



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 08:21 AM UTC

PDB ID : 6J6N / pdb_00006j6n
EMDB ID : EMD-0691
Title : Cryo-EM structure of the yeast B*-b1 complex at an average resolution of 3.86 angstrom
Authors : Wan, R.; Bai, R.; Yan, C.; Lei, J.; Shi, Y.
Deposited on : 2019-01-15
Resolution : 3.86 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

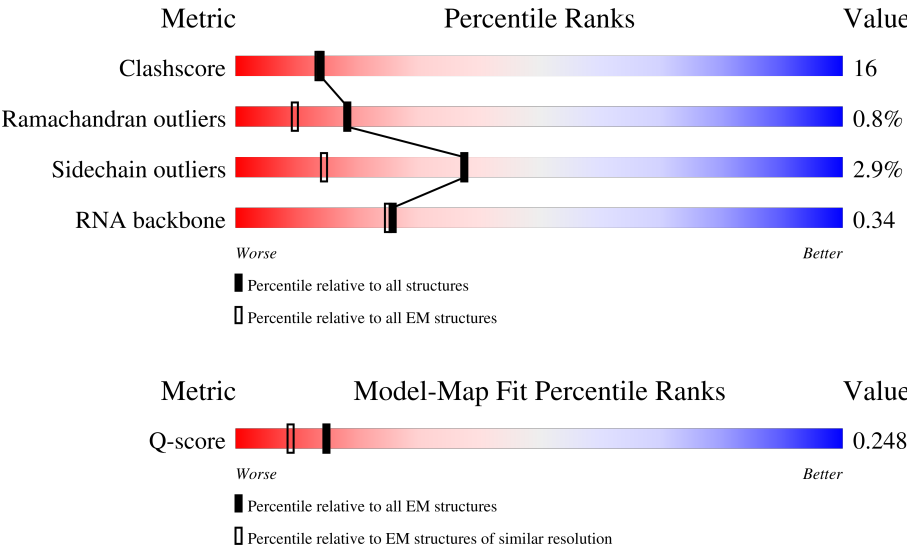
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.86 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.



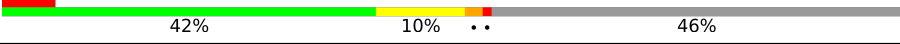
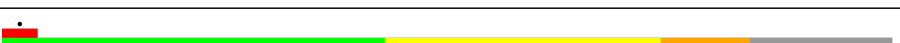
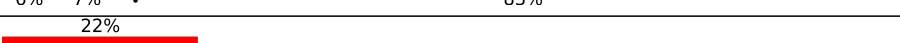
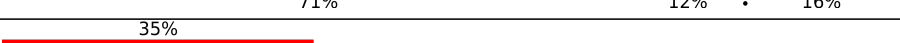
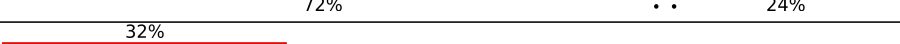
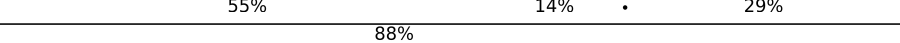
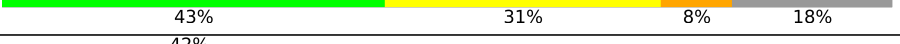
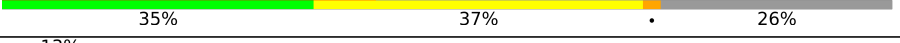
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8889 (3.36 - 4.35)

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	6% 61% 17% 21%
2	C	1008	74% 18% 9%
3	J	135	18% 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	c	590	
12	d	687	
13	I	215	
14	n	455	
15	H	235	
16	B	246	
17	D	214	
18	E	112	
19	L	1175	
20	v	859	
21	a	111	
22	b	238	
23	t	175	
24	i	94	
24	u	94	
25	m	146	
25	z	146	
26	j	77	

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Mol	Chain	Length	Quality of chain
26	x	77	
27	h	86	
27	w	86	
28	e	110	
28	g	110	
29	k	196	
29	s	196	
30	l	101	
30	y	101	
31	o	503	
31	p	503	
31	q	503	
31	r	503	

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 78937 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	1913	Total	C	N	O	S	0	0
			15793	10154	2714	2868	57		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	920	Total	C	N	O	S	0	0
			7348	4733	1223	1362	30		

- 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	357	Total	C	N	O	S	0	0
			2810	1777	493	530	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	P	205	Total	C	N	O	S	0	0
			1608	1003	294	304	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Q	292	Total	C	N	O	S	0	0
			2301	1461	399	426	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	70	Total	C	N	O	S	0	0
			567	355	113	98	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 protein called Pre-mRNA-splicing factor CEF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	c	436	Total	C	N	O	S	0	0
			2978	1843	552	575	8		

- Molecule 12 is a protein called Pre-mRNA-splicing factor CLF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	d	566	Total	C	N	O	S	0	0
			3881	2433	707	732	9		

- Molecule 13 is a protein called Pre-mRNA-splicing factor SYF2.

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

- Molecule 14 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	n	299	Total	C	N	O	P	S	0	0
			1894	1175	340	372	1	6		

- Molecule 15 is a protein called Pre-mRNA-splicing factor ISY1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	71	Total	C	N	O	S	0	0
			629	399	116	113	1		

- Molecule 16 is a RNA chain called UBC4 pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	B	57	Total	C	N	O	P	0	0
			1206	542	209	398	57		

- Molecule 17 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	D	179	Total	C	N	O	P	0	0
			3795	1699	660	1258	178		

- Molecule 18 is a RNA chain called U6 snRNA.

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

- Molecule 19 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	205	Total	C	N	O	P	0	0
			4325	1936	728	1456	205		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	v	722	Total	C	N	O	S	0	0
			4625	2893	825	895	12		

- Molecule 21 is a protein called U2 small nuclear ribonucleoprotein B”.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	a	84	Total	C	N	O	0	0
			416	248	84	84		

- Molecule 22 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	b	169	Total	C	N	O	0	0
			841	503	169	169		

- 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 E.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	u	74	Total	C	N	O	S	0	0
			526	346	87	90	3		
24	i	74	Total	C	N	O	S	0	0
			541	358	90	90	3		

- Molecule 25 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	m	119	Total	C	N	O	S	0	0
			917	575	163	176	3		
25	z	108	Total	C	N	O	S	0	0
			824	521	142	158	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	j	75	Total	C	N	O	S	0	0
			552	350	98	103	1		
26	x	75	Total	C	N	O	S	0	0
			552	350	98	103	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	h	68	Total	C	N	O	S	0	0
			518	337	96	84	1		
27	w	68	Total	C	N	O	S	0	0
			518	337	96	84	1		

- Molecule 28 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	g	101	Total	C	N	O	S	0	0
			785	504	149	128	4		
28	e	101	Total	C	N	O	S	0	0
			785	504	149	128	4		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	k	100	Total	C	N	O	S	0	0
			809	514	150	142	3		
29	s	93	Total	C	N	O	S	0	0
			749	476	138	132	3		

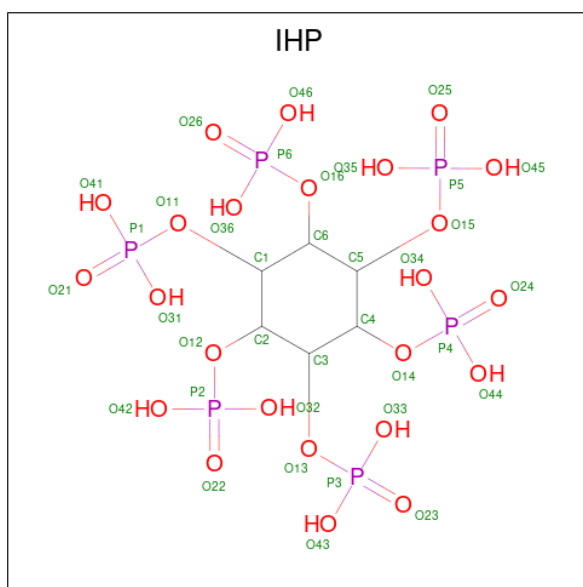
- Molecule 30 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	l	83	Total	C	N	O	S	0	0
			641	408	111	120	2		
30	y	81	Total	C	N	O	S	0	0
			616	394	107	113	2		

- Molecule 31 is a protein called Pre-mRNA-processing factor 19.

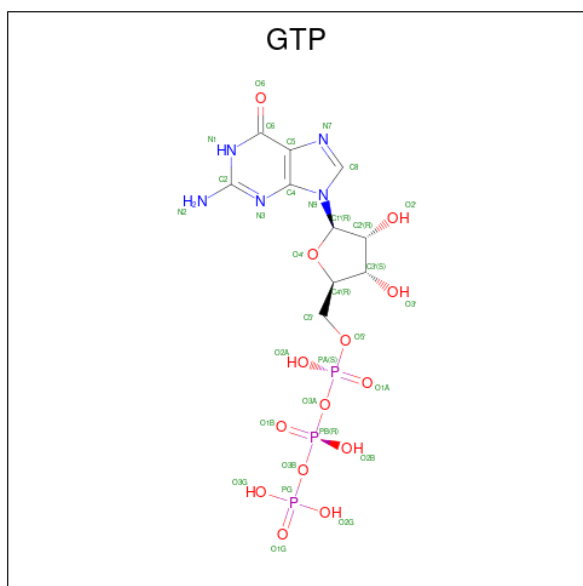
Mol	Chain	Residues	Atoms					AltConf	Trace
31	r	125	Total	C	N	O	S	0	0
			823	521	133	167	2		
31	p	128	Total	C	N	O	S	0	0
			843	532	136	173	2		
31	q	129	Total	C	N	O	S	0	0
			850	537	137	174	2		
31	o	126	Total	C	N	O	S	0	0
			830	525	134	169	2		

- Molecule 32 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: C₆H₁₈O₂₄P₆).



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

- Molecule 33 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

- Molecule 34 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
34	C	1	Total 1	Mg 1	0
34	E	5	Total 5	Mg 5	0

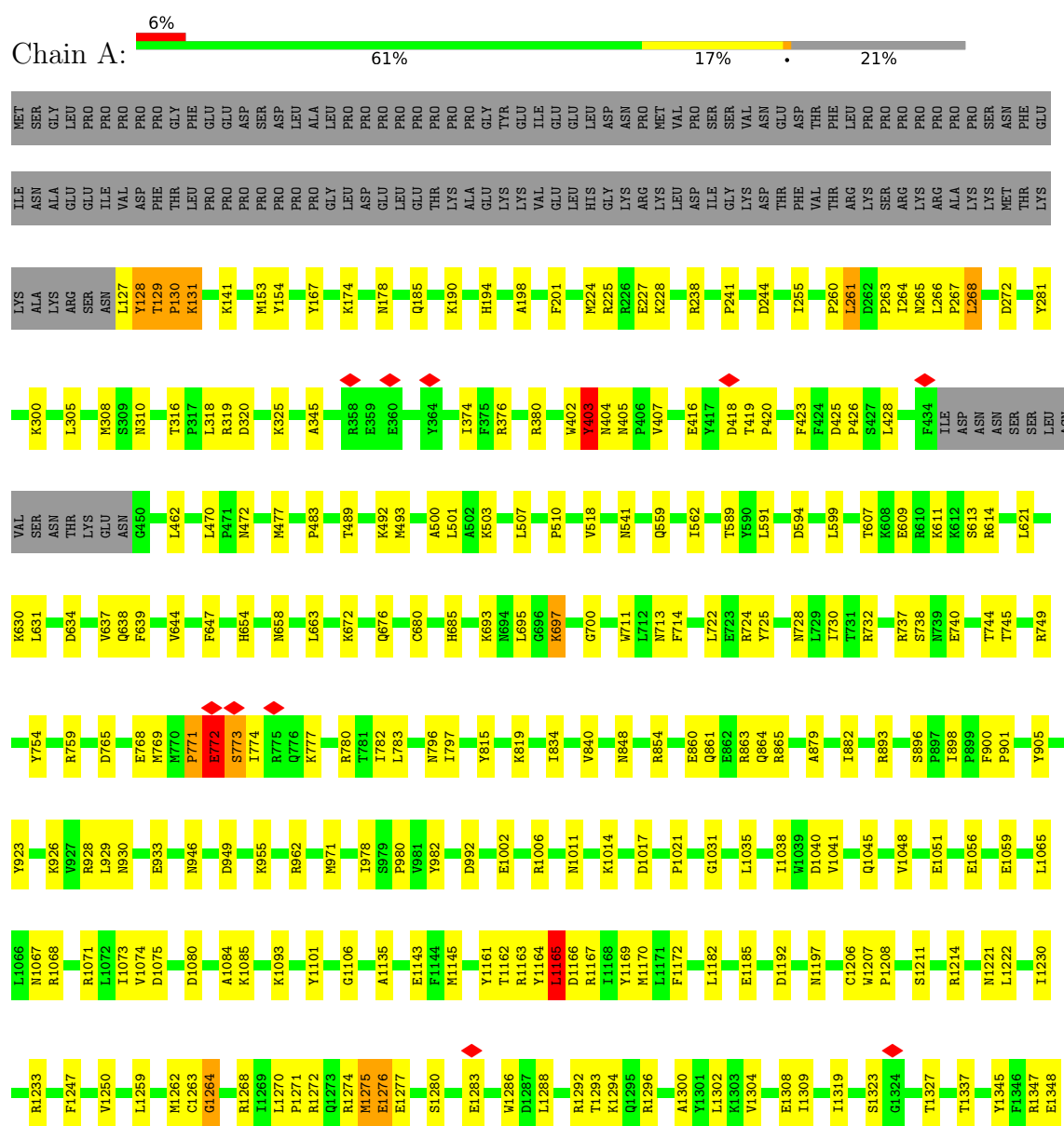
- Molecule 35 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

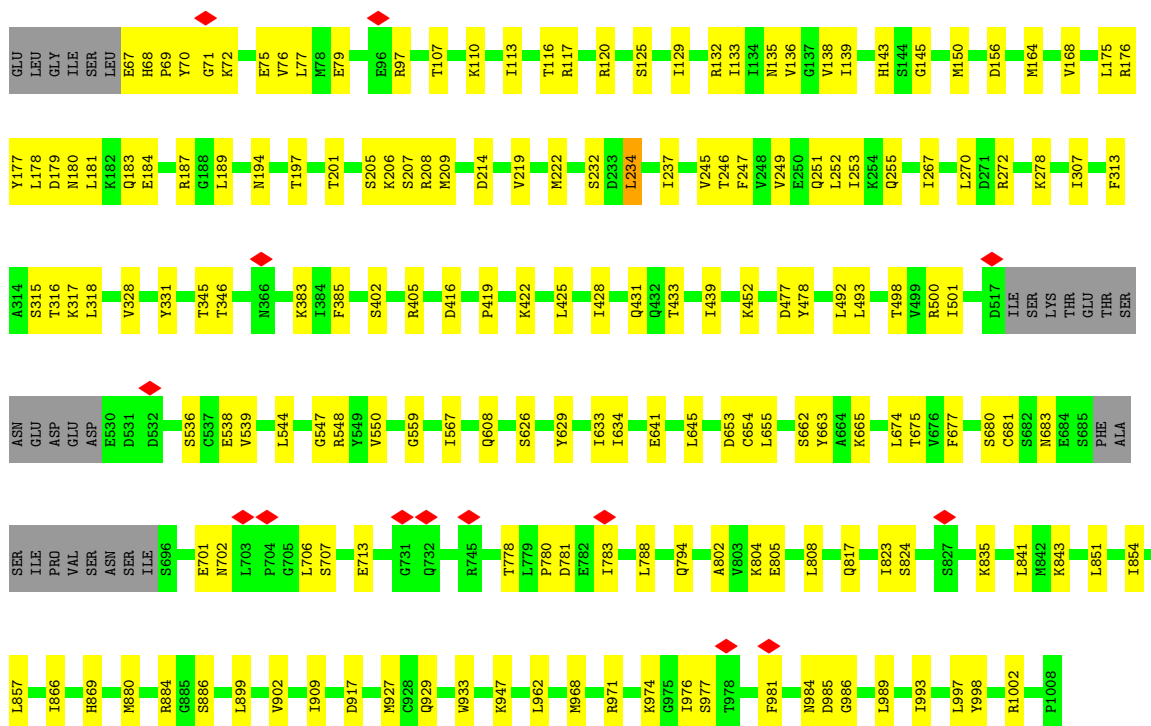
3 Residue-property plots

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.

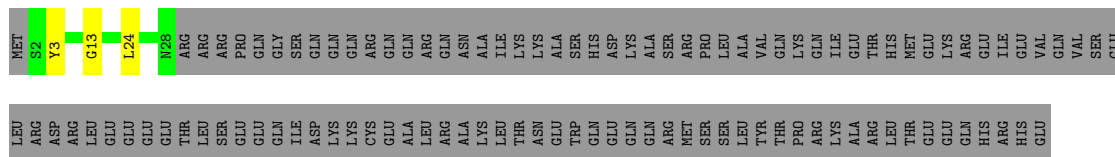
• Molecule 1: Pre-mRNA-splicing factor 8



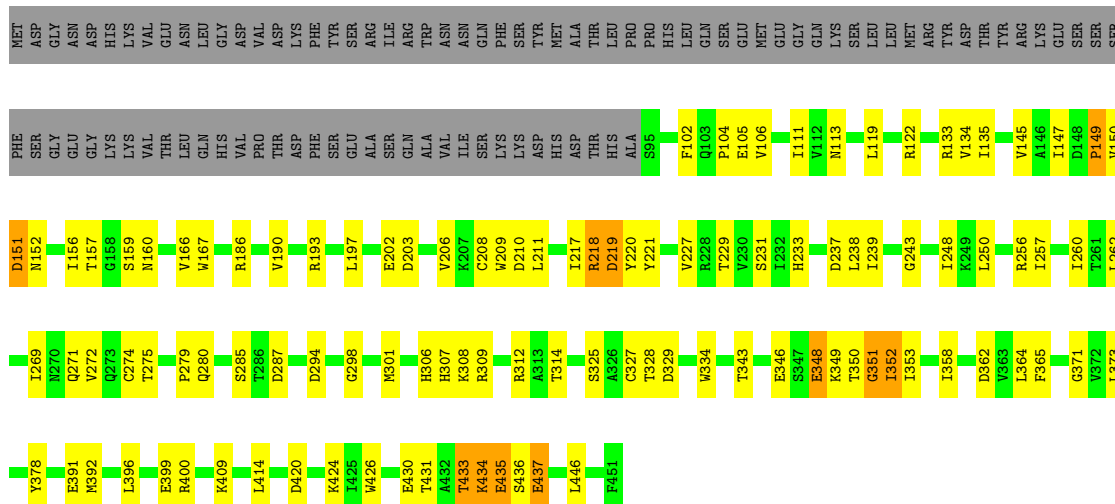


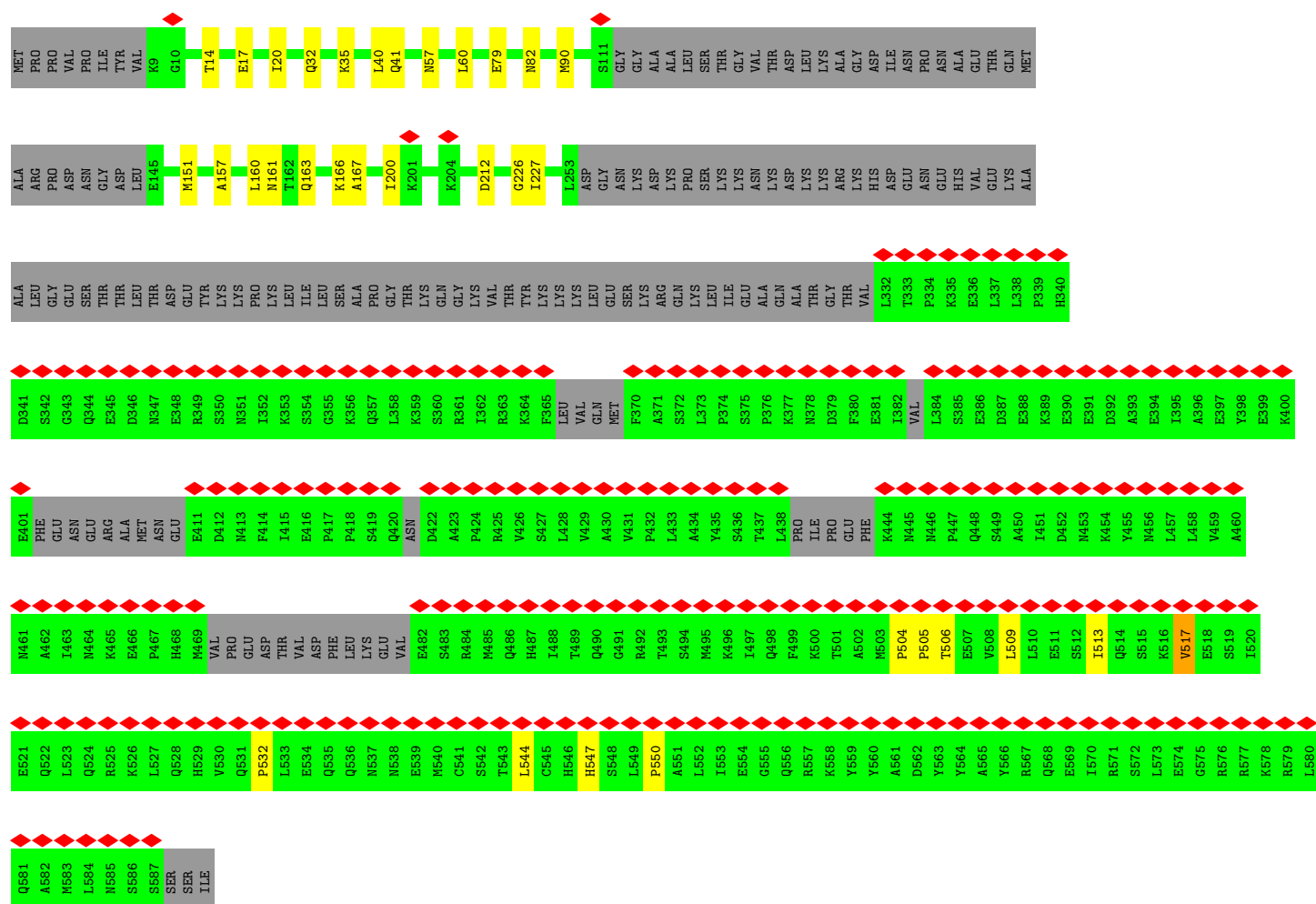


- Molecule 3: Pre-mRNA-splicing factor CWC21

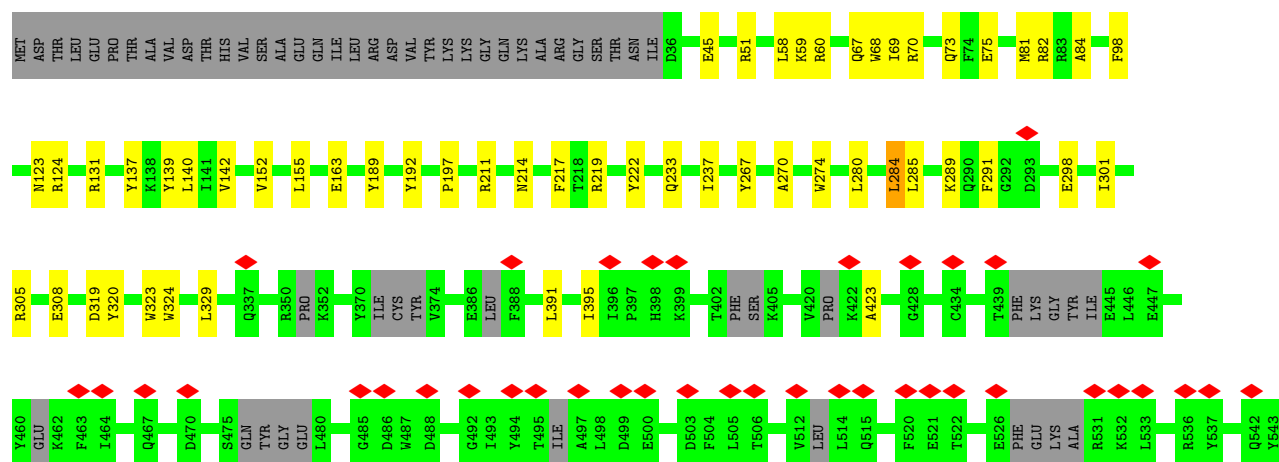


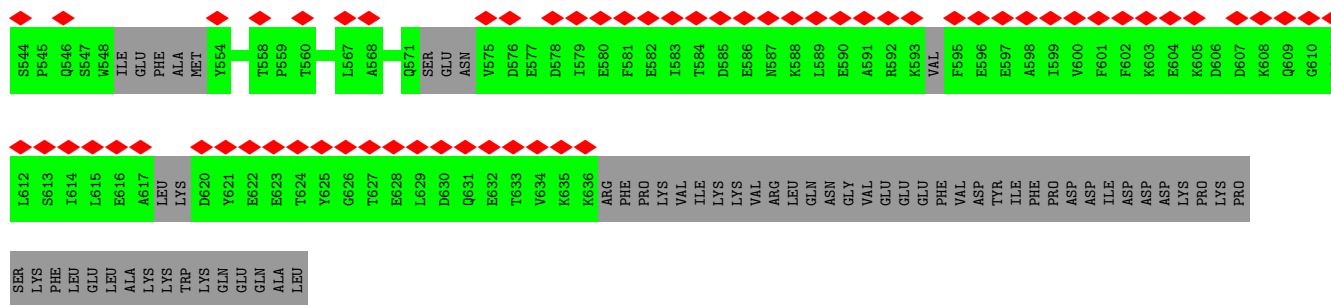
- Molecule 4: Pre-mRNA-splicing factor PRP46



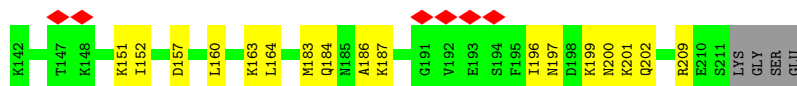
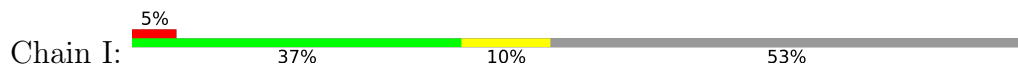


Chain d:

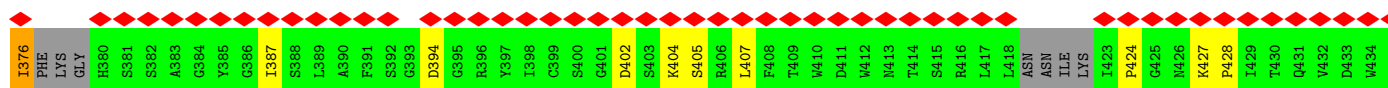
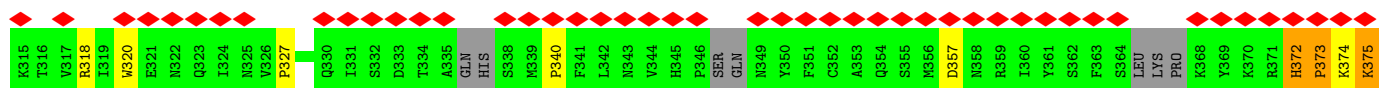
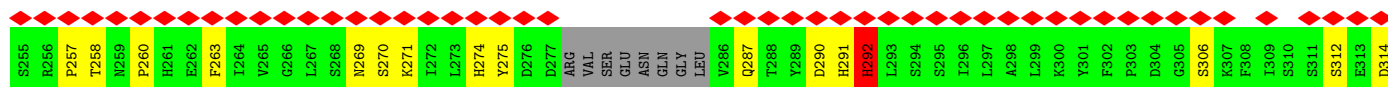
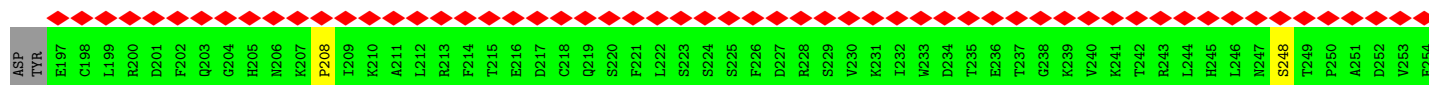
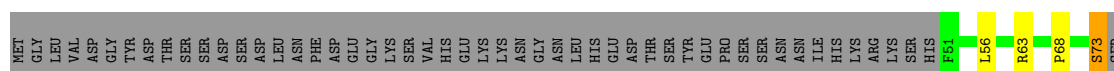


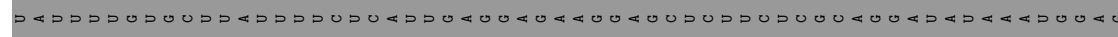


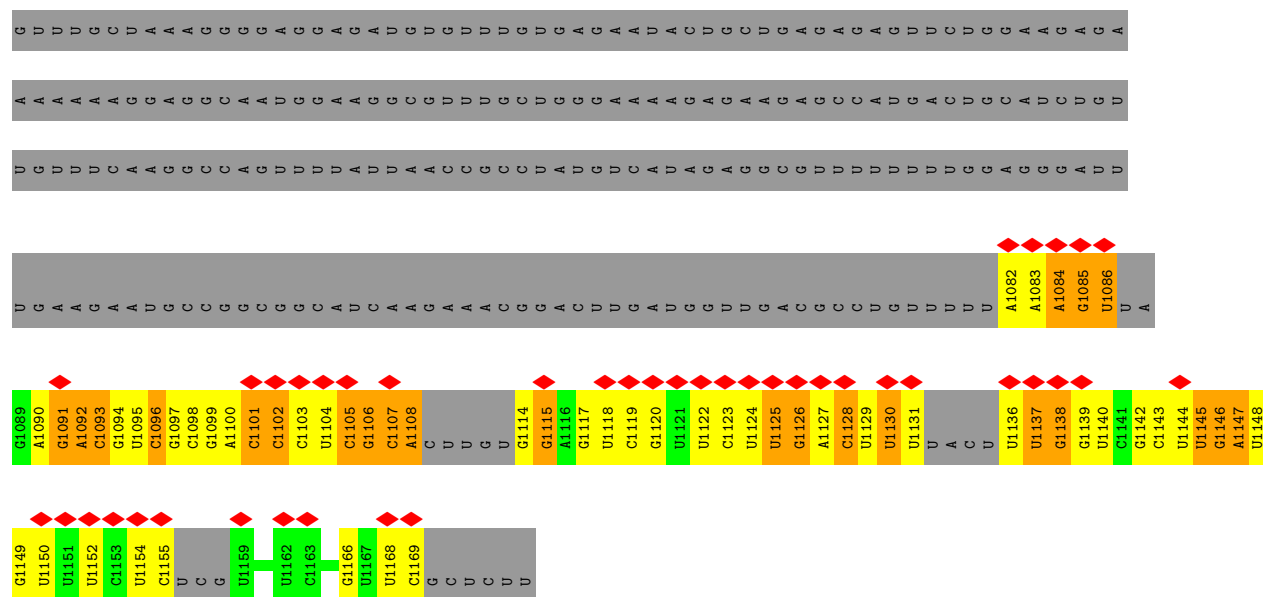
• Molecule 13: Pre-mRNA-splicing factor SYF2



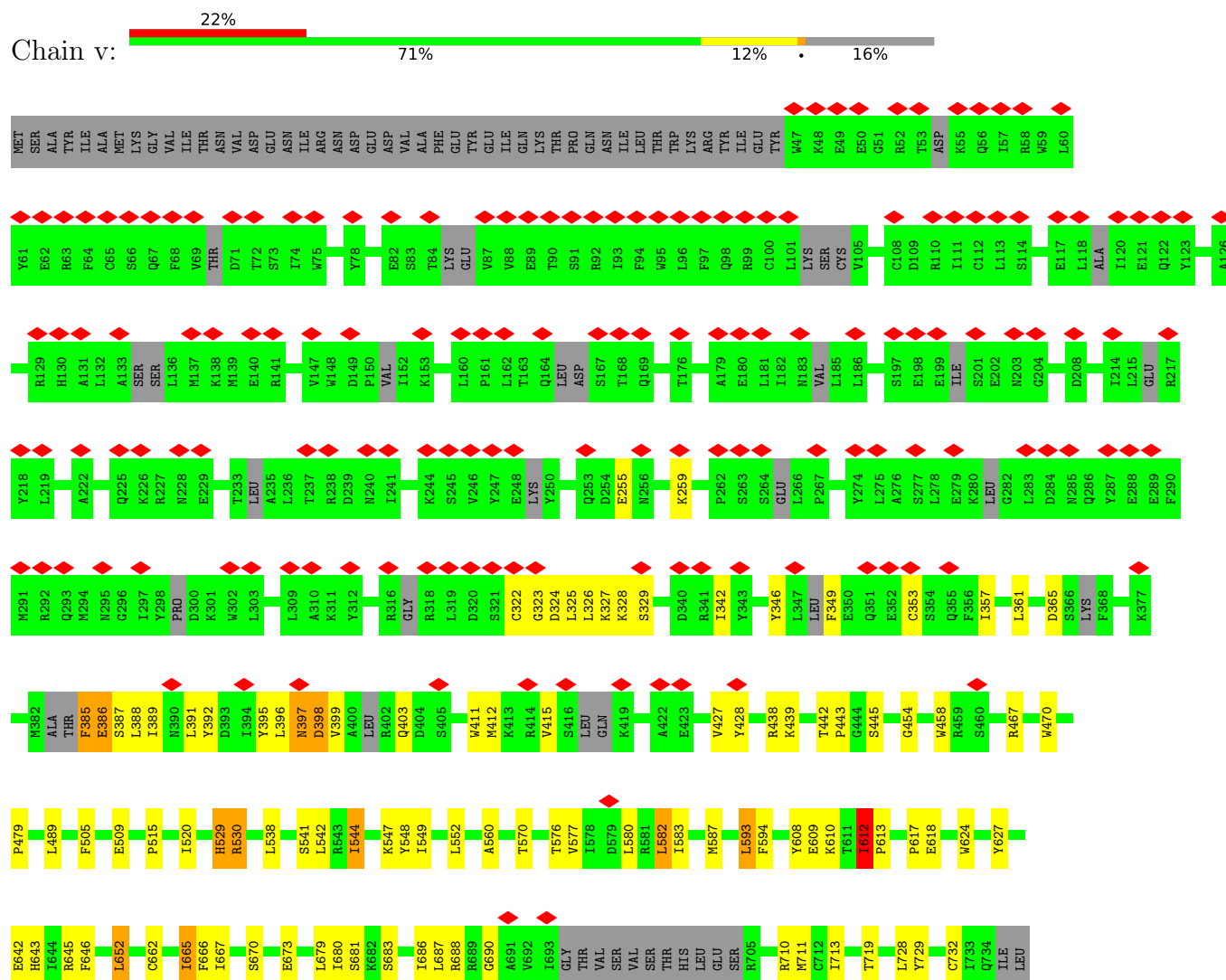
• Molecule 14: Pre-mRNA-processing factor 17

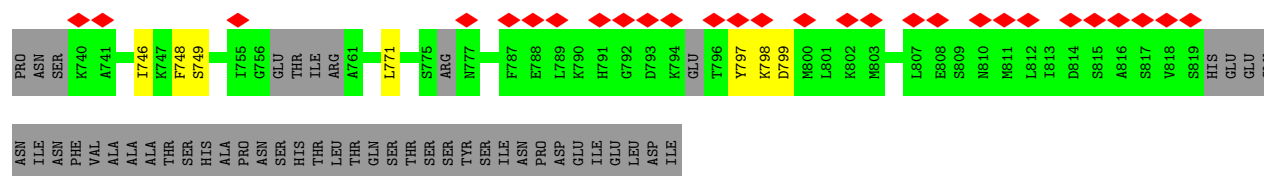




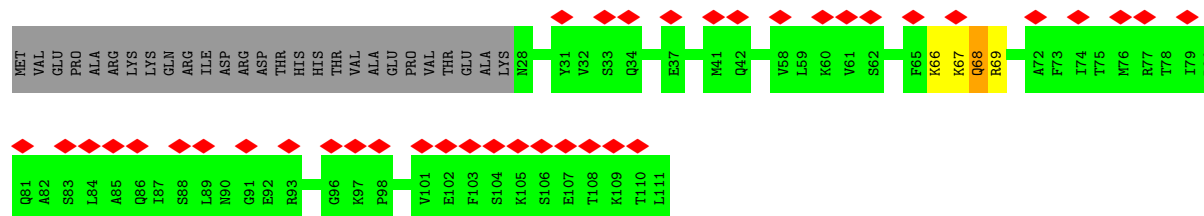
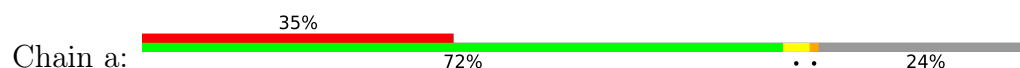


• Molecule 20: Pre-mRNA-splicing factor SYF1

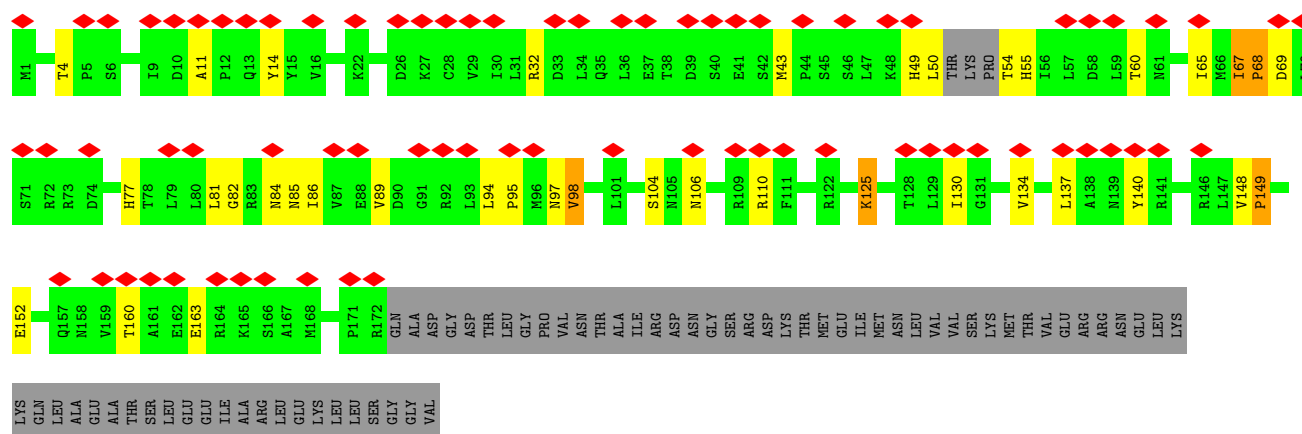




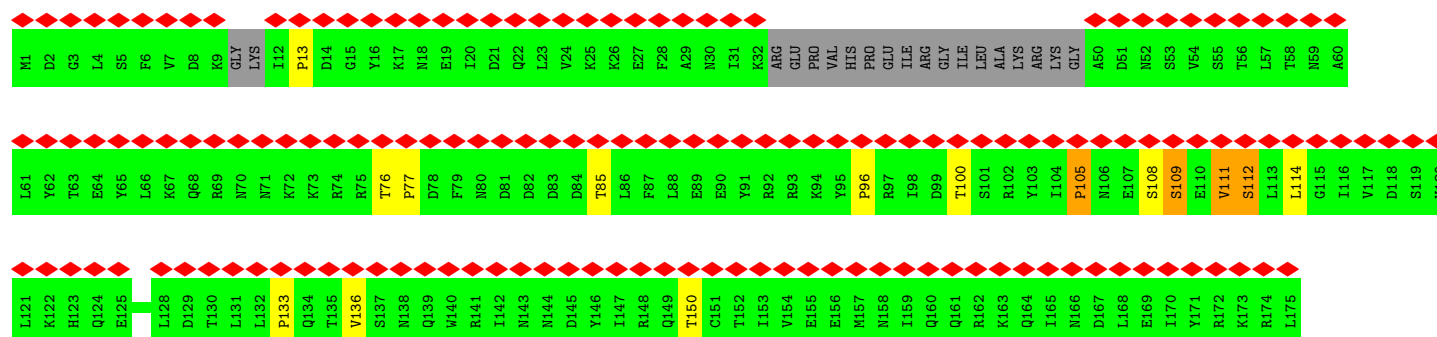
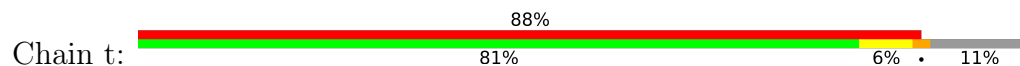
• Molecule 21: U2 small nuclear ribonucleoprotein B''



