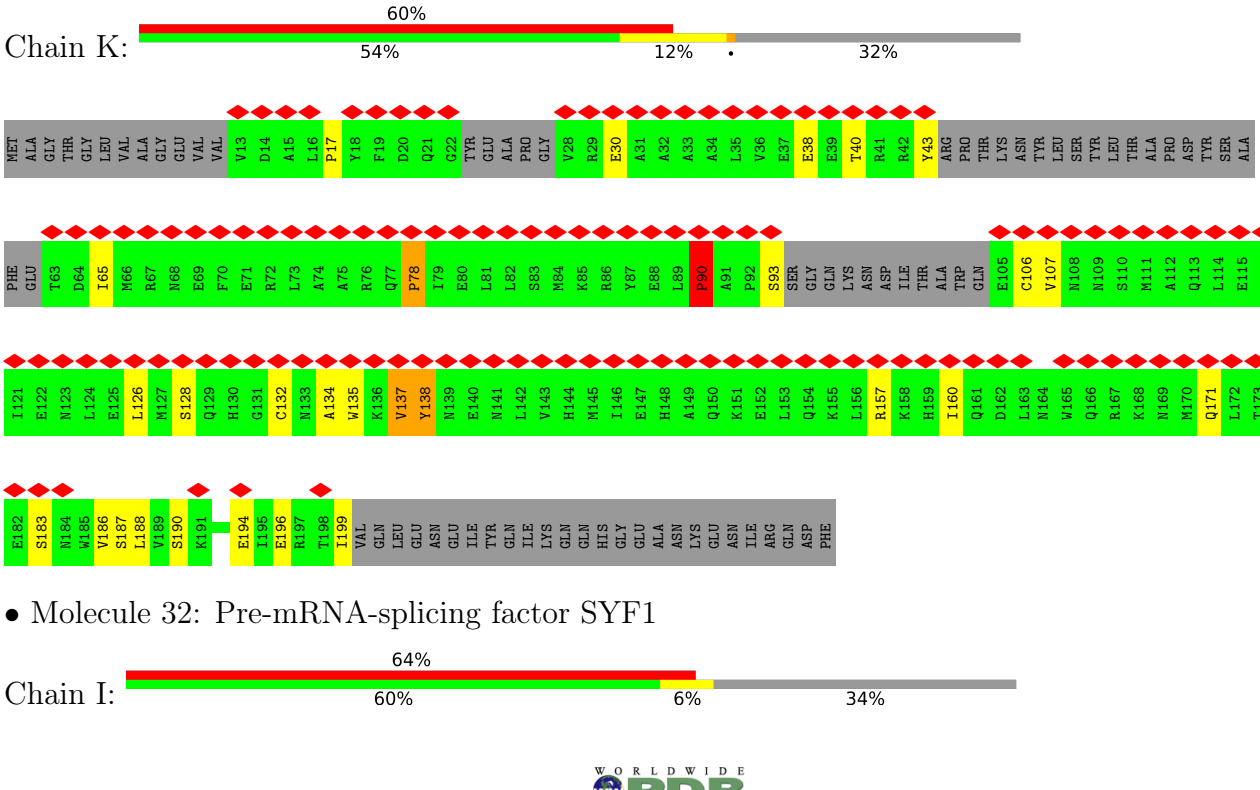


• Molecule 30: Pre-mRNA-processing factor 19

Chain t:

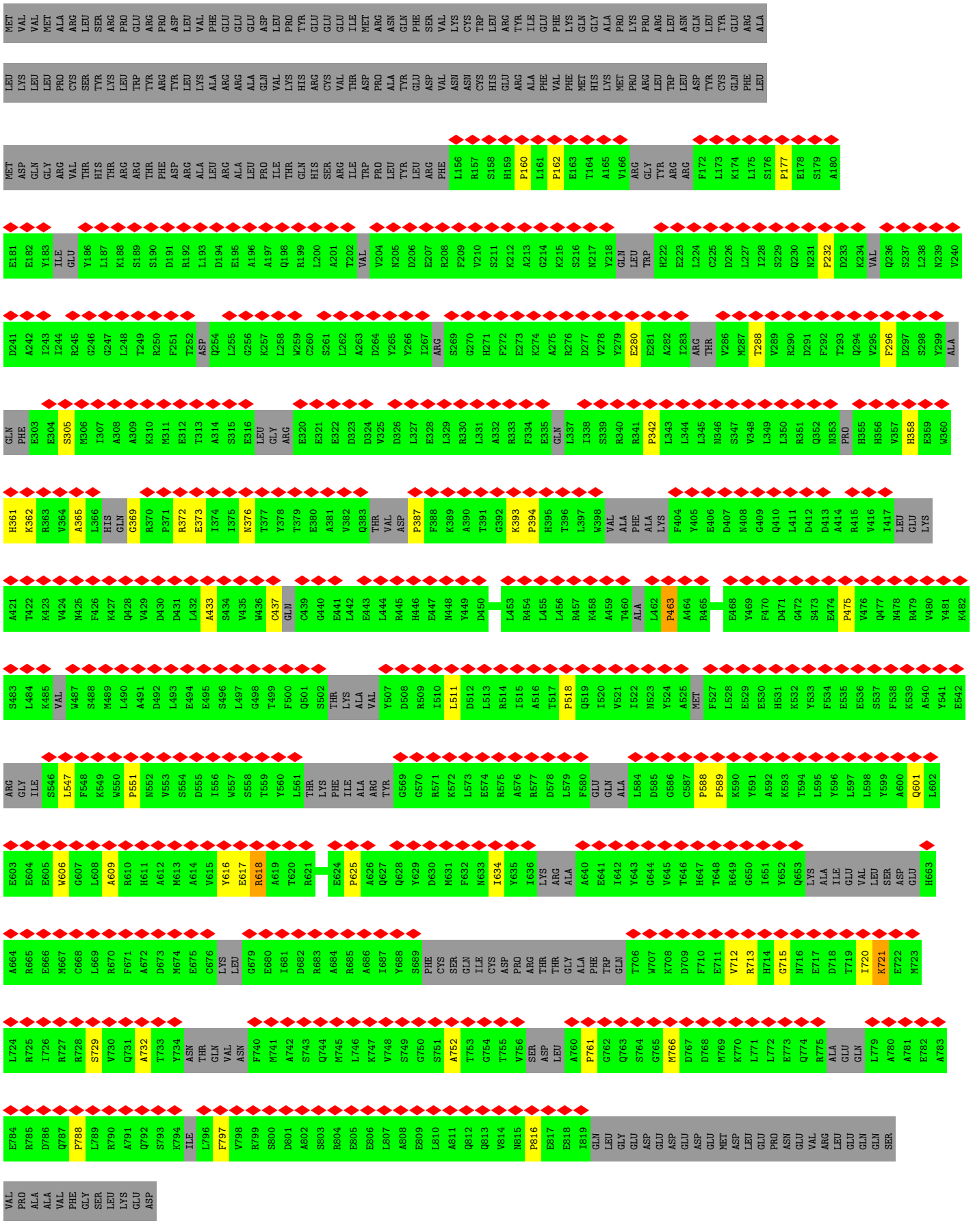
• Molecule 31: Pre-mRNA-splicing factor SPF27

Chain K:



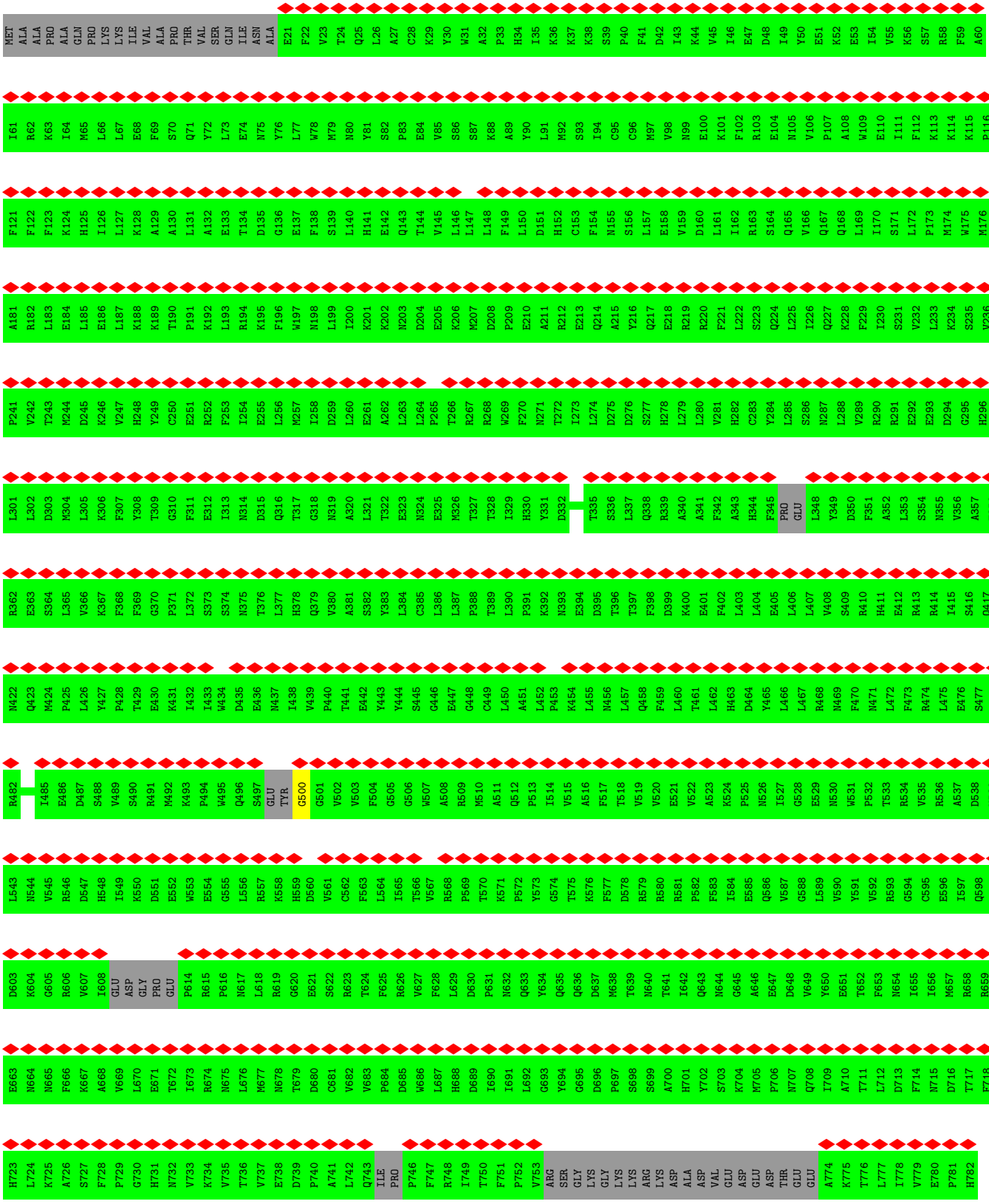
• Molecule 32: Pre-mRNA-splicing factor SYF1

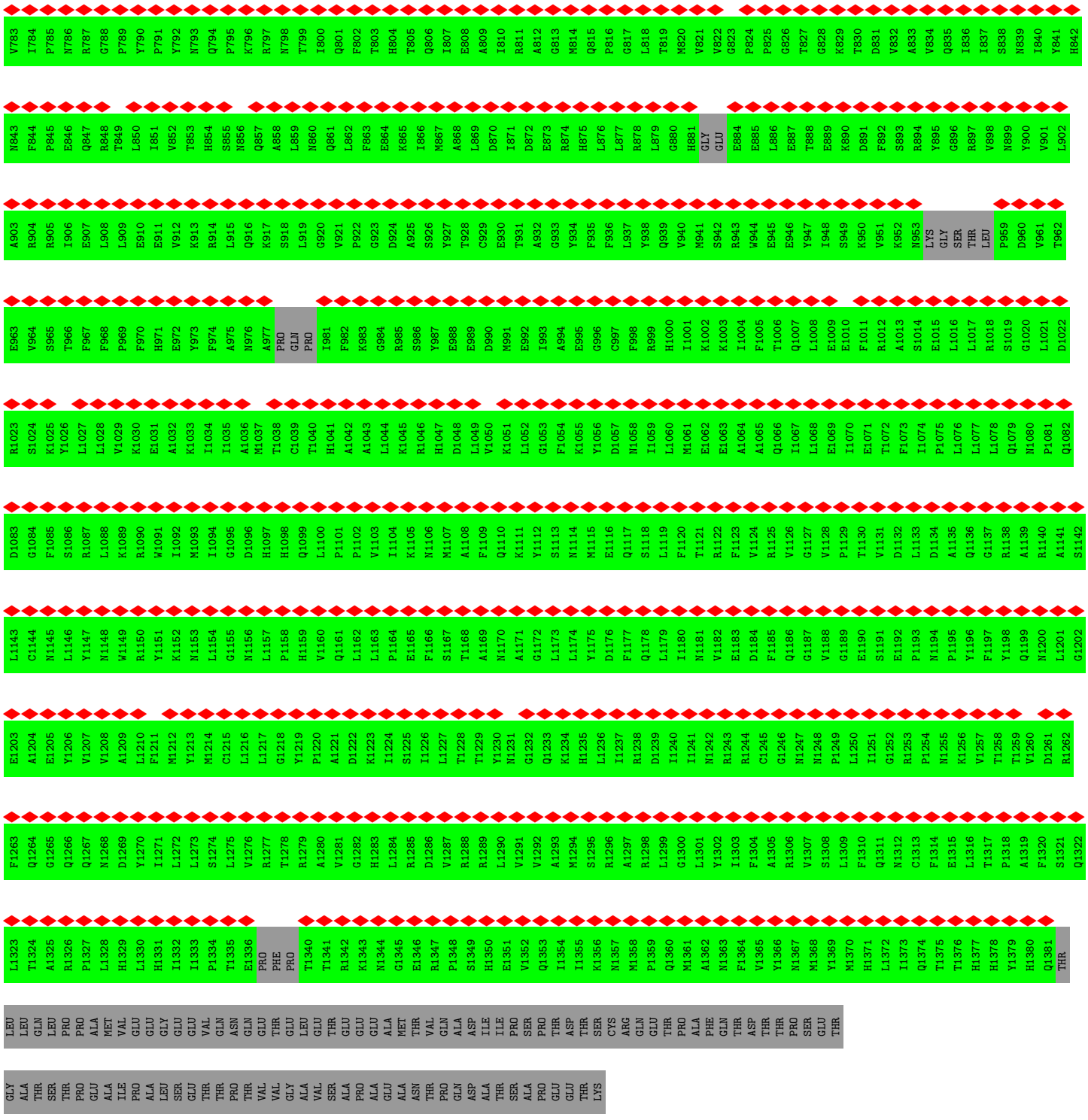
Chain I:


MET VAL VAL MET ALA ARG LEU SER ARG PRO GLU ARG PRO ASP LEU VAL PHE GLU GLU GLU ASP LEU PRO TYR GLU GLU GLU ILE MET ARG ASN GLN PHE SER VAL LYS CYS TRP LEU ARG TYR ILE GLU PHE LYS GLN GLY ALA PRO LYS PRO ARG LEU ASN GLN LEU TYR GLU ARG ALA
LEU LYS LEU LEU PRO CYS SER TYR LYS LEU TRP TYR ARG TYR LEU LYS ALA ARG ARG ALA GLN VAL LYS HIS ARG CYS VAL THR ASP PRO ALA TYR GLU ASP VAL ASN ASN CYS HIS GLU ARG ALA PHE VAL PHE MET HIS LYS MET PRO ARG LEU TRP LEU ASP TYR CYS GLN PHE LEU
MET ASP GLN GLY ARG VAL THR HIS THR ARG ARG THR PHE ASP ARG ALA LEU ARG ALA LEU PRO ILE THR GLN HIS SER ARG ILE TRP PRO LEU TYR LEU ARG PHE L156 R157 S158 H159 P160 L161 P162 E163 T164 A165 V166 ARG GLY TYR ARG ARG F172 L173 K174 L175 S176 P177 E178 S179 A180
E181 E182 Y183 ILE GLU Y186 L187 K188 S189 S190 D191 R192 L193 D194 E195 A196 A197 Q198 R199 L200 A201 T202 VAL V204 N205 D206 E207 R208 P209 V210 S211 K212 A213 G214 K215 S216 N217 Y218 GLN LEU TRP H222 E223 L224 C225 D226 L227 I228 S229 Q230 N231 P232 D233 K234 VAL Q236 S237 L238 N239 V240
D241 A242 I243 I244 R245 G246 G247 L248 T249 R250 F251 T252 ASP Q254 L255 G256 K257 L258 W259 C260 S261 L262 A263 D264 Y265 Y266 I267 ARG S269 G270 H271 F272 E273 K274 A275 R276 D277 V278 Y279 E280 E281 A282 I283 ARG THR V286 M287 T288 V289 R290 D291 F292 T293 Q294 V295 F296 D297 S298 Y299 ALA
GLN PHE E303 E304 S305 M306 I307 A308 A309 K310 M311 E312 T313 A314 S315 E316 LEU GLY ARG E320 E321 E322 D323 D324 V325 D326 L327 E328 L329 R330 L331 A332 R333 F334 E335 GLN L337 I338 S339 R340 R341 P342 L343 L344 L345 N346 S347 V348 L349 L350 R351 Q352 N353 PRO H355 H356 V357 H358 E359 W360
H361 K362 R363 V364 A365 L366 HIS GLN G369 R370 P371 R372 E373 I374 I375 N376 T377 Y378 T379 E380 A381 V382 Q383 THR VAL ASP P387 F388 K389 A390 T391 G392 K393 P394 H395 T396 L397 W398 VAL ALA PHE ALA LYS F404 Y405 E406 D407 N408 G409 Q410 L411 D412 D413 A414 R415 V416 I417 LEU GLU LYS
A421 T422 K423 V424 N425 F426 K427 Q428 V429 D430 D431 L432 A433 S434 V435 W436 C437 GLN C439 G440 E441 L442 E443 L444 R445 H446 E447 N448 Y449 D450 L453 R454 L455 L456 R457 K458 A459 T460 ALA L462 P463 A464 R465 E468 Y469 F470 D471 G472 S473 E474 P475 V476 Q477 N478 R479 V480 Y481 K482
S483 L484 K485 VAL W487 S488 M489 L490 A491 D492 L493 E494 E495 S496 L497 G498 T499 F500 Q501 S502 THR LYS ALA VAL Y507 D508 R509 I510 L511 D512 L513 R514 I515 A516 T517 P518 Q519 I520 V521 I522 N523 Y524 A525 MET F527 L528 E529 E530 H531 K532 Y533 F534 E535 E536 S537 F538 K539 A540 Y541 E542
ARG GLY ILE S546 L547 F548 K549 W550 P551 N552 V553 S554 D555 I556 W557 S558 T559 Y560 L561 THR LYS PHE ILE ALA ARG TYR G569 G570 R571 K572 L573 E574 R575 A576 R577 D578 L579 F580 GLU GLN ALA L584 D585 G586 C587 P588 P589 K590 Y591 A592 K593 T594 L595 Y596 L597 L598 Y599 A600 Q601 L602
E603 E604 E605 W606 G607 L608 A609 R610 H611 A612 M613 A614 V615 Y616 E617 R618 A619 T620 R621 E624 P625 A626 Q627 Q628 Y629 D630 M631 F632 N633 I634 Y635 I636 LYS ARG ALA A640 E641 I642 Y643 G644 V645 T646 H647 T648 R649 G650 I651 Y652 Q653 LYS ALA ILE GLU VAL LEU SER ASP GLU H663
A664 R665 E666 M667 C668 L669 R670 F671 A672 D673 M674 E675 C676 LYS LEU G679 E680 I681 D682 R683 A684 R685 A686 I687 Y688 S689 PHE CYS SER GLN ILE CYS ASP PRO ARG THR THR GLY ALA PHE TRP GLN T706 W707 K708 D709 F710 E711 V712 R713 H714 G715 N716 E717 D718 T719 I720 K721 E722 M723
L724 R725 I726 R727 R728 S729 V730 Q731 A732 T733 Y734 ASN THR GLN VAL ASN F740 M741 A742 S743 Q744 M745 L746 K747 V748 S749 G750 S751 A752 T753 G754 T755 V756 SER ASP LEU A760 P761 G762 Q763 S764 G765 M766 D767 D768 M769 K770 L771 L772 E773 Q774 R775 ALA GLU GLN L779 A780 A781 E782 A783
E784 R785 D786 Q787 P788 L789 R790 A791 Q792 S793 K794 ILE L796 F797 V798 R799 S800 D801 A802 S803 R804 E805 E806 L807 A808 E809 L810 A811 Q812 Q813 V814 N815 P816 E817 E818 I819 GLN LEU GLY GLU ASP GLU ASP GLU MET ASP LEU GLU PRO ASN GLU VAL ARG LEU GLU GLN GLN SER
VAL PRO ALA ALA VAL PHE GLY SER LEU LYS GLU ASP

• Molecule 33: Intron-binding protein aquarius

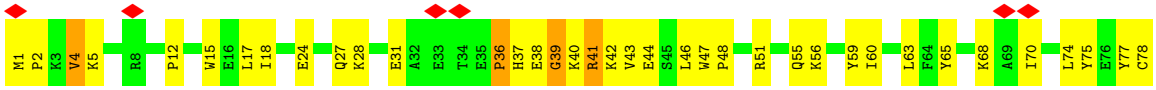
Chain Q:

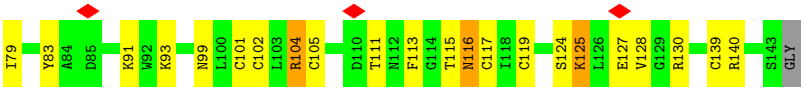




• Molecule 34: Protein BUD31 homolog

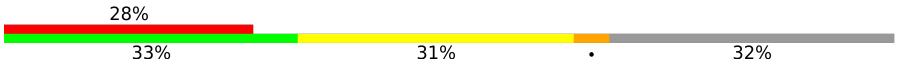
Chain N:

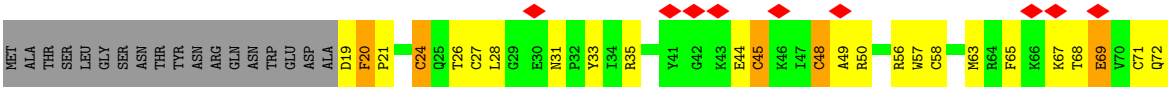


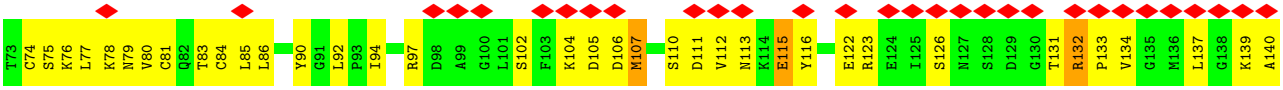


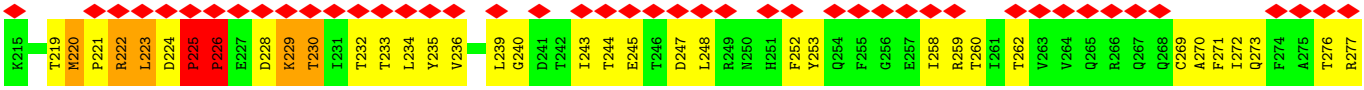
• Molecule 35: Pre-mRNA-splicing factor RBM22

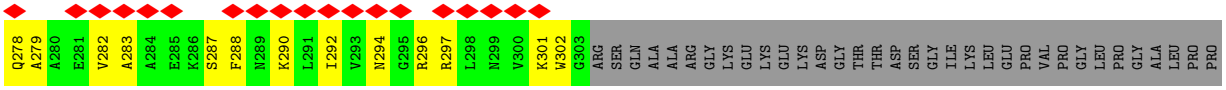
Chain O:





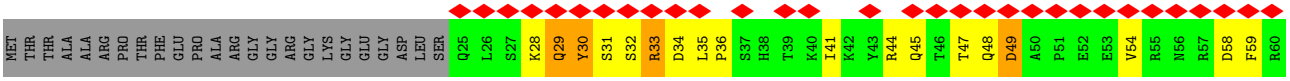


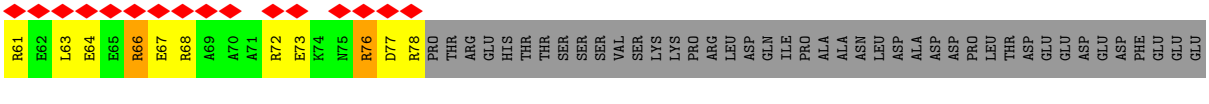


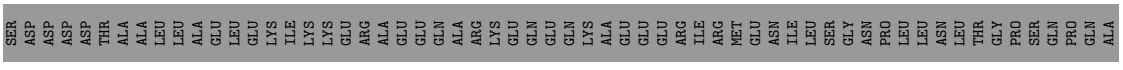


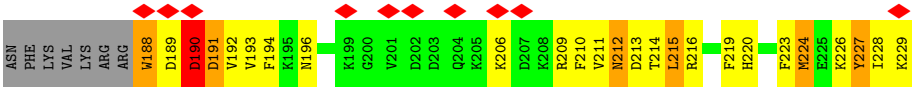
• Molecule 36: Spliceosome-associated protein CWC15 homolog

Chain P:

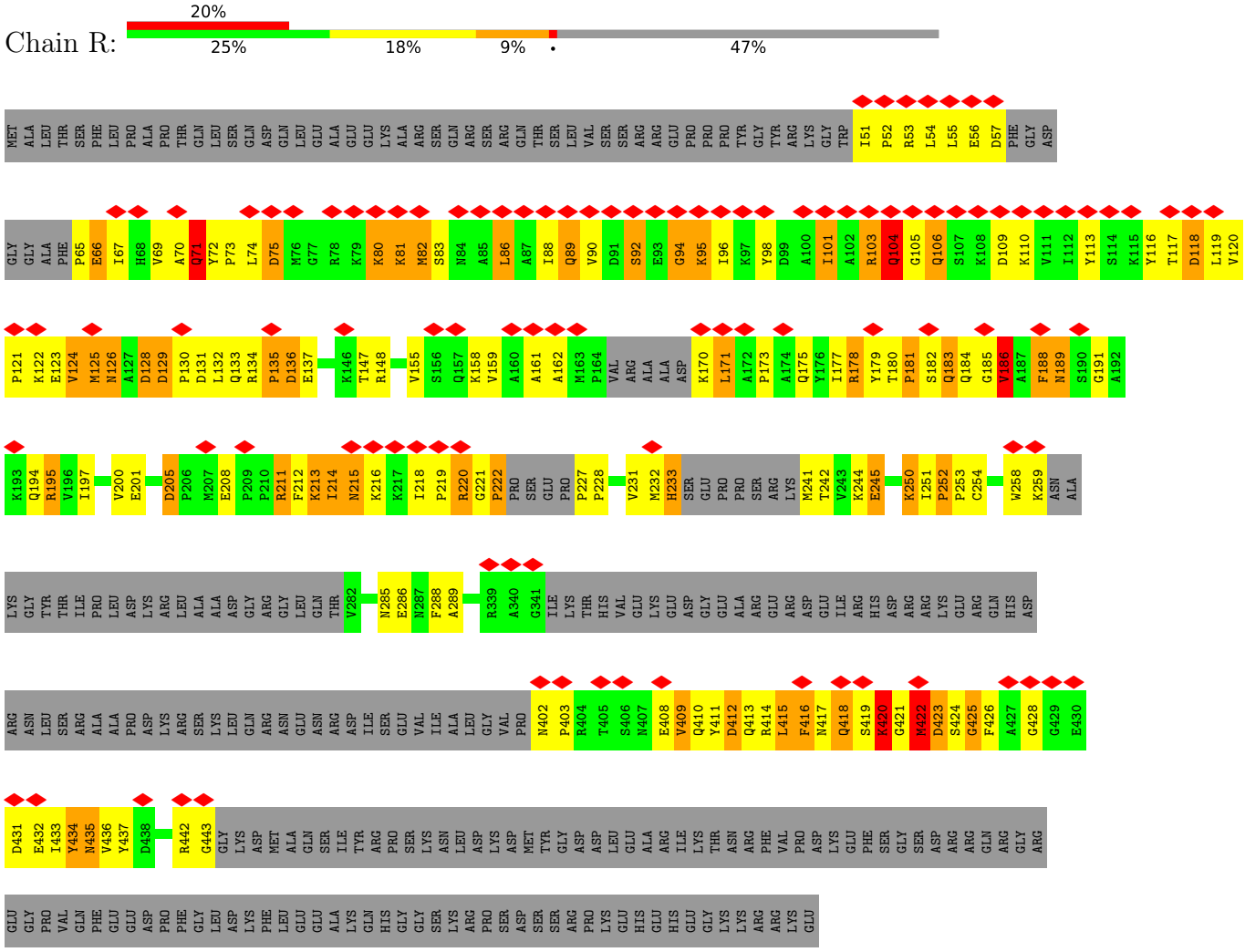




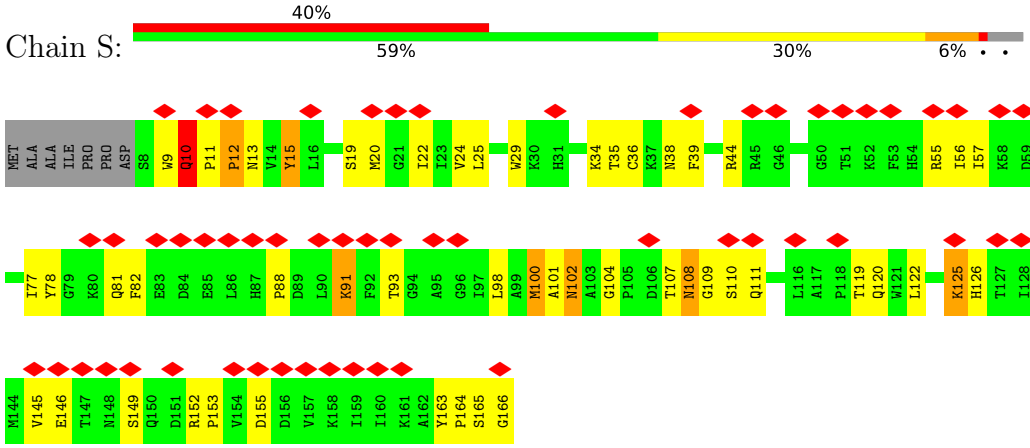




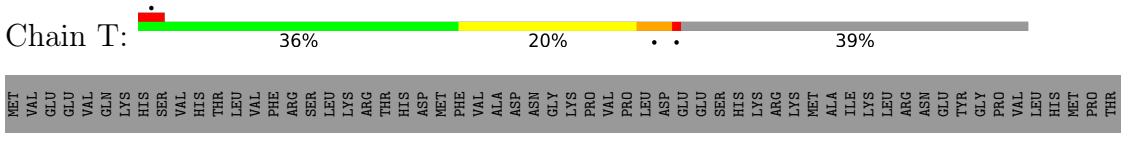
• Molecule 37: Skip

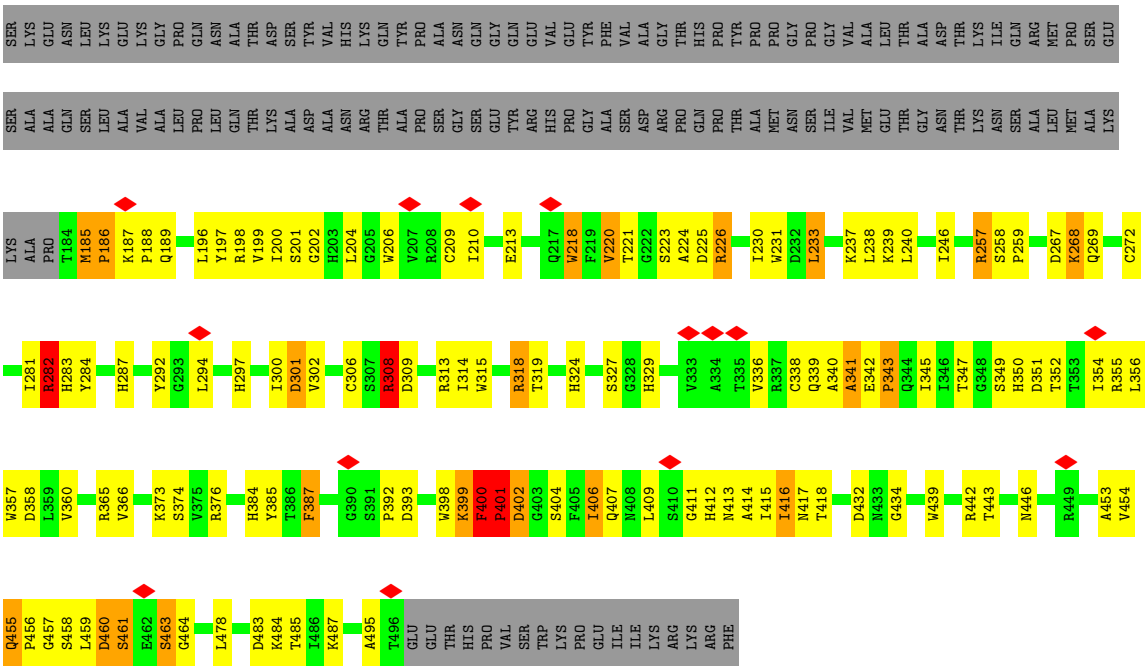


• Molecule 38: Peptidyl-prolyl cis-trans isomerase-like 1



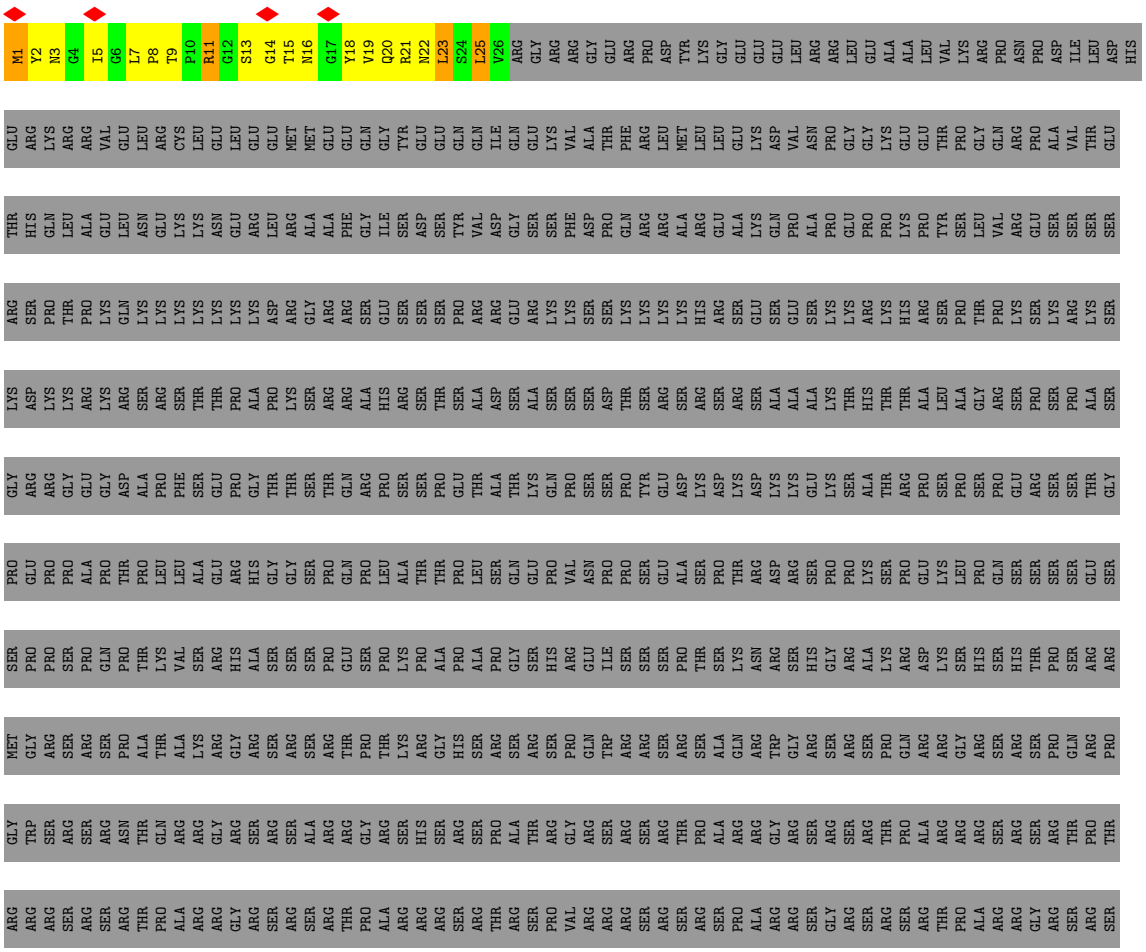
• Molecule 39: Pleiotropic regulator 1

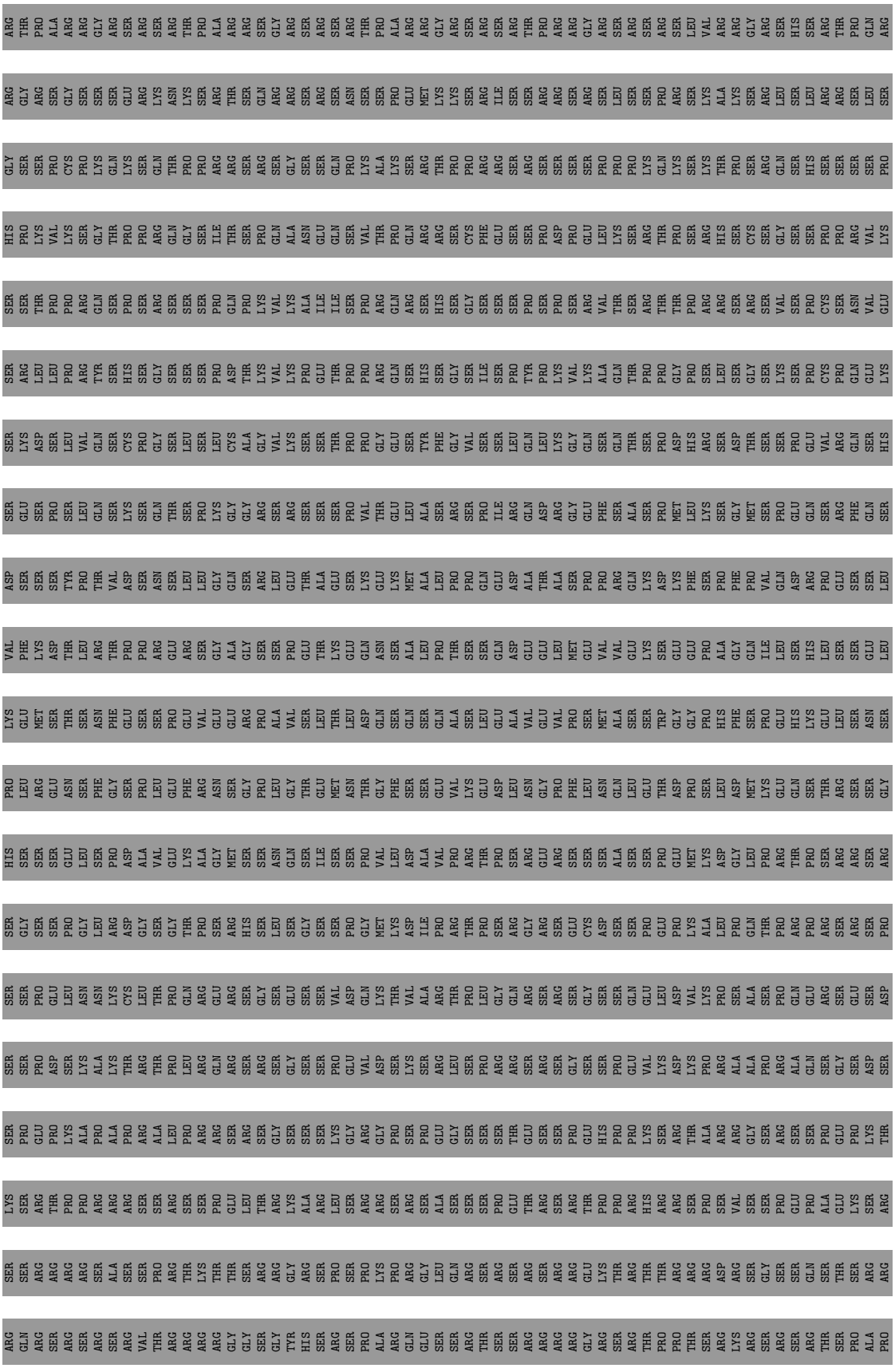


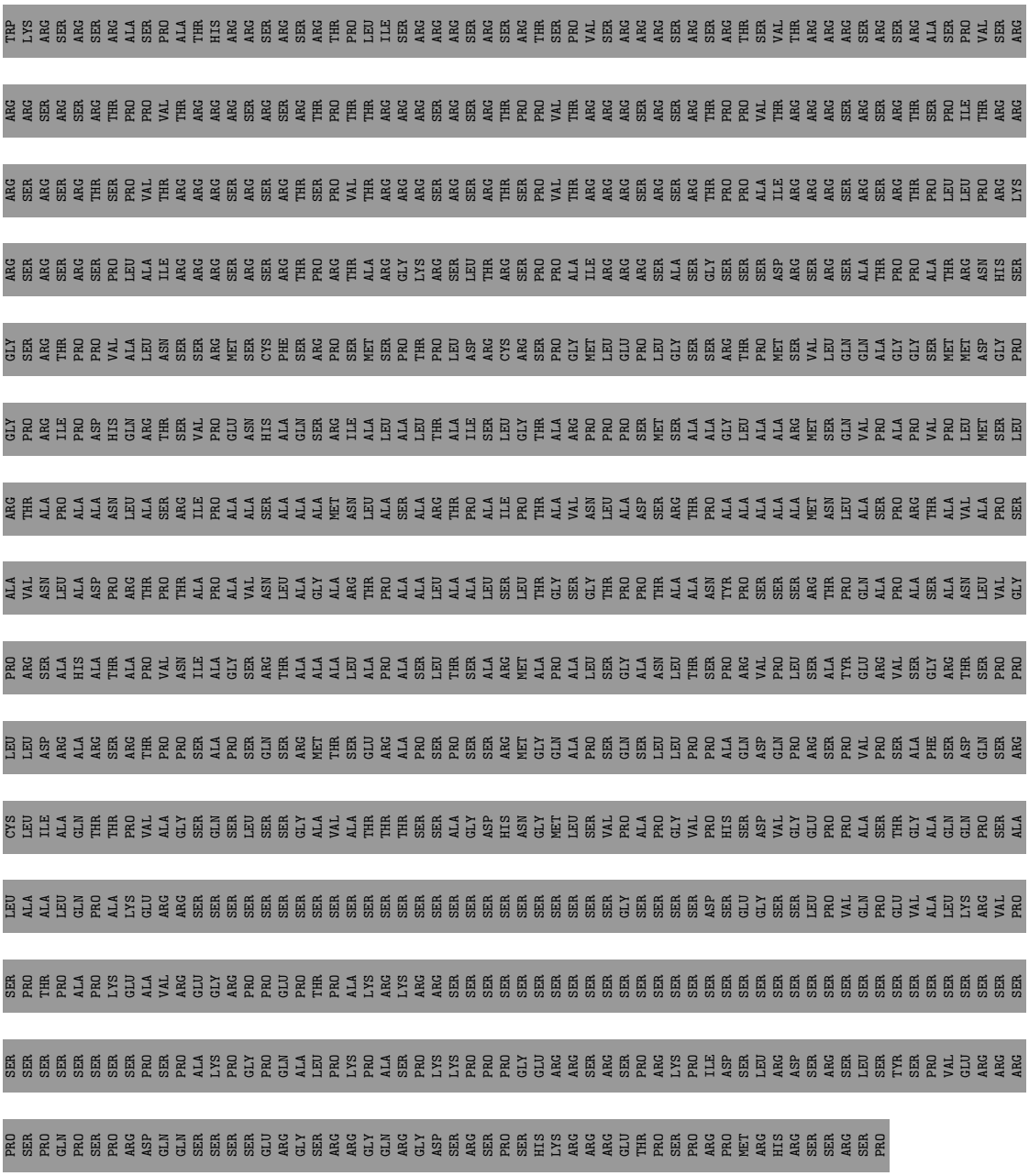


• Molecule 40: Serine/arginine repetitive matrix protein 2

Chain U: 99%

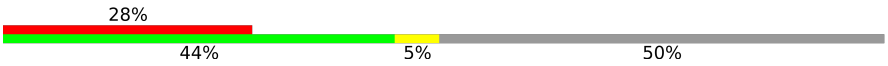


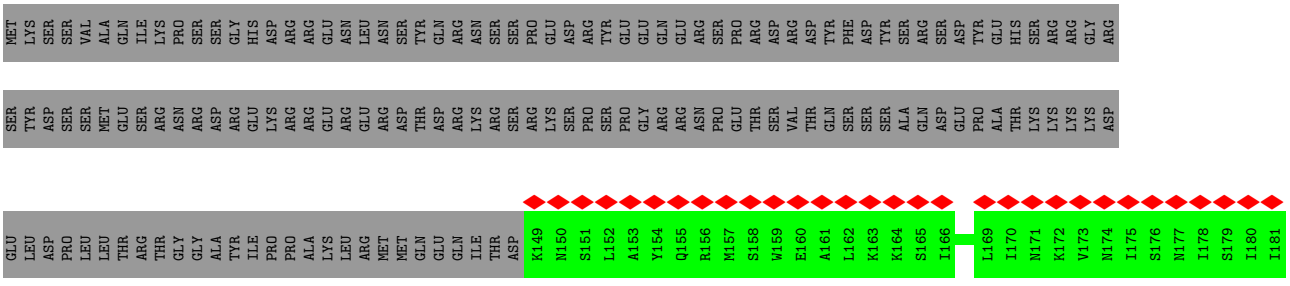


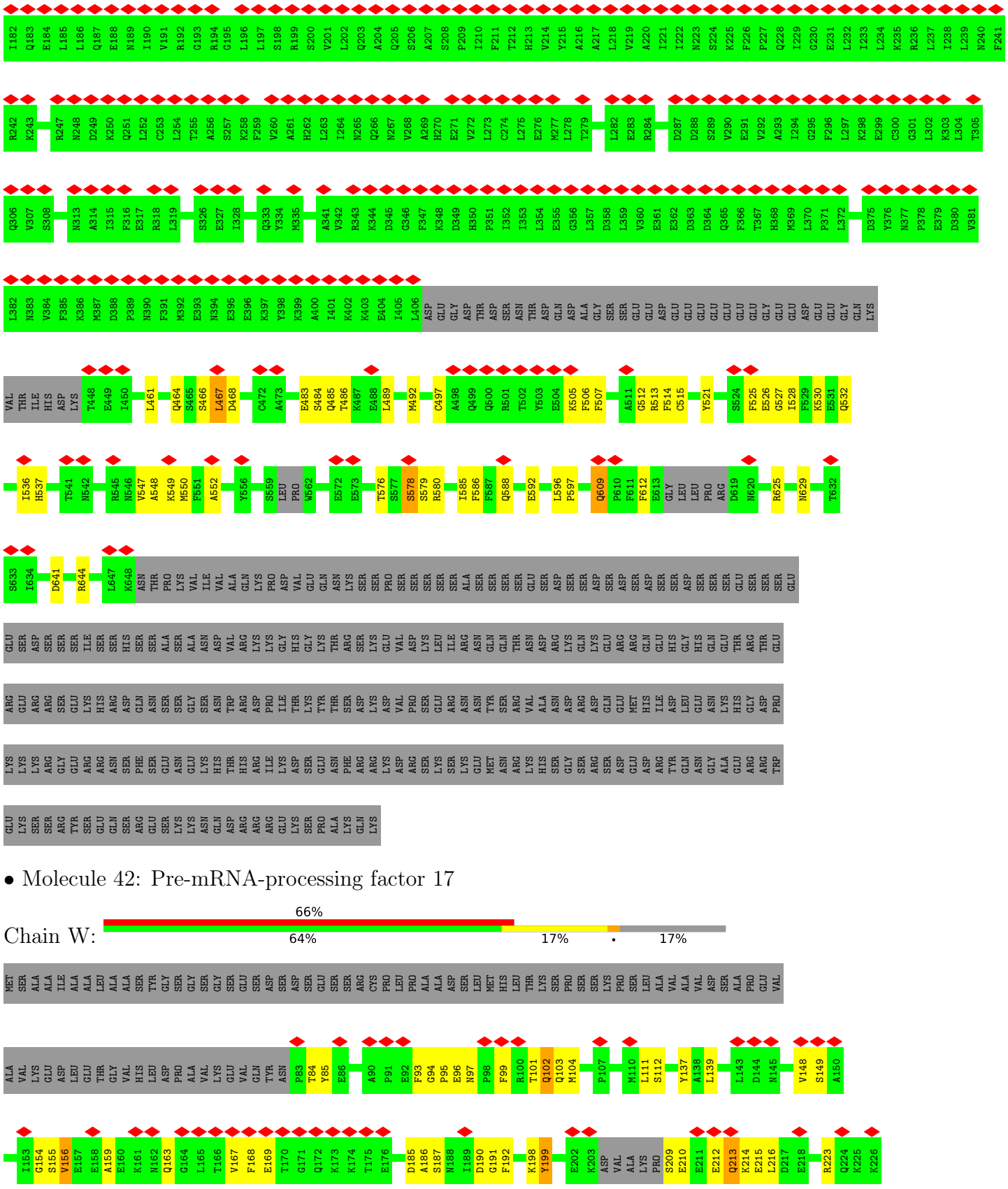


• Molecule 41: Pre-mRNA-splicing factor CWC22 homolog

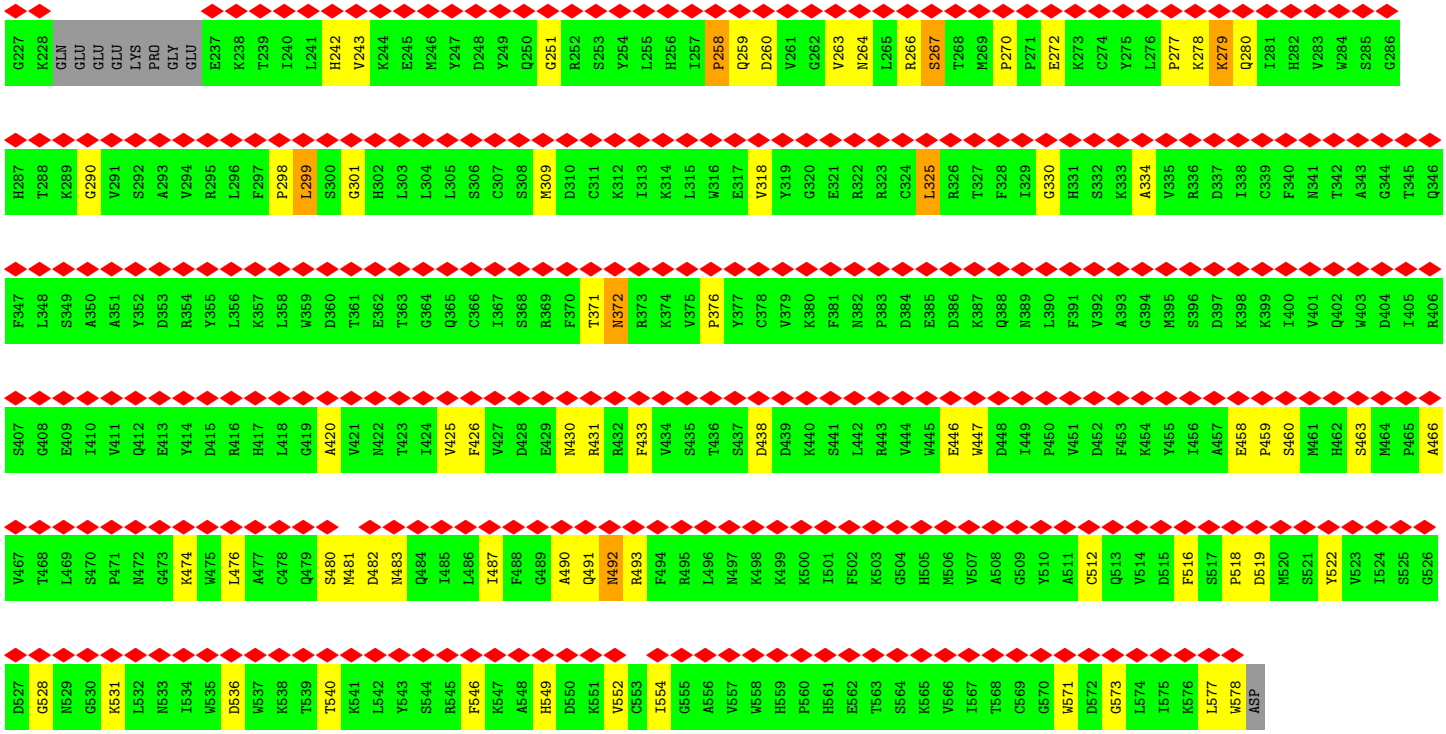
Chain V:



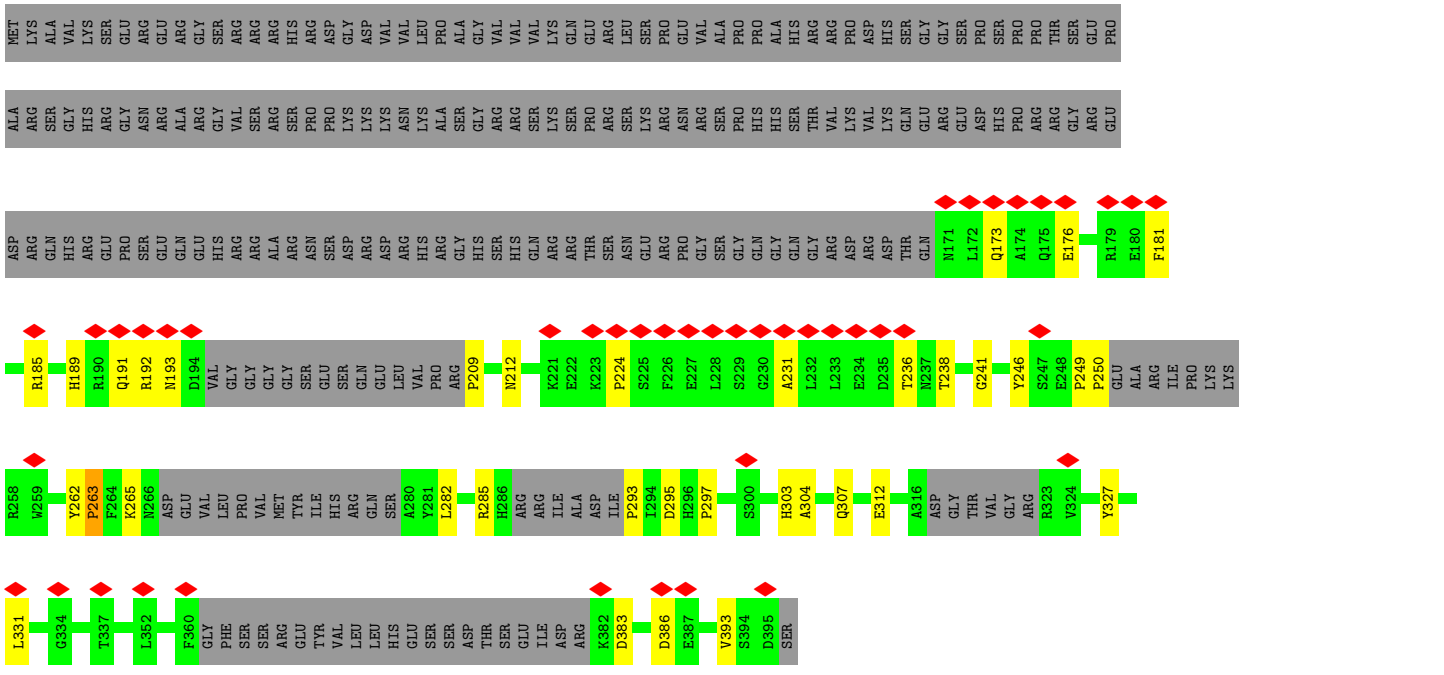




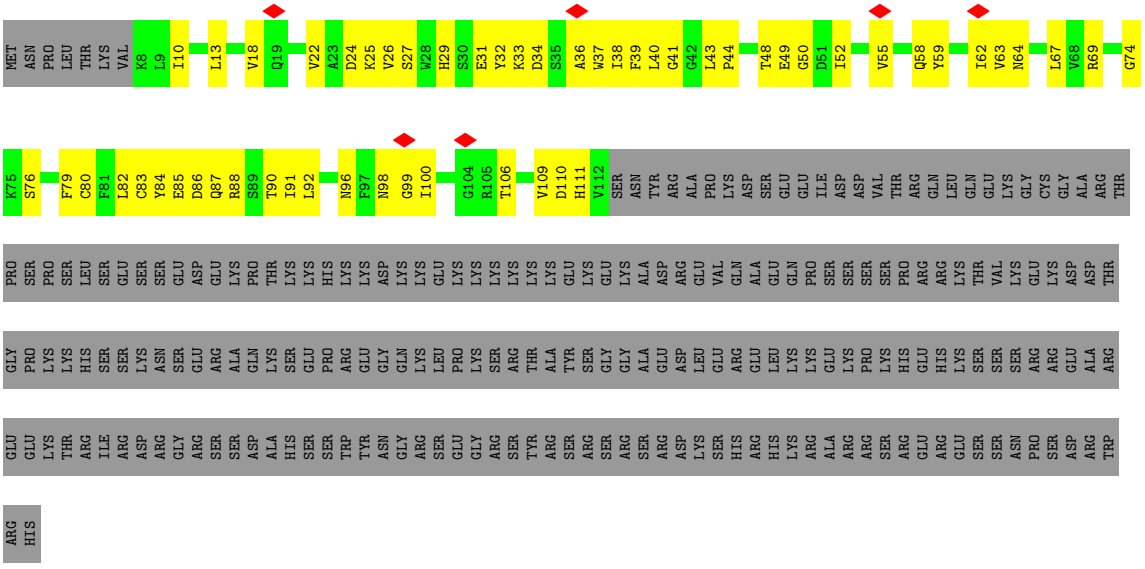
• Molecule 42: Pre-mRNA-processing factor 17

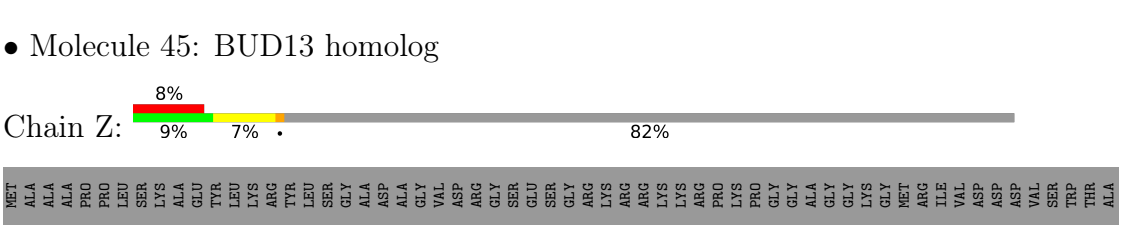


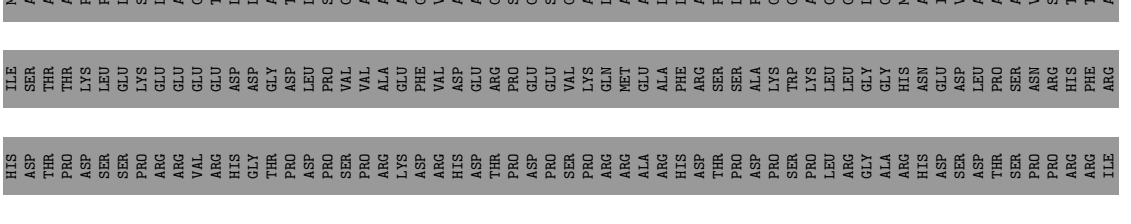
• Molecule 43: Smad nuclear-interacting protein 1

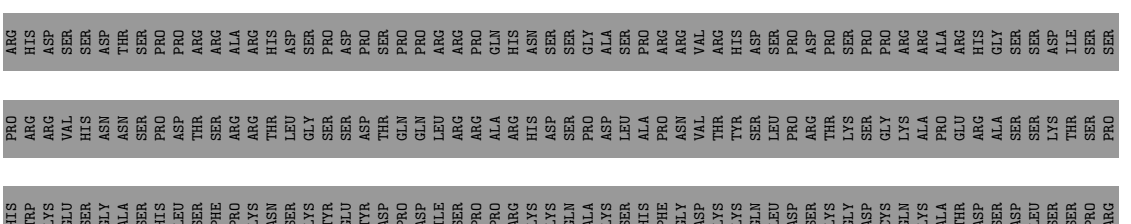


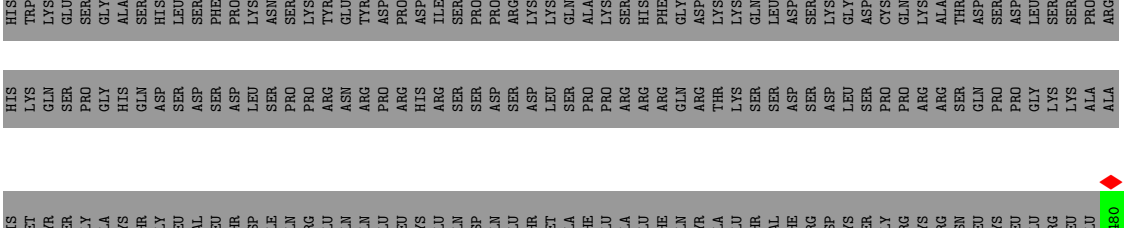
• Molecule 44: RNA-binding motif protein, X-linked 2

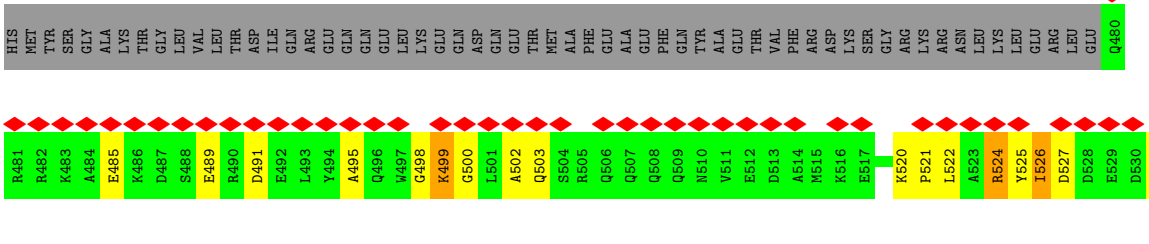


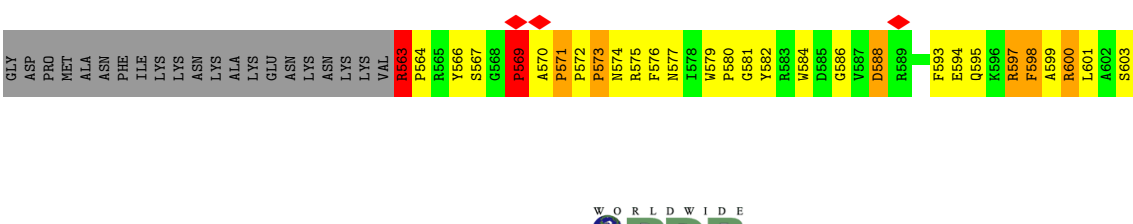




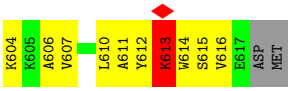




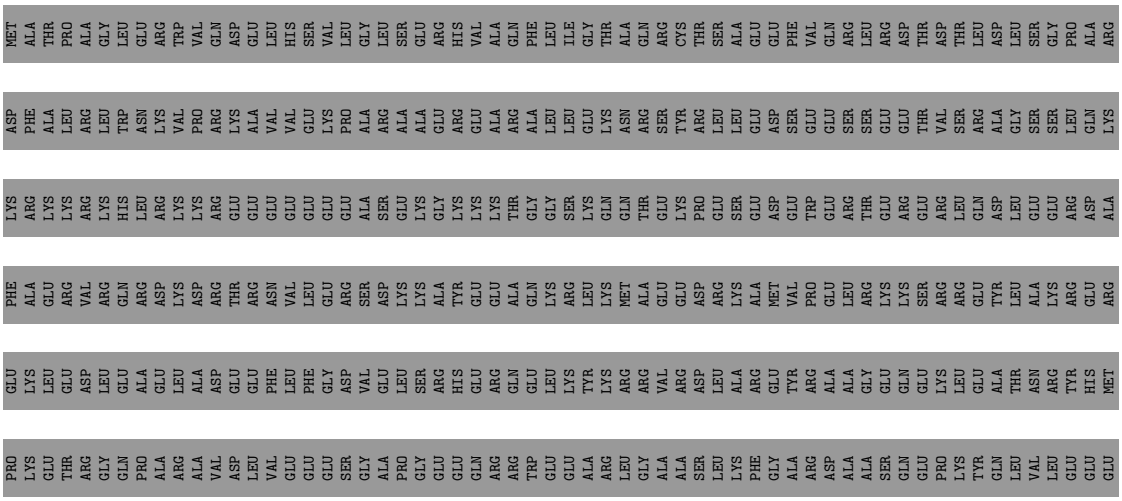


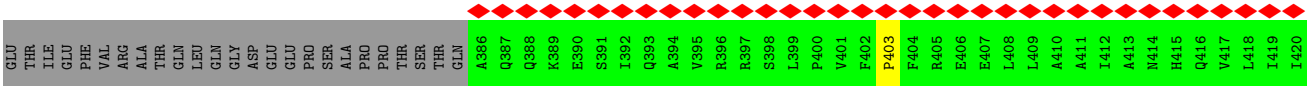


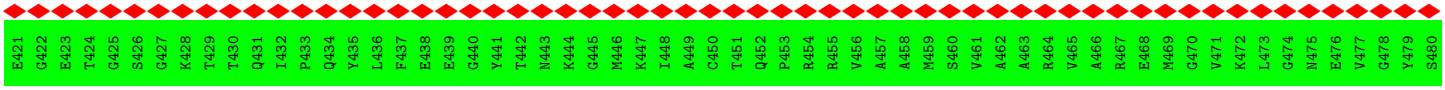
• Molecule 45: BUD13 homolog

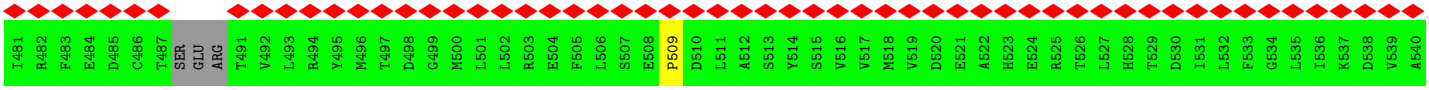


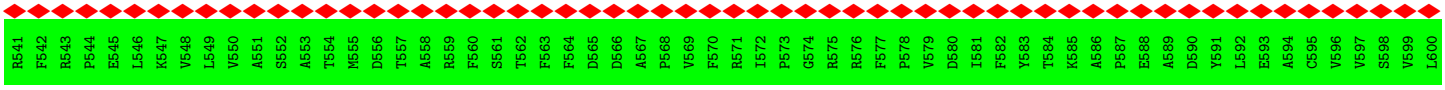
• Molecule 46: Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16

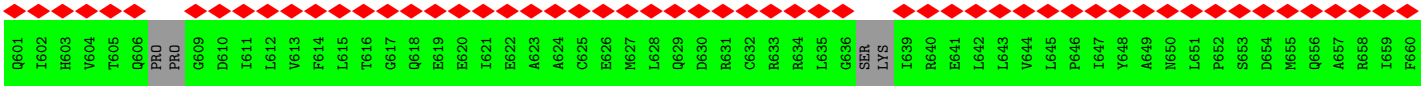


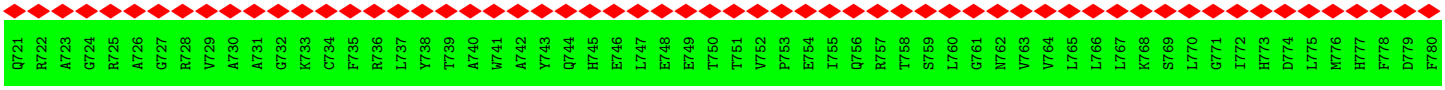


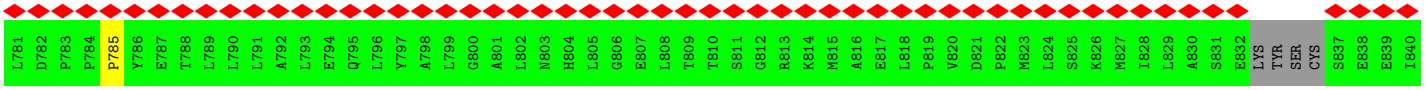


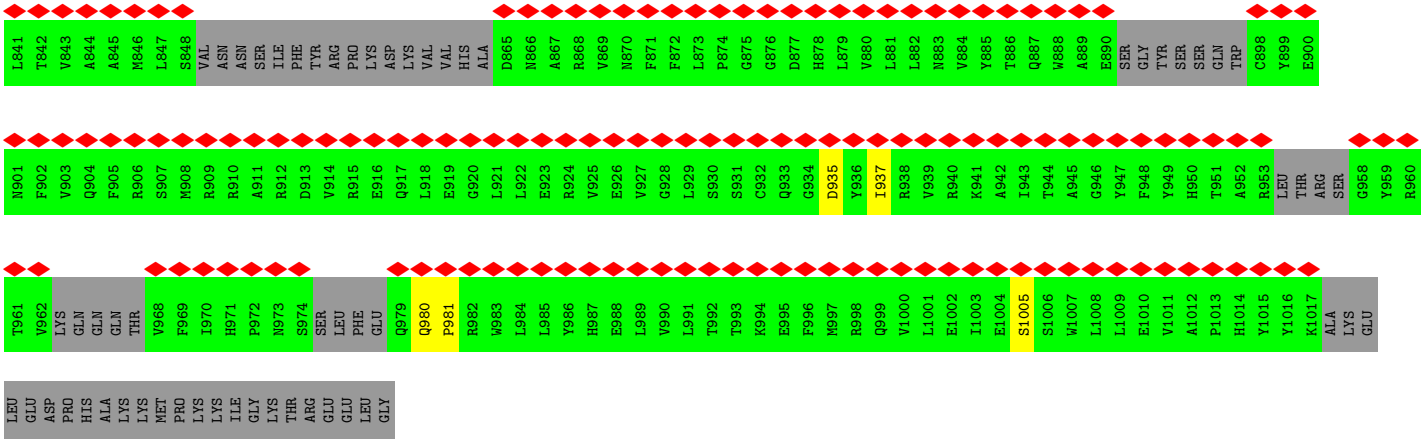






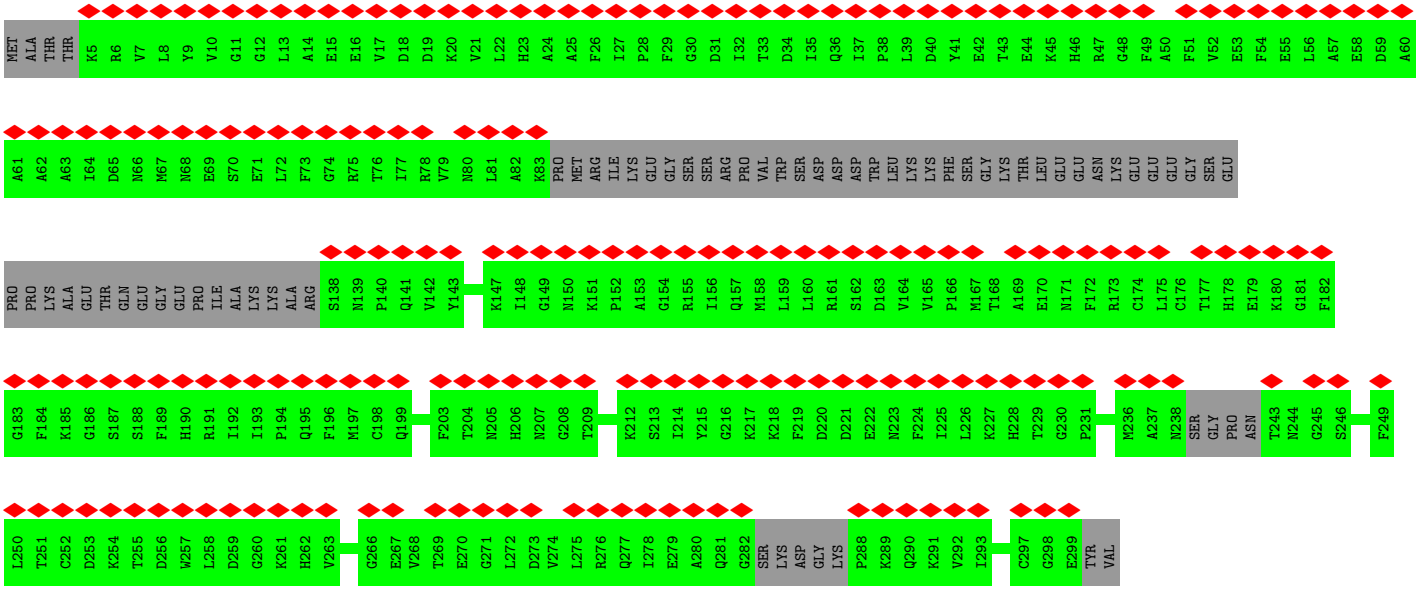






• Molecule 47: Peptidyl-prolyl cis-trans isomerase E

Chain y:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	14316	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 ($e^-/Å^2$)	48	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	0.142	Depositor
Minimum map value	-0.067	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0323	Depositor
Map size (Å)	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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: IHP, MG, ZN, GTP

