



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 03:25 AM UTC

PDB ID : 5WSG / pdb_00005wsg
EMDB ID : EMD-6684
Title : Cryo-EM structure of the Catalytic Step II spliceosome (C* complex) at 4.0 angstrom resolution
Authors : Yan, C.; Wan, R.; Bai, R.; Huang, G.; Shi, Y.
Deposited on : 2016-12-07
Resolution : 4.00 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

The types of validation reports are described at

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

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

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

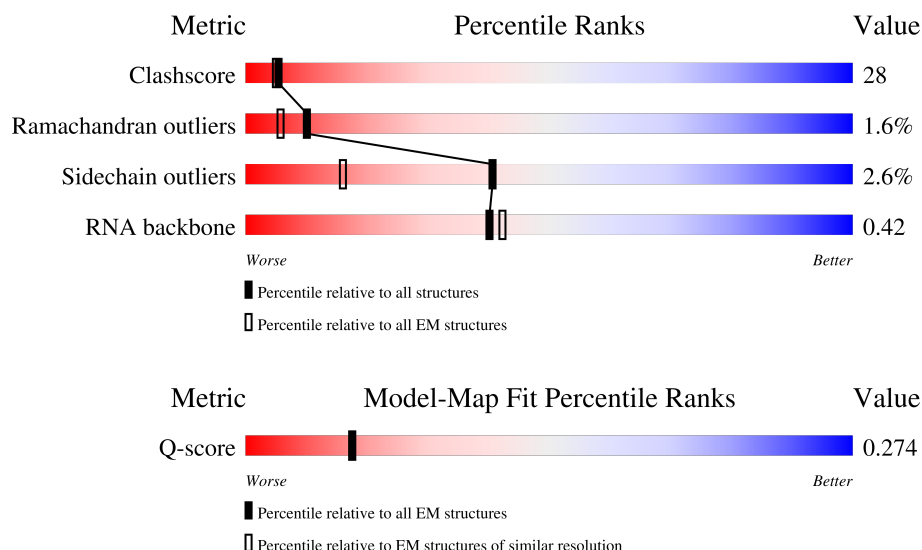
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 Å.

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



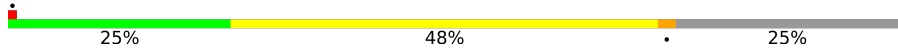
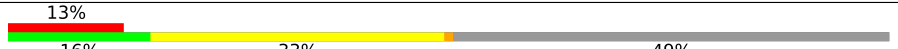
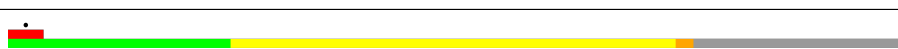
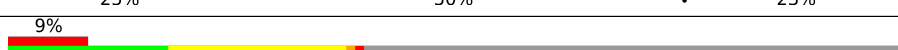
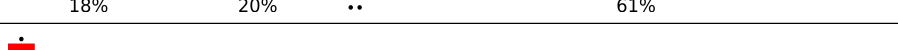
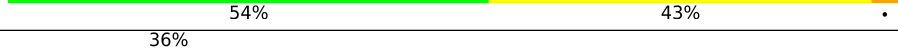
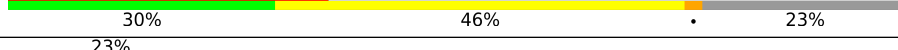
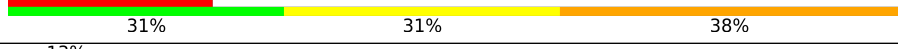
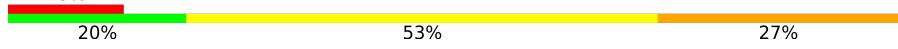
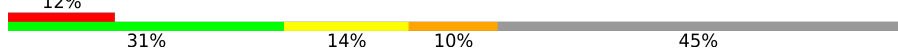
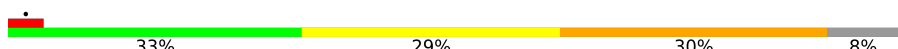
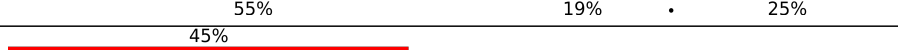
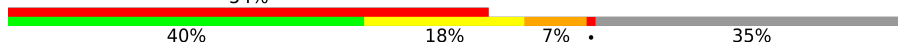
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7587 (3.50 - 4.50)

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

Mol	Chain	Length	Quality of chain
1	A	2413	8% 31% 47% 20%
2	C	1008	35% 51% 13%
3	J	135	7% 13% 80%

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Mol	Chain	Length	Quality of chain
4	O	451	
5	P	379	
6	Q	364	
7	R	339	
8	S	175	
9	T	157	
10	Z	577	
11	B	13	
12	N	15	
13	D	214	
14	E	112	
15	L	1175	
16	M	23	
17	c	579	
18	d	652	
19	I	215	
20	v	858	
21	n	455	
22	o	503	
22	p	503	
22	q	503	
22	r	503	
23	t	175	
24	F	196	
24	k	196	

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Mol	Chain	Length	Quality of chain
25	G	94	
25	i	94	
26	H	86	
26	h	86	
27	K	77	
27	j	77	
28	U	101	
28	l	101	
29	V	146	
29	m	146	
30	W	110	
30	g	110	
31	X	111	
32	Y	238	
33	b	14	
34	e	1071	
35	f	251	

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
36	GTP	C	1500	-	-	X	-

2 Entry composition [i](#)

There are 38 unique types of molecules in this entry. The entry contains 76730 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Pre-mRNA-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1931	Total	C	N	O	S	0	0
			15939	10244	2739	2898	58		

- Molecule 2 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	878	Total	C	N	O	S	0	0
			7019	4529	1166	1295	29		

- Molecule 3 is a protein called Pre-mRNA-splicing factor CWC21.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	J	27	Total	C	N	O	0	0
			190	112	38	40		

- Molecule 4 is a protein called Pre-mRNA-splicing factor PRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	O	337	Total	C	N	O	S	0	0
			2646	1669	466	501	10		

- Molecule 5 is a protein called Pre-mRNA-processing protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	P	201	Total	C	N	O	S	0	0
			1583	988	290	298	7		

- Molecule 6 is a protein called Pre-mRNA-splicing factor SLT11.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Q	185	Total	C	N	O	S	0	0
			1472	930	256	271	15		

- Molecule 7 is a protein called Pre-mRNA-splicing factor CWC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	R	261	Total	C	N	O	S	0	0
			2089	1320	369	388	12		

- Molecule 8 is a protein called Pre-mRNA-splicing factor CWC15.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	S	69	Total	C	N	O	S	0	0
			560	351	112	96	1		

- Molecule 9 is a protein called Pre-mRNA-splicing factor BUD31.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	T	157	Total	C	N	O	S	0	0
			1291	808	240	232	11		

- Molecule 10 is a protein called Pre-mRNA-splicing factor CWC22.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Z	447	Total	C	N	O	S	0	0
			3651	2343	602	688	18		

- Molecule 11 is a RNA chain called 5'-exon.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B	13	Total	C	N	O	P	0	0
			275	124	47	91	13		

- Molecule 12 is a RNA chain called 5'-intron-lariat.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	15	Total	C	N	O	P	0	0
			312	140	45	112	15		

- Molecule 13 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D	117	Total	C	N	O	P	0	0
			2465	1104	414	830	117		

- Molecule 14 is a RNA chain called *Saccharomyces cerevisiae* S288c SNR6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	E	103	Total	C	N	O	P	0	0
			2192	982	391	716	103		

- Molecule 15 is a RNA chain called RNA (91-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	91	Total	C	N	O	P	0	0
			1909	854	309	655	91		

- Molecule 16 is a RNA chain called 3'-intron-lariat.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	23	Total	C	N	O	P	0	0
			486	219	86	158	23		

- Molecule 17 is a protein called Pre-mRNA-splicing factor CEF1,Pre-mRNA-splicing factor CEF1,Cef1,Pre-mRNA-splicing factor CEF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	c	436	Total	C	N	O	S	0	0
			2971	1841	549	573	8		

- Molecule 18 is a protein called Pre-mRNA-splicing factor CLF1,Pre-mRNA-splicing factor CLF1,Clf1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	d	532	Total	C	N	O	S	0	0
			3506	2182	658	658	8		

- Molecule 19 is a protein called Pre-mRNA-splicing factor SYF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	I	102	Total	C	N	O	S	0	0
			822	504	152	165	1		

- Molecule 20 is a protein called Syf1,Pre-mRNA-splicing factor SYF1,Syf1,Pre-mRNA-splicing factor SYF1,Syf1,Pre-mRNA-splicing factor SYF1,Syf1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	v	593	Total	C	N	O	S	0	0
			3183	1953	603	626	1		

- Molecule 21 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	n	296	Total	C	N	O	S	0	0
			1870	1162	337	365	6		

- Molecule 22 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	o	126	Total	C	N	O	S	0	0
			830	525	134	169	2		
22	p	128	Total	C	N	O	S	0	0
			843	532	136	173	2		
22	q	387	Total	C	N	O	S	0	0
			2345	1471	402	464	8		
22	r	125	Total	C	N	O	S	0	0
			823	521	133	167	2		

- Molecule 23 is a protein called Pre-mRNA-splicing factor SNT309.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	t	156	Total	C	N	O	S	0	0
			926	585	160	180	1		

- Molecule 24 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	k	80	Total	C	N	O	S	0	0
			631	403	114	111	3		
24	F	78	Total	C	N	O	S	0	0
			610	389	110	108	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	i	75	Total	C	N	O	S	0	0
			575	379	92	101	3		
25	G	75	Total	C	N	O	S	0	0
			575	379	92	101	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	h	70	Total	C	N	O	S	0	0
			554	355	98	100	1		
26	H	70	Total	C	N	O	S	0	0
			554	355	98	100	1		

- Molecule 27 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	j	69	Total	C	N	O	S	0	0
			529	337	93	97	2		
27	K	69	Total	C	N	O	S	0	0
			529	337	93	97	2		

- Molecule 28 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	l	82	Total	C	N	O	S	0	0
			625	399	109	115	2		
28	U	82	Total	C	N	O	S	0	0
			625	399	109	115	2		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	m	82	Total	C	N	O	S	0	0
			644	409	110	123	2		
29	V	82	Total	C	N	O	S	0	0
			644	409	110	123	2		

- Molecule 30 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	g	94	Total	C	N	O	S	0	0
			741	477	141	119	4		
30	W	65	Total	C	N	O	S	0	0
			528	340	102	84	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
31	X	81	Total	C	N	O	0	0
			513	332	89	92		

- Molecule 32 is a protein called U2 small nuclear ribonucleoprotein A'.

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

- Molecule 33 is a RNA chain called 3'-exon-intron.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	14	Total	C	N	O	P	0	0
			208	91	13	90	14		

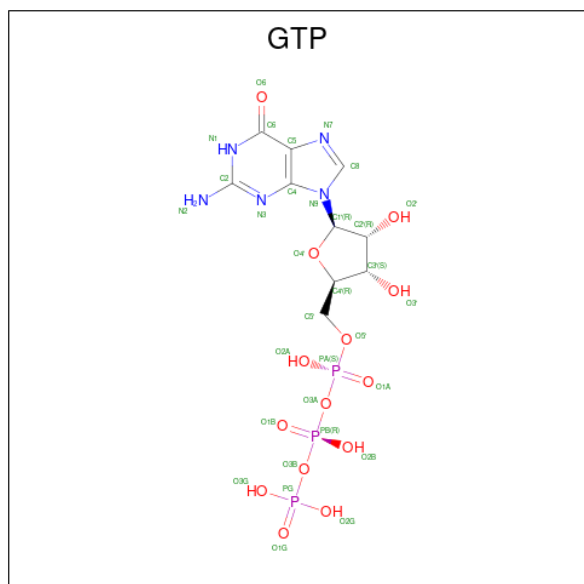
- Molecule 34 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	e	679	Total	C	N	O	0	0
			3360	2002	679	679		

- Molecule 35 is a protein called Pre-mRNA-splicing factor 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	f	148	Total	C	N	O	S	0	0
			1202	780	204	214	4		

- Molecule 36 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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

- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	C	1	Total	Mg	0
			1	1	
37	B	1	Total	Mg	0
			1	1	
37	E	4	Total	Mg	0
			4	4	

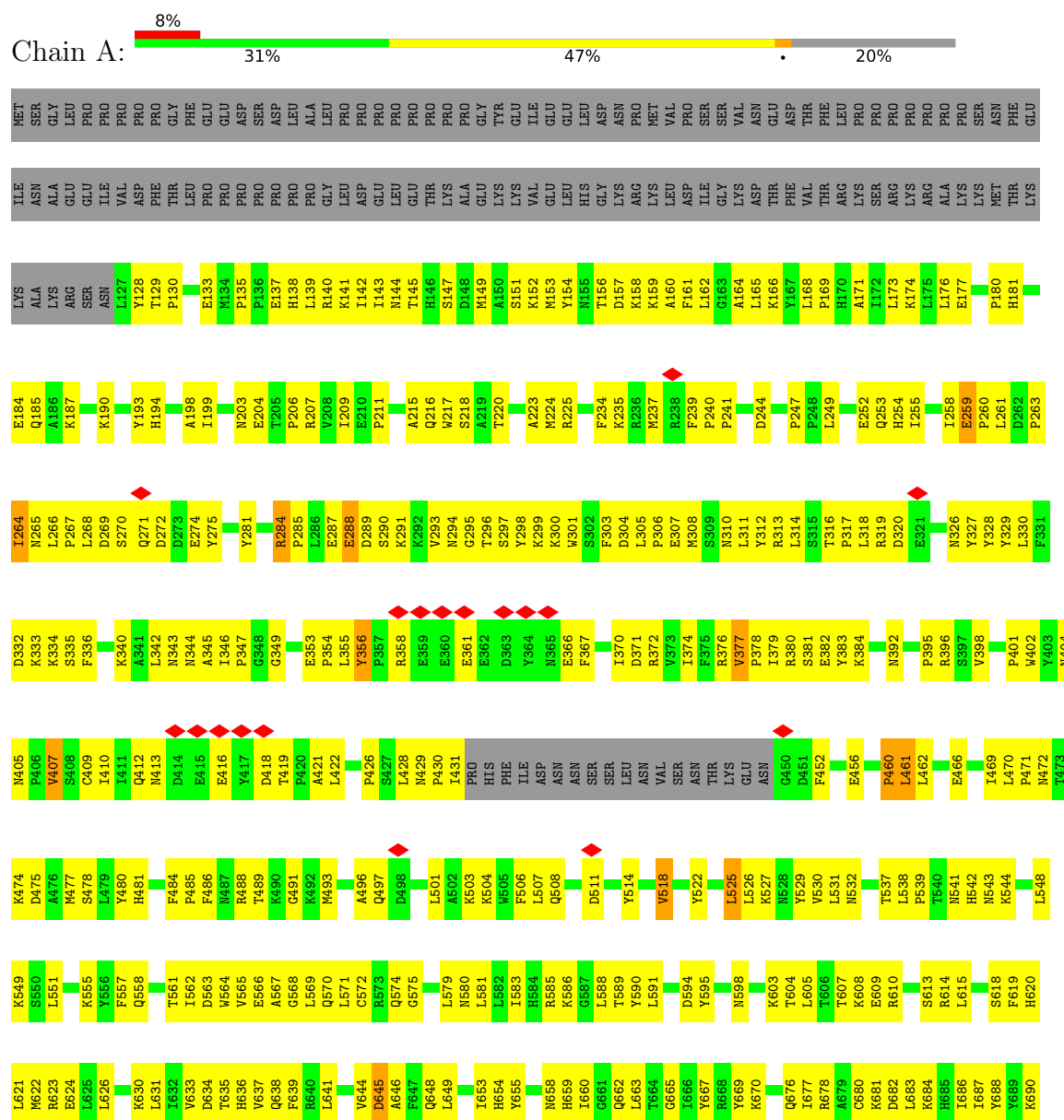
- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
38	Q	2	Total	Zn	0
			2	2	
38	R	1	Total	Zn	0
			1	1	
38	T	3	Total	Zn	0
			3	3	

3 Residue-property plots

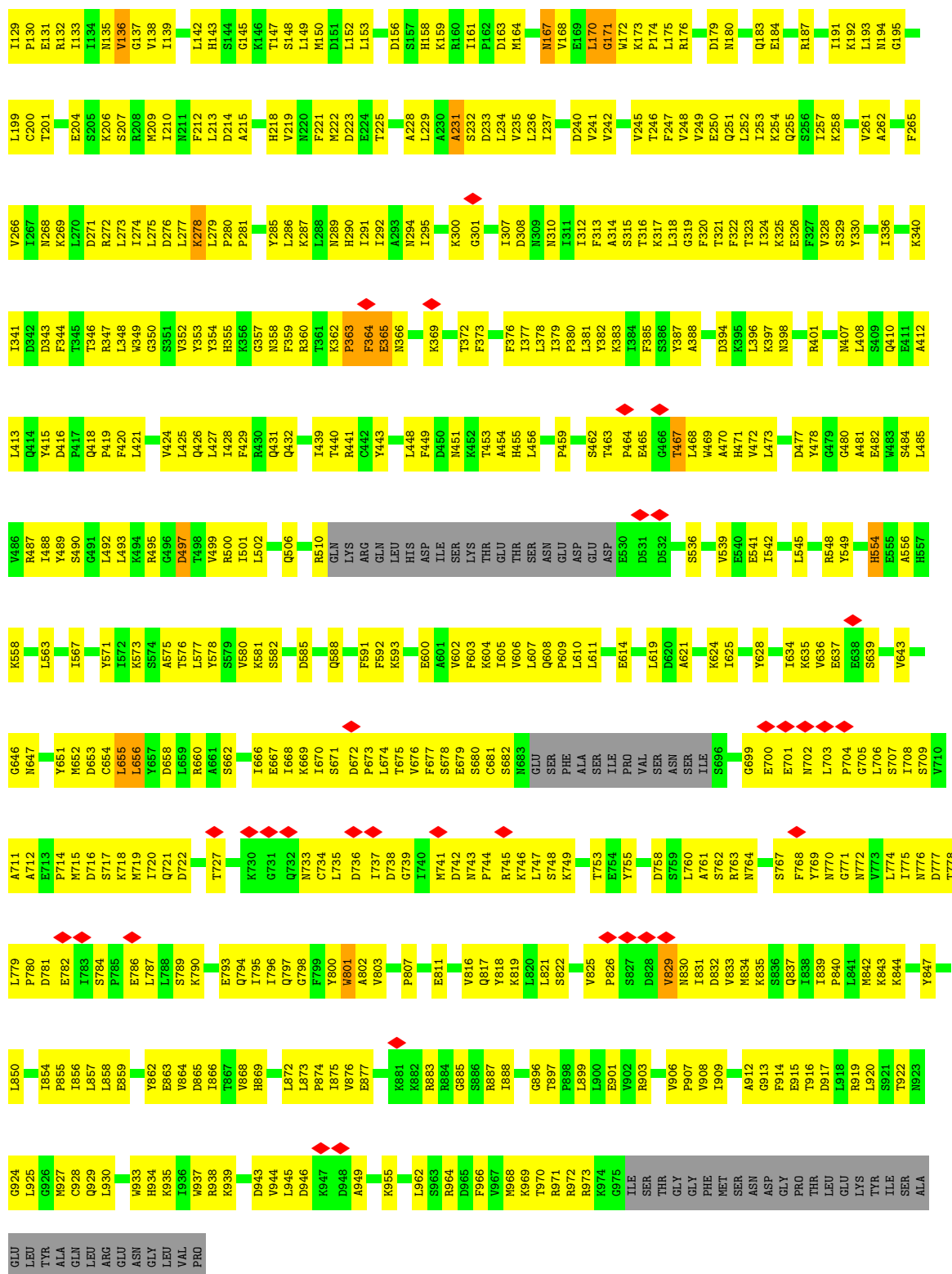
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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-splicing factor 8

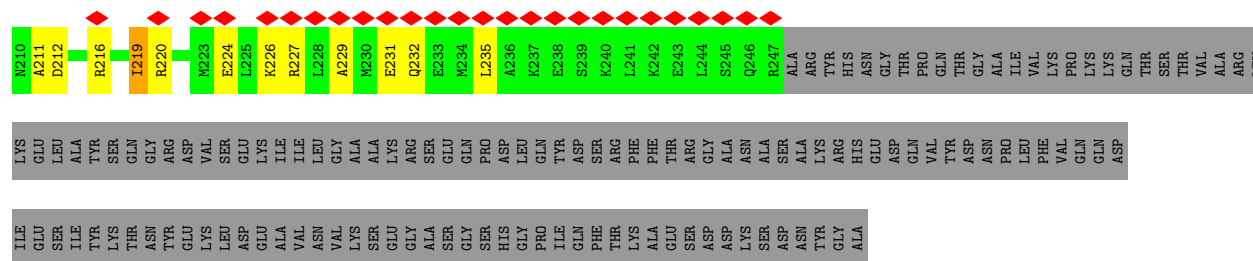




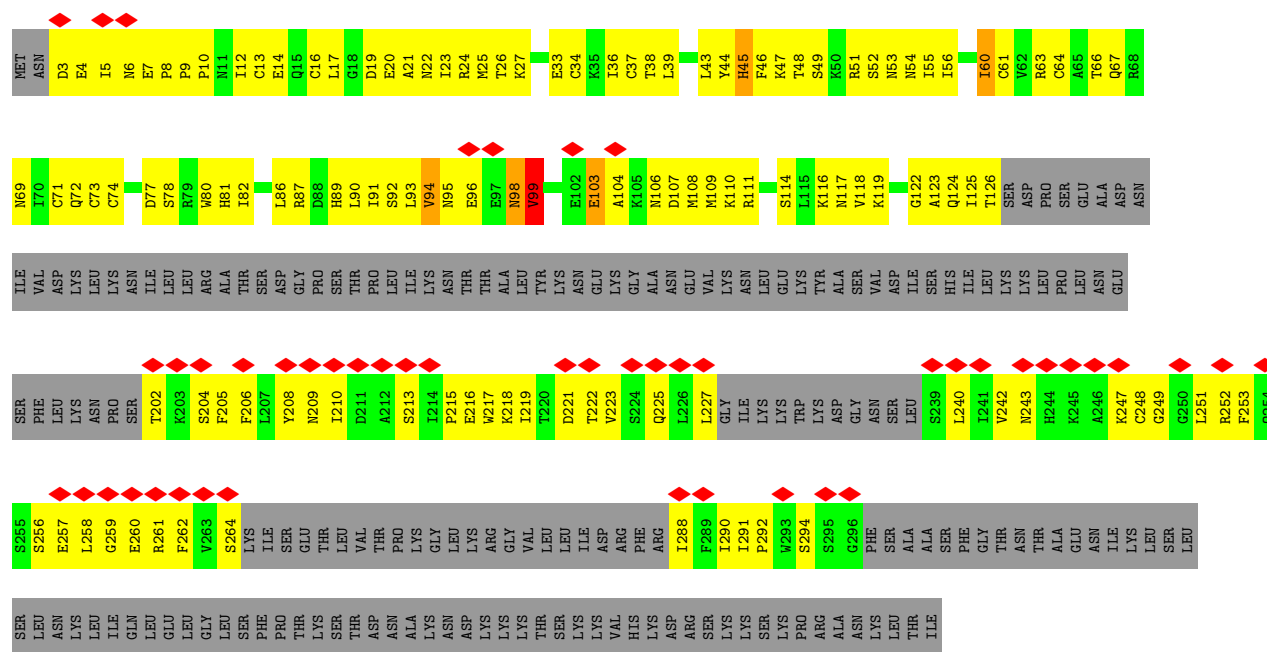




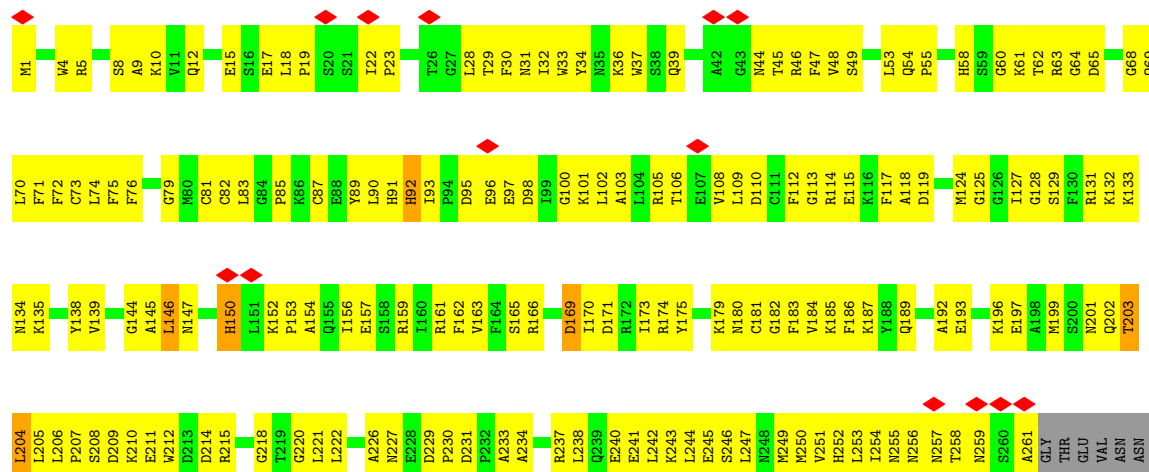
• Molecule 3: Pre-mRNA-splicing factor CWC21

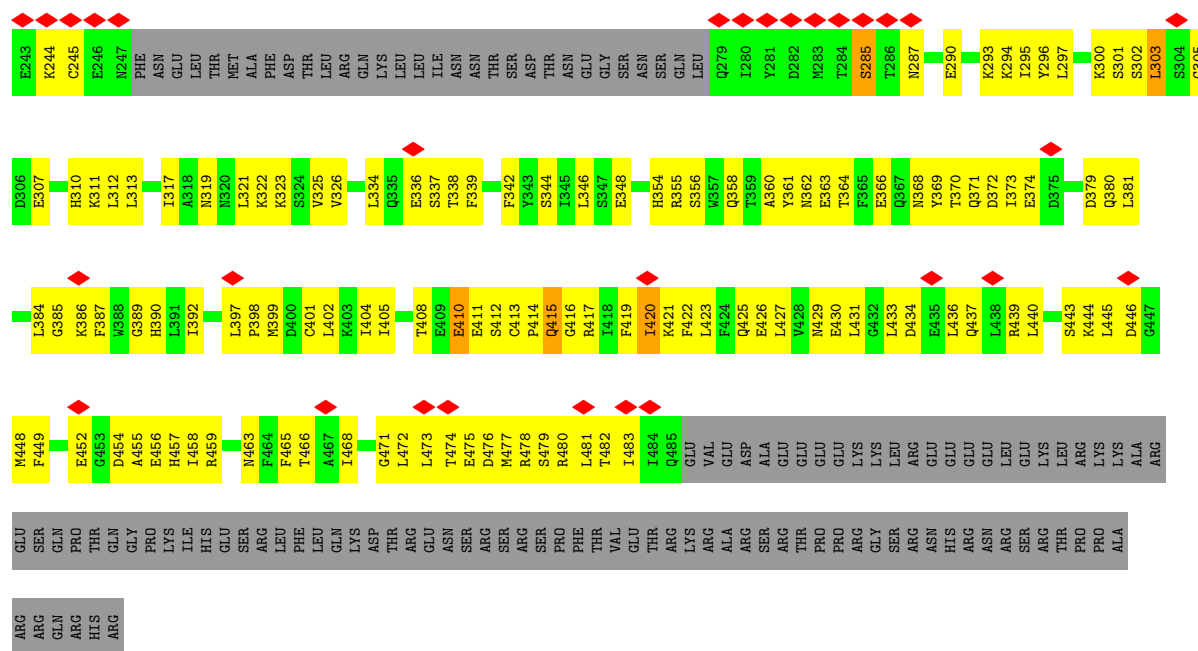


• Molecule 6: Pre-mRNA-splicing factor SLT11

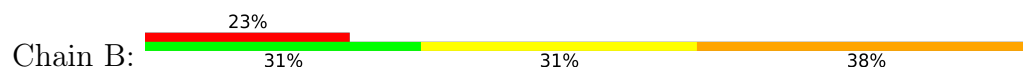


• Molecule 7: Pre-mRNA-splicing factor CWC2

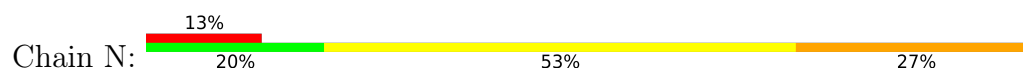




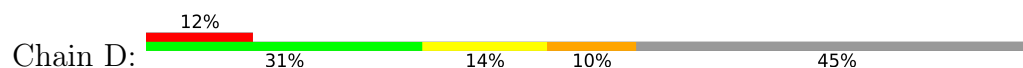
• Molecule 11: 5'-exon



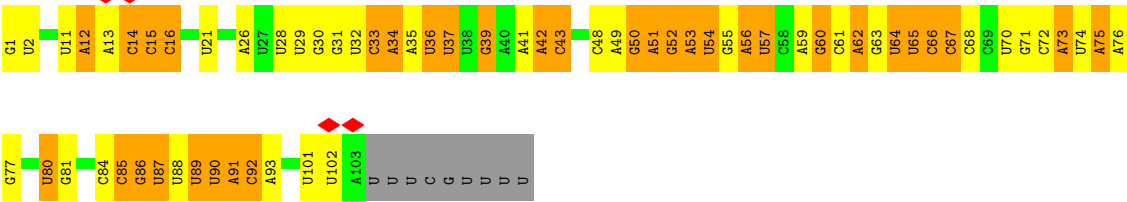
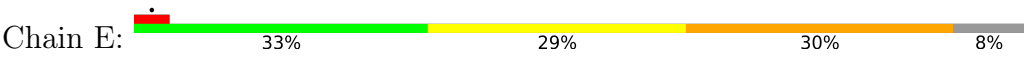
• Molecule 12: 5'-intron-lariat



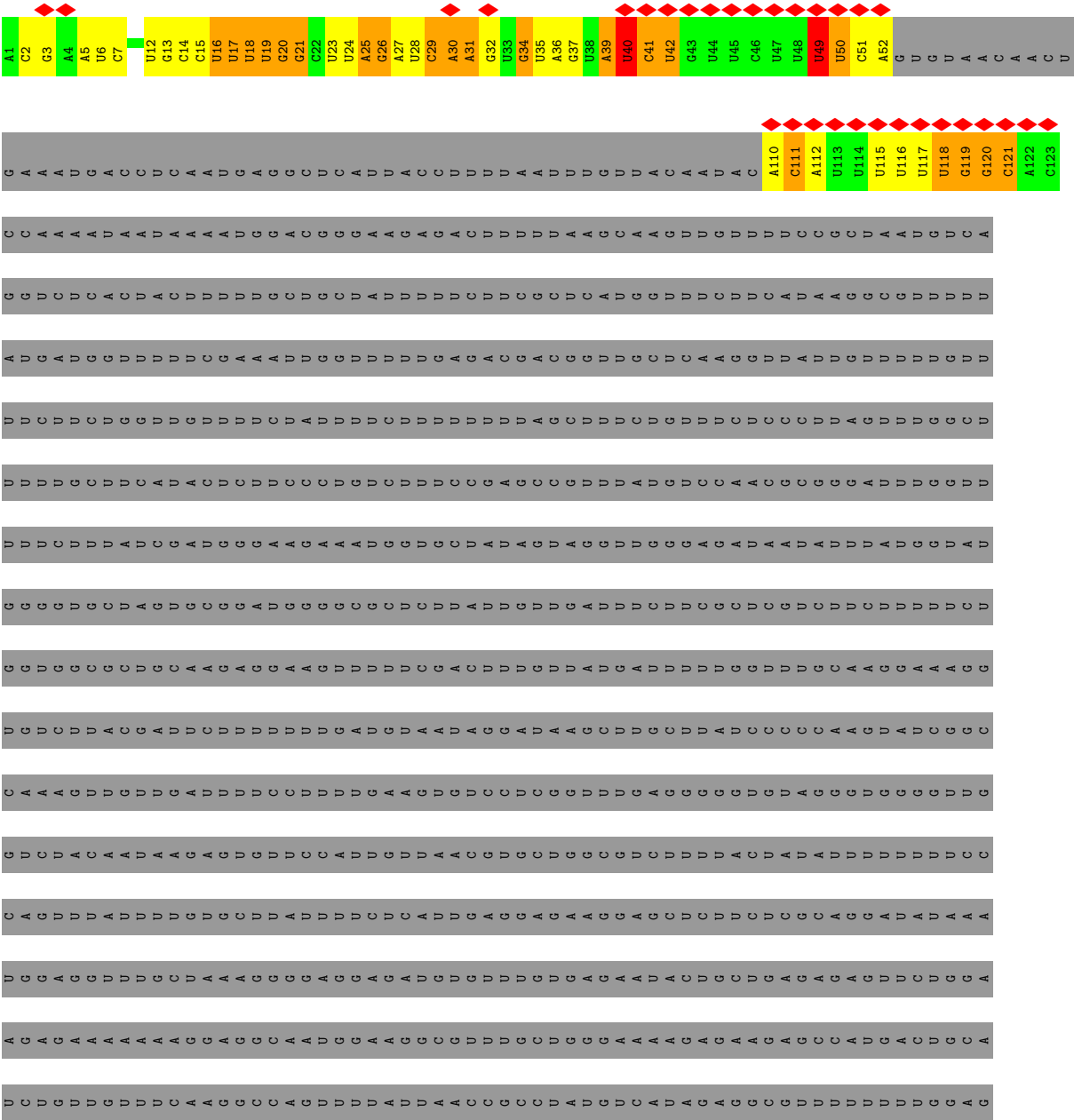
• Molecule 13: U5 snRNA



• Molecule 14: Saccharomyces cerevisiae S288c SNR6 snRNA

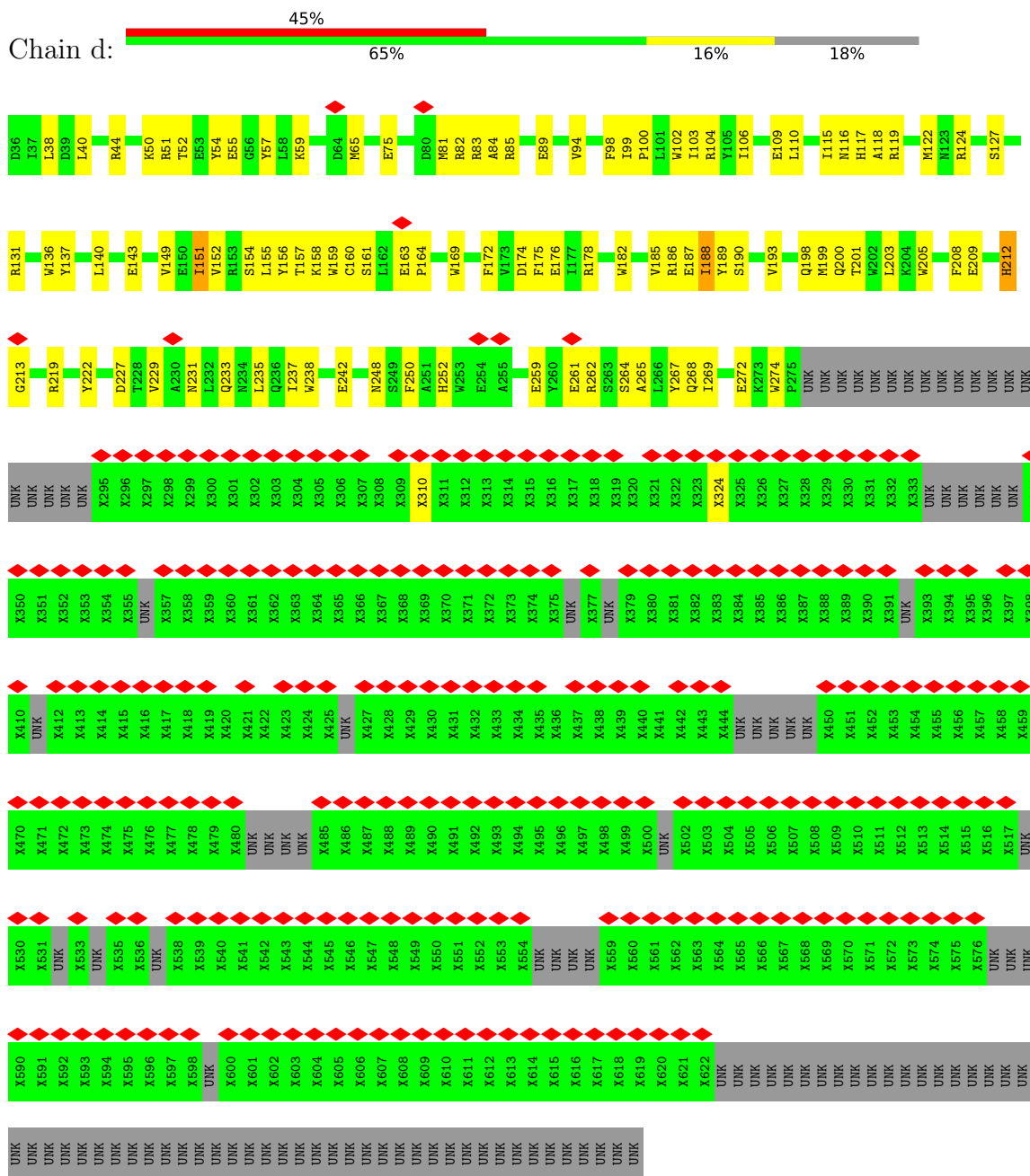


● Molecule 15: RNA (91-MER)

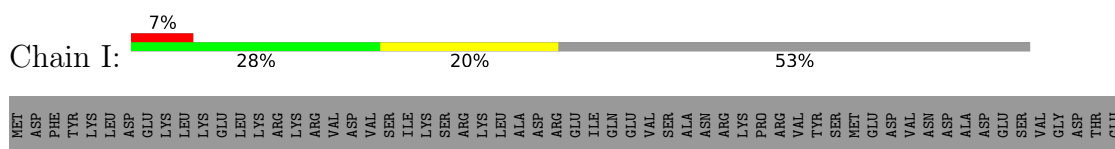


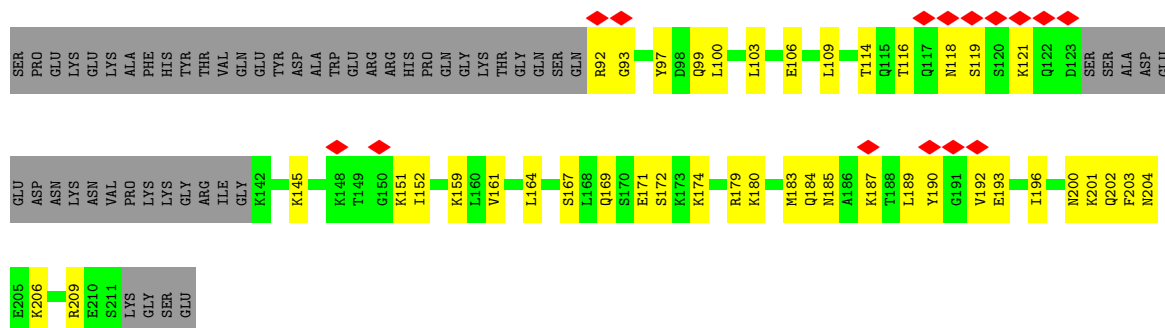


• Molecule 18: Pre-mRNA-splicing factor CLF1,Pre-mRNA-splicing factor CLF1,Clf1

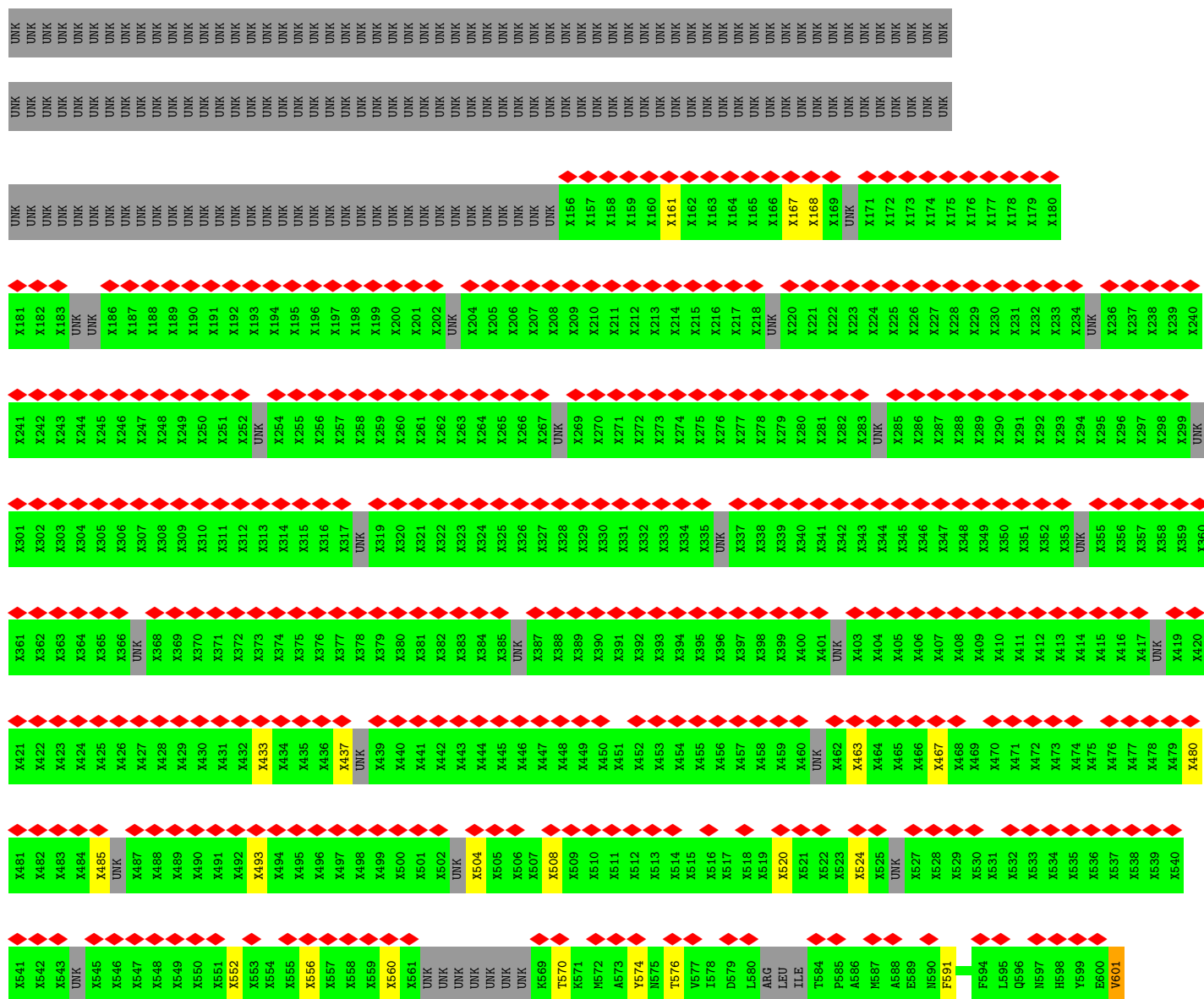


• Molecule 19: Pre-mRNA-splicing factor SYF2





- Molecule 20: Syf1,Pre-mRNA-splicing factor SYF1,Syf1,Pre-mRNA-splicing factor SYF1,Syf1,Pre-mRNA-splicing factor SYF1,Syf1





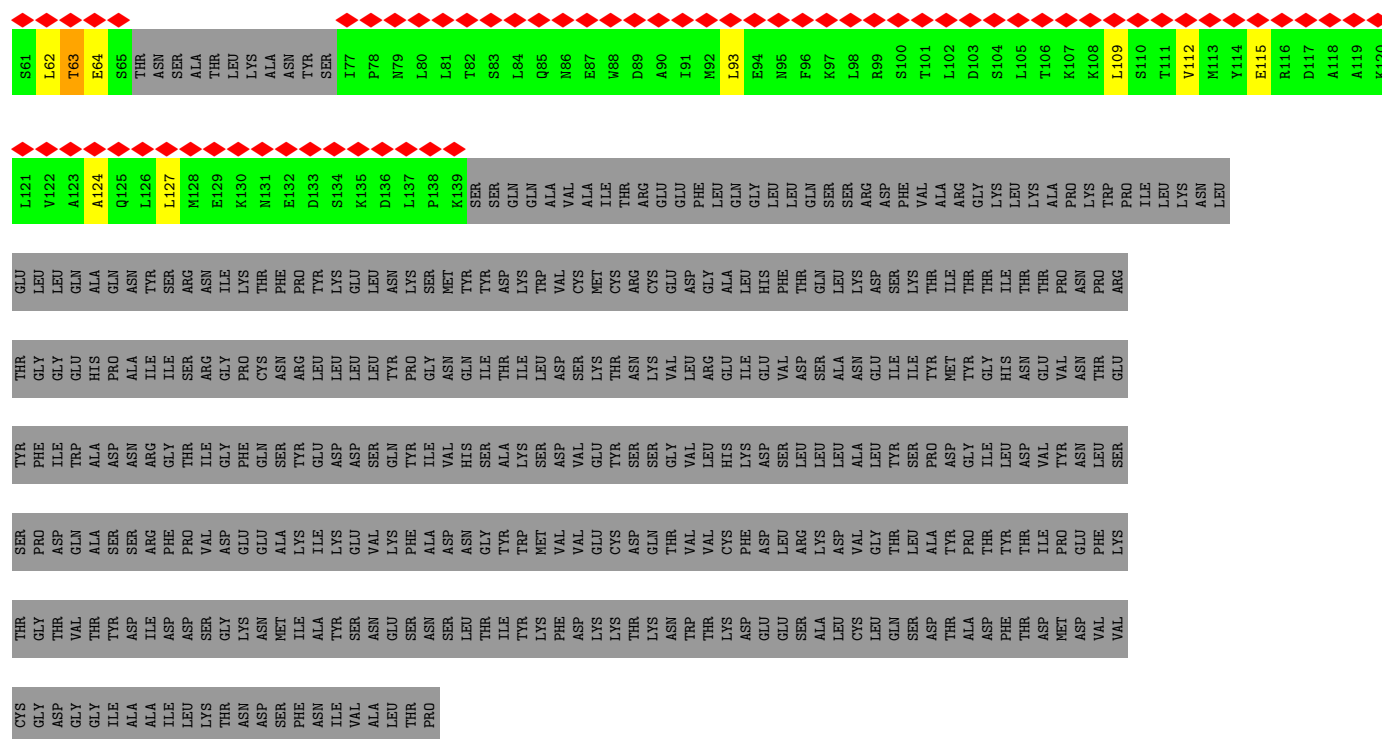
M1	L2	C3	A4	I5	S6	G7	K8	V9	P10	R11	R12	P13	V14	L15	S16	P17	K18	S19	R20	T21	I22	F23	E24	K25	S26	L27	L28	E29	Q30	Y31	V32	K33	D34	T35	G36	N37	D38	P39	I40	T41	N42	E43	P44	L45	S46	I47	E48	E49	I50	V51	E52	I53	V54	P55	S56	A57	Q58	Q59	A60
S61	L62	T63	E64	S65	THR	ASN	THR	ALA	THR	LEU	LYS	ALA	TYR	SER	I77	P78	N79	L80	L81	T82	S83	L84	Q85	N86	E87	W88	D89	A90	I91	H92	L93	E94	N95	F96	K97	L98	R99	S100	T101	L102	D103	S104	L105	T106	K107	K108	L109	S110	T111	V112	M113	Y114	E115	R116	D117	A118	A119	K120	
L121	V122	A123	A124	Q125	L126	L127	M128	E129	K130	M131	E132	D133	S134	K135	D136	L137	P138	K139	S140	SER	GLN	GLN	LYS	TRP	VAL	ALA	VAL	GLY	ASP	VAL	GLY	LEU	GLN	HIS	PHE	LEU	GLN	SER	LEU	ASP	THR	ILE	ALA	ARG	GLY	LYS	PRO	ASN	PRO	THR	ARG								
GLU	LEU	GLN	GLN	ASN	GLN	TYR	SER	ARG	ASN	LYS	PHE	PRO	TYR	LYS	LEU	GLU	LEU	ASN	TYR	ASP	GLN	LYS	TRP	VAL	CYS	MET	ILE	THR	ASN	ARG	GLY	LEU	GLN	THR	GLN	SER	ASP	PHE	VAL	ALA	ARG	GLY	LYS	PRO	ASN	PRO	THR	ARG											
THR	GLY	GLY	GLU	PRO	ASN	ALA	ILE	THR	PRO	CYS	THR	ASN	TYR	GLY	LEU	LEU	ASN	GLN	TYR	ILE	THR	LYS	TRP	VAL	LYS	THR	ASN	ARG	VAL	LEU	ARG	GLY	ALA	LEU	LYS	ASP	GLY	THR	ILE	ALA	THR	THR	ILE	ALA	ARG	GLY	LYS	PRO	ASN	PRO	THR	ARG							
TYR	PHE	ILE	TRP	ALA	ASP	ASN	ARG	GLY	THR	PHE	GLN	SER	TYR	ILE	GLU	GLU	ASP	HIS	SER	ALA	LYS	SER	ASP	VAL	GLU	TYR	SER	GLY	VAL	LEU	HIS	ASP	LEU	SER	LEU	ALA	ASN	GLY	THR	ILE	ALA	THR	THR	ILE	ALA	ARG	GLY	LYS	PRO	ASN	PRO	THR	ARG						
SER	PRO	ASP	GLN	SER	SER	ARG	PHE	THR	VAL	ASP	GLY	GLU	ALA	VAL	GLU	VAL	GLY	ASN	GLY	THR	LYS	TRP	VAL	GLY	GLU	CYS	ASP	VAL	VAL	VAL	PHE	HIS	LEU	LEU	ASP	GLY	THR	ILE	ALA	THR	THR	ILE	ALA	ARG	GLY	LYS	PRO	ASN	PRO	THR	ARG								
THR	GLY	THR	VAL	THR	ASP	ILE	ASP	THR	VAL	GLY	ASN	GLU	ALA	VAL	GLU	VAL	GLY	ASN	GLY	THR	LYS	TRP	VAL	GLY	GLU	CYS	ASP	VAL	VAL	VAL	PHE	HIS	LEU	LEU	ASP	GLY	THR	ILE	ALA	THR	THR	ILE	ALA	ARG	GLY	LYS	PRO	ASN	PRO	THR	ARG								
CYS	GLY	ASP	GLY	GLY	ILE	ALA	ILE	THR	VAL	GLY	ASN	GLU	ALA	VAL	GLU	VAL	GLY	ASN	GLY	THR	LYS	TRP	VAL	GLY	GLU	CYS	ASP	VAL	VAL	VAL	PHE	HIS	LEU	LEU	ASP	GLY	THR	ILE	ALA	THR	THR	ILE	ALA	ARG	GLY	LYS	PRO	ASN	PRO	THR	ARG								

● Molecule 22: Pre-mRNA-processing factor 19

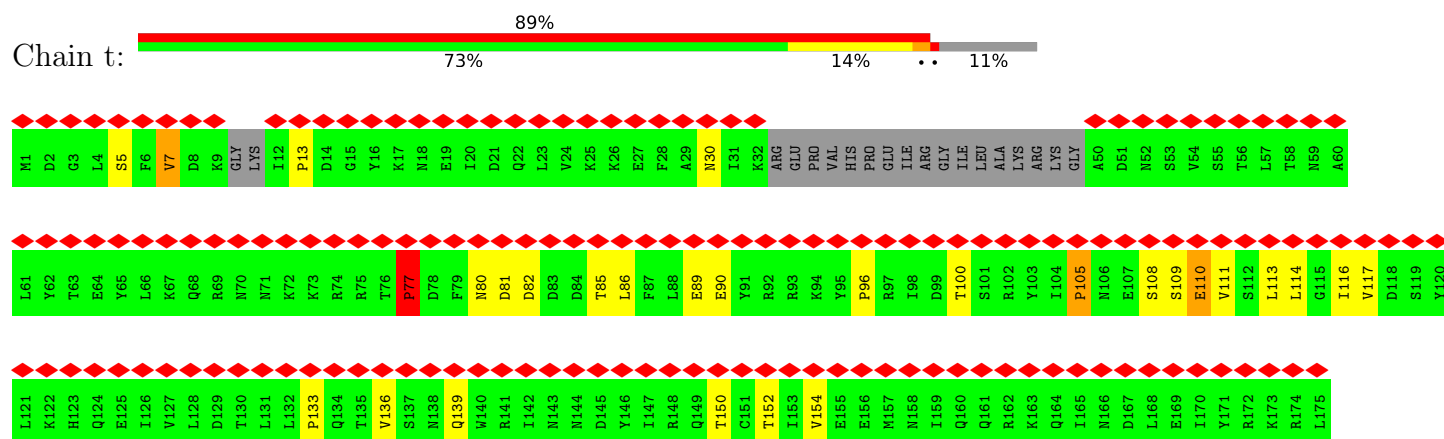


M1	L2	C3	A4	I5	S6	G7	K8	V9	P10	R11	R12	P13	V14	L15	S16	P17	K18	S19	R20	T21	I22	F23	E24	K25	S26	L27	L28	E29	Q30	Y31	V32	K33	D34	T35	G36	N37	D38	P39	I40	T41	N42	E43	P44	L45	S46	I47	E48	E49	I50	V51	E52	I53	V54	P55	S56	A57	Q58	Q59	A60
S61	L62	T63	E64	S65	THR	ASN	THR	ALA	THR	LEU	LYS	ALA	TYR	SER	I77	P78	N79	L80	L81	T82	S83	L84	Q85	N86	E87	W88	D89	A90	I91	H92	L93	E94	N95	F96	K97	L98	R99	S100	T101	L102	D103	S104	L105	T106	K107	K108	L109	S110	T111	V112	M113	Y114	E115	R116	D117	A118	A119	K120	
L121	V122	A123	A124	Q125	L126	L127	M128	E129	K130	M131	E132	D133	S134	K135	D136	L137	P138	K139	S140	S141	Q142	GLN	ALA	VAL	ALA	VAL	ILE	THR	LYS	ARG	GLY	LEU	GLN	GLY	LEU	GLN	SER	ASP	PHE	VAL	ALA	ARG	GLY	LYS	LEU	THR	LYS	PRO	ASN	PRO	THR	ARG							
GLU	LEU	LEU	GLN	ALA	ASN	TYR	ASN	THR	LYS	THR	PHE	PRO	TYR	LYS	LEU	GLU	LEU	ASN	TYR	ASP	GLN	LYS	TRP	VAL	CYS	MET	LYS	THR	ASN	ARG	GLY	LEU	GLN	VAL	ASP	GLY	LEU	ALA	ASN	LYS	THR	ILE	ALA	ARG	GLY	LYS	PRO	ASN	PRO	THR	ARG								
THR	GLY	GLY	HIS	PRO	ALA	ILE	THR	GLY	ILE	PRO	CYS	THR	ASN	GLY	LEU	GLU	LEU	ASN	GLN	TYR	ILE	THR	VAL	GLY	LYS	THR	ASN	ARG	GLY	LEU	GLN	VAL	ASP	GLY	LEU	ALA	ASN	LYS	THR	ILE	ALA	ARG	GLY	LYS	PRO	ASN	PRO	THR	ARG										
TYR	PHE	ILE	TRP	ALA	ASP	ASN	ARG	GLY	ILE	THR	GLY	ILE	THR	GLN	LYS	TRP	VAL	GLY	LEU	GLN	TYR	ILE	THR	VAL	GLY	LYS	THR	ASN	ARG	GLY	LEU	GLN	VAL	ASP	GLY	LEU	ALA	ASN	LYS	THR	ILE	ALA	ARG	GLY	LYS	PRO	ASN	PRO	THR	ARG									

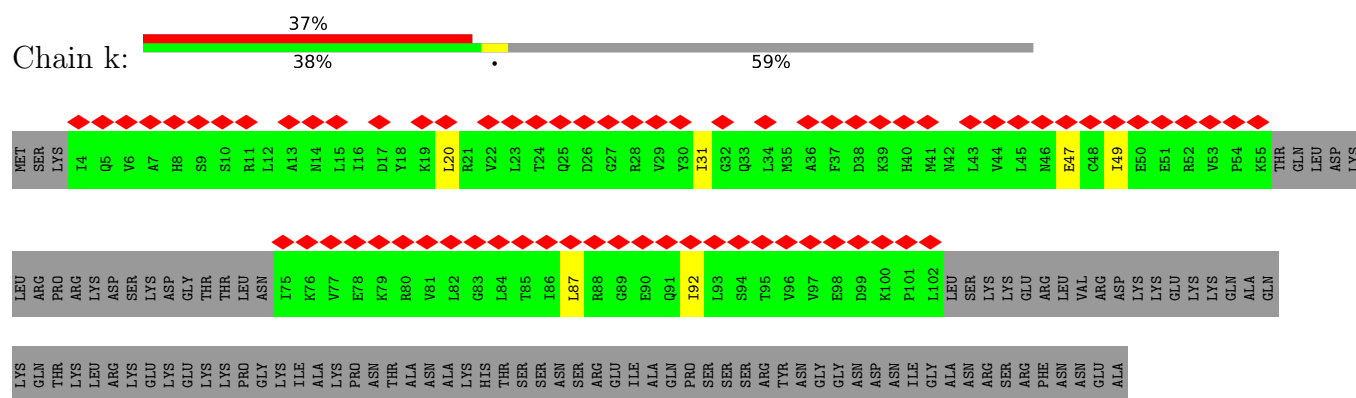




• Molecule 23: Pre-mRNA-splicing factor SNT309

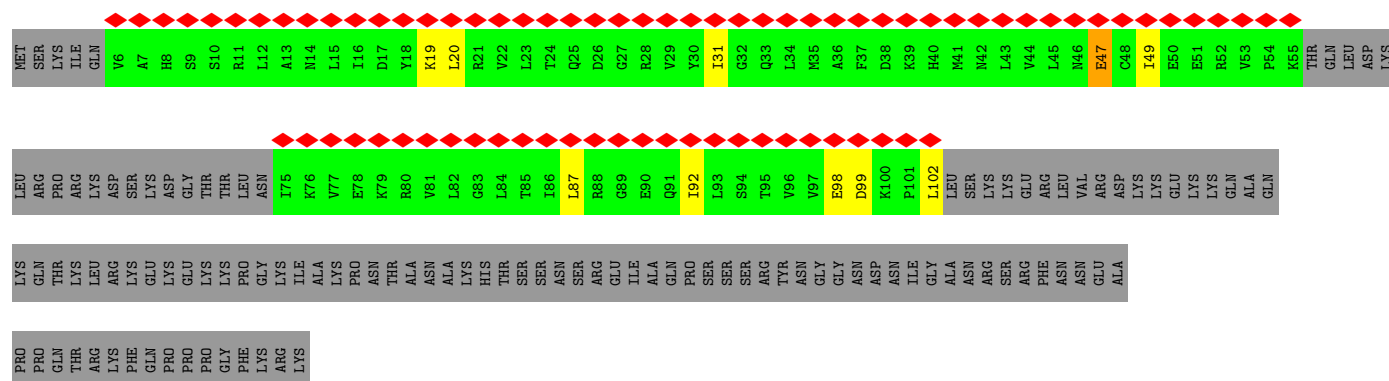
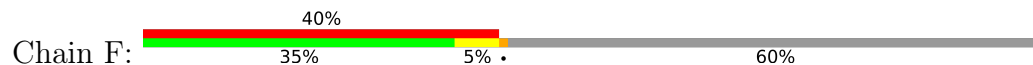