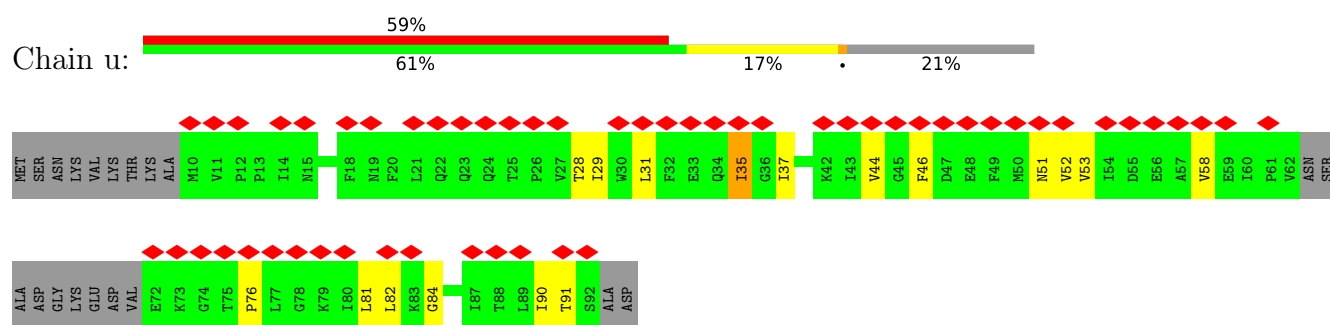
• Molecule 22: U2 small nuclear ribonucleoprotein A'



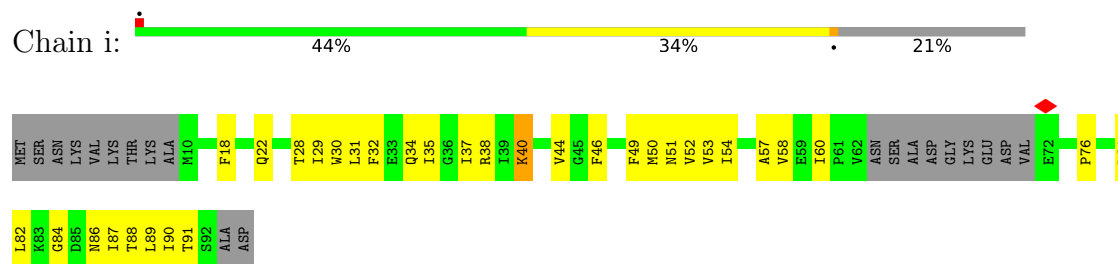
• Molecule 23: Pre-mRNA-splicing factor SNT309



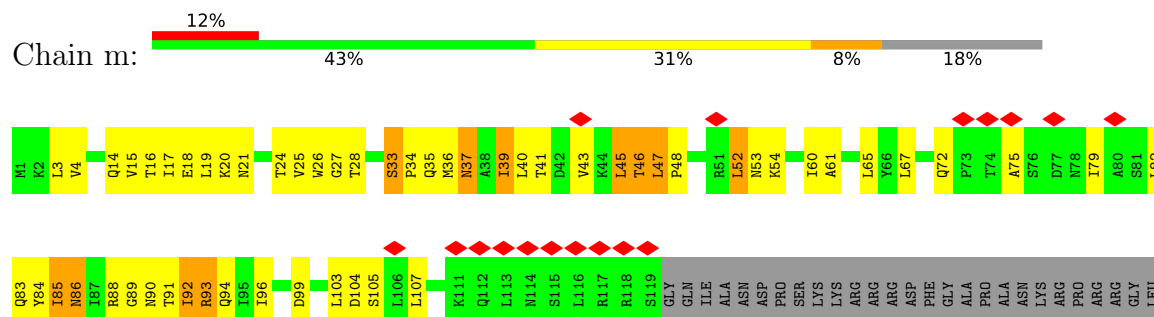
• Molecule 24: Small nuclear ribonucleoprotein E



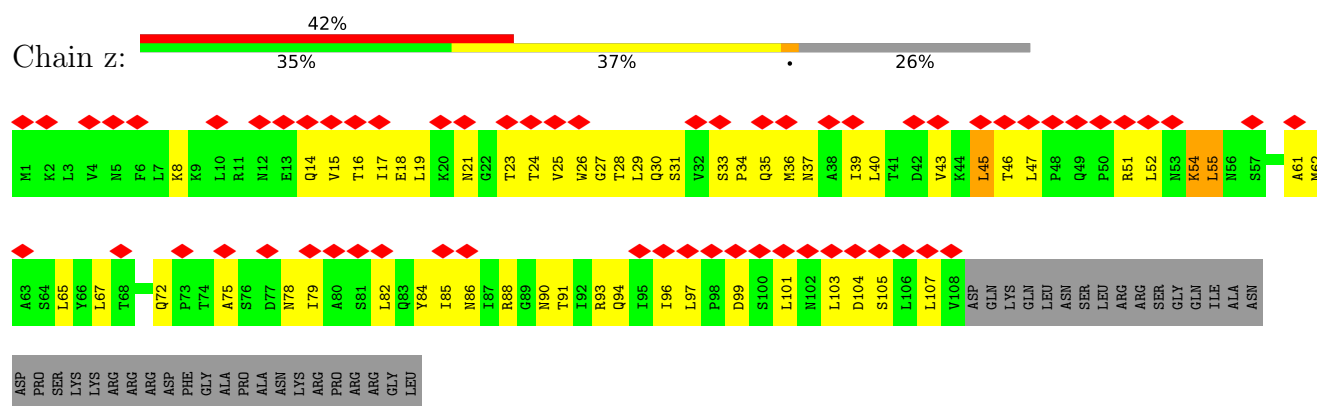
• Molecule 24: Small nuclear ribonucleoprotein E



• Molecule 25: Small nuclear ribonucleoprotein Sm D1

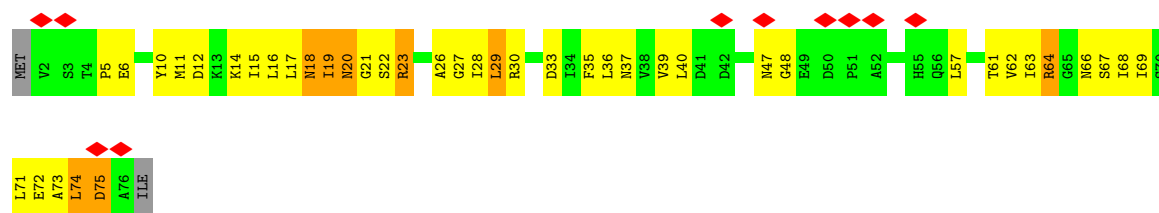


• Molecule 25: Small nuclear ribonucleoprotein Sm D1

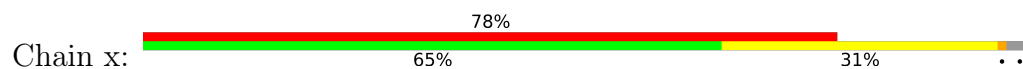


• Molecule 26: Small nuclear ribonucleoprotein G

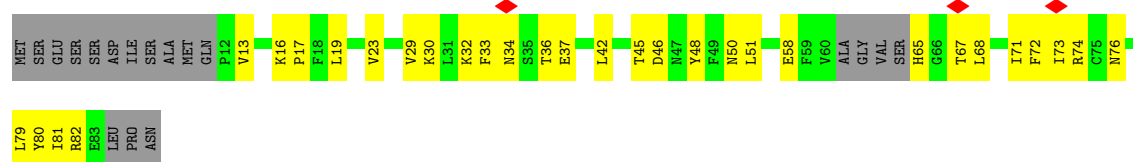




• Molecule 26: Small nuclear ribonucleoprotein G



• Molecule 27: Small nuclear ribonucleoprotein F



• Molecule 27: Small nuclear ribonucleoprotein F



• Molecule 28: Small nuclear ribonucleoprotein Sm D2



Chain e:

Amino Acid	Percentage
MET	1%
SER	1%
SER	1%
GLN	1%
ILE	1%
ILE	1%
ASP	1%
R	62%
P	47%
K	39%
H	5%
L	8%
Others	1%

[illegible]

Chain s:

Sequence logo for Chain s. The y-axis represents information content in bits (0.00 to 0.15). The x-axis shows amino acid positions from 1 to 254. A color scale at the top indicates conservation levels: 20% (red), 23% (green), and 53% (grey).

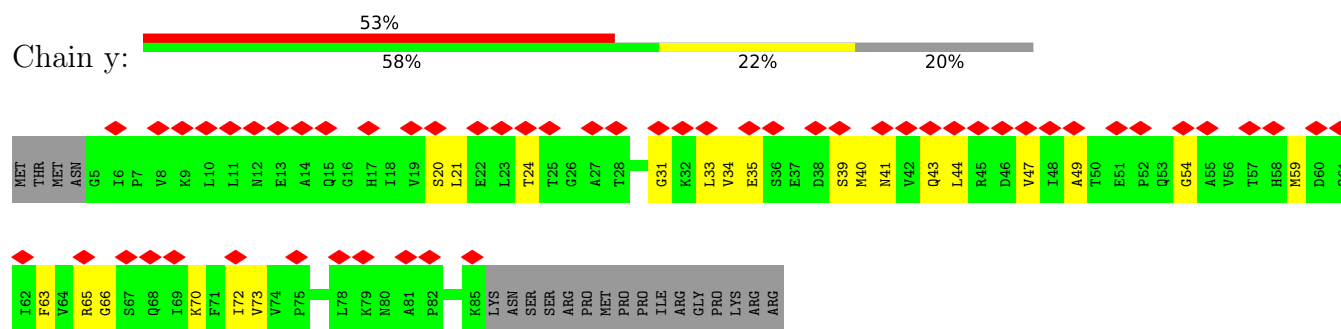
Position	Amino Acid	Information Content (bits)
1	Met	0.05
2	Ser	0.05
3	K3	0.10
4	I4	0.10
5	Q5	0.10
6	V6	0.10
7	A7	0.10
8	H8	0.10
9	S9	0.10
10	S10	0.10
11	R11	0.10
12	L12	0.10
13	A13	0.10
14	N14	0.10
15	L15	0.10
16	I16	0.10
17	D17	0.10
18	Y18	0.10
19	R21	0.10
20	T24	0.10
21	Q25	0.10
22	D26	0.10
23	G27	0.10
24	R28	0.10
25	V29	0.10
26	Y30	0.10
27	I31	0.10
28	G32	0.10
29	Q33	0.10
30	L34	0.10
31	N35	0.10
32	A36	0.10
33	F37	0.10
34	D38	0.10
35	K39	0.10
36	H40	0.10
37	N41	0.10
38	N42	0.10
39	L43	0.10
40	V44	0.10
41	C48	0.10
42	I49	0.10
43	E50	0.10
44	E51	0.10
45	R52	0.10
46	V53	0.10
47	P54	0.10
48	K55	0.10
49	T56	0.10
50	Q57	0.10
51	L58	0.10
52	D59	0.10
53	K60	0.10
54	L61	0.10
55	R62	0.10
56	P63	0.10
57	S64	0.10
58	Lys	0.10
59	Leu	0.10
60	Arg	0.10
61	Thr	0.10
62	Gln	0.10
63	Ala	0.10
64	Pro	0.10
65	Glu	0.10
66	Asn	0.10
67	Phe	0.10
68	Arg	0.10
69	Asp	0.10
70	Val	0.10
71	Leu	0.10
72	Arg	0.10
73	Ala	0.10
74	Gly	0.10
75	Thr	0.10
76	Gln	0.10
77	Ala	0.10
78	Pro	0.10
79	Glu	0.10
80	Asn	0.10
81	Thr	0.10
82	Asp	0.10
83	Arg	0.10
84	Val	0.10
85	Leu	0.10
86	Arg	0.10
87	Ala	0.10
88	Gly	0.10
89	Thr	0.10
90	Gln	0.10
91	Ala	0.10
92	Pro	0.10
93	Glu	0.10
94	Asn	0.10
95	Arg	0.10
96	Leu	0.10
97	Asp	0.10
98	Val	0.10
99	Arg	0.10
100	Ala	0.10
101	Gly	0.10
102	Thr	0.10
103	Gln	0.10
104	Ala	0.10
105	Pro	0.10
106	Glu	0.10
107	Asn	0.10
108	Thr	0.10
109	Arg	0.10
110	Leu	0.10
111	Val	0.10
112	Asp	0.10
113	Arg	0.10
114	Leu	0.10
115	Ala	0.10
116	Gly	0.10
117	Thr	0.10
118	Gln	0.10
119	Ala	0.10
120	Pro	0.10
121	Glu	0.10
122	Asn	0.10
123	Thr	0.10
124	Arg	0.10
125	Leu	0.10
126	Asp	0.10
127	Val	0.10
128	Arg	0.10
129	Leu	0.10
130	Ala	0.10
131	Gly	0.10
132	Thr	0.10
133	Gln	0.10
134	Ala	0.10
135	Pro	0.10
136	Glu	0.10
137	Asn	0.10
138	Thr	0.10
139	Arg	0.10
140	Leu	0.10
141	Val	0.10
142	Asp	0.10
143	Arg	0.10
144	Leu	0.10
145	Ala	0.10

Chain 1:

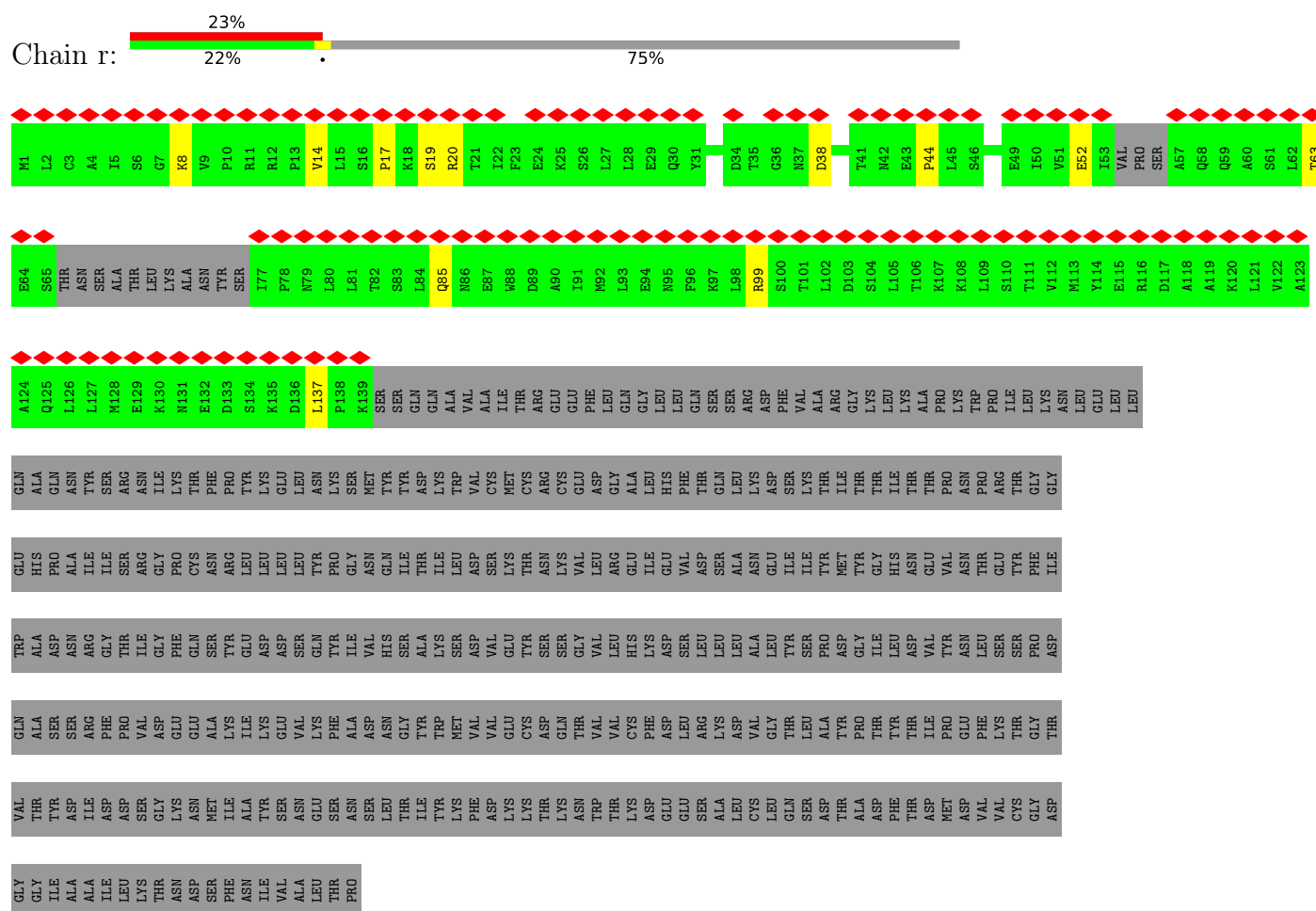
27% 36% 20% 18%

Sequence logo showing amino acid frequencies across 100 positions. The y-axis represents frequency in bits. The x-axis shows positions 1 to 100. The sequence is: MET, THR, MET, ASN, GS, K9, L10, L11, N12, E13, E14, Q15, G16, H17, I18, V19, S20, L21, E22, L23, T24, T25, K32, L33, V34, E35, S36, E37, D38, S39, N40, N41, V42, Q43, L44, R45, D46, V47, T48, A49, M59, D60, Q61, T62, F63, V64, R65, Q66, S67, Q68, I69, F71, I72, V73, V74, V75.

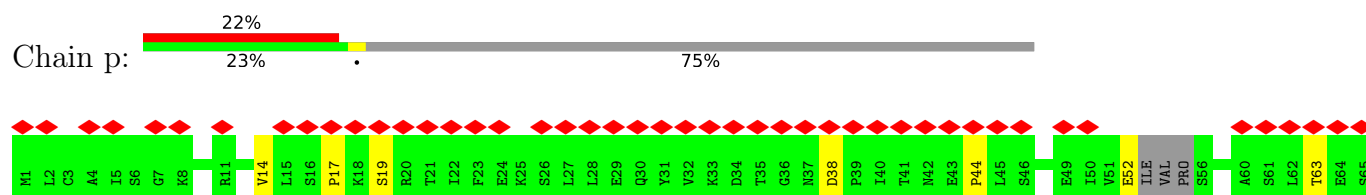
- Molecule 30: Small nuclear ribonucleoprotein Sm D3



- Molecule 31: Pre-mRNA-processing factor 19



- Molecule 31: Pre-mRNA-processing factor 19



CYS
GLY
ASP
GLY
GLY
ILE
ALA
ALA
ILE
LEU
LYS
THR
ASN
ASP
SER
PHE
ASN
ILE
VAL
ALA
LEU
THR
PRO

● Molecule 31: Pre-mRNA-processing factor 19



M1	L2	C3	A4	I5	S6	G7	K8	V9	P10	R11	R12	P13	V14	L15	S16	P17	T21	E24	K25	S26	L27	L28	Q30	Y31	V32	K33	D34	T35	G36	N37	D38	P39	I40	T41	M42	E43	P44	L45	S46	I47	E48	E49	I50	V51	E52	I53	VAL	PRO	S56	A57	Q58	Q59	A60	S61	L62	T63
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E64	S65	THR	ASN	SER	ALA	THR	LEU	LYS	ALA	ASN	TYR	SER	I77	P78	N79	L80	L81	S83	L84	Q85	N86	E87	W88	D89	A90	I91	N92	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
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A124	Q125	L126	L127	M128	E129	K130	N131	E132	D133	S134	K135	D136	L137	P138	K139	S140	SER	GLN	GLY	ALA	VAL	ALA	VAL	ILE	ILE	THR	ARG	GLY	GLU	GLU	PHE	GLY	ALA	GLN	VAL	ALA	ARG	GLY	LYS	ILE	THR	ALA	ARG	ASP	THR	LEU	LYS	ASN	THR	GLY	LEU	LEU	LEU	LEU
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GLN	ALA	GLN	ASN	TYR	SER	ARG	ASN	ILE	LYS	THR	PHE	PRO	TYR	LYS	GLU	LEU	ASN	LYS	SER	MET	TYR	TYR	ASP	LYS	TRP	VAL	ASP	VAL	GLY	GLN	ILE	THR	LYS	TRP	GLY	ASN	LYS	VAL	GLY	ASP	THR	GLN	LEU	SER	ALA	ASN	LYS	ASP	GLY	ILE	SER	THR	ALA	THR	PRO	ASN	PRO	ARG	THR	GLY	ILE
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GLU	HIS	PRO	ALA	ASN	ILE	ILE	SER	ARG	GLY	THR	ILE	GLY	PRO	CYS	ASN	ARG	LEU	LEU	GLY	PRO	GLY	GLN	TYR	ILE	ILE	LEU	ASP	VAL	GLY	ASN	LYS	VAL	GLY	ASP	LEU	VAL	GLY	ASN	GLY	ILE	THR	LYS	TRP	GLY	ASN	LYS	VAL	GLY	ILE	THR	GLU	THR	VAL	ASN	THR	GLU	THR	PHE	ILE
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TRP	ALA	ASP	ASN	ARG	GLY	THR	ILE	THR	ILE	PHE	GLY	GLU	GLN	ASN	TYR	GLY	ASP	VAL	ILE	VAL	HIS	SER	ALA	LYS	TRP	MET	VAL	ASP	VAL	GLY	LYS	TYR	THR	SER	GLY	VAL	LEU	LEU	LEU	ASP	ALA	ASN	GLY	LEU	THR	TYR	ILE	SER	PRO	ASP	THR	GLY	ILE	THR	THR	ASP
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GLN	ALA	SER	SER	ARG	PHE	PRO	VAL	ASP	GLY	GLU	LYS	GLU	ALA	ILE	LYS	VAL	PHE	ALA	ASP	ASN	GLY	TYR	TRP	MET	VAL	VAL	GLY	GLU	LYS	LYS	THR	LYS	ASN	THR	GLN	THR	VAL	VAL	CYS	LYS	PHE	ASP	LEU	LEU	LYS	ASP	VAL	GLY	THR	THR	ILE	PRO	GLU	PHE	LYS	THR	GLY	THR
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VAL	THR	TYR	ALA	ILE	ASP	ASP	SER	GLY	LYS	ASN	MET	ILE	ALA	TYR	VAL	ASN	GLU	SER	ASN	SER	THR	ILE	TYR	LYS	PHE	ASP	ASP	LYS	LYS	THR	LYS	ASN	THR	ASN	THR	THR	THR	THR	THR	THR	GLY	LEU	LEU	VAL	GLN	THR	SER	ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR
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GLY	GLY	ILE	ALA	ALA	ILE	LEU	LYS	THR	ASN	ASP	SER	PHE	ASN	VAL	ALA	LEU	THR	PRO
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	395458	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49.3	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	0.209	Depositor
Minimum map value	-0.095	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.028	Depositor
Map size (Å)	532.0, 532.0, 532.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.33, 1.33, 1.33	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.43	0/16198	0.64	4/21958 (0.0%)
2	C	0.39	0/7503	0.61	0/10159
3	J	0.38	0/191	0.75	0/254
4	O	0.50	0/2872	0.70	0/3902
5	P	0.39	0/1629	0.55	0/2194
6	Q	0.37	0/2339	0.67	1/3154 (0.0%)
7	R	0.36	0/2135	0.61	1/2871 (0.0%)
8	S	0.30	0/581	0.51	0/776
9	T	0.44	0/1315	0.64	1/1759 (0.1%)
10	Z	0.29	1/3712 (0.0%)	0.56	0/5004
11	c	0.26	0/2996	0.49	0/4033
12	d	0.32	1/3931 (0.0%)	0.52	2/5356 (0.0%)
13	I	0.33	0/826	0.53	0/1097
14	n	0.37	0/1894	0.60	0/2529
15	H	0.34	0/644	0.86	2/864 (0.2%)
16	B	0.31	0/1347	0.53	1/2091 (0.0%)
17	D	0.30	0/4239	0.41	0/6598
18	E	0.42	0/2452	0.48	0/3817
19	L	0.35	1/4815 (0.0%)	0.58	3/7467 (0.0%)
20	v	0.49	0/4662	0.76	4/6358 (0.1%)
21	a	0.63	0/415	1.14	0/577
22	b	1.07	0/839	1.44	8/1169 (0.7%)
23	t	0.29	0/924	0.54	0/1244
24	i	0.27	0/551	0.57	0/750
24	u	0.25	0/535	0.49	0/730
25	m	0.49	0/926	0.77	0/1257
25	z	0.32	0/833	0.62	0/1134
26	j	0.64	0/557	0.85	0/756
26	x	0.37	0/557	0.65	0/756
27	h	0.26	0/529	0.55	0/715
27	w	0.24	0/529	0.56	0/715
28	e	0.51	0/799	0.67	0/1078

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
28	g	0.56	0/799	0.78	0/1078
29	k	0.56	0/815	0.81	0/1092
29	s	0.44	0/755	0.73	0/1014
30	l	0.73	0/650	1.00	1/879 (0.1%)
30	y	0.31	0/625	0.58	0/847
31	o	0.23	0/835	0.56	2/1126 (0.2%)
31	p	0.18	0/848	0.44	0/1143
31	q	0.27	0/856	0.57	0/1155
31	r	0.30	0/828	0.57	0/1117
All	All	0.41	3/81286 (0.0%)	0.63	30/112573 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	d	163	GLU	C-O	6.22	1.26	1.23
19	L	12	U	O3'-P	5.65	1.69	1.61
10	Z	73	ILE	CA-CB	-5.26	1.51	1.54

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	b	43	MET	CA-C-N	8.56	128.69	119.28
22	b	43	MET	C-N-CA	8.56	128.69	119.28
22	b	4	THR	CA-C-N	7.90	127.46	118.85
22	b	4	THR	C-N-CA	7.90	127.46	118.85
12	d	98	PHE	CA-C-N	7.03	124.67	120.24
12	d	98	PHE	C-N-CA	7.03	124.67	120.24
20	v	681	SER	N-CA-C	-6.52	105.08	113.16
22	b	11	ALA	CA-C-N	6.50	127.97	119.84
22	b	11	ALA	C-N-CA	6.50	127.97	119.84
19	L	1092	A	C2'-C3'-O3'	-6.44	104.04	113.70
20	v	612	ILE	O-C-N	6.24	124.50	120.07
19	L	31	A	C2'-C3'-O3'	6.00	118.50	109.50
31	o	37	ASN	CA-C-N	6.00	129.94	121.61
31	o	37	ASN	C-N-CA	6.00	129.94	121.61
1	A	1964	PRO	O-C-N	5.82	130.50	122.64
16	B	8	U	C2'-C3'-O3'	-5.68	105.19	113.70
7	R	153	PRO	N-CA-C	5.57	121.79	114.27
6	Q	214	ILE	CA-CB-CG2	5.56	119.95	110.50
19	L	6	U	C2'-C3'-O3'	-5.49	105.47	113.70
1	A	1941	LEU	N-CA-C	5.39	117.16	111.28
9	T	35	LYS	CA-C-O	-5.26	111.13	119.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	H	34	ARG	CA-C-N	5.21	139.50	127.00
15	H	34	ARG	C-N-CA	5.21	139.50	127.00
22	b	81	LEU	CA-C-N	5.21	124.92	119.92
22	b	81	LEU	C-N-CA	5.21	124.92	119.92
20	v	560	ALA	CA-C-N	5.05	130.49	122.61
20	v	560	ALA	C-N-CA	5.05	130.49	122.61
30	l	39	SER	N-CA-C	-5.03	105.92	111.71
1	A	1781	TYR	CA-C-N	5.03	131.14	121.54
1	A	1781	TYR	C-N-CA	5.03	131.14	121.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	15793	0	15768	389	0
2	C	7348	0	7521	125	0
3	J	190	0	186	3	0
4	O	2810	0	2804	99	0
5	P	1608	0	1631	56	0
6	Q	2301	0	2366	46	0
7	R	2089	0	2053	39	0
8	S	567	0	552	14	0
9	T	1291	0	1312	37	0
10	Z	3651	0	3707	37	0
11	c	2978	0	2459	22	0
12	d	3881	0	3041	54	0
13	I	822	0	845	24	0
14	n	1894	0	1405	33	0
15	H	629	0	625	9	0
16	B	1206	0	609	71	0
17	D	3795	0	1919	100	0
18	E	2192	0	1106	53	0
19	L	4325	0	2197	291	0
20	v	4625	0	3448	127	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	a	416	0	182	6	0
22	b	841	0	350	27	0
23	t	926	0	606	3	0
24	i	541	0	542	77	0
24	u	526	0	515	21	0
25	m	917	0	961	106	0
25	z	824	0	864	88	0
26	j	552	0	553	85	0
26	x	552	0	553	23	0
27	h	518	0	502	38	0
27	w	518	0	502	49	0
28	e	785	0	802	101	0
28	g	785	0	802	118	0
29	k	809	0	881	138	0
29	s	749	0	809	59	0
30	l	641	0	666	121	0
30	y	616	0	639	25	0
31	o	830	0	663	6	0
31	p	843	0	675	6	0
31	q	850	0	682	4	0
31	r	823	0	654	10	0
32	A	36	0	6	6	0
33	C	32	0	12	7	0
34	C	1	0	0	0	0
34	E	5	0	0	0	0
35	Q	2	0	0	0	0
35	R	1	0	0	0	0
35	T	3	0	0	0	0
All	All	78937	0	68975	2306	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 16.

All (2306) 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)
26:j:17:LEU:CD1	26:j:19:ILE:HD11	1.43	1.47
29:k:31:ILE:CD1	29:k:49:ILE:HD11	1.45	1.45
28:g:35:ASN:HB2	28:g:61:PHE:CZ	1.52	1.43
28:e:56:ALA:HB2	28:e:72:VAL:CG2	1.48	1.41
19:L:1137:U:H2'	19:L:1138:G:C1'	1.58	1.34