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	0.72	9/16867 (0.1%)	0.80	25/22888 (0.1%)
2	B	0.75	2/1970 (0.1%)	0.91	7/3060 (0.2%)
3	C	0.79	1/6864 (0.0%)	0.96	10/9334 (0.1%)
4	D	0.33	0/8527	0.59	0/11887
5	E	0.64	0/2392	0.79	0/3242
6	a	0.47	0/397	0.61	0/549
6	h	0.46	0/391	0.61	0/540
7	b	0.49	0/404	0.72	0/561
7	i	0.50	0/421	0.73	0/583
8	c	0.57	0/405	0.73	0/563
8	j	0.57	0/405	0.73	0/563
9	d	0.68	0/479	0.84	0/666
9	k	0.70	0/420	0.85	0/583
10	f	0.75	0/360	0.81	0/497
10	m	0.75	0/360	0.81	0/497
11	e	0.65	0/390	0.80	0/542
11	l	0.64	0/390	0.80	0/542
12	g	0.54	0/362	0.71	0/501
12	n	0.54	0/332	0.72	0/458
13	F	0.39	0/2224	0.86	0/3462
14	G	0.35	0/1717	0.95	1/2664 (0.0%)
15	H	0.59	7/3217 (0.2%)	1.06	18/4997 (0.4%)
16	o	0.61	0/803	1.41	2/1119 (0.2%)
17	p	1.01	1/810 (0.1%)	1.46	4/1122 (0.4%)
18	w	0.53	5/2380 (0.2%)	0.67	13/3274 (0.4%)
19	u	0.23	0/514	0.63	4/710 (0.6%)
20	v	0.73	4/935 (0.4%)	0.81	9/1266 (0.7%)
21	1	0.33	0/7826	0.51	0/10617
22	2	0.52	3/1277 (0.2%)	0.73	7/1724 (0.4%)
23	3	0.32	0/9381	0.52	0/12732
24	4	0.83	2/535 (0.4%)	0.98	4/724 (0.6%)
25	5	0.29	0/823	0.48	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
26	6	0.29	0/678	0.51	0/909
27	7	0.31	0/556	0.45	0/751
28	J	0.62	0/3500	0.73	0/4750
29	L	0.52	3/2283 (0.1%)	0.58	8/3088 (0.3%)
30	q	0.35	0/658	0.58	3/919 (0.3%)
30	r	0.32	0/653	0.59	3/912 (0.3%)
30	s	0.26	0/334	0.37	0/466
30	t	0.30	0/334	0.38	0/466
31	K	1.28	14/981 (1.4%)	0.69	5/1317 (0.4%)
32	I	0.39	0/2745	0.56	17/3765 (0.5%)
33	Q	0.21	0/6518	0.42	0/9075
34	N	0.88	1/1210 (0.1%)	1.00	3/1622 (0.2%)
35	O	0.80	3/2321 (0.1%)	0.94	6/3135 (0.2%)
36	P	0.83	1/841 (0.1%)	1.01	2/1117 (0.2%)
37	R	0.68	5/2224 (0.2%)	0.88	7/2992 (0.2%)
38	S	0.59	0/1268	0.80	1/1714 (0.1%)
39	T	1.05	1/2522 (0.0%)	1.11	4/3438 (0.1%)
40	U	1.03	0/196	1.09	1/265 (0.4%)
41	V	0.54	0/2239	0.67	1/3118 (0.0%)
42	W	0.55	0/2381	0.76	4/3310 (0.1%)
43	X	0.27	0/1012	0.48	0/1351
44	Y	0.31	0/753	0.48	0/1014
45	Z	0.57	2/772 (0.3%)	0.79	7/1056 (0.7%)
46	x	0.35	0/2871	0.53	3/3981 (0.1%)
47	y	0.35	0/1129	0.61	0/1558
All	All	0.58	64/115557 (0.1%)	0.75	179/159679 (0.1%)

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	6
3	C	0	3
4	D	0	1
9	d	0	1
9	k	0	1
21	1	0	9
22	2	0	1
23	3	0	4
27	7	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
34	N	0	1
37	R	0	1
39	T	0	2
43	X	0	1
All	All	0	32

All (64) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	K	106	CYS	CB-SG	-23.13	1.43	1.82
31	K	132	CYS	CB-SG	-17.48	1.52	1.82
29	L	761	SER	CB-OG	8.91	1.53	1.42
31	K	128	SER	CB-OG	8.42	1.53	1.42
31	K	183	SER	CB-OG	8.28	1.53	1.42
18	w	457	SER	CB-OG	8.21	1.52	1.42
35	O	181	TYR	CE1-CZ	-8.11	1.28	1.38
29	L	726	SER	CB-OG	8.08	1.52	1.42
31	K	190	SER	CB-OG	8.01	1.52	1.42
31	K	187	SER	CB-OG	7.96	1.52	1.42
18	w	483	SER	CB-OG	7.46	1.51	1.42
15	H	142	C	C1'-N1	7.35	1.59	1.48
22	2	655	SER	CB-OG	7.35	1.51	1.42
34	N	102	CYS	CB-SG	-7.30	1.69	1.82
1	A	406	TRP	CB-CG	-7.06	1.37	1.50
20	v	19	SER	CB-OG	6.99	1.51	1.42
2	B	103	G	C1'-N9	-6.95	1.37	1.46
1	A	2223	CYS	CB-SG	-6.78	1.70	1.82
15	H	150	U	C1'-N1	6.76	1.58	1.48
36	P	227	TYR	CG-CD2	-6.70	1.30	1.39
1	A	476	PHE	CG-CD2	6.66	1.48	1.38
20	v	53	SER	CB-OG	6.65	1.50	1.42
29	L	724	TYR	CB-CG	-6.58	1.41	1.51
15	H	97	G	C1'-N9	-6.48	1.37	1.46
20	v	22	SER	CB-OG	6.46	1.50	1.42
15	H	151	C	C1'-N1	6.44	1.58	1.48
15	H	184	C	C1'-N1	6.37	1.58	1.48
31	K	43	TYR	CB-CG	-6.33	1.42	1.51
31	K	138	TYR	CB-CG	-6.33	1.42	1.51
15	H	141	C	C1'-N1	6.31	1.58	1.48
31	K	93	SER	CB-OG	6.29	1.50	1.42
24	4	50	THR	CB-OG1	5.94	1.55	1.43
18	w	395	TRP	CZ3-CH2	5.86	1.49	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	4	42	THR	CB-OG1	5.85	1.54	1.43
39	T	218	TRP	CB-CG	-5.71	1.40	1.50
20	v	80	THR	CB-OG1	5.66	1.54	1.43
31	K	40	THR	CB-OG1	5.61	1.54	1.43
2	B	56	C	O3'-P	-5.45	1.54	1.61
1	A	212	PRO	N-CA	-5.43	1.38	1.47
45	Z	569	PRO	N-CD	5.43	1.55	1.47
22	2	620	PRO	N-CD	5.41	1.55	1.47
18	w	284	ARG	CA-CB	-5.37	1.42	1.53
1	A	94	TYR	CB-CG	-5.33	1.43	1.51
35	O	225	PRO	N-CD	5.33	1.55	1.47
31	K	30	GLU	CB-CG	-5.25	1.42	1.52
22	2	643	PRO	N-CD	5.24	1.55	1.47
35	O	226	PRO	N-CD	5.22	1.55	1.47
17	p	156	ASN	C-N	-5.21	1.22	1.34
18	w	415	THR	CB-OG1	5.21	1.53	1.43
37	R	130	PRO	N-CD	5.18	1.55	1.47
31	K	137	VAL	CB-CG1	-5.18	1.42	1.52
31	K	119	VAL	CB-CG2	-5.15	1.42	1.52
45	Z	521	PRO	N-CD	5.15	1.55	1.47
15	H	110	A	C1'-N9	-5.13	1.39	1.46
37	R	222	PRO	N-CD	5.13	1.55	1.47
1	A	140	TYR	CG-CD2	-5.13	1.32	1.39
1	A	351	TYR	CB-CG	-5.11	1.44	1.51
1	A	225	TYR	CB-CG	-5.09	1.44	1.51
31	K	186	VAL	CA-CB	-5.08	1.44	1.54
37	R	253	PRO	N-CD	5.05	1.54	1.47
3	C	145	PHE	CB-CG	-5.04	1.42	1.51
37	R	252	PRO	N-CD	5.04	1.54	1.47
1	A	406	TRP	CG-CD2	-5.03	1.35	1.43
37	R	227	PRO	N-CD	5.03	1.54	1.47

All (179) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
24	4	83	PRO	CA-CB-CG	10.19	124.17	104.80
22	2	636	MET	CG-SD-CE	9.28	115.05	100.20
31	K	90	PRO	CA-CB-CG	8.66	121.26	104.80
45	Z	569	PRO	CA-N-CD	-8.56	99.52	111.50
45	Z	573	PRO	CA-N-CD	-8.45	99.67	111.50
35	O	225	PRO	CA-N-CD	-8.17	100.07	111.50
1	A	404	LEU	CB-CG-CD1	8.13	124.83	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
35	O	226	PRO	CA-N-CD	-8.07	100.21	111.50
35	O	35	ARG	NE-CZ-NH2	-7.69	116.45	120.30
1	A	552	ARG	NE-CZ-NH1	7.53	124.06	120.30
1	A	153	ARG	NE-CZ-NH2	-7.36	116.62	120.30
2	B	20	G	N9-C1'-C2'	7.29	123.48	114.00
42	W	278	LYS	CB-CA-C	-7.29	95.82	110.40
15	H	113	G	OP2-P-O3'	7.25	121.15	105.20
15	H	141	C	OP2-P-O3'	7.24	121.14	105.20
15	H	114	A	OP2-P-O3'	7.22	121.09	105.20
3	C	144	CYS	N-CA-CB	7.20	123.56	110.60
15	H	150	U	OP2-P-O3'	7.19	121.01	105.20
37	R	180	THR	C-N-CD	-7.16	104.85	120.60
18	w	441	PRO	N-CA-CB	7.16	111.89	103.30
19	u	222	PRO	N-CA-CB	7.14	111.87	103.30
1	A	611	LEU	CB-CG-CD1	-7.10	98.92	111.00
22	2	656	PRO	N-CA-CB	6.88	111.56	103.30
1	A	565	ARG	NE-CZ-NH2	-6.88	116.86	120.30
15	H	155	C	P-O3'-C3'	6.78	127.84	119.70
15	H	141	C	O3'-P-O5'	-6.77	91.14	104.00
15	H	150	U	O3'-P-O5'	-6.77	91.14	104.00
2	B	104	C	C2'-C3'-O3'	-6.77	94.61	109.50
2	B	26	A	O5'-P-OP2	6.74	118.78	110.70
15	H	113	G	O3'-P-O5'	-6.73	91.21	104.00
15	H	114	A	O3'-P-O5'	-6.72	91.23	104.00
15	H	30	A	O5'-P-OP1	-6.71	99.66	105.70
20	v	115	PRO	N-CA-CB	6.65	111.28	103.30
3	C	420	CYS	CA-CB-SG	-6.63	102.07	114.00
2	B	12	U	N1-C1'-C2'	-6.62	104.72	112.00
36	P	215	LEU	CB-CG-CD1	-6.61	99.76	111.00
30	q	46	PRO	N-CA-CB	6.59	111.21	103.30
31	K	90	PRO	N-CA-CB	6.57	111.19	103.30
42	W	279	LYS	N-CA-C	-6.57	93.26	111.00
20	v	139	PRO	N-CA-CB	6.54	111.15	103.30
24	4	27	PRO	N-CA-CB	6.50	111.10	103.30
1	A	598	LEU	CB-CG-CD2	-6.50	99.96	111.00
30	q	60	PRO	N-CA-CB	6.48	111.08	103.30
30	r	46	PRO	N-CA-CB	6.48	111.08	103.30
36	P	215	LEU	CB-CG-CD2	6.47	122.00	111.00
42	W	251	GLY	N-CA-C	-6.47	96.93	113.10
18	w	120	PRO	N-CA-CB	6.47	111.06	103.30
18	w	227	PRO	N-CA-CB	6.47	111.06	103.30
31	K	78	PRO	N-CA-CB	6.42	111.00	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
34	N	101	CYS	CB-CA-C	-6.41	97.58	110.40
3	C	921	LEU	CB-CG-CD1	6.41	121.89	111.00
46	x	403	PRO	N-CA-CB	6.35	110.92	103.30
19	u	200	PRO	N-CA-CB	6.31	110.87	103.30
32	I	475	PRO	N-CA-CB	6.31	110.87	103.30
38	S	152	ARG	NE-CZ-NH2	-6.31	117.15	120.30
37	R	205	ASP	CB-CG-OD2	6.30	123.97	118.30
1	A	476	PHE	CB-CG-CD1	6.30	125.21	120.80
35	O	181	TYR	CG-CD2-CE2	-6.28	116.28	121.30
20	v	218	PRO	N-CA-CB	6.28	110.83	103.30
45	Z	570	ALA	C-N-CD	6.25	141.52	128.40
18	w	105	PRO	N-CA-CB	6.24	110.79	103.30
32	I	551	PRO	N-CA-CB	6.24	110.78	103.30
31	K	107	VAL	CA-CB-CG1	6.23	120.25	110.90
18	w	305	PRO	N-CA-CB	6.23	110.77	103.30
32	I	589	PRO	N-CA-CB	6.23	110.77	103.30
1	A	153	ARG	NE-CZ-NH1	6.22	123.41	120.30
22	2	641	PRO	N-CA-CB	6.21	110.76	103.30
18	w	174	PRO	N-CA-CB	6.21	110.75	103.30
1	A	506	LEU	CB-CG-CD1	-6.20	100.45	111.00
32	I	162	PRO	N-CA-CB	6.20	110.73	103.30
39	T	220	VAL	CB-CA-C	-6.18	99.65	111.40
39	T	282	ARG	NE-CZ-NH2	-6.18	117.21	120.30
19	u	221	PRO	N-CA-CB	6.17	110.70	103.30
32	I	232	PRO	N-CA-CB	6.16	110.69	103.30
46	x	509	PRO	N-CA-CB	6.14	110.66	103.30
29	L	558	PRO	N-CA-CB	6.12	110.64	103.30
17	p	184	PRO	N-CA-CB	6.10	110.62	103.30
32	I	177	PRO	N-CA-CB	6.10	110.61	103.30
29	L	546	PRO	N-CA-CB	6.09	110.60	103.30
18	w	202	PRO	N-CA-CB	6.04	110.55	103.30
20	v	221	PRO	N-CA-CB	6.04	110.55	103.30
32	I	788	PRO	N-CA-CB	6.03	110.54	103.30
32	I	816	PRO	N-CA-CB	6.01	110.51	103.30
17	p	155	LEU	N-CA-CB	5.99	122.37	110.40
14	G	156	U	C2-N1-C1'	5.97	124.87	117.70
20	v	162	PRO	N-CA-CB	5.96	110.45	103.30
18	w	99	PRO	N-CA-CB	5.96	110.45	103.30
32	I	160	PRO	N-CA-CB	5.95	110.44	103.30
32	I	394	PRO	N-CA-CB	5.95	110.44	103.30
37	R	252	PRO	C-N-CD	5.93	140.85	128.40
29	L	563	PRO	N-CA-CB	5.89	110.37	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	I	387	PRO	N-CA-CB	5.87	110.35	103.30
18	w	230	PRO	N-CA-CB	5.86	110.33	103.30
17	p	219	LYS	O-C-N	5.86	132.07	122.70
20	v	220	PRO	N-CA-CB	5.86	110.33	103.30
18	w	419	PRO	N-CA-CB	5.85	110.32	103.30
20	v	217	PRO	N-CA-CB	5.84	110.31	103.30
15	H	172	C	P-O3'-C3'	5.84	126.71	119.70
32	I	342	PRO	N-CA-CB	5.84	110.30	103.30
29	L	564	PRO	N-CA-CB	5.83	110.30	103.30
30	q	19	PRO	N-CA-CB	5.83	110.29	103.30
3	C	148	CYS	CB-CA-C	5.82	122.04	110.40
3	C	446	LYS	C-N-CD	5.81	140.61	128.40
29	L	594	PRO	N-CA-CB	5.81	110.28	103.30
32	I	518	PRO	N-CA-CB	5.81	110.28	103.30
30	r	19	PRO	N-CA-CB	5.79	110.25	103.30
15	H	156	U	P-O3'-C3'	-5.77	112.78	119.70
29	L	548	PRO	N-CA-CB	5.77	110.22	103.30
29	L	620	PRO	N-CA-CB	5.77	110.23	103.30
22	2	629	PRO	N-CA-CB	5.77	110.22	103.30
45	Z	563	ARG	C-N-CD	5.76	140.49	128.40
32	I	588	PRO	N-CA-CB	5.75	110.20	103.30
35	O	48	CYS	CA-CB-SG	5.70	124.27	114.00
1	A	565	ARG	NE-CZ-NH1	5.69	123.15	120.30
37	R	221	GLY	C-N-CD	5.66	140.29	128.40
22	2	642	PRO	C-N-CD	5.65	140.27	128.40
24	4	27	PRO	CA-CB-CG	5.64	115.51	104.80
1	A	1364	LEU	CA-CB-CG	5.63	128.25	115.30
1	A	332	TYR	N-CA-C	-5.61	95.85	111.00
45	Z	520	LYS	C-N-CD	5.61	140.18	128.40
32	I	463	PRO	N-CA-CB	5.58	110.00	103.30
31	K	93	SER	N-CA-CB	-5.58	102.14	110.50
32	I	761	PRO	N-CA-CB	5.58	109.99	103.30
15	H	46	U	P-O3'-C3'	5.57	126.39	119.70
46	x	785	PRO	N-CA-CB	5.56	109.97	103.30
29	L	774	VAL	CA-CB-CG2	5.54	119.20	110.90
16	o	58	ASP	N-CA-CB	-5.52	100.66	110.60
34	N	104	ARG	NE-CZ-NH2	-5.49	117.55	120.30
20	v	73	THR	CA-CB-OG1	5.48	120.50	109.00
1	A	118	VAL	CB-CA-C	-5.47	101.01	111.40
15	H	157	G	O4'-C1'-N9	-5.47	103.83	108.20
3	C	146	VAL	CA-CB-CG2	-5.46	102.70	110.90
30	r	60	PRO	N-CA-CB	5.46	109.85	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	I	625	PRO	N-CA-CB	5.45	109.84	103.30
1	A	656	LEU	CB-CG-CD1	-5.45	101.74	111.00
1	A	2310	ARG	CG-CD-NE	5.42	123.19	111.80
18	w	399	LEU	CB-CG-CD1	-5.42	101.78	111.00
3	C	91	GLU	C-N-CD	-5.42	108.68	120.60
40	U	19	VAL	CB-CA-C	-5.41	101.13	111.40
34	N	102	CYS	CB-CA-C	-5.40	99.59	110.40
1	A	420	ARG	NE-CZ-NH2	-5.40	117.60	120.30
1	A	251	ASP	CB-CG-OD1	5.39	123.15	118.30
22	2	651	PRO	N-CA-CB	5.39	109.77	103.30
39	T	308	ARG	NE-CZ-NH2	-5.36	117.62	120.30
22	2	619	MET	C-N-CD	5.36	139.66	128.40
15	H	106	G	O5'-P-OP1	5.34	117.10	110.70
15	H	156	U	OP2-P-O3'	5.33	116.93	105.20
1	A	92	LEU	CB-CG-CD1	-5.31	101.97	111.00
2	B	40	U	N1-C1'-C2'	5.31	120.90	114.00
37	R	178	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	A	314	ILE	CA-CB-CG1	-5.28	100.96	111.00
1	A	656	LEU	CA-CB-CG	-5.28	103.16	115.30
2	B	37	G	O5'-P-OP2	-5.26	100.97	105.70
24	4	50	THR	CA-CB-OG1	5.25	120.02	109.00
3	C	921	LEU	CB-CG-CD2	-5.24	102.09	111.00
17	p	149	PRO	N-CA-CB	5.23	109.58	103.30
1	A	656	LEU	CB-CG-CD2	5.21	119.86	111.00
45	Z	588	ASP	CB-CG-OD2	5.20	122.98	118.30
3	C	776	GLU	N-CA-C	5.19	125.02	111.00
37	R	178	ARG	NE-CZ-NH1	5.19	122.90	120.30
45	Z	527	ASP	CB-CG-OD2	5.19	122.97	118.30
19	u	203	SER	N-CA-CB	-5.18	102.73	110.50
35	O	24	CYS	CA-CB-SG	5.17	123.31	114.00
1	A	330	THR	CA-CB-CG2	-5.17	105.16	112.40
1	A	647	LEU	CB-CG-CD1	-5.14	102.26	111.00
15	H	157	G	P-O5'-C5'	-5.13	112.69	120.90
41	V	467	LEU	CB-CA-C	-5.13	100.45	110.20
1	A	638	LEU	CA-CB-CG	-5.11	103.54	115.30
42	W	279	LYS	N-CA-CB	5.10	119.77	110.60
18	w	399	LEU	CD1-CG-CD2	5.09	125.76	110.50
2	B	20	G	O4'-C1'-N9	5.09	112.27	108.20
15	H	156	U	C4'-C3'-C2'	5.08	107.68	102.60
1	A	677	VAL	CB-CA-C	-5.07	101.78	111.40
39	T	233	LEU	CB-CG-CD1	-5.06	102.40	111.00
18	w	45	ALA	N-CA-CB	-5.04	103.04	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
37	R	101	ILE	CB-CA-C	-5.04	101.53	111.60
16	o	99	SER	N-CA-CB	-5.03	102.96	110.50
20	v	33	LEU	CB-CG-CD1	-5.02	102.47	111.00
3	C	220	ARG	NE-CZ-NH2	-5.01	117.79	120.30

There are no chirality outliers.

All (32) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	1	1028	HIS	Peptide
21	1	1105	GLU	Peptide
21	1	1107	GLN	Peptide
21	1	220	GLN	Peptide
21	1	415	LEU	Peptide
21	1	418	PRO	Peptide
21	1	460	PRO	Peptide
21	1	717	THR	Peptide
21	1	943	LYS	Peptide
22	2	558	ARG	Peptide
23	3	261	PHE	Peptide
23	3	530	ASP	Peptide
23	3	552	ARG	Peptide
23	3	916	ASN	Peptide
27	7	74	GLN	Peptide
1	A	166	PHE	Peptide
1	A	346	ASP	Peptide
1	A	408	PRO	Peptide
1	A	433	GLU	Peptide
1	A	697	MET	Peptide
1	A	941	LYS	Peptide
3	C	622	GLU	Peptide
3	C	736	GLY	Peptide
3	C	823	ALA	Peptide
4	D	430	LEU	Peptide
34	N	36	PRO	Peptide
37	R	94	GLY	Peptide
39	T	400	PHE	Mainchain,Peptide
43	X	193	ASN	Peptide
9	d	112	ASN	Peptide
9	k	112	ASN	Peptide

5.2 Too-close contacts (i)

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	16399	0	16176	1407	0
2	B	1768	0	897	120	0
3	C	6716	0	6691	892	0
4	D	8528	0	3745	78	0
5	E	2338	0	2272	153	0
6	a	399	0	173	0	0
6	h	393	0	170	0	0
7	b	405	0	170	0	0
7	i	422	0	177	0	0
8	c	406	0	170	0	0
8	j	406	0	170	0	0
9	d	480	0	200	0	0
9	k	422	0	175	0	0
10	f	361	0	158	0	0
10	m	361	0	158	0	0
11	e	391	0	163	0	0
11	l	391	0	163	0	0
12	g	363	0	160	0	0
12	n	334	0	143	0	0
13	F	1988	0	1005	186	0
14	G	1545	0	786	197	0
15	H	2886	0	1463	239	0
16	o	804	0	350	0	0
17	p	813	0	365	0	0
18	w	2373	0	1301	0	0
19	u	520	0	214	0	0
20	v	936	0	591	0	0
21	1	7702	0	7389	309	0
22	2	1252	0	1040	57	0
23	3	9195	0	9091	465	0
24	4	527	0	438	40	0
25	5	807	0	729	26	0
26	6	670	0	654	21	0
27	7	540	0	509	25	0
28	J	3463	0	2544	107	0
29	L	2260	0	1776	92	0
30	q	659	0	296	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	r	654	0	294	0	0
30	s	335	0	168	0	0
30	t	335	0	168	0	0
31	K	979	0	739	11	0
32	I	2778	0	1238	21	0
33	Q	6528	0	2814	6	0
34	N	1184	0	1190	75	0
35	O	2273	0	2244	244	0
36	P	829	0	814	192	0
37	R	2188	0	2102	400	0
38	S	1236	0	1210	135	0
39	T	2457	0	2416	251	0
40	U	193	0	196	40	0
41	V	2243	0	971	48	0
42	W	2384	0	1055	126	0
43	X	1012	0	733	17	0
44	Y	743	0	613	67	0
45	Z	755	0	591	113	0
46	x	2882	0	1308	0	0
47	y	1133	0	519	0	0
48	A	36	0	6	10	0
49	A	5	0	4	2	0
50	C	32	0	12	11	0
51	C	1	0	0	0	0
51	F	5	0	0	0	0
52	6	3	0	0	0	0
52	N	3	0	0	0	0
52	O	3	0	0	3	0
52	v	1	0	0	0	0
All	All	113433	0	84077	4900	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 26.

All (4900) 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)
44:Y:37:TRP:CH2	45:Z:498:GLY:HA2	1.23	1.65
1:A:1758:PRO:HA	21:1:938:TRP:CD1	1.28	1.59
1:A:2270:PHE:HB3	4:D:1264:PRO:CB	1.34	1.56
3:C:149:LEU:HD13	3:C:427:PHE:CD2	1.38	1.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2270:PHE:CG	4:D:1264:PRO:CB	1.89	1.54
3:C:77:VAL:HG11	39:T:196:LEU:CG	1.39	1.52
44:Y:37:TRP:CH2	45:Z:498:GLY:CA	1.93	1.51
1:A:2270:PHE:CB	4:D:1264:PRO:CB	1.86	1.49
45:Z:564:PRO:HB2	45:Z:582:TYR:CG	1.45	1.49
36:P:193:VAL:HG23	36:P:194:PHE:CD2	1.46	1.47
1:A:1758:PRO:HA	21:1:938:TRP:NE1	1.16	1.46
37:R:442:ARG:HH11	37:R:443:GLY:C	1.17	1.45
1:A:844:GLU:CB	37:R:422:MET:CE	1.94	1.45
36:P:193:VAL:CG2	36:P:194:PHE:HD2	1.28	1.45
35:O:149:LYS:HD2	35:O:290:LYS:CE	1.49	1.43
37:R:414:ARG:NH1	45:Z:598:PHE:CZ	1.86	1.43
38:S:57:ILE:HD13	42:W:97:ASN:CB	1.44	1.42
14:G:21:A:H2	35:O:212:LYS:CB	1.30	1.42
3:C:705:VAL:HG23	3:C:717:PHE:CD2	1.55	1.41
1:A:384:VAL:HG12	3:C:331:PHE:CE2	1.56	1.40
3:C:79:THR:CG2	39:T:199:VAL:HB	1.51	1.40
35:O:189:PRO:HG3	42:W:223:ARG:CA	1.48	1.40
1:A:73:HIS:HD2	1:A:81:PHE:CE2	1.37	1.40
1:A:2270:PHE:CD1	4:D:1264:PRO:CB	2.03	1.40
28:J:293:ASN:CB	29:L:225:TYR:CB	1.98	1.39
3:C:79:THR:HG23	39:T:199:VAL:CB	1.49	1.39
5:E:260:ARG:NH1	5:E:273:CYS:SG	1.95	1.39
1:A:299:ILE:CG1	1:A:1342:TRP:HZ3	1.34	1.39
28:J:339:TRP:HA	37:R:116:TYR:CE2	1.58	1.38
3:C:387:ASP:O	3:C:388:VAL:HG12	1.20	1.37
37:R:442:ARG:CD	37:R:443:GLY:H	1.37	1.37
4:D:863:THR:CB	23:3:599:GLU:HA	1.53	1.37
1:A:380:LEU:CB	3:C:354:ARG:HG3	1.54	1.36
3:C:77:VAL:HG12	39:T:196:LEU:C	1.46	1.36
37:R:92:SER:CA	38:S:19:SER:HB2	1.55	1.36
1:A:762:ARG:HH22	36:P:226:LYS:NZ	1.19	1.35
29:L:216:PHE:CD1	35:O:113:ASN:CA	2.08	1.35
28:J:339:TRP:HA	37:R:116:TYR:CD2	1.60	1.35
37:R:414:ARG:NH1	45:Z:598:PHE:CE2	1.93	1.35
3:C:77:VAL:CG1	39:T:196:LEU:C	1.94	1.35
1:A:1758:PRO:CA	21:1:938:TRP:NE1	1.89	1.34
3:C:149:LEU:CD1	3:C:427:PHE:CD2	2.08	1.34
37:R:442:ARG:HD3	37:R:443:GLY:N	1.05	1.34
37:R:414:ARG:NE	45:Z:598:PHE:CZ	1.95	1.34
3:C:452:THR:CG2	3:C:577:PHE:HD2	1.40	1.34

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:S:39:PHE:CB	38:S:129:PHE:CZ	2.10	1.34
1:A:121:HIS:NE2	1:A:481:PHE:HB3	1.42	1.33
1:A:1482:GLU:O	1:A:1486:GLU:HG2	1.29	1.32
3:C:145:PHE:CA	3:C:312:SER:HB2	1.57	1.31
38:S:57:ILE:CD1	42:W:97:ASN:CB	2.08	1.31
37:R:414:ARG:CZ	45:Z:598:PHE:CZ	2.14	1.31
3:C:670:SER:HA	3:C:823:ALA:CB	1.60	1.31
23:3:687:SER:OG	23:3:1206:LYS:HD2	1.26	1.31
1:A:73:HIS:CD2	1:A:81:PHE:CZ	2.20	1.30
1:A:299:ILE:HG13	1:A:1342:TRP:CZ3	1.67	1.30
36:P:212:ASN:O	39:T:458:SER:HA	1.30	1.30
1:A:264:PHE:CZ	1:A:459:LEU:HD13	1.66	1.30
1:A:844:GLU:CB	37:R:422:MET:HE3	1.54	1.30
1:A:1342:TRP:CD2	3:C:921:LEU:HD13	1.65	1.30
32:I:280:GLU:CB	32:I:288:THR:CB	2.08	1.29
1:A:296:PHE:CG	3:C:656:ALA:HB2	1.66	1.29
36:P:211:VAL:HG13	39:T:457:GLY:CA	1.62	1.29
14:G:-9:C:C4	40:U:18:TYR:CE1	2.20	1.29
32:I:280:GLU:C	32:I:288:THR:CB	2.00	1.28
1:A:73:HIS:CD2	1:A:81:PHE:CE2	2.20	1.28
3:C:77:VAL:CG1	39:T:196:LEU:HG	1.63	1.28
3:C:705:VAL:CG2	3:C:717:PHE:CE2	2.15	1.28
1:A:1342:TRP:CE3	3:C:921:LEU:HD13	1.69	1.28
1:A:1364:LEU:CD1	41:V:461:LEU:CB	2.11	1.28
37:R:92:SER:HA	38:S:19:SER:CB	1.61	1.28
1:A:1757:GLU:O	21:1:938:TRP:CZ2	1.87	1.26
3:C:78:GLU:O	39:T:198:ARG:HA	1.35	1.26
3:C:145:PHE:HA	3:C:312:SER:CB	1.65	1.26
14:G:-9:C:C5	40:U:18:TYR:CE1	2.23	1.26
36:P:211:VAL:CG1	39:T:457:GLY:HA3	1.65	1.26
36:P:193:VAL:CG2	36:P:194:PHE:CD2	2.09	1.26
5:E:146:ARG:NH1	5:E:148:LYS:CE	1.98	1.25
37:R:414:ARG:CZ	45:Z:598:PHE:HZ	1.47	1.25
1:A:299:ILE:CG1	1:A:1342:TRP:CZ3	2.18	1.25
1:A:2268:LEU:HD23	4:D:1261:PRO:O	1.22	1.25
38:S:131:ARG:HD3	38:S:132:VAL:O	1.09	1.25
38:S:39:PHE:CG	38:S:129:PHE:HE2	1.53	1.25
1:A:2268:LEU:HD22	4:D:1261:PRO:CB	1.65	1.25
1:A:299:ILE:CD1	3:C:921:LEU:HB2	1.67	1.24
1:A:380:LEU:HD22	3:C:354:ARG:O	1.24	1.24
24:4:14:THR:HA	24:4:59:VAL:O	1.32	1.24

