



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 02:36 PM UTC

PDB ID : 6J6G / pdb_00006j6g
EMDB ID : EMD-0686
Title : Cryo-EM structure of the yeast B*-a2 complex at an average resolution of 3.2 angstrom
Authors : Wan, R.; Bai, R.; Yan, C.; Lei, J.; Shi, Y.
Deposited on : 2019-01-15
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

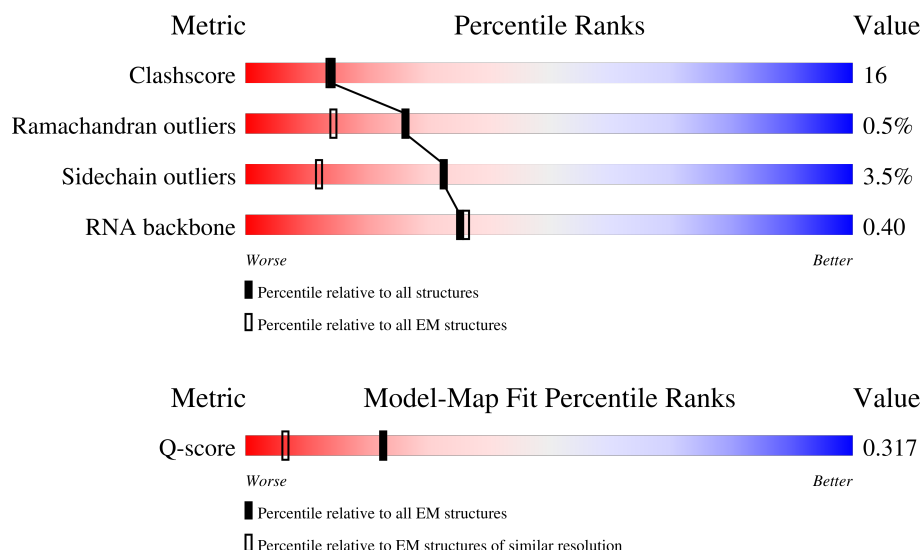
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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	
2	C	1008	
3	J	135	

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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	679	
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 79042 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	70	Total	C	N	O	S	0	0
			617	390	115	111	1		

- Molecule 16 is a RNA chain called ACT1 pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	B	60	Total	C	N	O	P	0	0
			1266	567	213	426	60		

- 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	208	Total	C	N	O	P	0	0
			4382	1962	732	1480	208		

- 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		

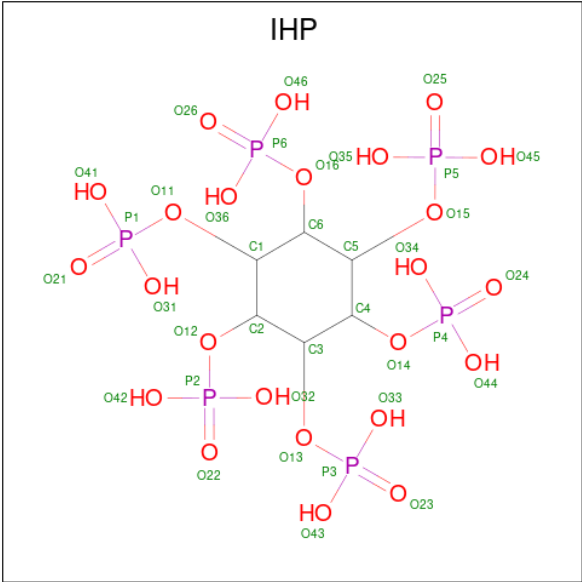
- Molecule 30 is a protein called Small nuclear ribonucleoprotein Sm D3.

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.

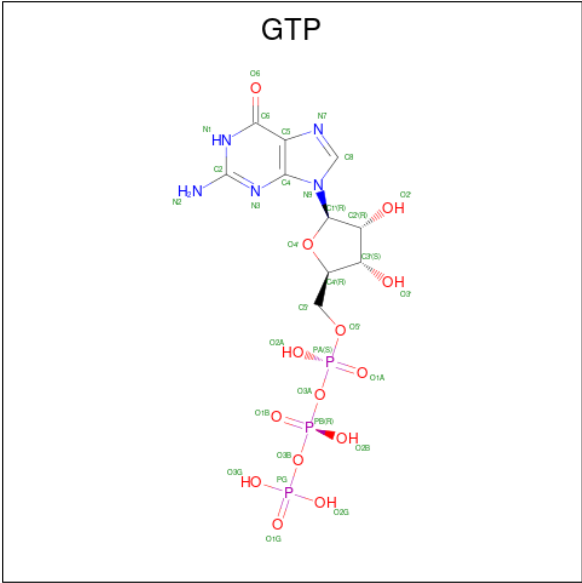
Mol	Chain	Residues	Atoms					AltConf	Trace
31	r	125	Total	C	N	O	S	0	0
			823	521	133	167	2		
31	p	128	Total	C	N	O	S	0	0
			843	532	136	173	2		
31	q	129	Total	C	N	O	S	0	0
			850	537	137	174	2		
31	o	126	Total	C	N	O	S	0	0
			830	525	134	169	2		

- 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

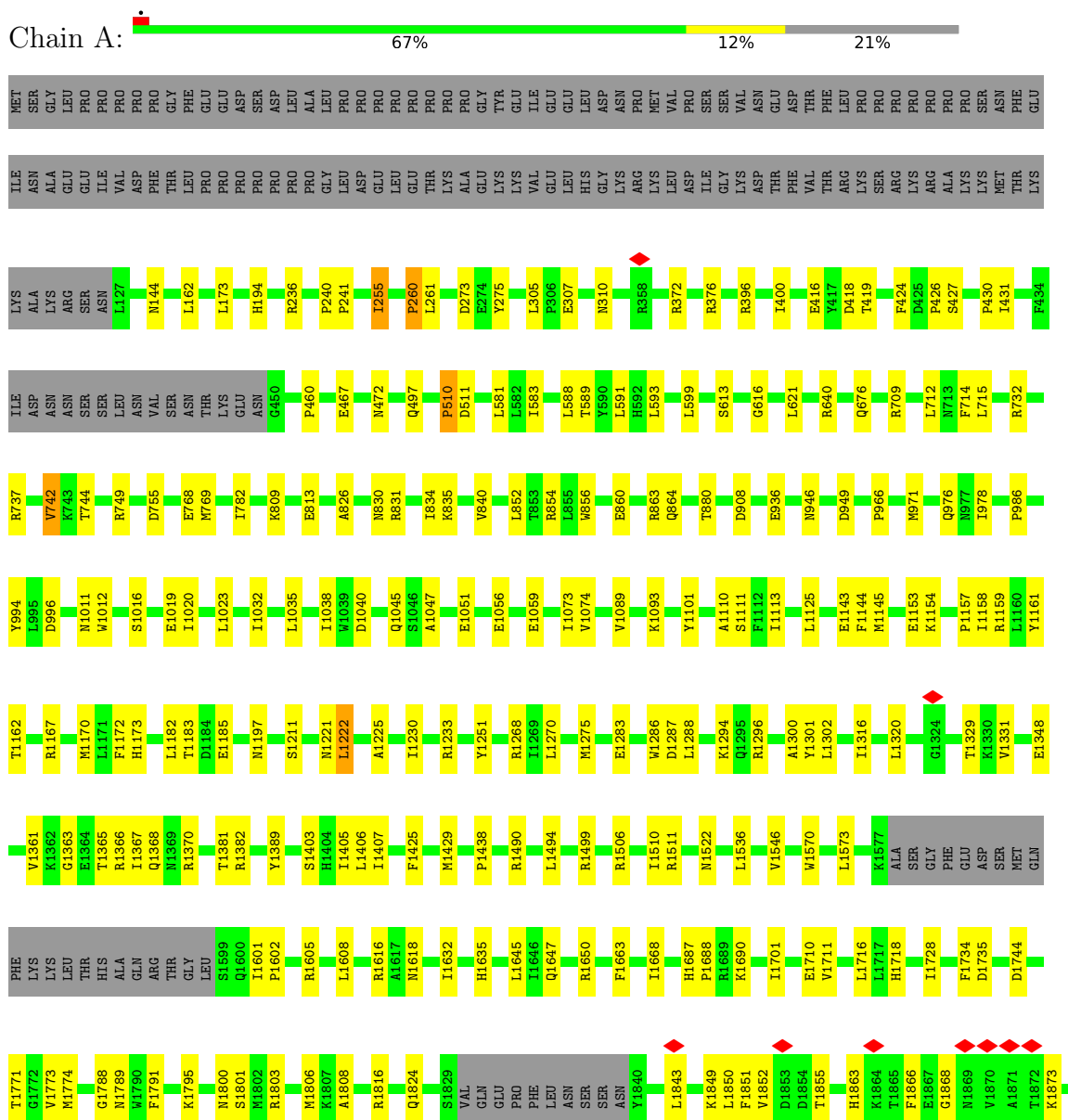
- Molecule 35 is ZINC ION (CCD ID: ZN) (formula: Zn).

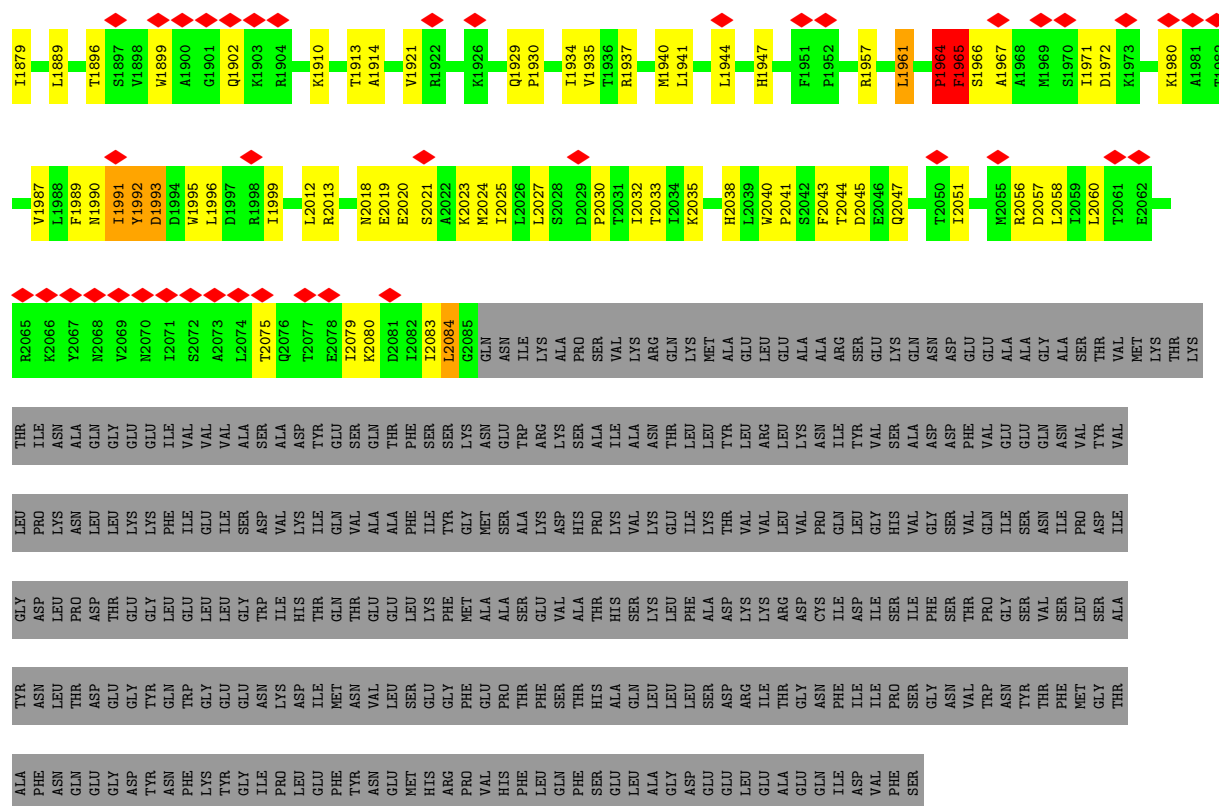
Mol	Chain	Residues	Atoms		AltConf
35	Q	2	Total 2	Zn 2	0
35	R	1	Total 1	Zn 1	0
35	T	3	Total 3	Zn 3	0

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.