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:B:10:A:C8	16:B:11:A:C5	2.21	1.28
20:v:612:ILE:HG13	20:v:613:PRO:CD	1.60	1.28
24:i:30:TRP:NE1	24:i:38:ARG:HD3	1.52	1.25
29:k:31:ILE:HD11	29:k:49:ILE:CD1	1.68	1.23
25:m:84:TYR:CD2	29:k:6:VAL:HG11	1.73	1.23
29:k:48:CYS:SG	29:k:82:LEU:HD12	1.79	1.23
19:L:15:C:O2'	19:L:16:U:H5'	1.40	1.22
19:L:1154:U:O2'	19:L:1155:C:H5'	1.07	1.21
26:j:64:ARG:NH2	24:i:50:MET:HB3	1.56	1.19
28:e:56:ALA:CB	28:e:69:LEU:HD23	1.73	1.19
20:v:711:MET:HE1	20:v:748:PHE:CB	1.72	1.19
19:L:1154:U:O2'	19:L:1155:C:C5'	1.90	1.18
1:A:1889:LEU:CD2	1:A:1991:ILE:HG12	1.73	1.18
19:L:4:A:H1'	20:v:529:HIS:CD2	1.77	1.17
16:B:9:A:H1'	16:B:10:A:OP1	1.42	1.17
28:e:56:ALA:HB3	28:e:69:LEU:HD23	1.21	1.17
25:m:19:LEU:HD22	25:m:91:THR:HG22	1.29	1.15
26:j:28:ILE:O	26:j:40:LEU:HB2	1.44	1.15
1:A:1165:LEU:HG	1:A:1166:ASP:H	0.99	1.14
26:j:64:ARG:HH22	24:i:50:MET:HB3	1.10	1.14
29:k:49:ILE:HG22	29:k:81:VAL:HA	1.26	1.14
31:r:99:ARG:HG2	31:o:98:LEU:HD11	1.18	1.13
1:A:1165:LEU:HD11	1:A:1166:ASP:OD1	1.46	1.13
5:P:105:LEU:HG	5:P:112:ILE:HG13	1.13	1.13
5:P:105:LEU:HD12	6:Q:17:LEU:HD21	1.20	1.13
26:j:57:LEU:HB3	24:i:91:THR:HG21	1.22	1.13
20:v:612:ILE:HG13	20:v:613:PRO:HD3	1.16	1.12
29:k:105:LYS:HA	29:k:108:ARG:HH21	1.07	1.12
1:A:1992:TYR:HD2	1:A:1996:LEU:HG	1.11	1.12
26:j:17:LEU:HD12	26:j:19:ILE:HD11	1.24	1.11
2:C:234:LEU:HD21	2:C:439:ILE:CG2	1.80	1.11
19:L:113:U:O4	27:w:48:TYR:HA	1.46	1.11
19:L:1137:U:H2'	19:L:1138:G:H1'	1.26	1.11
25:m:17:ILE:HG23	25:m:92:ILE:CG2	1.79	1.10
29:k:86:ILE:HD11	30:l:11:LEU:HD12	1.33	1.10
28:e:56:ALA:HB2	28:e:72:VAL:HG23	1.17	1.10
16:B:10:A:N7	16:B:11:A:C6	2.20	1.10
29:k:31:ILE:CD1	29:k:49:ILE:CD1	2.27	1.10
30:l:21:LEU:HD23	30:l:72:ILE:HG12	1.32	1.09
19:L:16:U:H5'	19:L:18:U:C5	1.86	1.09
20:v:385:PHE:HA	20:v:388:LEU:HD12	1.20	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:s:54:PRO:HB2	29:s:57:GLN:HG2	1.31	1.09
24:i:30:TRP:CD1	24:i:38:ARG:HD3	1.86	1.09
16:B:10:A:C8	16:B:11:A:C4	2.39	1.09
1:A:1165:LEU:CG	1:A:1166:ASP:H	1.66	1.08
28:g:35:ASN:CB	28:g:61:PHE:CZ	2.37	1.08
29:k:49:ILE:CG2	29:k:81:VAL:HA	1.84	1.07
30:l:47:VAL:HG23	30:l:59:MET:HG3	1.31	1.07
25:m:84:TYR:CE2	29:k:6:VAL:HG11	1.89	1.07
16:B:-1:A:H3'	16:B:0:G:H5'	1.29	1.06
20:v:711:MET:CE	20:v:748:PHE:CB	2.34	1.06
18:E:55:G:H5'	18:E:55:G:H8	1.20	1.06
20:v:386:GLU:HA	20:v:389:ILE:HD12	1.38	1.06
1:A:1165:LEU:HD11	1:A:1166:ASP:CG	1.80	1.06
19:L:1137:U:H2'	19:L:1138:G:O4'	1.55	1.06
26:j:17:LEU:HD13	26:j:19:ILE:HD11	1.32	1.06
1:A:1889:LEU:HD21	1:A:1991:ILE:HG12	1.10	1.05
25:m:17:ILE:HG23	25:m:92:ILE:HG22	1.36	1.05
1:A:697:LYS:HD2	32:A:3000:IHP:O25	1.55	1.05
17:D:175:G:O6	24:i:35:ILE:HD11	1.57	1.04
24:i:30:TRP:CD1	24:i:38:ARG:CD	2.40	1.04
12:d:267:TYR:CG	12:d:284:LEU:HD23	1.92	1.04
5:P:106:LEU:HG	5:P:107:ASN:H	1.17	1.04
29:k:105:LYS:HA	29:k:108:ARG:NH2	1.73	1.03
30:y:21:LEU:CD1	30:y:44:LEU:HD11	1.87	1.03
29:k:31:ILE:CG1	29:k:49:ILE:CD1	2.36	1.03
26:j:27:GLY:HA3	26:j:40:LEU:HD12	1.36	1.03
17:D:99:U:H5''	17:D:99:U:H6	1.22	1.02
25:m:17:ILE:CG2	25:m:92:ILE:CG2	2.36	1.02
19:L:113:U:C5	27:w:48:TYR:CD1	2.46	1.02
28:g:40:THR:O	28:g:41:ARG:HG2	1.60	1.02
26:j:17:LEU:CD1	26:j:19:ILE:CD1	2.37	1.02
28:g:35:ASN:HA	28:g:61:PHE:CE2	1.93	1.02
4:O:218:ARG:HB3	4:O:256:ARG:HD3	1.39	1.01
16:B:10:A:C8	16:B:11:A:C6	2.46	1.01
2:C:234:LEU:CD2	2:C:439:ILE:HG23	1.89	1.01
20:v:541:SER:O	20:v:544:ILE:HG22	1.61	1.00
19:L:1082:A:H2'	19:L:1083:A:H8	1.26	1.00
20:v:386:GLU:HA	20:v:389:ILE:CD1	1.92	1.00
7:R:151:LEU:HD23	19:L:78:G:H5''	1.44	0.99
29:k:48:CYS:SG	29:k:82:LEU:CD1	2.50	0.99
24:u:35:ILE:CD1	27:w:79:LEU:CD1	2.40	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1575:TRP:CZ3	1:A:1825:ILE:HG12	1.96	0.99
19:L:1137:U:O2'	19:L:1138:G:H4'	1.63	0.98
22:b:50:LEU:C	22:b:55:HIS:CB	2.36	0.97
24:i:28:THR:HG22	24:i:40:LYS:HD2	1.45	0.97
17:D:128:A:H2'	17:D:129:G:H5''	1.45	0.97
16:B:-11:U:O2'	16:B:-10:G:O5'	1.82	0.97
28:e:56:ALA:HB2	28:e:72:VAL:HG21	1.47	0.97
25:m:96:ILE:HD11	28:g:89:ARG:HH22	1.29	0.97
22:b:110:ARG:HA	22:b:134:VAL:CB	1.95	0.97
1:A:402:TRP:O	1:A:403:TYR:O	1.83	0.96
29:s:59:ASP:HA	29:s:62:ARG:HH21	1.31	0.96
29:k:49:ILE:HG22	29:k:81:VAL:CA	1.94	0.96
19:L:1082:A:H2'	19:L:1083:A:C8	2.00	0.96
5:P:105:LEU:HG	5:P:112:ILE:CG1	1.95	0.96
22:b:110:ARG:CA	22:b:134:VAL:CB	2.44	0.95
1:A:1889:LEU:HD21	1:A:1991:ILE:CG1	1.96	0.95
29:k:31:ILE:HG13	29:k:49:ILE:CD1	1.94	0.95
19:L:1085:G:C2	19:L:1086:U:C5	2.54	0.95
28:e:56:ALA:CB	28:e:72:VAL:CG2	2.42	0.95
30:l:14:ALA:O	30:l:17:HIS:HB2	1.67	0.95
28:e:56:ALA:CB	28:e:72:VAL:HG23	1.96	0.95
18:E:55:G:H5'	18:E:55:G:C8	2.02	0.95
5:P:105:LEU:CG	5:P:112:ILE:HG13	1.96	0.94
19:L:121:C:H1'	28:e:49:ARG:HG2	1.48	0.94
1:A:1992:TYR:CD2	1:A:1996:LEU:HG	2.02	0.93
25:m:47:LEU:HD11	25:m:61:ALA:CB	1.98	0.93
5:P:150:ASP:OD1	5:P:151:GLY:N	2.02	0.93
24:u:35:ILE:HD13	27:w:79:LEU:CD1	1.98	0.93
19:L:53:G:N3	19:L:54:U:H5'	1.83	0.93
28:g:50:ASN:HD22	28:g:52:HIS:HE1	0.99	0.92
31:r:99:ARG:HG2	31:o:98:LEU:CD1	1.98	0.92
1:A:1165:LEU:CD1	1:A:1166:ASP:OD1	2.17	0.92
29:k:13:ALA:HB2	29:k:37:PHE:HZ	1.31	0.92
29:s:48:CYS:SG	29:s:82:LEU:O	2.27	0.92
28:g:35:ASN:HB2	28:g:61:PHE:HZ	1.25	0.92
19:L:151:A:H61	19:L:1086:U:H3	1.11	0.92
29:k:44:VAL:HG22	29:k:86:ILE:HG22	1.52	0.92
1:A:1165:LEU:HG	1:A:1166:ASP:N	1.78	0.91
1:A:1889:LEU:HD11	1:A:1991:ILE:HG23	1.53	0.91
28:g:50:ASN:HD22	28:g:52:HIS:CE1	1.87	0.91
25:m:47:LEU:HD11	25:m:61:ALA:HB1	1.53	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:l:59:MET:SD	30:l:62:ILE:HD12	2.09	0.91
17:D:83:C:O2'	17:D:84:A:O5'	1.85	0.91
28:g:40:THR:C	28:g:41:ARG:HG2	1.94	0.91
29:k:35:MET:HB3	30:l:84:PHE:HE2	1.34	0.91
29:k:31:ILE:HG13	29:k:49:ILE:HD12	1.51	0.91
27:w:32:LYS:HG3	27:w:33:PHE:CD1	2.06	0.91
2:C:234:LEU:HD21	2:C:439:ILE:HG23	0.93	0.90
17:D:168:U:H2'	24:i:49:PHE:CD1	2.06	0.90
17:D:173:U:H1'	28:g:99:ASP:HB3	1.48	0.90
30:y:21:LEU:HD11	30:y:44:LEU:HD11	1.51	0.90
19:L:113:U:C4	27:w:48:TYR:HA	2.05	0.90
26:j:17:LEU:HD13	26:j:19:ILE:CD1	2.01	0.90
29:k:86:ILE:HD11	30:l:11:LEU:CD1	2.02	0.90
28:g:76:TRP:CZ2	28:g:87:ARG:HD3	2.07	0.89
19:L:117:U:O2	25:z:35:GLN:HB3	1.71	0.89
20:v:385:PHE:CA	20:v:388:LEU:HD12	2.03	0.89
30:l:21:LEU:CD2	30:l:72:ILE:HG12	2.02	0.89
1:A:266:LEU:HG	1:A:267:PRO:HD2	1.52	0.89
19:L:118:U:H3	28:e:66:ASN:HD22	1.17	0.89
29:k:40:HIS:O	29:k:41:MET:HB2	1.70	0.89
25:z:47:LEU:HD21	25:z:61:ALA:CB	2.02	0.88
30:l:17:HIS:CG	30:l:75:PRO:HG2	2.07	0.88
19:L:152:C:H42	19:L:1085:G:H1	1.20	0.88
30:l:65:ARG:HH11	30:l:65:ARG:HG3	1.36	0.88
1:A:1993:ASP:OD2	1:A:2040:TRP:CD1	2.27	0.88
28:g:76:TRP:CH2	28:g:87:ARG:HD3	2.09	0.88
30:l:75:PRO:HB2	30:l:78:LEU:HD13	1.56	0.88
30:y:33:LEU:HA	30:y:44:LEU:HD23	1.54	0.88
24:u:35:ILE:HD11	27:w:79:LEU:CD1	2.03	0.87
26:j:27:GLY:CA	26:j:40:LEU:HD12	2.05	0.87
26:j:61:THR:HG22	24:i:91:THR:HG23	1.55	0.87
5:P:106:LEU:CG	5:P:107:ASN:H	1.86	0.87
4:O:436:SER:C	4:O:437:GLU:HG2	1.99	0.87
19:L:151:A:N6	19:L:1086:U:H3	1.72	0.87
19:L:1130:U:H2'	19:L:1131:U:O4'	1.73	0.87
28:g:50:ASN:HB3	28:g:52:HIS:ND1	1.90	0.87
28:g:45:ILE:HD12	28:g:55:ILE:HG12	1.57	0.87
12:d:60:ARG:HH12	18:E:84:C:H5'	1.38	0.87
17:D:6:G:H4'	29:k:11:ARG:NH2	1.89	0.87
30:l:82:PRO:O	30:l:85:LYS:HD2	1.73	0.87
20:v:386:GLU:CA	20:v:389:ILE:HD12	2.04	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1987:VAL:HG11	1:A:1989:PHE:HE2	1.39	0.86
1:A:1987:VAL:CG1	1:A:1989:PHE:HE2	1.89	0.86
19:L:1146:G:H2'	19:L:1147:A:C8	2.11	0.86
13:I:121:LYS:NZ	20:v:529:HIS:HD2	1.72	0.86
19:L:1154:U:HO2'	19:L:1155:C:H5'	1.37	0.86
19:L:53:G:H1'	19:L:54:U:C5'	2.05	0.86
29:k:29:VAL:O	29:k:50:GLU:HA	1.76	0.86
1:A:1165:LEU:CD1	1:A:1166:ASP:CG	2.49	0.85
16:B:-1:A:H3'	16:B:0:G:C5'	2.05	0.85
1:A:1961:LEU:HD21	1:A:2084:LEU:HD13	1.56	0.85
25:m:52:LEU:HD21	28:g:79:LYS:C	2.00	0.85
30:y:21:LEU:HD12	30:y:44:LEU:HD11	1.56	0.85
19:L:1154:U:H2'	19:L:1155:C:C6	2.11	0.85
28:g:50:ASN:ND2	28:g:52:HIS:HE1	1.75	0.85
16:B:10:A:N7	16:B:11:A:C5	2.42	0.84
30:l:49:ALA:HB2	30:l:59:MET:HE3	1.59	0.84
19:L:1137:U:C2'	19:L:1138:G:H1'	2.05	0.84
1:A:1990:ASN:ND2	1:A:1993:ASP:H	1.73	0.84
17:D:99:U:H5''	17:D:99:U:C6	2.12	0.84
1:A:1987:VAL:CG1	1:A:1989:PHE:CE2	2.61	0.84
5:P:105:LEU:CD1	6:Q:17:LEU:HD21	2.04	0.84
25:m:39:ILE:HD11	25:m:84:TYR:CE1	2.13	0.84
28:g:43:PRO:O	28:g:107:THR:CB	2.26	0.84
1:A:697:LYS:HG2	32:A:3000:IHP:O46	1.78	0.83
20:v:385:PHE:HA	20:v:388:LEU:CD1	2.05	0.83
29:s:54:PRO:CB	29:s:57:GLN:HG2	2.08	0.83
22:b:14:TYR:O	29:s:102:LEU:CD1	2.26	0.83
29:k:35:MET:HB3	30:l:84:PHE:CE2	2.13	0.83
5:P:149:MET:O	5:P:150:ASP:HB3	1.78	0.82
24:i:30:TRP:NE1	24:i:38:ARG:CD	2.39	0.82
6:Q:298:SER:HB3	19:L:75:A:N6	1.93	0.82
19:L:53:G:H1'	19:L:54:U:O5'	1.80	0.82
26:x:19:ILE:O	26:x:23:ARG:HB2	1.78	0.82
25:m:52:LEU:HD21	28:g:80:LYS:N	1.94	0.82
30:l:47:VAL:HG23	30:l:59:MET:CG	2.10	0.82
1:A:185:GLN:HG3	1:A:263:PRO:HG3	1.60	0.81
26:j:6:GLU:HG2	30:l:37:GLU:OE2	1.80	0.81
26:j:64:ARG:HG3	24:i:50:MET:SD	2.20	0.81
29:k:42:ASN:HB3	29:k:89:GLY:H	1.45	0.81
29:k:49:ILE:CG2	29:k:81:VAL:CA	2.57	0.81
24:u:35:ILE:CD1	27:w:79:LEU:HD12	2.09	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:l:15:GLN:C	30:l:15:GLN:HE21	1.89	0.81
25:m:3:LEU:CD2	28:g:95:PHE:HE1	1.94	0.81
29:k:13:ALA:HA	29:k:37:PHE:CE2	2.16	0.81
29:k:42:ASN:HB3	29:k:89:GLY:N	1.95	0.81
1:A:1889:LEU:CG	1:A:1991:ILE:HG12	2.10	0.81
19:L:1085:G:N2	19:L:1086:U:C4	2.49	0.81
20:v:612:ILE:CG1	20:v:613:PRO:HD3	2.07	0.81
29:k:84:LEU:HD23	30:l:75:PRO:O	1.81	0.81
25:z:47:LEU:HD21	25:z:61:ALA:HB3	1.62	0.81
12:d:267:TYR:CD2	12:d:284:LEU:HD23	2.15	0.81
25:m:4:VAL:HG22	25:m:36:MET:HE2	1.63	0.81
26:j:27:GLY:HA3	26:j:40:LEU:CD1	2.09	0.81
1:A:1271:PRO:O	1:A:1275:MET:HG2	1.80	0.80
19:L:1085:G:C2	19:L:1086:U:C4	2.68	0.80
25:m:96:ILE:CD1	28:g:89:ARG:HH22	1.92	0.80
28:g:35:ASN:HB2	28:g:61:PHE:CE2	2.15	0.80
16:B:9:A:C1'	16:B:10:A:OP1	2.27	0.80
19:L:1137:U:C2'	19:L:1138:G:C4'	2.60	0.80
30:l:17:HIS:ND1	30:l:75:PRO:HG2	1.96	0.80
26:j:17:LEU:HD12	26:j:19:ILE:CD1	2.07	0.80
16:B:10:A:H8	16:B:11:A:C4	1.96	0.80
19:L:4:A:C1'	20:v:529:HIS:CD2	2.64	0.80
19:L:42:U:O2'	19:L:43:G:OP1	2.00	0.80
20:v:662:CYS:SG	20:v:665:ILE:HD11	2.22	0.79
29:k:86:ILE:CD1	30:l:11:LEU:HD12	2.11	0.79
29:k:105:LYS:CA	29:k:108:ARG:HH21	1.91	0.79
25:z:72:GLN:HE22	25:z:79:ILE:HD11	1.46	0.79
1:A:1275:MET:O	1:A:1276:GLU:HG2	1.80	0.79
19:L:3:G:O2'	19:L:4:A:N7	2.15	0.79
27:h:71:ILE:HG23	28:g:103:VAL:HG23	1.64	0.79
28:g:35:ASN:O	28:g:39:VAL:HG23	1.83	0.79
19:L:1085:G:N2	19:L:1086:U:C5	2.51	0.79
19:L:1137:U:C2'	19:L:1138:G:C1'	2.53	0.79
25:m:72:GLN:HE22	25:m:79:ILE:HD11	1.47	0.79
5:P:106:LEU:HG	5:P:107:ASN:N	1.97	0.79
17:D:167:A:H2'	27:h:48:TYR:CE2	2.18	0.79
22:b:14:TYR:O	29:s:102:LEU:HD12	1.84	0.78
17:D:6:G:H4'	29:k:11:ARG:HH22	1.46	0.78
25:m:17:ILE:CG2	25:m:92:ILE:HG22	2.07	0.78
1:A:1961:LEU:HD21	1:A:2084:LEU:CD1	2.12	0.78
30:l:11:LEU:HD11	30:l:72:ILE:CD1	2.13	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:i:40:LYS:HG3	24:i:60:ILE:CD1	2.13	0.78
4:O:111:ILE:HG21	12:d:197:PRO:HD3	1.65	0.78
1:A:1165:LEU:CG	1:A:1166:ASP:N	2.35	0.78
19:L:113:U:C5	27:w:48:TYR:CE1	2.71	0.78
19:L:1136:U:O3'	19:L:1137:U:H4'	1.82	0.78
19:L:113:U:O4	27:w:48:TYR:CA	2.31	0.78
30:y:21:LEU:CD2	30:y:72:ILE:HG12	2.14	0.78
4:O:434:LYS:HB2	4:O:434:LYS:NZ	1.98	0.78
19:L:16:U:H5'	19:L:18:U:C6	2.18	0.78
25:m:19:LEU:HD22	25:m:91:THR:CG2	2.10	0.78
30:l:21:LEU:HD23	30:l:72:ILE:CG1	2.13	0.78
29:s:59:ASP:HA	29:s:62:ARG:NH2	1.99	0.78
28:e:56:ALA:HB1	28:e:69:LEU:HD23	1.65	0.77
30:y:21:LEU:HD12	30:y:44:LEU:CD1	2.12	0.77
12:d:329:LEU:HD23	20:v:642:GLU:HG3	1.65	0.77
19:L:1137:U:H2'	19:L:1138:G:C4'	2.13	0.77
28:e:68:VAL:C	28:e:69:LEU:HD12	2.09	0.77
29:k:13:ALA:CB	29:k:37:PHE:HZ	1.97	0.77
16:B:10:A:H8	16:B:11:A:C5	1.99	0.77
25:m:93:ARG:HH11	25:m:93:ARG:HG3	1.50	0.77
25:m:39:ILE:HD11	25:m:84:TYR:HE1	1.49	0.77
1:A:1574:PHE:HD1	1:A:1574:PHE:H	1.33	0.77
16:B:69:A:H3'	16:B:70:A:H4'	1.67	0.77
19:L:1101:C:H5'	19:L:1102:C:OP2	1.84	0.77
29:k:35:MET:CB	30:l:84:PHE:HE2	1.97	0.77
28:e:59:LYS:CG	28:e:70:GLU:HG2	2.13	0.77
24:i:32:PHE:HD1	24:i:86:ASN:O	1.68	0.77
29:s:57:GLN:HB3	29:s:75:ILE:HG23	1.67	0.76
2:C:318:LEU:HD13	2:C:425:LEU:CD1	2.15	0.76
17:D:28:G:O2'	17:D:29:G:P	2.42	0.76
29:s:54:PRO:HB2	29:s:57:GLN:CG	2.15	0.76
30:l:33:LEU:HD21	30:l:35:GLU:O	1.85	0.76
19:L:1137:U:C2'	19:L:1138:G:H4'	2.15	0.76
19:L:125:C:H5''	28:e:80:LYS:HA	1.67	0.76
2:C:205:SER:O	30:l:83:LEU:HD23	1.86	0.76
20:v:612:ILE:HG13	20:v:613:PRO:HD2	1.67	0.76
20:v:617:PRO:O	20:v:618:GLU:HB2	1.84	0.76
7:R:151:LEU:HD23	19:L:78:G:C5'	2.14	0.76
20:v:612:ILE:CG1	20:v:613:PRO:CD	2.55	0.76
25:m:86:ASN:HD21	29:k:41:MET:CE	1.99	0.76
30:y:35:GLU:HB2	30:y:43:GLN:HG2	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:PRO:O	1:A:131:LYS:O	2.03	0.75
4:O:373:LEU:HD12	4:O:373:LEU:O	1.86	0.75
24:u:35:ILE:HD13	27:w:79:LEU:HD12	1.64	0.75
26:j:61:THR:CG2	24:i:91:THR:HG23	2.16	0.75
24:i:30:TRP:CG	24:i:38:ARG:NE	2.54	0.75
19:L:1114:G:H2'	19:L:1115:G:O4'	1.87	0.75
1:A:1992:TYR:HD2	1:A:1996:LEU:CG	1.96	0.75
1:A:2021:SER:HA	1:A:2024:MET:SD	2.27	0.75
2:C:317:LYS:HB2	33:C:1500:GTP:C5	2.22	0.75
15:H:26:TYR:O	15:H:27:LYS:HG2	1.85	0.75
30:l:17:HIS:ND1	30:l:75:PRO:CG	2.50	0.75
4:O:434:LYS:HB2	4:O:434:LYS:HZ3	1.52	0.75
24:u:35:ILE:HD13	27:w:79:LEU:HD11	1.67	0.75
25:m:41:THR:O	25:m:83:GLN:HG2	1.86	0.75
30:y:31:GLY:HA3	30:y:47:VAL:HG12	1.68	0.74
5:P:106:LEU:CG	5:P:107:ASN:N	2.48	0.74
26:j:14:LYS:HG2	26:j:74:LEU:HD11	1.68	0.74
29:k:13:ALA:HB2	29:k:37:PHE:CZ	2.21	0.74
29:k:49:ILE:HD12	29:k:49:ILE:H	1.52	0.74
1:A:1627:LEU:HD23	1:A:1630:THR:OG1	1.88	0.74
2:C:318:LEU:O	2:C:422:LYS:HG3	1.87	0.74
29:k:15:LEU:HB2	29:k:18:TYR:CD2	2.22	0.74
29:s:28:ARG:HD3	29:s:52:ARG:HE	1.51	0.74
27:w:32:LYS:HG3	27:w:33:PHE:HD1	1.53	0.74
17:D:128:A:C2'	17:D:129:G:H5''	2.16	0.74
25:z:23:THR:HG22	25:z:47:LEU:HD11	1.68	0.74
16:B:10:A:C5	16:B:11:A:C6	2.76	0.74
30:l:24:THR:HA	30:l:70:LYS:NZ	2.03	0.74
17:D:167:A:H2'	27:h:48:TYR:HE2	1.51	0.74
26:j:29:LEU:HD23	26:j:29:LEU:C	2.13	0.74
26:j:57:LEU:HB3	24:i:91:THR:CG2	2.11	0.74
19:L:117:U:C2	25:z:35:GLN:HB3	2.22	0.73
19:L:1085:G:N3	19:L:1086:U:C5	2.55	0.73
28:e:59:LYS:HG2	28:e:70:GLU:CG	2.18	0.73
19:L:1137:U:C2'	19:L:1138:G:O4'	2.35	0.73
1:A:1080:ASP:O	11:c:82:ASN:ND2	2.21	0.73
1:A:1165:LEU:CD1	1:A:1166:ASP:N	2.51	0.73
1:A:1165:LEU:HD12	1:A:1166:ASP:N	2.04	0.73
19:L:15:C:H1'	19:L:16:U:C5	2.23	0.73
19:L:1129:U:H2'	19:L:1130:U:H5'	1.71	0.73
26:j:23:ARG:H	26:j:23:ARG:HD3	1.52	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:s:52:ARG:O	29:s:77:VAL:HG13	1.87	0.73
19:L:1105:C:H1'	19:L:1106:G:C1'	2.19	0.73
25:z:45:LEU:HD11	25:z:65:LEU:HD13	1.68	0.73
1:A:2021:SER:HA	1:A:2024:MET:HB2	1.70	0.73
28:g:78:GLU:HG2	28:g:85:ILE:CG2	2.19	0.73
5:P:162:GLU:OE1	5:P:162:GLU:HA	1.87	0.73
16:B:-11:U:HO2'	16:B:-10:G:P	2.11	0.73
2:C:132:ARG:NH2	30:l:15:GLN:O	2.22	0.73
14:n:292:HIS:H	14:n:292:HIS:CD2	2.05	0.73
28:e:56:ALA:HB2	28:e:72:VAL:CB	2.17	0.73
1:A:1990:ASN:HD21	1:A:1993:ASP:H	1.35	0.73
30:l:24:THR:HA	30:l:70:LYS:HZ2	1.54	0.73
25:z:47:LEU:HD21	25:z:61:ALA:HB1	1.70	0.73
13:I:121:LYS:HZ3	20:v:529:HIS:HD2	1.35	0.73
17:D:173:U:C2	28:g:97:ARG:CZ	2.72	0.73
1:A:130:PRO:O	1:A:131:LYS:C	2.32	0.72
25:m:82:LEU:HD11	25:m:85:ILE:HB	1.70	0.72
1:A:1626:GLN:HB2	1:A:1633:PHE:CE1	2.25	0.72
1:A:1961:LEU:HD23	1:A:2084:LEU:HB2	1.69	0.72
1:A:1991:ILE:HD12	1:A:1992:TYR:CE1	2.25	0.72
5:P:106:LEU:C	5:P:106:LEU:HD12	2.14	0.72
25:m:45:LEU:HD11	25:m:65:LEU:HD13	1.69	0.72
26:j:18:ASN:C	26:j:19:ILE:HD13	2.14	0.72
29:k:109:LEU:C	29:k:109:LEU:HD12	2.15	0.72
28:e:59:LYS:HG2	28:e:70:GLU:HG2	1.69	0.72
12:d:60:ARG:NH1	18:E:84:C:H5'	2.04	0.72
29:k:15:LEU:C	29:k:15:LEU:HD12	2.14	0.72
4:O:206:VAL:HB	4:O:220:TYR:HB2	1.72	0.72
27:w:34:ASN:HB3	27:w:36:THR:HG23	1.72	0.72
1:A:697:LYS:CD	32:A:3000:IHP:O25	2.33	0.72
28:g:50:ASN:HB3	28:g:52:HIS:HD1	1.53	0.72
19:L:4:A:H1'	20:v:529:HIS:NE2	2.05	0.72
29:k:109:LEU:HD12	29:k:109:LEU:O	1.90	0.72
24:i:30:TRP:CD2	24:i:38:ARG:NE	2.58	0.72
20:v:608:TYR:O	20:v:612:ILE:HG23	1.90	0.71
27:h:34:ASN:HB3	27:h:36:THR:HG23	1.72	0.71
28:e:48:LEU:HD22	28:e:52:HIS:NE2	2.05	0.71
1:A:771:PRO:O	4:O:309:ARG:NH2	2.23	0.71
25:m:19:LEU:CD2	25:m:91:THR:HG22	2.16	0.71
30:l:70:LYS:HZ2	30:l:70:LYS:HB2	1.55	0.71
27:w:32:LYS:HG3	27:w:33:PHE:CE1	2.25	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:v:388:LEU:HA	20:v:391:LEU:HD12	1.72	0.71
24:u:35:ILE:CD1	27:w:79:LEU:HD11	2.20	0.71
28:g:33:LEU:C	28:g:33:LEU:HD12	2.15	0.71
28:g:50:ASN:CB	28:g:52:HIS:CE1	2.73	0.71
24:i:30:TRP:CD2	24:i:38:ARG:CZ	2.73	0.71
25:m:47:LEU:HD11	25:m:61:ALA:HB3	1.73	0.71
16:B:8:U:H5''	16:B:9:A:OP1	1.91	0.71
17:D:166:U:O2	28:g:63:ARG:NH1	2.23	0.71
20:v:365:ASP:HA	20:v:399:VAL:HG22	1.72	0.71
30:y:21:LEU:HD23	30:y:72:ILE:HG12	1.73	0.71
1:A:1993:ASP:OD2	1:A:2040:TRP:CG	2.44	0.71
9:T:147:HIS:H	9:T:147:HIS:CD2	2.06	0.71
27:h:68:LEU:HD23	27:h:71:ILE:HD11	1.73	0.71
30:l:65:ARG:HG3	30:l:65:ARG:NH1	1.99	0.71
19:L:117:U:C5	25:z:88:ARG:NH1	2.59	0.70
25:m:3:LEU:HG	28:g:95:PHE:HE1	1.55	0.70
25:m:84:TYR:CD2	29:k:6:VAL:CG1	2.64	0.70
1:A:1889:LEU:CD2	1:A:1991:ILE:CG1	2.64	0.70
24:i:40:LYS:HG3	24:i:60:ILE:HD11	1.74	0.70
16:B:-1:A:C3'	16:B:0:G:H5'	2.16	0.70
16:B:10:A:H2'	16:B:11:A:C4	2.26	0.70
29:k:52:ARG:NH2	29:k:78:GLU:OE2	2.24	0.70
1:A:2032:ILE:HD11	1:A:2043:PHE:CD1	2.26	0.70
20:v:385:PHE:O	20:v:389:ILE:HD12	1.92	0.70
1:A:1992:TYR:HB3	1:A:1996:LEU:HB2	1.74	0.70
29:k:40:HIS:O	29:k:41:MET:CB	2.40	0.70
30:l:11:LEU:HD11	30:l:72:ILE:HD12	1.73	0.70
17:D:28:G:O2'	17:D:29:G:O5'	2.09	0.70
26:x:14:LYS:HG2	26:x:74:LEU:HD11	1.74	0.70
31:r:99:ARG:CG	31:o:98:LEU:HD11	2.12	0.70
12:d:284:LEU:O	12:d:284:LEU:HD13	1.92	0.70
19:L:53:G:H1'	19:L:54:U:P	2.32	0.70
28:g:105:LEU:C	28:g:105:LEU:HD12	2.16	0.70
29:k:31:ILE:HD11	29:k:49:ILE:HD11	0.73	0.70
1:A:185:GLN:HE21	1:A:263:PRO:HD3	1.55	0.69
32:A:3000:IHP:H1	32:A:3000:IHP:O43	1.91	0.69
12:d:284:LEU:HD13	12:d:284:LEU:C	2.17	0.69
20:v:388:LEU:HB3	20:v:392:TYR:OH	1.92	0.69
20:v:797:TYR:C	20:v:799:ASP:H	1.99	0.69
1:A:185:GLN:HG3	1:A:263:PRO:CG	2.22	0.69
19:L:1146:G:H3'	19:L:1147:A:H5''	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:b:54:THR:HA	22:b:77:HIS:CB	2.22	0.69
14:n:270:SER:O	14:n:291:HIS:CB	2.40	0.69
25:z:39:ILE:HD11	25:z:84:TYR:HE1	1.56	0.69
25:m:20:LYS:HG2	25:m:91:THR:O	1.92	0.69
27:w:68:LEU:HD23	27:w:71:ILE:HD11	1.73	0.69
5:P:160:PRO:C	5:P:162:GLU:H	2.01	0.69
1:A:264:ILE:HG13	1:A:647:PHE:CE1	2.26	0.69
9:T:144:GLN:HB3	9:T:149:GLY:HA2	1.75	0.69
14:n:292:HIS:HB3	14:n:318:ARG:HH12	1.58	0.69
16:B:9:A:H1'	16:B:10:A:P	2.33	0.69
22:b:14:TYR:C	29:s:102:LEU:HD12	2.17	0.69
25:m:3:LEU:CG	28:g:95:PHE:HE1	2.06	0.69
28:e:59:LYS:HD3	28:e:70:GLU:OE1	1.93	0.69
20:v:396:LEU:HD23	20:v:396:LEU:C	2.18	0.69
1:A:768:GLU:OE1	4:O:352:ILE:HG12	1.93	0.69
19:L:70:A:H61	19:L:82:C:H42	1.41	0.69
28:g:35:ASN:CA	28:g:61:PHE:CE2	2.72	0.69
29:k:82:LEU:HD13	29:k:85:THR:HG21	1.75	0.69
30:l:82:PRO:O	30:l:85:LYS:CD	2.41	0.68
24:i:29:ILE:HG22	24:i:90:ILE:HA	1.76	0.68
24:i:30:TRP:CD1	24:i:38:ARG:CG	2.76	0.68
2:C:116:THR:HG23	2:C:120:ARG:HH21	1.57	0.68
12:d:289:LYS:HG3	20:v:609:GLU:HG2	1.75	0.68
19:L:1118:U:H2'	19:L:1119:C:C6	2.28	0.68
20:v:530:ARG:CA	20:v:530:ARG:HH11	2.06	0.68
29:k:49:ILE:HG23	29:k:81:VAL:HA	1.75	0.68
29:s:50:GLU:OE2	29:s:80:ARG:NE	2.23	0.68
1:A:1574:PHE:CZ	1:A:1826:TYR:HB2	2.29	0.68
17:D:174:G:H3'	28:g:49:ARG:HH12	1.58	0.68
19:L:69:G:H1	19:L:83:U:H3	1.41	0.68
24:i:54:ILE:HG13	24:i:57:ALA:HB2	1.73	0.68
28:e:89:ARG:NH2	28:e:91:ILE:HD11	2.07	0.68
2:C:69:PRO:CG	2:C:76:VAL:HG21	2.23	0.68
17:D:176:A:H1'	27:h:33:PHE:HE1	1.59	0.68
26:j:20:ASN:HD22	26:j:21:GLY:N	1.90	0.68
30:y:20:SER:HB2	30:y:73:VAL:HB	1.75	0.68
4:O:218:ARG:HB3	4:O:256:ARG:CD	2.21	0.68
5:P:148:HIS:HB2	12:d:131:ARG:HG3	1.76	0.68
17:D:128:A:H3'	17:D:128:A:N3	2.09	0.68
25:m:103:LEU:HD13	28:g:93:LYS:HD3	1.76	0.68
26:j:28:ILE:O	26:j:40:LEU:CB	2.33	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:69:PRO:HG2	2:C:76:VAL:HG21	1.76	0.68
2:C:70:TYR:O	2:C:72:LYS:N	2.27	0.68
25:m:88:ARG:HH11	25:m:90:ASN:ND2	1.92	0.68
16:B:61:U:H3	19:L:43:G:H1	1.42	0.68
19:L:1093:C:H6	19:L:1093:C:C5'	2.07	0.68
26:j:23:ARG:HD3	26:j:23:ARG:N	2.08	0.68
28:g:33:LEU:HD12	28:g:33:LEU:O	1.94	0.68
28:g:50:ASN:ND2	28:g:52:HIS:CE1	2.54	0.68
1:A:1165:LEU:CD1	1:A:1166:ASP:H	2.07	0.67
1:A:1961:LEU:CD2	1:A:2084:LEU:HB2	2.24	0.67
4:O:414:LEU:HB3	4:O:426:TRP:HB2	1.74	0.67
12:d:284:LEU:O	12:d:284:LEU:HD22	1.93	0.67
19:L:1117:G:O2'	19:L:1118:U:H5'	1.94	0.67
28:e:49:ARG:NH2	27:w:76:ASN:OD1	2.27	0.67
28:e:93:LYS:HB3	25:z:97:LEU:HD11	1.76	0.67
29:s:28:ARG:HG2	29:s:52:ARG:HG2	1.75	0.67
1:A:224:MET:HG3	1:A:264:ILE:HD11	1.76	0.67
18:E:55:G:H2'	18:E:56:A:H8	1.60	0.67
19:L:1125:U:H2'	19:L:1126:G:C8	2.30	0.67
24:u:29:ILE:HG22	24:u:90:ILE:HA	1.75	0.67
25:m:86:ASN:HD21	29:k:41:MET:HE1	1.59	0.67
26:j:57:LEU:CB	24:i:91:THR:HG21	2.14	0.67
1:A:1262:MET:O	1:A:1263:CYS:HB2	1.95	0.67
12:d:289:LYS:HE2	20:v:643:HIS:HE1	1.58	0.67
26:j:27:GLY:CA	26:j:40:LEU:CD1	2.69	0.67
28:e:56:ALA:HB3	28:e:69:LEU:CD2	2.14	0.67
30:l:70:LYS:NZ	30:l:70:LYS:HB2	2.07	0.67
1:A:267:PRO:O	1:A:268:LEU:HB2	1.93	0.67
19:L:114:U:O4'	26:x:64:ARG:NH1	2.26	0.67
19:L:1119:C:O5'	19:L:1119:C:H6	1.78	0.67
29:k:50:GLU:HG3	29:k:50:GLU:O	1.94	0.67
29:k:52:ARG:HG2	29:k:52:ARG:HH11	1.60	0.67
16:B:2:U:O2'	16:B:3:A:H4'	1.95	0.67
19:L:5:A:H2'	19:L:5:A:N3	2.09	0.67
29:k:15:LEU:HB2	29:k:18:TYR:CE2	2.29	0.67
30:l:20:SER:OG	30:l:73:VAL:CG2	2.43	0.67
19:L:1168:U:O5'	19:L:1168:U:H6	1.78	0.67
25:m:43:VAL:HG21	25:m:85:ILE:CG2	2.25	0.67
19:L:117:U:C5	25:z:88:ARG:CZ	2.78	0.67
19:L:125:C:OP1	25:z:55:LEU:HD11	1.94	0.67
20:v:395:TYR:O	20:v:398:ASP:HB3	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:m:103:LEU:CD1	28:g:93:LYS:HD3	2.25	0.67
30:l:47:VAL:CG2	30:l:59:MET:HG3	2.19	0.67
4:O:150:VAL:HG21	8:S:40:ARG:CD	2.24	0.66
16:B:-1:A:C3'	16:B:0:G:C5'	2.72	0.66
19:L:1146:G:H2'	19:L:1147:A:N9	2.10	0.66
25:m:21:ASN:HD21	29:k:93:LEU:HD11	1.60	0.66
28:e:78:GLU:CG	25:z:52:LEU:HD22	2.24	0.66
24:i:40:LYS:CG	24:i:60:ILE:CD1	2.73	0.66
1:A:1999:ILE:HD11	1:A:2045:ASP:OD2	1.95	0.66
7:R:234:ALA:HA	7:R:237:ARG:HE	1.59	0.66
14:n:402:ASP:OD2	14:n:404:LYS:HB2	1.96	0.66
25:m:17:ILE:CG2	25:m:92:ILE:HG23	2.26	0.66
29:s:82:LEU:HD13	29:s:85:THR:HG21	1.75	0.66
25:z:45:LEU:HD11	25:z:65:LEU:CD1	2.26	0.66
13:I:209:ARG:NH2	19:L:18:U:O2	2.28	0.66
17:D:168:U:C6	24:i:49:PHE:CE1	2.83	0.66
19:L:114:U:H1'	26:x:66:ASN:HB2	1.76	0.66
18:E:100:U:O2'	18:E:101:U:OP1	2.13	0.66
19:L:110:A:N6	25:z:34:PRO:HB2	2.10	0.66
19:L:125:C:H4'	28:e:81:GLY:N	2.09	0.66
19:L:1105:C:H1'	19:L:1106:G:H1'	1.78	0.66
20:v:711:MET:HE1	20:v:748:PHE:CA	2.26	0.66
30:l:21:LEU:HD22	30:l:69:ILE:HD13	1.77	0.66
5:P:105:LEU:HD11	6:Q:25:MET:HE1	1.77	0.66
6:Q:297:PHE:O	6:Q:298:SER:OG	2.12	0.66
16:B:8:U:H4'	16:B:9:A:OP1	1.96	0.66
17:D:99:U:H6	17:D:99:U:C5'	2.05	0.66
19:L:1093:C:H6	19:L:1093:C:O5'	1.78	0.66
22:b:32:ARG:HA	22:b:60:THR:O	1.96	0.66
23:t:111:VAL:O	23:t:114:LEU:N	2.29	0.66
29:s:44:VAL:HG22	29:s:86:ILE:HG22	1.77	0.66
1:A:2013:ARG:NH1	1:A:2082:ILE:O	2.29	0.66
20:v:746:ILE:CB	20:v:771:LEU:CB	2.73	0.66
30:l:43:GLN:C	30:l:44:LEU:HD23	2.20	0.66
9:T:123:ARG:NH2	18:E:26:A:O2'	2.27	0.66
12:d:267:TYR:CD2	12:d:284:LEU:CD2	2.78	0.66
19:L:125:C:OP1	25:z:55:LEU:CD1	2.42	0.66
28:g:40:THR:C	28:g:41:ARG:CG	2.69	0.66
28:e:56:ALA:CB	28:e:72:VAL:HB	2.25	0.66
1:A:1275:MET:O	1:A:1277:GLU:N	2.25	0.66
19:L:1129:U:H2'	19:L:1130:U:C5'	2.26	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:m:3:LEU:HG	28:g:95:PHE:CE1	2.31	0.66
1:A:404:ASN:ND2	2:C:927:MET:SD	2.69	0.65
29:s:93:LEU:HD11	25:z:21:ASN:HD21	1.60	0.65
1:A:1987:VAL:HG12	1:A:1989:PHE:CE2	2.31	0.65
9:T:121:ILE:C	9:T:123:ARG:H	2.05	0.65
19:L:54:U:H3'	19:L:54:U:OP2	1.96	0.65
25:m:88:ARG:HH11	25:m:90:ASN:HD22	1.42	0.65
29:k:86:ILE:CG2	30:l:10:LEU:HD23	2.26	0.65
1:A:518:VAL:HG12	1:A:685:HIS:HB3	1.78	0.65
4:O:446:LEU:HD21	12:d:237:ILE:HB	1.76	0.65
19:L:121:C:H1'	28:e:49:ARG:CG	2.24	0.65
25:m:43:VAL:HG21	25:m:85:ILE:HG21	1.78	0.65
28:e:89:ARG:CZ	28:e:91:ILE:HD11	2.26	0.65
24:i:58:VAL:HG12	24:i:76:PRO:HA	1.79	0.65
19:L:1150:U:OP1	29:s:55:LYS:HG3	1.95	0.65
28:g:38:MET:HA	28:g:58:VAL:O	1.96	0.65
29:k:48:CYS:HG	29:k:82:LEU:HD12	1.60	0.65
1:A:1771:THR:HA	1:A:1789:ASN:HD21	1.61	0.65
2:C:187:ARG:NH1	2:C:653:ASP:OD2	2.29	0.65
4:O:435:GLU:O	4:O:436:SER:HB3	1.96	0.65
19:L:1137:U:C4	21:a:67:LYS:O	2.50	0.65
28:g:50:ASN:HB3	28:g:52:HIS:CE1	2.32	0.65
25:z:51:ARG:O	25:z:54:LYS:N	2.29	0.65
17:D:176:A:N3	27:h:33:PHE:HD1	1.94	0.65
27:h:71:ILE:HG23	28:g:103:VAL:CG2	2.25	0.65
26:j:63:ILE:HG13	24:i:89:LEU:CD2	2.26	0.65
26:j:64:ARG:HH22	24:i:50:MET:CB	2.00	0.65
16:B:7:C:O2'	16:B:8:U:OP1	2.15	0.65
17:D:165:A:H4'	17:D:166:U:OP1	1.97	0.65
28:e:48:LEU:HD22	28:e:52:HIS:CE1	2.33	0.65
24:i:30:TRP:CE2	24:i:38:ARG:CZ	2.80	0.65
1:A:1626:GLN:NE2	1:A:1630:THR:O	2.30	0.64
9:T:156:THR:HB	14:n:56:LEU:HD11	1.79	0.64
19:L:121:C:C1'	28:e:49:ARG:HG2	2.24	0.64
22:b:110:ARG:CB	22:b:134:VAL:CB	2.74	0.64
25:m:3:LEU:CD2	28:g:95:PHE:CE1	2.79	0.64
29:k:30:TYR:CD1	29:k:50:GLU:HB3	2.32	0.64
28:e:93:LYS:HB3	25:z:97:LEU:CD1	2.27	0.64
29:s:88:ARG:NH1	30:y:40:MET:SD	2.70	0.64
30:y:34:VAL:HG12	30:y:35:GLU:HG2	1.77	0.64
19:L:114:U:O2	26:x:64:ARG:HG2	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:w:32:LYS:CG	27:w:33:PHE:CE1	2.80	0.64
1:A:772:GLU:O	1:A:773:SER:OG	2.10	0.64
16:B:10:A:N7	16:B:11:A:N6	2.46	0.64
25:m:45:LEU:CD1	25:m:65:LEU:HD13	2.27	0.64
26:j:11:MET:O	26:j:12:ASP:HB2	1.97	0.64
24:i:32:PHE:CD1	24:i:86:ASN:O	2.50	0.64
25:z:45:LEU:CD1	25:z:65:LEU:HD13	2.27	0.64
14:n:292:HIS:HB3	14:n:314:ASP:OD2	1.97	0.64
14:n:405:SER:C	14:n:407:LEU:H	2.05	0.64
19:L:30:A:O2'	19:L:31:A:OP2	2.15	0.64
25:m:15:VAL:HG23	25:m:96:ILE:O	1.96	0.64
25:m:45:LEU:HD11	25:m:65:LEU:CD1	2.27	0.64
29:k:60:LYS:HD2	29:k:75:ILE:HD13	1.78	0.64
29:k:84:LEU:HG	30:l:74:VAL:HG23	1.80	0.64
1:A:185:GLN:CG	1:A:263:PRO:HG3	2.28	0.64
19:L:1086:U:O5'	19:L:1086:U:H6	1.81	0.64
22:b:110:ARG:N	22:b:134:VAL:CB	2.60	0.64
2:C:234:LEU:C	2:C:234:LEU:HD12	2.23	0.64
28:e:93:LYS:HD2	25:z:97:LEU:CD1	2.27	0.64
26:j:69:ILE:HA	30:l:68:GLN:HG3	1.80	0.63
1:A:1647:GLN:O	1:A:1650:ARG:NH1	2.30	0.63
25:m:67:LEU:HB3	29:k:29:VAL:HG21	1.80	0.63
9:T:150:CYS:SG	9:T:151:ARG:N	2.71	0.63
18:E:53:A:H5'	18:E:54:U:OP2	1.99	0.63
29:k:28:ARG:HG2	29:k:52:ARG:HG2	1.81	0.63
1:A:1896:THR:HA	1:A:1899:TRP:HD1	1.63	0.63
26:j:63:ILE:HG13	24:i:89:LEU:HD23	1.79	0.63
17:D:167:A:H3'	27:h:48:TYR:OH	1.98	0.63
18:E:55:G:H8	18:E:55:G:C5'	2.06	0.63
19:L:141:A:C2	19:L:1168:U:O2	2.51	0.63
1:A:1035:LEU:HB2	1:A:1038:ILE:HD11	1.79	0.63
4:O:152:ASN:HD21	4:O:409:LYS:HB3	1.64	0.63
6:Q:13:CYS:HB2	6:Q:16:CYS:SG	2.39	0.63
9:T:147:HIS:NE2	18:E:29:U:O2'	2.31	0.63
19:L:53:G:C1'	19:L:54:U:P	2.87	0.63
25:m:83:GLN:NE2	25:m:84:TYR:HB2	2.13	0.63
1:A:316:THR:HG22	1:A:319:ARG:HH21	1.64	0.63
1:A:930:ASN:HB2	19:L:30:A:OP1	1.98	0.63
1:A:1808:ALA:HB1	1:A:1947:HIS:HE1	1.64	0.63
1:A:1991:ILE:HD12	1:A:1992:TYR:HE1	1.62	0.63
25:m:89:GLY:O	25:m:92:ILE:HG13	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:k:11:ARG:O	29:k:14:ASN:N	2.31	0.63
30:l:17:HIS:O	30:l:19:VAL:HG13	1.98	0.63
1:A:1628:ASP:OD1	1:A:1628:ASP:N	2.29	0.63
17:D:28:G:O2'	17:D:29:G:OP1	2.17	0.63
25:m:17:ILE:HG23	25:m:92:ILE:HG21	1.76	0.63
29:s:29:VAL:HG21	25:z:67:LEU:HB3	1.79	0.63
24:i:30:TRP:CD1	24:i:38:ARG:NE	2.66	0.63
4:O:193:ARG:HH22	4:O:237:ASP:H	1.46	0.62
1:A:266:LEU:HG	1:A:267:PRO:CD	2.26	0.62
1:A:1889:LEU:HB2	1:A:1989:PHE:O	1.98	0.62
10:Z:101:MET:O	10:Z:105:GLN:NE2	2.32	0.62
17:D:174:G:C3'	28:g:49:ARG:HH12	2.12	0.62
29:k:13:ALA:HA	29:k:37:PHE:HE2	1.64	0.62
26:x:27:GLY:HA3	26:x:40:LEU:HD13	1.80	0.62
24:u:58:VAL:HG12	24:u:76:PRO:HA	1.79	0.62
2:C:145:GLY:HA2	33:C:1500:GTP:O1A	1.99	0.62
2:C:205:SER:HB2	30:l:9:LYS:HD3	1.81	0.62
6:Q:304:THR:HG22	7:R:153:PRO:HG2	1.81	0.62
26:j:63:ILE:HG21	26:j:68:ILE:HD11	1.80	0.62
29:k:105:LYS:HA	29:k:108:ARG:CZ	2.30	0.62
6:Q:297:PHE:CG	6:Q:298:SER:N	2.68	0.62
17:D:124:C:O2'	17:D:125:C:H5'	1.99	0.62
19:L:1090:A:O2'	19:L:1091:G:H5'	2.00	0.62
29:s:54:PRO:HG2	29:s:76:LYS:O	1.98	0.62
7:R:150:HIS:O	7:R:151:LEU:HB2	1.98	0.62
25:m:86:ASN:ND2	29:k:41:MET:HE1	2.15	0.62
25:m:93:ARG:HG3	25:m:93:ARG:NH1	2.14	0.62
28:g:76:TRP:CZ2	28:g:87:ARG:CD	2.79	0.62
30:l:77:LEU:HD23	30:l:77:LEU:H	1.64	0.62
1:A:1627:LEU:HD22	1:A:1632:ILE:HB	1.81	0.62
1:A:1990:ASN:HD21	1:A:1993:ASP:N	1.98	0.62
2:C:493:LEU:HD21	2:C:539:VAL:HG21	1.82	0.62
2:C:143:HIS:N	33:C:1500:GTP:O3G	2.33	0.62
5:P:134:VAL:HG22	6:Q:111:ARG:HD3	1.80	0.62
20:v:612:ILE:N	20:v:613:PRO:HD2	2.15	0.62
26:j:64:ARG:NH2	24:i:50:MET:CB	2.47	0.62
26:j:19:ILE:CG2	24:i:88:THR:HG23	2.29	0.62
28:g:38:MET:SD	28:g:60:ALA:HA	2.38	0.62
29:s:42:ASN:HB3	29:s:89:GLY:H	1.65	0.62
19:L:1154:U:H2'	19:L:1155:C:H6	1.63	0.62
20:v:385:PHE:O	20:v:388:LEU:HB2	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:133:ILE:HG22	2:C:209:MET:HB3	1.80	0.61
2:C:180:ASN:ND2	2:C:547:GLY:O	2.33	0.61
2:C:270:LEU:HB2	2:C:315:SER:HB2	1.82	0.61
2:C:498:THR:HG22	2:C:538:GLU:HG2	1.82	0.61
20:v:322:CYS:O	20:v:326:LEU:N	2.28	0.61
20:v:580:LEU:HB3	20:v:582:LEU:HD23	1.82	0.61
28:g:78:GLU:CD	28:g:85:ILE:HG23	2.25	0.61
1:A:272:ASP:O	1:A:310:ASN:ND2	2.33	0.61
16:B:10:A:N9	16:B:11:A:C2	2.68	0.61
19:L:4:A:H1'	20:v:529:HIS:CG	2.34	0.61
1:A:268:LEU:HD11	1:A:281:TYR:HE2	1.64	0.61
4:O:105:GLU:HG2	4:O:106:VAL:HG23	1.82	0.61
17:D:173:U:O2	28:g:97:ARG:NE	2.32	0.61
19:L:31:A:H1'	19:L:32:G:OP1	2.00	0.61
19:L:115:U:C2	30:y:39:SER:OG	2.53	0.61
28:e:56:ALA:CB	28:e:72:VAL:CB	2.77	0.61
24:i:30:TRP:HA	24:i:38:ARG:HG3	1.82	0.61
22:b:65:ILE:HA	22:b:85:ASN:O	2.01	0.61
30:l:41:ASN:HB3	30:l:66:GLY:H	1.65	0.61
1:A:1011:ASN:ND2	1:A:1143:GLU:O	2.33	0.61
1:A:1286:TRP:NE1	1:A:1348:GLU:OE1	2.33	0.61
16:B:9:A:C1'	16:B:10:A:P	2.88	0.61
19:L:1083:A:H2'	19:L:1084:A:H8	1.65	0.61
20:v:582:LEU:HD12	20:v:582:LEU:O	2.00	0.61
1:A:1271:PRO:HG2	1:A:1274:ARG:HB2	1.81	0.61
1:A:1446:THR:OG1	1:A:1449:ASN:ND2	2.32	0.61
17:D:173:U:C2	28:g:97:ARG:NH1	2.68	0.61
29:k:13:ALA:CA	29:k:37:PHE:CZ	2.83	0.61
30:l:13:GLU:OE1	30:l:13:GLU:HA	2.01	0.61
14:n:263:PHE:HB2	14:n:275:TYR:HB2	1.82	0.61
19:L:1095:U:H2'	19:L:1096:C:C6	2.35	0.61
19:L:1137:U:C5	21:a:67:LYS:O	2.54	0.61
20:v:396:LEU:HD23	20:v:396:LEU:O	1.99	0.61
30:l:39:SER:O	30:l:40:MET:HB3	2.01	0.61
15:H:27:LYS:NZ	15:H:29:TYR:OH	2.33	0.61
19:L:3:G:O2'	19:L:4:A:OP1	2.19	0.61
28:g:62:ASP:OD1	28:g:63:ARG:N	2.26	0.61
29:k:13:ALA:HA	29:k:37:PHE:CZ	2.34	0.61
6:Q:298:SER:HB3	19:L:75:A:H62	1.64	0.61
12:d:289:LYS:CG	20:v:609:GLU:HG2	2.31	0.61
1:A:503:LYS:NZ	17:D:83:C:OP2	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2040:TRP:HA	1:A:2040:TRP:CE3	2.36	0.61
1:A:2047:GLN:O	1:A:2051:ILE:N	2.31	0.61
4:O:217:ILE:HG22	4:O:218:ARG:HG3	1.81	0.61
4:O:329:ASP:OD1	4:O:351:GLY:N	2.27	0.61
7:R:145:ALA:HB2	7:R:221:LEU:HB3	1.81	0.61
18:E:55:G:O2'	18:E:56:A:H5'	2.00	0.61
19:L:126:A:P	28:e:80:LYS:CB	2.89	0.61
1:A:1197:ASN:ND2	1:A:1221:ASN:OD1	2.34	0.60
2:C:183:GLN:HE22	2:C:654:CYS:HA	1.64	0.60
19:L:117:U:C6	25:z:88:ARG:NH1	2.69	0.60
19:L:1085:G:N3	19:L:1085:G:H2'	2.16	0.60
19:L:1125:U:H2'	19:L:1126:G:H8	1.64	0.60
29:k:43:LEU:CD1	29:k:87:LEU:HD22	2.31	0.60
29:k:105:LYS:O	29:k:108:ARG:HG2	2.01	0.60
28:e:62:ASP:OD1	28:e:63:ARG:N	2.33	0.60
4:O:343:THR:HB	5:P:47:ARG:HB2	1.83	0.60
5:P:106:LEU:HD12	5:P:107:ASN:N	2.16	0.60
19:L:119:G:H2'	19:L:120:G:H5'	1.82	0.60
20:v:387:SER:O	20:v:391:LEU:HG	2.01	0.60
30:l:42:VAL:HG22	30:l:64:VAL:HG22	1.83	0.60
1:A:416:GLU:HG2	1:A:418:ASP:H	1.66	0.60
4:O:190:VAL:HG22	4:O:197:LEU:HD12	1.81	0.60
2:C:307:ILE:HG12	2:C:346:THR:HA	1.83	0.60
17:D:27:G:H4'	17:D:28:G:OP1	2.01	0.60
1:A:1992:TYR:HB3	1:A:1996:LEU:CB	2.31	0.60
4:O:150:VAL:HG21	8:S:40:ARG:HD2	1.83	0.60
6:Q:293:TRP:CE2	6:Q:297:PHE:HB3	2.36	0.60
25:m:67:LEU:HD11	29:k:53:VAL:HG23	1.82	0.60
1:A:1208:PRO:HG3	1:A:1419:ASP:HB2	1.82	0.60
1:A:1990:ASN:ND2	1:A:1993:ASP:N	2.48	0.60
18:E:13:A:H4'	18:E:14:C:OP1	2.02	0.60
19:L:4:A:N3	19:L:5:A:C8	2.70	0.60
17:D:132:A:N6	17:D:146:C:O2	2.34	0.60
25:m:52:LEU:O	25:m:52:LEU:HD12	2.01	0.60
1:A:1800:ASN:OD1	1:A:1803:ARG:NH2	2.35	0.60
2:C:947:LYS:NZ	2:C:984:ASN:O	2.35	0.60
19:L:1107:C:H2'	19:L:1108:A:OP2	2.01	0.60
25:m:41:THR:O	25:m:83:GLN:HA	2.02	0.60
1:A:893:ARG:HH22	1:A:1135:ALA:HB3	1.65	0.60
19:L:1117:G:C2'	19:L:1118:U:H5'	2.31	0.60
20:v:680:ILE:O	20:v:680:ILE:HG22	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:j:20:ASN:OD1	24:i:32:PHE:CE2	2.55	0.60
2:C:788:LEU:HD11	2:C:823:ILE:HG21	1.83	0.60
5:P:101:PRO:O	5:P:102:ALA:HB2	2.01	0.59
12:d:233:GLN:OE1	12:d:274:TRP:NE1	2.32	0.59
16:B:7:C:O2'	16:B:8:U:P	2.60	0.59
19:L:4:A:C1'	20:v:529:HIS:CG	2.85	0.59
19:L:4:A:O5'	19:L:4:A:H8	1.84	0.59
20:v:530:ARG:NH1	20:v:530:ARG:HB2	2.17	0.59
20:v:797:TYR:O	20:v:799:ASP:N	2.34	0.59
30:l:20:SER:OG	30:l:73:VAL:HG23	2.01	0.59
6:Q:212:ALA:O	7:R:237:ARG:NH1	2.32	0.59
18:E:64:U:H2'	18:E:65:U:H6	1.67	0.59
19:L:1106:G:H4'	19:L:1107:C:OP1	2.00	0.59
28:e:46:ILE:HD12	28:e:54:ILE:HD11	1.84	0.59
1:A:1440:ILE:HA	1:A:1443:TYR:HD2	1.68	0.59
1:A:2023:LYS:O	1:A:2027:LEU:HB2	2.03	0.59
14:n:374:LYS:O	14:n:375:LYS:C	2.44	0.59
25:m:39:ILE:CD1	25:m:84:TYR:CE1	2.85	0.59
29:s:12:LEU:HD12	29:s:15:LEU:HD11	1.84	0.59
2:C:780:PRO:HA	2:C:783:ILE:HB	1.84	0.59
10:Z:63:PHE:O	10:Z:69:ASN:ND2	2.35	0.59
16:B:8:U:C4'	16:B:9:A:OP1	2.51	0.59
19:L:1142:G:C2'	19:L:1143:C:H5'	2.32	0.59
24:u:35:ILE:HD11	27:w:79:LEU:HD13	1.82	0.59
13:I:117:GLN:HB3	13:I:121:LYS:HE3	1.83	0.59
14:n:375:LYS:O	14:n:376:ILE:HG13	2.03	0.59
19:L:6:U:OP1	19:L:6:U:H6	1.86	0.59
27:h:33:PHE:CZ	28:g:49:ARG:CD	2.86	0.59
1:A:376:ARG:HG3	2:C:909:ILE:HG13	1.84	0.59
1:A:380:ARG:NH2	2:C:917:ASP:OD1	2.35	0.59
1:A:901:PRO:HB2	1:A:955:LYS:HE2	1.85	0.59
1:A:1296:ARG:NH1	10:Z:430:GLU:OE2	2.36	0.59
28:g:46:ILE:HD12	28:g:54:ILE:HD11	1.84	0.59
28:e:78:GLU:HG2	25:z:52:LEU:HD22	1.85	0.59
24:i:40:LYS:CD	24:i:60:ILE:HD13	2.32	0.59
1:A:854:ARG:HH22	19:L:25:A:H5''	1.67	0.59
1:A:2043:PHE:HE2	1:A:2047:GLN:H	1.50	0.59
17:D:167:A:O4'	28:g:64:HIS:NE2	2.25	0.59
25:m:16:THR:OG1	25:m:96:ILE:HB	2.03	0.59
29:k:43:LEU:HD11	29:k:87:LEU:HD22	1.85	0.59