• Molecule 24: Small nuclear ribonucleoprotein-associated protein B

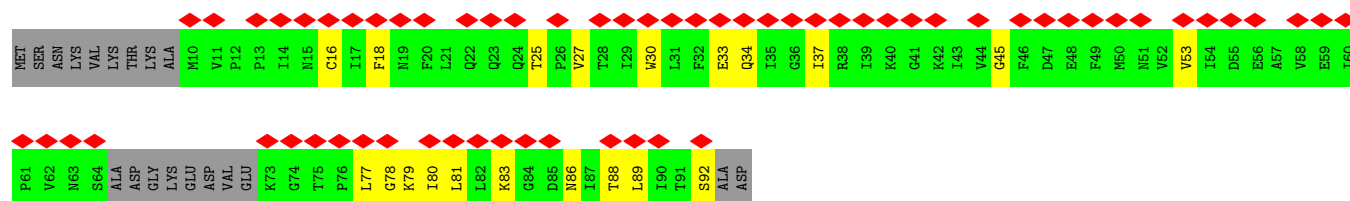


PRO
PRO
GLN
THR
LYS
ARG
LYS
PHE
GLN
PRO
PRO
PRO
GLY
PHE
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ARG
LYS

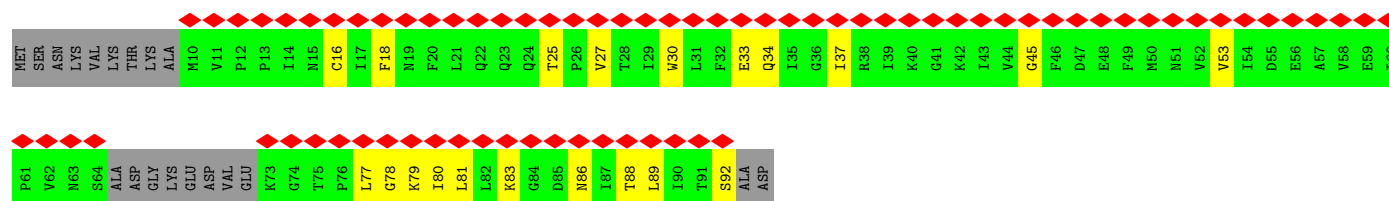
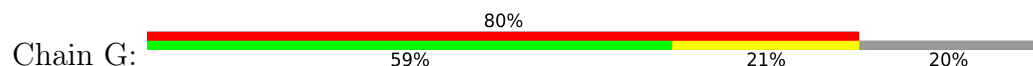
• Molecule 24: Small nuclear ribonucleoprotein-associated protein B



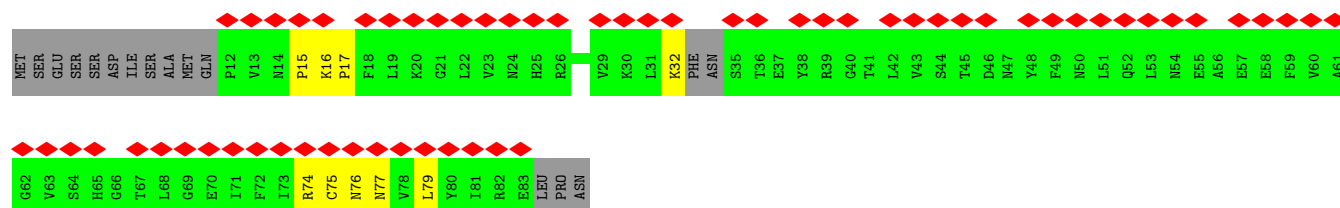
• Molecule 25: Small nuclear ribonucleoprotein E



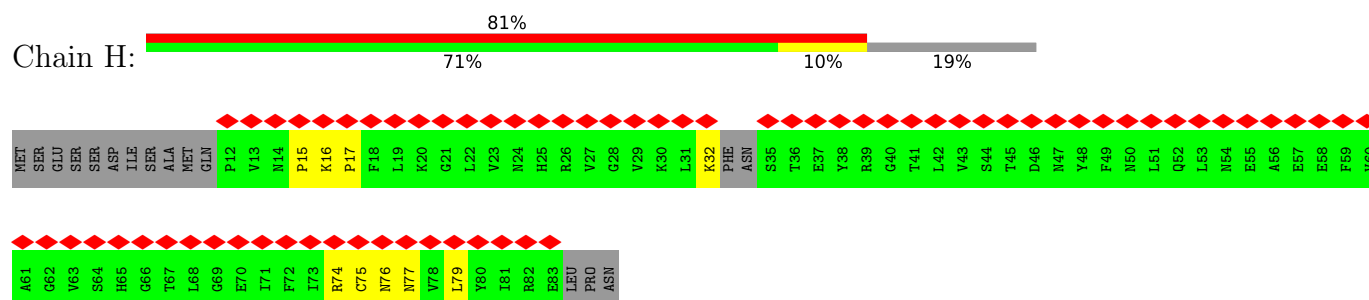
• Molecule 25: Small nuclear ribonucleoprotein E



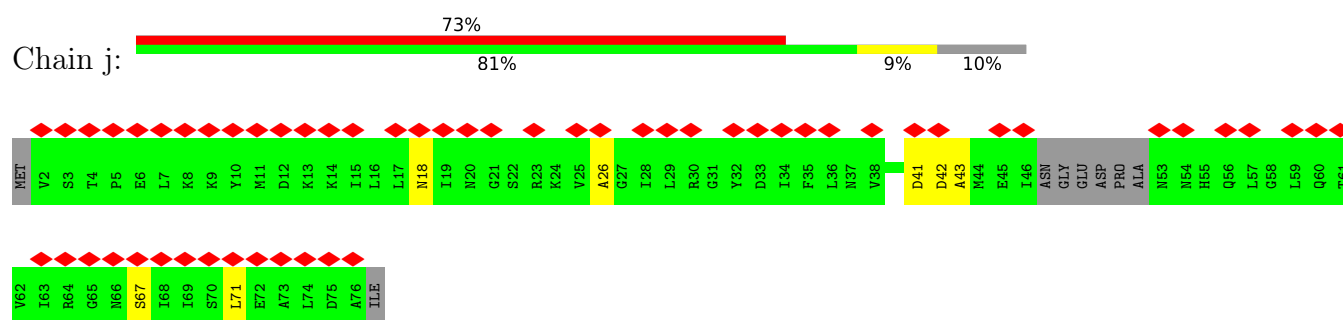
• Molecule 26: Small nuclear ribonucleoprotein F



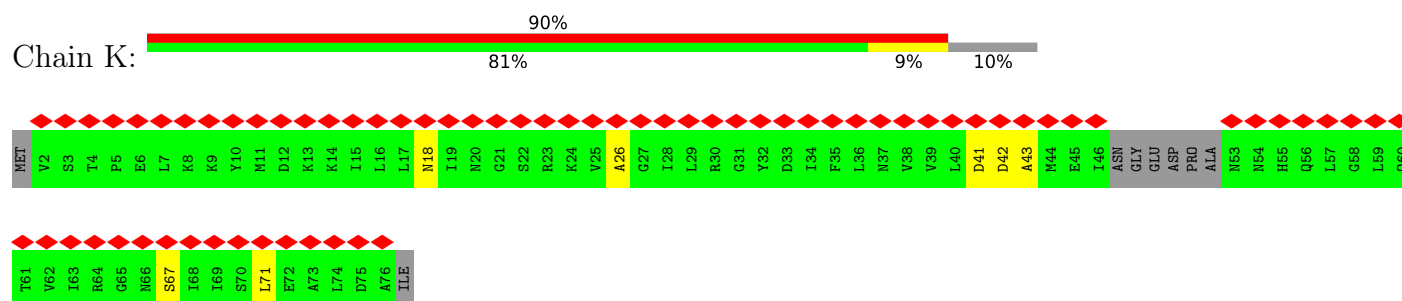
- Molecule 26: Small nuclear ribonucleoprotein F



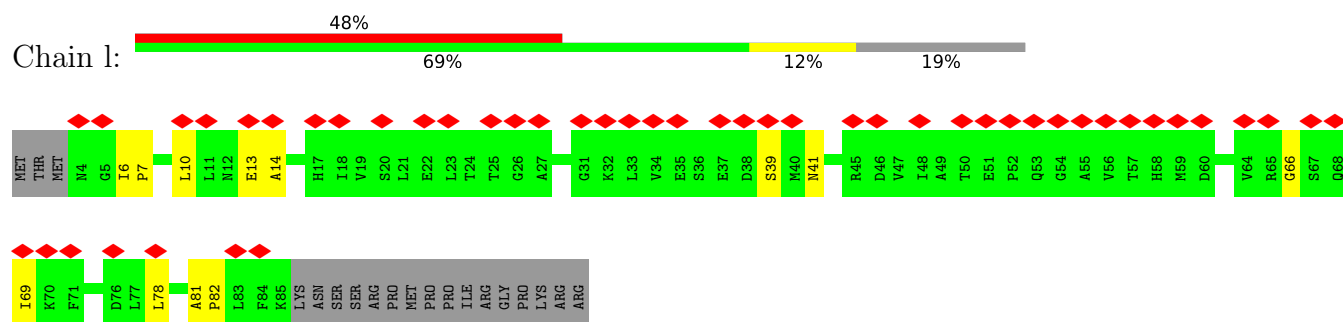
- Molecule 27: Small nuclear ribonucleoprotein G



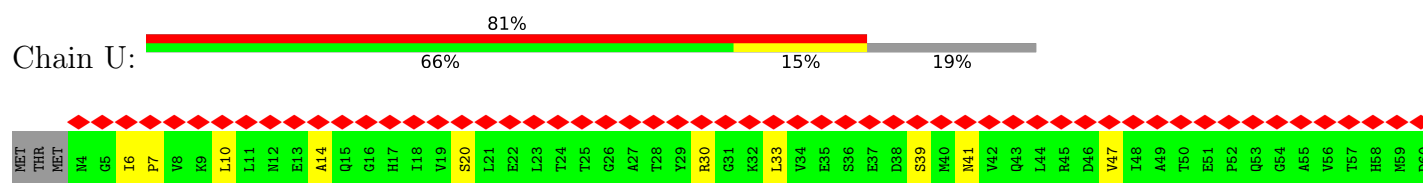
- Molecule 27: Small nuclear ribonucleoprotein G

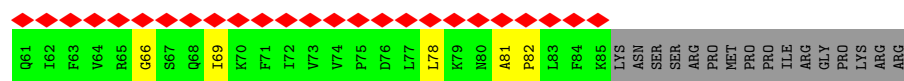


- Molecule 28: Small nuclear ribonucleoprotein Sm D3

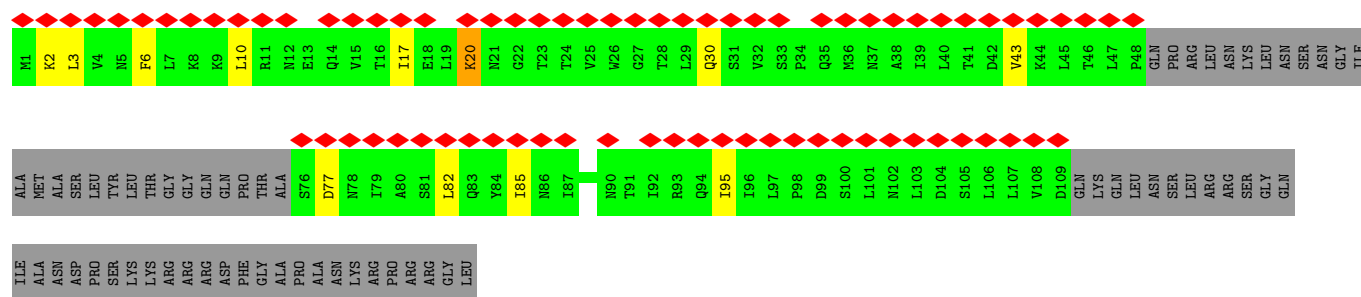


- Molecule 28: Small nuclear ribonucleoprotein Sm D3

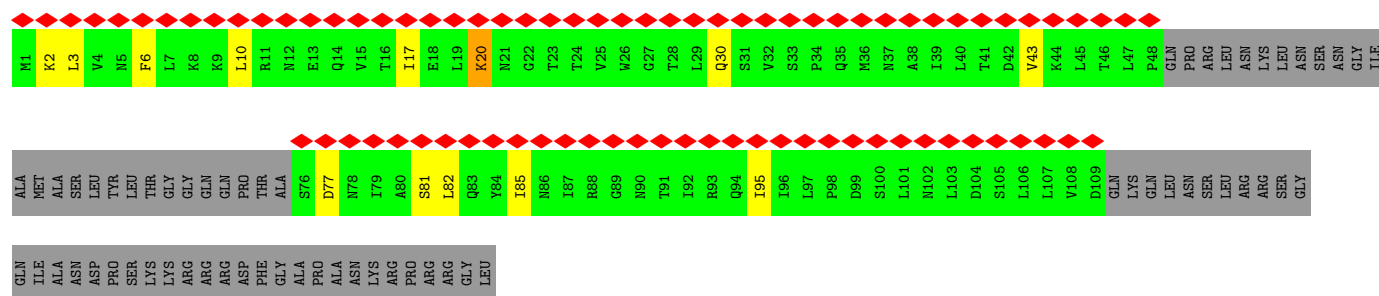




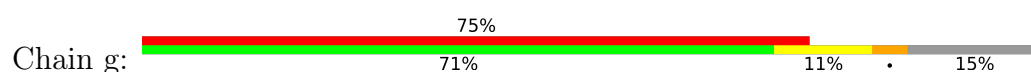
• Molecule 29: Small nuclear ribonucleoprotein Sm D1



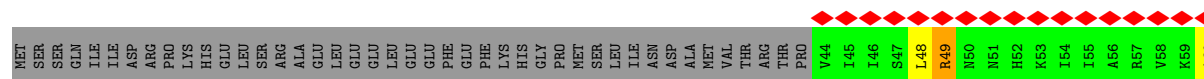
• Molecule 29: Small nuclear ribonucleoprotein Sm D1



• Molecule 30: Small nuclear ribonucleoprotein Sm D2

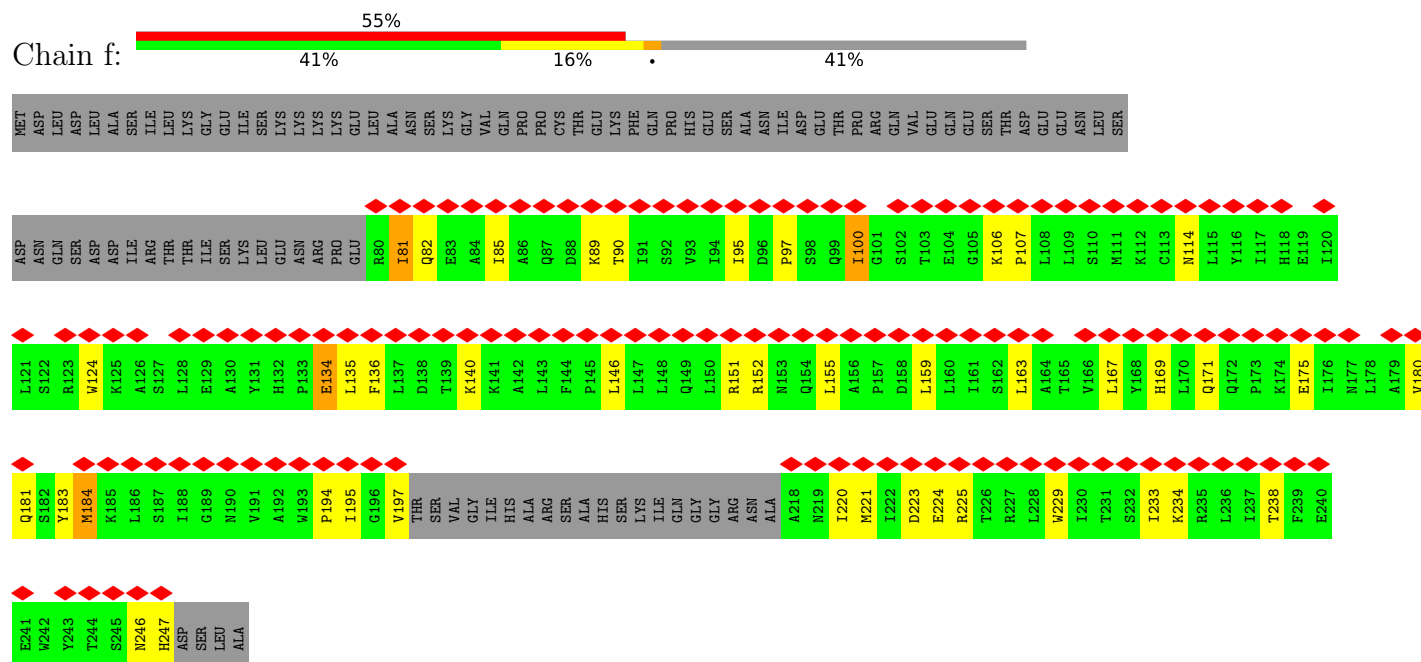


• Molecule 30: Small nuclear ribonucleoprotein Sm D2





Chain f:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	27558	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.6	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	0.191	Depositor
Minimum map value	-0.094	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.0297	Depositor
Map size ($\text{\AA}$)	522.4, 522.4, 522.4	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3060001, 1.3060001, 1.3060001	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	0.76	0/16346	0.89	5/22154 (0.0%)
2	C	0.75	0/7168	0.86	3/9707 (0.0%)
3	J	0.71	0/191	0.93	1/254 (0.4%)
4	O	0.93	0/2704	1.00	4/3676 (0.1%)
5	P	0.64	0/1604	0.91	4/2160 (0.2%)
6	Q	0.63	0/1496	0.85	0/2014
7	R	0.66	0/2135	0.83	2/2871 (0.1%)
8	S	0.66	0/574	0.99	1/766 (0.1%)
9	T	0.72	0/1315	0.92	0/1759
10	Z	0.51	0/3712	0.80	2/5004 (0.0%)
11	B	0.29	0/307	0.27	0/475
12	N	0.36	0/346	0.52	0/535
13	D	0.36	0/2747	0.36	0/4267
14	E	0.35	0/2452	0.37	1/3817 (0.0%)
15	L	0.69	13/2123 (0.6%)	0.85	12/3295 (0.4%)
16	M	0.33	0/543	0.57	0/842
17	c	0.38	0/2405	0.77	0/3218
18	d	0.36	0/2107	0.63	0/2852
19	I	0.30	0/826	0.58	0/1097
20	v	0.87	9/905 (1.0%)	1.10	9/1214 (0.7%)
21	n	1.07	13/1878 (0.7%)	1.12	22/2503 (0.9%)
22	o	0.54	0/835	0.85	0/1126
22	p	0.54	0/848	0.91	0/1143
22	q	0.64	0/2342	0.93	2/3139 (0.1%)
22	r	0.53	0/828	0.86	0/1117
23	t	0.58	0/924	1.06	2/1244 (0.2%)
24	F	0.55	0/615	0.76	0/829
24	k	0.55	0/636	0.76	0/856
25	G	0.63	0/585	0.86	0/795
25	i	0.64	0/585	0.86	0/795
26	H	0.61	0/564	0.87	0/761
26	h	0.61	0/564	0.87	0/761

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
27	K	0.53	0/532	0.82	1/715 (0.1%)
27	j	0.53	0/532	0.82	1/715 (0.1%)
28	U	0.54	0/634	0.96	0/859
28	l	0.55	0/634	0.96	0/859
29	V	0.58	0/649	0.81	0/880
29	m	0.58	0/649	0.81	0/880
30	W	0.65	0/535	0.86	2/717 (0.3%)
30	g	0.65	0/753	0.96	2/1013 (0.2%)
31	X	1.01	2/514 (0.4%)	1.86	8/686 (1.2%)
32	Y	1.24	6/839 (0.7%)	2.35	45/1127 (4.0%)
33	b	0.40	0/227	0.86	0/346
34	e	0.86	2/3357 (0.1%)	1.70	41/4674 (0.9%)
35	f	0.36	0/1227	0.81	2/1665 (0.1%)
All	All	0.68	45/74292 (0.1%)	0.94	172/102182 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	24
2	C	0	10
4	O	0	10
5	P	0	5
6	Q	0	6
7	R	0	3
8	S	0	1
9	T	0	5
10	Z	0	2
17	c	0	2
18	d	0	1
21	n	0	4
27	K	0	1
27	j	0	1
28	U	0	2
28	l	0	2
30	W	0	2
30	g	0	2
34	e	0	32
All	All	0	115

All (45) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	n	399	CYS	CB-SG	-12.13	1.41	1.81
21	n	444	CYS	CB-SG	-11.50	1.43	1.81
32	Y	69	ASP	CA-CB	-10.62	1.38	1.53
21	n	454	CYS	CB-SG	-9.96	1.48	1.81
21	n	218	CYS	CB-SG	-9.77	1.49	1.81
21	n	352	CYS	CB-SG	-9.38	1.50	1.81
21	n	198	CYS	CB-SG	-8.85	1.52	1.81
20	v	712	CYS	CB-SG	-8.52	1.53	1.81
21	n	396	ARG	CA-CB	-8.39	1.44	1.54
15	L	1096	C	O3'-P	-8.05	1.49	1.61
15	L	1096	C	C1'-N1	7.67	1.59	1.48
15	L	1120	G	C1'-N9	-7.58	1.36	1.48
15	L	1118	U	C1'-N1	7.54	1.59	1.48
15	L	1111	U	C1'-N1	6.97	1.58	1.48
15	L	1101	C	C1'-N1	6.96	1.58	1.48
15	L	1119	C	C1'-N1	6.96	1.58	1.48
32	Y	102	THR	CB-OG1	6.94	1.54	1.43
15	L	1109	C	C1'-N1	6.93	1.57	1.47
15	L	1115	G	C1'-N9	-6.89	1.37	1.48
32	Y	51	THR	CB-OG1	6.67	1.54	1.43
34	e	432	SER	N-CA	6.30	1.53	1.46
21	n	291	HIS	CA-CB	-6.29	1.42	1.53
31	X	75	THR	CB-OG1	6.19	1.53	1.43
31	X	110	THR	CB-OG1	6.19	1.53	1.43
21	n	155	ILE	CB-CG1	-6.09	1.41	1.53
32	Y	153	THR	CB-OG1	6.09	1.53	1.43
15	L	1112	G	C1'-N9	-5.97	1.39	1.48
32	Y	38	THR	CB-OG1	5.92	1.53	1.43
15	L	121	C	C1'-N1	5.86	1.57	1.48
32	Y	160	THR	CB-OG1	5.68	1.52	1.43
20	v	723	SER	CB-OG	5.63	1.53	1.42
20	v	718	SER	CB-OG	5.62	1.53	1.42
21	n	430	THR	CB-OG1	5.47	1.52	1.43
21	n	235	THR	CB-OG1	5.45	1.52	1.43
15	L	49	U	C1'-N1	5.32	1.56	1.48
15	L	50	U	C1'-N1	5.25	1.56	1.48
20	v	576	THR	CB-OG1	5.22	1.52	1.43
20	v	714	SER	CB-OG	5.22	1.52	1.42
21	n	440	SER	CB-OG	5.15	1.52	1.42
20	v	719	THR	CB-OG1	5.14	1.51	1.43
20	v	681	SER	CB-OG	5.14	1.52	1.42
20	v	632	THR	CB-OG1	5.09	1.51	1.43
21	n	342	LEU	CB-CG	-5.07	1.43	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	e	926	HIS	CA-C	5.06	1.59	1.52
20	v	644	ILE	CB-CG1	-5.04	1.43	1.53

All (172) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	Y	44	PRO	N-CA-CB	15.96	113.92	103.23
32	Y	81	LEU	CA-C-N	12.08	131.58	120.10
32	Y	81	LEU	C-N-CA	12.08	131.58	120.10
34	e	595	PHE	N-CA-C	10.17	123.45	108.60
34	e	373	GLY	O-C-N	9.77	135.41	122.70
32	Y	12	PRO	N-CA-CB	9.10	111.38	103.19
34	e	373	GLY	CA-C-N	8.95	138.64	121.54
34	e	373	GLY	C-N-CA	8.95	138.64	121.54
21	n	428	PRO	N-CA-CB	8.47	112.14	103.25
21	n	208	PRO	N-CA-CB	8.30	110.57	103.35
21	n	257	PRO	N-CA-CB	8.23	110.63	103.31
32	Y	5	PRO	N-CA-CB	8.17	111.97	103.23
22	q	238	ASN	CA-C-N	8.14	130.02	119.84
22	q	238	ASN	C-N-CA	8.14	130.02	119.84
15	L	40	U	C4'-C3'-O3'	8.09	121.53	109.40
34	e	431	TYR	CA-C-N	8.04	136.10	121.94
34	e	431	TYR	C-N-CA	8.04	136.10	121.94
34	e	445	LYS	N-CA-C	8.00	121.89	108.13
32	Y	15	TYR	CA-C-O	-8.00	111.81	120.36
32	Y	107	SER	N-CA-C	7.98	122.80	112.26
21	n	260	PRO	N-CA-CB	7.97	109.94	101.88
20	v	613	PRO	N-CA-CB	7.92	111.12	103.51
1	A	1903	LYS	CB-CA-C	-7.83	106.47	115.79
34	e	900	TRP	CA-C-N	7.73	130.85	120.65
34	e	900	TRP	C-N-CA	7.73	130.85	120.65
21	n	327	PRO	N-CA-CB	7.65	110.15	103.27
20	v	616	PRO	N-CA-CB	7.59	110.44	103.08
15	L	1111	U	P-O5'-C5'	-7.58	109.53	120.90
32	Y	126	ASN	CA-C-O	7.53	128.31	120.40
5	P	59	THR	CB-CA-C	-7.48	106.89	115.79
4	O	122	ARG	CA-C-N	7.34	127.61	119.90
4	O	122	ARG	C-N-CA	7.34	127.61	119.90
15	L	1110	U	O3'-P-O5'	-7.33	93.00	104.00
32	Y	57	LEU	N-CA-CB	7.31	123.10	110.81
21	n	424	PRO	N-CA-CB	7.28	110.50	103.51
31	X	65	PHE	CA-CB-CG	-7.25	106.55	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	P	85	SER	N-CA-C	7.19	121.78	107.62
14	E	52	G	C2'-C3'-O3'	-7.17	102.94	113.70
32	Y	33	ASP	CA-CB-CG	7.16	119.76	112.60
32	Y	10	ASP	CA-CB-CG	7.09	119.69	112.60
21	n	159	PRO	N-CA-CB	7.07	110.67	103.25
21	n	373	PRO	N-CA-CB	7.04	110.64	103.25
32	Y	42	SER	N-CA-CB	-7.03	99.66	110.42
15	L	1113	U	C3'-C2'-O2'	-7.02	104.06	114.60
20	v	722	PRO	N-CA-CB	7.01	111.05	103.33
32	Y	7	ILE	CA-CB-CG1	6.96	122.24	110.40
32	Y	3	PHE	N-CA-C	-6.83	98.08	108.67
31	X	73	PHE	CA-C-O	-6.81	112.83	120.32
32	Y	4	THR	N-CA-CB	-6.79	98.28	110.37
20	v	617	PRO	CA-CB-CG	6.77	117.37	104.50
21	n	162	PRO	N-CA-CB	6.65	110.23	103.25
15	L	1107	C	C5'-C4'-O4'	-6.63	99.15	109.10
30	W	82	LYS	N-CA-C	6.55	124.76	110.80
32	Y	68	PRO	N-CA-CB	6.54	110.12	103.25
30	g	82	LYS	N-CA-C	6.53	124.71	110.80
21	n	436	PRO	N-CA-CB	6.48	110.13	103.00
32	Y	130	ILE	CA-C-O	6.48	128.88	120.78
4	O	123	PRO	N-CA-C	6.37	120.42	110.80
15	L	1112	G	P-O3'-C3'	6.35	129.72	120.20
1	A	511	ASP	CB-CA-C	-6.29	107.53	116.34
32	Y	50	LEU	CA-C-N	6.25	131.47	122.40
32	Y	50	LEU	C-N-CA	6.25	131.47	122.40
7	R	204	LEU	CA-C-N	6.24	135.21	122.04
7	R	204	LEU	C-N-CA	6.24	135.21	122.04
21	n	396	ARG	N-CA-CB	-6.23	107.87	114.10
34	e	631	LYS	N-CA-C	6.23	124.07	110.80
15	L	1111	U	C5'-C4'-C3'	-6.21	106.68	116.00
10	Z	205	TYR	CB-CA-C	-6.20	103.69	109.83
32	Y	83	ARG	N-CA-C	6.19	119.90	111.17
20	v	641	PRO	CA-CB-CG	6.17	116.21	104.50
21	n	178	ILE	CB-CA-C	-6.13	102.42	111.19
21	n	340	PRO	N-CA-CB	6.07	109.62	103.25
32	Y	111	PHE	CA-CB-CG	6.07	119.87	113.80
32	Y	62	ASN	CA-CB-CG	6.05	118.65	112.60
32	Y	132	ASN	OD1-CG-ND2	6.05	128.65	122.60
32	Y	85	ASN	N-CA-CB	-6.02	102.60	111.51
32	Y	127	LEU	CA-C-N	-5.97	114.36	122.77
32	Y	127	LEU	C-N-CA	-5.97	114.36	122.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	e	858	SER	N-CA-C	5.95	118.25	111.11
23	t	105	PRO	CA-CB-CG	5.93	115.78	104.50
21	n	373	PRO	CA-CB-CG	5.93	115.76	104.50
31	X	66	LYS	N-CA-C	-5.91	104.75	111.07
15	L	1106	G	O3'-P-O5'	-5.89	95.17	104.00
20	v	617	PRO	N-CA-CB	5.86	109.40	103.25
34	e	391	GLY	CA-C-N	5.85	132.71	121.54
34	e	391	GLY	C-N-CA	5.85	132.71	121.54
2	C	656	LEU	CA-CB-CG	-5.84	95.84	116.30
5	P	135	VAL	CA-C-N	-5.83	105.46	122.38
5	P	135	VAL	C-N-CA	-5.83	105.46	122.38
34	e	525	ILE	CB-CA-C	5.83	116.70	110.53
21	n	436	PRO	CA-CB-CG	5.81	115.54	104.50
1	A	525	LEU	CA-CB-CG	-5.80	96.01	116.30
32	Y	60	THR	CA-C-O	5.79	127.68	121.55
32	Y	44	PRO	CB-CA-C	-5.77	106.15	111.40
21	n	274	HIS	CA-CB-CG	-5.76	108.04	113.80
34	e	424	PRO	N-CA-C	5.75	121.04	113.86
10	Z	201	ARG	CA-CB-CG	-5.74	102.63	114.10
15	L	1107	C	P-O3'-C3'	5.73	128.79	120.20
1	A	1041	VAL	N-CA-C	-5.72	106.92	112.29
34	e	713	LEU	CA-C-N	5.71	132.45	121.54
34	e	713	LEU	C-N-CA	5.71	132.45	121.54
34	e	497	ARG	CA-C-N	5.69	131.16	122.29
34	e	497	ARG	C-N-CA	5.69	131.16	122.29
8	S	8	GLN	N-CA-C	5.68	122.90	110.80
15	L	1111	U	O4'-C1'-C2'	-5.66	101.94	107.60
32	Y	158	ASN	CB-CA-C	-5.61	102.09	110.16
15	L	1108	A	N9-C1'-C2'	5.60	120.41	112.00
34	e	687	SER	CA-C-N	5.60	126.30	120.03
34	e	687	SER	C-N-CA	5.60	126.30	120.03
21	n	380	HIS	CA-CB-CG	-5.53	108.27	113.80
35	f	100	ILE	N-CA-C	5.52	116.16	110.36
34	e	988	ILE	CB-CA-C	-5.47	102.32	111.29
23	t	77	PRO	CA-CB-CG	5.47	114.89	104.50
34	e	392	TYR	CA-C-N	5.45	131.95	121.54
34	e	392	TYR	C-N-CA	5.45	131.95	121.54
30	g	81	GLY	N-CA-C	5.43	119.53	112.25
32	Y	15	TYR	O-C-N	5.43	129.41	123.22
34	e	618	ASP	CB-CA-C	5.42	121.44	110.38
30	W	81	GLY	N-CA-C	5.42	119.51	112.25
32	Y	71	SER	N-CA-CB	-5.40	102.67	110.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	e	532	VAL	CA-C-N	5.38	131.37	121.85
34	e	532	VAL	C-N-CA	5.38	131.37	121.85
31	X	93	ARG	CA-CB-CG	-5.38	103.34	114.10
32	Y	50	LEU	N-CA-C	-5.38	106.22	112.89
34	e	524	THR	CA-C-N	-5.37	118.10	123.04
34	e	524	THR	C-N-CA	-5.37	118.10	123.04
32	Y	141	ARG	CD-NE-CZ	5.35	131.89	124.40
21	n	219	GLN	CA-CB-CG	-5.34	103.43	114.10
32	Y	133	GLN	CA-CB-CG	-5.31	103.48	114.10
35	f	124	TRP	N-CA-C	-5.31	105.41	111.14
15	L	1113	U	O4'-C1'-C2'	-5.29	100.51	105.80
34	e	372	ILE	CB-CA-C	5.29	119.15	110.69
31	X	41	MET	N-CA-C	5.28	117.44	111.11
34	e	885	ILE	CA-C-N	5.27	127.29	120.44
34	e	885	ILE	C-N-CA	5.27	127.29	120.44
32	Y	155	ASP	CA-C-N	5.26	130.02	122.40
32	Y	155	ASP	C-N-CA	5.26	130.02	122.40
20	v	641	PRO	N-CA-CB	5.25	108.76	103.25
34	e	394	ASN	CA-C-N	5.25	127.83	120.28
34	e	394	ASN	C-N-CA	5.25	127.83	120.28
34	e	925	VAL	N-CA-C	5.24	115.67	108.12
32	Y	38	THR	CA-CB-OG1	5.23	117.45	109.60
32	Y	44	PRO	CA-C-O	-5.23	114.36	120.85
21	n	295	SER	N-CA-CB	-5.22	102.80	110.26
31	X	71	GLN	N-CA-C	5.20	117.58	109.52
21	n	258	THR	N-CA-CB	-5.20	102.48	110.01
32	Y	134	VAL	CA-C-N	5.20	127.76	120.28
32	Y	134	VAL	C-N-CA	5.20	127.76	120.28
32	Y	100	ASN	CA-CB-CG	5.19	117.79	112.60
2	C	116	THR	CA-C-N	5.18	128.97	120.63
2	C	116	THR	C-N-CA	5.18	128.97	120.63
21	n	219	GLN	N-CA-CB	-5.17	102.49	110.25
4	O	250	LEU	CA-CB-CG	-5.15	98.29	116.30
34	e	811	MET	O-C-N	-5.13	115.76	122.59
34	e	933	VAL	N-CA-CB	5.13	119.69	111.23
34	e	563	SER	CA-C-N	5.09	127.99	121.27
34	e	563	SER	C-N-CA	5.09	127.99	121.27
31	X	68	GLN	N-CA-C	5.07	119.46	113.28
27	K	42	ASP	N-CA-C	5.05	117.20	110.53
1	A	763	MET	CB-CG-SD	-5.05	97.54	112.70
27	j	42	ASP	N-CA-C	5.05	117.20	110.53
21	n	68	PRO	N-CA-C	5.05	120.66	114.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	e	393	ALA	CA-C-N	5.04	128.39	120.82
34	e	393	ALA	C-N-CA	5.04	128.39	120.82
32	Y	107	SER	N-CA-CB	-5.04	102.91	111.17
20	v	721	GLY	CA-C-N	5.03	124.63	119.05
20	v	721	GLY	C-N-CA	5.03	124.63	119.05
32	Y	56	ILE	CA-C-O	-5.03	115.23	120.76
31	X	103	PHE	CA-C-O	-5.01	115.34	121.05
32	Y	148	VAL	CA-C-N	5.00	124.67	119.56
32	Y	148	VAL	C-N-CA	5.00	124.67	119.56
3	J	12	LYS	N-CA-C	-5.00	100.14	110.80

There are no chirality outliers.

All (115) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1014	LYS	Peptide
1	A	1036	SER	Peptide
1	A	1346	PHE	Peptide
1	A	1375	LEU	Peptide
1	A	1409	ALA	Peptide
1	A	1410	SER	Peptide
1	A	1418	THR	Peptide
1	A	1432	GLU	Peptide
1	A	1539	LEU	Peptide
1	A	1588	LYS	Peptide
1	A	1720	THR	Peptide
1	A	1788	GLY	Peptide
1	A	1790	TRP	Peptide
1	A	1809	ASN	Peptide
1	A	1972	ASP	Peptide
1	A	1999	ILE	Peptide
1	A	259	GLU	Peptide
1	A	288	GLU	Peptide
1	A	356	TYR	Peptide
1	A	460	PRO	Peptide
1	A	539	PRO	Peptide
1	A	761	SER	Peptide
1	A	907	ASN	Peptide
1	A	985	ASP	Peptide
2	C	170	LEU	Peptide
2	C	171	GLY	Peptide
2	C	231	ALA	Peptide

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Mol	Chain	Res	Type	Group
2	C	350	GLY	Peptide
2	C	365	GLU	Peptide
2	C	369	LYS	Peptide
2	C	467	THR	Peptide
2	C	554	HIS	Peptide
2	C	70	TYR	Peptide
2	C	82	ASN	Peptide
27	K	41	ASP	Peptide
4	O	123	PRO	Peptide
4	O	155	PHE	Peptide
4	O	278	ASP	Peptide
4	O	305	THR	Peptide
4	O	376	TYR	Peptide
4	O	431	THR	Peptide
4	O	434	LYS	Peptide
4	O	435	GLU	Peptide
4	O	437	GLU	Peptide
4	O	441	ALA	Peptide
5	P	101	PRO	Peptide
5	P	103	ASN	Peptide
5	P	35	ALA	Peptide
5	P	84	ASN	Peptide
5	P	85	SER	Peptide
6	Q	103	GLU	Peptide
6	Q	291	ILE	Peptide
6	Q	45	HIS	Peptide
6	Q	6	ASN	Peptide
6	Q	94	VAL	Peptide
6	Q	98	ASN	Peptide
7	R	125	GLY	Peptide
7	R	150	HIS	Peptide
7	R	203	THR	Peptide
8	S	172	LYS	Peptide
9	T	104	CYS	Peptide
9	T	116	ASN	Peptide
9	T	118	SER	Peptide
9	T	155	SER	Peptide
9	T	5	LYS	Peptide
28	U	81	ALA	Mainchain,Peptide
30	W	81	GLY	Mainchain,Peptide
10	Z	23	SER	Peptide
10	Z	285	SER	Peptide

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Mol	Chain	Res	Type	Group
17	c	65	PHE	Peptide
17	c	81	PRO	Peptide
18	d	212	HIS	Peptide
34	e	309	MET	Peptide
34	e	313	LEU	Peptide
34	e	372	ILE	Peptide
34	e	386	TYR	Peptide
34	e	387	LEU	Peptide
34	e	431	TYR	Peptide
34	e	436	GLU	Peptide
34	e	443	CYS	Peptide
34	e	449	VAL	Peptide
34	e	532	VAL	Peptide
34	e	542	GLN	Peptide
34	e	563	SER	Peptide
34	e	570	MET	Peptide
34	e	595	PHE	Peptide
34	e	604	ASN	Peptide
34	e	610	PRO	Peptide
34	e	627	LEU	Peptide
34	e	631	LYS	Mainchain,Peptide
34	e	654	ILE	Peptide
34	e	709	GLU	Peptide
34	e	733	SER	Peptide
34	e	737	THR	Peptide
34	e	738	ASP	Peptide
34	e	796	ALA	Peptide
34	e	810	SER	Peptide
34	e	857	PHE	Peptide
34	e	898	LYS	Peptide
34	e	924	TYR	Peptide
34	e	947	LEU	Peptide
34	e	953	TYR	Peptide
34	e	986	LYS	Peptide
30	g	81	GLY	Mainchain,Peptide
27	j	41	ASP	Peptide
28	l	81	ALA	Mainchain,Peptide
21	n	290	ASP	Peptide
21	n	305	GLY	Peptide
21	n	67	GLY	Mainchain,Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	15939	0	15918	1408	0
2	C	7019	0	7201	562	0
3	J	190	0	186	29	0
4	O	2646	0	2639	238	0
5	P	1583	0	1608	107	0
6	Q	1472	0	1485	138	0
7	R	2089	0	2053	240	0
8	S	560	0	545	47	0
9	T	1291	0	1312	94	0
10	Z	3651	0	3707	284	0
11	B	275	0	138	26	0
12	N	312	0	156	56	0
13	D	2465	0	1251	129	0
14	E	2192	0	1106	187	0
15	L	1909	0	970	224	0
16	M	486	0	246	75	0
17	c	2971	0	2336	105	0
18	d	3506	0	2340	115	0
19	I	822	0	845	69	0
20	v	3183	0	1207	73	0
21	n	1870	0	1392	116	0
22	o	830	0	663	6	0
22	p	843	0	675	9	0
22	q	2345	0	1636	43	0
22	r	823	0	654	7	0
23	t	926	0	606	15	0
24	F	610	0	640	16	0
24	k	631	0	670	3	0
25	G	575	0	597	21	0
25	i	575	0	597	21	0
26	H	554	0	556	18	0
26	h	554	0	556	17	0
27	K	529	0	557	2	0
27	j	529	0	557	2	0
28	U	625	0	647	9	0
28	l	625	0	647	5	0
29	V	644	0	686	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	m	644	0	686	14	0
30	W	528	0	573	16	0
30	g	741	0	778	17	0
31	X	513	0	402	13	0
32	Y	841	0	614	17	0
33	b	208	0	106	70	0
34	e	3360	0	1483	3	0
35	f	1202	0	1248	87	0
36	C	32	0	12	11	0
37	B	1	0	0	0	0
37	C	1	0	0	0	0
37	E	4	0	0	0	0
38	Q	2	0	0	0	0
38	R	1	0	0	0	0
38	T	3	0	0	0	0
All	All	76730	0	65487	3976	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 28.

All (3976) 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)
7:R:75:PHE:CE2	14:E:35:A:C8	1.74	1.62
1:A:1587:PHE:CE2	15:L:31:A:H5'	1.33	1.60
7:R:46:ARG:CD	12:N:110:A:H2	1.17	1.56
7:R:75:PHE:CD2	14:E:35:A:N7	1.83	1.45
21:n:230:VAL:HB	21:n:244:LEU:CG	1.41	1.43
7:R:46:ARG:CD	12:N:110:A:C2	2.05	1.40
20:v:729:TYR:CZ	20:v:748:UNK:CB	2.03	1.39
7:R:46:ARG:HD3	12:N:110:A:C2	1.55	1.39
1:A:839:HIS:CD2	13:D:95:C:O2	1.76	1.38
15:L:5:A:C5'	19:I:114:THR:HG21	1.54	1.36
1:A:839:HIS:HD2	13:D:95:C:O2	1.05	1.35
6:Q:215:PRO:HG3	6:Q:217:TRP:CE2	1.62	1.34
2:C:99:LYS:NZ	13:D:43:G:OP2	1.58	1.34
1:A:1988:LEU:CD1	35:f:180:VAL:HG12	1.57	1.33
1:A:839:HIS:HD2	13:D:95:C:C2	1.46	1.33
1:A:1666:CYS:O	1:A:1670:ASP:HB2	1.27	1.30
1:A:1587:PHE:CE2	15:L:31:A:C5'	2.11	1.30
21:n:59:ARG:O	21:n:62:THR:HG23	1.26	1.30