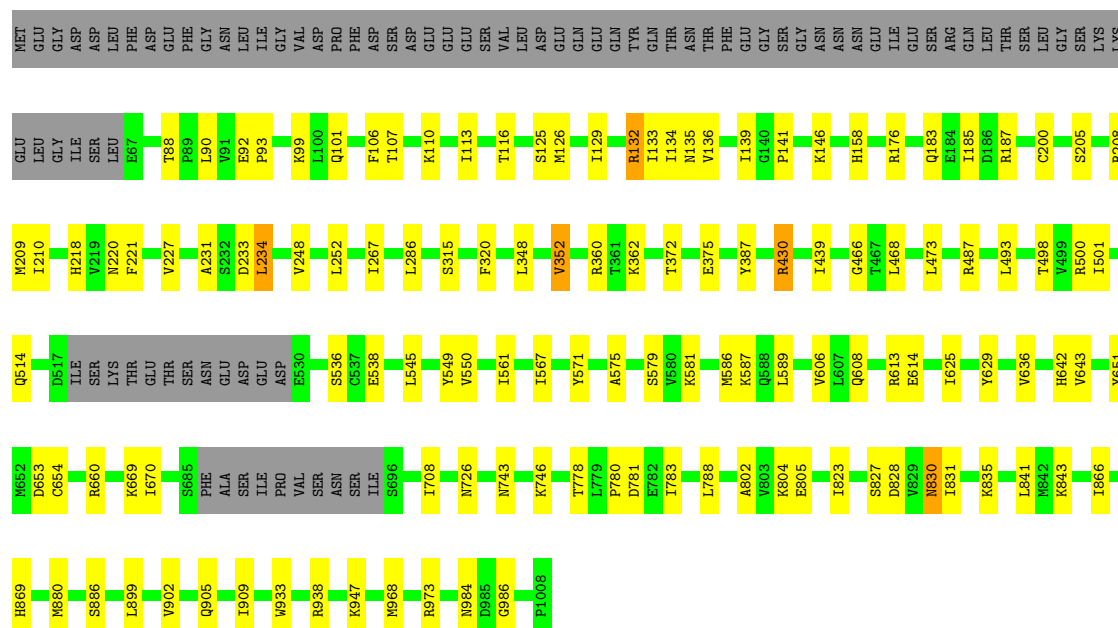
• Molecule 1: Pre-mRNA-splicing factor 8





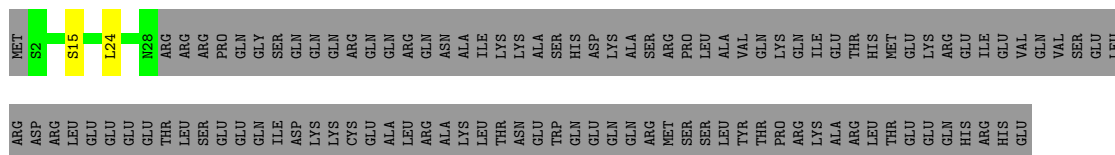
• Molecule 2: Pre-mRNA-splicing factor SNU114

Chain C: 79% 12% 9%

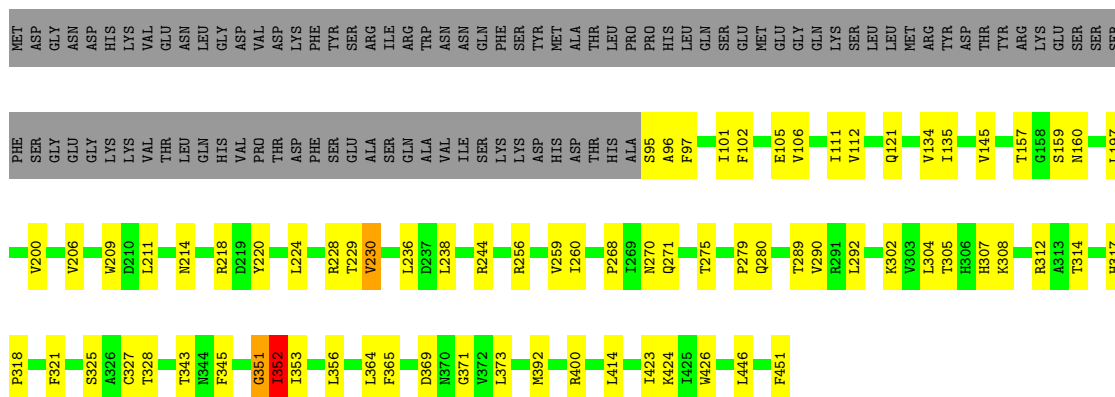


• Molecule 3: Pre-mRNA-splicing factor CWC21

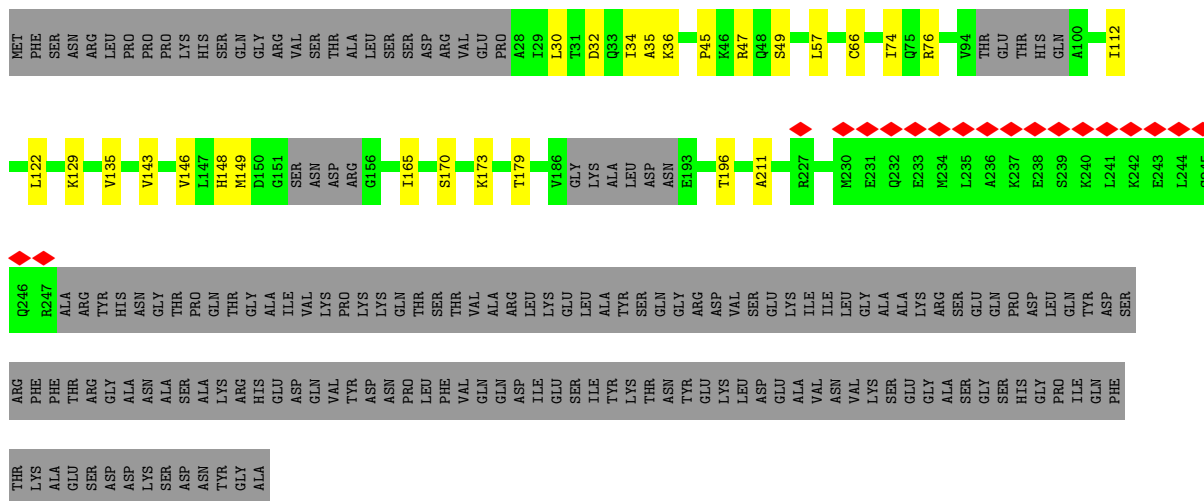
Chain J: 19% 80%



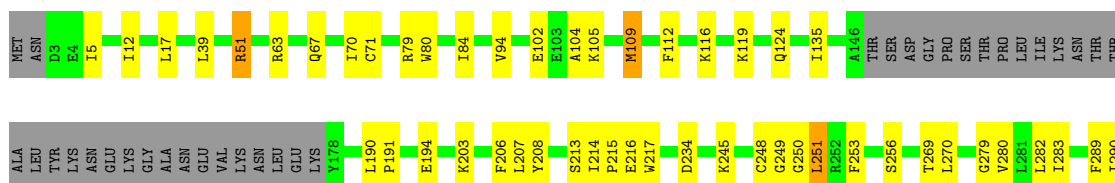
- Molecule 4: Pre-mRNA-splicing factor PRP46



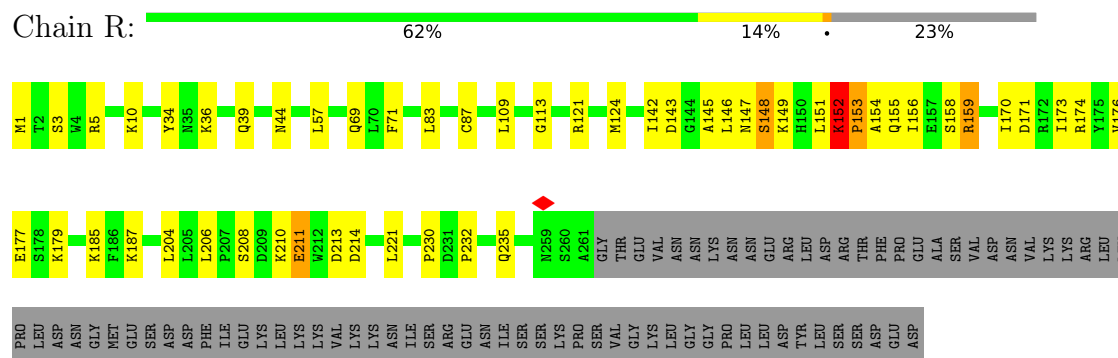
- Molecule 5: Pre-mRNA-processing protein 45



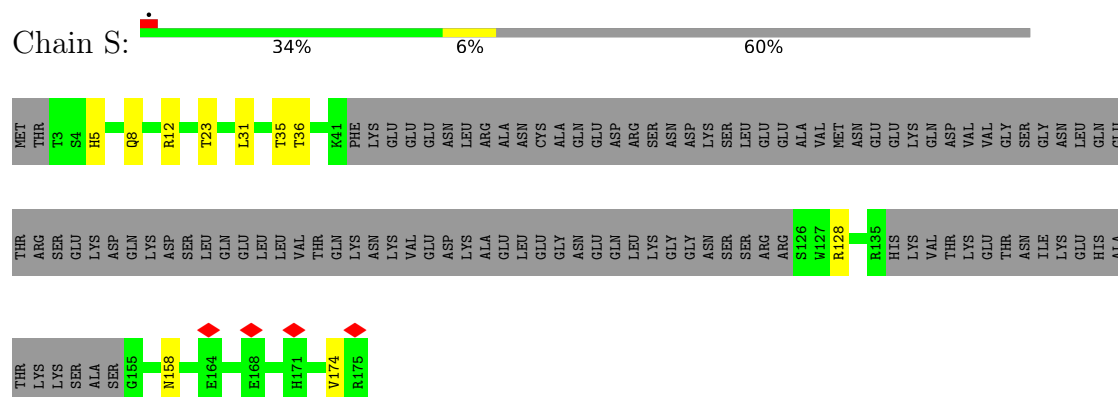
- Molecule 6: Pre-mRNA-splicing factor SLT11



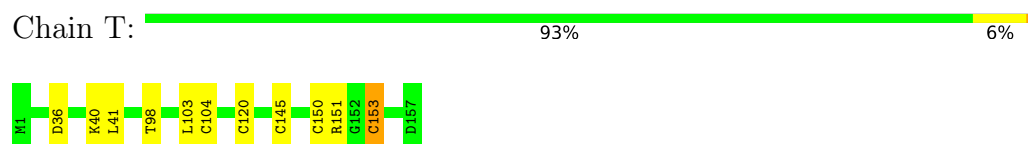
- Molecule 7: Pre-mRNA-splicing factor CWC2