30:l:17:HIS:HE1	30:l:77:LEU:HD11	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:TYR:CZ	1:A:129:THR:O	2.55	0.59
12:d:267:TYR:CB	12:d:284:LEU:HD23	2.32	0.59
26:j:6:GLU:OE2	30:l:35:GLU:HB3	2.03	0.59
28:e:91:ILE:HD13	25:z:96:ILE:HD11	1.84	0.59
11:c:41:GLN:HB3	11:c:151:MET:HE2	1.84	0.59
17:D:167:A:C5	27:h:48:TYR:CE1	2.91	0.59
28:e:93:LYS:HZ2	25:z:103:LEU:CD1	2.15	0.59
4:O:327:CYS:SG	4:O:328:THR:N	2.76	0.58
19:L:1093:C:C5'	19:L:1093:C:C6	2.85	0.58
25:m:18:GLU:OE1	25:m:94:GLN:OE1	2.20	0.58
28:g:50:ASN:O	28:g:51:ASN:HB3	2.03	0.58
9:T:145:CYS:SG	9:T:147:HIS:HD2	2.26	0.58
19:L:1146:G:C2'	19:L:1147:A:C8	2.85	0.58
28:g:37:ALA:HB1	28:g:44:VAL:HG11	1.83	0.58
28:g:105:LEU:HD12	28:g:105:LEU:O	2.04	0.58
29:k:52:ARG:HH11	29:k:52:ARG:CG	2.15	0.58
1:A:982:TYR:HB2	1:A:1106:GLY:HA3	1.85	0.58
19:L:113:U:O4	27:w:47:ASN:O	2.21	0.58
19:L:1107:C:C2'	19:L:1108:A:OP2	2.51	0.58
19:L:1142:G:H2'	19:L:1143:C:H5'	1.84	0.58
26:j:61:THR:HG22	24:i:91:THR:CG2	2.31	0.58
1:A:1192:ASP:OD2	1:A:1197:ASN:ND2	2.36	0.58
2:C:402:SER:O	2:C:405:ARG:NH1	2.36	0.58
1:A:1852:VAL:HB	1:A:1935:VAL:HG22	1.85	0.58
6:Q:297:PHE:C	6:Q:298:SER:OG	2.45	0.58
12:d:301:ILE:HD11	20:v:646:PHE:CG	2.39	0.58
17:D:128:A:O2'	17:D:129:G:C8	2.54	0.58
26:j:23:ARG:HH21	26:j:23:ARG:HB2	1.68	0.58
30:l:11:LEU:CD1	30:l:72:ILE:HD12	2.33	0.58
25:z:16:THR:OG1	25:z:96:ILE:HB	2.03	0.58
1:A:127:LEU:O	1:A:128:TYR:HB3	2.01	0.58
1:A:1403:SER:OG	1:A:1429:MET:SD	2.56	0.58
28:e:73:LYS:NZ	28:e:75:LEU:HD21	2.17	0.58
1:A:1272:ARG:HA	1:A:1275:MET:HG3	1.86	0.58
2:C:968:MET:HE1	2:C:986:GLY:HA2	1.86	0.58
1:A:2035:LYS:HB2	1:A:2038:HIS:HB2	1.85	0.58
2:C:222:MET:HE3	2:C:933:TRP:HZ2	1.69	0.58
18:E:11:U:O4	18:E:15:C:N4	2.37	0.58
19:L:1137:U:O2'	19:L:1138:G:C4'	2.43	0.58
5:P:162:GLU:C	5:P:164:LYS:H	2.11	0.58
16:B:10:A:H2'	16:B:11:A:Cl'	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:16:U:H5'	19:L:18:U:C4	2.37	0.58
20:v:323:GLY:O	20:v:327:LYS:N	2.29	0.58
25:m:17:ILE:HG21	25:m:92:ILE:CG2	2.33	0.58
1:A:1717:LEU:HB2	1:A:1786:ALA:H	1.69	0.58
2:C:318:LEU:HD13	2:C:425:LEU:HD11	1.86	0.58
4:O:150:VAL:O	4:O:151:ASP:HB2	2.03	0.58
5:P:104:LEU:HD23	5:P:110:HIS:O	2.04	0.58
19:L:4:A:H2'	19:L:5:A:H8	1.69	0.58
19:L:110:A:H62	25:z:34:PRO:HB2	1.69	0.58
19:L:1118:U:O2'	19:L:1119:C:H5'	2.04	0.58
28:g:40:THR:O	28:g:40:THR:HG22	2.04	0.58
28:e:56:ALA:CA	28:e:72:VAL:HG23	2.33	0.58
1:A:1921:VAL:O	1:A:1929:GLN:NE2	2.36	0.57
17:D:99:U:C6	17:D:99:U:C5'	2.85	0.57
25:m:52:LEU:HD12	25:m:52:LEU:C	2.28	0.57
25:m:82:LEU:C	25:m:82:LEU:HD12	2.29	0.57
1:A:407:VAL:O	2:C:272:ARG:NH2	2.37	0.57
1:A:589:THR:OG1	7:R:39:GLN:NE2	2.36	0.57
29:k:15:LEU:HD12	29:k:15:LEU:O	2.03	0.57
28:e:56:ALA:HB1	28:e:69:LEU:HB3	1.86	0.57
1:A:185:GLN:HE21	1:A:263:PRO:CD	2.17	0.57
17:D:79:C:H5''	17:D:80:G:H2'	1.86	0.57
25:m:84:TYR:HD2	29:k:6:VAL:HG21	1.68	0.57
24:i:30:TRP:CE3	24:i:38:ARG:NH2	2.72	0.57
1:A:1163:ARG:NH1	1:A:1165:LEU:O	2.38	0.57
1:A:1855:THR:HG22	1:A:1937:ARG:HH21	1.69	0.57
14:n:312:SER:OG	14:n:314:ASP:OD1	2.23	0.57
17:D:173:U:O2'	27:h:74:ARG:NH2	2.37	0.57
20:v:690:GLY:HA3	20:v:710:ARG:HE	1.68	0.57
25:m:52:LEU:HD21	28:g:79:LYS:CA	2.34	0.57
29:s:29:VAL:O	29:s:50:GLU:HA	2.05	0.57
29:s:91:GLN:HG3	30:y:70:LYS:HG3	1.87	0.57
1:A:264:ILE:HG23	1:A:264:ILE:O	2.05	0.57
1:A:493:MET:N	1:A:493:MET:SD	2.77	0.57
9:T:123:ARG:HH21	18:E:26:A:HO2'	1.51	0.57
9:T:144:GLN:HB3	9:T:149:GLY:CA	2.35	0.57
1:A:308:MET:HG3	1:A:489:THR:HG22	1.87	0.57
1:A:1843:LEU:HA	1:A:1849:LYS:HZ3	1.69	0.57
1:A:1987:VAL:HG12	1:A:1989:PHE:CD2	2.39	0.57
28:g:46:ILE:HG12	28:g:104:VAL:HG22	1.87	0.57
26:x:47:ASN:OD1	26:x:48:GLY:N	2.31	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:416:GLU:HB3	1:A:419:THR:HG23	1.85	0.57
2:C:316:THR:N	33:C:1500:GTP:O6	2.37	0.57
7:R:83:LEU:HB2	7:R:87:CYS:HB2	1.87	0.57
13:I:121:LYS:NZ	20:v:529:HIS:CD2	2.64	0.57
25:m:90:ASN:OD1	25:m:91:THR:N	2.38	0.57
30:l:44:LEU:HD12	30:l:47:VAL:CG1	2.35	0.57
5:P:160:PRO:O	5:P:162:GLU:N	2.37	0.57
13:I:121:LYS:HZ1	20:v:529:HIS:HD2	1.52	0.57
19:L:109:C:P	25:z:8:LYS:HZ2	2.27	0.57
1:A:1626:GLN:HG3	1:A:1633:PHE:CE1	2.40	0.57
1:A:1914:ALA:HA	1:A:1944:LEU:HD23	1.87	0.57
2:C:181:LEU:HD23	2:C:184:GLU:HG3	1.87	0.57
16:B:-6:U:H5''	16:B:-6:U:O2	2.05	0.57
22:b:14:TYR:C	29:s:102:LEU:CD1	2.76	0.57
26:j:16:LEU:HD22	26:j:72:GLU:OE2	2.05	0.57
29:k:30:TYR:HD1	29:k:50:GLU:HB3	1.69	0.57
29:k:49:ILE:CG2	29:k:81:VAL:CB	2.83	0.57
28:e:46:ILE:HG12	28:e:104:VAL:HG22	1.87	0.57
7:R:196:LYS:NZ	18:E:38:U:O2	2.35	0.56
16:B:7:C:HO2'	16:B:8:U:P	2.27	0.56
27:h:58:GLU:O	27:h:65:HIS:N	2.38	0.56
1:A:266:LEU:CG	1:A:267:PRO:HD2	2.29	0.56
1:A:1211:SER:OG	1:A:1268:ARG:NH1	2.38	0.56
1:A:1401:SER:OG	1:A:1438:PRO:O	2.23	0.56
1:A:1576:GLU:HB3	1:A:1824:GLN:HB3	1.87	0.56
16:B:10:A:C8	16:B:11:A:C2	2.93	0.56
20:v:530:ARG:HB2	20:v:530:ARG:CZ	2.34	0.56
20:v:610:LYS:O	20:v:613:PRO:HG2	2.05	0.56
1:A:1288:LEU:HD11	1:A:1300:ALA:HB2	1.87	0.56
11:c:513:ILE:O	11:c:517:VAL:N	2.38	0.56
15:H:79:ASN:HA	15:H:82:LEU:HD12	1.86	0.56
18:E:58:C:H2'	18:E:59:A:H5''	1.87	0.56
19:L:125:C:H5''	28:e:80:LYS:CA	2.34	0.56
19:L:1106:G:H5'	19:L:1107:C:OP1	2.05	0.56
29:k:11:ARG:H	29:k:14:ASN:HB2	1.69	0.56
28:e:68:VAL:O	28:e:69:LEU:HD12	2.06	0.56
1:A:1575:TRP:CZ3	1:A:1825:ILE:CG1	2.82	0.56
9:T:147:HIS:CD2	9:T:147:HIS:N	2.73	0.56
12:d:211:ARG:HG2	20:v:520:ILE:HG13	1.86	0.56
20:v:349:PHE:O	20:v:353:CYS:N	2.37	0.56
29:s:53:VAL:HG23	25:z:67:LEU:HD11	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:l:17:HIS:HB3	30:l:75:PRO:CG	2.35	0.56
12:d:137:TYR:HA	12:d:140:LEU:HD12	1.86	0.56
22:b:14:TYR:O	29:s:102:LEU:HD13	2.03	0.56
14:n:292:HIS:CB	14:n:318:ARG:NH1	2.68	0.56
28:g:38:MET:HB2	28:g:58:VAL:HG12	1.88	0.56
29:k:35:MET:HE2	29:k:46:ASN:HB2	1.87	0.56
29:k:86:ILE:CD1	30:l:11:LEU:CD1	2.78	0.56
26:x:7:LEU:HD23	26:x:29:LEU:HD11	1.87	0.56
20:v:392:TYR:HA	20:v:395:TYR:HD2	1.70	0.56
26:j:19:ILE:HD12	26:j:68:ILE:HD13	1.87	0.56
24:i:40:LYS:CG	24:i:60:ILE:HD13	2.36	0.56
1:A:1164:TYR:O	1:A:1165:LEU:HG	2.06	0.56
10:Z:10:ASP:OD2	10:Z:244:LYS:NZ	2.38	0.56
28:e:54:ILE:HD13	28:e:72:VAL:HG21	1.88	0.56
30:l:10:LEU:HD12	30:l:10:LEU:O	2.04	0.56
24:i:30:TRP:CG	24:i:38:ARG:HE	2.24	0.56
27:w:58:GLU:O	27:w:65:HIS:N	2.38	0.56
1:A:772:GLU:O	1:A:773:SER:CB	2.54	0.56
8:S:12:ARG:HH12	8:S:16:LYS:HB2	1.71	0.56
19:L:6:U:H6	19:L:6:U:P	2.29	0.56
20:v:530:ARG:HH11	20:v:530:ARG:HA	1.70	0.56
26:j:14:LYS:CG	26:j:74:LEU:HD11	2.34	0.56
28:g:78:GLU:HG2	28:g:85:ILE:HG22	1.88	0.56
28:g:102:ILE:HG13	28:g:103:VAL:H	1.70	0.56
1:A:1362:LYS:NZ	3:J:13:GLY:O	2.39	0.55
30:l:21:LEU:CD2	30:l:69:ILE:HD13	2.36	0.55
25:z:23:THR:HG22	25:z:47:LEU:CD1	2.34	0.55
5:P:92:ARG:NH1	17:D:110:U:OP1	2.40	0.55
20:v:542:LEU:HD23	20:v:582:LEU:HD12	1.88	0.55
1:A:241:PRO:O	1:A:638:GLN:NE2	2.40	0.55
1:A:462:LEU:HB3	2:C:383:LYS:HD2	1.89	0.55
4:O:220:TYR:HE2	4:O:239:ILE:HD12	1.69	0.55
5:P:143:VAL:HG11	12:d:124:ARG:HG3	1.88	0.55
19:L:116:U:N3	29:s:40:HIS:CD2	2.74	0.55
26:j:19:ILE:HG21	24:i:88:THR:HG23	1.88	0.55
29:k:49:ILE:HD12	29:k:49:ILE:N	2.16	0.55
28:e:73:LYS:HG3	28:e:90:PHE:CD2	2.41	0.55
25:z:39:ILE:HD11	25:z:84:TYR:CE1	2.40	0.55
1:A:426:PRO:HG3	10:Z:201:ARG:HH11	1.71	0.55
1:A:621:LEU:HD23	1:A:722:LEU:HD21	1.88	0.55
1:A:930:ASN:ND2	19:L:29:C:H5'	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:218:ARG:CB	4:O:256:ARG:HD3	2.25	0.55
5:P:129:LYS:NZ	8:S:23:THR:O	2.39	0.55
11:c:35:LYS:HD3	18:E:55:G:N7	2.22	0.55
12:d:291:PHE:CE1	20:v:610:LYS:HE2	2.41	0.55
12:d:305:ARG:NH2	12:d:308:GLU:OE1	2.38	0.55
19:L:16:U:H2'	19:L:18:U:O4	2.07	0.55
20:v:385:PHE:N	20:v:385:PHE:CD1	2.73	0.55
28:e:93:LYS:NZ	25:z:103:LEU:HD13	2.21	0.55
1:A:992:ASP:OD2	1:A:1085:LYS:NZ	2.40	0.55
1:A:2040:TRP:HA	1:A:2040:TRP:HE3	1.71	0.55
2:C:70:TYR:C	2:C:72:LYS:H	2.14	0.55
4:O:111:ILE:HG21	12:d:197:PRO:CD	2.35	0.55
17:D:50:G:H1	17:D:65:U:H3	1.55	0.55
19:L:120:G:H4'	19:L:121:C:O5'	2.06	0.55
20:v:386:GLU:HA	20:v:389:ILE:HD13	1.84	0.55
28:g:35:ASN:CB	28:g:61:PHE:CE2	2.81	0.55
19:L:152:C:N4	19:L:1085:G:H1	1.97	0.55
19:L:1129:U:C2'	19:L:1130:U:C5'	2.85	0.55
28:g:37:ALA:CB	28:g:44:VAL:HG11	2.37	0.55
24:i:30:TRP:O	24:i:88:THR:HB	2.07	0.55
1:A:1406:LEU:HB3	1:A:1425:PHE:HB3	1.89	0.55
1:A:1889:LEU:HG	1:A:1991:ILE:HG12	1.89	0.55
1:A:2056:ARG:O	1:A:2060:LEU:N	2.35	0.55
11:c:163:GLN:HB3	11:c:167:ALA:HB3	1.89	0.55
28:e:102:ILE:HG13	28:e:103:VAL:H	1.70	0.55
1:A:745:THR:HG21	4:O:203:ASP:HB2	1.87	0.55
2:C:176:ARG:NH2	2:C:179:ASP:OD2	2.40	0.55
2:C:206:LYS:HE2	30:l:12:ASN:HB3	1.89	0.55
29:k:49:ILE:HG23	29:k:81:VAL:HG23	1.88	0.55
28:e:97:ARG:NH2	25:z:36:MET:SD	2.79	0.55
26:x:74:LEU:O	26:x:74:LEU:HD12	2.07	0.55
1:A:1271:PRO:O	1:A:1275:MET:CG	2.54	0.55
18:E:64:U:H2'	18:E:65:U:C6	2.42	0.55
20:v:325:LEU:O	20:v:329:SER:N	2.38	0.55
10:Z:73:ILE:HG22	10:Z:123:ILE:HD12	1.89	0.55
19:L:33:U:H2'	19:L:34:G:H8	1.72	0.55
29:k:44:VAL:HG13	29:k:85:THR:O	2.06	0.55
24:i:30:TRP:CE2	24:i:38:ARG:NE	2.75	0.55
2:C:97:ARG:NH1	17:D:43:G:OP1	2.40	0.54
5:P:106:LEU:CD1	5:P:107:ASN:N	2.69	0.54
6:Q:297:PHE:O	6:Q:298:SER:CB	2.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:25:A:HB2'	19:L:27:A:OP2	2.07	0.54
19:L:113:U:C6	27:w:48:TYR:CE1	2.96	0.54
1:A:1051:GLU:HB3	1:A:1167:ARG:HH21	1.71	0.54
1:A:2018:ASN:ND2	1:A:2058:LEU:HD22	2.22	0.54
10:Z:421:LYS:HG3	10:Z:468:ILE:HG23	1.89	0.54
24:u:44:VAL:HB	24:u:53:VAL:HG23	1.89	0.54
29:k:49:ILE:HG22	29:k:80:ARG:C	2.32	0.54
29:s:53:VAL:HG23	25:z:67:LEU:CD1	2.37	0.54
1:A:676:GLN:HG2	1:A:714:PHE:HB2	1.90	0.54
1:A:680:CYS:SG	1:A:711:TRP:NE1	2.80	0.54
1:A:1294:LYS:O	10:Z:429:ASN:ND2	2.34	0.54
1:A:1627:LEU:HD13	1:A:1634:LEU:HD13	1.90	0.54
2:C:866:ILE:HB	2:C:902:VAL:HB	1.89	0.54
14:n:63:ARG:NH1	14:n:68:PRO:O	2.40	0.54
18:E:14:C:H4'	18:E:15:C:OP2	2.06	0.54
20:v:255:GLU:O	20:v:259:LYS:N	2.40	0.54
26:j:35:PHE:HB2	26:j:37:ASN:ND2	2.23	0.54
26:j:47:ASN:OD1	26:j:48:GLY:N	2.31	0.54
2:C:270:LEU:HD11	2:C:313:PHE:HB3	1.89	0.54
4:O:229:THR:HG21	4:O:272:VAL:H	1.72	0.54
17:D:172:U:N3	25:m:37:ASN:OD1	2.41	0.54
19:L:109:C:O2'	19:L:110:A:OP2	2.23	0.54
29:k:39:LYS:HG3	29:k:40:HIS:N	2.23	0.54
1:A:1934:ILE:HG12	1:A:1957:ARG:HB2	1.89	0.54
2:C:69:PRO:HG3	2:C:76:VAL:HG21	1.90	0.54
9:T:13:PRO:HG2	9:T:77:LEU:HA	1.89	0.54
13:I:117:GLN:O	13:I:121:LYS:HE3	2.07	0.54
19:L:15:C:H1'	19:L:16:U:C6	2.42	0.54
26:j:63:ILE:CG1	24:i:89:LEU:CD2	2.86	0.54
24:i:44:VAL:HB	24:i:53:VAL:HG23	1.89	0.54
1:A:864:GLN:HE22	1:A:1101:TYR:H	1.55	0.54
9:T:145:CYS:O	9:T:149:GLY:HA2	2.06	0.54
20:v:711:MET:HE2	20:v:748:PHE:CB	2.33	0.54
30:l:21:LEU:HD12	30:l:44:LEU:HD11	1.90	0.54
4:O:119:LEU:O	4:O:122:ARG:NH1	2.39	0.54
4:O:285:SER:OG	4:O:287:ASP:OD1	2.26	0.54
28:e:56:ALA:HB1	28:e:72:VAL:HB	1.89	0.54
4:O:238:LEU:HD21	5:P:74:ILE:HD13	1.90	0.54
9:T:102:LYS:O	9:T:153:CYS:HB3	2.08	0.54
25:m:86:ASN:ND2	29:k:41:MET:CE	2.70	0.54
1:A:1272:ARG:NE	1:A:1296:ARG:O	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2020:GLU:CG	1:A:2024:MET:HE1	2.38	0.54
6:Q:39:LEU:HD23	6:Q:63:ARG:HH12	1.72	0.54
6:Q:67:GLN:NE2	6:Q:114:SER:O	2.41	0.54
17:D:2:A:H61	17:D:164:C:N4	2.06	0.54
19:L:4:A:C2	19:L:5:A:C5	2.96	0.54
1:A:929:LEU:HD22	1:A:933:GLU:HG3	1.90	0.54
2:C:317:LYS:CB	33:C:1500:GTP:C6	2.91	0.54
2:C:851:LEU:HB2	2:C:989:LEU:HD13	1.90	0.54
4:O:102:PHE:O	4:O:104:PRO:HD3	2.07	0.54
19:L:4:A:H8	19:L:4:A:P	2.31	0.54
19:L:4:A:P	19:L:4:A:C8	3.01	0.54
27:h:71:ILE:CG2	28:g:103:VAL:HG23	2.37	0.54
29:k:51:GLU:OE1	29:k:77:VAL:HG11	2.07	0.54
1:A:738:SER:OG	1:A:740:GLU:OE1	2.26	0.53
1:A:860:GLU:OE2	1:A:863:ARG:NH2	2.37	0.53
10:Z:319:ASN:HA	10:Z:322:LYS:HD3	1.89	0.53
12:d:211:ARG:HG2	20:v:520:ILE:CG1	2.38	0.53
19:L:53:G:H1'	19:L:54:U:H5''	1.86	0.53
20:v:686:ILE:HG12	20:v:713:ILE:HG21	1.89	0.53
22:b:125:LYS:O	22:b:152:GLU:CB	2.55	0.53
28:g:79:LYS:HA	28:g:83:ASN:O	2.08	0.53
29:k:52:ARG:HB3	29:k:52:ARG:NH1	2.23	0.53
29:s:16:ILE:O	29:s:17:ASP:HB2	2.08	0.53
25:z:27:GLY:HA3	25:z:43:VAL:HG12	1.90	0.53
1:A:796:ASN:ND2	1:A:861:GLN:OE1	2.40	0.53
4:O:256:ARG:NH2	8:S:31:LEU:O	2.42	0.53
19:L:45:U:H2'	19:L:45:U:O2	2.07	0.53
19:L:1155:C:H6	19:L:1155:C:O5'	1.90	0.53
26:j:71:LEU:HB3	30:l:63:PHE:HB3	1.90	0.53
30:l:63:PHE:CD1	30:l:63:PHE:C	2.85	0.53
2:C:804:LYS:HD3	2:C:805:GLU:HG3	1.89	0.53
13:I:117:GLN:C	13:I:121:LYS:HE3	2.32	0.53
14:n:292:HIS:HB3	14:n:318:ARG:NH1	2.22	0.53
29:k:31:ILE:CG1	29:k:49:ILE:HD13	2.37	0.53
29:k:31:ILE:O	29:k:48:CYS:HA	2.09	0.53
30:l:11:LEU:HD23	30:l:36:SER:HB3	1.90	0.53
1:A:614:ARG:CZ	16:B:-1:A:H5''	2.37	0.53
1:A:765:ASP:OD2	1:A:815:TYR:OH	2.25	0.53
1:A:971:MET:HG2	1:A:980:PRO:HA	1.90	0.53
2:C:139:ILE:HD12	2:C:252:LEU:HD22	1.88	0.53
2:C:713:GLU:HB3	2:C:817:GLN:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:294:ASP:HB2	4:O:301:MET:HG3	1.91	0.53
7:R:151:LEU:HA	19:L:78:G:OP1	2.09	0.53
19:L:1129:U:C2'	19:L:1130:U:H5'	2.38	0.53
22:b:160:THR:O	22:b:163:GLU:N	2.42	0.53
26:j:23:ARG:HH21	26:j:23:ARG:CG	2.22	0.53
28:e:50:ASN:O	28:e:51:ASN:CB	2.57	0.53
30:l:71:PHE:C	30:l:71:PHE:CD1	2.85	0.53
26:x:35:PHE:HB2	26:x:37:ASN:ND2	2.23	0.53
1:A:238:ARG:NH1	1:A:1695:ASN:O	2.40	0.53
28:e:54:ILE:HB	28:e:72:VAL:CG2	2.38	0.53
24:i:30:TRP:HE1	24:i:38:ARG:HD3	1.62	0.53
1:A:1850:LEU:HD13	1:A:1930:PRO:HG3	1.89	0.53
18:E:55:G:H2'	18:E:56:A:C8	2.41	0.53
19:L:109:C:H3'	19:L:109:C:H6	1.73	0.53
19:L:1137:U:H5'	21:a:66:LYS:O	2.09	0.53
1:A:1843:LEU:HD22	1:A:1851:PHE:HZ	1.74	0.53
4:O:436:SER:O	4:O:437:GLU:HG2	2.07	0.53
16:B:10:A:H2'	16:B:11:A:N3	2.24	0.53
16:B:57:C:O2	16:B:57:C:H2'	2.09	0.53
20:v:391:LEU:HB3	20:v:395:TYR:CE2	2.43	0.53
25:m:27:GLY:HA3	25:m:43:VAL:HG12	1.90	0.53
26:x:63:ILE:HG21	26:x:68:ILE:HD11	1.90	0.53
1:A:2057:ASP:HA	1:A:2060:LEU:HB2	1.89	0.53
4:O:221:TYR:OH	18:E:74:U:O4'	2.22	0.53
18:E:13:A:HO2'	18:E:14:C:H5	1.56	0.53
19:L:6:U:O2	19:L:6:U:H2'	2.09	0.53
19:L:1107:C:H6	19:L:1107:C:H5'	1.74	0.53
20:v:357:ILE:O	20:v:361:LEU:N	2.35	0.53
26:j:10:TYR:HB3	26:j:15:ILE:HD11	1.90	0.53
29:s:58:LEU:HD11	25:z:62:MET:HE3	1.91	0.53
26:x:71:LEU:N	30:y:63:PHE:O	2.28	0.53
11:c:226:GLY:O	13:I:151:LYS:NZ	2.32	0.53
20:v:489:LEU:HD22	20:v:547:LYS:HD3	1.89	0.53
28:e:45:ILE:HB	28:e:105:LEU:HG	1.90	0.53
26:x:14:LYS:CG	26:x:74:LEU:HD11	2.39	0.53
1:A:244:ASP:HB2	1:A:594:ASP:HB2	1.91	0.53
1:A:796:ASN:HD21	1:A:865:ARG:HH22	1.56	0.53
1:A:1361:VAL:HG22	1:A:1403:SER:HB2	1.91	0.53
14:n:274:HIS:HB2	14:n:287:GLN:HB2	1.91	0.53
16:B:8:U:C5'	16:B:9:A:OP1	2.55	0.53
19:L:4:A:C2	19:L:5:A:C8	2.97	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:j:27:GLY:C	26:j:40:LEU:HD12	2.34	0.53
26:j:29:LEU:HD23	26:j:29:LEU:O	2.09	0.53
1:A:1445:THR:OG1	1:A:1450:GLU:OE2	2.27	0.52
16:B:10:A:C2'	16:B:11:A:N3	2.72	0.52
18:E:55:G:C8	18:E:55:G:C5'	2.86	0.52
28:g:35:ASN:HA	28:g:61:PHE:CD2	2.40	0.52
1:A:2020:GLU:HG3	1:A:2024:MET:HE1	1.90	0.52
6:Q:51:ARG:NH2	18:E:29:U:OP2	2.42	0.52
7:R:229:ASP:O	7:R:235:GLN:NE2	2.36	0.52
17:D:167:A:C6	27:h:48:TYR:CD1	2.98	0.52
25:m:84:TYR:CD2	29:k:6:VAL:HG21	2.44	0.52
29:k:18:TYR:CE1	29:k:101:PRO:HD3	2.44	0.52
30:l:10:LEU:O	30:l:13:GLU:HB2	2.09	0.52
11:c:509:LEU:O	11:c:513:ILE:N	2.38	0.52
19:L:114:U:O2	26:x:64:ARG:CG	2.57	0.52
25:z:52:LEU:HD23	25:z:55:LEU:HD22	1.92	0.52
2:C:197:THR:HG21	2:C:544:LEU:HD22	1.90	0.52
9:T:95:TRP:HA	9:T:101:GLU:HA	1.91	0.52
19:L:1125:U:H6	19:L:1125:U:H5''	1.74	0.52
28:e:93:LYS:NZ	25:z:103:LEU:CD1	2.73	0.52
1:A:713:ASN:ND2	17:D:84:A:OP1	2.42	0.52
1:A:1626:GLN:HB2	1:A:1633:PHE:HE1	1.68	0.52
16:B:10:A:H2'	16:B:11:A:O4'	2.09	0.52
19:L:1101:C:H2'	19:L:1101:C:O2	2.09	0.52
20:v:683:SER:O	20:v:687:LEU:N	2.40	0.52
26:j:19:ILE:HG21	24:i:88:THR:CG2	2.40	0.52
28:g:68:VAL:C	28:g:69:LEU:HD12	2.35	0.52
29:s:42:ASN:HB3	29:s:89:GLY:N	2.23	0.52
30:l:79:LYS:HG3	30:l:80:ASN:N	2.25	0.52
2:C:317:LYS:HB2	33:C:1500:GTP:C6	2.43	0.52
4:O:280:GLN:NE2	5:P:66:CYS:SG	2.82	0.52
6:Q:70:ILE:HD13	6:Q:84:ILE:HD11	1.92	0.52
16:B:1:G:O2'	16:B:2:U:H5''	2.10	0.52
19:L:113:U:C6	27:w:48:TYR:CD1	2.96	0.52
20:v:467:ARG:HA	20:v:470:TRP:HD1	1.75	0.52
20:v:612:ILE:HD13	20:v:624:TRP:CZ2	2.44	0.52
26:j:64:ARG:HH21	24:i:50:MET:HB3	1.64	0.52
27:w:29:VAL:HG12	27:w:81:ILE:HG12	1.91	0.52
5:P:105:LEU:CD1	5:P:112:ILE:HG13	2.38	0.52
6:Q:246:ALA:HB1	6:Q:312:LEU:HD22	1.92	0.52
13:I:183:MET:HE1	19:L:17:U:OP1	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:129:G:H1'	17:D:131:A:H2'	1.90	0.52
28:g:50:ASN:O	28:g:51:ASN:CB	2.57	0.52
28:e:44:VAL:HG22	28:e:56:ALA:O	2.10	0.52
28:e:93:LYS:CB	25:z:97:LEU:CD1	2.87	0.52
30:l:17:HIS:CG	30:l:75:PRO:CG	2.88	0.52
27:w:32:LYS:HA	27:w:79:LEU:HD12	1.92	0.52
1:A:1575:TRP:CH2	1:A:1825:ILE:HG12	2.43	0.52
17:D:100:A:OP1	18:E:72:C:N4	2.38	0.52
20:v:530:ARG:NH1	20:v:530:ARG:CB	2.73	0.52
25:m:99:ASP:OD1	28:g:92:SER:HB3	2.09	0.52
27:h:13:VAL:HG12	24:i:44:VAL:HG11	1.92	0.52
27:h:29:VAL:HG12	27:h:81:ILE:HG12	1.91	0.52
28:g:32:SER:O	28:g:35:ASN:ND2	2.37	0.52
28:g:41:ARG:HG3	28:g:41:ARG:NH2	2.25	0.52
30:l:44:LEU:HD12	30:l:47:VAL:HG11	1.91	0.52
1:A:268:LEU:HD11	1:A:281:TYR:CE2	2.44	0.52
4:O:159:SER:OG	4:O:160:ASN:N	2.42	0.52
25:m:17:ILE:HD12	25:m:40:LEU:HD11	1.92	0.52
28:g:37:ALA:HB1	28:g:44:VAL:CG1	2.39	0.52
28:e:93:LYS:HZ3	25:z:103:LEU:HD13	1.74	0.52
30:l:22:GLU:HB3	30:l:71:PHE:CE1	2.44	0.52
19:L:53:G:C1'	19:L:54:U:OP1	2.58	0.52
30:l:21:LEU:HD22	30:l:42:VAL:HG21	1.92	0.52
27:w:23:VAL:HA	27:w:42:LEU:HD22	1.92	0.52
27:w:32:LYS:CG	27:w:33:PHE:CD1	2.88	0.52
1:A:1011:ASN:O	1:A:1014:LYS:NZ	2.42	0.51
12:d:324:TRP:CE3	20:v:679:LEU:HD13	2.46	0.51
27:h:32:LYS:HA	27:h:79:LEU:HD12	1.92	0.51
1:A:153:MET:HE3	1:A:154:TYR:CZ	2.45	0.51
2:C:500:ARG:NH1	2:C:536:SER:OG	2.43	0.51
18:E:100:U:HO2'	18:E:101:U:P	2.33	0.51
1:A:477:MET:HE2	2:C:278:LYS:HE3	1.93	0.51
1:A:930:ASN:HD22	19:L:29:C:H5'	1.75	0.51
6:Q:67:GLN:NE2	6:Q:116:LYS:O	2.44	0.51
14:n:269:ASN:O	14:n:270:SER:HB2	2.09	0.51
16:B:7:C:O2'	16:B:8:U:H5'	2.10	0.51
19:L:1127:A:C2'	19:L:1128:C:O5'	2.58	0.51
28:g:76:TRP:CH2	28:g:87:ARG:CD	2.86	0.51
28:e:59:LYS:HG3	28:e:70:GLU:HG2	1.90	0.51
6:Q:293:TRP:HD1	6:Q:295:SER:H	1.58	0.51
27:h:23:VAL:HA	27:h:42:LEU:HD22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:e:70:GLU:OE2	28:e:71:ASN:OD1	2.28	0.51
10:Z:84:ASN:ND2	10:Z:220:TYR:OH	2.43	0.51
17:D:179:U:OP1	28:g:79:LYS:O	2.27	0.51
19:L:119:G:N7	28:e:49:ARG:HD2	2.24	0.51
29:s:18:TYR:CE1	29:s:101:PRO:HD3	2.44	0.51
1:A:238:ARG:HH12	1:A:1696:SER:HB3	1.76	0.51
2:C:880:MET:HE3	2:C:886:SER:HB3	1.93	0.51
26:j:19:ILE:HD13	26:j:19:ILE:N	2.23	0.51
27:h:74:ARG:HE	27:h:76:ASN:ND2	2.08	0.51
28:g:78:GLU:CG	28:g:85:ILE:CG2	2.88	0.51
29:s:24:THR:OG1	29:s:26:ASP:OD1	2.25	0.51
31:r:8:LYS:CG	31:o:88:TRP:HH2	2.24	0.51
1:A:1701:ILE:HB	1:A:1734:PHE:HB2	1.92	0.51
15:H:26:TYR:CG	15:H:27:LYS:N	2.73	0.51
28:g:76:TRP:CZ2	28:g:87:ARG:NE	2.79	0.51
24:i:28:THR:CG2	24:i:40:LYS:HD2	2.31	0.51
24:i:30:TRP:CE2	24:i:38:ARG:HD3	2.38	0.51
1:A:1084:ALA:HB2	11:c:82:ASN:HD21	1.75	0.51
4:O:343:THR:HA	5:P:45:PRO:HB3	1.93	0.51
10:Z:105:GLN:OE1	10:Z:108:ARG:NH2	2.44	0.51
17:D:60:U:C6	17:D:61:U:C6	2.98	0.51
17:D:128:A:C2'	17:D:128:A:N3	2.74	0.51
20:v:365:ASP:CA	20:v:399:VAL:HG22	2.39	0.51
20:v:729:TYR:CE1	20:v:749:SER:CB	2.94	0.51
25:m:4:VAL:HG11	25:m:34:PRO:O	2.11	0.51
25:m:47:LEU:HD23	25:m:48:PRO:HD2	1.92	0.51
1:A:1457:VAL:HG21	1:A:1486:ARG:HG2	1.93	0.51
1:A:2044:THR:O	1:A:2045:ASP:HB2	2.11	0.51
7:R:203:THR:HB	7:R:205:LEU:HD23	1.93	0.51
29:k:13:ALA:CB	29:k:37:PHE:CZ	2.85	0.51
29:k:24:THR:OG1	29:k:26:ASP:OD1	2.25	0.51
1:A:1601:ILE:HG22	1:A:1605:ARG:HH21	1.76	0.51
1:A:1991:ILE:O	1:A:2040:TRP:NE1	2.44	0.51
19:L:40:U:O2'	19:L:41:C:H5'	2.11	0.51
1:A:1165:LEU:CG	1:A:1166:ASP:OD1	2.59	0.50
1:A:1292:ARG:HD3	1:A:1293:THR:HG23	1.93	0.50
7:R:155:GLN:N	7:R:155:GLN:OE1	2.44	0.50
19:L:51:C:H6	19:L:51:C:O5'	1.93	0.50
19:L:1090:A:C2'	19:L:1091:G:H5'	2.41	0.50
19:L:1146:G:C6	19:L:1147:A:C6	3.00	0.50
19:L:1154:U:C2'	19:L:1155:C:O5'	2.58	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:y:21:LEU:CD1	30:y:44:LEU:CD1	2.71	0.50
16:B:69:A:O2'	16:B:71:C:O4'	2.24	0.50
26:j:71:LEU:HD23	26:j:71:LEU:C	2.36	0.50
28:e:89:ARG:NH2	28:e:91:ILE:CD1	2.72	0.50
25:z:30:GLN:HB2	25:z:39:ILE:HG23	1.92	0.50
1:A:614:ARG:NH1	16:B:-1:A:H5''	2.26	0.50
29:k:38:ASP:OD1	29:k:39:LYS:N	2.41	0.50
30:l:41:ASN:HB3	30:l:66:GLY:N	2.26	0.50
1:A:1712:SER:HB3	1:A:1724:PHE:HD1	1.76	0.50
1:A:2021:SER:O	1:A:2025:ILE:N	2.43	0.50
13:I:117:GLN:HB3	13:I:121:LYS:CE	2.42	0.50
17:D:128:A:N3	17:D:128:A:C3'	2.74	0.50
19:L:117:U:H5'	25:z:90:ASN:HB3	1.93	0.50
20:v:530:ARG:CA	20:v:530:ARG:NH1	2.73	0.50
26:j:62:VAL:CG1	24:i:90:ILE:HB	2.41	0.50
29:s:85:THR:HG22	30:y:73:VAL:HG22	1.93	0.50
1:A:728:ASN:ND2	18:E:72:C:O2'	2.44	0.50
4:O:150:VAL:O	4:O:151:ASP:CB	2.60	0.50
7:R:7:LYS:HD3	7:R:10:LYS:HE2	1.94	0.50
9:T:121:ILE:C	9:T:123:ARG:N	2.70	0.50
12:d:298:GLU:HA	12:d:301:ILE:HG22	1.94	0.50
25:z:17:ILE:HD12	25:z:40:LEU:HD11	1.92	0.50
6:Q:254:GLN:NE2	19:L:75:A:OP1	2.45	0.50
7:R:232:PRO:HA	7:R:235:GLN:HB2	1.92	0.50
26:x:10:TYR:HB3	26:x:15:ILE:HD11	1.94	0.50
25:z:16:THR:HA	25:z:25:VAL:O	2.11	0.50
1:A:402:TRP:C	1:A:403:TYR:O	2.50	0.50
1:A:2021:SER:CA	1:A:2024:MET:HB2	2.40	0.50
4:O:218:ARG:O	4:O:219:ASP:CB	2.60	0.50
4:O:257:ILE:HD12	5:P:78:VAL:HG13	1.94	0.50
7:R:230:PRO:HD2	16:B:14:U:H2'	1.94	0.50
10:Z:32:LEU:HD23	10:Z:76:LEU:HD23	1.93	0.50
18:E:84:C:H3'	18:E:85:C:H5''	1.93	0.50
19:L:109:C:OP1	25:z:8:LYS:NZ	2.45	0.50
19:L:1106:G:C4'	19:L:1107:C:OP1	2.60	0.50
28:g:41:ARG:HG3	28:g:41:ARG:HH21	1.75	0.50
30:l:61:GLN:HG3	30:l:62:ILE:N	2.25	0.50
25:z:19:LEU:HD22	25:z:91:THR:HG22	1.93	0.50
1:A:1406:LEU:N	10:Z:307:GLU:OE2	2.39	0.50
1:A:1795:LYS:HA	1:A:1798:ILE:HG22	1.93	0.50
2:C:138:VAL:HG21	2:C:150:MET:HE3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Z:305:GLY:HA3	10:Z:345:ILE:HG23	1.94	0.50
16:B:11:A:H4'	16:B:11:A:OP1	2.11	0.50
17:D:175:G:O5'	28:g:49:ARG:NH1	2.45	0.50
19:L:1105:C:H1'	19:L:1106:G:O4'	2.12	0.50
24:u:35:ILE:HG23	24:u:37:ILE:H	1.77	0.50
6:Q:71:CYS:SG	6:Q:74:CYS:N	2.83	0.50
14:n:292:HIS:CD2	14:n:292:HIS:N	2.78	0.50
17:D:123:U:C2'	17:D:124:C:H5'	2.41	0.50
19:L:4:A:C2	19:L:5:A:N7	2.80	0.50
19:L:1154:U:C2'	19:L:1155:C:C5'	2.87	0.50
20:v:530:ARG:NH1	20:v:530:ARG:N	2.60	0.50
28:g:71:ASN:N	28:g:92:SER:O	2.41	0.50
29:k:52:ARG:CG	29:k:52:ARG:NH1	2.74	0.50
30:l:21:LEU:CD1	30:l:44:LEU:HD11	2.42	0.50
24:i:46:PHE:HB3	24:i:52:VAL:HG12	1.94	0.50
1:A:1716:LEU:HD21	1:A:1753:ARG:HH22	1.77	0.49
1:A:2024:MET:HE2	25:z:99:ASP:O	2.12	0.49
19:L:53:G:C1'	19:L:54:U:O5'	2.56	0.49
19:L:1127:A:H8	19:L:1127:A:O5'	1.95	0.49
22:b:67:ILE:CB	22:b:89:VAL:CB	2.90	0.49
25:m:16:THR:HA	25:m:25:VAL:O	2.11	0.49
1:A:1993:ASP:CG	1:A:2040:TRP:H	2.19	0.49
17:D:80:G:OP1	17:D:114:G:O2'	2.29	0.49
20:v:396:LEU:C	20:v:396:LEU:CD2	2.86	0.49
28:e:73:LYS:HE3	28:e:90:PHE:HE2	1.78	0.49
24:i:54:ILE:CG1	24:i:57:ALA:HB2	2.41	0.49
30:y:24:THR:HA	30:y:70:LYS:HE3	1.93	0.49
1:A:1280:SER:OG	10:Z:348:GLU:OE1	2.29	0.49
2:C:778:THR:HG23	2:C:781:ASP:H	1.76	0.49
4:O:227:VAL:HA	4:O:243:GLY:HA3	1.94	0.49
10:Z:403:LYS:HG2	10:Z:445:LEU:HB3	1.94	0.49
14:n:375:LYS:C	14:n:376:ILE:CG1	2.86	0.49
19:L:54:U:H2'	19:L:55:G:C8	2.46	0.49
20:v:667:ILE:HA	20:v:670:SER:HB3	1.94	0.49
28:e:63:ARG:HH11	28:e:64:HIS:HE1	1.59	0.49
30:y:33:LEU:HA	30:y:44:LEU:CD2	2.35	0.49
1:A:768:GLU:O	4:O:309:ARG:NH1	2.46	0.49
1:A:1364:GLU:OE1	1:A:1403:SER:OG	2.29	0.49
1:A:1678:ILE:HG22	1:A:1709:TRP:HH2	1.76	0.49
2:C:626:SER:HB2	2:C:634:ILE:HD12	1.93	0.49
19:L:1084:A:O3'	19:L:1085:G:H8	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:k:49:ILE:HG22	29:k:81:VAL:N	2.27	0.49
29:k:84:LEU:O	30:l:74:VAL:HG22	2.12	0.49
1:A:854:ARG:NH2	19:L:25:A:H5'	2.27	0.49
2:C:501:ILE:HD13	2:C:567:ILE:HG23	1.94	0.49
15:H:46:GLU:OE2	15:H:50:TRP:NE1	2.37	0.49
18:E:64:U:C2'	18:E:65:U:O5'	2.60	0.49
19:L:1168:U:H2'	19:L:1169:C:C6	2.46	0.49
1:A:1549:ALA:HA	10:Z:297:LEU:HD21	1.94	0.49
1:A:1710:GLU:HG2	1:A:1728:ILE:HG12	1.94	0.49
1:A:1964:PRO:HG2	1:A:2013:ARG:HA	1.93	0.49
2:C:251:GLN:HE21	2:C:255:GLN:HE21	1.60	0.49
13:I:184:GLN:HA	13:I:187:LYS:HZ3	1.78	0.49
14:n:290:ASP:O	14:n:320:TRP:HH2	1.95	0.49
19:L:1095:U:H3'	19:L:1096:C:C6	2.48	0.49
28:e:59:LYS:HG3	25:z:103:LEU:HD22	1.94	0.49
30:l:44:LEU:HB2	30:l:47:VAL:CG1	2.43	0.49
1:A:639:PHE:HA	1:A:644:VAL:HB	1.95	0.49
1:A:1368:GLN:NE2	1:A:1389:TYR:OH	2.46	0.49
7:R:150:HIS:C	7:R:151:LEU:HD12	2.37	0.49
12:d:267:TYR:HB3	12:d:284:LEU:HD23	1.94	0.49
17:D:176:A:H1'	27:h:33:PHE:CE1	2.43	0.49
19:L:5:A:N3	19:L:5:A:C2'	2.76	0.49
19:L:53:G:H1'	19:L:54:U:OP1	2.13	0.49
20:v:365:ASP:CB	20:v:399:VAL:HG22	2.42	0.49
22:b:49:HIS:O	22:b:50:LEU:CB	2.61	0.49
26:j:19:ILE:HG22	24:i:88:THR:HG23	1.94	0.49
1:A:1068:ARG:NH1	5:P:212:ASP:OD2	2.46	0.49
19:L:53:G:O2'	19:L:54:U:O5'	2.18	0.49
19:L:68:U:H2'	19:L:69:G:H8	1.78	0.49
24:u:35:ILE:HD11	27:w:79:LEU:HD12	1.86	0.49
25:m:14:GLN:HB3	25:m:26:TRP:CH2	2.48	0.49
26:j:63:ILE:CG1	24:i:89:LEU:HD23	2.43	0.49
27:h:72:PHE:O	28:g:103:VAL:HA	2.13	0.49
28:g:77:THR:HB	28:g:86:ASN:HD22	1.78	0.49
28:e:93:LYS:CD	25:z:97:LEU:HD11	2.43	0.49
29:s:93:LEU:HD11	25:z:21:ASN:ND2	2.28	0.49
1:A:1382:ARG:NH2	1:A:1635:HIS:O	2.45	0.49
2:C:168:VAL:HG21	2:C:175:LEU:HD13	1.94	0.49
2:C:993:ILE:HG12	2:C:997:LEU:HD22	1.94	0.49
4:O:275:THR:OG1	4:O:279:PRO:O	2.31	0.49
9:T:128:GLN:NE2	18:E:28:U:O4	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:1107:C:H3'	19:L:1107:C:OP2	2.12	0.49
28:e:91:ILE:HG21	25:z:96:ILE:HG12	1.95	0.49
9:T:121:ILE:HD11	9:T:129:LEU:HD21	1.95	0.49
19:L:1106:G:N2	21:a:69:ARG:O	2.46	0.49
19:L:1150:U:OP1	29:s:55:LYS:CG	2.61	0.49
29:k:35:MET:CB	30:l:84:PHE:CE2	2.85	0.49
30:l:65:ARG:HD3	30:l:67:SER:HB3	1.94	0.49
2:C:237:ILE:HD13	2:C:253:ILE:HG22	1.95	0.48
11:c:14:THR:HG23	11:c:17:GLU:H	1.78	0.48
17:D:55:U:H1'	17:D:60:U:O4	2.13	0.48
24:u:35:ILE:HD12	27:w:32:LYS:O	2.12	0.48
25:m:46:THR:HB	25:m:79:ILE:HA	1.95	0.48
30:l:15:GLN:HE21	30:l:16:GLY:N	2.11	0.48
30:l:21:LEU:CD2	30:l:72:ILE:CG1	2.81	0.48
30:l:39:SER:O	30:l:40:MET:CB	2.60	0.48
24:i:40:LYS:O	24:i:57:ALA:HA	2.13	0.48
27:w:32:LYS:HD2	27:w:33:PHE:HE1	1.77	0.48
1:A:2032:ILE:HD11	1:A:2043:PHE:HD1	1.77	0.48
1:A:2043:PHE:HE2	1:A:2047:GLN:N	2.11	0.48
5:P:127:VAL:HG11	18:E:32:U:H3	1.77	0.48
9:T:149:GLY:O	9:T:150:CYS:O	2.31	0.48
18:E:61:C:H6	18:E:61:C:H5''	1.78	0.48
19:L:1114:G:H2'	19:L:1115:G:C1'	2.42	0.48
20:v:617:PRO:O	20:v:618:GLU:CB	2.60	0.48
28:g:64:HIS:O	28:g:65:CYS:CB	2.61	0.48
30:l:44:LEU:CB	30:l:47:VAL:HG13	2.43	0.48
25:z:14:GLN:HB3	25:z:26:TRP:CH2	2.48	0.48
1:A:128:TYR:HA	9:T:112:ASN:HD21	1.78	0.48
1:A:225:ARG:NH2	1:A:693:LYS:O	2.46	0.48
1:A:1233:ARG:NH1	8:S:131:THR:HG21	2.28	0.48
1:A:1487:GLY:O	1:A:1490:ARG:NH2	2.38	0.48
1:A:1961:LEU:CD2	1:A:2084:LEU:CD1	2.89	0.48
2:C:117:ARG:NE	2:C:156:ASP:O	2.44	0.48
16:B:6:U:C2'	16:B:7:C:H5'	2.43	0.48
31:r:8:LYS:CG	31:o:88:TRP:CH2	2.96	0.48
1:A:255:ILE:HD11	1:A:637:VAL:HG13	1.95	0.48
1:A:1574:PHE:CD1	1:A:1574:PHE:N	2.73	0.48
4:O:220:TYR:HE1	4:O:256:ARG:HG2	1.78	0.48
14:n:292:HIS:CG	14:n:318:ARG:HH11	2.31	0.48
24:u:46:PHE:HB3	24:u:52:VAL:HG12	1.94	0.48
25:m:19:LEU:HD23	25:m:92:ILE:HA	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:g:41:ARG:HB2	28:g:57:ARG:HD3	1.95	0.48
31:r:137:LEU:HD23	31:o:137:LEU:HD23	1.95	0.48
4:O:430:GLU:HG2	4:O:431:THR:HG23	1.94	0.48
6:Q:248:CYS:SG	6:Q:316:LEU:CD1	3.01	0.48
8:S:3:THR:OG1	8:S:4:SER:N	2.47	0.48
12:d:189:TYR:HA	12:d:192:TYR:HB3	1.94	0.48
12:d:320:TYR:HA	12:d:323:TRP:HD1	1.77	0.48
26:j:64:ARG:HD2	24:i:87:ILE:HB	1.95	0.48
28:g:38:MET:HG3	28:g:58:VAL:O	2.13	0.48
28:e:59:LYS:HG2	28:e:70:GLU:HG3	1.96	0.48
31:r:14:VAL:HG12	31:r:52:GLU:HA	1.95	0.48
1:A:174:LYS:O	1:A:178:ASN:ND2	2.40	0.48
13:I:121:LYS:HZ1	20:v:529:HIS:CD2	2.29	0.48
17:D:129:G:C2'	17:D:129:G:N3	2.76	0.48
1:A:1283:GLU:HB3	10:Z:341:LYS:HB2	1.95	0.48
2:C:69:PRO:O	2:C:70:TYR:CG	2.66	0.48
17:D:168:U:C4	24:i:49:PHE:CZ	3.02	0.48
18:E:43:C:H2'	18:E:44:A:H8	1.79	0.48
20:v:652:LEU:HD11	20:v:666:PHE:CZ	2.49	0.48
30:l:17:HIS:CB	30:l:75:PRO:HG2	2.44	0.48
1:A:591:LEU:HD11	1:A:613:SER:HB2	1.96	0.48
1:A:737:ARG:HH12	18:E:69:C:H3'	1.77	0.48
2:C:110:LYS:HD2	2:C:113:ILE:HD12	1.96	0.48
4:O:446:LEU:HD23	12:d:237:ILE:CG2	2.43	0.48
9:T:144:GLN:HE21	9:T:151:ARG:CZ	2.26	0.48
18:E:64:U:O2'	18:E:65:U:O5'	2.30	0.48
19:L:1085:G:P	19:L:1085:G:C8	3.06	0.48
20:v:608:TYR:CD2	20:v:627:TYR:HD1	2.32	0.48
26:j:11:MET:HA	26:j:29:LEU:HD22	1.96	0.48
29:s:28:ARG:CG	29:s:52:ARG:HG2	2.42	0.48
29:s:53:VAL:CG2	25:z:67:LEU:CD1	2.91	0.48
31:r:20:ARG:CB	31:q:51:VAL:HG13	2.44	0.48
1:A:607:THR:HG22	1:A:611:LYS:HE2	1.95	0.48
2:C:629:TYR:HE2	2:C:655:LEU:HA	1.79	0.48
4:O:147:ILE:O	4:O:149:PRO:HD3	2.14	0.48
4:O:308:LYS:HA	5:P:148:HIS:CE1	2.49	0.48
4:O:352:ILE:O	4:O:352:ILE:HG22	2.14	0.48
4:O:365:PHE:CE1	4:O:373:LEU:HB2	2.49	0.48
28:e:45:ILE:HD12	28:e:55:ILE:HG12	1.96	0.48
26:x:35:PHE:O	26:x:36:LEU:HB3	2.14	0.48
1:A:1677:GLN:HE22	1:A:1707:HIS:H	1.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:138:VAL:HB	2:C:214:ASP:HA	1.96	0.48
4:O:371:GLY:HA3	4:O:400:ARG:HG2	1.95	0.48
14:n:73:SEP:O	14:n:73:SEP:OG	2.31	0.48
19:L:1107:C:HO2'	19:L:1108:A:P	2.37	0.48
27:h:29:VAL:O	27:h:37:GLU:HA	2.14	0.48
25:z:82:LEU:HD11	25:z:85:ILE:HB	1.96	0.48
9:T:73:ILE:HB	9:T:77:LEU:HD23	1.96	0.47
1:A:926:LYS:HD2	1:A:1521:ARG:HH12	1.78	0.47
1:A:1048:VAL:HG22	1:A:1250:VAL:HG22	1.95	0.47
1:A:1206:CYS:SG	1:A:1207:TRP:N	2.87	0.47
1:A:1993:ASP:HB2	1:A:2040:TRP:HB2	1.96	0.47
4:O:365:PHE:HE1	4:O:373:LEU:HB2	1.79	0.47
10:Z:39:GLU:OE2	10:Z:42:ARG:NH1	2.44	0.47
19:L:31:A:O2'	19:L:32:G:OP1	2.30	0.47
19:L:40:U:C2'	19:L:41:C:H5'	2.44	0.47
28:g:67:MET:HG3	28:g:69:LEU:CD1	2.44	0.47
29:k:33:GLN:O	29:k:45:LEU:HA	2.14	0.47
29:k:49:ILE:CG2	29:k:81:VAL:HB	2.43	0.47
29:s:48:CYS:SG	29:s:82:LEU:HD12	2.54	0.47
1:A:1677:GLN:OE1	1:A:1709:TRP:NE1	2.39	0.47
17:D:83:C:HO2'	17:D:84:A:P	2.30	0.47
20:v:403:GLN:HG2	20:v:439:LYS:HB2	1.95	0.47
25:m:21:ASN:ND2	29:k:93:LEU:HD11	2.28	0.47
25:m:25:VAL:HG22	25:m:45:LEU:HB2	1.96	0.47
1:A:971:MET:HE2	1:A:978:ILE:HG22	1.97	0.47
1:A:1626:GLN:CB	1:A:1633:PHE:CE1	2.97	0.47
2:C:201:THR:HG22	2:C:207:SER:HB3	1.95	0.47
5:P:126:PHE:HD1	6:Q:30:GLN:HB2	1.80	0.47
19:L:108:A:O3'	25:z:8:LYS:NZ	2.47	0.47
20:v:365:ASP:O	20:v:399:VAL:HG13	2.14	0.47
20:v:385:PHE:HA	20:v:388:LEU:HB2	1.95	0.47
22:b:65:ILE:O	22:b:86:ILE:HA	2.14	0.47
26:j:23:ARG:HH21	26:j:23:ARG:CB	2.27	0.47
30:l:77:LEU:O	30:l:79:LYS:N	2.47	0.47
27:w:29:VAL:O	27:w:37:GLU:HA	2.14	0.47
1:A:609:GLU:OE2	18:E:43:C:O2'	2.26	0.47
1:A:1992:TYR:N	1:A:1992:TYR:HD1	2.12	0.47
4:O:348:GLU:O	4:O:349:LYS:HB2	2.15	0.47
9:T:149:GLY:O	9:T:150:CYS:C	2.57	0.47
16:B:10:A:C8	16:B:11:A:N1	2.82	0.47
19:L:4:A:O4'	20:v:529:HIS:CG	2.68	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:120:G:H4'	19:L:121:C:C5'	2.45	0.47
27:h:19:LEU:HD11	24:i:81:LEU:HD22	1.96	0.47
28:e:102:ILE:HG13	28:e:103:VAL:N	2.30	0.47
1:A:129:THR:HB	1:A:130:PRO:HD2	1.97	0.47
1:A:1863:HIS:CD2	1:A:1873:LYS:HD2	2.49	0.47
5:P:162:GLU:C	5:P:164:LYS:N	2.71	0.47
7:R:54:GLN:H	7:R:58:HIS:HD2	1.63	0.47
22:b:60:THR:HA	22:b:82:GLY:O	2.15	0.47
25:m:92:ILE:HG13	25:m:92:ILE:H	1.45	0.47
28:g:89:ARG:NH2	28:g:91:ILE:HD11	2.29	0.47
30:l:11:LEU:HD23	30:l:36:SER:CB	2.45	0.47
1:A:672:LYS:NZ	17:D:86:G:OP2	2.47	0.47
1:A:1323:SER:O	1:A:1370:ARG:NH2	2.45	0.47
1:A:1992:TYR:N	1:A:1992:TYR:CD1	2.83	0.47
2:C:662:SER:O	2:C:665:LYS:NZ	2.48	0.47
2:C:869:HIS:HA	2:C:899:LEU:HA	1.97	0.47
4:O:186:ARG:NH1	4:O:202:GLU:OE2	2.48	0.47
4:O:271:GLN:HG2	4:O:314:THR:H	1.80	0.47
4:O:312:ARG:NH1	4:O:352:ILE:HG23	2.30	0.47
5:P:157:GLU:CD	5:P:157:GLU:N	2.73	0.47
5:P:170:SER:OG	5:P:173:LYS:O	2.32	0.47
5:P:197:ILE:HG23	11:c:90:MET:HE2	1.97	0.47
6:Q:12:ILE:HA	6:Q:71:CYS:HB2	1.96	0.47
7:R:51:PHE:HD2	7:R:80:MET:HG2	1.79	0.47
12:d:69:ILE:O	12:d:73:GLN:N	2.42	0.47
17:D:128:A:H1'	17:D:129:G:C5	2.50	0.47
18:E:48:C:H2'	18:E:49:A:H8	1.80	0.47
25:m:86:ASN:ND2	25:m:86:ASN:C	2.73	0.47
26:j:63:ILE:CG2	26:j:68:ILE:HD11	2.45	0.47
29:s:7:ALA:HB3	29:s:10:SER:HB2	1.96	0.47
25:z:25:VAL:HG22	25:z:45:LEU:HB2	1.97	0.47
1:A:300:LYS:HG2	1:A:492:LYS:HG2	1.97	0.47
1:A:1275:MET:C	1:A:1277:GLU:H	2.19	0.47
2:C:808:LEU:O	2:C:971:ARG:NH1	2.43	0.47
5:P:104:LEU:HD21	5:P:111:HIS:CD2	2.50	0.47
6:Q:196:PHE:HD1	6:Q:292:PRO:HD3	1.79	0.47
16:B:10:A:H2'	16:B:11:A:N9	2.30	0.47
20:v:577:VAL:HG12	20:v:583:ILE:HB	1.97	0.47
26:j:37:ASN:OD1	26:j:64:ARG:HA	2.14	0.47
29:k:45:LEU:O	29:k:84:LEU:HA	2.13	0.47
7:R:62:THR:OG1	7:R:63:ARG:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Z:44:LEU:HD21	10:Z:56:ILE:HD11	1.96	0.47
12:d:51:ARG:NE	12:d:75:GLU:OE2	2.48	0.47
19:L:5:A:C8	19:L:5:A:O5'	2.68	0.47
19:L:1083:A:H2'	19:L:1084:A:C8	2.47	0.47
19:L:1127:A:H2'	19:L:1128:C:O5'	2.14	0.47
28:e:93:LYS:CB	25:z:97:LEU:HD12	2.45	0.47
30:l:42:VAL:HG22	30:l:64:VAL:CG2	2.44	0.47
1:A:1309:ILE:HG12	1:A:1356:LEU:HD13	1.97	0.47
2:C:977:SER:OG	2:C:985:ASP:OD1	2.28	0.47
4:O:218:ARG:O	4:O:219:ASP:HB3	2.14	0.47
13:I:199:LYS:NZ	19:L:17:U:O3'	2.48	0.47
17:D:65:U:H2'	17:D:66:A:H8	1.79	0.47
19:L:108:A:C6	19:L:109:C:N4	2.83	0.47
20:v:389:ILE:HA	20:v:392:TYR:CD2	2.50	0.47
28:e:49:ARG:NH2	27:w:76:ASN:CG	2.73	0.47
29:s:54:PRO:HG2	29:s:57:GLN:HG3	1.96	0.47
29:s:95:THR:OG1	25:z:86:ASN:HB3	2.15	0.47
14:n:292:HIS:HA	14:n:318:ARG:NH1	2.29	0.46
19:L:53:G:O4'	19:L:54:U:OP1	2.33	0.46
20:v:397:ASN:HB3	20:v:411:TRP:HD1	1.79	0.46
22:b:137:LEU:O	22:b:140:TYR:CB	2.63	0.46
28:g:54:ILE:HA	28:g:73:LYS:O	2.14	0.46
30:l:63:PHE:C	30:l:63:PHE:HD1	2.24	0.46
25:z:33:SER:HB2	25:z:37:ASN:HB2	1.97	0.46
7:R:159:ARG:NH1	7:R:204:LEU:O	2.48	0.46
9:T:131:GLU:OE2	9:T:135:LYS:NZ	2.48	0.46
12:d:219:ARG:HA	12:d:222:TYR:HB2	1.98	0.46
19:L:113:U:O4	27:w:47:ASN:C	2.58	0.46
19:L:118:U:N3	28:e:66:ASN:ND2	2.58	0.46
19:L:1146:G:H5'	19:L:1147:A:OP2	2.15	0.46
24:u:81:LEU:HD22	27:w:19:LEU:HD11	1.98	0.46
26:j:30:ARG:HE	26:j:30:ARG:HB2	1.60	0.46
28:g:102:ILE:HG13	28:g:103:VAL:N	2.30	0.46
29:k:30:TYR:CE1	29:k:50:GLU:HB3	2.50	0.46
29:s:38:ASP:OD1	29:s:39:LYS:N	2.39	0.46
30:y:44:LEU:CB	30:y:47:VAL:HG11	2.45	0.46
1:A:928:ARG:HG3	19:L:30:A:C2	2.50	0.46
2:C:125:SER:OG	30:l:77:LEU:HD13	2.15	0.46
2:C:416:ASP:HB2	2:C:419:PRO:HD2	1.96	0.46
5:P:160:PRO:C	5:P:162:GLU:N	2.67	0.46
18:E:64:U:O2'	18:E:65:U:P	2.72	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:16:U:H3'	19:L:18:U:C5	2.51	0.46
19:L:110:A:H62	25:z:34:PRO:CB	2.28	0.46
20:v:442:THR:HG1	20:v:445:SER:HG	1.57	0.46