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:v:729:TYR:CE1	20:v:748:UNK:CB	2.13	1.29
6:Q:215:PRO:HG3	6:Q:217:TRP:CZ2	1.69	1.28
6:Q:47:LYS:HE2	14:E:31:G:O6	1.16	1.27
20:v:168:UNK:CA	29:V:81:SER:OG	1.80	1.27
1:A:1864:LYS:HE3	21:n:321:GLU:CB	1.65	1.26
15:L:5:A:H5'	19:I:114:THR:CG2	1.66	1.25
12:N:100:G:C8	33:b:-1:A:H2''	1.71	1.25
22:q:422:GLY:O	22:q:442:SER:CB	1.84	1.24
1:A:713:ASN:ND2	13:D:83:C:H4'	1.55	1.22
1:A:1774:MET:O	1:A:1786:ALA:HA	1.40	1.20
20:v:168:UNK:HA	29:V:81:SER:OG	1.04	1.19
1:A:1337:THR:CG2	33:b:8:A:H62	1.56	1.19
24:F:98:GLU:O	32:Y:53:PRO:CB	1.92	1.17
7:R:89:TYR:CD2	14:E:34:A:C2	2.32	1.16
21:n:251:ALA:HA	21:n:267:LEU:CB	1.75	1.16
6:Q:47:LYS:CE	14:E:31:G:O6	1.94	1.15
7:R:46:ARG:NH1	12:N:110:A:C2	2.14	1.15
1:A:1596:THR:CG2	33:b:4:U:H5''	1.76	1.14
6:Q:217:TRP:O	6:Q:221:ASP:HB2	1.47	1.13
7:R:46:ARG:NH1	12:N:110:A:N3	1.96	1.13
7:R:75:PHE:CD2	14:E:35:A:C8	2.28	1.12
1:A:1988:LEU:H	35:f:181:GLN:HG2	1.01	1.11
15:L:1109:C:N4	31:X:109:LYS:H	1.48	1.10
33:b:-2:U:H2'	33:b:-1:A:H5'	1.32	1.10
6:Q:51:ARG:NH2	14:E:28:U:O2	1.83	1.10
23:t:7:VAL:HG11	23:t:154:VAL:CB	1.82	1.10
1:A:854:ARG:NH2	15:L:25:A:OP1	1.84	1.10
20:v:729:TYR:CE2	20:v:748:UNK:CB	2.33	1.10
1:A:477:MET:HE2	2:C:278:LYS:HE3	1.22	1.09
15:L:1111:U:C6	15:L:1111:U:H5''	1.86	1.09
16:M:489:A:H5''	21:n:246:LEU:N	1.66	1.09
1:A:614:ARG:NH1	11:B:98:A:H4'	1.68	1.08
7:R:183:PHE:CE2	12:N:113:U:C6	2.41	1.08
14:E:21:U:OP2	21:n:54:SER:OG	1.71	1.08
1:A:1588:LYS:HD3	15:L:30:A:N3	1.69	1.08
1:A:1337:THR:HG22	33:b:8:A:N6	1.69	1.07
1:A:1864:LYS:CE	21:n:321:GLU:HB2	1.83	1.07
35:f:183:TYR:CE2	35:f:234:LYS:HD2	1.88	1.07
1:A:1587:PHE:CZ	15:L:31:A:H5'	1.89	1.07
1:A:1709:TRP:O	1:A:1728:ILE:HA	1.54	1.07
21:n:230:VAL:CB	21:n:244:LEU:CG	2.33	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:179:LYS:HB3	12:N:111:U:O2'	1.54	1.07
1:A:1588:LYS:CD	15:L:30:A:C2	2.38	1.06
1:A:1988:LEU:HD22	35:f:180:VAL:HG11	1.31	1.06
7:R:46:ARG:HD2	12:N:110:A:C2	1.89	1.06
1:A:1988:LEU:HD13	35:f:180:VAL:HG12	1.08	1.06
7:R:183:PHE:HE2	12:N:113:U:C6	1.72	1.06
6:Q:215:PRO:CG	6:Q:217:TRP:CE2	2.38	1.06
1:A:1596:THR:HG23	33:b:4:U:H5'	1.38	1.06
12:N:100:G:C8	33:b:-1:A:C2'	2.39	1.05
20:v:161:UNK:CB	32:Y:48:LYS:CB	2.34	1.05
24:F:99:ASP:CB	32:Y:53:PRO:CB	2.35	1.05
1:A:1864:LYS:CE	21:n:321:GLU:CB	2.34	1.04
15:L:1102:C:H2'	15:L:1103:C:C6	1.91	1.04
1:A:1927:GLU:CG	35:f:135:LEU:HD11	1.86	1.04
15:L:1116:A:H2'	15:L:1117:G:H8	1.18	1.04
15:L:15:C:H41	19:I:209:ARG:CG	1.71	1.03
20:v:730:GLN:HA	20:v:733:ILE:HD11	1.37	1.03
14:E:49:A:C2'	14:E:50:G:H5'	1.89	1.03
22:o:51:VAL:HG21	22:p:20:ARG:CB	1.89	1.03
1:A:1337:THR:HG22	33:b:8:A:H62	0.86	1.02
1:A:839:HIS:CD2	13:D:95:C:C2	2.39	1.02
1:A:1924:LEU:HD22	35:f:234:LYS:NZ	1.74	1.02
13:D:165:A:H4'	13:D:166:U:C5'	1.89	1.02
18:d:227:ASP:O	18:d:231:ASN:HB2	1.57	1.02
21:n:302:PHE:CG	21:n:306:SER:O	2.13	1.02
15:L:110:A:H4'	15:L:111:C:C5'	1.89	1.01
1:A:1924:LEU:HD22	35:f:234:LYS:HZ2	1.16	1.01
1:A:1588:LYS:HD2	15:L:30:A:C2	1.95	1.01
18:d:99:ILE:HG13	18:d:100:PRO:CD	1.91	1.01
7:R:75:PHE:CE2	14:E:35:A:N7	2.06	1.01
1:A:334:LYS:NZ	13:D:77:A:OP2	1.93	1.00
1:A:1488:ILE:HG23	1:A:1489:PRO:HD3	1.40	1.00
13:D:165:A:C4'	13:D:166:U:H5'	1.92	1.00
2:C:784:SER:HB2	2:C:787:LEU:HB3	1.42	1.00
1:A:1587:PHE:HE2	15:L:31:A:C5'	1.60	1.00
15:L:1116:A:H2'	15:L:1117:G:C8	1.95	1.00
20:v:718:SER:OG	20:v:725:THR:HG21	1.61	1.00
21:n:55:GLU:OE2	21:n:58:ARG:NE	1.95	1.00
21:n:68:PRO:HD2	21:n:69:TRP:CE3	1.96	0.99
1:A:934:ARG:HH22	15:L:30:A:H5'	1.25	0.99
14:E:49:A:H2'	14:E:50:G:H5'	1.41	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:110:A:C4'	15:L:111:C:H5'	1.92	0.99
15:L:1114:G:O6	31:X:38:LYS:NZ	1.95	0.99
1:A:1851:PHE:O	1:A:1881:THR:HA	1.62	0.99
1:A:2059:ILE:O	1:A:2063:TYR:HB2	1.61	0.99
8:S:6:ARG:NH1	14:E:84:C:O2'	1.96	0.99
16:M:495:A:H2'	16:M:496:U:C6	1.98	0.99
16:M:489:A:H5''	21:n:246:LEU:H	1.22	0.98
21:n:59:ARG:O	21:n:62:THR:CG2	2.10	0.98
1:A:1775:ILE:HA	1:A:1785:ASP:O	1.62	0.98
1:A:477:MET:HE2	2:C:278:LYS:CE	1.93	0.98
7:R:179:LYS:HA	12:N:111:U:O2	1.63	0.98
1:A:1864:LYS:HE3	21:n:321:GLU:HB2	1.00	0.97
13:D:75:A:H4'	13:D:76:U:H5'	1.43	0.97
4:O:379:LYS:HA	5:P:47:ARG:HH21	1.27	0.97
1:A:1587:PHE:CZ	15:L:31:A:C5'	2.47	0.96
15:L:1111:U:H5''	15:L:1111:U:H6	1.25	0.96
15:L:1097:G:N2	15:L:1119:C:O2	1.96	0.96
18:d:99:ILE:HG13	18:d:100:PRO:HD3	1.42	0.96
1:A:1988:LEU:CD2	35:f:180:VAL:HG11	1.94	0.96
15:L:25:A:H2	17:c:31:HIS:HB3	1.27	0.96
1:A:1335:TRP:HD1	1:A:1367:ILE:HD12	1.28	0.95
12:N:100:G:H8	33:b:-1:A:C2'	1.77	0.94
15:L:1116:A:C2	15:L:1117:G:C4	2.54	0.94
33:b:-2:U:C2'	33:b:-1:A:H5'	1.96	0.94
1:A:1864:LYS:NZ	21:n:321:GLU:HB3	1.82	0.94
1:A:1666:CYS:O	1:A:1670:ASP:CB	2.15	0.94
15:L:1111:U:O4'	28:U:30:ARG:HD3	1.67	0.94
1:A:1588:LYS:HD3	15:L:30:A:C2	2.00	0.94
7:R:47:PHE:CE1	14:E:37:U:N3	2.35	0.94
2:C:472:VAL:HB	2:C:575:ALA:O	1.68	0.94
7:R:75:PHE:HD2	14:E:35:A:N7	1.52	0.94
1:A:1988:LEU:HD22	35:f:180:VAL:CG1	1.96	0.94
1:A:1927:GLU:HG3	35:f:135:LEU:CD1	1.97	0.94
17:c:65:PHE:HE1	17:c:101:ARG:HB2	1.33	0.94
15:L:110:A:C2	29:V:2:LYS:CE	2.51	0.94
15:L:1102:C:H2'	15:L:1103:C:C5	2.03	0.94
1:A:532:ASN:ND2	13:D:84:A:OP2	1.99	0.93
2:C:340:LYS:O	2:C:343:ASP:HB3	1.68	0.93
15:L:1101:C:N4	31:X:38:LYS:HZ3	1.66	0.93
1:A:1988:LEU:HD13	35:f:180:VAL:CG1	1.99	0.93
1:A:1081:TYR:O	1:A:1085:LYS:HB2	1.69	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Z:63:PHE:O	10:Z:69:ASN:ND2	2.01	0.93
1:A:1988:LEU:H	35:f:181:GLN:CG	1.81	0.93
1:A:1335:TRP:CD1	1:A:1367:ILE:HD12	2.03	0.93
13:D:165:A:C2	29:m:2:LYS:CE	2.51	0.93
15:L:110:A:H4'	15:L:111:C:H5'	0.95	0.93
2:C:132:ARG:NH2	28:l:13:GLU:O	2.02	0.92
1:A:1330:LYS:HD3	33:b:6:U:OP1	1.68	0.92
1:A:1596:THR:HG22	33:b:4:U:H5''	1.51	0.92
20:v:729:TYR:CD1	20:v:748:UNK:CB	2.52	0.92
1:A:1588:LYS:HD2	15:L:30:A:H2	1.28	0.92
1:A:1927:GLU:HG2	35:f:135:LEU:HD11	1.50	0.92
1:A:1986:MET:HG3	35:f:184:MET:HG3	1.50	0.92
22:q:468:GLN:CB	22:q:481:CYS:SG	2.58	0.92
1:A:854:ARG:CZ	15:L:25:A:OP1	2.17	0.92
15:L:1116:A:C6	15:L:1117:G:C6	2.57	0.92
15:L:1099:G:C5	15:L:1100:A:C8	2.58	0.91
9:T:151:ARG:O	21:n:63:ARG:NH1	2.02	0.91
23:t:81:ASP:CB	23:t:85:THR:CB	2.49	0.91
1:A:1924:LEU:CD2	35:f:234:LYS:NZ	2.34	0.91
7:R:46:ARG:HD3	12:N:110:A:H2	0.93	0.91
33:b:2:U:H5''	33:b:3:U:OP2	1.70	0.91
7:R:75:PHE:CZ	14:E:35:A:C8	2.59	0.91
1:A:1594:GLN:O	1:A:1598:LEU:HB3	1.71	0.91
15:L:15:C:H41	19:I:209:ARG:CB	1.84	0.90
20:v:682:LYS:O	20:v:685:GLU:CG	2.18	0.90
20:v:726:ARG:NH2	20:v:760:UNK:CB	2.35	0.90
1:A:751:ASP:OD1	1:A:752:ALA:N	2.04	0.90
1:A:1988:LEU:N	35:f:181:GLN:HG2	1.86	0.90
7:R:75:PHE:CD2	14:E:35:A:C5	2.59	0.90
12:N:100:G:N7	33:b:-1:A:H2''	1.87	0.90
6:Q:208:TYR:HB2	6:Q:290:ILE:HD12	1.52	0.90
1:A:416:GLU:HG2	1:A:418:ASP:H	1.35	0.90
18:d:229:VAL:O	18:d:233:GLN:HB2	1.72	0.90
16:M:499:U:O2'	16:M:500:A:OP1	1.90	0.90
20:v:730:GLN:HA	20:v:733:ILE:CD1	2.02	0.90
14:E:86:G:N2	18:d:57:TYR:CE2	2.40	0.90
1:A:1860:VAL:HG21	16:M:502:C:H5''	1.54	0.89
13:D:165:A:C2	29:m:2:LYS:HE2	2.07	0.89
17:c:229:ASP:HB2	19:I:151:LYS:HB3	1.53	0.89
7:R:138:TYR:OH	12:N:111:U:OP2	1.90	0.89
1:A:1988:LEU:CD2	35:f:180:VAL:CG1	2.51	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:101:GLN:NE2	13:D:75:A:H61	1.71	0.89
7:R:108:VAL:HG23	7:R:109:LEU:HG	1.54	0.89
15:L:110:A:C2	29:V:2:LYS:HE2	2.08	0.89
7:R:234:ALA:HA	7:R:237:ARG:HD3	1.51	0.89
1:A:713:ASN:HD21	13:D:83:C:H4'	1.32	0.89
1:A:854:ARG:HH22	15:L:25:A:H5''	1.37	0.89
7:R:76:PHE:HB2	7:R:91:HIS:HD2	1.38	0.89
15:L:34:G:OP2	15:L:34:G:C8	2.26	0.89
15:L:1099:G:C6	15:L:1100:A:N7	2.41	0.89
1:A:1365:THR:O	1:A:1369:ASN:ND2	2.06	0.88
14:E:89:U:C6	19:I:179:ARG:HG2	2.08	0.88
10:Z:74:PRO:HA	10:Z:123:ILE:HG21	1.55	0.88
1:A:1576:GLU:OE1	1:A:1826:TYR:O	1.92	0.88
21:n:184:ASP:O	21:n:185:HIS:CG	2.27	0.88
1:A:1863:HIS:O	1:A:1871:ALA:HB3	1.73	0.88
15:L:15:C:H41	19:I:209:ARG:HG2	1.36	0.88
16:M:489:A:H5''	21:n:246:LEU:CA	2.03	0.88
7:R:161:ARG:O	7:R:165:SER:HB3	1.73	0.88
1:A:1748:ILE:O	1:A:1751:TYR:N	2.06	0.87
8:S:9:LEU:HD12	8:S:10:GLU:HB2	1.54	0.87
1:A:1592:HIS:HE1	33:b:4:U:C6	1.91	0.87
20:v:168:UNK:HA	29:V:81:SER:CB	2.04	0.87
16:M:489:A:C5'	21:n:246:LEU:H	1.86	0.87
1:A:614:ARG:CZ	11:B:98:A:H4'	2.05	0.87
1:A:1927:GLU:CG	35:f:135:LEU:CD1	2.52	0.87
1:A:1596:THR:CG2	33:b:4:U:C5'	2.52	0.87
15:L:110:A:C2	29:V:2:LYS:HE3	2.10	0.87
7:R:23:PRO:O	7:R:37:TRP:NE1	2.06	0.86
13:D:165:A:H4'	13:D:166:U:H5'	0.95	0.86
2:C:266:VAL:HG22	2:C:312:ILE:HB	1.55	0.86
2:C:711:ALA:HB3	2:C:819:LYS:O	1.74	0.86
7:R:89:TYR:HD2	14:E:34:A:C2	1.93	0.86
13:D:165:A:C2	29:m:2:LYS:HE3	2.10	0.86
15:L:1099:G:N7	15:L:1100:A:C8	2.43	0.86
1:A:585:ARG:NH2	1:A:733:GLN:O	2.09	0.86
14:E:91:A:N7	19:I:97:TYR:CE1	2.42	0.86
16:M:483:U:H3'	16:M:484:U:C5	2.10	0.86
20:v:730:GLN:O	20:v:733:ILE:HD12	1.76	0.86
7:R:118:ALA:O	7:R:129:SER:OG	1.93	0.85
1:A:839:HIS:CD2	13:D:95:C:N3	2.45	0.85
9:T:41:LEU:HD21	14:E:35:A:C2	2.11	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1864:LYS:HZ1	21:n:321:GLU:HB3	1.40	0.85
21:n:155:ILE:CG1	21:n:453:VAL:O	2.25	0.85
1:A:320:ASP:OD1	1:A:508:GLN:NE2	2.09	0.85
4:O:407:PHE:HE1	4:O:414:LEU:HD13	1.41	0.85
1:A:1673:LEU:HA	1:A:1678:ILE:HB	1.58	0.85
2:C:365:GLU:HG3	2:C:366:ASN:H	1.41	0.85
1:A:1864:LYS:HD2	21:n:328:ILE:CG1	2.07	0.85
1:A:137:GLU:OE2	1:A:140:ARG:NH2	2.10	0.85
15:L:1099:G:C5	15:L:1100:A:N7	2.44	0.85
16:M:484:U:H4'	16:M:485:U:H5'	1.59	0.84
1:A:366:GLU:HG3	1:A:372:ARG:HH11	1.41	0.84
1:A:1046:SER:HA	1:A:1251:TYR:O	1.77	0.84
1:A:839:HIS:HD2	13:D:95:C:N3	1.75	0.84
1:A:1211:SER:O	1:A:1257:ASN:ND2	2.10	0.84
1:A:1405:ILE:HG22	1:A:1406:LEU:H	1.43	0.84
1:A:1860:VAL:HG21	16:M:502:C:C5'	2.06	0.84
7:R:127:ILE:HB	14:E:39:G:N7	1.92	0.84
21:n:250:PRO:O	21:n:267:LEU:CB	2.26	0.84
10:Z:60:VAL:HG13	10:Z:76:LEU:HD22	1.59	0.84
12:N:100:G:H8	33:b:-1:A:H2''	1.33	0.84
33:b:3:U:H3'	33:b:3:U:OP1	1.78	0.84
7:R:89:TYR:CD2	14:E:34:A:N3	2.46	0.84
7:R:253:LEU:O	7:R:257:ASN:CB	2.26	0.84
9:T:128:GLN:O	9:T:131:GLU:N	2.10	0.84
25:i:86:ASN:HD21	26:h:32:LYS:HD3	1.43	0.84
25:G:86:ASN:HD21	26:H:32:LYS:HD3	1.43	0.84
1:A:620:HIS:HB3	1:A:669:TYR:CE2	2.13	0.84
1:A:854:ARG:HH22	15:L:25:A:C5'	1.91	0.83
10:Z:61:VAL:HG11	10:Z:101:MET:HE3	1.59	0.83
15:L:1102:C:H2'	15:L:1103:C:H6	1.42	0.83
12:N:101:U:O4	14:E:50:G:O2'	1.95	0.83
1:A:1587:PHE:HE2	15:L:31:A:O5'	1.59	0.83
4:O:354:ASN:ND2	4:O:369:ASP:OD1	2.11	0.83
22:q:51:VAL:HG13	22:r:20:ARG:CB	2.09	0.83
1:A:128:TYR:HA	9:T:112:ASN:HD21	1.43	0.83
2:C:734:CYS:SG	2:C:755:TYR:OH	2.35	0.83
10:Z:60:VAL:O	10:Z:64:THR:OG1	1.97	0.83
15:L:1101:C:H41	31:X:38:LYS:HZ3	1.26	0.83
1:A:542:HIS:C	1:A:544:LYS:H	1.86	0.83
2:C:770:ASN:OD1	2:C:771:GLY:N	2.11	0.83
15:L:1109:C:H41	31:X:109:LYS:H	1.21	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:2:SER:O	3:J:4:ASN:ND2	2.11	0.83
20:v:724:VAL:O	20:v:727:GLU:CG	2.27	0.83
7:R:161:ARG:O	7:R:165:SER:CB	2.27	0.82
4:O:379:LYS:HD3	5:P:47:ARG:HH22	1.42	0.82
6:Q:13:CYS:N	6:Q:71:CYS:SG	2.52	0.82
1:A:978:ILE:HB	8:S:174:VAL:HA	1.61	0.82
1:A:1485:ASP:O	1:A:1490:ARG:NH2	2.12	0.82
1:A:1596:THR:HG22	33:b:4:U:C5'	2.08	0.82
2:C:308:ASP:HB3	2:C:310:ASN:HD22	1.44	0.82
7:R:75:PHE:HE2	14:E:35:A:C8	1.54	0.82
10:Z:102:PHE:HB2	10:Z:117:ILE:HG21	1.60	0.82
14:E:89:U:H6	19:I:179:ARG:HG2	1.42	0.82
1:A:1670:ASP:HA	1:A:1681:VAL:HG21	1.59	0.82
1:A:1988:LEU:O	35:f:181:GLN:NE2	2.12	0.82
7:R:127:ILE:O	14:E:39:G:O6	1.96	0.82
7:R:75:PHE:CE2	14:E:35:A:H8	1.55	0.82
15:L:5:A:H5'	19:I:114:THR:HG21	0.83	0.82
2:C:378:LEU:O	2:C:381:LEU:N	2.13	0.82
1:A:1056:GLU:OE1	1:A:1060:LYS:NZ	2.12	0.81
1:A:1864:LYS:CE	21:n:321:GLU:HB3	2.09	0.81
10:Z:174:TRP:HZ3	10:Z:201:ARG:HD2	1.44	0.81
15:L:41:C:O2	16:M:494:G:N2	2.13	0.81
21:n:405:SER:O	21:n:406:ARG:CB	2.26	0.81
1:A:1889:LEU:O	1:A:1988:LEU:HA	1.79	0.81
2:C:779:LEU:O	2:C:782:GLU:N	2.12	0.81
4:O:193:ARG:HH22	4:O:237:ASP:H	1.28	0.81
7:R:73:CYS:HA	14:E:34:A:N1	1.95	0.81
23:t:114:LEU:O	23:t:117:VAL:HG22	1.78	0.81
1:A:2059:ILE:O	1:A:2063:TYR:CB	2.29	0.81
10:Z:201:ARG:NH2	10:Z:205:TYR:OH	2.13	0.81
2:C:748:SER:HB2	2:C:762:SER:HB3	1.63	0.81
24:F:19:LYS:NZ	32:Y:34:LEU:CB	2.44	0.81
1:A:1456:ARG:NH2	1:A:1460:GLU:OE2	2.13	0.81
1:A:353:GLU:CG	13:D:104:G:O5'	2.28	0.81
1:A:1986:MET:HB2	35:f:184:MET:HB3	1.61	0.81
2:C:712:ALA:HA	2:C:817:GLN:O	1.81	0.81
7:R:87:CYS:HB3	7:R:91:HIS:CE1	2.15	0.81
1:A:381:SER:O	1:A:384:LYS:N	2.13	0.81
6:Q:47:LYS:NZ	14:E:30:G:O6	2.12	0.80
20:v:724:VAL:HA	20:v:727:GLU:CG	2.11	0.80
1:A:1538:ASN:OD1	1:A:1539:LEU:N	2.14	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1711:VAL:HG13	1:A:1789:ASN:HB3	1.62	0.80
2:C:468:LEU:O	2:C:578:TYR:HA	1.82	0.80
21:n:230:VAL:O	21:n:244:LEU:CG	2.29	0.80
26:H:74:ARG:NH2	30:W:64:HIS:O	2.14	0.80
1:A:1986:MET:CB	35:f:184:MET:HB3	2.11	0.80
7:R:165:SER:HA	7:R:170:ILE:HD11	1.62	0.80
1:A:1464:LYS:NZ	1:A:1479:GLU:O	2.15	0.80
10:Z:78:ALA:O	10:Z:81:ALA:HB3	1.81	0.80
10:Z:174:TRP:CZ3	10:Z:201:ARG:HD2	2.15	0.80
15:L:1109:C:N4	31:X:109:LYS:N	2.30	0.80
1:A:353:GLU:HG3	13:D:104:G:O5'	1.81	0.80
13:D:81:A:O2'	13:D:82:A:OP1	1.98	0.80
1:A:1195:PHE:HB3	1:A:1217:ARG:HE	1.47	0.80
1:A:1337:THR:CG2	33:b:8:A:N6	2.37	0.80
7:R:36:LYS:HZ2	14:E:41:A:H2	1.26	0.80
18:d:199:MET:HB2	18:d:242:GLU:HG3	1.64	0.80
22:q:369:PHE:O	22:q:370:PRO:CB	2.30	0.80
17:c:64:GLU:HG2	17:c:65:PHE:H	1.45	0.80
14:E:89:U:C6	19:I:179:ARG:CG	2.65	0.80
15:L:119:G:H5'	30:W:99:ASP:OD2	1.82	0.80
1:A:1575:TRP:HA	1:A:1825:ILE:HG12	1.64	0.79
22:q:178:LYS:HB3	22:q:468:GLN:CB	2.12	0.79
24:F:102:LEU:C	32:Y:13:GLN:HB3	2.07	0.79
1:A:1864:LYS:NZ	21:n:321:GLU:CB	2.45	0.79
1:A:1988:LEU:HD13	35:f:180:VAL:C	2.07	0.79
13:D:174:G:H5'	30:g:99:ASP:OD2	1.82	0.79
15:L:1099:G:N3	15:L:1099:G:H5''	1.97	0.79
15:L:39:A:H2'	15:L:40:U:C5'	2.12	0.79
1:A:1988:LEU:HB2	35:f:181:GLN:HG3	1.65	0.79
6:Q:73:CYS:SG	6:Q:74:CYS:N	2.54	0.79
15:L:25:A:C2	17:c:31:HIS:HB3	2.16	0.79
26:h:74:ARG:NH2	30:g:64:HIS:O	2.14	0.79
1:A:681:LYS:O	1:A:684:LYS:HB3	1.81	0.79
1:A:716:ARG:NH2	13:D:112:C:C2	2.51	0.79
1:A:1859:ARG:O	1:A:1874:ALA:HA	1.83	0.79
15:L:34:G:OP2	15:L:34:G:O4'	2.01	0.79
21:n:183:ASN:HA	21:n:208:PRO:CG	2.13	0.79
1:A:1750:ARG:O	1:A:1754:ALA:HB2	1.83	0.79
4:O:248:ILE:O	4:O:262:LEU:HB2	1.83	0.79
1:A:740:GLU:HG3	1:A:741:ILE:H	1.47	0.79
1:A:1051:GLU:OE1	1:A:1204:ARG:NH2	2.15	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2018:ASN:ND2	1:A:2062:GLU:OE1	2.15	0.79
1:A:2034:ILE:HG12	1:A:2041:PRO:HA	1.65	0.79
2:C:646:GLY:HA3	2:C:652:MET:HE3	1.65	0.79
6:Q:61:CYS:O	6:Q:72:GLN:NE2	2.15	0.79
10:Z:37:LEU:HG	10:Z:79:LEU:HB2	1.65	0.79
1:A:1581:PHE:HE2	1:A:1585:MET:HE2	1.47	0.79
16:M:485:U:OP2	16:M:485:U:H2'	1.82	0.79
1:A:1435:LYS:NZ	1:A:1550:LEU:O	2.16	0.78
2:C:252:LEU:O	2:C:255:GLN:N	2.16	0.78
15:L:18:U:O2	19:I:206:LYS:HD2	1.84	0.78
15:L:41:C:C2	16:M:494:G:N2	2.50	0.78
1:A:1130:ARG:NH1	1:A:1133:ASP:OD2	2.17	0.78
4:O:121:GLN:NE2	5:P:49:SER:O	2.17	0.78
7:R:76:PHE:HB2	7:R:91:HIS:CD2	2.17	0.78
1:A:1082:ILE:O	1:A:1085:LYS:N	2.17	0.78
20:v:726:ARG:HH22	20:v:760:UNK:CB	1.97	0.78
16:M:483:U:H3'	16:M:484:U:C4	2.18	0.78
33:b:-5:U:O2'	33:b:-4:U:O4'	2.02	0.78
1:A:1447:TRP:HB3	1:A:1451:PHE:HE2	1.49	0.78
2:C:67:GLU:CD	2:C:68:HIS:H	1.92	0.77
2:C:163:ASP:OD2	2:C:548:ARG:NH1	2.17	0.77
15:L:1100:A:H61	15:L:1116:A:H61	1.30	0.77
1:A:1945:GLU:O	1:A:1948:MET:N	2.16	0.77
6:Q:71:CYS:HB3	6:Q:74:CYS:HB2	1.65	0.77
2:C:397:LYS:HG2	2:C:401:ARG:HH12	1.48	0.77
10:Z:421:LYS:HG3	10:Z:468:ILE:HG12	1.67	0.77
15:L:1111:U:C6	15:L:1111:U:C5'	2.65	0.77
17:c:65:PHE:CE1	17:c:101:ARG:HB2	2.20	0.77
35:f:183:TYR:CE2	35:f:234:LYS:CD	2.66	0.77
1:A:1305:SER:OG	1:A:1307:GLU:OE1	2.03	0.77
1:A:997:GLN:OE1	1:A:1511:ARG:NH2	2.17	0.77
10:Z:129:VAL:HG12	10:Z:130:ILE:HG23	1.66	0.77
16:M:484:U:O2'	16:M:485:U:O4'	2.03	0.77
1:A:353:GLU:HG2	13:D:104:G:P	2.25	0.77
2:C:123:MET:HB2	2:C:199:LEU:HD23	1.66	0.77
10:Z:61:VAL:HA	10:Z:64:THR:HB	1.66	0.77
15:L:1100:A:N1	15:L:1116:A:N1	2.33	0.77
1:A:1151:GLU:O	1:A:1155:ALA:N	2.17	0.77
3:J:6:ILE:HD11	11:B:90:A:N1	2.00	0.77
17:c:78:ARG:NH2	17:c:79:GLU:OE2	2.18	0.77
1:A:1063:PHE:HE1	1:A:1086:ASN:HD22	1.31	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:833:VAL:O	2:C:837:GLN:HB2	1.84	0.77
7:R:253:LEU:O	7:R:257:ASN:HB3	1.85	0.77
1:A:992:ASP:OD1	1:A:1085:LYS:NZ	2.18	0.77
7:R:245:GLU:HG3	7:R:249:MET:HE2	1.67	0.77
1:A:404:ASN:ND2	2:C:927:MET:SD	2.57	0.76
1:A:1362:LYS:NZ	3:J:13:GLY:O	2.18	0.76
17:c:69:GLU:HG3	17:c:93:ARG:HH21	1.48	0.76
1:A:763:MET:SD	1:A:783:LEU:HD11	2.25	0.76
1:A:1348:GLU:HG2	1:A:1446:THR:HB	1.67	0.76
2:C:969:LYS:O	2:C:972:ARG:N	2.18	0.76
4:O:127:ALA:HB3	4:O:428:GLN:HE21	1.50	0.76
1:A:1335:TRP:CH2	1:A:1339:LEU:HD13	2.20	0.76
2:C:667:GLU:OE1	2:C:667:GLU:N	2.17	0.76
17:c:68:GLU:O	17:c:72:GLN:HB2	1.85	0.76
19:I:114:THR:O	19:I:118:ASN:HB2	1.85	0.76
20:v:729:TYR:CD2	20:v:748:UNK:CB	2.69	0.76
21:n:382:SER:OG	21:n:432:VAL:HG13	1.84	0.76
1:A:1111:SER:O	1:A:1114:PHE:HB3	1.83	0.76
1:A:1315:ARG:O	1:A:1318:GLY:N	2.18	0.76
1:A:1594:GLN:O	1:A:1598:LEU:CB	2.33	0.76
1:A:1180:GLU:HA	1:A:1183:THR:HG22	1.65	0.76
1:A:1717:LEU:HB2	1:A:1786:ALA:HB3	1.67	0.76
1:A:1810:PRO:O	1:A:1813:TYR:N	2.18	0.76
7:R:69:GLN:HG2	7:R:70:LEU:H	1.48	0.76
5:P:174:ASN:OD1	5:P:185:ARG:NH1	2.18	0.76
18:d:189:TYR:HB3	18:d:205:TRP:CD1	2.21	0.76
33:b:4:U:O2'	33:b:5:U:O5'	2.03	0.76
1:A:1815:LEU:O	1:A:1818:ARG:N	2.19	0.76
16:M:502:C:O2'	16:M:503:A:OP2	2.04	0.76
1:A:1736:VAL:HG22	1:A:1775:ILE:HB	1.68	0.76
10:Z:82:LEU:O	10:Z:85:SER:HB3	1.85	0.76
2:C:132:ARG:HG3	2:C:206:LYS:HZ1	1.49	0.76
10:Z:475:GLU:OE2	10:Z:478:ARG:NH1	2.19	0.76
15:L:1109:C:H41	31:X:109:LYS:N	1.84	0.76
17:c:239:LYS:O	17:c:243:GLN:HB2	1.85	0.76
18:d:99:ILE:CG1	18:d:100:PRO:HD3	2.16	0.76
6:Q:16:CYS:SG	7:R:105:ARG:NH2	2.58	0.75
1:A:1379:MET:HE1	1:A:1620:TYR:H	1.51	0.75
2:C:315:SER:O	2:C:319:GLY:N	2.20	0.75
4:O:357:SER:OG	4:O:405:SER:OG	2.02	0.75
9:T:41:LEU:HD11	14:E:35:A:N3	1.99	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:676:GLN:N	1:A:676:GLN:OE1	2.18	0.75
1:A:984:VAL:HG12	1:A:985:ASP:H	1.51	0.75
15:L:15:C:N4	19:I:209:ARG:HB2	2.01	0.75
1:A:158:LYS:NZ	7:R:33:TRP:O	2.18	0.75
1:A:579:LEU:HD22	1:A:619:PHE:HE1	1.52	0.75
6:Q:116:LYS:NZ	17:c:220:GLU:O	2.19	0.75
1:A:1870:VAL:HB	16:M:500:A:C5'	2.17	0.75
4:O:391:GLU:HB3	4:O:400:ARG:HB2	1.66	0.75
1:A:333:LYS:O	1:A:336:PHE:N	2.19	0.75
10:Z:454:ASP:HB3	10:Z:457:HIS:HB2	1.67	0.75
6:Q:104:ALA:HB1	6:Q:110:LYS:HB3	1.69	0.75
6:Q:217:TRP:O	6:Q:221:ASP:CB	2.32	0.75
18:d:248:ASN:O	18:d:252:HIS:HB2	1.87	0.75
21:n:253:VAL:CG2	21:n:297:LEU:O	2.34	0.75
1:A:1988:LEU:HD11	35:f:180:VAL:HG12	1.67	0.75
2:C:214:ASP:OD1	2:C:215:ALA:N	2.20	0.75
1:A:670:LYS:NZ	13:D:101:C:OP1	2.19	0.75
10:Z:89:ASP:O	10:Z:93:THR:OG1	2.04	0.75
1:A:340:LYS:O	1:A:343:ASN:N	2.17	0.74
1:A:1988:LEU:CD1	35:f:180:VAL:CG1	2.53	0.74
33:b:-3:A:H4'	33:b:-2:U:OP2	1.86	0.74
1:A:716:ARG:NH2	13:D:112:C:N3	2.36	0.74
1:A:900:PHE:N	1:A:1075:ASP:OD2	2.19	0.74
2:C:117:ARG:NH2	2:C:156:ASP:O	2.20	0.74
4:O:379:LYS:HA	5:P:47:ARG:NH2	2.01	0.74
6:Q:205:PHE:HB2	6:Q:251:LEU:HB3	1.68	0.74
14:E:64:U:O2'	14:E:65:U:OP1	2.05	0.74
18:d:267:TYR:OH	18:d:310:UNK:O	2.05	0.74
1:A:1338:SER:OG	1:A:1339:LEU:N	2.19	0.74
4:O:263:VAL:HG12	4:O:264:GLY:H	1.50	0.74
9:T:120:CYS:HB2	9:T:122:CYS:HB3	1.68	0.74
10:Z:212:LEU:O	10:Z:214:ILE:N	2.20	0.74
14:E:89:U:H6	19:I:179:ARG:CG	1.99	0.74
14:E:91:A:C2	18:d:99:ILE:HD13	2.21	0.74
1:A:1377:SER:CB	11:B:95:U:OP1	2.36	0.74
4:O:229:THR:HG21	4:O:272:VAL:H	1.51	0.74
10:Z:92:GLU:O	10:Z:227:TYR:OH	2.05	0.74
10:Z:166:SER:OG	10:Z:169:THR:OG1	2.04	0.74
1:A:1122:ASP:OD1	1:A:1161:TYR:OH	2.05	0.74
1:A:1144:PHE:HE2	1:A:1145:MET:HE2	1.52	0.74
1:A:790:TRP:O	1:A:793:TRP:N	2.21	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1592:HIS:HE1	33:b:4:U:C5	2.05	0.74
18:d:189:TYR:HB3	18:d:205:TRP:HD1	1.53	0.74
22:q:173:LYS:O	22:q:174:TRP:CB	2.36	0.74
1:A:1776:GLY:O	1:A:1784:TYR:HA	1.88	0.74
14:E:91:A:N3	18:d:99:ILE:HD13	2.03	0.74
20:v:669:TYR:HE2	20:v:686:ILE:HG13	1.53	0.74
33:b:4:U:H4'	33:b:5:U:OP1	1.87	0.74
1:A:847:LYS:O	1:A:850:GLY:N	2.21	0.74
1:A:1144:PHE:HD2	1:A:1145:MET:HG2	1.50	0.74
4:O:327:CYS:SG	4:O:328:THR:N	2.61	0.74
21:n:253:VAL:HG21	21:n:297:LEU:O	1.87	0.74
1:A:796:ASN:ND2	1:A:861:GLN:OE1	2.21	0.73
2:C:360:ARG:HG2	2:C:362:LYS:HB2	1.69	0.73
4:O:125:TRP:HE1	4:O:437:GLU:CD	1.95	0.73
15:L:5:A:H5''	19:I:114:THR:HG21	1.66	0.73
15:L:15:C:H41	19:I:209:ARG:HB2	1.52	0.73
10:Z:399:MET:SD	10:Z:439:ARG:HB3	2.28	0.73
1:A:326:ASN:ND2	2:C:924:GLY:O	2.22	0.73
1:A:776:GLN:HG2	1:A:777:LYS:H	1.54	0.73
1:A:976:GLN:HE22	1:A:1310:LYS:HD3	1.53	0.73
1:A:1454:SER:HA	1:A:1487:GLY:HA2	1.69	0.73
4:O:407:PHE:CE1	4:O:414:LEU:HD13	2.22	0.73
1:A:1042:SER:OG	1:A:1043:ARG:NH1	2.20	0.73
1:A:1337:THR:CB	33:b:8:A:H62	2.01	0.73
24:F:47:GLU:HG3	32:Y:15:TYR:CB	2.18	0.73
25:G:86:ASN:HD21	26:H:32:LYS:CD	2.02	0.73
1:A:1337:THR:CB	33:b:8:A:N6	2.52	0.73
9:T:126:ARG:HG3	21:n:72:TRP:CZ2	2.24	0.73
14:E:90:U:C5	18:d:104:ARG:NH2	2.55	0.73
21:n:165:THR:OG1	21:n:445:SER:CB	2.36	0.73
10:Z:57:CYS:HB3	10:Z:94:LEU:HD13	1.69	0.73
10:Z:384:LEU:HB3	10:Z:419:PHE:HE1	1.53	0.73
15:L:1101:C:N4	31:X:38:LYS:NZ	2.36	0.73
1:A:1052:THR:O	1:A:1167:ARG:HA	1.88	0.73
1:A:1282:ASP:OD1	1:A:1283:GLU:N	2.20	0.73
1:A:1058:ALA:O	1:A:1061:ILE:N	2.17	0.73
1:A:2043:PHE:HB3	1:A:2047:GLN:HB2	1.71	0.73
10:Z:384:LEU:O	10:Z:387:PHE:N	2.22	0.73
1:A:1882:LEU:HB2	1:A:1991:ILE:HD11	1.71	0.73
18:d:261:GLU:O	18:d:265:ALA:HB2	1.89	0.73
14:E:89:U:C5	19:I:179:ARG:HB3	2.24	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:q:422:GLY:H	22:q:443:ASN:CG	1.96	0.72
1:A:269:ASP:CG	1:A:271:GLN:H	1.97	0.72
5:P:101:PRO:O	5:P:103:ASN:N	2.23	0.72
6:Q:209:ASN:HD22	6:Q:288:ILE:HA	1.54	0.72
1:A:329:TYR:CZ	2:C:919:ARG:HD2	2.24	0.72
1:A:488:ARG:NH1	13:D:81:A:H61	1.87	0.72
1:A:1526:TRP:CD1	1:A:1526:TRP:H	2.03	0.72
2:C:407:ASN:OD1	2:C:408:LEU:N	2.20	0.72
1:A:1539:LEU:O	1:A:1541:ALA:N	2.23	0.72
4:O:365:PHE:CZ	4:O:373:LEU:HD22	2.25	0.72
7:R:253:LEU:O	7:R:257:ASN:HB2	1.90	0.72
1:A:139:LEU:HG	1:A:570:GLN:HE22	1.54	0.72
6:Q:86:LEU:O	6:Q:89:HIS:N	2.21	0.72
12:N:100:G:H8	33:b:-1:A:H2'	1.52	0.72
10:Z:122:SER:HB3	10:Z:158:CYS:HB3	1.72	0.72
12:N:109:U:C6	12:N:109:U:OP2	2.43	0.72
14:E:65:U:O2'	14:E:67:C:OP2	2.07	0.72
1:A:1717:LEU:N	1:A:1786:ALA:O	2.21	0.72
1:A:1864:LYS:HE2	21:n:328:ILE:HA	1.69	0.72
2:C:317:LYS:HE2	2:C:418:GLN:HE22	1.55	0.72
25:i:86:ASN:HD21	26:h:32:LYS:CD	2.02	0.72
1:A:477:MET:HE1	2:C:278:LYS:HD3	1.71	0.72
1:A:1576:GLU:CD	1:A:1826:TYR:O	2.33	0.72
1:A:1659:GLU:O	1:A:1663:PHE:HB3	1.90	0.72
2:C:135:ASN:N	2:C:233:ASP:OD2	2.22	0.72
2:C:833:VAL:O	2:C:837:GLN:CB	2.38	0.72
1:A:488:ARG:HH11	13:D:81:A:N6	1.88	0.72
1:A:1442:ARG:NH2	10:Z:302:SER:O	2.21	0.72
1:A:992:ASP:O	1:A:995:LEU:N	2.22	0.71
2:C:234:LEU:HD23	2:C:443:TYR:HB2	1.70	0.71
2:C:317:LYS:N	36:C:1500:GTP:O6	2.18	0.71
4:O:443:ASN:O	4:O:445:ASN:ND2	2.23	0.71
5:P:84:ASN:O	5:P:125:ARG:NH1	2.18	0.71
9:T:44:LYS:O	9:T:47:GLU:N	2.22	0.71
10:Z:471:GLY:O	10:Z:478:ARG:NH2	2.23	0.71
2:C:183:GLN:NE2	2:C:654:CYS:HA	2.04	0.71
4:O:365:PHE:HZ	4:O:373:LEU:HD22	1.55	0.71
1:A:978:ILE:HD12	8:S:174:VAL:HG22	1.72	0.71
1:A:1801:SER:O	1:A:1804:THR:OG1	2.08	0.71
2:C:271:ASP:OD2	36:C:1500:GTP:N1	2.23	0.71
2:C:760:LEU:O	2:C:764:ASN:ND2	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:27:ASN:OD1	3:J:28:ASN:N	2.23	0.71
10:Z:77:SER:OG	10:Z:120:CYS:SG	2.49	0.71
18:d:198:GLN:O	18:d:201:THR:OG1	2.07	0.71
21:n:312:SER:OG	21:n:314:ASP:OD1	2.07	0.71
2:C:831:ILE:HG13	2:C:832:ASP:H	1.53	0.71
17:c:39:LEU:HD12	17:c:158:ARG:HH11	1.55	0.71
1:A:861:GLN:HE21	1:A:1097:HIS:HB3	1.54	0.71
1:A:1144:PHE:CE2	1:A:1145:MET:HE2	2.26	0.71
1:A:1902:GLN:OE1	1:A:1902:GLN:N	2.24	0.71
4:O:362:ASP:OD2	4:O:379:LYS:NZ	2.22	0.71
18:d:99:ILE:HG13	18:d:100:PRO:N	1.98	0.71
2:C:775:ILE:HG22	2:C:776:ASN:H	1.55	0.71
7:R:209:ASP:H	7:R:212:TRP:HB2	1.56	0.71
13:D:174:G:OP1	13:D:174:G:H4'	1.90	0.71
15:L:41:C:H4'	15:L:42:U:OP1	1.89	0.71
6:Q:33:GLU:OE1	6:Q:33:GLU:N	2.22	0.71
9:T:126:ARG:HG3	21:n:72:TRP:CE2	2.26	0.71
35:f:183:TYR:HE2	35:f:234:LYS:HD2	1.55	0.71
2:C:682:SER:HA	2:C:714:PRO:HG3	1.73	0.71
2:C:855:PRO:HG2	2:C:944:VAL:HG21	1.71	0.71
15:L:1116:A:C6	15:L:1117:G:C5	2.79	0.71
7:R:206:LEU:HD12	7:R:207:PRO:HD2	1.73	0.71
33:b:-5:U:O2'	33:b:-4:U:O5'	2.08	0.71
1:A:342:LEU:HD13	1:A:392:ASN:HD22	1.56	0.71
4:O:152:ASN:HD21	4:O:409:LYS:HB3	1.54	0.71
20:v:616:PRO:CG	20:v:617:PRO:N	2.53	0.71
15:L:52:A:C6	21:n:204:GLY:HA2	2.26	0.70
20:v:718:SER:OG	20:v:725:THR:CG2	2.38	0.70
8:S:8:GLN:HB2	14:E:63:G:O2'	1.91	0.70
10:Z:73:ILE:HG23	10:Z:120:CYS:HB2	1.72	0.70
10:Z:392:ILE:HG12	10:Z:397:LEU:HD22	1.73	0.70
10:Z:440:LEU:HD12	10:Z:473:LEU:HD13	1.72	0.70
1:A:771:PRO:O	4:O:309:ARG:NH2	2.24	0.70
1:A:1513:GLU:O	1:A:1516:GLN:N	2.17	0.70
21:n:55:GLU:OE2	21:n:58:ARG:CD	2.38	0.70
2:C:90:LEU:HD22	4:O:211:LEU:HD22	1.72	0.70
14:E:89:U:C6	19:I:179:ARG:HB3	2.27	0.70
1:A:688:TYR:O	1:A:691:PHE:N	2.20	0.70
2:C:719:MET:O	2:C:722:ASP:N	2.23	0.70
5:P:118:GLN:OE1	5:P:118:GLN:N	2.22	0.70
13:D:76:U:O2'	13:D:77:A:OP1	2.07	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:v:167:UNK:O	29:V:81:SER:HB3	1.91	0.70
1:A:484:PHE:CB	13:D:81:A:N7	2.55	0.70
1:A:579:LEU:HD22	1:A:619:PHE:CE1	2.25	0.70
1:A:1142:ASN:OD1	1:A:1148:LYS:NZ	2.25	0.70
7:R:254:ILE:O	7:R:258:THR:CB	2.40	0.70
18:d:227:ASP:O	18:d:231:ASN:CB	2.36	0.70
20:v:168:UNK:N	29:V:81:SER:OG	2.23	0.70
1:A:1860:VAL:HA	1:A:1873:LYS:O	1.92	0.70
5:P:134:VAL:HG22	6:Q:111:ARG:HD3	1.73	0.70
19:I:200:ASN:O	19:I:204:ASN:HB2	1.91	0.70
20:v:168:UNK:HA	29:V:81:SER:HG	1.52	0.70
6:Q:217:TRP:CD1	6:Q:218:LYS:N	2.59	0.70
10:Z:16:GLU:O	10:Z:20:MET:HB2	1.92	0.70
10:Z:39:GLU:OE2	10:Z:42:ARG:NH1	2.23	0.70
13:D:173:U:H4'	13:D:174:G:OP1	1.91	0.70
21:n:55:GLU:OE2	21:n:55:GLU:HA	1.91	0.70
33:b:4:U:O2	33:b:5:U:N3	2.24	0.69
1:A:486:PHE:O	1:A:488:ARG:N	2.24	0.69
1:A:701:CYS:SG	1:A:702:GLY:N	2.64	0.69
2:C:362:LYS:O	2:C:364:PHE:N	2.26	0.69
10:Z:103:VAL:O	10:Z:107:ASN:ND2	2.24	0.69
15:L:1116:A:C2	15:L:1117:G:C5	2.80	0.69
1:A:933:GLU:OE1	1:A:933:GLU:N	2.15	0.69
1:A:1525:PHE:HE2	33:b:8:A:N1	1.90	0.69
1:A:1590:LEU:HD21	1:A:1598:LEU:HD13	1.74	0.69
7:R:183:PHE:CE2	12:N:113:U:C5	2.80	0.69
25:G:86:ASN:HD21	26:H:32:LYS:CE	2.06	0.69
1:A:1887:GLY:HA2	1:A:1991:ILE:HD12	1.73	0.69
6:Q:67:GLN:NE2	6:Q:114:SER:O	2.25	0.69
10:Z:88:PRO:HB3	10:Z:223:HIS:CD2	2.28	0.69
16:M:489:A:H5'	21:n:245:HIS:HB2	1.73	0.69
1:A:1058:ALA:HB1	1:A:1103:LEU:HB3	1.74	0.69
10:Z:456:GLU:HA	10:Z:459:ARG:HH11	1.58	0.69
14:E:91:A:C5	19:I:97:TYR:CD1	2.81	0.69
1:A:749:ARG:NH1	14:E:76:A:OP2	2.26	0.69
2:C:787:LEU:HD12	2:C:790:LYS:HD2	1.75	0.69
15:L:1116:A:C4	15:L:1117:G:C8	2.80	0.69
20:v:601:VAL:O	20:v:604:SER:OG	2.09	0.69
28:U:30:ARG:O	28:U:47:VAL:HG23	1.92	0.69
1:A:269:ASP:OD2	1:A:272:ASP:N	2.21	0.69
1:A:709:ARG:HH22	13:D:83:C:P	2.14	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:656:LEU:HD13	2:C:670:ILE:HD13	1.74	0.69
6:Q:202:THR:OG1	6:Q:252:ARG:NE	2.19	0.69
14:E:91:A:C4	18:d:99:ILE:HD11	2.28	0.69
15:L:1102:C:O5'	15:L:1102:C:H6	1.76	0.69
33:b:4:U:H6	33:b:4:U:H5'	1.55	0.69
1:A:889:TRP:HD1	1:A:890:LEU:HG	1.58	0.69
1:A:1280:SER:OG	10:Z:348:GLU:OE1	2.10	0.69
4:O:292:LEU:HD11	4:O:304:LEU:HD11	1.74	0.69
6:Q:53:ASN:O	14:E:31:G:N1	2.26	0.69
14:E:54:U:O4	17:c:165:LYS:HE2	1.92	0.69
15:L:40:U:HO2'	15:L:41:C:H5	1.40	0.69
15:L:110:A:H2	29:V:2:LYS:HE2	1.58	0.69
15:L:118:U:H4'	15:L:119:G:OP1	1.91	0.69
15:L:119:G:OP1	15:L:119:G:H4'	1.90	0.69
15:L:119:G:N7	29:V:20:LYS:HE2	2.08	0.69
16:M:484:U:O3'	16:M:485:U:O4'	2.11	0.69
2:C:326:GLU:HG2	2:C:330:TYR:CE2	2.27	0.69
4:O:204:LYS:HE2	4:O:225:SER:HA	1.74	0.69
5:P:108:ASN:O	5:P:111:HIS:N	2.25	0.69
1:A:614:ARG:HH12	11:B:98:A:H4'	1.54	0.69
15:L:15:C:N4	19:I:209:ARG:HG2	2.08	0.69
1:A:590:TYR:OH	1:A:609:GLU:OE1	2.06	0.68
1:A:1362:LYS:HZ3	3:J:14:SER:HA	1.59	0.68
1:A:1928:GLU:OE1	35:f:234:LYS:HG2	1.94	0.68
2:C:215:ALA:HB1	2:C:225:THR:HG22	1.74	0.68
4:O:225:SER:OG	4:O:245:ASP:OD1	2.10	0.68
17:c:243:GLN:O	17:c:247:LYS:HG2	1.93	0.68
1:A:1899:TRP:HH2	1:A:1909:ALA:HA	1.56	0.68
2:C:183:GLN:HE22	2:C:654:CYS:HA	1.57	0.68
2:C:340:LYS:O	2:C:344:PHE:N	2.24	0.68
14:E:64:U:O2'	14:E:65:U:P	2.51	0.68
1:A:1972:ASP:O	1:A:1975:SER:N	2.26	0.68
25:i:86:ASN:HD21	26:h:32:LYS:CE	2.06	0.68
1:A:1924:LEU:CD2	35:f:234:LYS:HZ1	2.06	0.68
2:C:84:GLN:HE22	2:C:90:LEU:HA	1.58	0.68
2:C:706:LEU:HD21	2:C:834:MET:HE1	1.75	0.68
5:P:226:LYS:O	5:P:229:ALA:N	2.27	0.68
20:v:602:MET:HA	20:v:605:PHE:HD2	1.57	0.68
1:A:416:GLU:HG2	1:A:418:ASP:N	2.08	0.68
2:C:711:ALA:CB	2:C:819:LYS:O	2.41	0.68
5:P:148:HIS:H	18:d:131:ARG:HG3	1.59	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:110:ASP:OD1	7:R:114:ARG:N	2.19	0.68
10:Z:402:LEU:HD22	10:Z:445:LEU:HD13	1.75	0.68
13:D:174:G:N7	29:m:20:LYS:HE2	2.08	0.68
18:d:103:ILE:HA	18:d:106:ILE:HD12	1.74	0.68
1:A:768:GLU:O	4:O:309:ARG:NH1	2.25	0.68
1:A:1020:ILE:HG13	1:A:1022:PRO:HD2	1.76	0.68
1:A:1656:LYS:HD3	1:A:1949:LEU:HD12	1.76	0.68
1:A:1889:LEU:HB2	1:A:1989:PHE:HB2	1.76	0.68
1:A:1905:LEU:HA	1:A:1908:LEU:HB3	1.75	0.68
2:C:101:GLN:HA	2:C:104:THR:O	1.93	0.68
2:C:168:VAL:HG21	2:C:175:LEU:HB2	1.76	0.68
7:R:54:GLN:HB2	7:R:58:HIS:CD2	2.28	0.68
2:C:67:GLU:HB3	2:C:69:PRO:HD2	1.74	0.68
2:C:736:ASP:OD1	2:C:737:ILE:N	2.27	0.68
2:C:775:ILE:N	2:C:818:TYR:O	2.26	0.68
10:Z:437:GLN:HG2	10:Z:473:LEU:HD21	1.76	0.68
1:A:151:SER:OG	1:A:152:LYS:N	2.24	0.68
1:A:1711:VAL:HG21	1:A:1771:THR:HG21	1.76	0.68
2:C:122:TYR:OH	2:C:126:MET:HE2	1.92	0.68
2:C:355:HIS:HD2	2:C:360:ARG:HB3	1.59	0.68
2:C:858:LEU:HD22	2:C:937:TRP:HB3	1.74	0.68
15:L:39:A:H2'	15:L:40:U:H5'	1.75	0.68
1:A:618:SER:OG	1:A:725:TYR:HB3	1.93	0.68
1:A:940:ILE:O	1:A:943:ALA:N	2.26	0.68
15:L:15:C:N4	19:I:209:ARG:CG	2.53	0.68
15:L:120:G:C2	25:G:33:GLU:HG3	2.29	0.68
1:A:1842:GLU:OE1	1:A:1845:ASN:ND2	2.24	0.68
4:O:206:VAL:HG21	4:O:241:THR:HG21	1.74	0.68
26:h:74:ARG:NH1	30:g:65:CYS:SG	2.66	0.68
1:A:426:PRO:HB3	10:Z:201:ARG:HE	1.59	0.67
1:A:934:ARG:NH2	15:L:30:A:H5'	2.05	0.67
1:A:1338:SER:O	1:A:1341:SER:OG	2.04	0.67
1:A:1340:ILE:HD11	1:A:1400:ILE:HD12	1.76	0.67
1:A:1449:ASN:O	1:A:1452:LEU:N	2.28	0.67
4:O:284:SER:HB2	4:O:311:VAL:HB	1.77	0.67
6:Q:258:LEU:O	6:Q:262:PHE:CB	2.42	0.67
1:A:1161:TYR:HD1	1:A:1170:MET:HG2	1.60	0.67
4:O:118:LEU:HD21	5:P:48:GLN:HB3	1.76	0.67
20:v:709:TRP:HA	20:v:712:CYS:SG	2.34	0.67
1:A:895:PHE:HE2	1:A:1073:ILE:HG13	1.57	0.67
1:A:2041:PRO:HG2	1:A:2043:PHE:CZ	2.29	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:135:ASN:O	2:C:233:ASP:N	2.27	0.67
2:C:145:GLY:O	2:C:148:SER:OG	2.12	0.67
13:D:75:A:H4'	13:D:76:U:C5'	2.21	0.67
13:D:174:G:C5'	30:g:99:ASP:HB2	2.25	0.67
15:L:1116:A:C4	15:L:1117:G:N7	2.63	0.67
17:c:224:MET:HE3	17:c:225:PRO:HD2	1.77	0.67
22:o:51:VAL:HG11	22:p:20:ARG:CB	2.25	0.67
1:A:783:LEU:O	1:A:786:LEU:N	2.26	0.67
2:C:701:GLU:HG2	2:C:703:LEU:H	1.60	0.67
7:R:208:SER:HA	7:R:212:TRP:CG	2.29	0.67
20:v:504:UNK:O	20:v:508:UNK:N	2.26	0.67
22:q:20:ARG:CB	22:r:53:ILE:HA	2.24	0.67
22:q:306:ASP:CG	22:q:308:ARG:H	2.03	0.67
26:H:74:ARG:NH1	30:W:65:CYS:SG	2.66	0.67
1:A:1169:TYR:CE2	1:A:1262:MET:HG2	2.29	0.67
1:A:1443:TYR:OH	1:A:1545:ASP:OD2	2.09	0.67
2:C:383:LYS:O	2:C:387:TYR:HB2	1.94	0.67
13:D:175:G:C2	25:i:33:GLU:HG3	2.29	0.67
1:A:1592:HIS:CE1	33:b:4:U:C5	2.82	0.67
2:C:307:ILE:HA	2:C:324:ILE:HD11	1.76	0.67
4:O:116:GLU:HG3	18:d:235:LEU:CD1	2.25	0.67
10:Z:319:ASN:HA	10:Z:322:LYS:HD3	1.74	0.67
1:A:269:ASP:OD1	1:A:270:SER:N	2.28	0.67
1:A:1414:TRP:O	1:A:1417:GLN:N	2.23	0.67
1:A:1663:PHE:O	1:A:1666:CYS:HB3	1.95	0.67
1:A:1682:THR:OG1	1:A:1702:THR:OG1	2.11	0.67
2:C:576:THR:HG22	2:C:592:PHE:HD2	1.60	0.67
7:R:146:LEU:HD23	7:R:147:ASN:H	1.60	0.67
10:Z:301:SER:O	10:Z:302:SER:OG	2.13	0.67
21:n:68:PRO:HD2	21:n:69:TRP:HE3	1.53	0.67
1:A:1279:VAL:O	1:A:1299:LYS:NZ	2.27	0.67
1:A:1864:LYS:HE2	21:n:328:ILE:CA	2.24	0.67
1:A:1893:ILE:HB	1:A:1985:GLN:H	1.59	0.67
2:C:355:HIS:CD2	2:C:360:ARG:HB3	2.30	0.67
4:O:285:SER:OG	4:O:287:ASP:OD1	2.13	0.67
6:Q:39:LEU:HD11	6:Q:111:ARG:HG3	1.75	0.67
8:S:8:GLN:NE2	8:S:10:GLU:O	2.28	0.67
15:L:119:G:C5'	30:W:99:ASP:HB2	2.25	0.67
4:O:377:ASP:OD2	4:O:380:SER:N	2.27	0.67
9:T:151:ARG:C	21:n:63:ARG:HH12	2.03	0.67
19:I:196:ILE:H	19:I:200:ASN:HD22	1.42	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:129:ILE:HG22	2:C:131:GLU:H	1.59	0.67
7:R:87:CYS:HB3	7:R:91:HIS:HE1	1.56	0.67
8:S:35:THR:OG1	13:D:109:A:OP1	2.13	0.67
16:M:485:U:O2'	16:M:486:A:N7	2.27	0.67
1:A:1445:THR:OG1	1:A:1450:GLU:OE2	2.13	0.66
6:Q:9:PRO:HB2	6:Q:10:PRO:HD2	1.76	0.66
2:C:795:ILE:HG23	2:C:842:MET:HE3	1.77	0.66
4:O:358:ILE:HG22	4:O:359:ASN:H	1.59	0.66
10:Z:317:ILE:HD13	10:Z:325:VAL:HG21	1.75	0.66
1:A:572:CYS:SG	1:A:630:LYS:HD3	2.36	0.66
1:A:1034:ASN:ND2	1:A:1289:VAL:O	2.21	0.66
7:R:254:ILE:O	7:R:258:THR:HB	1.95	0.66
10:Z:301:SER:OG	10:Z:311:LYS:NZ	2.28	0.66
10:Z:386:LYS:O	10:Z:389:GLY:N	2.28	0.66
1:A:676:GLN:HE21	1:A:714:PHE:HB2	1.60	0.66
1:A:1762:ASP:OD1	1:A:1763:ASN:N	2.29	0.66
2:C:703:LEU:O	2:C:705:GLY:N	2.28	0.66
4:O:320:GLU:OE2	5:P:55:VAL:N	2.21	0.66
7:R:180:ASN:HB2	12:N:111:U:C5	2.31	0.66
15:L:15:C:O2'	15:L:16:U:O4'	2.13	0.66
17:c:220:GLU:OE2	18:d:82:ARG:NH2	2.28	0.66
35:f:169:HIS:CE1	35:f:195:ILE:H	2.13	0.66
1:A:1857:VAL:HG13	1:A:1894:ILE:HD13	1.78	0.66
1:A:1914:ALA:HB2	1:A:1943:PRO:HB2	1.78	0.66
1:A:1928:GLU:OE2	35:f:238:THR:HG22	1.94	0.66
7:R:8:SER:HA	7:R:61:LYS:HB3	1.77	0.66
9:T:118:SER:HB2	9:T:119:THR:HG23	1.77	0.66
10:Z:479:SER:O	10:Z:482:THR:OG1	2.13	0.66
13:D:44:A:O2'	13:D:45:A:OP2	2.10	0.66
17:c:214:ASN:HD21	18:d:44:ARG:HD2	1.60	0.66
18:d:248:ASN:O	18:d:252:HIS:CB	2.44	0.66
20:v:729:TYR:CG	20:v:748:UNK:CB	2.79	0.66
29:V:82:LEU:HD12	29:V:85:ILE:HD11	1.77	0.66
1:A:1067:ASN:O	1:A:1071:ARG:HG2	1.95	0.66
15:L:18:U:C6	19:I:202:GLN:CG	2.79	0.66
22:q:348:TYR:CB	22:q:377:ILE:CB	2.74	0.66
1:A:128:TYR:HA	9:T:112:ASN:ND2	2.10	0.66
1:A:934:ARG:HH22	15:L:30:A:C5'	2.04	0.66
1:A:1990:ASN:ND2	1:A:1993:ASP:O	2.28	0.66
2:C:274:ILE:HG12	2:C:275:LEU:HD12	1.78	0.66
2:C:636:VAL:HG12	2:C:637:GLU:H	1.59	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:101:GLN:HE22	13:D:75:A:H61	1.43	0.66
22:q:20:ARG:CB	22:r:52:GLU:O	2.43	0.66
1:A:905:TYR:HE2	1:A:907:ASN:HB2	1.60	0.66
1:A:1870:VAL:HB	16:M:500:A:H5''	1.76	0.66
17:c:163:GLN:HB3	17:c:167:ALA:HB3	1.78	0.66
1:A:834:ILE:HG12	1:A:840:VAL:HG11	1.78	0.66
1:A:960:THR:O	1:A:962:ARG:NH1	2.29	0.66
1:A:1393:GLU:OE1	1:A:1393:GLU:N	2.23	0.66
7:R:183:PHE:CD2	12:N:113:U:C6	2.84	0.66
17:c:68:GLU:O	17:c:72:GLN:CB	2.43	0.66
17:c:185:LEU:O	17:c:188:ARG:N	2.29	0.66
22:q:463:SER:O	22:q:464:ALA:HB3	1.96	0.66
1:A:402:TRP:HE1	1:A:405:ASN:ND2	1.94	0.65
1:A:634:ASP:O	1:A:637:VAL:N	2.29	0.65
2:C:779:LEU:HD12	2:C:782:GLU:HB2	1.78	0.65
2:C:829:VAL:HG12	2:C:830:ASN:H	1.61	0.65
4:O:148:ASP:OD1	4:O:150:VAL:N	2.22	0.65
4:O:187:ASP:OD1	4:O:188:VAL:N	2.27	0.65
15:L:39:A:H2'	15:L:40:U:H5''	1.75	0.65
17:c:204:LYS:HG2	17:c:205:LYS:H	1.59	0.65
1:A:220:THR:O	1:A:224:MET:HG2	1.96	0.65
1:A:374:ILE:HG21	2:C:966:PHE:HE1	1.59	0.65
1:A:477:MET:CE	2:C:278:LYS:HD3	2.26	0.65
1:A:585:ARG:HB2	7:R:33:TRP:CE3	2.31	0.65
1:A:1286:TRP:NE1	1:A:1348:GLU:OE1	2.30	0.65
7:R:46:ARG:NE	12:N:110:A:H2	1.91	0.65
13:D:165:A:H2	29:m:2:LYS:HE2	1.58	0.65
14:E:56:A:O2'	14:E:57:U:OP1	2.13	0.65
14:E:91:A:N3	18:d:99:ILE:CD1	2.60	0.65
25:G:77:LEU:HD21	25:G:80:ILE:HD12	1.79	0.65
2:C:130:PRO:HG2	2:C:558:LYS:NZ	2.10	0.65
6:Q:89:HIS:CD2	7:R:242:LEU:HD21	2.31	0.65
18:d:209:GLU:O	18:d:213:GLY:N	2.19	0.65
1:A:217:TRP:HZ3	1:A:703:PHE:HA	1.61	0.65
1:A:713:ASN:O	1:A:716:ARG:N	2.30	0.65
1:A:784:GLN:NE2	15:L:20:G:H5''	2.11	0.65
6:Q:53:ASN:OD1	6:Q:54:ASN:N	2.29	0.65
14:E:49:A:O2'	14:E:50:G:H5'	1.96	0.65
1:A:180:PRO:HA	1:A:187:LYS:HE2	1.79	0.65
1:A:295:GLY:O	1:A:298:TYR:N	2.25	0.65
1:A:687:ILE:HD11	1:A:706:PRO:HG2	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1330:LYS:CD	33:b:6:U:OP1	2.43	0.65
21:n:60:ARG:O	21:n:62:THR:N	2.29	0.65
35:f:184:MET:HA	35:f:184:MET:HE3	1.79	0.65
1:A:353:GLU:CG	13:D:104:G:P	2.85	0.65
9:T:46:ASN:OD1	9:T:47:GLU:N	2.30	0.65
10:Z:113:SER:O	10:Z:117:ILE:HG12	1.97	0.65
29:m:82:LEU:HD12	29:m:85:ILE:HD11	1.77	0.65
1:A:1498:ASP:O	1:A:1501:THR:OG1	2.08	0.65
1:A:1561:LEU:O	1:A:1564:GLY:N	2.20	0.65
1:A:1850:LEU:HD13	1:A:1930:PRO:HB3	1.78	0.65
4:O:201:SER:OG	4:O:202:GLU:N	2.29	0.65
6:Q:258:LEU:O	6:Q:262:PHE:HB2	1.96	0.65
25:i:77:LEU:HD21	25:i:80:ILE:HD12	1.79	0.65
1:A:177:GLU:HB3	1:A:712:LEU:HD11	1.78	0.65
1:A:430:PRO:O	10:Z:182:GLN:NE2	2.22	0.65
1:A:1682:THR:O	1:A:1702:THR:OG1	2.15	0.65
1:A:1870:VAL:HG23	16:M:499:U:O2'	1.96	0.65
7:R:72:PHE:CD1	7:R:90:LEU:HB2	2.32	0.65
20:v:167:UNK:O	29:V:81:SER:CB	2.44	0.65
21:n:163:GLU:CB	21:n:183:ASN:HB3	2.27	0.65
1:A:725:TYR:CD1	14:E:72:C:C1'	2.80	0.65
1:A:1090:ILE:HD11	1:A:1104:ILE:HD11	1.77	0.65
1:A:2077:THR:HA	1:A:2080:LYS:HG2	1.77	0.65
4:O:230:VAL:HG22	4:O:241:THR:HG22	1.79	0.65
1:A:1082:ILE:HD13	1:A:1113:ILE:HD11	1.79	0.65
4:O:307:HIS:HD1	4:O:327:CYS:HB2	1.62	0.65
4:O:340:SER:OG	4:O:341:LEU:N	2.29	0.65
8:S:7:PRO:O	8:S:8:GLN:HB3	1.95	0.65
10:Z:307:GLU:OE2	10:Z:311:LYS:HE3	1.97	0.65
35:f:183:TYR:CZ	35:f:234:LYS:HD2	2.32	0.65
1:A:676:GLN:O	1:A:680:CYS:N	2.18	0.64
1:A:1113:ILE:O	1:A:1116:TYR:HB3	1.97	0.64
1:A:1843:LEU:O	1:A:1849:LYS:HD2	1.96	0.64
1:A:1928:GLU:OE2	35:f:238:THR:CG2	2.45	0.64
6:Q:242:VAL:O	7:R:161:ARG:NH2	2.30	0.64
7:R:47:PHE:CZ	14:E:37:U:N3	2.65	0.64
7:R:64:GLY:O	7:R:68:GLY:N	2.30	0.64
20:v:722:PRO:O	20:v:725:THR:OG1	2.15	0.64
24:F:98:GLU:C	32:Y:53:PRO:CB	2.70	0.64
1:A:2013:ARG:HB3	1:A:2059:ILE:HD11	1.77	0.64
6:Q:77:ASP:OD1	6:Q:78:SER:N	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:929:LEU:O	1:A:934:ARG:NH1	2.31	0.64
1:A:1232:SER:HB2	8:S:135:ARG:NH2	2.12	0.64
1:A:1882:LEU:HB3	1:A:1889:LEU:HD23	1.79	0.64
12:N:104:G:C6	14:E:49:A:N1	2.65	0.64
4:O:414:LEU:HB3	4:O:426:TRP:HB2	1.80	0.64
9:T:101:GLU:OE1	14:E:1:G:O2'	2.14	0.64
16:M:500:A:H2'	16:M:502:C:H5	1.62	0.64
5:P:105:LEU:HD21	6:Q:12:ILE:HB	1.78	0.64
7:R:127:ILE:CB	14:E:39:G:N7	2.59	0.64
9:T:88:ASP:CG	9:T:91:LEU:H	2.05	0.64
1:A:563:ASP:OD1	1:A:564:TRP:N	2.30	0.64
1:A:954:ILE:HG12	1:A:991:THR:HG22	1.80	0.64
1:A:1296:ARG:NH2	10:Z:426:GLU:OE2	2.30	0.64
1:A:1587:PHE:CE2	15:L:31:A:O5'	2.40	0.64
1:A:1750:ARG:O	1:A:1754:ALA:CB	2.46	0.64
7:R:89:TYR:CG	14:E:34:A:C2	2.84	0.64
2:C:272:ARG:HG3	36:C:1500:GTP:N2	2.13	0.64
6:Q:34:CYS:HB3	6:Q:36:ILE:H	1.62	0.64
1:A:1001:TYR:OH	1:A:1005:GLN:NE2	2.31	0.64
1:A:1792:ASN:OD1	1:A:1793:GLY:N	2.31	0.64
12:N:104:G:C6	14:E:49:A:C2	2.86	0.64
16:M:485:U:H4'	16:M:486:A:OP1	1.98	0.64
2:C:701:GLU:OE1	2:C:706:LEU:N	2.30	0.64
7:R:175:TYR:OH	7:R:180:ASN:OD1	2.16	0.64
20:v:724:VAL:C	20:v:727:GLU:CG	2.71	0.64
26:h:77:ASN:OD1	30:g:49:ARG:HD3	1.97	0.64
1:A:1488:ILE:HG23	1:A:1489:PRO:CD	2.24	0.64
1:A:1525:PHE:CE2	33:b:8:A:N1	2.66	0.64
2:C:77:LEU:HD11	4:O:135:ILE:HG12	1.81	0.64
4:O:392:MET:HG3	4:O:393:VAL:H	1.63	0.64
14:E:88:U:O2'	15:L:17:U:OP2	2.10	0.64
18:d:54:TYR:O	18:d:57:TYR:N	2.31	0.64
19:I:187:LYS:HA	19:I:201:LYS:HZ1	1.61	0.64
21:n:395:GLY:O	21:n:396:ARG:CB	2.46	0.64
1:A:1365:THR:HG22	1:A:1429:MET:HE3	1.80	0.63
1:A:1716:LEU:N	1:A:1719:GLU:OE1	2.30	0.63
26:H:77:ASN:OD1	30:W:49:ARG:HD3	1.97	0.63
1:A:353:GLU:HG2	13:D:104:G:OP1	1.97	0.63
1:A:644:VAL:HG12	1:A:648:GLN:HB2	1.80	0.63
1:A:1154:LYS:HA	1:A:1159:ARG:NH2	2.13	0.63
6:Q:13:CYS:SG	6:Q:17:LEU:N	2.71	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Q:89:HIS:O	6:Q:92:SER:OG	2.10	0.63
17:c:224:MET:SD	18:d:124:ARG:NH1	2.72	0.63
23:t:81:ASP:CB	23:t:85:THR:OG1	2.46	0.63
1:A:209:ILE:HG23	1:A:301:TRP:CD1	2.34	0.63
1:A:2014:ALA:HB3	1:A:2055:MET:HE3	1.79	0.63
2:C:817:GLN:HE21	2:C:819:LYS:HE3	1.63	0.63
21:n:380:HIS:CG	21:n:381:SER:N	2.66	0.63
1:A:1377:SER:HB3	11:B:95:U:OP1	1.97	0.63
1:A:1777:ILE:HA	1:A:1783:MET:O	1.98	0.63
7:R:44:ASN:OD1	7:R:45:THR:N	2.31	0.63
10:Z:80:ILE:O	10:Z:84:ASN:N	2.21	0.63
18:d:143:GLU:HG3	18:d:151:ILE:HG21	1.80	0.63
20:v:602:MET:HA	20:v:605:PHE:CD2	2.33	0.63
35:f:136:PHE:CE2	35:f:140:LYS:HD2	2.34	0.63
1:A:407:VAL:HG23	2:C:927:MET:HE2	1.81	0.63
1:A:1797:LEU:O	1:A:1801:SER:OG	2.15	0.63
2:C:398:ASN:OD1	2:C:401:ARG:NH2	2.31	0.63
2:C:946:ASP:HB3	2:C:949:ALA:HB2	1.79	0.63
13:D:83:C:O2'	13:D:84:A:O5'	2.15	0.63
15:L:14:C:OP2	19:I:209:ARG:NH2	2.32	0.63
20:v:611:THR:CB	20:v:623:LEU:HD13	2.29	0.63
33:b:6:U:O2'	33:b:7:U:H5'	1.97	0.63
1:A:725:TYR:HD1	14:E:72:C:O4'	1.82	0.63
1:A:1775:ILE:HG12	1:A:1786:ALA:HB2	1.81	0.63
6:Q:256:SER:C	6:Q:259:GLY:H	2.06	0.63
7:R:15:GLU:HA	7:R:18:LEU:HG	1.81	0.63
10:Z:186:LEU:HD23	10:Z:190:LEU:HD22	1.81	0.63
15:L:1107:C:H6	15:L:1107:C:H5'	1.63	0.63
16:M:483:U:H5''	16:M:484:U:OP2	1.98	0.63
1:A:239:PHE:CD1	1:A:241:PRO:HD3	2.34	0.63
1:A:828:HIS:CE1	8:S:166:HIS:HD1	2.17	0.63
2:C:717:SER:O	2:C:721:GLN:HB2	1.99	0.63
4:O:242:ALA:HB2	4:O:248:ILE:HA	1.79	0.63
4:O:325:SER:HB3	4:O:334:TRP:HE1	1.62	0.63
7:R:97:GLU:O	7:R:100:GLY:N	2.32	0.63
10:Z:100:LEU:HB2	10:Z:233:ASP:CG	2.23	0.63
1:A:314:LEU:O	1:A:317:PRO:HD2	1.99	0.63
1:A:676:GLN:NE2	1:A:714:PHE:HB2	2.13	0.63
1:A:2070:ASN:OD1	1:A:2071:ILE:N	2.32	0.63
2:C:317:LYS:HB2	36:C:1500:GTP:C6	2.34	0.63
4:O:156:ILE:HG12	4:O:166:VAL:HG22	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:308:LYS:HA	5:P:148:HIS:HE1	1.63	0.63
10:Z:178:ARG:NH2	10:Z:182:GLN:OE1	2.31	0.63
1:A:784:GLN:NE2	15:L:20:G:C5'	2.61	0.63
1:A:1592:HIS:CE1	33:b:4:U:C6	2.82	0.63
2:C:85:SER:O	2:C:88:THR:OG1	2.13	0.63
2:C:448:LEU:O	2:C:451:ASN:N	2.31	0.63
4:O:212:GLU:OE1	8:S:38:LYS:NZ	2.27	0.63
11:B:88:U:H2'	11:B:89:A:H4'	1.81	0.63
14:E:85:C:O4'	14:E:85:C:OP1	2.17	0.63
1:A:296:THR:CG2	13:D:33:U:OP2	2.47	0.62
2:C:743:ASN:HB3	2:C:746:LYS:HB3	1.81	0.62
1:A:1105:ARG:O	1:A:1110:ALA:HB3	1.99	0.62
1:A:1626:GLN:HE21	1:A:1631:GLY:HA2	1.64	0.62
2:C:269:LYS:HG2	36:C:1500:GTP:C6	2.34	0.62
10:Z:433:LEU:O	10:Z:437:GLN:HG3	1.99	0.62
1:A:1157:PRO:HG3	8:S:127:TRP:CE2	2.34	0.62
1:A:1924:LEU:HD21	35:f:234:LYS:HZ1	1.64	0.62
4:O:357:SER:HB2	4:O:365:PHE:HB3	1.80	0.62
5:P:34:ILE:HG23	5:P:35:ALA:H	1.64	0.62
7:R:124:MET:HE3	7:R:227:ASN:ND2	2.14	0.62
10:Z:18:TRP:CZ2	10:Z:22:ARG:HD3	2.34	0.62
15:L:50:U:H2'	15:L:51:C:C6	2.34	0.62
15:L:1098:C:O5'	15:L:1098:C:H6	1.83	0.62
9:T:151:ARG:HB2	21:n:63:ARG:NH1	2.14	0.62
10:Z:386:LYS:HG2	10:Z:426:GLU:HB2	1.81	0.62
18:d:140:LEU:O	18:d:143:GLU:N	2.31	0.62
1:A:452:PHE:CZ	2:C:347:ARG:HG3	2.34	0.62
1:A:1289:VAL:HA	1:A:1295:GLN:O	1.99	0.62
1:A:1566:GLY:HA3	1:A:1816:ARG:HE	1.64	0.62
2:C:840:PRO:O	2:C:843:LYS:HB3	2.00	0.62
10:Z:88:PRO:HB3	10:Z:223:HIS:CG	2.33	0.62
10:Z:446:ASP:O	10:Z:449:PHE:N	2.32	0.62
14:E:91:A:N7	19:I:97:TYR:CD1	2.67	0.62
16:M:500:A:C4	16:M:502:C:N4	2.67	0.62
1:A:1852:VAL:HA	1:A:1881:THR:HG22	1.80	0.62
2:C:946:ASP:H	2:C:964:ARG:HD3	1.64	0.62
4:O:379:LYS:HD3	5:P:47:ARG:NH2	2.14	0.62
10:Z:161:LYS:HE2	10:Z:165:VAL:HG23	1.81	0.62
10:Z:287:ASN:O	10:Z:290:GLU:HB3	2.00	0.62
13:D:174:G:O5'	26:h:76:ASN:ND2	2.32	0.62
14:E:42:A:O2'	14:E:43:C:OP1	2.17	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:I:164:LEU:O	19:I:167:SER:OG	2.17	0.62
1:A:475:ASP:O	1:A:478:SER:N	2.26	0.62
1:A:1852:VAL:HB	1:A:1935:VAL:HG22	1.81	0.62
3:J:22:ARG:NH1	3:J:23:SER:O	2.33	0.62
4:O:223:HIS:CE1	4:O:249:LYS:HD2	2.35	0.62
10:Z:374:GLU:HA	10:Z:415:GLN:OE1	1.98	0.62
14:E:89:U:H6	19:I:179:ARG:CB	2.12	0.62
15:L:119:G:O5'	26:H:76:ASN:ND2	2.32	0.62
17:c:94:PRO:HG2	17:c:97:VAL:HB	1.81	0.62
17:c:184:GLU:O	17:c:187:LYS:HB2	1.99	0.62
4:O:420:ASP:O	8:S:158:ASN:ND2	2.32	0.62
7:R:81:CYS:SG	14:E:35:A:N6	2.70	0.62
15:L:1099:G:C8	15:L:1100:A:C8	2.87	0.62
1:A:900:PHE:HA	1:A:1078:ILE:HD11	1.81	0.62
1:A:1150:LYS:HB3	1:A:1154:LYS:NZ	2.15	0.62
2:C:706:LEU:HD23	2:C:825:VAL:HA	1.80	0.62
10:Z:15:ARG:O	10:Z:19:GLU:HB2	2.00	0.62
6:Q:215:PRO:CG	6:Q:217:TRP:CD2	2.82	0.62
9:T:81:LEU:O	9:T:84:GLU:N	2.31	0.62
15:L:1120:G:H5''	15:L:1120:G:H8	1.65	0.62
33:b:2:U:O3'	33:b:4:U:OP2	2.17	0.62
1:A:713:ASN:HD22	13:D:83:C:H4'	1.62	0.61
1:A:1212:ARG:HG2	1:A:1213:MET:H	1.64	0.61
10:Z:8:ASP:OD1	10:Z:9:GLU:N	2.32	0.61
10:Z:355:ARG:O	10:Z:358:GLN:N	2.33	0.61
1:A:2022:ALA:HB1	1:A:2055:MET:HE1	1.81	0.61
1:A:2026:LEU:HB3	1:A:2041:PRO:HG3	1.82	0.61
2:C:136:VAL:HA	2:C:234:LEU:O	1.99	0.61
2:C:195:GLY:HA3	2:C:545:LEU:HD13	1.82	0.61
7:R:161:ARG:HG2	7:R:173:ILE:HD12	1.82	0.61
9:T:156:THR:O	21:n:60:ARG:NH1	2.32	0.61
18:d:115:ILE:O	18:d:118:ALA:N	2.33	0.61
1:A:705:GLN:NE2	1:A:709:ARG:HG3	2.14	0.61
1:A:1476:ALA:HB3	1:A:1479:GLU:HG2	1.83	0.61
2:C:829:VAL:O	2:C:830:ASN:ND2	2.34	0.61
7:R:75:PHE:O	7:R:81:CYS:N	2.34	0.61
13:D:174:G:H5''	30:g:99:ASP:HB2	1.82	0.61
16:M:495:A:C8	16:M:496:U:C5	2.88	0.61
2:C:798:GLY:HA2	2:C:839:ILE:HG23	1.82	0.61
7:R:161:ARG:O	7:R:165:SER:OG	2.18	0.61
14:E:89:U:C6	19:I:179:ARG:CB	2.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:m:3:LEU:HD11	30:g:60:ALA:HB1	1.82	0.61
28:U:20:SER:OG	28:U:30:ARG:HD2	2.01	0.61
35:f:169:HIS:HE1	35:f:195:ILE:H	1.47	0.61
1:A:815:TYR:O	1:A:818:SER:N	2.33	0.61
1:A:1051:GLU:O	1:A:1246:ALA:HA	2.00	0.61
2:C:142:LEU:HD12	2:C:929:GLN:HE21	1.65	0.61
2:C:500:ARG:NH1	2:C:536:SER:OG	2.34	0.61
2:C:716:ASP:CG	2:C:719:MET:H	2.09	0.61
3:J:17:SER:O	11:B:91:A:H4'	2.00	0.61
25:i:86:ASN:ND2	26:h:32:LYS:HD3	2.13	0.61
1:A:790:TRP:CD1	1:A:819:LYS:HZ3	2.18	0.61
1:A:1372:LYS:HG2	1:A:1383:PHE:CD2	2.35	0.61
2:C:79:GLU:OE1	4:O:174:LEU:N	2.34	0.61
10:Z:14:GLN:NE2	10:Z:245:CYS:HB2	2.16	0.61
10:Z:73:ILE:HA	10:Z:76:LEU:HD12	1.82	0.61
12:N:108:U:C4'	12:N:109:U:OP2	2.48	0.61
15:L:18:U:C6	19:I:202:GLN:HG2	2.36	0.61
15:L:25:A:C2	17:c:31:HIS:O	2.54	0.61
20:v:724:VAL:CA	20:v:727:GLU:CG	2.79	0.61
1:A:258:ILE:HG12	1:A:641:LEU:HA	1.83	0.61
1:A:281:TYR:O	9:T:8:ARG:NH2	2.34	0.61
1:A:430:PRO:HB3	10:Z:198:PHE:HD2	1.65	0.61
1:A:585:ARG:HD3	7:R:33:TRP:CD2	2.36	0.61
1:A:780:ARG:HH12	8:S:9:LEU:HD22	1.65	0.61
1:A:1576:GLU:OE2	1:A:1826:TYR:O	2.18	0.61
6:Q:103:GLU:HG2	6:Q:104:ALA:HB3	1.83	0.61
16:M:502:C:O2'	16:M:503:A:P	2.59	0.61
35:f:95:ILE:H	35:f:171:GLN:HE22	1.49	0.61
1:A:1340:ILE:O	1:A:1344:THR:OG1	2.16	0.61
2:C:415:TYR:HB2	2:C:420:PHE:HB2	1.82	0.61
6:Q:103:GLU:OE1	7:R:131:ARG:NH1	2.32	0.61
7:R:173:ILE:HG12	7:R:184:VAL:HG13	1.82	0.61
13:D:175:G:N7	26:h:32:LYS:HD2	2.15	0.61
17:c:148:GLU:HG2	17:c:151:MET:HE3	1.83	0.61
1:A:934:ARG:HD2	15:L:31:A:C5	2.36	0.61
1:A:1988:LEU:CG	35:f:180:VAL:HG12	2.27	0.61
4:O:125:TRP:HE1	4:O:437:GLU:CG	2.14	0.61
15:L:120:G:N7	26:H:32:LYS:HD2	2.15	0.61
21:n:357:ASP:CG	21:n:358:ASN:H	2.09	0.61
1:A:353:GLU:HG2	13:D:104:G:O5'	2.01	0.61
1:A:905:TYR:CE2	1:A:907:ASN:HB2	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1667:GLN:O	1:A:1670:ASP:N	2.33	0.61
2:C:137:GLY:O	2:C:235:VAL:HA	2.01	0.61
2:C:802:ALA:HB2	2:C:843:LYS:HA	1.83	0.61
2:C:901:GLU:OE2	2:C:903:ARG:NE	2.31	0.61
5:P:127:VAL:HG11	14:E:32:U:O4	2.00	0.61
6:Q:213:SER:OG	7:R:237:ARG:NE	2.33	0.61
7:R:76:PHE:O	7:R:79:GLY:N	2.23	0.61
7:R:152:LYS:HG2	7:R:154:ALA:H	1.66	0.61
10:Z:15:ARG:O	10:Z:19:GLU:CB	2.49	0.61
14:E:56:A:O2'	14:E:57:U:P	2.59	0.61
15:L:119:G:OP2	26:H:76:ASN:CB	2.49	0.61
1:A:608:LYS:NZ	14:E:43:C:H5'	2.16	0.60
1:A:744:THR:O	1:A:749:ARG:NH2	2.34	0.60
1:A:782:ILE:HA	1:A:785:HIS:HD2	1.66	0.60
1:A:890:LEU:O	1:A:894:SER:N	2.33	0.60
1:A:1386:ALA:O	1:A:1390:THR:HG23	2.02	0.60
1:A:1899:TRP:HB3	1:A:1905:LEU:HD21	1.83	0.60
10:Z:40:SER:O	10:Z:44:LEU:CB	2.49	0.60
15:L:1116:A:N1	15:L:1117:G:C6	2.68	0.60
21:n:54:SER:O	21:n:58:ARG:HG2	2.01	0.60
22:q:178:LYS:CB	22:q:468:GLN:CB	2.79	0.60
15:L:15:C:O2'	15:L:16:U:H5''	2.01	0.60
1:A:304:ASP:OD1	1:A:305:LEU:N	2.32	0.60
1:A:1712:SER:HB3	1:A:1724:PHE:HA	1.81	0.60
7:R:46:ARG:CZ	12:N:110:A:C2	2.84	0.60
7:R:75:PHE:CZ	14:E:35:A:O2'	2.54	0.60
7:R:254:ILE:O	7:R:258:THR:OG1	2.16	0.60
15:L:52:A:N6	21:n:204:GLY:HA2	2.16	0.60
1:A:137:GLU:HB3	9:T:52:ILE:HD13	1.81	0.60
1:A:288:GLU:OE1	1:A:288:GLU:N	2.35	0.60
1:A:484:PHE:CG	13:D:81:A:N7	2.70	0.60
6:Q:219:ILE:O	6:Q:222:THR:OG1	2.15	0.60
8:S:5:HIS:HB3	15:L:21:G:N7	2.16	0.60
10:Z:40:SER:O	10:Z:44:LEU:HB2	2.01	0.60
25:G:86:ASN:ND2	26:H:32:LYS:HD3	2.13	0.60
1:A:266:LEU:HD23	1:A:268:LEU:H	1.66	0.60
1:A:852:LEU:O	1:A:855:LEU:N	2.34	0.60
1:A:1698:ALA:HB1	1:A:1766:MET:HB2	1.83	0.60
1:A:2013:ARG:NH1	1:A:2085:GLY:O	2.23	0.60
2:C:167:ASN:O	2:C:171:GLY:HA3	2.01	0.60
2:C:738:ASP:HA	2:C:768:PHE:CZ	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:303:VAL:O	4:O:304:LEU:HD23	2.01	0.60
10:Z:63:PHE:HD2	10:Z:76:LEU:HD21	1.65	0.60
15:L:119:G:H5'	30:W:99:ASP:HB2	1.82	0.60
17:c:12:VAL:HG22	17:c:13:TRP:H	1.66	0.60
17:c:14:THR:HG23	17:c:17:GLU:H	1.66	0.60
35:f:183:TYR:CE2	35:f:234:LYS:HE3	2.37	0.60
1:A:1362:LYS:O	1:A:1365:THR:OG1	2.13	0.60
1:A:1986:MET:HE2	35:f:184:MET:HG2	1.82	0.60
4:O:160:ASN:HA	4:O:184:THR:OG1	2.01	0.60
7:R:124:MET:HE3	7:R:227:ASN:HD21	1.66	0.60
10:Z:305:GLY:HA2	10:Z:342:PHE:CD1	2.37	0.60
14:E:60:G:OP1	33:b:1:U:H5'	2.02	0.60
1:A:933:GLU:HA	1:A:936:GLU:OE1	2.00	0.60
2:C:223:ASP:OD2	2:C:647:ASN:ND2	2.32	0.60
4:O:111:ILE:HB	4:O:114:ARG:HH21	1.67	0.60
6:Q:257:GLU:OE2	6:Q:261:ARG:NH2	2.35	0.60
7:R:46:ARG:HD2	12:N:110:A:N1	2.15	0.60
17:c:216:ASP:OD1	17:c:217:ILE:N	2.35	0.60
20:v:480:UNK:O	20:v:485:UNK:N	2.35	0.60
1:A:705:GLN:HE21	1:A:709:ARG:HG3	1.65	0.60
1:A:1090:ILE:O	1:A:1096:SER:HA	2.02	0.60
1:A:1176:GLU:O	1:A:1180:GLU:HB2	2.02	0.60
2:C:105:ILE:HG22	2:C:180:ASN:O	2.02	0.60
2:C:116:THR:HG21	2:C:120:ARG:NH2	2.17	0.60
6:Q:256:SER:O	6:Q:259:GLY:N	2.33	0.60
9:T:41:LEU:HD11	14:E:35:A:C2	2.36	0.60
10:Z:99:MET:HE1	10:Z:227:TYR:CD1	2.37	0.60
13:D:78:A:O2'	13:D:79:C:P	2.60	0.60
14:E:64:U:HO2'	14:E:65:U:P	2.25	0.60
1:A:620:HIS:HB3	1:A:669:TYR:CZ	2.36	0.60
1:A:1156:HIS:CG	1:A:1157:PRO:HD2	2.37	0.60
1:A:1306:GLU:HA	1:A:1309:ILE:HD12	1.84	0.60
1:A:1411:ASP:HB2	3:J:6:ILE:HG22	1.81	0.60
2:C:200:CYS:SG	2:C:210:ILE:HD12	2.42	0.60
2:C:326:GLU:O	2:C:329:SER:OG	2.13	0.60
1:A:281:TYR:HB3	9:T:8:ARG:HH22	1.67	0.60
1:A:312:TYR:O	1:A:319:ARG:NH2	2.35	0.60
2:C:915:GLU:HG2	2:C:928:CYS:HB3	1.83	0.60
6:Q:98:ASN:O	6:Q:99:VAL:HG12	2.02	0.60
13:D:174:G:OP2	26:h:76:ASN:CB	2.49	0.60
25:i:83:LYS:NZ	26:h:75:CYS:O	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:V:3:LEU:HD11	30:W:60:ALA:HB1	1.82	0.60
2:C:245:VAL:HG11	2:C:295:ILE:HG22	1.84	0.59
2:C:398:ASN:HA	2:C:401:ARG:NH2	2.17	0.59
7:R:230:PRO:HG2	12:N:114:U:C5	2.37	0.59
10:Z:305:GLY:HA2	10:Z:342:PHE:CE1	2.37	0.59
19:I:190:TYR:CZ	19:I:192:VAL:HB	2.37	0.59
21:n:68:PRO:HD2	21:n:69:TRP:CZ3	2.36	0.59
1:A:168:LEU:HD23	1:A:622:MET:HE2	1.83	0.59
1:A:1025:VAL:HG21	1:A:1265:PHE:HD2	1.67	0.59
1:A:1063:PHE:HB2	17:c:83:GLN:HE21	1.67	0.59
2:C:231:ALA:HB2	2:C:473:LEU:HD11	1.83	0.59
4:O:148:ASP:CG	4:O:150:VAL:H	2.08	0.59
15:L:24:U:H5''	15:L:25:A:OP2	2.01	0.59
21:n:60:ARG:C	21:n:62:THR:N	2.59	0.59
1:A:484:PHE:HB2	13:D:81:A:N7	2.16	0.59
1:A:725:TYR:CE1	14:E:72:C:N1	2.69	0.59
1:A:779:ALA:O	1:A:782:ILE:HG22	2.02	0.59
1:A:1588:LYS:HE2	15:L:32:G:OP2	2.02	0.59
2:C:778:THR:HG21	2:C:822:SER:HB2	1.85	0.59
18:d:158:LYS:O	18:d:161:SER:N	2.35	0.59
1:A:1705:SER:HB3	1:A:1709:TRP:CE3	2.37	0.59
19:I:184:GLN:HA	19:I:187:LYS:HZ3	1.66	0.59
3:J:19:HIS:ND1	11:B:91:A:C8	2.71	0.59
4:O:155:PHE:HZ	4:O:425:ILE:HD11	1.68	0.59
18:d:237:ILE:HD11	18:d:238:TRP:CE2	2.36	0.59
1:A:1368:GLN:O	1:A:1372:LYS:HG3	2.02	0.59
4:O:166:VAL:HB	4:O:176:THR:HG22	1.84	0.59
17:c:525:ARG:O	17:c:528:GLN:CG	2.51	0.59
18:d:99:ILE:O	18:d:102:TRP:N	2.34	0.59
20:v:552:UNK:O	20:v:556:UNK:N	2.36	0.59
35:f:106:LYS:HB3	35:f:107:PRO:HD3	1.83	0.59
3:J:12:LYS:NZ	13:D:103:A:O4'	2.34	0.59
10:Z:439:ARG:O	10:Z:443:SER:OG	2.12	0.59
13:D:79:C:O2	13:D:79:C:H3'	2.03	0.59
14:E:86:G:N2	18:d:57:TYR:CD2	2.70	0.59
15:L:1116:A:N1	15:L:1117:G:C5	2.71	0.59
21:n:60:ARG:C	21:n:62:THR:H	2.11	0.59
28:l:66:GLY:HA2	28:l:69:ILE:HD12	1.85	0.59
28:U:66:GLY:HA2	28:U:69:ILE:HD12	1.85	0.59
1:A:488:ARG:NH1	13:D:81:A:N6	2.49	0.59
2:C:184:GLU:CD	2:C:191:ILE:H	2.10	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:718:LYS:HA	2:C:721:GLN:HB3	1.83	0.59
7:R:241:GLU:O	7:R:244:LEU:HG	2.03	0.59
8:S:16:LYS:HE3	14:E:65:U:OP2	2.03	0.59
9:T:51:GLU:O	9:T:54:GLN:N	2.36	0.59
14:E:86:G:C2	18:d:57:TYR:CE2	2.91	0.59
18:d:189:TYR:O	18:d:193:VAL:HG22	2.03	0.59
1:A:194:HIS:CD2	5:P:122:LEU:HD22	2.37	0.59
1:A:1857:VAL:HG13	1:A:1894:ILE:CD1	2.32	0.59
1:A:2050:THR:O	1:A:2053:SER:OG	2.12	0.59
13:D:167:A:N7	30:g:63:ARG:NE	2.51	0.59
21:n:251:ALA:CA	21:n:267:LEU:CB	2.67	0.59
1:A:143:ILE:HG13	1:A:144:ASN:N	2.18	0.59
1:A:275:TYR:CE2	1:A:306:PRO:HB2	2.38	0.59
1:A:954:ILE:O	1:A:957:TYR:N	2.35	0.59
1:A:968:ASP:OD2	17:c:46:ARG:NH2	2.23	0.59
1:A:1063:PHE:O	1:A:1066:LEU:N	2.36	0.59
2:C:277:LEU:HB3	2:C:279:LEU:HD13	1.85	0.59
4:O:414:LEU:HG	4:O:426:TRP:HD1	1.67	0.59
5:P:209:GLU:O	5:P:212:ASP:HB3	2.03	0.59
6:Q:13:CYS:SG	6:Q:16:CYS:HB3	2.43	0.59
7:R:46:ARG:HH12	7:R:222:LEU:HD11	1.68	0.59
10:Z:405:ILE:HD13	10:Z:420:ILE:HD11	1.85	0.59
19:I:92:ARG:N	19:I:93:GLY:HA3	2.18	0.59
19:I:106:GLU:HA	19:I:109:LEU:HD12	1.84	0.59
25:G:83:LYS:NZ	26:H:75:CYS:O	2.35	0.59
1:A:164:ALA:HB2	5:P:122:LEU:HD21	1.85	0.58
1:A:615:LEU:HD23	1:A:619:PHE:CD2	2.38	0.58
1:A:713:ASN:HD21	13:D:83:C:C4'	2.11	0.58
1:A:1376:ASN:O	1:A:1377:SER:OG	2.11	0.58
1:A:1716:LEU:HD23	1:A:1787:TYR:HB2	1.85	0.58
1:A:1893:ILE:HD12	1:A:1985:GLN:HG2	1.84	0.58
2:C:201:THR:HG22	2:C:207:SER:HB3	1.85	0.58
2:C:236:LEU:HD11	2:C:439:ILE:HG12	1.83	0.58
4:O:308:LYS:HA	5:P:148:HIS:CE1	2.38	0.58
1:A:284:ARG:NH2	13:D:33:U:C4	2.71	0.58
1:A:1011:ASN:HD21	1:A:1142:ASN:HB2	1.67	0.58
1:A:1232:SER:HB2	8:S:135:ARG:CZ	2.32	0.58
1:A:1748:ILE:HG22	1:A:1752:VAL:HG23	1.85	0.58
1:A:1845:ASN:HB2	1:A:1849:LYS:HZ1	1.68	0.58
7:R:185:LYS:C	7:R:186:PHE:HD1	2.11	0.58
10:Z:475:GLU:O	10:Z:478:ARG:N	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:157:GLU:OE2	7:R:161:ARG:NE	2.36	0.58
8:S:6:ARG:NH2	14:E:85:C:OP1	2.36	0.58
10:Z:60:VAL:HG11	10:Z:80:ILE:HD11	1.84	0.58
10:Z:63:PHE:HZ	10:Z:72:LEU:HD12	1.69	0.58
20:v:611:THR:CB	20:v:623:LEU:CD1	2.81	0.58
33:b:-2:U:C3'	33:b:-1:A:H5'	2.33	0.58
1:A:1052:THR:OG1	1:A:1168:ILE:HB	2.03	0.58
1:A:1129:GLU:O	1:A:1132:THR:N	2.36	0.58
1:A:1925:PRO:O	1:A:1929:GLN:HG3	2.04	0.58
2:C:300:LYS:HG3	2:C:301:GLY:H	1.67	0.58
4:O:285:SER:O	4:O:287:ASP:N	2.36	0.58
4:O:307:HIS:ND1	4:O:327:CYS:HB2	2.17	0.58
7:R:4:TRP:NE1	7:R:60:GLY:O	2.37	0.58
13:D:175:G:N1	25:i:33:GLU:O	2.36	0.58
22:q:194:THR:OG1	22:q:213:CYS:HB3	2.03	0.58
1:A:264:ILE:HG22	1:A:265:ASN:O	2.03	0.58
1:A:728:ASN:ND2	14:E:72:C:O2'	2.29	0.58
2:C:75:GLU:OE1	4:O:133:ARG:NE	2.36	0.58
2:C:132:ARG:HG3	2:C:206:LYS:NZ	2.17	0.58
2:C:797:GLN:O	2:C:800:TYR:N	2.36	0.58
2:C:832:ASP:HA	2:C:835:LYS:HG2	1.85	0.58
6:Q:202:THR:HG1	6:Q:252:ARG:HE	1.47	0.58
22:q:378:LYS:CG	22:q:423:THR:O	2.51	0.58
35:f:134:GLU:OE2	35:f:135:LEU:HG	2.04	0.58
1:A:143:ILE:HD13	1:A:570:GLN:HG2	1.86	0.58
1:A:1253:LYS:O	1:A:1274:ARG:NH2	2.35	0.58
1:A:1645:LEU:O	1:A:1648:ILE:N	2.37	0.58
2:C:373:PHE:HD1	2:C:377:ILE:HD12	1.67	0.58
13:D:174:G:C5	29:m:20:LYS:HE2	2.39	0.58
17:c:66:SER:H	17:c:69:GLU:HB2	1.68	0.58
20:v:687:LEU:HD23	20:v:713:ILE:HA	1.84	0.58
1:A:1463:THR:O	1:A:1466:GLN:N	2.37	0.58
2:C:680:SER:OG	2:C:681:CYS:N	2.36	0.58
6:Q:87:ARG:NH2	6:Q:126:THR:OG1	2.36	0.58
7:R:256:ASN:OD1	7:R:257:ASN:N	2.36	0.58
10:Z:452:GLU:N	10:Z:452:GLU:OE1	2.37	0.58
1:A:834:ILE:O	1:A:837:GLY:N	2.37	0.58
1:A:923:TYR:HD1	1:A:926:LYS:HD3	1.68	0.58
1:A:2013:ARG:O	1:A:2016:LYS:N	2.34	0.58
2:C:269:LYS:HG2	36:C:1500:GTP:N1	2.19	0.58
2:C:373:PHE:CD1	2:C:377:ILE:HD12	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:72:PHE:HD1	7:R:90:LEU:HB2	1.67	0.58
7:R:117:PHE:CD2	14:E:39:G:C4	2.92	0.58
1:A:1624:LEU:HD21	1:A:1635:HIS:ND1	2.19	0.58
1:A:1797:LEU:O	1:A:1801:SER:CB	2.52	0.58
1:A:2013:ARG:HB3	1:A:2059:ILE:CD1	2.33	0.58
2:C:702:ASN:OD1	2:C:844:LYS:NZ	2.36	0.58
2:C:746:LYS:O	2:C:749:LYS:N	2.37	0.58
6:Q:34:CYS:SG	6:Q:61:CYS:N	2.76	0.58
14:E:53:A:H5'	14:E:54:U:OP2	2.02	0.58
15:L:120:G:N1	25:G:33:GLU:O	2.36	0.58
16:M:490:A:H2'	16:M:491:C:C6	2.38	0.58
1:A:235:LYS:O	1:A:648:GLN:NE2	2.37	0.58
1:A:717:GLY:HA3	13:D:84:A:O2'	2.04	0.58
1:A:1476:ALA:C	1:A:1478:GLU:H	2.11	0.58
1:A:2019:GLU:O	1:A:2022:ALA:N	2.34	0.58
4:O:125:TRP:HZ2	4:O:432:ALA:HB1	1.68	0.58
4:O:414:LEU:HD12	4:O:415:ILE:H	1.68	0.58
7:R:180:ASN:ND2	12:N:111:U:C4	2.72	0.58
7:R:255:ASN:O	7:R:259:ASN:ND2	2.30	0.58
10:Z:334:LEU:HD22	10:Z:380:GLN:HB3	1.85	0.58
14:E:14:C:H4'	14:E:15:C:O5'	2.04	0.58
22:p:98:LEU:HD12	22:q:98:LEU:HD23	1.85	0.58
1:A:782:ILE:HD12	1:A:785:HIS:CD2	2.39	0.57
1:A:901:PRO:HB2	1:A:955:LYS:HE3	1.86	0.57
1:A:946:ASN:HB3	1:A:949:ASP:HB3	1.85	0.57
1:A:1181:GLU:O	1:A:1184:ASP:HB2	2.04	0.57
1:A:1988:LEU:CD2	35:f:180:VAL:HG12	2.27	0.57
2:C:249:VAL:O	2:C:253:ILE:HG12	2.03	0.57
6:Q:53:ASN:O	14:E:31:G:N2	2.37	0.57
15:L:52:A:N1	21:n:204:GLY:HA2	2.19	0.57
1:A:580:ASN:O	1:A:583:ILE:N	2.36	0.57
1:A:746:THR:OG1	1:A:749:ARG:NH2	2.37	0.57
2:C:89:PRO:O	2:C:91:VAL:N	2.35	0.57
2:C:326:GLU:HG2	2:C:330:TYR:HE2	1.69	0.57
7:R:19:PRO:HB3	14:E:36:U:O4	2.03	0.57
7:R:249:MET:HA	7:R:252:HIS:HD2	1.68	0.57
15:L:112:A:N7	30:W:63:ARG:NE	2.51	0.57
15:L:119:G:C5	29:V:20:LYS:HE2	2.39	0.57
35:f:169:HIS:HD2	35:f:175:GLU:OE2	1.87	0.57
1:A:480:TYR:CE2	2:C:275:LEU:HD23	2.39	0.57
1:A:1265:PHE:HE1	1:A:1346:PHE:HD1	1.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1337:THR:HB	33:b:8:A:N6	2.18	0.57
2:C:655:LEU:O	2:C:658:ASP:N	2.36	0.57
10:Z:159:GLY:O	10:Z:163:ALA:HB3	2.05	0.57
10:Z:476:ASP:O	10:Z:479:SER:OG	2.16	0.57
17:c:214:ASN:ND2	18:d:44:ARG:HD2	2.19	0.57
22:q:472:ALA:HB2	22:q:477:MET:CG	2.35	0.57
1:A:426:PRO:HB3	10:Z:201:ARG:NE	2.19	0.57
1:A:933:GLU:O	1:A:936:GLU:N	2.37	0.57
1:A:1601:ILE:HG12	1:A:1604:ARG:HH22	1.69	0.57
1:A:1716:LEU:HA	1:A:1787:TYR:HA	1.86	0.57
1:A:1860:VAL:HG11	16:M:502:C:H5'	1.87	0.57
2:C:225:THR:O	2:C:228:ALA:N	2.37	0.57
4:O:148:ASP:HB2	4:O:154:TRP:CE2	2.39	0.57
7:R:115:GLU:OE1	7:R:115:GLU:N	2.37	0.57
13:D:78:A:O2'	13:D:79:C:O5'	2.18	0.57
21:n:72:TRP:O	21:n:73:SER:OG	2.16	0.57
24:F:47:GLU:HG3	32:Y:15:TYR:CG	2.39	0.57
1:A:137:GLU:O	1:A:140:ARG:N	2.37	0.57
1:A:1805:ILE:HG23	1:A:1809:ASN:HD22	1.69	0.57
2:C:682:SER:O	2:C:854:ILE:HB	2.04	0.57
3:J:6:ILE:HD11	11:B:90:A:H61	1.69	0.57
4:O:157:THR:HG21	4:O:423:ILE:HD11	1.85	0.57
6:Q:27:LYS:HG3	6:Q:44:TYR:HE1	1.69	0.57
7:R:47:PHE:CZ	14:E:37:U:C2	2.93	0.57