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:S:39:PHE:HB2	38:S:129:PHE:CZ	1.66	1.24
1:A:1758:PRO:CA	21:1:938:TRP:CD1	2.16	1.24
3:C:679:PRO:HB2	3:C:807:GLN:OE1	1.25	1.24
3:C:84:GLU:O	39:T:238:LEU:HD23	1.34	1.24
1:A:2113:LYS:HE3	4:D:1229:ASP:O	1.33	1.23
14:G:21:A:C2	35:O:212:LYS:CB	2.21	1.23
1:A:380:LEU:HB2	3:C:354:ARG:CG	1.67	1.23
1:A:593:ARG:NH1	1:A:1565:LYS:HE2	1.53	1.23
44:Y:37:TRP:CZ3	45:Z:498:GLY:CA	2.20	1.23
44:Y:37:TRP:CZ3	45:Z:498:GLY:HA2	1.73	1.23
1:A:121:HIS:CE1	1:A:481:PHE:HB3	1.73	1.23
3:C:140:HIS:CG	3:C:230:ASP:HB2	1.74	1.22
1:A:1342:TRP:CD2	3:C:921:LEU:CD1	2.22	1.22
1:A:762:ARG:HH22	36:P:226:LYS:CE	1.51	1.22
3:C:78:GLU:HG2	3:C:80:ILE:CD1	1.69	1.22
3:C:145:PHE:CA	3:C:312:SER:CB	2.18	1.22
28:J:256:LYS:O	29:L:232:TYR:CD2	1.93	1.22
3:C:77:VAL:HG13	39:T:196:LEU:O	1.40	1.21
3:C:497:LEU:HD13	3:C:577:PHE:CZ	1.76	1.21
13:F:28:A:O2'	34:N:39:GLY:HA2	1.40	1.21
44:Y:18:VAL:CB	45:Z:600:ARG:HH21	1.53	1.21
35:O:149:LYS:HD2	35:O:290:LYS:NZ	1.53	1.21
1:A:1320:LYS:HE2	37:R:434:TYR:CE1	1.76	1.21
3:C:137:HIS:CD2	3:C:236:MET:HB2	1.75	1.21
1:A:2298:LEU:HB3	4:D:1283:PRO:CB	1.71	1.20
37:R:442:ARG:CD	37:R:443:GLY:N	1.95	1.20
38:S:39:PHE:CB	38:S:129:PHE:HZ	1.46	1.20
1:A:227:ARG:HA	1:A:416:GLY:O	1.39	1.20
1:A:755:HIS:ND1	36:P:223:PHE:CG	2.10	1.19
3:C:705:VAL:HG23	3:C:717:PHE:CE2	1.75	1.19
5:E:146:ARG:NH1	5:E:148:LYS:HE3	1.53	1.19
38:S:39:PHE:CG	38:S:129:PHE:CE2	2.30	1.19
1:A:380:LEU:HB3	3:C:354:ARG:NH1	1.58	1.19
32:I:280:GLU:O	32:I:288:THR:CB	1.90	1.19
1:A:380:LEU:O	3:C:354:ARG:HG2	1.37	1.18
13:F:68:C:N4	36:P:33:ARG:HB3	1.55	1.18
1:A:402:ILE:HG21	3:C:268:LYS:NZ	1.55	1.18
29:L:209:ASP:OD2	35:O:111:ASP:HB2	1.39	1.18
1:A:695:ASP:HB3	39:T:374:SER:OG	1.40	1.18
1:A:2325:VAL:HG13	4:D:788:GLY:O	1.40	1.18
23:3:699:VAL:HA	23:3:715:MET:O	1.40	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2268:LEU:CD2	4:D:1261:PRO:O	1.91	1.18
1:A:299:ILE:HD11	3:C:921:LEU:CB	1.75	1.17
1:A:1290:LYS:HE2	40:U:13:SER:CA	1.74	1.17
3:C:149:LEU:HD13	3:C:427:PHE:CG	1.79	1.17
1:A:705:LYS:CB	37:R:251:ILE:HD12	1.72	1.17
2:B:42:U:N3	14:G:-3:A:H2	1.42	1.17
3:C:140:HIS:CG	3:C:230:ASP:CB	2.27	1.17
1:A:696:MET:CB	39:T:415:ILE:CD1	2.22	1.17
3:C:465:MET:HE1	3:C:475:MET:HG3	1.26	1.17
3:C:77:VAL:CG1	39:T:196:LEU:O	1.89	1.16
1:A:86:ARG:HH22	37:R:211:ARG:CG	1.57	1.16
1:A:417:ARG:HH22	2:B:58:U:H5"	1.03	1.16
1:A:1290:LYS:CE	40:U:13:SER:HA	1.75	1.16
3:C:78:GLU:CG	3:C:80:ILE:HD11	1.72	1.16
3:C:221:ILE:HD11	3:C:479:THR:OG1	1.46	1.16
1:A:758:ARG:HB3	36:P:227:TYR:CE2	1.79	1.16
3:C:679:PRO:CB	3:C:807:GLN:OE1	1.95	1.15
1:A:338:VAL:CG2	3:C:867:PRO:HG3	1.74	1.15
1:A:755:HIS:CE1	36:P:223:PHE:CG	2.35	1.14
38:S:131:ARG:CD	38:S:132:VAL:O	1.95	1.14
35:O:189:PRO:CG	42:W:223:ARG:HA	1.76	1.14
1:A:1262:LYS:HG2	37:R:431:ASP:CB	1.77	1.14
1:A:2298:LEU:O	4:D:1283:PRO:CB	1.95	1.14
3:C:670:SER:HA	3:C:823:ALA:HB1	1.27	1.14
5:E:74:PHE:CE1	5:E:81:LEU:HD21	1.82	1.14
24:4:28:LEU:O	24:4:32:LEU:HB2	1.48	1.14
32:I:373:GLU:CA	32:I:393:LYS:CB	2.26	1.14
37:R:101:ILE:O	37:R:104:GLN:HG3	1.48	1.14
1:A:305:ARG:CB	3:C:879:ASP:OD1	1.94	1.14
1:A:1405:LEU:HB3	37:R:415:LEU:HD23	1.29	1.14
15:H:156:U:H6	15:H:156:U:H5"	1.10	1.14
44:Y:18:VAL:CB	45:Z:600:ARG:NH2	2.10	1.14
1:A:1405:LEU:HB3	37:R:415:LEU:CD2	1.78	1.14
3:C:77:VAL:HG12	39:T:197:TYR:N	1.61	1.14
37:R:442:ARG:NH1	37:R:443:GLY:C	2.00	1.14
1:A:1342:TRP:CE2	3:C:921:LEU:CD1	2.31	1.13
13:F:27:A:N3	35:O:181:TYR:CE2	2.16	1.13
35:O:185:LYS:HD2	42:W:215:GLU:CB	1.79	1.13
14:G:11:A:C2	14:G:12:G:C8	2.36	1.13
3:C:452:THR:CG2	3:C:577:PHE:CD2	2.31	1.13
3:C:679:PRO:HD2	3:C:807:GLN:HB3	1.16	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:705:LYS:HB2	37:R:251:ILE:HD12	1.28	1.13
1:A:1548:TYR:CD2	1:A:1549:VAL:HG22	1.83	1.13
2:B:42:U:N3	14:G:-3:A:C2	2.15	1.13
1:A:762:ARG:NH2	36:P:226:LYS:NZ	1.95	1.13
1:A:439:GLN:NE2	1:A:614:TYR:CZ	2.18	1.12
1:A:1758:PRO:N	21:1:938:TRP:HE1	1.45	1.12
3:C:216:THR:HG22	3:C:245:HIS:HE1	0.97	1.12
3:C:81:VAL:HG13	39:T:201:SER:CB	1.77	1.12
3:C:140:HIS:CB	3:C:230:ASP:HB2	1.79	1.12
1:A:299:ILE:HD11	3:C:921:LEU:HB2	1.18	1.12
3:C:507:VAL:HG11	3:C:565:ILE:HG23	1.30	1.12
3:C:216:THR:HG22	3:C:245:HIS:CE1	1.85	1.12
13:F:68:C:C4	36:P:33:ARG:HB3	1.85	1.12
1:A:696:MET:CB	39:T:415:ILE:HD11	1.80	1.11
1:A:758:ARG:HB3	36:P:227:TYR:HE2	0.96	1.11
3:C:77:VAL:HG11	39:T:196:LEU:CB	1.79	1.11
14:G:-9:C:C4	40:U:18:TYR:CZ	2.38	1.11
23:3:687:SER:OG	23:3:1206:LYS:CD	1.97	1.11
1:A:762:ARG:NH2	36:P:226:LYS:CE	2.14	1.11
37:R:420:LYS:HE3	37:R:420:LYS:HA	1.18	1.11
29:L:216:PHE:HE1	35:O:112:VAL:C	1.53	1.11
45:Z:566:TYR:CE2	45:Z:584:TRP:CZ3	2.39	1.11
1:A:151:MET:HE3	1:A:628:GLY:O	1.49	1.10
1:A:692:ASP:HA	39:T:376:ARG:NH2	1.65	1.10
1:A:73:HIS:NE2	1:A:81:PHE:CE1	2.20	1.10
1:A:1548:TYR:HD2	1:A:1549:VAL:HG22	1.14	1.10
28:J:225:LEU:HD21	29:L:211:ASN:HB2	1.29	1.10
32:I:296:PHE:HA	32:I:305:SER:CB	1.80	1.10
1:A:299:ILE:HG12	3:C:920:PRO:O	1.52	1.10
1:A:402:ILE:HG21	3:C:268:LYS:CE	1.81	1.10
3:C:470:PRO:HB3	3:C:500:THR:HG23	1.34	1.10
35:O:149:LYS:HD2	35:O:290:LYS:HE2	1.12	1.10
37:R:92:SER:C	38:S:19:SER:HB2	1.71	1.10
1:A:1305:SER:HB2	1:A:1310:ARG:NH1	1.66	1.09
1:A:1757:GLU:O	21:1:938:TRP:CE2	2.04	1.09
1:A:762:ARG:NH2	36:P:226:LYS:HE2	1.66	1.09
1:A:2287:ARG:NH2	4:D:1147:ASN:CB	2.15	1.09
1:A:73:HIS:HD2	1:A:81:PHE:CD2	1.69	1.09
3:C:66:TYR:CD2	39:T:457:GLY:HA2	1.87	1.09
14:G:-9:C:N4	40:U:18:TYR:OH	1.86	1.08
44:Y:85:GLU:O	45:Z:502:ALA:N	1.85	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:MET:CE	1:A:88:TYR:CD2	2.36	1.08
1:A:1342:TRP:CE2	3:C:921:LEU:HD13	1.86	1.08
3:C:465:MET:CE	3:C:475:MET:HG3	1.82	1.08
35:O:149:LYS:CD	35:O:290:LYS:NZ	2.16	1.08
45:Z:566:TYR:CE2	45:Z:584:TRP:HZ3	1.71	1.08
1:A:299:ILE:HD11	3:C:921:LEU:CA	1.84	1.08
1:A:783:TYR:CE1	36:P:228:ILE:HG21	1.88	1.08
38:S:39:PHE:HB3	38:S:129:PHE:CZ	1.85	1.08
28:J:259:GLN:HE22	29:L:220:PRO:CD	1.66	1.08
3:C:497:LEU:CD1	3:C:577:PHE:CZ	2.36	1.07
32:I:280:GLU:CA	32:I:288:THR:CB	2.32	1.07
35:O:185:LYS:HE3	42:W:215:GLU:O	1.54	1.07
1:A:546:LEU:HD11	1:A:595:LYS:HD2	1.12	1.07
24:4:17:VAL:HA	24:4:85:ARG:O	1.53	1.07
29:L:216:PHE:CE1	35:O:113:ASN:N	2.21	1.07
1:A:264:PHE:HE1	1:A:455:VAL:HG13	1.15	1.07
3:C:670:SER:CB	3:C:823:ALA:HB3	1.85	1.07
1:A:744:LYS:CE	36:P:213:ASP:HA	1.84	1.06
13:F:68:C:C4	36:P:33:ARG:CB	2.38	1.06
1:A:587:GLN:CG	1:A:1550:GLY:O	2.04	1.06
28:J:406:PHE:CD2	28:J:411:MET:HE3	1.90	1.06
1:A:86:ARG:HH22	37:R:211:ARG:HG2	1.15	1.05
1:A:264:PHE:CE1	1:A:455:VAL:HG13	1.90	1.05
35:O:132:ARG:HH11	38:S:149:SER:HB3	1.15	1.05
38:S:39:PHE:CB	38:S:129:PHE:CE2	2.40	1.05
1:A:305:ARG:HB3	3:C:879:ASP:OD1	1.55	1.05
1:A:532:THR:HG23	14:G:2:U:P	1.97	1.05
1:A:1757:GLU:C	21:1:938:TRP:HE1	1.60	1.05
2:B:39:C:H4'	2:B:40:U:OP1	1.23	1.05
1:A:705:LYS:CG	37:R:251:ILE:HD12	1.86	1.05
1:A:1364:LEU:HD13	41:V:461:LEU:CB	1.86	1.05
1:A:1758:PRO:CA	21:1:938:TRP:HE1	1.60	1.05
3:C:452:THR:HG22	3:C:577:PHE:HD2	1.21	1.05
1:A:1342:TRP:CZ3	3:C:921:LEU:HD13	1.92	1.05
1:A:168:PRO:HG3	1:A:559:ASP:HB3	1.39	1.04
1:A:301:LYS:HE3	3:C:940:ARG:HA	1.38	1.04
1:A:844:GLU:CB	37:R:422:MET:HE1	1.83	1.04
39:T:399:LYS:CG	39:T:406:ILE:HD11	1.87	1.04
1:A:369:GLU:O	1:A:371:LEU:N	1.88	1.04
1:A:692:ASP:HA	39:T:376:ARG:HH22	1.18	1.04
3:C:228:PHE:HA	3:C:256:CYS:O	1.57	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:863:THR:CB	23:3:599:GLU:CA	2.35	1.04
37:R:178:ARG:HD3	37:R:194:GLN:HE22	1.17	1.04
1:A:1307:MET:HB3	1:A:1310:ARG:HD2	1.07	1.04
1:A:1449:LYS:HE3	37:R:428:GLY:HA3	1.37	1.04
3:C:78:GLU:HG2	3:C:80:ILE:HD11	1.06	1.04
1:A:755:HIS:ND1	36:P:223:PHE:CD1	2.26	1.04
2:B:43:U:H4'	13:F:67:G:H1	0.93	1.04
3:C:488:VAL:HG13	3:C:609:LYS:HE2	1.39	1.04
13:F:25:C:H4'	13:F:26:U:OP2	1.22	1.04
37:R:436:VAL:HG23	37:R:437:TYR:CD1	1.93	1.04
1:A:402:ILE:CG2	3:C:268:LYS:NZ	2.19	1.04
1:A:593:ARG:HH12	1:A:1565:LYS:HE2	0.91	1.04
23:3:442:LEU:HD12	23:3:734:LEU:HD23	1.05	1.04
1:A:168:PRO:CG	1:A:559:ASP:HB3	1.87	1.03
1:A:1342:TRP:CE3	3:C:921:LEU:HD22	1.93	1.03
24:4:70:ALA:O	24:4:74:MET:CB	2.04	1.03
1:A:755:HIS:CE1	36:P:223:PHE:CD2	2.46	1.03
29:L:224:PHE:CD1	37:R:86:LEU:HD12	1.93	1.03
1:A:254:TYR:CZ	1:A:434:HIS:HB3	1.93	1.03
1:A:384:VAL:HG12	3:C:331:PHE:CD2	1.94	1.03
1:A:388:LEU:HB2	3:C:379:LYS:HD3	1.33	1.03
37:R:92:SER:HA	38:S:19:SER:HB3	1.35	1.03
1:A:76:MET:HE1	1:A:88:TYR:CD2	1.93	1.03
1:A:1306:LYS:NZ	2:B:38:C:O2'	1.90	1.03
28:J:273:TYR:CZ	37:R:228:PRO:HB3	1.94	1.03
35:O:116:TYR:OH	37:R:222:PRO:HD3	1.58	1.03
1:A:299:ILE:CD1	1:A:1342:TRP:CZ3	2.42	1.03
1:A:1305:SER:HB2	1:A:1310:ARG:HH11	1.16	1.03
15:H:105:G:H2'	15:H:106:G:H5"	1.37	1.03
23:3:442:LEU:HD12	23:3:734:LEU:CD2	1.87	1.03
1:A:254:TYR:CE2	1:A:434:HIS:HB2	1.94	1.02
1:A:642:ARG:HD3	2:B:28:A:H1'	1.37	1.02
2:B:43:U:H5'	13:F:67:G:H22	1.19	1.02
3:C:452:THR:HG22	3:C:577:PHE:CD2	1.94	1.02
28:J:331:GLN:HG2	37:R:98:TYR:OH	1.59	1.02
45:Z:564:PRO:CB	45:Z:582:TYR:CG	2.41	1.02
3:C:387:ASP:O	3:C:388:VAL:CG1	2.07	1.02
37:R:420:LYS:HG3	37:R:421:GLY:H	1.20	1.02
1:A:384:VAL:CG1	3:C:331:PHE:CE2	2.42	1.02
2:B:42:U:O2'	13:F:69:A:N3	1.93	1.02
13:F:68:C:C5	36:P:33:ARG:CB	2.42	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:R:434:TYR:O	37:R:435:ASN:ND2	1.90	1.02
44:Y:37:TRP:CD1	44:Y:83:CYS:HB2	1.92	1.02
1:A:339:PHE:CE1	1:A:406:TRP:CE3	2.46	1.02
13:F:36:A:H3'	13:F:37:C:H5"	1.39	1.02
34:N:40:LYS:O	34:N:41:ARG:HG3	1.59	1.02
35:O:132:ARG:NH1	38:S:149:SER:HB3	1.73	1.02
1:A:1307:MET:CB	1:A:1310:ARG:HD2	1.90	1.01
45:Z:525:TYR:CD1	45:Z:526:ILE:HG23	1.95	1.01
3:C:511:GLY:O	3:C:576:ILE:CD1	2.07	1.01
1:A:532:THR:HG21	14:G:2:U:C5'	1.89	1.01
1:A:1457:HIS:HE1	1:A:1459:ARG:CG	1.74	1.01
3:C:132:VAL:HG12	3:C:226:VAL:HG23	1.43	1.01
3:C:349:PHE:CD1	3:C:356:PHE:CE1	2.49	1.01
1:A:1305:SER:CB	1:A:1310:ARG:HH11	1.73	1.00
1:A:2287:ARG:HH21	4:D:1147:ASN:CB	1.72	1.00
35:O:149:LYS:CG	35:O:290:LYS:NZ	2.25	1.00
42:W:420:ALA:O	42:W:438:ASP:N	1.93	1.00
3:C:261:ASP:OD2	50:C:1500:GTP:N1	1.92	1.00
3:C:703:GLU:OE2	3:C:740:THR:HG21	1.61	1.00
15:H:179:C:H2'	15:H:180:G:H8	1.25	1.00
3:C:705:VAL:CG2	3:C:717:PHE:CD2	2.39	1.00
14:G:17:U:O2	35:O:198:ILE:HD11	1.62	1.00
36:P:193:VAL:HG21	36:P:194:PHE:HD2	1.26	1.00
3:C:81:VAL:CG1	39:T:201:SER:HB3	1.90	1.00
23:3:303:ALA:O	23:3:310:ILE:HA	1.61	1.00
1:A:623:LYS:O	48:A:2401:IHP:P4	2.20	1.00
29:L:209:ASP:OD1	35:O:111:ASP:N	1.95	1.00
2:B:43:U:H4'	13:F:67:G:N1	1.75	1.00
3:C:85:ASP:HB3	39:T:238:LEU:HG	1.43	1.00
3:C:129:ILE:HG22	3:C:199:LEU:HB3	1.44	1.00
1:A:1162:PRO:HG2	36:P:194:PHE:CE2	1.97	1.00
45:Z:525:TYR:CE1	45:Z:526:ILE:HG23	1.96	1.00
1:A:779:LEU:HD21	36:P:223:PHE:CE2	1.97	0.99
37:R:414:ARG:NE	45:Z:598:PHE:HZ	1.38	0.99
38:S:11:PRO:HB3	38:S:166:GLY:HA3	1.40	0.99
1:A:783:TYR:HB2	36:P:228:ILE:HG12	1.43	0.99
28:J:270:ASP:OD2	37:R:222:PRO:CG	2.10	0.99
1:A:86:ARG:NH2	37:R:211:ARG:CG	2.24	0.99
23:3:442:LEU:CD1	23:3:734:LEU:HD23	1.90	0.99
38:S:11:PRO:HB3	38:S:165:SER:O	1.62	0.99
1:A:264:PHE:CE1	1:A:459:LEU:HD13	1.96	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:F:28:A:HO2'	34:N:39:GLY:HA2	1.25	0.99
1:A:696:MET:CB	39:T:415:ILE:HD13	1.89	0.99
39:T:434:GLY:HA2	39:T:464:GLY:HA2	1.41	0.99
1:A:715:GLU:OE2	37:R:258:TRP:HZ3	1.43	0.99
1:A:2328:ALA:HB2	4:D:788:GLY:HA2	1.44	0.99
45:Z:600:ARG:HB3	45:Z:600:ARG:HH11	1.24	0.99
1:A:2074:ARG:NH2	4:D:1044:VAL:O	1.96	0.99
3:C:64:LYS:HE3	36:P:206:LYS:HE2	1.45	0.99
3:C:137:HIS:CD2	3:C:236:MET:CB	2.45	0.99
13:F:68:C:C5	36:P:33:ARG:HB2	1.97	0.99
1:A:593:ARG:HH12	1:A:1565:LYS:CE	1.76	0.99
1:A:1457:HIS:NE2	37:R:425:GLY:N	2.09	0.99
35:O:149:LYS:CG	35:O:290:LYS:HZ3	1.75	0.99
37:R:92:SER:CA	38:S:19:SER:CB	2.29	0.99
29:L:216:PHE:CE1	35:O:113:ASN:CA	2.46	0.99
35:O:149:LYS:HZ3	35:O:290:LYS:HG2	1.23	0.98
3:C:78:GLU:O	39:T:198:ARG:CA	2.11	0.98
42:W:242:HIS:CB	42:W:325:LEU:O	2.10	0.98
1:A:1084:PRO:HG2	36:P:188:TRP:HZ2	1.26	0.98
13:F:27:A:C4	35:O:181:TYR:CE2	2.50	0.98
36:P:210:PHE:CD2	39:T:455:GLN:OE1	2.16	0.98
37:R:420:LYS:HB2	45:Z:610:LEU:HD11	1.44	0.98
1:A:1211:ASP:OD1	41:V:505:LYS:CB	2.12	0.98
1:A:1481:VAL:HG11	1:A:1498:TRP:CE2	1.99	0.98
3:C:306:ASN:OD1	3:C:437:HIS:CE1	2.16	0.98
35:O:149:LYS:CD	35:O:290:LYS:HE2	1.94	0.98
36:P:30:TYR:OH	37:R:162:ALA:HA	1.63	0.98
1:A:1307:MET:HB3	1:A:1310:ARG:CD	1.94	0.98
1:A:1757:GLU:O	21:1:938:TRP:HZ2	1.45	0.98
15:H:83:A:H2'	15:H:84:C:O4'	1.64	0.98
38:S:11:PRO:CB	38:S:165:SER:O	2.11	0.98
1:A:461:HIS:NE2	2:B:26:A:N6	2.12	0.97
3:C:84:GLU:O	39:T:238:LEU:CD2	2.12	0.97
3:C:670:SER:CA	3:C:823:ALA:HB3	1.94	0.97
38:S:100:MET:HG2	38:S:108:ASN:OD1	1.64	0.97
41:V:548:ALA:CB	41:V:585:ILE:CB	2.42	0.97
3:C:66:TYR:HB3	39:T:456:PRO:O	1.64	0.97
3:C:81:VAL:HG13	39:T:201:SER:HB3	0.99	0.97
44:Y:37:TRP:CZ3	45:Z:498:GLY:HA3	2.00	0.97
45:Z:566:TYR:HE2	45:Z:584:TRP:HZ3	1.05	0.97
3:C:711:ARG:HD3	3:C:730:ARG:HH11	1.29	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1348:VAL:HG12	3:C:921:LEU:HD23	1.43	0.97
1:A:1364:LEU:HD12	41:V:461:LEU:CB	1.89	0.97
35:O:149:LYS:CD	35:O:290:LYS:HZ3	1.74	0.97
3:C:500:THR:HG22	3:C:545:PRO:HA	1.47	0.97
29:L:216:PHE:HD1	35:O:113:ASN:CA	1.59	0.97
3:C:670:SER:HA	3:C:823:ALA:HB3	1.43	0.97
1:A:1320:LYS:HE2	37:R:434:TYR:HE1	1.15	0.97
35:O:189:PRO:HG3	42:W:223:ARG:HA	1.01	0.97
3:C:670:SER:CA	3:C:823:ALA:CB	2.43	0.96
28:J:300:ASP:OD2	37:R:101:ILE:HG13	1.65	0.96
34:N:28:LYS:HZ3	42:W:190:ASP:HA	1.28	0.96
1:A:380:LEU:CD2	3:C:354:ARG:O	2.12	0.96
1:A:1293:ASN:HD22	40:U:14:GLY:HA2	1.28	0.96
1:A:296:PHE:CE1	3:C:591:ALA:HB1	2.01	0.96
1:A:546:LEU:HD11	1:A:595:LYS:CD	1.94	0.96
3:C:855:GLY:O	3:C:856:HIS:HB3	1.63	0.96
5:E:321:TYR:CE1	42:W:84:THR:HA	1.99	0.96
32:I:358:HIS:CB	32:I:376:ASN:CB	2.44	0.96
14:G:18:A:H5'	35:O:69:GLU:OE1	1.66	0.96
1:A:380:LEU:CB	3:C:354:ARG:NH1	2.27	0.96
1:A:2335:ALA:O	4:D:570:THR:HA	1.65	0.96
39:T:352:THR:HG22	39:T:373:LYS:O	1.65	0.96
44:Y:37:TRP:HH2	45:Z:498:GLY:CA	1.70	0.96
1:A:303:ILE:HG21	3:C:933:PHE:CE1	2.01	0.96
1:A:47:GLU:O	1:A:50:LYS:HB2	1.64	0.96
3:C:135:CYS:SG	3:C:227:LEU:HD12	2.06	0.96
15:H:78:C:H2'	15:H:79:G:H8	1.27	0.96
1:A:121:HIS:NE2	1:A:481:PHE:CB	2.29	0.96
1:A:748:ASP:OD1	36:P:214:THR:HG22	1.64	0.96
1:A:369:GLU:OE2	1:A:369:GLU:N	1.97	0.96
1:A:2298:LEU:CB	4:D:1283:PRO:CB	2.44	0.95
3:C:115:GLU:O	3:C:118:PHE:N	1.98	0.95
1:A:587:GLN:HG3	1:A:1550:GLY:O	1.65	0.95
1:A:783:TYR:CD1	36:P:228:ILE:HG21	2.01	0.95
5:E:146:ARG:HH11	5:E:148:LYS:HE2	1.27	0.95
14:G:11:A:N3	14:G:12:G:H8	1.64	0.95
35:O:225:PRO:HB3	35:O:302:TRP:NE1	1.80	0.95
44:Y:37:TRP:CH2	45:Z:498:GLY:HA3	1.96	0.95
37:R:442:ARG:HD3	37:R:443:GLY:CA	1.96	0.95
1:A:171:ASP:O	1:A:520:TYR:CD2	2.20	0.95
15:H:156:U:H5"	15:H:156:U:C6	2.02	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:299:ILE:HD12	1:A:1342:TRP:CZ3	1.99	0.95
1:A:299:ILE:CB	1:A:1342:TRP:HZ3	1.79	0.95
3:C:145:PHE:CB	3:C:312:SER:HB3	1.97	0.95
13:F:22:A:H5"	34:N:116:ASN:O	1.66	0.95
35:O:149:LYS:CD	35:O:290:LYS:CE	2.44	0.95
1:A:388:LEU:O	3:C:379:LYS:NZ	2.00	0.95
3:C:700:ILE:HG23	3:C:735:PHE:CD2	2.01	0.95
1:A:264:PHE:CZ	1:A:459:LEU:CD1	2.50	0.95
1:A:705:LYS:HG2	37:R:251:ILE:HB	1.49	0.95
1:A:253:ASN:HB3	3:C:893:GLY:O	1.67	0.95
14:G:-9:C:N4	40:U:18:TYR:CZ	2.34	0.95
1:A:785:LYS:CE	36:P:215:LEU:HD11	1.97	0.94
14:G:11:A:C2	14:G:12:G:N7	2.34	0.94
1:A:384:VAL:CG1	3:C:331:PHE:CD2	2.50	0.94
1:A:1162:PRO:HG3	36:P:194:PHE:CD2	2.02	0.94
1:A:1457:HIS:CE1	37:R:424:SER:HA	2.01	0.94
28:J:339:TRP:CA	37:R:116:TYR:CE2	2.48	0.94
3:C:711:ARG:NH2	3:C:730:ARG:O	2.00	0.94
1:A:299:ILE:HG13	1:A:1342:TRP:CH2	2.02	0.94
13:F:49:G:N7	29:L:33:ARG:NH1	2.15	0.94
5:E:119:THR:CG2	5:E:161:ARG:HB3	1.97	0.94
15:H:180:G:H2'	15:H:181:G:H8	1.30	0.94
39:T:352:THR:HG22	39:T:373:LYS:C	1.86	0.94
13:F:27:A:P	34:N:41:ARG:HH21	1.90	0.94
1:A:587:GLN:CB	1:A:1550:GLY:O	2.16	0.94
1:A:1405:LEU:CB	37:R:415:LEU:CD2	2.45	0.94
1:A:1459:ARG:HE	37:R:423:ASP:HB2	1.31	0.94
1:A:2268:LEU:CD2	4:D:1261:PRO:CB	2.46	0.94
3:C:145:PHE:HA	3:C:312:SER:HB2	0.95	0.94
3:C:445:ALA:HB3	3:C:466:SER:HA	1.50	0.94
14:G:-9:C:C5	40:U:18:TYR:HE1	1.79	0.94
15:H:79:G:H2'	15:H:80:A:H8	1.33	0.94
24:4:69:TYR:CZ	24:4:73:ILE:HG13	2.03	0.94
3:C:349:PHE:HD1	3:C:356:PHE:CD1	1.85	0.94
2:B:39:C:C4'	2:B:40:U:OP1	2.16	0.94
1:A:158:ARG:NH2	1:A:570:ASP:OD2	2.01	0.93
1:A:2113:LYS:HE2	4:D:1229:ASP:CB	1.98	0.93
13:F:8:C:H6	13:F:8:C:H5"	1.31	0.93
1:A:461:HIS:CD2	2:B:27:U:O4	2.20	0.93
13:F:25:C:C4'	13:F:26:U:OP2	2.16	0.93
29:L:216:PHE:CE1	35:O:112:VAL:C	2.40	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:R:171:LEU:HD12	37:R:201:GLU:OE1	1.67	0.93
3:C:76:GLU:OE1	3:C:76:GLU:N	2.01	0.93
5:E:146:ARG:NH1	5:E:148:LYS:HE2	1.82	0.93
3:C:149:LEU:CD1	3:C:427:PHE:HD2	1.80	0.93
29:L:209:ASP:HA	35:O:110:SER:HB2	1.49	0.93
1:A:73:HIS:CD2	1:A:81:PHE:CE1	2.56	0.93
1:A:151:MET:CE	1:A:628:GLY:O	2.15	0.93
1:A:695:ASP:CB	39:T:374:SER:OG	2.15	0.93
1:A:2113:LYS:CE	4:D:1229:ASP:O	2.16	0.93
3:C:449:ILE:HG21	3:C:457:VAL:CG1	1.99	0.93
28:J:259:GLN:NE2	29:L:220:PRO:CD	2.30	0.93
1:A:67:ARG:HD3	1:A:179:ALA:HB2	1.51	0.93
28:J:294:HIS:CE1	29:L:227:THR:HB	2.04	0.93
1:A:417:ARG:NH2	2:B:58:U:H5"	1.82	0.93
1:A:2314:PHE:CB	4:D:1125:SER:CA	2.47	0.93
3:C:497:LEU:HD13	3:C:577:PHE:HZ	1.17	0.93
13:F:68:C:C4	36:P:33:ARG:CG	2.52	0.93
1:A:548:ARG:NH2	1:A:549:GLU:OE2	2.01	0.92
2:B:43:U:C4'	13:F:67:G:H1	1.80	0.92
35:O:189:PRO:CG	42:W:223:ARG:CA	2.41	0.92
35:O:225:PRO:HG3	35:O:302:TRP:HE1	1.29	0.92
37:R:101:ILE:O	37:R:104:GLN:CG	2.16	0.92
1:A:299:ILE:HD12	1:A:1342:TRP:CE3	2.03	0.92
1:A:2328:ALA:CB	4:D:788:GLY:HA2	1.99	0.92
3:C:69:ALA:HA	39:T:456:PRO:HG3	1.49	0.92
3:C:449:ILE:CG2	3:C:457:VAL:CG1	2.46	0.92
3:C:678:THR:HG21	3:C:683:ASN:HD22	1.35	0.92
13:F:28:A:O2'	34:N:39:GLY:CA	2.17	0.92
42:W:258:PRO:O	42:W:260:ASP:N	2.02	0.92
37:R:412:ASP:CG	37:R:413:GLN:H	1.69	0.92
35:O:223:LEU:HD13	35:O:224:ASP:N	1.84	0.92
3:C:77:VAL:CG1	39:T:196:LEU:CB	2.45	0.92
3:C:140:HIS:CG	3:C:230:ASP:HB3	2.03	0.92
37:R:414:ARG:NH1	45:Z:598:PHE:HE2	1.58	0.92
1:A:523:ASN:OD1	1:A:552:ARG:NH2	2.02	0.92
1:A:532:THR:CG2	14:G:2:U:O5'	2.17	0.92
3:C:445:ALA:O	3:C:449:ILE:N	2.03	0.92
3:C:476:CYS:HB3	3:C:565:ILE:HB	1.51	0.92
28:J:339:TRP:CA	37:R:116:TYR:CD2	2.51	0.92
1:A:228:TRP:O	1:A:415:SER:HA	1.70	0.92
1:A:339:PHE:CE1	1:A:406:TRP:CZ3	2.58	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:670:SER:HB3	3:C:823:ALA:HB3	1.48	0.92
13:F:27:A:P	34:N:41:ARG:NH2	2.43	0.92
28:J:259:GLN:HE22	29:L:220:PRO:HD2	1.32	0.92
34:N:128:VAL:HG13	34:N:130:ARG:H	1.35	0.92
1:A:762:ARG:HH22	36:P:226:LYS:HZ1	1.08	0.92
1:A:651:TRP:NE1	13:F:66:C:C2	2.38	0.92
1:A:779:LEU:HD21	36:P:223:PHE:CZ	2.05	0.92
3:C:244:LYS:HA	3:C:292:TYR:HD2	1.34	0.91
37:R:106:GLN:HG2	37:R:110:LYS:HE2	1.51	0.91
3:C:483:SER:HA	3:C:490:PHE:HB3	1.52	0.91
3:C:674:CYS:SG	3:C:822:MET:SD	2.67	0.91
1:A:86:ARG:NH2	37:R:211:ARG:HG3	1.84	0.91
1:A:235:MET:CE	1:A:411:PHE:HA	1.99	0.91
1:A:1307:MET:SD	1:A:1547:VAL:HB	2.09	0.91
3:C:86:THR:O	39:T:239:LYS:O	1.88	0.91
3:C:132:VAL:CG1	3:C:226:VAL:HG23	2.00	0.91
38:S:131:ARG:NH1	38:S:133:CYS:HA	1.86	0.91
1:A:171:ASP:HB3	1:A:519:ASP:HB2	1.53	0.91
1:A:305:ARG:HA	1:A:305:ARG:HH11	1.33	0.91
1:A:296:PHE:CE1	3:C:591:ALA:CB	2.54	0.91
35:O:234:LEU:O	35:O:271:PHE:HA	1.70	0.91
1:A:1320:LYS:CE	37:R:434:TYR:CE1	2.54	0.91
1:A:372:PRO:CG	3:C:342:ARG:HE	1.83	0.91
3:C:452:THR:HG22	3:C:577:PHE:HB3	1.52	0.91
29:L:224:PHE:CD1	37:R:86:LEU:CD1	2.53	0.91
3:C:145:PHE:N	3:C:312:SER:HB2	1.85	0.90
1:A:1757:GLU:O	21:1:938:TRP:NE1	2.03	0.90
13:F:35:A:C8	14:G:12:G:C6	2.59	0.90
23:3:34:ARG:HB2	23:3:37:ILE:HB	1.51	0.90
1:A:232:LEU:HD22	1:A:404:LEU:HD13	1.53	0.90
3:C:230:ASP:OD2	3:C:233:GLU:HG2	1.70	0.90
1:A:1457:HIS:CE1	37:R:425:GLY:H	1.88	0.90
3:C:678:THR:OG1	3:C:680:ASN:O	1.89	0.90
1:A:76:MET:HE1	1:A:88:TYR:CG	2.06	0.90
1:A:1320:LYS:CE	37:R:434:TYR:HE1	1.85	0.90
44:Y:37:TRP:NE1	44:Y:83:CYS:HB2	1.87	0.90
1:A:587:GLN:CA	1:A:1550:GLY:O	2.20	0.90
1:A:623:LYS:HB3	48:A:2401:IHP:O34	1.72	0.90
1:A:1426:ASP:CG	37:R:421:GLY:HA3	1.91	0.90
3:C:221:ILE:CD1	3:C:479:THR:OG1	2.19	0.90
13:F:94:C:P	28:J:351:ASN:HD22	1.95	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:782:LEU:HD13	36:P:220:HIS:HE1	1.34	0.90
1:A:1290:LYS:HG2	40:U:13:SER:O	1.71	0.90
3:C:711:ARG:HD3	3:C:730:ARG:NH1	1.86	0.90
13:F:27:A:H1'	35:O:181:TYR:HE2	1.36	0.90
3:C:228:PHE:CA	3:C:256:CYS:O	2.20	0.90
1:A:705:LYS:HG2	37:R:251:ILE:CB	2.01	0.89
39:T:399:LYS:HG3	39:T:406:ILE:HD11	1.54	0.89
23:3:699:VAL:HG22	23:3:716:SER:HB2	1.53	0.89
38:S:34:LYS:HE3	38:S:78:TYR:CE2	2.07	0.89
34:N:124:SER:O	34:N:127:GLU:HG2	1.71	0.89
44:Y:36:ALA:HB2	45:Z:499:LYS:O	1.72	0.89
1:A:227:ARG:CA	1:A:416:GLY:O	2.20	0.89
1:A:744:LYS:HE2	36:P:213:ASP:HA	1.52	0.89
1:A:296:PHE:CB	3:C:656:ALA:HB2	2.02	0.89
36:P:192:VAL:HG12	36:P:194:PHE:H	1.35	0.89
1:A:387:PHE:CE2	3:C:399:LEU:HD23	2.07	0.89
1:A:748:ASP:HA	36:P:214:THR:HG21	1.54	0.89
1:A:254:TYR:CZ	1:A:434:HIS:CB	2.54	0.89
15:H:80:A:H2'	15:H:81:G:H8	1.36	0.89
37:R:81:LYS:HA	37:R:81:LYS:CE	2.02	0.89
1:A:1342:TRP:CE2	3:C:921:LEU:HD11	2.08	0.89
28:J:220:LEU:HD11	28:J:224:LYS:HE3	1.53	0.89
1:A:532:THR:OG1	14:G:2:U:O5'	1.89	0.89
15:H:81:G:H2'	15:H:82:G:H8	1.35	0.89
15:H:82:G:H2'	15:H:83:A:H8	1.38	0.89
37:R:92:SER:O	38:S:19:SER:HB2	1.73	0.89
3:C:64:LYS:HZ1	36:P:206:LYS:HG2	1.38	0.88
36:P:193:VAL:HG21	36:P:194:PHE:CD2	2.02	0.88
1:A:2314:PHE:HB2	4:D:1125:SER:CA	2.03	0.88
14:G:11:A:N3	14:G:12:G:C8	2.38	0.88
37:R:81:LYS:HA	37:R:81:LYS:NZ	1.88	0.88
1:A:785:LYS:HE2	36:P:215:LEU:HD11	1.54	0.88
3:C:78:GLU:O	39:T:199:VAL:N	2.06	0.88
3:C:140:HIS:CE1	3:C:233:GLU:HB2	2.07	0.88
1:A:175:PRO:HG2	1:A:498:ARG:NH2	1.88	0.88
1:A:1314:VAL:HG11	1:A:1487:HIS:CD2	2.07	0.88
3:C:679:PRO:CG	3:C:807:GLN:OE1	2.21	0.88
1:A:419:ARG:NH2	1:A:423:ASP:O	2.06	0.88
3:C:678:THR:CG2	3:C:683:ASN:HB2	2.04	0.88
13:F:68:C:C4	36:P:33:ARG:HG2	2.07	0.88
1:A:384:VAL:HG12	3:C:331:PHE:HE2	1.08	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:587:GLN:HA	1:A:1550:GLY:O	1.74	0.88
1:A:1342:TRP:CD2	3:C:921:LEU:HD11	2.08	0.88
1:A:715:GLU:OE2	37:R:258:TRP:CZ3	2.25	0.88
1:A:1755:SER:OG	21:1:938:TRP:CH2	2.26	0.88
22:2:614:ARG:HH11	22:2:614:ARG:HG3	1.38	0.88
3:C:261:ASP:OD1	50:C:1500:GTP:O6	1.92	0.88
35:O:189:PRO:HG3	42:W:223:ARG:N	1.88	0.88
38:S:111:GLN:HE22	42:W:93:PHE:CB	1.86	0.88
1:A:1457:HIS:CE1	37:R:425:GLY:N	2.41	0.88
1:A:1459:ARG:HG3	37:R:422:MET:O	1.74	0.88
36:P:224:MET:CE	36:P:228:ILE:HD13	2.04	0.88
1:A:278:LYS:NZ	14:G:-9:C:OP1	2.06	0.87
1:A:372:PRO:HG3	3:C:342:ARG:HE	1.38	0.87
3:C:97:VAL:CG2	36:P:45:GLN:HG3	2.03	0.87
15:H:179:C:O2'	15:H:180:G:H5'	1.74	0.87
3:C:149:LEU:HD12	3:C:427:PHE:HD2	1.39	0.87
3:C:700:ILE:HG23	3:C:735:PHE:CE2	2.09	0.87
23:3:812:LYS:O	23:3:816:LYS:HB2	1.74	0.87
14:G:137:C:H42	15:H:40:C:H42	1.22	0.87
24:4:75:ASN:OD1	24:4:86:VAL:HB	1.74	0.87
1:A:329:LEU:HD13	3:C:177:ARG:HE	1.40	0.87
3:C:523:GLN:OE1	3:C:524:ILE:N	2.07	0.87
1:A:433:GLU:OE1	1:A:436:PRO:HB3	1.74	0.87
3:C:705:VAL:HG21	3:C:717:PHE:CE2	2.07	0.87
5:E:243:LEU:CD1	5:E:247:GLY:HA2	2.04	0.87
15:H:68:G:O2'	15:H:69:U:H5'	1.74	0.87
15:H:78:C:H2'	15:H:79:G:C8	2.10	0.87
1:A:1162:PRO:CG	36:P:194:PHE:CE2	2.57	0.87
1:A:1370:ARG:HG2	41:V:464:GLN:HA	1.54	0.87
3:C:488:VAL:HG13	3:C:609:LYS:CE	2.05	0.87
15:H:154:C:O2	15:H:176:G:N2	2.07	0.87
23:3:442:LEU:CD1	23:3:734:LEU:CD2	2.50	0.87
23:3:545:VAL:HG12	23:3:546:LYS:HG2	1.57	0.87
28:J:339:TRP:CD2	37:R:116:TYR:HD2	1.93	0.87
37:R:423:ASP:O	37:R:424:SER:OG	1.92	0.87
15:H:180:G:H2'	15:H:181:G:C8	2.10	0.87
1:A:1548:TYR:HD2	14:G:-6:C:HO2'	1.20	0.87
3:C:701:GLU:HA	3:C:740:THR:OG1	1.75	0.87
28:J:255:LEU:HD22	29:L:235:LEU:HD13	1.56	0.87
1:A:232:LEU:HD22	1:A:404:LEU:CD1	2.04	0.86
3:C:216:THR:CG2	3:C:245:HIS:HE1	1.84	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:R:442:ARG:NH1	37:R:443:GLY:O	2.07	0.86
13:F:27:A:OP2	34:N:41:ARG:NH2	2.09	0.86
1:A:1481:VAL:HG11	1:A:1498:TRP:CD2	2.10	0.86
1:A:318:TYR:CA	3:C:638:ASP:OD1	2.22	0.86
15:H:179:C:H2'	15:H:180:G:C8	2.09	0.86
1:A:86:ARG:NH2	37:R:211:ARG:HG2	1.85	0.86
33:Q:500:GLY:N	37:R:51:ILE:HD11	1.89	0.86
34:N:28:LYS:HZ1	42:W:190:ASP:H	1.18	0.86
35:O:20:PHE:CD1	37:R:177:ILE:HD11	2.11	0.86
1:A:1342:TRP:HB3	3:C:921:LEU:HD21	1.54	0.86
5:E:267:PHE:CE1	31:K:194:GLU:CB	2.59	0.86
15:H:148:C:O2'	15:H:149:A:H5'	1.75	0.86
21:1:1179:ASP:OD2	21:1:1185:ARG:NH1	2.08	0.86
39:T:399:LYS:HG2	39:T:406:ILE:HD11	1.53	0.86
5:E:269:PRO:O	5:E:270:LYS:HB3	1.76	0.86
13:F:26:U:H3'	13:F:27:A:H5"	1.56	0.86
28:J:256:LYS:O	29:L:232:TYR:CE2	2.29	0.86
36:P:210:PHE:HD2	39:T:455:GLN:OE1	1.53	0.86
37:R:147:THR:HG23	39:T:360:VAL:HG12	1.57	0.86
38:S:57:ILE:HD11	42:W:97:ASN:CB	2.03	0.86
39:T:417:ASN:OD1	39:T:432:ASP:OD1	1.94	0.86
1:A:299:ILE:CD1	1:A:1342:TRP:HZ3	1.85	0.86
1:A:402:ILE:CG2	3:C:268:LYS:HZ2	1.84	0.86
38:S:35:THR:O	38:S:129:PHE:CE1	2.29	0.86
1:A:296:PHE:HB3	3:C:656:ALA:CB	2.05	0.85
1:A:338:VAL:HG21	3:C:867:PRO:HG3	1.57	0.85
1:A:532:THR:CG2	14:G:2:U:C5'	2.52	0.85
37:R:135:PRO:O	37:R:136:ASP:OD1	1.94	0.85
1:A:299:ILE:CG1	3:C:920:PRO:O	2.24	0.85
37:R:420:LYS:HE3	37:R:420:LYS:CA	1.98	0.85
38:S:39:PHE:HB2	38:S:129:PHE:CE2	2.09	0.85
38:S:9:TRP:O	38:S:11:PRO:HD3	1.76	0.85
3:C:72:VAL:HG22	39:T:453:ALA:HB1	1.58	0.85
3:C:149:LEU:HD12	3:C:427:PHE:CD2	2.07	0.85
15:H:79:G:O2'	15:H:80:A:H5'	1.76	0.85
35:O:225:PRO:CG	35:O:302:TRP:HE1	1.88	0.85
38:S:35:THR:O	38:S:129:PHE:HE1	1.57	0.85
3:C:145:PHE:HB2	3:C:312:SER:HB3	1.57	0.85
21:1:672:ALA:HA	21:1:679:ILE:HD11	1.58	0.85
35:O:185:LYS:HG3	42:W:216:LEU:N	1.92	0.85
2:B:95:G:H4'	2:B:96:A:O4'	1.76	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:R:414:ARG:NH1	45:Z:598:PHE:HZ	1.44	0.85
5:E:162:ARG:NH2	5:E:203:ASP:O	2.10	0.85
5:E:267:PHE:CE1	31:K:194:GLU:HB3	2.10	0.85
1:A:152:ARG:HB3	1:A:152:ARG:HH11	1.40	0.85
37:R:414:ARG:HB2	37:R:414:ARG:NH2	1.92	0.85
38:S:35:THR:C	38:S:129:PHE:HE1	1.80	0.85
3:C:133:THR:O	3:C:226:VAL:N	2.10	0.85
42:W:137:TYR:HA	42:W:154:GLY:HA3	1.59	0.85
1:A:121:HIS:CG	1:A:481:PHE:O	2.30	0.85
1:A:338:VAL:HG23	3:C:867:PRO:HG3	1.58	0.85
1:A:452:LYS:NZ	2:B:48:A:OP1	2.10	0.84
3:C:94:ILE:HD13	36:P:44:ARG:NH1	1.92	0.84
15:H:156:U:H6	15:H:156:U:C5’	1.88	0.84
45:Z:600:ARG:HH11	45:Z:600:ARG:CB	1.90	0.84
2:B:40:U:H3	14:G:-1:G:H1	1.25	0.84
3:C:444:GLY:O	3:C:447:PRO:HD2	1.77	0.84
3:C:516:LEU:HD12	3:C:517:GLU:HG3	1.59	0.84
1:A:595:LYS:HE3	1:A:644:ILE:HD11	1.58	0.84
13:F:36:A:H2’	13:F:38:G:OP2	1.78	0.84
15:H:80:A:O2’	15:H:81:G:H5’	1.78	0.84
15:H:181:G:O2’	15:H:182:U:H5’	1.77	0.84
15:H:182:U:O2’	15:H:183:G:H5’	1.75	0.84
23:3:356:HIS:HB2	23:3:401:LEU:HB2	1.60	0.84
1:A:1348:VAL:CG1	3:C:921:LEU:HD23	2.06	0.84
3:C:80:ILE:O	39:T:200:ILE:HA	1.78	0.84
37:R:415:LEU:O	37:R:417:ASN:N	2.09	0.84
1:A:755:HIS:CE1	36:P:223:PHE:CB	2.60	0.84
3:C:711:ARG:HD3	3:C:730:ARG:HE	1.42	0.84
1:A:588:LEU:O	1:A:1551:PHE:CE1	2.31	0.84
3:C:244:LYS:HA	3:C:292:TYR:CD2	2.13	0.84
3:C:365:SER:OG	3:C:371:GLU:OE2	1.95	0.84
3:C:725:ASP:OD1	3:C:727:LEU:N	2.10	0.84
15:H:78:C:O2’	15:H:79:G:H5’	1.77	0.84
37:R:178:ARG:HD3	37:R:194:GLN:NE2	1.91	0.84
1:A:1426:ASP:CB	37:R:421:GLY:HA3	2.08	0.84
1:A:1457:HIS:CE1	1:A:1459:ARG:CG	2.61	0.84
1:A:1457:HIS:NE2	37:R:424:SER:HA	1.93	0.83
3:C:705:VAL:HG21	3:C:717:PHE:HE2	1.40	0.83
1:A:254:TYR:CE2	1:A:434:HIS:CB	2.61	0.83
1:A:1342:TRP:CZ2	3:C:921:LEU:HD13	2.13	0.83
3:C:79:THR:C	3:C:80:ILE:HD12	1.98	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:348:TYR:CD1	3:C:359:LYS:HB3	2.13	0.83
15:H:71:C:O2'	15:H:72:U:H5'	1.78	0.83
45:Z:566:TYR:CE2	45:Z:584:TRP:CE3	2.66	0.83
3:C:488:VAL:CG1	3:C:609:LYS:HE2	2.08	0.83
14:G:22:C:O2'	14:G:23:U:OP1	1.95	0.83
15:H:152:G:N2	15:H:153:A:N7	2.27	0.83
1:A:168:PRO:HG3	1:A:559:ASP:CB	2.07	0.83
5:E:74:PHE:CE1	5:E:81:LEU:CD2	2.62	0.83
44:Y:37:TRP:CZ2	45:Z:498:GLY:HA2	2.08	0.83
3:C:151:GLU:OE1	3:C:417:ARG:NH2	2.11	0.83
15:H:70:C:O2'	15:H:71:C:H5'	1.78	0.83
37:R:117:THR:O	37:R:120:VAL:HG12	1.78	0.83
1:A:365:VAL:HG12	1:A:366:LYS:H	1.44	0.83
3:C:77:VAL:CG1	39:T:196:LEU:CG	2.35	0.83
1:A:1310:ARG:NH2	1:A:1564:GLY:HA3	1.94	0.83
1:A:1342:TRP:CH2	3:C:921:LEU:HD13	2.12	0.83
3:C:80:ILE:N	39:T:199:VAL:O	2.12	0.83
1:A:303:ILE:CG2	3:C:933:PHE:CE1	2.62	0.83
3:C:824:THR:HG23	3:C:824:THR:O	1.77	0.83
28:J:270:ASP:CG	37:R:222:PRO:HB3	1.99	0.83
37:R:134:ARG:O	37:R:136:ASP:N	2.12	0.83
1:A:1457:HIS:HE1	1:A:1459:ARG:HG2	1.43	0.83
3:C:145:PHE:CA	3:C:312:SER:HB3	2.04	0.83
15:H:72:U:O2'	15:H:73:C:H5'	1.77	0.83
3:C:470:PRO:HB3	3:C:500:THR:CG2	2.08	0.82
21:1:1108:ASN:ND2	21:1:1111:CYS:SG	2.52	0.82
15:H:73:C:O2'	15:H:74:U:H5'	1.79	0.82
1:A:1084:PRO:HG2	36:P:188:TRP:CZ2	2.12	0.82
1:A:1293:ASN:ND2	40:U:14:GLY:HA2	1.94	0.82
3:C:220:ARG:NH1	3:C:578:ARG:O	2.12	0.82
3:C:228:PHE:CB	3:C:256:CYS:O	2.27	0.82
3:C:482:TYR:HE2	3:C:493:PHE:CG	1.97	0.82
5:E:165:GLN:O	5:E:166:LEU:HD23	1.79	0.82
28:J:259:GLN:NE2	29:L:220:PRO:HD2	1.94	0.82
3:C:705:VAL:CB	3:C:717:PHE:CE2	2.61	0.82
14:G:11:A:C4	14:G:12:G:C8	2.67	0.82
15:H:69:U:O2'	15:H:70:C:H5'	1.80	0.82
37:R:103:ARG:HB3	37:R:103:ARG:HH11	1.44	0.82
1:A:532:THR:HG21	14:G:2:U:H5"	1.62	0.82
15:H:81:G:O2'	15:H:82:G:H5'	1.78	0.82
3:C:140:HIS:ND1	3:C:230:ASP:HB3	1.94	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:304:GLN:HE21	23:3:308:GLY:HA2	1.44	0.82
42:W:209:SER:O	42:W:213:GLN:N	2.12	0.82
1:A:132:ILE:CD1	2:B:57:G:OP1	2.27	0.82
3:C:489:GLN:O	3:C:489:GLN:NE2	2.13	0.82
15:H:105:G:C2'	15:H:106:G:H5"	2.10	0.82
36:P:30:TYR:OH	37:R:162:ALA:CA	2.27	0.82
1:A:615:ARG:O	1:A:618:THR:OG1	1.96	0.82
1:A:1342:TRP:CE3	3:C:921:LEU:CD2	2.62	0.82
1:A:1457:HIS:CE1	1:A:1459:ARG:HG2	2.15	0.82
1:A:2113:LYS:HE3	4:D:1229:ASP:C	2.01	0.82
3:C:259:LYS:HG2	3:C:262:ARG:CD	2.09	0.82
36:P:212:ASN:HB3	39:T:458:SER:HB2	1.61	0.82
1:A:1370:ARG:NH1	41:V:466:SER:O	2.10	0.82
1:A:303:ILE:CG2	3:C:933:PHE:HE1	1.93	0.81
5:E:74:PHE:CE2	5:E:343:ILE:HG12	2.14	0.81
44:Y:37:TRP:HA	44:Y:82:LEU:O	1.80	0.81
3:C:64:LYS:HE3	36:P:206:LYS:CE	2.10	0.81
3:C:244:LYS:HB2	3:C:292:TYR:CE2	2.15	0.81
3:C:306:ASN:OD1	3:C:437:HIS:ND1	2.14	0.81
3:C:507:VAL:CG1	3:C:565:ILE:HG23	2.10	0.81
22:2:643:PRO:HD2	24:4:69:TYR:CD2	2.16	0.81
23:3:42:ARG:HE	23:3:53:LEU:HD11	1.45	0.81
23:3:210:PHE:HB2	23:3:224:TYR:HB2	1.60	0.81
26:6:49:CYS:HB3	26:6:87:LYS:HD3	1.61	0.81
34:N:111:THR:HG21	34:N:115:THR:O	1.79	0.81
1:A:1757:GLU:C	21:1:938:TRP:NE1	2.33	0.81
36:P:193:VAL:HG23	36:P:194:PHE:CG	2.15	0.81
39:T:213:GLU:HG3	39:T:218:TRP:CE2	2.16	0.81
1:A:121:HIS:HA	1:A:482:PHE:HA	1.62	0.81
1:A:651:TRP:NE1	13:F:66:C:O2	2.14	0.81
3:C:511:GLY:O	3:C:576:ILE:HD13	1.79	0.81
38:S:39:PHE:CD2	38:S:129:PHE:CE2	2.68	0.81
1:A:247:THR:OG1	1:A:429:ASN:HB3	1.80	0.81
1:A:402:ILE:HG21	3:C:268:LYS:HE3	1.62	0.81
1:A:623:LYS:O	48:A:2401:IHP:O44	1.99	0.81
1:A:1184:ASN:OD1	1:A:1195:ARG:NH1	2.14	0.81
1:A:1426:ASP:HB2	37:R:421:GLY:CA	2.11	0.81
3:C:452:THR:HG21	3:C:577:PHE:HD2	1.43	0.81
5:E:74:PHE:CZ	5:E:81:LEU:HD21	2.16	0.81
5:E:281:VAL:CG2	42:W:148:VAL:HA	2.10	0.81
35:O:229:LYS:HG3	35:O:277:ARG:HH12	1.45	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:MET:HE1	1:A:411:PHE:HA	1.61	0.81
1:A:705:LYS:HB2	37:R:251:ILE:CD1	2.07	0.81
1:A:228:TRP:N	1:A:416:GLY:O	2.14	0.81
1:A:907:PRO:HD3	36:P:229:LYS:HB2	1.63	0.81
3:C:96:PRO:HA	36:P:48:GLN:HE21	1.44	0.81
3:C:140:HIS:NE2	3:C:233:GLU:HG3	1.95	0.81
38:S:39:PHE:CD1	38:S:129:PHE:HE2	1.97	0.81
1:A:296:PHE:CD1	3:C:656:ALA:HB2	2.16	0.81
3:C:140:HIS:ND1	3:C:230:ASP:N	2.28	0.81
3:C:452:THR:CB	3:C:577:PHE:HD2	1.93	0.81
3:C:507:VAL:HG11	3:C:565:ILE:CG2	2.09	0.81
3:C:711:ARG:HD3	3:C:730:ARG:NE	1.96	0.81
14:G:26:U:C1’	35:O:269:CYS:SG	2.68	0.81
15:H:183:G:H2’	15:H:184:C:H6	1.44	0.80
35:O:220:MET:SD	35:O:222:ARG:CB	2.70	0.80
1:A:461:HIS:CE1	2:B:23:C:C6	2.69	0.80
15:H:83:A:H2’	15:H:84:C:C1’	2.10	0.80
1:A:2314:PHE:HB3	4:D:1125:SER:CA	2.11	0.80
2:B:18:C:O2’	2:B:19:A:O5’	1.98	0.80
13:F:68:C:H41	36:P:33:ARG:HB3	1.45	0.80
28:J:273:TYR:CE1	37:R:228:PRO:HB3	2.17	0.80
1:A:318:TYR:HB2	3:C:638:ASP:OD1	1.80	0.80
14:G:134:U:H3	15:H:42:G:H1	1.24	0.80
23:3:979:ARG:HD2	23:3:982:GLU:HB2	1.63	0.80
35:O:235:TYR:HD2	35:O:301:LYS:HB2	1.45	0.80
37:R:65:PRO:HG2	37:R:66:GLU:OE2	1.79	0.80
15:H:149:A:H2’	15:H:150:U:H6	1.44	0.80
22:2:682:LEU:HD13	22:2:687:PHE:HA	1.63	0.80
23:3:637:PRO:HA	23:3:669:LEU:HA	1.63	0.80
33:Q:500:GLY:N	37:R:51:ILE:CD1	2.44	0.80
1:A:748:ASP:CA	36:P:214:THR:HG21	2.11	0.80
3:C:705:VAL:CG2	3:C:717:PHE:HE2	1.84	0.80
15:H:82:G:O2’	15:H:83:A:H5’	1.81	0.80
1:A:596:TYR:CD2	14:G:-5:G:C6	2.70	0.80
1:A:1482:GLU:O	1:A:1486:GLU:CG	2.23	0.80
3:C:87:GLN:OE1	3:C:91:GLU:HG2	1.82	0.80
3:C:140:HIS:CE1	3:C:230:ASP:HB3	2.16	0.80
3:C:776:GLU:O	3:C:781:ASP:OD1	2.00	0.80
5:E:265:ARG:H	5:E:272:ARG:NH2	1.80	0.80
13:F:68:C:N3	36:P:33:ARG:HG2	1.97	0.80
15:H:152:G:H5”	15:H:153:A:OP2	1.80	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:732:TRP:HE1	21:1:768:GLU:HG2	1.47	0.80
23:3:590:MET:HG2	23:3:607:VAL:HA	1.63	0.80
1:A:439:GLN:O	1:A:444:ARG:NH1	2.14	0.80
2:B:31:U:H5"	36:P:32:SER:OG	1.81	0.80
1:A:245:LEU:HA	1:A:430:TRP:HZ2	1.46	0.80
1:A:264:PHE:HE1	1:A:455:VAL:CG1	1.94	0.80
1:A:293:TRP:CZ3	1:A:295:GLU:OE1	2.35	0.80
1:A:301:LYS:CE	3:C:940:ARG:HA	2.12	0.80
1:A:481:PHE:CE2	37:R:205:ASP:HA	2.17	0.80
1:A:593:ARG:NH1	1:A:1565:LYS:CE	2.40	0.80
3:C:445:ALA:HB1	3:C:449:ILE:HD11	1.63	0.80
3:C:738:ASP:HB2	3:C:740:THR:O	1.82	0.80
35:O:20:PHE:CE1	37:R:177:ILE:HD11	2.17	0.80
5:E:248:SER:HB2	5:E:249:TYR:CD1	2.17	0.80
13:F:22:A:C5'	34:N:116:ASN:O	2.30	0.80
24:4:28:LEU:O	24:4:32:LEU:CB	2.27	0.80
35:O:225:PRO:HB3	35:O:302:TRP:CE2	2.17	0.80
1:A:374:ASP:HB2	3:C:355:LYS:HD3	1.64	0.79
1:A:387:PHE:CD2	3:C:399:LEU:HD23	2.17	0.79
2:B:90:U:H5"	2:B:91:U:H5'	1.65	0.79
5:E:209:ILE:HG21	5:E:250:LEU:CD1	2.12	0.79
29:L:222:LEU:H	29:L:222:LEU:HD22	1.45	0.79
1:A:825:ILE:HB	1:A:1001:VAL:HG12	1.65	0.79
3:C:145:PHE:N	3:C:312:SER:CB	2.41	0.79
14:G:-8:U:C6	40:U:16:ASN:HA	2.17	0.79
14:G:21:A:OP2	35:O:156:TYR:OH	1.99	0.79
23:3:687:SER:OG	23:3:1206:LYS:CE	2.29	0.79
38:S:11:PRO:CB	38:S:166:GLY:HA3	2.12	0.79
1:A:283:VAL:O	1:A:284:ARG:NE	2.15	0.79
29:L:216:PHE:HE1	35:O:112:VAL:O	1.66	0.79
39:T:292:TYR:CZ	39:T:308:ARG:HG3	2.18	0.79
1:A:546:LEU:CD1	1:A:595:LYS:HD2	2.06	0.79
3:C:77:VAL:HG11	39:T:196:LEU:HG	0.79	0.79
5:E:310:TYR:CE1	5:E:322:LYS:HD2	2.18	0.79
39:T:306:CYS:SG	39:T:336:VAL:HB	2.22	0.79
1:A:596:TYR:CZ	14:G:-5:G:C8	2.71	0.79
23:3:641:CYS:HB2	23:3:701:LEU:HB3	1.64	0.79
42:W:212:GLU:O	42:W:214:LYS:N	2.14	0.79
3:C:244:LYS:HB2	3:C:292:TYR:HE2	1.47	0.79
15:H:153:A:H2'	15:H:154:C:H5'	1.65	0.79
37:R:67:ILE:HG22	37:R:69:VAL:HG23	1.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:S:34:LYS:HE3	38:S:78:TYR:HE2	1.47	0.79
36:P:212:ASN:O	39:T:458:SER:CA	2.23	0.79
37:R:420:LYS:HG3	37:R:421:GLY:N	1.97	0.79
39:T:351:ASP:O	39:T:352:THR:OG1	1.98	0.79
3:C:515:THR:O	3:C:517:GLU:N	2.16	0.79
3:C:705:VAL:HB	3:C:717:PHE:CE2	2.18	0.79
1:A:73:HIS:CD2	1:A:81:PHE:CD2	2.57	0.79
3:C:140:HIS:ND1	3:C:230:ASP:CB	2.46	0.79
3:C:259:LYS:HE2	3:C:262:ARG:CD	2.13	0.79
15:H:68:G:H1	15:H:84:C:H42	1.29	0.79
15:H:79:G:H2'	15:H:80:A:C8	2.17	0.79
1:A:596:TYR:CE2	14:G:-5:G:C5	2.71	0.78
13:F:34:G:N7	14:G:12:G:O6	2.16	0.78
15:H:101:U:H5"	15:H:102:U:H5'	1.64	0.78
45:Z:593:PHE:O	45:Z:597:ARG:HB2	1.83	0.78
1:A:1342:TRP:CE3	3:C:921:LEU:CD1	2.53	0.78
13:F:27:A:C4	35:O:181:TYR:CZ	2.71	0.78
38:S:111:GLN:NE2	42:W:93:PHE:CB	2.46	0.78
1:A:718:ARG:NH2	37:R:259:LYS:HE3	1.98	0.78
15:H:82:G:H2'	15:H:83:A:C8	2.17	0.78
23:3:1109:LEU:HD11	23:3:1128:ILE:HG21	1.65	0.78
1:A:695:ASP:OD2	39:T:350:HIS:HB3	1.83	0.78
23:3:477:SER:HA	23:3:482:THR:HG22	1.65	0.78
38:S:39:PHE:HB3	38:S:129:PHE:HZ	1.26	0.78
40:U:1:MET:SD	40:U:1:MET:N	2.54	0.78
1:A:664:HIS:NE2	1:A:666:LYS:HD3	1.98	0.78
23:3:435:LEU:HD22	23:3:799:ILE:HD11	1.66	0.78
1:A:312:TYR:OH	3:C:853:ARG:NH2	2.17	0.78
37:R:132:LEU:HB3	39:T:399:LYS:NZ	1.99	0.78
1:A:299:ILE:HD12	3:C:921:LEU:HB2	1.66	0.78
1:A:705:LYS:HG2	37:R:251:ILE:HD12	1.65	0.78
1:A:758:ARG:CB	36:P:227:TYR:CE2	2.64	0.78
39:T:387:PHE:CE1	39:T:398:TRP:CD1	2.72	0.78
42:W:277:PRO:CB	42:W:578:TRP:C	2.51	0.78
24:4:17:VAL:HG22	24:4:86:VAL:HG22	1.66	0.78
39:T:434:GLY:HA2	39:T:464:GLY:CA	2.14	0.78
1:A:468:LYS:HD3	1:A:469:LYS:N	1.99	0.78
3:C:133:THR:HB	3:C:225:VAL:HG23	1.65	0.78
23:3:295:THR:HG22	23:3:297:SER:H	1.48	0.78
35:O:149:LYS:HZ3	35:O:290:LYS:CG	1.97	0.78
3:C:452:THR:HG21	3:C:577:PHE:CD2	2.16	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:2:649:LYS:HB3	22:2:655:SER:HB2	1.65	0.78
23:3:474:ILE:O	23:3:485:LEU:HB2	1.83	0.78
24:4:17:VAL:O	24:4:56:TYR:HA	1.83	0.78
35:O:131:THR:HG23	42:W:111:LEU:H	1.48	0.78
36:P:224:MET:HE2	36:P:228:ILE:HD13	1.63	0.78
39:T:267:ASP:HB3	39:T:269:GLN:HG2	1.64	0.78
1:A:692:ASP:CA	39:T:376:ARG:HH22	1.97	0.77
1:A:919:ASP:OD2	1:A:1012:LYS:NZ	2.17	0.77
21:1:1053:ARG:NH1	22:2:559:PRO:O	2.17	0.77
23:3:805:ASN:ND2	23:3:858:GLY:O	2.14	0.77
1:A:168:PRO:HG2	1:A:559:ASP:HB3	1.64	0.77
3:C:449:ILE:HG21	3:C:457:VAL:HG12	1.66	0.77
3:C:677:GLU:OE2	3:C:684:LYS:HG2	1.83	0.77
21:1:941:ASN:HA	21:1:948:ARG:HH22	1.48	0.77
1:A:587:GLN:O	1:A:1551:PHE:HA	1.83	0.77
1:A:666:LYS:HB3	1:A:668:VAL:HG23	1.66	0.77
1:A:1405:LEU:CA	37:R:415:LEU:CD2	2.62	0.77
2:B:43:U:H5'	13:F:67:G:N2	1.98	0.77
3:C:449:ILE:CD1	3:C:466:SER:OG	2.33	0.77
15:H:80:A:H2'	15:H:81:G:C8	2.19	0.77
24:4:69:TYR:CE1	24:4:73:ILE:HG13	2.19	0.77
35:O:189:PRO:HG3	42:W:223:ARG:CB	2.15	0.77
38:S:11:PRO:HB2	38:S:165:SER:O	1.83	0.77
45:Z:595:GLN:O	45:Z:599:ALA:N	2.14	0.77
1:A:456:LEU:O	1:A:460:LYS:HG2	1.84	0.77
1:A:1352:HIS:ND1	40:U:21:ARG:HA	1.98	0.77
3:C:140:HIS:HA	3:C:259:LYS:HZ3	1.47	0.77
3:C:349:PHE:CD1	3:C:356:PHE:CD1	2.68	0.77
5:E:277:PHE:HE2	5:E:300:ILE:CD1	1.98	0.77
13:F:8:C:H5"	13:F:8:C:C6	2.19	0.77
35:O:292:ILE:HG12	35:O:297:ARG:HA	1.66	0.77
1:A:651:TRP:CE2	13:F:66:C:C2	2.72	0.77
3:C:85:ASP:CB	39:T:238:LEU:HG	2.14	0.77
3:C:151:GLU:OE1	3:C:417:ARG:CZ	2.33	0.77
14:G:11:A:H2'	14:G:12:G:O4'	1.84	0.77
35:O:45:CYS:SG	52:O:502:ZN:ZN	1.71	0.77
44:Y:86:ASP:HA	45:Z:502:ALA:HB3	1.65	0.77
1:A:152:ARG:HH11	1:A:152:ARG:CB	1.97	0.77
1:A:362:ARG:O	1:A:362:ARG:NE	2.18	0.77
28:J:291:GLN:NE2	29:L:230:GLU:OE2	2.17	0.77
39:T:318:ARG:HG3	39:T:319:THR:HG23	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:482:TYR:HE2	3:C:493:PHE:CB	1.98	0.77
45:Z:603:SER:O	45:Z:607:VAL:HG23	1.84	0.77
1:A:43:LYS:HD2	42:W:168:PHE:CB	2.14	0.77
1:A:203:VAL:HG21	1:A:237:THR:CG2	2.14	0.77
1:A:1426:ASP:HB2	37:R:421:GLY:HA3	1.64	0.77
3:C:145:PHE:CZ	3:C:427:PHE:CE1	2.73	0.77
3:C:471:ASP:H	3:C:499:GLY:HA2	1.47	0.77
5:E:74:PHE:CD1	5:E:81:LEU:CD2	2.67	0.77
23:3:785:PRO:HA	23:3:800:ILE:O	1.84	0.77
1:A:623:LYS:CB	48:A:2401:IHP:O34	2.33	0.77
1:A:1314:VAL:HG11	1:A:1487:HIS:CG	2.19	0.77
1:A:1342:TRP:HE3	3:C:921:LEU:HD22	1.49	0.77
3:C:567:GLU:HG2	3:C:572:GLU:OE2	1.85	0.77
15:H:177:A:H5”	15:H:178:A:OP1	1.84	0.77
23:3:981:CYS:SG	23:3:982:GLU:N	2.57	0.77
38:S:11:PRO:HB3	38:S:166:GLY:CA	2.14	0.77
1:A:782:LEU:HD13	36:P:220:HIS:CE1	2.18	0.76
3:C:82:GLN:CB	39:T:231:TRP:HZ3	1.98	0.76
3:C:711:ARG:HD3	3:C:730:ARG:CZ	2.16	0.76
5:E:146:ARG:HH12	5:E:148:LYS:HE3	1.49	0.76
35:O:132:ARG:NH1	38:S:149:SER:CB	2.46	0.76
35:O:149:LYS:NZ	35:O:290:LYS:HG2	1.99	0.76
35:O:177:GLU:OE1	35:O:177:GLU:N	2.18	0.76
1:A:119:LEU:HD12	1:A:484:SER:HB2	1.67	0.76
1:A:630:TRP:O	1:A:632:ALA:N	2.18	0.76
21:1:473:GLN:HE22	25:5:93:ASN:H	1.33	0.76
37:R:420:LYS:HG2	37:R:423:ASP:OD2	1.84	0.76
1:A:43:LYS:CD	42:W:168:PHE:CB	2.63	0.76
1:A:230:PHE:N	1:A:414:ARG:O	2.18	0.76
1:A:705:LYS:CB	37:R:251:ILE:CD1	2.59	0.76
3:C:449:ILE:HD11	3:C:466:SER:N	1.99	0.76
15:H:143:A:H3’	15:H:143:A:N3	2.01	0.76
38:S:9:TRP:CZ2	38:S:44:ARG:HD3	2.20	0.76
38:S:13:ASN:HA	38:S:25:LEU:O	1.85	0.76
3:C:261:ASP:CG	50:C:1500:GTP:HN1	1.88	0.76
5:E:162:ARG:NH2	5:E:204:THR:HA	1.99	0.76
15:H:148:C:H2’	15:H:149:A:H8	1.48	0.76
38:S:9:TRP:HE3	38:S:11:PRO:HD3	1.49	0.76
1:A:1342:TRP:CB	3:C:921:LEU:HD21	2.13	0.76
3:C:471:ASP:OD1	3:C:472:GLY:N	2.19	0.76
22:2:611:ASP:O	22:2:614:ARG:HB3	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:R:412:ASP:CG	37:R:413:GLN:N	2.39	0.76
38:S:10:GLN:HA	38:S:29:TRP:CZ2	2.20	0.76
1:A:755:HIS:HA	36:P:223:PHE:CE1	2.20	0.76
15:H:168:A:H5'	15:H:169:C:OP2	1.86	0.76
45:Z:566:TYR:HD2	45:Z:580:PRO:HG2	1.50	0.76
3:C:750:LEU:O	3:C:754:VAL:HG23	1.84	0.76
13:F:40:U:H2'	13:F:41:A:C8	2.20	0.76
23:3:328:LYS:HB2	23:3:372:GLU:HG3	1.68	0.76
41:V:548:ALA:HB1	41:V:586:PHE:N	2.00	0.76
1:A:779:LEU:CD2	36:P:223:PHE:CE2	2.69	0.76
1:A:1301:ILE:HD11	1:A:1306:LYS:HE2	1.68	0.76
5:E:231:MET:HB3	5:E:262:TRP:CZ3	2.21	0.76
23:3:442:LEU:O	23:3:735:SER:N	2.18	0.76
1:A:1162:PRO:CG	36:P:194:PHE:CD2	2.69	0.75
23:3:11:ALA:O	23:3:34:ARG:NH1	2.17	0.75
35:O:149:LYS:HG2	35:O:290:LYS:HZ3	1.49	0.75
45:Z:594:GLU:O	45:Z:598:PHE:HB2	1.86	0.75
1:A:318:TYR:N	3:C:638:ASP:OD1	2.19	0.75
32:I:720:ILE:O	32:I:721:LYS:CB	2.34	0.75
1:A:229:GLN:HG2	1:A:415:SER:HB2	1.68	0.75
1:A:532:THR:OG1	14:G:2:U:C5'	2.34	0.75
3:C:149:LEU:CD1	3:C:427:PHE:CG	2.53	0.75
3:C:593:GLU:HG3	3:C:594:PRO:HD2	1.67	0.75
14:G:132:G:H1	15:H:44:U:H3	1.34	0.75
23:3:784:THR:O	23:3:786:ARG:NH1	2.18	0.75
34:N:28:LYS:NZ	42:W:190:ASP:HA	2.01	0.75
37:R:66:GLU:OE2	37:R:66:GLU:N	2.19	0.75
37:R:181:PRO:O	37:R:182:SER:HB2	1.84	0.75
38:S:119:THR:OG1	38:S:122:LEU:HD12	1.87	0.75
1:A:318:TYR:CB	3:C:638:ASP:OD1	2.35	0.75
4:D:452:PRO:CB	23:3:570:PRO:HB2	2.16	0.75
14:G:11:A:C4	14:G:12:G:H8	2.04	0.75
15:H:81:G:H2'	15:H:82:G:C8	2.19	0.75
23:3:905:VAL:HB	23:3:928:TYR:HB2	1.68	0.75
1:A:402:ILE:CG2	3:C:268:LYS:HZ1	1.97	0.75
35:O:20:PHE:CD1	37:R:177:ILE:CD1	2.70	0.75
3:C:470:PRO:HA	3:C:499:GLY:HA2	1.67	0.75
3:C:711:ARG:CD	3:C:730:ARG:HE	1.99	0.75
15:H:10:C:H2'	15:H:11:G:H8	1.52	0.75
23:3:1105:GLN:O	23:3:1118:VAL:HB	1.87	0.75
13:F:36:A:C3'	13:F:37:C:H5"	2.16	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:J:339:TRP:CE3	37:R:116:TYR:HD2	2.04	0.75
41:V:515:CYS:HA	41:V:521:TYR:CB	2.17	0.75
3:C:82:GLN:HB2	39:T:231:TRP:HZ3	1.50	0.75
3:C:465:MET:HE1	3:C:475:MET:CG	2.13	0.75
15:H:71:C:H2'	15:H:72:U:C6	2.21	0.75
15:H:153:A:C2'	15:H:154:C:H5'	2.17	0.75
3:C:348:TYR:CE1	3:C:359:LYS:HB3	2.22	0.74
3:C:510:LEU:HD22	3:C:514:TYR:CE2	2.22	0.74
28:J:256:LYS:O	29:L:232:TYR:HD2	1.66	0.74
28:J:273:TYR:CG	37:R:228:PRO:HG2	2.21	0.74
1:A:1405:LEU:CA	37:R:415:LEU:HD21	2.15	0.74
3:C:449:ILE:CG2	3:C:457:VAL:HG12	2.17	0.74
35:O:225:PRO:CB	35:O:302:TRP:HE1	2.00	0.74
1:A:339:PHE:HE1	1:A:406:TRP:CZ3	2.01	0.74
1:A:532:THR:CG2	14:G:2:U:P	2.75	0.74
1:A:783:TYR:CB	36:P:228:ILE:HG12	2.17	0.74
1:A:2325:VAL:HG13	4:D:788:GLY:C	2.07	0.74
35:O:185:LYS:CE	42:W:215:GLU:O	2.33	0.74
45:Z:525:TYR:HD1	45:Z:526:ILE:HG23	1.52	0.74
1:A:666:LYS:CB	1:A:668:VAL:HG23	2.17	0.74
1:A:2073:TRP:CD1	1:A:2074:ARG:HD2	2.22	0.74
23:3:437:VAL:O	23:3:776:GLN:HA	1.87	0.74
42:W:198:LYS:O	42:W:199:TYR:O	2.04	0.74
1:A:318:TYR:C	3:C:638:ASP:OD1	2.25	0.74
1:A:380:LEU:O	3:C:354:ARG:CG	2.30	0.74
1:A:1457:HIS:CD2	37:R:425:GLY:H	2.04	0.74
3:C:137:HIS:CG	3:C:236:MET:HB2	2.22	0.74
15:H:180:G:O2'	15:H:181:G:H5'	1.88	0.74
37:R:70:ALA:O	37:R:71:GLN:O	2.05	0.74
1:A:73:HIS:NE2	1:A:81:PHE:CZ	2.51	0.74
1:A:203:VAL:CG2	1:A:237:THR:CG2	2.66	0.74
1:A:305:ARG:HB2	3:C:879:ASP:OD1	1.88	0.74
1:A:1405:LEU:HA	37:R:415:LEU:CD2	2.17	0.74
23:3:294:LYS:O	23:3:343:LYS:NZ	2.21	0.74
23:3:931:VAL:HG12	23:3:932:ASN:H	1.53	0.74
28:J:270:ASP:OD2	37:R:222:PRO:HG2	1.88	0.74
38:S:131:ARG:NH1	38:S:132:VAL:O	2.20	0.74
1:A:132:ILE:HD11	2:B:57:G:OP1	1.88	0.74
5:E:258:THR:HG22	5:E:260:ARG:HG2	1.68	0.74
1:A:744:LYS:HE3	36:P:213:ASP:HA	1.70	0.74
3:C:140:HIS:CA	3:C:230:ASP:HB2	2.17	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:F:34:G:H5"	13:F:34:G:N3	2.03	0.74
35:O:225:PRO:CB	35:O:302:TRP:NE1	2.50	0.74
37:R:422:MET:O	37:R:424:SER:N	2.17	0.74
39:T:385:TYR:O	39:T:400:PHE:HB2	1.88	0.74
1:A:260:LEU:HD23	1:A:455:VAL:HG22	1.70	0.74
1:A:2270:PHE:HD1	4:D:1264:PRO:CB	1.96	0.74
3:C:445:ALA:HB1	3:C:449:ILE:CD1	2.17	0.74
13:F:1:G:O2'	34:N:99:ASN:ND2	2.20	0.74
1:A:380:LEU:CA	3:C:354:ARG:HG3	2.16	0.73
1:A:748:ASP:OD1	36:P:214:THR:CG2	2.36	0.73
5:E:243:LEU:HD11	5:E:247:GLY:HA2	1.68	0.73
1:A:176:LEU:HD13	1:A:181:ASN:HD22	1.52	0.73
28:J:406:PHE:CD2	28:J:411:MET:CE	2.70	0.73
1:A:312:TYR:CE2	3:C:882:GLY:HA3	2.23	0.73
1:A:593:ARG:HD3	14:G:-4:A:H4'	1.70	0.73
5:E:119:THR:HG21	5:E:161:ARG:CB	2.17	0.73
1:A:380:LEU:CB	3:C:354:ARG:CG	2.45	0.73
3:C:97:VAL:HG21	36:P:45:GLN:HG3	1.69	0.73
21:1:563:LEU:HD22	21:1:566:LEU:HD22	1.70	0.73
42:W:137:TYR:CB	42:W:159:ALA:HB2	2.17	0.73
1:A:2078:ILE:CG2	4:D:1047:PRO:CB	2.66	0.73
2:B:42:U:C4'	13:F:70:A:H4'	2.18	0.73
3:C:94:ILE:HD11	36:P:44:ARG:NH2	2.03	0.73
1:A:294:ASN:OD1	3:C:654:LYS:HD3	1.89	0.73
3:C:516:LEU:CD1	3:C:517:GLU:HG3	2.18	0.73
3:C:671:SER:O	3:C:672:LEU:HD13	1.89	0.73
15:H:69:U:H2'	15:H:70:C:C6	2.23	0.73
15:H:165:A:O2'	15:H:166:G:H5'	1.88	0.73
35:O:149:LYS:HG3	35:O:290:LYS:HZ1	1.54	0.73
35:O:247:ASP:OD2	35:O:294:ASN:ND2	2.21	0.73
38:S:131:ARG:NH1	38:S:133:CYS:CA	2.51	0.73
5:E:287:ASN:O	5:E:289:LEU:HD23	1.88	0.73
26:6:51:TYR:H	26:6:54:TYR:HB2	1.53	0.73
35:O:149:LYS:CG	35:O:290:LYS:HZ1	2.02	0.73
37:R:67:ILE:HG22	37:R:69:VAL:CG2	2.18	0.73
38:S:9:TRP:HZ2	38:S:44:ARG:HD3	1.52	0.73
38:S:100:MET:CG	38:S:108:ASN:OD1	2.36	0.73
1:A:1301:ILE:O	1:A:1303:LEU:O	2.06	0.73
38:S:81:GLN:HA	38:S:108:ASN:O	1.88	0.73
2:B:42:U:C2	14:G:-3:A:H2	2.07	0.73
15:H:106:G:H4'	15:H:107:A:O4'	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:555:VAL:HG23	23:3:592:LEU:HD22	1.70	0.73
23:3:1145:GLU:OE2	23:3:1149:ARG:NH2	2.21	0.73
28:J:339:TRP:CE3	37:R:116:TYR:CD2	2.76	0.73
42:W:101:THR:O	42:W:104:MET:N	2.22	0.73
3:C:711:ARG:CD	3:C:730:ARG:HH11	2.01	0.73
28:J:259:GLN:NE2	29:L:220:PRO:HD3	2.02	0.73
1:A:1290:LYS:HG2	40:U:13:SER:C	2.08	0.72
3:C:449:ILE:HG22	3:C:457:VAL:CG1	2.18	0.72
5:E:146:ARG:HH12	5:E:148:LYS:CE	1.99	0.72
5:E:250:LEU:HD23	5:E:250:LEU:O	1.88	0.72
15:H:70:C:H2'	15:H:71:C:C6	2.24	0.72
41:V:548:ALA:HB3	41:V:585:ILE:CB	2.19	0.72
1:A:1342:TRP:CZ2	3:C:921:LEU:CD1	2.71	0.72
3:C:508:LYS:HE3	3:C:566:THR:HG21	1.70	0.72
39:T:434:GLY:CA	39:T:464:GLY:HA2	2.19	0.72
2:B:40:U:H4'	2:B:41:U:OP2	1.89	0.72
3:C:93:ILE:HD13	39:T:230:ILE:HD13	1.72	0.72
15:H:106:G:H21	15:H:107:A:N6	1.87	0.72
15:H:182:U:H2'	15:H:183:G:H8	1.53	0.72
21:1:428:ALA:O	21:1:432:THR:N	2.21	0.72
23:3:547:CYS:HA	23:3:555:VAL:O	1.89	0.72
1:A:675:GLN:OE1	13:F:70:A:OP1	2.08	0.72
3:C:519:GLU:N	3:C:519:GLU:OE2	2.21	0.72
13:F:34:G:N3	13:F:34:G:H3'	2.05	0.72
1:A:549:GLU:OE1	1:A:552:ARG:NH1	2.23	0.72
1:A:1457:HIS:HE2	37:R:424:SER:CA	2.02	0.72
1:A:1755:SER:CB	21:1:938:TRP:CH2	2.72	0.72
3:C:125:ASN:O	3:C:126:SER:OG	2.04	0.72
3:C:726:LEU:HD12	3:C:726:LEU:O	1.89	0.72
14:G:20:A:H1'	35:O:193:LEU:CD2	2.19	0.72
35:O:45:CYS:HG	52:O:502:ZN:ZN	1.01	0.72
39:T:352:THR:CG2	39:T:373:LYS:C	2.58	0.72
1:A:150:MET:SD	1:A:153:ARG:NH2	2.62	0.72
1:A:303:ILE:HD13	3:C:933:PHE:CD1	2.25	0.72
1:A:712:HIS:CE1	37:R:254:CYS:HB2	2.24	0.72
3:C:77:VAL:CG1	39:T:196:LEU:CA	2.68	0.72
3:C:449:ILE:HG21	3:C:457:VAL:HG11	1.70	0.72
13:F:5:U:H3'	13:F:7:G:H5"	1.71	0.72
1:A:1413:ASP:O	1:A:1418:ARG:NH1	2.21	0.72
3:C:250:ARG:HE	3:C:451:HIS:CD2	2.07	0.72
23:3:720:TRP:HB3	23:3:731:LEU:HD11	1.69	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:PRO:O	1:A:111:GLU:OE1	2.08	0.72
1:A:193:LEU:HD12	1:A:194:GLU:H	1.55	0.72
1:A:1338:SER:OG	1:A:1351:THR:N	2.16	0.72
13:F:39:A:H61	14:G:8:C:H42	1.36	0.72
22:2:614:ARG:HG3	22:2:614:ARG:NH1	1.98	0.72
35:O:240:GLY:HA3	35:O:296:ARG:HH12	1.55	0.72
1:A:718:ARG:CZ	37:R:259:LYS:HE3	2.20	0.72
5:E:264:VAL:HA	5:E:272:ARG:HH21	1.55	0.72
13:F:28:A:O4'	34:N:41:ARG:HA	1.90	0.72
23:3:783:TYR:HB2	23:3:801:GLU:HB3	1.72	0.72
42:W:491:GLN:O	42:W:493:ARG:N	2.23	0.72
1:A:785:LYS:HE3	36:P:215:LEU:HD11	1.71	0.72
1:A:1481:VAL:HG21	1:A:1498:TRP:CH2	2.25	0.72
1:A:2324:GLU:HG2	1:A:2330:ARG:HH12	1.54	0.72
2:B:42:U:O4'	13:F:70:A:H4'	1.89	0.72
15:H:165:A:C2'	15:H:166:G:H5'	2.20	0.72
1:A:228:TRP:O	1:A:415:SER:CA	2.38	0.71
1:A:2156:THR:OG1	1:A:2157:VAL:N	2.21	0.71
3:C:64:LYS:NZ	36:P:206:LYS:HG2	2.05	0.71
3:C:129:ILE:HA	3:C:199:LEU:O	1.90	0.71
1:A:203:VAL:HG23	1:A:237:THR:HG21	1.72	0.71
2:B:31:U:C5'	36:P:32:SER:OG	2.38	0.71
28:J:273:TYR:CE1	37:R:228:PRO:CB	2.72	0.71
29:L:224:PHE:CE1	37:R:86:LEU:CD1	2.73	0.71
36:P:66:ARG:HB2	36:P:66:ARG:HH11	1.55	0.71
1:A:168:PRO:CG	1:A:559:ASP:CB	2.64	0.71
1:A:730:GLY:O	37:R:252:PRO:HG2	1.90	0.71
1:A:1402:ARG:HH22	45:Z:572:PRO:HA	1.53	0.71
1:A:1481:VAL:HG21	1:A:1498:TRP:CZ2	2.25	0.71
21:1:1206:ASP:OD1	21:1:1207:SER:N	2.21	0.71
1:A:434:HIS:ND1	1:A:435:CYS:SG	2.62	0.71
1:A:462:ARG:HD2	1:A:462:ARG:N	2.05	0.71
15:H:153:A:H2'	15:H:154:C:C5'	2.19	0.71
21:1:405:ASP:HA	25:5:49:ARG:HH22	1.55	0.71
1:A:299:ILE:HD13	1:A:1346:THR:HG21	1.73	0.71
1:A:461:HIS:HD2	2:B:27:U:O4	1.71	0.71
3:C:706:GLN:HE21	3:C:708:THR:H	1.38	0.71
5:E:74:PHE:CE2	5:E:343:ILE:CG1	2.73	0.71
36:P:224:MET:CE	36:P:224:MET:HA	2.21	0.71
37:R:414:ARG:CZ	37:R:414:ARG:HB2	2.18	0.71
1:A:81:PHE:O	1:A:83:HIS:N	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1529:ILE:O	1:A:1532:ARG:N	2.24	0.71
1:A:2328:ALA:HB3	4:D:788:GLY:N	2.05	0.71
3:C:700:ILE:HA	3:C:705:VAL:CG1	2.21	0.71
3:C:705:VAL:HG23	3:C:717:PHE:HD2	1.48	0.71
15:H:72:U:H2'	15:H:73:C:C6	2.26	0.71
35:O:185:LYS:HG3	42:W:216:LEU:CA	2.20	0.71
1:A:76:MET:CE	1:A:506:LEU:HD11	2.21	0.71
1:A:264:PHE:CE2	1:A:459:LEU:CD1	2.73	0.71
1:A:2325:VAL:CG1	4:D:789:MET:HA	2.20	0.71
3:C:80:ILE:HD12	3:C:80:ILE:N	2.05	0.71
3:C:94:ILE:HD13	36:P:44:ARG:CZ	2.20	0.71
3:C:441:PRO:O	3:C:444:GLY:HA3	1.90	0.71
3:C:490:PHE:CZ	3:C:612:LYS:HD2	2.26	0.71
35:O:235:TYR:HD1	35:O:271:PHE:HE1	1.37	0.71
36:P:191:ASP:N	36:P:191:ASP:OD1	2.23	0.71
42:W:277:PRO:CB	42:W:578:TRP:O	2.39	0.71
45:Z:612:TYR:O	45:Z:614:TRP:N	2.23	0.71
1:A:76:MET:HE3	1:A:506:LEU:HD11	1.72	0.71
1:A:1290:LYS:CG	40:U:13:SER:O	2.38	0.71
2:B:40:U:C4'	2:B:41:U:OP2	2.39	0.71
29:L:209:ASP:CG	35:O:111:ASP:HB2	2.11	0.71
41:V:549:LYS:O	41:V:552:ALA:HB3	1.91	0.71
1:A:365:VAL:HG12	1:A:366:LYS:N	2.06	0.71
1:A:402:ILE:HG21	3:C:268:LYS:HZ1	1.51	0.71
1:A:1459:ARG:CG	37:R:422:MET:O	2.39	0.71
3:C:679:PRO:HG2	3:C:807:GLN:OE1	1.91	0.71
28:J:270:ASP:OD2	37:R:222:PRO:HG3	1.88	0.71
29:L:209:ASP:OD2	35:O:111:ASP:CB	2.30	0.71
37:R:422:MET:HG2	37:R:423:ASP:N	2.05	0.71
38:S:71:GLY:O	42:W:93:PHE:CB	2.39	0.71
1:A:705:LYS:HG2	37:R:251:ILE:CD1	2.21	0.71
1:A:1085:ILE:HG12	1:A:1099:PHE:HE1	1.56	0.71
1:A:1552:GLN:HB3	49:A:2402:ALA:CB	2.21	0.71
1:A:2078:ILE:HG21	4:D:1047:PRO:CB	2.20	0.71
21:1:1221:GLU:HG3	21:1:1223:SER:H	1.56	0.71
28:J:353:GLU:OE1	28:J:358:GLU:HB3	1.91	0.71
36:P:189:ASP:OD2	36:P:192:VAL:HG21	1.91	0.71
39:T:366:VAL:HG21	39:T:402:ASP:HA	1.72	0.71
1:A:719:CYS:SG	37:R:258:TRP:CH2	2.84	0.70
3:C:259:LYS:HG3	50:C:1500:GTP:C6	2.26	0.70
14:G:20:A:H1'	35:O:193:LEU:HD21	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1342:TRP:CG	3:C:921:LEU:HD21	2.25	0.70
15:H:160:A:O2'	15:H:161:U:H5'	1.90	0.70
29:L:209:ASP:CG	35:O:111:ASP:H	1.91	0.70
35:O:197:ASN:OD1	35:O:198:ILE:N	2.24	0.70
35:O:262:THR:HB	35:O:271:PHE:HB2	1.73	0.70
1:A:1549:VAL:CG2	14:G:-6:C:O2'	2.39	0.70
14:G:11:A:N3	14:G:11:A:H5"	2.05	0.70
15:H:168:A:N3	15:H:168:A:H2'	2.06	0.70
23:3:722:SER:HA	23:3:730:HIS:O	1.92	0.70
38:S:88:PRO:O	38:S:91:LYS:HE3	1.90	0.70
1:A:593:ARG:O	14:G:-4:A:H1'	1.91	0.70
13:F:24:A:H2	13:F:26:U:C2	2.09	0.70
23:3:446:GLU:OE1	23:3:763:ARG:NH1	2.24	0.70
35:O:144:SER:HA	35:O:148:LEU:HD13	1.73	0.70
37:R:189:ASN:HD21	37:R:195:ARG:NH2	1.90	0.70
39:T:267:ASP:O	39:T:268:LYS:HG3	1.91	0.70
1:A:171:ASP:O	1:A:520:TYR:CG	2.44	0.70
1:A:181:ASN:O	1:A:185:VAL:HG22	1.90	0.70
3:C:449:ILE:HD13	3:C:466:SER:OG	1.92	0.70
13:F:94:C:OP1	28:J:351:ASN:ND2	2.25	0.70
15:H:181:G:H2'	15:H:182:U:C6	2.26	0.70
21:1:901:GLN:HA	21:1:939:ARG:NH2	2.07	0.70
29:L:216:PHE:CE1	35:O:112:VAL:HG12	2.25	0.70
37:R:103:ARG:HH11	37:R:103:ARG:CB	2.04	0.70
1:A:338:VAL:HG21	3:C:867:PRO:CG	2.22	0.70
3:C:457:VAL:CB	3:C:462:GLY:HA3	2.22	0.70
13:F:38:G:P	13:F:38:G:H8	2.14	0.70
13:F:68:C:C2	36:P:33:ARG:HG2	2.27	0.70
14:G:12:G:N3	14:G:12:G:H2'	2.07	0.70
21:1:1108:ASN:OD1	21:1:1110:VAL:N	2.25	0.70
41:V:536:ILE:O	41:V:578:SER:CB	2.39	0.70
42:W:101:THR:O	42:W:102:GLN:C	2.30	0.70
1:A:296:PHE:HE1	3:C:591:ALA:HB1	1.52	0.70
1:A:305:ARG:CG	3:C:879:ASP:OD1	2.39	0.70
3:C:132:VAL:CG1	3:C:226:VAL:CG2	2.70	0.70
3:C:135:CYS:SG	3:C:227:LEU:CD1	2.80	0.70
13:F:27:A:H1'	35:O:181:TYR:CE2	2.23	0.70
14:G:-9:C:C6	40:U:18:TYR:CD1	2.80	0.70
35:O:189:PRO:CG	42:W:223:ARG:N	2.54	0.70
37:R:220:ARG:NH1	37:R:220:ARG:HB2	2.06	0.70
38:S:10:GLN:HB3	38:S:29:TRP:CE3	2.27	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:S:39:PHE:HB2	38:S:129:PHE:HZ	1.10	0.70
1:A:76:MET:SD	1:A:88:TYR:CG	2.85	0.70
1:A:377:GLU:O	1:A:378:PHE:HB3	1.91	0.70
1:A:596:TYR:CD2	14:G:-5:G:C5	2.79	0.70
1:A:675:GLN:O	13:F:55:C:O2'	2.10	0.70
1:A:1318:THR:HB	1:A:1324:GLY:HA3	1.73	0.70
15:H:154:C:H2'	15:H:155:C:C6	2.27	0.70
21:1:1155:PHE:HA	21:1:1158:ILE:HG12	1.73	0.70
37:R:80:LYS:O	37:R:81:LYS:NZ	2.25	0.70
1:A:132:ILE:HD13	2:B:57:G:OP1	1.92	0.70
1:A:719:CYS:SG	37:R:258:TRP:HH2	2.13	0.70
2:B:42:U:H4'	13:F:70:A:H5'	1.73	0.70
3:C:137:HIS:CE1	3:C:236:MET:SD	2.85	0.70
35:O:149:LYS:NZ	35:O:290:LYS:CG	2.55	0.70
1:A:481:PHE:CD2	37:R:205:ASP:HA	2.27	0.69
1:A:718:ARG:NE	37:R:259:LYS:HE3	2.06	0.69
3:C:452:THR:HB	3:C:577:PHE:CD2	2.26	0.69
23:3:524:ILE:HD11	23:3:556:ILE:HG21	1.74	0.69
1:A:461:HIS:CD2	2:B:26:A:N6	2.60	0.69
1:A:673:THR:O	1:A:677:VAL:HG23	1.91	0.69
3:C:64:LYS:NZ	36:P:206:LYS:CG	2.55	0.69
3:C:452:THR:O	3:C:577:PHE:HA	1.92	0.69
5:E:74:PHE:HE2	5:E:343:ILE:HG12	1.54	0.69
5:E:264:VAL:HA	5:E:272:ARG:NH2	2.07	0.69
35:O:48:CYS:SG	35:O:71:CYS:SG	2.91	0.69
1:A:974:ASN:HB2	1:A:1178:TYR:HB3	1.73	0.69
1:A:71:ARG:HD2	1:A:177:ASP:OD2	1.92	0.69
1:A:338:VAL:CB	3:C:867:PRO:HG3	2.21	0.69
1:A:805:GLU:CB	36:P:194:PHE:HZ	2.04	0.69
3:C:709:TRP:HB3	3:C:713:LYS:HD2	1.73	0.69
23:3:280:ASP:H	23:3:857:ALA:HB3	1.58	0.69
36:P:30:TYR:OH	37:R:161:ALA:O	2.10	0.69
37:R:436:VAL:HG23	37:R:437:TYR:CE1	2.26	0.69
1:A:76:MET:HE1	1:A:88:TYR:CB	2.22	0.69
1:A:755:HIS:HE1	36:P:223:PHE:CD2	2.06	0.69
14:G:19:G:H5"	35:O:159:ARG:HD2	1.74	0.69
15:H:149:A:H2'	15:H:150:U:C6	2.27	0.69
15:H:153:A:N6	15:H:177:A:C2	2.60	0.69
15:H:183:G:H2'	15:H:184:C:C6	2.26	0.69
29:L:209:ASP:OD1	35:O:111:ASP:CG	2.31	0.69
37:R:408:GLU:CG	37:R:409:VAL:H	2.04	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1180:LYS:HA	1:A:1201:ARG:HH12	1.58	0.69
23:3:428:GLY:HA3	23:3:433:SER:HA	1.73	0.69
34:N:51:ARG:NH2	42:W:192:PHE:O	2.26	0.69
1:A:76:MET:CE	1:A:88:TYR:CG	2.70	0.69
1:A:229:GLN:CG	1:A:415:SER:HB2	2.21	0.69
1:A:296:PHE:HB3	3:C:656:ALA:HB2	1.66	0.69
1:A:762:ARG:NH2	36:P:226:LYS:HZ3	1.87	0.69
1:A:1342:TRP:HB3	3:C:921:LEU:CD2	2.22	0.69
3:C:89:LEU:HD23	3:C:89:LEU:C	2.14	0.69
3:C:482:TYR:CE2	3:C:493:PHE:HB2	2.28	0.69
5:E:178:LEU:CD1	5:E:222:LEU:CD2	2.71	0.69
15:H:83:A:C2'	15:H:84:C:O4'	2.39	0.69
25:5:18:ASN:OD1	25:5:19:ARG:N	2.25	0.69
43:X:185:ARG:O	43:X:189:HIS:HB2	1.93	0.69
1:A:1348:VAL:CG1	3:C:921:LEU:CD2	2.71	0.69
1:A:1459:ARG:HG3	37:R:424:SER:H	1.57	0.69
3:C:93:ILE:CG2	39:T:218:TRP:CE2	2.76	0.69
3:C:736:GLY:CA	3:C:770:PHE:CE2	2.75	0.69
15:H:152:G:O3'	15:H:153:A:O4'	2.11	0.69
23:3:236:ILE:HB	23:3:249:LEU:HB2	1.75	0.69
23:3:687:SER:HG	23:3:1206:LYS:HD2	1.55	0.69
28:J:353:GLU:OE1	28:J:358:GLU:CB	2.41	0.69
36:P:30:TYR:CZ	37:R:162:ALA:HA	2.28	0.69
36:P:224:MET:CE	36:P:228:ILE:CD1	2.71	0.69
42:W:474:LYS:HA	42:W:490:ALA:HB3	1.75	0.69
1:A:2113:LYS:CE	4:D:1229:ASP:CB	2.71	0.69
3:C:72:VAL:HG22	39:T:453:ALA:CB	2.23	0.69
3:C:256:CYS:SG	3:C:308:CYS:HB2	2.33	0.69
5:E:74:PHE:CD1	5:E:81:LEU:HD23	2.28	0.69
35:O:26:THR:OG1	35:O:159:ARG:NH2	2.26	0.69
1:A:338:VAL:CG2	3:C:867:PRO:CG	2.64	0.68
1:A:755:HIS:CE1	36:P:223:PHE:HB3	2.28	0.68
1:A:1076:ASP:O	1:A:1079:THR:OG1	2.11	0.68
13:F:37:C:H4'	13:F:38:G:OP2	1.91	0.68
22:2:487:LEU:O	22:2:490:HIS:N	2.26	0.68
1:A:299:ILE:CD1	3:C:921:LEU:CB	2.50	0.68
3:C:140:HIS:CD2	3:C:230:ASP:HB3	2.28	0.68
3:C:445:ALA:CB	3:C:466:SER:HA	2.20	0.68
3:C:725:ASP:OD1	3:C:728:ALA:N	2.25	0.68
23:3:452:LEU:HD11	23:3:762:LEU:HB2	1.74	0.68
37:R:434:TYR:HE2	37:R:436:VAL:HG22	1.57	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:HIS:NE2	1:A:81:PHE:CD1	2.59	0.68
1:A:203:VAL:CG2	1:A:237:THR:HG21	2.23	0.68
22:2:643:PRO:HD2	24:4:69:TYR:CG	2.27	0.68
36:P:72:ARG:NH1	36:P:72:ARG:HB2	2.08	0.68
37:R:106:GLN:CG	37:R:110:LYS:HE2	2.22	0.68
37:R:420:LYS:HG2	37:R:423:ASP:CG	2.13	0.68
44:Y:33:LYS:HA	44:Y:87:GLN:HE22	1.59	0.68
1:A:32:GLU:HG3	1:A:36:LYS:HE3	1.74	0.68
1:A:245:LEU:HA	1:A:430:TRP:CZ2	2.28	0.68
1:A:2267:PHE:HA	4:D:1261:PRO:CB	2.23	0.68
3:C:453:TYR:CZ	3:C:575:GLN:HB2	2.28	0.68
23:3:718:ARG:NH2	23:3:734:LEU:O	2.26	0.68
38:S:102:ASN:ND2	38:S:104:GLY:O	2.25	0.68
44:Y:86:ASP:HB2	45:Z:502:ALA:CB	2.23	0.68
1:A:44:ARG:HD2	1:A:45:TYR:CE2	2.28	0.68
1:A:121:HIS:HE2	1:A:481:PHE:HB3	1.51	0.68
1:A:171:ASP:OD2	1:A:519:ASP:OD2	2.12	0.68
3:C:482:TYR:CE2	3:C:493:PHE:CB	2.77	0.68
3:C:678:THR:HG21	3:C:683:ASN:ND2	2.06	0.68
14:G:-2:C:H2'	14:G:-1:G:C8	2.28	0.68
23:3:868:VAL:O	23:3:877:LEU:N	2.27	0.68
42:W:466:ALA:CB	42:W:512:CYS:O	2.41	0.68
1:A:296:PHE:CE1	3:C:591:ALA:HB3	2.27	0.68
1:A:384:VAL:HG11	3:C:331:PHE:CD2	2.28	0.68
5:E:108:HIS:CE1	5:E:128:SER:CB	2.77	0.68
15:H:147:G:O2'	15:H:148:C:H5'	1.94	0.68
29:L:216:PHE:CZ	35:O:112:VAL:HG12	2.29	0.68
35:O:137:LEU:HD12	35:O:140:ALA:HB3	1.76	0.68
36:P:63:LEU:O	36:P:63:LEU:HD23	1.94	0.68
37:R:414:ARG:NE	45:Z:598:PHE:CE1	2.47	0.68
42:W:212:GLU:C	42:W:214:LYS:H	1.97	0.68
1:A:91:ALA:O	1:A:93:LYS:N	2.27	0.68
1:A:380:LEU:C	3:C:354:ARG:HG2	2.14	0.68
1:A:779:LEU:CD2	36:P:223:PHE:HE2	2.06	0.68
1:A:1457:HIS:HE2	37:R:424:SER:HA	1.55	0.68
13:F:68:C:C5	36:P:33:ARG:HB3	2.20	0.68
37:R:88:ILE:CG2	37:R:96:ILE:CG2	2.71	0.68
1:A:299:ILE:HD11	3:C:921:LEU:HA	1.73	0.68
1:A:2146:VAL:HG22	1:A:2272:MET:HB2	1.74	0.68
2:B:32:C:OP1	36:P:33:ARG:CZ	2.41	0.68
3:C:79:THR:HG23	39:T:199:VAL:CG2	2.24	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:452:THR:HG22	3:C:577:PHE:CB	2.23	0.68
5:E:74:PHE:CD1	5:E:81:LEU:HD21	2.29	0.68
23:3:546:LYS:O	23:3:556:ILE:HA	1.94	0.68
37:R:92:SER:O	38:S:19:SER:O	2.11	0.68
45:Z:597:ARG:NH1	45:Z:601:LEU:CD1	2.57	0.68
1:A:228:TRP:O	1:A:416:GLY:N	2.26	0.68
1:A:758:ARG:HG3	1:A:779:LEU:HD11	1.75	0.68
1:A:1210:LYS:NZ	1:A:1369:TYR:OH	2.27	0.68
2:B:21:A:O3'	2:B:22:U:H4'	1.94	0.68
3:C:141:GLY:O	3:C:258:ASN:ND2	2.27	0.68
22:2:614:ARG:NH2	22:2:685:ASP:OD1	2.26	0.68
23:3:301:PHE:HB2	23:3:313:ILE:HB	1.76	0.68
27:7:48:ASP:O	27:7:51:ASN:N	2.27	0.68
28:J:360:ASP:O	28:J:363:ARG:HG3	1.93	0.68
44:Y:86:ASP:CA	45:Z:502:ALA:HB3	2.23	0.68
1:A:645:THR:HB	1:A:646:PRO:HD3	1.74	0.68
1:A:2300:ASN:OD1	4:D:1228:VAL:O	2.12	0.68
3:C:94:ILE:CD1	36:P:44:ARG:NH1	2.57	0.68
13:F:35:A:H5"	13:F:35:A:N3	2.09	0.68
15:H:159:U:O2'	15:H:160:A:H5'	1.94	0.68
23:3:374:SER:HB3	23:3:377:MET:HG3	1.76	0.68
23:3:753:GLY:HA3	23:3:765:LEU:O	1.93	0.68
28:J:353:GLU:OE2	28:J:361:ARG:NH2	2.27	0.68
38:S:11:PRO:HB3	38:S:165:SER:C	2.15	0.68
3:C:94:ILE:CD1	36:P:44:ARG:CZ	2.72	0.67
3:C:360:ALA:H	3:C:361:PRO:HD3	1.59	0.67
3:C:534:VAL:HG12	3:C:535:ALA:H	1.59	0.67
37:R:420:LYS:HB2	45:Z:610:LEU:CD1	2.22	0.67
41:V:547:VAL:O	41:V:550:MET:N	2.27	0.67
1:A:75:ASP:OD1	1:A:75:ASP:N	2.26	0.67
3:C:140:HIS:HB3	3:C:230:ASP:HB2	1.71	0.67
23:3:18:ILE:HD12	23:3:67:ALA:HB2	1.77	0.67
37:R:147:THR:CG2	39:T:360:VAL:HG12	2.23	0.67
1:A:122:ILE:CD1	1:A:483:GLN:HG3	2.24	0.67
1:A:2314:PHE:HD2	4:D:1123:TRP:CB	2.05	0.67
3:C:140:HIS:CD2	3:C:230:ASP:CB	2.77	0.67
3:C:737:PRO:HG3	3:C:774:THR:OG1	1.93	0.67
21:1:437:PRO:O	43:X:262:TYR:HA	1.94	0.67
1:A:89:LEU:HD22	1:A:656:LEU:HD22	1.76	0.67
1:A:255:PHE:HE1	1:A:432:ARG:O	1.75	0.67
1:A:1072:LEU:HD22	1:A:1087:LEU:HD22	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1661:TRP:CE2	1:A:1700:GLY:HA3	2.30	0.67
3:C:259:LYS:HE2	3:C:262:ARG:HD2	1.74	0.67
21:1:1097:LEU:O	21:1:1100:ASN:ND2	2.24	0.67
23:3:412:ILE:HG12	23:3:423:LEU:HG	1.76	0.67
34:N:40:LYS:C	34:N:41:ARG:HG3	2.13	0.67
35:O:131:THR:HG23	42:W:111:LEU:N	2.10	0.67
1:A:76:MET:HE2	1:A:88:TYR:CD2	2.26	0.67
1:A:380:LEU:CA	3:C:354:ARG:CG	2.72	0.67
1:A:1422:LEU:HD22	21:1:88:VAL:CB	2.25	0.67
3:C:389:ASP:OD1	3:C:389:ASP:N	2.26	0.67
5:E:66:GLU:HB2	5:E:87:ASP:OD2	1.94	0.67
21:1:474:TYR:OH	25:5:93:ASN:ND2	2.27	0.67
21:1:798:THR:HG22	21:1:800:GLY:H	1.60	0.67
37:R:119:LEU:CB	37:R:232:MET:HG3	2.24	0.67
37:R:285:ASN:OD1	37:R:286:GLU:N	2.27	0.67
39:T:185:MET:CB	39:T:186:PRO:HD3	2.24	0.67
1:A:76:MET:SD	1:A:88:TYR:CD1	2.88	0.67
1:A:298:ASP:O	1:A:302:ILE:HG12	1.95	0.67
1:A:1281:THR:HG22	1:A:1284:LEU:H	1.59	0.67
3:C:94:ILE:HD11	36:P:44:ARG:HH22	1.60	0.67
3:C:132:VAL:HG12	3:C:226:VAL:CG2	2.23	0.67
5:E:246:GLU:HB2	5:E:248:SER:OG	1.94	0.67
39:T:455:GLN:HG3	39:T:485:THR:HG21	1.76	0.67
1:A:229:GLN:HA	1:A:414:ARG:O	1.94	0.67
1:A:299:ILE:CB	1:A:1342:TRP:CZ3	2.66	0.67
1:A:1258:LYS:HE2	37:R:432:GLU:HA	1.77	0.67
1:A:1758:PRO:CB	21:1:938:TRP:CD1	2.77	0.67
3:C:736:GLY:CA	3:C:770:PHE:HE2	2.07	0.67
35:O:131:THR:HG23	42:W:111:LEU:HA	1.77	0.67
44:Y:62:ILE:HA	44:Y:84:TYR:HA	1.75	0.67
44:Y:100:ILE:O	44:Y:106:THR:HA	1.94	0.67
45:Z:597:ARG:NH1	45:Z:601:LEU:HD12	2.08	0.67
1:A:296:PHE:CG	3:C:656:ALA:CB	2.62	0.67
1:A:696:MET:C	1:A:698:PRO:HD3	2.15	0.67
3:C:572:GLU:HG3	3:C:573:GLU:H	1.60	0.67
15:H:151:C:C2	15:H:152:G:C8	2.83	0.67
37:R:81:LYS:HA	37:R:81:LYS:HZ1	1.59	0.67
37:R:119:LEU:HA	37:R:232:MET:SD	2.34	0.67
39:T:272:CYS:HB3	39:T:282:ARG:HG3	1.76	0.67
1:A:134:TRP:HB3	1:A:418:THR:CG2	2.25	0.67
1:A:380:LEU:N	3:C:354:ARG:HB3	2.09	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:40:U:C5'	2:B:41:U:OP2	2.43	0.67
3:C:452:THR:CB	3:C:577:PHE:CD2	2.73	0.67
5:E:243:LEU:HD12	5:E:247:GLY:HA2	1.76	0.67
14:G:10:U:O5'	14:G:10:U:H6	1.78	0.67
15:H:169:C:O2'	15:H:170:C:H5'	1.95	0.67
23:3:63:ARG:NH2	23:3:119:GLN:OE1	2.22	0.67
23:3:802:THR:HA	23:3:863:ALA:O	1.95	0.67
1:A:2306:HIS:CD2	1:A:2308:VAL:H	2.13	0.67
3:C:149:LEU:HD13	3:C:427:PHE:CE2	2.22	0.67
3:C:510:LEU:HD22	3:C:514:TYR:CD2	2.30	0.67
13:F:27:A:N3	35:O:181:TYR:CD2	2.62	0.67
15:H:153:A:C3'	15:H:154:C:H5'	2.25	0.67
21:1:1126:PHE:HA	21:1:1165:TYR:OH	1.94	0.67
37:R:92:SER:C	38:S:19:SER:CB	2.56	0.67
37:R:135:PRO:O	37:R:136:ASP:CG	2.33	0.67
42:W:420:ALA:N	42:W:438:ASP:CB	2.57	0.67
1:A:225:TYR:O	1:A:418:THR:OG1	2.11	0.66
1:A:1309:SER:O	1:A:1544:ARG:HD3	1.94	0.66
3:C:77:VAL:CG1	39:T:196:LEU:HB3	2.24	0.66
3:C:129:ILE:HG22	3:C:199:LEU:CB	2.23	0.66
23:3:470:PHE:HB3	23:3:747:SER:HA	1.75	0.66
23:3:1035:THR:HG21	23:3:1103:SER:HA	1.75	0.66
24:4:17:VAL:HG13	24:4:84:ILE:HG23	1.77	0.66
1:A:2328:ALA:CB	4:D:788:GLY:CA	2.74	0.66
3:C:230:ASP:OD1	3:C:259:LYS:CB	2.43	0.66
15:H:143:A:H2'	15:H:144:C:H6	1.59	0.66
15:H:151:C:O2	15:H:152:G:C8	2.48	0.66
38:S:34:LYS:CE	38:S:78:TYR:CE2	2.77	0.66
38:S:77:ILE:HG13	38:S:78:TYR:HD1	1.58	0.66
1:A:439:GLN:NE2	1:A:614:TYR:OH	2.27	0.66
1:A:676:ARG:NE	13:F:56:A:OP1	2.28	0.66
3:C:62:ASP:OD1	3:C:62:ASP:N	2.28	0.66
3:C:244:LYS:CB	3:C:292:TYR:CE2	2.79	0.66
15:H:151:C:H2'	15:H:152:G:H8	1.59	0.66
23:3:147:ASP:OD1	23:3:151:ARG:N	2.25	0.66
23:3:687:SER:HA	23:3:1206:LYS:HE3	1.76	0.66
23:3:947:GLU:HB3	23:3:963:VAL:HG22	1.75	0.66
1:A:532:THR:HG23	14:G:2:U:O5'	1.89	0.66
1:A:748:ASP:OD2	39:T:204:LEU:O	2.13	0.66
1:A:1386:TRP:HE1	1:A:1417:PRO:HD2	1.61	0.66
1:A:1457:HIS:CE1	1:A:1459:ARG:HB2	2.30	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:19:A:O2'	2:B:20:G:OP1	2.12	0.66
5:E:146:ARG:HH11	5:E:148:LYS:CE	1.83	0.66
15:H:73:C:H2'	15:H:74:U:C6	2.30	0.66
15:H:114:A:H61	15:H:142:C:H42	1.44	0.66
21:1:397:ARG:HD3	21:1:398:PRO:HD2	1.78	0.66
26:6:25:LYS:NZ	26:6:26:CYS:SG	2.68	0.66
1:A:254:TYR:OH	1:A:434:HIS:HB3	1.95	0.66
1:A:420:ARG:NH1	2:B:56:C:O2'	2.28	0.66
35:O:28:LEU:HD23	37:R:195:ARG:HE	1.61	0.66
1:A:532:THR:CB	14:G:2:U:O5'	2.42	0.66
3:C:473:PRO:O	3:C:474:LEU:HB3	1.96	0.66
3:C:474:LEU:HD23	3:C:474:LEU:C	2.16	0.66
15:H:47:U:H1'	15:H:48:A:H8	1.61	0.66
23:3:1017:ASN:OD1	23:3:1018:GLU:N	2.29	0.66
35:O:147:LEU:O	35:O:151:ALA:N	2.29	0.66
35:O:243:ILE:HG12	35:O:294:ASN:HD22	1.61	0.66
36:P:212:ASN:OD1	39:T:483:ASP:HA	1.96	0.66
39:T:314:ILE:HD12	39:T:324:HIS:HB2	1.75	0.66
44:Y:39:PHE:O	44:Y:109:VAL:HA	1.95	0.66
44:Y:98:ASN:OD1	44:Y:99:GLY:N	2.25	0.66
45:Z:525:TYR:HE1	45:Z:526:ILE:HG23	1.57	0.66
1:A:375:ASP:H	3:C:355:LYS:HZ2	1.44	0.66
1:A:377:GLU:O	1:A:378:PHE:CB	2.44	0.66
3:C:145:PHE:CE1	3:C:427:PHE:HE1	2.14	0.66
3:C:221:ILE:CG1	3:C:479:THR:OG1	2.43	0.66
39:T:342:GLU:HB3	39:T:343:PRO:CD	2.26	0.66
1:A:380:LEU:HB2	3:C:354:ARG:HG3	0.72	0.66
1:A:718:ARG:HH21	37:R:259:LYS:HE3	1.58	0.66
1:A:785:LYS:HE3	36:P:215:LEU:CD1	2.26	0.66
3:C:140:HIS:HA	3:C:259:LYS:NZ	2.10	0.66
5:E:116:HIS:O	5:E:124:LEU:HD12	1.95	0.66
5:E:281:VAL:HG22	42:W:148:VAL:HA	1.76	0.66
23:3:355:ASN:OD1	23:3:436:ARG:NH2	2.26	0.66
35:O:196:GLN:HE21	35:O:208:PRO:HG2	1.61	0.66
38:S:10:GLN:HB3	38:S:29:TRP:CD2	2.30	0.66
1:A:304:ILE:HD11	1:A:1342:TRP:CZ2	2.30	0.66
14:G:146:C:H41	21:1:1107:GLN:HG3	1.60	0.66
23:3:670:GLN:HA	23:3:698:PRO:HA	1.78	0.66
23:3:952:ILE:HG12	23:3:961:ILE:HG12	1.78	0.66
27:7:63:ARG:O	27:7:67:ASN:ND2	2.29	0.66
28:J:300:ASP:OD2	37:R:101:ILE:CG1	2.44	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:V:548:ALA:HB1	41:V:585:ILE:CB	2.25	0.66
1:A:406:TRP:HH2	3:C:265:LEU:O	1.79	0.66
1:A:755:HIS:HE1	36:P:223:PHE:HB3	1.61	0.66
1:A:829:PRO:O	1:A:882:LYS:NZ	2.27	0.66
1:A:1457:HIS:NE2	37:R:424:SER:CA	2.59	0.66
3:C:87:GLN:HE21	39:T:239:LYS:HD3	1.61	0.66
5:E:320:LEU:O	42:W:85:TYR:CB	2.44	0.66
23:3:330:PHE:O	23:3:394:ASN:ND2	2.29	0.66
34:N:28:LYS:HZ1	42:W:190:ASP:N	1.91	0.66
2:B:42:U:O4	14:G:-3:A:N1	2.29	0.65
3:C:77:VAL:HG12	39:T:197:TYR:CA	2.25	0.65
3:C:136:GLY:HA2	3:C:239:THR:HG22	1.77	0.65
5:E:178:LEU:HD11	5:E:222:LEU:CD2	2.26	0.65
37:R:124:VAL:HG13	37:R:125:MET:H	1.60	0.65
1:A:293:TRP:HZ3	1:A:295:GLU:OE1	1.76	0.65
1:A:651:TRP:CD1	13:F:66:C:H1'	2.31	0.65
1:A:1459:ARG:HE	37:R:423:ASP:CB	2.06	0.65
14:G:-12:G:H2'	14:G:-11:G:C8	2.30	0.65
39:T:439:TRP:CZ3	39:T:446:ASN:HB2	2.32	0.65
1:A:339:PHE:CD1	1:A:406:TRP:CE3	2.84	0.65
2:B:43:U:H3	14:G:-4:A:H2	1.37	0.65
2:B:43:U:O4	14:G:-4:A:N1	2.30	0.65
21:1:1171:PRO:O	21:1:1174:GLU:HB2	1.96	0.65
36:P:210:PHE:HB3	39:T:455:GLN:HE22	1.61	0.65
1:A:97:HIS:HD2	1:A:473:PHE:CZ	2.15	0.65
1:A:344:ASP:N	1:A:344:ASP:OD1	2.28	0.65
1:A:468:LYS:HD3	1:A:469:LYS:H	1.61	0.65
1:A:639:PHE:O	2:B:28:A:O2'	2.12	0.65
1:A:1356:GLY:O	40:U:15:THR:HG22	1.96	0.65
1:A:1459:ARG:CD	37:R:422:MET:O	2.45	0.65
2:B:63:A:H4'	5:E:106:LYS:NZ	2.12	0.65
21:1:713:ALA:HA	21:1:716:ALA:HB3	1.77	0.65
36:P:66:ARG:HH11	36:P:66:ARG:CB	2.09	0.65
1:A:301:LYS:HG2	3:C:940:ARG:N	2.12	0.65
3:C:457:VAL:HB	3:C:462:GLY:HA3	1.78	0.65
23:3:714:ALA:O	23:3:720:TRP:HB2	1.97	0.65
39:T:327:SER:O	39:T:357:TRP:HH2	1.79	0.65
3:C:700:ILE:HG21	3:C:741:GLY:O	1.97	0.65
14:G:137:C:H42	15:H:40:C:N4	1.95	0.65
21:1:584:ASP:OD1	21:1:585:GLU:N	2.29	0.65
22:2:487:LEU:HD12	27:7:28:LYS:HE3	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:2:511:LEU:HD23	22:2:593:GLU:HG3	1.79	0.65
35:O:31:ASN:OD1	35:O:33:TYR:N	2.27	0.65
39:T:459:LEU:HD12	39:T:460:ASP:H	1.61	0.65
5:E:108:HIS:CE1	5:E:128:SER:HB3	2.31	0.65
13:F:24:A:H2	13:F:26:U:N3	1.94	0.65
23:3:525:ARG:HG3	23:3:533:VAL:HG13	1.78	0.65
35:O:185:LYS:HG3	42:W:216:LEU:HA	1.79	0.65
1:A:155:LYS:NZ	1:A:624:GLY:O	2.29	0.65
1:A:318:TYR:HB2	3:C:638:ASP:CG	2.16	0.65
1:A:338:VAL:HG11	3:C:267:LEU:CD2	2.27	0.65
1:A:378:PHE:CD1	1:A:379:GLU:N	2.65	0.65
1:A:2314:PHE:CD2	4:D:1123:TRP:CB	2.80	0.65
3:C:572:GLU:HG3	3:C:573:GLU:N	2.12	0.65
23:3:866:ILE:HB	23:3:880:VAL:HB	1.79	0.65
32:I:296:PHE:CA	32:I:305:SER:CB	2.66	0.65
35:O:68:THR:HA	35:O:83:THR:HG22	1.77	0.65
38:S:9:TRP:HE3	38:S:11:PRO:CD	2.10	0.65
39:T:458:SER:OG	39:T:459:LEU:N	2.30	0.65
1:A:2319:LEU:HG	1:A:2320:LEU:N	2.11	0.65
23:3:687:SER:CB	23:3:1206:LYS:HE2	2.27	0.65
23:3:791:HIS:HE1	23:3:934:GLY:HA3	1.62	0.65
24:4:75:ASN:OD1	24:4:86:VAL:CB	2.45	0.65
34:N:28:LYS:NZ	42:W:190:ASP:H	1.95	0.65
2:B:44:A:C2	14:G:-5:G:N1	2.62	0.65
3:C:749:THR:O	3:C:753:GLU:N	2.27	0.65
13:F:33:G:OP2	13:F:33:G:H8	1.80	0.65
15:H:153:A:H3'	15:H:154:C:H5'	1.79	0.65
15:H:156:U:C6	15:H:156:U:C5'	2.72	0.65
21:1:1026:ASN:HD22	21:1:1031:VAL:HG11	1.60	0.65
35:O:253:TYR:OH	38:S:120:GLN:HG2	1.97	0.65
36:P:210:PHE:CE2	39:T:455:GLN:OE1	2.50	0.65
3:C:97:VAL:CG1	36:P:47:THR:OG1	2.45	0.64
3:C:463:GLU:OE1	3:C:463:GLU:N	2.29	0.64
3:C:488:VAL:HG13	3:C:609:LYS:NZ	2.12	0.64
5:E:277:PHE:HE2	5:E:300:ILE:HD13	1.61	0.64
21:1:912:ASN:OD1	21:1:957:ARG:NH1	2.30	0.64
37:R:171:LEU:CD1	37:R:201:GLU:OE1	2.44	0.64
2:B:19:A:H2'	2:B:20:G:H5"	1.78	0.64
3:C:72:VAL:CG2	39:T:453:ALA:HB1	2.26	0.64
14:G:11:A:N3	14:G:11:A:H3'	2.12	0.64
15:H:148:C:H2'	15:H:149:A:C8	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:458:ALA:HA	23:3:741:PHE:HB3	1.78	0.64
3:C:141:GLY:C	3:C:258:ASN:HD22	2.01	0.64
5:E:153:PHE:O	5:E:171:SER:HB2	1.97	0.64
23:3:429:ARG:HH12	27:7:58:ASN:HA	1.62	0.64
1:A:779:LEU:HD21	36:P:223:PHE:HE2	1.59	0.64
1:A:1051:LEU:CD2	36:P:193:VAL:HG11	2.27	0.64
3:C:256:CYS:SG	3:C:308:CYS:CB	2.86	0.64
4:D:455:PHE:CB	23:3:573:GLN:CD	2.66	0.64
23:3:206:GLN:HG3	23:3:228:LEU:HD12	1.78	0.64
37:R:88:ILE:H	37:R:88:ILE:HD12	1.61	0.64
44:Y:24:ASP:O	44:Y:27:SER:N	2.30	0.64
45:Z:594:GLU:O	45:Z:598:PHE:N	2.25	0.64
1:A:299:ILE:HB	1:A:1342:TRP:CZ3	2.33	0.64
1:A:976:MET:HG2	1:A:1187:PHE:HB3	1.78	0.64
1:A:1069:ASN:OD1	1:A:1075:GLN:NE2	2.31	0.64
2:B:40:U:H5'	2:B:41:U:OP2	1.97	0.64
3:C:97:VAL:HG22	36:P:45:GLN:HG3	1.77	0.64
3:C:482:TYR:HE2	3:C:493:PHE:CD2	2.14	0.64
23:3:687:SER:CB	23:3:1206:LYS:CE	2.76	0.64
1:A:176:LEU:HD13	1:A:181:ASN:ND2	2.12	0.64
15:H:68:G:H1	15:H:84:C:N4	1.95	0.64
35:O:223:LEU:O	35:O:223:LEU:HD22	1.98	0.64
35:O:225:PRO:HB2	35:O:226:PRO:HD2	1.80	0.64
37:R:419:SER:O	37:R:420:LYS:O	2.16	0.64
3:C:350:ASN:ND2	3:C:353:THR:HG23	2.13	0.64
3:C:705:VAL:HB	3:C:717:PHE:CZ	2.33	0.64
14:G:149:G:C2	14:G:150:U:H2'	2.32	0.64
21:1:847:ALA:O	21:1:851:SER:CB	2.46	0.64
37:R:433:ILE:HD12	37:R:435:ASN:ND2	2.12	0.64
38:S:10:GLN:OE1	38:S:10:GLN:N	2.31	0.64
1:A:380:LEU:CB	3:C:354:ARG:HH11	2.08	0.64
1:A:1342:TRP:CD2	3:C:921:LEU:CD2	2.80	0.64
3:C:824:THR:O	3:C:824:THR:CG2	2.45	0.64
13:F:38:G:H8	13:F:38:G:O5'	1.79	0.64
21:1:599:ASN:O	21:1:603:ALA:HB2	1.98	0.64
21:1:702:ARG:O	21:1:705:SER:OG	2.13	0.64
24:4:15:VAL:O	24:4:58:PHE:HA	1.97	0.64
29:L:224:PHE:HD1	37:R:86:LEU:HD12	1.54	0.64
1:A:175:PRO:HG2	1:A:498:ARG:CZ	2.27	0.64
1:A:481:PHE:CE2	37:R:205:ASP:CA	2.81	0.64
1:A:1134:TRP:O	1:A:1139:ARG:NH1	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1252:GLY:HA2	1:A:1298:ARG:NH2	2.13	0.64
3:C:363:SER:O	3:C:364:SER:OG	2.11	0.64
14:G:-9:C:C6	40:U:18:TYR:CE1	2.84	0.64
15:H:25:G:H2'	15:H:26:A:H8	1.62	0.64
23:3:635:ALA:HB3	23:3:669:LEU:HD23	1.79	0.64
28:J:294:HIS:CE1	29:L:227:THR:CB	2.80	0.64
42:W:264:ASN:O	42:W:267:SER:CB	2.46	0.64
1:A:1215:ASN:HB3	1:A:1224:ARG:HD2	1.79	0.64
1:A:1457:HIS:CE1	37:R:424:SER:CA	2.79	0.64
2:B:12:U:O2'	2:B:13:C:O5'	2.14	0.64
3:C:678:THR:HG21	3:C:683:ASN:HB2	1.76	0.64
14:G:155:U:H4'	14:G:156:U:H5'	1.79	0.64
35:O:223:LEU:HD13	35:O:223:LEU:C	2.15	0.64
35:O:276:THR:HG23	35:O:279:ALA:H	1.62	0.64
38:S:13:ASN:HD22	38:S:24:VAL:HG11	1.62	0.64
1:A:134:TRP:HB3	1:A:418:THR:HG21	1.79	0.63
1:A:1337:GLN:O	1:A:1352:HIS:HB2	1.98	0.63
3:C:482:TYR:CE2	3:C:493:PHE:CD2	2.86	0.63
1:A:461:HIS:CE1	2:B:23:C:C5	2.86	0.63
1:A:643:GLY:HA3	2:B:29:A:O4'	1.99	0.63
3:C:481:MET:SD	3:C:492:ALA:HB2	2.37	0.63
3:C:596:ASN:HD22	3:C:596:ASN:N	1.96	0.63
13:F:94:C:OP1	28:J:351:ASN:HB2	1.98	0.63
14:G:-9:C:C5	40:U:18:TYR:CD1	2.84	0.63
14:G:26:U:C1'	35:O:269:CYS:HB3	2.28	0.63
15:H:152:G:C2	15:H:153:A:C5	2.87	0.63
24:4:75:ASN:OD1	24:4:86:VAL:N	2.31	0.63
3:C:77:VAL:HG12	39:T:196:LEU:O	1.70	0.63
5:E:119:THR:HG23	5:E:161:ARG:HB3	1.80	0.63