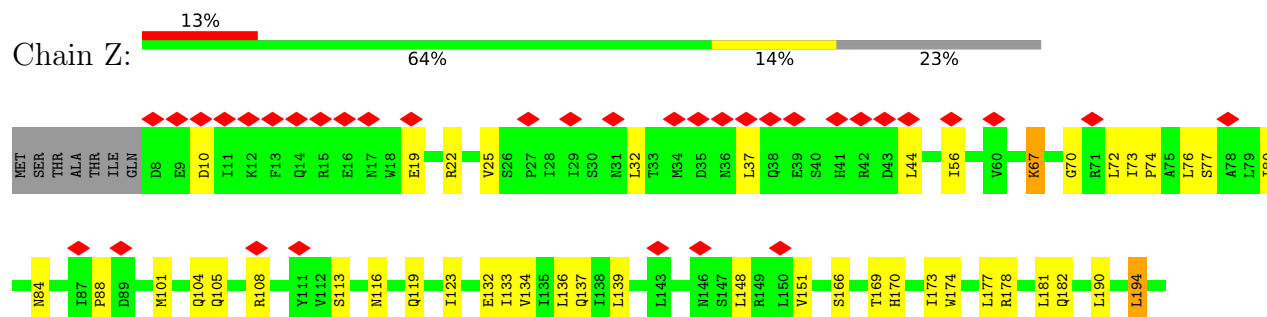
- Molecule 8: Pre-mRNA-splicing factor CWC15



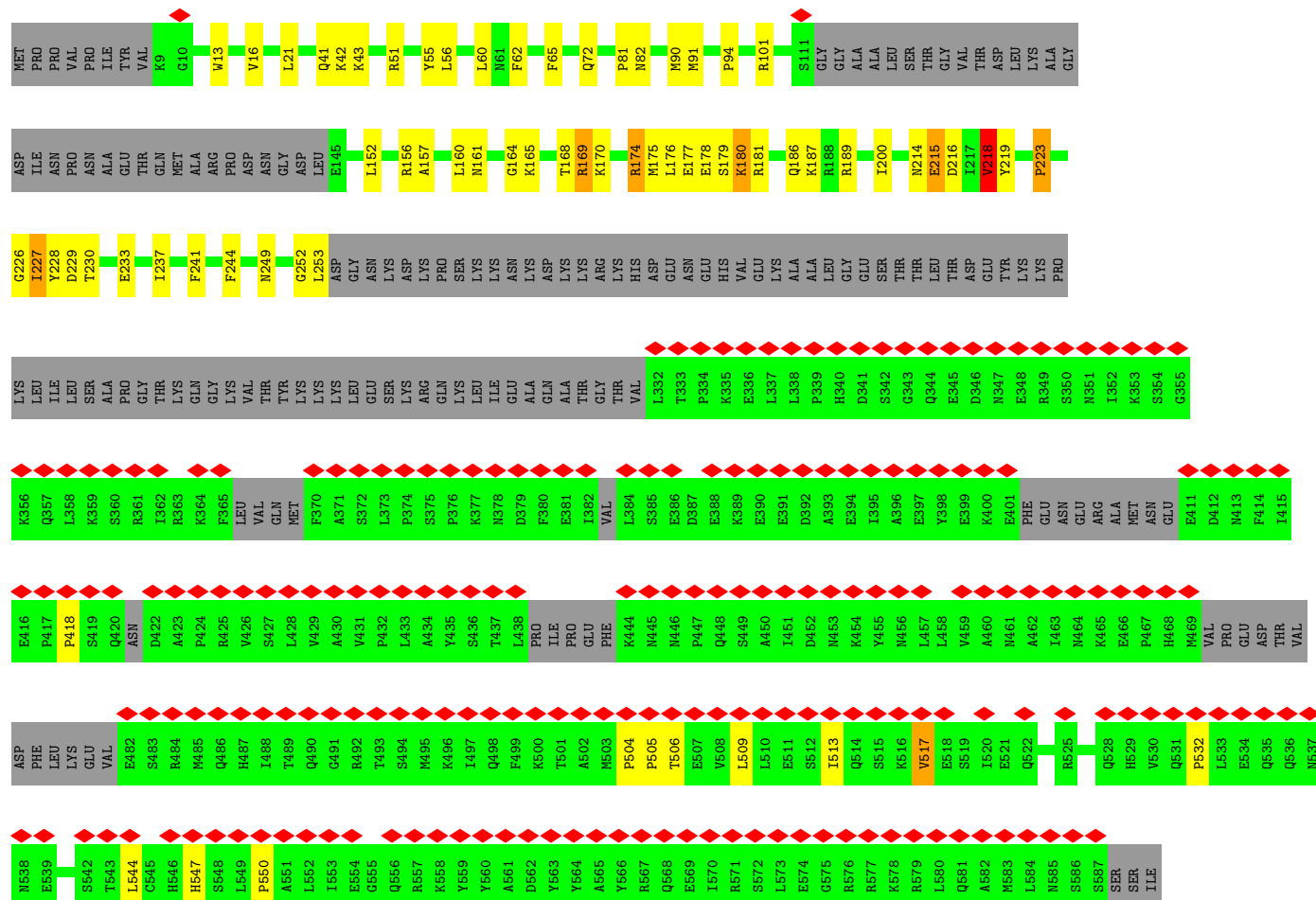
- Molecule 9: Pre-mRNA-splicing factor BUD31



- Molecule 10: Pre-mRNA-splicing factor CWC22

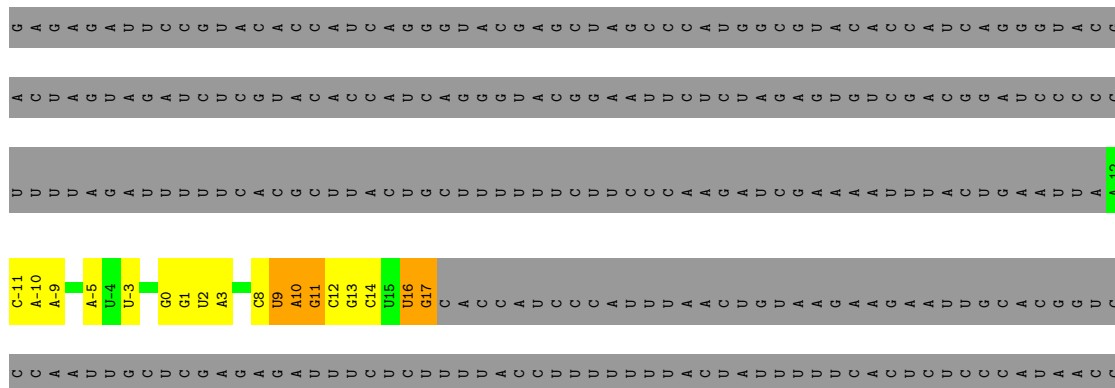


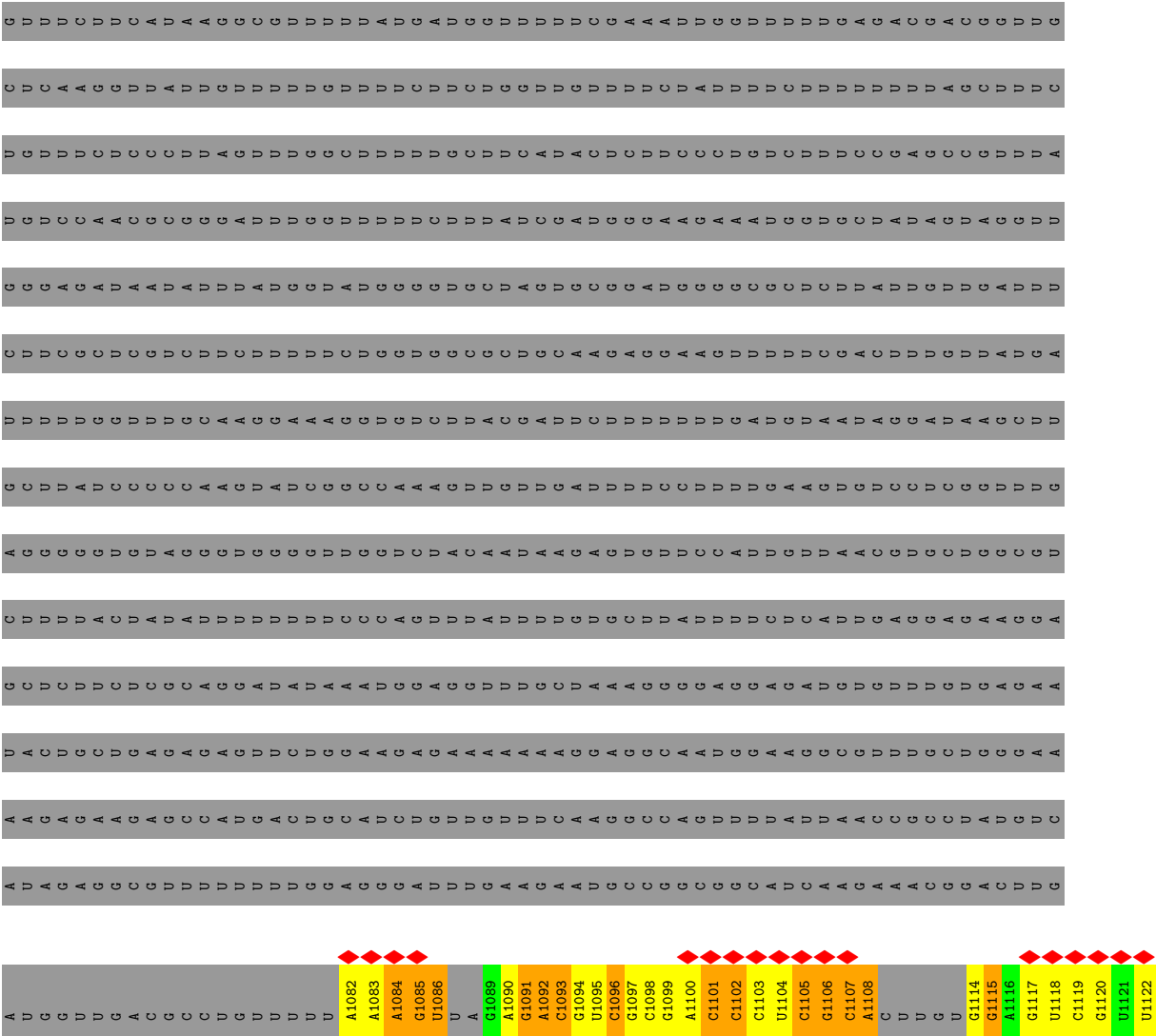
- Molecule 11: Pre-mRNA-splicing factor CEF1



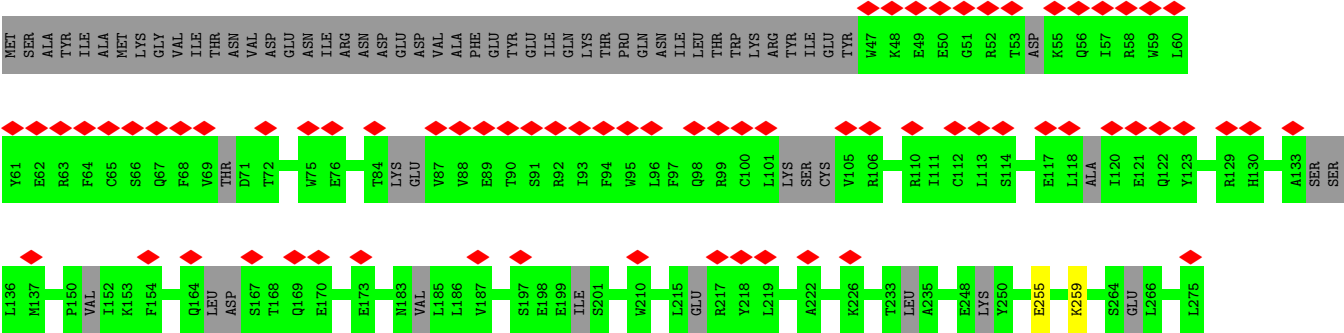
- Molecule 12: Pre-mRNA-splicing factor CLF1