20:v:479:PRO:HB3	20:v:530:ARG:HD3	1.97	0.46
20:v:505:PHE:O	20:v:509:GLU:N	2.46	0.46
20:v:797:TYR:C	20:v:799:ASP:N	2.66	0.46
23:t:111:VAL:O	23:t:112:SER:C	2.58	0.46
28:g:78:GLU:HG2	28:g:85:ILE:HG23	1.94	0.46
29:k:11:ARG:H	29:k:14:ASN:CB	2.27	0.46
1:A:1813:TYR:CD2	1:A:1911:TRP:HH2	2.32	0.46
13:l:92:ARG:NH2	19:L:12:U:O3'	2.49	0.46
20:v:385:PHE:O	20:v:389:ILE:CD1	2.63	0.46
20:v:729:TYR:HE1	20:v:749:SER:CB	2.28	0.46
25:m:53:ASN:O	25:m:54:LYS:HB3	2.15	0.46
26:j:74:LEU:O	26:j:75:ASP:CB	2.64	0.46
28:g:26:PHE:HE1	28:g:63:ARG:HA	1.80	0.46
31:p:19:SER:OG	31:p:38:ASP:OD2	2.26	0.46
1:A:374:ILE:HD12	2:C:674:LEU:HD22	1.97	0.46
1:A:1618:ASN:N	1:A:1744:ASP:OD2	2.47	0.46
4:O:197:LEU:HB2	4:O:211:LEU:HD11	1.97	0.46
4:O:231:SER:OG	4:O:274:CYS:SG	2.66	0.46
19:L:7:C:O2'	19:L:8:U:H5'	2.16	0.46
19:L:1095:U:C3'	19:L:1096:C:C6	2.99	0.46
30:l:21:LEU:HD21	30:l:72:ILE:CD1	2.45	0.46
1:A:732:ARG:NH2	18:E:71:G:OP2	2.47	0.46
2:C:608:GLN:HE21	2:C:641:GLU:HG2	1.80	0.46
4:O:392:MET:HG2	8:S:158:ASN:HB2	1.97	0.46
4:O:446:LEU:CD2	12:d:237:ILE:CG2	2.94	0.46
14:n:292:HIS:CG	14:n:318:ARG:NH1	2.84	0.46
16:B:71:C:H2'	16:B:72:A:H8	1.81	0.46
19:L:1107:C:O2'	19:L:1108:A:P	2.74	0.46
19:L:1137:U:O4	21:a:67:LYS:O	2.33	0.46
28:g:67:MET:HG3	28:g:69:LEU:HD11	1.97	0.46
1:A:1889:LEU:HG	1:A:1991:ILE:CG1	2.45	0.46
1:A:1910:LYS:HB3	1:A:1940:MET:HG2	1.97	0.46
4:O:435:GLU:N	4:O:435:GLU:CD	2.73	0.46
10:Z:317:ILE:HD13	10:Z:325:VAL:HG21	1.97	0.46
17:D:83:C:H4'	17:D:84:A:OP1	2.15	0.46
17:D:99:U:O2'	17:D:100:A:OP1	2.34	0.46
17:D:123:U:O2'	17:D:124:C:H5'	2.16	0.46
19:L:1105:C:O3'	19:L:1106:G:O4'	2.34	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:1117:G:H2'	19:L:1118:U:H5'	1.98	0.46
28:g:41:ARG:CB	28:g:57:ARG:HD3	2.45	0.46
28:e:93:LYS:CD	25:z:97:LEU:CD1	2.94	0.46
29:s:53:VAL:CG2	25:z:67:LEU:HD11	2.45	0.46
30:l:77:LEU:C	30:l:79:LYS:H	2.24	0.46
24:i:51:ASN:HB3	24:i:84:GLY:H	1.81	0.46
1:A:1458:TRP:NE1	1:A:1489:PRO:HD2	2.31	0.46
10:Z:77:SER:HA	10:Z:80:ILE:HD12	1.98	0.46
12:d:270:ALA:HB1	12:d:280:LEU:HD11	1.98	0.46
16:B:10:A:C1'	16:B:11:A:C2	2.99	0.46
19:L:11:U:O2'	19:L:12:U:O5'	2.34	0.46
19:L:121:C:N4	27:w:33:PHE:CG	2.84	0.46
24:u:51:ASN:HB3	24:u:84:GLY:H	1.81	0.46
1:A:834:ILE:HD12	1:A:848:ASN:HD22	1.81	0.46
1:A:1961:LEU:HD21	1:A:2084:LEU:HD12	1.96	0.46
2:C:802:ALA:HB2	2:C:843:LYS:HA	1.98	0.46
5:P:76:ARG:HE	6:Q:5:ILE:HD12	1.79	0.46
5:P:216:ARG:HD3	5:P:220:ARG:HH22	1.81	0.46
10:Z:299:LEU:HD21	10:Z:343:TYR:HE1	1.81	0.46
14:n:405:SER:C	14:n:407:LEU:N	2.71	0.46
21:a:67:LYS:O	21:a:68:GLN:CB	2.64	0.46
29:k:16:ILE:O	29:k:17:ASP:HB2	2.16	0.46
28:e:33:LEU:HD23	27:w:72:PHE:HB2	1.98	0.46
30:l:11:LEU:HD11	30:l:72:ILE:HD13	1.94	0.46
1:A:946:ASN:HB3	1:A:949:ASP:HB2	1.98	0.46
1:A:1214:ARG:HE	2:C:981:PHE:HB2	1.81	0.46
2:C:246:THR:OG1	2:C:247:PHE:N	2.45	0.46
4:O:309:ARG:HD2	4:O:328:THR:HG21	1.98	0.46
5:P:150:ASP:CG	5:P:151:GLY:N	2.73	0.46
26:j:23:ARG:CG	26:j:23:ARG:NH2	2.79	0.46
29:k:84:LEU:HD21	30:l:78:LEU:HB2	1.98	0.46
31:p:105:LEU:O	31:p:109:LEU:N	2.47	0.46
1:A:2013:ARG:NH2	1:A:2083:ILE:O	2.49	0.45
2:C:232:SER:O	2:C:452:LYS:NZ	2.43	0.45
2:C:245:VAL:HG12	2:C:249:VAL:HG11	1.99	0.45
5:P:149:MET:HE3	5:P:149:MET:HB2	1.75	0.45
6:Q:242:VAL:HG22	6:Q:249:GLY:HA3	1.98	0.45
6:Q:270:LEU:HD12	6:Q:289:PHE:HE1	1.81	0.45
7:R:170:ILE:HD13	7:R:173:ILE:HD11	1.97	0.45
16:B:-10:G:O2'	16:B:-9:A:O5'	2.34	0.45
16:B:10:A:C1'	16:B:11:A:N3	2.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:168:U:C6	24:i:49:PHE:HE1	2.33	0.45
17:D:173:U:C5	28:g:64:HIS:CE1	3.04	0.45
25:m:82:LEU:HD12	25:m:83:GLN:N	2.31	0.45
1:A:774:ILE:HD11	1:A:777:LYS:HB2	1.98	0.45
1:A:1283:GLU:OE2	1:A:1442:ARG:NH2	2.49	0.45
1:A:1961:LEU:CD2	1:A:2084:LEU:HD13	2.37	0.45
2:C:477:ASP:OD2	2:C:663:TYR:OH	2.31	0.45
4:O:373:LEU:HD12	4:O:373:LEU:C	2.41	0.45
7:R:87:CYS:HB3	7:R:91:HIS:HE1	1.80	0.45
11:c:200:ILE:HG21	12:d:45:GLU:HG3	1.97	0.45
26:x:37:ASN:OD1	26:x:64:ARG:HA	2.16	0.45
1:A:1093:LYS:HD3	19:L:25:A:C8	2.51	0.45
1:A:1406:LEU:HB2	10:Z:307:GLU:HG3	1.99	0.45
1:A:1574:PHE:CG	1:A:1575:TRP:N	2.84	0.45
1:A:1965:PHE:O	1:A:1966:SER:HB3	2.16	0.45
2:C:206:LYS:HD2	2:C:208:ARG:HH21	1.81	0.45
11:c:160:LEU:HD23	13:I:196:ILE:HG12	1.98	0.45
17:D:167:A:C1'	28:g:64:HIS:HE2	2.27	0.45
25:m:18:GLU:HG3	25:m:24:THR:HG22	1.98	0.45
26:j:18:ASN:ND2	26:j:18:ASN:N	2.60	0.45
28:e:91:ILE:HG21	25:z:96:ILE:HD13	1.97	0.45
29:s:50:GLU:O	29:s:79:LYS:HA	2.17	0.45
30:l:44:LEU:HB2	30:l:47:VAL:HG13	1.98	0.45
1:A:769:MET:HG3	4:O:352:ILE:HD11	1.98	0.45
10:Z:322:LYS:HE3	10:Z:357:TRP:CE2	2.52	0.45
13:I:186:ALA:O	13:I:201:LYS:NZ	2.49	0.45
17:D:28:G:C2'	17:D:29:G:O5'	2.64	0.45
17:D:168:U:C4	24:i:49:PHE:HZ	2.35	0.45
19:L:54:U:P	19:L:54:U:H3'	2.57	0.45
19:L:117:U:C5	25:z:88:ARG:NH2	2.84	0.45
20:v:509:GLU:OE2	20:v:548:TYR:OH	2.23	0.45
26:j:20:ASN:OD1	24:i:32:PHE:CD2	2.70	0.45
27:h:46:ASP:N	28:g:30:PRO:HG2	2.31	0.45
30:l:23:LEU:HB3	30:l:25:THR:HG22	1.98	0.45
26:x:15:ILE:HG23	26:x:72:GLU:O	2.16	0.45
1:A:771:PRO:O	1:A:772:GLU:HB3	2.17	0.45
1:A:900:PHE:N	1:A:1075:ASP:OD2	2.43	0.45
1:A:1286:TRP:CE2	1:A:1302:LEU:HD11	2.51	0.45
4:O:420:ASP:OD2	4:O:424:LYS:NZ	2.49	0.45
9:T:40:LYS:NZ	18:E:35:A:O3'	2.50	0.45
10:Z:402:LEU:HD12	10:Z:405:ILE:HD13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:1129:U:H2'	19:L:1130:U:O5'	2.16	0.45
28:g:62:ASP:HB3	28:g:66:ASN:OD1	2.17	0.45
30:l:65:ARG:HH11	30:l:65:ARG:CG	2.14	0.45
31:p:14:VAL:HG12	31:p:52:GLU:HA	1.97	0.45
1:A:141:LYS:HE2	9:T:48:GLN:HB3	1.98	0.45
2:C:70:TYR:CE2	4:O:134:VAL:HG21	2.51	0.45
2:C:998:TYR:HE2	2:C:1002:ARG:HH21	1.63	0.45
6:Q:297:PHE:CD2	6:Q:298:SER:N	2.84	0.45
10:Z:37:LEU:HD23	10:Z:214:ILE:HG13	1.99	0.45
14:n:357:ASP:O	14:n:376:ILE:N	2.47	0.45
16:B:-10:G:O2'	16:B:-9:A:C8	2.61	0.45
19:L:16:U:H3'	19:L:18:U:H5	1.82	0.45
24:u:91:THR:HG21	26:x:57:LEU:HB3	1.99	0.45
28:g:78:GLU:CG	28:g:85:ILE:HG23	2.47	0.45
28:e:62:ASP:HB3	28:e:66:ASN:OD1	2.17	0.45
28:e:91:ILE:HG21	25:z:96:ILE:CG1	2.47	0.45
27:w:33:PHE:CD1	27:w:33:PHE:N	2.84	0.45
1:A:190:LYS:HD3	1:A:559:GLN:HE21	1.82	0.45
1:A:1275:MET:C	1:A:1277:GLU:N	2.75	0.45
1:A:1574:PHE:CE1	1:A:1826:TYR:O	2.69	0.45
1:A:2032:ILE:HG21	1:A:2041:PRO:HB2	1.97	0.45
4:O:217:ILE:CG2	4:O:218:ARG:HG3	2.47	0.45
14:n:405:SER:O	14:n:407:LEU:N	2.47	0.45
17:D:173:U:C2	28:g:97:ARG:NE	2.84	0.45
19:L:1146:G:H3'	19:L:1147:A:C5'	2.44	0.45
22:b:148:VAL:O	22:b:149:PRO:CB	2.64	0.45
25:m:17:ILE:CG2	25:m:92:ILE:HG21	2.38	0.45
26:j:19:ILE:HG22	26:j:67:SER:HB2	1.98	0.45
29:k:45:LEU:HD12	29:k:87:LEU:CD1	2.47	0.45
29:s:54:PRO:CG	29:s:76:LYS:O	2.65	0.45
1:A:345:ALA:HB3	3:J:3:TYR:HB2	1.99	0.45
1:A:1382:ARG:NH1	1:A:1614:ILE:O	2.45	0.45
5:P:149:MET:O	5:P:150:ASP:CB	2.55	0.45
16:B:7:C:O2'	16:B:8:U:C5'	2.65	0.45
19:L:116:U:C2	29:s:40:HIS:CD2	3.04	0.45
20:v:570:THR:HG21	20:v:594:PHE:CZ	2.51	0.45
20:v:645:ARG:NH2	20:v:673:GLU:OE2	2.43	0.45
22:b:54:THR:CA	22:b:77:HIS:CB	2.94	0.45
22:b:97:ASN:O	22:b:98:VAL:CB	2.64	0.45
30:l:14:ALA:HB1	30:l:19:VAL:HG11	1.98	0.45
1:A:227:GLU:HG2	1:A:647:PHE:CG	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:265:ASN:CG	9:T:7:ARG:HH22	2.25	0.45
16:B:10:A:H1'	16:B:11:A:C2	2.52	0.45
20:v:324:ASP:O	20:v:328:LYS:N	2.47	0.45
26:j:35:PHE:O	26:j:36:LEU:CB	2.64	0.45
29:k:45:LEU:HD12	29:k:87:LEU:HD13	1.98	0.45
29:k:86:ILE:HG22	30:l:10:LEU:HD23	1.99	0.45
28:e:48:LEU:HD22	28:e:52:HIS:HE2	1.77	0.45
29:s:54:PRO:CG	29:s:57:GLN:CG	2.94	0.45
30:l:33:LEU:CD2	30:l:35:GLU:O	2.63	0.45
25:z:18:GLU:HG3	25:z:24:THR:HG22	1.98	0.45
1:A:228:LYS:HZ2	1:A:695:LEU:HD13	1.82	0.45
1:A:305:LEU:HD12	1:A:472:ASN:HB3	1.98	0.45
4:O:396:LEU:HB2	4:O:399:GLU:HG3	1.99	0.45
19:L:1095:U:H2'	19:L:1096:C:N1	2.32	0.45
20:v:412:MET:HE2	20:v:428:TYR:HA	1.99	0.45
20:v:415:VAL:HG21	20:v:427:VAL:HG21	1.98	0.45
30:l:21:LEU:CD2	30:l:42:VAL:HG21	2.46	0.45
2:C:136:VAL:HG23	2:C:234:LEU:O	2.17	0.44
5:P:156:GLY:C	5:P:157:GLU:CD	2.86	0.44
6:Q:79:ARG:HG2	6:Q:80:TRP:CD1	2.52	0.44
15:H:91:ARG:NH2	16:B:54:A:OP2	2.50	0.44
17:D:116:U:H2'	17:D:117:G:C8	2.53	0.44
25:m:14:GLN:NE2	25:m:28:THR:OG1	2.50	0.44
29:k:15:LEU:HD13	29:k:18:TYR:HB2	1.99	0.44
25:z:14:GLN:NE2	25:z:28:THR:OG1	2.50	0.44
1:A:1673:LEU:HB2	1:A:1678:ILE:HD11	1.99	0.44
1:A:1796:PRO:O	1:A:1800:ASN:ND2	2.50	0.44
1:A:1964:PRO:O	1:A:1965:PHE:HB2	2.17	0.44
2:C:180:ASN:HD22	2:C:194:ASN:HD21	1.65	0.44
2:C:884:ARG:HH21	2:C:962:LEU:HD13	1.83	0.44
4:O:208:CYS:SG	4:O:209:TRP:N	2.90	0.44
15:H:36:ARG:NE	16:B:55:U:H5'	2.32	0.44
19:L:114:U:C2	26:x:64:ARG:HG3	2.52	0.44
25:m:39:ILE:CD1	25:m:84:TYR:HE1	2.22	0.44
28:e:52:HIS:CD2	28:e:52:HIS:O	2.71	0.44
30:l:34:VAL:HG12	30:l:35:GLU:HG2	1.98	0.44
30:l:38:ASP:OD1	30:l:38:ASP:N	2.43	0.44
25:z:8:LYS:HE2	25:z:8:LYS:HB3	1.59	0.44
2:C:713:GLU:O	2:C:817:GLN:N	2.39	0.44
5:P:205:SER:OG	11:c:79:GLU:O	2.26	0.44
12:d:59:LYS:HG3	18:E:66:C:C5	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:117:U:H5'	25:z:90:ASN:CB	2.48	0.44
25:m:72:GLN:NE2	25:m:75:ALA:HB2	2.33	0.44
27:h:33:PHE:CZ	28:g:49:ARG:NE	2.85	0.44
27:h:80:TYR:HE1	27:h:82:ARG:HD2	1.82	0.44
28:g:63:ARG:HE	28:g:63:ARG:HB3	1.60	0.44
28:e:49:ARG:N	28:e:100:SER:O	2.49	0.44
28:e:66:ASN:HB3	28:e:98:GLY:H	1.81	0.44
28:e:73:LYS:HG3	28:e:90:PHE:HD2	1.83	0.44
30:l:70:LYS:NZ	30:l:70:LYS:CB	2.79	0.44
1:A:905:TYR:OH	1:A:1002:GLU:OE2	2.33	0.44
1:A:1508:HIS:HA	1:A:1511:ARG:HG2	2.00	0.44
4:O:248:ILE:HB	4:O:262:LEU:HB2	1.99	0.44
4:O:433:THR:O	4:O:435:GLU:O	2.35	0.44
6:Q:4:GLU:HG2	6:Q:5:ILE:HG23	2.00	0.44
7:R:149:LYS:HB3	7:R:151:LEU:HD11	2.00	0.44
19:L:4:A:OP1	19:L:4:A:C8	2.70	0.44
19:L:6:U:O5'	19:L:6:U:C6	2.70	0.44
19:L:7:C:OP2	19:L:7:C:C6	2.70	0.44
19:L:1093:C:C5	19:L:1093:C:OP2	2.70	0.44
26:j:5:PRO:HA	30:l:37:GLU:OE1	2.17	0.44
27:h:16:LYS:HB3	27:h:17:PRO:HD3	2.00	0.44
29:k:30:TYR:CD1	29:k:50:GLU:CB	2.98	0.44
27:w:16:LYS:HB3	27:w:17:PRO:HD3	1.99	0.44
25:z:72:GLN:NE2	25:z:75:ALA:HB2	2.33	0.44
1:A:1337:THR:HG22	16:B:76:U:H1'	1.99	0.44
1:A:1574:PHE:O	1:A:1575:TRP:CD1	2.70	0.44
1:A:1574:PHE:O	1:A:1575:TRP:CG	2.71	0.44
5:P:196:THR:HA	11:c:90:MET:HE1	1.99	0.44
7:R:63:ARG:HD3	9:T:143:HIS:CD2	2.53	0.44
12:d:67:GLN:OE1	12:d:70:ARG:NH2	2.50	0.44
12:d:139:TYR:HD2	12:d:155:LEU:HD22	1.82	0.44
19:L:84:C:H2'	19:L:85:A:C8	2.53	0.44
20:v:479:PRO:HB3	20:v:530:ARG:CD	2.47	0.44
28:g:56:ALA:HB3	28:g:69:LEU:HD23	2.00	0.44
1:A:420:PRO:HG2	1:A:423:PHE:HB2	2.00	0.44
1:A:864:GLN:HE22	1:A:1101:TYR:N	2.15	0.44
1:A:2019:GLU:HB3	1:A:2020:GLU:OE1	2.18	0.44
6:Q:214:ILE:HD11	6:Q:283:ILE:HD13	1.99	0.44
14:n:372:HIS:CG	14:n:373:PRO:N	2.85	0.44
19:L:4:A:N9	20:v:529:HIS:CE1	2.85	0.44
19:L:1107:C:OP2	19:L:1107:C:C6	2.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:1129:U:O2'	19:L:1130:U:C5'	2.65	0.44
20:v:549:ILE:HD12	20:v:587:MET:HE3	1.99	0.44
25:m:36:MET:HE3	25:m:36:MET:HB2	1.90	0.44
29:k:49:ILE:HG22	29:k:80:ARG:O	2.17	0.44
29:k:105:LYS:HA	29:k:108:ARG:NE	2.32	0.44
29:s:54:PRO:HG2	29:s:57:GLN:CG	2.48	0.44
26:x:33:ASP:OD1	26:x:37:ASN:N	2.51	0.44
31:q:14:VAL:HG12	31:q:52:GLU:HA	2.00	0.44
1:A:425:ASP:H	1:A:428:LEU:HD12	1.83	0.44
1:A:1773:VAL:HA	1:A:1788:GLY:HA3	2.00	0.44
2:C:67:GLU:C	2:C:68:HIS:ND1	2.76	0.44
2:C:68:HIS:CG	2:C:68:HIS:O	2.71	0.44
13:I:197:ASN:OD1	13:I:200:ASN:ND2	2.51	0.44
19:L:6:U:H6	19:L:6:U:O5'	2.00	0.44
19:L:1085:G:C8	19:L:1085:G:OP2	2.70	0.44
19:L:1093:C:OP2	19:L:1093:C:H5	2.01	0.44
19:L:1154:U:H2'	19:L:1155:C:C5	2.49	0.44
20:v:391:LEU:O	20:v:395:TYR:CD2	2.70	0.44
25:m:43:VAL:HG21	25:m:85:ILE:HG22	1.96	0.44
27:h:13:VAL:O	24:i:53:VAL:HG21	2.17	0.44
29:k:15:LEU:C	29:k:15:LEU:CD1	2.86	0.44
28:e:93:LYS:NZ	25:z:101:LEU:O	2.51	0.44
30:y:44:LEU:HB3	30:y:47:VAL:HG11	2.00	0.44
1:A:654:HIS:CE1	1:A:658:ASN:HD21	2.36	0.44
1:A:1995:TRP:O	1:A:1999:ILE:HD12	2.17	0.44
5:P:193:GLU:OE1	5:P:195:ASN:N	2.48	0.44
17:D:176:A:N3	27:h:33:PHE:CD1	2.81	0.44
19:L:4:A:C4	19:L:5:A:C8	3.06	0.44
19:L:116:U:C4	29:s:40:HIS:NE2	2.86	0.44
19:L:1136:U:OP1	19:L:1136:U:C6	2.70	0.44
20:v:549:ILE:HD12	20:v:587:MET:CE	2.48	0.44
26:j:33:ASP:OD1	26:j:37:ASN:N	2.51	0.44
1:A:1192:ASP:OD1	1:A:1192:ASP:N	2.51	0.44
1:A:1990:ASN:O	1:A:1993:ASP:OD1	2.35	0.44
6:Q:190:LEU:HD11	6:Q:312:LEU:HD11	1.99	0.44
7:R:207:PRO:HB3	7:R:212:TRP:CE2	2.52	0.44
17:D:169:U:O2	26:j:66:ASN:N	2.51	0.44
19:L:5:A:C2	19:L:6:U:C5	3.05	0.44
19:L:1093:C:C6	19:L:1093:C:H5''	2.52	0.44
24:u:31:LEU:HD21	24:u:82:LEU:HD21	2.00	0.44
24:i:31:LEU:HD21	24:i:82:LEU:HD21	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:754:TYR:HE2	1:A:819:LYS:HG3	1.82	0.43
1:A:1031:GLY:HA3	1:A:1145:MET:HE3	1.99	0.43
1:A:1162:THR:HG22	1:A:1169:TYR:HB2	2.00	0.43
1:A:1991:ILE:H	1:A:1991:ILE:HG13	1.40	0.43
1:A:2043:PHE:CE2	1:A:2047:GLN:HB3	2.53	0.43
14:n:292:HIS:CB	14:n:314:ASP:OD2	2.65	0.43
19:L:51:C:O5'	19:L:51:C:C6	2.70	0.43
20:v:385:PHE:C	20:v:389:ILE:HD12	2.43	0.43
24:i:30:TRP:CE2	24:i:38:ARG:CD	2.99	0.43
1:A:1073:ILE:HG23	1:A:1074:VAL:HG23	2.00	0.43
1:A:1233:ARG:HH12	8:S:131:THR:HG21	1.83	0.43
1:A:1995:TRP:CZ3	1:A:2040:TRP:CD1	3.06	0.43
3:J:24:LEU:H	10:Z:310:HIS:HD2	1.67	0.43
7:R:102:LEU:O	7:R:106:THR:OG1	2.29	0.43
7:R:149:LYS:HB3	7:R:151:LEU:CD1	2.47	0.43
17:D:128:A:O2'	17:D:129:G:O4'	2.36	0.43
17:D:147:C:H2'	17:D:148:G:C8	2.53	0.43
18:E:85:C:H5''	18:E:85:C:C6	2.53	0.43
19:L:54:U:OP2	19:L:54:U:C6	2.70	0.43
19:L:113:U:H5	27:w:48:TYR:CE1	2.30	0.43
20:v:612:ILE:N	20:v:613:PRO:CD	2.81	0.43
25:m:26:TRP:O	25:m:43:VAL:HA	2.17	0.43
25:m:103:LEU:HD23	25:m:107:LEU:HD11	2.01	0.43
29:k:32:GLY:HA3	29:k:47:GLU:O	2.18	0.43
28:e:91:ILE:HG21	25:z:96:ILE:CD1	2.48	0.43
1:A:320:ASP:HB3	1:A:483:PRO:HG2	2.00	0.43
1:A:1889:LEU:HD21	1:A:1991:ILE:CD1	2.47	0.43
2:C:177:TYR:O	2:C:548:ARG:NE	2.50	0.43
2:C:317:LYS:HB2	33:C:1500:GTP:C4	2.53	0.43
2:C:385:PHE:HE1	2:C:425:LEU:HD11	1.84	0.43
4:O:256:ARG:HH11	4:O:256:ARG:HD2	1.71	0.43
17:D:167:A:C8	27:h:48:TYR:CZ	3.06	0.43
19:L:30:A:HO2'	19:L:31:A:P	2.40	0.43
19:L:1146:G:H2'	19:L:1147:A:C1'	2.48	0.43
22:b:77:HIS:HA	22:b:98:VAL:HA	1.99	0.43
25:m:47:LEU:CD1	25:m:61:ALA:HB1	2.38	0.43
26:j:62:VAL:HG12	24:i:90:ILE:HB	2.00	0.43
29:k:28:ARG:CD	29:k:52:ARG:HG2	2.48	0.43
29:k:52:ARG:HB3	29:k:52:ARG:CZ	2.48	0.43
30:l:33:LEU:HD23	30:l:33:LEU:C	2.43	0.43
1:A:1040:ASP:O	1:A:1045:GLN:NE2	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1669:LEU:HD22	1:A:1669:LEU:HA	1.90	0.43
1:A:1806:MET:O	1:A:1816:ARG:NH2	2.51	0.43
2:C:187:ARG:NH2	2:C:654:CYS:SG	2.91	0.43
2:C:675:THR:HG22	2:C:909:ILE:HD13	2.00	0.43
4:O:145:VAL:HG22	4:O:157:THR:HG23	1.99	0.43
4:O:229:THR:HG21	4:O:272:VAL:N	2.34	0.43
11:c:157:ALA:O	11:c:161:ASN:ND2	2.52	0.43
19:L:1097:G:C2	19:L:1146:G:C4	3.07	0.43
28:g:105:LEU:C	28:g:105:LEU:CD1	2.88	0.43
29:k:35:MET:CE	29:k:46:ASN:HB2	2.49	0.43
29:s:54:PRO:CG	29:s:57:GLN:HG2	2.47	0.43
1:A:1275:MET:HE3	1:A:1275:MET:HB3	1.67	0.43
1:A:1276:GLU:CG	1:A:1277:GLU:N	2.81	0.43
2:C:75:GLU:OE2	4:O:133:ARG:NE	2.51	0.43
6:Q:316:LEU:O	6:Q:319:LEU:N	2.52	0.43
14:n:375:LYS:C	14:n:376:ILE:HG13	2.44	0.43
16:B:3:A:H2	18:E:79:A:C2	2.36	0.43
19:L:7:C:H2'	19:L:8:U:C6	2.54	0.43
19:L:1086:U:OP2	19:L:1086:U:C6	2.70	0.43
29:k:104:SER:O	29:k:107:GLU:HB3	2.17	0.43
1:A:1051:GLU:HB2	1:A:1247:PHE:HB2	2.01	0.43
1:A:1304:VAL:H	1:A:1353:THR:HG21	1.84	0.43
2:C:201:THR:HA	2:C:207:SER:HA	2.01	0.43
5:P:34:ILE:HG21	12:d:155:LEU:HD12	2.01	0.43
9:T:67:TYR:HB2	9:T:73:ILE:HD11	2.01	0.43
10:Z:181:LEU:HA	10:Z:181:LEU:HD23	1.80	0.43
19:L:1107:C:O2'	19:L:1108:A:O5'	2.37	0.43
19:L:1126:G:H8	19:L:1126:G:O5'	2.01	0.43
26:j:15:ILE:HG12	26:j:73:ALA:HA	2.00	0.43
30:l:36:SER:C	30:l:37:GLU:HG2	2.44	0.43
27:w:32:LYS:CG	27:w:33:PHE:HE1	2.30	0.43
25:z:26:TRP:O	25:z:43:VAL:HA	2.17	0.43
25:z:31:SER:O	25:z:39:ILE:HG22	2.18	0.43
2:C:164:MET:HG3	2:C:168:VAL:HG23	2.01	0.43
2:C:680:SER:OG	2:C:681:CYS:N	2.52	0.43
2:C:683:ASN:HD22	2:C:854:ILE:HG13	1.84	0.43
2:C:707:SER:H	2:C:824:SER:HB3	1.83	0.43
12:d:319:ASP:OD1	12:d:319:ASP:N	2.52	0.43
16:B:-1:A:H2'	16:B:0:G:C5'	2.49	0.43
16:B:10:A:C8	16:B:10:A:OP2	2.72	0.43
17:D:124:C:C2'	17:D:125:C:H5'	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:128:A:H2'	17:D:128:A:N3	2.33	0.43
17:D:128:A:C8	17:D:128:A:OP2	2.71	0.43
19:L:109:C:C3'	19:L:109:C:C6	3.01	0.43
20:v:728:LEU:O	20:v:732:CYS:N	2.48	0.43
24:i:32:PHE:HB3	24:i:34:GLN:OE1	2.18	0.43
25:z:15:VAL:HG11	25:z:29:LEU:HD12	2.00	0.43
1:A:834:ILE:HG12	1:A:840:VAL:HG11	2.00	0.43
1:A:879:ALA:HB1	5:P:208:LEU:HD21	2.00	0.43
1:A:882:ILE:HG21	1:A:1065:LEU:HD11	2.01	0.43
10:Z:369:TYR:CZ	10:Z:405:ILE:HG23	2.54	0.43
17:D:82:A:O2'	17:D:83:C:H5'	2.18	0.43
20:v:454:GLY:O	20:v:458:TRP:N	2.52	0.43
25:m:84:TYR:CG	25:m:84:TYR:O	2.71	0.43
29:k:86:ILE:HG21	30:l:10:LEU:HD23	1.99	0.43
29:k:105:LYS:O	29:k:108:ARG:NE	2.52	0.43
28:e:77:THR:HB	28:e:86:ASN:HD22	1.84	0.43
28:e:79:LYS:HA	28:e:83:ASN:O	2.19	0.43
27:w:80:TYR:HE1	27:w:82:ARG:HD2	1.83	0.43
30:y:49:ALA:HB2	30:y:59:MET:HE3	2.01	0.43
1:A:630:LYS:NZ	1:A:634:ASP:OD2	2.45	0.43
1:A:896:SER:OG	1:A:1006:ARG:NH1	2.52	0.43
1:A:1327:THR:HA	1:A:1603:ASN:HD21	1.84	0.43
1:A:1687:HIS:HD2	1:A:1688:PRO:HD2	1.84	0.43
1:A:1991:ILE:O	1:A:1993:ASP:OD2	2.36	0.43
6:Q:102:GLU:OE2	12:d:82:ARG:NH2	2.52	0.43
6:Q:269:THR:HG22	6:Q:279:GLY:HA2	2.01	0.43
13:I:196:ILE:HB	13:I:200:ASN:ND2	2.33	0.43
25:m:17:ILE:HG21	25:m:92:ILE:HG23	1.98	0.43
27:h:67:THR:C	27:h:68:LEU:HD12	2.44	0.43
29:s:21:ARG:HD3	25:z:67:LEU:O	2.19	0.43
27:w:67:THR:C	27:w:68:LEU:HD12	2.44	0.43
1:A:541:ASN:HD21	17:D:79:C:H5	1.66	0.43
1:A:724:ARG:HH21	1:A:725:TYR:HE1	1.66	0.43
1:A:1165:LEU:HD12	1:A:1166:ASP:CB	2.49	0.43
4:O:307:HIS:NE2	4:O:325:SER:OG	2.42	0.43
4:O:435:GLU:CD	4:O:435:GLU:H	2.25	0.43
9:T:108:CYS:HB3	9:T:120:CYS:SG	2.58	0.43
15:H:60:GLN:O	15:H:63:THR:OG1	2.33	0.43
19:L:120:G:H4'	19:L:121:C:H5'	2.01	0.43
19:L:1147:A:O2'	19:L:1148:U:H5'	2.19	0.43
25:m:33:SER:HB2	25:m:37:ASN:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:m:96:ILE:CD1	28:g:89:ARG:NH2	2.73	0.43
1:A:1270:LEU:HD22	1:A:1275:MET:SD	2.59	0.42
1:A:1879:ILE:HG12	1:A:1913:THR:HG22	2.00	0.42
2:C:492:LEU:HD22	2:C:493:LEU:H	1.84	0.42
13:I:157:ASP:OD1	13:I:157:ASP:N	2.51	0.42
17:D:131:A:H5''	17:D:132:A:C8	2.54	0.42
19:L:33:U:H2'	19:L:34:G:C8	2.54	0.42
19:L:125:C:H4'	28:e:81:GLY:H	1.83	0.42
20:v:593:LEU:HD22	20:v:593:LEU:HA	1.84	0.42
25:m:15:VAL:HG22	25:m:16:THR:N	2.33	0.42
25:m:67:LEU:O	29:k:21:ARG:HD3	2.19	0.42
28:e:91:ILE:HD12	28:e:94:LEU:CD1	2.48	0.42
30:l:21:LEU:HD13	30:l:42:VAL:HG21	2.00	0.42
1:A:264:ILE:HG13	1:A:647:PHE:CZ	2.54	0.42
4:O:250:LEU:HD12	4:O:260:ILE:HB	2.01	0.42
16:B:2:U:O2	16:B:2:U:H3'	2.19	0.42
16:B:10:A:C5	16:B:11:A:N6	2.86	0.42
17:D:128:A:H1'	17:D:129:G:C4	2.55	0.42
17:D:175:G:P	28:g:49:ARG:HH12	2.42	0.42
20:v:385:PHE:CD1	20:v:388:LEU:HD12	2.54	0.42
25:z:45:LEU:HG	25:z:45:LEU:O	2.20	0.42
1:A:261:LEU:O	1:A:263:PRO:HD3	2.18	0.42
1:A:744:THR:O	1:A:749:ARG:NH2	2.52	0.42
1:A:1161:TYR:CD1	1:A:1170:MET:HG2	2.55	0.42
1:A:1264:GLY:HA3	1:A:1308:GLU:HG3	2.01	0.42
1:A:1991:ILE:O	1:A:2040:TRP:CD1	2.73	0.42
1:A:2080:LYS:HB2	1:A:2084:LEU:HD21	2.00	0.42
2:C:187:ARG:HB3	2:C:189:LEU:HD23	2.01	0.42
2:C:478:TYR:CE2	2:C:550:VAL:HG23	2.54	0.42
14:n:357:ASP:HA	14:n:376:ILE:H	1.84	0.42
17:D:43:G:H2'	17:D:45:A:OP1	2.19	0.42
17:D:173:U:C1'	28:g:99:ASP:HB3	2.34	0.42
19:L:4:A:H2'	19:L:5:A:C8	2.51	0.42
20:v:397:ASN:HD22	20:v:397:ASN:HA	1.66	0.42
20:v:529:HIS:CG	20:v:529:HIS:O	2.71	0.42
26:j:23:ARG:NH2	26:j:23:ARG:HG2	2.34	0.42
29:k:51:GLU:HB3	29:k:77:VAL:HG11	2.02	0.42
30:l:77:LEU:C	30:l:79:LYS:N	2.76	0.42
1:A:780:ARG:HH22	8:S:9:LEU:HD21	1.84	0.42
1:A:893:ARG:HD3	1:A:893:ARG:HA	1.83	0.42
1:A:1388:PHE:HA	1:A:1397:LEU:HD23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1910:LYS:HE2	1:A:1940:MET:HG2	2.01	0.42
6:Q:31:GLY:HA3	6:Q:43:LEU:HB2	2.01	0.42
16:B:2:U:O2'	16:B:3:A:OP1	2.34	0.42
19:L:10:U:O2'	19:L:11:U:H5'	2.19	0.42
28:e:54:ILE:HB	28:e:72:VAL:HG22	2.01	0.42
30:y:41:ASN:HB3	30:y:66:GLY:H	1.83	0.42
1:A:318:LEU:HD13	1:A:501:LEU:HD23	2.02	0.42
1:A:1738:LEU:HD23	1:A:1777:ILE:HB	2.02	0.42
2:C:77:LEU:HD21	4:O:135:ILE:HG12	2.02	0.42
2:C:633:ILE:HB	2:C:645:LEU:HD12	2.01	0.42
4:O:420:ASP:O	8:S:158:ASN:ND2	2.53	0.42
17:D:147:C:H2'	17:D:148:G:H8	1.83	0.42
17:D:169:U:H1'	26:j:66:ASN:HB2	2.01	0.42
18:E:61:C:H5''	18:E:61:C:C6	2.54	0.42
19:L:68:U:H2'	19:L:69:G:C8	2.55	0.42
19:L:1082:A:C2	19:L:1083:A:C5	3.07	0.42
20:v:342:ILE:O	20:v:346:TYR:N	2.45	0.42
25:m:84:TYR:CG	29:k:6:VAL:HG11	2.41	0.42
26:j:74:LEU:H	26:j:74:LEU:HG	1.65	0.42
29:k:35:MET:HE2	29:k:46:ASN:CA	2.50	0.42
28:e:78:GLU:HG3	25:z:52:LEU:HD22	2.00	0.42
29:s:31:ILE:O	29:s:48:CYS:HA	2.19	0.42
2:C:206:LYS:CE	30:l:12:ASN:HB3	2.49	0.42
2:C:328:VAL:HG21	2:C:345:THR:HG22	2.01	0.42
2:C:701:GLU:HG2	2:C:702:ASN:H	1.83	0.42
4:O:186:ARG:HG3	4:O:202:GLU:HG3	2.02	0.42
4:O:306:HIS:CD2	4:O:334:TRP:HH2	2.38	0.42
7:R:90:LEU:HB3	7:R:92:HIS:CD2	2.55	0.42
7:R:234:ALA:HB2	7:R:237:ARG:HH21	1.84	0.42
16:B:10:A:C8	16:B:11:A:N3	2.85	0.42
19:L:38:U:H2'	19:L:39:A:H8	1.85	0.42
28:g:50:ASN:CB	28:g:52:HIS:ND1	2.69	0.42
29:k:35:MET:SD	30:l:84:PHE:CE2	3.13	0.42
1:A:265:ASN:OD1	9:T:7:ARG:NH2	2.49	0.42
6:Q:106:ASN:ND2	11:c:212:ASP:H	2.18	0.42
6:Q:213:SER:OG	6:Q:214:ILE:N	2.49	0.42
9:T:44:LYS:HD3	9:T:44:LYS:HA	1.84	0.42
16:B:57:C:O2'	16:B:58:U:P	2.78	0.42
19:L:1084:A:H2'	19:L:1084:A:N3	2.34	0.42
19:L:1146:G:C4	19:L:1147:A:C5	3.07	0.42
23:t:105:PRO:O	23:t:109:SER:OG	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:j:74:LEU:O	26:j:74:LEU:HD12	2.20	0.42
4:O:391:GLU:HG2	4:O:392:MET:H	1.85	0.42
6:Q:33:GLU:HA	6:Q:40:PRO:HA	2.01	0.42
8:S:5:HIS:HB3	19:L:21:G:N7	2.34	0.42
13:I:102:LYS:NZ	13:I:106:GLU:OE2	2.49	0.42
14:n:271:LYS:HA	14:n:291:HIS:CB	2.49	0.42
15:H:34:ARG:HH12	15:H:36:ARG:NH1	2.18	0.42
16:B:68:U:H3	19:L:36:A:H61	1.67	0.42
19:L:1097:G:H21	19:L:1146:G:H1'	1.84	0.42
28:e:91:ILE:CG2	25:z:96:ILE:CG2	2.98	0.42
1:A:281:TYR:O	9:T:8:ARG:NH2	2.53	0.42
1:A:898:ILE:HB	1:A:1074:VAL:HG22	2.02	0.42
1:A:1021:PRO:HG2	1:A:1345:TYR:HE1	1.85	0.42
1:A:1508:HIS:HA	1:A:1511:ARG:HE	1.84	0.42
1:A:1967:ALA:O	1:A:1971:ILE:N	2.39	0.42
1:A:2047:GLN:HG2	1:A:2051:ILE:HG13	2.01	0.42
2:C:794:GLN:HE22	2:C:835:LYS:HG2	1.85	0.42
10:Z:358:GLN:O	10:Z:362:ASN:ND2	2.53	0.42
10:Z:474:THR:OG1	10:Z:478:ARG:NH1	2.51	0.42
11:c:40:LEU:HD12	11:c:40:LEU:HA	1.89	0.42
30:l:41:ASN:ND2	30:l:63:PHE:CZ	2.88	0.42
1:A:962:ARG:NE	1:A:1080:ASP:OD2	2.47	0.42
1:A:1993:ASP:HB3	1:A:2038:HIS:HB3	2.00	0.42
2:C:177:TYR:HD2	2:C:178:LEU:HD12	1.85	0.42
16:B:10:A:C5	16:B:11:A:N1	2.88	0.42
17:D:168:U:H2'	24:i:49:PHE:CE1	2.53	0.42
29:s:54:PRO:CB	29:s:57:GLN:CG	2.88	0.42
25:z:103:LEU:HD23	25:z:107:LEU:HD11	2.01	0.42
1:A:167:TYR:HB3	1:A:201:PHE:HZ	1.85	0.41
1:A:591:LEU:HB3	1:A:599:LEU:HD11	2.02	0.41
1:A:1017:ASP:OD2	1:A:1507:GLY:N	2.37	0.41
1:A:1067:ASN:O	1:A:1071:ARG:HG2	2.20	0.41
2:C:706:LEU:HD23	2:C:706:LEU:HA	1.86	0.41
9:T:102:LYS:NZ	9:T:157:ASP:O	2.52	0.41
12:d:140:LEU:HD23	12:d:152:VAL:HG12	2.01	0.41
12:d:289:LYS:HE3	12:d:289:LYS:HB2	1.90	0.41
19:L:4:A:O5'	19:L:4:A:C8	2.70	0.41
19:L:51:C:H2'	19:L:52:A:O4'	2.20	0.41
19:L:1095:U:C2'	19:L:1096:C:C6	3.03	0.41
24:u:28:THR:N	24:u:91:THR:O	2.49	0.41
25:m:104:ASP:OD1	25:m:105:SER:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:k:44:VAL:CG2	29:k:86:ILE:HG22	2.36	0.41
30:l:44:LEU:HD23	30:l:44:LEU:N	2.32	0.41
24:i:28:THR:N	24:i:91:THR:O	2.49	0.41
27:w:45:THR:HA	27:w:50:ASN:O	2.20	0.41
1:A:500:ALA:HB1	1:A:503:LYS:HB2	2.02	0.41
1:A:1276:GLU:HG3	1:A:1277:GLU:N	2.34	0.41
1:A:1896:THR:HA	1:A:1899:TRP:CD1	2.49	0.41
12:d:285:LEU:HD11	12:d:301:ILE:HD12	2.01	0.41
16:B:77:C:H2'	16:B:78:A:C8	2.55	0.41
17:D:174:G:H2'	28:g:49:ARG:NH1	2.35	0.41
19:L:119:G:OP2	27:w:76:ASN:ND2	2.39	0.41
19:L:1093:C:O2'	30:y:54:GLY:HA3	2.20	0.41
25:m:52:LEU:CD2	28:g:79:LYS:CA	2.98	0.41
26:j:14:LYS:CD	26:j:74:LEU:HD11	2.49	0.41
26:j:15:ILE:O	26:j:26:ALA:HA	2.19	0.41
1:A:1572:GLY:C	1:A:1573:LEU:HD22	2.45	0.41
18:E:9:A:H2'	18:E:10:G:C8	2.56	0.41
19:L:31:A:O2'	19:L:32:G:P	2.78	0.41
19:L:1137:U:H3'	19:L:1137:U:H6	1.85	0.41
25:m:45:LEU:HG	25:m:45:LEU:O	2.20	0.41
27:h:45:THR:HA	27:h:50:ASN:O	2.20	0.41
27:h:74:ARG:NE	28:g:99:ASP:HA	2.35	0.41
31:p:98:LEU:HG	31:q:99:ARG:HE	1.84	0.41
1:A:194:HIS:HB3	1:A:198:ALA:H	1.85	0.41
1:A:503:LYS:HG2	1:A:507:LEU:HD13	2.02	0.41
1:A:1677:GLN:NE2	1:A:1706:VAL:HB	2.35	0.41
2:C:234:LEU:CD2	2:C:439:ILE:CG2	2.73	0.41
4:O:362:ASP:HB3	4:O:378:TYR:HB3	2.01	0.41
7:R:1:MET:HA	7:R:5:ARG:HB2	2.02	0.41
9:T:147:HIS:O	9:T:148:CYS:CB	2.69	0.41
14:n:248:SER:H	14:n:269:ASN:CG	2.27	0.41
20:v:442:THR:HA	20:v:443:PRO:HD3	1.91	0.41
20:v:552:LEU:HD13	20:v:570:THR:HA	2.02	0.41
20:v:686:ILE:HG21	20:v:713:ILE:HG21	2.03	0.41
22:b:84:ASN:O	22:b:106:ASN:HA	2.21	0.41
28:e:89:ARG:NH1	28:e:91:ILE:HD11	2.35	0.41
30:l:44:LEU:HB2	30:l:62:ILE:HG22	2.02	0.41
30:l:44:LEU:CB	30:l:47:VAL:CG1	2.97	0.41
24:i:35:ILE:HG22	24:i:37:ILE:HG12	2.02	0.41
1:A:1014:LYS:HD3	1:A:1014:LYS:HA	1.88	0.41
32:A:3000:IHP:O12	32:A:3000:IHP:P3	2.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:150:VAL:HG21	8:S:40:ARG:HD3	2.00	0.41
4:O:350:THR:HG22	4:O:353:ILE:HG13	2.01	0.41
6:Q:80:TRP:CD1	7:R:253:LEU:HD11	2.56	0.41
11:c:57:ASN:HB3	11:c:60:LEU:HG	2.03	0.41
17:D:65:U:H2'	17:D:66:A:C8	2.55	0.41
17:D:128:A:C2'	17:D:129:G:C5'	2.95	0.41
19:L:1082:A:O2'	19:L:1083:A:H5'	2.21	0.41
29:k:86:ILE:CG1	30:l:72:ILE:HB	2.51	0.41
30:l:34:VAL:CG2	30:l:45:ARG:HB2	2.51	0.41
30:l:83:LEU:HD12	30:l:84:PHE:N	2.35	0.41
1:A:614:ARG:HB2	18:E:70:U:O2'	2.21	0.41
1:A:1185:GLU:OE1	8:S:128:ARG:NH1	2.53	0.41
1:A:1347:ARG:HG2	1:A:1447:TRP:CD1	2.55	0.41
2:C:135:ASN:ND2	2:C:559:GLY:O	2.39	0.41
5:P:35:ALA:H	12:d:123:ASN:HD21	1.69	0.41
7:R:87:CYS:HB3	7:R:91:HIS:CE1	2.55	0.41
12:d:58:LEU:HD22	12:d:68:TRP:CE2	2.55	0.41
16:B:2:U:O2'	16:B:3:A:P	2.78	0.41
19:L:1143:C:HO2'	19:L:1145:U:P	2.44	0.41
26:j:72:GLU:O	26:j:72:GLU:HG3	2.19	0.41
29:k:28:ARG:HD2	29:k:50:GLU:OE1	2.21	0.41
28:e:57:ARG:HD2	28:e:70:GLU:CD	2.46	0.41
1:A:228:LYS:HE2	1:A:700:GLY:H	1.85	0.41
1:A:923:TYR:CD1	1:A:926:LYS:HD3	2.55	0.41
1:A:1965:PHE:HE1	1:A:2012:LEU:HD13	1.85	0.41
1:A:2075:THR:O	1:A:2079:ILE:N	2.44	0.41
4:O:294:ASP:O	4:O:298:GLY:N	2.48	0.41
17:D:99:U:O2'	17:D:100:A:P	2.79	0.41
29:k:59:ASP:HA	29:k:62:ARG:HH21	1.86	0.41
29:s:15:LEU:O	29:s:16:ILE:HD13	2.20	0.41
29:s:48:CYS:SG	29:s:85:THR:HG23	2.60	0.41
26:x:35:PHE:O	26:x:36:LEU:CB	2.68	0.41
1:A:783:LEU:HD13	1:A:783:LEU:HA	1.80	0.41
1:A:1056:GLU:HB3	1:A:1059:GLU:HB3	2.02	0.41
2:C:129:ILE:HG22	2:C:132:ARG:H	1.86	0.41
4:O:358:ILE:HG12	4:O:364:LEU:HD12	2.02	0.41
9:T:50:TRP:CD1	9:T:148:CYS:C	2.99	0.41
10:Z:84:ASN:HD22	10:Z:129:VAL:HG13	1.86	0.41
10:Z:354:HIS:CD2	10:Z:356:SER:H	2.38	0.41
11:c:166:LYS:HD3	18:E:52:G:H4'	2.03	0.41
19:L:109:C:H3'	19:L:109:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:1085:G:N2	19:L:1086:U:C6	2.87	0.41
19:L:1097:G:N2	19:L:1146:G:H1'	2.36	0.41
25:m:3:LEU:HD21	28:g:95:PHE:HE1	1.83	0.41
27:h:33:PHE:HZ	28:g:49:ARG:NE	2.19	0.41
25:z:104:ASP:OD1	25:z:105:SER:N	2.53	0.41
1:A:426:PRO:HG3	10:Z:201:ARG:NH1	2.36	0.41
1:A:1574:PHE:HE1	1:A:1826:TYR:O	2.04	0.41
32:A:3000:IHP:O46	32:A:3000:IHP:P5	2.79	0.41
2:C:107:THR:HA	17:D:45:A:OP2	2.20	0.41
4:O:269:ILE:HG12	4:O:285:SER:HB3	2.03	0.41
6:Q:37:CYS:HB3	6:Q:64:CYS:SG	2.61	0.41
6:Q:296:GLY:O	6:Q:298:SER:OG	2.39	0.41
6:Q:310:ILE:O	6:Q:313:SER:OG	2.29	0.41
7:R:55:PRO:HB3	7:R:93:ILE:HD11	2.02	0.41
7:R:157:GLU:OE2	7:R:161:ARG:NH2	2.51	0.41
10:Z:148:LEU:HA	10:Z:151:VAL:HG12	2.02	0.41
14:n:376:ILE:HD12	14:n:394:ASP:OD2	2.21	0.41
16:B:2:U:HO2'	16:B:3:A:P	2.43	0.41
17:D:28:G:H2'	17:D:29:G:H8	1.84	0.41
17:D:51:G:H2'	17:D:52:G:H8	1.85	0.41
17:D:168:U:C5	24:i:49:PHE:CE1	3.08	0.41
18:E:43:C:H2'	18:E:44:A:C8	2.56	0.41
19:L:5:A:C2'	19:L:6:U:OP1	2.69	0.41
20:v:687:LEU:HD22	20:v:688:ARG:HH21	1.85	0.41
22:b:68:PRO:O	22:b:69:ASP:CB	2.69	0.41
25:m:3:LEU:HD23	28:g:95:PHE:CE1	2.53	0.41
29:k:18:TYR:HE1	29:k:101:PRO:HD3	1.84	0.41
29:k:84:LEU:O	30:l:74:VAL:CG2	2.68	0.41
28:e:67:MET:HG3	28:e:69:LEU:CD1	2.50	0.41
29:s:30:TYR:HD2	29:s:87:LEU:HD21	1.86	0.41
30:l:71:PHE:C	30:l:71:PHE:HD1	2.27	0.41
27:w:30:LYS:HD2	27:w:80:TYR:CE2	2.55	0.41
27:w:79:LEU:HD22	27:w:80:TYR:HD2	1.86	0.41
31:p:98:LEU:HD12	31:q:98:LEU:HG	2.03	0.41
1:A:470:LEU:HD23	1:A:470:LEU:HA	1.92	0.41
1:A:1283:GLU:OE1	10:Z:340:SER:OG	2.39	0.41
1:A:1717:LEU:HD13	1:A:1786:ALA:HB3	2.03	0.41
1:A:2043:PHE:CG	1:A:2044:THR:N	2.89	0.41
1:A:2056:ARG:O	1:A:2060:LEU:HG	2.20	0.41
2:C:79:GLU:HG3	4:O:167:TRP:HZ3	1.86	0.41
2:C:677:PHE:HB3	2:C:857:LEU:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:250:LEU:HD23	4:O:250:LEU:HA	1.93	0.41
7:R:231:ASP:OD1	7:R:231:ASP:N	2.54	0.41
12:d:284:LEU:C	12:d:284:LEU:CD1	2.89	0.41
17:D:21:G:H2'	17:D:22:G:C8	2.56	0.41
19:L:114:U:O2'	30:y:65:ARG:NH2	2.53	0.41
20:v:711:MET:HE1	20:v:748:PHE:HA	1.99	0.41
25:m:33:SER:HB2	25:m:37:ASN:CB	2.50	0.41
25:m:67:LEU:HB3	29:k:29:VAL:CG2	2.49	0.41
28:g:26:PHE:CE1	28:g:63:ARG:HA	2.56	0.41
28:g:49:ARG:N	28:g:100:SER:O	2.49	0.41
29:k:20:LEU:HD12	29:k:34:LEU:HB2	2.03	0.41
30:l:17:HIS:CE1	30:l:77:LEU:HD11	2.52	0.41
30:l:21:LEU:CD2	30:l:72:ILE:CD1	2.99	0.41
1:A:759:ARG:HE	1:A:783:LEU:HG	1.85	0.40
1:A:782:ILE:HD13	5:P:165:ILE:HD13	2.03	0.40
4:O:219:ASP:O	4:O:220:TYR:CD1	2.74	0.40
5:P:172:TRP:O	11:c:32:GLN:NE2	2.54	0.40
7:R:206:LEU:O	7:R:208:SER:N	2.55	0.40
18:E:57:U:H2'	18:E:58:C:O5'	2.22	0.40
19:L:42:U:O2'	19:L:43:G:P	2.79	0.40
26:j:29:LEU:C	26:j:29:LEU:CD2	2.86	0.40
29:k:29:VAL:O	29:k:50:GLU:CA	2.58	0.40
29:k:85:THR:HG22	30:l:73:VAL:HG13	2.03	0.40
28:e:50:ASN:O	28:e:51:ASN:HB3	2.21	0.40
28:e:57:ARG:HD3	28:e:70:GLU:OE1	2.20	0.40
1:A:325:LYS:HB2	1:A:405:ASN:HD22	1.86	0.40
12:d:214:ASN:HB2	12:d:217:PHE:HD2	1.87	0.40
18:E:14:C:C4'	18:E:15:C:OP2	2.69	0.40
19:L:1129:U:C2'	19:L:1130:U:O5'	2.69	0.40
27:h:51:LEU:HB2	27:h:73:ILE:HB	2.04	0.40
29:k:28:ARG:CG	29:k:52:ARG:HG2	2.48	0.40
29:k:30:TYR:HH	30:l:71:PHE:HD2	1.69	0.40
28:e:69:LEU:HD12	28:e:69:LEU:N	2.36	0.40
25:z:93:ARG:HG2	25:z:94:GLN:HG3	2.03	0.40
1:A:1379:MET:HE3	1:A:1379:MET:HB3	1.77	0.40
1:A:1408:PRO:HB3	1:A:1422:ILE:HG23	2.03	0.40
2:C:69:PRO:O	2:C:70:TYR:CD2	2.74	0.40
2:C:431:GLN:O	2:C:433:THR:N	2.50	0.40
4:O:156:ILE:HG12	4:O:166:VAL:HG22	2.03	0.40
12:d:142:VAL:HG22	13:l:164:LEU:HD21	2.03	0.40
12:d:305:ARG:HG3	20:v:642:GLU:HB3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:d:391:LEU:O	12:d:395:ILE:N	2.52	0.40
17:D:169:U:C6	26:j:35:PHE:CD1	3.10	0.40
18:E:57:U:C2'	18:E:58:C:O5'	2.69	0.40
19:L:117:U:O2	25:z:35:GLN:O	2.39	0.40
19:L:1085:G:N3	19:L:1086:U:H5	2.11	0.40
28:g:77:THR:CB	28:g:86:ASN:HD22	2.34	0.40
29:k:30:TYR:CE1	29:k:50:GLU:CB	3.04	0.40
29:k:105:LYS:HA	29:k:108:ARG:HE	1.86	0.40
24:i:31:LEU:HD12	24:i:37:ILE:HG13	2.04	0.40
24:i:54:ILE:CD1	24:i:57:ALA:CB	3.00	0.40
1:A:631:LEU:HD21	1:A:663:LEU:HD13	2.02	0.40
1:A:1172:PHE:CZ	1:A:1230:ILE:HD11	2.57	0.40
1:A:1574:PHE:CE1	1:A:1826:TYR:HB2	2.55	0.40
1:A:2021:SER:O	1:A:2024:MET:HB2	2.21	0.40
2:C:219:VAL:HG11	2:C:929:GLN:HB3	2.03	0.40
2:C:331:TYR:OH	2:C:428:ILE:O	2.38	0.40
4:O:193:ARG:NH2	4:O:233:HIS:O	2.53	0.40
4:O:210:ASP:HB2	4:O:217:ILE:CG1	2.51	0.40
9:T:121:ILE:O	9:T:123:ARG:N	2.54	0.40
11:c:544:LEU:HA	11:c:547:HIS:HB2	2.03	0.40
19:L:53:G:C2'	19:L:54:U:O5'	2.69	0.40
24:u:90:ILE:HB	26:x:62:VAL:CG1	2.52	0.40
25:m:83:GLN:HE22	25:m:84:TYR:HB2	1.82	0.40
27:h:30:LYS:HD2	27:h:80:TYR:CE2	2.56	0.40
28:e:47:SER:HB2	28:e:103:VAL:HG12	2.04	0.40
28:e:89:ARG:HH22	28:e:91:ILE:CD1	2.33	0.40
28:e:92:SER:CB	25:z:99:ASP:OD1	2.69	0.40
31:r:19:SER:OG	31:r:38:ASP:OD2	2.34	0.40
31:r:85:GLN:HG2	31:p:80:LEU:HD21	2.03	0.40
2:C:974:LYS:HB3	2:C:976:ILE:HG12	2.02	0.40
7:R:117:PHE:HD2	18:E:39:G:C2	2.39	0.40
11:c:227:ILE:HG12	13:I:152:ILE:HG22	2.02	0.40
12:d:81:MET:HA	12:d:84:ALA:HB3	2.03	0.40
13:I:160:LEU:HA	13:I:163:LYS:HB2	2.04	0.40
19:L:31:A:O2'	19:L:31:A:N3	2.52	0.40
19:L:121:C:N4	27:w:33:PHE:CD1	2.90	0.40
20:v:385:PHE:HD1	20:v:388:LEU:HD12	1.85	0.40
22:b:104:SER:HA	22:b:130:ILE:O	2.21	0.40
25:m:4:VAL:CG2	25:m:36:MET:HE2	2.45	0.40
26:j:15:ILE:HG12	26:j:73:ALA:CB	2.51	0.40
27:h:79:LEU:HD22	27:h:80:TYR:HD2	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:g:50:ASN:HB2	28:g:52:HIS:CE1	2.55	0.40
28:e:73:LYS:HE3	28:e:90:PHE:CE2	2.56	0.40
27:w:51:LEU:HB2	27:w:73:ILE:HB	2.04	0.40
25:z:46:THR:OG1	25:z:78:ASN:O	2.29	0.40
25:z:47:LEU:CD2	25:z:61:ALA:HB3	2.43	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	1905/2413 (79%)	1793 (94%)	95 (5%)	17 (1%)	14	47
2	C	914/1008 (91%)	872 (95%)	41 (4%)	1 (0%)	48	80
3	J	25/135 (18%)	23 (92%)	2 (8%)	0	100	100
4	O	355/451 (79%)	316 (89%)	33 (9%)	6 (2%)	7	35
5	P	197/379 (52%)	183 (93%)	6 (3%)	8 (4%)	2	21
6	Q	288/364 (79%)	263 (91%)	20 (7%)	5 (2%)	7	35
7	R	259/339 (76%)	247 (95%)	10 (4%)	2 (1%)	16	50
8	S	64/175 (37%)	60 (94%)	4 (6%)	0	100	100
9	T	155/157 (99%)	146 (94%)	6 (4%)	3 (2%)	6	33
10	Z	443/577 (77%)	422 (95%)	21 (5%)	0	100	100
11	c	418/590 (71%)	398 (95%)	20 (5%)	0	100	100
12	d	534/687 (78%)	520 (97%)	13 (2%)	1 (0%)	43	74
13	I	98/215 (46%)	94 (96%)	4 (4%)	0	100	100
14	n	279/455 (61%)	249 (89%)	25 (9%)	5 (2%)	6	34
15	H	69/235 (29%)	61 (88%)	8 (12%)	0	100	100
20	v	666/859 (78%)	642 (96%)	22 (3%)	2 (0%)	36	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	a	82/111 (74%)	78 (95%)	3 (4%)	1 (1%)	10	41
22	b	165/238 (69%)	138 (84%)	20 (12%)	7 (4%)	2	21
23	t	150/175 (86%)	145 (97%)	4 (3%)	1 (1%)	18	53
24	i	70/94 (74%)	67 (96%)	3 (4%)	0	100	100
24	u	70/94 (74%)	67 (96%)	3 (4%)	0	100	100
25	m	117/146 (80%)	111 (95%)	6 (5%)	0	100	100
25	z	106/146 (73%)	100 (94%)	6 (6%)	0	100	100
26	j	73/77 (95%)	67 (92%)	5 (7%)	1 (1%)	9	38
26	x	73/77 (95%)	65 (89%)	7 (10%)	1 (1%)	9	38
27	h	64/86 (74%)	60 (94%)	4 (6%)	0	100	100
27	w	64/86 (74%)	61 (95%)	3 (5%)	0	100	100
28	e	99/110 (90%)	95 (96%)	3 (3%)	1 (1%)	12	45
28	g	99/110 (90%)	93 (94%)	4 (4%)	2 (2%)	6	33
29	k	96/196 (49%)	90 (94%)	5 (5%)	1 (1%)	12	45
29	s	89/196 (45%)	83 (93%)	6 (7%)	0	100	100
30	l	81/101 (80%)	79 (98%)	0	2 (2%)	4	29
30	y	79/101 (78%)	75 (95%)	4 (5%)	0	100	100
31	o	120/503 (24%)	115 (96%)	5 (4%)	0	100	100
31	p	122/503 (24%)	118 (97%)	4 (3%)	0	100	100
31	q	125/503 (25%)	116 (93%)	9 (7%)	0	100	100
31	r	119/503 (24%)	112 (94%)	7 (6%)	0	100	100
All	All	8732/13195 (66%)	8224 (94%)	441 (5%)	67 (1%)	18	50