7:R:159:ARG:HD3	7:R:204:LEU:HB3	1.87	0.57
10:Z:85:SER:HB2	10:Z:220:TYR:HE1	1.70	0.57
10:Z:100:LEU:HB2	10:Z:233:ASP:OD2	2.05	0.57
17:c:233:GLU:OE2	18:d:115:ILE:N	2.38	0.57
1:A:347:PRO:HG3	3:J:2:SER:N	2.20	0.57
1:A:1014:LYS:HG3	1:A:1016:SER:OG	2.04	0.57
4:O:382:HIS:CE1	4:O:442:TRP:H	2.22	0.57
10:Z:410:GLU:OE1	10:Z:411:GLU:N	2.38	0.57
10:Z:459:ARG:O	10:Z:463:ASN:HB3	2.05	0.57
21:n:302:PHE:CG	21:n:307:LYS:HA	2.39	0.57
1:A:185:GLN:HG2	1:A:263:PRO:HD3	1.86	0.57
1:A:1182:LEU:O	1:A:1185:GLU:N	2.38	0.57
1:A:1335:TRP:HD1	1:A:1367:ILE:CD1	2.12	0.57
2:C:352:VAL:O	2:C:372:THR:OG1	2.17	0.57
7:R:28:LEU:HG	7:R:29:THR:HG23	1.87	0.57
7:R:110:ASP:CG	7:R:114:ARG:H	2.09	0.57
13:D:174:G:O6	29:m:20:LYS:HB3	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:570:GLN:O	1:A:574:GLN:HG2	2.05	0.57
5:P:35:ALA:HB3	18:d:158:LYS:HE2	1.86	0.57
6:Q:260:GLU:O	6:Q:264:SER:N	2.32	0.57
1:A:374:ILE:HG12	2:C:969:LYS:HG3	1.86	0.57
1:A:725:TYR:CE1	14:E:72:C:C2	2.92	0.57
1:A:725:TYR:HE1	14:E:72:C:N1	2.03	0.57
1:A:1616:ARG:NH2	1:A:1744:ASP:OD1	2.38	0.57
6:Q:104:ALA:HB1	6:Q:110:LYS:CB	2.35	0.57
18:d:136:TRP:CE3	18:d:159:TRP:HB2	2.40	0.57
1:A:252:GLU:OE1	1:A:252:GLU:N	2.35	0.57
1:A:266:LEU:HG	1:A:267:PRO:HD2	1.86	0.57
1:A:1335:TRP:HH2	1:A:1339:LEU:HD13	1.70	0.57
1:A:1679:GLU:HG2	1:A:1706:VAL:HA	1.87	0.57
2:C:679:GLU:OE1	2:C:807:PRO:HD2	2.05	0.57
2:C:858:LEU:HB3	2:C:937:TRP:CE3	2.40	0.57
5:P:30:LEU:O	5:P:33:GLN:N	2.38	0.57
9:T:122:CYS:HB2	9:T:145:CYS:HB2	1.86	0.57
10:Z:326:VAL:HG11	10:Z:364:THR:HG21	1.87	0.57
17:c:64:GLU:HG2	17:c:65:PHE:N	2.19	0.57
17:c:207:TYR:CE2	17:c:210:ASP:HA	2.40	0.57
2:C:360:ARG:C	2:C:362:LYS:H	2.13	0.56
6:Q:107:ASP:O	6:Q:110:LYS:HG2	2.04	0.56
8:S:7:PRO:HD2	15:L:20:G:N3	2.19	0.56
10:Z:143:LEU:HB3	10:Z:176:LYS:NZ	2.20	0.56
14:E:42:A:HO2'	14:E:43:C:P	2.28	0.56
15:L:52:A:H8	15:L:52:A:O5'	1.88	0.56
35:f:183:TYR:CE2	35:f:234:LYS:CE	2.88	0.56
1:A:320:ASP:O	1:A:508:GLN:NE2	2.37	0.56
1:A:558:GLN:NE2	9:T:107:ARG:HH12	2.03	0.56
1:A:1710:GLU:HA	1:A:1727:LEU:O	2.04	0.56
1:A:1863:HIS:O	1:A:1871:ALA:CB	2.51	0.56
4:O:304:LEU:HB3	4:O:334:TRP:CZ3	2.41	0.56
8:S:10:GLU:HG2	8:S:11:ALA:H	1.69	0.56
15:L:12:U:H4'	19:I:92:ARG:HH22	1.70	0.56
15:L:119:G:O6	29:V:20:LYS:HB3	2.05	0.56
24:F:19:LYS:HZ1	32:Y:34:LEU:CB	2.16	0.56
1:A:284:ARG:HB2	1:A:287:GLU:OE2	2.04	0.56
1:A:296:THR:HB	13:D:32:G:H5''	1.86	0.56
1:A:909:THR:O	1:A:913:VAL:HG23	2.05	0.56
1:A:978:ILE:O	8:S:175:ARG:HB3	2.05	0.56
1:A:1324:GLY:HA3	33:b:3:U:C3'	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1490:ARG:O	1:A:1492:SER:N	2.38	0.56
1:A:1701:ILE:O	1:A:1733:TRP:HA	2.05	0.56
1:A:1715:SER:HG	1:A:1790:TRP:CD1	2.22	0.56
1:A:1864:LYS:CE	21:n:328:ILE:CB	2.83	0.56
1:A:1881:THR:OG1	1:A:1890:PHE:HB2	2.05	0.56
1:A:1902:GLN:HE21	1:A:1908:LEU:HD21	1.71	0.56
1:A:2043:PHE:HD2	1:A:2048:TRP:CD2	2.23	0.56
2:C:716:ASP:HB3	2:C:719:MET:CB	2.35	0.56
2:C:772:ASN:HB3	2:C:816:VAL:H	1.70	0.56
2:C:772:ASN:OD1	2:C:772:ASN:N	2.35	0.56
2:C:858:LEU:HB3	2:C:937:TRP:HE3	1.70	0.56
4:O:154:TRP:CD1	4:O:154:TRP:N	2.73	0.56
5:P:216:ARG:HA	5:P:219:ILE:HD12	1.88	0.56
6:Q:48:THR:OG1	6:Q:49:SER:N	2.37	0.56
7:R:150:HIS:O	7:R:152:LYS:N	2.38	0.56
16:M:497:A:C5	16:M:498:C:N4	2.73	0.56
21:n:59:ARG:NH1	21:n:59:ARG:HG2	2.21	0.56
33:b:3:U:H4'	33:b:4:U:OP1	2.05	0.56
1:A:801:VAL:HG11	1:A:804:MET:HE3	1.88	0.56
2:C:99:LYS:HG2	13:D:43:G:C5'	2.36	0.56
9:T:90:LEU:O	9:T:93:ALA:N	2.38	0.56
17:c:16:VAL:O	17:c:20:ILE:HD12	2.06	0.56
1:A:744:THR:HG22	14:E:75:A:OP1	2.06	0.56
1:A:865:ARG:O	1:A:868:GLN:N	2.36	0.56
1:A:1596:THR:HG22	33:b:4:U:O5'	2.04	0.56
1:A:1962:ARG:HG3	1:A:2085:GLY:HA3	1.87	0.56
2:C:271:ASP:CG	36:C:1500:GTP:HN1	2.14	0.56
2:C:885:GLY:HA2	2:C:907:PRO:HD3	1.88	0.56
7:R:230:PRO:CG	12:N:114:U:C4	2.88	0.56
15:L:40:U:O2'	15:L:41:C:H5	1.87	0.56
1:A:376:ARG:O	1:A:377:VAL:HB	2.05	0.56
1:A:402:TRP:CG	1:A:402:TRP:O	2.59	0.56
2:C:463:THR:O	2:C:465:GLU:HG2	2.06	0.56
4:O:116:GLU:HG3	18:d:235:LEU:HD11	1.87	0.56
6:Q:87:ARG:NH2	6:Q:122:GLY:O	2.37	0.56
10:Z:122:SER:O	10:Z:125:PHE:N	2.38	0.56
18:d:182:TRP:O	18:d:186:ARG:NH1	2.38	0.56
29:V:43:VAL:HG11	29:V:85:ILE:HD12	1.87	0.56
1:A:153:MET:HE2	1:A:154:TYR:CE1	2.40	0.56
1:A:421:ALA:HB3	1:A:469:ILE:HD12	1.87	0.56
1:A:1626:GLN:HB2	1:A:1633:PHE:CE1	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:116:THR:HG22	2:C:158:HIS:CD2	2.41	0.56
2:C:242:VAL:HG13	2:C:897:THR:HG21	1.88	0.56
2:C:865:ASP:OD1	2:C:866:ILE:N	2.39	0.56
6:Q:119:LYS:HE3	6:Q:123:ALA:HB1	1.87	0.56
10:Z:368:ASN:HA	10:Z:372:ASP:HB3	1.88	0.56
12:N:101:U:H3'	12:N:101:U:H6	1.71	0.56
22:q:294:HIS:CG	22:q:338:LEU:H	2.24	0.56
1:A:209:ILE:HG22	1:A:211:PRO:HD2	1.88	0.56
1:A:562:ILE:HD11	1:A:566:GLU:CD	2.31	0.56
1:A:589:THR:OG1	7:R:39:GLN:NE2	2.39	0.56
1:A:854:ARG:NH1	15:L:25:A:OP1	2.39	0.56
1:A:1424:HIS:CD2	3:J:6:ILE:HG21	2.40	0.56
1:A:1447:TRP:HB3	1:A:1451:PHE:CE2	2.36	0.56
1:A:1864:LYS:HD2	21:n:328:ILE:CB	2.35	0.56
6:Q:53:ASN:ND2	7:R:69:GLN:HA	2.21	0.56
15:L:51:C:H6	15:L:51:C:O5'	1.89	0.56
1:A:1431:HIS:HB2	1:A:1433:ASP:O	2.05	0.56
10:Z:118:LEU:HA	10:Z:121:LEU:HD12	1.87	0.56
11:B:99:G:O3'	33:b:1:U:O5'	2.24	0.56
21:n:200:ARG:CG	21:n:201:ASP:N	2.69	0.56
1:A:740:GLU:HG3	1:A:741:ILE:N	2.20	0.56
1:A:861:GLN:NE2	1:A:1097:HIS:HB3	2.20	0.56
1:A:878:GLU:O	1:A:881:THR:OG1	2.21	0.56
1:A:1049:LEU:HA	1:A:1170:MET:O	2.05	0.56
1:A:1395:GLY:HA3	1:A:1609:TRP:CD1	2.41	0.56
2:C:187:ARG:NH1	2:C:653:ASP:OD2	2.38	0.56
6:Q:61:CYS:HB3	6:Q:63:ARG:H	1.71	0.56
7:R:36:LYS:NZ	14:E:41:A:H2	2.02	0.56
16:M:499:U:C2'	16:M:500:A:H5'	2.35	0.56
18:d:159:TRP:O	18:d:164:PRO:HG3	2.06	0.56
18:d:185:VAL:HA	18:d:188:ILE:HD12	1.87	0.56
1:A:461:LEU:HD12	1:A:462:LEU:HD12	1.88	0.55
1:A:1050:LEU:HD23	1:A:1248:VAL:HG22	1.87	0.55
1:A:1203:ASN:ND2	1:A:1213:MET:O	2.38	0.55
1:A:1354:GLU:OE2	1:A:1408:PRO:HG2	2.06	0.55
1:A:1986:MET:HB3	35:f:184:MET:HB3	1.87	0.55
9:T:98:THR:OG1	9:T:99:GLY:N	2.39	0.55
15:L:15:C:N4	19:I:209:ARG:CB	2.58	0.55
15:L:1097:G:N1	15:L:1119:C:N3	2.50	0.55
15:L:1100:A:C2	15:L:1101:C:C2	2.95	0.55
15:L:1105:C:N4	31:X:97:LYS:NZ	2.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:d:235:LEU:HD23	18:d:237:ILE:HG23	1.87	0.55
25:G:77:LEU:HD21	25:G:80:ILE:CD1	2.36	0.55
1:A:1705:SER:HB3	1:A:1709:TRP:CD2	2.41	0.55
1:A:1920:LEU:CD1	35:f:184:MET:HE2	2.36	0.55
2:C:84:GLN:HG2	2:C:88:THR:OG1	2.07	0.55
2:C:261:VAL:HG12	2:C:262:ALA:H	1.71	0.55
2:C:660:ARG:HH22	2:C:670:ILE:HD12	1.71	0.55
4:O:138:HIS:CE1	4:O:159:SER:HB2	2.41	0.55
4:O:200:VAL:HG11	4:O:230:VAL:HG23	1.88	0.55
7:R:55:PRO:HG2	7:R:166:ARG:HD2	1.88	0.55
10:Z:69:ASN:HB3	10:Z:73:ILE:HG13	1.88	0.55
10:Z:130:ILE:HD11	10:Z:135:ILE:HD11	1.89	0.55
15:L:18:U:C6	19:I:202:GLN:HG3	2.42	0.55
29:m:43:VAL:HG11	29:m:85:ILE:HD12	1.87	0.55
1:A:1508:HIS:HB2	1:A:1529:ASN:ND2	2.21	0.55
1:A:1562:PHE:HB2	1:A:1609:TRP:HH2	1.71	0.55
1:A:1755:LYS:HB3	1:A:1759:TYR:CE2	2.41	0.55
1:A:1927:GLU:HG2	35:f:135:LEU:CD1	2.24	0.55
4:O:155:PHE:HD2	4:O:167:TRP:CD1	2.25	0.55
6:Q:118:VAL:HG23	6:Q:119:LYS:O	2.06	0.55
10:Z:361:TYR:O	10:Z:364:THR:N	2.39	0.55
16:M:499:U:O5'	16:M:499:U:H6	1.89	0.55
18:d:119:ARG:O	18:d:122:MET:N	2.39	0.55
1:A:477:MET:CE	2:C:278:LYS:CE	2.79	0.55
1:A:1870:VAL:HG23	16:M:499:U:C2'	2.36	0.55
4:O:134:VAL:HG22	4:O:424:LYS:HG2	1.88	0.55
4:O:328:THR:OG1	4:O:329:ASP:N	2.39	0.55
16:M:496:U:H3'	16:M:497:A:H5''	1.87	0.55
21:n:253:VAL:HG21	21:n:298:ALA:HA	1.87	0.55
35:f:234:LYS:O	35:f:238:THR:HG23	2.06	0.55
1:A:382:GLU:OE1	1:A:382:GLU:N	2.28	0.55
1:A:1679:GLU:HB2	1:A:1704:GLU:O	2.06	0.55
2:C:291:ILE:O	2:C:294:ASN:N	2.40	0.55
2:C:545:LEU:HD12	2:C:545:LEU:O	2.06	0.55
15:L:7:C:OP1	19:I:174:LYS:CE	2.55	0.55
16:M:499:U:H2'	16:M:500:A:H5'	1.89	0.55
1:A:382:GLU:H	1:A:382:GLU:CD	2.11	0.55
1:A:1183:THR:O	1:A:1187:LEU:HB2	2.06	0.55
2:C:234:LEU:HD11	2:C:439:ILE:HG23	1.88	0.55
7:R:97:GLU:O	7:R:100:GLY:CA	2.55	0.55
21:n:357:ASP:CG	21:n:358:ASN:N	2.62	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:t:7:VAL:CG1	23:t:154:VAL:CB	2.73	0.55
2:C:636:VAL:HG12	2:C:637:GLU:N	2.21	0.55
4:O:396:LEU:O	4:O:399:GLU:N	2.21	0.55
15:L:41:C:HO2'	15:L:42:U:C5'	2.20	0.55
15:L:1102:C:H2'	15:L:1103:C:H5	1.70	0.55
16:M:487:A:H2'	16:M:488:G:H8	1.70	0.55
16:M:495:A:N7	16:M:496:U:C4	2.74	0.55
1:A:327:TYR:HD2	1:A:328:TYR:CD1	2.25	0.55
1:A:665:GLY:HA2	1:A:667:TYR:CE1	2.42	0.55
1:A:742:VAL:HG12	4:O:224:LEU:HD23	1.89	0.55
1:A:1511:ARG:O	1:A:1515:LYS:HG2	2.06	0.55
1:A:1739:ARG:O	1:A:1778:ASP:HA	2.06	0.55
4:O:187:ASP:OD2	4:O:230:VAL:N	2.26	0.55
4:O:244:ARG:HH12	8:S:8:GLN:NE2	2.05	0.55
4:O:414:LEU:O	4:O:425:ILE:HA	2.07	0.55
8:S:8:GLN:CB	14:E:63:G:O2'	2.54	0.55
15:L:28:U:C2'	15:L:29:C:H5'	2.37	0.55
21:n:55:GLU:OE2	21:n:58:ARG:HD2	2.05	0.55
22:q:292:TYR:CB	22:q:335:SER:HA	2.37	0.55
1:A:249:LEU:HD12	1:A:249:LEU:O	2.07	0.55
1:A:1232:SER:O	1:A:1234:VAL:N	2.40	0.55
1:A:1343:PHE:HE2	1:A:1402:ALA:HB3	1.72	0.55
1:A:1940:MET:HE3	1:A:1944:LEU:HG	1.89	0.55
2:C:897:THR:O	2:C:899:LEU:N	2.37	0.55
4:O:125:TRP:HE1	4:O:437:GLU:HG3	1.71	0.55
6:Q:240:LEU:HD13	6:Q:251:LEU:HD13	1.87	0.55
7:R:180:ASN:ND2	12:N:111:U:O4	2.40	0.55
10:Z:105:GLN:HB3	10:Z:110:ASP:HB3	1.88	0.55
14:E:56:A:HO2'	14:E:57:U:P	2.30	0.55
15:L:39:A:C2'	15:L:40:U:C5'	2.83	0.55
18:d:174:ASP:O	18:d:178:ARG:NH1	2.40	0.55
1:A:790:TRP:NE1	1:A:819:LYS:HZ3	2.05	0.55
1:A:1335:TRP:CZ3	1:A:1339:LEU:HD22	2.42	0.55
2:C:246:THR:O	2:C:249:VAL:N	2.38	0.55
2:C:493:LEU:HB2	2:C:556:ALA:HB3	1.88	0.55
2:C:607:LEU:HD22	2:C:668:ILE:HD12	1.89	0.55
4:O:224:LEU:HB2	4:O:245:ASP:OD1	2.07	0.55
10:Z:89:ASP:O	10:Z:93:THR:CB	2.54	0.55
15:L:23:U:C4	15:L:26:G:O4'	2.59	0.55
15:L:1116:A:N3	15:L:1117:G:C8	2.74	0.55
16:M:489:A:C5'	21:n:245:HIS:HB2	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:v:606:GLN:HA	20:v:609:GLU:CG	2.37	0.55
21:n:208:PRO:O	21:n:225:SER:OG	2.21	0.55
25:i:77:LEU:HD21	25:i:80:ILE:CD1	2.36	0.55
32:Y:44:PRO:O	32:Y:69:ASP:CB	2.54	0.55
1:A:367:PHE:O	1:A:372:ARG:NH2	2.41	0.54
1:A:1026:TYR:HA	1:A:1286:TRP:HZ3	1.72	0.54
1:A:1153:GLU:O	1:A:1159:ARG:NE	2.40	0.54
2:C:145:GLY:HA3	2:C:268:ASN:ND2	2.22	0.54
4:O:259:VAL:HG12	4:O:260:ILE:HG13	1.89	0.54
10:Z:355:ARG:O	10:Z:358:GLN:HB3	2.07	0.54
10:Z:412:SER:O	10:Z:417:ARG:NH1	2.39	0.54
10:Z:459:ARG:O	10:Z:463:ASN:CB	2.55	0.54
1:A:235:LYS:NZ	1:A:1758:ASP:OD1	2.40	0.54
1:A:366:GLU:HG3	1:A:372:ARG:NH1	2.17	0.54
1:A:551:LEU:HG	1:A:557:PHE:CE2	2.41	0.54
1:A:1435:LYS:HZ3	1:A:1550:LEU:C	2.11	0.54
1:A:1699:ALA:HB2	1:A:1767:TYR:HD1	1.72	0.54
2:C:477:ASP:HB2	2:C:628:TYR:CE2	2.42	0.54
2:C:700:GLU:HG2	2:C:701:GLU:O	2.06	0.54
10:Z:455:ALA:HA	10:Z:458:ILE:HD12	1.90	0.54
17:c:66:SER:O	17:c:70:ASP:N	2.41	0.54
18:d:265:ALA:O	18:d:269:ILE:HD12	2.07	0.54
1:A:1751:TYR:CZ	1:A:1755:LYS:HG3	2.42	0.54
2:C:109:LEU:HD22	2:C:112:ASN:OD1	2.07	0.54
2:C:856:ILE:HA	2:C:944:VAL:HG11	1.88	0.54
4:O:220:TYR:CE1	4:O:256:ARG:HG2	2.42	0.54
6:Q:45:HIS:CE1	14:E:32:U:H5'	2.43	0.54
7:R:92:HIS:ND1	7:R:93:ILE:O	2.34	0.54
18:d:106:ILE:HG12	18:d:122:MET:HE3	1.88	0.54
21:n:55:GLU:O	21:n:59:ARG:HB2	2.07	0.54
1:A:557:PHE:O	1:A:558:GLN:NE2	2.40	0.54
1:A:768:GLU:OE2	4:O:310:SER:HB3	2.08	0.54
1:A:1372:LYS:HG2	1:A:1383:PHE:CE2	2.43	0.54
1:A:1678:ILE:HG23	1:A:1703:MET:HE1	1.90	0.54
2:C:271:ASP:OD1	2:C:272:ARG:N	2.40	0.54
2:C:314:ALA:HB1	2:C:321:THR:HG22	1.89	0.54
4:O:265:HIS:CE1	4:O:291:ARG:HG2	2.43	0.54
4:O:414:LEU:HD12	4:O:415:ILE:N	2.21	0.54
7:R:47:PHE:CE1	14:E:37:U:C4	2.95	0.54
7:R:117:PHE:CE2	14:E:39:G:C4	2.96	0.54
10:Z:53:ARG:HG3	10:Z:54:ASN:H	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Z:152:ILE:O	10:Z:156:LYS:HB2	2.08	0.54
15:L:1114:G:H2'	15:L:1115:G:C8	2.43	0.54
1:A:456:GLU:OE1	1:A:456:GLU:N	2.38	0.54
2:C:139:ILE:HD12	2:C:252:LEU:HD22	1.89	0.54
2:C:149:LEU:HD12	2:C:152:LEU:HD12	1.90	0.54
2:C:471:HIS:N	2:C:487:ARG:O	2.34	0.54
2:C:745:ARG:O	2:C:748:SER:OG	2.24	0.54
7:R:95:ASP:OD1	7:R:97:GLU:N	2.39	0.54
9:T:29:GLN:HA	9:T:32:ASP:OD2	2.08	0.54
10:Z:18:TRP:CD1	10:Z:242:PHE:HB2	2.41	0.54
10:Z:98:LEU:HD23	10:Z:101:MET:HG3	1.89	0.54
35:f:223:ASP:CG	35:f:224:GLU:H	2.16	0.54
1:A:332:ASP:N	1:A:332:ASP:OD1	2.38	0.54
1:A:346:ILE:O	1:A:349:GLY:N	2.40	0.54
1:A:594:ASP:OD1	1:A:594:ASP:N	2.36	0.54
1:A:709:ARG:NH2	13:D:83:C:OP1	2.36	0.54
1:A:1011:ASN:ND2	1:A:1142:ASN:HB2	2.23	0.54
1:A:1029:THR:O	1:A:1032:ILE:N	2.40	0.54
1:A:1063:PHE:HB2	17:c:83:GLN:NE2	2.23	0.54
1:A:1464:LYS:HD3	1:A:1479:GLU:HB2	1.89	0.54
2:C:101:GLN:NE2	13:D:75:A:N6	2.48	0.54
5:P:111:HIS:O	5:P:112:ILE:HG13	2.07	0.54
5:P:197:ILE:HG23	17:c:90:MET:HE2	1.88	0.54
6:Q:37:CYS:HB3	6:Q:64:CYS:SG	2.47	0.54
7:R:95:ASP:OD1	7:R:98:ASP:N	2.35	0.54
15:L:7:C:OP1	19:I:174:LYS:HE3	2.07	0.54
17:c:39:LEU:HD12	17:c:158:ARG:NH1	2.20	0.54
20:v:726:ARG:HA	20:v:729:TYR:CD2	2.43	0.54
21:n:318:ARG:HD3	21:n:327:PRO:CG	2.38	0.54
22:q:467:LEU:CG	22:q:481:CYS:SG	2.96	0.54
32:Y:68:PRO:O	32:Y:69:ASP:CB	2.54	0.54
1:A:402:TRP:HE1	1:A:405:ASN:HD21	1.54	0.54
1:A:430:PRO:HB3	10:Z:198:PHE:CD2	2.42	0.54
2:C:105:ILE:HG12	2:C:106:PHE:H	1.73	0.54
2:C:733:ASN:OD1	2:C:734:CYS:N	2.40	0.54
4:O:184:THR:O	4:O:201:SER:OG	2.07	0.54
7:R:18:LEU:HD11	7:R:82:CYS:SG	2.48	0.54
7:R:207:PRO:O	7:R:212:TRP:NE1	2.41	0.54
9:T:32:ASP:O	9:T:35:LYS:HD3	2.07	0.54
10:Z:63:PHE:CD2	10:Z:76:LEU:HD21	2.43	0.54
15:L:1102:C:C2'	15:L:1103:C:C6	2.80	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:c:25:VAL:HG11	17:c:52:TRP:CH2	2.43	0.54
24:F:47:GLU:HG3	32:Y:15:TYR:HB2	1.87	0.54
1:A:168:LEU:HB3	1:A:622:MET:HE1	1.90	0.54
1:A:409:CYS:SG	2:C:272:ARG:NH2	2.81	0.54
1:A:1282:ASP:OD2	10:Z:305:GLY:N	2.40	0.54
2:C:265:PHE:CD2	2:C:295:ILE:HD12	2.43	0.54
3:J:19:HIS:CE1	11:B:91:A:N7	2.76	0.54
5:P:110:HIS:CD2	6:Q:17:LEU:HD22	2.43	0.54
6:Q:215:PRO:HG2	6:Q:217:TRP:CE2	2.40	0.54
17:c:227:ILE:O	19:I:152:ILE:N	2.27	0.54
18:d:81:MET:O	18:d:84:ALA:N	2.41	0.54
1:A:422:LEU:HD12	1:A:469:ILE:HD11	1.90	0.54
1:A:977:ASN:HB2	8:S:175:ARG:HH11	1.72	0.54
1:A:1451:PHE:O	1:A:1454:SER:OG	2.21	0.54
1:A:2049:ILE:O	1:A:2052:GLU:HB2	2.08	0.54
2:C:133:ILE:HG22	2:C:209:MET:HB3	1.89	0.54
2:C:142:LEU:HB3	2:C:143:HIS:HD2	1.73	0.54
2:C:716:ASP:HB3	2:C:719:MET:HB2	1.89	0.54
4:O:325:SER:HB3	4:O:334:TRP:NE1	2.22	0.54
10:Z:22:ARG:O	10:Z:25:VAL:HB	2.07	0.54
10:Z:66:ASN:OD1	10:Z:67:LYS:N	2.41	0.54
10:Z:92:GLU:OE1	10:Z:96:LYS:HE3	2.07	0.54
14:E:61:C:OP2	14:E:80:U:O2'	2.25	0.54
17:c:21:LEU:O	17:c:24:ALA:N	2.41	0.54
20:v:560:UNK:HA	20:v:570:THR:HG21	1.89	0.54
24:F:98:GLU:O	32:Y:53:PRO:CA	2.56	0.54
1:A:888:GLU:O	1:A:892:SER:HB3	2.08	0.54
1:A:1039:TRP:CD2	1:A:1271:PRO:HB3	2.43	0.54
1:A:1580:GLY:C	1:A:1582:GLU:H	2.16	0.54
1:A:1736:VAL:HA	1:A:1775:ILE:O	2.07	0.54
2:C:315:SER:O	2:C:319:GLY:CA	2.56	0.54
2:C:801:TRP:HE1	2:C:843:LYS:HD2	1.72	0.54
4:O:202:GLU:OE1	4:O:226:GLY:HA3	2.08	0.54
7:R:19:PRO:CB	14:E:36:U:O4	2.56	0.54
7:R:244:LEU:O	7:R:247:LEU:HB3	2.08	0.54
10:Z:60:VAL:O	10:Z:64:THR:CB	2.56	0.54
1:A:762:VAL:HG21	1:A:786:LEU:HD11	1.88	0.53
1:A:1034:ASN:HB3	1:A:1291:GLU:HG3	1.89	0.53
1:A:1693:LYS:HE3	1:A:1695:ASN:HB2	1.88	0.53
4:O:437:GLU:OE1	4:O:438:PRO:HA	2.08	0.53
6:Q:221:ASP:OD1	6:Q:225:GLN:NE2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:T:88:ASP:HB3	9:T:91:LEU:HB3	1.90	0.53
10:Z:326:VAL:CG1	10:Z:364:THR:HG21	2.38	0.53
10:Z:437:GLN:HA	10:Z:473:LEU:HD21	1.89	0.53
10:Z:454:ASP:O	10:Z:458:ILE:HG13	2.08	0.53
16:M:498:C:H6	16:M:498:C:O5'	1.92	0.53
17:c:230:THR:O	17:c:232:THR:N	2.33	0.53
18:d:238:TRP:HD1	18:d:242:GLU:CD	2.16	0.53
22:q:341:ASP:O	22:q:342:SER:CB	2.56	0.53
24:k:31:ILE:HD11	24:k:49:ILE:HD12	1.90	0.53
1:A:968:ASP:CG	17:c:46:ARG:HH21	2.14	0.53
1:A:1326:THR:O	1:A:1327:THR:OG1	2.21	0.53
1:A:1375:LEU:O	1:A:1376:ASN:ND2	2.41	0.53
1:A:2034:ILE:CG1	1:A:2041:PRO:HA	2.38	0.53
2:C:116:THR:HG21	2:C:120:ARG:CZ	2.38	0.53
2:C:120:ARG:O	2:C:123:MET:HB3	2.08	0.53
2:C:324:ILE:O	2:C:328:VAL:HG23	2.08	0.53
2:C:767:SER:OG	2:C:796:ILE:HD13	2.08	0.53
7:R:47:PHE:CE2	14:E:37:U:O2	2.61	0.53
9:T:120:CYS:HB2	9:T:122:CYS:CB	2.38	0.53
10:Z:408:THR:HB	10:Z:410:GLU:HB3	1.89	0.53
1:A:304:ASP:CG	1:A:306:PRO:HD2	2.33	0.53
1:A:1281:ASN:HD22	1:A:1285:VAL:CG2	2.21	0.53
1:A:1592:HIS:CE1	33:b:4:U:H5'	2.44	0.53
1:A:1605:ARG:NE	1:A:1824:GLN:OE1	2.42	0.53
1:A:1753:ARG:O	1:A:1757:LEU:HG	2.09	0.53
2:C:292:ILE:O	2:C:295:ILE:HG12	2.07	0.53
2:C:385:PHE:HE1	2:C:425:LEU:HD11	1.73	0.53
2:C:490:SER:HA	2:C:558:LYS:HD3	1.89	0.53
2:C:608:GLN:O	2:C:668:ILE:HB	2.09	0.53
2:C:807:PRO:HG3	2:C:850:LEU:HD23	1.90	0.53
4:O:333:SER:OG	4:O:334:TRP:N	2.40	0.53
9:T:151:ARG:O	21:n:63:ARG:CZ	2.55	0.53
15:L:15:C:C5	19:I:209:ARG:HG2	2.43	0.53
1:A:470:LEU:HB3	1:A:471:PRO:HD2	1.90	0.53
1:A:1910:LYS:O	1:A:1913:THR:OG1	2.25	0.53
4:O:380:SER:OG	4:O:381:GLY:N	2.39	0.53
5:P:80:ALA:O	5:P:83:ALA:N	2.41	0.53
5:P:127:VAL:HG11	14:E:32:U:H3	1.74	0.53
10:Z:74:PRO:CA	10:Z:123:ILE:HG21	2.32	0.53
10:Z:77:SER:O	10:Z:81:ALA:N	2.28	0.53
10:Z:97:GLU:HG3	10:Z:101:MET:HE2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:D:174:G:H8	30:g:99:ASP:OD2	1.91	0.53
15:L:1114:G:H8	15:L:1114:G:O5'	1.91	0.53
1:A:234:PHE:CE2	1:A:700:GLY:HA2	2.43	0.53
1:A:380:ARG:NH2	1:A:382:GLU:OE2	2.41	0.53
1:A:383:TYR:CE1	2:C:913:GLY:HA3	2.44	0.53
1:A:725:TYR:CD1	14:E:72:C:H1'	2.44	0.53
1:A:752:ALA:O	1:A:756:LEU:HB2	2.08	0.53
1:A:905:TYR:HB3	1:A:908:ASP:HB2	1.90	0.53
1:A:1925:PRO:HD3	35:f:234:LYS:HD3	1.91	0.53
2:C:139:ILE:O	2:C:237:ILE:HA	2.08	0.53
5:P:105:LEU:H	5:P:108:ASN:HA	1.74	0.53
5:P:111:HIS:HB2	6:Q:22:ASN:HA	1.90	0.53
10:Z:28:ILE:HG21	10:Z:44:LEU:HD13	1.90	0.53
10:Z:448:MET:HE2	10:Z:449:PHE:CZ	2.44	0.53
13:D:75:A:C4'	13:D:76:U:H5'	2.28	0.53
15:L:1102:C:C2'	15:L:1103:C:H6	2.15	0.53
18:d:259:GLU:HB3	18:d:262:ARG:HB3	1.90	0.53
22:p:102:LEU:O	22:p:105:LEU:CG	2.57	0.53
33:b:4:U:H2'	33:b:5:U:C4	2.44	0.53
35:f:90:THR:O	35:f:90:THR:HG22	2.08	0.53
1:A:284:ARG:NH2	13:D:33:U:O4	2.42	0.53
1:A:477:MET:HE3	2:C:275:LEU:HA	1.91	0.53
1:A:1082:ILE:C	1:A:1085:LYS:H	2.14	0.53
1:A:1458:TRP:CZ2	1:A:1489:PRO:HB2	2.43	0.53
1:A:2063:TYR:HA	1:A:2067:TYR:CD1	2.44	0.53
2:C:473:LEU:HD12	2:C:485:LEU:HD22	1.90	0.53
2:C:715:MET:HB2	2:C:720:ILE:HD11	1.89	0.53
13:D:31:G:C2'	13:D:32:G:H5'	2.39	0.53
15:L:1103:C:C6	15:L:1114:G:N2	2.76	0.53
20:v:682:LYS:O	20:v:686:ILE:HG12	2.08	0.53
22:q:292:TYR:CB	22:q:336:GLY:N	2.72	0.53
1:A:564:TRP:O	1:A:567:ALA:N	2.42	0.53
2:C:761:ALA:O	2:C:764:ASN:N	2.41	0.53
7:R:230:PRO:HG3	12:N:114:U:C4	2.42	0.53
9:T:151:ARG:O	21:n:63:ARG:NH2	2.41	0.53
10:Z:102:PHE:HZ	10:Z:142:LEU:HD21	1.73	0.53
13:D:107:C:H2'	13:D:108:C:O4'	2.08	0.53
15:L:1116:A:C5	15:L:1117:G:C5	2.97	0.53
17:c:104:ARG:HA	17:c:107:GLU:HB2	1.91	0.53
18:d:193:VAL:HG12	18:d:201:THR:HB	1.91	0.53
24:F:31:ILE:HD11	24:F:49:ILE:HD12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:f:223:ASP:CG	35:f:224:GLU:N	2.66	0.53
1:A:770:MET:O	4:O:309:ARG:NH2	2.42	0.53
1:A:1720:THR:OG1	1:A:1721:ASN:N	2.42	0.53
1:A:1751:TYR:CE1	1:A:1755:LYS:HG3	2.43	0.53
10:Z:172:MET:O	10:Z:175:GLU:HB3	2.09	0.53
10:Z:445:LEU:O	10:Z:449:PHE:HB2	2.08	0.53
15:L:28:U:O2'	15:L:29:C:H5'	2.08	0.53
19:I:193:GLU:OE1	19:I:204:ASN:HB3	2.08	0.53
1:A:161:PHE:CE1	1:A:198:ALA:HA	2.44	0.53
1:A:285:PRO:HD2	1:A:298:TYR:OH	2.08	0.53
1:A:854:ARG:NH2	15:L:25:A:H5''	2.17	0.53
1:A:1413:SER:OG	1:A:1414:TRP:N	2.42	0.53
2:C:485:LEU:HA	2:C:563:LEU:HD23	1.91	0.53
2:C:758:ASP:HB3	2:C:761:ALA:HB3	1.89	0.53
15:L:119:G:H8	30:W:99:ASP:OD2	1.91	0.53
15:L:1105:C:H42	31:X:97:LYS:NZ	2.07	0.53
18:d:137:TYR:HA	18:d:140:LEU:HD12	1.90	0.53
1:A:526:LEU:O	1:A:529:TYR:N	2.41	0.53
1:A:541:ASN:ND2	13:D:40:C:C4	2.77	0.53
1:A:618:SER:O	1:A:621:LEU:N	2.42	0.53
1:A:776:GLN:H	1:A:776:GLN:CD	2.17	0.53
1:A:847:LYS:HG2	15:L:24:U:C6	2.44	0.53
1:A:1232:SER:OG	1:A:1233:ARG:N	2.40	0.53
4:O:358:ILE:HA	4:O:364:LEU:HD12	1.91	0.53
13:D:96:U:O5'	13:D:96:U:H6	1.91	0.53
1:A:239:PHE:HD1	1:A:241:PRO:HD3	1.72	0.52
1:A:374:ILE:HG21	2:C:966:PHE:CE1	2.43	0.52
1:A:514:TYR:HB3	1:A:518:VAL:CG2	2.40	0.52
1:A:1505:ASP:OD1	1:A:1506:ARG:N	2.42	0.52
1:A:1576:GLU:OE1	1:A:1826:TYR:HB2	2.09	0.52
1:A:1992:TYR:HB3	1:A:1995:TRP:HB2	1.91	0.52
2:C:142:LEU:HD12	2:C:929:GLN:NE2	2.24	0.52
2:C:428:ILE:HG22	2:C:429:PHE:HD1	1.74	0.52
18:d:160:CYS:HB3	18:d:169:TRP:CH2	2.43	0.52
22:q:298:ASN:O	22:q:299:THR:CB	2.57	0.52
35:f:225:ARG:NH1	35:f:225:ARG:HB2	2.24	0.52
1:A:137:GLU:O	1:A:138:HIS:C	2.52	0.52
1:A:783:LEU:HD12	1:A:783:LEU:N	2.24	0.52
2:C:922:THR:OG1	2:C:925:LEU:O	2.14	0.52
13:D:43:G:O2'	13:D:45:A:H5'	2.09	0.52
15:L:17:U:H4'	15:L:18:U:OP2	2.07	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:1116:A:N6	15:L:1117:G:C6	2.78	0.52
21:n:55:GLU:O	21:n:58:ARG:HG3	2.09	0.52
25:G:27:VAL:HG22	25:G:92:SER:HB2	1.91	0.52
1:A:936:GLU:O	1:A:939:LEU:N	2.43	0.52
1:A:1709:TRP:O	1:A:1728:ILE:CA	2.42	0.52
2:C:147:THR:OG1	2:C:214:ASP:OD2	2.24	0.52
2:C:272:ARG:HG3	36:C:1500:GTP:HN21	1.75	0.52
2:C:365:GLU:CG	2:C:366:ASN:H	2.18	0.52
2:C:699:GLY:O	2:C:707:SER:OG	2.27	0.52
4:O:304:LEU:HD13	4:O:334:TRP:CE3	2.43	0.52
16:M:484:U:H2'	16:M:485:U:C2	2.43	0.52
35:f:100:ILE:HD12	35:f:194:PRO:HG3	1.91	0.52
1:A:138:HIS:O	1:A:142:ILE:HG12	2.08	0.52
1:A:466:GLU:OE1	1:A:466:GLU:N	2.36	0.52
1:A:910:LYS:O	1:A:913:VAL:HB	2.09	0.52
1:A:1624:LEU:HD21	1:A:1635:HIS:CE1	2.45	0.52
1:A:1653:LEU:O	1:A:1657:ILE:HG13	2.08	0.52
1:A:2017:THR:HG21	1:A:2059:ILE:HG12	1.91	0.52
2:C:798:GLY:O	2:C:801:TRP:HB3	2.09	0.52
2:C:831:ILE:O	2:C:835:LYS:HE2	2.10	0.52
9:T:131:GLU:OE2	9:T:135:LYS:NZ	2.32	0.52
14:E:89:U:O2	14:E:89:U:H2'	2.08	0.52
15:L:30:A:H4'	15:L:31:A:OP1	2.09	0.52
16:M:493:A:H2'	16:M:494:G:O4'	2.09	0.52
19:I:145:LYS:HG2	19:I:152:ILE:HG13	1.90	0.52
35:f:163:LEU:O	35:f:167:LEU:HD13	2.10	0.52
1:A:514:TYR:HB3	1:A:518:VAL:HG23	1.92	0.52
1:A:930:ASN:OD1	15:L:30:A:OP1	2.27	0.52
1:A:971:MET:HE3	1:A:978:ILE:HG22	1.92	0.52
2:C:234:LEU:HB2	2:C:262:ALA:O	2.10	0.52
2:C:916:THR:O	2:C:919:ARG:N	2.42	0.52
6:Q:108:MET:SD	14:E:66:C:H1'	2.50	0.52
7:R:117:PHE:HB2	14:E:39:G:N1	2.24	0.52
7:R:183:PHE:CD2	12:N:113:U:C5	2.98	0.52
10:Z:82:LEU:HD21	10:Z:215:LEU:HD21	1.92	0.52
35:f:246:ASN:O	35:f:247:HIS:ND1	2.42	0.52
1:A:381:SER:OG	1:A:382:GLU:N	2.41	0.52
1:A:839:HIS:HB2	13:D:95:C:N3	2.25	0.52
1:A:897:PRO:O	1:A:1006:ARG:NH1	2.43	0.52
1:A:1716:LEU:H	1:A:1719:GLU:HB2	1.74	0.52
2:C:429:PHE:N	2:C:429:PHE:CD1	2.77	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:T:100:TYR:O	9:T:102:LYS:N	2.43	0.52
10:Z:18:TRP:HB2	10:Z:242:PHE:CD1	2.45	0.52
10:Z:69:ASN:OD1	10:Z:72:LEU:HB2	2.09	0.52
21:n:230:VAL:CA	21:n:244:LEU:CG	2.88	0.52
1:A:472:ASN:O	1:A:474:LYS:N	2.43	0.52
1:A:1086:ASN:O	1:A:1088:VAL:HG13	2.10	0.52
1:A:1275:MET:O	1:A:1276:GLU:HG2	2.10	0.52
2:C:323:THR:O	2:C:326:GLU:N	2.43	0.52
5:P:127:VAL:HG11	14:E:32:U:C4	2.45	0.52
6:Q:215:PRO:CG	6:Q:217:TRP:CZ2	2.65	0.52
13:D:103:A:O2'	13:D:104:G:OP2	2.25	0.52
15:L:41:C:H2'	15:L:42:U:C6	2.45	0.52
17:c:202:LYS:O	17:c:204:LYS:N	2.36	0.52
21:n:244:LEU:C	21:n:245:HIS:CG	2.86	0.52
22:p:124:ALA:O	22:p:127:LEU:CG	2.58	0.52
1:A:1312:PHE:CD1	1:A:1342:LEU:HD13	2.44	0.52
1:A:1431:HIS:CG	1:A:1434:GLU:HA	2.45	0.52
1:A:1856:ASN:HD21	1:A:1968:ALA:HB3	1.75	0.52
2:C:109:LEU:HD23	2:C:111:LYS:HG2	1.92	0.52
2:C:454:ALA:HB1	2:C:459:PRO:HA	1.92	0.52
2:C:775:ILE:HB	2:C:819:LYS:HG2	1.91	0.52
7:R:46:ARG:NH2	7:R:220:GLY:O	2.42	0.52
7:R:117:PHE:CD2	14:E:39:G:C5	2.97	0.52
10:Z:431:LEU:HD12	10:Z:436:LEU:HD13	1.92	0.52
21:n:51:PHE:HE1	21:n:55:GLU:HG3	1.75	0.52
1:A:395:PRO:HB2	1:A:398:VAL:HG21	1.92	0.52
1:A:898:ILE:HG22	1:A:899:PRO:O	2.10	0.52
1:A:1460:GLU:O	1:A:1463:THR:OG1	2.25	0.52
2:C:240:ASP:OD2	2:C:269:LYS:NZ	2.25	0.52
2:C:268:ASN:HA	2:C:314:ALA:O	2.10	0.52
2:C:277:LEU:HB3	2:C:279:LEU:CD1	2.40	0.52
14:E:92:C:O2	15:L:13:G:N2	2.42	0.52
18:d:122:MET:HE2	18:d:122:MET:HA	1.92	0.52
22:q:405:ASP:CB	23:t:30:ASN:CG	2.83	0.52
1:A:329:TYR:CE1	2:C:919:ARG:HD2	2.45	0.52
1:A:1888:HIS:HA	1:A:1989:PHE:O	2.09	0.52
1:A:2043:PHE:HB2	1:A:2048:TRP:CD1	2.45	0.52
2:C:440:THR:O	2:C:443:TYR:N	2.43	0.52
4:O:328:THR:O	4:O:353:ILE:HG12	2.10	0.52
7:R:182:GLY:O	7:R:183:PHE:HD1	1.93	0.52
7:R:237:ARG:O	7:R:240:GLU:HB3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Z:339:PHE:HE2	10:Z:387:PHE:HA	1.74	0.52
1:A:371:ASP:HB3	2:C:972:ARG:HD3	1.92	0.51
1:A:401:PRO:O	1:A:402:TRP:HB3	2.10	0.51
1:A:1137:PRO:HG2	1:A:1140:ASN:HB2	1.92	0.51
1:A:1988:LEU:HD12	35:f:181:GLN:HA	1.92	0.51
2:C:355:HIS:ND1	2:C:366:ASN:HB2	2.25	0.51
4:O:152:ASN:ND2	4:O:409:LYS:HB3	2.24	0.51
4:O:182:VAL:HG23	4:O:183:MET:H	1.74	0.51
7:R:169:ASP:N	7:R:169:ASP:OD1	2.42	0.51
15:L:2:C:O5'	15:L:2:C:H6	1.92	0.51
17:c:213:TYR:HD2	18:d:52:THR:HG22	1.75	0.51
21:n:444:CYS:O	21:n:444:CYS:SG	2.66	0.51
1:A:143:ILE:O	1:A:147:SER:OG	2.19	0.51
1:A:623:ARG:NH2	1:A:624:GLU:OE2	2.44	0.51
1:A:1587:PHE:CZ	15:L:31:A:H5''	2.42	0.51
1:A:1699:ALA:HB1	1:A:1733:TRP:CG	2.45	0.51
2:C:233:ASP:OD1	2:C:487:ARG:NH2	2.43	0.51
2:C:325:LYS:NZ	2:C:441:ARG:HH12	2.08	0.51
4:O:243:GLY:O	4:O:245:ASP:N	2.44	0.51
6:Q:217:TRP:CD1	6:Q:217:TRP:C	2.87	0.51
10:Z:69:ASN:CB	10:Z:73:ILE:HG13	2.40	0.51
15:L:15:C:H1'	15:L:16:U:C5	2.45	0.51
17:c:218:VAL:HG12	17:c:219:TYR:CD2	2.45	0.51
18:d:99:ILE:HA	18:d:102:TRP:HD1	1.75	0.51
18:d:106:ILE:O	18:d:109:GLU:N	2.42	0.51
19:I:183:MET:O	19:I:187:LYS:HG2	2.10	0.51
20:v:680:ILE:O	20:v:683:SER:OG	2.22	0.51
1:A:239:PHE:CE2	1:A:655:TYR:HD2	2.29	0.51
1:A:933:GLU:H	1:A:933:GLU:CD	2.13	0.51
1:A:1142:ASN:HB3	1:A:1146:GLN:HB2	1.92	0.51
1:A:1302:LEU:O	1:A:1303:LYS:HG3	2.10	0.51
1:A:1400:ILE:HG23	1:A:1542:TYR:CZ	2.45	0.51
2:C:343:ASP:O	2:C:346:THR:OG1	2.24	0.51
2:C:365:GLU:HG3	2:C:366:ASN:N	2.19	0.51
2:C:717:SER:O	2:C:721:GLN:CB	2.59	0.51
4:O:302:LYS:NZ	4:O:338:GLU:O	2.43	0.51
6:Q:90:LEU:HD21	7:R:246:SER:HB3	1.92	0.51
7:R:89:TYR:CE2	14:E:34:A:C4	2.98	0.51
17:c:148:GLU:HA	17:c:151:MET:HE3	1.91	0.51
1:A:1047:ALA:HA	1:A:1172:PHE:O	2.10	0.51
2:C:711:ALA:O	2:C:818:TYR:HA	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:749:LYS:O	2:C:753:THR:OG1	2.21	0.51
15:L:1107:C:H5'	15:L:1107:C:C6	2.44	0.51
19:I:187:LYS:HA	19:I:201:LYS:NZ	2.24	0.51
24:F:47:GLU:CB	32:Y:15:TYR:CG	2.93	0.51
1:A:569:LEU:O	1:A:572:CYS:N	2.43	0.51
1:A:1051:GLU:HG2	1:A:1169:TYR:HE1	1.75	0.51
1:A:1156:HIS:HD2	1:A:1158:ILE:HB	1.74	0.51
1:A:1347:ARG:HD2	1:A:1447:TRP:CE2	2.45	0.51
1:A:1944:LEU:O	1:A:1948:MET:HG2	2.09	0.51
1:A:2024:MET:O	1:A:2028:SER:N	2.44	0.51
2:C:92:GLU:HG2	2:C:93:PRO:O	2.10	0.51
3:J:9:LYS:O	3:J:10:SER:OG	2.21	0.51
4:O:161:ASP:O	4:O:162:THR:OG1	2.24	0.51
5:P:43:PHE:N	5:P:43:PHE:CD1	2.77	0.51
7:R:174:ARG:HH22	12:N:114:U:C5'	2.24	0.51
8:S:8:GLN:HG2	8:S:10:GLU:H	1.76	0.51
10:Z:480:ARG:HD3	10:Z:483:ILE:HD12	1.92	0.51
13:D:78:A:H4'	13:D:79:C:OP1	2.11	0.51
15:L:49:U:H6	15:L:49:U:H5''	1.75	0.51
18:d:154:SER:O	18:d:157:THR:HB	2.11	0.51
19:I:106:GLU:O	19:I:109:LEU:HB2	2.10	0.51
33:b:4:U:H2'	33:b:5:U:N3	2.26	0.51
1:A:1025:VAL:HG21	1:A:1265:PHE:CD2	2.45	0.51
1:A:1033:ASN:HB2	1:A:1288:LEU:HD13	1.93	0.51
1:A:1423:THR:C	1:A:1424:HIS:CG	2.89	0.51
1:A:1559:HIS:CE1	1:A:1743:TYR:CZ	2.99	0.51
2:C:778:THR:HG23	2:C:781:ASP:H	1.75	0.51
6:Q:25:MET:HB2	6:Q:45:HIS:O	2.10	0.51
7:R:180:ASN:HB2	12:N:111:U:C6	2.46	0.51
8:S:8:GLN:O	8:S:10:GLU:N	2.44	0.51
15:L:1105:C:N4	31:X:97:LYS:HZ1	2.09	0.51
16:M:492:U:H2'	16:M:493:A:C8	2.45	0.51
21:n:59:ARG:HH11	21:n:59:ARG:CG	2.24	0.51
25:i:27:VAL:HG22	25:i:92:SER:HB2	1.91	0.51
1:A:176:LEU:HD23	1:A:176:LEU:O	2.10	0.51
1:A:255:ILE:O	1:A:258:ILE:HG22	2.11	0.51
1:A:314:LEU:O	1:A:316:THR:N	2.44	0.51
1:A:705:GLN:HB3	1:A:706:PRO:HD3	1.92	0.51
1:A:1865:THR:OG1	1:A:1869:ASN:N	2.43	0.51
2:C:106:PHE:CZ	2:C:478:TYR:HD2	2.28	0.51
2:C:418:GLN:HB3	2:C:419:PRO:HD3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Q:38:THR:C	6:Q:39:LEU:HD12	2.36	0.51
1:A:223:ALA:HB2	1:A:266:LEU:HD12	1.92	0.51
1:A:639:PHE:HB2	1:A:649:LEU:HD13	1.93	0.51
1:A:1150:LYS:HB3	1:A:1154:LYS:HZ3	1.76	0.51
1:A:1303:LYS:NZ	1:A:1353:THR:HG22	2.26	0.51
2:C:315:SER:HB3	2:C:320:PHE:CE1	2.46	0.51
2:C:707:SER:O	2:C:708:ILE:HD13	2.11	0.51
5:P:34:ILE:HD11	18:d:155:LEU:HD13	1.92	0.51
5:P:43:PHE:HE1	5:P:147:LEU:HD22	1.76	0.51
10:Z:159:GLY:O	10:Z:163:ALA:CB	2.58	0.51
16:M:489:A:H2'	16:M:490:A:H8	1.76	0.51
22:q:309:GLY:O	22:q:325:HIS:CG	2.63	0.51
24:F:99:ASP:CA	32:Y:53:PRO:CB	2.88	0.51
1:A:259:GLU:CG	1:A:260:PRO:HD2	2.40	0.51
1:A:307:GLU:O	1:A:310:ASN:N	2.44	0.51
1:A:614:ARG:CZ	11:B:98:A:C4'	2.85	0.51
2:C:246:THR:HG23	2:C:248:VAL:HG12	1.93	0.51
2:C:734:CYS:SG	2:C:735:LEU:N	2.84	0.51
2:C:793:GLU:HA	2:C:796:ILE:HG22	1.92	0.51
2:C:862:TYR:CD2	2:C:930:LEU:HB3	2.46	0.51
4:O:380:SER:OG	4:O:382:HIS:N	2.39	0.51
5:P:147:LEU:HD12	5:P:147:LEU:O	2.11	0.51
6:Q:22:ASN:OD1	6:Q:23:ILE:N	2.44	0.51
7:R:127:ILE:HD12	14:E:39:G:C8	2.46	0.51
11:B:99:G:N2	33:b:2:U:OP1	2.44	0.51
14:E:90:U:H5	18:d:104:ARG:HH22	1.55	0.51
15:L:1102:C:O2'	15:L:1103:C:H5'	2.10	0.51
16:M:484:U:H3'	16:M:484:U:H6	1.75	0.51
1:A:215:ALA:O	1:A:218:SER:N	2.42	0.51
1:A:583:ILE:O	1:A:586:LYS:N	2.40	0.51
1:A:776:GLN:HG2	1:A:777:LYS:N	2.23	0.51
1:A:1063:PHE:CB	17:c:83:GLN:HE21	2.23	0.51
1:A:1283:GLU:OE1	1:A:1446:THR:HG21	2.10	0.51
1:A:1733:TRP:CD1	1:A:1769:SER:HG	2.29	0.51
1:A:1849:LYS:O	1:A:1884:PRO:HD2	2.11	0.51
1:A:1986:MET:HG3	35:f:184:MET:CG	2.31	0.51
2:C:307:ILE:HG12	2:C:346:THR:HA	1.93	0.51
2:C:497:ASP:N	2:C:497:ASP:OD1	2.43	0.51
7:R:55:PRO:HB3	7:R:93:ILE:HD11	1.92	0.51
14:E:59:A:H3'	14:E:60:G:H5''	1.93	0.51
14:E:85:C:OP1	14:E:85:C:C4'	2.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:20:G:O5'	15:L:20:G:H8	1.93	0.51
17:c:189:ARG:HG2	18:d:38:LEU:HD21	1.93	0.51
1:A:953:ARG:HG2	1:A:957:TYR:CE2	2.46	0.50
1:A:985:ASP:OD1	17:c:46:ARG:NH1	2.45	0.50
1:A:1795:LYS:O	1:A:1799:GLN:HG3	2.10	0.50
2:C:101:GLN:O	2:C:101:GLN:HG2	2.11	0.50
2:C:172:TRP:CD1	2:C:172:TRP:N	2.79	0.50
5:P:202:MET:SD	17:c:79:GLU:HG3	2.51	0.50
7:R:34:TYR:CZ	14:E:41:A:H1'	2.46	0.50
7:R:234:ALA:O	7:R:237:ARG:HB2	2.10	0.50
14:E:49:A:N7	14:E:50:G:N7	2.59	0.50
22:q:175:PRO:O	22:q:467:LEU:CG	2.59	0.50
1:A:839:HIS:ND1	1:A:839:HIS:O	2.44	0.50
1:A:953:ARG:HG2	1:A:957:TYR:HE2	1.76	0.50
1:A:1048:VAL:HA	1:A:1249:SER:O	2.12	0.50
1:A:1094:ASP:OD1	15:L:25:A:C2	2.64	0.50
1:A:1878:CYS:SG	1:A:1891:LEU:HD22	2.50	0.50
4:O:162:THR:HG21	4:O:182:VAL:O	2.12	0.50
7:R:22:ILE:HG22	7:R:30:PHE:CZ	2.46	0.50
7:R:75:PHE:HE2	14:E:35:A:H8	1.04	0.50
7:R:233:ALA:O	7:R:237:ARG:HG3	2.11	0.50
9:T:151:ARG:NH2	21:n:69:TRP:O	2.44	0.50
10:Z:159:GLY:HA2	10:Z:162:LEU:HB3	1.92	0.50
14:E:91:A:O2'	19:I:100:LEU:HD22	2.11	0.50
15:L:1116:A:C5	15:L:1117:G:N7	2.79	0.50
18:d:136:TRP:CZ3	18:d:159:TRP:HB2	2.47	0.50
26:H:74:ARG:HD3	30:W:101:VAL:O	2.12	0.50
1:A:224:MET:O	1:A:225:ARG:C	2.54	0.50
1:A:709:ARG:NH2	13:D:82:A:O3'	2.45	0.50
1:A:1861:THR:HG21	1:A:1875:ILE:HG13	1.93	0.50
2:C:362:LYS:HD3	2:C:365:GLU:HB3	1.93	0.50
5:P:182:LEU:O	5:P:185:ARG:N	2.39	0.50
9:T:100:TYR:O	9:T:103:LEU:N	2.42	0.50
10:Z:354:HIS:CD2	10:Z:356:SER:H	2.29	0.50
16:M:493:A:H2'	16:M:494:G:C1'	2.41	0.50
22:o:51:VAL:CG2	22:p:20:ARG:CB	2.77	0.50
1:A:193:TYR:CE1	1:A:558:GLN:HB2	2.46	0.50
1:A:929:LEU:HD22	1:A:933:GLU:HB3	1.94	0.50
1:A:1011:ASN:ND2	1:A:1143:GLU:O	2.44	0.50
1:A:1067:ASN:ND2	17:c:81:PRO:HB2	2.27	0.50
1:A:1508:HIS:HB2	1:A:1529:ASN:HD21	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1669:LEU:HD23	1:A:1672:GLU:HG3	1.92	0.50
2:C:585:ASP:O	2:C:588:GLN:HB3	2.11	0.50
9:T:121:ILE:HD11	9:T:129:LEU:HD21	1.93	0.50
13:D:83:C:HO2'	13:D:84:A:P	2.35	0.50
1:A:779:ALA:O	1:A:782:ILE:N	2.44	0.50
1:A:982:TYR:HD2	1:A:1106:GLY:H	1.59	0.50
2:C:142:LEU:HB3	2:C:143:HIS:CD2	2.46	0.50
2:C:285:TYR:HD2	2:C:286:LEU:HD12	1.76	0.50
2:C:677:PHE:HB2	2:C:811:GLU:OE1	2.10	0.50
6:Q:106:ASN:HD21	17:c:212:ASP:HB3	1.76	0.50
6:Q:109:MET:SD	17:c:218:VAL:O	2.70	0.50
6:Q:222:THR:HA	6:Q:225:GLN:OE1	2.10	0.50
10:Z:143:LEU:HB3	10:Z:176:LYS:HZ3	1.77	0.50
14:E:91:A:C4	18:d:99:ILE:CD1	2.94	0.50
22:r:124:ALA:O	22:r:127:LEU:CG	2.59	0.50
1:A:709:ARG:NH2	13:D:83:C:P	2.84	0.50
1:A:1023:LEU:HB2	1:A:1451:PHE:CE1	2.46	0.50
1:A:1304:VAL:H	1:A:1353:THR:HG21	1.77	0.50
1:A:1343:PHE:HD1	1:A:1350:ILE:HD13	1.76	0.50
1:A:1606:PHE:O	1:A:1609:TRP:N	2.45	0.50
1:A:1922:ARG:HG2	1:A:1951:PHE:CZ	2.46	0.50
1:A:1935:VAL:O	1:A:1959:THR:HG23	2.11	0.50
2:C:499:VAL:HG11	2:C:577:LEU:HG	1.93	0.50
3:J:6:ILE:HD11	11:B:90:A:C6	2.46	0.50
7:R:146:LEU:HD23	7:R:147:ASN:N	2.25	0.50
7:R:229:ASP:CG	12:N:113:U:C2	2.89	0.50
10:Z:419:PHE:HD2	10:Z:420:ILE:HD12	1.75	0.50
14:E:11:U:C2	14:E:12:A:H1'	2.47	0.50
18:d:50:LYS:HE3	18:d:54:TYR:CE2	2.46	0.50
22:o:100:SER:O	22:o:103:ASP:CG	2.55	0.50
1:A:413:ASN:OD1	1:A:413:ASN:N	2.37	0.50
1:A:614:ARG:CZ	11:B:98:A:C5'	2.90	0.50
1:A:1924:LEU:CD2	35:f:234:LYS:CE	2.90	0.50
2:C:722:ASP:OD2	2:C:755:TYR:OH	2.15	0.50
2:C:817:GLN:NE2	2:C:819:LYS:HE3	2.25	0.50
3:J:6:ILE:HD11	11:B:90:A:N6	2.27	0.50
4:O:213:LYS:HZ2	13:D:107:C:H5''	1.77	0.50
10:Z:104:GLN:HB3	10:Z:108:ARG:HH22	1.77	0.50
17:c:213:TYR:CD2	18:d:52:THR:HG22	2.47	0.50
20:v:606:GLN:HA	20:v:609:GLU:HG3	1.94	0.50
1:A:1077:ASN:O	1:A:1080:ASP:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1366:ARG:HA	1:A:1369:ASN:HD22	1.77	0.50
1:A:1877:GLY:C	1:A:1894:ILE:HB	2.37	0.50
1:A:2013:ARG:NH2	1:A:2083:ILE:O	2.45	0.50
2:C:261:VAL:HG12	2:C:262:ALA:N	2.27	0.50
4:O:392:MET:HG3	4:O:393:VAL:N	2.26	0.50
15:L:25:A:H2'	15:L:27:A:OP2	2.12	0.50
33:b:7:U:H5'	33:b:7:U:H6	1.77	0.50
1:A:429:ASN:HB3	1:A:430:PRO:HD2	1.94	0.50
1:A:633:VAL:O	1:A:637:VAL:HG23	2.12	0.50
1:A:745:THR:HG21	4:O:182:VAL:HG21	1.94	0.50
1:A:1203:ASN:HD22	1:A:1213:MET:HB3	1.77	0.50
1:A:1339:LEU:O	1:A:1342:LEU:N	2.45	0.50
1:A:1362:LYS:NZ	3:J:14:SER:HA	2.26	0.50
2:C:501:ILE:HD13	2:C:567:ILE:HG21	1.94	0.50
2:C:758:ASP:O	2:C:762:SER:N	2.33	0.50
5:P:127:VAL:CG1	14:E:32:U:O4	2.60	0.50
5:P:227:ARG:O	5:P:231:GLU:HB2	2.11	0.50
7:R:89:TYR:CE2	14:E:34:A:N3	2.80	0.50
10:Z:104:GLN:HA	10:Z:107:ASN:HD22	1.77	0.50
10:Z:384:LEU:HB3	10:Z:419:PHE:CE1	2.41	0.50
14:E:89:U:H5	19:I:179:ARG:HB3	1.74	0.50
18:d:261:GLU:O	18:d:265:ALA:CB	2.58	0.50
19:I:116:THR:O	19:I:119:SER:OG	2.22	0.50
21:n:200:ARG:CG	21:n:201:ASP:H	2.24	0.50
35:f:155:LEU:HD22	35:f:159:LEU:HD23	1.94	0.50
1:A:168:LEU:HD21	1:A:626:LEU:HD21	1.94	0.49
1:A:284:ARG:CZ	13:D:33:U:O4	2.60	0.49
1:A:725:TYR:HE1	14:E:72:C:C2	2.30	0.49
1:A:743:LYS:HD3	1:A:749:ARG:CZ	2.42	0.49
1:A:1286:TRP:NE1	1:A:1302:LEU:HD11	2.27	0.49
1:A:1613:THR:OG1	1:A:1614:ILE:N	2.43	0.49
2:C:484:SER:O	2:C:563:LEU:HA	2.12	0.49
2:C:863:GLU:OE2	2:C:934:HIS:ND1	2.44	0.49
4:O:341:LEU:HG	4:O:342:LEU:O	2.12	0.49
5:P:105:LEU:N	5:P:108:ASN:HA	2.27	0.49
7:R:169:ASP:OD2	7:R:187:LYS:HD2	2.12	0.49
9:T:143:HIS:O	9:T:151:ARG:HG2	2.12	0.49
13:D:174:G:OP2	26:h:76:ASN:HB2	2.12	0.49
14:E:50:G:H8	14:E:50:G:OP2	1.95	0.49
1:A:828:HIS:O	1:A:829:TYR:C	2.55	0.49
1:A:1161:TYR:HE1	1:A:1168:ILE:HG23	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1390:THR:OG1	1:A:1396:GLY:HA3	2.12	0.49
1:A:1588:LYS:O	1:A:1590:LEU:N	2.45	0.49
1:A:2009:THR:O	1:A:2013:ARG:HG3	2.12	0.49
5:P:159:ASP:O	5:P:162:GLU:N	2.45	0.49
7:R:184:VAL:HG12	7:R:186:PHE:HE1	1.76	0.49
10:Z:12:LYS:HG3	10:Z:15:ARG:HH12	1.77	0.49
10:Z:413:CYS:O	10:Z:416:GLY:N	2.44	0.49
12:N:108:U:H4'	12:N:109:U:OP2	2.11	0.49
25:i:86:ASN:HD21	26:h:32:LYS:NZ	2.09	0.49
1:A:374:ILE:HD13	2:C:966:PHE:CD1	2.47	0.49
1:A:532:ASN:CG	13:D:84:A:OP2	2.54	0.49
1:A:608:LYS:HZ2	14:E:43:C:H5'	1.76	0.49
1:A:1144:PHE:CD2	1:A:1145:MET:HG2	2.40	0.49
1:A:1624:LEU:HD11	1:A:1635:HIS:CE1	2.47	0.49
1:A:1708:GLU:HA	1:A:1730:ASN:OD1	2.12	0.49
1:A:1902:GLN:HE21	1:A:1908:LEU:CD2	2.26	0.49
2:C:268:ASN:OD1	2:C:316:THR:HG23	2.12	0.49
2:C:348:LEU:HD21	2:C:377:ILE:HD11	1.92	0.49
4:O:237:ASP:O	4:O:238:LEU:HD23	2.12	0.49
9:T:120:CYS:C	9:T:122:CYS:N	2.68	0.49
9:T:151:ARG:HB2	21:n:63:ARG:HH12	1.77	0.49
10:Z:364:THR:O	10:Z:368:ASN:ND2	2.44	0.49
10:Z:452:GLU:CD	10:Z:452:GLU:H	2.20	0.49
13:D:103:A:O2'	13:D:104:G:P	2.70	0.49
15:L:119:G:OP2	26:H:76:ASN:HB2	2.12	0.49
15:L:1120:G:H8	15:L:1120:G:C5'	2.25	0.49
1:A:355:LEU:HD13	13:D:105:A:H5'	1.94	0.49
1:A:677:ILE:O	1:A:681:LYS:HG3	2.13	0.49
1:A:1117:TYR:OH	1:A:1238:LEU:HD22	2.13	0.49
1:A:1995:TRP:HE3	1:A:2004:ALA:HB1	1.76	0.49
2:C:312:ILE:HG12	2:C:323:THR:OG1	2.12	0.49
2:C:825:VAL:HG13	2:C:826:PRO:HD2	1.95	0.49
5:P:115:VAL:HG21	6:Q:24:ARG:HH11	1.77	0.49
9:T:14:ASP:C	9:T:16:PHE:H	2.21	0.49
10:Z:96:LYS:HG3	10:Z:227:TYR:OH	2.13	0.49
15:L:30:A:C4'	15:L:31:A:OP1	2.61	0.49
25:G:86:ASN:HD21	26:H:32:LYS:NZ	2.09	0.49
1:A:168:LEU:O	1:A:171:ALA:N	2.46	0.49
1:A:355:LEU:CD1	13:D:105:A:H5'	2.42	0.49
1:A:889:TRP:O	1:A:893:ARG:N	2.36	0.49
2:C:79:GLU:OE2	4:O:173:LYS:HD3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:138:VAL:HG21	2:C:150:MET:CE	2.43	0.49
2:C:221:PHE:HE1	2:C:651:TYR:HD1	1.60	0.49
2:C:254:LYS:O	2:C:258:LYS:CB	2.60	0.49
21:n:263:PHE:HB2	21:n:275:TYR:HB2	1.94	0.49
1:A:168:LEU:HB3	1:A:622:MET:CE	2.42	0.49
1:A:538:LEU:HD11	13:D:41:A:C6	2.48	0.49
1:A:763:MET:CE	1:A:779:ALA:HB1	2.43	0.49
1:A:871:GLY:N	5:P:198:ASN:HD22	2.11	0.49
1:A:1023:LEU:HD13	1:A:1451:PHE:CD1	2.47	0.49
1:A:1596:THR:HG23	33:b:4:U:C5'	2.24	0.49
2:C:254:LYS:O	2:C:258:LYS:HB2	2.12	0.49
7:R:63:ARG:NH2	9:T:143:HIS:CD2	2.81	0.49
7:R:229:ASP:OD1	12:N:113:U:O2'	2.23	0.49
10:Z:449:PHE:HZ	10:Z:465:PHE:HE2	1.61	0.49
14:E:87:U:OP1	14:E:87:U:O4'	2.31	0.49
15:L:39:A:C2'	15:L:40:U:H5''	2.42	0.49
16:M:499:U:HO2'	16:M:500:A:P	2.26	0.49
21:n:225:SER:OG	21:n:226:PHE:N	2.45	0.49
21:n:252:ASP:C	21:n:253:VAL:HG23	2.37	0.49
22:q:405:ASP:HB2	23:t:30:ASN:CG	2.38	0.49
1:A:203:ASN:O	1:A:204:GLU:HG3	2.12	0.49
1:A:503:LYS:HA	1:A:506:PHE:CE2	2.48	0.49
1:A:532:ASN:HD21	13:D:84:A:P	2.31	0.49
1:A:645:ASP:OD1	1:A:646:ALA:N	2.45	0.49
1:A:1111:SER:HB3	1:A:1514:PHE:HD2	1.78	0.49
1:A:1383:PHE:HB3	1:A:1388:PHE:CE2	2.47	0.49
1:A:1392:LYS:HA	1:A:1396:GLY:O	2.13	0.49
1:A:1411:ASP:HA	3:J:5:GLY:O	2.13	0.49
4:O:254:ARG:HG3	4:O:255:THR:HG23	1.94	0.49
5:P:62:GLU:O	5:P:65:GLU:N	2.28	0.49
5:P:105:LEU:HD12	5:P:106:LEU:H	1.78	0.49
6:Q:38:THR:O	6:Q:39:LEU:HD12	2.13	0.49
7:R:15:GLU:OE1	9:T:44:LYS:NZ	2.42	0.49
7:R:134:ASN:ND2	7:R:226:ALA:O	2.46	0.49
10:Z:414:PRO:HA	10:Z:417:ARG:HD2	1.95	0.49
10:Z:443:SER:O	10:Z:444:LYS:HG2	2.13	0.49
17:c:15:ASN:HA	17:c:18:ASP:HB3	1.95	0.49
20:v:726:ARG:HA	20:v:729:TYR:CE2	2.48	0.49
1:A:428:LEU:HD22	2:C:896:GLY:O	2.12	0.49
1:A:462:LEU:HD22	2:C:383:LYS:HB3	1.94	0.49
1:A:542:HIS:C	1:A:544:LYS:N	2.56	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1082:ILE:HG21	1:A:1113:ILE:CD1	2.43	0.49
1:A:1798:ILE:O	1:A:1801:SER:OG	2.28	0.49
2:C:184:GLU:OE2	2:C:192:LYS:N	2.45	0.49
2:C:286:LEU:HD23	10:Z:182:GLN:HB3	1.95	0.49
5:P:126:PHE:HB3	5:P:129:LYS:HB2	1.94	0.49
20:v:718:SER:HG	20:v:725:THR:HG21	1.72	0.49
21:n:252:ASP:O	21:n:253:VAL:CG2	2.61	0.49
1:A:194:HIS:HA	1:A:557:PHE:CD1	2.47	0.49
1:A:252:GLU:CD	1:A:253:GLN:HG3	2.38	0.49
1:A:296:THR:HG21	13:D:33:U:OP2	2.11	0.49
1:A:1111:SER:HA	1:A:1514:PHE:CE2	2.48	0.49
1:A:1572:GLY:O	1:A:1827:GLN:NE2	2.46	0.49
1:A:1699:ALA:HB2	1:A:1767:TYR:CD1	2.46	0.49
1:A:2017:THR:HB	1:A:2062:GLU:OE2	2.12	0.49
4:O:217:ILE:HG22	4:O:218:ARG:HG3	1.95	0.49
9:T:128:GLN:C	9:T:131:GLU:H	2.17	0.49
12:N:108:U:H1'	12:N:109:U:OP1	2.13	0.49
17:c:230:THR:HG21	18:d:117:HIS:CE1	2.47	0.49
26:h:74:ARG:HD3	30:g:101:VAL:O	2.12	0.49
1:A:342:LEU:HD13	1:A:392:ASN:ND2	2.27	0.49
1:A:377:VAL:HG13	1:A:378:PRO:HD2	1.95	0.49
1:A:923:TYR:CZ	1:A:936:GLU:OE1	2.66	0.49
1:A:1026:TYR:HD1	1:A:1286:TRP:CZ3	2.31	0.49
1:A:1402:ALA:HB2	1:A:1440:ILE:HG13	1.93	0.49
2:C:74:VAL:HA	4:O:132:SER:O	2.13	0.49
4:O:404:CYS:SG	4:O:417:GLY:N	2.83	0.49
14:E:49:A:C8	14:E:50:G:N7	2.80	0.49
18:d:102:TRP:O	18:d:106:ILE:HG13	2.13	0.49
1:A:1157:PRO:HG3	8:S:127:TRP:CZ2	2.48	0.48
1:A:1380:PRO:HG2	11:B:93:U:C4	2.48	0.48
1:A:1471:GLN:OE1	1:A:1473:ARG:NE	2.46	0.48
1:A:1540:ASN:O	1:A:1543:ARG:N	2.46	0.48
1:A:1629:LEU:H	1:A:1629:LEU:HG	1.34	0.48
1:A:1927:GLU:HG3	35:f:135:LEU:HD13	1.91	0.48
2:C:99:LYS:HG2	13:D:43:G:H5'	1.95	0.48
2:C:928:CYS:SG	2:C:929:GLN:N	2.85	0.48
6:Q:258:LEU:O	6:Q:262:PHE:HB3	2.11	0.48
9:T:47:GLU:O	9:T:50:TRP:N	2.46	0.48
9:T:123:ARG:NH2	14:E:26:A:O2'	2.46	0.48
10:Z:79:LEU:O	10:Z:83:LEU:N	2.34	0.48
17:c:186:GLN:HG2	17:c:189:ARG:HD2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1986:MET:CE	35:f:184:MET:HG2	2.41	0.48
2:C:122:TYR:O	2:C:125:SER:HB3	2.13	0.48
2:C:277:LEU:CB	2:C:279:LEU:HD13	2.44	0.48
4:O:248:ILE:HG13	4:O:269:ILE:HD13	1.95	0.48
5:P:87:ASN:HB2	5:P:90:SER:HB2	1.95	0.48
7:R:119:ASP:OD1	7:R:119:ASP:N	2.45	0.48
7:R:196:LYS:NZ	7:R:197:GLU:OE2	2.46	0.48
15:L:51:C:C6	15:L:51:C:O5'	2.66	0.48
15:L:1109:C:N4	31:X:108:THR:HA	2.28	0.48
22:q:214:ARG:HB3	22:q:217:ASP:CG	2.38	0.48
1:A:776:GLN:HG2	1:A:777:LYS:HG2	1.95	0.48
1:A:933:GLU:O	1:A:936:GLU:HB2	2.13	0.48
1:A:1015:PRO:HB3	1:A:1164:TYR:CE1	2.48	0.48
1:A:1718:HIS:HE1	1:A:1799:GLN:HG2	1.78	0.48
1:A:1734:PHE:HD1	1:A:1773:VAL:HB	1.79	0.48
1:A:1855:THR:HA	1:A:1937:ARG:NH2	2.27	0.48
1:A:1986:MET:CG	35:f:184:MET:HG3	2.34	0.48
1:A:2010:LEU:HD21	1:A:2083:ILE:HG23	1.94	0.48
2:C:274:ILE:HB	2:C:382:TYR:CE1	2.49	0.48
2:C:468:LEU:HD12	2:C:490:SER:O	2.12	0.48
2:C:674:LEU:HD11	2:C:973:ARG:NH2	2.29	0.48
2:C:716:ASP:OD1	2:C:718:LYS:N	2.30	0.48
2:C:794:GLN:HE22	2:C:835:LYS:HD2	1.78	0.48
4:O:114:ARG:NH2	18:d:163:GLU:OE2	2.47	0.48
5:P:101:PRO:C	5:P:103:ASN:H	2.16	0.48
5:P:107:ASN:OD1	5:P:109:SER:HB2	2.13	0.48
5:P:216:ARG:O	5:P:219:ILE:HB	2.14	0.48
7:R:65:ASP:OD1	7:R:90:LEU:HD22	2.13	0.48
10:Z:58:LYS:C	10:Z:61:VAL:H	2.22	0.48
10:Z:413:CYS:SG	10:Z:415:GLN:HB2	2.53	0.48
14:E:49:A:H3'	14:E:50:G:H8	1.79	0.48
17:c:22:LYS:O	17:c:26:GLN:HB2	2.13	0.48
17:c:513:ILE:HA	17:c:516:LYS:CG	2.43	0.48
23:t:86:LEU:O	23:t:89:GLU:CG	2.61	0.48
1:A:153:MET:HE2	1:A:154:TYR:HE1	1.78	0.48
1:A:477:MET:HE2	2:C:278:LYS:CD	2.43	0.48
1:A:683:LEU:HD13	1:A:706:PRO:HB2	1.96	0.48
2:C:355:HIS:CE1	2:C:360:ARG:HH21	2.31	0.48
14:E:87:U:C5	14:E:88:U:C4	3.01	0.48
21:n:368:LYS:O	21:n:406:ARG:CB	2.61	0.48
1:A:168:LEU:N	1:A:169:PRO:HD2	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:923:TYR:OH	1:A:936:GLU:OE1	2.31	0.48
1:A:1147:PHE:C	1:A:1148:LYS:HD2	2.38	0.48
1:A:1235:PRO:HD3	8:S:133:PHE:CE2	2.49	0.48
1:A:1323:SER:HB2	1:A:1326:THR:CG2	2.44	0.48
1:A:1364:GLU:OE1	1:A:1403:SER:HB3	2.13	0.48
2:C:786:GLU:O	2:C:789:SER:N	2.47	0.48
4:O:153:GLU:HB2	4:O:154:TRP:HD1	1.79	0.48
4:O:221:TYR:CG	4:O:222:GLY:N	2.82	0.48
4:O:403:LEU:HD11	4:O:419:ALA:HB2	1.93	0.48
6:Q:61:CYS:HB2	6:Q:64:CYS:H	1.78	0.48
7:R:110:ASP:OD1	7:R:113:GLY:N	2.47	0.48
10:Z:157:ILE:HG23	10:Z:208:GLY:O	2.13	0.48
10:Z:398:PRO:HD2	10:Z:401:CYS:SG	2.54	0.48
15:L:1116:A:N6	15:L:1117:G:O6	2.46	0.48
16:M:483:U:C3'	16:M:484:U:C5	2.91	0.48
16:M:487:A:H2'	16:M:488:G:C8	2.49	0.48
25:G:34:GLN:HE21	25:G:37:ILE:HD12	1.79	0.48
1:A:164:ALA:HB2	5:P:122:LEU:CD2	2.44	0.48
1:A:430:PRO:O	1:A:431:ILE:HG22	2.14	0.48
1:A:472:ASN:O	1:A:475:ASP:N	2.42	0.48
1:A:1478:GLU:HA	1:A:1481:GLU:HB2	1.94	0.48
1:A:1541:ALA:O	1:A:1544:THR:OG1	2.23	0.48
1:A:2011:LEU:HD13	1:A:2040:TRP:CE3	2.49	0.48
2:C:77:LEU:HD12	2:C:77:LEU:O	2.14	0.48
2:C:316:THR:OG1	36:C:1500:GTP:N7	2.46	0.48
2:C:377:ILE:O	2:C:380:PRO:HG2	2.13	0.48
2:C:624:LYS:O	2:C:628:TYR:HD1	1.97	0.48
2:C:908:VAL:HG13	2:C:909:ILE:N	2.28	0.48
4:O:155:PHE:CD2	4:O:167:TRP:HB2	2.49	0.48
4:O:285:SER:O	4:O:288:ALA:N	2.45	0.48
4:O:359:ASN:CG	4:O:360:GLN:H	2.20	0.48
7:R:117:PHE:HD2	14:E:39:G:C6	2.31	0.48
9:T:156:THR:HG23	9:T:157:ASP:H	1.78	0.48
10:Z:12:LYS:HG3	10:Z:15:ARG:NH1	2.29	0.48
10:Z:121:LEU:O	10:Z:124:LEU:HB2	2.14	0.48
15:L:15:C:C2'	15:L:16:U:H5''	2.43	0.48
35:f:89:LYS:N	35:f:89:LYS:HD2	2.29	0.48
1:A:766:ILE:HG21	1:A:782:ILE:HG21	1.94	0.48
1:A:932:SER:O	1:A:935:GLU:HB3	2.13	0.48
1:A:999:LEU:O	1:A:1000:TRP:C	2.55	0.48
1:A:1382:ARG:HD3	1:A:1614:ILE:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1678:ILE:N	1:A:1706:VAL:HG23	2.29	0.48
4:O:391:GLU:O	4:O:392:MET:HB2	2.11	0.48
9:T:28:ILE:HG13	9:T:29:GLN:N	2.28	0.48
10:Z:181:LEU:HD11	10:Z:194:LEU:HD22	1.95	0.48
10:Z:422:PHE:O	10:Z:425:GLN:N	2.46	0.48
18:d:55:GLU:O	18:d:59:LYS:HB2	2.14	0.48
21:n:59:ARG:HG2	21:n:59:ARG:HH11	1.78	0.48
1:A:249:LEU:HD13	1:A:254:HIS:HB2	1.95	0.48
1:A:580:ASN:O	1:A:581:LEU:C	2.57	0.48
1:A:588:LEU:HD11	1:A:613:SER:HA	1.95	0.48
1:A:631:LEU:HD21	1:A:663:LEU:HD13	1.96	0.48
1:A:789:ALA:O	1:A:792:CYS:HB2	2.14	0.48
1:A:1716:LEU:N	1:A:1719:GLU:HB2	2.28	0.48
1:A:2013:ARG:HH22	1:A:2085:GLY:CA	2.27	0.48
2:C:161:ILE:HG22	2:C:163:ASP:H	1.79	0.48
12:N:101:U:H3'	12:N:101:U:C6	2.49	0.48
16:M:489:A:H2'	16:M:490:A:C8	2.48	0.48
16:M:496:U:C3'	16:M:497:A:H5''	2.43	0.48
1:A:135:PRO:HG3	9:T:56:HIS:CD2	2.48	0.48
1:A:772:GLU:HG3	1:A:773:SER:H	1.78	0.48
1:A:1233:ARG:HD3	8:S:131:THR:HG21	1.96	0.48
1:A:1440:ILE:O	1:A:1443:TYR:N	2.37	0.48
1:A:1648:ILE:HG22	1:A:1649:PHE:CD1	2.48	0.48
1:A:1797:LEU:O	1:A:1801:SER:HB3	2.12	0.48
4:O:149:PRO:HG3	4:O:191:SER:O	2.14	0.48
10:Z:106:PHE:CZ	10:Z:145:LYS:HG3	2.49	0.48
10:Z:465:PHE:HB2	10:Z:474:THR:HG21	1.96	0.48
20:v:712:CYS:O	20:v:713:ILE:C	2.57	0.48
21:n:227:ASP:OD1	21:n:229:SER:OG	2.31	0.48
35:f:229:TRP:O	35:f:233:ILE:HG12	2.14	0.48
1:A:174:LYS:HA	1:A:174:LYS:HD2	1.63	0.48
1:A:265:ASN:O	1:A:266:LEU:HB2	2.14	0.48
1:A:289:ASP:O	1:A:290:SER:C	2.57	0.48
1:A:296:THR:HG22	13:D:33:U:OP2	2.14	0.48
2:C:325:LYS:NZ	2:C:441:ARG:HH22	2.12	0.48
4:O:187:ASP:HB3	4:O:200:VAL:CG1	2.44	0.48
5:P:104:LEU:HG	5:P:108:ASN:HB2	1.96	0.48
7:R:102:LEU:O	7:R:105:ARG:N	2.40	0.48
7:R:144:GLY:O	7:R:203:THR:HA	2.14	0.48
7:R:163:VAL:HG13	7:R:166:ARG:NH2	2.29	0.48
7:R:230:PRO:CG	12:N:114:U:C5	2.97	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Z:361:TYR:O	10:Z:362:ASN:C	2.56	0.48
14:E:42:A:H2'	14:E:43:C:O5'	2.13	0.48
21:n:51:PHE:HE1	21:n:55:GLU:CG	2.27	0.48
33:b:1:U:O2'	33:b:2:U:OP2	2.26	0.48
1:A:294:ASN:HB2	1:A:299:LYS:O	2.14	0.47
1:A:522:TYR:O	1:A:525:LEU:N	2.46	0.47
1:A:568:GLY:HA3	1:A:633:VAL:HG11	1.96	0.47
1:A:1051:GLU:HG2	1:A:1169:TYR:CE1	2.49	0.47
1:A:1073:ILE:HG23	1:A:1074:VAL:HG23	1.95	0.47
1:A:1077:ASN:O	1:A:1078:ILE:C	2.56	0.47
1:A:1406:LEU:HD12	10:Z:307:GLU:OE2	2.13	0.47
1:A:1562:PHE:HZ	1:A:1570:TRP:HA	1.78	0.47
1:A:1856:ASN:ND2	1:A:1968:ALA:HB3	2.29	0.47
1:A:1907:GLN:O	1:A:1911:TRP:HD1	1.97	0.47
1:A:2080:LYS:O	1:A:2084:LEU:HG	2.14	0.47
2:C:105:ILE:O	2:C:106:PHE:HB2	2.14	0.47
2:C:142:LEU:HG	2:C:218:HIS:HA	1.95	0.47
2:C:269:LYS:HG2	36:C:1500:GTP:C2	2.49	0.47
2:C:920:LEU:O	2:C:922:THR:N	2.46	0.47
10:Z:152:ILE:O	10:Z:156:LYS:CB	2.62	0.47
10:Z:228:ILE:O	10:Z:231:ASP:N	2.42	0.47
16:M:494:G:O2'	16:M:495:A:OP1	2.29	0.47
16:M:497:A:C6	16:M:498:C:N4	2.82	0.47
18:d:156:TYR:CD1	18:d:172:PHE:HB2	2.49	0.47
1:A:156:THR:HG21	14:E:33:C:O2	2.14	0.47
1:A:310:ASN:HA	1:A:313:ARG:NH2	2.30	0.47
1:A:992:ASP:HB3	1:A:1108:LYS:HB2	1.96	0.47
1:A:1347:ARG:HB2	1:A:1447:TRP:CD1	2.49	0.47
1:A:1527:TRP:CE3	1:A:1528:THR:HG23	2.49	0.47
1:A:1986:MET:CB	35:f:184:MET:CB	2.89	0.47
1:A:2014:ALA:HB1	1:A:2058:LEU:HD12	1.96	0.47
1:A:2064:GLY:HA2	1:A:2069:VAL:O	2.13	0.47
2:C:541:GLU:HG2	2:C:542:ILE:N	2.29	0.47
2:C:739:GLY:O	2:C:741:MET:N	2.47	0.47
2:C:872:LEU:HB3	2:C:875:ILE:HD12	1.96	0.47
10:Z:57:CYS:O	10:Z:61:VAL:HG23	2.13	0.47
10:Z:93:THR:O	10:Z:96:LYS:HB2	2.14	0.47
10:Z:413:CYS:O	10:Z:417:ARG:N	2.37	0.47
18:d:264:SER:HA	18:d:267:TYR:HB3	1.97	0.47
21:n:60:ARG:O	21:n:63:ARG:HG2	2.14	0.47
22:q:395:GLN:CG	22:q:421:THR:O	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:683:LEU:O	1:A:684:LYS:C	2.56	0.47
1:A:926:LYS:HD2	1:A:1521:ARG:HH22	1.79	0.47
1:A:969:ILE:HD11	1:A:982:TYR:HE1	1.79	0.47
1:A:984:VAL:HG12	1:A:985:ASP:N	2.25	0.47
1:A:1130:ARG:NH2	1:A:1158:ILE:O	2.47	0.47
1:A:1866:PHE:HE2	14:E:48:C:HO2'	1.61	0.47
1:A:1995:TRP:HZ3	1:A:2008:LEU:HB2	1.79	0.47
2:C:107:THR:OG1	2:C:549:TYR:HB3	2.14	0.47
2:C:137:GLY:N	2:C:232:SER:OG	2.47	0.47
2:C:221:PHE:CE1	2:C:651:TYR:HD1	2.32	0.47
2:C:319:GLY:O	2:C:426:GLN:NE2	2.25	0.47
2:C:801:TRP:CD1	2:C:843:LYS:HB2	2.49	0.47
6:Q:125:ILE:HG13	6:Q:126:THR:H	1.79	0.47
7:R:33:TRP:C	7:R:33:TRP:CD1	2.92	0.47
7:R:132:LYS:HG2	7:R:133:LYS:O	2.14	0.47
14:E:53:A:C5'	14:E:54:U:OP2	2.63	0.47
15:L:5:A:H2'	15:L:6:U:C6	2.50	0.47
1:A:763:MET:HE1	1:A:779:ALA:HB1	1.96	0.47
1:A:1559:HIS:O	1:A:1612:PRO:HG2	2.14	0.47
1:A:1677:GLN:HB3	1:A:1706:VAL:HB	1.96	0.47
1:A:1734:PHE:HB3	1:A:1736:VAL:HG23	1.96	0.47
1:A:2075:THR:O	1:A:2079:ILE:HD12	2.15	0.47
2:C:139:ILE:HG22	2:C:215:ALA:HB3	1.95	0.47
4:O:125:TRP:CZ2	4:O:432:ALA:HB1	2.49	0.47
7:R:72:PHE:O	7:R:112:PHE:HD1	1.96	0.47
10:Z:124:LEU:HD22	10:Z:129:VAL:HG11	1.96	0.47
10:Z:184:GLN:HG3	10:Z:185:GLU:H	1.79	0.47
15:L:30:A:O3'	15:L:31:A:C4'	2.62	0.47
16:M:500:A:C2'	16:M:502:C:H5	2.24	0.47
1:A:209:ILE:HG23	1:A:301:TRP:NE1	2.30	0.47
1:A:1094:ASP:OD1	15:L:25:A:C4	2.67	0.47
1:A:1402:ALA:HA	1:A:1439:THR:HB	1.96	0.47
1:A:1586:GLN:HB2	1:A:1590:LEU:CD1	2.44	0.47
1:A:1592:HIS:NE2	33:b:4:U:OP1	2.48	0.47
1:A:1626:GLN:NE2	1:A:1631:GLY:HA2	2.27	0.47
1:A:1908:LEU:HD12	1:A:1908:LEU:HA	1.66	0.47
1:A:1925:PRO:HG2	1:A:1928:GLU:HB2	1.95	0.47
2:C:115:LYS:O	2:C:116:THR:OG1	2.27	0.47
2:C:279:LEU:O	2:C:280:PRO:C	2.55	0.47
2:C:489:TYR:O	2:C:558:LYS:HG3	2.14	0.47
7:R:91:HIS:O	7:R:92:HIS:HB3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:231:ASP:C	7:R:231:ASP:OD1	2.56	0.47
9:T:44:LYS:O	9:T:45:SER:C	2.56	0.47
10:Z:21:ILE:O	10:Z:24:HIS:HB2	2.14	0.47
10:Z:97:GLU:O	10:Z:101:MET:HG2	2.14	0.47
12:N:101:U:C6	12:N:101:U:C3'	2.98	0.47
18:d:324:UNK:CB	20:v:642:GLU:HG3	2.44	0.47
21:n:375:LYS:HA	21:n:376:ILE:HA	1.66	0.47
1:A:1286:TRP:CD1	1:A:1448:GLU:OE2	2.68	0.47
1:A:1339:LEU:HD21	1:A:1440:ILE:CD1	2.44	0.47
1:A:1347:ARG:HD3	1:A:1445:THR:O	2.14	0.47
2:C:431:GLN:H	2:C:431:GLN:CD	2.23	0.47
2:C:864:VAL:CG2	2:C:906:VAL:HG12	2.44	0.47
17:c:63:THR:HG22	17:c:93:ARG:HH12	1.78	0.47
17:c:581:GLN:O	17:c:584:LEU:CG	2.62	0.47
19:I:114:THR:O	19:I:118:ASN:CB	2.57	0.47
1:A:166:LYS:HE3	1:A:723:GLU:O	2.14	0.47
1:A:260:PRO:O	1:A:261:LEU:HB3	2.14	0.47
1:A:356:TYR:HB3	1:A:396:ARG:NH1	2.30	0.47
1:A:477:MET:CE	2:C:278:LYS:CD	2.92	0.47
1:A:501:LEU:HD13	1:A:705:GLN:HG2	1.97	0.47
1:A:591:LEU:HA	1:A:591:LEU:HD23	1.54	0.47
1:A:722:LEU:O	1:A:723:GLU:C	2.58	0.47
1:A:839:HIS:NE2	13:D:95:C:O2	2.38	0.47
1:A:857:ILE:O	1:A:858:LYS:C	2.57	0.47
1:A:991:THR:O	1:A:992:ASP:C	2.57	0.47
1:A:1077:ASN:O	1:A:1080:ASP:HB2	2.15	0.47
1:A:1630:THR:O	1:A:1692:TYR:HB2	2.15	0.47
1:A:1632:ILE:HG12	1:A:1740:TYR:HB3	1.95	0.47
1:A:2050:THR:O	1:A:2054:GLN:HG3	2.14	0.47
2:C:675:THR:OG1	2:C:676:VAL:N	2.47	0.47
4:O:150:VAL:HG12	4:O:151:ASP:OD1	2.13	0.47
6:Q:290:ILE:HG22	6:Q:292:PRO:HD3	1.97	0.47
7:R:46:ARG:CZ	12:N:110:A:H2	2.26	0.47
7:R:117:PHE:CD2	14:E:39:G:C2	3.02	0.47
10:Z:58:LYS:O	10:Z:61:VAL:HB	2.15	0.47
10:Z:117:ILE:HG22	10:Z:121:LEU:HD11	1.96	0.47
10:Z:413:CYS:HB3	10:Z:416:GLY:H	1.78	0.47
13:D:31:G:H2'	13:D:32:G:H5'	1.96	0.47
15:L:112:A:N7	30:W:63:ARG:CZ	2.78	0.47
15:L:119:G:N7	29:V:20:LYS:CE	2.77	0.47
15:L:1099:G:N3	15:L:1099:G:C5'	2.73	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:1100:A:C2	15:L:1101:C:N1	2.82	0.47
15:L:1115:G:H2'	15:L:1116:A:C8	2.50	0.47
18:d:172:PHE:O	18:d:175:PHE:HB3	2.15	0.47
19:I:185:ASN:O	19:I:189:LEU:HG	2.15	0.47
20:v:645:ARG:NE	20:v:669:TYR:OH	2.48	0.47
1:A:225:ARG:NH2	1:A:693:LYS:O	2.47	0.47
1:A:742:VAL:HG23	1:A:743:LYS:N	2.30	0.47
1:A:783:LEU:HD12	1:A:783:LEU:H	1.78	0.47
1:A:1627:LEU:HD11	1:A:1634:LEU:HD12	1.96	0.47
2:C:286:LEU:CD2	10:Z:182:GLN:HB3	2.44	0.47
2:C:968:MET:HE2	2:C:971:ARG:HD3	1.96	0.47
4:O:437:GLU:N	4:O:438:PRO:HD3	2.30	0.47
5:P:127:VAL:HG11	14:E:32:U:N3	2.30	0.47
5:P:196:THR:OG1	5:P:197:ILE:N	2.48	0.47
7:R:76:PHE:C	7:R:79:GLY:H	2.18	0.47
9:T:108:CYS:HA	9:T:120:CYS:SG	2.54	0.47
10:Z:98:LEU:O	10:Z:101:MET:HB2	2.13	0.47
15:L:120:G:H4'	15:L:121:C:O4'	2.15	0.47
17:c:181:ARG:O	17:c:185:LEU:HG	2.13	0.47
1:A:159:LYS:HZ2	1:A:734:PHE:HE1	1.63	0.47
1:A:404:ASN:CG	1:A:405:ASN:N	2.72	0.47
1:A:767:LEU:HD21	1:A:775:ARG:HG3	1.97	0.47
1:A:974:ASN:O	1:A:975:TYR:HB2	2.14	0.47
1:A:1292:ARG:HG3	1:A:1293:THR:HG23	1.97	0.47
1:A:1437:ILE:HG22	1:A:1438:PRO:O	2.14	0.47
1:A:1805:ILE:HG23	1:A:1809:ASN:ND2	2.30	0.47
1:A:2048:TRP:O	1:A:2052:GLU:HG3	2.15	0.47
1:A:2062:GLU:O	1:A:2066:LYS:HB3	2.15	0.47
2:C:138:VAL:HG21	2:C:150:MET:HE1	1.97	0.47
2:C:727:THR:HG23	2:C:736:ASP:H	1.80	0.47
4:O:193:ARG:HH22	4:O:237:ASP:N	2.04	0.47
4:O:377:ASP:OD2	4:O:379:LYS:N	2.48	0.47
5:P:196:THR:HA	17:c:90:MET:HE1	1.97	0.47
6:Q:53:ASN:O	14:E:31:G:C2	2.68	0.47
6:Q:206:PHE:HB3	6:Q:208:TYR:CZ	2.50	0.47
8:S:10:GLU:HG2	8:S:11:ALA:N	2.30	0.47
10:Z:10:ASP:OD2	10:Z:244:LYS:NZ	2.45	0.47
12:N:102:A:H8	12:N:102:A:H5''	1.80	0.47
17:c:152:LEU:O	17:c:156:ARG:CB	2.63	0.47
19:I:99:GLN:O	19:I:103:LEU:HG	2.15	0.47
21:n:292:HIS:NE2	21:n:310:SER:OG	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:412:GLN:OE1	1:A:412:GLN:N	2.40	0.47
1:A:603:LYS:O	1:A:604:THR:C	2.58	0.47
1:A:725:TYR:HE1	14:E:72:C:C6	2.32	0.47
1:A:1400:ILE:HG23	1:A:1542:TYR:CE2	2.50	0.47
2:C:79:GLU:CB	4:O:167:TRP:HZ3	2.27	0.47
2:C:312:ILE:HG23	2:C:323:THR:OG1	2.15	0.47
2:C:779:LEU:HB3	2:C:780:PRO:HD3	1.97	0.47
2:C:938:ARG:HG2	2:C:939:LYS:O	2.15	0.47
4:O:244:ARG:HH12	8:S:8:GLN:HE22	1.62	0.47
14:E:88:U:C6	15:L:17:U:C6	3.03	0.47
15:L:34:G:H2'	15:L:35:U:O4'	2.15	0.47
17:c:103:ASN:O	17:c:107:GLU:HG3	2.14	0.47
18:d:198:GLN:HB2	18:d:201:THR:HG23	1.97	0.47
1:A:638:GLN:O	1:A:639:PHE:C	2.58	0.46
1:A:1296:ARG:HH12	10:Z:390:HIS:CE1	2.32	0.46
1:A:1328:PHE:O	1:A:1331:VAL:N	2.49	0.46
1:A:1343:PHE:CD1	1:A:1350:ILE:HD13	2.50	0.46
1:A:1562:PHE:CZ	1:A:1570:TRP:HA	2.50	0.46
1:A:1864:LYS:HZ2	21:n:321:GLU:CG	2.27	0.46
2:C:682:SER:HA	2:C:714:PRO:CG	2.44	0.46
2:C:743:ASN:O	2:C:747:LEU:N	2.39	0.46
2:C:758:ASP:CG	2:C:761:ALA:H	2.23	0.46
4:O:188:VAL:HG13	4:O:197:LEU:HD11	1.97	0.46
4:O:193:ARG:NH2	4:O:237:ASP:H	2.05	0.46
5:P:103:ASN:HD22	5:P:114:VAL:HG21	1.79	0.46
8:S:167:GLN:O	8:S:171:HIS:HB2	2.15	0.46
9:T:104:CYS:C	9:T:105:CYS:SG	2.97	0.46
10:Z:99:MET:HB2	10:Z:99:MET:HE3	1.55	0.46
13:D:44:A:OP2	13:D:44:A:H4'	2.14	0.46
13:D:174:G:N7	29:m:20:LYS:CE	2.77	0.46
14:E:1:G:H2'	14:E:2:U:C6	2.50	0.46
17:c:33:TRP:O	17:c:36:VAL:N	2.48	0.46
22:q:472:ALA:CB	22:q:477:MET:CG	2.93	0.46
25:i:34:GLN:HE21	25:i:37:ILE:HD12	1.79	0.46
1:A:215:ALA:O	1:A:216:GLN:C	2.58	0.46
1:A:1021:PRO:HG2	1:A:1022:PRO:HD3	1.97	0.46
1:A:1058:ALA:HA	1:A:1061:ILE:HG13	1.96	0.46
1:A:1143:GLU:H	1:A:1146:GLN:CD	2.23	0.46
1:A:1468:ALA:HA	1:A:1473:ARG:HG2	1.96	0.46
1:A:1999:ILE:HD11	1:A:2007:ARG:NH2	2.30	0.46
2:C:221:PHE:O	2:C:222:MET:C	2.58	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:412:ALA:HA	2:C:415:TYR:CE2	2.50	0.46
2:C:482:GLU:OE1	2:C:628:TYR:OH	2.32	0.46
2:C:916:THR:O	2:C:917:ASP:C	2.58	0.46
4:O:307:HIS:CE1	4:O:326:ALA:O	2.68	0.46
5:P:167:ALA:O	5:P:184:ARG:NH2	2.48	0.46
6:Q:3:ASP:O	6:Q:5:ILE:N	2.48	0.46
7:R:62:THR:OG1	7:R:63:ARG:N	2.45	0.46
9:T:120:CYS:HA	14:E:29:U:C4'	2.46	0.46
10:Z:80:ILE:HG23	10:Z:90:ILE:HG22	1.97	0.46
10:Z:87:ILE:HG22	10:Z:89:ASP:H	1.80	0.46
10:Z:177:LEU:O	10:Z:180:ILE:HB	2.15	0.46
10:Z:312:LEU:HD23	10:Z:312:LEU:HA	1.75	0.46
10:Z:363:GLU:O	10:Z:366:GLU:N	2.48	0.46
13:D:167:A:N7	30:g:63:ARG:CZ	2.78	0.46
13:D:179:U:OP1	30:g:79:LYS:HG2	2.16	0.46
20:v:730:GLN:C	20:v:733:ILE:HD12	2.38	0.46
33:b:4:U:C2'	33:b:5:U:C2	2.98	0.46
1:A:299:LYS:HA	1:A:493:MET:HG2	1.96	0.46
1:A:461:LEU:H	1:A:461:LEU:HG	1.44	0.46
1:A:801:VAL:HG13	1:A:802:PRO:HD2	1.97	0.46
1:A:960:THR:OG1	1:A:961:GLN:N	2.48	0.46
1:A:1066:LEU:O	1:A:1068:ARG:N	2.49	0.46
1:A:1070:LEU:HD23	1:A:1070:LEU:HA	1.72	0.46
2:C:470:ALA:CB	2:C:488:ILE:HA	2.46	0.46
2:C:634:ILE:HG22	2:C:635:LYS:N	2.31	0.46
4:O:111:ILE:HB	4:O:114:ARG:HE	1.80	0.46
4:O:221:TYR:O	4:O:251:TRP:HH2	1.99	0.46
5:P:35:ALA:O	5:P:37:ASN:N	2.49	0.46
5:P:108:ASN:O	5:P:110:HIS:N	2.49	0.46
6:Q:33:GLU:HG2	6:Q:34:CYS:O	2.14	0.46
9:T:150:CYS:SG	9:T:151:ARG:N	2.88	0.46
10:Z:370:THR:OG1	10:Z:371:GLN:N	2.48	0.46
12:N:100:G:C8	33:b:-1:A:H2'	2.32	0.46
13:D:175:G:H4'	13:D:176:A:O4'	2.15	0.46
14:E:50:G:OP2	14:E:50:G:H2'	2.15	0.46
21:n:274:HIS:HB2	21:n:287:GLN:HB2	1.97	0.46
26:h:16:LYS:N	26:h:17:PRO:CD	2.79	0.46
33:b:4:U:C5'	33:b:4:U:H6	2.28	0.46
33:b:8:A:H8	33:b:8:A:O5'	1.99	0.46
1:A:168:LEU:O	1:A:169:PRO:C	2.55	0.46
1:A:555:LYS:HD2	5:P:118:GLN:HE21	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1313:ASP:HB2	1:A:1359:ILE:HD13	1.97	0.46
1:A:1875:ILE:HG22	1:A:1876:ASN:H	1.80	0.46
4:O:131:LEU:HB2	4:O:426:TRP:CZ3	2.49	0.46
7:R:105:ARG:HG2	7:R:109:LEU:HD11	1.97	0.46
8:S:168:GLU:O	8:S:171:HIS:N	2.48	0.46
10:Z:148:LEU:HD23	10:Z:148:LEU:HA	1.68	0.46
28:U:30:ARG:C	28:U:47:VAL:HG23	2.40	0.46
35:f:97:PRO:HB2	35:f:197:VAL:HG21	1.97	0.46
1:A:173:LEU:HD11	1:A:712:LEU:HD21	1.97	0.46
1:A:758:LEU:HD23	1:A:759:ARG:N	2.30	0.46
1:A:1023:LEU:HB2	1:A:1451:PHE:HE1	1.80	0.46
1:A:1051:GLU:OE1	1:A:1247:PHE:HB2	2.15	0.46
1:A:1347:ARG:O	1:A:1441:PHE:CE1	2.69	0.46
2:C:859:GLU:OE2	2:C:907:PRO:HB3	2.15	0.46
4:O:129:TRP:HB2	4:O:375:PHE:HE2	1.81	0.46
4:O:354:ASN:ND2	4:O:402:VAL:O	2.42	0.46
7:R:162:PHE:C	7:R:165:SER:HG	2.24	0.46
9:T:100:TYR:HE1	14:E:26:A:H4'	1.81	0.46
10:Z:131:HIS:O	10:Z:134:VAL:HG12	2.15	0.46
10:Z:338:THR:HG22	10:Z:339:PHE:N	2.31	0.46
10:Z:405:ILE:HG21	10:Z:420:ILE:HG12	1.98	0.46
14:E:67:C:OP2	18:d:59:LYS:HE2	2.16	0.46
17:c:72:GLN:HE21	17:c:76:LEU:HD11	1.80	0.46
28:U:39:SER:O	28:U:41:ASN:N	2.48	0.46
1:A:180:PRO:O	1:A:184:GLU:HB2	2.16	0.46
1:A:588:LEU:HD22	1:A:590:TYR:CZ	2.50	0.46
1:A:728:ASN:O	1:A:729:LEU:C	2.58	0.46
1:A:1048:VAL:HG22	1:A:1250:VAL:HA	1.97	0.46
1:A:1377:SER:CA	11:B:95:U:OP1	2.63	0.46
1:A:1818:ARG:HA	1:A:1821:LYS:HG2	1.97	0.46
2:C:287:LYS:O	2:C:290:HIS:N	2.49	0.46
2:C:477:ASP:HB2	2:C:628:TYR:CD2	2.49	0.46
4:O:263:VAL:HG12	4:O:264:GLY:N	2.24	0.46
10:Z:38:GLN:O	10:Z:41:HIS:HB3	2.16	0.46
20:v:606:GLN:HA	20:v:609:GLU:HG2	1.98	0.46
35:f:136:PHE:CZ	35:f:140:LYS:HD2	2.50	0.46
1:A:745:THR:CG2	4:O:203:ASP:HB2	2.46	0.46
1:A:771:PRO:HD3	5:P:163:TRP:CD1	2.51	0.46
1:A:1130:ARG:HD2	1:A:1130:ARG:HA	1.75	0.46
2:C:81:LYS:O	2:C:82:ASN:ND2	2.48	0.46
2:C:136:VAL:HG13	2:C:212:PHE:HA	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:489:TYR:HE2	2:C:592:PHE:CE1	2.33	0.46
2:C:821:LEU:HD23	2:C:821:LEU:HA	1.66	0.46
4:O:358:ILE:HG22	4:O:359:ASN:N	2.30	0.46
5:P:216:ARG:HA	5:P:219:ILE:CD1	2.45	0.46