13:F:35:A:H2'	13:F:36:A:C5'	2.28	0.63
23:3:187:MET:HE2	23:3:206:GLN:HB3	1.80	0.63
23:3:553:GLN:NE2	23:3:565:TYR:OH	2.31	0.63
23:3:931:VAL:N	23:3:936:LYS:O	2.29	0.63
25:5:20:ILE:HG12	25:5:63:VAL:HG22	1.78	0.63
1:A:755:HIS:CD2	36:P:219:PHE:HE2	2.15	0.63
13:F:27:A:OP1	34:N:41:ARG:NH2	2.30	0.63
13:F:58:G:H2'	13:F:59:G:C8	2.32	0.63
23:3:86:ARG:HA	23:3:105:GLU:O	1.98	0.63
23:3:174:ASP:OD2	23:3:240:GLY:N	2.31	0.63
23:3:489:GLU:HG2	23:3:748:GLU:HB3	1.80	0.63
35:O:78:LYS:O	35:O:97:ARG:NH2	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:W:463:SER:O	42:W:480:SER:HA	1.98	0.63
43:X:241:GLY:N	43:X:262:TYR:O	2.31	0.63
1:A:44:ARG:HD2	1:A:45:TYR:CZ	2.34	0.63
1:A:380:LEU:HB3	3:C:354:ARG:HH11	1.60	0.63
1:A:596:TYR:CE2	14:G:-5:G:N7	2.66	0.63
3:C:129:ILE:CG2	3:C:199:LEU:HB3	2.27	0.63
3:C:295:ASP:OD1	3:C:297:ASN:N	2.32	0.63
3:C:350:ASN:CG	3:C:353:THR:HG23	2.19	0.63
3:C:456:GLY:O	3:C:457:VAL:HG22	1.99	0.63
13:F:36:A:C5'	13:F:36:A:H8	2.12	0.63
37:R:132:LEU:HD23	37:R:132:LEU:H	1.63	0.63
4:D:1992:GLU:HA	4:D:1995:ALA:HB3	1.80	0.63
13:F:28:A:H1'	34:N:39:GLY:O	1.98	0.63
23:3:673:VAL:HA	23:3:691:THR:H	1.63	0.63
23:3:794:SER:OG	23:3:796:ASN:OD1	2.15	0.63
37:R:123:GLU:OE1	37:R:124:VAL:N	2.30	0.63
1:A:43:LYS:NZ	42:W:168:PHE:O	2.30	0.63
1:A:460:LYS:NZ	2:B:49:A:OP2	2.29	0.63
1:A:1260:VAL:HG21	1:A:1325:LEU:HB3	1.80	0.63
1:A:1309:SER:O	1:A:1544:ARG:CD	2.47	0.63
5:E:178:LEU:HD21	5:E:208:ILE:CD1	2.28	0.63
15:H:47:U:H1'	15:H:48:A:C8	2.34	0.63
21:1:812:PRO:HB2	21:1:813:PRO:HD3	1.81	0.63
25:5:23:ILE:HD12	25:5:89:VAL:HG12	1.81	0.63
35:O:115:GLU:HB3	37:R:218:ILE:HG21	1.80	0.63
1:A:319:LEU:N	3:C:638:ASP:OD1	2.31	0.63
1:A:693:ILE:HG13	1:A:738:MET:SD	2.38	0.63
1:A:1000:ILE:HG22	1:A:1001:VAL:HG13	1.81	0.63
3:C:93:ILE:CD1	39:T:230:ILE:HD13	2.29	0.63
3:C:476:CYS:CB	3:C:565:ILE:HB	2.27	0.63
21:1:698:GLN:O	21:1:702:ARG:NH1	2.32	0.63
23:3:399:ASP:OD1	23:3:400:GLU:N	2.32	0.63
37:R:67:ILE:HD13	37:R:67:ILE:N	2.13	0.63
1:A:109:PRO:HD3	1:A:630:TRP:CZ2	2.33	0.63
3:C:259:LYS:HE2	3:C:262:ARG:HD3	1.79	0.63
13:F:26:U:C3'	13:F:27:A:H5"	2.29	0.63
13:F:40:U:H2'	13:F:41:A:H8	1.61	0.63
37:R:418:GLN:O	45:Z:606:ALA:HB2	1.97	0.63
1:A:595:LYS:HA	2:B:44:A:O3'	1.98	0.62
1:A:768:ASP:HB2	1:A:771:VAL:HG12	1.79	0.62
3:C:250:ARG:NE	3:C:451:HIS:NE2	2.47	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:265:ARG:H	5:E:272:ARG:HH21	1.47	0.62
15:H:179:C:C2	15:H:180:G:N7	2.67	0.62
23:3:524:ILE:HD11	23:3:556:ILE:HD13	1.80	0.62
37:R:250:LYS:HD3	37:R:251:ILE:N	2.13	0.62
41:V:549:LYS:O	41:V:552:ALA:N	2.32	0.62
45:Z:566:TYR:HB2	45:Z:581:GLY:O	1.98	0.62
1:A:630:TRP:O	1:A:631:ALA:C	2.37	0.62
1:A:1085:ILE:HG12	1:A:1099:PHE:CE1	2.34	0.62
5:E:251:LEU:HG	5:E:291:CYS:SG	2.39	0.62
34:N:116:ASN:OD1	34:N:116:ASN:N	2.32	0.62
35:O:219:THR:O	35:O:221:PRO:HD3	1.99	0.62
1:A:365:VAL:CG1	1:A:366:LYS:H	2.13	0.62
1:A:375:ASP:N	3:C:355:LYS:HZ2	1.97	0.62
1:A:2068:SER:HB2	1:A:2072:GLU:HB2	1.82	0.62
3:C:79:THR:HG23	39:T:199:VAL:HB	0.68	0.62
21:1:1010:THR:OG1	21:1:1011:PRO:HD3	1.98	0.62
1:A:141:ILE:HG12	1:A:426:LEU:CD2	2.30	0.62
1:A:283:VAL:HG13	1:A:284:ARG:H	1.64	0.62
1:A:755:HIS:ND1	36:P:223:PHE:CD2	2.60	0.62
3:C:360:ALA:N	3:C:361:PRO:HD3	2.14	0.62
21:1:1257:PRO:HG3	22:2:482:ALA:HB2	1.81	0.62
45:Z:566:TYR:CD2	45:Z:584:TRP:CE3	2.88	0.62
1:A:121:HIS:CE1	1:A:481:PHE:CB	2.68	0.62
1:A:203:VAL:HG21	1:A:237:THR:HG22	1.81	0.62
1:A:1306:LYS:NZ	2:B:38:C:C2'	2.62	0.62
1:A:2105:ILE:HD13	1:A:2266:ARG:HH22	1.64	0.62
2:B:43:U:N3	14:G:-4:A:C2	2.60	0.62
3:C:132:VAL:HG11	3:C:434:CYS:SG	2.39	0.62
23:3:27:GLN:OE1	23:3:42:ARG:NH1	2.32	0.62
23:3:380:GLU:O	23:3:383:ASP:N	2.32	0.62
35:O:19:ASP:OD1	35:O:20:PHE:N	2.33	0.62
37:R:250:LYS:HA	37:R:250:LYS:HE3	1.81	0.62
39:T:185:MET:HB3	39:T:186:PRO:HD3	1.81	0.62
42:W:280:GLN:HA	42:W:577:LEU:O	2.00	0.62
1:A:97:HIS:CD2	1:A:473:PHE:CZ	2.87	0.62
1:A:305:ARG:HA	1:A:305:ARG:NH1	2.09	0.62
1:A:312:TYR:CD2	3:C:882:GLY:HA3	2.34	0.62
1:A:402:ILE:HG22	3:C:268:LYS:NZ	2.10	0.62
1:A:755:HIS:HE1	36:P:223:PHE:CG	2.11	0.62
3:C:259:LYS:HG2	3:C:262:ARG:HD2	1.81	0.62
15:H:182:U:H2'	15:H:183:G:C8	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:273:ARG:O	23:3:386:PHE:HA	2.00	0.62
1:A:253:ASN:CB	3:C:893:GLY:O	2.46	0.62
1:A:800:TYR:CG	3:C:59:LEU:HD13	2.34	0.62
1:A:1548:TYR:CG	14:G:-6:C:C6	2.87	0.62
5:E:119:THR:HG21	5:E:161:ARG:HB3	1.72	0.62
23:3:505:THR:HG21	23:3:508:CYS:SG	2.40	0.62
23:3:567:GLU:OE2	23:3:601:ARG:NE	2.29	0.62
36:P:211:VAL:HG13	39:T:457:GLY:HA3	0.75	0.62
39:T:356:LEU:N	39:T:356:LEU:HD12	2.15	0.62
1:A:282:LEU:C	1:A:282:LEU:HD23	2.20	0.62
5:E:146:ARG:CZ	5:E:148:LYS:HE3	2.27	0.62
21:1:847:ALA:O	21:1:851:SER:HB3	1.99	0.62
23:3:642:ILE:O	23:3:703:ARG:NH2	2.32	0.62
33:Q:500:GLY:N	37:R:51:ILE:HG13	2.14	0.62
45:Z:600:ARG:HH11	45:Z:600:ARG:CG	2.13	0.62
1:A:155:LYS:HD2	1:A:626:GLY:O	2.00	0.62
1:A:762:ARG:NH2	36:P:226:LYS:HZ1	1.79	0.62
1:A:2325:VAL:CG1	4:D:788:GLY:O	2.33	0.62
15:H:154:C:H2'	15:H:155:C:H6	1.63	0.62
15:H:161:U:H6	15:H:161:U:O5'	1.83	0.62
21:1:664:GLY:HA2	21:1:667:ILE:HD12	1.80	0.62
21:1:696:ASP:OD1	21:1:697:GLU:N	2.33	0.62
21:1:1052:ALA:HA	21:1:1055:TRP:HD1	1.64	0.62
22:2:612:GLU:O	22:2:615:ILE:N	2.33	0.62
23:3:521:PRO:HA	23:3:544:ILE:HG22	1.81	0.62
28:J:406:PHE:CE2	28:J:411:MET:CE	2.83	0.62
35:O:81:CYS:SG	52:O:501:ZN:ZN	1.88	0.62
38:S:9:TRP:CE3	38:S:11:PRO:CG	2.83	0.62
45:Z:573:PRO:HD2	45:Z:573:PRO:O	1.99	0.62
1:A:1217:GLN:NE2	41:V:592:GLU:O	2.32	0.62
1:A:2328:ALA:HB3	4:D:788:GLY:CA	2.30	0.62
3:C:230:ASP:OD1	3:C:259:LYS:HB3	2.00	0.62
35:O:185:LYS:HG3	42:W:215:GLU:C	2.21	0.62
1:A:338:VAL:HG11	3:C:267:LEU:HD21	1.81	0.61
1:A:835:ASP:OD1	1:A:836:THR:N	2.32	0.61
5:E:277:PHE:HE2	5:E:300:ILE:HD12	1.63	0.61
23:3:811:THR:OG1	23:3:884:GLN:OE1	2.14	0.61
23:3:1004:ASP:OD1	23:3:1005:VAL:N	2.33	0.61
36:P:194:PHE:O	36:P:196:ASN:N	4.26	0.61
3:C:141:GLY:C	3:C:258:ASN:ND2	2.53	0.61
13:F:24:A:C2	13:F:26:U:C2	2.88	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:G:13:C:H2'	14:G:14:A:C8	2.36	0.61
23:3:786:ARG:NH1	23:3:802:THR:O	2.33	0.61
28:J:262:ARG:HD3	29:L:220:PRO:HG2	1.82	0.61
38:S:131:ARG:HD3	38:S:132:VAL:C	2.09	0.61
45:Z:597:ARG:HH12	45:Z:601:LEU:HD12	1.66	0.61
1:A:344:ASP:OD1	1:A:347:LEU:CD1	2.49	0.61
1:A:783:TYR:HB2	36:P:228:ILE:CG1	2.26	0.61
1:A:2106:LEU:HD12	1:A:2107:PRO:HD2	1.83	0.61
13:F:38:G:P	13:F:38:G:C8	2.94	0.61
14:G:26:U:H5"	35:O:235:TYR:OH	2.00	0.61
21:1:866:LYS:HG3	21:1:909:VAL:HG11	1.82	0.61
23:3:317:THR:HA	23:3:322:VAL:HA	1.81	0.61
1:A:588:LEU:O	1:A:1551:PHE:HE1	1.78	0.61
1:A:1754:TYR:CD1	21:1:941:ASN:OD1	2.53	0.61
1:A:1754:TYR:HD1	21:1:941:ASN:OD1	1.82	0.61
14:G:146:C:H1'	15:H:33:G:N2	2.15	0.61
15:H:165:A:H8	15:H:165:A:O5'	1.84	0.61
37:R:55:LEU:O	37:R:73:PRO:O	2.19	0.61
37:R:92:SER:N	38:S:19:SER:HB2	2.15	0.61
45:Z:566:TYR:CD1	45:Z:567:SER:N	2.69	0.61
1:A:203:VAL:CG2	1:A:237:THR:HB	2.30	0.61
1:A:305:ARG:HG3	3:C:879:ASP:OD1	1.99	0.61
1:A:344:ASP:OD1	1:A:347:LEU:HD12	2.00	0.61
3:C:679:PRO:HD3	3:C:811:THR:OG1	1.99	0.61
3:C:750:LEU:C	3:C:750:LEU:HD12	2.21	0.61
15:H:56:A:H61	22:2:505:CYS:HA	1.66	0.61
15:H:68:G:H2'	15:H:69:U:C6	2.35	0.61
21:1:648:LEU:O	21:1:651:VAL:N	2.33	0.61
23:3:288:VAL:HG23	23:3:289:CYS:H	1.65	0.61
23:3:994:GLN:NE2	23:3:1036:ALA:O	2.33	0.61
39:T:327:SER:O	39:T:357:TRP:CH2	2.53	0.61
1:A:299:ILE:CD1	3:C:920:PRO:O	2.48	0.61
1:A:1755:SER:OG	21:1:938:TRP:CZ2	2.50	0.61
3:C:64:LYS:HZ2	36:P:206:LYS:HG3	1.63	0.61
3:C:97:VAL:HG13	36:P:47:THR:OG1	2.00	0.61
3:C:140:HIS:CG	3:C:230:ASP:H	2.18	0.61
3:C:809:ILE:HB	3:C:810:PRO:HD3	1.82	0.61
23:3:1191:LYS:NZ	23:3:1195:GLU:OE2	2.33	0.61
34:N:28:LYS:NZ	42:W:190:ASP:CA	2.64	0.61
41:V:537:HIS:HA	41:V:578:SER:CB	2.31	0.61
1:A:299:ILE:HD11	3:C:921:LEU:N	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:623:LYS:HD3	48:A:2401:IHP:O43	2.01	0.61
3:C:471:ASP:N	3:C:499:GLY:HA2	2.15	0.61
3:C:495:ARG:HD2	3:C:497:LEU:HD23	1.81	0.61
21:1:720:GLY:N	23:3:216:GLY:O	2.29	0.61
32:I:361:HIS:O	32:I:372:ARG:CB	2.48	0.61
35:O:283:ALA:O	35:O:287:SER:OG	2.18	0.61
37:R:185:GLY:O	37:R:186:VAL:HG22	2.00	0.61
39:T:339:GLN:NE2	39:T:342:GLU:O	2.34	0.61
39:T:355:ARG:C	39:T:356:LEU:HD12	2.21	0.61
42:W:290:GLY:CA	42:W:571:TRP:O	2.49	0.61
1:A:260:LEU:CD2	1:A:455:VAL:HG22	2.30	0.61
1:A:461:HIS:NE2	2:B:23:C:C6	2.69	0.61
1:A:593:ARG:CZ	1:A:1565:LYS:HE2	2.26	0.61
1:A:1286:ASP:OD1	1:A:1354:ARG:NH2	2.33	0.61
1:A:1548:TYR:CD1	14:G:-6:C:C5	2.89	0.61
3:C:151:GLU:OE1	3:C:417:ARG:NH1	2.34	0.61
3:C:470:PRO:HA	3:C:499:GLY:CA	2.29	0.61
3:C:675:PHE:HD1	3:C:675:PHE:H	1.47	0.61
14:G:8:C:H2'	14:G:9:C:C6	2.35	0.61
15:H:106:G:N2	15:H:107:A:C6	2.67	0.61
15:H:142:C:C2'	15:H:143:A:H5'	2.30	0.61
15:H:157:G:H5"	15:H:157:G:H8	1.65	0.61
28:J:408:ASP:OD1	28:J:442:ARG:HG2	2.01	0.61
3:C:478:THR:OG1	3:C:563:ALA:O	2.14	0.61
3:C:705:VAL:HG22	3:C:705:VAL:O	2.00	0.61
15:H:153:A:N6	15:H:177:A:H2	1.98	0.61
23:3:740:GLU:HB2	23:3:757:ILE:HD12	1.83	0.61
29:L:74:LEU:HD23	29:L:77:LEU:HD12	1.83	0.61
35:O:196:GLN:NE2	35:O:209:VAL:HG23	2.14	0.61
44:Y:87:GLN:O	44:Y:90:THR:N	2.33	0.61
1:A:73:HIS:CD2	1:A:81:PHE:CG	2.89	0.61
1:A:73:HIS:CD2	1:A:81:PHE:CD1	2.88	0.61
1:A:256:TYR:CE1	3:C:888:ARG:CZ	2.83	0.61
1:A:1481:VAL:HG12	1:A:1485:LEU:CD1	2.31	0.61
5:E:108:HIS:CE1	5:E:128:SER:HB2	2.35	0.61
13:F:6:C:OP2	13:F:6:C:H4'	1.99	0.61
21:1:1203:GLY:O	23:3:1171:LYS:NZ	2.34	0.61
23:3:226:GLU:HG3	23:3:261:PHE:HZ	1.65	0.61
23:3:452:LEU:HB3	23:3:478:PHE:HE1	1.66	0.61
24:4:71:ILE:HD11	24:4:88:LYS:HB3	1.83	0.61
37:R:92:SER:O	38:S:19:SER:CB	2.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:R:92:SER:O	38:S:19:SER:C	2.39	0.61
39:T:349:SER:OG	39:T:351:ASP:OD1	2.18	0.61
1:A:296:PHE:CD2	3:C:656:ALA:HB2	2.30	0.60
1:A:1405:LEU:HA	37:R:415:LEU:HD21	1.78	0.60
3:C:133:THR:O	3:C:226:VAL:HB	2.01	0.60
3:C:135:CYS:O	3:C:228:PHE:N	2.28	0.60
3:C:449:ILE:HD11	3:C:466:SER:CA	2.31	0.60
3:C:710:ASN:O	3:C:713:LYS:N	2.31	0.60
13:F:27:A:C1'	35:O:181:TYR:HE2	2.11	0.60
15:H:143:A:H2'	15:H:144:C:C6	2.35	0.60
21:1:1293:ASN:HB3	27:7:76:CYS:HB3	1.83	0.60
28:J:406:PHE:CG	28:J:411:MET:HE3	2.36	0.60
35:O:235:TYR:CD2	35:O:301:LYS:HB2	2.33	0.60
45:Z:524:ARG:NE	45:Z:524:ARG:O	2.34	0.60
1:A:800:TYR:CD2	3:C:59:LEU:HD13	2.36	0.60
1:A:1457:HIS:CE1	1:A:1459:ARG:CB	2.83	0.60
21:1:918:VAL:HG12	21:1:961:VAL:HG21	1.83	0.60
28:J:338:GLU:O	37:R:116:TYR:CD1	2.54	0.60
45:Z:491:ASP:O	45:Z:495:ALA:CB	2.48	0.60
1:A:151:MET:SD	1:A:628:GLY:C	2.80	0.60
1:A:158:ARG:HH12	1:A:573:GLN:HE21	1.48	0.60
1:A:1310:ARG:HH22	1:A:1564:GLY:HA3	1.64	0.60
1:A:2073:TRP:CZ3	1:A:2310:ARG:HG2	2.36	0.60
28:J:291:GLN:OE1	29:L:230:GLU:HG3	2.01	0.60
39:T:339:GLN:HG2	39:T:340:ALA:N	2.16	0.60
45:Z:491:ASP:O	45:Z:495:ALA:HB2	2.01	0.60
1:A:82:ARG:HB3	1:A:83:HIS:ND1	2.17	0.60
1:A:532:THR:CG2	14:G:2:U:H5"	2.27	0.60
14:G:13:C:H2'	14:G:14:A:H8	1.66	0.60
24:4:31:GLU:O	24:4:35:GLN:HG2	2.02	0.60
39:T:292:TYR:CE2	39:T:308:ARG:HG3	2.36	0.60
1:A:48:LYS:O	1:A:53:PHE:CG	2.54	0.60
1:A:339:PHE:CE1	1:A:406:TRP:HE3	2.12	0.60
5:E:178:LEU:HD21	5:E:208:ILE:HD13	1.82	0.60
5:E:266:PRO:HG3	29:L:785:GLN:NE2	2.16	0.60
23:3:673:VAL:HG12	23:3:690:ARG:HA	1.84	0.60
23:3:833:GLU:HA	23:3:834:LEU:HB2	1.84	0.60
29:L:233:GLN:OE1	29:L:233:GLN:HA	2.01	0.60
37:R:171:LEU:CD1	37:R:201:GLU:CD	2.70	0.60
42:W:531:LYS:CB	42:W:546:PHE:O	2.50	0.60
1:A:623:LYS:CD	48:A:2401:IHP:O43	2.49	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1447:VAL:HG11	1:A:1449:LYS:HE2	1.82	0.60
1:A:1548:TYR:HD2	14:G:-6:C:O2'	1.85	0.60
1:A:2298:LEU:CD1	4:D:1265:GLN:CB	2.79	0.60
3:C:86:THR:HG22	39:T:238:LEU:O	2.01	0.60
3:C:452:THR:HG22	3:C:577:PHE:CG	2.37	0.60
3:C:706:GLN:NE2	3:C:708:THR:OG1	2.35	0.60
5:E:267:PHE:HE1	31:K:194:GLU:HB3	1.63	0.60
1:A:924:GLN:HE22	1:A:1439:ARG:CZ	2.14	0.60
3:C:221:ILE:HD11	3:C:479:THR:HG1	1.65	0.60
23:3:613:THR:HG22	23:3:632:ALA:HA	1.84	0.60
23:3:898:ASN:OD1	23:3:899:THR:N	2.34	0.60
41:V:483:GLU:O	41:V:486:THR:CB	2.49	0.60
1:A:705:LYS:HE2	37:R:251:ILE:HB	1.82	0.60
1:A:960:ASN:ND2	1:A:1225:THR:OG1	2.32	0.60
3:C:77:VAL:HG21	39:T:196:LEU:HD23	1.83	0.60
3:C:148:CYS:HA	3:C:417:ARG:NH2	2.16	0.60
23:3:325:ILE:O	23:3:375:SER:N	2.35	0.60
39:T:267:ASP:O	39:T:268:LYS:CB	2.47	0.60
39:T:455:GLN:HG2	39:T:456:PRO:HD3	1.83	0.60
2:B:42:U:C4'	13:F:70:A:C4'	2.80	0.60
3:C:140:HIS:HA	3:C:230:ASP:HB2	1.83	0.60
3:C:567:GLU:OE2	3:C:570:GLY:HA3	2.02	0.60
13:F:7:G:H5'	13:F:7:G:H8	1.66	0.60
13:F:37:C:H41	14:G:5:G:P	2.24	0.60
15:H:83:A:C2	15:H:84:C:C2	2.90	0.60
29:L:77:LEU:HD22	37:R:289:ALA:HA	1.84	0.60
35:O:132:ARG:HG3	35:O:137:LEU:HD23	1.84	0.60
39:T:342:GLU:HB3	39:T:343:PRO:HD3	1.83	0.60
45:Z:563:ARG:HH21	45:Z:563:ARG:CG	2.14	0.60
1:A:1384:ARG:HH21	1:A:1414:ARG:HH12	1.50	0.60
1:A:1426:ASP:OD2	37:R:421:GLY:HA3	2.01	0.60
3:C:79:THR:CG2	39:T:199:VAL:CB	2.37	0.60
3:C:82:GLN:HB2	39:T:231:TRP:CZ3	2.36	0.60
3:C:94:ILE:CD1	36:P:44:ARG:NH2	2.65	0.60
3:C:443:VAL:O	3:C:447:PRO:HD3	2.02	0.60
3:C:678:THR:CG2	3:C:683:ASN:CB	2.79	0.60
14:G:26:U:C5'	35:O:235:TYR:OH	2.50	0.60
21:1:862:GLU:OE1	21:1:904:THR:OG1	2.19	0.60
33:Q:500:GLY:N	37:R:51:ILE:CG1	2.65	0.60
33:Q:500:GLY:CA	37:R:51:ILE:HD11	2.32	0.60
37:R:106:GLN:HG2	37:R:110:LYS:CE	2.28	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:T:185:MET:SD	39:T:442:ARG:NH1	2.71	0.60
1:A:122:ILE:HD13	1:A:483:GLN:CG	2.32	0.59
1:A:306:GLN:HG3	3:C:853:ARG:HG2	1.83	0.59
1:A:372:PRO:CG	3:C:342:ARG:NE	2.62	0.59
23:3:772:ALA:O	23:3:774:PHE:N	2.35	0.59
23:3:968:ARG:HD3	23:3:979:ARG:HD3	1.84	0.59
3:C:73:TYR:CD2	39:T:199:VAL:HG21	2.36	0.59
3:C:73:TYR:CZ	39:T:487:LYS:HE3	2.37	0.59
3:C:669:THR:HG22	3:C:690:GLU:HB3	1.84	0.59
23:3:687:SER:HB3	23:3:1206:LYS:HE2	1.83	0.59
28:J:406:PHE:CE2	28:J:411:MET:HE3	2.36	0.59
29:L:216:PHE:CE1	35:O:112:VAL:O	2.52	0.59
36:P:72:ARG:HB2	36:P:72:ARG:HH11	1.66	0.59
39:T:455:GLN:HG2	39:T:456:PRO:CD	2.32	0.59
1:A:122:ILE:N	1:A:481:PHE:O	2.34	0.59
1:A:532:THR:HG23	14:G:2:U:OP1	2.01	0.59
1:A:718:ARG:HE	37:R:259:LYS:HE3	1.67	0.59
3:C:186:VAL:HG22	3:C:535:ALA:HA	1.85	0.59
23:3:883:GLU:HG3	23:3:884:GLN:H	1.66	0.59
35:O:133:PRO:HD2	35:O:137:LEU:HD22	1.84	0.59
37:R:104:GLN:NE2	37:R:105:GLY:N	2.50	0.59
45:Z:574:ASN:O	45:Z:575:ARG:C	2.40	0.59
1:A:181:ASN:N	1:A:181:ASN:OD1	2.35	0.59
2:B:43:U:C4	14:G:-4:A:N1	2.71	0.59
5:E:233:GLY:O	5:E:260:ARG:NH2	2.35	0.59
13:F:27:A:C1’	35:O:181:TYR:CE2	2.86	0.59
14:G:22:C:O2’	14:G:23:U:P	2.60	0.59
28:J:493:ALA:HB1	28:J:499:ARG:CB	2.32	0.59
34:N:117:CYS:SG	34:N:119:CYS:HB3	2.42	0.59
37:R:124:VAL:HG22	37:R:125:MET:N	2.16	0.59
37:R:420:LYS:HA	37:R:420:LYS:CE	2.12	0.59
1:A:86:ARG:HG3	1:A:87:VAL:N	2.17	0.59
1:A:944:ASP:OD2	1:A:1435:GLY:N	2.34	0.59
1:A:1262:LYS:CG	37:R:431:ASP:CB	2.69	0.59
1:A:1405:LEU:HA	37:R:415:LEU:HD22	1.84	0.59
3:C:298:LEU:HD13	3:C:298:LEU:N	2.18	0.59
15:H:56:A:H2’	15:H:57:A:C8	2.38	0.59
23:3:895:ARG:NH2	23:3:901:GLU:OE1	2.34	0.59
23:3:1040:ASP:OD1	23:3:1043:THR:N	2.35	0.59
29:L:209:ASP:OD1	35:O:111:ASP:CB	2.51	0.59
1:A:661:GLU:CD	37:R:214:ILE:HD11	2.22	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:692:ASP:O	1:A:696:MET:CB	2.50	0.59
1:A:942:PRO:HB2	1:A:1438:VAL:HG12	1.84	0.59
1:A:1076:ASP:OD1	1:A:1077:ILE:N	2.35	0.59
1:A:1363:GLN:HG2	1:A:1364:LEU:H	1.66	0.59
3:C:66:TYR:HE2	36:P:211:VAL:HG11	1.67	0.59
3:C:91:GLU:OE1	3:C:91:GLU:HA	2.01	0.59
3:C:145:PHE:CB	3:C:312:SER:CB	2.65	0.59
13:F:36:A:C5'	13:F:36:A:C8	2.85	0.59
15:H:112:G:H2'	15:H:113:G:H8	1.65	0.59
21:1:936:VAL:O	21:1:940:LEU:HB2	2.03	0.59
21:1:1125:PRO:HA	21:1:1128:VAL:HG22	1.84	0.59
35:O:132:ARG:HH11	38:S:149:SER:CB	2.00	0.59
35:O:155:PRO:HD3	37:R:188:PHE:CD1	2.38	0.59
39:T:345:ILE:HB	39:T:357:TRP:HB2	1.85	0.59
41:V:514:PHE:O	41:V:521:TYR:CB	2.51	0.59
1:A:338:VAL:HG21	3:C:867:PRO:CD	2.33	0.59
1:A:387:PHE:HE2	3:C:399:LEU:HD23	1.63	0.59
1:A:569:VAL:O	1:A:570:ASP:CB	2.50	0.59
1:A:1405:LEU:CB	37:R:415:LEU:HD22	2.33	0.59
1:A:1758:PRO:CB	21:1:938:TRP:HD1	2.16	0.59
3:C:149:LEU:CD1	3:C:427:PHE:CB	2.80	0.59
23:3:224:TYR:HB3	23:3:261:PHE:HE2	1.66	0.59
23:3:461:THR:HA	23:3:473:TYR:O	2.03	0.59
23:3:1015:LYS:HE2	23:3:1065:GLU:HG2	1.85	0.59
28:J:225:LEU:CD2	29:L:211:ASN:HB2	2.20	0.59
37:R:90:VAL:CG1	37:R:94:GLY:O	2.50	0.59
37:R:110:LYS:HD2	37:R:110:LYS:C	2.23	0.59
38:S:10:GLN:HA	38:S:29:TRP:CH2	2.38	0.59
42:W:290:GLY:HA3	42:W:571:TRP:HA	1.84	0.59
44:Y:88:ARG:HH11	45:Z:576:PHE:HB3	1.68	0.59
1:A:44:ARG:CG	1:A:45:TYR:CD2	2.85	0.59
1:A:305:ARG:HH21	3:C:854:ARG:HD3	1.68	0.59
1:A:888:GLN:NE2	1:A:890:ALA:O	2.19	0.59
3:C:227:LEU:O	3:C:255:VAL:HA	2.03	0.59
23:3:457:ASN:ND2	23:3:478:PHE:O	2.35	0.59
23:3:784:THR:HB	23:3:786:ARG:HH12	1.67	0.59
23:3:1027:ASP:OD1	23:3:1028:THR:N	2.35	0.59
26:6:56:GLY:O	26:6:65:GLY:N	2.21	0.59
35:O:233:THR:HA	35:O:272:ILE:O	2.03	0.59
37:R:420:LYS:HG2	37:R:423:ASP:OD1	2.02	0.59
37:R:421:GLY:O	37:R:423:ASP:N	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:S:71:GLY:O	42:W:93:PHE:N	2.31	0.59
1:A:43:LYS:HD3	42:W:168:PHE:CB	2.32	0.59
3:C:137:HIS:CD2	3:C:236:MET:HB3	2.35	0.59
3:C:497:LEU:HD11	3:C:577:PHE:CZ	2.32	0.59
5:E:321:TYR:CD1	42:W:84:THR:HA	2.38	0.59
21:1:1223:SER:HB2	21:1:1226:VAL:HG12	1.83	0.59
23:3:638:GLU:H	23:3:669:LEU:HA	1.68	0.59
1:A:232:LEU:HD13	1:A:401:GLY:HA2	1.85	0.59
1:A:1310:ARG:NH2	1:A:1563:HIS:O	2.32	0.59
2:B:44:A:H2	14:G:-5:G:H1	1.48	0.59
3:C:145:PHE:CE1	3:C:427:PHE:CE1	2.91	0.59
3:C:465:MET:CE	3:C:475:MET:CG	2.70	0.59
3:C:736:GLY:HA2	3:C:770:PHE:CE2	2.38	0.59
13:F:45:A:H1'	13:F:73:A:C2	2.38	0.59
21:1:522:LYS:HD3	21:1:526:PHE:CZ	2.38	0.59
23:3:22:PHE:HD2	23:3:29:GLU:HB2	1.68	0.59
23:3:753:GLY:CA	23:3:765:LEU:O	2.51	0.59
28:J:259:GLN:HE22	29:L:220:PRO:CG	2.15	0.59
34:N:28:LYS:HZ3	42:W:190:ASP:CA	2.08	0.59
37:R:125:MET:CE	37:R:131:ASP:OD1	2.51	0.59
37:R:148:ARG:HG3	37:R:148:ARG:HH11	1.68	0.59
38:S:77:ILE:HG13	38:S:78:TYR:CD1	2.38	0.59
1:A:44:ARG:HG3	1:A:45:TYR:CD2	2.37	0.58
1:A:723:ASN:HB2	1:A:785:LYS:HG2	1.83	0.58
3:C:69:ALA:CA	39:T:456:PRO:HG3	2.28	0.58
3:C:359:LYS:HE3	3:C:359:LYS:O	2.02	0.58
13:F:35:A:O2'	13:F:36:A:OP1	2.21	0.58
21:1:1278:ASP:OD2	23:3:112:CYS:N	2.36	0.58
22:2:648:LEU:HD11	22:2:650:ILE:HG13	1.85	0.58
23:3:336:ALA:HA	23:3:351:SER:HA	1.85	0.58
28:J:339:TRP:CG	37:R:116:TYR:HD2	2.21	0.58
39:T:185:MET:SD	39:T:442:ARG:NH2	2.75	0.58
44:Y:52:ILE:HA	44:Y:55:VAL:HG22	1.84	0.58
1:A:76:MET:SD	1:A:88:TYR:CD2	2.95	0.58
1:A:695:ASP:CG	39:T:374:SER:OG	2.41	0.58
1:A:1352:HIS:CD2	40:U:5:ILE:CD1	2.86	0.58
1:A:1354:ARG:HH11	40:U:7:LEU:HG	1.68	0.58
1:A:2325:VAL:O	4:D:788:GLY:HA2	2.03	0.58
2:B:42:U:C4	14:G:-3:A:N1	2.71	0.58
3:C:78:GLU:CD	39:T:198:ARG:HE	2.07	0.58
3:C:474:LEU:HD11	3:C:501:ILE:HG12	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:982:LEU:HD11	21:1:997:LEU:HD11	1.83	0.58
21:1:1147:VAL:O	21:1:1150:SER:OG	2.17	0.58
23:3:417:ASN:OD1	23:3:418:GLU:N	2.36	0.58
23:3:797:LEU:HG	23:3:871:PRO:HG3	1.85	0.58
23:3:903:TRP:HB3	23:3:930:LEU:HD23	1.84	0.58
35:O:84:CYS:O	35:O:85:LEU:HB2	2.03	0.58
37:R:433:ILE:CD1	37:R:435:ASN:ND2	2.67	0.58
44:Y:86:ASP:CB	45:Z:502:ALA:HB3	2.33	0.58
1:A:32:GLU:OE2	1:A:36:LYS:HE3	2.03	0.58
1:A:229:GLN:HA	1:A:415:SER:HA	1.85	0.58
3:C:133:THR:O	3:C:226:VAL:CA	2.51	0.58
5:E:87:ASP:O	5:E:88:ARG:HG3	2.04	0.58
21:1:773:LEU:HD21	21:1:792:VAL:HG22	1.84	0.58
23:3:304:GLN:NE2	23:3:335:VAL:HA	2.18	0.58
36:P:210:PHE:HD2	39:T:455:GLN:CD	2.05	0.58
37:R:233:HIS:CD2	37:R:233:HIS:H	2.22	0.58
42:W:97:ASN:C	42:W:99:PHE:H	2.06	0.58
1:A:1180:LYS:HA	1:A:1201:ARG:NH1	2.18	0.58
3:C:679:PRO:HD2	3:C:807:GLN:CB	2.10	0.58
23:3:442:LEU:HD13	23:3:734:LEU:CD2	2.33	0.58
28:J:338:GLU:O	37:R:116:TYR:CG	2.57	0.58
35:O:245:GLU:O	35:O:248:LEU:N	2.37	0.58
1:A:299:ILE:CD1	1:A:1346:THR:HG21	2.32	0.58
1:A:1367:ASN:OD1	1:A:1368:LEU:N	2.37	0.58
1:A:1481:VAL:HG12	1:A:1485:LEU:HD12	1.85	0.58
3:C:750:LEU:O	3:C:750:LEU:HD12	2.03	0.58
5:E:263:ASP:HB3	5:E:274:VAL:HG21	1.84	0.58
23:3:587:VAL:HG11	23:3:590:MET:HG3	1.85	0.58
45:Z:566:TYR:CD2	45:Z:584:TRP:HE3	2.20	0.58
5:E:87:ASP:O	5:E:88:ARG:CB	2.51	0.58
23:3:224:TYR:HB3	23:3:261:PHE:CE2	2.39	0.58
24:4:18:GLY:H	24:4:85:ARG:HB2	1.67	0.58
36:P:35:LEU:HB3	36:P:36:PRO:HD2	1.86	0.58
41:V:497:CYS:CB	41:V:507:PHE:CB	2.81	0.58
1:A:388:LEU:HD13	3:C:379:LYS:HB3	1.85	0.58
1:A:798:GLY:HA2	37:R:288:PHE:CE2	2.39	0.58
1:A:2095:ASP:OD2	1:A:2258:ARG:NE	2.36	0.58
3:C:509:VAL:O	3:C:510:LEU:HD23	2.04	0.58
15:H:147:G:H2'	15:H:148:C:C6	2.38	0.58
1:A:121:HIS:ND1	1:A:481:PHE:O	2.36	0.58
1:A:152:ARG:HH11	1:A:152:ARG:CG	2.16	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:264:PHE:CE1	1:A:455:VAL:CG1	2.75	0.58
1:A:535:ARG:CZ	1:A:535:ARG:HB3	2.33	0.58
3:C:140:HIS:NE2	3:C:233:GLU:CG	2.66	0.58
15:H:80:A:C2	15:H:81:G:C5	2.92	0.58
25:5:24:ARG:HG2	25:5:59:THR:HG22	1.86	0.58
36:P:188:TRP:C	36:P:190:ASP:N	2.52	0.58
41:V:609:GLN:O	41:V:612:PHE:N	2.36	0.58
1:A:2073:TRP:HD1	1:A:2074:ARG:HD2	1.67	0.58
1:A:2310:ARG:NH1	1:A:2314:PHE:HE1	2.02	0.58
3:C:140:HIS:NE2	3:C:233:GLU:CB	2.67	0.58
14:G:141:C:H2'	14:G:142:U:H6	1.69	0.58
21:1:415:LEU:O	25:5:36:TYR:OH	2.21	0.58
21:1:1109:ARG:NH2	21:1:1142:ASN:HB2	2.19	0.58
21:1:1165:TYR:HE1	22:2:575:PHE:CD1	2.21	0.58
23:3:878:ASP:OD1	23:3:879:LEU:N	2.37	0.58
37:R:124:VAL:HG22	37:R:126:ASN:H	1.68	0.58
45:Z:566:TYR:HE2	45:Z:584:TRP:CZ3	1.92	0.58
1:A:249:LEU:HD22	1:A:254:TYR:HB2	1.86	0.58
1:A:280:GLU:OE2	1:A:281:PRO:HD2	2.03	0.58
1:A:2073:TRP:CD1	1:A:2074:ARG:N	2.72	0.58
3:C:573:GLU:N	3:C:573:GLU:OE1	2.37	0.58
14:G:18:A:C5'	35:O:69:GLU:OE1	2.46	0.58
37:R:125:MET:HE3	37:R:131:ASP:OD1	2.03	0.58
37:R:171:LEU:HD23	37:R:171:LEU:O	2.03	0.58
1:A:232:LEU:HD22	1:A:404:LEU:HD12	1.86	0.57
2:B:44:A:H2	14:G:-5:G:N1	2.02	0.57
3:C:145:PHE:CD1	3:C:312:SER:HB3	2.39	0.57
5:E:165:GLN:HG3	5:E:181:ILE:HD11	1.85	0.57
37:R:189:ASN:HD21	37:R:195:ARG:HH22	1.50	0.57
37:R:415:LEU:C	37:R:417:ASN:H	2.05	0.57
39:T:399:LYS:HG2	39:T:406:ILE:CD1	2.31	0.57
1:A:48:LYS:O	1:A:53:PHE:CD2	2.57	0.57
5:E:277:PHE:CE2	5:E:300:ILE:CD1	2.85	0.57
13:F:39:A:N6	14:G:8:C:H42	2.02	0.57
14:G:12:G:N2	14:G:13:C:O4'	2.38	0.57
23:3:781:LEU:HB3	23:3:801:GLU:OE2	2.04	0.57
36:P:188:TRP:O	36:P:189:ASP:C	2.42	0.57
1:A:60:ASP:OD1	1:A:60:ASP:N	2.36	0.57
3:C:749:THR:OG1	3:C:752:SER:HB2	2.04	0.57
4:D:454:PRO:HA	23:3:571:SER:O	2.04	0.57
23:3:463:ARG:HB2	23:3:510:LEU:HD22	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:O:131:THR:HG23	42:W:111:LEU:CA	2.34	0.57
43:X:285:ARG:NH1	43:X:304:ALA:O	2.35	0.57
1:A:439:GLN:NE2	1:A:614:TYR:CE2	2.49	0.57
1:A:800:TYR:HB3	3:C:59:LEU:CD1	2.34	0.57
2:B:41:U:C4	14:G:-1:G:N1	2.73	0.57
2:B:42:U:H3	14:G:-3:A:H2	0.70	0.57
3:C:617:LEU:HD11	3:C:629:ILE:HG23	1.87	0.57
23:3:306:GLU:OE2	27:7:63:ARG:HG3	2.03	0.57
23:3:478:PHE:O	23:3:504:PRO:HB3	2.05	0.57
23:3:1050:PHE:HB3	23:3:1167:TYR:CE2	2.38	0.57
29:L:73:HIS:O	29:L:77:LEU:HG	2.04	0.57
37:R:171:LEU:HD12	37:R:201:GLU:CD	2.25	0.57
1:A:50:LYS:O	1:A:51:PHE:C	2.43	0.57
3:C:79:THR:HG23	39:T:199:VAL:CG1	2.27	0.57
21:1:850:ILE:O	21:1:854:VAL:HG23	2.04	0.57
23:3:520:TYR:HB2	23:3:521:PRO:HD2	1.87	0.57
23:3:791:HIS:CE1	23:3:934:GLY:HA3	2.39	0.57
37:R:55:LEU:CB	37:R:73:PRO:O	2.53	0.57
1:A:785:LYS:CE	36:P:215:LEU:CD1	2.78	0.57
1:A:1548:TYR:CD2	1:A:1549:VAL:CG2	2.75	0.57
2:B:20:G:O6	2:B:24:G:OP1	2.21	0.57
3:C:93:ILE:O	3:C:94:ILE:HB	2.04	0.57
3:C:572:GLU:O	3:C:573:GLU:HB2	2.04	0.57
3:C:669:THR:CG2	3:C:690:GLU:OE1	2.52	0.57
5:E:267:PHE:CE1	31:K:194:GLU:HB2	2.40	0.57
14:G:137:C:N4	15:H:40:C:H42	1.99	0.57
23:3:211:TYR:CE1	23:3:222:ARG:HG2	2.40	0.57
23:3:429:ARG:NH1	27:7:58:ASN:OD1	2.38	0.57
36:P:73:GLU:O	36:P:76:ARG:HG2	2.04	0.57
36:P:188:TRP:N	36:P:188:TRP:CE3	2.73	0.57
1:A:569:VAL:O	1:A:570:ASP:HB2	2.04	0.57
1:A:623:LYS:O	48:A:2401:IHP:O24	2.22	0.57
1:A:745:ALA:HB2	39:T:206:TRP:CZ2	2.40	0.57
1:A:783:TYR:CG	36:P:228:ILE:HG12	2.39	0.57
3:C:140:HIS:HE2	3:C:233:GLU:HG3	1.68	0.57
15:H:166:G:OP2	15:H:166:G:N2	2.27	0.57
29:L:33:ARG:O	29:L:36:SER:OG	2.20	0.57
29:L:215:PRO:O	35:O:113:ASN:CA	2.53	0.57
34:N:28:LYS:NZ	42:W:190:ASP:N	2.52	0.57
35:O:240:GLY:HA3	35:O:296:ARG:HH22	1.68	0.57
36:P:31:SER:N	36:P:34:ASP:OD2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:293:TRP:HB2	1:A:1136:ARG:NH2	2.19	0.57
1:A:705:LYS:CG	37:R:251:ILE:HB	2.27	0.57
3:C:140:HIS:CE1	3:C:233:GLU:CB	2.83	0.57
3:C:487:GLY:HA3	3:C:489:GLN:OE1	2.05	0.57
3:C:490:PHE:HZ	3:C:612:LYS:HD2	1.69	0.57
3:C:511:GLY:O	3:C:576:ILE:HD12	2.02	0.57
15:H:148:C:O5'	15:H:148:C:H6	1.87	0.57
21:1:1109:ARG:HH22	21:1:1142:ASN:HB2	1.69	0.57
21:1:1258:ALA:HB3	21:1:1261:VAL:HG12	1.86	0.57
23:3:184:CYS:SG	23:3:209:THR:OG1	2.56	0.57
23:3:275:ARG:HE	23:3:386:PHE:HD2	1.51	0.57
37:R:434:TYR:CD2	37:R:435:ASN:N	2.73	0.57
1:A:387:PHE:CD2	3:C:399:LEU:CD2	2.87	0.57
1:A:587:GLN:HA	1:A:1550:GLY:C	2.25	0.57
1:A:692:ASP:CA	39:T:376:ARG:NH2	2.53	0.57
1:A:705:LYS:CG	37:R:251:ILE:CD1	2.70	0.57
5:E:310:TYR:CE1	5:E:322:LYS:CD	2.86	0.57
15:H:152:G:N2	15:H:153:A:C5	2.73	0.57
21:1:1098:LEU:HD13	21:1:1135:GLU:HG3	1.85	0.57
21:1:1126:PHE:CE2	22:2:572:HIS:HA	2.39	0.57
28:J:224:LYS:HE2	28:J:255:LEU:HD13	1.85	0.57
38:S:131:ARG:NH1	38:S:133:CYS:CB	2.68	0.57
45:Z:525:TYR:CD1	45:Z:526:ILE:N	2.73	0.57
1:A:532:THR:CB	14:G:2:U:C5'	2.83	0.57
1:A:832:TYR:CE2	1:A:834:HIS:HB2	2.40	0.57
3:C:508:LYS:HE3	3:C:566:THR:CG2	2.34	0.57
21:1:807:LYS:HA	21:1:811:LEU:HD12	1.87	0.57
21:1:942:ASN:HD22	21:1:947:VAL:HG11	1.70	0.57
23:3:635:ALA:H	23:3:669:LEU:HD21	1.70	0.57
37:R:181:PRO:O	42:W:112:SER:O	2.21	0.57
39:T:347:THR:CG2	39:T:357:TRP:HE1	2.18	0.57
41:V:489:LEU:O	41:V:492:MET:CB	2.53	0.57
42:W:420:ALA:H	42:W:438:ASP:CB	2.17	0.57
45:Z:611:ALA:O	45:Z:614:TRP:HB3	2.05	0.57
1:A:32:GLU:CG	1:A:36:LYS:HE3	2.35	0.56
2:B:27:U:O2'	2:B:28:A:O5'	2.23	0.56
3:C:261:ASP:OD1	50:C:1500:GTP:C6	2.57	0.56
3:C:456:GLY:C	3:C:457:VAL:HG13	2.25	0.56
28:J:270:ASP:OD2	37:R:222:PRO:CB	2.52	0.56
38:S:10:GLN:CB	38:S:29:TRP:CD2	2.88	0.56
39:T:306:CYS:SG	39:T:336:VAL:CG1	2.93	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:790:ARG:NE	1:A:986:GLU:OE2	2.38	0.56
1:A:1233:ASP:OD1	1:A:1234:ASP:N	2.37	0.56
1:A:1252:GLY:HA2	1:A:1298:ARG:HH21	1.69	0.56
13:F:57:U:H2'	13:F:58:G:H8	1.69	0.56
14:G:7:G:H2'	14:G:8:C:C6	2.40	0.56
15:H:78:C:HO2'	15:H:79:G:H5'	1.70	0.56
15:H:141:C:C2	15:H:142:C:C5	2.94	0.56
23:3:327:LEU:O	23:3:373:PHE:HB2	2.05	0.56
28:J:273:TYR:CG	37:R:228:PRO:CG	2.88	0.56
37:R:409:VAL:O	37:R:410:GLN:HG2	2.05	0.56
41:V:483:GLU:O	41:V:486:THR:N	2.33	0.56
45:Z:524:ARG:HB3	45:Z:524:ARG:CZ	2.35	0.56
1:A:36:LYS:NZ	42:W:163:GLN:CB	2.69	0.56
1:A:36:LYS:HZ1	42:W:163:GLN:CB	2.18	0.56
1:A:178:TYR:CD2	1:A:491:GLU:HB2	2.40	0.56
1:A:356:ILE:HG22	1:A:357:ASN:N	2.20	0.56
1:A:434:HIS:CE1	1:A:435:CYS:SG	2.98	0.56
1:A:532:THR:CB	14:G:2:U:H5"	2.35	0.56
1:A:587:GLN:O	1:A:587:GLN:HG2	2.04	0.56
1:A:1301:ILE:HD11	1:A:1306:LYS:CE	2.35	0.56
1:A:1386:TRP:HZ2	1:A:1417:PRO:HB2	1.69	0.56
3:C:426:GLU:O	3:C:427:PHE:HB2	2.05	0.56
3:C:449:ILE:CG2	3:C:457:VAL:HG11	2.30	0.56
5:E:250:LEU:CD2	5:E:262:TRP:HB2	2.35	0.56
15:H:152:G:N2	15:H:153:A:C8	2.73	0.56
21:1:847:ALA:O	21:1:851:SER:OG	2.24	0.56
22:2:643:PRO:CD	24:4:69:TYR:CG	2.88	0.56
29:L:209:ASP:CG	35:O:111:ASP:CB	2.73	0.56
34:N:38:GLU:C	34:N:40:LYS:H	2.08	0.56
36:P:76:ARG:HG3	36:P:77:ASP:N	2.19	0.56
37:R:89:GLN:OE1	38:S:146:GLU:N	2.38	0.56
38:S:131:ARG:HH12	38:S:133:CYS:HA	1.68	0.56
1:A:120:TYR:N	1:A:483:GLN:O	2.33	0.56
1:A:226:GLN:HA	1:A:418:THR:OG1	2.06	0.56
1:A:570:ASP:OD1	1:A:571:ALA:N	2.38	0.56
1:A:2113:LYS:CE	4:D:1229:ASP:CA	2.84	0.56
3:C:223:ASP:OD1	3:C:495:ARG:NH2	2.38	0.56
3:C:457:VAL:HA	3:C:462:GLY:HA3	1.88	0.56
3:C:673:LYS:HG3	3:C:686:THR:CG2	2.36	0.56
3:C:701:GLU:HA	3:C:740:THR:HG1	1.70	0.56
14:G:22:C:O2	14:G:22:C:H2'	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:944:SER:O	21:1:948:ARG:HG3	2.04	0.56
21:1:1279:ALA:HA	23:3:1167:TYR:CE1	2.41	0.56
24:4:75:ASN:ND2	24:4:86:VAL:O	2.38	0.56
1:A:226:GLN:OE1	1:A:417:ARG:NE	2.31	0.56
1:A:692:ASP:OD1	39:T:376:ARG:NH2	2.38	0.56
1:A:1163:ARG:NH2	3:C:61:GLU:OE2	2.35	0.56
5:E:267:PHE:CZ	31:K:194:GLU:CG	2.88	0.56
13:F:26:U:O2'	13:F:27:A:OP1	2.18	0.56
27:7:32:LEU:O	27:7:36:HIS:ND1	2.23	0.56
28:J:311:GLN:OE1	28:J:311:GLN:N	2.33	0.56
1:A:282:LEU:HD23	1:A:282:LEU:O	2.05	0.56
1:A:301:LYS:HG2	3:C:940:ARG:CA	2.35	0.56
3:C:301:SER:O	3:C:304:LEU:N	2.30	0.56
3:C:619:THR:C	3:C:620:LYS:HG3	2.25	0.56
13:F:50:A:O2'	13:F:51:U:OP1	2.23	0.56
42:W:101:THR:O	42:W:103:GLN:N	2.38	0.56
1:A:283:VAL:HG22	1:A:284:ARG:HG2	1.88	0.56
1:A:651:TRP:CZ2	13:F:66:C:N3	2.73	0.56
1:A:812:THR:HG23	1:A:1055:LEU:HD11	1.88	0.56
1:A:2320:LEU:HD23	1:A:2322:GLU:H	1.71	0.56
3:C:140:HIS:CB	3:C:230:ASP:CB	2.66	0.56
24:4:79:LEU:HB2	24:4:84:ILE:HD11	1.88	0.56
29:L:721:LEU:HA	29:L:724:TYR:CG	2.41	0.56
34:N:128:VAL:HG13	34:N:130:ARG:N	2.14	0.56
1:A:44:ARG:NH2	5:E:285:GLU:O	2.38	0.56
1:A:229:GLN:HG2	1:A:415:SER:CB	2.36	0.56
1:A:579:GLN:NE2	1:A:613:TYR:CE1	2.74	0.56
1:A:849:ALA:O	1:A:1449:LYS:NZ	2.36	0.56
1:A:2153:THR:HG22	1:A:2154:HIS:H	1.70	0.56
3:C:85:ASP:HB3	39:T:238:LEU:CG	2.27	0.56
3:C:677:GLU:HA	3:C:683:ASN:O	2.05	0.56
4:D:455:PHE:CB	23:3:573:GLN:NE2	2.68	0.56
5:E:277:PHE:CE2	5:E:300:ILE:HD13	2.40	0.56
14:G:20:A:C1'	35:O:193:LEU:HD21	2.35	0.56
21:1:1026:ASN:ND2	21:1:1031:VAL:HG11	2.21	0.56
1:A:378:PHE:C	1:A:379:GLU:HG2	2.25	0.56
2:B:40:U:H3'	2:B:40:U:O2	2.05	0.56
3:C:385:VAL:HG23	3:C:386:GLY:N	2.20	0.56
5:E:153:PHE:HD1	5:E:153:PHE:H	1.54	0.56
15:H:150:U:C2	15:H:151:C:C5	2.94	0.56
21:1:689:ILE:O	21:1:692:HIS:ND1	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:718:PRO:HA	21:1:756:LEU:HG	1.88	0.56
25:5:93:ASN:OD1	25:5:94:ALA:N	2.34	0.56
28:J:433:ARG:HH12	28:J:461:LYS:CB	2.19	0.56
35:O:236:VAL:O	35:O:269:CYS:HA	2.06	0.56
39:T:342:GLU:CB	39:T:343:PRO:CD	2.83	0.56
45:Z:612:TYR:O	45:Z:613:LYS:C	2.43	0.56
1:A:89:LEU:HD13	1:A:660:PHE:CZ	2.41	0.56
1:A:339:PHE:CD1	1:A:406:TRP:CZ3	2.93	0.56
1:A:1305:SER:OG	1:A:1310:ARG:HD3	2.06	0.56
1:A:1451:ASN:OD1	1:A:1453:PHE:N	2.39	0.56
1:A:1552:GLN:HB3	49:A:2402:ALA:HB1	1.86	0.56
1:A:1607:GLU:N	1:A:1632:PHE:O	2.38	0.56
3:C:631:GLY:HA3	3:C:637:LEU:HD21	1.88	0.56
15:H:83:A:N1	15:H:84:C:C4	2.74	0.56
21:1:1293:ASN:HA	27:7:76:CYS:O	2.05	0.56
21:1:1295:TYR:CE2	27:7:28:LYS:HE2	2.41	0.56
23:3:29:GLU:HB3	23:3:40:LEU:HD11	1.87	0.56
23:3:804:HIS:HD2	23:3:862:TRP:CZ2	2.24	0.56
23:3:1028:THR:HG22	23:3:1088:LYS:HD3	1.86	0.56
34:N:59:TYR:CE1	42:W:187:SER:HA	2.41	0.56
1:A:295:GLU:OE2	3:C:593:GLU:OE2	2.23	0.55
1:A:783:TYR:CD1	36:P:228:ILE:HG12	2.41	0.55
14:G:16:G:H4'	14:G:17:U:O5'	2.04	0.55
15:H:154:C:O2'	15:H:155:C:H5'	2.04	0.55
21:1:570:TYR:HD1	21:1:573:LYS:HD2	1.71	0.55
23:3:633:LEU:HD13	23:3:667:ILE:HG21	1.87	0.55
38:S:131:ARG:HH11	38:S:133:CYS:HA	1.69	0.55
1:A:417:ARG:HH12	2:B:58:U:H4'	1.70	0.55
15:H:141:C:H2'	15:H:142:C:H6	1.71	0.55
15:H:149:A:C4	15:H:150:U:C5	2.95	0.55
15:H:180:G:C2	15:H:181:G:C5	2.94	0.55
35:O:225:PRO:HG3	35:O:302:TRP:NE1	2.12	0.55
1:A:89:LEU:HD13	1:A:660:PHE:HZ	1.71	0.55
1:A:296:PHE:HB3	3:C:656:ALA:HB1	1.86	0.55
1:A:1418:ARG:HE	1:A:1464:LEU:HD23	1.72	0.55
1:A:1690:ASP:OD1	1:A:1691:ASN:N	2.39	0.55
3:C:674:CYS:HG	3:C:822:MET:CE	2.16	0.55
5:E:250:LEU:HD22	5:E:262:TRP:HB2	1.88	0.55
21:1:1137:ARG:HH21	22:2:524:LEU:HD13	1.72	0.55
36:P:224:MET:HA	36:P:224:MET:HE3	1.88	0.55
3:C:77:VAL:HG13	39:T:196:LEU:C	1.90	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:706:GLN:NE2	3:C:708:THR:H	2.02	0.55
22:2:650:ILE:HG12	22:2:688:GLY:HA3	1.89	0.55
23:3:745:PHE:HE2	23:3:750:CYS:HB3	1.71	0.55
1:A:151:MET:CE	1:A:628:GLY:C	2.75	0.55
1:A:587:GLN:HB2	1:A:1550:GLY:H	1.71	0.55
1:A:1035:GLN:HA	1:A:1446:GLN:NE2	2.21	0.55
1:A:1364:LEU:HD13	41:V:461:LEU:C	2.27	0.55
1:A:1370:ARG:HH22	41:V:506:PHE:CB	2.19	0.55
2:B:47:A:O2'	2:B:48:A:H5"	2.06	0.55
2:B:94:U:H2'	2:B:95:G:H5"	1.89	0.55
3:C:185:PRO:HG3	3:C:482:TYR:CZ	2.41	0.55
3:C:439:PRO:HB2	3:C:443:VAL:HB	1.88	0.55
21:1:1166:ILE:O	21:1:1170:THR:HG23	2.07	0.55
24:4:29:LEU:HD22	24:4:33:PHE:HE2	1.72	0.55
38:S:13:ASN:HD22	38:S:24:VAL:CG1	2.19	0.55
45:Z:566:TYR:CD2	45:Z:580:PRO:HG2	2.36	0.55
1:A:89:LEU:O	1:A:89:LEU:HD23	2.05	0.55
1:A:1364:LEU:HD11	41:V:461:LEU:CB	2.29	0.55
1:A:1645:LEU:HB2	1:A:1714:ALA:HB3	1.88	0.55
3:C:516:LEU:HD13	3:C:516:LEU:C	2.26	0.55
3:C:702:ASN:O	3:C:703:GLU:HB2	2.07	0.55
5:E:162:ARG:CZ	5:E:203:ASP:O	2.55	0.55
15:H:165:A:H2'	15:H:166:G:H5'	1.88	0.55
23:3:996:ILE:HG23	23:3:999:ARG:H	1.72	0.55
1:A:1233:ASP:O	1:A:1236:SER:OG	2.23	0.55
1:A:2306:HIS:HD2	1:A:2308:VAL:H	1.54	0.55
3:C:78:GLU:OE1	39:T:198:ARG:NE	2.36	0.55
3:C:79:THR:CG2	39:T:199:VAL:CG1	2.84	0.55
3:C:567:GLU:OE1	3:C:572:GLU:HB3	2.06	0.55
5:E:260:ARG:NH1	5:E:276:ILE:HD11	2.22	0.55
14:G:23:U:O2	14:G:23:U:H2'	2.07	0.55
21:1:1255:PHE:CD2	22:2:487:LEU:HD22	2.42	0.55
36:P:33:ARG:HG3	36:P:33:ARG:HH11	1.72	0.55
44:Y:22:VAL:HG22	44:Y:26:VAL:HG13	1.88	0.55
45:Z:600:ARG:HB3	45:Z:600:ARG:NH1	2.08	0.55
1:A:283:VAL:HG13	1:A:284:ARG:N	2.22	0.55
1:A:464:PRO:O	1:A:465:LYS:HB3	2.05	0.55
1:A:715:GLU:CD	37:R:258:TRP:CZ3	2.79	0.55
1:A:1099:PHE:HE2	1:A:1153:VAL:HG13	1.72	0.55
1:A:1457:HIS:HE1	1:A:1459:ARG:HG3	1.68	0.55
21:1:1017:LEU:HD13	21:1:1050:VAL:HG21	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:1076:ALA:O	21:1:1080:THR:HG23	2.07	0.55
31:K:135:TRP:O	31:K:138:TYR:CG	2.60	0.55
37:R:74:LEU:HD23	37:R:75:ASP:OD1	2.06	0.55
37:R:436:VAL:CG2	37:R:437:TYR:CE1	2.89	0.55
41:V:641:ASP:O	41:V:644:ARG:N	2.39	0.55
44:Y:85:GLU:O	45:Z:502:ALA:CB	2.55	0.55
1:A:436:PRO:O	1:A:437:ALA:HB3	2.07	0.55
1:A:623:LYS:CG	48:A:2401:IHP:O34	2.55	0.55
1:A:1305:SER:CB	1:A:1310:ARG:NH1	2.44	0.55
3:C:149:LEU:HA	3:C:427:PHE:CD2	2.41	0.55
5:E:114:GLU:CD	5:E:116:HIS:HE2	2.09	0.55
14:G:142:U:H2'	14:G:143:U:C6	2.42	0.55
15:H:150:U:H2'	15:H:151:C:H6	1.71	0.55
25:5:17:VAL:HG23	25:5:67:ILE:HD11	1.89	0.55
44:Y:37:TRP:HZ3	45:Z:498:GLY:HA3	1.66	0.55
1:A:119:LEU:HD11	1:A:477:LYS:HG3	1.88	0.55
1:A:168:PRO:HG2	1:A:559:ASP:CB	2.36	0.55
1:A:1457:HIS:HE2	37:R:425:GLY:H	1.46	0.55
3:C:220:ARG:HG2	3:C:479:THR:HG21	1.89	0.55
21:1:1174:GLU:OE2	21:1:1210:HIS:NE2	2.35	0.55
29:L:224:PHE:CD1	37:R:86:LEU:O	2.59	0.55
34:N:139:CYS:SG	34:N:140:ARG:N	2.80	0.55
36:P:188:TRP:O	36:P:190:ASP:N	2.39	0.55
37:R:74:LEU:HD23	37:R:74:LEU:C	2.27	0.55
38:S:131:ARG:HH11	38:S:133:CYS:CA	2.17	0.55
45:Z:574:ASN:O	45:Z:577:ASN:N	2.33	0.55
1:A:148:TRP:CH2	1:A:616:PHE:HB2	2.42	0.54
1:A:356:ILE:HG22	1:A:357:ASN:H	1.72	0.54
1:A:2325:VAL:HG13	4:D:789:MET:HA	1.88	0.54
1:A:2325:VAL:O	4:D:788:GLY:CA	2.56	0.54
23:3:309:ASP:HA	23:3:332:THR:HG22	1.88	0.54
23:3:550:ASN:HD21	23:3:595:VAL:H	1.53	0.54
23:3:848:PRO:HB2	23:3:851:ILE:HG22	1.89	0.54
24:4:14:THR:CA	24:4:59:VAL:O	2.28	0.54
26:6:39:PRO:HB3	26:6:70:TYR:HB2	1.88	0.54
28:J:294:HIS:HE1	29:L:227:THR:HB	1.70	0.54
35:O:166:SER:HA	35:O:169:VAL:HG12	1.89	0.54
35:O:232:THR:HG22	35:O:277:ARG:HA	1.89	0.54
36:P:228:ILE:O	36:P:229:LYS:C	2.45	0.54
37:R:86:LEU:HD12	37:R:86:LEU:O	2.06	0.54
42:W:185:ASP:O	42:W:186:ALA:HB3	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2073:TRP:HD1	1:A:2074:ARG:N	2.04	0.54
2:B:36:C:H2'	40:U:11:ARG:HH12	1.71	0.54
5:E:119:THR:HG21	5:E:161:ARG:HB2	1.87	0.54
15:H:153:A:C3'	15:H:154:C:C5'	2.86	0.54
21:1:1179:ASP:HB3	22:2:511:LEU:CD1	2.37	0.54
21:1:1279:ALA:HA	23:3:1167:TYR:HE1	1.70	0.54
34:N:38:GLU:O	34:N:40:LYS:N	2.38	0.54
43:X:312:GLU:O	43:X:327:TYR:HB2	2.07	0.54
1:A:592:TYR:HA	1:A:595:LYS:O	2.08	0.54
1:A:1132:LYS:HA	1:A:1139:ARG:HD3	1.90	0.54
3:C:140:HIS:CD2	3:C:233:GLU:HG3	2.41	0.54
3:C:510:LEU:HB3	3:C:576:ILE:HD11	1.89	0.54
13:F:27:A:N9	35:O:181:TYR:OH	2.37	0.54
13:F:36:A:H2'	13:F:37:C:H4'	1.89	0.54
13:F:38:G:H2'	13:F:39:A:C8	2.42	0.54
13:F:56:A:C2	15:H:20:G:C2	2.96	0.54
23:3:553:GLN:HA	23:3:566:PHE:O	2.07	0.54
23:3:1014:TYR:OH	23:3:1019:ASN:OD1	2.24	0.54
28:J:218:GLU:HG3	28:J:219:GLU:OE2	2.07	0.54
35:O:196:GLN:HE22	35:O:209:VAL:HG23	1.71	0.54
42:W:198:LYS:O	42:W:199:TYR:C	2.45	0.54
1:A:151:MET:SD	1:A:628:GLY:O	2.65	0.54
1:A:596:TYR:CZ	14:G:-5:G:N7	2.75	0.54
1:A:676:ARG:HG3	13:F:56:A:P	2.48	0.54
1:A:2117:ILE:O	1:A:2304:PHE:HB2	2.08	0.54
3:C:749:THR:HG1	3:C:752:SER:HB2	1.72	0.54
35:O:102:SER:OG	35:O:139:LYS:NZ	2.25	0.54
37:R:402:ASN:HB3	43:X:191:GLN:HB2	1.90	0.54
44:Y:10:ILE:HD13	44:Y:98:ASN:HD21	1.73	0.54
1:A:173:GLU:O	1:A:520:TYR:CD2	2.61	0.54
1:A:329:LEU:HD13	3:C:177:ARG:NE	2.17	0.54
1:A:699:GLU:O	1:A:701:ILE:HD12	2.07	0.54
1:A:1459:ARG:HG3	37:R:424:SER:N	2.22	0.54
3:C:145:PHE:CZ	3:C:427:PHE:HE1	2.21	0.54
5:E:161:ARG:NH1	5:E:203:ASP:OD1	2.40	0.54
23:3:913:LEU:HD23	23:3:920:VAL:HG12	1.89	0.54
28:J:262:ARG:HD3	29:L:220:PRO:CG	2.38	0.54
29:L:224:PHE:HD1	37:R:86:LEU:O	1.91	0.54
36:P:63:LEU:HD23	36:P:63:LEU:C	2.28	0.54
39:T:455:GLN:NE2	39:T:456:PRO:HD2	2.22	0.54
1:A:705:LYS:HG2	37:R:251:ILE:CG1	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1285:LEU:HB3	1:A:1335:ILE:HD12	1.90	0.54
1:A:1333:VAL:HG11	1:A:1367:ASN:HD22	1.73	0.54
1:A:1351:THR:HG22	40:U:25:LEU:HD21	1.88	0.54
2:B:42:U:H4'	13:F:70:A:C4'	2.37	0.54
5:E:108:HIS:ND1	5:E:128:SER:CB	2.70	0.54
5:E:310:TYR:CZ	5:E:322:LYS:HD2	2.42	0.54
23:3:138:GLN:HG2	23:3:161:HIS:CE1	2.43	0.54
23:3:336:ALA:HB2	23:3:349:VAL:HG13	1.90	0.54
23:3:547:CYS:HB3	23:3:556:ILE:HG22	1.90	0.54
37:R:131:ASP:OD2	37:R:132:LEU:HD23	2.07	0.54
1:A:978:GLU:OE2	1:A:1187:PHE:HB2	2.07	0.54
1:A:1328:LEU:HD22	1:A:1368:LEU:HD21	1.89	0.54
1:A:1342:TRP:CG	3:C:921:LEU:HD11	2.42	0.54
3:C:259:LYS:CE	3:C:262:ARG:HD2	2.36	0.54
3:C:482:TYR:CD2	3:C:493:PHE:HB2	2.42	0.54
3:C:700:ILE:CG2	3:C:735:PHE:CD2	2.83	0.54
4:D:1048:VAL:O	4:D:1050:GLU:N	2.40	0.54
21:1:470:ASP:OD1	21:1:471:ASP:N	2.41	0.54
21:1:624:VAL:O	21:1:628:THR:OG1	2.14	0.54
21:1:632:PHE:HA	21:1:635:VAL:HG22	1.90	0.54
23:3:144:LEU:HB3	23:3:152:LEU:HD11	1.89	0.54
23:3:253:GLU:OE2	23:3:254:ASN:ND2	2.41	0.54
28:J:408:ASP:OD1	28:J:443:ILE:HG22	2.07	0.54
3:C:230:ASP:CG	3:C:259:LYS:NZ	2.61	0.54
15:H:183:G:C4	15:H:184:C:C5	2.95	0.54
21:1:331:ALA:O	21:1:335:LYS:N	2.34	0.54
23:3:526:HIS:HB3	23:3:534:ASN:HB2	1.88	0.54
23:3:669:LEU:HB2	23:3:673:VAL:HG22	1.88	0.54
36:P:228:ILE:HD12	36:P:228:ILE:N	2.23	0.54
38:S:55:ARG:CZ	42:W:95:PRO:O	2.56	0.54
39:T:356:LEU:N	39:T:356:LEU:CD1	2.70	0.54
45:Z:612:TYR:O	45:Z:615:SER:N	2.29	0.54
1:A:375:ASP:N	3:C:355:LYS:NZ	2.56	0.54
1:A:628:GLY:O	1:A:629:PHE:HB2	2.08	0.54
1:A:2287:ARG:HH22	4:D:1147:ASN:CB	2.15	0.54
3:C:135:CYS:SG	3:C:227:LEU:HB2	2.47	0.54
21:1:893:ILE:HG13	21:1:928:TYR:CD2	2.43	0.54
22:2:476:GLU:N	22:2:479:ASP:OD2	2.41	0.54
23:3:452:LEU:HB3	23:3:478:PHE:CE1	2.42	0.54
27:7:15:GLN:O	27:7:21:THR:OG1	2.22	0.54
28:J:255:LEU:HD22	29:L:235:LEU:CD1	2.35	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:R:232:MET:O	37:R:232:MET:HG2	2.07	0.54
1:A:339:PHE:HE1	1:A:406:TRP:HZ3	1.54	0.54
1:A:623:LYS:HG2	48:A:2401:IHP:O34	2.07	0.54
1:A:2310:ARG:HH12	1:A:2314:PHE:HE1	1.56	0.54
3:C:79:THR:HA	39:T:199:VAL:H	1.73	0.54
14:G:137:C:H2'	14:G:138:A:O4'	2.07	0.54
15:H:3:C:H2'	15:H:4:G:H8	1.73	0.54
21:1:826:ASP:OD1	21:1:827:ARG:N	2.39	0.54
21:1:1010:THR:O	21:1:1012:PRO:HD3	2.08	0.54
23:3:605:LEU:O	23:3:616:ILE:HA	2.08	0.54
27:7:60:SER:HG	27:7:63:ARG:H	1.55	0.54
35:O:50:ARG:NH1	35:O:122:GLU:OE1	2.41	0.54
35:O:57:TRP:CD1	35:O:57:TRP:C	2.81	0.54
35:O:235:TYR:HD1	35:O:271:PHE:CE1	2.24	0.54
37:R:135:PRO:HD2	39:T:341:ALA:HB1	1.90	0.54
37:R:442:ARG:CD	37:R:443:GLY:CA	2.70	0.54
42:W:474:LYS:CA	42:W:490:ALA:HB3	2.37	0.54
1:A:148:TRP:CZ2	1:A:616:PHE:HA	2.43	0.53
1:A:2067:PHE:CE2	1:A:2069:SER:HA	2.43	0.53
3:C:700:ILE:HA	3:C:705:VAL:HG12	1.89	0.53
3:C:742:PRO:HB2	3:C:786:ASN:H	1.72	0.53
5:E:178:LEU:CD1	5:E:222:LEU:HD22	2.37	0.53
14:G:-8:U:C6	40:U:16:ASN:CA	2.90	0.53
39:T:287:HIS:CE1	39:T:313:ARG:HG3	2.43	0.53
42:W:481:MET:O	42:W:483:ASN:N	2.41	0.53
42:W:531:LYS:HA	42:W:546:PHE:O	2.07	0.53
45:Z:485:GLU:O	45:Z:489:GLU:CB	2.56	0.53
1:A:71:ARG:NH1	1:A:177:ASP:OD2	2.32	0.53
1:A:254:TYR:O	1:A:434:HIS:HD2	1.91	0.53
1:A:705:LYS:HG2	37:R:251:ILE:CG2	2.38	0.53
1:A:1403:LEU:O	37:R:412:ASP:HB2	2.08	0.53
14:G:135:G:H1	15:H:41:U:H3	1.56	0.53
15:H:84:C:O2	15:H:84:C:H2'	2.09	0.53
23:3:166:LEU:O	23:3:186:GLU:HA	2.08	0.53
23:3:550:ASN:HB3	23:3:553:GLN:HB2	1.90	0.53
39:T:454:VAL:HG12	39:T:455:GLN:N	2.24	0.53
5:E:87:ASP:O	5:E:88:ARG:HB2	2.07	0.53
13:F:53:A:H2'	13:F:54:G:O4'	2.09	0.53
21:1:626:ASN:ND2	21:1:630:ARG:HH12	2.06	0.53
21:1:1299:GLU:HA	21:1:1302:TYR:CE2	2.44	0.53
23:3:639:SER:OG	23:3:701:LEU:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:N:27:GLN:NE2	34:N:31:GLU:OE2	2.41	0.53
35:O:165:CYS:HB2	35:O:181:TYR:HB2	1.90	0.53
39:T:384:HIS:O	39:T:385:TYR:CB	2.55	0.53
41:V:525:PHE:O	41:V:528:ILE:N	2.41	0.53
43:X:181:PHE:HA	44:Y:50:GLY:H	1.73	0.53
1:A:1352:HIS:CD2	40:U:5:ILE:HD13	2.44	0.53
3:C:449:ILE:CD1	3:C:466:SER:N	2.71	0.53
21:1:822:ARG:HH11	44:Y:31:GLU:HG2	1.74	0.53
21:1:1077:THR:O	21:1:1080:THR:OG1	2.22	0.53
21:1:1127:THR:HA	22:2:571:LEU:HB3	1.88	0.53
23:3:3:LEU:HD12	23:3:1093:MET:SD	2.48	0.53
23:3:476:VAL:HG22	23:3:762:LEU:HD22	1.91	0.53
28:J:218:GLU:HG3	28:J:219:GLU:N	2.23	0.53
37:R:103:ARG:HH11	37:R:103:ARG:CG	2.21	0.53
1:A:122:ILE:HD13	1:A:483:GLN:HG3	1.90	0.53
1:A:348:PRO:HB3	1:A:394:TYR:CE2	2.43	0.53
3:C:481:MET:SD	3:C:559:ILE:HD11	2.48	0.53
1:A:881:ILE:HG23	1:A:918:THR:HG23	1.88	0.53
1:A:1457:HIS:HE2	37:R:425:GLY:N	2.04	0.53
1:A:2073:TRP:CH2	1:A:2310:ARG:HG2	2.44	0.53
1:A:2113:LYS:HE3	4:D:1229:ASP:CA	2.38	0.53
3:C:115:GLU:O	3:C:116:MET:C	2.43	0.53
3:C:220:ARG:O	3:C:448:LYS:HE2	2.08	0.53
3:C:360:ALA:N	3:C:361:PRO:CD	2.71	0.53
15:H:147:G:C2	15:H:148:C:C2	2.97	0.53
15:H:153:A:H3'	15:H:154:C:C5'	2.38	0.53
21:1:1157:TYR:O	26:6:38:ARG:NH2	2.40	0.53
23:3:195:ASP:OD1	23:3:197:THR:OG1	2.23	0.53
23:3:250:ILE:HD13	23:3:259:LYS:HB3	1.91	0.53
36:P:41:ILE:HD11	39:T:318:ARG:HB2	1.90	0.53
38:S:20:MET:HE1	38:S:141:ARG:HB3	1.91	0.53
1:A:465:LYS:HG3	1:A:465:LYS:O	2.08	0.53
3:C:449:ILE:HG22	3:C:457:VAL:HG13	1.88	0.53
5:E:108:HIS:ND1	5:E:128:SER:HB2	2.24	0.53
5:E:178:LEU:CD2	5:E:208:ILE:CD1	2.87	0.53
15:H:68:G:C2'	15:H:69:U:H5'	2.37	0.53
23:3:141:VAL:HG11	23:3:213:LEU:HD12	1.89	0.53
1:A:642:ARG:CD	2:B:28:A:H1'	2.24	0.53
2:B:18:C:C2'	2:B:19:A:O5'	2.56	0.53
2:B:32:C:H5"	36:P:33:ARG:NH1	2.24	0.53
3:C:82:GLN:CG	39:T:237:LYS:HA	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:79:G:C2	15:H:80:A:C5	2.97	0.53
21:1:944:SER:HA	21:1:948:ARG:NE	2.23	0.53
23:3:519:VAL:HG22	23:3:524:ILE:HG12	1.89	0.53
23:3:712:VAL:HG23	23:3:722:SER:HB3	1.91	0.53
23:3:719:SER:OG	23:3:739:LEU:HD11	2.09	0.53
28:J:359:VAL:O	28:J:363:ARG:HG2	2.08	0.53
34:N:55:GLN:NE2	42:W:192:PHE:CB	2.71	0.53
34:N:128:VAL:CG1	34:N:130:ARG:HB3	2.38	0.53
37:R:132:LEU:HB3	39:T:399:LYS:HZ2	1.70	0.53
39:T:318:ARG:HH11	39:T:318:ARG:CG	2.22	0.53
40:U:23:LEU:O	40:U:23:LEU:HD13	2.08	0.53
45:Z:571:PRO:HD3	45:Z:579:TRP:CH2	2.43	0.53
1:A:372:PRO:CB	3:C:342:ARG:HH21	2.22	0.53
1:A:595:LYS:NZ	2:B:45:C:OP1	2.31	0.53
1:A:1199:LYS:NZ	1:A:1206:GLU:OE2	2.32	0.53
3:C:259:LYS:HG2	3:C:262:ARG:HG3	1.90	0.53
5:E:232:ARG:O	5:E:262:TRP:HH2	1.91	0.53
21:1:516:LEU:O	21:1:520:THR:HG23	2.08	0.53
24:4:47:ASP:HB3	24:4:52:GLN:O	2.08	0.53
32:I:362:LYS:HA	32:I:372:ARG:CB	2.39	0.53
1:A:204:LEU:HD23	1:A:205:ASP:OD1	2.09	0.53
1:A:723:ASN:ND2	1:A:788:GLN:OE1	2.41	0.53
1:A:748:ASP:HA	36:P:214:THR:CG2	2.34	0.53
1:A:1275:ARG:HD2	1:A:1375:TRP:CD1	2.44	0.53
1:A:1425:LYS:CG	37:R:417:ASN:OD1	2.56	0.53
2:B:42:U:H4'	13:F:70:A:C5'	2.37	0.53
3:C:250:ARG:NE	3:C:451:HIS:CD2	2.76	0.53
3:C:516:LEU:HB2	3:C:575:GLN:HE22	1.73	0.53
13:F:50:A:H2'	13:F:51:U:C6	2.44	0.53
13:F:56:A:C6	15:H:20:G:C6	2.96	0.53
22:2:614:ARG:HH11	22:2:614:ARG:CG	2.14	0.53
23:3:211:TYR:HE1	23:3:222:ARG:HG2	1.74	0.53
38:S:34:LYS:CE	38:S:78:TYR:CD2	2.92	0.53
1:A:606:LYS:HD2	1:A:1548:TYR:CE1	2.44	0.52
1:A:891:PHE:O	29:L:83:ARG:NH1	2.42	0.52
3:C:671:SER:C	3:C:672:LEU:HD22	2.30	0.52
21:1:599:ASN:O	21:1:603:ALA:CB	2.57	0.52
23:3:1148:LEU:O	23:3:1152:HIS:N	2.39	0.52
37:R:95:LYS:HD3	37:R:95:LYS:N	2.25	0.52
1:A:191:ILE:HG23	1:A:572:PHE:CZ	2.44	0.52
1:A:245:LEU:HD22	1:A:430:TRP:CH2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:596:TYR:HB2	14:G:-5:G:C2	2.43	0.52
1:A:2298:LEU:HD13	4:D:1265:GLN:CB	2.39	0.52
3:C:943:LEU:HD23	3:C:943:LEU:N	2.24	0.52
13:F:48:A:N3	29:L:33:ARG:NH2	2.57	0.52
13:F:94:C:OP1	28:J:351:ASN:CB	2.57	0.52
14:G:153:C:H4'	14:G:154:U:OP1	2.10	0.52
15:H:81:G:C2	15:H:82:G:C5	2.97	0.52
41:V:530:LYS:O	41:V:532:GLN:N	2.42	0.52
42:W:212:GLU:C	42:W:214:LYS:N	2.61	0.52
3:C:97:VAL:HG12	36:P:47:THR:OG1	2.10	0.52
13:F:34:G:H2'	13:F:35:A:O5'	2.10	0.52
14:G:-4:A:H2'	14:G:-3:A:C8	2.44	0.52
15:H:148:C:C2'	15:H:149:A:H5'	2.39	0.52
21:1:516:LEU:HD11	21:1:558:ARG:HD3	1.91	0.52
21:1:1090:PRO:HG3	21:1:1123:CYS:HB2	1.91	0.52
23:3:128:ARG:HH21	23:3:180:PRO:HG3	1.73	0.52
23:3:159:GLU:OE2	26:6:14:GLN:HB2	2.09	0.52
35:O:229:LYS:HA	35:O:277:ARG:NH2	2.24	0.52
36:P:189:ASP:O	36:P:191:ASP:N	2.43	0.52
37:R:233:HIS:H	37:R:233:HIS:HD2	1.56	0.52
38:S:39:PHE:CD2	38:S:129:PHE:HE2	2.10	0.52
39:T:351:ASP:C	39:T:352:THR:HG1	2.11	0.52
40:U:9:THR:HG23	40:U:9:THR:O	2.09	0.52
42:W:531:LYS:CA	42:W:546:PHE:O	2.58	0.52
1:A:830:LEU:HA	1:A:882:LYS:HZ2	1.74	0.52
1:A:1214:TRP:CE2	1:A:1230:LEU:HD11	2.45	0.52
1:A:2133:PRO:HD2	1:A:2139:VAL:HG13	1.92	0.52
5:E:178:LEU:N	5:E:178:LEU:HD23	2.25	0.52
14:G:-12:G:H4'	14:G:-11:G:OP1	2.09	0.52
21:1:1108:ASN:OD1	21:1:1109:ARG:N	2.43	0.52
23:3:114:ARG:NE	23:3:136:GLU:OE1	2.32	0.52
35:O:75:SER:O	35:O:79:ASN:N	2.42	0.52
35:O:80:VAL:HG11	35:O:94:ILE:HD11	1.90	0.52
35:O:243:ILE:HG22	35:O:244:THR:O	2.08	0.52
37:R:52:PRO:O	37:R:53:ARG:HB2	2.09	0.52
37:R:81:LYS:HA	37:R:81:LYS:HE3	1.87	0.52
1:A:299:ILE:HD11	3:C:920:PRO:C	2.29	0.52
1:A:1275:ARG:NH1	1:A:1378:GLU:OE1	2.43	0.52
1:A:1306:LYS:HB2	14:G:-6:C:H4'	1.92	0.52
1:A:1631:LEU:HD12	1:A:1660:TYR:HD2	1.74	0.52
3:C:80:ILE:CD1	3:C:80:ILE:N	2.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:143:THR:HB	50:C:1500:GTP:O1A	2.09	0.52
3:C:700:ILE:CG2	3:C:741:GLY:O	2.57	0.52
13:F:36:A:C8	13:F:36:A:C4'	2.93	0.52
13:F:57:U:H2'	13:F:58:G:C8	2.45	0.52
21:1:717:THR:HG22	21:1:718:PRO:CD	2.39	0.52
21:1:762:ALA:O	21:1:766:THR:OG1	2.19	0.52
23:3:159:GLU:HB3	23:3:161:HIS:CD2	2.44	0.52
34:N:40:LYS:O	34:N:41:ARG:CG	2.47	0.52
45:Z:524:ARG:HD2	45:Z:525:TYR:HB3	1.92	0.52
1:A:91:ALA:O	1:A:92:LEU:C	2.45	0.52
1:A:107:PRO:O	1:A:111:GLU:CD	2.48	0.52
1:A:115:ASP:HB3	1:A:486:LYS:HE2	1.91	0.52
1:A:121:HIS:HE2	1:A:481:PHE:CB	2.14	0.52
1:A:121:HIS:CD2	1:A:481:PHE:HB3	2.36	0.52
2:B:42:U:O2'	13:F:69:A:C2	2.58	0.52
2:B:43:U:C5'	13:F:67:G:H22	2.08	0.52
3:C:78:GLU:O	39:T:198:ARG:C	2.47	0.52
3:C:78:GLU:CG	3:C:80:ILE:CD1	2.54	0.52
3:C:139:HIS:O	3:C:259:LYS:NZ	2.36	0.52
3:C:449:ILE:HD11	3:C:466:SER:HA	1.91	0.52
3:C:508:LYS:HB3	3:C:566:THR:CG2	2.39	0.52
3:C:710:ASN:O	3:C:712:LYS:N	2.42	0.52
21:1:1254:LEU:O	21:1:1262:ARG:HG2	2.09	0.52
23:3:755:VAL:HG22	23:3:764:ILE:HD12	1.90	0.52
23:3:1059:PRO:O	23:3:1062:THR:HG23	2.08	0.52
35:O:72:GLN:O	35:O:75:SER:OG	2.19	0.52
39:T:267:ASP:O	39:T:268:LYS:CG	2.56	0.52
39:T:351:ASP:C	39:T:352:THR:OG1	2.48	0.52
45:Z:597:ARG:NH1	45:Z:601:LEU:HD13	2.24	0.52
1:A:1131:LYS:HE3	1:A:1174:PHE:CD1	2.44	0.52
1:A:1162:PRO:HG3	36:P:194:PHE:CG	2.44	0.52
1:A:1459:ARG:HD2	37:R:422:MET:O	2.09	0.52
14:G:11:A:N1	14:G:12:G:C8	2.77	0.52
23:3:285:MET:SD	23:3:305:THR:HB	2.49	0.52
23:3:304:GLN:HE22	23:3:335:VAL:HA	1.73	0.52
24:4:41:ASN:HB2	24:4:60:GLU:HB3	1.92	0.52
37:R:442:ARG:CD	37:R:443:GLY:C	2.77	0.52
39:T:318:ARG:HH11	39:T:319:THR:HG23	1.74	0.52
1:A:47:GLU:OE1	1:A:47:GLU:N	2.35	0.52
1:A:206:TRP:CD1	1:A:213:LEU:HD21	2.45	0.52
1:A:651:TRP:CZ2	13:F:66:C:C4	2.97	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1502:PHE:CZ	1:A:1505:LYS:HB3	2.45	0.52
1:A:2147:MET:O	1:A:2274:PRO:HD3	2.10	0.52
1:A:2268:LEU:HD22	4:D:1261:PRO:O	1.96	0.52
3:C:711:ARG:CZ	3:C:730:ARG:O	2.57	0.52
3:C:902:HIS:ND1	3:C:903:HIS:HB2	2.25	0.52
21:1:1289:ASN:HB3	21:1:1295:TYR:H	1.75	0.52
23:3:108:GLY:O	26:6:82:ARG:HD3	2.09	0.52
23:3:232:GLY:HA2	23:3:252:SER:HA	1.90	0.52
24:4:34:LEU:HA	24:4:37:GLY:O	2.10	0.52
35:O:24:CYS:HB2	35:O:27:CYS:SG	2.49	0.52
37:R:135:PRO:O	37:R:136:ASP:CB	2.58	0.52
1:A:380:LEU:HB2	3:C:354:ARG:NH1	2.18	0.52
1:A:1136:ARG:H	1:A:1345:GLN:HA	1.75	0.52
3:C:259:LYS:HG2	3:C:262:ARG:CG	2.39	0.52
3:C:510:LEU:HD22	3:C:514:TYR:HE2	1.75	0.52
21:1:901:GLN:HA	21:1:939:ARG:HH22	1.72	0.52
36:P:193:VAL:HG23	36:P:194:PHE:N	2.25	0.52
38:S:9:TRP:CE3	38:S:11:PRO:HG2	2.45	0.52
39:T:347:THR:O	39:T:354:ILE:HG23	2.10	0.52
42:W:518:PRO:O	42:W:519:ASP:CB	2.57	0.52
1:A:666:LYS:HB2	1:A:668:VAL:HG23	1.92	0.52
1:A:676:ARG:HG3	13:F:55:C:O3'	2.09	0.52
3:C:449:ILE:CD1	3:C:466:SER:CA	2.88	0.52
3:C:600:LEU:N	3:C:601:PRO:HD2	2.25	0.52
13:F:27:A:N9	35:O:181:TYR:CZ	2.77	0.52
21:1:661:ARG:NH1	21:1:696:ASP:OD2	2.39	0.52
21:1:1070:LYS:HB3	21:1:1073:ILE:HD12	1.91	0.52
21:1:1096:THR:HA	21:1:1099:ASN:ND2	2.25	0.52
23:3:259:LYS:HG3	23:3:266:ASP:OD1	2.09	0.52
23:3:1048:ASP:HB3	23:3:1052:ASN:H	1.75	0.52
35:O:113:ASN:O	35:O:116:TYR:N	2.43	0.52
36:P:189:ASP:OD2	36:P:192:VAL:CG2	2.59	0.52
37:R:70:ALA:O	37:R:71:GLN:C	2.48	0.52
44:Y:69:ARG:NH2	44:Y:74:GLY:O	2.34	0.52
1:A:128:PHE:CD1	1:A:473:PHE:CZ	2.98	0.51
1:A:941:LYS:HG3	1:A:1071:PHE:CE1	2.46	0.51
1:A:1275:ARG:HD2	1:A:1375:TRP:NE1	2.25	0.51
1:A:1425:LYS:C	1:A:1425:LYS:HD3	2.31	0.51
1:A:1701:VAL:HA	1:A:1716:GLY:HA3	1.91	0.51
1:A:2081:ALA:HB1	4:D:1010:SER:CB	2.40	0.51
3:C:64:LYS:NZ	36:P:206:LYS:HG3	2.22	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:89:LEU:O	3:C:91:GLU:N	2.43	0.51
21:1:1256:HIS:ND1	21:1:1261:VAL:HG11	2.24	0.51
23:3:1134:SER:HB2	23:3:1136:GLU:OE1	2.09	0.51
34:N:43:VAL:O	34:N:47:TRP:NE1	2.44	0.51
36:P:32:SER:O	36:P:35:LEU:HD12	2.09	0.51
1:A:203:VAL:CG2	1:A:237:THR:CB	2.88	0.51
1:A:672:VAL:HG21	39:T:267:ASP:OD1	2.10	0.51
1:A:805:GLU:CB	36:P:194:PHE:CZ	2.89	0.51
1:A:2090:ILE:HA	1:A:2223:CYS:O	2.10	0.51
3:C:77:VAL:HG13	39:T:196:LEU:HB3	1.91	0.51
13:F:36:A:H3'	13:F:37:C:C5'	2.26	0.51
21:1:1253:GLY:HA3	21:1:1265:TYR:CG	2.45	0.51
26:6:54:TYR:HA	26:6:57:ARG:HB2	1.92	0.51
29:L:224:PHE:CE1	37:R:86:LEU:HD13	2.44	0.51
39:T:392:PRO:HA	39:T:414:ALA:O	2.09	0.51
42:W:425:VAL:O	42:W:433:PHE:CB	2.59	0.51
1:A:339:PHE:C	1:A:340:ILE:HD13	2.31	0.51
1:A:461:HIS:HD2	2:B:27:U:C4	2.28	0.51
1:A:750:TRP:CZ2	1:A:778:ARG:HG2	2.45	0.51
1:A:1179:SER:O	1:A:1182:ASN:N	2.44	0.51
3:C:674:CYS:SG	3:C:822:MET:CE	2.99	0.51
13:F:45:A:N1	22:2:554:ARG:NH2	2.53	0.51
21:1:1179:ASP:HB2	21:1:1185:ARG:HD3	1.93	0.51
23:3:331:ASP:OD2	23:3:394:ASN:HB2	2.11	0.51
32:I:729:SER:O	32:I:732:ALA:HB3	2.09	0.51
37:R:125:MET:O	37:R:126:ASN:HB3	2.11	0.51
39:T:267:ASP:O	39:T:268:LYS:HB2	2.09	0.51
39:T:454:VAL:CG2	39:T:463:SER:OG	2.58	0.51
1:A:308:ILE:HG22	1:A:308:ILE:O	2.09	0.51
1:A:384:VAL:CG1	3:C:331:PHE:HD2	2.16	0.51
1:A:782:LEU:HB3	36:P:224:MET:SD	2.50	0.51
3:C:300:LEU:HD13	3:C:300:LEU:N	2.25	0.51
3:C:388:VAL:O	3:C:388:VAL:HG22	2.10	0.51
15:H:55:U:H1'	15:H:58:U:H5	1.74	0.51
15:H:107:A:C6	15:H:108:G:C5	2.99	0.51
23:3:667:ILE:HB	23:3:675:LEU:HB2	1.91	0.51
45:Z:593:PHE:O	45:Z:597:ARG:CB	2.57	0.51
1:A:122:ILE:CD1	1:A:483:GLN:CG	2.89	0.51
1:A:593:ARG:NE	14:G:-4:A:O5'	2.43	0.51
1:A:1758:PRO:HB3	21:1:938:TRP:HD1	1.74	0.51
3:C:678:THR:HG23	3:C:683:ASN:H	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:231:MET:SD	5:E:262:TRP:CE3	3.04	0.51
13:F:68:C:N4	36:P:33:ARG:CB	2.45	0.51
14:G:20:A:P	35:O:159:ARG:HD3	2.50	0.51
21:1:1054:GLU:OE1	21:1:1057:ARG:NH1	2.36	0.51
23:3:460:TRP:CZ2	23:3:507:SER:HA	2.46	0.51
23:3:854:ALA:HB1	23:3:856:LYS:HD2	1.93	0.51
23:3:1002:VAL:HB	23:3:1010:ILE:HB	1.93	0.51
1:A:1447:VAL:HG12	1:A:1449:LYS:HG2	1.92	0.51
13:F:43:A:O2'	13:F:44:G:H5'	2.11	0.51
14:G:26:U:C1'	35:O:269:CYS:CB	2.88	0.51
21:1:231:ARG:HA	21:1:607:ALA:HB2	1.92	0.51
23:3:264:GLN:HE22	23:3:322:VAL:H	1.58	0.51
37:R:442:ARG:HD2	37:R:443:GLY:C	2.31	0.51
38:S:36:CYS:HA	38:S:129:PHE:CE1	2.45	0.51
39:T:318:ARG:HG3	39:T:318:ARG:HH11	1.76	0.51
1:A:203:VAL:HG23	1:A:237:THR:CG2	2.35	0.51
1:A:589:THR:OG1	1:A:590:GLY:N	2.44	0.51
1:A:978:GLU:CD	1:A:1188:ASN:H	2.14	0.51
1:A:1320:LYS:NZ	37:R:434:TYR:CD1	2.77	0.51
1:A:1629:ILE:HB	1:A:1662:ILE:HB	1.92	0.51
1:A:2095:ASP:OD1	1:A:2095:ASP:N	2.41	0.51
3:C:220:ARG:O	3:C:448:LYS:CE	2.58	0.51
13:F:34:G:N3	13:F:34:G:C3'	2.72	0.51
13:F:94:C:H5"	28:J:347:HIS:HB3	1.92	0.51
22:2:469:VAL:HG12	22:2:471:ARG:H	1.76	0.51
23:3:113:ARG:HB2	23:3:116:VAL:HB	1.91	0.51
23:3:971:ASP:OD1	23:3:972:LEU:N	2.43	0.51
35:O:20:PHE:CE1	37:R:197:ILE:HD13	2.46	0.51
35:O:75:SER:OG	35:O:76:LYS:N	2.44	0.51
38:S:35:THR:O	38:S:129:PHE:CZ	2.63	0.51
39:T:459:LEU:HD12	39:T:460:ASP:N	2.25	0.51
44:Y:37:TRP:CH2	45:Z:498:GLY:N	2.74	0.51
1:A:95:MET:N	1:A:96:PRO:HD2	2.26	0.51
1:A:595:LYS:HB3	2:B:45:C:OP1	2.11	0.51
3:C:133:THR:O	3:C:226:VAL:O	2.29	0.51
13:F:34:G:N3	13:F:34:G:C5'	2.73	0.51
13:F:35:A:N3	13:F:35:A:C5'	2.73	0.51
23:3:354:GLY:HA3	23:3:432:ARG:HH12	1.76	0.51
24:4:16:TYR:HA	24:4:57:GLY:O	2.10	0.51
24:4:16:TYR:HD1	24:4:58:PHE:CE2	2.28	0.51
28:J:257:GLU:HA	29:L:232:TYR:CE2	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:J:273:TYR:CD2	37:R:228:PRO:CG	2.94	0.51
38:S:11:PRO:CA	38:S:166:GLY:HA3	2.41	0.51
1:A:184:ASP:OD1	34:N:1:MET:N	2.35	0.51
1:A:744:LYS:HZ1	36:P:212:ASN:C	2.14	0.51
1:A:975:VAL:HB	1:A:1099:PHE:HB2	1.93	0.51
1:A:1373:GLN:HB3	1:A:1378:GLU:OE2	2.11	0.51
1:A:1549:VAL:HG22	14:G:-6:C:O2'	2.08	0.51
1:A:2073:TRP:HH2	1:A:2310:ARG:NH1	2.09	0.51
3:C:131:ASN:ND2	3:C:223:ASP:OD2	2.44	0.51
14:G:11:A:N3	14:G:11:A:C5'	2.73	0.51
14:G:11:A:N1	14:G:12:G:N7	2.59	0.51
14:G:20:A:OP2	35:O:159:ARG:CD	2.58	0.51
21:1:669:GLN:O	21:1:672:ALA:N	2.44	0.51
23:3:246:SER:O	23:3:260:ASN:ND2	2.44	0.51
23:3:404:LEU:HD23	23:3:407:ILE:HD11	1.92	0.51
23:3:520:TYR:CE1	23:3:522:ASP:HB2	2.46	0.51
23:3:896:PHE:HB2	23:3:899:THR:HG22	1.93	0.51
28:J:273:TYR:CD1	37:R:228:PRO:HG2	2.46	0.51
38:S:131:ARG:HH11	38:S:132:VAL:C	2.12	0.51
39:T:300:ILE:O	39:T:301:ASP:HB2	2.11	0.51
1:A:331:TRP:C	1:A:331:TRP:HE3	2.14	0.51
1:A:338:VAL:CG1	3:C:267:LEU:HD23	2.41	0.51
1:A:748:ASP:OD2	39:T:484:LYS:NZ	2.43	0.51
1:A:823:SER:OG	1:A:933:ARG:NH1	2.44	0.51
1:A:1276:GLU:O	1:A:1279:VAL:HG12	2.11	0.51
3:C:93:ILE:CD1	39:T:230:ILE:CD1	2.89	0.51
15:H:111:G:O3'	15:H:112:G:O4'	2.29	0.51
21:1:475:PHE:CE1	21:1:502:LEU:HB2	2.46	0.51
21:1:582:LEU:HD23	21:1:630:ARG:HB3	1.93	0.51
23:3:757:ILE:HG23	23:3:762:LEU:HD13	1.93	0.51
23:3:1144:VAL:O	23:3:1148:LEU:HB2	2.11	0.51
35:O:283:ALA:O	35:O:287:SER:CB	2.58	0.51
39:T:385:TYR:CE2	39:T:400:PHE:HB3	2.46	0.51
1:A:86:ARG:HH21	37:R:211:ARG:HG3	1.74	0.50
1:A:227:ARG:C	1:A:416:GLY:O	2.48	0.50
1:A:1435:GLY:O	1:A:1438:VAL:HG22	2.10	0.50
3:C:215:VAL:HG11	3:C:242:LEU:HD22	1.93	0.50
3:C:559:ILE:C	3:C:559:ILE:HD12	2.31	0.50
23:3:28:GLN:HE22	23:3:343:LYS:HG2	1.77	0.50
23:3:80:VAL:HB	23:3:88:VAL:HG23	1.93	0.50
23:3:110:SER:HB3	26:6:82:ARG:HH12	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:556:ILE:HD11	23:3:564:VAL:HB	1.93	0.50
28:J:252:GLU:OE1	28:J:260:ARG:HB3	2.12	0.50
28:J:360:ASP:HA	28:J:363:ARG:HD2	1.91	0.50
37:R:220:ARG:CB	37:R:220:ARG:HH11	2.24	0.50
39:T:233:LEU:HD23	39:T:233:LEU:C	2.32	0.50
42:W:474:LYS:C	42:W:490:ALA:CB	2.80	0.50
1:A:863:GLU:OE2	1:A:916:LYS:NZ	2.36	0.50
2:B:20:G:H1'	2:B:21:A:OP1	2.12	0.50
2:B:44:A:P	13:F:66:C:H42	2.33	0.50
3:C:452:THR:O	3:C:578:ARG:N	2.43	0.50
3:C:457:VAL:HG12	3:C:462:GLY:CA	2.41	0.50
3:C:619:THR:O	3:C:620:LYS:HG3	2.11	0.50
5:E:229:TYR:CE2	5:E:272:ARG:NH1	2.77	0.50
15:H:51:A:N6	15:H:63:G:O6	2.44	0.50
35:O:149:LYS:NZ	35:O:290:LYS:HG3	2.26	0.50
38:S:10:GLN:HA	38:S:29:TRP:CE2	2.46	0.50
45:Z:574:ASN:O	45:Z:576:PHE:N	2.44	0.50
1:A:227:ARG:H	1:A:417:ARG:HA	1.75	0.50
1:A:264:PHE:CE1	1:A:459:LEU:CD1	2.81	0.50
1:A:844:GLU:CB	37:R:422:MET:HE2	2.23	0.50
1:A:1700:GLY:O	1:A:1717:ASN:N	2.41	0.50
3:C:94:ILE:HG21	39:T:259:PRO:HB3	1.92	0.50
3:C:387:ASP:O	3:C:389:ASP:OD1	2.30	0.50
3:C:659:VAL:HG12	3:C:660:VAL:N	2.26	0.50
14:G:-12:G:O2'	14:G:-11:G:O5'	2.30	0.50
15:H:153:A:C2'	15:H:154:C:C5'	2.86	0.50
15:H:182:U:C2'	15:H:183:G:H5'	2.41	0.50
21:1:1156:GLU:O	26:6:38:ARG:NH1	2.45	0.50
23:3:506:LEU:HB3	23:3:547:CYS:SG	2.52	0.50
27:7:32:LEU:HA	27:7:35:GLN:HG2	1.93	0.50
35:O:44:GLU:HA	35:O:50:ARG:O	2.10	0.50
37:R:178:ARG:CD	37:R:194:GLN:HE22	2.07	0.50
37:R:422:MET:C	37:R:424:SER:H	2.12	0.50
37:R:434:TYR:CD1	45:Z:616:VAL:CB	2.95	0.50
39:T:329:HIS:CE1	39:T:355:ARG:HG3	2.46	0.50
41:V:576:THR:O	41:V:580:ARG:N	2.36	0.50
1:A:305:ARG:HE	3:C:854:ARG:NH1	2.10	0.50
1:A:338:VAL:HB	3:C:867:PRO:HG3	1.93	0.50
1:A:1379:PHE:O	1:A:1382:SER:OG	2.17	0.50
2:B:63:A:H4'	5:E:106:LYS:HZ2	1.75	0.50
3:C:134:LEU:HD23	3:C:226:VAL:HB	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:140:HIS:HB3	3:C:230:ASP:N	2.26	0.50
3:C:456:GLY:O	3:C:457:VAL:HG13	2.11	0.50
5:E:277:PHE:CE2	5:E:300:ILE:HD12	2.46	0.50
13:F:35:A:C8	14:G:12:G:N1	2.80	0.50
13:F:37:C:N4	14:G:5:G:OP1	2.44	0.50
14:G:-4:A:H2'	14:G:-3:A:H8	1.76	0.50
21:1:897:LEU:HD11	21:1:932:ILE:HD13	1.93	0.50
23:3:996:ILE:HD13	23:3:1041:TYR:HD1	1.75	0.50
35:O:253:TYR:OH	38:S:120:GLN:HA	2.12	0.50
37:R:434:TYR:CE2	37:R:436:VAL:HG22	2.43	0.50
39:T:306:CYS:SG	39:T:336:VAL:CB	2.97	0.50
44:Y:86:ASP:HB2	45:Z:502:ALA:HB3	1.93	0.50
1:A:693:ILE:O	1:A:697:MET:N	2.42	0.50
1:A:1591:MET:SD	1:A:1611:LYS:NZ	2.75	0.50
1:A:2298:LEU:CD1	4:D:1285:SER:CA	2.89	0.50
3:C:93:ILE:HG21	39:T:218:TRP:CE2	2.46	0.50
3:C:846:VAL:HG22	3:C:887:LEU:HD11	1.94	0.50
14:G:-11:G:OP1	40:U:21:ARG:NE	2.40	0.50
14:G:132:G:H2'	14:G:133:A:C8	2.46	0.50
21:1:822:ARG:HD3	44:Y:32:TYR:OH	2.12	0.50
23:3:685:ASP:OD1	23:3:686:LEU:N	2.44	0.50
23:3:807:TYR:HE1	23:3:861:GLN:HG3	1.76	0.50
29:L:216:PHE:CZ	35:O:112:VAL:CG1	2.95	0.50
31:K:196:GLU:O	31:K:199:ILE:CG1	2.59	0.50
35:O:106:ASP:CG	35:O:107:MET:H	2.15	0.50
37:R:101:ILE:O	37:R:104:GLN:HG2	2.08	0.50
37:R:442:ARG:HH11	37:R:443:GLY:CA	2.15	0.50
39:T:297:HIS:HD2	39:T:338:CYS:SG	2.34	0.50
1:A:117:PRO:HG2	1:A:131:GLU:HB2	1.94	0.50
1:A:848:GLU:CD	37:R:424:SER:OG	2.50	0.50
2:B:100:C:H2'	2:B:101:U:C6	2.47	0.50
13:F:36:A:C3'	13:F:37:C:C5'	2.85	0.50
15:H:25:G:H2'	15:H:26:A:C8	2.45	0.50
15:H:46:U:O2'	15:H:47:U:OP2	2.25	0.50
15:H:70:C:O5'	15:H:70:C:H6	1.94	0.50
15:H:147:G:N2	15:H:148:C:C2	2.80	0.50
21:1:1003:VAL:HG23	21:1:1004:ILE:H	1.77	0.50
21:1:1132:LEU:O	21:1:1135:GLU:N	2.45	0.50
23:3:300:PHE:CG	23:3:312:LYS:HE2	2.46	0.50
34:N:105:CYS:SG	34:N:119:CYS:SG	3.10	0.50
36:P:41:ILE:HD11	39:T:318:ARG:HA	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:P:210:PHE:CG	39:T:201:SER:OG	2.64	0.50
41:V:484:SER:C	41:V:486:THR:H	2.15	0.50
1:A:121:HIS:HA	1:A:481:PHE:O	2.12	0.50
1:A:402:ILE:HD13	3:C:268:LYS:HE3	1.94	0.50
1:A:588:LEU:O	1:A:1551:PHE:CD1	2.65	0.50
1:A:1209:HIS:CG	1:A:1210:LYS:H	2.30	0.50
1:A:1667:ARG:HD2	1:A:1679:TYR:CE2	2.46	0.50
35:O:222:ARG:HA	35:O:288:PHE:HD2	1.76	0.50
1:A:89:LEU:CD2	1:A:656:LEU:HD22	2.42	0.50
1:A:948:PRO:O	1:A:951:LEU:HB2	2.12	0.50
1:A:1700:GLY:H	1:A:1717:ASN:HD22	1.60	0.50
1:A:2113:LYS:HE2	4:D:1229:ASP:CA	2.41	0.50
3:C:66:TYR:CD2	39:T:457:GLY:CA	2.79	0.50
3:C:244:LYS:CA	3:C:292:TYR:CD2	2.92	0.50
15:H:148:C:HO2'	15:H:149:A:H5'	1.77	0.50
23:3:550:ASN:HD21	23:3:595:VAL:N	2.10	0.50
23:3:1050:PHE:HB3	23:3:1167:TYR:HE2	1.75	0.50
23:3:1147:HIS:O	23:3:1151:GLU:HB2	2.10	0.50
39:T:281:ILE:HD12	39:T:282:ARG:HG2	1.92	0.50
42:W:290:GLY:HA2	42:W:573:GLY:HA2	1.94	0.50
1:A:1402:ARG:HH21	45:Z:573:PRO:HG3	1.77	0.50
3:C:259:LYS:HE2	3:C:262:ARG:HH11	1.77	0.50
5:E:228:THR:HG22	5:E:229:TYR:HD1	1.77	0.50
13:F:41:A:H2'	13:F:42:C:C6	2.47	0.50
15:H:74:U:O5'	15:H:74:U:H6	1.95	0.50
21:1:595:GLU:O	21:1:599:ASN:ND2	2.45	0.50
23:3:12:THR:HA	23:3:34:ARG:NH1	2.27	0.50
23:3:441:GLY:HA2	23:3:733:PRO:O	2.11	0.50
23:3:458:ALA:HB3	23:3:477:SER:HB3	1.94	0.50
23:3:527:ILE:HA	23:3:532:ARG:O	2.12	0.50
23:3:745:PHE:CZ	23:3:747:SER:HB3	2.46	0.50
23:3:819:MET:O	23:3:823:MET:HG3	2.12	0.50
43:X:282:LEU:HD23	43:X:295:ASP:HA	1.94	0.50
1:A:55:ASP:OD1	1:A:55:ASP:N	2.45	0.49
1:A:686:ARG:HH11	1:A:710:LEU:HD13	1.77	0.49
3:C:144:CYS:C	3:C:312:SER:HB2	2.33	0.49
3:C:499:GLY:O	3:C:500:THR:CG2	2.60	0.49
21:1:1040:GLY:HA2	21:1:1080:THR:HG22	1.94	0.49
23:3:4:TYR:HB2	23:3:1132:PHE:CZ	2.47	0.49
23:3:734:LEU:HD13	23:3:767:LEU:HD21	1.94	0.49
23:3:1188:ASN:O	23:3:1192:ASN:ND2	2.31	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:O:186:PRO:HD2	42:W:216:LEU:HA	1.93	0.49
36:P:66:ARG:HH11	36:P:66:ARG:CG	2.24	0.49
45:Z:612:TYR:C	45:Z:614:TRP:N	2.63	0.49
45:Z:614:TRP:CD1	45:Z:614:TRP:C	2.85	0.49
1:A:348:PRO:O	1:A:350:PHE:N	2.45	0.49
1:A:965:VAL:HG13	1:A:966:TRP:CD1	2.47	0.49
1:A:1403:LEU:O	37:R:412:ASP:CB	2.60	0.49
2:B:40:U:H3	14:G:-1:G:H22	1.59	0.49
3:C:116:MET:O	3:C:119:LEU:HB3	2.12	0.49
3:C:854:ARG:NH1	3:C:879:ASP:OD2	2.45	0.49
5:E:265:ARG:N	5:E:272:ARG:HH21	2.10	0.49
13:F:27:A:N9	35:O:181:TYR:CE2	2.80	0.49
15:H:181:G:N2	15:H:182:U:C2	2.80	0.49
21:1:717:THR:HG22	21:1:718:PRO:HD3	1.93	0.49
23:3:274:ARG:HG2	23:3:387:PHE:CE1	2.47	0.49
37:R:132:LEU:HB3	39:T:399:LYS:HZ1	1.77	0.49
38:S:34:LYS:HE3	38:S:78:TYR:CD2	2.47	0.49
42:W:430:ASN:O	42:W:447:TRP:CB	2.59	0.49
44:Y:48:THR:OG1	44:Y:49:GLU:OE1	2.30	0.49
1:A:152:ARG:CG	1:A:152:ARG:NH1	2.73	0.49
1:A:296:PHE:CD1	3:C:591:ALA:HB3	2.47	0.49
1:A:380:LEU:CB	3:C:354:ARG:CZ	2.88	0.49
1:A:409:ARG:N	1:A:410:PRO:HD2	2.26	0.49
1:A:596:TYR:CD1	14:G:-5:G:C4	3.01	0.49
3:C:65:TYR:C	3:C:66:TYR:CG	2.86	0.49
3:C:78:GLU:OE1	39:T:198:ARG:NH2	2.45	0.49
3:C:297:ASN:HB3	3:C:298:LEU:HD13	1.95	0.49
3:C:493:PHE:HD2	3:C:551:LEU:HD21	1.76	0.49
3:C:715:GLY:HA2	3:C:729:ALA:HB1	1.93	0.49
5:E:164:PRO:O	5:E:166:LEU:HG	2.13	0.49
21:1:499:LYS:HD3	21:1:534:GLN:NE2	2.27	0.49
21:1:652:CYS:HB3	21:1:692:HIS:CE1	2.46	0.49
21:1:827:ARG:O	21:1:830:TYR:HB3	2.12	0.49
23:3:235:LEU:HG	23:3:250:ILE:HG13	1.93	0.49
23:3:498:GLY:HA3	23:3:531:LYS:HZ3	1.77	0.49
23:3:1008:SER:OG	23:3:1009:PHE:N	2.45	0.49
34:N:59:TYR:CD1	42:W:187:SER:HA	2.48	0.49
35:O:225:PRO:CB	35:O:226:PRO:HD2	2.42	0.49
38:S:110:SER:O	38:S:111:GLN:C	2.50	0.49
42:W:474:LYS:C	42:W:490:ALA:HB3	2.33	0.49
1:A:76:MET:SD	1:A:88:TYR:CE1	3.05	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:588:LEU:C	1:A:1551:PHE:CD1	2.86	0.49
1:A:800:TYR:CB	3:C:59:LEU:HD13	2.43	0.49
1:A:1056:HIS:NE2	1:A:1060:GLU:OE2	2.44	0.49
3:C:62:ASP:HB3	36:P:206:LYS:NZ	2.27	0.49
3:C:66:TYR:CE2	36:P:211:VAL:HG11	2.45	0.49
3:C:349:PHE:CD1	3:C:356:PHE:HE1	2.22	0.49
15:H:37:U:H2'	15:H:38:A:H8	1.77	0.49
23:3:253:GLU:OE2	23:3:284:GLY:HA3	2.12	0.49
28:J:220:LEU:HD13	28:J:220:LEU:C	2.32	0.49
34:N:1:MET:HB3	34:N:2:PRO:HD3	1.94	0.49
35:O:147:LEU:HA	35:O:150:LEU:HG	1.94	0.49
37:R:433:ILE:HG13	37:R:434:TYR:O	2.12	0.49
1:A:115:ASP:CB	1:A:486:LYS:HE2	2.43	0.49
1:A:1405:LEU:N	37:R:415:LEU:HD21	2.27	0.49
3:C:133:THR:O	3:C:226:VAL:CB	2.60	0.49
3:C:335:ASN:OD1	3:C:336:TYR:N	2.45	0.49
3:C:709:TRP:N	3:C:709:TRP:CD1	2.79	0.49
23:3:994:GLN:HE22	23:3:1037:SER:HA	1.78	0.49
32:I:511:LEU:CB	32:I:547:LEU:CA	2.91	0.49
35:O:106:ASP:OD1	35:O:107:MET:N	2.42	0.49
35:O:161:ARG:NH2	35:O:182:ARG:HD2	2.27	0.49
37:R:231:VAL:HG23	37:R:232:MET:N	2.26	0.49
37:R:241:MET:SD	37:R:245:GLU:CD	2.91	0.49
45:Z:563:ARG:CG	45:Z:563:ARG:NH2	2.73	0.49
1:A:690:MET:HG3	1:A:694:LEU:HD12	1.95	0.49
1:A:1618:LYS:HD2	1:A:1626:CYS:H	1.78	0.49
1:A:1718:TRP:HZ3	1:A:1726:ILE:HD12	1.77	0.49
2:B:42:U:O4'	13:F:70:A:C4'	2.58	0.49
5:E:266:PRO:HB3	29:L:785:GLN:HB2	1.95	0.49
13:F:36:A:C8	13:F:36:A:H5'	2.48	0.49
21:1:805:TYR:CE1	21:1:809:GLU:HG3	2.46	0.49
23:3:23:SER:HA	23:3:94:PRO:HG3	1.95	0.49
23:3:483:LEU:HD11	23:3:493:GLU:HG3	1.94	0.49
23:3:755:VAL:HG13	23:3:762:LEU:HD11	1.93	0.49
23:3:794:SER:HB2	23:3:933:ASN:O	2.12	0.49
23:3:1048:ASP:OD1	23:3:1049:LYS:N	2.45	0.49
28:J:331:GLN:CG	37:R:98:TYR:OH	2.47	0.49
34:N:40:LYS:C	34:N:41:ARG:CG	2.81	0.49
35:O:240:GLY:HA3	35:O:296:ARG:NH1	2.24	0.49
45:Z:526:ILE:N	45:Z:526:ILE:HD12	2.27	0.49
1:A:365:VAL:CG1	1:A:366:LYS:N	2.73	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:461:HIS:NE2	2:B:23:C:C5	2.80	0.49
1:A:800:TYR:HB3	3:C:59:LEU:HD13	1.95	0.49
1:A:1760:GLU:HB2	1:A:1761:PRO:HD2	1.93	0.49
3:C:140:HIS:O	3:C:258:ASN:HB3	2.13	0.49
3:C:363:SER:O	3:C:364:SER:CB	2.60	0.49
4:D:455:PHE:CB	23:3:573:GLN:HG2	2.43	0.49
14:G:-9:C:N3	40:U:18:TYR:CZ	2.77	0.49
21:1:498:MET:HE1	21:1:531:LEU:HD12	1.93	0.49
21:1:1017:LEU:HD21	21:1:1058:ILE:HD11	1.93	0.49
21:1:1273:TYR:OH	21:1:1277:GLN:NE2	2.46	0.49
23:3:31:VAL:HG21	23:3:78:ILE:HD11	1.95	0.49
36:P:30:TYR:OH	37:R:162:ALA:C	2.50	0.49
42:W:210:GLU:HA	42:W:213:GLN:CB	2.42	0.49
45:Z:597:ARG:HH12	45:Z:601:LEU:CD1	2.22	0.49
1:A:380:LEU:HB3	3:C:354:ARG:HH12	1.64	0.49
1:A:532:THR:HG21	14:G:2:U:H5'	1.88	0.49
2:B:20:G:OP1	2:B:20:G:H4'	2.12	0.49
2:B:63:A:H5"	5:E:106:LYS:HZ3	1.76	0.49
3:C:73:TYR:CZ	39:T:487:LYS:CE	2.95	0.49
3:C:137:HIS:NE2	3:C:236:MET:CE	2.75	0.49
3:C:705:VAL:HG21	3:C:718:PHE:CZ	2.47	0.49
5:E:74:PHE:HE1	5:E:95:VAL:CG2	2.25	0.49
13:F:53:A:C6	13:F:54:G:C5	3.00	0.49
14:G:5:G:H2'	14:G:5:G:N3	2.28	0.49
14:G:155:U:H4'	14:G:156:U:OP2	2.13	0.49
15:H:107:A:C2	15:H:108:G:C4	3.01	0.49
15:H:143:A:N3	15:H:143:A:C3'	2.73	0.49
21:1:175:LYS:O	21:1:179:GLY:HA3	2.11	0.49
21:1:1134:ASN:ND2	22:2:534:GLN:HA	2.28	0.49
23:3:47:THR:HG23	23:3:49:LYS:H	1.77	0.49
23:3:700:LYS:NZ	23:3:740:GLU:O	2.41	0.49
23:3:785:PRO:HA	23:3:801:GLU:HA	1.95	0.49
24:4:32:LEU:HD21	24:4:79:LEU:HD21	1.94	0.49
35:O:189:PRO:CB	42:W:223:ARG:HA	2.40	0.49
37:R:55:LEU:CA	37:R:73:PRO:O	2.61	0.49
1:A:258:PHE:HZ	1:A:275:GLY:O	1.96	0.49
1:A:331:TRP:CZ2	3:C:896:PHE:CE1	3.01	0.49
1:A:347:LEU:HD13	1:A:351:TYR:OH	2.12	0.49
1:A:1393:ARG:O	1:A:1397:ILE:HG13	2.12	0.49
1:A:2129:TYR:HB3	1:A:2172:MET:HE3	1.94	0.49
3:C:301:SER:O	3:C:303:LEU:N	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:499:GLY:O	3:C:500:THR:HG23	2.13	0.49
5:E:219:VAL:HB	5:E:229:TYR:HB2	1.95	0.49
26:6:43:VAL:HG21	26:6:69:ALA:HB3	1.94	0.49
28:J:560:ALA:H	32:I:766:MET:CB	2.26	0.49
35:O:235:TYR:CD1	35:O:271:PHE:HE1	2.24	0.49
37:R:131:ASP:OD2	37:R:132:LEU:CD2	2.60	0.49
37:R:171:LEU:HD11	37:R:201:GLU:CD	2.32	0.49
39:T:442:ARG:HB3	39:T:443:THR:HG23	1.95	0.49
44:Y:38:ILE:HG22	44:Y:90:THR:HG23	1.95	0.49
1:A:304:ILE:HD11	1:A:1342:TRP:HZ2	1.77	0.49
1:A:494:LEU:HD21	1:A:562:VAL:HG21	1.95	0.49
1:A:623:LYS:HG2	48:A:2401:IHP:O43	2.13	0.49
1:A:2073:TRP:CH2	1:A:2310:ARG:NH1	2.80	0.49
3:C:381:LEU:CD2	3:C:416:LEU:HD22	2.42	0.49
5:E:74:PHE:HE1	5:E:95:VAL:HG22	1.77	0.49
15:H:71:C:H2'	15:H:72:U:H6	1.75	0.49
34:N:55:GLN:CD	42:W:192:PHE:CB	2.81	0.49
35:O:155:PRO:HG3	37:R:188:PHE:HA	1.94	0.49
37:R:433:ILE:O	37:R:434:TYR:HB3	2.13	0.49
42:W:536:ASP:O	42:W:540:THR:N	2.42	0.49
44:Y:24:ASP:CG	44:Y:25:LYS:H	2.14	0.49
1:A:44:ARG:CG	1:A:45:TYR:CE2	2.95	0.48
1:A:322:ASN:OD1	3:C:655:VAL:HB	2.12	0.48
1:A:380:LEU:N	3:C:354:ARG:CB	2.75	0.48
1:A:433:GLU:OE1	1:A:436:PRO:CB	2.54	0.48
1:A:2298:LEU:HD11	4:D:1265:GLN:CB	2.44	0.48
1:A:2298:LEU:C	4:D:1283:PRO:CB	2.78	0.48
3:C:82:GLN:HG3	39:T:237:LYS:HA	1.94	0.48
3:C:334:ILE:HD12	3:C:334:ILE:O	2.13	0.48
4:D:441:GLY:O	4:D:693:THR:N	2.36	0.48
5:E:153:PHE:N	5:E:153:PHE:CD1	2.78	0.48
13:F:26:U:H3'	13:F:27:A:C5'	2.37	0.48
15:H:182:U:HO2'	15:H:183:G:H5'	1.76	0.48
21:1:408:PHE:HB2	25:5:49:ARG:NH1	2.28	0.48
23:3:669:LEU:HD22	23:3:673:VAL:HG21	1.93	0.48
37:R:82:MET:HE2	37:R:82:MET:O	2.13	0.48
44:Y:32:TYR:C	44:Y:34:ASP:H	2.15	0.48
1:A:595:LYS:CE	1:A:644:ILE:HD11	2.38	0.48
1:A:794:TYR:CD2	1:A:1028:TYR:HB2	2.47	0.48
1:A:2149:PRO:O	1:A:2160:PRO:HD3	2.13	0.48
2:B:40:U:H3	14:G:-1:G:N2	2.11	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:78:GLU:C	39:T:198:ARG:HA	2.25	0.48
3:C:508:LYS:HB3	3:C:566:THR:HG23	1.95	0.48
3:C:855:GLY:O	3:C:856:HIS:CB	2.44	0.48
5:E:162:ARG:HH22	5:E:204:THR:HA	1.74	0.48
13:F:54:G:N2	15:H:22:U:C2	2.81	0.48
14:G:11:A:N3	14:G:11:A:C3'	2.76	0.48
15:H:5:C:H2'	15:H:6:U:H6	1.78	0.48
21:1:483:ASP:OD1	21:1:484:GLU:N	2.46	0.48
28:J:360:ASP:HA	28:J:363:ARG:CG	2.44	0.48
38:S:131:ARG:HH12	38:S:133:CYS:CB	2.26	0.48
1:A:122:ILE:HD12	1:A:483:GLN:HG3	1.94	0.48
1:A:828:PRO:HG3	1:A:925:TYR:CZ	2.48	0.48
1:A:1214:TRP:CZ2	1:A:1230:LEU:HD11	2.48	0.48
1:A:2097:ILE:HD12	1:A:2099:GLU:HB2	1.93	0.48
3:C:73:TYR:CE1	39:T:453:ALA:O	2.67	0.48
3:C:297:ASN:HD22	3:C:298:LEU:CD1	2.26	0.48
3:C:333:ASP:OD1	3:C:333:ASP:N	2.42	0.48
3:C:401:ILE:HD11	3:C:423:PHE:HB2	1.96	0.48
13:F:49:G:H2'	13:F:50:A:H8	1.78	0.48
14:G:-8:U:C5	40:U:16:ASN:HB3	2.48	0.48
14:G:138:A:H5"	29:L:12:ARG:NE	2.28	0.48
15:H:10:C:H2'	15:H:11:G:C8	2.40	0.48
23:3:157:PRO:HD2	26:6:16:GLY:HA2	1.95	0.48
23:3:870:ASN:ND2	23:3:873:GLN:H	2.10	0.48
34:N:65:TYR:OH	34:N:93:LYS:HE2	2.13	0.48
37:R:433:ILE:HG13	37:R:434:TYR:N	2.27	0.48
39:T:302:VAL:HG23	39:T:315:TRP:O	2.14	0.48
42:W:97:ASN:C	42:W:99:PHE:N	2.66	0.48
45:Z:604:LYS:HA	45:Z:607:VAL:HG23	1.94	0.48
1:A:273:ILE:CG2	1:A:274:PRO:HD2	2.43	0.48
1:A:296:PHE:CD2	3:C:656:ALA:N	2.81	0.48
1:A:2298:LEU:HD11	4:D:1285:SER:CA	2.43	0.48
3:C:291:MET:CG	3:C:292:TYR:CE1	2.96	0.48
3:C:443:VAL:O	3:C:447:PRO:CD	2.62	0.48
3:C:452:THR:O	3:C:577:PHE:CA	2.60	0.48
13:F:8:C:H6	13:F:8:C:C5'	2.15	0.48
13:F:66:C:H2'	13:F:67:G:O4'	2.12	0.48
14:G:-8:U:H2'	14:G:-7:C:O4'	2.13	0.48
14:G:9:C:H2'	14:G:10:U:C6	2.48	0.48
14:G:19:G:C5'	35:O:159:ARG:HD2	2.40	0.48
15:H:25:G:N3	15:H:26:A:C8	2.82	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:886:GLU:OE1	23:3:926:TYR:OH	2.24	0.48
23:3:1149:ARG:HH12	23:3:1161:LEU:HD13	1.79	0.48
28:J:406:PHE:HB3	28:J:411:MET:HG2	1.96	0.48
43:X:212:ASN:H	43:X:307:GLN:HE22	1.60	0.48
1:A:774:LYS:HG2	15:H:23:A:C8	2.48	0.48
1:A:1214:TRP:NE1	1:A:1276:GLU:OE1	2.23	0.48
13:F:45:A:H4'	13:F:46:G:OP2	2.14	0.48
13:F:53:A:C6	15:H:25:G:C4	3.02	0.48
23:3:930:LEU:HA	23:3:937:LEU:HD23	1.95	0.48
27:7:40:TYR:HA	27:7:43:TYR:CD2	2.49	0.48
29:L:733:LYS:O	29:L:736:ASN:CG	2.52	0.48
35:O:229:LYS:HA	35:O:277:ARG:HH22	1.78	0.48
37:R:103:ARG:CG	37:R:103:ARG:NH1	2.75	0.48
39:T:185:MET:CB	39:T:186:PRO:CD	2.90	0.48
39:T:213:GLU:HB2	39:T:218:TRP:O	2.14	0.48
1:A:279:PHE:CZ	1:A:452:LYS:HG3	2.49	0.48
1:A:593:ARG:HE	14:G:-4:A:P	2.37	0.48
1:A:718:ARG:HH21	37:R:259:LYS:CE	2.25	0.48
3:C:350:ASN:HB3	3:C:353:THR:HG23	1.94	0.48
3:C:445:ALA:O	3:C:449:ILE:HG13	2.12	0.48
3:C:678:THR:HG23	3:C:683:ASN:CA	2.43	0.48
3:C:736:GLY:N	3:C:770:PHE:HE2	2.10	0.48
21:1:1212:LEU:HD13	21:1:1237:LEU:HD13	1.96	0.48
23:3:142:TYR:CE1	23:3:157:PRO:HB3	2.48	0.48
23:3:565:TYR:CG	23:3:619:LEU:HD13	2.48	0.48
37:R:215:ASN:HD22	37:R:216:LYS:N	2.11	0.48
41:V:549:LYS:O	41:V:552:ALA:CB	2.60	0.48
1:A:247:THR:HG1	1:A:429:ASN:HB3	1.76	0.48
1:A:279:PHE:CE1	1:A:452:LYS:HE3	2.48	0.48
1:A:330:THR:O	1:A:331:TRP:CB	2.62	0.48
1:A:409:ARG:HD2	1:A:409:ARG:O	2.14	0.48
1:A:1295:ILE:HG13	1:A:1296:GLN:N	2.29	0.48
3:C:135:CYS:SG	3:C:227:LEU:HA	2.54	0.48
3:C:149:LEU:CA	3:C:427:PHE:CE2	2.97	0.48
3:C:349:PHE:HB2	3:C:356:PHE:CE1	2.48	0.48
3:C:514:TYR:CD1	3:C:515:THR:N	2.82	0.48
15:H:83:A:C2	15:H:84:C:N3	2.82	0.48
23:3:457:ASN:HD21	23:3:504:PRO:HB3	1.79	0.48
23:3:842:PHE:HD2	23:3:843:LEU:HD12	1.78	0.48
23:3:926:TYR:HE1	23:3:942:LYS:HG3	1.77	0.48
28:J:273:TYR:CZ	37:R:228:PRO:CB	2.82	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:O:223:LEU:HD22	35:O:223:LEU:C	2.34	0.48
39:T:387:PHE:CD1	39:T:387:PHE:C	2.87	0.48
1:A:121:HIS:O	1:A:123:THR:N	2.47	0.48
1:A:299:ILE:CD1	3:C:920:PRO:C	2.82	0.48
1:A:596:TYR:O	1:A:597:LYS:C	2.50	0.48
1:A:1119:ASP:OD2	1:A:1124:ASN:N	2.44	0.48
1:A:1332:HIS:HB3	1:A:1359:HIS:HE1	1.78	0.48
3:C:82:GLN:O	39:T:202:GLY:HA3	2.13	0.48
3:C:457:VAL:HG12	3:C:462:GLY:HA3	1.96	0.48
3:C:477:HIS:HD1	3:C:478:THR:N	2.12	0.48
5:E:243:LEU:HD11	5:E:247:GLY:CA	2.41	0.48
14:G:17:U:H2'	14:G:18:A:C8	2.49	0.48
15:H:83:A:C2	15:H:84:C:C4	3.01	0.48
21:1:1297:ARG:NH1	27:7:39:SER:OG	2.46	0.48