All (67) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	131	LYS
1	A	260	PRO
1	A	403	TYR
1	A	773	SER
1	A	1575	TRP
1	A	1965	PHE
4	O	151	ASP
5	P	106	LEU
9	T	148	CYS

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Mol	Chain	Res	Type
9	T	150	CYS
12	d	423	ALA
14	n	292	HIS
14	n	372	HIS
21	a	68	GLN
22	b	68	PRO
22	b	95	PRO
22	b	125	LYS
22	b	149	PRO
26	j	75	ASP
1	A	510	PRO
1	A	771	PRO
1	A	1491	ILE
1	A	1964	PRO
2	C	71	GLY
4	O	219	ASP
4	O	351	GLY
5	P	102	ALA
5	P	105	LEU
5	P	157	GLU
5	P	162	GLU
20	v	798	LYS
22	b	98	VAL
23	t	112	SER
28	g	51	ASN
28	g	65	CYS
29	k	41	MET
28	e	51	ASN
30	l	78	LEU
1	A	128	TYR
4	O	218	ARG
5	P	150	ASP
6	Q	256	SER
6	Q	297	PHE
6	Q	298	SER
7	R	151	LEU
9	T	122	CYS
14	n	375	LYS
20	v	515	PRO
22	b	67	ILE
22	b	94	LEU
1	A	772	GLU