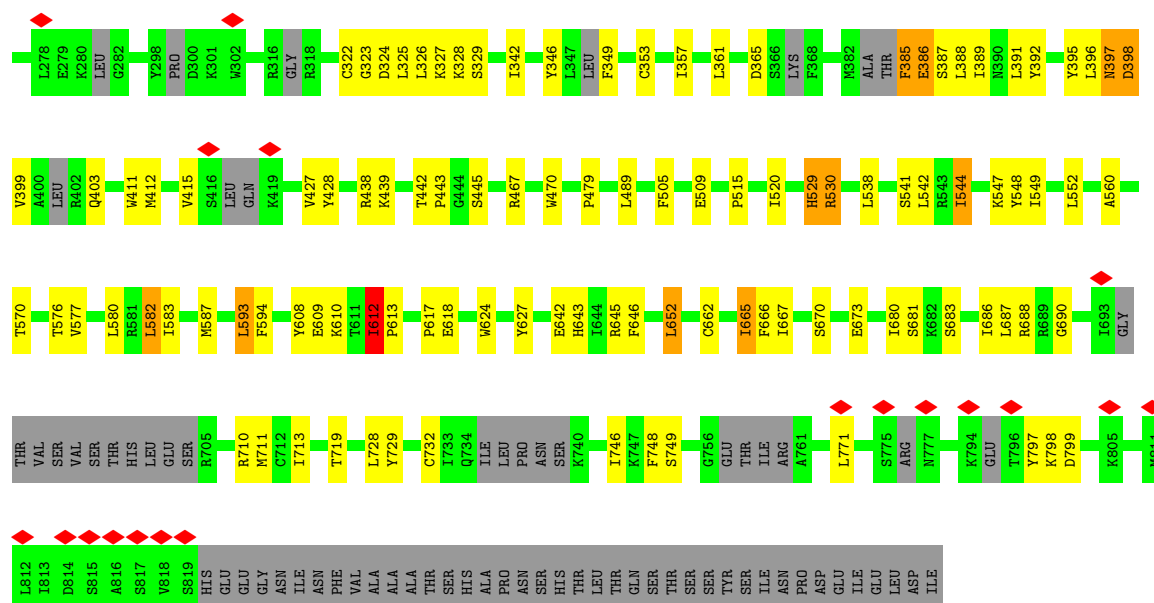




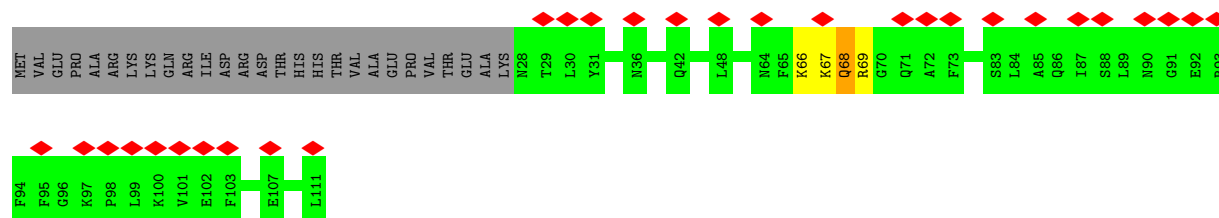


● Molecule 20: Pre-mRNA-splicing factor SYF1

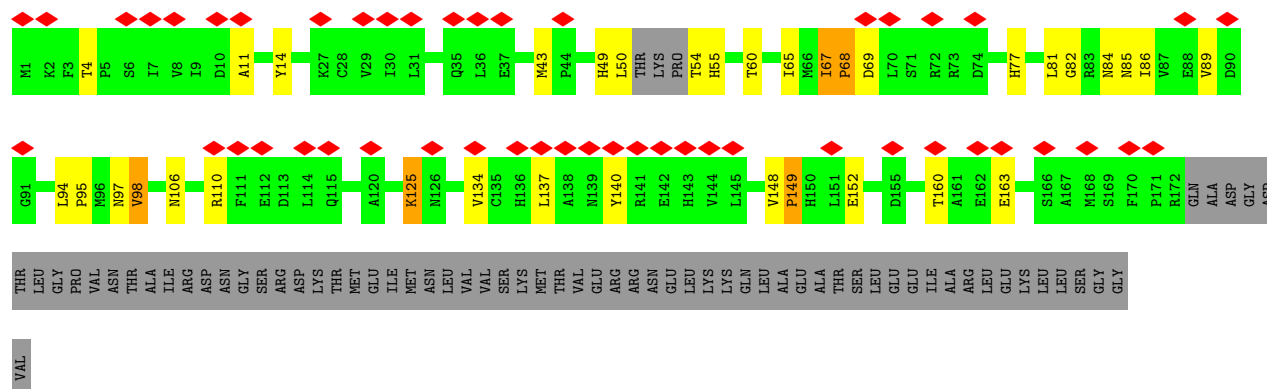




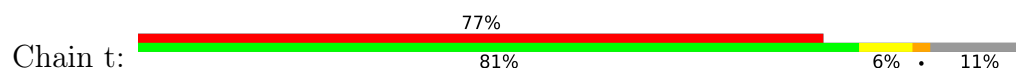
• Molecule 21: U2 small nuclear ribonucleoprotein B''

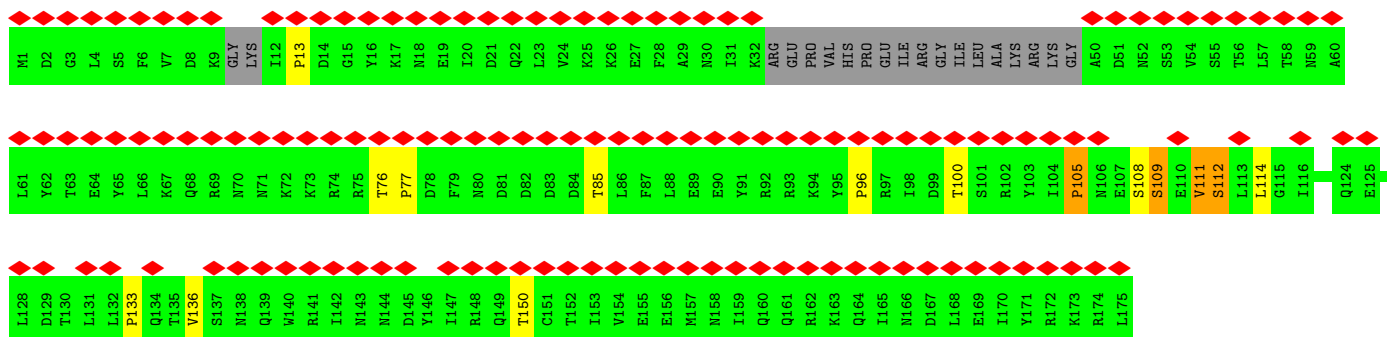


• Molecule 22: U2 small nuclear ribonucleoprotein A'

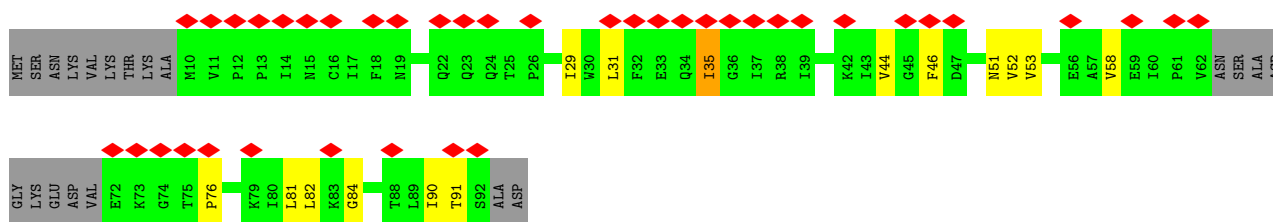


• Molecule 23: Pre-mRNA-splicing factor SNT309

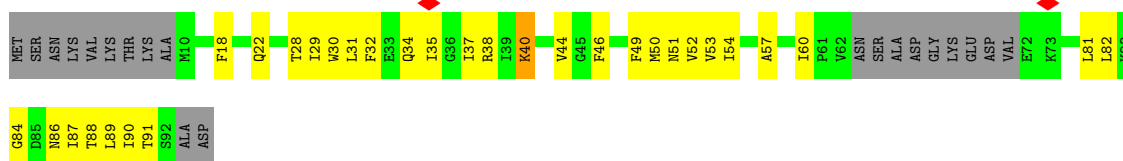




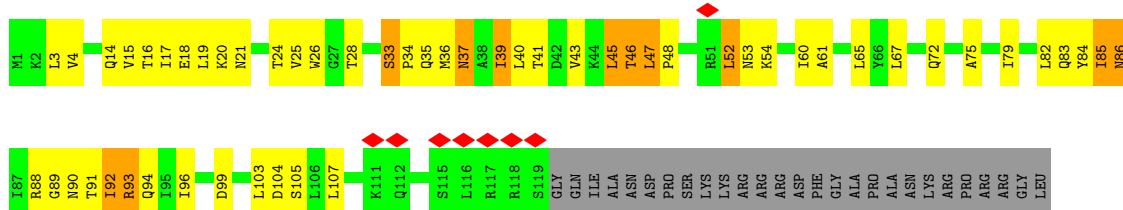
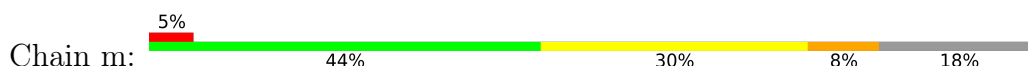
• Molecule 24: Small nuclear ribonucleoprotein E



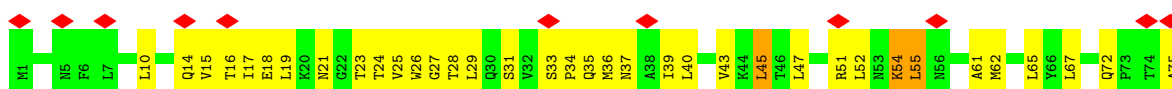
• Molecule 24: Small nuclear ribonucleoprotein E

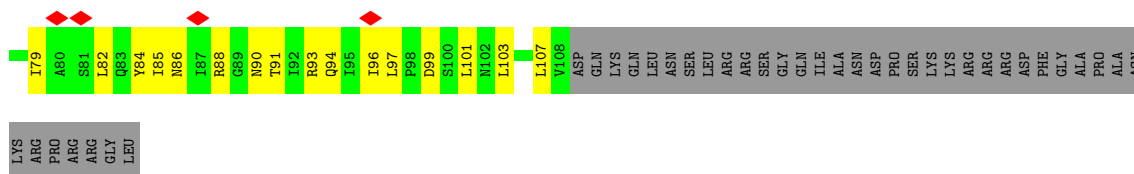


• Molecule 25: Small nuclear ribonucleoprotein Sm D1

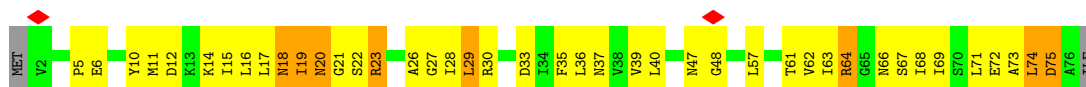


• Molecule 25: Small nuclear ribonucleoprotein Sm D1

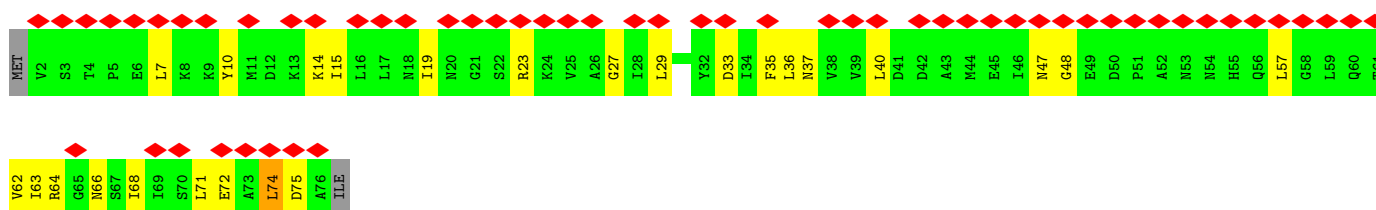
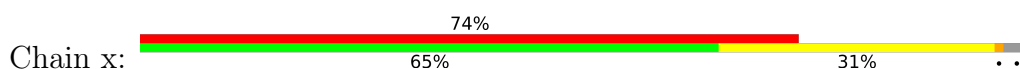