22:2:504:TRP:C	22:2:506:PHE:H	2.17	0.48
23:3:462:VAL:O	23:3:472:ALA:N	2.46	0.48
23:3:476:VAL:O	23:3:482:THR:HA	2.14	0.48
39:T:384:HIS:O	39:T:385:TYR:HB3	2.13	0.48
41:V:576:THR:O	41:V:579:SER:N	2.47	0.48
42:W:528:GLY:O	42:W:552:VAL:CB	2.62	0.48
1:A:592:TYR:O	1:A:595:LYS:O	2.32	0.48
1:A:1315:VAL:HG12	1:A:1538:TRP:CE3	2.49	0.48
3:C:128:LEU:O	3:C:199:LEU:N	2.37	0.48
3:C:690:GLU:HB2	3:C:691:PRO:HD2	1.95	0.48
13:F:44:G:H2'	22:2:554:ARG:HG2	1.96	0.48
14:G:20:A:OP2	35:O:159:ARG:HD3	2.14	0.48
15:H:37:U:H2'	15:H:38:A:C8	2.49	0.48
22:2:652:GLY:N	22:2:655:SER:O	2.45	0.48
23:3:21:ASN:HD21	23:3:28:GLN:HG2	1.77	0.48
23:3:58:VAL:HG12	23:3:1155:LEU:HB3	1.95	0.48
23:3:891:VAL:HA	23:3:906:LEU:O	2.13	0.48
23:3:1057:ARG:HG2	23:3:1058:LEU:O	2.13	0.48
37:R:184:GLN:O	37:R:188:PHE:HB2	2.13	0.48
44:Y:110:ASP:OD1	44:Y:111:HIS:N	2.43	0.48
1:A:232:LEU:HD13	1:A:404:LEU:HD12	1.95	0.48
1:A:238:LEU:HB3	1:A:411:PHE:HE2	1.79	0.48
1:A:380:LEU:HB2	3:C:354:ARG:CZ	2.44	0.48
1:A:380:LEU:N	3:C:354:ARG:CG	2.77	0.48
1:A:412:ASN:OD1	1:A:413:LEU:HD23	2.13	0.48
1:A:731:LEU:HD23	1:A:736:GLU:HB2	1.94	0.48
1:A:1551:PHE:O	1:A:1553:VAL:HG23	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1607:GLU:HB2	1:A:1634:SER:HA	1.96	0.48
1:A:1723:LYS:HB3	1:A:1724:PRO:HD3	1.95	0.48
3:C:93:ILE:O	3:C:94:ILE:CB	2.62	0.48
3:C:145:PHE:HB2	3:C:312:SER:CB	2.32	0.48
13:F:27:A:N3	35:O:181:TYR:HE2	1.98	0.48
21:1:208:PRO:N	21:1:656:LYS:HE3	2.29	0.48
23:3:981:CYS:SG	23:3:1021:LEU:HG	2.54	0.48
37:R:402:ASN:HB2	43:X:192:ARG:CG	2.43	0.48
1:A:203:VAL:HG12	1:A:207:PHE:CD1	2.49	0.47
1:A:296:PHE:CZ	3:C:591:ALA:C	2.88	0.47
1:A:735:ILE:O	1:A:738:MET:HE2	2.14	0.47
1:A:758:ARG:HD2	1:A:775:ASN:ND2	2.28	0.47
1:A:1183:PRO:HA	1:A:1201:ARG:HE	1.78	0.47
1:A:1548:TYR:CG	14:G:-6:C:C5	3.02	0.47
1:A:2325:VAL:HG11	4:D:789:MET:HA	1.94	0.47
3:C:557:GLN:N	3:C:558:PRO:HD2	2.29	0.47
5:E:263:ASP:OD1	5:E:272:ARG:HB3	2.13	0.47
13:F:44:G:N2	14:G:3:A:C8	2.82	0.47
21:1:209:GLY:HA3	21:1:614:ARG:NH1	2.29	0.47
23:3:353:PHE:HB3	23:3:406:PRO:HD3	1.96	0.47
23:3:550:ASN:OD1	23:3:551:GLN:N	2.41	0.47
23:3:814:GLN:O	23:3:818:GLN:HB2	2.13	0.47
26:6:19:ILE:HD12	26:6:42:LEU:HD21	1.96	0.47
28:J:273:TYR:CD2	37:R:228:PRO:HG3	2.49	0.47
37:R:120:VAL:CG2	37:R:121:PRO:HD2	2.44	0.47
43:X:246:TYR:H	43:X:386:ASP:HA	1.79	0.47
1:A:312:TYR:N	1:A:312:TYR:CD1	2.78	0.47
1:A:1045:GLY:HA3	1:A:1090:ARG:NH2	2.29	0.47
1:A:1270:LEU:HD12	1:A:1274:PHE:CD2	2.49	0.47
3:C:753:GLU:O	3:C:755:ASP:N	2.45	0.47
5:E:269:PRO:O	5:E:270:LYS:CB	2.54	0.47
13:F:12:G:H2'	13:F:13:G:O4'	2.14	0.47
15:H:151:C:C2	15:H:152:G:N7	2.82	0.47
23:3:1095:TYR:CZ	23:3:1164:ARG:HD2	2.49	0.47
26:6:23:CYS:HB3	26:6:58:CYS:HB2	1.97	0.47
27:7:69:MET:HA	27:7:72:MET:HG2	1.96	0.47
28:J:436:TYR:OH	28:J:458:PHE:HA	2.14	0.47
35:O:253:TYR:OH	38:S:120:GLN:CG	2.62	0.47
39:T:416:ILE:O	39:T:416:ILE:HD13	2.14	0.47
41:V:484:SER:C	41:V:486:THR:N	2.67	0.47
41:V:527:GLY:O	41:V:530:LYS:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:V:625:ARG:O	41:V:629:ASN:CB	2.62	0.47
1:A:385:GLU:OE1	1:A:386:PRO:HD2	2.14	0.47
1:A:388:LEU:CD1	3:C:379:LYS:HB3	2.45	0.47
1:A:1211:ASP:CG	41:V:505:LYS:CB	2.82	0.47
1:A:1258:LYS:HE2	37:R:432:GLU:CA	2.44	0.47
3:C:66:TYR:OH	36:P:216:ARG:HD2	2.13	0.47
3:C:73:TYR:HE1	39:T:453:ALA:O	1.97	0.47
3:C:441:PRO:O	3:C:444:GLY:CA	2.61	0.47
3:C:449:ILE:HD12	3:C:466:SER:OG	2.13	0.47
3:C:673:LYS:HB3	3:C:688:ILE:HG22	1.96	0.47
5:E:178:LEU:CD2	5:E:208:ILE:HD13	2.44	0.47
14:G:138:A:H2'	14:G:139:U:C6	2.49	0.47
21:1:1252:GLN:HG2	22:2:492:LYS:HA	1.96	0.47
23:3:240:GLY:HA3	23:3:246:SER:HB2	1.95	0.47
27:7:33:VAL:HG23	27:7:75:PRO:HG2	1.96	0.47
37:R:73:PRO:HG2	37:R:74:LEU:H	1.79	0.47
37:R:189:ASN:HD21	37:R:195:ARG:CZ	2.26	0.47
38:S:9:TRP:CE3	38:S:11:PRO:CD	2.95	0.47
44:Y:63:VAL:HG23	44:Y:64:ASN:H	1.78	0.47
1:A:1192:PHE:HE1	1:A:1274:PHE:CD1	2.32	0.47
1:A:1439:ARG:O	1:A:1443:LYS:HG2	2.15	0.47
3:C:240:GLU:OE2	3:C:292:TYR:OH	2.18	0.47
3:C:438:ILE:CD1	3:C:438:ILE:N	2.76	0.47
14:G:17:U:H2'	14:G:18:A:H8	1.79	0.47
14:G:149:G:N2	14:G:150:U:H2'	2.29	0.47
21:1:464:LEU:HD23	21:1:478:LEU:HD21	1.95	0.47
21:1:781:ASP:HB3	21:1:784:MET:HB2	1.95	0.47
23:3:54:LEU:HD22	23:3:98:MET:HA	1.97	0.47
23:3:120:PHE:HB2	23:3:133:SER:OG	2.15	0.47
26:6:21:ARG:HG3	26:6:56:GLY:HA2	1.96	0.47
36:P:224:MET:HE2	36:P:228:ILE:CD1	2.39	0.47
36:P:228:ILE:CD1	36:P:228:ILE:N	2.78	0.47
1:A:171:ASP:CG	1:A:519:ASP:OD2	2.53	0.47
1:A:277:PRO:HA	1:A:448:GLN:HG3	1.96	0.47
1:A:340:ILE:HD13	1:A:340:ILE:N	2.29	0.47
1:A:546:LEU:HD11	1:A:595:LYS:CG	2.43	0.47
1:A:2252:LEU:HD23	1:A:2253:PRO:HD2	1.96	0.47
3:C:73:TYR:OH	39:T:487:LYS:CE	2.62	0.47
3:C:185:PRO:HD3	3:C:482:TYR:CE1	2.50	0.47
5:E:161:ARG:HH11	5:E:161:ARG:CG	2.26	0.47
13:F:22:A:H3'	34:N:115:THR:HG21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:1172:LEU:HA	22:2:522:PHE:HE1	1.79	0.47
23:3:354:GLY:HA3	23:3:432:ARG:NH1	2.30	0.47
23:3:539:PRO:HD2	23:3:558:LEU:HD21	1.95	0.47
36:P:192:VAL:HG12	36:P:193:VAL:N	2.29	0.47
37:R:103:ARG:NH2	37:R:110:LYS:O	2.40	0.47
37:R:178:ARG:CD	37:R:194:GLN:NE2	2.72	0.47
1:A:323:LEU:N	1:A:324:PRO:CD	2.77	0.47
1:A:338:VAL:HB	3:C:867:PRO:CG	2.45	0.47
1:A:380:LEU:H	3:C:354:ARG:HB3	1.79	0.47
1:A:2148:VAL:O	1:A:2150:GLN:HG2	2.14	0.47
1:A:2310:ARG:HH11	1:A:2310:ARG:CG	2.27	0.47
2:B:42:U:H2'	2:B:43:U:O4'	2.13	0.47
3:C:507:VAL:HG12	3:C:508:LYS:N	2.29	0.47
3:C:710:ASN:O	3:C:711:ARG:C	2.53	0.47
14:G:-5:G:O2'	14:G:-4:A:H8	1.98	0.47
15:H:57:A:H2'	15:H:58:U:O4'	2.14	0.47
21:1:1140:GLU:O	21:1:1144:GLN:HG3	2.15	0.47
28:J:216:ASP:O	28:J:219:GLU:N	2.47	0.47
37:R:51:ILE:N	37:R:52:PRO:CD	2.77	0.47
37:R:90:VAL:HB	38:S:20:MET:SD	2.55	0.47
38:S:34:LYS:HE2	38:S:78:TYR:CD2	2.48	0.47
39:T:318:ARG:HH11	39:T:319:THR:CG2	2.28	0.47
1:A:735:ILE:O	1:A:738:MET:HB3	2.15	0.47
1:A:1241:HIS:ND1	1:A:1287:LEU:HD11	2.29	0.47
3:C:78:GLU:CD	3:C:80:ILE:HD11	2.30	0.47
3:C:749:THR:O	3:C:753:GLU:HB2	2.14	0.47
21:1:903:GLN:HE22	21:1:910:MET:HG3	1.80	0.47
23:3:18:ILE:HD13	23:3:65:LEU:HG	1.96	0.47
23:3:498:GLY:HA3	23:3:531:LYS:NZ	2.30	0.47
23:3:554:VAL:HB	23:3:566:PHE:HB2	1.97	0.47
23:3:624:CYS:SG	23:3:625:LEU:HD13	2.54	0.47
23:3:675:LEU:HD23	23:3:686:LEU:HD11	1.96	0.47
23:3:931:VAL:O	23:3:936:LYS:N	2.40	0.47
23:3:1032:TRP:O	23:3:1048:ASP:HA	2.15	0.47
28:J:273:TYR:CE2	37:R:228:PRO:HB3	2.46	0.47
34:N:27:GLN:HE21	34:N:31:GLU:HG2	1.79	0.47
35:O:236:VAL:HB	35:O:270:ALA:O	2.15	0.47
36:P:227:TYR:N	36:P:227:TYR:CD1	2.81	0.47
38:S:125:LYS:HE3	38:S:125:LYS:N	2.30	0.47
39:T:257:ARG:HD3	39:T:301:ASP:OD1	2.14	0.47
41:V:467:LEU:O	41:V:468:ASP:CB	2.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:Y:40:LEU:HB2	44:Y:43:LEU:HD11	1.96	0.47
1:A:195:LEU:H	1:A:195:LEU:HD12	1.80	0.47
1:A:229:GLN:CB	1:A:415:SER:HB2	2.45	0.47
1:A:1455:TRP:CE3	1:A:1456:THR:HB	2.50	0.47
1:A:2314:PHE:HB3	4:D:1125:SER:N	2.29	0.47
3:C:115:GLU:O	3:C:118:PHE:CA	2.61	0.47
3:C:457:VAL:CA	3:C:462:GLY:HA3	2.44	0.47
21:1:207:THR:HA	21:1:656:LYS:NZ	2.28	0.47
21:1:699:GLN:HA	21:1:702:ARG:CZ	2.45	0.47
23:3:164:ASN:ND2	23:3:189:TYR:OH	2.34	0.47
23:3:304:GLN:HA	23:3:309:ASP:O	2.15	0.47
23:3:931:VAL:HG12	23:3:932:ASN:N	2.26	0.47
25:5:14:PRO:HB2	25:5:16:GLU:OE1	2.15	0.47
39:T:246:ILE:HB	39:T:267:ASP:OD1	2.15	0.47
1:A:134:TRP:HB3	1:A:418:THR:HG22	1.95	0.47
1:A:596:TYR:CZ	14:G:-5:G:C5	3.03	0.47
1:A:695:ASP:HB3	39:T:374:SER:CB	2.38	0.47
1:A:1608:THR:HG22	1:A:1632:PHE:HB2	1.97	0.47
2:B:42:U:O5’	2:B:42:U:H6	1.97	0.47
21:1:535:ILE:O	21:1:538:LEU:N	2.47	0.47
21:1:760:GLU:N	21:1:760:GLU:OE1	2.47	0.47
21:1:1132:LEU:HD11	21:1:1150:SER:OG	2.14	0.47
23:3:5:ASN:OD1	23:3:6:LEU:N	2.47	0.47
23:3:212:GLU:OE1	23:3:223:LYS:HD2	2.15	0.47
37:R:67:ILE:HG22	37:R:69:VAL:HG21	1.97	0.47
37:R:82:MET:HE3	37:R:82:MET:C	2.36	0.47
1:A:91:ALA:O	1:A:94:TYR:N	2.43	0.47
1:A:331:TRP:CZ2	3:C:896:PHE:HE1	2.33	0.47
1:A:596:TYR:CE1	14:G:-5:G:C4	3.03	0.47
2:B:29:A:O2’	2:B:30:A:H5’	2.15	0.47
3:C:470:PRO:CA	3:C:499:GLY:HA2	2.42	0.47
3:C:490:PHE:CE1	3:C:612:LYS:HD2	2.49	0.47
13:F:49:G:H2’	13:F:50:A:C8	2.50	0.47
14:G:156:U:P	14:G:156:U:H3’	2.54	0.47
15:H:6:U:H2’	15:H:7:U:H6	1.80	0.47
15:H:47:U:H4’	15:H:48:A:OP1	2.15	0.47
15:H:153:A:C8	15:H:154:C:H5’	2.50	0.47
21:1:1185:ARG:HD2	21:1:1218:ASN:CG	2.35	0.47
22:2:642:PRO:HG3	22:2:648:LEU:HD22	1.97	0.47
23:3:182:PHE:O	23:3:210:PHE:HA	2.15	0.47
23:3:482:THR:HG23	23:3:503:THR:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:J:255:LEU:CD2	29:L:235:LEU:HD13	2.38	0.47
1:A:755:HIS:HE1	36:P:223:PHE:CB	2.14	0.46
1:A:1256:PHE:CZ	1:A:1302:GLY:HA3	2.51	0.46
1:A:2121:ARG:HA	1:A:2121:ARG:HD2	1.55	0.46
3:C:82:GLN:HG3	39:T:238:LEU:N	2.30	0.46
3:C:244:LYS:HG3	3:C:292:TYR:CD2	2.50	0.46
3:C:449:ILE:HD11	3:C:465:MET:C	2.35	0.46
3:C:571:ASN:O	3:C:572:GLU:HB3	2.16	0.46
21:1:815:PHE:HA	21:1:819:TRP:HD1	1.81	0.46
21:1:1058:ILE:O	21:1:1062:LEU:HG	2.16	0.46
23:3:248:VAL:HG23	23:3:250:ILE:HD11	1.96	0.46
23:3:536:TRP:CG	23:3:566:PHE:HZ	2.33	0.46
36:P:64:GLU:OE2	36:P:68:ARG:NE	2.48	0.46
42:W:481:MET:C	42:W:483:ASN:H	2.18	0.46
1:A:299:ILE:HD12	3:C:921:LEU:HD22	1.97	0.46
1:A:519:ASP:C	1:A:519:ASP:OD1	2.54	0.46
1:A:1209:HIS:CG	1:A:1210:LYS:N	2.83	0.46
1:A:1212:GLY:HA3	1:A:1280:ASN:ND2	2.31	0.46
2:B:41:U:H2'	2:B:42:U:C6	2.49	0.46
3:C:262:ARG:HG2	50:C:1500:GTP:N2	2.30	0.46
3:C:350:ASN:CB	3:C:353:THR:HG23	2.45	0.46
13:F:78:A:H8	13:F:78:A:OP2	1.98	0.46
15:H:150:U:H2'	15:H:151:C:C6	2.50	0.46
21:1:732:TRP:HB2	21:1:765:TYR:HE1	1.79	0.46
21:1:738:HIS:CE1	21:1:746:PHE:HE2	2.32	0.46
21:1:1169:VAL:HG12	21:1:1173:LEU:HG	1.97	0.46
23:3:28:GLN:NE2	23:3:343:LYS:HG2	2.31	0.46
23:3:1005:VAL:O	23:3:1032:TRP:HA	2.15	0.46
34:N:128:VAL:HG11	34:N:130:ARG:HB3	1.96	0.46
38:S:13:ASN:ND2	38:S:24:VAL:CG1	2.79	0.46
38:S:101:ALA:HB1	42:W:94:GLY:HA3	1.96	0.46
44:Y:48:THR:HG1	44:Y:49:GLU:H	1.63	0.46
1:A:232:LEU:O	1:A:404:LEU:HD11	2.16	0.46
1:A:298:ASP:OD1	1:A:300:ASN:N	2.48	0.46
1:A:437:ALA:O	1:A:439:GLN:HG2	2.15	0.46
1:A:532:THR:CG2	14:G:2:U:OP1	2.63	0.46
1:A:844:GLU:O	1:A:848:GLU:HG2	2.15	0.46
1:A:982:GLU:HG3	1:A:1169:GLN:HG3	1.97	0.46
3:C:221:ILE:HG23	3:C:495:ARG:HB3	1.96	0.46
5:E:87:ASP:O	5:E:88:ARG:CG	2.63	0.46
13:F:28:A:O2'	34:N:39:GLY:C	2.53	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:728:LEU:O	21:1:731:LEU:N	2.48	0.46
23:3:274:ARG:NH2	23:3:307:GLN:OE1	2.48	0.46
35:O:185:LYS:CD	42:W:215:GLU:CB	2.72	0.46
37:R:195:ARG:HB3	37:R:195:ARG:HH11	1.80	0.46
44:Y:37:TRP:CZ3	45:Z:498:GLY:C	2.86	0.46
1:A:97:HIS:HD2	1:A:473:PHE:HZ	1.59	0.46
1:A:338:VAL:HG21	3:C:867:PRO:HD3	1.97	0.46
1:A:468:LYS:HD3	1:A:468:LYS:C	2.35	0.46
1:A:1305:SER:HB2	1:A:1310:ARG:HH12	1.71	0.46
1:A:1370:ARG:NH2	41:V:506:PHE:CB	2.78	0.46
1:A:1478:LEU:HD12	1:A:1484:ILE:HD11	1.97	0.46
1:A:1718:TRP:CZ3	1:A:1723:LYS:HA	2.51	0.46
3:C:66:TYR:CG	39:T:457:GLY:HA2	2.46	0.46
3:C:80:ILE:HD13	39:T:198:ARG:HG3	1.98	0.46
3:C:678:THR:HG21	3:C:683:ASN:CB	2.43	0.46
5:E:260:ARG:CZ	5:E:276:ILE:HD11	2.46	0.46
13:F:27:A:C2	35:O:181:TYR:CD2	3.03	0.46
13:F:37:C:O2	13:F:37:C:H2'	2.15	0.46
14:G:149:G:H2'	14:G:150:U:C6	2.50	0.46
15:H:71:C:O5'	15:H:71:C:H6	1.98	0.46
15:H:79:G:N3	15:H:80:A:C8	2.83	0.46
15:H:142:C:H2'	15:H:143:A:H5'	1.98	0.46
21:1:572:HIS:HB2	21:1:612:THR:HG23	1.96	0.46
21:1:722:GLU:O	21:1:725:ASP:HB2	2.14	0.46
21:1:842:ASN:HA	21:1:879:LEU:HD11	1.96	0.46
21:1:1210:HIS:CD2	22:2:584:LEU:HD22	2.51	0.46
23:3:30:ILE:HG22	23:3:32:VAL:HG13	1.98	0.46
23:3:228:LEU:HD23	23:3:259:LYS:NZ	2.30	0.46
23:3:238:VAL:HB	23:3:247:GLY:O	2.16	0.46
23:3:509:SER:CB	23:3:549:VAL:HG21	2.45	0.46
23:3:616:ILE:O	23:3:628:LEU:HB2	2.16	0.46
23:3:801:GLU:O	23:3:864:SER:HA	2.16	0.46
35:O:146:MET:O	35:O:149:LYS:N	2.40	0.46
38:S:81:GLN:HB3	38:S:108:ASN:N	2.31	0.46
39:T:213:GLU:HG3	39:T:218:TRP:NE1	2.29	0.46
1:A:67:ARG:HD3	1:A:179:ALA:CB	2.34	0.46
1:A:1354:ARG:NH1	40:U:7:LEU:CD2	2.79	0.46
1:A:1718:TRP:CZ3	1:A:1726:ILE:HD12	2.51	0.46
3:C:385:VAL:CG2	3:C:386:GLY:N	2.78	0.46
15:H:80:A:N3	15:H:81:G:C8	2.84	0.46
21:1:478:LEU:HA	21:1:496:LYS:HE3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:579:GLU:HB3	21:1:627:THR:OG1	2.16	0.46
21:1:903:GLN:HG3	21:1:950:GLN:HE22	1.81	0.46
21:1:1186:GLN:HE22	21:1:1225:HIS:HB3	1.79	0.46
21:1:1253:GLY:HA3	21:1:1265:TYR:CD1	2.51	0.46
23:3:195:ASP:OD2	23:3:200:ALA:N	2.43	0.46
23:3:701:LEU:HA	23:3:713:LEU:O	2.16	0.46
23:3:787:LYS:HB3	23:3:800:ILE:HD11	1.96	0.46
23:3:828:GLY:O	23:3:834:LEU:N	2.49	0.46
23:3:851:ILE:HG23	23:3:852:PHE:CD2	2.50	0.46
25:5:78:SER:HA	25:5:89:VAL:HG21	1.97	0.46
35:O:193:LEU:HD23	35:O:193:LEU:O	2.15	0.46
37:R:134:ARG:O	37:R:135:PRO:C	2.54	0.46
1:A:270:ASN:HD21	40:U:8:PRO:HA	1.81	0.46
1:A:596:TYR:OH	14:G:-5:G:C8	2.68	0.46
1:A:748:ASP:CB	36:P:214:THR:HG21	2.46	0.46
1:A:1397:ILE:HG12	37:R:408:GLU:CG	2.45	0.46
1:A:1631:LEU:HD12	1:A:1660:TYR:CD2	2.51	0.46
3:C:145:PHE:CG	3:C:312:SER:HB3	2.49	0.46
3:C:149:LEU:N	3:C:427:PHE:HE2	2.14	0.46
5:E:281:VAL:HG21	42:W:148:VAL:HA	1.95	0.46
21:1:862:GLU:O	21:1:865:ARG:N	2.48	0.46
21:1:972:GLY:O	21:1:976:VAL:HG22	2.15	0.46
23:3:253:GLU:HG3	23:3:254:ASN:HD22	1.81	0.46
23:3:459:VAL:HB	23:3:757:ILE:HG23	1.97	0.46
23:3:497:SER:O	23:3:531:LYS:NZ	2.38	0.46
25:5:81:ASN:OD1	25:5:82:VAL:N	2.48	0.46
35:O:78:LYS:HG3	35:O:202:TYR:CZ	2.51	0.46
35:O:123:ARG:O	35:O:126:SER:OG	2.16	0.46
39:T:185:MET:HB2	39:T:186:PRO:HD3	1.98	0.46
1:A:75:ASP:HB2	1:A:77:THR:OG1	2.16	0.46
1:A:201:ALA:HA	1:A:204:LEU:HB3	1.98	0.46
1:A:388:LEU:HB3	1:A:391:THR:OG1	2.16	0.46
1:A:2196:HIS:HB3	1:A:2230:LEU:HD11	1.98	0.46
2:B:12:U:H3	2:B:65:G:H1	1.62	0.46
3:C:66:TYR:N	3:C:66:TYR:CD1	2.81	0.46
3:C:507:VAL:HG13	3:C:566:THR:O	2.16	0.46
3:C:559:ILE:HD12	3:C:559:ILE:O	2.15	0.46
3:C:569:ARG:O	3:C:569:ARG:HG2	2.16	0.46
3:C:671:SER:OG	3:C:672:LEU:HD22	2.15	0.46
3:C:853:ARG:O	3:C:854:ARG:CB	2.62	0.46
3:C:934:MET:HE2	3:C:934:MET:HB2	1.77	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:276:ILE:C	5:E:277:PHE:HD1	2.19	0.46
14:G:135:G:O6	14:G:137:C:N4	2.48	0.46
15:H:30:A:C8	29:L:7:LYS:HD3	2.51	0.46
15:H:107:A:C6	15:H:108:G:C6	3.04	0.46
21:1:859:ASP:OD1	21:1:860:GLU:N	2.47	0.46
29:L:78:MET:HB3	29:L:81:GLN:OE1	2.16	0.46
35:O:20:PHE:CG	35:O:21:PRO:HD2	2.51	0.46
45:Z:604:LYS:HA	45:Z:607:VAL:CG2	2.46	0.46
1:A:780:THR:HG22	1:A:898:PHE:CD2	2.50	0.46
1:A:802:THR:HG22	1:A:803:ALA:H	1.80	0.46
1:A:1237:MET:HG2	1:A:1284:LEU:HD21	1.98	0.46
1:A:1312:PRO:O	1:A:1315:VAL:HG22	2.14	0.46
1:A:1399:GLN:HB3	1:A:1401:ARG:HG2	1.98	0.46
1:A:1489:LEU:O	1:A:1492:GLY:N	2.45	0.46
4:D:1349:GLY:HA2	4:D:1491:SER:O	2.16	0.46
13:F:56:A:N1	15:H:20:G:C6	2.84	0.46
15:H:78:C:O5’	15:H:78:C:H6	1.98	0.46
21:1:588:TYR:HA	21:1:591:VAL:HG12	1.98	0.46
21:1:608:THR:O	21:1:612:THR:OG1	2.15	0.46
21:1:759:ALA:O	21:1:763:ASN:HB2	2.16	0.46
23:3:69:ARG:HG2	23:3:70:LEU:O	2.16	0.46
34:N:5:LYS:HD2	34:N:77:TYR:OH	2.16	0.46
34:N:17:LEU:HD12	34:N:18:ILE:HG23	1.98	0.46
37:R:88:ILE:HG22	37:R:96:ILE:HG23	1.98	0.46
37:R:92:SER:O	38:S:19:SER:CA	2.64	0.46
37:R:220:ARG:NH1	37:R:220:ARG:CB	2.76	0.46
1:A:532:THR:OG1	14:G:2:U:H5”	2.12	0.46
1:A:841:LEU:HD13	1:A:1433:ASP:HB2	1.98	0.46
1:A:1306:LYS:NZ	2:B:38:C:H2’	2.30	0.46
1:A:1388:GLU:O	1:A:1392:LYS:HG2	2.16	0.46
3:C:725:ASP:OD1	3:C:727:LEU:CA	2.64	0.46
5:E:266:PRO:HB3	29:L:785:GLN:CB	2.46	0.46
5:E:276:ILE:C	5:E:277:PHE:CD1	2.89	0.46
13:F:43:A:H2	14:G:4:A:H61	1.64	0.46
15:H:114:A:H2’	15:H:115:G:H8	1.81	0.46
21:1:647:PHE:O	21:1:651:VAL:HG23	2.16	0.46
21:1:1125:PRO:O	21:1:1128:VAL:N	2.49	0.46
21:1:1181:ASP:H	21:1:1184:HIS:HD2	1.64	0.46
23:3:71:THR:HG23	23:3:126:LYS:HD2	1.98	0.46
23:3:587:VAL:HG11	23:3:590:MET:HE2	1.98	0.46
23:3:718:ARG:HG2	23:3:719:SER:N	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:4:29:LEU:HD22	24:4:33:PHE:CE2	2.49	0.46
24:4:32:LEU:CD2	24:4:79:LEU:HD21	2.46	0.46
25:5:46:ARG:HB3	25:5:63:VAL:HG12	1.97	0.46
28:J:406:PHE:CG	28:J:411:MET:CE	2.97	0.46
35:O:63:MET:SD	35:O:160:ASN:HB2	2.56	0.46
36:P:54:VAL:HG13	36:P:59:PHE:HZ	1.80	0.46
37:R:185:GLY:C	37:R:186:VAL:HG13	2.35	0.46
1:A:34:ALA:HA	5:E:213:ILE:CD1	2.46	0.46
1:A:296:PHE:CB	3:C:656:ALA:CB	2.71	0.46
1:A:331:TRP:NE1	3:C:884:GLU:OE2	2.49	0.46
1:A:586:GLY:O	1:A:592:TYR:CE2	2.69	0.46
1:A:738:MET:HE3	1:A:739:ILE:HG13	1.97	0.46
1:A:1328:LEU:HD23	1:A:1470:TYR:CE2	2.51	0.46
3:C:678:THR:HG23	3:C:683:ASN:N	2.31	0.46
5:E:248:SER:HB2	5:E:249:TYR:HD1	1.75	0.46
21:1:888:LEU:O	21:1:892:LEU:HG	2.15	0.46
23:3:287:PHE:CD1	23:3:303:ALA:HB1	2.50	0.46
35:O:84:CYS:HB3	35:O:86:LEU:HG	1.98	0.46
36:P:48:GLN:O	36:P:49:ASP:CB	2.64	0.46
37:R:148:ARG:HG3	37:R:148:ARG:NH1	2.31	0.46
1:A:121:HIS:HD2	1:A:482:PHE:CE1	2.35	0.45
1:A:892:LYS:HD2	1:A:912:GLU:OE1	2.16	0.45
1:A:903:SER:OG	1:A:904:HIS:N	2.48	0.45
1:A:1026:ASN:ND2	1:A:1029:GLY:O	2.45	0.45
1:A:1348:VAL:HG11	3:C:921:LEU:HD21	1.98	0.45
1:A:2121:ARG:O	1:A:2154:HIS:HA	2.15	0.45
1:A:2169:LEU:HD21	1:A:2272:MET:HG3	1.99	0.45
5:E:232:ARG:O	5:E:262:TRP:CH2	2.69	0.45
21:1:744:ALA:O	21:1:787:ILE:HG21	2.16	0.45
21:1:1165:TYR:HE1	22:2:575:PHE:CG	2.33	0.45
23:3:58:VAL:HG12	23:3:1155:LEU:HD23	1.98	0.45
23:3:233:ASN:ND2	23:3:286:ILE:HD12	2.31	0.45
23:3:448:ALA:HB3	23:3:764:ILE:HB	1.97	0.45
23:3:488:GLY:C	23:3:490:THR:H	2.19	0.45
23:3:1012:VAL:HA	23:3:1022:ILE:O	2.17	0.45
37:R:65:PRO:HA	38:S:93:THR:O	2.16	0.45
1:A:303:ILE:HG23	3:C:933:PHE:CE1	2.50	0.45
1:A:671:THR:OG1	13:F:69:A:OP1	2.34	0.45
1:A:1084:PRO:HB3	1:A:1101:PHE:CE1	2.51	0.45
1:A:1318:THR:CG2	1:A:1484:ILE:HG21	2.46	0.45
1:A:1667:ARG:HD2	1:A:1679:TYR:CD2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:136:GLY:HA3	3:C:228:PHE:O	2.16	0.45
3:C:301:SER:C	3:C:303:LEU:N	2.68	0.45
3:C:499:GLY:C	3:C:500:THR:HG23	2.36	0.45
3:C:753:GLU:C	3:C:755:ASP:H	2.19	0.45
13:F:57:U:C2	13:F:58:G:N7	2.84	0.45
14:G:10:U:O2'	14:G:11:A:OP1	2.28	0.45
21:1:701:VAL:O	21:1:705:SER:HB3	2.16	0.45
38:S:39:PHE:CD1	38:S:129:PHE:CE2	2.88	0.45
38:S:82:PHE:H	38:S:108:ASN:H	1.64	0.45
40:U:1:MET:O	40:U:3:ASN:N	2.48	0.45
1:A:359:ILE:O	1:A:360:SER:HB3	2.16	0.45
1:A:907:PRO:CD	36:P:229:LYS:HB2	2.39	0.45
1:A:1301:ILE:CD1	1:A:1306:LYS:HE2	2.41	0.45
1:A:2070:LYS:HA	1:A:2070:LYS:HD3	1.67	0.45
1:A:2074:ARG:O	1:A:2078:ILE:HD13	2.17	0.45
1:A:2117:ILE:H	1:A:2117:ILE:HG12	1.64	0.45
3:C:336:TYR:CD1	3:C:336:TYR:C	2.89	0.45
5:E:146:ARG:NH1	5:E:148:LYS:NZ	2.62	0.45
15:H:60:U:H2'	15:H:61:C:H6	1.81	0.45
21:1:1074:ARG:HD2	21:1:1111:CYS:SG	2.55	0.45
23:3:169:HIS:CD2	23:3:170:VAL:H	2.34	0.45
23:3:526:HIS:HB3	23:3:534:ASN:O	2.17	0.45
23:3:805:ASN:O	23:3:856:LYS:HB3	2.16	0.45
31:K:188:LEU:C	31:K:188:LEU:HD13	2.36	0.45
36:P:227:TYR:N	36:P:227:TYR:HD1	2.14	0.45
39:T:306:CYS:SG	39:T:336:VAL:HG12	2.56	0.45
42:W:426:PHE:HA	42:W:433:PHE:HA	1.99	0.45
1:A:331:TRP:C	1:A:331:TRP:CE3	2.90	0.45
1:A:374:ASP:O	1:A:375:ASP:HB3	2.16	0.45
1:A:434:HIS:C	1:A:434:HIS:HD1	2.19	0.45
1:A:592:TYR:CE1	14:G:-5:G:H4'	2.51	0.45
1:A:651:TRP:CD1	13:F:66:C:C1'	2.98	0.45
1:A:1434:LYS:O	1:A:1439:ARG:NH1	2.45	0.45
3:C:193:THR:HG22	3:C:428:THR:HG21	1.97	0.45
3:C:482:TYR:CE2	3:C:493:PHE:CG	2.89	0.45
5:E:119:THR:CG2	5:E:161:ARG:CB	2.73	0.45
5:E:157:CYS:HA	5:E:168:CYS:O	2.16	0.45
15:H:181:G:C2	15:H:182:U:N3	2.84	0.45
21:1:427:PRO:O	21:1:431:LEU:N	2.45	0.45
21:1:834:VAL:O	21:1:838:VAL:HG23	2.16	0.45
21:1:1181:ASP:OD1	21:1:1182:LEU:N	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:257:THR:OG1	23:3:268:ARG:HG2	2.16	0.45
23:3:897:SER:HB2	23:3:957:GLY:HA3	1.97	0.45
23:3:905:VAL:HG23	23:3:930:LEU:HB2	1.98	0.45
27:7:73:LEU:HD12	27:7:74:GLN:N	2.32	0.45
32:I:712:VAL:O	32:I:715:GLY:N	2.49	0.45
34:N:47:TRP:HB2	34:N:48:PRO:HD3	1.99	0.45
34:N:125:LYS:HD2	42:W:167:VAL:O	2.17	0.45
35:O:234:LEU:HB2	35:O:272:ILE:HB	1.98	0.45
36:P:193:VAL:CG2	36:P:194:PHE:N	2.79	0.45
37:R:88:ILE:HD12	37:R:88:ILE:N	2.29	0.45
37:R:181:PRO:O	37:R:182:SER:CB	2.58	0.45
1:A:259:ASP:C	1:A:259:ASP:OD1	2.55	0.45
1:A:535:ARG:NH1	14:G:2:U:OP2	2.50	0.45
1:A:658:ARG:N	36:P:29:GLN:OE1	2.49	0.45
1:A:966:TRP:HE3	1:A:1178:TYR:CZ	2.35	0.45
1:A:1426:ASP:OD2	37:R:421:GLY:CA	2.64	0.45
1:A:1604:LEU:HD11	1:A:1725:LEU:HD22	1.99	0.45
3:C:183:SER:OG	3:C:480:LYS:NZ	2.50	0.45
3:C:230:ASP:CG	3:C:259:LYS:HZ1	2.19	0.45
5:E:243:LEU:CD1	5:E:247:GLY:CA	2.84	0.45
14:G:26:U:C2’	35:O:269:CYS:SG	3.04	0.45
15:H:25:G:C2	15:H:26:A:C5	3.04	0.45
15:H:150:U:H3	15:H:181:G:H1	1.62	0.45
15:H:152:G:O2’	15:H:153:A:H1’	2.16	0.45
23:3:636:GLN:O	23:3:670:GLN:HG2	2.17	0.45
23:3:796:ASN:HA	23:3:871:PRO:HD3	1.98	0.45
28:J:360:ASP:HA	28:J:363:ARG:CD	2.46	0.45
29:L:789:ALA:O	29:L:792:LEU:CG	2.64	0.45
38:S:34:LYS:HG3	38:S:78:TYR:CE2	2.52	0.45
39:T:409:LEU:HD12	39:T:409:LEU:N	2.31	0.45
42:W:266:ARG:O	42:W:267:SER:O	2.35	0.45
1:A:61:MET:HB3	1:A:62:PRO:HD2	1.98	0.45
1:A:730:GLY:O	1:A:731:LEU:HB2	2.16	0.45
1:A:1413:ASP:OD1	1:A:1414:ARG:HG3	2.17	0.45
1:A:2172:MET:HE3	1:A:2172:MET:HB2	1.86	0.45
3:C:66:TYR:CB	39:T:456:PRO:O	2.51	0.45
3:C:495:ARG:HG3	3:C:495:ARG:O	2.16	0.45
3:C:497:LEU:CD1	3:C:577:PHE:CE1	2.94	0.45
3:C:852:ARG:NH2	14:G:-12:G:OP1	2.50	0.45
5:E:260:ARG:CD	5:E:276:ILE:HG12	2.47	0.45
13:F:94:C:H2’	13:F:95:G:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:G:-12:G:HO2'	14:G:-11:G:C5'	2.29	0.45
23:3:115:ILE:HD11	27:7:18:TYR:CE1	2.51	0.45
23:3:482:THR:HG21	23:3:505:THR:OG1	2.17	0.45
37:R:179:TYR:CE2	37:R:181:PRO:HG3	2.52	0.45
39:T:297:HIS:CD2	39:T:338:CYS:SG	3.09	0.45
42:W:516:PHE:HA	42:W:522:TYR:O	2.16	0.45
45:Z:525:TYR:CE1	45:Z:526:ILE:CG2	2.86	0.45
1:A:317:PRO:HB2	1:A:327:VAL:HG11	1.98	0.45
1:A:536:LYS:HD3	13:F:72:G:O2'	2.16	0.45
1:A:1733:ILE:HG23	1:A:1737:ASN:HB2	1.98	0.45
2:B:57:G:H2'	2:B:58:U:H5'	1.99	0.45
3:C:926:ALA:N	3:C:927:PRO:HD2	2.32	0.45
5:E:178:LEU:HG	5:E:188:GLN:HB2	1.98	0.45
5:E:277:PHE:CD1	5:E:277:PHE:N	2.83	0.45
13:F:22:A:P	34:N:115:THR:OG1	2.74	0.45
21:1:86:ALA:O	21:1:89:ALA:HB3	2.17	0.45
21:1:476:ASP:OD1	21:1:477:LYS:N	2.49	0.45
21:1:1110:VAL:O	21:1:1113:THR:HB	2.17	0.45
21:1:1251:LEU:HD12	22:2:497:SER:OG	2.16	0.45
23:3:223:LYS:HE2	23:3:224:TYR:CZ	2.52	0.45
23:3:429:ARG:HH12	27:7:59:GLU:H	1.65	0.45
23:3:1114:SER:HB2	23:3:1215:TYR:CE1	2.51	0.45
28:J:338:GLU:O	37:R:116:TYR:CE1	2.69	0.45
35:O:225:PRO:HB3	35:O:302:TRP:CZ2	2.51	0.45
37:R:128:ASP:OD2	37:R:133:GLN:OE1	2.34	0.45
39:T:393:ASP:O	39:T:413:ASN:ND2	2.49	0.45
45:Z:564:PRO:O	45:Z:582:TYR:CG	2.69	0.45
45:Z:600:ARG:CG	45:Z:600:ARG:NH1	2.73	0.45
1:A:76:MET:SD	1:A:88:TYR:CE2	3.10	0.45
1:A:402:ILE:HG22	3:C:268:LYS:HZ1	1.77	0.45
1:A:755:HIS:CG	36:P:219:PHE:HE2	2.35	0.45
1:A:833:LYS:HG3	1:A:834:HIS:CD2	2.52	0.45
1:A:975:VAL:HG11	1:A:1153:VAL:HG21	1.98	0.45
1:A:1342:TRP:CE3	3:C:921:LEU:CG	3.00	0.45
1:A:2073:TRP:CZ3	1:A:2313:HIS:CE1	3.05	0.45
2:B:22:U:O2	2:B:22:U:H2'	2.15	0.45
3:C:144:CYS:SG	3:C:148:CYS:SG	3.15	0.45
13:F:38:G:OP2	13:F:38:G:C8	2.70	0.45
14:G:6:A:H2'	14:G:7:G:H8	1.82	0.45
21:1:501:LEU:O	21:1:504:ILE:N	2.48	0.45
21:1:592:GLU:O	21:1:596:ILE:HG23	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:629:ALA:HA	21:1:667:ILE:HG12	1.99	0.45
23:3:383:ASP:OD1	23:3:384:THR:N	2.50	0.45
23:3:607:VAL:HB	23:3:615:ARG:O	2.17	0.45
23:3:1057:ARG:HB2	23:3:1092:ILE:HD13	1.98	0.45
37:R:82:MET:C	37:R:82:MET:CE	2.86	0.45
42:W:466:ALA:HB2	42:W:512:CYS:O	2.17	0.45
44:Y:41:GLY:HA2	44:Y:79:PHE:HB3	1.99	0.45
1:A:733:THR:OG1	1:A:734:PRO:HD3	2.16	0.45
1:A:1013:ASN:OD1	1:A:1030:ILE:HG13	2.16	0.45
1:A:1125:ILE:HG22	1:A:1147:VAL:HG21	1.99	0.45
1:A:2334:TYR:CE1	4:D:591:GLU:CB	3.00	0.45
2:B:40:U:OP2	2:B:40:U:C6	2.70	0.45
3:C:137:HIS:HD2	3:C:236:MET:HB2	1.61	0.45
3:C:191:PRO:HG2	3:C:426:GLU:OE1	2.17	0.45
3:C:445:ALA:HB1	3:C:449:ILE:CG1	2.45	0.45
5:E:162:ARG:HH21	5:E:204:THR:HA	1.78	0.45
13:F:51:U:H2'	13:F:52:U:O4'	2.17	0.45
14:G:20:A:OP2	35:O:159:ARG:HG3	2.16	0.45
21:1:552:LEU:HA	21:1:555:VAL:HG12	1.98	0.45
21:1:822:ARG:NH1	44:Y:31:GLU:HG2	2.32	0.45
21:1:897:LEU:O	21:1:901:GLN:HG3	2.17	0.45
21:1:1186:GLN:NE2	21:1:1225:HIS:HB3	2.31	0.45
25:5:48:ILE:HG12	25:5:62:VAL:HG23	1.99	0.45
28:J:406:PHE:CB	28:J:411:MET:HG2	2.47	0.45
35:O:205:ILE:O	35:O:207:ASP:N	2.50	0.45
35:O:259:ARG:HD2	35:O:273:GLN:HG2	1.99	0.45
39:T:342:GLU:CB	39:T:343:PRO:HD2	2.47	0.45
39:T:454:VAL:HG22	39:T:463:SER:OG	2.16	0.45
39:T:455:GLN:CG	39:T:456:PRO:CD	2.94	0.45
1:A:44:ARG:CD	1:A:45:TYR:CE2	2.99	0.45
1:A:845:ARG:NH2	1:A:1439:ARG:HE	2.15	0.45
1:A:1258:LYS:HE2	37:R:432:GLU:CB	2.47	0.45
3:C:65:TYR:O	3:C:66:TYR:CB	2.65	0.45
3:C:230:ASP:OD2	3:C:233:GLU:CG	2.55	0.45
3:C:502:HIS:ND1	3:C:543:ARG:HB3	2.32	0.45
3:C:926:ALA:HA	3:C:929:LEU:HG	1.98	0.45
13:F:50:A:H2'	13:F:51:U:H6	1.82	0.45
14:G:6:A:H2'	14:G:7:G:C8	2.52	0.45
14:G:12:G:N3	14:G:12:G:C2'	2.79	0.45
14:G:157:U:H5'	21:1:622:GLU:OE1	2.17	0.45
15:H:113:G:H2'	15:H:114:A:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:1002:ASN:OD1	21:1:1041:ARG:NH2	2.50	0.45
22:2:611:ASP:O	22:2:614:ARG:CB	2.60	0.45
23:3:883:GLU:HG3	23:3:884:GLN:N	2.32	0.45
23:3:1051:GLY:HA2	23:3:1100:THR:HA	1.99	0.45
25:5:26:LEU:HD12	25:5:87:LEU:HD22	1.98	0.45
27:7:31:TRP:HE3	27:7:32:LEU:HD12	1.82	0.45
29:L:226:ASP:OD1	37:R:83:SER:HB2	2.16	0.45
32:I:433:ALA:O	32:I:437:CYS:N	2.50	0.45
34:N:91:LYS:HD3	34:N:91:LYS:HA	1.81	0.45
35:O:197:ASN:O	35:O:201:ARG:HG3	2.17	0.45
37:R:88:ILE:HG21	37:R:96:ILE:CG2	2.46	0.45
37:R:89:GLN:OE1	38:S:145:VAL:HG13	2.17	0.45
37:R:408:GLU:CG	37:R:409:VAL:N	2.78	0.45
45:Z:524:ARG:HD2	45:Z:525:TYR:CB	2.46	0.45
1:A:1348:VAL:HG11	3:C:921:LEU:CD2	2.47	0.44
1:A:1549:VAL:HG22	14:G:-6:C:HO2'	1.82	0.44
3:C:93:ILE:CG2	39:T:218:TRP:NE1	2.80	0.44
5:E:276:ILE:O	5:E:277:PHE:HD1	2.00	0.44
13:F:68:C:C5	36:P:33:ARG:HG2	2.52	0.44
13:F:94:C:H2'	13:F:95:G:C8	2.52	0.44
15:H:7:U:H2'	15:H:8:C:C6	2.52	0.44
15:H:81:G:N3	15:H:82:G:C8	2.85	0.44
15:H:141:C:H2'	15:H:142:C:C6	2.50	0.44
21:1:810:ILE:O	21:1:813:PRO:HD2	2.17	0.44
23:3:544:ILE:HD11	23:3:556:ILE:HG21	1.98	0.44
23:3:1140:PHE:O	23:3:1144:VAL:HG23	2.17	0.44
35:O:56:ARG:HG2	35:O:67:LYS:HB3	1.99	0.44
35:O:131:THR:O	35:O:132:ARG:HB2	2.17	0.44
35:O:294:ASN:O	35:O:296:ARG:HG3	2.17	0.44
37:R:147:THR:HG23	39:T:360:VAL:CG1	2.40	0.44
37:R:416:PHE:O	37:R:416:PHE:CG	2.70	0.44
41:V:548:ALA:HB2	41:V:585:ILE:CB	2.42	0.44
1:A:280:GLU:OE1	40:U:9:THR:HG21	2.17	0.44
1:A:1088:PHE:HD1	1:A:1097:ILE:HG12	1.82	0.44
1:A:1310:ARG:NH1	1:A:1566:ILE:HD11	2.32	0.44
1:A:1430:LEU:HD11	37:R:422:MET:HA	1.98	0.44
1:A:1557:LEU:HD13	1:A:1580:HIS:CE1	2.53	0.44
1:A:2280:ASN:HB3	1:A:2309:HIS:CD2	2.53	0.44
2:B:44:A:OP1	13:F:66:C:N4	2.30	0.44
3:C:93:ILE:CG2	39:T:218:TRP:CZ2	3.00	0.44
3:C:388:VAL:HA	3:C:392:LEU:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:132:THR:HG21	5:E:146:ARG:HG2	1.98	0.44
13:F:58:G:O2'	13:F:59:G:OP1	2.31	0.44
15:H:143:A:OP2	15:H:143:A:C2	2.71	0.44
15:H:157:G:H5"	15:H:157:G:C8	2.50	0.44
21:1:762:ALA:O	21:1:766:THR:CB	2.64	0.44
21:1:1252:GLN:NE2	22:2:492:LYS:O	2.51	0.44
22:2:613:LEU:HD21	24:4:32:LEU:HD13	1.99	0.44
23:3:404:LEU:HB3	23:3:407:ILE:HD11	1.99	0.44
23:3:1159:ASP:OD1	23:3:1160:HIS:N	2.49	0.44
28:J:297:ASN:OD1	29:L:223:GLY:O	2.34	0.44
29:L:213:GLU:CB	35:O:110:SER:HB3	2.47	0.44
35:O:230:THR:H	35:O:277:ARG:NH1	2.15	0.44
38:S:38:ASN:HD22	38:S:100:MET:CE	2.31	0.44
1:A:193:LEU:HD12	1:A:194:GLU:N	2.29	0.44
1:A:380:LEU:HD22	3:C:354:ARG:C	2.21	0.44
1:A:380:LEU:CD2	3:C:354:ARG:C	2.84	0.44
1:A:1136:ARG:CZ	1:A:1139:ARG:HH21	2.30	0.44
1:A:1136:ARG:NE	1:A:1139:ARG:HH21	2.16	0.44
1:A:1459:ARG:HD3	1:A:1459:ARG:HA	1.75	0.44
2:B:63:A:H5"	5:E:106:LYS:NZ	2.32	0.44
3:C:140:HIS:HB3	3:C:230:ASP:CB	2.43	0.44
3:C:671:SER:CB	3:C:672:LEU:HD22	2.46	0.44
5:E:209:ILE:HG21	5:E:250:LEU:HD11	1.94	0.44
13:F:39:A:H2'	13:F:40:U:C6	2.52	0.44
14:G:20:A:OP2	35:O:159:ARG:CG	2.64	0.44
21:1:529:GLY:HA2	21:1:570:TYR:CZ	2.51	0.44
23:3:205:GLN:HB2	23:3:228:LEU:O	2.17	0.44
23:3:462:VAL:HG21	23:3:508:CYS:HB3	1.98	0.44
23:3:484:VAL:HG21	23:3:499:PHE:HB2	1.99	0.44
23:3:536:TRP:CD1	23:3:566:PHE:HZ	2.35	0.44
23:3:723:TYR:CD1	23:3:725:TYR:HB2	2.53	0.44
25:5:98:PHE:O	25:5:100:LYS:N	2.50	0.44
35:O:33:TYR:OH	42:W:139:LEU:O	2.30	0.44
36:P:188:TRP:N	36:P:188:TRP:CD2	2.86	0.44
37:R:416:PHE:O	37:R:416:PHE:CD1	2.70	0.44
39:T:387:PHE:CZ	39:T:398:TRP:CD1	3.04	0.44
45:Z:500:GLY:O	45:Z:503:GLN:N	2.50	0.44
45:Z:573:PRO:O	45:Z:573:PRO:CD	2.65	0.44
45:Z:597:ARG:CZ	45:Z:601:LEU:HD13	2.47	0.44
1:A:121:HIS:CA	1:A:481:PHE:O	2.66	0.44
1:A:394:TYR:CD1	1:A:394:TYR:N	2.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:532:THR:OG1	14:G:2:U:H3'	2.17	0.44
1:A:661:GLU:HA	37:R:213:LYS:HA	2.00	0.44
1:A:777:GLY:O	1:A:780:THR:OG1	2.25	0.44
1:A:1074:PHE:HB3	1:A:1079:THR:OG1	2.17	0.44
1:A:1354:ARG:NH1	40:U:7:LEU:HD21	2.32	0.44
1:A:2125:ALA:O	1:A:2150:GLN:NE2	2.50	0.44
1:A:2328:ALA:CB	4:D:788:GLY:N	2.79	0.44
4:D:721:VAL:HA	4:D:825:THR:O	2.17	0.44
13:F:5:U:H5'	13:F:6:C:OP2	2.17	0.44
15:H:159:U:H2'	15:H:160:A:C8	2.52	0.44
15:H:165:A:C6	15:H:166:G:O6	2.71	0.44
21:1:937:LEU:O	21:1:940:LEU:HB3	2.18	0.44
22:2:611:ASP:O	22:2:614:ARG:N	2.50	0.44
23:3:643:VAL:HG12	23:3:664:TYR:O	2.17	0.44
23:3:1063:ASN:H	23:3:1087:GLN:HE22	1.65	0.44
23:3:1096:HIS:NE2	23:3:1098:GLY:HA2	2.33	0.44
36:P:189:ASP:C	36:P:191:ASP:N	2.68	0.44
39:T:439:TRP:CE3	39:T:446:ASN:HB2	2.52	0.44
44:Y:36:ALA:CB	45:Z:499:LYS:O	2.54	0.44
1:A:141:ILE:HG12	1:A:426:LEU:HD23	1.99	0.44
1:A:507:LEU:HD12	1:A:507:LEU:HA	1.79	0.44
1:A:1402:ARG:HD2	37:R:412:ASP:HA	1.98	0.44
1:A:2303:GLU:CD	1:A:2303:GLU:H	2.19	0.44
3:C:135:CYS:SG	3:C:227:LEU:CB	3.06	0.44
3:C:259:LYS:HD2	50:C:1500:GTP:C5	2.52	0.44
3:C:673:LYS:HG3	3:C:686:THR:HG23	2.00	0.44
14:G:21:A:O3'	14:G:22:C:C6	2.71	0.44
15:H:60:U:H2'	15:H:61:C:C6	2.52	0.44
21:1:1211:LEU:O	21:1:1215:VAL:HG23	2.17	0.44
23:3:460:TRP:CE2	23:3:507:SER:HA	2.53	0.44
23:3:511:LEU:HB2	23:3:517:VAL:HG23	1.99	0.44
26:6:58:CYS:N	26:6:63:GLY:O	2.46	0.44
35:O:258:ILE:HG22	35:O:260:THR:N	2.32	0.44
44:Y:58:GLN:HB2	45:Z:584:TRP:NE1	2.33	0.44
1:A:79:ARG:HD2	1:A:79:ARG:O	2.18	0.44
1:A:305:ARG:NH2	3:C:854:ARG:HD3	2.32	0.44
1:A:611:LEU:HA	1:A:611:LEU:HD12	1.85	0.44
1:A:707:ARG:O	1:A:711:GLN:HG3	2.17	0.44
1:A:978:GLU:OE2	1:A:1188:ASN:N	2.36	0.44
1:A:1134:TRP:CZ2	1:A:1195:ARG:HB2	2.53	0.44
1:A:1407:ASP:OD1	1:A:1407:ASP:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:457:VAL:CG1	3:C:462:GLY:HA3	2.46	0.44
15:H:34:U:C4	15:H:35:A:N7	2.85	0.44
15:H:73:C:O5'	15:H:73:C:H6	2.01	0.44
15:H:142:C:O2'	15:H:143:A:H5'	2.18	0.44
15:H:147:G:C6	15:H:148:C:N4	2.86	0.44
21:1:1108:ASN:OD1	21:1:1110:VAL:HG12	2.17	0.44
22:2:569:GLN:CB	42:W:460:SER:CB	2.95	0.44
23:3:589:CYS:O	23:3:608:GLY:N	2.41	0.44
23:3:812:LYS:O	23:3:816:LYS:CB	2.57	0.44
35:O:68:THR:HA	35:O:83:THR:CG2	2.45	0.44
36:P:193:VAL:HG23	36:P:194:PHE:CB	2.47	0.44
38:S:9:TRP:HE3	38:S:11:PRO:CG	2.29	0.44
44:Y:63:VAL:HG23	44:Y:64:ASN:N	2.33	0.44
1:A:67:ARG:HE	1:A:67:ARG:HB2	1.58	0.44
1:A:193:LEU:HB3	1:A:208:TYR:OH	2.17	0.44
1:A:373:ASP:OD1	1:A:374:ASP:N	2.51	0.44
1:A:460:LYS:NZ	2:B:49:A:P	2.91	0.44
1:A:1362:ASP:OD1	1:A:1362:ASP:N	2.51	0.44
1:A:1481:VAL:CG1	1:A:1498:TRP:CE2	2.88	0.44
1:A:2237:TRP:HZ2	1:A:2248:PRO:HB2	1.81	0.44
1:A:2310:ARG:HH11	1:A:2310:ARG:HB3	1.83	0.44
3:C:145:PHE:HD1	3:C:312:SER:HB3	1.83	0.44
5:E:266:PRO:CG	29:L:785:GLN:HB3	2.48	0.44
13:F:9:U:H2'	13:F:10:U:C6	2.52	0.44
13:F:68:C:C5	36:P:33:ARG:CG	2.95	0.44
15:H:26:A:C6	15:H:27:U:C4	3.05	0.44
21:1:1072:ALA:O	21:1:1075:ARG:HB3	2.18	0.44
23:3:607:VAL:HG21	23:3:617:ILE:HD12	1.99	0.44
23:3:929:LYS:HD3	23:3:938:GLU:OE2	2.17	0.44
29:L:224:PHE:CE1	37:R:86:LEU:HD12	2.43	0.44
39:T:342:GLU:O	39:T:343:PRO:C	2.56	0.44
41:V:525:PHE:O	41:V:526:GLU:C	2.55	0.44
42:W:476:LEU:O	42:W:487:ILE:HA	2.16	0.44
45:Z:584:TRP:CZ3	45:Z:586:GLY:HA2	2.53	0.44
1:A:148:TRP:HE3	1:A:629:PHE:CD1	2.35	0.44
1:A:402:ILE:HG21	3:C:268:LYS:HZ2	1.47	0.44
1:A:1034:LEU:HB2	1:A:1037:ALA:HB2	1.98	0.44
1:A:1457:HIS:CE1	37:R:424:SER:C	2.90	0.44
1:A:1533:ARG:HD2	1:A:1751:LEU:O	2.18	0.44
14:G:21:A:P	35:O:156:TYR:HH	2.35	0.44
14:G:26:U:H5'	35:O:235:TYR:OH	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:601:ALA:HB2	21:1:635:VAL:HG12	2.00	0.44
21:1:969:LYS:O	21:1:973:HIS:ND1	2.36	0.44
23:3:353:PHE:CD1	23:3:406:PRO:HD3	2.53	0.44
23:3:930:LEU:HG	23:3:934:GLY:HA2	1.98	0.44
24:4:79:LEU:HG	24:4:84:ILE:HG13	2.00	0.44
36:P:66:ARG:HB2	36:P:66:ARG:NH1	2.30	0.44
37:R:124:VAL:HG22	37:R:125:MET:H	1.83	0.44
37:R:132:LEU:HD23	37:R:132:LEU:N	2.31	0.44
37:R:208:GLU:OE2	37:R:211:ARG:NH1	2.51	0.44
37:R:415:LEU:H	37:R:415:LEU:HG	1.56	0.44
39:T:358:ASP:HB2	39:T:365:ARG:HD2	2.00	0.44
45:Z:524:ARG:CD	45:Z:524:ARG:C	2.85	0.44
1:A:82:ARG:NH1	14:G:16:G:O6	2.49	0.44
1:A:106:MET:HG2	1:A:489:TRP:CZ2	2.53	0.44
1:A:300:ASN:O	3:C:936:LYS:CB	2.66	0.44
1:A:382:GLU:O	1:A:383:PHE:CD2	2.70	0.44
1:A:941:LYS:HE3	1:A:951:LEU:HD21	2.00	0.44
1:A:1038:SER:HA	1:A:1442:PHE:HE2	1.83	0.44
1:A:2072:GLU:O	1:A:2076:ARG:HG3	2.18	0.44
1:A:2222:SER:OG	1:A:2223:CYS:N	2.50	0.44
3:C:439:PRO:O	3:C:440:SER:CB	2.66	0.44
3:C:465:MET:HE1	3:C:475:MET:CE	2.47	0.44
3:C:779:LEU:HD11	3:C:825:PRO:HB2	1.99	0.44
14:G:-8:U:C2	40:U:15:THR:O	2.71	0.44
14:G:11:A:C5	14:G:12:G:C8	3.06	0.44
14:G:21:A:O3’	14:G:22:C:H6	2.00	0.44
15:H:6:U:H2’	15:H:7:U:C6	2.53	0.44
21:1:503:LYS:HD2	21:1:515:ALA:HB2	2.00	0.44
21:1:779:SER:HB3	21:1:784:MET:HG2	2.00	0.44
21:1:1131:ALA:O	21:1:1135:GLU:HG2	2.17	0.44
23:3:411:GLN:HA	23:3:1105:GLN:OE1	2.18	0.44
23:3:798:ILE:HA	23:3:867:ARG:O	2.18	0.44
25:5:46:ARG:N	25:5:63:VAL:O	2.50	0.44
34:N:125:LYS:HA	34:N:125:LYS:HD3	1.74	0.44
35:O:28:LEU:CD2	37:R:195:ARG:HE	2.29	0.44
38:S:81:GLN:HB3	38:S:108:ASN:H	1.82	0.44
42:W:420:ALA:HB3	42:W:438:ASP:CB	2.48	0.44
1:A:44:ARG:HG2	1:A:45:TYR:CD2	2.53	0.43
1:A:330:THR:O	1:A:331:TRP:HB2	2.17	0.43
1:A:402:ILE:HD13	3:C:268:LYS:CE	2.47	0.43
1:A:1306:LYS:HZ1	2:B:38:C:H2’	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1532:ARG:HG2	1:A:1572:SER:OG	2.18	0.43
3:C:229:ILE:CG2	3:C:234:GLY:O	2.66	0.43
5:E:248:SER:HB2	5:E:249:TYR:CE1	2.53	0.43
13:F:35:A:C8	14:G:12:G:O6	2.71	0.43
13:F:68:C:H42	39:T:283:HIS:CE1	2.35	0.43
21:1:903:GLN:HG3	21:1:950:GLN:NE2	2.33	0.43
23:3:176:GLY:O	23:3:178:GLU:HG2	2.17	0.43
23:3:446:GLU:CD	23:3:763:ARG:HD3	2.38	0.43
23:3:747:SER:N	23:3:750:CYS:O	2.51	0.43
23:3:998:HIS:HE1	23:3:1064:ASP:OD2	2.00	0.43
23:3:1207:LYS:HA	23:3:1210:ASP:OD2	2.18	0.43
25:5:53:THR:O	25:5:57:ARG:HG3	2.18	0.43
28:J:339:TRP:C	37:R:116:TYR:CE2	2.92	0.43
37:R:109:ASP:OD1	37:R:110:LYS:N	2.51	0.43
39:T:454:VAL:CG1	39:T:455:GLN:N	2.81	0.43
1:A:73:HIS:HA	1:A:81:PHE:CE2	2.53	0.43
1:A:89:LEU:CD2	1:A:656:LEU:CD2	2.95	0.43
1:A:331:TRP:HE3	1:A:332:TYR:CA	2.30	0.43
1:A:664:HIS:CE1	1:A:666:LYS:HD3	2.53	0.43
1:A:694:LEU:O	1:A:698:PRO:HG3	2.18	0.43
1:A:970:GLU:HB2	1:A:972:GLU:OE2	2.17	0.43
1:A:1553:VAL:O	1:A:1561:PHE:HA	2.18	0.43
1:A:2328:ALA:HB3	4:D:787:ALA:C	2.38	0.43
3:C:135:CYS:N	3:C:226:VAL:O	2.50	0.43
3:C:392:LEU:HD12	3:C:392:LEU:O	2.18	0.43
3:C:508:LYS:O	3:C:566:THR:HG22	2.18	0.43
3:C:674:CYS:HB2	3:C:818:SER:HB3	2.00	0.43
3:C:703:GLU:OE2	3:C:740:THR:CG2	2.50	0.43
5:E:251:LEU:CG	5:E:291:CYS:SG	3.05	0.43
15:H:159:U:H2'	15:H:160:A:H8	1.83	0.43
15:H:182:U:H6	15:H:182:U:O5'	2.01	0.43
21:1:528:ALA:HB2	21:1:563:LEU:HD13	2.00	0.43
21:1:732:TRP:O	21:1:735:ILE:HB	2.19	0.43
22:2:556:LYS:O	22:2:559:PRO:HD3	2.18	0.43
23:3:409:PHE:HD2	23:3:788:PHE:CE2	2.36	0.43
23:3:633:LEU:HD12	23:3:637:PRO:HG2	2.00	0.43
23:3:791:HIS:ND1	23:3:794:SER:HB3	2.33	0.43
23:3:837:GLU:O	23:3:837:GLU:HG2	2.17	0.43
37:R:419:SER:C	37:R:420:LYS:O	2.55	0.43
1:A:908:VAL:HA	1:A:1445:TYR:O	2.18	0.43
1:A:1071:PHE:CD2	1:A:1072:LEU:HG	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:131:ASN:HB3	3:C:549:TRP:CZ2	2.52	0.43
3:C:524:ILE:O	3:C:525:CYS:SG	2.74	0.43
15:H:64:A:H2'	15:H:65:U:C6	2.53	0.43
15:H:153:A:H2'	15:H:154:C:H5"	1.99	0.43
21:1:840:LEU:O	21:1:844:VAL:HG12	2.19	0.43
22:2:482:ALA:O	22:2:485:PRO:HD3	2.18	0.43
23:3:88:VAL:HA	23:3:103:HIS:O	2.18	0.43
23:3:1056:VAL:HG22	23:3:1091:VAL:HG22	2.01	0.43
24:4:67:ALA:HA	24:4:70:ALA:HB3	2.00	0.43
31:K:134:ALA:O	31:K:137:VAL:HG12	2.17	0.43
35:O:27:CYS:O	35:O:28:LEU:C	2.56	0.43
35:O:185:LYS:CG	42:W:216:LEU:HA	2.46	0.43
37:R:88:ILE:HG22	37:R:96:ILE:CG2	2.49	0.43
39:T:406:ILE:HG22	39:T:407:GLN:N	2.33	0.43
42:W:309:MET:HA	42:W:334:ALA:HB1	2.00	0.43
1:A:338:VAL:CB	3:C:867:PRO:CG	2.96	0.43
1:A:406:TRP:CH2	3:C:265:LEU:O	2.64	0.43
1:A:741:ARG:NH2	39:T:432:ASP:O	2.41	0.43
1:A:1263:TRP:CE3	1:A:1295:ILE:HD13	2.53	0.43
1:A:1307:MET:SD	1:A:1547:VAL:CB	2.96	0.43
1:A:1480:GLY:O	1:A:1483:GLY:N	2.51	0.43
1:A:1674:HIS:HB3	1:A:1709:TYR:CE2	2.53	0.43
1:A:2284:MET:HE1	1:A:2311:PRO:HG3	1.99	0.43
2:B:99:C:H2'	2:B:100:C:C6	2.53	0.43
3:C:133:THR:CB	3:C:225:VAL:HG23	2.43	0.43
3:C:297:ASN:HD22	3:C:298:LEU:HD12	1.83	0.43
3:C:350:ASN:HB3	3:C:353:THR:CG2	2.49	0.43
3:C:505:GLN:HG2	3:C:506:PRO:HD2	2.00	0.43
3:C:776:GLU:O	3:C:781:ASP:HA	2.18	0.43
13:F:42:C:H2'	13:F:43:A:C8	2.53	0.43
21:1:885:ASP:OD1	21:1:888:LEU:HB3	2.18	0.43
21:1:1119:VAL:O	21:1:1122:THR:HG22	2.17	0.43
21:1:1120:ALA:HB1	21:1:1125:PRO:HB3	2.01	0.43
21:1:1179:ASP:HB3	22:2:511:LEU:HD12	2.00	0.43
22:2:630:PRO:HA	22:2:631:PRO:HD3	1.77	0.43
23:3:136:GLU:OE2	23:3:189:TYR:OH	2.10	0.43
23:3:521:PRO:HA	23:3:544:ILE:CG2	2.49	0.43
23:3:745:PHE:HB2	23:3:755:VAL:HG23	2.00	0.43
29:L:63:TRP:CH2	29:L:99:HIS:HB2	2.54	0.43
29:L:101:GLU:O	29:L:105:ASP:HB2	2.18	0.43
35:O:90:TYR:HB3	35:O:92:LEU:HD12	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:R:54:LEU:HD12	37:R:54:LEU:HA	1.86	0.43
37:R:55:LEU:C	37:R:73:PRO:O	2.56	0.43
39:T:399:LYS:HG3	39:T:406:ILE:CD1	2.37	0.43
44:Y:36:ALA:HB3	45:Z:498:GLY:O	2.18	0.43
1:A:459:LEU:HD12	1:A:459:LEU:HA	1.75	0.43
1:A:2073:TRP:CD1	1:A:2073:TRP:C	2.91	0.43
1:A:2073:TRP:CH2	1:A:2313:HIS:CG	3.06	0.43
3:C:145:PHE:N	3:C:312:SER:OG	2.50	0.43
3:C:736:GLY:HA3	3:C:770:PHE:CE2	2.53	0.43
5:E:67:GLY:N	5:E:87:ASP:OD1	2.42	0.43
14:G:-5:G:O2'	14:G:-4:A:H5"	2.18	0.43
15:H:83:A:C4	15:H:84:C:C6	3.07	0.43
15:H:98:G:H5'	15:H:104:U:OP2	2.18	0.43
15:H:154:C:O2'	15:H:155:C:C5'	2.66	0.43
15:H:181:G:C2	15:H:182:U:C4	3.07	0.43
21:1:897:LEU:HD21	21:1:932:ILE:HD13	2.00	0.43
21:1:1235:GLU:O	21:1:1238:ARG:HB3	2.18	0.43
23:3:139:LYS:HB2	23:3:160:ALA:HB3	2.00	0.43
23:3:868:VAL:HG12	23:3:877:LEU:HB2	1.99	0.43
35:O:58:CYS:HB2	35:O:65:PHE:CE1	2.52	0.43
35:O:230:THR:H	35:O:277:ARG:CZ	2.32	0.43
37:R:126:ASN:HD22	37:R:128:ASP:H	1.66	0.43
44:Y:29:HIS:CG	44:Y:91:ILE:HG23	2.53	0.43
1:A:648:LEU:HA	1:A:648:LEU:HD23	1.79	0.43
1:A:1382:SER:HB3	1:A:1416:ILE:HG12	2.00	0.43
1:A:1555:LEU:HD12	1:A:1560:ILE:HB	2.00	0.43
2:B:27:U:HO2'	2:B:28:A:P	2.41	0.43
3:C:60:HIS:ND1	3:C:60:HIS:O	2.51	0.43
13:F:36:A:C3'	13:F:36:A:C8	3.01	0.43
15:H:157:G:H2'	15:H:158:G:O4'	2.19	0.43
21:1:889:GLU:HA	21:1:892:LEU:HD12	2.00	0.43
22:2:613:LEU:HD11	24:4:32:LEU:HD13	1.99	0.43
23:3:32:VAL:HG23	23:3:39:GLU:HB3	1.99	0.43
23:3:640:LEU:HD22	23:3:667:ILE:HG12	2.01	0.43
25:5:114:LYS:HA	25:5:119:ILE:O	2.19	0.43
29:L:73:HIS:CD2	29:L:77:LEU:HD11	2.53	0.43
35:O:45:CYS:SG	35:O:48:CYS:N	2.92	0.43
35:O:45:CYS:O	35:O:49:ALA:HA	2.18	0.43
35:O:147:LEU:HD12	35:O:148:LEU:N	2.34	0.43
37:R:52:PRO:HB3	37:R:57:ASP:OD2	2.17	0.43
37:R:119:LEU:HA	37:R:232:MET:CE	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:R:120:VAL:HG23	37:R:121:PRO:HD2	2.01	0.43
38:S:10:GLN:CA	38:S:29:TRP:CE2	3.01	0.43
39:T:459:LEU:HG	39:T:461:SER:OG	2.18	0.43
1:A:345:PRO:O	1:A:346:ASP:O	2.35	0.43
1:A:372:PRO:HB2	3:C:342:ARG:HH21	1.84	0.43
1:A:790:ARG:HG3	3:C:60:HIS:HD2	1.82	0.43
2:B:87:A:H5'	2:B:93:U:OP2	2.19	0.43
3:C:61:GLU:OE1	3:C:62:ASP:N	2.51	0.43
3:C:295:ASP:OD1	3:C:297:ASN:HB2	2.19	0.43
3:C:461:LEU:HD23	3:C:461:LEU:HA	1.78	0.43
21:1:471:ASP:OD2	21:1:505:LYS:NZ	2.34	0.43
29:L:216:PHE:HZ	35:O:112:VAL:CG1	2.31	0.43
34:N:59:TYR:CZ	34:N:63:LEU:HD11	2.53	0.43
37:R:242:THR:HG22	37:R:244:LYS:H	1.84	0.43
38:S:56:ILE:HD12	38:S:153:PRO:HG3	2.00	0.43
38:S:131:ARG:HH12	38:S:133:CYS:HB2	1.83	0.43
1:A:293:TRP:HB2	1:A:1136:ARG:HH22	1.83	0.43
1:A:470:ARG:CZ	1:A:470:ARG:HB2	2.49	0.43
1:A:643:GLY:O	1:A:646:PRO:HD2	2.19	0.43
1:A:781:ARG:NH2	15:H:24:A:H5'	2.34	0.43
1:A:1433:ASP:O	1:A:1434:LYS:HD3	2.19	0.43
1:A:1437:ARG:O	1:A:1440:THR:OG1	2.36	0.43
3:C:73:TYR:CE1	39:T:487:LYS:HE2	2.52	0.43
3:C:137:HIS:HD2	3:C:236:MET:CB	2.22	0.43
3:C:275:TYR:OH	3:C:345:GLY:HA2	2.19	0.43
3:C:349:PHE:CG	3:C:356:PHE:HE1	2.36	0.43
3:C:941:LYS:HG2	3:C:942:GLY:N	2.34	0.43
13:F:28:A:C4'	34:N:41:ARG:HA	2.48	0.43
13:F:46:G:H2'	13:F:47:A:C8	2.54	0.43
15:H:166:G:N3	15:H:166:G:H2'	2.33	0.43
15:H:180:G:N3	15:H:181:G:C8	2.87	0.43
21:1:892:LEU:HD23	21:1:892:LEU:HA	1.91	0.43
23:3:458:ALA:HA	23:3:741:PHE:CB	2.45	0.43
23:3:482:THR:OG1	23:3:501:GLY:HA3	2.19	0.43
27:7:51:ASN:OD1	27:7:61:LYS:HE2	2.18	0.43
34:N:46:LEU:HD23	34:N:46:LEU:HA	1.92	0.43
34:N:128:VAL:HG13	34:N:130:ARG:CB	2.48	0.43
36:P:191:ASP:O	36:P:192:VAL:HG23	2.18	0.43
38:S:55:ARG:NH2	42:W:95:PRO:O	2.52	0.43
39:T:225:ASP:O	39:T:226:ARG:HB2	2.18	0.43
1:A:235:MET:CE	1:A:411:PHE:CA	2.85	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:VAL:O	1:A:284:ARG:CZ	2.67	0.43
1:A:284:ARG:HE	1:A:284:ARG:HB3	1.70	0.43
1:A:371:LEU:HD12	1:A:372:PRO:HD2	2.00	0.43
1:A:380:LEU:HD22	1:A:380:LEU:H	1.84	0.43
1:A:843:LEU:HD22	1:A:867:ILE:HG23	2.01	0.43
1:A:1314:VAL:HG11	1:A:1487:HIS:NE2	2.34	0.43
1:A:1539:SER:OG	1:A:1540:PRO:HD3	2.19	0.43
3:C:289:ILE:CD1	3:C:300:LEU:HD21	2.49	0.43
3:C:381:LEU:HD23	3:C:416:LEU:HD22	1.99	0.43
5:E:255:MET:C	5:E:257:ASN:H	2.22	0.43
13:F:39:A:H61	14:G:8:C:N4	2.11	0.43
14:G:12:G:C2	14:G:13:C:O4'	2.71	0.43
21:1:184:VAL:O	21:1:188:ALA:CB	2.66	0.43
23:3:458:ALA:C	23:3:757:ILE:HG12	2.39	0.43
28:J:339:TRP:CG	37:R:116:TYR:CD2	3.06	0.43
37:R:250:LYS:HD3	37:R:250:LYS:C	2.39	0.43
39:T:347:THR:HG21	39:T:357:TRP:HE1	1.82	0.43
43:X:307:GLN:HB3	43:X:331:LEU:HD13	2.01	0.43
1:A:30:LEU:HB3	5:E:194:TYR:CZ	2.53	0.43
1:A:61:MET:HE1	34:N:104:ARG:HD2	2.01	0.43
1:A:151:MET:SD	1:A:628:GLY:HA3	2.59	0.43
1:A:210:HIS:CD2	1:A:210:HIS:C	2.92	0.43
1:A:344:ASP:OD1	1:A:347:LEU:HD11	2.19	0.43
2:B:12:U:O2'	2:B:13:C:P	2.77	0.43
3:C:669:THR:HG22	3:C:690:GLU:CB	2.48	0.43
5:E:178:LEU:CD1	5:E:222:LEU:HD21	2.46	0.43
5:E:321:TYR:OH	5:E:356:ILE:HG23	2.19	0.43
15:H:68:G:C6	15:H:84:C:N4	2.85	0.43
21:1:900:PHE:HA	21:1:903:GLN:HE21	1.83	0.43
21:1:968:GLU:OE1	21:1:968:GLU:N	2.51	0.43
23:3:253:GLU:HA	23:3:286:ILE:HG22	2.01	0.43
23:3:820:ALA:HB2	23:3:843:LEU:HD11	2.00	0.43
23:3:1055:VAL:HB	23:3:1093:MET:HB3	2.00	0.43
26:6:14:GLN:O	26:6:46:CYS:HB3	2.18	0.43
29:L:209:ASP:HA	35:O:110:SER:CB	2.34	0.43
37:R:113:TYR:CG	37:R:118:ASP:OD2	2.72	0.43
39:T:399:LYS:CG	39:T:406:ILE:CD1	2.78	0.43
44:Y:37:TRP:CE2	44:Y:83:CYS:SG	3.11	0.43
44:Y:85:GLU:O	45:Z:502:ALA:CA	2.65	0.43
1:A:76:MET:CE	1:A:88:TYR:CE2	2.99	0.42
1:A:369:GLU:HB2	1:A:370:PRO:HD2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1373:GLN:NE2	1:A:1381:ASP:OD2	2.52	0.42
1:A:2328:ALA:CB	4:D:787:ALA:C	2.87	0.42
3:C:77:VAL:CB	39:T:196:LEU:HG	2.41	0.42
3:C:457:VAL:O	3:C:458:ASP:CB	2.67	0.42
13:F:55:C:OP2	13:F:74:U:O2'	2.36	0.42
23:3:169:HIS:H	23:3:185:LEU:HB2	1.83	0.42
23:3:226:GLU:HG3	23:3:261:PHE:CZ	2.51	0.42
23:3:587:VAL:CG1	23:3:590:MET:HG3	2.49	0.42
23:3:1188:ASN:OD1	23:3:1189:LYS:N	2.51	0.42
26:6:57:ARG:HD2	26:6:62:GLY:C	2.40	0.42
34:N:2:PRO:HG2	34:N:4:VAL:H	1.84	0.42
34:N:60:ILE:HD13	34:N:78:CYS:HB3	2.00	0.42
35:O:77:LEU:HD12	35:O:77:LEU:HA	1.89	0.42
35:O:278:GLN:O	35:O:282:VAL:HG23	2.19	0.42
37:R:124:VAL:HG22	37:R:126:ASN:N	2.34	0.42
39:T:284:TYR:N	39:T:284:TYR:CD1	2.87	0.42
41:V:585:ILE:O	41:V:586:PHE:C	2.58	0.42
42:W:491:GLN:O	42:W:492:ASN:C	2.57	0.42
44:Y:92:LEU:O	44:Y:96:ASN:CB	2.67	0.42
1:A:39:GLN:OE1	42:W:169:GLU:CB	2.67	0.42
1:A:332:TYR:C	1:A:332:TYR:CD1	2.92	0.42
1:A:1425:LYS:HG2	37:R:417:ASN:OD1	2.18	0.42
1:A:1560:ILE:HG12	1:A:1668:TRP:CB	2.49	0.42
1:A:1730:MET:O	1:A:1734:MET:HG2	2.19	0.42
3:C:93:ILE:HG21	39:T:218:TRP:CZ2	2.54	0.42
3:C:481:MET:SD	3:C:492:ALA:CB	3.06	0.42
15:H:168:A:N3	15:H:168:A:C2'	2.77	0.42
21:1:404:LEU:HD23	25:5:47:GLN:CD	2.39	0.42
21:1:744:ALA:HB2	21:1:784:MET:SD	2.59	0.42
21:1:1289:ASN:HB2	21:1:1294:THR:HA	2.00	0.42
23:3:274:ARG:NH2	23:3:309:ASP:OD2	2.50	0.42
23:3:520:TYR:HE1	23:3:522:ASP:HB2	1.83	0.42
33:Q:500:GLY:HA2	37:R:51:ILE:HD11	2.00	0.42
37:R:118:ASP:OD1	37:R:232:MET:HE1	2.19	0.42
37:R:220:ARG:HB2	37:R:220:ARG:CZ	2.49	0.42
44:Y:37:TRP:NE1	44:Y:83:CYS:CB	2.70	0.42
1:A:32:GLU:OE2	1:A:36:LYS:CE	2.68	0.42
1:A:407:ALA:HA	1:A:408:PRO:HD3	1.87	0.42
1:A:962:LEU:HB2	1:A:965:VAL:HB	1.99	0.42
1:A:1052:VAL:HG22	1:A:1161:LEU:HD21	2.01	0.42
1:A:1099:PHE:HZ	1:A:1157:ILE:HD11	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1353:PHE:HE2	40:U:22:ASN:CG	2.23	0.42
1:A:1457:HIS:HE2	37:R:424:SER:CB	2.32	0.42
1:A:2067:PHE:HB2	1:A:2072:GLU:HG2	2.00	0.42
3:C:242:LEU:HD23	3:C:242:LEU:HA	1.84	0.42
3:C:413:ARG:HB2	3:C:414:PRO:HD3	1.99	0.42
15:H:3:C:H2'	15:H:4:G:C8	2.53	0.42
15:H:178:A:N3	15:H:178:A:H2'	2.34	0.42
21:1:707:LEU:O	21:1:710:ALA:HB3	2.20	0.42
21:1:811:LEU:HB2	21:1:812:PRO:HD3	2.00	0.42
21:1:1040:GLY:CA	21:1:1080:THR:HG22	2.48	0.42
22:2:613:LEU:HA	22:2:616:SER:OG	2.20	0.42
23:3:310:ILE:O	23:3:330:PHE:HB3	2.19	0.42
23:3:961:ILE:HB	23:3:970:TYR:CD2	2.54	0.42
28:J:375:ASP:O	28:J:376:VAL:C	2.58	0.42
34:N:15:TRP:HE3	34:N:74:LEU:HD11	1.83	0.42
35:O:185:LYS:HG2	35:O:186:PRO:HD2	2.00	0.42
42:W:155:SER:O	42:W:156:VAL:CB	2.67	0.42
1:A:32:GLU:CD	1:A:36:LYS:HE3	2.39	0.42
1:A:173:GLU:O	1:A:520:TYR:HD2	2.02	0.42
1:A:232:LEU:N	1:A:233:PRO:CD	2.83	0.42
1:A:1354:ARG:NH1	40:U:7:LEU:HG	2.34	0.42
1:A:2272:MET:HB3	1:A:2272:MET:HE3	1.68	0.42
2:B:94:U:O2'	2:B:95:G:H3'	2.18	0.42
3:C:323:PHE:CE1	3:C:424:PHE:HE1	2.37	0.42
3:C:706:GLN:HE21	3:C:708:THR:N	2.12	0.42
3:C:863:ILE:HA	3:C:864:PRO:HD3	1.88	0.42
5:E:67:GLY:H	5:E:87:ASP:CG	2.20	0.42
15:H:5:C:H2'	15:H:6:U:C6	2.54	0.42
21:1:413:LYS:HG3	21:1:415:LEU:HD11	2.01	0.42
21:1:619:ASN:ND2	21:1:624:VAL:HG21	2.34	0.42
21:1:619:ASN:OD1	21:1:620:MET:N	2.52	0.42
21:1:722:GLU:O	21:1:725:ASP:CB	2.67	0.42
23:3:185:LEU:HD11	23:3:235:LEU:HD13	2.01	0.42
23:3:287:PHE:HA	23:3:304:GLN:O	2.19	0.42
23:3:1014:TYR:CE2	23:3:1016:ARG:HA	2.55	0.42
23:3:1052:ASN:OD1	23:3:1096:HIS:ND1	2.39	0.42
23:3:1201:PRO:HB2	23:3:1202:PRO:HD3	2.02	0.42
26:6:47:ASP:HA	26:6:50:ASN:O	2.20	0.42
28:J:331:GLN:HG2	37:R:98:TYR:HH	1.76	0.42
28:J:339:TRP:CD2	37:R:116:TYR:CD2	2.85	0.42
29:L:63:TRP:CZ2	29:L:99:HIS:HB2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:N:12:PRO:HG2	34:N:74:LEU:HA	2.02	0.42
35:O:240:GLY:HA3	35:O:296:ARG:NH2	2.34	0.42
36:P:188:TRP:C	36:P:190:ASP:H	2.21	0.42
37:R:183:GLN:HB3	37:R:188:PHE:CD2	2.54	0.42
38:S:125:LYS:HB3	38:S:126:HIS:CE1	2.54	0.42
42:W:528:GLY:HA2	42:W:552:VAL:CB	2.49	0.42
44:Y:69:ARG:HA	44:Y:76:SER:HA	2.02	0.42
1:A:61:MET:CE	34:N:104:ARG:HD2	2.49	0.42
1:A:120:TYR:HE1	1:A:485:THR:HB	1.84	0.42
1:A:378:PHE:CD1	1:A:378:PHE:C	2.93	0.42
1:A:549:GLU:CD	1:A:552:ARG:NH1	2.72	0.42
1:A:596:TYR:CE1	14:G:-5:G:N9	2.88	0.42
1:A:718:ARG:NH2	37:R:259:LYS:CE	2.78	0.42
1:A:1263:TRP:CD2	1:A:1295:ILE:HD13	2.54	0.42
1:A:1363:GLN:O	1:A:1364:LEU:HG	2.18	0.42
1:A:1555:LEU:HB2	1:A:1558:THR:OG1	2.19	0.42
3:C:669:THR:HG22	3:C:690:GLU:OE1	2.19	0.42
3:C:712:LYS:O	3:C:716:GLU:HG3	2.18	0.42
5:E:277:PHE:CE1	5:E:317:ARG:HG2	2.53	0.42
14:G:5:G:C2	14:G:6:A:C5	3.08	0.42
14:G:136:U:O4	21:1:515:ALA:HA	2.19	0.42
21:1:494:GLU:HA	21:1:497:ILE:HG22	2.01	0.42
21:1:940:LEU:O	21:1:948:ARG:NH2	2.51	0.42
21:1:1255:PHE:HD2	22:2:487:LEU:HD22	1.81	0.42
23:3:508:CYS:SG	23:3:518:GLN:NE2	2.92	0.42
23:3:673:VAL:HA	23:3:690:ARG:HA	2.02	0.42
23:3:784:THR:HB	23:3:786:ARG:NH1	2.32	0.42
35:O:104:LYS:HG3	35:O:139:LYS:HZ1	1.84	0.42
35:O:133:PRO:HG2	35:O:137:LEU:HB2	2.01	0.42
35:O:248:LEU:O	35:O:252:PHE:HD2	2.03	0.42
37:R:129:ASP:HB3	37:R:131:ASP:CG	2.40	0.42
39:T:318:ARG:CG	39:T:318:ARG:NH1	2.82	0.42
1:A:385:GLU:HB3	1:A:386:PRO:HD2	2.00	0.42
1:A:494:LEU:HD23	1:A:494:LEU:HA	1.84	0.42
1:A:715:GLU:OE1	37:R:258:TRP:CE3	2.73	0.42
1:A:791:GLN:NE2	1:A:1026:ASN:OD1	2.52	0.42
3:C:85:ASP:OD2	39:T:240:LEU:HA	2.20	0.42
3:C:90:THR:O	3:C:92:PRO:HD3	2.19	0.42
15:H:107:A:N1	15:H:108:G:C5	2.88	0.42
21:1:1075:ARG:HE	21:1:1075:ARG:HB2	1.64	0.42
23:3:146:ARG:HB2	23:3:150:ALA:HA	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:353:PHE:O	23:3:432:ARG:NH1	2.44	0.42
27:7:30:GLU:HA	27:7:33:VAL:HG12	2.02	0.42
29:L:209:ASP:CG	35:O:111:ASP:N	2.63	0.42
29:L:219:LYS:NZ	35:O:105:ASP:O	2.53	0.42
32:I:712:VAL:O	32:I:713:ARG:C	2.57	0.42
35:O:224:ASP:N	35:O:225:PRO:HD2	2.34	0.42
37:R:71:GLN:HE21	37:R:71:GLN:HB2	1.61	0.42
38:S:98:LEU:HD21	38:S:129:PHE:HD2	1.84	0.42
38:S:102:ASN:OD1	38:S:107:THR:O	2.37	0.42
39:T:188:PRO:HG3	39:T:443:THR:HG21	2.01	0.42
44:Y:38:ILE:HG12	44:Y:82:LEU:HB3	2.02	0.42
1:A:48:LYS:HG2	1:A:49:ARG:N	2.35	0.42
1:A:384:VAL:O	1:A:385:GLU:HG2	2.20	0.42
1:A:651:TRP:CD1	13:F:66:C:C2	3.07	0.42
2:B:19:A:H2'	2:B:20:G:C5'	2.49	0.42
2:B:32:C:OP1	36:P:33:ARG:NE	2.53	0.42
3:C:77:VAL:HG13	39:T:196:LEU:CB	2.41	0.42
3:C:140:HIS:CB	3:C:230:ASP:H	2.33	0.42
3:C:259:LYS:HD2	50:C:1500:GTP:C4	2.55	0.42
3:C:452:THR:HB	3:C:577:PHE:CE2	2.55	0.42
5:E:152:SER:OG	5:E:153:PHE:HD1	2.03	0.42
13:F:58:G:O2'	13:F:59:G:P	2.78	0.42
14:G:141:C:H2'	14:G:142:U:C6	2.52	0.42
15:H:179:C:C2	15:H:180:G:C8	3.07	0.42
21:1:401:ASP:HA	21:1:404:LEU:HB2	2.00	0.42
21:1:848:GLU:O	21:1:851:SER:OG	2.32	0.42
21:1:1179:ASP:OD1	21:1:1181:ASP:N	2.52	0.42
23:3:3:LEU:HA	23:3:1130:VAL:O	2.20	0.42
23:3:228:LEU:HD23	23:3:259:LYS:HZ2	1.84	0.42
23:3:456:PRO:HB2	23:3:757:ILE:HD13	2.02	0.42
25:5:25:ASN:HB3	25:5:87:LEU:HA	2.02	0.42
28:J:294:HIS:HE1	29:L:227:THR:CB	2.26	0.42
29:L:703:MET:O	29:L:707:ALA:HB3	2.18	0.42
31:K:157:ARG:O	31:K:160:ILE:CG1	2.68	0.42
35:O:219:THR:O	35:O:220:MET:C	2.58	0.42
36:P:226:LYS:HD3	36:P:227:TYR:HE1	1.83	0.42
37:R:67:ILE:CG1	37:R:71:GLN:OE1	2.68	0.42
41:V:484:SER:O	41:V:486:THR:N	2.53	0.42
41:V:547:VAL:O	41:V:548:ALA:C	2.58	0.42
42:W:571:TRP:O	42:W:573:GLY:N	2.52	0.42
1:A:120:TYR:CE1	1:A:485:THR:HG22	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:372:PRO:HB2	3:C:342:ARG:NH2	2.34	0.42
1:A:382:GLU:O	1:A:383:PHE:CG	2.73	0.42
1:A:651:TRP:CE2	13:F:66:C:N3	2.88	0.42
1:A:816:TRP:CE2	1:A:820:ARG:HG3	2.55	0.42
1:A:1436:TRP:HA	1:A:1439:ARG:CZ	2.50	0.42
1:A:2302:LYS:HD2	1:A:2306:HIS:CE1	2.54	0.42
2:B:19:A:HO2'	2:B:20:G:P	2.37	0.42
3:C:149:LEU:HA	3:C:427:PHE:HD2	1.82	0.42
13:F:28:A:O4'	34:N:41:ARG:CA	2.64	0.42
14:G:-3:A:H2'	14:G:-2:C:C6	2.55	0.42
15:H:82:G:C2	15:H:83:A:C5	3.08	0.42
21:1:527:GLY:O	21:1:531:LEU:HD13	2.20	0.42
22:2:525:PRO:HD2	22:2:528:ILE:HD12	2.00	0.42
23:3:412:ILE:HD12	23:3:1118:VAL:HG11	2.01	0.42
23:3:519:VAL:HG22	23:3:524:ILE:HG23	2.02	0.42
23:3:691:THR:HG22	23:3:716:SER:HB3	2.02	0.42
35:O:24:CYS:HB3	35:O:26:THR:H	1.85	0.42
39:T:187:LYS:N	39:T:188:PRO:CD	2.83	0.42
39:T:233:LEU:HD23	39:T:233:LEU:O	2.20	0.42
42:W:431:ARG:O	42:W:446:GLU:HA	2.19	0.42
44:Y:37:TRP:HH2	45:Z:498:GLY:N	2.15	0.42
44:Y:59:TYR:HB3	44:Y:92:LEU:HD23	2.01	0.42
1:A:137:GLU:N	1:A:138:PRO:HD2	2.35	0.42
1:A:303:ILE:CG2	3:C:933:PHE:CD1	3.03	0.42
1:A:434:HIS:ND1	1:A:434:HIS:C	2.73	0.42
1:A:629:PHE:CD2	1:A:629:PHE:O	2.73	0.42
1:A:697:MET:N	1:A:698:PRO:HD3	2.34	0.42
1:A:833:LYS:HE3	1:A:834:HIS:NE2	2.35	0.42
1:A:1416:ILE:HB	1:A:1417:PRO:HD3	2.01	0.42
1:A:1457:HIS:HE1	37:R:424:SER:HA	1.74	0.42
1:A:1554:GLN:NE2	1:A:1620:TYR:O	2.49	0.42
2:B:92:U:C3'	2:B:93:U:H5'	2.50	0.42
3:C:140:HIS:HB3	3:C:230:ASP:H	1.85	0.42
3:C:149:LEU:HA	3:C:427:PHE:CE2	2.54	0.42
14:G:139:U:H2'	14:G:140:A:C8	2.55	0.42
15:H:26:A:C5	15:H:27:U:C5	3.08	0.42
21:1:687:VAL:HA	21:1:690:ILE:HG22	2.01	0.42
21:1:727:VAL:HG12	21:1:731:LEU:HD11	2.02	0.42
21:1:790:LYS:O	21:1:793:LYS:HB3	2.19	0.42
23:3:706:MET:HE2	23:3:770:LEU:CB	2.49	0.42
23:3:1039:LEU:HB2	23:3:1043:THR:OG1	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:J:240:THR:O	28:J:241:VAL:HB	2.19	0.42
28:J:259:GLN:HE21	29:L:220:PRO:HD3	1.82	0.42
35:O:253:TYR:CZ	38:S:120:GLN:CG	3.02	0.42
36:P:58:ASP:OD2	36:P:61:ARG:HB2	2.19	0.42
36:P:192:VAL:CG1	36:P:193:VAL:N	2.83	0.42
1:A:86:ARG:HH22	37:R:211:ARG:HA	1.85	0.42
1:A:1188:ASN:ND2	1:A:1233:ASP:OD2	2.47	0.42
1:A:1371:TYR:OH	41:V:464:GLN:CB	2.67	0.42
1:A:1399:GLN:C	1:A:1401:ARG:H	2.24	0.42
1:A:1544:ARG:HB3	1:A:1672:ASP:OD2	2.19	0.42
1:A:2120:LEU:HD12	1:A:2120:LEU:N	2.35	0.42
3:C:220:ARG:HD3	3:C:477:HIS:NE2	2.34	0.42
3:C:474:LEU:HD12	3:C:500:THR:O	2.20	0.42
5:E:274:VAL:C	5:E:275:LYS:HG3	2.40	0.42
15:H:147:G:C2	15:H:148:C:N3	2.87	0.42
15:H:155:C:H2'	15:H:156:U:H5"	2.02	0.42
15:H:179:C:O2	15:H:180:G:C8	2.72	0.42
21:1:555:VAL:O	21:1:559:ILE:HG12	2.19	0.42
22:2:643:PRO:HG2	24:4:66:ASP:HA	2.01	0.42
23:3:259:LYS:HE3	23:3:266:ASP:OD2	2.20	0.42
23:3:261:PHE:HD1	23:3:261:PHE:HA	1.72	0.42
23:3:288:VAL:HG23	23:3:289:CYS:N	2.33	0.42
23:3:706:MET:CE	23:3:770:LEU:CB	2.98	0.42
23:3:968:ARG:CZ	23:3:979:ARG:HH11	2.33	0.42
23:3:1011:TRP:HB3	23:3:1024:PHE:CZ	2.55	0.42
28:J:216:ASP:O	28:J:218:GLU:N	2.53	0.42
34:N:56:LYS:HE2	34:N:83:TYR:O	2.20	0.42
35:O:292:ILE:HG23	35:O:296:ARG:C	2.40	0.42
39:T:281:ILE:CD1	39:T:282:ARG:HG2	2.50	0.42
1:A:1320:LYS:NZ	37:R:434:TYR:CE1	2.88	0.41
1:A:1402:ARG:CD	37:R:412:ASP:HA	2.50	0.41
3:C:291:MET:HG2	3:C:292:TYR:CE1	2.54	0.41
3:C:445:ALA:HB1	3:C:449:ILE:HG13	2.02	0.41
3:C:829:GLU:HG3	3:C:830:PRO:HD2	2.01	0.41
13:F:8:C:C6	13:F:8:C:C5'	2.98	0.41
13:F:31:U:H2'	13:F:32:U:C6	2.55	0.41
15:H:68:G:H2'	15:H:69:U:H6	1.82	0.41
21:1:783:GLU:O	21:1:787:ILE:HG12	2.20	0.41
23:3:812:LYS:NZ	23:3:855:PRO:HG2	2.35	0.41
27:7:23:HIS:H	27:7:26:THR:HG1	1.68	0.41
28:J:239:ARG:C	28:J:239:ARG:HD3	2.40	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:J:262:ARG:HB3	29:L:220:PRO:HG3	2.02	0.41
28:J:368:ARG:O	28:J:372:VAL:HG23	2.20	0.41
37:R:131:ASP:OD2	37:R:132:LEU:N	2.53	0.41
38:S:15:TYR:HB2	38:S:163:TYR:HB2	2.02	0.41
1:A:61:MET:HB3	1:A:62:PRO:CD	2.51	0.41
1:A:121:HIS:CD2	1:A:481:PHE:O	2.70	0.41
1:A:151:MET:SD	1:A:628:GLY:CA	3.08	0.41
1:A:151:MET:HE1	1:A:629:PHE:HA	2.02	0.41
1:A:155:LYS:CE	1:A:624:GLY:O	2.68	0.41
1:A:372:PRO:HG2	3:C:342:ARG:HE	1.80	0.41
1:A:1051:LEU:HD22	36:P:193:VAL:HG11	2.00	0.41
1:A:1428:HIS:O	1:A:1429:THR:C	2.59	0.41
1:A:1503:TRP:CZ2	1:A:1753:LEU:HD21	2.55	0.41
1:A:1661:TRP:NE1	1:A:1697:SER:O	2.53	0.41
3:C:73:TYR:HB3	3:C:77:VAL:HG21	2.02	0.41
3:C:89:LEU:C	3:C:89:LEU:CD2	2.82	0.41
3:C:259:LYS:HG2	3:C:262:ARG:HD3	1.99	0.41
3:C:449:ILE:CD1	3:C:466:SER:HA	2.50	0.41
4:D:452:PRO:CB	23:3:570:PRO:CB	2.92	0.41
4:D:863:THR:CB	23:3:599:GLU:CB	2.96	0.41
14:G:-8:U:H5	40:U:16:ASN:HB3	1.85	0.41
15:H:80:A:C2	15:H:81:G:N7	2.88	0.41
15:H:153:A:H62	15:H:177:A:H2	1.67	0.41
21:1:1185:ARG:HD2	21:1:1218:ASN:OD1	2.20	0.41
23:3:425:VAL:O	23:3:435:LEU:HD12	2.20	0.41
23:3:436:ARG:HG2	23:3:778:ALA:HA	2.01	0.41
29:L:31:TRP:CH2	29:L:47:LYS:HA	2.55	0.41
34:N:37:HIS:CD2	34:N:37:HIS:O	2.74	0.41
34:N:75:TYR:CZ	34:N:79:ILE:HD11	2.55	0.41
35:O:132:ARG:HG3	35:O:137:LEU:CD2	2.50	0.41
35:O:164:ILE:HD12	35:O:164:ILE:HA	1.91	0.41
35:O:219:THR:O	35:O:221:PRO:CD	2.66	0.41
37:R:88:ILE:CG2	37:R:96:ILE:HG23	2.48	0.41
37:R:418:GLN:HE21	37:R:418:GLN:HB2	1.64	0.41
37:R:442:ARG:NH1	37:R:443:GLY:CA	2.78	0.41
42:W:371:THR:O	42:W:372:ASN:CB	2.68	0.41
42:W:458:GLU:O	42:W:459:PRO:C	2.58	0.41
44:Y:64:ASN:O	44:Y:83:CYS:HB3	2.19	0.41
45:Z:572:PRO:CG	45:Z:588:ASP:OD2	2.67	0.41
1:A:206:TRP:CE3	1:A:212:PRO:HB3	2.55	0.41
1:A:211:GLN:HA	1:A:212:PRO:HD3	1.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:428:LYS:HE3	1:A:454:TYR:CE1	2.55	0.41
1:A:434:HIS:CG	3:C:892:GLN:OE1	2.74	0.41
1:A:638:LEU:HA	1:A:638:LEU:HD23	1.70	0.41
1:A:2216:CYS:HA	1:A:2225:LEU:HB3	2.01	0.41
3:C:148:CYS:SG	3:C:312:SER:O	2.78	0.41
3:C:512:GLU:HG3	3:C:562:THR:O	2.19	0.41
5:E:263:ASP:O	5:E:272:ARG:NE	2.32	0.41
21:1:520:THR:HG21	21:1:558:ARG:HE	1.85	0.41
21:1:1124:SER:O	21:1:1127:THR:OG1	2.28	0.41
29:L:219:LYS:NZ	35:O:104:LYS:O	2.51	0.41
29:L:741:GLN:O	29:L:744:GLN:CG	2.69	0.41
35:O:214:LEU:HD23	35:O:214:LEU:HA	1.82	0.41
39:T:225:ASP:O	39:T:226:ARG:CB	2.67	0.41
1:A:54:VAL:O	1:A:54:VAL:HG23	2.20	0.41
1:A:258:PHE:CD2	1:A:434:HIS:HA	2.55	0.41
1:A:800:TYR:HB3	3:C:59:LEU:HD11	2.02	0.41
1:A:1581:LEU:HD22	1:A:1746:ARG:NH1	2.36	0.41
3:C:261:ASP:CG	50:C:1500:GTP:N1	2.61	0.41
3:C:445:ALA:CB	3:C:449:ILE:HD11	2.43	0.41
3:C:853:ARG:O	3:C:854:ARG:HB3	2.20	0.41
15:H:152:G:H2'	15:H:152:G:N3	2.36	0.41
15:H:154:C:N3	15:H:176:G:N1	2.61	0.41
21:1:642:PRO:HB3	21:1:682:HIS:NE2	2.36	0.41
21:1:1136:TYR:CE1	21:1:1144:GLN:HB3	2.55	0.41
23:3:199:GLU:HB3	23:3:203:ASN:HD21	1.85	0.41
28:J:220:LEU:O	28:J:223:TYR:HB3	2.21	0.41
37:R:155:VAL:O	37:R:159:VAL:HG23	2.20	0.41
42:W:97:ASN:O	42:W:99:PHE:N	2.53	0.41
1:A:331:TRP:HE3	1:A:332:TYR:N	2.18	0.41
1:A:2112:LYS:HE2	1:A:2112:LYS:HB3	1.67	0.41
3:C:589:LYS:HB3	3:C:659:VAL:O	2.20	0.41
3:C:704:VAL:O	3:C:709:TRP:CZ2	2.74	0.41
3:C:707:ILE:HD11	3:C:735:PHE:HB2	2.01	0.41
13:F:40:U:O4	13:F:41:A:N6	2.54	0.41
15:H:103:U:C3'	15:H:104:U:H5'	2.51	0.41
21:1:621:ASP:OD2	21:1:623:TYR:HB3	2.19	0.41
21:1:719:TYR:CD1	23:3:218:ASN:HB2	2.56	0.41
23:3:116:VAL:HA	23:3:117:PRO:HD3	1.95	0.41
23:3:554:VAL:HG12	23:3:556:ILE:HG23	2.02	0.41
23:3:896:PHE:CZ	23:3:972:LEU:HB2	2.55	0.41
24:4:69:TYR:OH	24:4:73:ILE:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:J:340:GLN:N	28:J:341:PRO:HD3	2.35	0.41
29:L:717:MET:O	29:L:721:LEU:N	2.48	0.41
36:P:189:ASP:O	36:P:190:ASP:C	2.58	0.41
39:T:223:SER:OG	39:T:224:ALA:N	2.53	0.41
43:X:173:GLN:NE2	43:X:176:GLU:HA	2.36	0.41
1:A:107:PRO:O	1:A:108:MET:HB2	2.21	0.41
1:A:118:VAL:HG12	1:A:119:LEU:N	2.36	0.41
1:A:1315:VAL:HG12	1:A:1538:TRP:CD2	2.56	0.41
1:A:1325:LEU:HD23	1:A:1325:LEU:HA	1.86	0.41
1:A:1529:ILE:O	1:A:1530:PRO:C	2.59	0.41
1:A:2111:LEU:HD21	1:A:2225:LEU:HD21	2.03	0.41
3:C:97:VAL:HG21	36:P:45:GLN:CG	2.46	0.41
3:C:137:HIS:NE2	3:C:236:MET:SD	2.93	0.41
13:F:39:A:H2'	13:F:40:U:O4'	2.21	0.41
14:G:-2:C:H2'	14:G:-1:G:H8	1.82	0.41
15:H:72:U:H6	15:H:72:U:O5'	2.03	0.41
15:H:171:U:H2'	15:H:172:C:O4'	2.21	0.41
21:1:815:PHE:HA	21:1:819:TRP:CD1	2.56	0.41
23:3:168:TYR:CE1	27:7:69:MET:HB3	2.55	0.41
32:I:296:PHE:CB	32:I:305:SER:O	2.68	0.41
38:S:9:TRP:C	38:S:11:PRO:HD3	2.39	0.41
39:T:297:HIS:CE1	39:T:300:ILE:HD12	2.56	0.41
39:T:455:GLN:CG	39:T:456:PRO:HD2	2.51	0.41
44:Y:24:ASP:O	44:Y:26:VAL:N	2.54	0.41
1:A:148:TRP:CZ2	1:A:616:PHE:CA	3.02	0.41
1:A:175:PRO:CG	1:A:498:ARG:NH2	2.73	0.41
1:A:294:ASN:OD1	3:C:654:LYS:CD	2.66	0.41
1:A:596:TYR:O	1:A:598:LEU:N	2.54	0.41
1:A:866:LEU:O	1:A:869:GLN:HB3	2.21	0.41
1:A:1035:GLN:HA	1:A:1446:GLN:HE22	1.84	0.41
1:A:1099:PHE:CE2	1:A:1153:VAL:HG13	2.53	0.41
1:A:1221:THR:O	1:A:1223:GLU:HG3	2.20	0.41
1:A:1342:TRP:CG	3:C:921:LEU:CD2	2.99	0.41
1:A:1430:LEU:HD21	37:R:422:MET:HA	2.03	0.41
1:A:1458:GLN:HE21	1:A:1463:LYS:HG3	1.86	0.41
2:B:23:C:H6	2:B:26:A:H62	1.67	0.41
2:B:40:U:O2	2:B:40:U:C2'	2.69	0.41
2:B:63:A:C4'	5:E:106:LYS:NZ	2.81	0.41
3:C:230:ASP:OD1	3:C:259:LYS:HB2	2.17	0.41
3:C:270:PRO:HA	3:C:271:PRO:HD3	1.87	0.41
14:G:26:U:H2'	35:O:269:CYS:SG	2.61	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:G:155:U:C4'	14:G:156:U:H5'	2.49	0.41
15:H:4:G:H2'	15:H:5:C:C6	2.55	0.41
15:H:83:A:H2'	15:H:84:C:H1'	2.00	0.41
21:1:1127:THR:O	22:2:571:LEU:HD13	2.21	0.41
23:3:314:THR:HG22	23:3:315:LEU:N	2.36	0.41
24:4:67:ALA:O	24:4:70:ALA:HB3	2.21	0.41
28:J:273:TYR:CD1	37:R:228:PRO:CB	3.04	0.41
35:O:149:LYS:CE	35:O:290:LYS:HE2	2.48	0.41
38:S:11:PRO:HB3	38:S:166:GLY:N	2.34	0.41
1:A:143:GLN:O	1:A:146:SER:HB3	2.20	0.41
1:A:362:ARG:C	1:A:362:ARG:CD	2.88	0.41
1:A:642:ARG:CZ	2:B:28:A:C4	3.04	0.41
1:A:1342:TRP:CD1	3:C:921:LEU:HD11	2.55	0.41
1:A:2310:ARG:HG2	1:A:2310:ARG:HH11	1.84	0.41
2:B:41:U:C4	2:B:42:U:O4	2.73	0.41
3:C:300:LEU:N	3:C:300:LEU:CD1	2.84	0.41
4:D:538:ILE:O	4:D:585:ILE:HA	2.21	0.41
13:F:60:C:H5"	37:R:219:PRO:HB3	2.01	0.41
14:G:21:A:OP1	35:O:156:TYR:CE2	2.73	0.41
15:H:160:A:H2'	15:H:161:U:C6	2.55	0.41
21:1:719:TYR:HB3	23:3:216:GLY:O	2.20	0.41
21:1:1016:LEU:O	21:1:1019:ARG:HB3	2.20	0.41
21:1:1055:TRP:O	21:1:1058:ILE:HB	2.20	0.41
21:1:1092:ASP:OD1	21:1:1092:ASP:N	2.53	0.41
23:3:86:ARG:CD	23:3:104:GLN:HE21	2.33	0.41
23:3:205:GLN:HE21	23:3:227:PRO:HB3	1.85	0.41
23:3:718:ARG:HG2	23:3:719:SER:H	1.84	0.41
26:6:90:ASN:OD1	26:6:91:LEU:N	2.54	0.41
31:K:134:ALA:C	31:K:137:VAL:HG12	2.40	0.41
34:N:68:LYS:HD3	34:N:68:LYS:HA	1.91	0.41
34:N:117:CYS:C	34:N:119:CYS:N	2.73	0.41
35:O:104:LYS:H	35:O:104:LYS:HG2	1.71	0.41
37:R:129:ASP:C	37:R:131:ASP:N	2.73	0.41
38:S:66:ASP:C	38:S:66:ASP:OD1	2.59	0.41
39:T:309:ASP:C	39:T:309:ASP:OD1	2.59	0.41
42:W:290:GLY:HA2	42:W:571:TRP:O	2.19	0.41
45:Z:522:LEU:HD13	45:Z:522:LEU:C	2.41	0.41
45:Z:525:TYR:HD1	45:Z:526:ILE:CG2	2.29	0.41
1:A:128:PHE:CD1	1:A:473:PHE:CE1	3.09	0.41
1:A:225:TYR:O	1:A:418:THR:CB	2.68	0.41
1:A:293:TRP:HD1	1:A:1136:ARG:NH2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:965:VAL:O	1:A:1100:ARG:NH1	2.54	0.41
1:A:1052:VAL:CG2	1:A:1161:LEU:HD21	2.51	0.41
1:A:2090:ILE:H	1:A:2090:ILE:HD13	1.86	0.41
3:C:64:LYS:HE2	3:C:64:LYS:HA	2.02	0.41
3:C:65:TYR:O	3:C:66:TYR:CG	2.73	0.41
3:C:79:THR:HA	39:T:199:VAL:O	2.20	0.41
3:C:132:VAL:HG11	3:C:226:VAL:CG2	2.49	0.41
3:C:133:THR:HB	3:C:225:VAL:HA	2.02	0.41
3:C:513:ASN:O	3:C:513:ASN:ND2	2.54	0.41
3:C:518:ASP:N	3:C:519:GLU:OE2	2.54	0.41
5:E:115:LEU:O	5:E:116:HIS:CD2	2.74	0.41
5:E:177:LYS:C	5:E:178:LEU:HD23	2.41	0.41
5:E:243:LEU:HD22	5:E:243:LEU:HA	1.80	0.41
5:E:266:PRO:CB	29:L:785:GLN:HB3	2.51	0.41
15:H:152:G:H2'	15:H:153:A:C1'	2.51	0.41
21:1:184:VAL:O	21:1:188:ALA:HB2	2.21	0.41
21:1:517:ARG:O	21:1:520:THR:OG1	2.20	0.41
21:1:664:GLY:O	21:1:667:ILE:HB	2.21	0.41
21:1:770:MET:O	21:1:774:ILE:HG12	2.21	0.41
21:1:963:LYS:HG2	21:1:1003:VAL:HB	2.02	0.41
21:1:1080:THR:HA	21:1:1083:TYR:CD2	2.56	0.41
21:1:1092:ASP:OD1	21:1:1093:VAL:N	2.54	0.41
21:1:1227:ILE:O	21:1:1231:MET:HG2	2.20	0.41
21:1:1252:GLN:OE1	22:2:499:PRO:HA	2.20	0.41
23:3:65:LEU:HD12	23:3:79:VAL:O	2.21	0.41
23:3:464:ARG:NH1	23:3:473:TYR:OH	2.53	0.41
23:3:633:LEU:HD13	23:3:667:ILE:CG2	2.51	0.41
23:3:910:ALA:HB2	23:3:948:VAL:HG23	2.02	0.41
32:I:606:TRP:O	32:I:609:ALA:HB3	2.21	0.41
32:I:616:TYR:O	32:I:618:ARG:N	2.54	0.41
37:R:69:VAL:HG12	37:R:70:ALA:N	2.36	0.41
37:R:132:LEU:HD13	39:T:399:LYS:HE3	2.02	0.41
37:R:414:ARG:NH2	37:R:414:ARG:CB	2.73	0.41
39:T:209:CYS:O	39:T:221:THR:HA	2.21	0.41
39:T:210:ILE:HG12	39:T:221:THR:HG22	2.03	0.41
39:T:294:LEU:N	39:T:294:LEU:HD23	2.36	0.41
39:T:400:PHE:HD1	39:T:401:PRO:HA	1.86	0.41
41:V:530:LYS:C	41:V:532:GLN:N	2.74	0.41
42:W:298:PRO:O	42:W:299:LEU:CB	2.68	0.41
43:X:303:HIS:CB	43:X:383:ASP:HB3	2.51	0.41
44:Y:10:ILE:O	44:Y:13:LEU:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:Y:67:LEU:HA	44:Y:80:CYS:HA	2.02	0.41
45:Z:566:TYR:CE2	45:Z:584:TRP:HE3	2.29	0.41
1:A:293:TRP:CE3	1:A:293:TRP:C	2.94	0.41
1:A:842:ALA:HB1	1:A:920:ALA:HB1	2.03	0.41
1:A:1312:PRO:CD	1:A:1541:THR:CG2	2.99	0.41
1:A:1425:LYS:CB	37:R:417:ASN:OD1	2.69	0.41
1:A:1755:SER:HB2	21:1:938:TRP:CH2	2.54	0.41
1:A:2117:ILE:HG21	1:A:2301:PRO:HB2	2.02	0.41
3:C:149:LEU:HD11	3:C:427:PHE:CB	2.51	0.41
3:C:354:ARG:CG	3:C:354:ARG:HH11	2.34	0.41
13:F:42:C:C2	13:F:43:A:C8	3.09	0.41
21:1:1286:ARG:N	23:3:1006:GLN:HE22	2.19	0.41
23:3:274:ARG:HD2	23:3:389:PRO:HD3	2.02	0.41
25:5:14:PRO:O	25:5:17:VAL:HG22	2.21	0.41
28:J:423:GLU:OE1	28:J:423:GLU:HA	2.21	0.41
29:L:49:ARG:NH1	29:L:53:TRP:HB3	2.36	0.41
34:N:40:LYS:O	34:N:44:GLU:HB3	2.21	0.41
34:N:113:PHE:HD1	37:R:200:VAL:HG21	1.86	0.41
38:S:11:PRO:O	38:S:29:TRP:NE1	2.41	0.41
38:S:20:MET:CE	38:S:141:ARG:HD2	2.51	0.41
39:T:399:LYS:HB2	39:T:404:SER:HB3	2.03	0.41
39:T:434:GLY:HA2	39:T:464:GLY:N	2.36	0.41
41:V:585:ILE:O	41:V:588:GLN:N	2.54	0.41
1:A:121:HIS:C	1:A:123:THR:H	2.23	0.40
1:A:329:LEU:HD12	3:C:177:ARG:HG2	2.03	0.40
1:A:460:LYS:HZ1	2:B:49:A:P	2.41	0.40
1:A:593:ARG:CD	14:G:-4:A:H4'	2.43	0.40
3:C:221:ILE:HG13	3:C:479:THR:OG1	2.21	0.40
3:C:235:VAL:HG13	3:C:239:THR:OG1	2.22	0.40
3:C:392:LEU:N	3:C:393:PRO:CD	2.84	0.40
5:E:178:LEU:CD2	5:E:208:ILE:HD11	2.51	0.40
5:E:257:ASN:ND2	42:W:149:SER:O	2.53	0.40
14:G:146:C:C4	14:G:147:C:N4	2.89	0.40
15:H:112:G:O5'	15:H:112:G:H8	2.04	0.40
21:1:498:MET:HE1	21:1:530:PRO:HB2	2.02	0.40
21:1:765:TYR:O	21:1:769:VAL:HG23	2.20	0.40
21:1:806:ILE:HG12	21:1:810:ILE:HD12	2.03	0.40
21:1:997:LEU:O	21:1:1001:VAL:HG23	2.21	0.40
21:1:1126:PHE:HA	21:1:1165:TYR:CZ	2.56	0.40
23:3:6:LEU:HD12	23:3:1128:ILE:HD11	2.03	0.40
23:3:194:ASN:O	23:3:196:PRO:HD3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:259:LYS:HG3	23:3:266:ASP:CG	2.42	0.40
25:5:27:PRO:HG3	25:5:85:ARG:NH1	2.36	0.40
34:N:70:ILE:HG23	34:N:74:LEU:HD23	2.01	0.40
35:O:155:PRO:HD3	37:R:188:PHE:CE1	2.56	0.40
43:X:263:PRO:CG	43:X:265:LYS:H	2.34	0.40
45:Z:563:ARG:HH21	45:Z:563:ARG:HG3	1.83	0.40
1:A:1251:SER:O	1:A:1298:ARG:NH2	2.55	0.40
1:A:1263:TRP:CZ2	1:A:1292:GLU:HG2	2.56	0.40
1:A:1451:ASN:HB2	37:R:428:GLY:O	2.21	0.40
3:C:64:LYS:NZ	36:P:209:ARG:NH1	2.70	0.40
3:C:85:ASP:HA	39:T:238:LEU:HB3	2.03	0.40
3:C:534:VAL:HG12	3:C:535:ALA:N	2.31	0.40
4:D:863:THR:CB	23:3:599:GLU:C	2.88	0.40
13:F:42:C:H2'	13:F:43:A:O4'	2.21	0.40
15:H:2:U:H2'	15:H:3:C:C6	2.55	0.40
15:H:149:A:N3	15:H:150:U:C6	2.89	0.40
21:1:658:TRP:CZ3	21:1:700:LYS:HD2	2.55	0.40
21:1:935:THR:O	21:1:939:ARG:HG2	2.21	0.40
21:1:1126:PHE:HA	21:1:1165:TYR:CE2	2.56	0.40
22:2:614:ARG:O	22:2:618:GLY:N	2.51	0.40
22:2:648:LEU:O	22:2:649:LYS:HD3	2.21	0.40
23:3:614:VAL:HB	23:3:633:LEU:HD11	2.03	0.40
23:3:983:ASN:HB2	23:3:1021:LEU:HB2	2.03	0.40
24:4:17:VAL:HG13	24:4:84:ILE:CG2	2.48	0.40
28:J:338:GLU:O	37:R:116:TYR:CD2	2.75	0.40
28:J:376:VAL:HG13	28:J:377:LYS:N	2.36	0.40
36:P:44:ARG:HG3	39:T:258:SER:CA	2.51	0.40
38:S:12:PRO:CD	38:S:166:GLY:HA2	2.51	0.40
38:S:25:LEU:HD12	38:S:25:LEU:N	2.36	0.40
38:S:55:ARG:HH12	42:W:96:GLU:HA	1.86	0.40
41:V:512:GLY:O	41:V:513:ARG:C	2.60	0.40
42:W:528:GLY:O	42:W:552:VAL:HA	2.21	0.40
43:X:238:THR:O	43:X:393:VAL:HG23	2.21	0.40
1:A:164:MET:CE	1:A:560:SER:HA	2.51	0.40
1:A:212:PRO:HD2	1:A:225:TYR:OH	2.21	0.40
1:A:652:LEU:HD23	1:A:652:LEU:HA	1.84	0.40
1:A:1057:ARG:O	1:A:1060:GLU:HB2	2.22	0.40
1:A:1273:TYR:HD2	1:A:1274:PHE:CD2	2.39	0.40
1:A:1342:TRP:CD2	3:C:921:LEU:HD21	2.50	0.40
3:C:375:GLU:N	3:C:376:PRO:HD2	2.37	0.40
4:D:455:PHE:CB	23:3:573:GLN:CG	2.99	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:255:MET:O	5:E:257:ASN:N	2.54	0.40
21:1:922:GLY:O	21:1:925:VAL:HG12	2.22	0.40
21:1:933:CYS:HA	21:1:936:VAL:HB	2.02	0.40
21:1:1130:PRO:HB3	22:2:528:ILE:HG23	2.04	0.40
23:3:63:ARG:HD2	23:3:83:ASP:HA	2.03	0.40
23:3:379:LEU:HB2	23:3:383:ASP:HB3	2.04	0.40
23:3:388:GLN:NE2	23:3:389:PRO:HD2	2.36	0.40
23:3:690:ARG:HE	23:3:695:GLY:N	2.20	0.40
38:S:15:TYR:CE2	38:S:22:ILE:HG21	2.57	0.40
38:S:65:GLY:O	38:S:110:SER:OG	2.40	0.40
39:T:339:GLN:CG	39:T:340:ALA:N	2.84	0.40
44:Y:37:TRP:HH2	45:Z:498:GLY:HA3	1.59	0.40
45:Z:491:ASP:O	45:Z:495:ALA:HB3	2.21	0.40
1:A:121:HIS:C	1:A:123:THR:N	2.74	0.40
1:A:372:PRO:CG	3:C:342:ARG:HG2	2.51	0.40
1:A:460:LYS:HA	1:A:460:LYS:HD2	1.94	0.40
1:A:938:PRO:O	1:A:941:LYS:HD3	2.22	0.40
1:A:2259:VAL:HG22	1:A:2260:GLN:H	1.86	0.40
3:C:229:ILE:HG12	3:C:239:THR:HG21	2.04	0.40
3:C:567:GLU:O	3:C:567:GLU:HG3	2.20	0.40
13:F:96:U:H2'	13:F:97:U:C6	2.56	0.40
21:1:1052:ALA:HA	21:1:1055:TRP:CD1	2.51	0.40
21:1:1248:GLN:NE2	23:3:1030:PRO:HD3	2.36	0.40
23:3:179:ASN:HB3	23:3:213:LEU:O	2.22	0.40
23:3:192:ALA:HA	23:3:200:ALA:HB3	2.02	0.40
25:5:42:TYR:CZ	25:5:73:ALA:HA	2.56	0.40
37:R:89:GLN:HG2	38:S:155:ASP:OD2	2.21	0.40
38:S:100:MET:HE3	38:S:109:GLY:O	2.22	0.40
39:T:220:VAL:HG12	39:T:221:THR:N	2.37	0.40
1:A:109:PRO:HD3	1:A:630:TRP:HZ2	1.83	0.40
1:A:120:TYR:CE1	1:A:485:THR:CG2	3.04	0.40
1:A:460:LYS:O	1:A:462:ARG:HD2	2.22	0.40
1:A:692:ASP:HA	39:T:376:ARG:HH21	1.72	0.40
1:A:718:ARG:NH2	37:R:259:LYS:HG3	2.36	0.40
1:A:787:GLU:OE1	1:A:790:ARG:NH2	2.53	0.40
1:A:923:ASP:OD2	1:A:1439:ARG:HD3	2.22	0.40
1:A:1161:LEU:HD23	1:A:1161:LEU:HA	1.85	0.40
1:A:1637:TRP:O	1:A:1656:THR:HA	2.22	0.40
2:B:20:G:C1'	2:B:21:A:OP1	2.69	0.40
2:B:57:G:C2'	2:B:58:U:H5'	2.51	0.40
3:C:259:LYS:HG3	50:C:1500:GTP:C5	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:592:VAL:HG12	3:C:603:MET:SD	2.62	0.40
3:C:673:LYS:HD3	3:C:673:LYS:H	1.86	0.40
3:C:738:ASP:N	3:C:738:ASP:OD1	2.54	0.40
3:C:926:ALA:N	3:C:927:PRO:CD	2.84	0.40
4:D:419:GLY:C	4:D:421:HIS:H	2.25	0.40
13:F:58:G:HO2'	13:F:59:G:P	2.44	0.40
21:1:570:TYR:O	21:1:574:ILE:HG12	2.22	0.40
21:1:839:GLU:O	21:1:842:ASN:HB2	2.22	0.40
21:1:1023:ILE:O	21:1:1026:ASN:HB2	2.21	0.40
23:3:443:GLU:HA	23:3:735:SER:OG	2.20	0.40
23:3:717:SER:O	23:3:738:THR:HG22	2.22	0.40
23:3:999:ARG:NE	23:3:1041:TYR:OH	2.54	0.40
32:I:365:ALA:CA	32:I:369:GLY:N	2.85	0.40
37:R:123:GLU:C	37:R:124:VAL:HG12	2.41	0.40
38:S:12:PRO:HB2	38:S:13:ASN:H	1.75	0.40
39:T:218:TRP:HZ3	39:T:220:VAL:CG2	2.35	0.40
43:X:231:ALA:O	43:X:236:THR:OG1	2.39	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	1970/2335 (84%)	1835 (93%)	108 (6%)	27 (1%)	11 46
3	C	854/972 (88%)	777 (91%)	57 (7%)	20 (2%)	6 34
4	D	1720/2136 (80%)	1632 (95%)	85 (5%)	3 (0%)	47 81
5	E	297/357 (83%)	272 (92%)	16 (5%)	9 (3%)	4 28
6	a	77/126 (61%)	76 (99%)	1 (1%)	0	100 100
6	h	76/126 (60%)	75 (99%)	1 (1%)	0	100 100
7	b	80/231 (35%)	78 (98%)	2 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	i	84/231 (36%)	82 (98%)	2 (2%)	0	100	100
8	c	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
8	j	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
9	d	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
9	k	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
10	f	72/86 (84%)	69 (96%)	3 (4%)	0	100	100
10	m	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
11	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
11	l	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
12	g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
12	n	64/76 (84%)	62 (97%)	2 (3%)	0	100	100
16	o	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	12	48
17	p	159/225 (71%)	138 (87%)	9 (6%)	12 (8%)	1	13
18	w	420/501 (84%)	380 (90%)	37 (9%)	3 (1%)	22	63
19	u	92/793 (12%)	86 (94%)	4 (4%)	2 (2%)	6	35
20	v	153/464 (33%)	124 (81%)	22 (14%)	7 (5%)	2	21
21	1	1022/1304 (78%)	897 (88%)	119 (12%)	6 (1%)	25	66
22	2	171/895 (19%)	154 (90%)	17 (10%)	0	100	100
23	3	1165/1217 (96%)	1081 (93%)	80 (7%)	4 (0%)	41	76
24	4	76/424 (18%)	69 (91%)	6 (8%)	1 (1%)	12	48
25	5	106/125 (85%)	90 (85%)	16 (15%)	0	100	100
26	6	87/110 (79%)	80 (92%)	7 (8%)	0	100	100
27	7	64/86 (74%)	55 (86%)	9 (14%)	0	100	100
28	J	483/848 (57%)	452 (94%)	24 (5%)	7 (1%)	11	46
29	L	324/802 (40%)	304 (94%)	18 (6%)	2 (1%)	25	66
30	q	130/504 (26%)	119 (92%)	7 (5%)	4 (3%)	4	27
30	r	129/504 (26%)	118 (92%)	9 (7%)	2 (2%)	9	44
30	s	65/504 (13%)	62 (95%)	2 (3%)	1 (2%)	10	46
30	t	65/504 (13%)	64 (98%)	0	1 (2%)	10	46
31	K	144/225 (64%)	134 (93%)	6 (4%)	4 (3%)	5	30
32	I	498/855 (58%)	479 (96%)	11 (2%)	8 (2%)	9	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
33	Q	1297/1485 (87%)	1271 (98%)	26 (2%)	0	100 100
34	N	141/144 (98%)	126 (89%)	12 (8%)	3 (2%)	7 36
35	O	283/420 (67%)	247 (87%)	26 (9%)	10 (4%)	3 25
36	P	92/229 (40%)	82 (89%)	8 (9%)	2 (2%)	6 35
37	R	274/540 (51%)	234 (85%)	25 (9%)	15 (6%)	2 19
38	S	157/166 (95%)	144 (92%)	10 (6%)	3 (2%)	8 38
39	T	311/514 (60%)	282 (91%)	17 (6%)	12 (4%)	3 23
40	U	24/2752 (1%)	20 (83%)	3 (12%)	1 (4%)	3 22
41	V	444/908 (49%)	412 (93%)	27 (6%)	5 (1%)	14 52
42	W	477/579 (82%)	421 (88%)	32 (7%)	24 (5%)	2 20
43	X	144/396 (36%)	134 (93%)	10 (7%)	0	100 100
44	Y	103/322 (32%)	92 (89%)	11 (11%)	0	100 100
45	Z	109/619 (18%)	93 (85%)	10 (9%)	6 (6%)	2 19
46	x	561/1041 (54%)	536 (96%)	20 (4%)	5 (1%)	17 57
47	y	224/301 (74%)	217 (97%)	7 (3%)	0	100 100
All	All	16082/29057 (55%)	14914 (93%)	957 (6%)	211 (1%)	16 48