7:R:89:TYR:HD2	14:E:34:A:N3	2.02	0.46
9:T:55:LEU:O	9:T:58:GLN:N	2.47	0.46
10:Z:368:ASN:O	10:Z:373:ILE:HG12	2.16	0.46
14:E:14:C:C4'	14:E:15:C:OP2	2.63	0.46
14:E:92:C:O2'	14:E:93:A:O4'	2.31	0.46
24:k:20:LEU:O	24:k:31:ILE:HA	2.16	0.46
26:H:16:LYS:N	26:H:17:PRO:CD	2.79	0.46
1:A:752:ALA:HB1	14:E:62:A:O2'	2.16	0.46
1:A:1036:SER:OG	1:A:1154:LYS:NZ	2.29	0.46
1:A:1458:TRP:HZ2	1:A:1489:PRO:HB2	1.81	0.46
2:C:251:GLN:NE2	2:C:255:GLN:HG2	2.31	0.46
2:C:739:GLY:O	2:C:742:ASP:N	2.21	0.46
2:C:840:PRO:O	2:C:843:LYS:N	2.48	0.46
2:C:869:HIS:CD2	2:C:925:LEU:HD22	2.50	0.46
4:O:187:ASP:HB3	4:O:200:VAL:HG12	1.98	0.46
5:P:37:ASN:ND2	5:P:145:PRO:HD3	2.30	0.46
5:P:175:PRO:HG2	15:L:19:U:O2	2.15	0.46
8:S:15:ALA:O	8:S:18:ALA:N	2.49	0.46
9:T:32:ASP:HA	9:T:35:LYS:HD3	1.98	0.46
14:E:64:U:H2'	14:E:65:U:C6	2.51	0.46
15:L:2:C:H2'	15:L:3:G:C8	2.51	0.46
25:G:30:TRP:CE2	25:G:89:LEU:HD22	2.51	0.46
25:G:86:ASN:ND2	26:H:32:LYS:NZ	2.64	0.46
29:V:6:PHE:CZ	29:V:10:LEU:HD11	2.51	0.46
1:A:355:LEU:HG	1:A:356:TYR:CE2	2.50	0.46
1:A:817:LYS:HG2	4:O:399:GLU:OE2	2.15	0.46
1:A:823:TRP:CE2	1:A:851:ARG:HG2	2.50	0.46
1:A:1054:LEU:HA	1:A:1054:LEU:HD23	1.62	0.46
1:A:1151:GLU:O	1:A:1154:LYS:N	2.49	0.46
1:A:1513:GLU:O	1:A:1516:GLN:HG3	2.16	0.46
1:A:1739:ARG:HD2	1:A:1751:TYR:CZ	2.51	0.46
2:C:173:LYS:HD3	13:D:76:U:OP1	2.15	0.46
2:C:388:ALA:HA	2:C:396:LEU:HD11	1.97	0.46
2:C:600:GLU:HB2	2:C:935:LYS:HE3	1.96	0.46
4:O:133:ARG:NH1	4:O:170:ALA:O	2.43	0.46
4:O:148:ASP:OD2	4:O:151:ASP:N	2.35	0.46
4:O:284:SER:HB3	4:O:290:VAL:HG22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Q:218:LYS:O	6:Q:221:ASP:HB3	2.16	0.46
9:T:55:LEU:HD23	9:T:55:LEU:HA	1.76	0.46
10:Z:40:SER:O	10:Z:44:LEU:HB3	2.16	0.46
10:Z:422:PHE:O	10:Z:423:LEU:C	2.58	0.46
18:d:172:PHE:CE2	18:d:188:ILE:HG12	2.51	0.46
18:d:233:GLN:HG2	18:d:274:TRP:CZ2	2.51	0.46
25:i:30:TRP:CE2	25:i:89:LEU:HD22	2.51	0.46
29:m:6:PHE:CZ	29:m:10:LEU:HD11	2.51	0.46
1:A:416:GLU:HB3	1:A:419:THR:HG23	1.98	0.46
1:A:860:GLU:OE2	1:A:863:ARG:NH2	2.49	0.46
1:A:1094:ASP:OD1	1:A:1094:ASP:N	2.49	0.46
1:A:1281:ASN:HD22	1:A:1285:VAL:HG21	1.80	0.46
1:A:1570:TRP:O	1:A:1572:GLY:N	2.49	0.46
1:A:1590:LEU:HD22	1:A:1595:ARG:HD2	1.97	0.46
1:A:1624:LEU:HA	1:A:1624:LEU:HD23	1.69	0.46
1:A:1782:ASN:ND2	1:A:1816:ARG:HH21	2.13	0.46
2:C:251:GLN:HE21	2:C:255:GLN:HG2	1.81	0.46
2:C:336:ILE:HD11	2:C:341:ILE:HG22	1.98	0.46
5:P:134:VAL:HG12	5:P:135:VAL:N	2.31	0.46
6:Q:45:HIS:HB3	6:Q:55:ILE:HD11	1.97	0.46
6:Q:210:ILE:HD12	6:Q:247:LYS:C	2.42	0.46
6:Q:216:GLU:O	6:Q:219:ILE:N	2.48	0.46
9:T:41:LEU:HD21	14:E:35:A:N1	2.28	0.46
12:N:105:U:H2'	12:N:106:A:C8	2.51	0.46
15:L:1100:A:H61	15:L:1116:A:N6	2.07	0.46
20:v:730:GLN:CA	20:v:733:ILE:CD1	2.86	0.46
34:e:948:PRO:C	34:e:950:TYR:H	2.24	0.46
1:A:1053:THR:HG22	1:A:1167:ARG:HD2	1.98	0.45
1:A:1068:ARG:O	1:A:1071:ARG:N	2.48	0.45
1:A:1124:LEU:O	1:A:1127:GLY:N	2.49	0.45
1:A:1447:TRP:O	1:A:1448:GLU:C	2.60	0.45
1:A:1859:ARG:NH2	1:A:1876:ASN:O	2.29	0.45
2:C:132:ARG:O	2:C:132:ARG:HG2	2.15	0.45
2:C:652:MET:HA	2:C:652:MET:HE2	1.97	0.45
4:O:220:TYR:CD1	4:O:256:ARG:HG2	2.51	0.45
5:P:205:SER:HA	5:P:208:LEU:HD12	1.98	0.45
8:S:160:MET:O	8:S:163:SER:N	2.33	0.45
9:T:151:ARG:HD2	21:n:71:SER:HA	1.96	0.45
10:Z:323:LYS:HE2	10:Z:364:THR:HG22	1.97	0.45
13:D:167:A:N7	30:g:63:ARG:NH1	2.65	0.45
14:E:21:U:P	21:n:54:SER:HG	2.18	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:i:86:ASN:ND2	26:h:32:LYS:NZ	2.64	0.45
1:A:361:GLU:OE1	1:A:361:GLU:N	2.48	0.45
1:A:713:ASN:O	1:A:716:ARG:HG2	2.16	0.45
1:A:767:LEU:CD2	1:A:775:ARG:HG3	2.46	0.45
1:A:779:ALA:O	1:A:780:ARG:C	2.59	0.45
1:A:865:ARG:HH21	1:A:869:LYS:NZ	2.14	0.45
1:A:953:ARG:O	1:A:956:LYS:HB3	2.16	0.45
1:A:1041:VAL:HG11	1:A:1253:LYS:HA	1.99	0.45
1:A:1066:LEU:O	1:A:1067:ASN:C	2.59	0.45
1:A:1377:SER:HA	11:B:95:U:OP1	2.16	0.45
1:A:1403:SER:OG	1:A:1404:HIS:N	2.49	0.45
1:A:1416:LYS:HD2	1:A:1416:LYS:HA	1.74	0.45
4:O:120:SER:OG	4:O:121:GLN:OE1	2.35	0.45
6:Q:4:GLU:O	6:Q:7:GLU:N	2.41	0.45
6:Q:240:LEU:CD1	6:Q:251:LEU:HD13	2.46	0.45
7:R:185:LYS:C	7:R:186:PHE:CD1	2.94	0.45
9:T:51:GLU:O	9:T:52:ILE:C	2.60	0.45
15:L:1115:G:H2'	15:L:1116:A:H8	1.80	0.45
18:d:40:LEU:HD21	18:d:44:ARG:HH21	1.81	0.45
19:I:203:PHE:O	19:I:206:LYS:N	2.48	0.45
22:r:62:LEU:O	22:r:63:THR:C	2.59	0.45
1:A:237:MET:HE1	1:A:638:GLN:OE1	2.16	0.45
1:A:304:ASP:OD1	1:A:306:PRO:HD2	2.17	0.45
1:A:345:ALA:H	3:J:3:TYR:HD2	1.64	0.45
1:A:452:PHE:HE1	2:C:347:ARG:NE	2.13	0.45
1:A:713:ASN:O	1:A:714:PHE:C	2.59	0.45
1:A:1012:TRP:CZ3	1:A:1013:ILE:HG13	2.51	0.45
1:A:1286:TRP:CD1	1:A:1286:TRP:N	2.83	0.45
1:A:1286:TRP:CE2	1:A:1302:LEU:HD11	2.52	0.45
1:A:1689:ARG:HA	1:A:1692:TYR:CE1	2.51	0.45
1:A:1748:ILE:O	1:A:1749:SER:C	2.59	0.45
1:A:2011:LEU:HD13	1:A:2040:TRP:CZ3	2.51	0.45
7:R:73:CYS:SG	7:R:76:PHE:N	2.88	0.45
7:R:117:PHE:CD2	14:E:39:G:C6	3.04	0.45
10:Z:69:ASN:HB3	10:Z:70:GLY:H	1.56	0.45
10:Z:184:GLN:HG3	10:Z:185:GLU:N	2.31	0.45
14:E:73:A:C6	14:E:75:A:C5	3.04	0.45
22:o:96:PHE:HD2	22:r:5:ILE:HG23	1.80	0.45
35:f:183:TYR:HE2	35:f:234:LYS:HE3	1.79	0.45
1:A:857:ILE:O	1:A:860:GLU:N	2.50	0.45
1:A:867:ILE:HG21	1:A:1101:TYR:CD1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:936:GLU:O	1:A:937:LEU:C	2.59	0.45
1:A:1275:MET:C	1:A:1277:GLU:H	2.22	0.45
1:A:1275:MET:HE1	1:A:1299:LYS:HD2	1.98	0.45
1:A:1431:HIS:NE2	1:A:1434:GLU:HB3	2.32	0.45
1:A:1540:ASN:O	1:A:1541:ALA:C	2.59	0.45
1:A:1683:LYS:HB3	1:A:1701:ILE:HG23	1.97	0.45
2:C:394:ASP:O	2:C:397:LYS:HB3	2.16	0.45
2:C:500:ARG:HB2	2:C:578:TYR:O	2.16	0.45
2:C:655:LEU:O	2:C:656:LEU:C	2.59	0.45
10:Z:22:ARG:HA	10:Z:25:VAL:HG23	1.99	0.45
10:Z:369:TYR:CE2	10:Z:405:ILE:HG12	2.51	0.45
12:N:102:A:C2	14:E:51:A:C8	3.05	0.45
14:E:53:A:H4'	14:E:54:U:OP2	2.16	0.45
14:E:88:U:H5''	15:L:17:U:H5	1.82	0.45
15:L:18:U:C5	19:I:202:GLN:CG	2.99	0.45
1:A:988:GLU:O	1:A:991:THR:OG1	2.34	0.45
1:A:1508:HIS:CD2	1:A:1532:HIS:CD2	3.05	0.45
1:A:1648:ILE:HG22	1:A:1649:PHE:CE1	2.52	0.45
1:A:1798:ILE:O	1:A:1802:MET:HG2	2.17	0.45
2:C:449:PHE:O	2:C:453:THR:HG23	2.16	0.45
4:O:355:THR:O	4:O:356:LEU:HD23	2.17	0.45
7:R:48:VAL:HG11	7:R:203:THR:HG23	1.99	0.45
7:R:96:GLU:OE2	7:R:187:LYS:NZ	2.47	0.45
7:R:97:GLU:O	7:R:100:GLY:HA3	2.16	0.45
9:T:88:ASP:OD2	9:T:90:LEU:HB2	2.17	0.45
9:T:89:LYS:HE2	13:D:123:U:O2'	2.17	0.45
15:L:41:C:HO2'	15:L:42:U:P	2.38	0.45
15:L:112:A:N7	30:W:63:ARG:NH1	2.65	0.45
17:c:44:THR:HG22	17:c:45:ALA:H	1.81	0.45
1:A:797:ILE:HD12	5:P:172:TRP:HH2	1.82	0.45
1:A:1161:TYR:OH	1:A:1163:ARG:HB2	2.17	0.45
1:A:1678:ILE:C	1:A:1706:VAL:HG23	2.42	0.45
2:C:265:PHE:CE2	2:C:295:ILE:HD12	2.52	0.45
2:C:777:ASP:O	2:C:778:THR:HB	2.17	0.45
4:O:132:SER:HB3	4:O:427:LYS:HB2	1.99	0.45
7:R:95:ASP:CG	7:R:97:GLU:H	2.25	0.45
10:Z:381:LEU:O	10:Z:422:PHE:HD2	1.99	0.45
10:Z:449:PHE:CZ	10:Z:477:MET:HE1	2.51	0.45
10:Z:465:PHE:CD1	10:Z:468:ILE:HD12	2.52	0.45
18:d:176:GLU:HG3	18:d:188:ILE:HD11	1.98	0.45
22:p:98:LEU:HD21	22:q:102:LEU:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:q:194:THR:HG1	22:q:213:CYS:HB3	1.81	0.45
22:q:463:SER:O	22:q:464:ALA:CB	2.62	0.45
28:l:39:SER:O	28:l:41:ASN:N	2.48	0.45
30:g:49:ARG:HD2	30:g:49:ARG:HA	1.64	0.45
1:A:168:LEU:HD12	1:A:199:ILE:HD11	1.99	0.45
1:A:355:LEU:CD1	13:D:105:A:C5'	2.94	0.45
1:A:548:LEU:HA	1:A:548:LEU:HD23	1.70	0.45
1:A:1365:THR:C	1:A:1369:ASN:HD22	2.24	0.45
1:A:1899:TRP:CH2	1:A:1909:ALA:HA	2.43	0.45
2:C:73:GLU:OE2	4:O:130:LYS:NZ	2.34	0.45
2:C:201:THR:HA	2:C:207:SER:HA	1.97	0.45
2:C:451:ASN:O	2:C:455:HIS:HB2	2.16	0.45
2:C:585:ASP:O	2:C:588:GLN:N	2.50	0.45
2:C:621:ALA:O	2:C:624:LYS:HB2	2.16	0.45
2:C:706:LEU:HD21	2:C:834:MET:CE	2.44	0.45
2:C:775:ILE:HG22	2:C:776:ASN:N	2.28	0.45
4:O:164:MET:HE1	4:O:209:TRP:NE1	2.31	0.45
9:T:119:THR:OG1	14:E:28:U:OP1	2.34	0.45
10:Z:161:LYS:HD2	10:Z:164:LEU:HB3	1.98	0.45
10:Z:408:THR:CB	10:Z:410:GLU:HB3	2.46	0.45
14:E:42:A:O2'	14:E:43:C:P	2.74	0.45
15:L:1103:C:N1	15:L:1114:G:N2	2.64	0.45
15:L:1116:A:C4	15:L:1117:G:C5	3.05	0.45
17:c:44:THR:HG22	17:c:45:ALA:N	2.32	0.45
35:f:82:GLN:HA	35:f:85:ILE:HG12	1.97	0.45
1:A:237:MET:HE3	1:A:237:MET:HB2	1.63	0.45
1:A:376:ARG:NH2	2:C:962:LEU:HD21	2.31	0.45
1:A:381:SER:HB3	3:J:3:TYR:O	2.16	0.45
1:A:529:TYR:O	1:A:530:VAL:C	2.58	0.45
1:A:537:THR:HG21	13:D:84:A:H62	1.81	0.45
1:A:1454:SER:HB2	1:A:1488:ILE:HG22	1.99	0.45
1:A:1814:VAL:HG21	1:A:1949:LEU:HD21	1.97	0.45
2:C:148:SER:OG	2:C:149:LEU:N	2.49	0.45
2:C:671:SER:OG	2:C:672:ASP:N	2.50	0.45
6:Q:215:PRO:HB2	6:Q:217:TRP:CE3	2.52	0.45
6:Q:223:VAL:O	6:Q:227:LEU:HG	2.17	0.45
9:T:120:CYS:HB2	9:T:122:CYS:H	1.81	0.45
20:v:624:TRP:HE1	20:v:651:ALA:CB	2.30	0.45
20:v:729:TYR:O	20:v:733:ILE:HG13	2.17	0.45
21:n:397:TYR:HA	21:n:412:TRP:O	2.17	0.45
1:A:239:PHE:HA	1:A:240:PRO:C	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:247:PRO:HB3	1:A:595:TYR:CZ	2.51	0.45
1:A:683:LEU:HA	1:A:683:LEU:HD23	1.64	0.45
1:A:763:MET:HB3	1:A:763:MET:HE3	1.60	0.45
1:A:790:TRP:CG	1:A:819:LYS:HZ3	2.34	0.45
1:A:1069:LEU:O	1:A:1072:LEU:HB2	2.17	0.45
1:A:1348:GLU:OE2	1:A:1448:GLU:HG3	2.17	0.45
1:A:1366:ARG:O	1:A:1369:ASN:HB2	2.16	0.45
1:A:1774:MET:O	1:A:1786:ALA:CA	2.34	0.45
2:C:135:ASN:H	2:C:233:ASP:CG	2.23	0.45
2:C:174:PRO:HG2	2:C:176:ARG:HD3	1.99	0.45
2:C:314:ALA:CB	2:C:321:THR:HG22	2.46	0.45
2:C:323:THR:O	2:C:324:ILE:C	2.60	0.45
2:C:353:TYR:N	2:C:353:TYR:CD1	2.83	0.45
2:C:428:ILE:HG22	2:C:429:PHE:CD1	2.51	0.45
2:C:829:VAL:CG1	2:C:834:MET:HG3	2.47	0.45
2:C:887:ARG:HE	2:C:938:ARG:NH2	2.14	0.45
4:O:119:LEU:HA	4:O:119:LEU:HD23	1.60	0.45
4:O:270:ASN:HD21	4:O:286:THR:CG2	2.30	0.45
4:O:315:ALA:O	4:O:323:VAL:HA	2.17	0.45
6:Q:33:GLU:HA	6:Q:39:LEU:O	2.16	0.45
8:S:7:PRO:O	8:S:8:GLN:CB	2.64	0.45
8:S:32:PRO:O	13:D:109:A:H4'	2.17	0.45
9:T:44:LYS:HD3	9:T:44:LYS:HA	1.68	0.45
15:L:1120:G:C5'	15:L:1120:G:C8	3.00	0.45
16:M:483:U:C5	16:M:483:U:OP2	2.70	0.45
18:d:65:MET:HE1	18:d:94:VAL:HG12	1.98	0.45
20:v:673:GLU:CB	20:v:683:SER:HB3	2.47	0.45
25:G:30:TRP:CD2	25:G:89:LEU:HD22	2.52	0.45
1:A:157:ASP:O	1:A:160:ALA:HB3	2.16	0.45
1:A:308:MET:HE2	1:A:486:PHE:O	2.17	0.45
1:A:688:TYR:O	1:A:690:LYS:N	2.49	0.45
1:A:1033:ASN:O	1:A:1035:LEU:N	2.50	0.45
1:A:1270:LEU:HD23	1:A:1270:LEU:HA	1.77	0.45
1:A:1411:ASP:H	3:J:6:ILE:HA	1.81	0.45
1:A:1710:GLU:HB2	1:A:1724:PHE:HB3	1.99	0.45
1:A:1922:ARG:HG2	1:A:1951:PHE:HZ	1.81	0.45
2:C:179:ASP:OD1	2:C:184:GLU:HB3	2.17	0.45
4:O:370:ASN:OD1	4:O:370:ASN:N	2.44	0.45
5:P:65:GLU:O	5:P:68:ALA:N	2.49	0.45
5:P:110:HIS:CE1	6:Q:19:ASP:HA	2.52	0.45
10:Z:360:ALA:O	10:Z:364:THR:HG23	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Z:414:PRO:N	10:Z:417:ARG:HH11	2.15	0.45
15:L:41:C:O2'	15:L:42:U:O5'	2.23	0.45
16:M:483:U:C6	16:M:484:U:O4	2.70	0.45
21:n:276:ASP:HB2	21:n:286:VAL:CG2	2.47	0.45
1:A:140:ARG:O	1:A:144:ASN:HB2	2.17	0.44
1:A:194:HIS:CD2	1:A:557:PHE:HE1	2.35	0.44
1:A:1031:GLY:HA3	1:A:1145:MET:HE3	1.98	0.44
1:A:1330:LYS:CE	33:b:6:U:OP1	2.65	0.44
1:A:1594:GLN:O	1:A:1598:LEU:HB2	2.17	0.44
1:A:1610:TRP:CD1	1:A:1610:TRP:N	2.85	0.44
1:A:1800:ASN:O	1:A:1803:ARG:HB2	2.17	0.44
2:C:103:HIS:ND1	2:C:662:SER:OG	2.50	0.44
2:C:320:PHE:HB2	2:C:429:PHE:CD2	2.52	0.44
2:C:510:ARG:HD2	2:C:591:PHE:CE2	2.52	0.44
2:C:833:VAL:O	2:C:837:GLN:HB3	2.14	0.44
4:O:211:LEU:HD23	4:O:211:LEU:HA	1.77	0.44
6:Q:106:ASN:ND2	17:c:212:ASP:H	2.15	0.44
7:R:4:TRP:CE2	7:R:92:HIS:CD2	3.06	0.44
7:R:145:ALA:HB2	7:R:204:LEU:HD12	1.99	0.44
7:R:245:GLU:HG3	7:R:249:MET:CE	2.44	0.44
10:Z:169:THR:HG1	10:Z:170:HIS:H	1.65	0.44
10:Z:285:SER:O	10:Z:287:ASN:N	2.49	0.44
10:Z:374:GLU:C	10:Z:415:GLN:HE22	2.25	0.44
12:N:104:G:O6	14:E:49:A:N1	2.50	0.44
17:c:75:ASP:O	17:c:79:GLU:HG2	2.16	0.44
18:d:205:TRP:O	18:d:208:PHE:HB3	2.18	0.44
1:A:265:ASN:HA	1:A:281:TYR:CZ	2.52	0.44
1:A:1130:ARG:O	1:A:1133:ASP:HB2	2.17	0.44
1:A:1196:GLU:HB3	1:A:1199:ILE:HD12	1.98	0.44
1:A:1424:HIS:NE2	3:J:6:ILE:HD13	2.32	0.44
1:A:1458:TRP:CZ2	1:A:1491:ILE:HD13	2.52	0.44
1:A:1548:GLN:O	1:A:1551:GLY:N	2.49	0.44
1:A:1986:MET:HB3	35:f:184:MET:CG	2.47	0.44
2:C:130:PRO:HG2	2:C:558:LYS:HZ1	1.80	0.44
2:C:885:GLY:HA2	2:C:907:PRO:CD	2.46	0.44
4:O:147:ILE:HG13	4:O:154:TRP:O	2.17	0.44
5:P:87:ASN:HD22	5:P:90:SER:HB2	1.82	0.44
7:R:31:ASN:OD1	7:R:32:ILE:N	2.50	0.44
10:Z:198:PHE:O	10:Z:201:ARG:HB3	2.17	0.44
15:L:41:C:H42	16:M:494:G:H1	1.66	0.44
16:M:483:U:O3'	16:M:484:U:C6	2.71	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:M:484:U:O2'	16:M:485:U:C2	2.70	0.44
18:d:119:ARG:NH1	18:d:143:GLU:OE2	2.51	0.44
19:I:159:LYS:C	19:I:161:VAL:H	2.26	0.44
20:v:712:CYS:O	20:v:715:LYS:N	2.49	0.44
1:A:745:THR:O	1:A:746:THR:HG23	2.17	0.44
1:A:782:ILE:O	1:A:785:HIS:HB2	2.17	0.44
1:A:950:THR:O	1:A:953:ARG:N	2.50	0.44
1:A:1111:SER:HA	1:A:1514:PHE:HE2	1.83	0.44
1:A:1379:MET:HG2	11:B:94:U:H1'	2.00	0.44
1:A:1476:ALA:C	1:A:1478:GLU:N	2.75	0.44
4:O:317:HIS:HD2	4:O:378:TYR:CE2	2.34	0.44
5:P:165:ILE:HG22	5:P:166:PRO:O	2.18	0.44
7:R:110:ASP:OD2	7:R:114:ARG:NE	2.41	0.44
7:R:146:LEU:CD2	7:R:147:ASN:H	2.28	0.44
14:E:53:A:C4'	14:E:54:U:OP2	2.65	0.44
15:L:119:G:C8	30:W:99:ASP:OD2	2.69	0.44
19:I:203:PHE:O	19:I:206:LYS:HB3	2.17	0.44
20:v:433:UNK:O	20:v:437:UNK:N	2.50	0.44
21:n:60:ARG:O	21:n:61:LYS:C	2.61	0.44
1:A:139:LEU:CG	1:A:570:GLN:HE22	2.28	0.44
1:A:180:PRO:O	1:A:181:HIS:HB2	2.18	0.44
1:A:574:GLN:O	1:A:575:GLY:C	2.60	0.44
1:A:649:LEU:HD12	1:A:649:LEU:HA	1.61	0.44
1:A:923:TYR:HH	1:A:936:GLU:CD	2.25	0.44
1:A:1063:PHE:HE1	1:A:1086:ASN:ND2	2.07	0.44
1:A:1412:LEU:O	1:A:1413:SER:C	2.60	0.44
1:A:1555:THR:O	1:A:1556:ILE:C	2.60	0.44
1:A:1596:THR:O	1:A:1599:SER:OG	2.21	0.44
1:A:1703:MET:HB2	1:A:1732:MET:HB2	2.00	0.44
2:C:273:LEU:HA	2:C:273:LEU:HD12	1.78	0.44
2:C:278:LYS:O	2:C:279:LEU:HD12	2.16	0.44
2:C:847:TYR:O	2:C:850:LEU:N	2.48	0.44
6:Q:26:THR:HG22	6:Q:27:LYS:N	2.33	0.44
6:Q:39:LEU:CD1	6:Q:111:ARG:HG3	2.44	0.44
7:R:117:PHE:HD2	14:E:39:G:C5	2.35	0.44
7:R:186:PHE:CD1	7:R:186:PHE:N	2.85	0.44
9:T:152:GLY:HA3	21:n:63:ARG:HH22	1.81	0.44
9:T:156:THR:HG23	9:T:157:ASP:N	2.32	0.44
10:Z:139:LEU:HD21	10:Z:154:VAL:HG11	1.99	0.44
10:Z:344:SER:O	10:Z:348:GLU:HG3	2.17	0.44
18:d:200:GLN:H	18:d:200:GLN:CD	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:F:20:LEU:O	24:F:31:ILE:HA	2.16	0.44
1:A:149:MET:HB2	1:A:154:TYR:HD2	1.82	0.44
1:A:263:PRO:HD2	9:T:7:ARG:NH2	2.32	0.44
1:A:773:SER:O	1:A:775:ARG:HB2	2.17	0.44
1:A:1580:GLY:O	1:A:1582:GLU:N	2.51	0.44
2:C:580:VAL:HG22	2:C:581:LYS:H	1.83	0.44
2:C:869:HIS:CD2	2:C:925:LEU:HD13	2.52	0.44
4:O:209:TRP:CZ3	4:O:216:ILE:HG13	2.53	0.44
4:O:317:HIS:CE1	4:O:320:GLU:H	2.35	0.44
5:P:89:ALA:HB2	13:D:111:C:OP1	2.17	0.44
5:P:120:ASP:OD1	5:P:121:PRO:HD2	2.18	0.44
7:R:34:TYR:CE2	14:E:41:A:H1'	2.53	0.44
7:R:63:ARG:HG3	7:R:85:PRO:O	2.17	0.44
7:R:186:PHE:CD2	7:R:192:ALA:HA	2.52	0.44
7:R:234:ALA:O	7:R:238:LEU:HG	2.18	0.44
10:Z:449:PHE:CZ	10:Z:465:PHE:HE2	2.35	0.44
14:E:66:C:H5'	14:E:66:C:H6	1.81	0.44
18:d:175:PHE:O	18:d:178:ARG:N	2.43	0.44
20:v:574:TYR:CZ	20:v:591:PHE:HB2	2.52	0.44
21:n:65:GLY:C	21:n:66:ASP:CG	2.86	0.44
21:n:380:HIS:CG	21:n:381:SER:H	2.33	0.44
22:p:100:SER:O	22:p:103:ASP:CG	2.60	0.44
22:q:102:LEU:O	22:q:105:LEU:CG	2.66	0.44
25:i:30:TRP:CD2	25:i:89:LEU:HD22	2.52	0.44
1:A:542:HIS:O	1:A:544:LYS:N	2.51	0.44
1:A:823:TRP:O	1:A:824:VAL:C	2.61	0.44
1:A:1794:LEU:O	1:A:1795:LYS:C	2.61	0.44
2:C:89:PRO:C	2:C:91:VAL:H	2.23	0.44
2:C:410:GLN:OE1	2:C:413:LEU:HD12	2.17	0.44
9:T:97:LYS:NZ	13:D:123:U:OP2	2.45	0.44
10:Z:104:GLN:O	10:Z:107:ASN:HB2	2.18	0.44
15:L:51:C:H2'	15:L:52:A:C8	2.52	0.44
15:L:1098:C:H2'	15:L:1099:G:H5''	1.98	0.44
16:M:484:U:O3'	16:M:485:U:C6	2.70	0.44
22:q:14:VAL:HG12	22:q:52:GLU:HA	1.98	0.44
1:A:504:LYS:HA	1:A:504:LYS:HD3	1.76	0.44
1:A:549:LYS:HE2	1:A:549:LYS:HB3	1.66	0.44
1:A:634:ASP:O	1:A:635:THR:C	2.60	0.44
1:A:999:LEU:HA	1:A:999:LEU:HD23	1.68	0.44
1:A:1049:LEU:HB2	1:A:1249:SER:OG	2.18	0.44
1:A:1399:MET:HE3	1:A:1399:MET:HB2	1.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1716:LEU:HB2	1:A:1719:GLU:HG3	1.99	0.44
2:C:576:THR:HG22	2:C:592:PHE:CD2	2.48	0.44
2:C:787:LEU:HA	2:C:790:LYS:HE3	1.99	0.44
5:P:34:ILE:HG23	5:P:35:ALA:N	2.32	0.44
7:R:12:GLN:HE22	7:R:76:PHE:HD1	1.64	0.44
7:R:189:GLN:HG3	7:R:193:GLU:OE2	2.17	0.44
9:T:88:ASP:OD1	9:T:90:LEU:N	2.50	0.44
10:Z:176:LYS:O	10:Z:180:ILE:HG13	2.17	0.44
10:Z:302:SER:O	10:Z:302:SER:OG	2.32	0.44
14:E:15:C:OP2	14:E:15:C:C6	2.70	0.44
14:E:50:G:OP2	14:E:50:G:C8	2.70	0.44
15:L:50:U:H2'	15:L:51:C:H6	1.81	0.44
17:c:96:GLN:OE1	17:c:96:GLN:N	2.40	0.44
1:A:129:THR:CG2	1:A:130:PRO:HD2	2.48	0.44
1:A:725:TYR:CD1	14:E:72:C:O4'	2.65	0.44
1:A:1266:GLU:HG3	1:A:1305:SER:HB2	2.00	0.44
1:A:1434:GLU:OE1	1:A:1434:GLU:N	2.50	0.44
1:A:1490:ARG:HH11	1:A:1536:LEU:C	2.25	0.44
1:A:1860:VAL:HG21	16:M:502:C:H4'	2.00	0.44
1:A:2010:LEU:HD23	1:A:2013:ARG:HD2	1.99	0.44
2:C:465:GLU:HB3	2:C:467:THR:HG23	1.99	0.44
2:C:539:VAL:HG11	2:C:542:ILE:HD11	2.00	0.44
4:O:198:PHE:CE1	4:O:239:ILE:HD11	2.52	0.44
4:O:252:ASP:HB2	4:O:259:VAL:CG2	2.48	0.44
15:L:20:G:O5'	15:L:20:G:C8	2.70	0.44
17:c:73:LEU:HD21	17:c:102:TYR:HB2	1.98	0.44
18:d:137:TYR:O	18:d:140:LEU:HB2	2.18	0.44
18:d:187:GLU:O	18:d:190:SER:HB3	2.18	0.44
22:o:112:VAL:O	22:o:115:GLU:CG	2.66	0.44
1:A:377:VAL:HG11	2:C:912:ALA:HB3	1.99	0.44
1:A:1012:TRP:CE3	1:A:1013:ILE:HG13	2.53	0.44
1:A:1454:SER:OG	1:A:1455:GLN:N	2.50	0.44
1:A:1563:LYS:HB2	1:A:1781:TYR:HD1	1.82	0.44
2:C:153:LEU:HA	2:C:153:LEU:HD23	1.78	0.44
2:C:678:SER:O	2:C:857:LEU:HD12	2.18	0.44
2:C:769:TYR:HD2	2:C:803:VAL:HG11	1.82	0.44
2:C:876:VAL:O	2:C:877:GLU:C	2.59	0.44
4:O:210:ASP:HB2	4:O:217:ILE:HG13	2.00	0.44
6:Q:66:THR:O	6:Q:69:ASN:N	2.46	0.44
6:Q:80:TRP:CZ3	6:Q:91:ILE:HD11	2.53	0.44
6:Q:95:ASN:CG	6:Q:96:GLU:H	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:246:SER:O	7:R:250:MET:HG3	2.18	0.44
9:T:5:LYS:O	9:T:9:SER:HB3	2.17	0.44
14:E:91:A:N7	19:I:97:TYR:HE1	2.06	0.44
15:L:36:A:H2'	15:L:37:G:H8	1.83	0.44
17:c:228:TYR:HA	19:I:152:ILE:HG22	1.99	0.44
17:c:509:LEU:O	17:c:513:ILE:N	2.49	0.44
18:d:149:VAL:HA	18:d:152:VAL:HG22	1.98	0.44
35:f:81:ILE:H	35:f:81:ILE:HD12	1.83	0.44
1:A:180:PRO:HA	1:A:187:LYS:CE	2.47	0.43
1:A:1509:ARG:O	1:A:1510:ILE:C	2.61	0.43
1:A:1969:MET:HE1	1:A:1978:VAL:HG21	1.99	0.43
2:C:195:GLY:CA	2:C:545:LEU:HD13	2.48	0.43
2:C:883:ARG:HG3	2:C:914:PHE:CD1	2.53	0.43
7:R:48:VAL:HG13	7:R:218:GLY:O	2.18	0.43
7:R:153:PRO:O	7:R:156:ILE:HB	2.17	0.43
13:D:45:A:N3	13:D:45:A:O2'	2.46	0.43
14:E:90:U:C6	18:d:104:ARG:NH2	2.86	0.43
1:A:888:GLU:O	1:A:892:SER:CB	2.66	0.43
1:A:987:LEU:HA	1:A:987:LEU:HD23	1.78	0.43
1:A:1066:LEU:O	1:A:1069:LEU:N	2.51	0.43
1:A:1165:LEU:HA	1:A:1165:LEU:HD23	1.74	0.43
1:A:1311:LYS:O	1:A:1314:SER:HB2	2.18	0.43
1:A:1538:ASN:C	1:A:1539:LEU:HD12	2.43	0.43
1:A:1687:HIS:CG	1:A:1688:PRO:HD2	2.53	0.43
1:A:1811:ALA:O	1:A:1814:VAL:HB	2.17	0.43
2:C:727:THR:HG22	2:C:736:ASP:HB2	1.99	0.43
4:O:379:LYS:CD	5:P:47:ARG:HH22	2.21	0.43
6:Q:23:ILE:HG22	6:Q:24:ARG:N	2.33	0.43
6:Q:206:PHE:HB3	6:Q:208:TYR:OH	2.17	0.43
7:R:163:VAL:HG13	7:R:166:ARG:HH21	1.83	0.43
10:Z:297:LEU:O	10:Z:300:LYS:N	2.48	0.43
10:Z:369:TYR:CZ	10:Z:405:ILE:HG12	2.52	0.43
17:c:155:ALA:O	17:c:158:ARG:N	2.51	0.43
19:I:169:GLN:O	19:I:172:SER:OG	2.33	0.43
19:I:200:ASN:O	19:I:204:ASN:CB	2.63	0.43
22:q:225:LEU:O	22:q:226:LYS:CB	2.65	0.43
22:q:405:ASP:HB3	23:t:30:ASN:CG	2.43	0.43
29:V:17:ILE:HG12	29:V:95:ILE:HG23	2.00	0.43
35:f:220:ILE:HG22	35:f:221:MET:N	2.34	0.43
1:A:137:GLU:HB2	9:T:52:ILE:HG21	2.01	0.43
1:A:244:ASP:HB3	1:A:594:ASP:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:525:LEU:HA	1:A:525:LEU:HD23	1.44	0.43
1:A:716:ARG:NH2	13:D:112:C:C4	2.86	0.43
1:A:727:GLY:O	1:A:731:THR:HG23	2.18	0.43
1:A:1619:VAL:HG11	1:A:1635:HIS:HB3	2.00	0.43
2:C:234:LEU:C	2:C:234:LEU:HD12	2.44	0.43
2:C:469:TRP:HA	2:C:577:LEU:O	2.18	0.43
4:O:434:LYS:O	4:O:435:GLU:C	2.59	0.43
6:Q:34:CYS:SG	6:Q:60:ILE:HA	2.59	0.43
6:Q:81:HIS:O	6:Q:82:ILE:HG13	2.17	0.43
10:Z:326:VAL:HG13	10:Z:361:TYR:HE1	1.83	0.43
12:N:108:U:O4'	12:N:109:U:OP2	2.37	0.43
16:M:495:A:C8	16:M:496:U:C4	3.06	0.43
16:M:499:U:O5'	16:M:499:U:C6	2.70	0.43
17:c:230:THR:OG1	17:c:231:SER:N	2.50	0.43
18:d:51:ARG:HH12	18:d:83:ARG:CZ	2.31	0.43
20:v:708:LEU:O	20:v:712:CYS:SG	2.70	0.43
26:h:16:LYS:CG	26:h:17:PRO:HD3	2.49	0.43
24:F:47:GLU:HB3	32:Y:15:TYR:CG	2.52	0.43
25:G:45:GLY:HA3	25:G:53:VAL:HG12	2.00	0.43
25:G:88:THR:HG23	27:K:67:SER:CB	2.49	0.43
28:U:14:ALA:HA	28:U:78:LEU:HD21	2.01	0.43
35:f:114:ASN:HD21	35:f:151:ARG:HH21	1.66	0.43
1:A:555:LYS:HA	9:T:113:GLU:OE1	2.17	0.43
1:A:852:LEU:O	1:A:853:THR:C	2.58	0.43
1:A:1654:TRP:HA	1:A:1657:ILE:HD12	1.99	0.43
1:A:1963:LEU:HA	1:A:1964:PRO:HD3	1.83	0.43
1:A:2053:SER:HA	1:A:2056:ARG:HH11	1.83	0.43
2:C:204:GLU:HB2	2:C:206:LYS:H	1.83	0.43
2:C:313:PHE:HD2	2:C:322:PHE:CE1	2.36	0.43
2:C:604:LYS:HE2	2:C:643:VAL:HG11	2.01	0.43
2:C:749:LYS:O	2:C:753:THR:CB	2.66	0.43
2:C:786:GLU:O	2:C:789:SER:OG	2.25	0.43
2:C:862:TYR:HE1	2:C:908:VAL:CB	2.31	0.43
4:O:273:GLN:HB3	4:O:316:LEU:HD11	2.01	0.43
5:P:180:VAL:HG12	5:P:181:ALA:O	2.19	0.43
6:Q:123:ALA:O	6:Q:124:GLN:C	2.61	0.43
7:R:71:PHE:CE1	7:R:109:LEU:HD13	2.54	0.43
7:R:183:PHE:HD2	12:N:113:U:C2	2.36	0.43
9:T:90:LEU:O	9:T:91:LEU:C	2.61	0.43
15:L:1102:C:C2	15:L:1103:C:C5	3.06	0.43
20:v:167:UNK:C	29:V:81:SER:OG	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:m:17:ILE:HG12	29:m:95:ILE:HG23	2.00	0.43
33:b:8:A:O5'	33:b:8:A:C8	2.70	0.43
1:A:305:LEU:O	1:A:306:PRO:C	2.61	0.43
1:A:404:ASN:CG	1:A:405:ASN:H	2.26	0.43
1:A:589:THR:HG1	7:R:39:GLN:HE22	1.65	0.43
1:A:760:ASN:ND2	4:O:244:ARG:HE	2.16	0.43
1:A:1039:TRP:CE3	1:A:1271:PRO:HB3	2.53	0.43
2:C:194:ASN:OD1	2:C:195:GLY:N	2.52	0.43
2:C:313:PHE:HB2	2:C:322:PHE:CZ	2.53	0.43
2:C:462:SER:OG	2:C:464:PRO:HD3	2.19	0.43
2:C:605:ILE:HG22	2:C:606:VAL:O	2.18	0.43
2:C:614:GLU:HB3	2:C:666:ILE:HD13	2.00	0.43
2:C:635:LYS:HB2	2:C:643:VAL:HB	2.00	0.43
2:C:669:LYS:HE3	2:C:669:LYS:HB2	1.74	0.43
2:C:676:VAL:HG12	2:C:677:PHE:N	2.33	0.43
2:C:862:TYR:HE1	2:C:908:VAL:HB	1.83	0.43
5:P:100:ALA:HB3	5:P:102:ALA:HB2	2.00	0.43
6:Q:45:HIS:CG	6:Q:55:ILE:HD11	2.53	0.43
9:T:46:ASN:OD1	9:T:46:ASN:C	2.60	0.43
10:Z:32:LEU:O	10:Z:72:LEU:HD13	2.18	0.43
10:Z:80:ILE:HA	10:Z:83:LEU:HB2	2.00	0.43
10:Z:454:ASP:CG	10:Z:457:HIS:HD2	2.27	0.43
14:E:42:A:C2'	14:E:43:C:O5'	2.65	0.43
16:M:495:A:C5	16:M:496:U:C4	3.06	0.43
24:F:87:LEU:HG	24:F:92:ILE:HD11	2.00	0.43
1:A:312:TYR:CE2	1:A:319:ARG:NH1	2.87	0.43
1:A:333:LYS:O	1:A:336:PHE:HB2	2.18	0.43
1:A:480:TYR:HE1	2:C:418:GLN:HB2	1.84	0.43
1:A:687:ILE:HG22	1:A:687:ILE:O	2.19	0.43
1:A:729:LEU:HA	1:A:729:LEU:HD12	1.78	0.43
1:A:1130:ARG:HD2	1:A:1133:ASP:OD2	2.18	0.43
2:C:74:VAL:HG22	4:O:131:LEU:O	2.18	0.43
2:C:502:LEU:HD11	2:C:506:GLN:HB2	1.99	0.43
2:C:737:ILE:HG23	2:C:768:PHE:CD2	2.53	0.43
4:O:196:TYR:HE2	8:S:37:LEU:HD22	1.84	0.43
5:P:65:GLU:OE1	5:P:65:GLU:HA	2.17	0.43
6:Q:117:ASN:C	6:Q:119:LYS:H	2.27	0.43
10:Z:85:SER:HB2	10:Z:220:TYR:CE1	2.51	0.43
10:Z:181:LEU:CD1	10:Z:194:LEU:HD22	2.48	0.43
10:Z:185:GLU:C	10:Z:186:LEU:HD12	2.43	0.43
1:A:355:LEU:HG	1:A:356:TYR:CD2	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:605:LEU:HA	1:A:605:LEU:HD23	1.49	0.43
1:A:758:LEU:O	1:A:761:SER:N	2.51	0.43
1:A:1435:LYS:C	1:A:1436:LEU:HD12	2.44	0.43
1:A:1442:ARG:HA	1:A:1442:ARG:HD3	1.77	0.43
1:A:1557:LEU:HD13	1:A:1562:PHE:CD2	2.54	0.43
1:A:1813:TYR:O	1:A:1817:GLU:HG3	2.18	0.43
1:A:1840:TYR:O	1:A:1843:LEU:HG	2.18	0.43
1:A:1964:PRO:HA	1:A:2016:LYS:HZ1	1.82	0.43
1:A:1988:LEU:HD21	35:f:180:VAL:HG11	1.91	0.43
2:C:251:GLN:HG2	2:C:933:TRP:CD2	2.54	0.43
2:C:427:LEU:HG	2:C:427:LEU:O	2.17	0.43
2:C:456:LEU:C	2:C:593:LYS:HE2	2.43	0.43
2:C:609:PRO:HA	2:C:668:ILE:HG22	2.00	0.43
2:C:798:GLY:CA	2:C:839:ILE:HG23	2.46	0.43
2:C:829:VAL:HG12	2:C:830:ASN:N	2.32	0.43
4:O:148:ASP:CG	4:O:151:ASP:H	2.24	0.43
5:P:232:GLN:OE1	5:P:235:LEU:HD22	2.19	0.43
6:Q:103:GLU:CD	7:R:131:ARG:HH22	2.27	0.43
7:R:117:PHE:O	7:R:129:SER:HA	2.19	0.43
8:S:30:LEU:HA	8:S:30:LEU:HD23	1.71	0.43
10:Z:135:ILE:O	10:Z:138:ILE:HB	2.19	0.43
10:Z:293:LYS:O	10:Z:294:LYS:C	2.62	0.43
10:Z:323:LYS:O	10:Z:326:VAL:HB	2.18	0.43
13:D:174:G:C8	30:g:99:ASP:OD2	2.69	0.43
13:D:175:G:C2	25:i:33:GLU:O	2.71	0.43
15:L:28:U:H2'	15:L:29:C:H5'	2.00	0.43
15:L:1097:G:H2'	15:L:1098:C:C6	2.54	0.43
16:M:490:A:H2'	16:M:491:C:H6	1.78	0.43
21:n:432:VAL:HA	21:n:443:ILE:O	2.19	0.43
23:t:81:ASP:C	23:t:82:ASP:CG	2.86	0.43
25:i:88:THR:HG23	27:j:67:SER:CB	2.49	0.43
1:A:431:ILE:HG22	10:Z:182:GLN:NE2	2.34	0.43
1:A:460:PRO:HG3	2:C:376:PHE:CD1	2.53	0.43
1:A:667:TYR:OH	1:A:1622:GLY:HA2	2.19	0.43
1:A:1757:LEU:O	1:A:1760:THR:OG1	2.29	0.43
5:P:103:ASN:ND2	5:P:114:VAL:HG21	2.33	0.43
6:Q:243:ASN:HB3	6:Q:248:CYS:SG	2.58	0.43
9:T:80:TRP:CZ2	9:T:84:GLU:HG3	2.54	0.43
9:T:106:LEU:HD23	9:T:106:LEU:HA	1.71	0.43
10:Z:169:THR:O	10:Z:173:ILE:HG13	2.19	0.43
13:D:176:A:O2'	29:m:20:LYS:HE3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:c:39:LEU:HD21	17:c:159:LEU:HD21	2.01	0.43
17:c:110:ASP:OD1	17:c:111:SER:N	2.50	0.43
17:c:204:LYS:CG	17:c:205:LYS:H	2.24	0.43
20:v:669:TYR:CE2	20:v:686:ILE:HG13	2.43	0.43
25:i:45:GLY:HA3	25:i:53:VAL:HG12	2.00	0.43
26:H:16:LYS:CG	26:H:17:PRO:HD3	2.49	0.43
1:A:190:LYS:O	1:A:203:ASN:N	2.40	0.43
1:A:851:ARG:O	1:A:855:LEU:HG	2.18	0.43
1:A:864:GLN:NE2	1:A:1100:LYS:H	2.16	0.43
1:A:977:ASN:HB2	8:S:175:ARG:NH1	2.34	0.43
1:A:1028:TRP:CD1	1:A:1260:PHE:CE2	3.07	0.43
2:C:229:LEU:O	2:C:232:SER:N	2.51	0.43
2:C:318:LEU:HD13	2:C:425:LEU:HD12	2.00	0.43
4:O:144:CYS:HB3	4:O:186:ARG:O	2.19	0.43
4:O:206:VAL:HB	4:O:220:TYR:HB2	2.00	0.43
4:O:312:ARG:HG2	4:O:312:ARG:O	2.19	0.43
5:P:70:THR:O	5:P:73:TYR:N	2.51	0.43
6:Q:66:THR:O	6:Q:67:GLN:C	2.60	0.43
10:Z:63:PHE:CZ	10:Z:72:LEU:HD12	2.50	0.43
10:Z:130:ILE:HG22	10:Z:225:HIS:HD2	1.83	0.43
14:E:70:U:H2'	14:E:71:G:O4'	2.19	0.43
17:c:93:ARG:NH1	17:c:101:ARG:HH22	2.17	0.43
21:n:416:ARG:O	21:n:417:LEU:HB2	2.18	0.43
25:G:34:GLN:NE2	25:G:37:ILE:HD12	2.34	0.43
1:A:358:ARG:NH2	13:D:91:U:O2'	2.51	0.43
1:A:654:HIS:CE1	1:A:658:ASN:HD21	2.37	0.43
1:A:714:PHE:C	1:A:714:PHE:CD2	2.96	0.43
1:A:895:PHE:CE2	1:A:1073:ILE:HG13	2.47	0.43
1:A:1187:LEU:HD23	1:A:1187:LEU:HA	1.78	0.43
1:A:1226:VAL:O	1:A:1227:PHE:C	2.60	0.43
1:A:1456:ARG:HG3	1:A:1457:VAL:N	2.34	0.43
2:C:70:TYR:CE2	4:O:134:VAL:HG21	2.54	0.43
2:C:159:LYS:HE2	2:C:159:LYS:HB3	1.83	0.43
2:C:480:GLY:O	2:C:481:ALA:C	2.62	0.43
2:C:656:LEU:HD23	2:C:656:LEU:HA	1.43	0.43
2:C:834:MET:HE3	2:C:834:MET:HB3	1.88	0.43
15:L:120:G:C2	25:G:33:GLU:O	2.71	0.43
15:L:121:C:O2'	29:V:20:LYS:HE3	2.19	0.43
17:c:41:GLN:HG2	17:c:42:LYS:H	1.84	0.43
18:d:75:GLU:OE2	18:d:83:ARG:HB2	2.18	0.43
25:i:34:GLN:NE2	25:i:37:ILE:HD12	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:l:14:ALA:HA	28:l:78:LEU:HD21	2.01	0.43
33:b:7:U:O2'	33:b:8:A:O5'	2.36	0.43
1:A:207:ARG:HH12	1:A:299:LYS:HE2	1.84	0.42
1:A:311:LEU:O	1:A:312:TYR:C	2.60	0.42
1:A:794:LYS:O	1:A:796:ASN:N	2.52	0.42
1:A:1145:MET:SD	1:A:1160:LEU:HD22	2.59	0.42
1:A:1343:PHE:HE2	1:A:1402:ALA:CB	2.32	0.42
1:A:1493:THR:O	1:A:1494:LEU:C	2.62	0.42
1:A:1580:GLY:C	1:A:1582:GLU:N	2.76	0.42
1:A:1592:HIS:CE1	33:b:4:U:OP1	2.72	0.42
1:A:1940:MET:HE3	1:A:1940:MET:HB3	1.77	0.42
2:C:153:LEU:HD13	2:C:212:PHE:CZ	2.54	0.42
2:C:317:LYS:HB2	36:C:1500:GTP:C5	2.54	0.42
2:C:340:LYS:O	2:C:343:ASP:CB	2.53	0.42
2:C:925:LEU:HA	2:C:925:LEU:HD23	1.70	0.42
4:O:224:LEU:HB2	4:O:245:ASP:CG	2.44	0.42
5:P:106:LEU:HD13	6:Q:14:GLU:HG3	2.01	0.42
6:Q:46:PHE:HD1	6:Q:47:LYS:O	2.02	0.42
6:Q:210:ILE:HD11	6:Q:249:GLY:N	2.34	0.42
7:R:103:ALA:HA	7:R:106:THR:HG23	2.00	0.42
7:R:139:VAL:O	7:R:181:CYS:HA	2.19	0.42
10:Z:15:ARG:O	10:Z:19:GLU:HB3	2.19	0.42
10:Z:106:PHE:HZ	10:Z:145:LYS:HG3	1.84	0.42
10:Z:131:HIS:HB2	10:Z:224:THR:CG2	2.49	0.42
10:Z:297:LEU:HD12	10:Z:297:LEU:HA	1.62	0.42
13:D:81:A:HO2'	13:D:82:A:P	2.36	0.42
15:L:1105:C:H42	31:X:97:LYS:HZ1	1.66	0.42
16:M:485:U:O2'	16:M:486:A:C5	2.71	0.42
19:I:118:ASN:OD1	19:I:121:LYS:HD2	2.19	0.42
21:n:205:HIS:CE1	21:n:231:LYS:HD2	2.54	0.42
23:t:109:SER:O	23:t:110:GLU:CB	2.67	0.42
1:A:206:PRO:HB2	1:A:496:ALA:CB	2.49	0.42
1:A:660:ILE:C	1:A:662:GLN:H	2.26	0.42
1:A:1320:LEU:HD23	1:A:1320:LEU:HA	1.62	0.42
1:A:1644:SER:O	1:A:1647:GLN:HB2	2.19	0.42
2:C:79:GLU:HB3	4:O:167:TRP:HZ3	1.84	0.42
2:C:363:PRO:O	2:C:364:PHE:HB3	2.19	0.42
2:C:715:MET:HG3	2:C:817:GLN:HB2	2.01	0.42
3:J:21:GLN:NE2	10:Z:310:HIS:CE1	2.87	0.42
4:O:176:THR:OG1	4:O:177:THR:N	2.52	0.42
4:O:211:LEU:O	4:O:212:GLU:C	2.61	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:P:201:PHE:O	5:P:204:LEU:N	2.52	0.42
6:Q:46:PHE:O	6:Q:56:ILE:N	2.52	0.42
7:R:1:MET:HA	7:R:5:ARG:HB3	2.02	0.42
7:R:83:LEU:HA	7:R:83:LEU:HD23	1.81	0.42
7:R:89:TYR:CB	14:E:34:A:C2	3.02	0.42
9:T:64:TYR:OH	9:T:69:LYS:HE2	2.19	0.42
10:Z:310:HIS:O	10:Z:311:LYS:C	2.60	0.42
10:Z:379:ASP:O	10:Z:381:LEU:N	2.53	0.42
13:D:80:G:C2	13:D:82:A:C2	3.07	0.42
13:D:167:A:N7	30:g:63:ARG:HB3	2.34	0.42
16:M:499:U:O2'	16:M:500:A:P	2.77	0.42
16:M:500:A:H8	16:M:500:A:H3'	1.83	0.42
17:c:68:GLU:H	17:c:68:GLU:CD	2.27	0.42
17:c:152:LEU:O	17:c:156:ARG:HB3	2.19	0.42
17:c:190:GLU:OE1	21:n:436:PRO:CG	2.67	0.42
18:d:219:ARG:O	18:d:222:TYR:HB2	2.19	0.42
21:n:290:ASP:O	21:n:320:TRP:HH2	2.02	0.42
35:f:220:ILE:HG22	35:f:221:MET:H	1.84	0.42
1:A:193:TYR:HD1	1:A:194:HIS:O	2.01	0.42
1:A:968:ASP:HB2	1:A:983:SER:OG	2.20	0.42
1:A:1382:ARG:NH1	1:A:1614:ILE:O	2.53	0.42
1:A:1555:THR:O	1:A:1558:GLU:N	2.52	0.42
1:A:1852:VAL:HB	1:A:1935:VAL:CG2	2.49	0.42
1:A:1889:LEU:HD12	1:A:1989:PHE:HB2	2.00	0.42
2:C:121:ASP:O	2:C:124:LEU:HB2	2.19	0.42
2:C:320:PHE:CD1	2:C:425:LEU:HD13	2.54	0.42
3:J:19:HIS:ND1	11:B:91:A:N7	2.68	0.42
5:P:106:LEU:HD13	6:Q:14:GLU:CG	2.50	0.42
5:P:134:VAL:HG13	6:Q:111:ARG:HG2	2.01	0.42
10:Z:49:ILE:HG21	10:Z:56:ILE:HG21	2.01	0.42
10:Z:62:ASP:O	10:Z:66:ASN:HB3	2.19	0.42
10:Z:155:MET:SD	10:Z:173:ILE:HG21	2.60	0.42
13:D:78:A:HO2'	13:D:79:C:P	2.34	0.42
14:E:91:A:O2'	19:I:100:LEU:CD2	2.67	0.42
20:v:167:UNK:C	29:V:81:SER:CB	2.96	0.42
22:q:123:ALA:O	22:q:127:LEU:CG	2.67	0.42
25:i:88:THR:HG22	25:i:89:LEU:HD12	2.01	0.42
1:A:288:GLU:HG2	1:A:288:GLU:O	2.19	0.42
1:A:354:PRO:C	1:A:356:TYR:H	2.27	0.42
1:A:484:PHE:CG	13:D:81:A:C5	3.07	0.42
1:A:621:LEU:HA	1:A:669:TYR:HD2	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:644:VAL:O	1:A:645:ASP:HB2	2.19	0.42
1:A:744:THR:OG1	1:A:745:THR:N	2.51	0.42
1:A:1272:ARG:HA	1:A:1275:MET:SD	2.59	0.42
1:A:1361:VAL:HG21	1:A:1407:ILE:HD11	2.01	0.42
1:A:1423:THR:O	1:A:1424:HIS:CG	2.72	0.42
2:C:700:GLU:HG2	2:C:701:GLU:N	2.33	0.42
4:O:335:GLY:O	4:O:339:GLY:HA2	2.19	0.42
4:O:396:LEU:O	4:O:398:GLY:N	2.52	0.42
5:P:51:PHE:N	5:P:51:PHE:CD1	2.86	0.42
8:S:128:ARG:HH21	8:S:129:LYS:NZ	2.18	0.42
9:T:1:MET:HB2	9:T:2:PRO:HD3	2.01	0.42
15:L:24:U:C5'	15:L:25:A:OP2	2.67	0.42
16:M:500:A:C5	16:M:502:C:N4	2.87	0.42
21:n:291:HIS:CB	21:n:320:TRP:CH2	3.02	0.42
23:t:136:VAL:O	23:t:139:GLN:CG	2.67	0.42
1:A:531:LEU:HD23	1:A:531:LEU:HA	1.51	0.42
1:A:548:LEU:O	1:A:549:LYS:C	2.62	0.42
1:A:686:ILE:HA	1:A:686:ILE:HD13	1.74	0.42
1:A:886:MET:SD	1:A:1120:VAL:HG22	2.59	0.42
1:A:1634:LEU:HA	1:A:1634:LEU:HD23	1.87	0.42
1:A:1798:ILE:C	1:A:1801:SER:HG	2.25	0.42
2:C:152:LEU:HD23	2:C:152:LEU:HA	1.81	0.42
2:C:360:ARG:C	2:C:362:LYS:N	2.76	0.42
2:C:606:VAL:HG12	2:C:607:LEU:N	2.34	0.42
2:C:873:LEU:O	2:C:874:PRO:C	2.63	0.42
2:C:885:GLY:HA3	2:C:906:VAL:HA	2.01	0.42
2:C:968:MET:HE2	2:C:968:MET:HA	2.02	0.42
4:O:221:TYR:O	4:O:251:TRP:CH2	2.73	0.42
5:P:145:PRO:HB3	18:d:127:SER:O	2.20	0.42
6:Q:17:LEU:HD23	6:Q:17:LEU:O	2.20	0.42
6:Q:215:PRO:CG	6:Q:217:TRP:NE1	2.81	0.42
7:R:135:LYS:HD3	7:R:187:LYS:O	2.20	0.42
7:R:138:TYR:HD1	7:R:183:PHE:HE1	1.66	0.42
9:T:90:LEU:H	9:T:90:LEU:HG	1.66	0.42
10:Z:61:VAL:O	10:Z:65:LEU:HB3	2.19	0.42
20:v:730:GLN:HA	20:v:733:ILE:HD12	1.97	0.42
28:U:6:ILE:N	28:U:7:PRO:CD	2.82	0.42
35:f:81:ILE:H	35:f:81:ILE:CD1	2.32	0.42
1:A:145:THR:C	1:A:147:SER:N	2.76	0.42
1:A:456:GLU:HA	2:C:357:GLY:HA2	2.01	0.42
1:A:497:GLN:OE1	1:A:712:LEU:HD22	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:750:LEU:HD23	1:A:751:ASP:HA	2.01	0.42
1:A:794:LYS:HD3	1:A:854:ARG:HH12	1.84	0.42
1:A:801:VAL:CG1	1:A:802:PRO:HD2	2.49	0.42
1:A:1128:GLN:O	1:A:1129:GLU:C	2.62	0.42
1:A:1150:LYS:HB3	1:A:1154:LYS:HZ2	1.85	0.42
1:A:1337:THR:HB	33:b:8:A:H61	1.84	0.42
1:A:1596:THR:O	1:A:1599:SER:N	2.48	0.42
1:A:1859:ARG:O	1:A:1874:ALA:CA	2.61	0.42
2:C:195:GLY:C	2:C:545:LEU:HD13	2.45	0.42
2:C:352:VAL:HG21	2:C:359:PHE:HB3	2.01	0.42
2:C:681:CYS:O	2:C:714:PRO:HG3	2.18	0.42
4:O:414:LEU:HD23	4:O:426:TRP:HB2	2.00	0.42
5:P:115:VAL:HG21	6:Q:24:ARG:NH1	2.35	0.42
7:R:31:ASN:OD1	7:R:31:ASN:C	2.62	0.42
8:S:127:TRP:O	8:S:129:LYS:N	2.53	0.42
8:S:170:LEU:HA	8:S:170:LEU:HD23	1.69	0.42
10:Z:32:LEU:CD2	10:Z:76:LEU:HD23	2.49	0.42
10:Z:71:ARG:O	10:Z:74:PRO:HG2	2.20	0.42
16:M:484:U:C2'	16:M:485:U:C2	3.03	0.42
16:M:500:A:H3'	16:M:500:A:C8	2.55	0.42
24:k:87:LEU:HG	24:k:92:ILE:HD11	2.00	0.42
1:A:265:ASN:ND2	9:T:7:ARG:NH2	2.68	0.42
1:A:422:LEU:HD23	1:A:422:LEU:HA	1.91	0.42
1:A:564:TRP:O	1:A:565:VAL:C	2.62	0.42
1:A:614:ARG:CZ	11:B:98:A:H5''	2.48	0.42
1:A:891:GLU:OE2	5:P:219:ILE:HG12	2.20	0.42
1:A:1023:LEU:HD13	1:A:1451:PHE:CE1	2.55	0.42
1:A:1206:CYS:HB3	1:A:1303:LYS:HE2	2.01	0.42
1:A:1226:VAL:O	1:A:1229:GLU:HB3	2.20	0.42
1:A:1348:GLU:CG	1:A:1446:THR:HB	2.45	0.42
1:A:1423:THR:O	1:A:1424:HIS:ND1	2.52	0.42
1:A:1454:SER:CB	1:A:1488:ILE:HG22	2.49	0.42
1:A:1498:ASP:OD1	1:A:1498:ASP:N	2.48	0.42
1:A:1570:TRP:CD2	1:A:1570:TRP:C	2.95	0.42
2:C:70:TYR:HB3	2:C:74:VAL:HG21	2.02	0.42
2:C:130:PRO:HG2	2:C:558:LYS:HZ2	1.82	0.42
2:C:281:PRO:HG3	2:C:382:TYR:HD2	1.85	0.42
2:C:774:LEU:HD23	2:C:775:ILE:N	2.35	0.42
2:C:933:TRP:O	2:C:935:LYS:HG3	2.19	0.42
4:O:131:LEU:HA	4:O:131:LEU:HD12	1.81	0.42
4:O:217:ILE:HD12	4:O:217:ILE:HG23	1.70	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:246:SER:HG	4:O:267:GLY:C	2.28	0.42
4:O:433:THR:OG1	4:O:434:LYS:N	2.53	0.42
6:Q:43:LEU:HA	6:Q:43:LEU:HD12	1.87	0.42
7:R:17:GLU:O	7:R:18:LEU:C	2.63	0.42
14:E:91:A:C8	19:I:97:TYR:CE1	3.05	0.42
17:c:242:GLU:O	17:c:246:ARG:CB	2.68	0.42
20:v:605:PHE:O	20:v:609:GLU:HG2	2.20	0.42
1:A:274:GLU:C	1:A:274:GLU:CD	2.88	0.42
1:A:297:SER:HB3	13:D:32:G:OP1	2.20	0.42
1:A:488:ARG:O	1:A:489:THR:OG1	2.31	0.42
1:A:724:ARG:O	1:A:725:TYR:C	2.62	0.42
1:A:750:LEU:HD23	1:A:751:ASP:N	2.35	0.42
1:A:1135:ALA:O	1:A:1141:PRO:HA	2.20	0.42
1:A:1324:GLY:HA3	33:b:3:U:H2'	2.01	0.42
1:A:1438:PRO:HG3	1:A:1545:ASP:HB3	2.00	0.42
1:A:1618:ASN:N	1:A:1744:ASP:OD2	2.52	0.42
1:A:1875:ILE:HG22	1:A:1876:ASN:N	2.34	0.42
1:A:1905:LEU:N	1:A:1905:LEU:HD12	2.35	0.42
1:A:1920:LEU:O	1:A:1924:LEU:HG	2.19	0.42
2:C:68:HIS:HA	2:C:71:GLY:HA2	2.02	0.42
2:C:161:ILE:HD13	2:C:164:MET:HE3	2.01	0.42
2:C:796:ILE:HG13	2:C:800:TYR:CZ	2.55	0.42
3:J:6:ILE:CD1	11:B:90:A:N1	2.78	0.42
4:O:204:LYS:HG2	4:O:225:SER:HA	2.02	0.42
5:P:107:ASN:OD1	5:P:107:ASN:N	2.46	0.42
6:Q:251:LEU:HD11	6:Q:253:PHE:CZ	2.55	0.42
7:R:210:LYS:HG3	7:R:211:GLU:N	2.35	0.42
9:T:99:GLY:O	9:T:101:GLU:N	2.52	0.42
14:E:54:U:O2'	14:E:55:G:N7	2.51	0.42
15:L:1096:C:H2'	15:L:1097:G:H8	1.85	0.42
21:n:291:HIS:CB	21:n:320:TRP:CZ2	3.02	0.42
1:A:143:ILE:HD13	1:A:570:GLN:NE2	2.35	0.42
1:A:484:PHE:O	1:A:485:PRO:C	2.61	0.42
1:A:655:TYR:CE1	1:A:659:HIS:CD2	3.08	0.42
1:A:874:ILE:O	1:A:875:THR:OG1	2.29	0.42
1:A:992:ASP:O	1:A:993:ALA:C	2.62	0.42
1:A:1041:VAL:O	1:A:1041:VAL:HG12	2.19	0.42
1:A:1562:PHE:O	1:A:1562:PHE:CG	2.73	0.42
1:A:1717:LEU:HA	1:A:1790:TRP:CZ2	2.55	0.42
1:A:1884:PRO:O	1:A:1992:TYR:OH	2.14	0.42
2:C:718:LYS:CA	2:C:721:GLN:HB3	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Q:47:LYS:HB3	6:Q:52:SER:HB3	2.01	0.42
6:Q:94:VAL:O	6:Q:95:ASN:HB3	2.19	0.42
10:Z:323:LYS:CE	10:Z:364:THR:HG22	2.50	0.42
10:Z:384:LEU:O	10:Z:385:GLY:C	2.63	0.42
15:L:52:A:O5'	15:L:52:A:C8	2.70	0.42
16:M:484:U:C6	16:M:484:U:C3'	3.03	0.42
17:c:332:UNK:H2	20:v:493:UNK:HA	1.85	0.42
18:d:103:ILE:O	18:d:106:ILE:N	2.50	0.42
18:d:115:ILE:HG23	18:d:116:ASN:N	2.34	0.42
1:A:143:ILE:HD13	1:A:570:GLN:HE21	1.85	0.42
1:A:161:PHE:O	1:A:162:LEU:C	2.59	0.42
1:A:190:LYS:HG2	1:A:561:THR:HG22	2.02	0.42
1:A:636:HIS:O	1:A:637:VAL:C	2.60	0.42
1:A:1042:SER:OG	1:A:1043:ARG:HG3	2.20	0.42
1:A:1050:LEU:HD11	1:A:1230:ILE:HD12	2.01	0.42
1:A:1208:PRO:HB2	1:A:1417:GLN:O	2.20	0.42
1:A:1340:ILE:O	1:A:1344:THR:CB	2.68	0.42
1:A:1341:SER:HA	1:A:1525:PHE:CE1	2.54	0.42
1:A:1654:TRP:O	1:A:1657:ILE:HB	2.19	0.42
1:A:1679:GLU:HG2	1:A:1705:SER:O	2.19	0.42
1:A:1714:PRO:HB2	1:A:1787:TYR:CE2	2.55	0.42
1:A:1755:LYS:O	1:A:1756:PHE:C	2.63	0.42
1:A:1865:THR:O	1:A:1866:PHE:C	2.63	0.42
1:A:1925:PRO:CD	35:f:234:LYS:HD3	2.50	0.42
1:A:1986:MET:CB	35:f:184:MET:CG	2.97	0.42
1:A:1986:MET:HB3	35:f:184:MET:CB	2.49	0.42
2:C:222:MET:HE1	2:C:252:LEU:HD21	2.01	0.42
2:C:421:LEU:O	2:C:424:VAL:N	2.53	0.42
2:C:798:GLY:HA3	2:C:842:MET:HB3	2.01	0.42
4:O:154:TRP:HZ3	4:O:156:ILE:HD11	1.85	0.42
4:O:387:LEU:HA	4:O:387:LEU:HD23	1.70	0.42
5:P:159:ASP:HB2	5:P:160:PRO:HD3	2.02	0.42
8:S:17:ALA:HA	8:S:20:TYR:CE2	2.54	0.42
10:Z:92:GLU:O	10:Z:96:LYS:HG3	2.20	0.42
10:Z:176:LYS:O	10:Z:179:TYR:HB3	2.20	0.42
10:Z:404:ILE:HD12	10:Z:404:ILE:H	1.85	0.42
10:Z:427:LEU:HD21	10:Z:431:LEU:HD12	2.02	0.42
13:D:32:G:C3'	13:D:33:U:H5''	2.49	0.42
15:L:7:C:OP1	19:I:174:LYS:HE2	2.19	0.42
15:L:16:U:H2'	19:I:179:ARG:HH21	1.85	0.42
17:c:533:LEU:O	17:c:536:GLN:CG	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:n:294:SER:CB	21:n:313:GLU:CG	2.98	0.42
25:G:77:LEU:HD23	25:G:78:GLY:N	2.35	0.42
30:W:49:ARG:HA	30:W:49:ARG:HD2	1.64	0.42
1:A:165:LEU:HB3	1:A:730:ILE:HD11	2.02	0.41
1:A:291:LYS:H	1:A:291:LYS:HG2	1.70	0.41
1:A:380:ARG:HA	3:J:4:ASN:OD1	2.19	0.41
1:A:452:PHE:CE1	2:C:347:ARG:HG3	2.54	0.41
1:A:481:HIS:NE2	2:C:276:ASP:OD1	2.53	0.41
1:A:583:ILE:HD13	1:A:583:ILE:HG21	1.78	0.41
1:A:940:ILE:O	1:A:941:GLU:C	2.63	0.41
1:A:1041:VAL:HG21	1:A:1274:ARG:NH1	2.35	0.41
1:A:1229:GLU:O	1:A:1232:SER:OG	2.16	0.41
1:A:1973:LYS:O	1:A:1976:ASP:HB2	2.20	0.41
4:O:232:ILE:O	4:O:233:HIS:C	2.60	0.41
5:P:110:HIS:HE1	6:Q:19:ASP:HA	1.84	0.41
6:Q:103:GLU:CD	7:R:131:ARG:HH12	2.27	0.41
6:Q:204:SER:O	6:Q:294:SER:HB3	2.20	0.41
7:R:251:VAL:HA	7:R:254:ILE:HG12	2.01	0.41
9:T:55:LEU:O	9:T:56:HIS:C	2.61	0.41
9:T:104:CYS:N	9:T:153:CYS:SG	2.82	0.41
14:E:84:C:H3'	14:E:85:C:H5''	2.01	0.41
15:L:112:A:N7	30:W:63:ARG:HB3	2.34	0.41
17:c:242:GLU:O	17:c:246:ARG:HB2	2.20	0.41
21:n:252:ASP:O	21:n:253:VAL:HG23	2.20	0.41
28:l:6:ILE:N	28:l:7:PRO:CD	2.82	0.41
1:A:294:ASN:CB	1:A:299:LYS:O	2.68	0.41
1:A:753:TYR:O	1:A:754:TYR:C	2.63	0.41
1:A:1148:LYS:HB2	1:A:1152:VAL:HG21	2.02	0.41
1:A:1229:GLU:OE2	1:A:1233:ARG:NH2	2.53	0.41
2:C:135:ASN:HB2	2:C:233:ASP:H	1.85	0.41
2:C:257:ILE:HD12	2:C:257:ILE:HA	1.93	0.41
2:C:358:ASN:OD1	2:C:358:ASN:N	2.53	0.41
2:C:362:LYS:HA	2:C:363:PRO:HD3	1.89	0.41
2:C:969:LYS:O	2:C:970:THR:C	2.62	0.41
4:O:122:ARG:CZ	4:O:122:ARG:HB2	2.49	0.41
4:O:323:VAL:O	4:O:323:VAL:HG13	2.19	0.41
6:Q:82:ILE:HG23	6:Q:86:LEU:HB3	2.02	0.41
7:R:49:SER:HB3	7:R:202:GLN:HE22	1.84	0.41
9:T:29:GLN:HA	9:T:32:ASP:CG	2.45	0.41
9:T:119:THR:O	9:T:120:CYS:C	2.63	0.41
10:Z:337:SER:O	10:Z:338:THR:OG1	2.30	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:E:88:U:H2'	15:L:17:U:C6	2.55	0.41
18:d:110:LEU:HD23	18:d:110:LEU:HA	1.80	0.41
25:G:88:THR:HG22	25:G:89:LEU:HD12	2.01	0.41
35:f:82:GLN:HG2	35:f:152:ARG:O	2.20	0.41
1:A:409:CYS:O	1:A:410:ILE:C	2.64	0.41
1:A:682:ASP:O	1:A:683:LEU:C	2.62	0.41
1:A:757:GLU:OE1	4:O:202:GLU:HB3	2.21	0.41
1:A:767:LEU:HD23	1:A:767:LEU:HA	1.82	0.41
1:A:784:GLN:HE22	15:L:19:U:C2'	2.34	0.41
1:A:954:ILE:O	1:A:955:LYS:C	2.63	0.41
1:A:1002:GLU:O	1:A:1005:GLN:HB3	2.19	0.41
1:A:1182:LEU:HD23	1:A:1182:LEU:HA	1.82	0.41
1:A:1222:LEU:HD23	1:A:1222:LEU:HA	1.82	0.41
1:A:1310:LYS:O	1:A:1314:SER:OG	2.23	0.41
1:A:1441:PHE:CD2	10:Z:303:LEU:HG	2.55	0.41
1:A:1893:ILE:HD13	1:A:1981:ALA:HB2	2.02	0.41
1:A:2015:LEU:O	1:A:2019:GLU:HG2	2.19	0.41
1:A:2021:SER:O	1:A:2025:ILE:HG13	2.19	0.41
1:A:2058:LEU:HD23	1:A:2058:LEU:HA	1.81	0.41
2:C:274:ILE:HG21	2:C:385:PHE:CD2	2.55	0.41
2:C:602:VAL:O	2:C:676:VAL:HG23	2.20	0.41
4:O:115:TYR:CD2	18:d:235:LEU:HD21	2.55	0.41
4:O:147:ILE:HD11	4:O:169:LEU:HD22	2.02	0.41
6:Q:4:GLU:O	6:Q:8:PRO:HD2	2.20	0.41
7:R:98:ASP:O	7:R:101:LYS:N	2.42	0.41
7:R:214:ASP:O	7:R:215:ARG:C	2.63	0.41
10:Z:18:TRP:HB2	10:Z:242:PHE:CE1	2.55	0.41
10:Z:194:LEU:HD23	10:Z:194:LEU:O	2.21	0.41
10:Z:336:GLU:O	10:Z:337:SER:HB3	2.21	0.41
15:L:41:C:O2'	15:L:42:U:P	2.78	0.41
19:I:167:SER:O	19:I:171:GLU:HG3	2.20	0.41
20:v:648:PHE:CD1	20:v:669:TYR:HB2	2.55	0.41
1:A:128:TYR:CZ	13:D:35:A:O4'	2.74	0.41
1:A:209:ILE:H	1:A:209:ILE:HG13	1.60	0.41
1:A:590:TYR:OH	1:A:609:GLU:HB3	2.20	0.41
1:A:784:GLN:HE22	15:L:20:G:H5''	1.81	0.41
1:A:1326:THR:C	1:A:1327:THR:HG1	2.20	0.41
1:A:1431:HIS:CE1	1:A:1434:GLU:HB3	2.56	0.41
2:C:75:GLU:HB2	4:O:133:ARG:HG3	2.02	0.41
2:C:90:LEU:HD12	4:O:176:THR:HG21	2.01	0.41
2:C:241:VAL:HG13	2:C:242:VAL:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:247:PHE:O	2:C:250:GLU:HB2	2.20	0.41
2:C:365:GLU:CG	2:C:366:ASN:N	2.81	0.41
2:C:378:LEU:HD23	2:C:378:LEU:HA	1.67	0.41
9:T:47:GLU:O	9:T:48:GLN:C	2.61	0.41
10:Z:434:ASP:O	10:Z:437:GLN:HB2	2.20	0.41
12:N:108:U:C1'	12:N:109:U:P	3.08	0.41
16:M:498:C:C4	16:M:499:U:N3	2.89	0.41
18:d:182:TRP:CH2	18:d:212:HIS:NE2	2.88	0.41
32:Y:62:ASN:HB2	32:Y:84:ASN:OD1	2.20	0.41
33:b:4:U:O2'	33:b:5:U:O4'	2.38	0.41
1:A:259:GLU:HG2	1:A:260:PRO:HD2	2.02	0.41
1:A:275:TYR:HD2	1:A:310:ASN:HD21	1.68	0.41
1:A:295:GLY:O	1:A:296:THR:C	2.64	0.41
1:A:340:LYS:NZ	1:A:355:LEU:HD13	2.35	0.41
1:A:344:ASN:HA	3:J:3:TYR:CE2	2.56	0.41
1:A:615:LEU:HD23	1:A:619:PHE:CE2	2.54	0.41
1:A:653:ILE:HD13	1:A:653:ILE:HG21	1.77	0.41
1:A:1427:ALA:O	3:J:16:THR:HB	2.21	0.41
1:A:1542:TYR:O	1:A:1543:ARG:C	2.62	0.41
1:A:1862:VAL:HA	1:A:1871:ALA:O	2.19	0.41
1:A:2034:ILE:HD13	1:A:2039:LEU:O	2.20	0.41
2:C:172:TRP:HZ2	2:C:416:ASP:OD2	2.03	0.41
2:C:175:LEU:HD23	2:C:175:LEU:C	2.45	0.41
2:C:324:ILE:HG13	2:C:325:LYS:N	2.35	0.41
2:C:355:HIS:CD2	2:C:360:ARG:NE	2.88	0.41
4:O:257:ILE:HG22	4:O:259:VAL:N	2.35	0.41
4:O:265:HIS:CD2	4:O:269:ILE:HG12	2.55	0.41
7:R:9:ALA:HB2	7:R:60:GLY:C	2.46	0.41
7:R:36:LYS:HG3	14:E:41:A:C2	2.56	0.41
7:R:53:LEU:HD12	7:R:54:GLN:N	2.36	0.41
7:R:163:VAL:HG11	7:R:199:MET:HE2	2.01	0.41
10:Z:21:ILE:C	10:Z:24:HIS:H	2.28	0.41
10:Z:465:PHE:CE1	10:Z:468:ILE:HD12	2.55	0.41
13:D:44:A:OP2	13:D:44:A:C4'	2.68	0.41
14:E:1:G:H2'	14:E:2:U:H6	1.85	0.41
15:L:1115:G:C6	15:L:1116:A:N6	2.89	0.41
16:M:483:U:H5''	16:M:484:U:P	2.60	0.41
18:d:200:GLN:HA	18:d:203:LEU:HB3	2.02	0.41
18:d:222:TYR:HB3	18:d:250:PHE:CE1	2.55	0.41
22:q:298:ASN:CG	22:q:300:GLU:H	2.29	0.41
1:A:161:PHE:HE1	1:A:198:ALA:HA	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:MET:HE3	1:A:702:GLY:O	2.20	0.41
1:A:299:LYS:HA	1:A:493:MET:CG	2.51	0.41
1:A:311:LEU:HA	1:A:311:LEU:HD23	1.81	0.41
1:A:353:GLU:HG3	13:D:104:G:P	2.59	0.41
1:A:407:VAL:HG21	2:C:927:MET:HB2	2.02	0.41
1:A:1082:ILE:HG21	1:A:1113:ILE:HD11	2.02	0.41
1:A:1423:THR:HB	1:A:1424:HIS:CD2	2.55	0.41
1:A:1540:ASN:C	1:A:1542:TYR:N	2.79	0.41
1:A:1751:TYR:O	1:A:1755:LYS:HG2	2.20	0.41
1:A:1879:ILE:O	1:A:1891:LEU:HA	2.21	0.41
1:A:2013:ARG:NH2	1:A:2084:LEU:C	2.79	0.41
2:C:212:PHE:O	2:C:213:LEU:HD23	2.21	0.41
2:C:394:ASP:OD1	2:C:394:ASP:C	2.62	0.41
2:C:603:PHE:HD2	2:C:652:MET:HG3	1.85	0.41
2:C:610:LEU:HA	2:C:610:LEU:HD12	1.76	0.41
2:C:619:LEU:HD23	2:C:619:LEU:HA	1.75	0.41
2:C:868:VAL:O	2:C:899:LEU:HA	2.21	0.41
4:O:169:LEU:HD12	4:O:169:LEU:HA	1.81	0.41
4:O:198:PHE:HZ	4:O:253:MET:HE2	1.86	0.41
4:O:238:LEU:HD11	5:P:74:ILE:CD1	2.51	0.41
4:O:251:TRP:HZ3	4:O:258:PRO:HD3	1.85	0.41
5:P:39:LYS:HE2	5:P:39:LYS:HB3	1.75	0.41
5:P:70:THR:O	5:P:71:LYS:C	2.63	0.41
5:P:129:LYS:HG2	5:P:130:LYS:N	2.35	0.41
6:Q:215:PRO:HB3	7:R:171:ASP:OD1	2.21	0.41
9:T:65:THR:O	9:T:69:LYS:HB2	2.20	0.41
10:Z:433:LEU:HD21	10:Z:472:LEU:HB2	2.02	0.41
15:L:34:G:OP2	15:L:34:G:H8	1.94	0.41
16:M:494:G:O2'	16:M:495:A:P	2.78	0.41
17:c:46:ARG:O	17:c:50:LEU:HB2	2.20	0.41
18:d:175:PHE:HA	18:d:178:ARG:NH2	2.35	0.41
22:r:112:VAL:O	22:r:115:GLU:CG	2.68	0.41
25:i:77:LEU:HD23	25:i:78:GLY:N	2.35	0.41
33:b:4:U:O2'	33:b:5:U:P	2.79	0.41
1:A:133:GLU:OE2	1:A:561:THR:HG23	2.19	0.41
1:A:141:LYS:O	1:A:142:ILE:C	2.63	0.41
1:A:370:ILE:O	1:A:371:ASP:C	2.64	0.41
1:A:503:LYS:HG2	1:A:507:LEU:HD13	2.03	0.41
1:A:933:GLU:O	1:A:934:ARG:C	2.62	0.41
1:A:1875:ILE:HA	1:A:1896:THR:HG21	2.03	0.41
1:A:1880:PHE:CZ	1:A:1882:LEU:HD23	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2080:LYS:HG3	1:A:2081:ASP:N	2.34	0.41
2:C:101:GLN:HE22	13:D:75:A:N6	2.13	0.41
2:C:563:LEU:HD23	2:C:563:LEU:HA	1.83	0.41
2:C:603:PHE:CD2	2:C:652:MET:HG3	2.55	0.41
2:C:611:LEU:HD23	2:C:611:LEU:HA	1.78	0.41
2:C:955:LYS:HD3	2:C:955:LYS:HA	1.90	0.41
4:O:155:PHE:O	4:O:156:ILE:HG13	2.20	0.41
4:O:198:PHE:CZ	4:O:253:MET:HE2	2.56	0.41
4:O:372:VAL:HA	4:O:387:LEU:O	2.20	0.41
4:O:391:GLU:OE1	4:O:397:GLU:HA	2.21	0.41
4:O:412:LEU:HD23	4:O:412:LEU:HA	1.87	0.41
6:Q:106:ASN:ND2	17:c:212:ASP:HB3	2.36	0.41
7:R:10:LYS:HE2	7:R:10:LYS:HB3	1.90	0.41
10:Z:32:LEU:HD23	10:Z:76:LEU:HD23	2.03	0.41
10:Z:49:ILE:O	10:Z:52:GLY:N	2.53	0.41
10:Z:130:ILE:HG22	10:Z:225:HIS:CD2	2.55	0.41
10:Z:204:ASP:O	10:Z:205:TYR:HB2	2.20	0.41
10:Z:385:GLY:O	10:Z:423:LEU:HA	2.21	0.41
17:c:145:GLU:HB3	17:c:149:LYS:HE3	2.02	0.41
19:I:180:LYS:O	19:I:183:MET:HB2	2.21	0.41
20:v:463:UNK:O	20:v:467:UNK:N	2.53	0.41
21:n:72:TRP:O	21:n:73:SER:CB	2.67	0.41
23:t:114:LEU:O	23:t:117:VAL:CG2	2.61	0.41
35:f:225:ARG:NH1	35:f:225:ARG:CB	2.84	0.41
1:A:161:PHE:HD1	1:A:161:PHE:HA	1.74	0.41
1:A:318:LEU:HA	1:A:318:LEU:HD23	1.69	0.41
1:A:1003:ALA:O	1:A:1006:ARG:N	2.54	0.41
1:A:1012:TRP:CD1	1:A:1012:TRP:H	2.38	0.41
1:A:1296:ARG:NH1	10:Z:430:GLU:OE2	2.54	0.41
1:A:1810:PRO:O	1:A:1811:ALA:C	2.64	0.41
1:A:1864:LYS:HE2	21:n:328:ILE:CB	2.51	0.41
1:A:1903:LYS:HB3	1:A:1904:ARG:H	1.58	0.41
2:C:67:GLU:N	2:C:76:VAL:HG21	2.35	0.41
2:C:79:GLU:CD	4:O:173:LYS:HA	2.46	0.41
2:C:101:GLN:O	2:C:102:GLU:C	2.64	0.41
2:C:126:MET:SD	2:C:132:ARG:HD2	2.61	0.41
2:C:744:PRO:O	2:C:747:LEU:HB3	2.21	0.41
2:C:760:LEU:O	2:C:763:ARG:HB2	2.21	0.41
4:O:149:PRO:HG3	4:O:192:ASP:HA	2.02	0.41
4:O:198:PHE:HD2	4:O:232:ILE:HG12	1.85	0.41
4:O:252:ASP:OD1	4:O:253:MET:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:342:LEU:HB3	5:P:47:ARG:HD3	2.01	0.41
5:P:115:VAL:O	6:Q:26:THR:HA	2.20	0.41
7:R:184:VAL:CG1	7:R:186:PHE:HE1	2.34	0.41
7:R:257:ASN:O	7:R:261:ALA:N	2.53	0.41
8:S:4:SER:O	8:S:5:HIS:CD2	2.74	0.41
10:Z:14:GLN:HA	10:Z:17:ASN:CB	2.50	0.41
10:Z:463:ASN:O	10:Z:466:THR:OG1	2.22	0.41
14:E:66:C:O2	17:c:211:ILE:HD12	2.21	0.41
14:E:67:C:O2'	17:c:207:TYR:HB3	2.21	0.41
18:d:407:UNK:C	18:d:409:UNK:H2	2.33	0.41
21:n:155:ILE:CG1	21:n:156:ARG:N	2.84	0.41
21:n:352:CYS:SG	21:n:363:PHE:HB2	2.61	0.41
22:q:59:GLN:O	22:q:60:ALA:HB3	2.20	0.41
30:g:102:ILE:HG22	30:g:103:VAL:HG23	2.01	0.41
33:b:4:U:H2'	33:b:5:U:C2	2.55	0.41
1:A:300:LYS:HA	1:A:491:GLY:O	2.21	0.41
1:A:330:LEU:O	1:A:335:SER:OG	2.39	0.41
1:A:431:ILE:HD12	2:C:287:LYS:HA	2.02	0.41
1:A:558:GLN:CD	9:T:107:ARG:HH12	2.29	0.41
1:A:571:LEU:HA	1:A:571:LEU:HD12	1.60	0.41
1:A:585:ARG:HD3	7:R:33:TRP:CE2	2.56	0.41
1:A:687:ILE:HD13	1:A:703:PHE:HD2	1.86	0.41
1:A:807:PRO:HG3	5:P:163:TRP:HH2	1.86	0.41
1:A:852:LEU:HD23	1:A:852:LEU:HA	1.52	0.41
1:A:898:ILE:HD12	1:A:1074:VAL:HG22	2.02	0.41
1:A:974:ASN:C	1:A:976:GLN:H	2.27	0.41
1:A:1063:PHE:O	1:A:1064:THR:C	2.64	0.41
1:A:1527:TRP:CD1	1:A:1527:TRP:H	2.39	0.41
1:A:1888:HIS:HB3	1:A:1988:LEU:HD23	2.02	0.41
1:A:1988:LEU:N	35:f:181:GLN:CG	2.64	0.41
1:A:2023:LYS:HB2	1:A:2023:LYS:HE3	1.87	0.41
2:C:582:SER:O	2:C:585:ASP:N	2.54	0.41
2:C:656:LEU:HD13	2:C:670:ILE:CD1	2.49	0.41
2:C:709:SER:OG	2:C:821:LEU:HD12	2.20	0.41
2:C:718:LYS:C	2:C:721:GLN:HB3	2.46	0.41
2:C:761:ALA:HA	2:C:764:ASN:HB2	2.02	0.41
2:C:913:GLY:O	2:C:914:PHE:C	2.64	0.41
4:O:156:ILE:HD13	4:O:156:ILE:HG21	1.88	0.41
4:O:162:THR:HG22	4:O:184:THR:HA	2.03	0.41
4:O:277:VAL:CG1	5:P:63:ILE:HG22	2.50	0.41
4:O:285:SER:C	4:O:287:ASP:N	2.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:295:VAL:HG23	4:O:296:VAL:N	2.36	0.41
4:O:376:TYR:CE1	4:O:383:LYS:HG3	2.56	0.41
4:O:389:THR:O	4:O:390:ARG:C	2.61	0.41
7:R:74:LEU:HB3	7:R:112:PHE:CD1	2.56	0.41
7:R:159:ARG:HB2	7:R:159:ARG:CZ	2.51	0.41
7:R:221:LEU:O	7:R:221:LEU:HD12	2.21	0.41
9:T:29:GLN:O	9:T:32:ASP:HB2	2.21	0.41
10:Z:122:SER:C	10:Z:125:PHE:H	2.29	0.41
10:Z:135:ILE:HD12	10:Z:135:ILE:HG23	1.80	0.41
12:N:104:G:N1	14:E:49:A:C2	2.89	0.41
14:E:16:C:O5'	14:E:16:C:H6	2.03	0.41
14:E:86:G:C2	18:d:57:TYR:CD2	3.09	0.41
15:L:16:U:OP2	15:L:18:U:C2	2.73	0.41
18:d:98:PHE:CD2	18:d:100:PRO:HD2	2.56	0.41
18:d:229:VAL:O	18:d:233:GLN:CB	2.57	0.41
18:d:267:TYR:OH	18:d:310:UNK:C	2.68	0.41
22:q:262:PRO:CG	22:q:271:SER:HB2	2.50	0.41
23:t:89:GLU:CG	23:t:90:GLU:N	2.84	0.41
23:t:113:LEU:O	23:t:116:ILE:CG1	2.69	0.41
26:H:32:LYS:HG3	26:H:77:ASN:HA	2.03	0.41
27:K:26:ALA:C	27:K:43:ALA:HB3	2.46	0.41
33:b:3:U:O5'	33:b:4:U:P	2.79	0.41
33:b:4:U:O2	33:b:5:U:C2	2.73	0.41
34:e:795:ILE:O	34:e:797:VAL:N	2.50	0.41
1:A:526:LEU:HD23	1:A:526:LEU:HA	1.54	0.41
1:A:780:ARG:HA	1:A:783:LEU:HD13	2.02	0.41
1:A:828:HIS:CE1	8:S:169:PHE:CD2	3.09	0.41
1:A:931:ALA:HA	1:A:934:ARG:NH2	2.36	0.41
1:A:1161:TYR:OH	1:A:1163:ARG:HD3	2.21	0.41
1:A:1203:ASN:ND2	1:A:1212:ARG:HG2	2.35	0.41
1:A:1212:ARG:HG2	1:A:1213:MET:N	2.33	0.41
1:A:1379:MET:HE3	1:A:1620:TYR:HB3	2.03	0.41
1:A:1932:GLN:NE2	1:A:1957:ARG:HD2	2.36	0.41
1:A:1962:ARG:NH1	1:A:2081:ASP:OD2	2.54	0.41
2:C:354:TYR:HD1	2:C:359:PHE:CD1	2.39	0.41
2:C:637:GLU:HB2	2:C:639:SER:OG	2.21	0.41
2:C:883:ARG:HE	2:C:914:PHE:HD1	1.68	0.41
2:C:943:ASP:O	2:C:945:LEU:N	2.53	0.41
4:O:112:VAL:O	4:O:115:TYR:N	2.52	0.41
4:O:265:HIS:CE1	4:O:291:ARG:CG	3.04	0.41
7:R:46:ARG:CZ	7:R:222:LEU:HD21	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:72:PHE:HE1	7:R:90:LEU:HD12	1.86	0.41
7:R:201:ASN:HA	7:R:220:GLY:HA3	2.02	0.41
7:R:205:LEU:HB3	7:R:206:LEU:H	1.66	0.41
10:Z:53:ARG:NH1	10:Z:89:ASP:OD1	2.54	0.41
10:Z:456:GLU:HA	10:Z:459:ARG:NH1	2.30	0.41
17:c:204:LYS:HG2	17:c:205:LYS:N	2.29	0.41
20:v:520:UNK:O	20:v:524:UNK:N	2.54	0.41
27:j:26:ALA:C	27:j:43:ALA:HB3	2.46	0.41
33:b:3:U:P	33:b:4:U:OP2	2.79	0.41
35:f:146:LEU:HD22	35:f:229:TRP:CE3	2.56	0.41
1:A:215:ALA:HB2	1:A:311:LEU:HD22	2.03	0.40
1:A:569:LEU:HD23	1:A:569:LEU:HA	1.56	0.40
1:A:607:THR:O	1:A:610:ARG:N	2.52	0.40
1:A:670:LYS:HE3	1:A:670:LYS:HB3	1.77	0.40
1:A:860:GLU:CD	1:A:863:ARG:HH21	2.29	0.40
1:A:910:LYS:O	1:A:913:VAL:N	2.53	0.40
1:A:1115:GLN:O	1:A:1116:TYR:C	2.63	0.40
1:A:1459:ALA:O	1:A:1462:ALA:HB3	2.21	0.40
1:A:1550:LEU:HD23	1:A:1550:LEU:HA	1.92	0.40
1:A:1863:HIS:C	1:A:1871:ALA:HB3	2.44	0.40
1:A:1972:ASP:O	1:A:1973:LYS:C	2.64	0.40
1:A:1999:ILE:HG22	1:A:2000:SER:N	2.34	0.40
1:A:2011:LEU:HB3	1:A:2040:TRP:CH2	2.56	0.40
2:C:149:LEU:O	2:C:150:MET:C	2.62	0.40
2:C:170:LEU:HD12	2:C:171:GLY:HA2	2.03	0.40
2:C:219:VAL:O	2:C:219:VAL:HG22	2.20	0.40
2:C:769:TYR:O	2:C:770:ASN:C	2.64	0.40
4:O:359:ASN:CG	4:O:360:GLN:N	2.79	0.40
5:P:130:LYS:HG2	5:P:131:ALA:H	1.86	0.40
8:S:165:TYR:O	8:S:168:GLU:N	2.54	0.40
10:Z:41:HIS:ND1	10:Z:83:LEU:HD23	2.36	0.40
17:c:63:THR:CG2	17:c:93:ARG:HH12	2.34	0.40
18:d:264:SER:O	18:d:268:GLN:HB2	2.21	0.40
20:v:616:PRO:O	20:v:618:GLU:N	2.54	0.40
22:q:183:LEU:CG	22:q:237:PRO:O	2.69	0.40
1:A:293:VAL:HG22	1:A:294:ASN:H	1.86	0.40
1:A:314:LEU:C	1:A:316:THR:H	2.28	0.40
1:A:319:ARG:HH11	1:A:319:ARG:HD3	1.65	0.40
1:A:551:LEU:HG	1:A:557:PHE:HE2	1.81	0.40
1:A:677:ILE:O	1:A:678:ARG:C	2.63	0.40
1:A:797:ILE:HG22	1:A:799:TRP:H	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:814:ARG:HG2	4:O:141:TRP:CZ2	2.56	0.40
1:A:1186:TYR:O	1:A:1187:LEU:C	2.62	0.40
1:A:1429:MET:HE2	1:A:1429:MET:HB3	1.93	0.40
1:A:1550:LEU:HB2	1:A:1556:ILE:HD11	2.03	0.40
1:A:1620:TYR:HD2	1:A:1621:VAL:HG22	1.85	0.40
2:C:84:GLN:NE2	2:C:90:LEU:H	2.17	0.40
2:C:84:GLN:NE2	2:C:90:LEU:HA	2.33	0.40
2:C:273:LEU:O	2:C:277:LEU:HB2	2.21	0.40
2:C:289:ASN:ND2	2:C:349:TRP:CZ2	2.89	0.40
2:C:571:TYR:CE1	2:C:573:LYS:O	2.73	0.40
4:O:126:HIS:HB2	4:O:384:TYR:CE2	2.56	0.40
4:O:292:LEU:HA	4:O:292:LEU:HD23	1.91	0.40
4:O:343:THR:OG1	4:O:344:ASN:N	2.54	0.40
7:R:174:ARG:HH22	12:N:114:U:H5'	1.85	0.40
7:R:231:ASP:OD1	7:R:233:ALA:N	2.54	0.40
9:T:121:ILE:HD13	14:E:28:U:H1'	2.03	0.40
10:Z:64:THR:OG1	10:Z:76:LEU:HD13	2.21	0.40
10:Z:434:ASP:O	10:Z:437:GLN:N	2.55	0.40
11:B:88:U:H2'	11:B:89:A:C4'	2.49	0.40
11:B:99:G:O3'	33:b:1:U:P	2.79	0.40
14:E:76:A:C2	14:E:77:G:C4	3.09	0.40
18:d:85:ARG:O	18:d:89:GLU:HG2	2.21	0.40
1:A:173:LEU:HD13	1:A:715:LEU:HD23	2.02	0.40
1:A:526:LEU:O	1:A:527:LYS:C	2.62	0.40
1:A:807:PRO:O	1:A:810:LYS:HB2	2.21	0.40
1:A:1001:TYR:O	1:A:1005:GLN:HB2	2.21	0.40
1:A:1339:LEU:HD21	1:A:1440:ILE:HD12	2.03	0.40
1:A:1438:PRO:HB2	1:A:1443:TYR:HE2	1.86	0.40
1:A:1718:HIS:CE1	1:A:1799:GLN:HG2	2.56	0.40
2:C:90:LEU:O	2:C:90:LEU:HD23	2.22	0.40
2:C:251:GLN:HE22	2:C:255:GLN:HE21	1.68	0.40
2:C:468:LEU:HD13	2:C:492:LEU:N	2.36	0.40
2:C:716:ASP:OD2	2:C:718:LYS:HB3	2.22	0.40
2:C:795:ILE:O	2:C:798:GLY:N	2.54	0.40
2:C:869:HIS:HD2	2:C:925:LEU:HB3	1.85	0.40
7:R:127:ILE:CG1	14:E:39:G:N7	2.84	0.40
10:Z:313:LEU:HD23	10:Z:313:LEU:HA	1.67	0.40
10:Z:346:LEU:HA	10:Z:346:LEU:HD12	1.77	0.40
13:D:79:C:H3'	13:D:80:G:H5'	2.03	0.40
14:E:15:C:C4	14:E:16:C:N4	2.89	0.40
17:c:72:GLN:O	17:c:75:ASP:HB3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:d:99:ILE:O	18:d:100:PRO:C	2.64	0.40
20:v:670:SER:CB	20:v:687:LEU:HD11	2.51	0.40
1:A:303:PHE:HD1	1:A:303:PHE:HA	1.65	0.40
1:A:880:THR:HG23	5:P:211:ALA:HB2	2.02	0.40
1:A:1031:GLY:O	1:A:1032:ILE:C	2.63	0.40
1:A:1180:GLU:O	1:A:1184:ASP:CG	2.64	0.40
1:A:2053:SER:O	1:A:2056:ARG:HB3	2.20	0.40
2:C:68:HIS:N	2:C:69:PRO:HD2	2.36	0.40
2:C:214:ASP:OD1	2:C:214:ASP:C	2.65	0.40
2:C:321:THR:OG1	2:C:432:GLN:HG2	2.22	0.40
2:C:412:ALA:O	2:C:413:LEU:C	2.64	0.40
2:C:495:ARG:N	2:C:554:HIS:O	2.55	0.40
4:O:125:TRP:CD1	4:O:437:GLU:OE1	2.74	0.40
4:O:281:VAL:O	4:O:293:TRP:HB2	2.21	0.40
5:P:220:ARG:O	5:P:224:GLU:HG2	2.21	0.40
7:R:240:GLU:O	7:R:243:LYS:HB3	2.22	0.40
10:Z:295:ILE:O	10:Z:296:TYR:C	2.63	0.40
10:Z:426:GLU:O	10:Z:429:ASN:N	2.55	0.40
10:Z:478:ARG:O	10:Z:481:LEU:HB2	2.21	0.40
14:E:101:U:H2'	14:E:102:U:C6	2.57	0.40
15:L:18:U:O2'	15:L:19:U:OP2	2.38	0.40
17:c:332:UNK:N	20:v:493:UNK:HA	2.37	0.40
18:d:269:ILE:O	18:d:272:GLU:HB3	2.20	0.40
34:e:809:VAL:C	34:e:811:MET:O	2.64	0.40
1:A:594:ASP:OD1	1:A:598:ASN:N	2.55	0.40
1:A:631:LEU:O	1:A:634:ASP:HB2	2.22	0.40
1:A:750:LEU:O	1:A:751:ASP:C	2.64	0.40
1:A:773:SER:OG	1:A:774:ILE:N	2.55	0.40
1:A:786:LEU:O	1:A:787:SER:C	2.63	0.40
1:A:910:LYS:O	1:A:911:ILE:C	2.64	0.40
1:A:936:GLU:O	1:A:940:ILE:HD12	2.21	0.40
1:A:965:LYS:HB3	1:A:966:PRO:HD2	2.03	0.40
1:A:1063:PHE:HB3	1:A:1083:THR:HG23	2.03	0.40
1:A:1323:SER:OG	1:A:1370:ARG:NH2	2.55	0.40
1:A:1369:ASN:HB3	1:A:1378:LYS:NZ	2.37	0.40
1:A:1405:ILE:HG22	1:A:1406:LEU:N	2.24	0.40
2:C:233:ASP:O	2:C:261:VAL:HG13	2.21	0.40
2:C:253:ILE:HG12	2:C:253:ILE:H	1.74	0.40
2:C:285:TYR:CD2	2:C:286:LEU:HD12	2.56	0.40
2:C:473:LEU:HD12	2:C:485:LEU:CD2	2.51	0.40
2:C:603:PHE:CZ	2:C:673:PRO:HB3	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:646:GLY:HA3	2:C:652:MET:CE	2.44	0.40
2:C:655:LEU:HD23	2:C:655:LEU:HA	1.77	0.40
2:C:737:ILE:HG13	2:C:768:PHE:CD1	2.55	0.40
2:C:831:ILE:HG13	2:C:832:ASP:N	2.29	0.40
2:C:864:VAL:HG22	2:C:930:LEU:CD2	2.52	0.40
4:O:164:MET:HE1	4:O:209:TRP:HE1	1.86	0.40
4:O:333:SER:O	4:O:334:TRP:CG	2.75	0.40
5:P:52:GLU:O	5:P:52:GLU:HG3	2.22	0.40
6:Q:20:GLU:HG3	6:Q:21:ALA:H	1.86	0.40
6:Q:117:ASN:O	6:Q:119:LYS:N	2.54	0.40
7:R:127:ILE:HG22	7:R:128:GLY:N	2.37	0.40
7:R:206:LEU:HB3	7:R:208:SER:O	2.22	0.40
9:T:58:GLN:O	9:T:59:ARG:C	2.64	0.40
10:Z:148:LEU:HA	10:Z:151:VAL:HG12	2.03	0.40
10:Z:321:LEU:HD23	10:Z:321:LEU:HA	1.77	0.40
10:Z:444:LYS:O	10:Z:444:LYS:HG3	2.21	0.40
17:c:65:PHE:CE1	17:c:101:ARG:HD3	2.57	0.40
18:d:81:MET:O	18:d:82:ARG:C	2.64	0.40
20:v:609:GLU:HG2	20:v:609:GLU:H	1.67	0.40
22:p:98:LEU:HD12	22:q:98:LEU:CD2	2.49	0.40
28:U:33:LEU:HD23	28:U:33:LEU:C	2.47	0.40
30:W:102:ILE:HG22	30:W:103:VAL:HG23	2.01	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	1925/2413 (80%)	1569 (82%)	339 (18%)	17 (1%)	14	48
2	C	872/1008 (86%)	735 (84%)	129 (15%)	8 (1%)	14	48
3	J	25/135 (18%)	21 (84%)	4 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	O	335/451 (74%)	281 (84%)	49 (15%)	5 (2%)	8	38
5	P	193/379 (51%)	160 (83%)	27 (14%)	6 (3%)	3	25
6	Q	177/364 (49%)	145 (82%)	30 (17%)	2 (1%)	11	44
7	R	259/339 (76%)	218 (84%)	40 (15%)	1 (0%)	30	65
8	S	63/175 (36%)	49 (78%)	12 (19%)	2 (3%)	3	25
9	T	155/157 (99%)	123 (79%)	28 (18%)	4 (3%)	4	29
10	Z	443/577 (77%)	369 (83%)	68 (15%)	6 (1%)	9	39
17	c	312/579 (54%)	273 (88%)	35 (11%)	4 (1%)	9	41
18	d	238/652 (36%)	201 (84%)	35 (15%)	2 (1%)	16	52
19	I	98/215 (46%)	85 (87%)	13 (13%)	0	100	100
20	v	121/858 (14%)	110 (91%)	7 (6%)	4 (3%)	3	24
21	n	272/455 (60%)	234 (86%)	28 (10%)	10 (4%)	2	22
22	o	120/503 (24%)	115 (96%)	4 (3%)	1 (1%)	16	52
22	p	122/503 (24%)	116 (95%)	6 (5%)	0	100	100
22	q	355/503 (71%)	327 (92%)	16 (4%)	12 (3%)	3	24
22	r	119/503 (24%)	111 (93%)	5 (4%)	3 (2%)	4	29
23	t	150/175 (86%)	134 (89%)	13 (9%)	3 (2%)	6	33
24	F	74/196 (38%)	67 (90%)	7 (10%)	0	100	100
24	k	76/196 (39%)	69 (91%)	7 (9%)	0	100	100
25	G	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
25	i	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
26	H	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	8	38
26	h	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	8	38
27	K	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
27	j	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
28	U	80/101 (79%)	70 (88%)	9 (11%)	1 (1%)	9	41
28	l	80/101 (79%)	70 (88%)	9 (11%)	1 (1%)	9	41
29	V	78/146 (53%)	74 (95%)	4 (5%)	0	100	100
29	m	78/146 (53%)	74 (95%)	4 (5%)	0	100	100
30	W	63/110 (57%)	58 (92%)	4 (6%)	1 (2%)	7	37
30	g	92/110 (84%)	85 (92%)	6 (6%)	1 (1%)	11	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	X	77/111 (69%)	75 (97%)	2 (3%)	0	100	100
32	Y	125/238 (52%)	111 (89%)	12 (10%)	2 (2%)	7	37
34	e	673/1071 (63%)	563 (84%)	75 (11%)	35 (5%)	1	18
35	f	144/251 (57%)	140 (97%)	4 (3%)	0	100	100
All	All	8398/14235 (59%)	7212 (86%)	1053 (12%)	133 (2%)	10	37