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Mol	Chain	Res	Type
1	A	1165	LEU
1	A	1264	GLY
4	O	352	ILE
5	P	101	PRO
30	l	40	MET
26	x	75	ASP
1	A	268	LEU
1	A	1276	GLU
5	P	161	ASN
6	Q	213	SER
7	R	206	LEU
14	n	387	ILE
14	n	427	LYS
1	A	130	PRO
4	O	149	PRO
6	Q	191	PRO

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	1737/2182 (80%)	1708 (98%)	29 (2%)	53	68
2	C	830/910 (91%)	827 (100%)	3 (0%)	84	83
3	J	21/121 (17%)	21 (100%)	0	100	100
4	O	312/397 (79%)	305 (98%)	7 (2%)	45	64
5	P	175/328 (53%)	171 (98%)	4 (2%)	44	64
6	Q	265/332 (80%)	264 (100%)	1 (0%)	84	83
7	R	224/296 (76%)	224 (100%)	0	100	100
8	S	57/151 (38%)	56 (98%)	1 (2%)	51	67
9	T	141/141 (100%)	139 (99%)	2 (1%)	59	70
10	Z	417/538 (78%)	416 (100%)	1 (0%)	87	87
11	c	214/525 (41%)	207 (97%)	7 (3%)	33	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	d	274/633 (43%)	273 (100%)	1 (0%)	84	83
13	I	92/193 (48%)	91 (99%)	1 (1%)	65	73
14	n	122/412 (30%)	107 (88%)	15 (12%)	4	20
15	H	69/216 (32%)	69 (100%)	0	100	100
20	v	294/786 (37%)	278 (95%)	16 (5%)	20	46
23	t	39/165 (24%)	26 (67%)	13 (33%)	0	1
24	i	55/83 (66%)	52 (94%)	3 (6%)	19	46
24	u	52/83 (63%)	51 (98%)	1 (2%)	50	66
25	m	106/129 (82%)	93 (88%)	13 (12%)	4	20
25	z	95/129 (74%)	92 (97%)	3 (3%)	34	56
26	j	56/66 (85%)	47 (84%)	9 (16%)	2	14
26	x	56/66 (85%)	55 (98%)	1 (2%)	51	67
27	h	51/77 (66%)	51 (100%)	0	100	100
27	w	51/77 (66%)	51 (100%)	0	100	100
28	e	82/103 (80%)	75 (92%)	7 (8%)	10	33
28	g	82/103 (80%)	75 (92%)	7 (8%)	10	33
29	k	92/176 (52%)	80 (87%)	12 (13%)	4	19
29	s	85/176 (48%)	81 (95%)	4 (5%)	23	48
30	l	72/89 (81%)	54 (75%)	18 (25%)	0	4
30	y	68/89 (76%)	68 (100%)	0	100	100
31	o	60/451 (13%)	57 (95%)	3 (5%)	22	47
31	p	62/451 (14%)	58 (94%)	4 (6%)	15	42
31	q	62/451 (14%)	59 (95%)	3 (5%)	23	48
31	r	60/451 (13%)	57 (95%)	3 (5%)	22	47
All	All	6530/11576 (56%)	6338 (97%)	192 (3%)	38	58

All (192) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	129	THR
1	A	261	LEU
1	A	403	TYR
1	A	562	ILE
1	A	697	LYS

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Mol	Chain	Res	Type
1	A	730	ILE
1	A	772	GLU
1	A	797	ILE
1	A	1041	VAL
1	A	1165	LEU
1	A	1182	LEU
1	A	1222	LEU
1	A	1259	LEU
1	A	1275	MET
1	A	1319	ILE
1	A	1574	PHE
1	A	1608	LEU
1	A	1627	LEU
1	A	1628	ASP
1	A	1661	ILE
1	A	1665	ILE
1	A	1669	LEU
1	A	1792	ASN
1	A	1961	LEU
1	A	1965	PHE
1	A	1991	ILE
1	A	1992	TYR
1	A	1993	ASP
1	A	2084	LEU
2	C	234	LEU
2	C	267	ILE
2	C	841	LEU
4	O	113	ASN
4	O	346	GLU
4	O	348	GLU
4	O	433	THR
4	O	434	LYS
4	O	435	GLU
4	O	437	GLU
5	P	30	LEU
5	P	104	LEU
5	P	106	LEU
5	P	162	GLU
6	Q	298	SER
8	S	35	THR
9	T	147	HIS
9	T	153	CYS

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Mol	Chain	Res	Type
10	Z	445	LEU
11	c	20	ILE
11	c	504	PRO
11	c	505	PRO
11	c	506	THR
11	c	517	VAL
11	c	532	PRO
11	c	550	PRO
12	d	284	LEU
13	I	202	GLN
14	n	159	PRO
14	n	162	PRO
14	n	208	PRO
14	n	257	PRO
14	n	258	THR
14	n	260	PRO
14	n	292	HIS
14	n	306	SER
14	n	327	PRO
14	n	340	PRO
14	n	373	PRO
14	n	376	ILE
14	n	424	PRO
14	n	428	PRO
14	n	436	PRO
20	v	385	PHE
20	v	386	GLU
20	v	397	ASN
20	v	398	ASP
20	v	438	ARG
20	v	529	HIS
20	v	530	ARG
20	v	538	LEU
20	v	544	ILE
20	v	576	THR
20	v	582	LEU
20	v	593	LEU
20	v	612	ILE
20	v	652	LEU
20	v	665	ILE
20	v	719	THR
23	t	13	PRO

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Mol	Chain	Res	Type
23	t	76	THR
23	t	77	PRO
23	t	85	THR
23	t	96	PRO
23	t	100	THR
23	t	105	PRO
23	t	108	SER
23	t	109	SER
23	t	111	VAL
23	t	133	PRO
23	t	136	VAL
23	t	150	THR
24	u	35	ILE
25	m	33	SER
25	m	35	GLN
25	m	37	ASN
25	m	39	ILE
25	m	45	LEU
25	m	46	THR
25	m	47	LEU
25	m	52	LEU
25	m	60	ILE
25	m	85	ILE
25	m	86	ASN
25	m	92	ILE
25	m	93	ARG
26	j	18	ASN
26	j	19	ILE
26	j	20	ASN
26	j	22	SER
26	j	23	ARG
26	j	29	LEU
26	j	39	VAL
26	j	64	ARG
26	j	74	LEU
28	g	33	LEU
28	g	35	ASN
28	g	41	ARG
28	g	42	THR
28	g	57	ARG
28	g	84	VAL
28	g	85	ILE

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Mol	Chain	Res	Type
29	k	14	ASN
29	k	15	LEU
29	k	39	LYS
29	k	41	MET
29	k	43	LEU
29	k	49	ILE
29	k	50	GLU
29	k	82	LEU
29	k	104	SER
29	k	105	LYS
29	k	106	LYS
29	k	109	LEU
28	e	41	ARG
28	e	57	ARG
28	e	70	GLU
28	e	88	GLU
28	e	91	ILE
28	e	92	SER
28	e	94	LEU
29	s	11	ARG
29	s	15	LEU
29	s	56	THR
29	s	82	LEU
30	l	11	LEU
30	l	15	GLN
30	l	23	LEU
30	l	32	LYS
30	l	36	SER
30	l	37	GLU
30	l	38	ASP
30	l	45	ARG
30	l	47	VAL
30	l	64	VAL
30	l	65	ARG
30	l	70	LYS
30	l	73	VAL
30	l	77	LEU
30	l	79	LYS
30	l	83	LEU
30	l	84	PHE
30	l	85	LYS
24	i	18	PHE

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Mol	Chain	Res	Type
24	i	22	GLN
24	i	40	LYS
26	x	74	LEU
25	z	45	LEU
25	z	54	LYS
25	z	55	LEU
31	r	17	PRO
31	r	44	PRO
31	r	63	THR
31	p	17	PRO
31	p	44	PRO
31	p	63	THR
31	p	98	LEU
31	q	17	PRO
31	q	44	PRO
31	q	55	PRO
31	o	17	PRO
31	o	44	PRO
31	o	63	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (142) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	185	GLN
1	A	429	ASN
1	A	509	HIS
1	A	541	ASN
1	A	559	GLN
1	A	658	ASN
1	A	796	ASN
1	A	830	ASN
1	A	861	GLN
1	A	864	GLN
1	A	868	GLN
1	A	948	HIS
1	A	952	ASN
1	A	997	GLN
1	A	1034	ASN
1	A	1099	ASN
1	A	1128	GLN
1	A	1140	ASN
1	A	1368	GLN

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Mol	Chain	Res	Type
1	A	1376	ASN
1	A	1431	HIS
1	A	1449	ASN
1	A	1455	GLN
1	A	1531	HIS
1	A	1532	HIS
1	A	1540	ASN
1	A	1652	HIS
1	A	1687	HIS
1	A	1707	HIS
1	A	1718	HIS
1	A	1730	ASN
1	A	1737	GLN
1	A	1792	ASN
1	A	1809	ASN
1	A	1863	HIS
1	A	1947	HIS
1	A	1990	ASN
1	A	2068	ASN
2	C	82	ASN
2	C	103	HIS
2	C	180	ASN
2	C	183	GLN
2	C	220	ASN
2	C	255	GLN
2	C	289	ASN
2	C	294	ASN
2	C	444	GLN
2	C	560	GLN
2	C	647	ASN
2	C	683	ASN
2	C	764	ASN
2	C	794	GLN
2	C	797	GLN
2	C	1004	ASN
3	J	4	ASN
3	J	19	HIS
4	O	136	ASN
4	O	152	ASN
4	O	194	HIS
4	O	214	ASN
4	O	271	GLN

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Mol	Chain	Res	Type
4	O	306	HIS
4	O	382	HIS
5	P	87	ASN
5	P	107	ASN
5	P	111	HIS
5	P	210	ASN
6	Q	85	GLN
6	Q	106	ASN
6	Q	317	ASN
7	R	44	ASN
7	R	91	HIS
7	R	201	ASN
7	R	257	ASN
8	S	34	HIS
8	S	171	HIS
8	S	173	HIS
9	T	56	HIS
9	T	57	HIS
9	T	112	ASN
9	T	128	GLN
9	T	143	HIS
9	T	144	GLN
10	Z	84	ASN
10	Z	107	ASN
10	Z	223	HIS
10	Z	310	HIS
10	Z	354	HIS
11	c	32	GLN
11	c	161	ASN
11	c	214	ASN
12	d	123	ASN
12	d	170	ASN
12	d	231	ASN
12	d	248	ASN
12	d	252	HIS
12	d	290	GLN
12	d	315	ASN
12	d	316	ASN
13	I	118	ASN
15	H	74	GLN
20	v	397	ASN
20	v	529	HIS

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Mol	Chain	Res	Type
20	v	596	GLN
20	v	643	HIS
23	t	143	ASN
24	u	24	GLN
24	u	86	ASN
25	m	5	ASN
25	m	12	ASN
25	m	14	GLN
25	m	21	ASN
25	m	30	GLN
25	m	83	GLN
25	m	86	ASN
25	m	94	GLN
26	j	20	ASN
26	j	54	ASN
27	h	50	ASN
28	g	50	ASN
28	g	52	HIS
28	g	86	ASN
29	k	14	ASN
28	e	50	ASN
28	e	64	HIS
28	e	66	ASN
28	e	86	ASN
30	l	15	GLN
30	l	41	ASN
30	l	43	GLN
30	l	68	GLN
24	i	22	GLN
24	i	24	GLN
26	x	20	ASN
30	y	53	GLN
25	z	5	ASN
25	z	12	ASN
25	z	14	GLN
25	z	21	ASN
25	z	30	GLN
31	r	85	GLN
31	q	85	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	B	55/246 (22%)	34 (61%)	5 (9%)
17	D	177/214 (82%)	56 (31%)	8 (4%)
18	E	102/112 (91%)	43 (42%)	5 (4%)
19	L	194/1175 (16%)	76 (39%)	13 (6%)
All	All	528/1747 (30%)	209 (39%)	31 (5%)

All (209) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
16	B	-11	U
16	B	-10	G
16	B	-9	A
16	B	-8	U
16	B	-6	U
16	B	-4	G
16	B	-3	A
16	B	-1	A
16	B	0	G
16	B	1	G
16	B	2	U
16	B	3	A
16	B	7	C
16	B	8	U
16	B	9	A
16	B	10	A
16	B	11	A
16	B	12	G
16	B	13	U
16	B	14	U
16	B	15	A
16	B	52	U
16	B	53	U
16	B	54	A
16	B	55	U
16	B	56	G
16	B	57	C
16	B	58	U
16	B	69	A
16	B	70	A
16	B	71	C
16	B	74	A
16	B	75	A
16	B	78	A

Continued on next page...