All (211) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	ARG
1	A	92	LEU
1	A	167	PRO
1	A	188	LEU
1	A	331	TRP
1	A	346	ASP
1	A	383	PHE
1	A	570	ASP
1	A	629	PHE
1	A	701	ILE
3	C	388	VAL
3	C	427	PHE
3	C	444	GLY
3	C	457	VAL
3	C	458	ASP
3	C	516	LEU
3	C	824	THR

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Mol	Chain	Res	Type
4	D	957	VAL
4	D	1584	ILE
5	E	193	THR
17	p	157	ASN
17	p	183	VAL
17	p	195	GLU
18	w	284	ARG
20	v	139	PRO
20	v	165	ARG
20	v	218	PRO
28	J	413	GLU
30	q	59	HIS
30	q	60	PRO
30	s	71	ILE
30	t	69	THR
31	K	78	PRO
31	K	90	PRO
32	I	463	PRO
32	I	721	LYS
32	I	797	PHE
34	N	36	PRO
35	O	20	PHE
35	O	107	MET
35	O	225	PRO
35	O	226	PRO
36	P	49	ASP
37	R	71	GLN
37	R	135	PRO
37	R	136	ASP
37	R	186	VAL
37	R	412	ASP
37	R	416	PHE
37	R	420	LYS
37	R	425	GLY
38	S	164	PRO
39	T	186	PRO
39	T	268	LYS
39	T	341	ALA
39	T	343	PRO
39	T	495	ALA
41	V	596	LEU
41	V	597	PRO