All (133) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	364	PHE
6	Q	99	VAL
10	Z	213	PHE
20	v	616	PRO
21	n	245	HIS
21	n	247	ASN
21	n	428	PRO
22	q	53	ILE
22	q	77	ILE
22	q	172	PRO
22	q	174	TRP
22	q	239	PRO
22	q	246	PRO
22	q	362	PRO
22	q	442	SER
22	r	64	GLU
23	t	77	PRO
32	Y	68	PRO
34	e	374	GLU
34	e	392	TYR
34	e	393	ALA
34	e	434	ARG
34	e	532	VAL
34	e	654	ILE
34	e	714	GLN
34	e	812	LEU
34	e	932	SER
34	e	933	VAL
34	e	948	PRO
34	e	988	ILE
1	A	1405	ILE
1	A	1540	ASN

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Mol	Chain	Res	Type
2	C	363	PRO
4	O	286	THR
5	P	112	ILE
8	S	8	GLN
8	S	9	LEU
20	v	601	VAL
20	v	618	GLU
21	n	61	LYS
21	n	291	HIS
21	n	406	ARG
22	q	196	PRO
23	t	110	GLU
34	e	388	TYR
34	e	428	GLU
34	e	442	GLU
34	e	561	CYS
34	e	611	ILE
34	e	629	GLY
34	e	739	GLU
34	e	919	THR
1	A	1404	HIS
1	A	1581	PHE
1	A	1964	PRO
5	P	102	ALA
10	Z	303	LEU
17	c	230	THR
17	c	231	SER
20	v	634	HIS
21	n	244	LEU
22	o	17	PRO
22	r	20	ARG
23	t	80	ASN
34	e	435	PHE
34	e	462	ASP
34	e	655	ASP
34	e	816	GLN
1	A	645	ASP
1	A	1628	ASP
2	C	655	LEU
2	C	829	VAL
4	O	278	ASP
4	O	435	GLU