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Mol	Chain	Res	Type
17	D	12	C
17	D	13	A
17	D	14	G
17	D	18	A
17	D	20	U
17	D	24	G
17	D	27	G
17	D	28	G
17	D	29	G
17	D	31	G
17	D	33	U
17	D	38	A
17	D	41	A
17	D	42	A
17	D	43	G
17	D	44	A
17	D	45	A
17	D	71	A
17	D	75	A
17	D	77	A
17	D	79	C
17	D	80	G
17	D	81	A
17	D	82	A
17	D	84	A
17	D	96	U
17	D	99	U
17	D	100	A
17	D	101	C
17	D	103	A
17	D	104	G
17	D	109	A
17	D	113	G
17	D	127	U
17	D	128	A
17	D	129	G
17	D	130	A
17	D	131	A
17	D	132	A
17	D	139	A
17	D	141	G
17	D	142	C

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Mol	Chain	Res	Type
17	D	151	A
17	D	160	U
17	D	161	U
17	D	162	G
17	D	163	C
17	D	164	C
17	D	165	A
17	D	166	U
17	D	168	U
17	D	170	U
17	D	171	U
17	D	174	G
17	D	175	G
17	D	178	C
18	E	5	G
18	E	12	A
18	E	13	A
18	E	14	C
18	E	15	C
18	E	16	C
18	E	23	G
18	E	31	G
18	E	36	U
18	E	39	G
18	E	40	A
18	E	42	A
18	E	51	A
18	E	52	G
18	E	54	U
18	E	55	G
18	E	56	A
18	E	58	C
18	E	59	A
18	E	60	G
18	E	62	A
18	E	63	G
18	E	64	U
18	E	65	U
18	E	66	C
18	E	67	C
18	E	68	C
18	E	73	A

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Mol	Chain	Res	Type
18	E	74	U
18	E	79	A
18	E	80	U
18	E	81	G
18	E	85	C
18	E	86	G
18	E	87	U
18	E	88	U
18	E	90	U
18	E	91	A
18	E	92	C
18	E	98	G
18	E	100	U
18	E	101	U
18	E	102	U
19	L	2	C
19	L	3	G
19	L	4	A
19	L	5	A
19	L	6	U
19	L	7	C
19	L	9	C
19	L	12	U
19	L	16	U
19	L	18	U
19	L	19	U
19	L	21	G
19	L	23	U
19	L	25	A
19	L	26	G
19	L	29	C
19	L	30	A
19	L	31	A
19	L	32	G
19	L	41	C
19	L	43	G
19	L	44	U
19	L	45	U
19	L	53	G
19	L	54	U
19	L	86	U
19	L	109	C

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Mol	Chain	Res	Type
19	L	110	A
19	L	111	C
19	L	115	U
19	L	119	G
19	L	120	G
19	L	121	C
19	L	124	C
19	L	129	A
19	L	141	A
19	L	153	U
19	L	1084	A
19	L	1085	G
19	L	1086	U
19	L	1091	G
19	L	1092	A
19	L	1093	C
19	L	1094	G
19	L	1096	C
19	L	1098	C
19	L	1099	G
19	L	1100	A
19	L	1101	C
19	L	1102	C
19	L	1103	C
19	L	1104	U
19	L	1105	C
19	L	1106	G
19	L	1107	C
19	L	1108	A
19	L	1115	G
19	L	1120	G
19	L	1122	U
19	L	1123	C
19	L	1124	U
19	L	1125	U
19	L	1126	G
19	L	1128	C
19	L	1130	U
19	L	1137	U
19	L	1138	G
19	L	1139	G
19	L	1140	U

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Mol	Chain	Res	Type
19	L	1144	U
19	L	1145	U
19	L	1146	G
19	L	1147	A
19	L	1149	G
19	L	1152	U
19	L	1166	G

All (31) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	B	2	U
16	B	7	C
16	B	9	A
16	B	57	C
16	B	69	A
17	D	17	C
17	D	27	G
17	D	28	G
17	D	83	C
17	D	99	U
17	D	127	U
17	D	150	U
17	D	163	C
18	E	14	C
18	E	55	G
18	E	64	U
18	E	85	C
18	E	100	U
19	L	3	G
19	L	5	A
19	L	31	A
19	L	42	U
19	L	53	G
19	L	109	C
19	L	120	G
19	L	1085	G
19	L	1092	A
19	L	1093	C
19	L	1106	G
19	L	1107	C
19	L	1146	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	$\# Z > 2$
14	SEP	n	73	14	8,9,10	1.57	1 (12%)	7,12,14	0.96	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
14	SEP	n	73	14	-	4/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	n	73	SEP	P-O1P	3.44	1.61	1.50

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
14	n	73	SEP	C-CA-CB-OG
14	n	73	SEP	CB-OG-P-O2P
14	n	73	SEP	CB-OG-P-O3P
14	n	73	SEP	CB-OG-P-O1P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	n	73	SEP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 12 are monoatomic - leaving 2 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	$\# Z > 2$
33	GTP	C	1500	34	33,34,34	0.59	0	50,54,54	0.49	0
32	IHP	A	3000	-	36,36,36	0.78	0	60,60,60	0.57	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
33	GTP	C	1500	34	-	10/22/38/38	0/3/3/3
32	IHP	A	3000	-	-	5/30/54/54	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
32	A	3000	IHP	C2-C3-O13-P3
33	C	1500	GTP	C5'-O5'-PA-O1A

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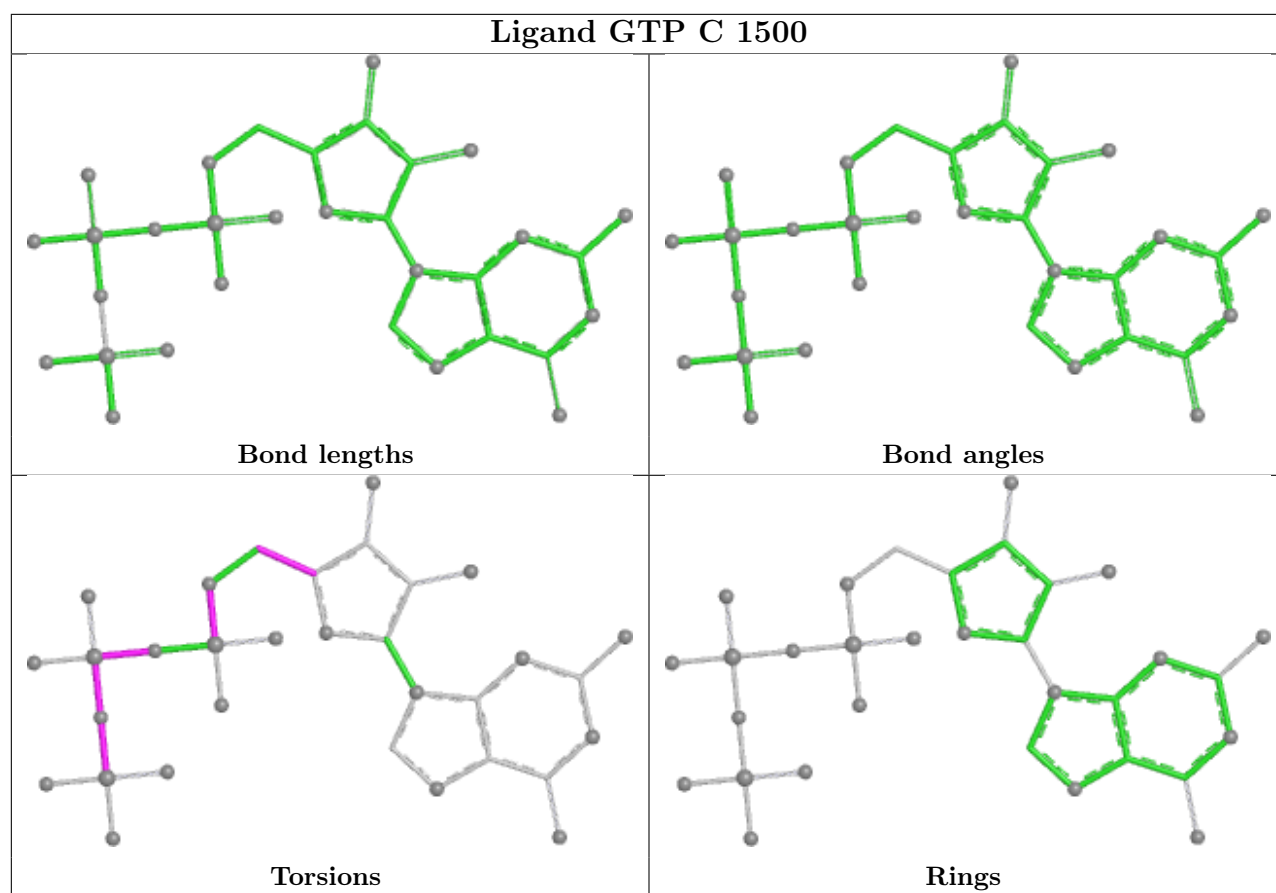
Mol	Chain	Res	Type	Atoms
33	C	1500	GTP	C3'-C4'-C5'-O5'
33	C	1500	GTP	O4'-C4'-C5'-O5'
32	A	3000	IHP	C4-C3-O13-P3
33	C	1500	GTP	PB-O3B-PG-O2G
33	C	1500	GTP	PB-O3B-PG-O3G
32	A	3000	IHP	C4-O14-P4-O24
33	C	1500	GTP	C5'-O5'-PA-O3A
33	C	1500	GTP	C5'-O5'-PA-O2A
33	C	1500	GTP	PG-O3B-PB-O1B
33	C	1500	GTP	PA-O3A-PB-O2B
32	A	3000	IHP	C3-O13-P3-O43
32	A	3000	IHP	C5-O15-P5-O25
33	C	1500	GTP	PG-O3B-PB-O2B

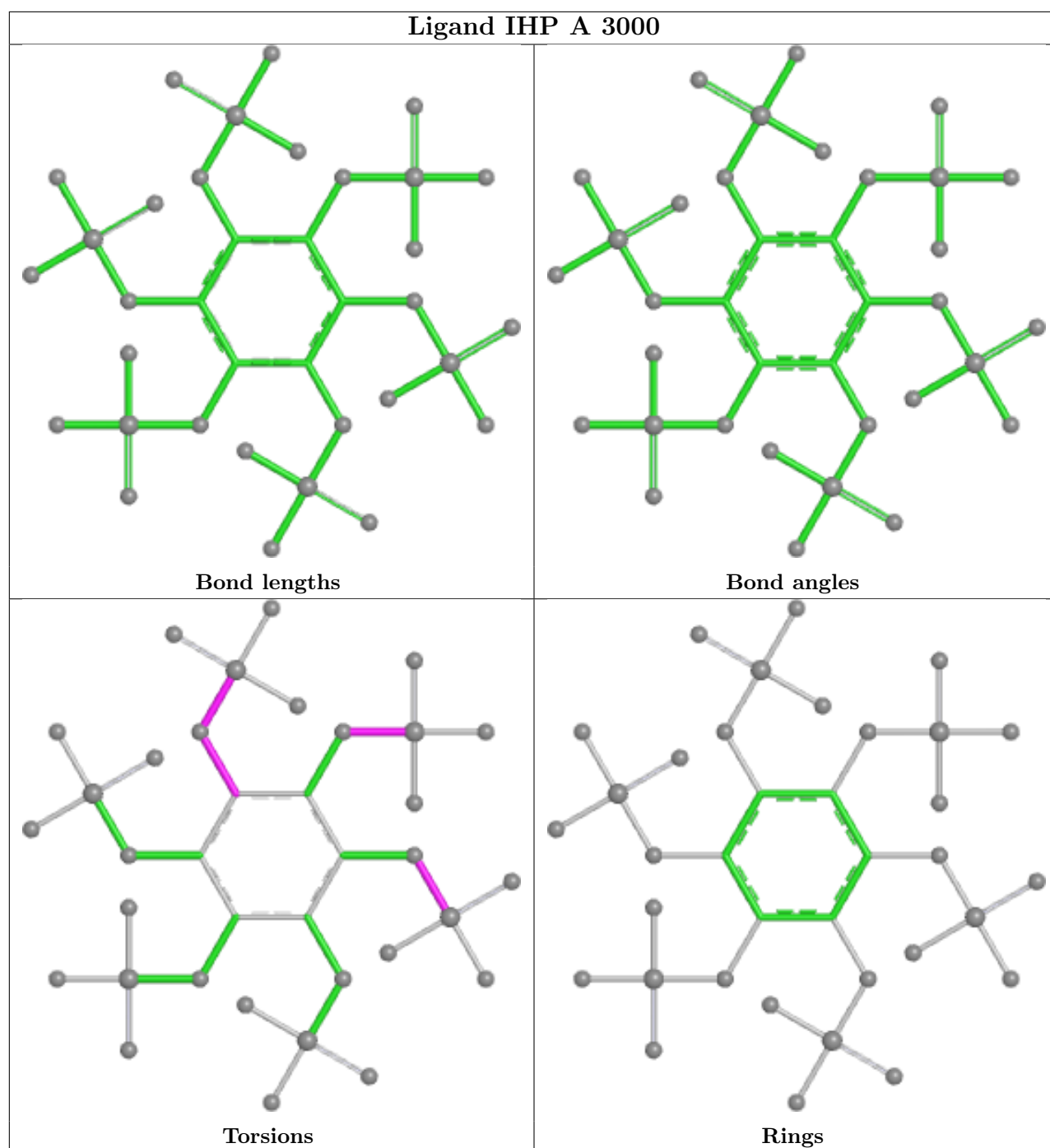
There are no ring outliers.

2 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
33	C	1500	GTP	7	0
32	A	3000	IHP	6	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

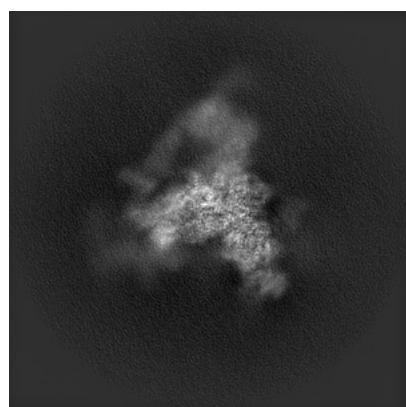
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0691. These allow visual inspection of the internal detail of the map and identification of artifacts.

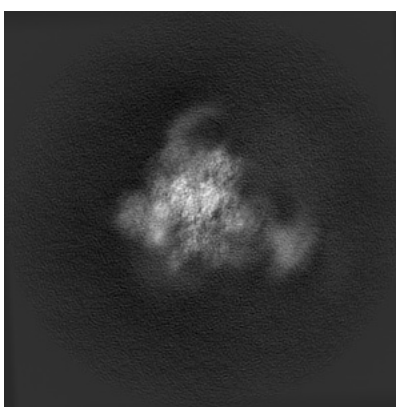
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

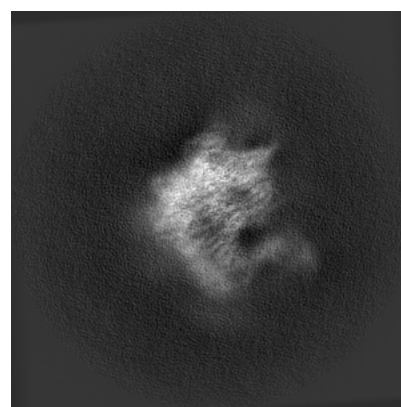
6.1.1 Primary map



X



Y

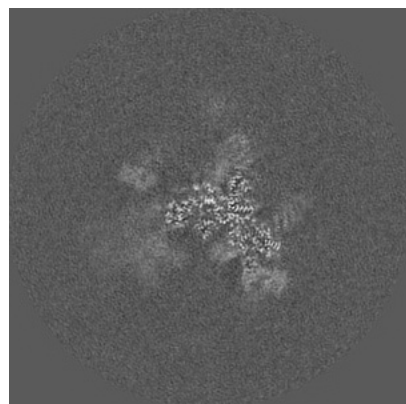


Z

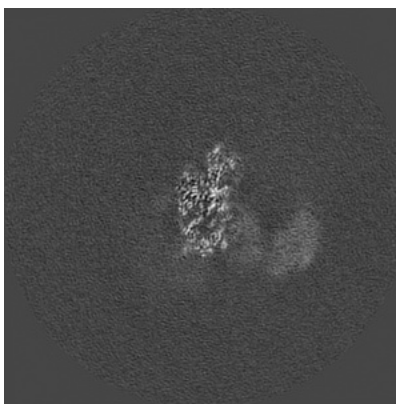
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

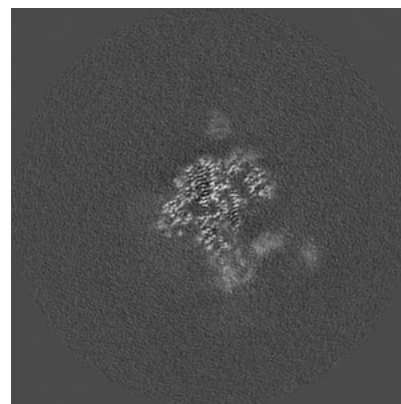
6.2.1 Primary map



X Index: 200



Y Index: 200

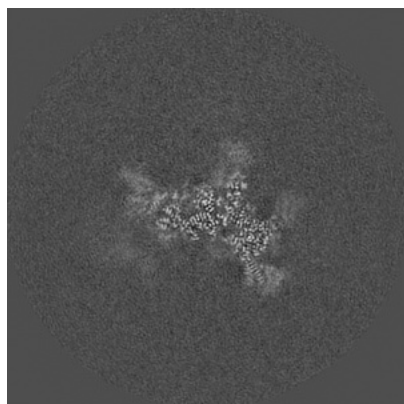


Z Index: 200

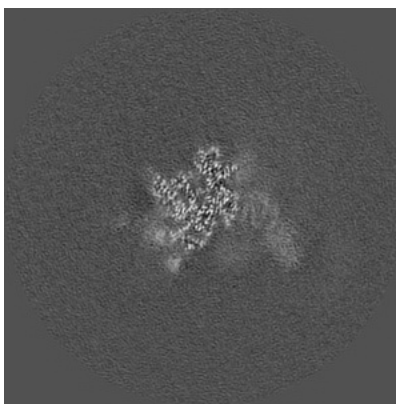
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

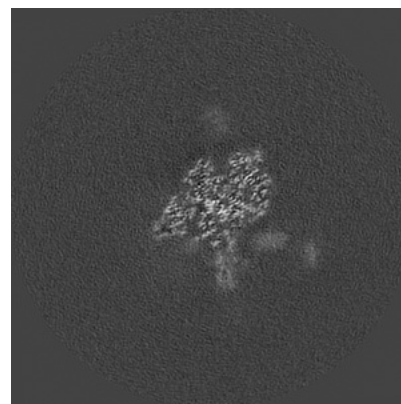
6.3.1 Primary map



X Index: 210



Y Index: 228

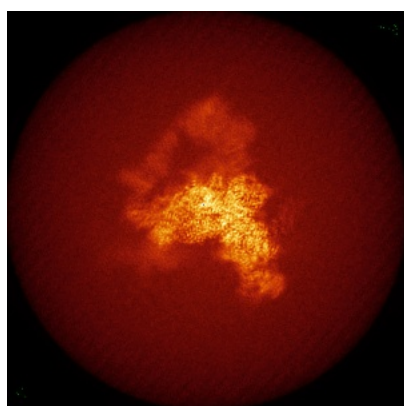


Z Index: 206

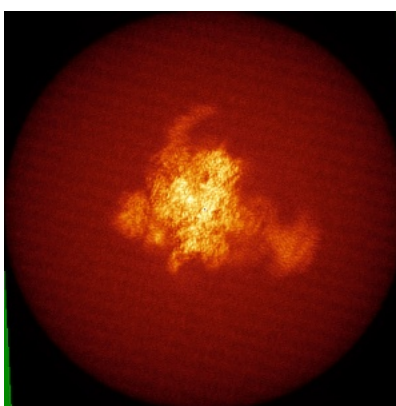
The images above show the largest variance slices of the map in three orthogonal directions.

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

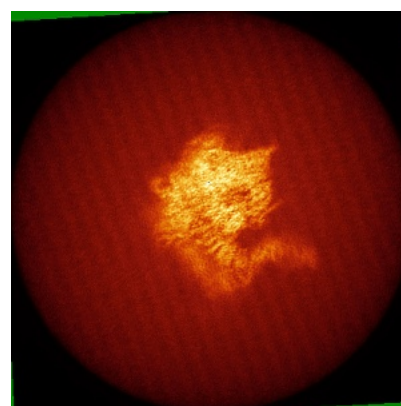
6.4.1 Primary map



X



Y

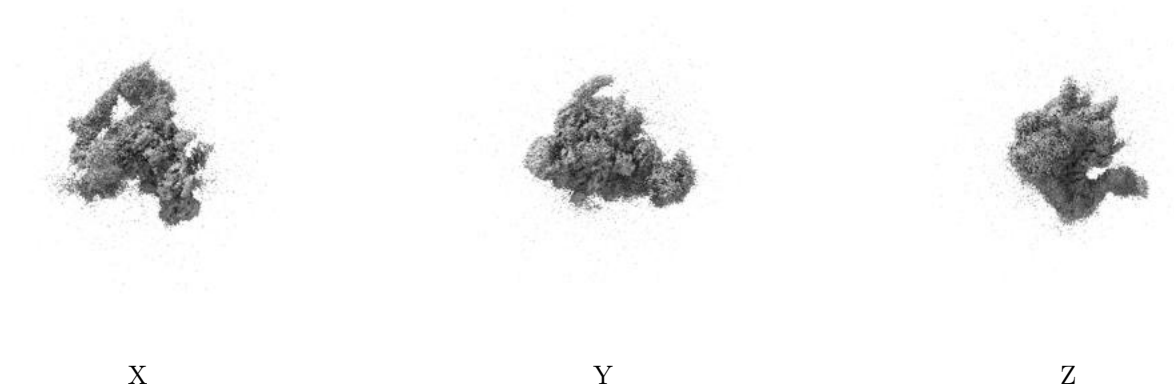


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.028. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

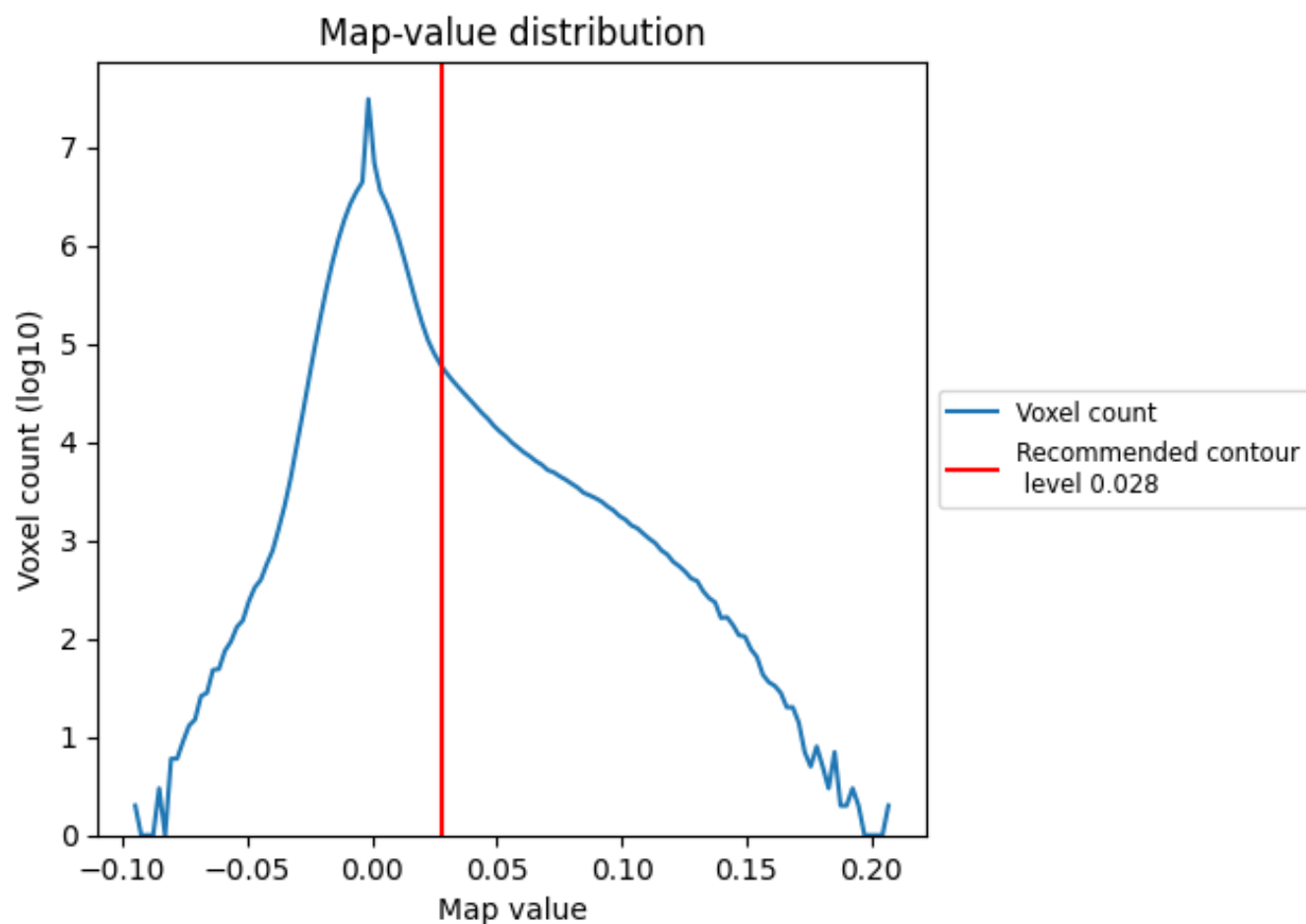
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

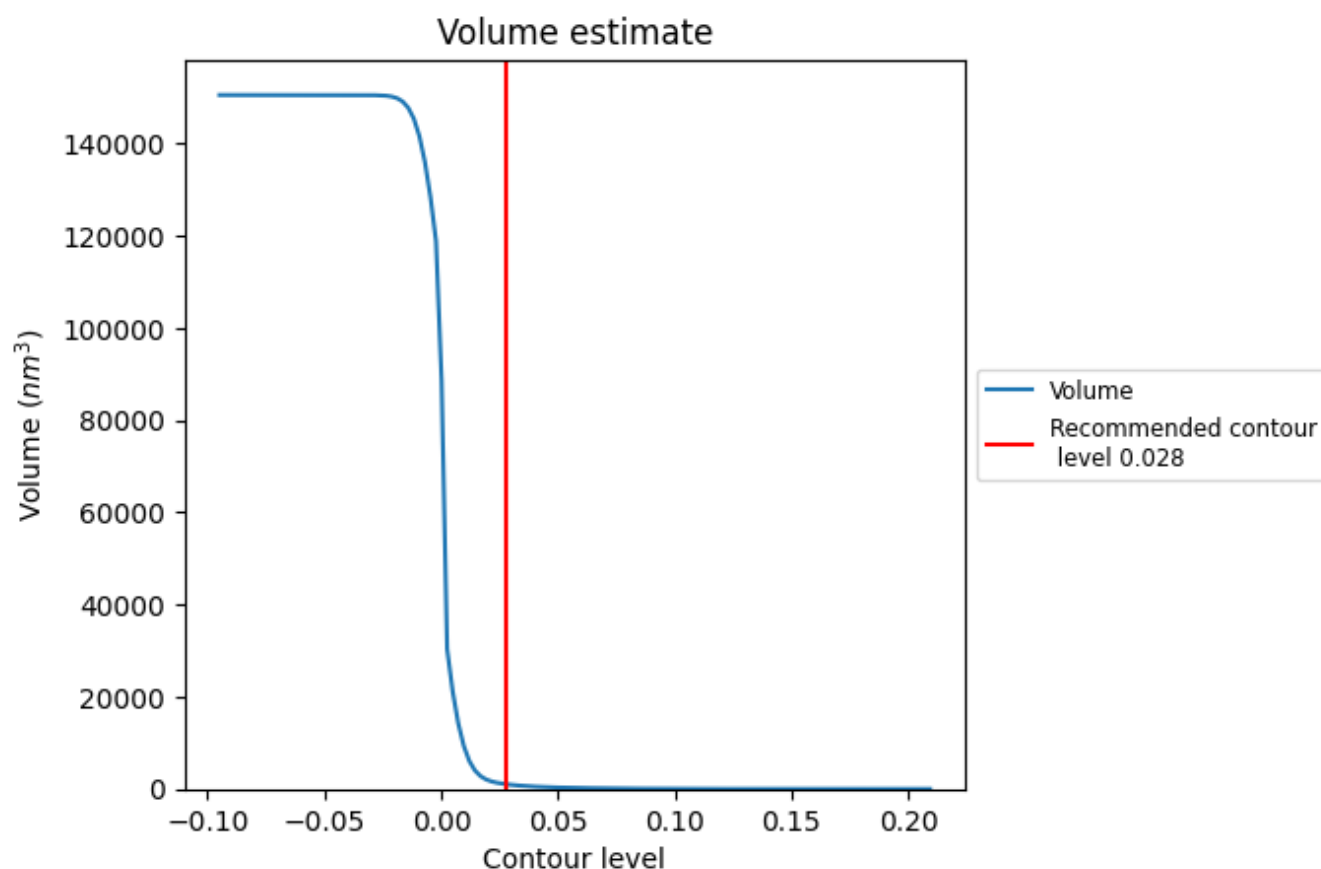
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

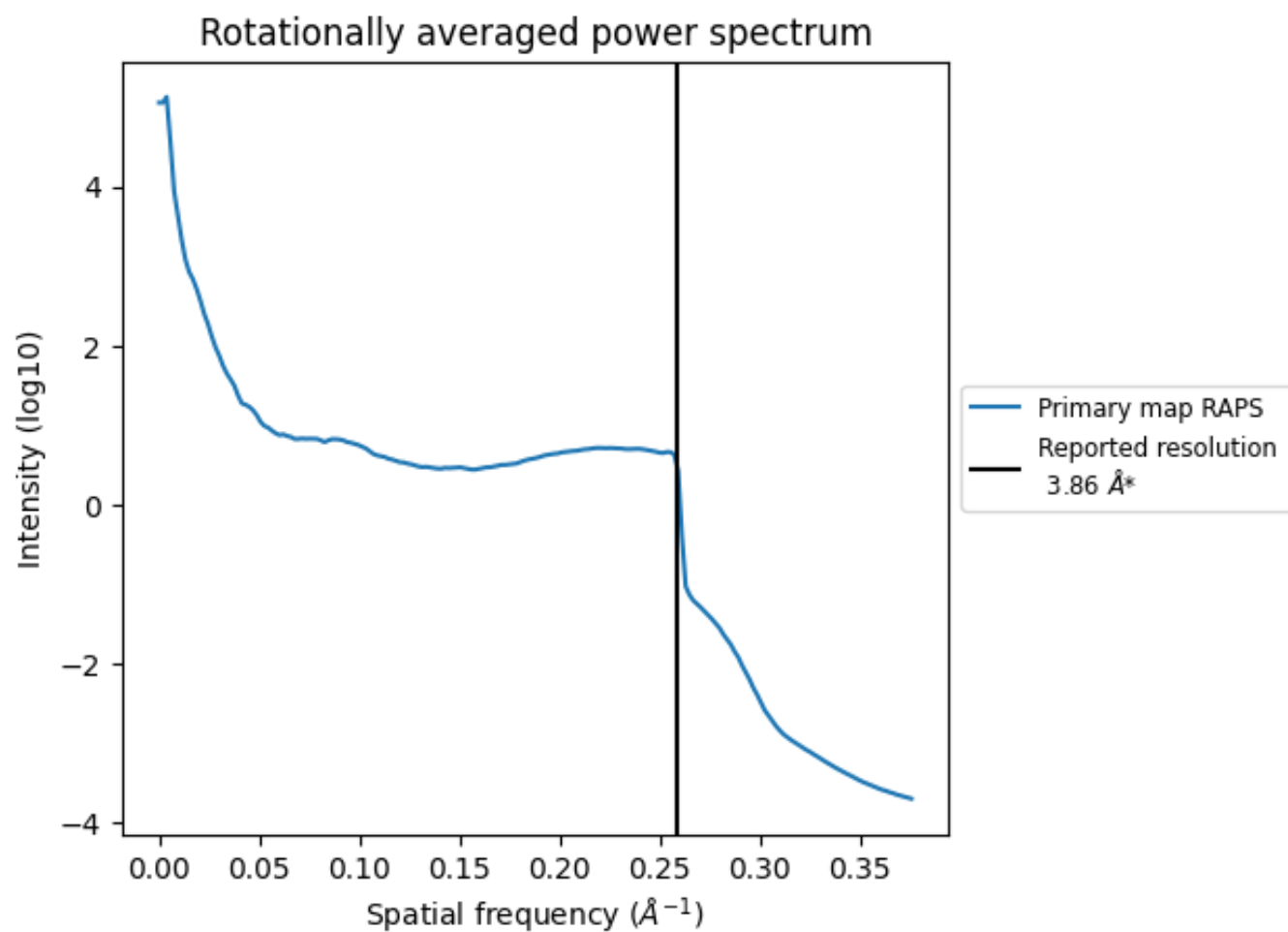
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1021 nm^3 ; this corresponds to an approximate mass of 922 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 0.259 Å⁻¹

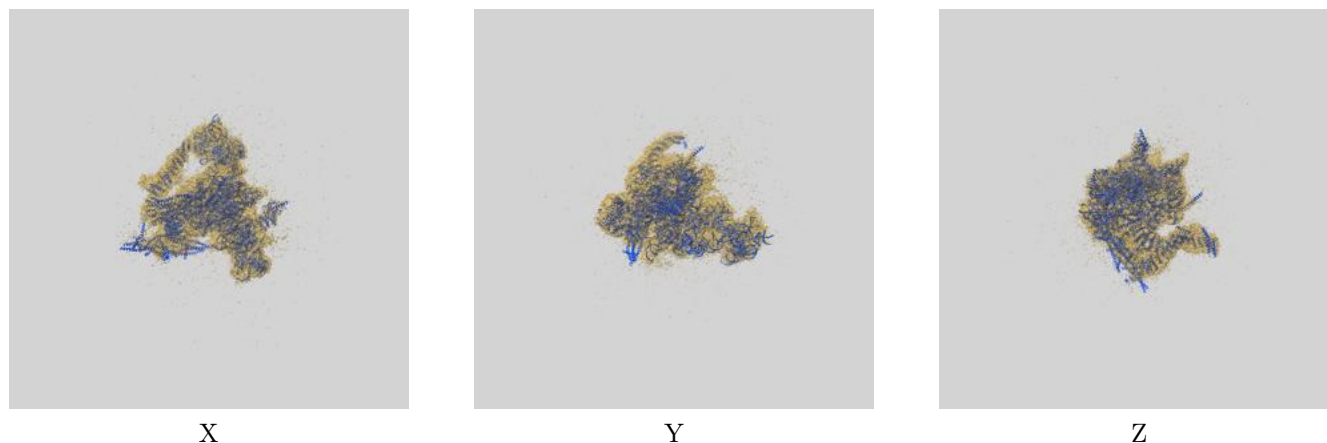
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

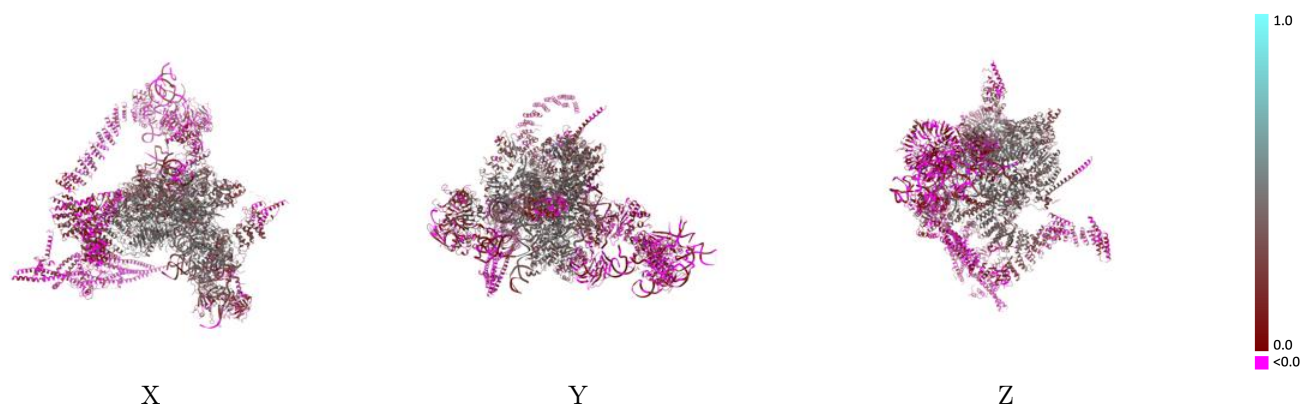
This section contains information regarding the fit between EMDB map EMD-0691 and PDB model 6J6N. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



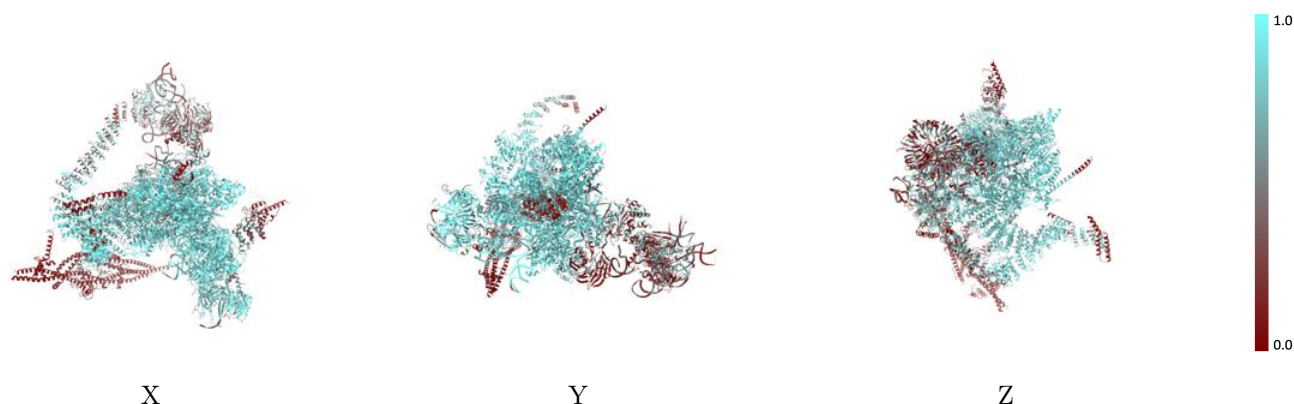
The images above show the 3D surface view of the map at the recommended contour level 0.028 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



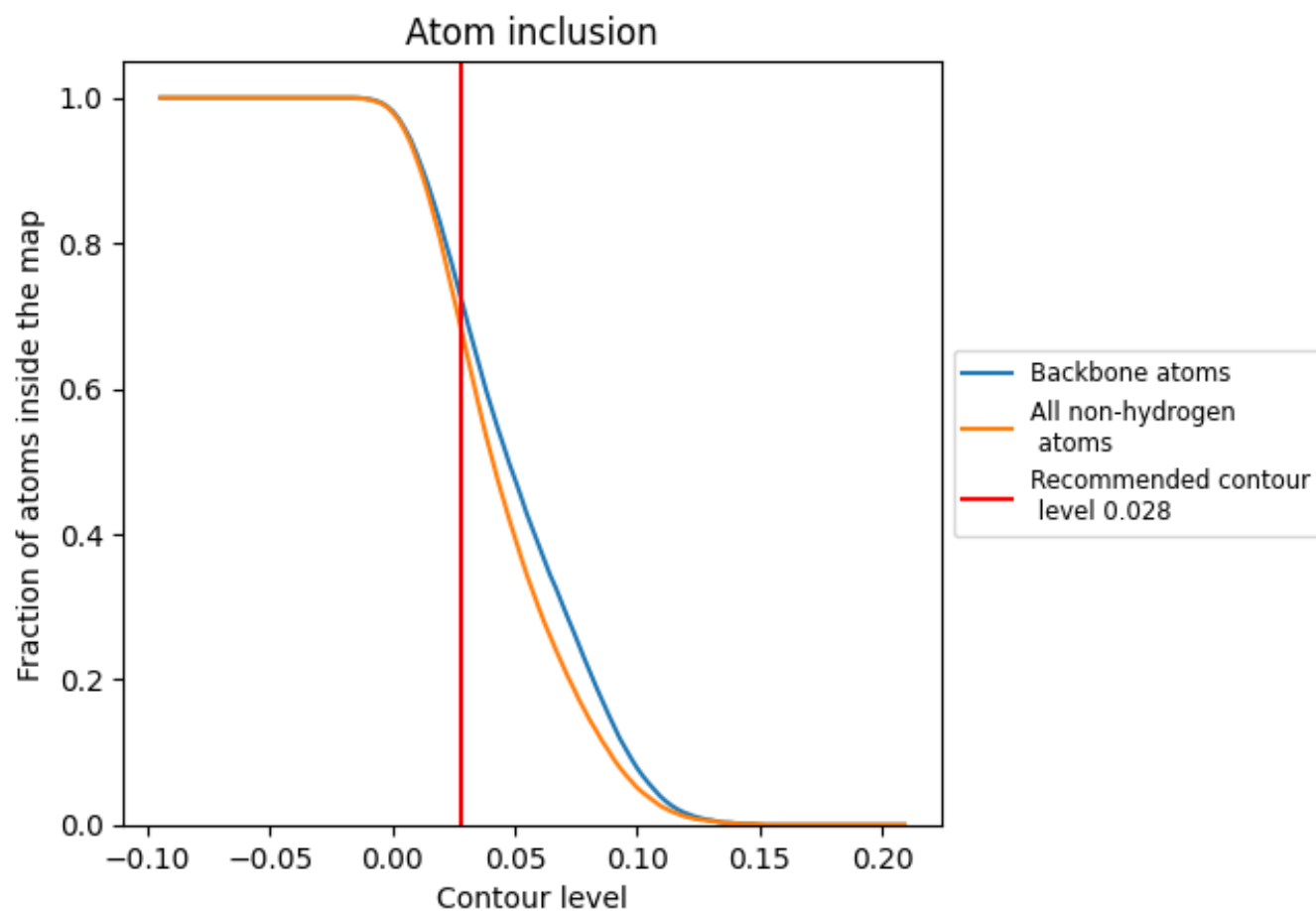
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.028).

9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 68% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.028) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6830	 0.2480
A	 0.8210	 0.3620
B	 0.6890	 0.2110
C	 0.8760	 0.3900
D	 0.9030	 0.2580
E	 0.9600	 0.3630
H	 0.4020	 0.0970
I	 0.7530	 0.2890
J	 0.8720	 0.3970
L	 0.4980	 0.0780
O	 0.8800	 0.4260
P	 0.7560	 0.3360
Q	 0.8190	 0.3290
R	 0.8720	 0.3760
S	 0.7630	 0.3950
T	 0.9030	 0.4020
Z	 0.5320	 0.2310
a	 0.5070	 0.0430
b	 0.5120	 0.0450
c	 0.4810	 0.2030
d	 0.7700	 0.2460
e	 0.3070	 0.0600
g	 0.7020	 0.1280
h	 0.8600	 0.1290
i	 0.8350	 0.1430
j	 0.7430	 0.2110
k	 0.7340	 0.2230
l	 0.8200	 0.3080
m	 0.6640	 0.1580
n	 0.1440	 0.0390
o	 0.1020	 -0.0100
p	 0.1200	 0.0050
q	 0.0150	 -0.0080
r	 0.0920	 -0.0100
s	 0.4600	 0.0150



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Chain	Atom inclusion	Q-score
t	 0.0320	 0.0250
u	 0.3050	 0.0300
v	 0.6840	 0.1200
w	 0.3610	 0.0580
x	 0.2390	 0.0380
y	 0.3240	 0.0380
z	 0.3880	 0.0460