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Mol	Chain	Res	Type
42	W	156	VAL
42	W	199	TYR
42	W	213	GLN
42	W	243	VAL
42	W	258	PRO
42	W	259	GLN
42	W	263	VAL
42	W	267	SER
42	W	279	LYS
42	W	299	LEU
42	W	325	LEU
42	W	372	ASN
42	W	492	ASN
45	Z	499	LYS
45	Z	531	LEU
45	Z	536	ARG
45	Z	569	PRO
46	x	937	ILE
1	A	122	ILE
1	A	308	ILE
1	A	349	ALA
1	A	370	PRO
1	A	374	ASP
1	A	631	ALA
3	C	90	THR
3	C	364	SER
3	C	572	GLU
3	C	711	ARG
16	o	160	LYS
17	p	159	PRO
17	p	160	GLU
17	p	177	PHE
17	p	186	ARG
19	u	280	VAL
20	v	115	PRO
21	1	112	ILE
23	3	775	ASN
28	J	217	GLU
28	J	341	PRO
28	J	376	VAL
28	J	709	VAL
30	q	9	ASN

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Mol	Chain	Res	Type
32	I	618	ARG
32	I	634	ILE
34	N	39	GLY
35	O	132	ARG
35	O	206	ASN
36	P	190	ASP
37	R	191	GLY
37	R	422	MET
38	S	12	PRO
39	T	301	ASP
40	U	2	TYR
41	V	485	GLN
42	W	191	GLY
42	W	318	VAL
42	W	482	ASP
45	Z	613	LYS
1	A	51	PHE
1	A	212	PRO
1	A	378	PHE
1	A	699	GLU
5	E	60	MET
5	E	88	ARG
5	E	256	ASP
17	p	222	TYR
18	w	177	ARG
30	q	19	PRO
30	r	9	ASN
32	I	601	GLN
32	I	752	ALA
35	O	222	ARG
37	R	104	GLN
37	R	173	PRO
39	T	406	ILE
41	V	578	SER
42	W	102	GLN
46	x	1005	SER
1	A	363	HIS
1	A	480	LYS
1	A	698	PRO
1	A	1092	ILE
3	C	63	LYS
3	C	754	VAL