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Mol	Chain	Res	Type
10	Z	53	ARG
21	n	267	LEU
28	l	82	PRO
30	g	82	LYS
28	U	82	PRO
30	W	82	LYS
34	e	333	THR
34	e	425	LEU
34	e	610	PRO
34	e	737	THR
34	e	944	LEU
34	e	946	ASP
34	e	985	ILE
1	A	264	ILE
1	A	543	ASN
1	A	1033	ASN
2	C	801	TRP
4	O	279	PRO
5	P	86	ASN
6	Q	93	LEU
7	R	92	HIS
9	T	98	THR
9	T	104	CYS
9	T	119	THR
21	n	416	ARG
22	q	60	ALA
34	e	922	ARG
1	A	1177	ASP
1	A	2002	TYR
2	C	167	ASN
2	C	278	LYS
9	T	115	ASN
10	Z	154	VAL
10	Z	410	GLU
10	Z	415	GLN
18	d	151	ILE
34	e	604	ASN
34	e	937	PRO
4	O	263	VAL
5	P	34	ILE
17	c	16	VAL
17	c	218	VAL

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Mol	Chain	Res	Type
22	q	36	GLY
26	h	15	PRO
26	H	15	PRO
32	Y	52	LYS
1	A	407	VAL
22	q	175	PRO
1	A	741	ILE
21	n	387	ILE
34	e	943	GLY
1	A	377	VAL
1	A	379	ILE
1	A	1752	VAL
5	P	166	PRO
2	C	704	PRO
5	P	219	ILE
18	d	188	ILE
22	r	36	GLY