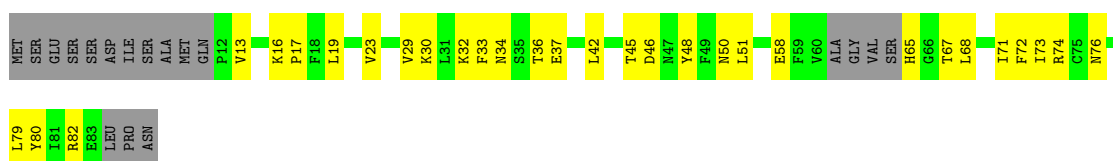
• Molecule 26: Small nuclear ribonucleoprotein G



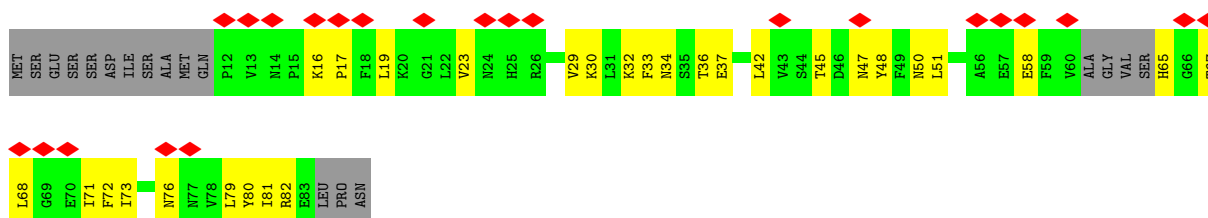
• Molecule 26: Small nuclear ribonucleoprotein G



• Molecule 27: Small nuclear ribonucleoprotein F

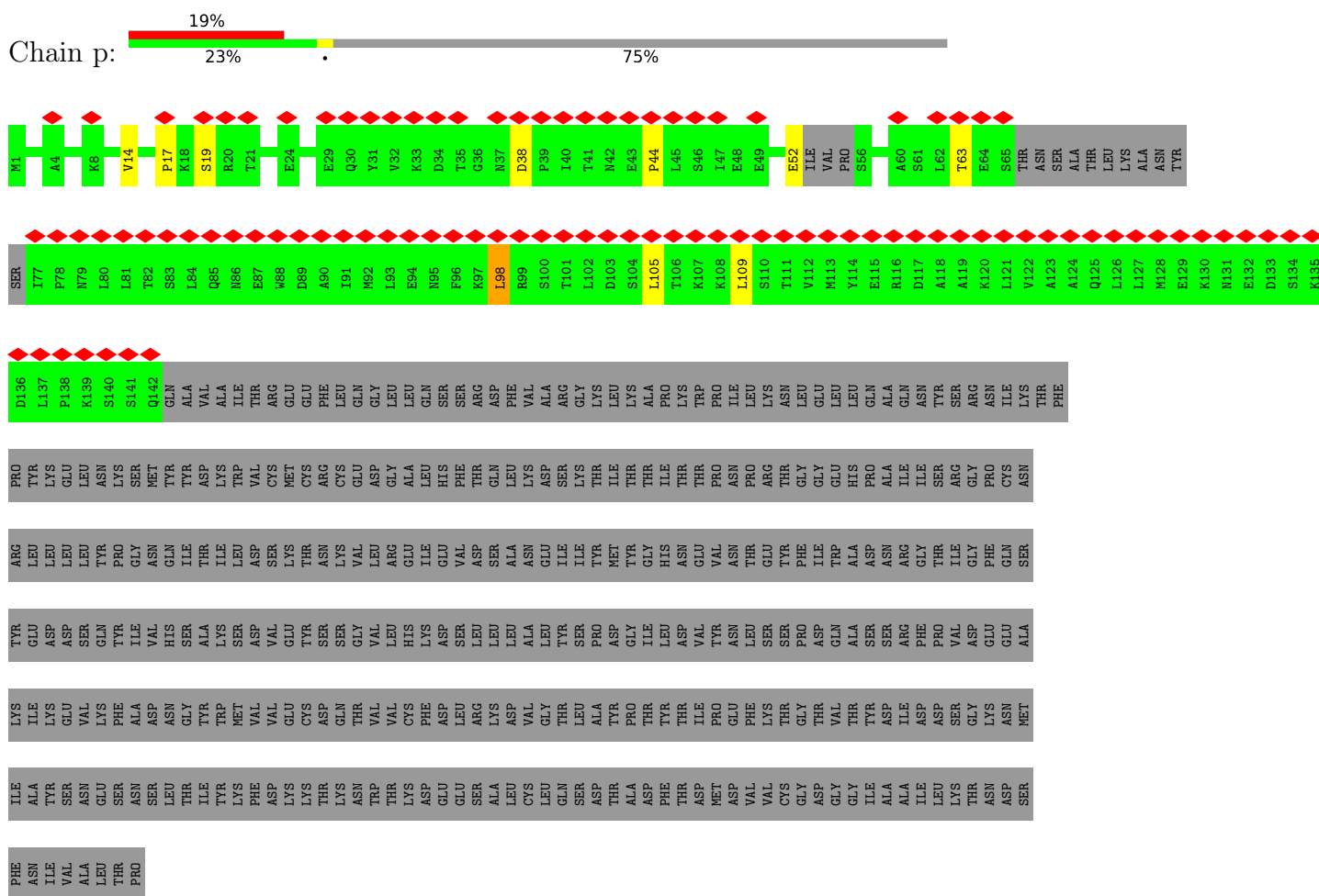


• Molecule 27: Small nuclear ribonucleoprotein F

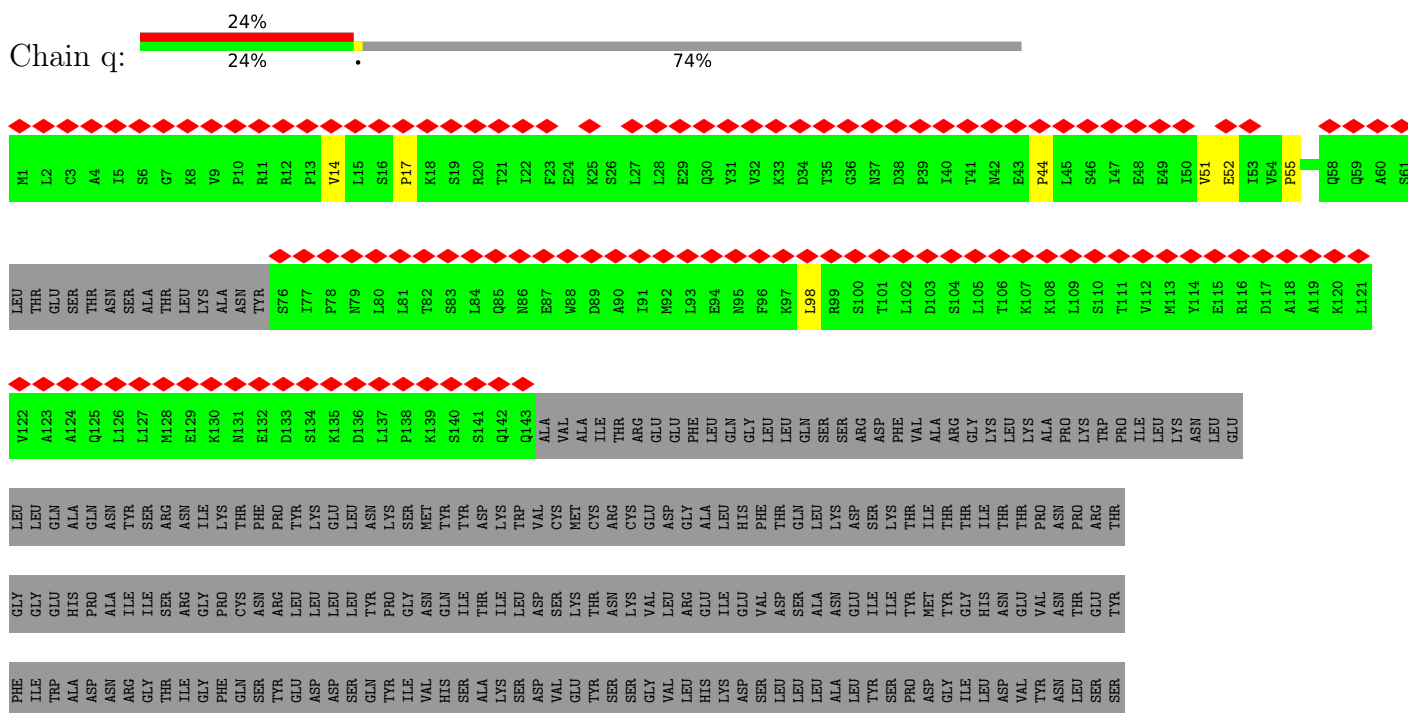


• Molecule 28: Small nuclear ribonucleoprotein Sm D2



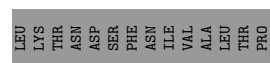
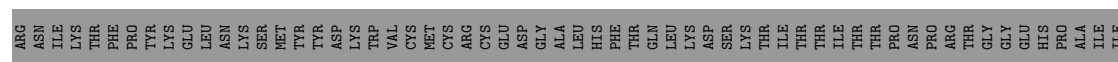
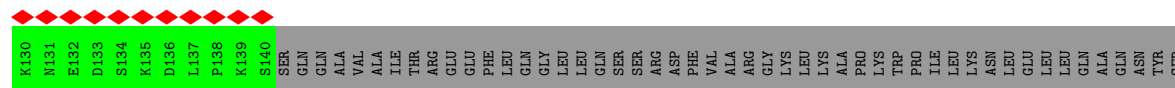
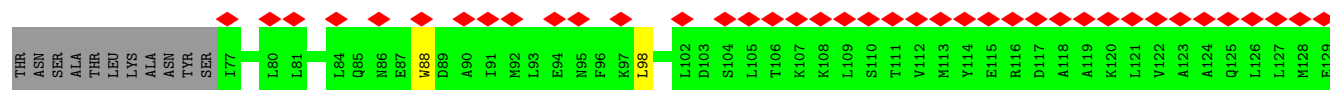
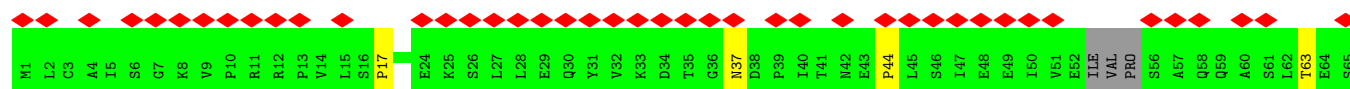