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Mol	Chain	Res	Type
3	C	856	HIS
5	E	162	ARG
16	o	32	PRO
17	p	208	GLN
17	p	209	GLY
21	1	417	PRO
21	1	456	VAL
28	J	604	PRO
29	L	585	TYR
31	K	65	ILE
32	I	617	GLU
35	O	134	VAL
35	O	230	THR
37	R	124	VAL
38	S	10	GLN
39	T	401	PRO
42	W	272	GLU
42	W	554	ILE
46	x	935	ASP
1	A	359	ILE
3	C	361	PRO
3	C	615	PRO
5	E	159	PRO
20	v	217	PRO
23	3	442	LEU
35	O	239	LEU
37	R	126	ASN
37	R	423	ASP
39	T	185	MET
39	T	189	GLN
39	T	226	ARG
42	W	301	GLY
42	W	330	GLY
46	x	980	GLN
46	x	981	PRO
3	C	94	ILE
3	C	360	ALA
3	C	623	GLU
5	E	270	LYS
17	p	173	GLN
20	v	141	ILE
20	v	220	PRO

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Mol	Chain	Res	Type
21	1	944	SER
29	L	215	PRO
41	V	609	GLN
42	W	376	PRO
42	W	549	HIS
3	C	66	TYR
5	E	149	GLY
45	Z	571	PRO
1	A	186	GLU
19	u	221	PRO
31	K	17	PRO
1	A	384	VAL
18	w	229	TRP
21	1	418	PRO
24	4	27	PRO
28	J	241	VAL
39	T	411	GLY
42	W	270	PRO
4	D	585	ILE
5	E	324	PRO
17	p	184	PRO
23	3	773	VAL
30	r	60	PRO
34	N	4	VAL
21	1	932	ILE
23	3	491	VAL

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	1773/2108 (84%)	1675 (94%)	98 (6%)	21 47
3	C	745/866 (86%)	677 (91%)	68 (9%)	9 30
5	E	256/300 (85%)	244 (95%)	12 (5%)	26 51
18	w	49/446 (11%)	47 (96%)	2 (4%)	30 55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
20	v	30/382 (8%)	28 (93%)	2 (7%)	16 41
21	1	735/1104 (67%)	735 (100%)	0	100 100
22	2	94/776 (12%)	90 (96%)	4 (4%)	29 53
23	3	1012/1051 (96%)	1011 (100%)	1 (0%)	93 97
24	4	39/336 (12%)	37 (95%)	2 (5%)	24 49
25	5	74/109 (68%)	74 (100%)	0	100 100
26	6	76/95 (80%)	76 (100%)	0	100 100
27	7	57/77 (74%)	57 (100%)	0	100 100
28	J	205/751 (27%)	194 (95%)	11 (5%)	22 47
29	L	131/709 (18%)	122 (93%)	9 (7%)	15 40
31	K	54/196 (28%)	49 (91%)	5 (9%)	9 29
34	N	130/130 (100%)	125 (96%)	5 (4%)	33 57
35	O	250/361 (69%)	239 (96%)	11 (4%)	28 53
36	P	90/203 (44%)	77 (86%)	13 (14%)	3 16
37	R	215/463 (46%)	165 (77%)	50 (23%)	1 4
38	S	129/134 (96%)	119 (92%)	10 (8%)	12 36
39	T	268/441 (61%)	251 (94%)	17 (6%)	18 43
40	U	21/2432 (1%)	16 (76%)	5 (24%)	0 4
43	X	51/349 (15%)	44 (86%)	7 (14%)	3 17
44	Y	57/291 (20%)	56 (98%)	1 (2%)	59 77
45	Z	47/545 (9%)	39 (83%)	8 (17%)	2 12
46	x	1/897 (0%)	1 (100%)	0	100 100
All	All	6589/15552 (42%)	6248 (95%)	341 (5%)	27 48

All (341) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	ARG
1	A	48	LYS
1	A	49	ARG
1	A	50	LYS
1	A	55	ASP
1	A	59	GLU
1	A	60	ASP

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Mol	Chain	Res	Type
1	A	75	ASP
1	A	77	THR
1	A	78	ASN
1	A	82	ARG
1	A	86	ARG
1	A	88	TYR
1	A	89	LEU
1	A	152	ARG
1	A	163	ARG
1	A	177	ASP
1	A	181	ASN
1	A	185	VAL
1	A	204	LEU
1	A	233	PRO
1	A	250	VAL
1	A	258	PHE
1	A	284	ARG
1	A	294	ASN
1	A	295	GLU
1	A	325	HIS
1	A	330	THR
1	A	331	TRP
1	A	336	ASN
1	A	344	ASP
1	A	352	PHE
1	A	359	ILE
1	A	362	ARG
1	A	363	HIS
1	A	364	SER
1	A	366	LYS
1	A	371	LEU
1	A	377	GLU
1	A	382	GLU
1	A	383	PHE
1	A	389	LYS
1	A	391	THR
1	A	394	TYR
1	A	409	ARG
1	A	413	LEU
1	A	433	GLU
1	A	459	LEU
1	A	462	ARG

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Mol	Chain	Res	Type
1	A	467	GLN
1	A	468	LYS
1	A	535	ARG
1	A	546	LEU
1	A	579	GLN
1	A	606	LYS
1	A	627	CYS
1	A	630	TRP
1	A	671	THR
1	A	673	THR
1	A	674	LYS
1	A	675	GLN
1	A	679	SER
1	A	1163	ARG
1	A	1425	LYS
1	A	1549	VAL
1	A	2067	PHE
1	A	2073	TRP
1	A	2074	ARG
1	A	2078	ILE
1	A	2085	LEU
1	A	2087	THR
1	A	2090	ILE
1	A	2103	THR
1	A	2108	LYS
1	A	2117	ILE
1	A	2143	ARG
1	A	2156	THR
1	A	2157	VAL
1	A	2159	LEU
1	A	2171	GLU
1	A	2193	VAL
1	A	2194	THR
1	A	2219	THR
1	A	2223	CYS
1	A	2233	SER
1	A	2239	ARG
1	A	2242	THR
1	A	2254	SER
1	A	2259	VAL
1	A	2261	MET
1	A	2273	VAL

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Mol	Chain	Res	Type
1	A	2284	MET
1	A	2293	LYS
1	A	2298	LEU
1	A	2310	ARG
1	A	2312	SER
1	A	2319	LEU
1	A	2329	ASP
3	C	61	GLU
3	C	62	ASP
3	C	63	LYS
3	C	64	LYS
3	C	66	TYR
3	C	68	THR
3	C	71	GLU
3	C	79	THR
3	C	97	VAL
3	C	131	ASN
3	C	227	LEU
3	C	256	CYS
3	C	259	LYS
3	C	295	ASP
3	C	296	GLU
3	C	297	ASN
3	C	298	LEU
3	C	300	LEU
3	C	333	ASP
3	C	336	TYR
3	C	354	ARG
3	C	359	LYS
3	C	362	THR
3	C	366	GLN
3	C	387	ASP
3	C	389	ASP
3	C	427	PHE
3	C	428	THR
3	C	438	ILE
3	C	446	LYS
3	C	452	THR
3	C	454	THR
3	C	457	VAL
3	C	458	ASP
3	C	459	SER

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Mol	Chain	Res	Type
3	C	463	GLU
3	C	468	CYS
3	C	474	LEU
3	C	475	MET
3	C	477	HIS
3	C	489	GLN
3	C	490	PHE
3	C	495	ARG
3	C	512	GLU
3	C	517	GLU
3	C	519	GLU
3	C	571	ASN
3	C	572	GLU
3	C	573	GLU
3	C	596	ASN
3	C	673	LYS
3	C	675	PHE
3	C	677	GLU
3	C	704	VAL
3	C	706	GLN
3	C	709	TRP
3	C	712	LYS
3	C	724	TRP
3	C	725	ASP
3	C	730	ARG
3	C	738	ASP
3	C	749	THR
3	C	750	LEU
3	C	763	LYS
3	C	826	ARG
3	C	856	HIS
3	C	941	LYS
3	C	943	LEU
5	E	74	PHE
5	E	153	PHE
5	E	161	ARG
5	E	229	TYR
5	E	243	LEU
5	E	248	SER
5	E	250	LEU
5	E	265	ARG
5	E	270	LYS

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Mol	Chain	Res	Type
5	E	271	GLU
5	E	289	LEU
5	E	290	ARG
18	w	419	PRO
18	w	441	PRO
20	v	18	SER
20	v	56	CYS
22	2	498	VAL
22	2	520	PRO
22	2	614	ARG
22	2	616	SER
23	3	442	LEU
24	4	27	PRO
24	4	83	PRO
28	J	217	GLU
28	J	218	GLU
28	J	219	GLU
28	J	221	ASN
28	J	229	LYS
28	J	239	ARG
28	J	281	LYS
28	J	308	ARG
28	J	363	ARG
28	J	410	HIS
28	J	411	MET
29	L	219	LYS
29	L	222	LEU
29	L	227	THR
29	L	228	SER
29	L	235	LEU
29	L	731	LEU
29	L	761	SER
29	L	766	ARG
29	L	781	GLU
31	K	38	GLU
31	K	90	PRO
31	K	117	GLN
31	K	126	LEU
31	K	171	GLN
34	N	24	GLU
34	N	41	ARG
34	N	42	LYS

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Mol	Chain	Res	Type
34	N	116	ASN
34	N	125	LYS
35	O	45	CYS
35	O	69	GLU
35	O	74	CYS
35	O	115	GLU
35	O	150	LEU
35	O	220	MET
35	O	223	LEU
35	O	225	PRO
35	O	226	PRO
35	O	228	ASP
35	O	229	LYS
36	P	28	LYS
36	P	29	GLN
36	P	30	TYR
36	P	33	ARG
36	P	66	ARG
36	P	67	GLU
36	P	76	ARG
36	P	78	ARG
36	P	188	TRP
36	P	190	ASP
36	P	191	ASP
36	P	212	ASN
36	P	224	MET
37	R	56	GLU
37	R	66	GLU
37	R	71	GLN
37	R	72	TYR
37	R	75	ASP
37	R	80	LYS
37	R	81	LYS
37	R	82	MET
37	R	86	LEU
37	R	89	GLN
37	R	92	SER
37	R	95	LYS
37	R	103	ARG
37	R	104	GLN
37	R	106	GLN
37	R	118	ASP

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Mol	Chain	Res	Type
37	R	122	LYS
37	R	125	MET
37	R	128	ASP
37	R	129	ASP
37	R	137	GLU
37	R	158	LYS
37	R	170	LYS
37	R	171	LEU
37	R	175	GLN
37	R	181	PRO
37	R	183	GLN
37	R	186	VAL
37	R	188	PHE
37	R	189	ASN
37	R	195	ARG
37	R	211	ARG
37	R	212	PHE
37	R	213	LYS
37	R	214	ILE
37	R	215	ASN
37	R	220	ARG
37	R	233	HIS
37	R	245	GLU
37	R	250	LYS
37	R	403	PRO
37	R	409	VAL
37	R	411	TYR
37	R	415	LEU
37	R	418	GLN
37	R	420	LYS
37	R	422	MET
37	R	426	PHE
37	R	434	TYR
37	R	435	ASN
38	S	10	GLN
38	S	15	TYR
38	S	91	LYS
38	S	100	MET
38	S	102	ASN
38	S	108	ASN
38	S	125	LYS
38	S	129	PHE

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Mol	Chain	Res	Type
38	S	131	ARG
38	S	133	CYS
39	T	257	ARG
39	T	282	ARG
39	T	308	ARG
39	T	318	ARG
39	T	387	PHE
39	T	399	LYS
39	T	400	PHE
39	T	401	PRO
39	T	402	ASP
39	T	412	HIS
39	T	416	ILE
39	T	418	THR
39	T	455	GLN
39	T	460	ASP
39	T	461	SER
39	T	463	SER
39	T	478	LEU
40	U	1	MET
40	U	11	ARG
40	U	20	GLN
40	U	23	LEU
40	U	25	LEU
43	X	209	PRO
43	X	224	PRO
43	X	249	PRO
43	X	250	PRO
43	X	263	PRO
43	X	293	PRO
43	X	297	PRO
44	Y	44	PRO
45	Z	524	ARG
45	Z	526	ILE
45	Z	563	ARG
45	Z	569	PRO
45	Z	597	ARG
45	Z	598	PHE
45	Z	600	ARG
45	Z	613	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (106) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	A	73	HIS
1	A	78	ASN
1	A	97	HIS
1	A	210	HIS
1	A	270	ASN
1	A	297	ASN
1	A	325	HIS
1	A	448	GLN
1	A	573	GLN
1	A	584	HIS
1	A	601	GLN
1	A	675	GLN
1	A	775	ASN
1	A	924	GLN
1	A	1024	HIS
1	A	1069	ASN
1	A	1075	GLN
1	A	1096	HIS
1	A	1217	GLN
1	A	1293	ASN
1	A	1296	GLN
1	A	1337	GLN
1	A	1359	HIS
1	A	1458	GLN
1	A	1460	HIS
1	A	1717	ASN
1	A	2123	GLN
1	A	2300	ASN
1	A	2306	HIS
3	C	87	GLN
3	C	245	HIS
3	C	297	ASN
3	C	437	HIS
3	C	513	ASN
3	C	575	GLN
3	C	583	ASN
3	C	596	ASN
3	C	706	GLN
3	C	924	GLN
5	E	165	GLN
18	w	425	HIS
18	w	485	ASN

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Mol	Chain	Res	Type
20	v	23	ASN
20	v	78	HIS
21	1	473	GLN
21	1	599	ASN
21	1	903	GLN
21	1	941	ASN
21	1	942	ASN
21	1	1026	ASN
21	1	1186	GLN
21	1	1209	ASN
21	1	1248	GLN
21	1	1277	GLN
22	2	490	HIS
23	3	21	ASN
23	3	97	ASN
23	3	104	GLN
23	3	254	ASN
23	3	264	GLN
23	3	293	HIS
23	3	304	GLN
23	3	388	GLN
23	3	518	GLN
23	3	775	ASN
23	3	870	ASN
23	3	1087	GLN
28	J	221	ASN
28	J	259	GLN
28	J	294	HIS
28	J	351	ASN
29	L	39	HIS
29	L	73	HIS
31	K	117	GLN
31	K	171	GLN
34	N	27	GLN
34	N	37	HIS
34	N	99	ASN
34	N	107	GLN
35	O	163	HIS
35	O	196	GLN
35	O	254	GLN
35	O	268	GLN
35	O	294	ASN

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Mol	Chain	Res	Type
36	P	212	ASN
36	P	220	HIS
37	R	104	GLN
37	R	106	GLN
37	R	126	ASN
37	R	189	ASN
37	R	194	GLN
37	R	215	ASN
37	R	233	HIS
37	R	283	HIS
37	R	418	GLN
39	T	217	GLN
39	T	278	ASN
39	T	297	HIS
39	T	413	ASN
39	T	417	ASN
39	T	446	ASN
39	T	451	HIS
39	T	455	GLN
43	X	307	GLN
44	Y	87	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	F	91/107 (85%)	37 (40%)	12 (13%)
14	G	76/274 (27%)	48 (63%)	9 (11%)
15	H	130/188 (69%)	33 (25%)	4 (3%)
2	B	82/117 (70%)	19 (23%)	10 (12%)
All	All	379/686 (55%)	137 (36%)	35 (9%)

All (137) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	12	U
2	B	13	C
2	B	19	A
2	B	20	G
2	B	21	A
2	B	22	U
2	B	23	C

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Mol	Chain	Res	Type
2	B	24	G
2	B	25	C
2	B	26	A
2	B	28	A
2	B	36	C
2	B	38	C
2	B	40	U
2	B	41	U
2	B	45	C
2	B	57	G
2	B	70	A
2	B	71	C
13	F	6	C
13	F	7	G
13	F	8	C
13	F	10	U
13	F	12	G
13	F	25	C
13	F	26	U
13	F	27	A
13	F	28	A
13	F	29	A
13	F	33	G
13	F	34	G
13	F	36	A
13	F	37	C
13	F	38	G
13	F	44	G
13	F	45	A
13	F	46	G
13	F	47	A
13	F	48	A
13	F	49	G
13	F	51	U
13	F	54	G
13	F	55	C
13	F	56	A
13	F	58	G
13	F	59	G
13	F	60	C
13	F	61	C
13	F	62	C

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Mol	Chain	Res	Type
13	F	68	C
13	F	74	U
13	F	78	A
13	F	79	C
13	F	85	U
13	F	86	U
13	F	87	C
14	G	-11	G
14	G	-6	C
14	G	-4	A
14	G	-3	A
14	G	1	G
14	G	2	U
14	G	3	A
14	G	4	A
14	G	5	G
14	G	7	G
14	G	8	C
14	G	10	U
14	G	11	A
14	G	12	G
14	G	13	C
14	G	17	U
14	G	21	A
14	G	22	C
14	G	23	U
14	G	24	G
14	G	25	G
14	G	26	U
14	G	27	U
14	G	28	A
14	G	29	C
14	G	30	C
14	G	31	U
14	G	131	U
14	G	132	G
14	G	135	G
14	G	136	U
14	G	137	C
14	G	143	U
14	G	144	A
14	G	145	U

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Mol	Chain	Res	Type
14	G	146	C
14	G	147	C
14	G	148	U
14	G	149	G
14	G	150	U
14	G	151	C
14	G	152	C
14	G	154	U
14	G	156	U
14	G	159	U
14	G	161	U
14	G	162	C
14	G	163	C
15	H	14	C
15	H	20	G
15	H	23	A
15	H	24	A
15	H	25	G
15	H	29	A
15	H	30	A
15	H	31	G
15	H	44	U
15	H	45	C
15	H	46	U
15	H	47	U
15	H	48	A
15	H	65	U
15	H	112	G
15	H	143	A
15	H	147	G
15	H	149	A
15	H	152	G
15	H	153	A
15	H	154	C
15	H	156	U
15	H	157	G
15	H	160	A
15	H	163	G
15	H	164	C
15	H	166	G
15	H	167	U
15	H	169	C

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Mol	Chain	Res	Type
15	H	177	A
15	H	178	A
15	H	179	C
15	H	183	G

All (35) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	12	U
2	B	18	C
2	B	19	A
2	B	20	G
2	B	23	C
2	B	24	G
2	B	25	C
2	B	27	U
2	B	39	C
2	B	40	U
13	F	5	U
13	F	7	G
13	F	25	C
13	F	33	G
13	F	35	A
13	F	36	A
13	F	37	C
13	F	47	A
13	F	48	A
13	F	50	A
13	F	58	G
13	F	59	G
14	G	-12	G
14	G	16	G
14	G	21	A
14	G	22	C
14	G	136	U
14	G	148	U
14	G	151	C
14	G	153	C
14	G	155	U
15	H	29	A
15	H	46	U
15	H	47	U

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Mol	Chain	Res	Type
15	H	156	U

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 19 ligands modelled in this entry, 16 are monoatomic - leaving 3 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	$\#\|Z\| > 2$
49	ALA	A	2402	-	3,4,5	0.65	0	2,4,6	0.83	0
50	GTP	C	1500	51	26,34,34	1.18	1 (3%)	32,54,54	1.81	8 (25%)
48	IHP	A	2401	-	36,36,36	1.01	2 (5%)	54,60,60	1.62	12 (22%)

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
49	ALA	A	2402	-	-	0/0/2/4	-
50	GTP	C	1500	51	-	7/18/38/38	0/3/3/3
48	IHP	A	2401	-	-	6/30/54/54	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	C	1500	GTP	C6-N1	-3.52	1.32	1.37
48	A	2401	IHP	P5-O45	-2.86	1.43	1.54
48	A	2401	IHP	P2-O12	2.65	1.64	1.59

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
48	A	2401	IHP	O45-P5-O35	4.10	123.30	107.64
48	A	2401	IHP	O35-P5-O15	-3.97	88.19	105.99
50	C	1500	GTP	C5-C6-N1	3.79	120.64	113.95
50	C	1500	GTP	PA-O3A-PB	-3.79	119.84	132.83
50	C	1500	GTP	O6-C6-C5	-3.73	117.08	124.37
48	A	2401	IHP	O16-C6-C1	3.32	116.50	108.69
48	A	2401	IHP	C6-C1-C2	-3.22	103.37	110.41
50	C	1500	GTP	PB-O3B-PG	-3.16	121.97	132.83
50	C	1500	GTP	C2-N1-C6	-3.02	119.53	125.10
50	C	1500	GTP	O2G-PG-O3B	2.89	114.34	104.64
48	A	2401	IHP	O44-P4-O34	2.73	118.06	107.64
48	A	2401	IHP	C5-C6-C1	-2.65	104.62	110.41
50	C	1500	GTP	C3'-C2'-C1'	2.32	104.47	100.98
50	C	1500	GTP	O4'-C4'-C3'	2.30	109.66	105.11
48	A	2401	IHP	O35-P5-O25	2.25	119.48	110.68
48	A	2401	IHP	O12-C2-C3	2.14	113.74	108.69
48	A	2401	IHP	O15-C5-C4	-2.13	103.66	108.69
48	A	2401	IHP	O42-P2-O22	2.10	118.91	110.68
48	A	2401	IHP	O31-P1-O11	-2.09	96.62	105.99
48	A	2401	IHP	C4-C3-C2	2.08	114.96	110.41

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
48	A	2401	IHP	C4-C5-O15-P5
48	A	2401	IHP	C6-C5-O15-P5
50	C	1500	GTP	PB-O3B-PG-O3G
50	C	1500	GTP	C5'-O5'-PA-O3A
50	C	1500	GTP	C5'-O5'-PA-O1A
50	C	1500	GTP	C5'-O5'-PA-O2A
50	C	1500	GTP	O4'-C4'-C5'-O5'
50	C	1500	GTP	C3'-C4'-C5'-O5'
48	A	2401	IHP	C2-O12-P2-O22
48	A	2401	IHP	C1-O11-P1-O21

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Mol	Chain	Res	Type	Atoms
48	A	2401	IHP	C1-O11-P1-O31
48	A	2401	IHP	C5-O15-P5-O35
50	C	1500	GTP	PG-O3B-PB-O2B

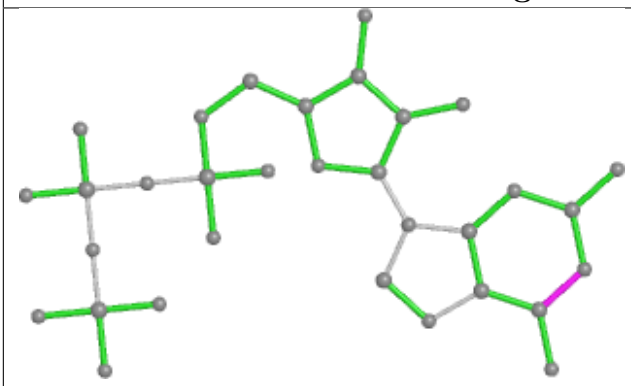
There are no ring outliers.

3 monomers are involved in 23 short contacts:

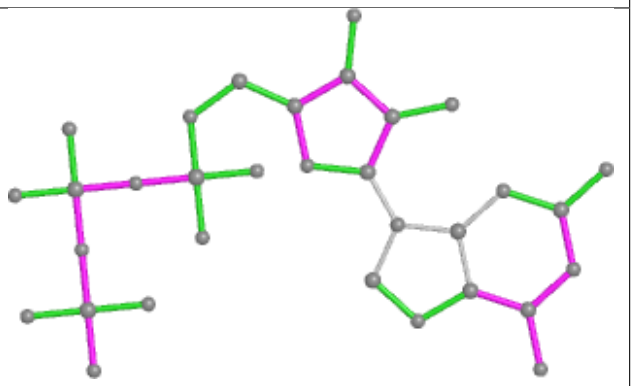
Mol	Chain	Res	Type	Clashes	Symm-Clashes
49	A	2402	ALA	2	0
50	C	1500	GTP	11	0
48	A	2401	IHP	10	0

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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

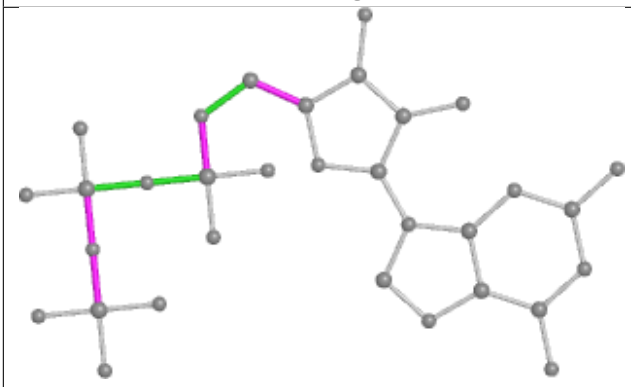
Ligand GTP C 1500



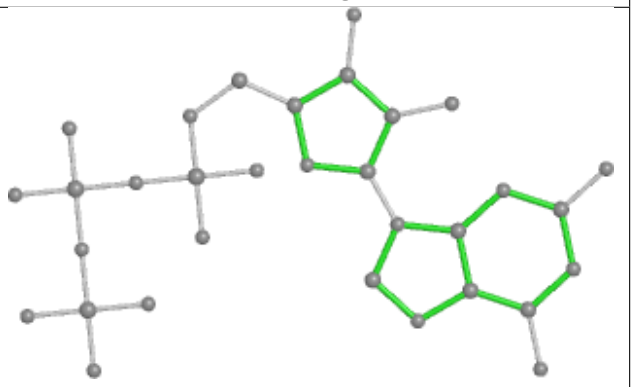
Bond lengths



Bond angles

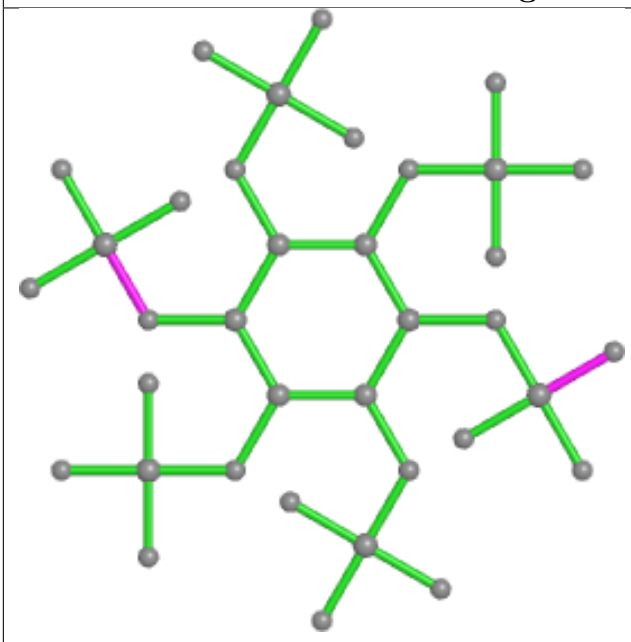


Torsions

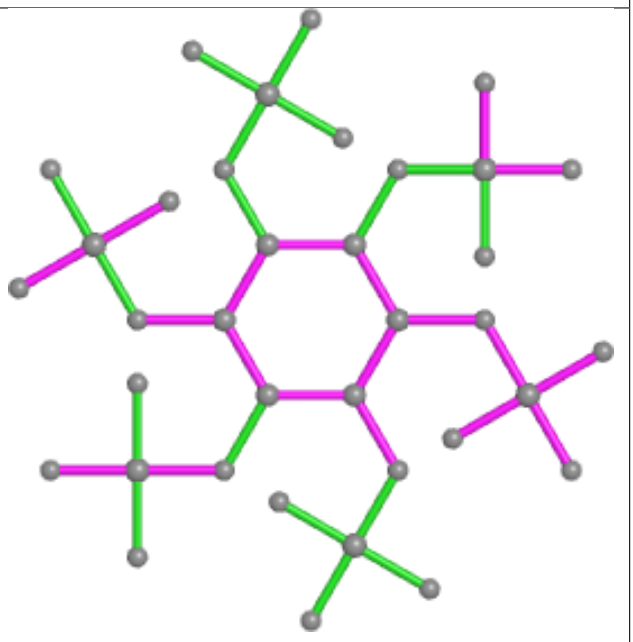


Rings

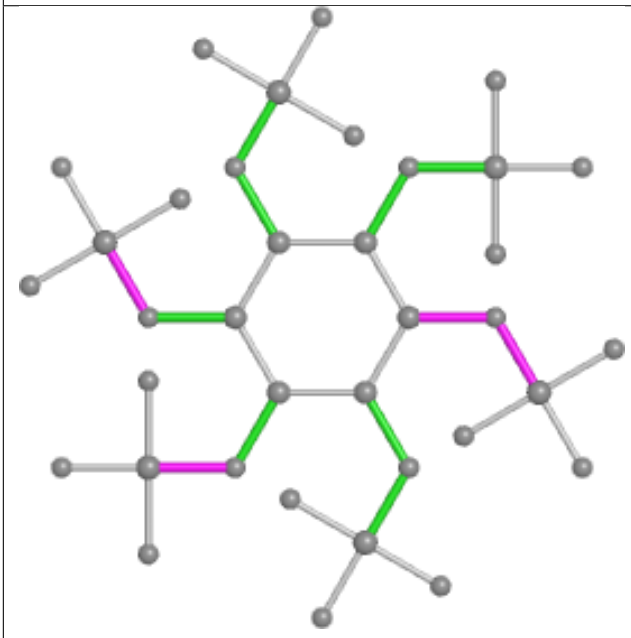
Ligand IHP A 2401



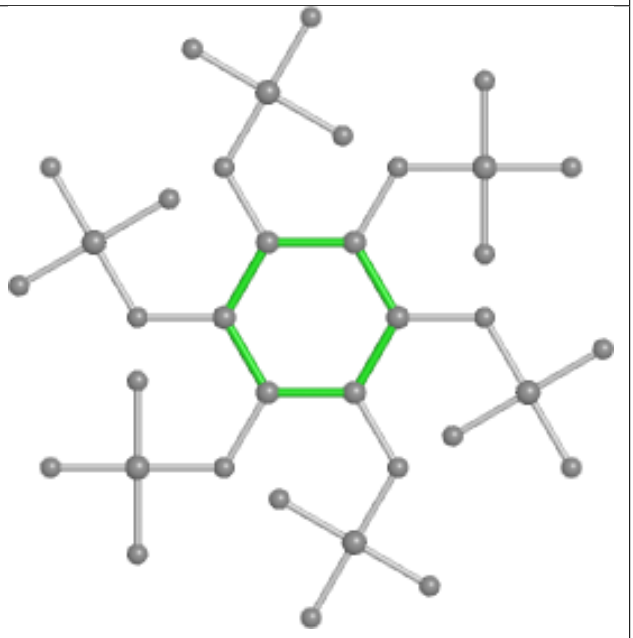
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

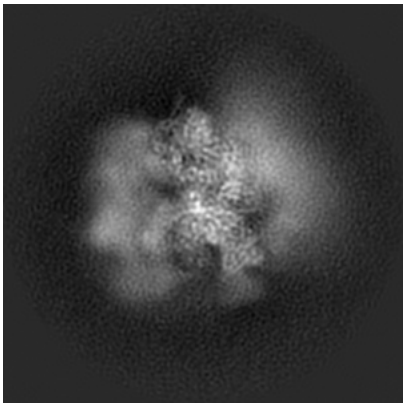
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-6890. These allow visual inspection of the internal detail of the map and identification of artifacts.

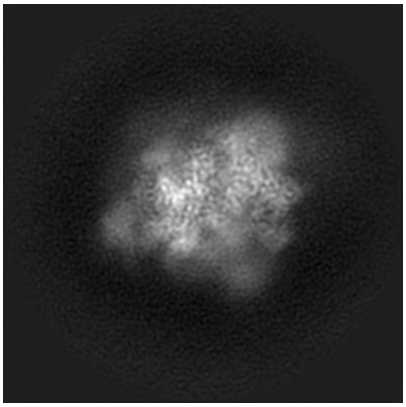
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

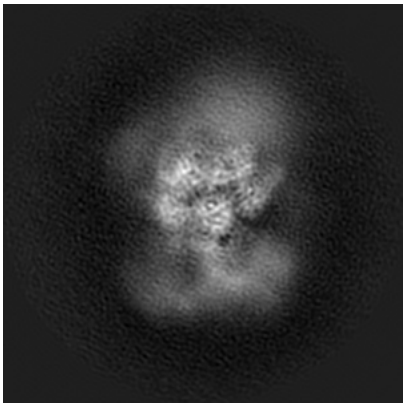
6.1.1 Primary map



X



Y

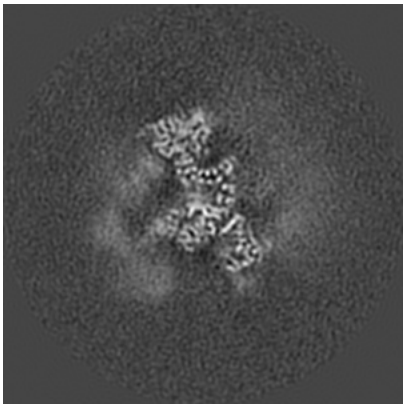


Z

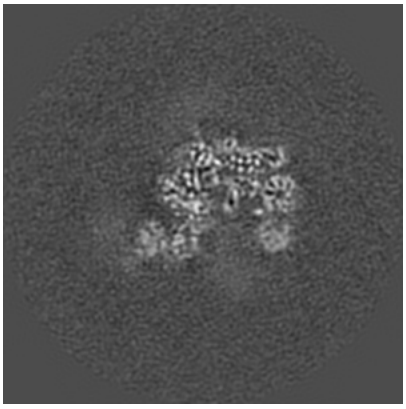
The images above show the map projected in three orthogonal directions.

6.2 Central slices

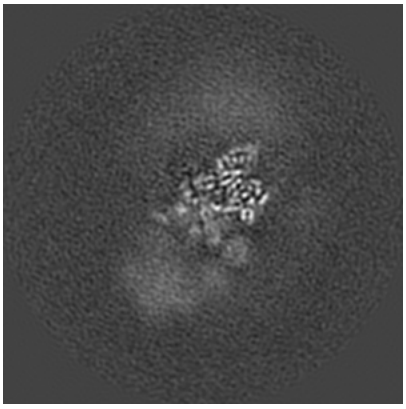
6.2.1 Primary map



X Index: 200



Y Index: 200

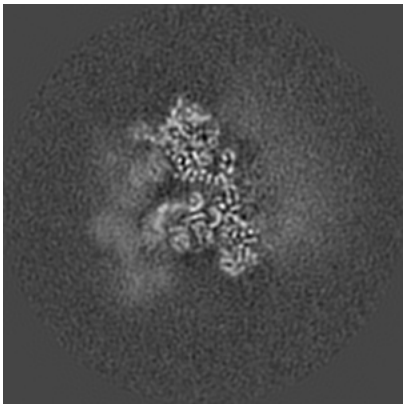


Z Index: 200

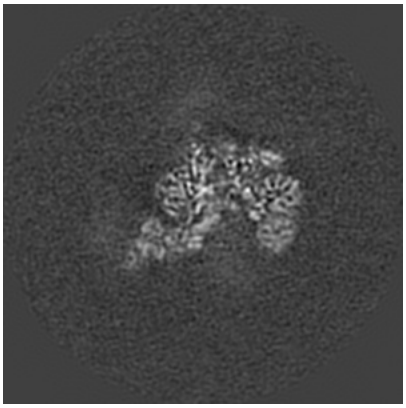
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

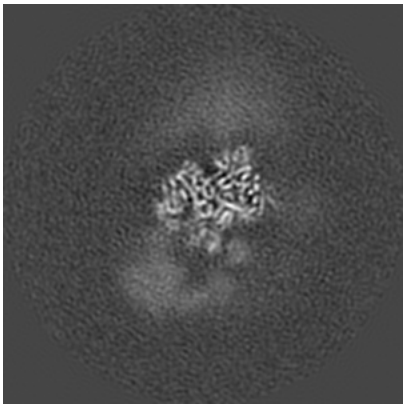
6.3.1 Primary map



X Index: 210



Y Index: 195



Z Index: 192

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.0323. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

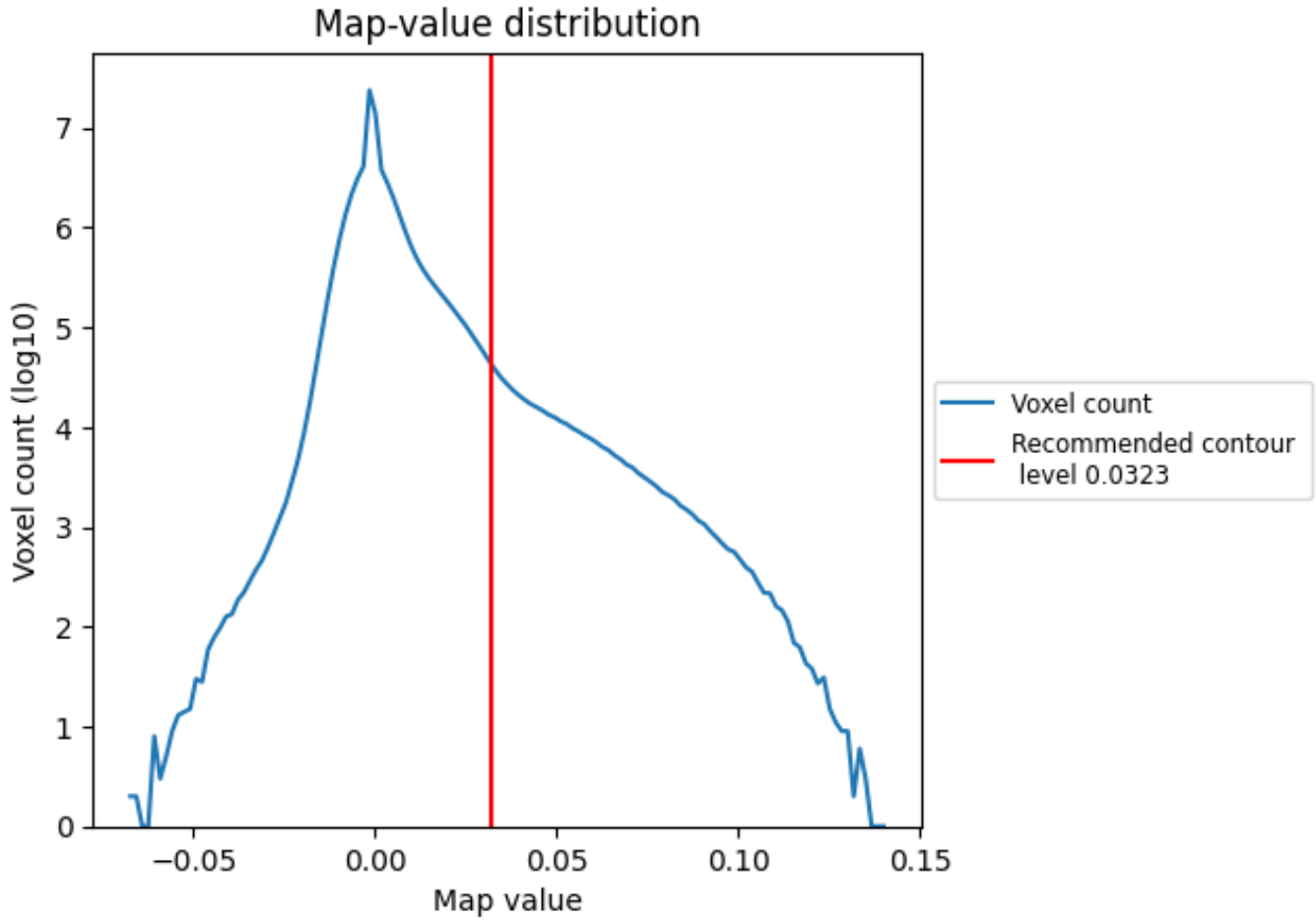
6.5 Mask visualisation (i)

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

7 Map analysis

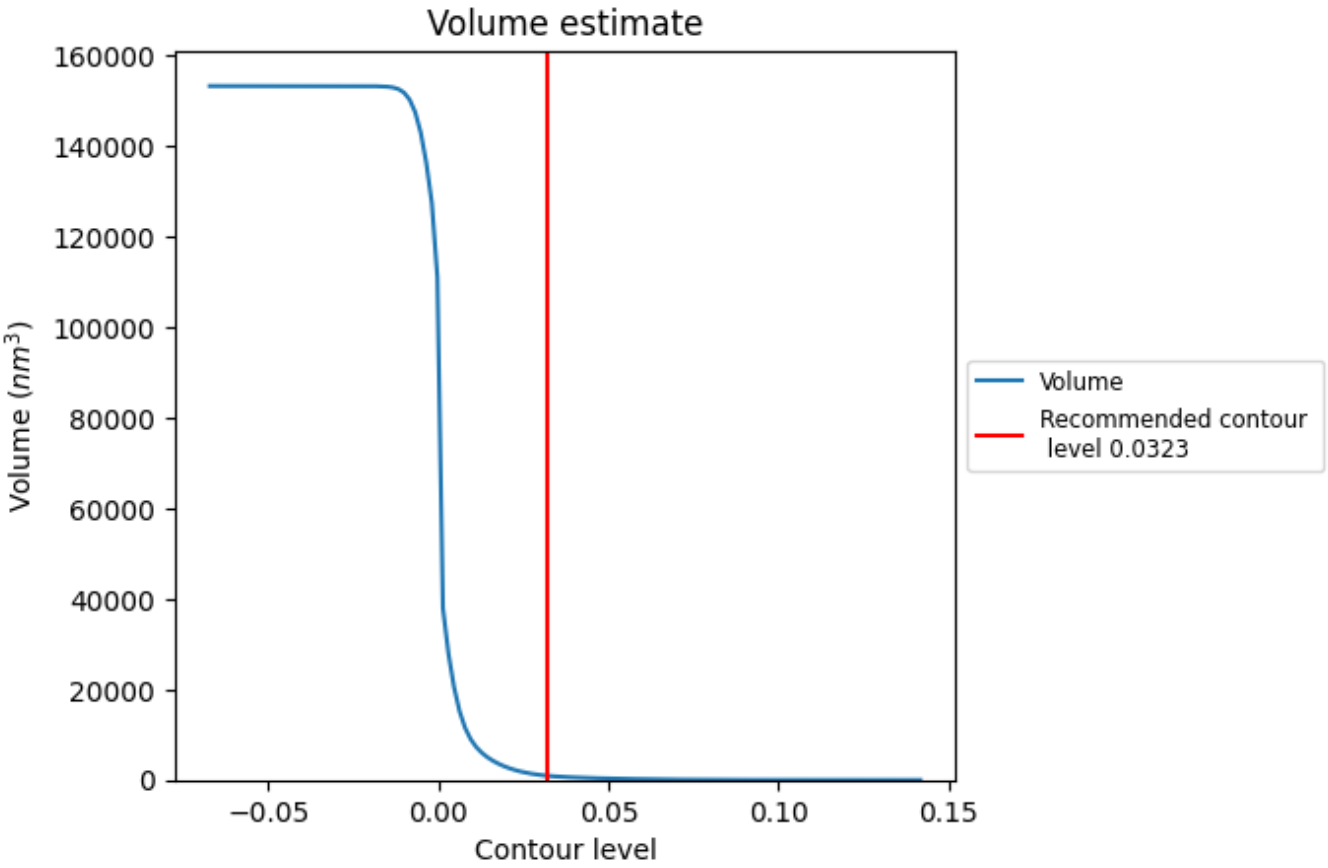
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

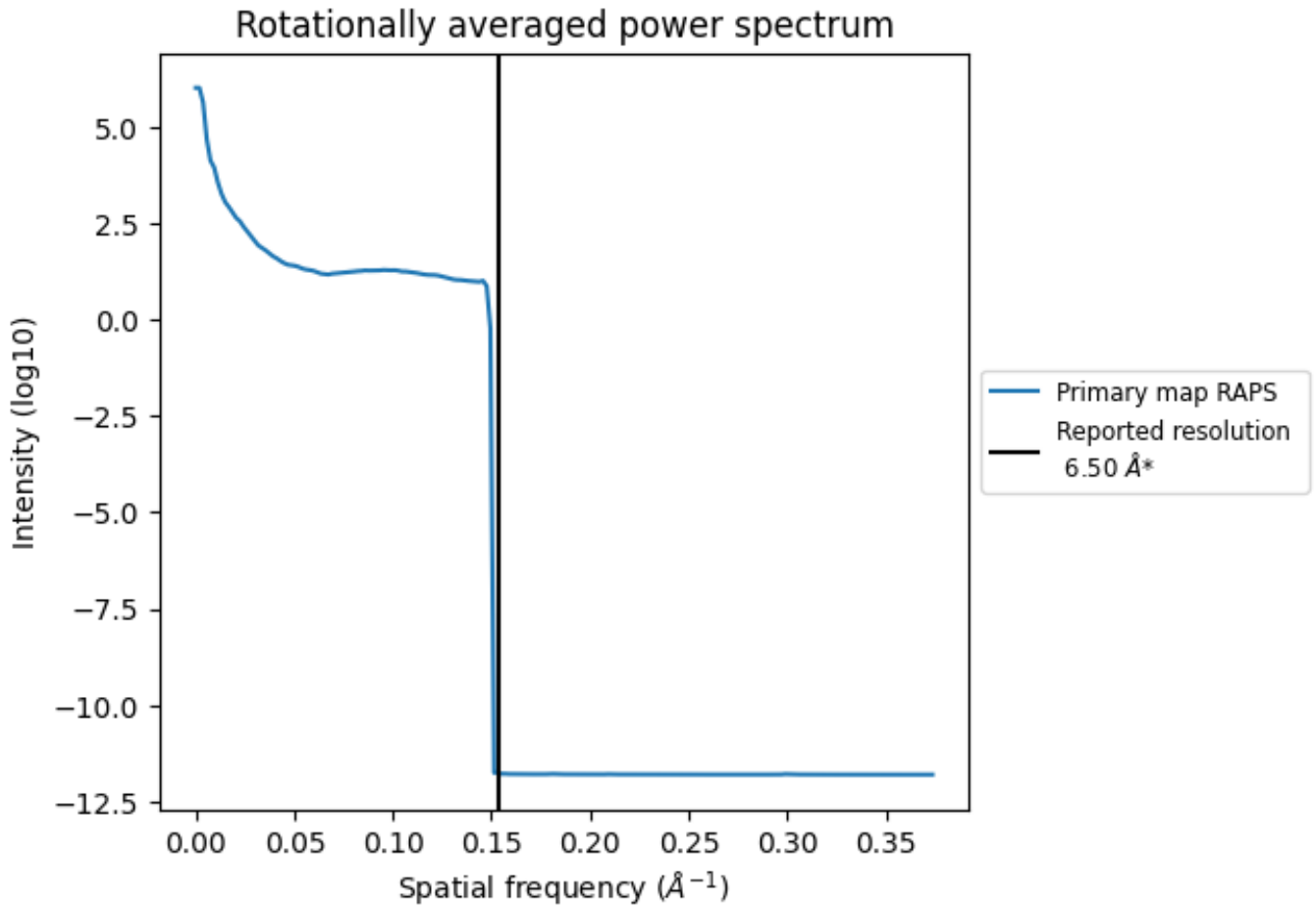
7.2 Volume estimate



The volume at the recommended contour level is 909 nm^3; this corresponds to an approximate mass of 821 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 (i)



*Reported resolution corresponds to spatial frequency of 0.154 $Å^{-1}$

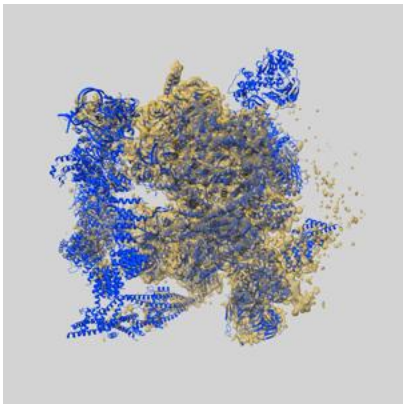
8 Fourier-Shell correlation (i)

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

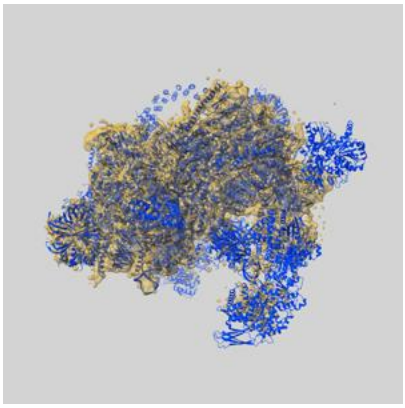
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-6890 and PDB model 5Z57. Per-residue inclusion information can be found in section 3 on page 16.

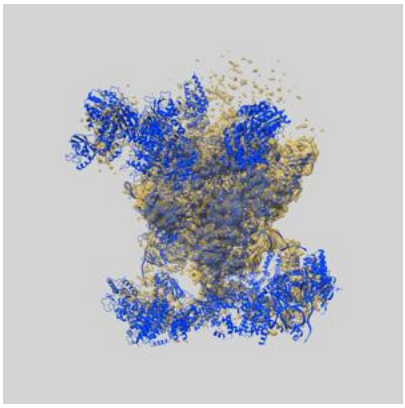
9.1 Map-model overlay



X



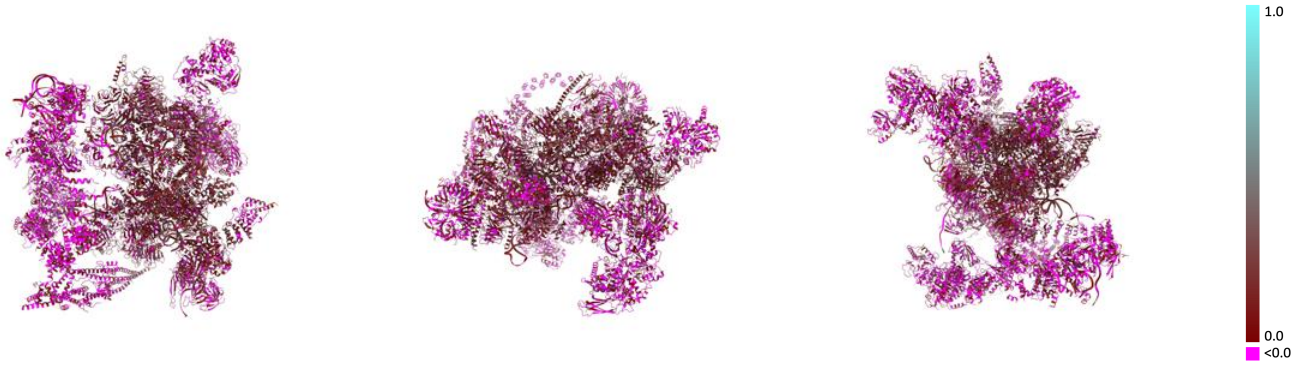
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0323 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.

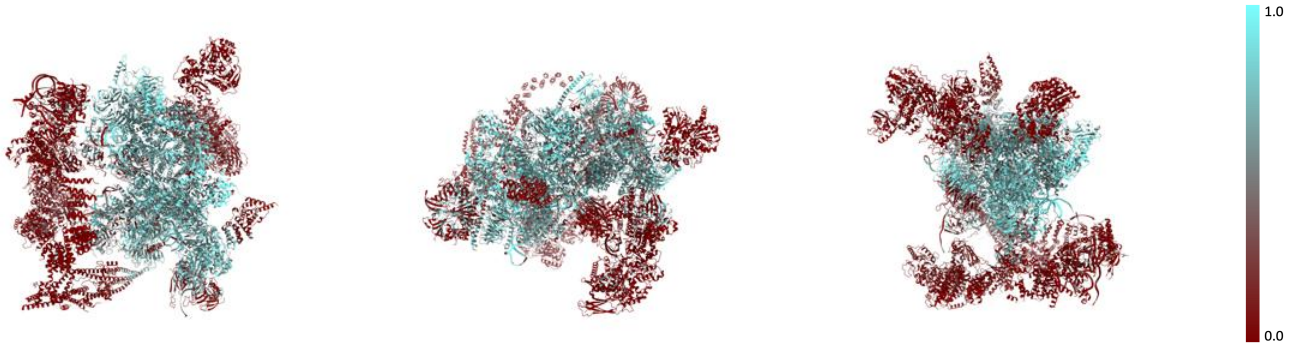
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

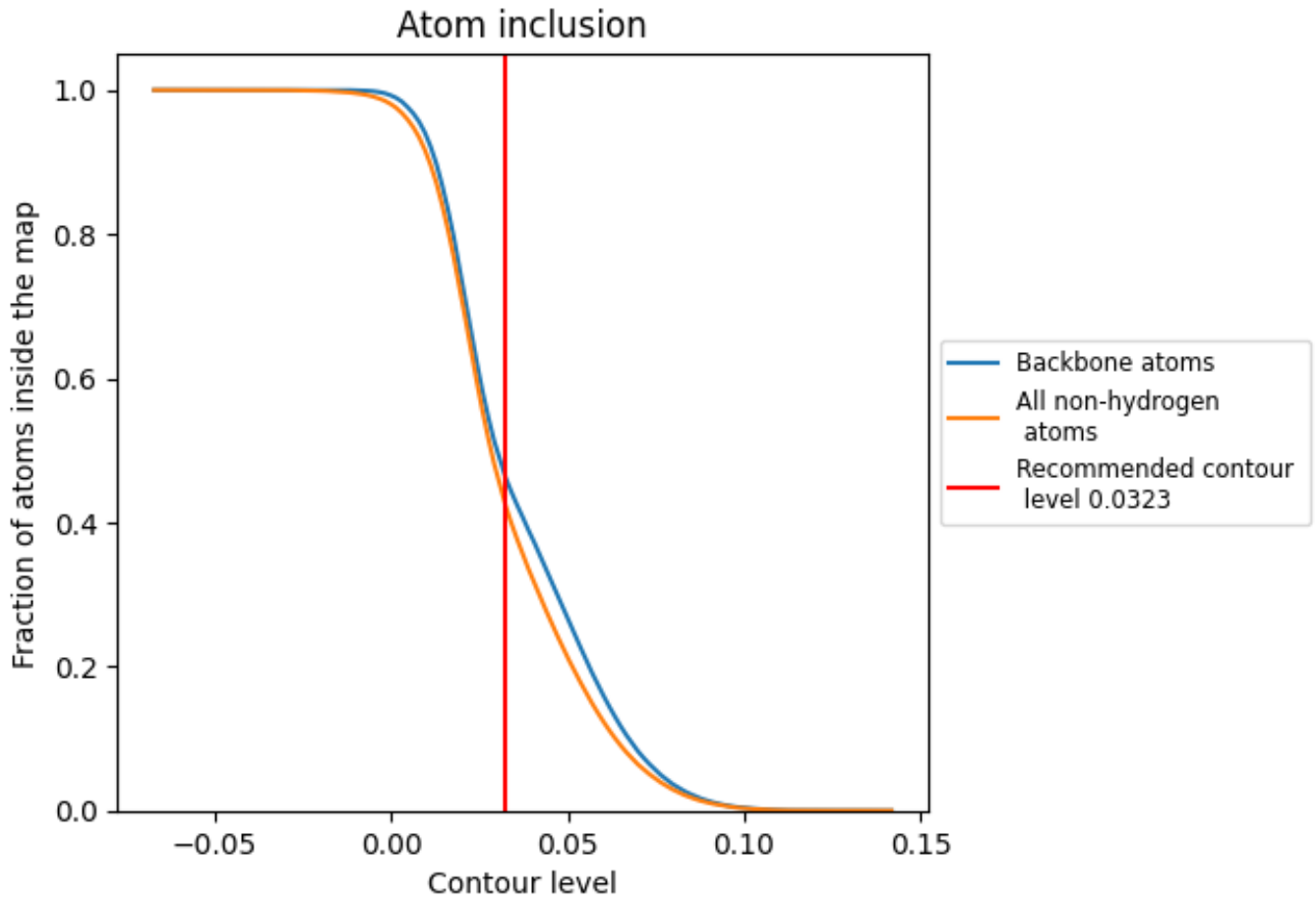
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.0323).

9.4 Atom inclusion (i)



At the recommended contour level, 46% of all backbone atoms, 42% 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 (0.0323) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4240	0.0970
1	0.6633	0.1660
2	0.6029	0.1390
3	0.6993	0.1390
4	0.3289	0.0210
5	0.7032	0.1570
6	0.6662	0.1340
7	0.6705	0.1450
A	0.5702	0.1360
B	0.7771	0.1670
C	0.6934	0.1510
D	0.0485	0.0190
E	0.6062	0.1060
F	0.8093	0.1690
G	0.7566	0.1610
H	0.4217	0.0840
I	0.0378	0.0050
J	0.3452	0.0650
K	0.1220	0.0430
L	0.3254	0.0880
N	0.6693	0.1380
O	0.4912	0.1160
P	0.3292	0.1440
Q	0.0244	0.0100
R	0.4886	0.1440
S	0.4905	0.1130
T	0.7377	0.1470
U	0.6684	0.1850
V	0.4084	0.1230
W	0.1942	0.0690
X	0.6451	0.1400
Y	0.7104	0.1780
Z	0.4447	0.1540
a	0.1404	0.0070
b	0.2864	0.0520

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Chain	Atom inclusion	Q-score
c	0.3202	0.0290
d	0.3125	0.0350
e	0.3478	0.0300
f	0.2798	0.0180
g	0.2810	0.0330
h	0.0585	-0.0130
i	0.0687	0.0440
j	0.0911	0.0080
k	0.0640	0.0180
l	0.0793	-0.0210
m	0.1191	-0.0100
n	0.0868	0.0230
o	0.0311	0.0290
p	0.1009	0.0230
q	0.0212	-0.0080
r	0.0459	0.0430
s	0.1104	0.0360
t	0.0000	0.0240
u	0.0135	0.0250
v	0.3534	0.0880
w	0.2144	0.0530
x	0.0000	0.0020
y	0.1289	0.0030