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	1753/2182 (80%)	1740 (99%)	13 (1%)	76	79
2	C	794/910 (87%)	787 (99%)	7 (1%)	70	76
3	J	21/121 (17%)	21 (100%)	0	100	100
4	O	295/397 (74%)	294 (100%)	1 (0%)	86	85
5	P	173/328 (53%)	171 (99%)	2 (1%)	63	73
6	Q	171/332 (52%)	169 (99%)	2 (1%)	63	73
7	R	224/296 (76%)	222 (99%)	2 (1%)	70	76
8	S	56/151 (37%)	54 (96%)	2 (4%)	31	53
9	T	141/141 (100%)	140 (99%)	1 (1%)	76	79
10	Z	417/538 (78%)	416 (100%)	1 (0%)	87	87
17	c	212/308 (69%)	205 (97%)	7 (3%)	33	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	d	219/219 (100%)	219 (100%)	0	100	100
19	I	92/193 (48%)	92 (100%)	0	100	100
20	v	57/152 (38%)	46 (81%)	11 (19%)	1	10
21	n	122/413 (30%)	101 (83%)	21 (17%)	2	13
22	o	59/451 (13%)	53 (90%)	6 (10%)	7	25
22	p	62/451 (14%)	54 (87%)	8 (13%)	4	19
22	q	119/451 (26%)	101 (85%)	18 (15%)	3	16
22	r	60/451 (13%)	55 (92%)	5 (8%)	10	33
23	t	37/165 (22%)	25 (68%)	12 (32%)	0	2
24	F	67/176 (38%)	66 (98%)	1 (2%)	57	70
24	k	70/176 (40%)	69 (99%)	1 (1%)	59	71
25	G	65/83 (78%)	60 (92%)	5 (8%)	12	35
25	i	65/83 (78%)	60 (92%)	5 (8%)	12	35
26	H	61/77 (79%)	60 (98%)	1 (2%)	55	70
26	h	61/77 (79%)	60 (98%)	1 (2%)	55	70
27	K	58/66 (88%)	56 (97%)	2 (3%)	32	55
27	j	58/66 (88%)	56 (97%)	2 (3%)	32	55
28	U	69/89 (78%)	68 (99%)	1 (1%)	59	71
28	l	69/89 (78%)	68 (99%)	1 (1%)	59	71
29	V	77/129 (60%)	74 (96%)	3 (4%)	28	51
29	m	77/129 (60%)	74 (96%)	3 (4%)	28	51
30	W	59/103 (57%)	54 (92%)	5 (8%)	10	33
30	g	79/103 (77%)	73 (92%)	6 (8%)	12	36
31	X	26/100 (26%)	26 (100%)	0	100	100
32	Y	47/219 (22%)	44 (94%)	3 (6%)	16	40
35	f	134/225 (60%)	131 (98%)	3 (2%)	45	65
All	All	6226/10640 (58%)	6064 (97%)	162 (3%)	41	61

All (162) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	284	ARG
1	A	461	LEU

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Mol	Chain	Res	Type
1	A	518	VAL
1	A	1094	ASP
1	A	1319	ILE
1	A	1326	THR
1	A	1339	LEU
1	A	1367	ILE
1	A	1576	GLU
1	A	1588	LYS
1	A	1629	LEU
1	A	1661	ILE
1	A	1988	LEU
2	C	109	LEU
2	C	136	VAL
2	C	193	LEU
2	C	379	ILE
2	C	497	ASP
2	C	625	ILE
2	C	888	ILE
4	O	343	THR
5	P	112	ILE
5	P	147	LEU
6	Q	60	ILE
6	Q	99	VAL
7	R	146	LEU
7	R	169	ASP
8	S	35	THR
8	S	36	THR
9	T	120	CYS
10	Z	420	ILE
17	c	504	PRO
17	c	505	PRO
17	c	506	THR
17	c	517	VAL
17	c	523	LEU
17	c	532	PRO
17	c	550	PRO
20	v	616	PRO
20	v	617	PRO
20	v	641	PRO
20	v	681	SER
20	v	706	LEU
20	v	712	CYS

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Mol	Chain	Res	Type
20	v	722	PRO
20	v	723	SER
20	v	725	THR
20	v	726	ARG
20	v	733	ILE
21	n	51	PHE
21	n	55	GLU
21	n	57	LYS
21	n	58	ARG
21	n	59	ARG
21	n	62	THR
21	n	66	ASP
21	n	159	PRO
21	n	162	PRO
21	n	208	PRO
21	n	257	PRO
21	n	258	THR
21	n	260	PRO
21	n	295	SER
21	n	306	SER
21	n	327	PRO
21	n	340	PRO
21	n	373	PRO
21	n	424	PRO
21	n	428	PRO
21	n	436	PRO
22	o	17	PRO
22	o	26	SER
22	o	44	PRO
22	o	63	THR
22	o	109	LEU
22	o	134	SER
22	p	17	PRO
22	p	44	PRO
22	p	63	THR
22	p	80	LEU
22	p	85	GLN
22	p	93	LEU
22	p	98	LEU
22	p	109	LEU
22	q	14	VAL
22	q	17	PRO

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Mol	Chain	Res	Type
22	q	44	PRO
22	q	55	PRO
22	q	56	SER
22	q	61	SER
22	q	102	LEU
22	q	126	LEU
22	q	172	PRO
22	q	175	PRO
22	q	196	PRO
22	q	215	CYS
22	q	235	THR
22	q	239	PRO
22	q	262	PRO
22	q	271	SER
22	q	350	PRO
22	q	412	PRO
22	r	17	PRO
22	r	44	PRO
22	r	63	THR
22	r	93	LEU
22	r	109	LEU
23	t	5	SER
23	t	7	VAL
23	t	13	PRO
23	t	77	PRO
23	t	96	PRO
23	t	100	THR
23	t	105	PRO
23	t	108	SER
23	t	111	VAL
23	t	133	PRO
23	t	150	THR
23	t	152	THR
24	k	47	GLU
25	i	16	CYS
25	i	18	PHE
25	i	25	THR
25	i	79	LYS
25	i	81	LEU
26	h	79	LEU
27	j	18	ASN
27	j	71	LEU

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Mol	Chain	Res	Type
28	l	10	LEU
29	m	20	LYS
29	m	30	GLN
29	m	77	ASP
30	g	24	PHE
30	g	48	LEU
30	g	49	ARG
30	g	77	THR
30	g	99	ASP
30	g	100	SER
24	F	47	GLU
25	G	16	CYS
25	G	18	PHE
25	G	25	THR
25	G	79	LYS
25	G	81	LEU
26	H	79	LEU
27	K	18	ASN
27	K	71	LEU
28	U	10	LEU
29	V	20	LYS
29	V	30	GLN
29	V	77	ASP
30	W	48	LEU
30	W	49	ARG
30	W	77	THR
30	W	99	ASP
30	W	100	SER
32	Y	4	THR
32	Y	44	PRO
32	Y	71	SER
35	f	81	ILE
35	f	134	GLU
35	f	184	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (133) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	138	HIS
1	A	146	HIS
1	A	181	HIS
1	A	265	ASN

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Mol	Chain	Res	Type
1	A	343	ASN
1	A	365	ASN
1	A	405	ASN
1	A	429	ASN
1	A	541	ASN
1	A	558	GLN
1	A	559	GLN
1	A	570	GLN
1	A	584	HIS
1	A	654	HIS
1	A	658	ASN
1	A	659	HIS
1	A	733	GLN
1	A	760	ASN
1	A	784	GLN
1	A	785	HIS
1	A	796	ASN
1	A	839	HIS
1	A	861	GLN
1	A	864	GLN
1	A	868	GLN
1	A	952	ASN
1	A	976	GLN
1	A	1005	GLN
1	A	1011	ASN
1	A	1067	ASN
1	A	1097	HIS
1	A	1156	HIS
1	A	1173	HIS
1	A	1231	GLN
1	A	1376	ASN
1	A	1470	GLN
1	A	1529	ASN
1	A	1532	HIS
1	A	1559	HIS
1	A	1592	HIS
1	A	1626	GLN
1	A	1652	HIS
1	A	1718	HIS
1	A	1856	ASN
1	A	1888	HIS
2	C	82	ASN

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Mol	Chain	Res	Type
2	C	84	GLN
2	C	101	GLN
2	C	143	HIS
2	C	158	HIS
2	C	220	ASN
2	C	251	GLN
2	C	289	ASN
2	C	310	ASN
2	C	355	HIS
2	C	418	GLN
2	C	423	HIS
2	C	608	GLN
2	C	776	ASN
2	C	794	GLN
2	C	817	GLN
2	C	830	ASN
2	C	869	HIS
2	C	929	GLN
2	C	960	ASN
3	J	4	ASN
3	J	21	GLN
4	O	138	HIS
4	O	223	HIS
4	O	265	HIS
4	O	270	ASN
4	O	271	GLN
4	O	382	HIS
4	O	428	GLN
4	O	445	ASN
5	P	103	ASN
5	P	148	HIS
5	P	198	ASN
6	Q	106	ASN
6	Q	209	ASN
7	R	91	HIS
7	R	191	ASN
7	R	202	GLN
7	R	227	ASN
7	R	252	HIS
8	S	5	HIS
8	S	27	HIS
8	S	34	HIS

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Mol	Chain	Res	Type
8	S	173	HIS
9	T	57	HIS
9	T	112	ASN
9	T	143	HIS
10	Z	31	ASN
10	Z	107	ASN
10	Z	131	HIS
10	Z	223	HIS
10	Z	225	HIS
10	Z	354	HIS
10	Z	358	GLN
10	Z	457	HIS
17	c	72	GLN
17	c	83	GLN
17	c	214	ASN
18	d	67	GLN
18	d	116	ASN
19	I	184	GLN
19	I	202	GLN
24	k	91	GLN
25	i	34	GLN
25	i	86	ASN
26	h	25	HIS
26	h	52	GLN
27	j	66	ASN
28	l	41	ASN
29	m	86	ASN
24	F	8	HIS
24	F	91	GLN
25	G	34	GLN
25	G	86	ASN
26	H	25	HIS
26	H	52	GLN
26	H	54	ASN
27	K	66	ASN
28	U	41	ASN
29	V	30	GLN
29	V	86	ASN
30	W	71	ASN
32	Y	62	ASN
35	f	87	GLN
35	f	132	HIS

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Mol	Chain	Res	Type
35	f	149	GLN
35	f	169	HIS
35	f	171	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	B	12/13 (92%)	5 (41%)	0
12	N	14/15 (93%)	4 (28%)	1 (7%)
13	D	114/214 (53%)	31 (27%)	3 (2%)
14	E	102/112 (91%)	34 (33%)	6 (5%)
15	L	88/1175 (7%)	30 (34%)	8 (9%)
16	M	22/23 (95%)	13 (59%)	3 (13%)
33	b	11/14 (78%)	11 (100%)	0
All	All	363/1566 (23%)	128 (35%)	21 (5%)

All (128) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	B	88	U
11	B	89	A
11	B	90	A
11	B	93	U
11	B	94	U
12	N	101	U
12	N	108	U
12	N	109	U
12	N	110	A
13	D	31	G
13	D	32	G
13	D	33	U
13	D	42	A
13	D	44	A
13	D	45	A
13	D	74	U
13	D	75	A
13	D	76	U
13	D	77	A
13	D	79	C
13	D	80	G
13	D	81	A

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Mol	Chain	Res	Type
13	D	82	A
13	D	84	A
13	D	90	C
13	D	92	U
13	D	94	C
13	D	101	C
13	D	104	G
13	D	113	G
13	D	127	U
13	D	164	C
13	D	165	A
13	D	166	U
13	D	170	U
13	D	171	U
13	D	172	U
13	D	173	U
13	D	174	G
13	D	175	G
14	E	12	A
14	E	13	A
14	E	14	C
14	E	15	C
14	E	16	C
14	E	33	C
14	E	34	A
14	E	36	U
14	E	37	U
14	E	39	G
14	E	43	C
14	E	50	G
14	E	51	A
14	E	52	G
14	E	54	U
14	E	57	U
14	E	60	G
14	E	62	A
14	E	65	U
14	E	66	C
14	E	67	C
14	E	68	C
14	E	73	A
14	E	74	U

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Mol	Chain	Res	Type
14	E	75	A
14	E	80	U
14	E	81	G
14	E	85	C
14	E	86	G
14	E	87	U
14	E	89	U
14	E	90	U
14	E	91	A
14	E	92	C
15	L	16	U
15	L	17	U
15	L	18	U
15	L	19	U
15	L	20	G
15	L	21	G
15	L	25	A
15	L	26	G
15	L	29	C
15	L	30	A
15	L	31	A
15	L	34	G
15	L	39	A
15	L	41	C
15	L	42	U
15	L	49	U
15	L	111	C
15	L	115	U
15	L	116	U
15	L	117	U
15	L	118	U
15	L	119	G
15	L	120	G
15	L	1099	G
15	L	1107	C
15	L	1108	A
15	L	1111	U
15	L	1112	G
15	L	1114	G
15	L	1120	G
16	M	484	U
16	M	485	U

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Mol	Chain	Res	Type
16	M	486	A
16	M	487	A
16	M	492	U
16	M	494	G
16	M	495	A
16	M	496	U
16	M	497	A
16	M	500	A
16	M	501	A
16	M	502	C
16	M	503	A
33	b	-4	U
33	b	-3	A
33	b	-2	U
33	b	1	U
33	b	2	U
33	b	3	U
33	b	4	U
33	b	5	U
33	b	6	U
33	b	7	U
33	b	8	A

All (21) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
12	N	108	U
13	D	78	A
13	D	83	C
13	D	172	U
14	E	14	C
14	E	42	A
14	E	51	A
14	E	53	A
14	E	56	A
14	E	64	U
15	L	17	U
15	L	29	C
15	L	30	A
15	L	40	U
15	L	41	C
15	L	117	U

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Mol	Chain	Res	Type
15	L	1107	C
15	L	1111	U
16	M	483	U
16	M	494	G
16	M	499	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 12 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
36	GTP	C	1500	37	33,34,34	1.44	5 (15%)	50,54,54	1.58	10 (20%)

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
36	GTP	C	1500	37	-	5/22/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	C	1500	GTP	PB-O3A	-3.34	1.55	1.59
36	C	1500	GTP	PB-O3B	-2.61	1.56	1.59
36	C	1500	GTP	C5-N7	-2.51	1.34	1.39
36	C	1500	GTP	C5-C6	-2.21	1.36	1.44
36	C	1500	GTP	O4'-C4'	-2.17	1.40	1.45

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	C	1500	GTP	C5-C4-N3	-3.90	122.18	128.39
36	C	1500	GTP	C2'-C1'-N9	-3.47	103.58	113.25
36	C	1500	GTP	O3G-PG-O3B	3.08	114.95	104.64
36	C	1500	GTP	C2-N1-C6	-3.05	119.57	125.11
36	C	1500	GTP	N9-C8-N7	-2.88	108.06	113.40
36	C	1500	GTP	C2-N3-C4	2.78	117.08	112.30
36	C	1500	GTP	O6-C6-C5	-2.31	120.44	126.53
36	C	1500	GTP	C8-N7-C5	2.23	108.23	104.26
36	C	1500	GTP	O4'-C4'-C5'	-2.18	102.36	109.33
36	C	1500	GTP	PA-O5'-C5'	-2.02	109.75	121.35

There are no chirality outliers.

All (5) torsion outliers are listed below:

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

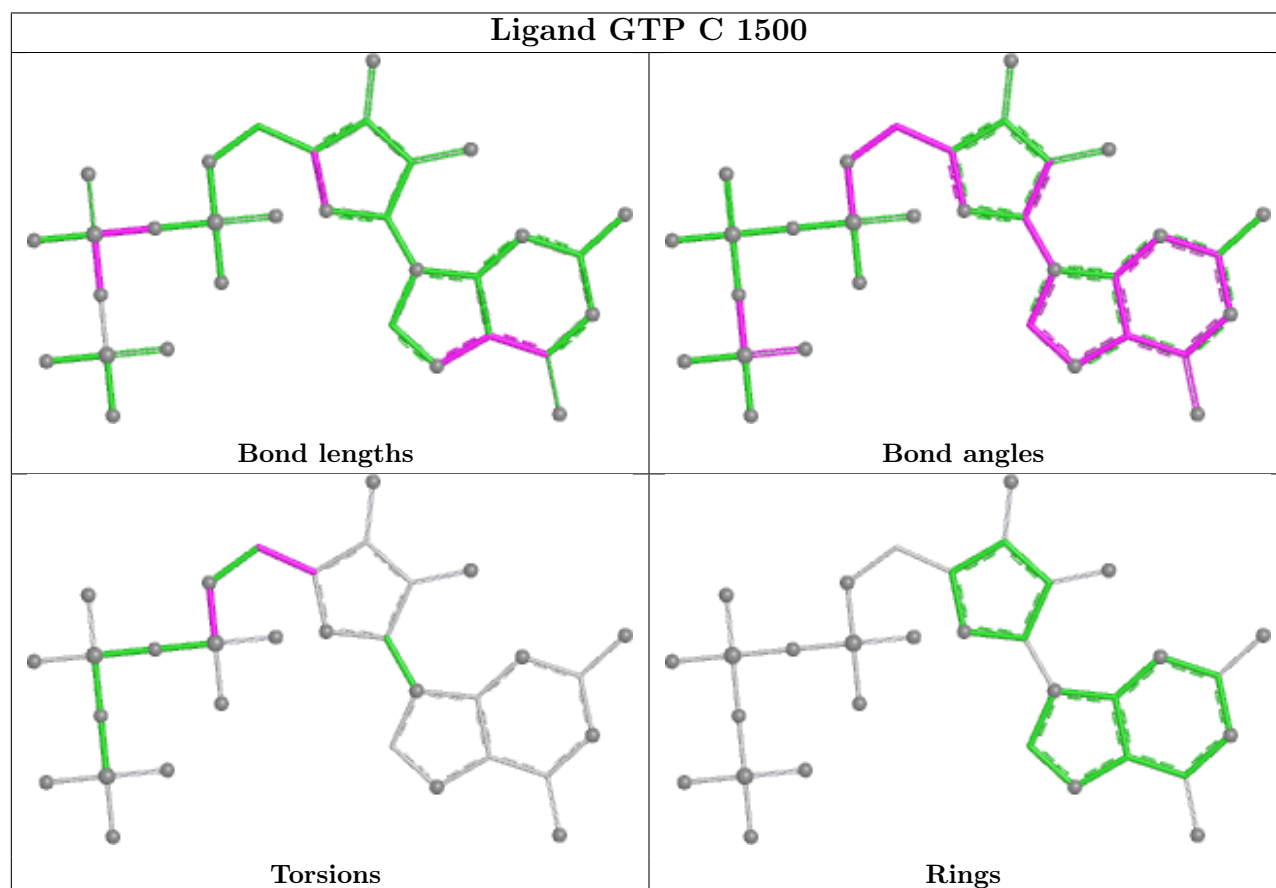
There are no ring outliers.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	C	1500	GTP	11	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

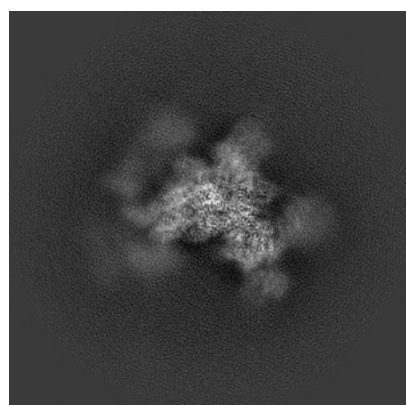
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6684. These allow visual inspection of the internal detail of the map and identification of artifacts.

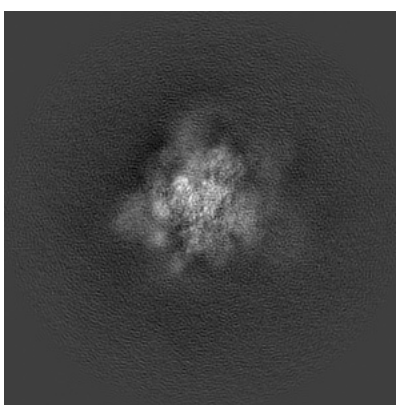
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

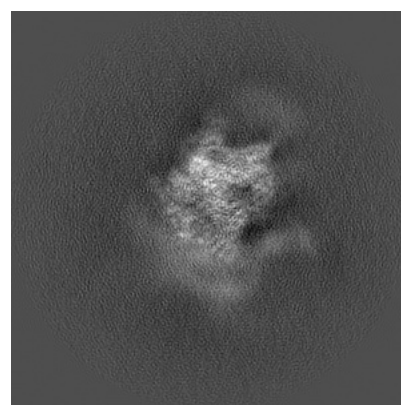
6.1.1 Primary map



X



Y

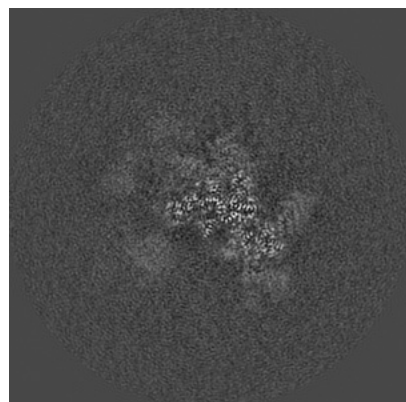


Z

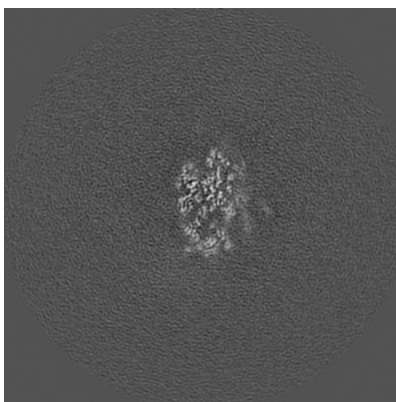
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

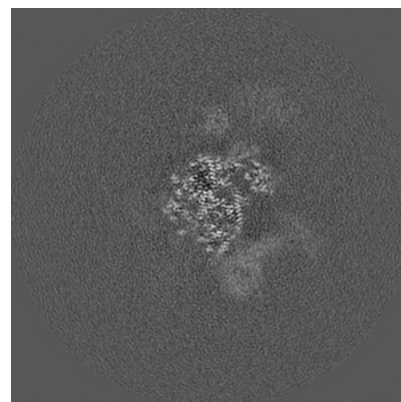
6.2.1 Primary map



X Index: 200



Y Index: 200

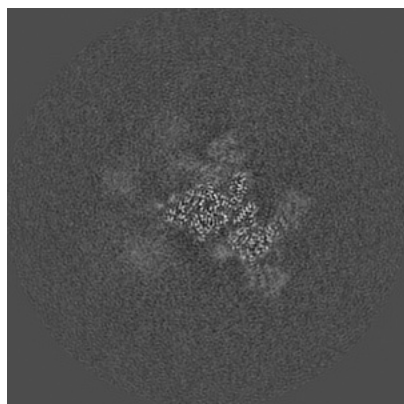


Z Index: 200

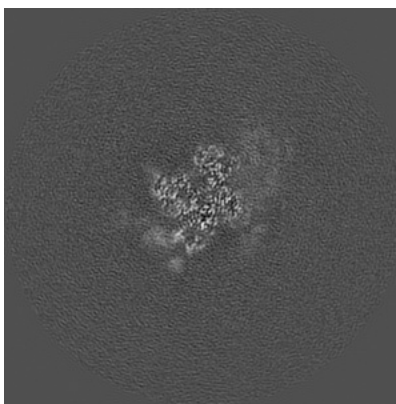
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

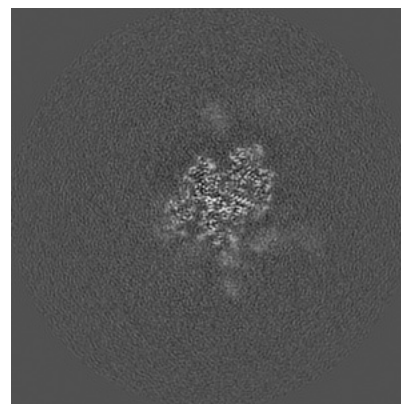
6.3.1 Primary map



X Index: 206



Y Index: 231

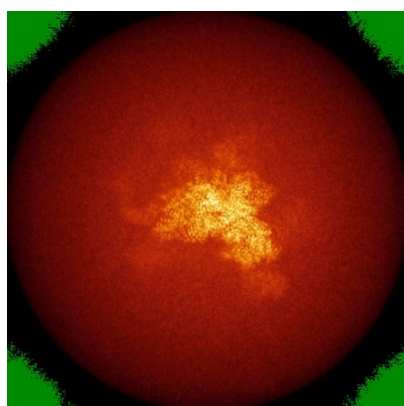


Z Index: 208

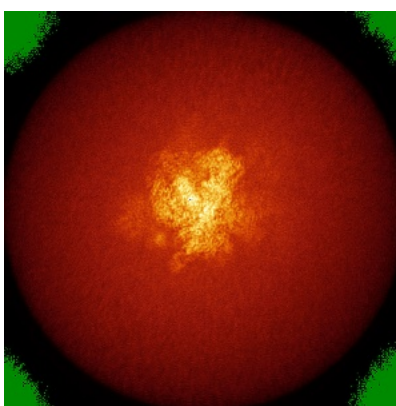
The images above show the largest variance slices of the map in three orthogonal directions.

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

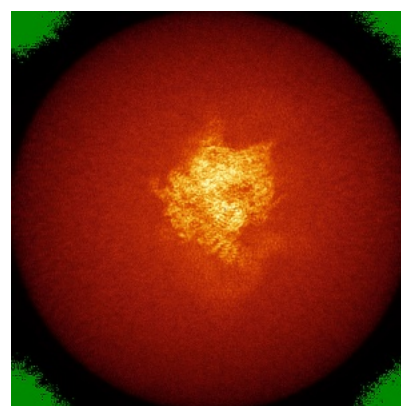
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

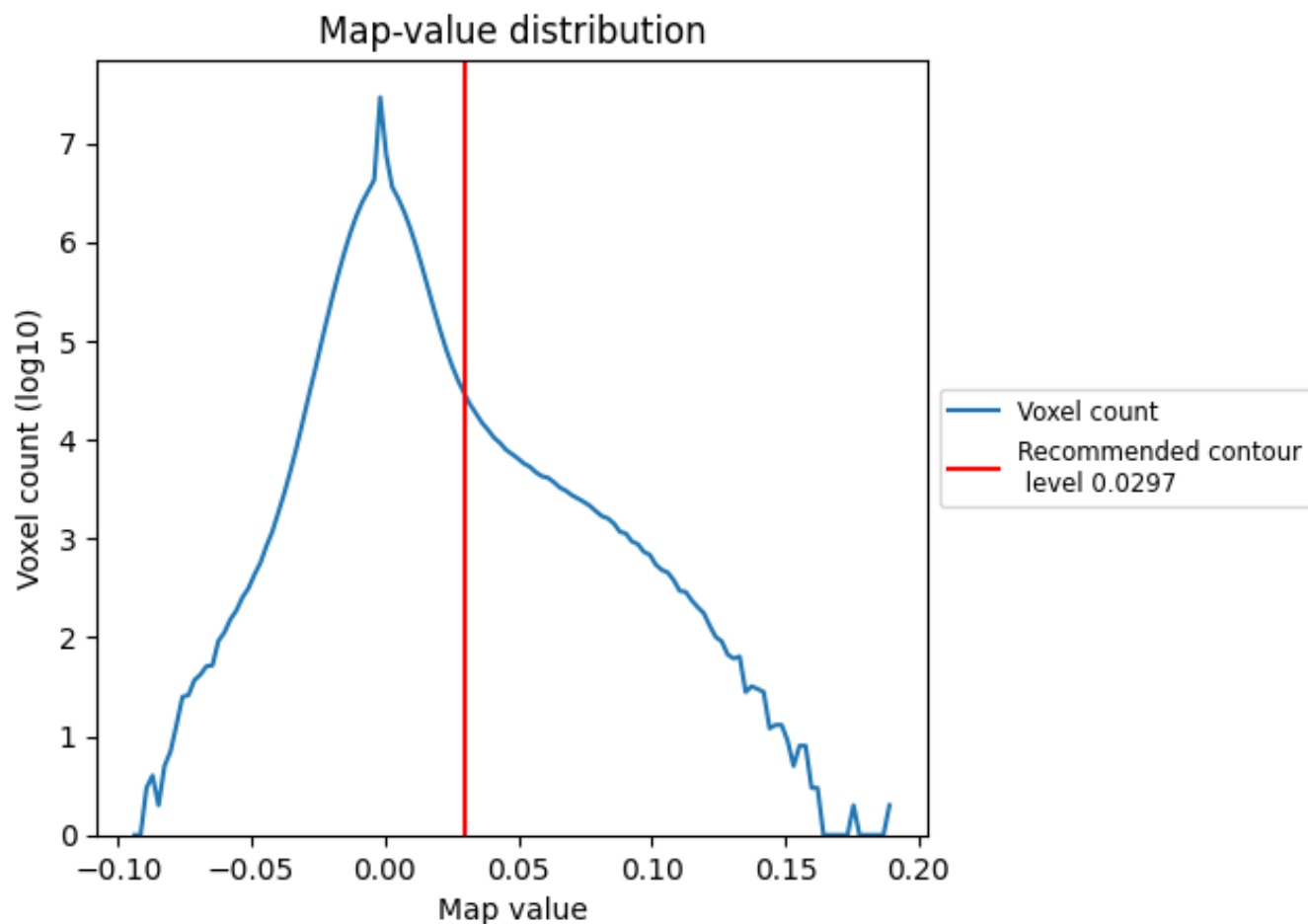
6.6 Mask visualisation

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

7 Map analysis [i](#)

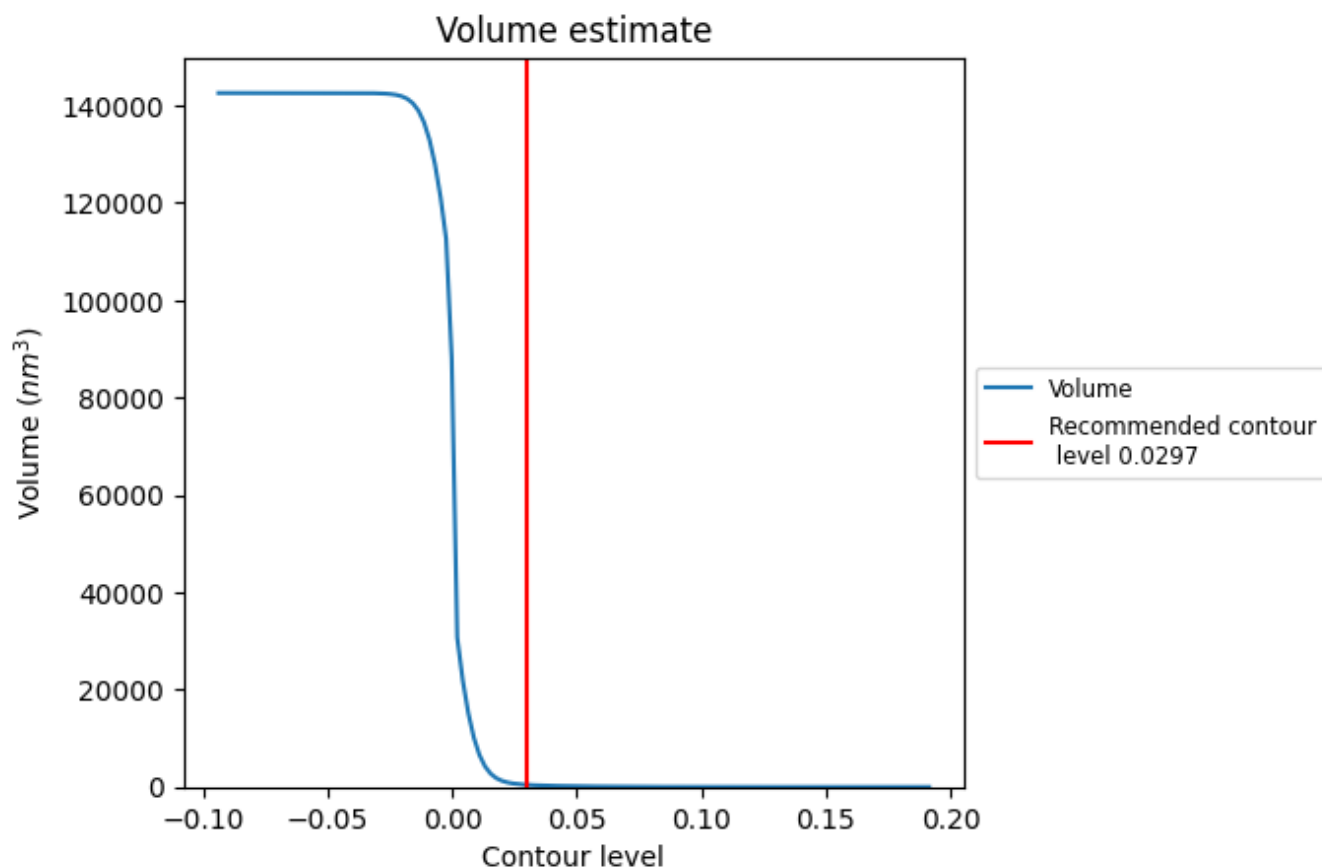
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

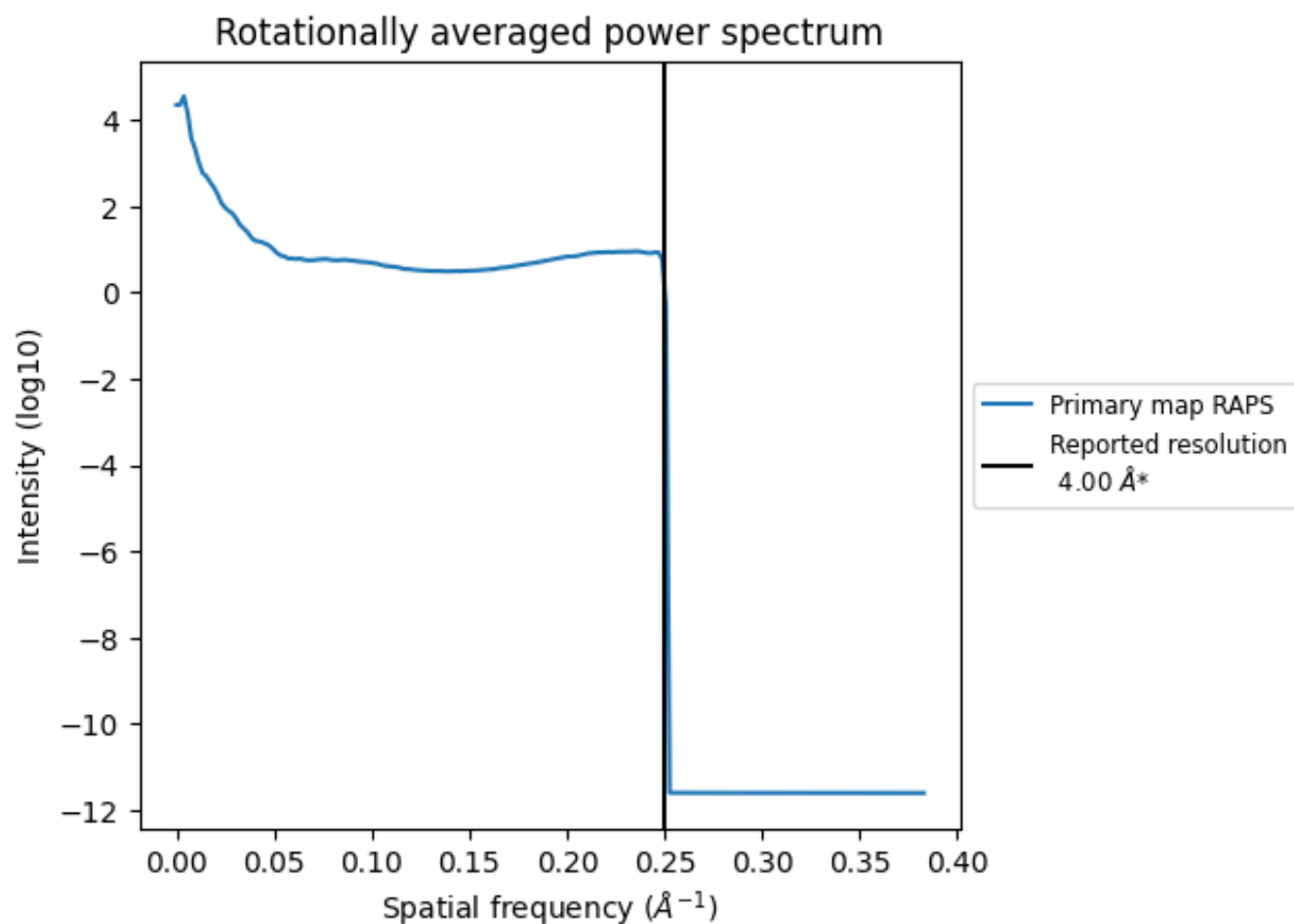
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 445 nm^3 ; this corresponds to an approximate mass of 402 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

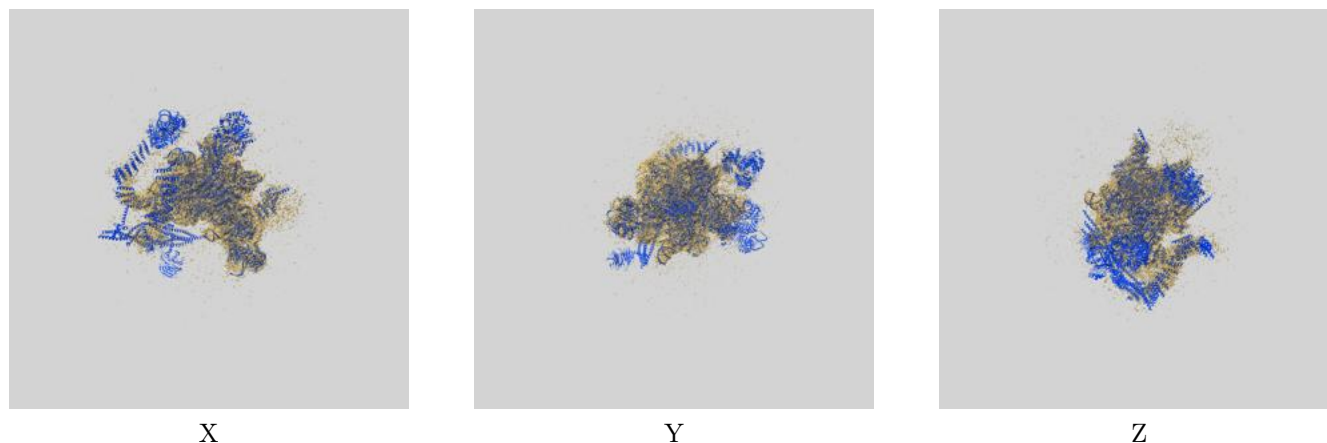
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

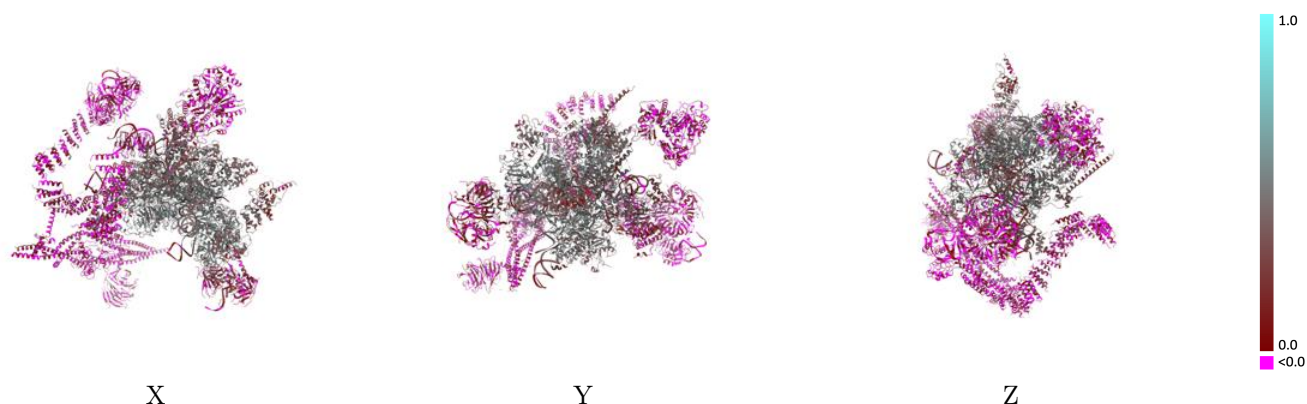
This section contains information regarding the fit between EMDB map EMD-6684 and PDB model 5WSG. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



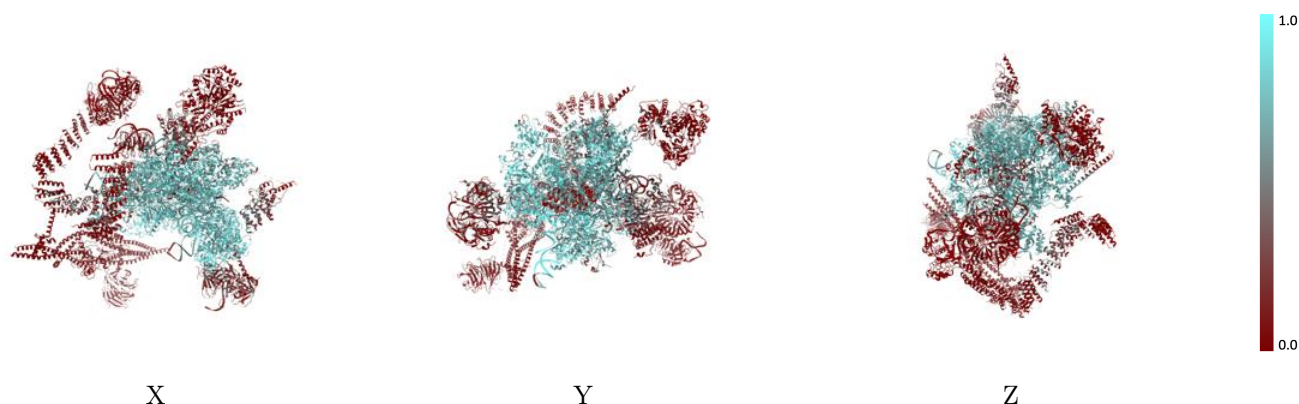
The images above show the 3D surface view of the map at the recommended contour level 0.0297 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



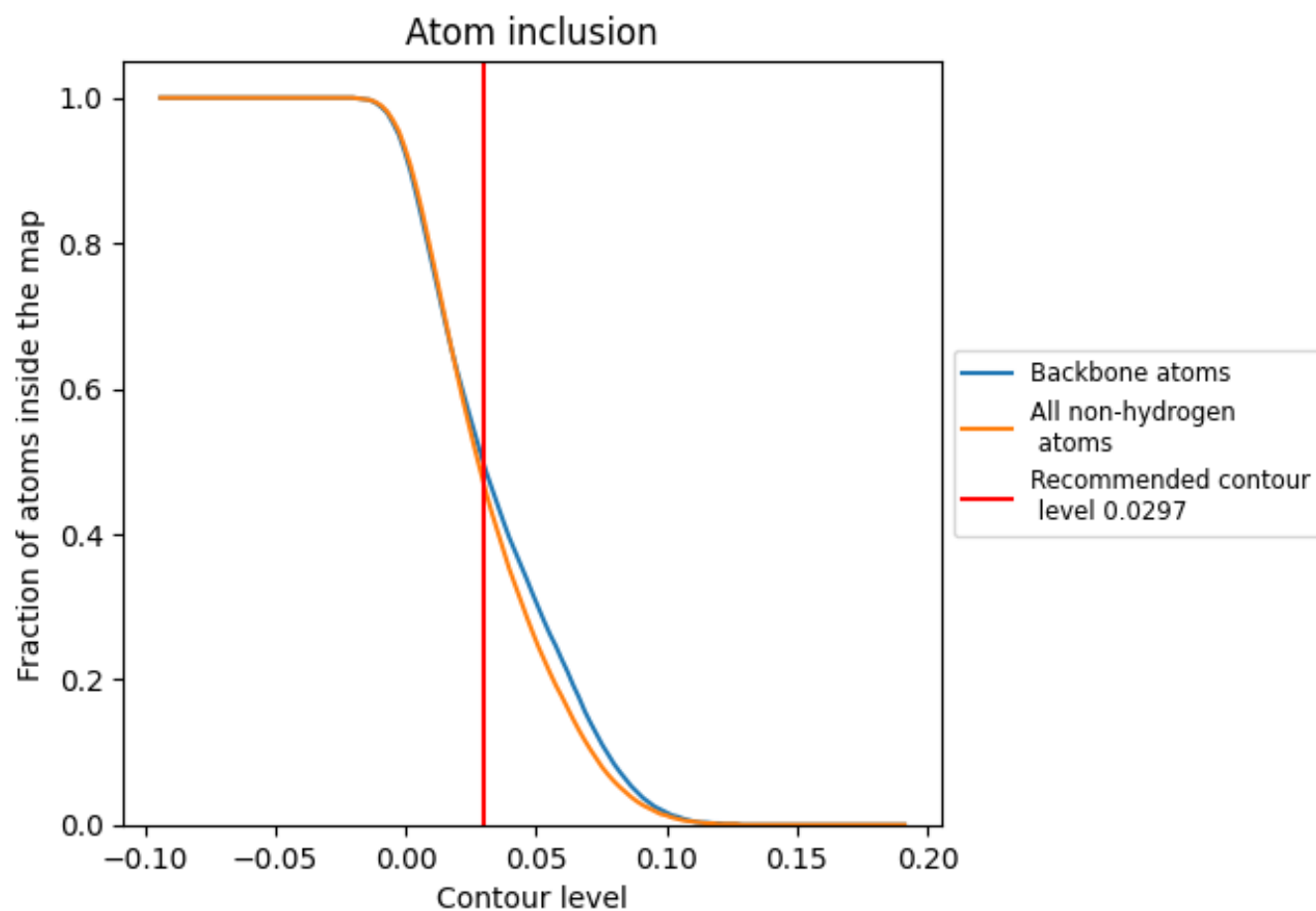
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0297).

9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 47% 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 (0.0297) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4730	 0.2740
A	 0.7330	 0.4410
B	 0.7390	 0.3930
C	 0.8060	 0.4510
D	 0.7220	 0.3140
E	 0.8230	 0.3420
F	 0.0020	 0.0070
G	 0.0040	 0.0080
H	 0.0000	 -0.0050
I	 0.6190	 0.3700
J	 0.7540	 0.4820
K	 0.0000	 -0.0030
L	 0.3220	 0.1470
M	 0.2550	 0.1390
N	 0.7080	 0.3270
O	 0.8350	 0.4860
P	 0.6520	 0.4210
Q	 0.6310	 0.4150
R	 0.7640	 0.4190
S	 0.6410	 0.4670
T	 0.7980	 0.4470
U	 0.0020	 -0.0170
V	 0.0020	 -0.0300
W	 0.0040	 0.0200
X	 0.0020	 0.0070
Y	 0.0000	 -0.0230
Z	 0.4450	 0.3510
b	 0.2600	 0.3130
c	 0.4110	 0.2380
d	 0.4710	 0.2350
e	 0.0370	 0.0300
f	 0.1000	 0.1370
g	 0.1550	 0.1070
h	 0.1620	 0.0520
i	 0.1910	 0.1150



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Chain	Atom inclusion	Q-score
j	 0.2110	 0.1460
k	 0.2060	 0.1700
l	 0.3380	 0.2630
m	 0.1410	 0.0830
n	 0.1980	 0.0690
o	 0.0120	 0.0030
p	 0.0060	 -0.0080
q	 0.0020	 0.0120
r	 0.0280	 0.0490
t	 0.0080	 0.0200
v	 0.1270	 0.0360