- Molecule 31: Pre-mRNA-processing factor 19



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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	555036	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	0.343	Depositor
Minimum map value	-0.140	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.019	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: IHP, SEP, MG, ZN, GTP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.33	0/16198	0.56	6/21958 (0.0%)
2	C	0.31	0/7503	0.54	0/10159
3	J	0.23	0/191	0.45	0/254
4	O	0.34	0/2872	0.57	0/3902
5	P	0.24	0/1629	0.47	0/2194
6	Q	0.38	0/2339	0.72	0/3154
7	R	0.37	0/2135	0.65	2/2871 (0.1%)
8	S	0.19	0/581	0.48	0/776
9	T	0.33	0/1315	0.54	0/1759
10	Z	0.32	0/3712	0.64	2/5004 (0.0%)
11	c	0.34	0/2996	0.58	0/4033
12	d	0.35	0/3931	0.61	2/5356 (0.0%)
13	I	0.17	0/826	0.33	0/1097
14	n	0.24	0/1894	0.59	0/2529
15	H	0.91	0/631	1.30	1/846 (0.1%)
16	B	0.23	0/1411	0.40	0/2191
17	D	0.23	0/4239	0.37	2/6598 (0.0%)
18	E	0.27	0/2452	0.36	0/3817
19	L	0.28	0/4877	0.48	1/7562 (0.0%)
20	v	0.49	0/4662	0.75	4/6358 (0.1%)
21	a	0.63	0/415	1.15	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	0.24	0/535	0.49	0/730
25	m	0.49	0/926	0.77	0/1257
25	z	0.31	0/833	0.61	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	0.23	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	0.43	0/755	0.72	0/1014
30	l	0.73	0/650	1.00	1/879 (0.1%)
30	y	0.30	0/625	0.59	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	0.37	0/81399	0.61	31/112750 (0.0%)

There are no bond length outliers.

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	b	43	MET	CA-C-N	8.57	128.71	119.28
22	b	43	MET	C-N-CA	8.57	128.71	119.28
22	b	4	THR	CA-C-N	7.87	127.43	118.85
22	b	4	THR	C-N-CA	7.87	127.43	118.85
17	D	96	U	C4'-C3'-O3'	-7.74	101.40	113.00
20	v	681	SER	N-CA-C	-6.52	105.08	113.16
22	b	11	ALA	CA-C-N	6.48	127.94	119.84
22	b	11	ALA	C-N-CA	6.48	127.94	119.84
19	L	1092	A	C2'-C3'-O3'	-6.43	104.05	113.70
17	D	95	C	C2'-C3'-O3'	6.42	119.14	109.50
20	v	612	ILE	O-C-N	6.24	124.50	120.07
1	A	510	PRO	CA-C-N	6.08	133.16	121.54
1	A	510	PRO	C-N-CA	6.08	133.16	121.54
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
12	d	424	ARG	CA-C-N	5.97	128.55	120.38
12	d	424	ARG	C-N-CA	5.97	128.55	120.38
1	A	1964	PRO	O-C-N	5.82	130.50	122.64
15	H	53	GLN	N-CA-C	-5.58	105.30	111.71
1	A	1941	LEU	N-CA-C	5.39	117.16	111.28
22	b	81	LEU	CA-C-N	5.20	124.91	119.92
22	b	81	LEU	C-N-CA	5.20	124.91	119.92
10	Z	72	LEU	CA-C-N	5.06	124.38	120.33
10	Z	72	LEU	C-N-CA	5.06	124.38	120.33
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
1	A	260	PRO	CA-C-N	5.04	131.16	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	260	PRO	C-N-CA	5.04	131.16	121.54
30	l	39	SER	N-CA-C	-5.03	105.92	111.71
7	R	44	ASN	CA-C-N	5.03	130.45	122.61
7	R	44	ASN	C-N-CA	5.03	130.45	122.61

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	15793	0	15768	308	0
2	C	7348	0	7521	94	0
3	J	190	0	186	2	0
4	O	2810	0	2804	75	0
5	P	1608	0	1631	34	0
6	Q	2301	0	2366	83	0
7	R	2089	0	2053	70	0
8	S	567	0	552	8	0
9	T	1291	0	1312	7	0
10	Z	3651	0	3707	96	0
11	c	2978	0	2459	104	0
12	d	3881	0	3041	182	0
13	I	822	0	845	27	0
14	n	1894	0	1406	6	0
15	H	617	0	616	65	0
16	B	1266	0	641	19	0
17	D	3795	0	1919	73	0
18	E	2192	0	1106	28	0
19	L	4382	0	2227	185	0
20	v	4625	0	3448	107	0
21	a	416	0	182	5	0
22	b	841	0	350	24	0
23	t	926	0	606	3	0
24	i	541	0	542	72	0
24	u	526	0	515	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	m	917	0	961	97	0
25	z	824	0	864	78	0
26	j	552	0	553	81	0
26	x	552	0	553	22	0
27	h	518	0	502	36	0
27	w	518	0	502	47	0
28	e	785	0	802	139	0
28	g	785	0	802	110	0
29	k	809	0	881	131	0
29	s	749	0	809	57	0
30	l	641	0	666	115	0
30	y	616	0	639	24	0
31	o	830	0	663	5	0
31	p	843	0	675	4	0
31	q	850	0	682	3	0
31	r	823	0	654	8	0
32	A	36	0	6	4	0
33	C	32	0	12	0	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	79042	0	69029	2108	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 (2108) 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)
11:c:237:ILE:HD11	12:d:114:CYS:SG	1.50	1.47
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
1:A:1808:ALA:HB1	1:A:1947:HIS:CE1	1.60	1.36
1:A:2030:PRO:CG	28:e:73:LYS:HB2	1.54	1.35
19:L:1137:U:H2'	19:L:1138:G:C1'	1.58	1.34
12:d:255:ALA:HB1	12:d:291:PHE:CE2	1.63	1.33
20:v:612:ILE:HG13	20:v:613:PRO:CD	1.60	1.28
2:C:286:LEU:CD2	10:Z:182:GLN:HB3	1.65	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:e:56:ALA:HB2	28:e:72:VAL:CG2	1.64	1.25
6:Q:300:ALA:HB2	7:R:154:ALA:CB	1.63	1.25
24:i:30:TRP:NE1	24:i:38:ARG:HD3	1.52	1.25
28:e:56:ALA:CB	28:e:69:LEU:HD23	1.66	1.25
11:c:164:GLY:O	11:c:168:THR:HG23	1.31	1.24
6:Q:304:THR:CG2	7:R:153:PRO:HG2	1.67	1.23
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:1154:U:O2'	19:L:1155:C:H5'	1.07	1.22
11:c:237:ILE:CD1	12:d:114:CYS:SG	2.30	1.20
26:j:64:ARG:NH2	24:i:50:MET:HB3	1.56	1.19
20:v:711:MET:HE1	20:v:748:PHE:CB	1.72	1.19
15:H:29:TYR:HD1	15:H:32:TYR:CD2	1.62	1.18
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
12:d:255:ALA:CB	12:d:291:PHE:CE2	2.27	1.17
11:c:227:ILE:CG1	13:I:152:ILE:HG22	1.75	1.16
7:R:152:LYS:CG	7:R:153:PRO:HD2	1.76	1.16
25:m:19:LEU:HD22	25:m:91:THR:HG22	1.29	1.15
11:c:252:GLY:HA2	12:d:38:LEU:O	1.46	1.15
26:j:28:ILE:O	26:j:40:LEU:HB2	1.44	1.15
1:A:2027:LEU:HD11	28:e:57:ARG:NE	1.60	1.15
26:j:64:ARG:HH22	24:i:50:MET:HB3	1.10	1.14
1:A:1980:LYS:NZ	28:e:39:VAL:HG11	1.61	1.13
31:r:99:ARG:HG2	31:o:98:LEU:HD11	1.18	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
28:e:56:ALA:HB3	28:e:69:LEU:HD23	1.23	1.12
1:A:1808:ALA:CB	1:A:1947:HIS:CE1	2.32	1.12
1:A:2033:THR:HG22	28:e:43:PRO:CG	1.78	1.12
19:L:1137:U:H2'	19:L:1138:G:H1'	1.26	1.12
29:k:105:LYS:HA	29:k:108:ARG:HH21	1.07	1.12
1:A:769:MET:HE2	4:O:352:ILE:CD1	1.78	1.12
1:A:1808:ALA:CB	1:A:1947:HIS:HE1	1.63	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
19:L:113:U:O4	27:w:48:TYR:HA	1.46	1.11
6:Q:300:ALA:CB	7:R:154:ALA:HB1	1.78	1.11
1:A:769:MET:CE	4:O:352:ILE:HD11	1.81	1.10
11:c:179:SER:HB2	15:H:68:PRO:HD3	1.20	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
1:A:2024:MET:HE2	28:e:93:LYS:CE	1.82	1.09
15:H:32:TYR:HB2	15:H:50:TRP:CH2	1.86	1.09
1:A:2027:LEU:CD1	28:e:57:ARG:HE	1.64	1.09
11:c:227:ILE:HG13	13:I:152:ILE:HG22	1.11	1.09
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
1:A:2030:PRO:HG3	28:e:73:LYS:HB2	1.13	1.09
12:d:271:ILE:HD13	12:d:281:LYS:HG3	1.12	1.09
15:H:58:ILE:HD11	15:H:85:LEU:HD22	1.34	1.08
15:H:58:ILE:HD11	15:H:85:LEU:CD2	1.82	1.08
12:d:141:ILE:CG2	13:I:105:TYR:CD1	2.37	1.08
1:A:427:SER:HA	10:Z:202:GLN:HB3	1.14	1.08
28:g:35:ASN:CB	28:g:61:PHE:CZ	2.37	1.08
6:Q:304:THR:HG22	7:R:153:PRO:HG2	1.26	1.07
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
15:H:29:TYR:CD1	15:H:32:TYR:CD2	2.43	1.07
28:e:56:ALA:HB2	28:e:72:VAL:HG23	1.31	1.07
1:A:2030:PRO:CG	28:e:73:LYS:CB	2.33	1.06
2:C:831:ILE:HG13	2:C:835:LYS:HE2	1.32	1.06
7:R:146:LEU:HD11	7:R:151:LEU:HD23	1.32	1.06
20:v:386:GLU:HA	20:v:389:ILE:HD12	1.38	1.06
11:c:179:SER:CB	15:H:68:PRO:HD3	1.86	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
15:H:60:GLN:O	15:H:63:THR:HG22	1.52	1.05
25:m:17:ILE:HG23	25:m:92:ILE:HG22	1.36	1.05
12:d:247:VAL:HG21	12:d:280:LEU:HD11	1.36	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
11:c:200:ILE:HG21	12:d:45:GLU:HG3	1.39	1.03
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
2:C:234:LEU:HD21	2:C:439:ILE:HG23	1.41	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:m:17:ILE:CG2	25:m:92:ILE:CG2	2.36	1.02
1:A:2027:LEU:HB3	28:e:71:ASN:CB	1.88	1.02
4:O:446:LEU:HD11	12:d:237:ILE:HG21	1.37	1.02
6:Q:215:PRO:HB3	7:R:171:ASP:OD1	1.59	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
12:d:263:SER:HB3	12:d:287:PHE:CZ	1.93	1.01
15:H:29:TYR:CD1	15:H:32:TYR:CE2	2.48	1.01
6:Q:300:ALA:CB	7:R:154:ALA:CB	2.38	1.00
5:P:148:HIS:HB2	12:d:131:ARG:HG3	1.42	1.00
19:L:1082:A:H2'	19:L:1083:A:H8	1.26	1.00
20:v:541:SER:O	20:v:544:ILE:HG22	1.61	1.00
2:C:831:ILE:O	2:C:835:LYS:HB2	1.60	1.00
20:v:386:GLU:HA	20:v:389:ILE:CD1	1.92	1.00
1:A:2030:PRO:HG2	28:e:73:LYS:CB	1.89	1.00
12:d:267:TYR:CD2	12:d:284:LEU:HD23	1.97	0.99
29:k:48:CYS:SG	29:k:82:LEU:CD1	2.50	0.99
6:Q:303:GLY:HA3	6:Q:309:ASN:OD1	1.62	0.99
24:u:35:ILE:CD1	27:w:79:LEU:CD1	2.40	0.99
1:A:2030:PRO:HG2	28:e:73:LYS:HB2	1.41	0.99
12:d:241:MET:HG2	12:d:279:LEU:HD13	1.42	0.98
12:d:255:ALA:HB1	12:d:291:PHE:CD2	1.99	0.98
1:A:431:ILE:O	10:Z:182:GLN:HG2	1.62	0.98
1:A:1972:ASP:CB	28:e:41:ARG:HD3	1.93	0.98
22:b:50:LEU:C	22:b:55:HIS:CB	2.36	0.98
19:L:1137:U:O2'	19:L:1138:G:H4'	1.63	0.97
1:A:2033:THR:HG22	28:e:43:PRO:HG3	0.99	0.97
7:R:152:LYS:HG3	7:R:153:PRO:HD2	1.43	0.97
12:d:271:ILE:CD1	12:d:281:LYS:HG3	1.93	0.97
24:i:28:THR:HG22	24:i:40:LYS:HD2	1.45	0.97
12:d:141:ILE:HG23	13:I:105:TYR:CD1	1.98	0.97
19:L:110:A:H61	25:z:35:GLN:NE2	1.61	0.97
25:m:96:ILE:HD11	28:g:89:ARG:HH22	1.29	0.97
11:c:169:ARG:HB3	11:c:169:ARG:HH11	1.28	0.96
22:b:110:ARG:HA	22:b:134:VAL:CB	1.95	0.96
29:s:59:ASP:HA	29:s:62:ARG:HH21	1.31	0.96
1:A:2024:MET:HE2	28:e:93:LYS:HE3	1.47	0.96
6:Q:109:MET:CE	6:Q:112:PHE:CD2	2.48	0.96
1:A:2030:PRO:HG3	28:e:73:LYS:CB	1.95	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:1082:A:H2'	19:L:1083:A:C8	2.00	0.96
12:d:267:TYR:O	12:d:271:ILE:HG22	1.64	0.96
12:d:241:MET:CG	12:d:279:LEU:CD1	2.44	0.95
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
30:l:14:ALA:O	30:l:17:HIS:HB2	1.67	0.95
7:R:152:LYS:HG2	7:R:153:PRO:HD2	1.46	0.95
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
12:d:141:ILE:CG2	13:I:105:TYR:CE1	2.50	0.93
25:m:47:LEU:HD11	25:m:61:ALA:CB	1.98	0.93
12:d:241:MET:HG2	12:d:279:LEU:HD11	1.51	0.93
24:u:35:ILE:HD13	27:w:79:LEU:CD1	1.98	0.93
5:P:143:VAL:HG11	12:d:124:ARG:HG3	1.50	0.93
17:D:6:G:H4'	29:k:11:ARG:NH2	1.82	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:1808:ALA:HB1	1:A:1947:HIS:HE1	0.76	0.92
29:s:48:CYS:SG	29:s:82:LEU:O	2.27	0.92
6:Q:248:CYS:SG	6:Q:316:LEU:CD1	2.58	0.92
29:k:13:ALA:HB2	29:k:37:PHE:HZ	1.31	0.92
28:g:35:ASN:HB2	28:g:61:PHE:HZ	1.25	0.92
29:k:44:VAL:HG22	29:k:86:ILE:HG22	1.52	0.92
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
2:C:430:ARG:HG3	2:C:430:ARG:HH11	1.34	0.91
25:m:47:LEU:HD11	25:m:61:ALA:HB1	1.53	0.91
30:l:59:MET:SD	30:l:62:ILE:HD12	2.09	0.91
1:A:2027:LEU:HB2	28:e:71:ASN:CG	1.96	0.91
15:H:32:TYR:HB2	15:H:50:TRP:HH2	1.23	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
30:y:21:LEU:HD11	30:y:44:LEU:HD11	1.51	0.91
1:A:1980:LYS:HZ1	28:e:39:VAL:HG11	1.24	0.91
19:L:151:A:H61	19:L:1086:U:H3	1.11	0.91
27:w:32:LYS:HG3	27:w:33:PHE:CD1	2.06	0.91
15:H:29:TYR:CE1	15:H:32:TYR:HE2	1.89	0.91
19:L:113:U:C4	27:w:48:TYR:HA	2.05	0.91
17:D:168:U:H2'	24:i:49:PHE:CD1	2.06	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:152:LYS:HG3	7:R:153:PRO:CD	2.01	0.90
1:A:2027:LEU:CB	28:e:71:ASN:CG	2.45	0.90
12:d:255:ALA:CB	12:d:291:PHE:HE2	1.81	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
4:O:446:LEU:CD1	12:d:237:ILE:HG21	2.01	0.90
6:Q:207:LEU:HD23	6:Q:290:ILE:HG22	1.51	0.90
7:R:145:ALA:HB2	7:R:221:LEU:HB3	1.54	0.90
10:Z:133:ILE:HA	10:Z:136:LEU:HD21	1.51	0.90
2:C:286:LEU:HD21	10:Z:182:GLN:HB3	1.51	0.89
28:g:76:TRP:CZ2	28:g:87:ARG:HD3	2.07	0.89
15:H:29:TYR:CE1	15:H:32:TYR:CE2	2.60	0.89
20:v:385:PHE:CA	20:v:388:LEU:HD12	2.03	0.89
11:c:214:ASN:HD21	12:d:44:ARG:CG	1.85	0.89
19:L:117:U:O2	25:z:35:GLN:HB3	1.72	0.89
7:R:146:LEU:HD13	7:R:151:LEU:HD23	1.54	0.89
11:c:252:GLY:CA	12:d:38:LEU:O	2.20	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	0.89
6:Q:109:MET:CE	6:Q:112:PHE:HD2	1.84	0.88
11:c:214:ASN:HD21	12:d:44:ARG:CD	1.86	0.88
30:l:17:HIS:CG	30:l:75:PRO:HG2	2.07	0.88
19:L:118:U:H3	28:e:66:ASN:HD22	1.17	0.88
4:O:111:ILE:HG21	12:d:197:PRO:HD3	1.56	0.88
10:Z:37:LEU:HD23	10:Z:214:ILE:HG13	1.55	0.88
12:d:141:ILE:HG23	13:I:105:TYR:CE1	2.08	0.88
30:l:65:ARG:HH11	30:l:65:ARG:HG3	1.36	0.88
1:A:1980:LYS:NZ	28:e:39:VAL:CG1	2.36	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
11:c:214:ASN:ND2	12:d:44:ARG:HG3	1.87	0.88
12:d:289:LYS:HE2	20:v:643:HIS:HE1	1.36	0.88
24:u:35:ILE:HD11	27:w:79:LEU:CD1	2.03	0.88
30:y:33:LEU:HA	30:y:44:LEU:HD23	1.54	0.88
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
2:C:286:LEU:HD23	10:Z:182:GLN:HB3	1.54	0.87
1:A:426:PRO:HB3	10:Z:201:ARG:CZ	2.05	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:151:A:N6	19:L:1086:U:H3	1.72	0.87
28:g:45:ILE:HD12	28:g:55:ILE:HG12	1.57	0.87
30:l:82:PRO:O	30:l:85:LYS:HD2	1.73	0.87
11:c:181:ARG:HB2	11:c:181:ARG:NH1	1.90	0.86
20:v:386:GLU:CA	20:v:389:ILE:HD12	2.04	0.86
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
15:H:54:VAL:O	15:H:58:ILE:HD13	1.75	0.86
17:D:130:A:OP1	17:D:130:A:H2'	1.76	0.86
12:d:113:LYS:HE3	13:I:162:ASN:OD1	1.76	0.86
4:O:446:LEU:CD1	12:d:237:ILE:CG2	2.54	0.86
10:Z:148:LEU:HB2	10:Z:190:LEU:HD11	1.58	0.86
12:d:57:TYR:HE1	18:E:85:C:OP2	1.58	0.86
11:c:165:LYS:HG3	18:E:54:U:O4	1.76	0.86
11:c:169:ARG:HH11	11:c:169:ARG:CB	1.88	0.86
29:k:29:VAL:O	29:k:50:GLU:HA	1.76	0.86
1:A:1961:LEU:HD21	1:A:2084:LEU:HD13	1.56	0.85
7:R:152:LYS:CG	7:R:153:PRO:CD	2.53	0.85
19:L:1154:U:HO2'	19:L:1155:C:H5'	1.37	0.85
28:e:56:ALA:HB2	28:e:72:VAL:HG21	1.56	0.85
30:y:21:LEU:HD12	30:y:44:LEU:HD11	1.56	0.85
25:m:52:LEU:HD21	28:g:79:LYS:C	2.00	0.85
28:e:56:ALA:HB1	28:e:69:LEU:HD23	1.57	0.85
12:d:141:ILE:CG2	13:I:105:TYR:HD1	1.82	0.85
12:d:229:VAL:HG12	12:d:274:TRP:CZ2	2.12	0.85
28:g:50:ASN:ND2	28:g:52:HIS:HE1	1.75	0.85
19:L:1137:U:C2'	19:L:1138:G:H1'	2.05	0.84
30:l:49:ALA:HB2	30:l:59:MET:HE3	1.59	0.84
1:A:769:MET:HE2	4:O:352:ILE:HD11	0.90	0.84
1:A:1990:ASN:ND2	1:A:1993:ASP:H	1.73	0.84
19:L:1154:U:H2'	19:L:1155:C:C6	2.11	0.84
1:A:1035:LEU:O	1:A:1035:LEU:HD12	1.78	0.84
11:c:227:ILE:CG1	13:I:152:ILE:CG2	2.54	0.84
28:e:56:ALA:CB	28:e:72:VAL:HG23	2.08	0.84
1:A:1987:VAL:CG1	1:A:1989:PHE:CE2	2.61	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
12:d:289:LYS:HG3	20:v:609:GLU:HG2	1.58	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:k:35:MET:HB3	30:l:84:PHE:CE2	2.13	0.83
6:Q:304:THR:CG2	7:R:153:PRO:CG	2.49	0.83
10:Z:174:TRP:HZ2	10:Z:205:TYR:HH	0.87	0.83
12:d:147:ASN:ND2	13:I:160:LEU:HD21	1.93	0.83
22:b:14:TYR:O	29:s:102:LEU:CD1	2.26	0.83
12:d:255:ALA:CB	12:d:291:PHE:CD2	2.60	0.83
19:L:110:A:N6	25:z:35:GLN:NE2	2.26	0.83
12:d:247:VAL:HG21	12:d:280:LEU:CD1	2.07	0.82
1:A:2024:MET:HE2	28:e:93:LYS:HE2	1.61	0.82
12:d:284:LEU:O	12:d:284:LEU:HD22	1.79	0.82
24:i:30:TRP:NE1	24:i:38:ARG:CD	2.39	0.82
26:x:19:ILE:O	26:x:23:ARG:HB2	1.78	0.82
1:A:427:SER:CA	10:Z:202:GLN:HB3	2.05	0.82
25:m:52:LEU:HD21	28:g:80:LYS:N	1.94	0.82
1:A:426:PRO:HG3	10:Z:201:ARG:NH1	1.94	0.82
12:d:147:ASN:HD22	13:I:160:LEU:HD21	1.45	0.82
30:l:47:VAL:HG23	30:l:59:MET:CG	2.10	0.82
4:O:97:PHE:HB3	12:d:231:ASN:OD1	1.80	0.81
10:Z:174:TRP:CH2	10:Z:201:ARG:HD3	2.14	0.81
24:u:35:ILE:CD1	27:w:79:LEU:HD12	2.09	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
15:H:58:ILE:CD1	15:H:85:LEU:HD22	2.11	0.81
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
28:e:56:ALA:CB	28:e:72:VAL:CG2	2.55	0.81
10:Z:70:GLY:HA2	10:Z:73:ILE:HG13	1.63	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
15:H:86:PHE:CE2	15:H:90:LYS:HE3	2.15	0.80
17:D:6:G:H4'	29:k:11:ARG:HH22	1.43	0.80
1:A:1980:LYS:HZ2	28:e:39:VAL:CG1	1.91	0.80
25:m:96:ILE:CD1	28:g:89:ARG:HH22	1.92	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:g:35:ASN:HB2	28:g:61:PHE:CE2	2.15	0.80
25:z:47:LEU:HD21	25:z:61:ALA:HB3	1.62	0.80
12:d:263:SER:HB3	12:d:287:PHE:HZ	1.42	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
1:A:1032:ILE:O	1:A:1035:LEU:HG	1.80	0.80
1:A:2027:LEU:O	28:e:71:ASN:HB3	1.82	0.80
12:d:267:TYR:HE2	12:d:287:PHE:HB3	1.47	0.80
19:L:109:C:OP1	25:z:34:PRO:HG3	1.81	0.80
19:L:109:C:OP1	25:z:34:PRO:CG	2.30	0.80
1:A:2024:MET:HA	28:e:71:ASN:HD21	1.47	0.79
5:P:135:VAL:HG21	11:c:219:TYR:CE1	2.17	0.79
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
11:c:181:ARG:HH21	12:d:49:ARG:NH1	1.79	0.79
27:h:71:ILE:HG23	28:g:103:VAL:HG23	1.64	0.79
6:Q:206:PHE:HD2	6:Q:291:ILE:CD1	1.96	0.79
19:L:1085:G:N2	19:L:1086:U:C5	2.51	0.79
1:A:2027:LEU:HD11	28:e:57:ARG:NH2	1.96	0.79
28:g:35:ASN:O	28:g:39:VAL:HG23	1.83	0.79
1:A:1035:LEU:HD11	1:A:1038:ILE:HG21	1.63	0.79
6:Q:215:PRO:CB	7:R:171:ASP:OD1	2.30	0.79
25:m:72:GLN:HE22	25:m:79:ILE:HD11	1.47	0.79
6:Q:300:ALA:HB2	7:R:154:ALA:HB1	0.86	0.79
5:P:148:HIS:HB2	12:d:131:ARG:CG	2.12	0.79
6:Q:214:ILE:HD11	6:Q:283:ILE:HG12	1.65	0.79
17:D:167:A:H2'	27:h:48:TYR:CE2	2.18	0.79
25:m:17:ILE:CG2	25:m:92:ILE:HG22	2.07	0.78
12:d:141:ILE:HG22	13:I:105:TYR:CE1	2.19	0.78
12:d:330:ILE:HA	12:d:334:PHE:HB2	1.64	0.78
19:L:113:U:O4	27:w:48:TYR:CA	2.31	0.78
22:b:14:TYR:O	29:s:102:LEU:HD12	1.84	0.78
1:A:1961:LEU:HD21	1:A:2084:LEU:CD1	2.12	0.78
19:L:113:U:C5	27:w:48:TYR:CE1	2.71	0.78
30:l:11:LEU:HD11	30:l:72:ILE:CD1	2.13	0.78
24:i:40:LYS:HG3	24:i:60:ILE:CD1	2.13	0.78
4:O:373:LEU:HD12	4:O:373:LEU:O	1.82	0.78
11:c:165:LYS:CG	18:E:54:U:O4	2.31	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:c:237:ILE:HD11	12:d:114:CYS:HG	1.48	0.78
25:m:19:LEU:HD22	25:m:91:THR:CG2	2.10	0.78
1:A:1035:LEU:HD11	1:A:1038:ILE:CG2	2.13	0.78
30:y:21:LEU:CD2	30:y:72:ILE:HG12	2.14	0.78
4:O:446:LEU:HD12	12:d:237:ILE:HB	1.64	0.78
19:L:1136:U:O3'	19:L:1137:U:H4'	1.82	0.78
30:y:21:LEU:HD12	30:y:44:LEU:CD1	2.12	0.78
1:A:1980:LYS:HZ2	28:e:39:VAL:HG11	1.44	0.77
11:c:229:ASP:HB2	13:I:151:LYS:HB3	1.65	0.77
19:L:1137:U:H2'	19:L:1138:G:C4'	2.13	0.77
29:s:59:ASP:HA	29:s:62:ARG:NH2	1.99	0.77
29:k:13:ALA:CB	29:k:37:PHE:HZ	1.97	0.77
12:d:267:TYR:CE2	12:d:287:PHE:HB3	2.20	0.77
15:H:74:GLN:O	15:H:78:LEU:HG	1.84	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
29:k:35:MET:CB	30:l:84:PHE:HE2	1.97	0.77
10:Z:133:ILE:O	10:Z:136:LEU:HG	1.85	0.77
29:s:57:GLN:HB3	29:s:75:ILE:HG23	1.67	0.77
24:i:32:PHE:HD1	24:i:86:ASN:O	1.68	0.77
19:L:1101:C:H5'	19:L:1102:C:OP2	1.84	0.76
1:A:1972:ASP:HB2	28:e:41:ARG:HD3	1.65	0.76
12:d:329:LEU:HD23	20:v:642:GLU:HG3	1.67	0.76
19:L:4:A:H1'	20:v:529:HIS:CD2	2.19	0.76
2:C:430:ARG:HG3	2:C:430:ARG:NH1	1.99	0.76
19:L:1137:U:C2'	19:L:1138:G:H4'	2.15	0.76
28:e:59:LYS:CG	28:e:70:GLU:HG2	2.13	0.76
30:l:33:LEU:HD21	30:l:35:GLU:O	1.85	0.76
11:c:165:LYS:CD	18:E:54:U:O4	2.33	0.76
19:L:125:C:H5''	28:e:80:LYS:HA	1.67	0.76
5:P:32:ASP:O	5:P:36:LYS:HG2	1.83	0.76
10:Z:133:ILE:HA	10:Z:136:LEU:CD2	2.16	0.76
12:d:70:ARG:NH1	18:E:88:U:H1'	2.00	0.76
15:H:32:TYR:HB2	15:H:50:TRP:CZ2	2.20	0.76
20:v:612:ILE:HG13	20:v:613:PRO:HD2	1.67	0.76
30:y:35:GLU:HB2	30:y:43:GLN:HG2	1.68	0.76
11:c:215:GLU:OE1	11:c:215:GLU:HA	1.85	0.76
10:Z:174:TRP:CZ3	10:Z:201:ARG:CZ	2.69	0.76
15:H:58:ILE:HD11	15:H:85:LEU:HD21	1.65	0.76
20:v:617:PRO:O	20:v:618:GLU:HB2	1.84	0.76
6:Q:304:THR:HG23	7:R:153:PRO:HG2	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
6:Q:109:MET:HE2	6:Q:112:PHE:CD2	2.21	0.75
12:d:255:ALA:HB3	12:d:291:PHE:HE2	1.51	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:2030:PRO:HG2	28:e:73:LYS:HB3	1.68	0.75
24:u:35:ILE:HD13	27:w:79:LEU:HD11	1.67	0.75
1:A:2021:SER:HA	1:A:2024:MET:SD	2.27	0.75
24:u:35:ILE:HD13	27:w:79:LEU:HD12	1.64	0.75
30:l:17:HIS:ND1	30:l:75:PRO:CG	2.50	0.75
25:m:41:THR:O	25:m:83:GLN:HG2	1.86	0.75
4:O:446:LEU:HD12	12:d:237:ILE:CG2	2.15	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:2027:LEU:HB3	28:e:71:ASN:CG	2.10	0.74
12:d:267:TYR:CD2	12:d:284:LEU:CD2	2.69	0.74
12:d:267:TYR:HE2	12:d:287:PHE:CD2	2.05	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
25:z:23:THR:HG22	25:z:47:LEU:HD11	1.68	0.74
1:A:1972:ASP:HB3	28:e:41:ARG:HD3	1.68	0.74
7:R:147:ASN:O	7:R:148:SER:OG	2.04	0.74
27:w:32:LYS:HG3	27:w:33:PHE:HD1	1.53	0.74
19:L:1085:G:N3	19:L:1086:U:C5	2.55	0.74
30:l:24:THR:HA	30:l:70:LYS:NZ	2.03	0.74
11:c:16:VAL:HG13	11:c:152:LEU:HD12	1.70	0.74
11:c:253:LEU:CD1	12:d:37:ILE:HB	2.17	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
28:e:59:LYS:HG2	28:e:70:GLU:CG	2.18	0.74
5:P:34:ILE:HD13	12:d:155:LEU:CD1	2.17	0.74
11:c:227:ILE:HG12	13:I:152:ILE:CG2	2.17	0.73
25:z:45:LEU:HD11	25:z:65:LEU:HD13	1.68	0.73
29:s:52:ARG:O	29:s:77:VAL:HG13	1.87	0.73
11:c:233:GLU:HG2	12:d:114:CYS:HA	1.69	0.73
19:L:117:U:C2	25:z:35:GLN:HB3	2.21	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:j:23:ARG:H	26:j:23:ARG:HD3	1.52	0.73
1:A:2021:SER:HA	1:A:2024:MET:HB2	1.70	0.73
19:L:1105:C:HI'	19:L:1106:G:C1'	2.19	0.73
28:g:78:GLU:HG2	28:g:85:ILE:CG2	2.19	0.73
1:A:424:PHE:CD2	10:Z:178:ARG:HD2	2.23	0.73
19:L:1137:U:C2'	19:L:1138:G:O4'	2.35	0.73
1:A:1990:ASN:HD21	1:A:1993:ASP:H	1.35	0.73
11:c:227:ILE:HG13	11:c:227:ILE:O	1.88	0.73
18:E:49:A:O2'	18:E:50:G:OP1	2.07	0.73
30:l:24:THR:HA	30:l:70:LYS:HZ2	1.54	0.73
4:O:111:ILE:HG22	12:d:194:MET:O	1.89	0.73
17:D:173:U:C2	28:g:97:ARG:CZ	2.72	0.73
25:m:82:LEU:HD11	25:m:85:ILE:HB	1.70	0.72
1:A:1991:ILE:HD12	1:A:1992:TYR:CE1	2.25	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
25:z:47:LEU:HD21	25:z:61:ALA:HB1	1.70	0.72
29:k:15:LEU:C	29:k:15:LEU:HD12	2.14	0.72
28:e:41:ARG:O	28:e:57:ARG:NH1	2.23	0.72
7:R:146:LEU:HD13	7:R:151:LEU:CD2	2.20	0.72
4:O:197:LEU:HB3	4:O:209:TRP:HB2	1.70	0.72
7:R:146:LEU:CD1	7:R:151:LEU:CD2	2.62	0.72
12:d:263:SER:CB	12:d:287:PHE:CZ	2.71	0.72
27:w:34:ASN:HB3	27:w:36:THR:HG23	1.72	0.72
28:g:50:ASN:HB3	28:g:52:HIS:HD1	1.53	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
2:C:831:ILE:CG1	2:C:835:LYS:HE2	2.15	0.71
20:v:608:TYR:O	20:v:612:ILE:HG23	1.90	0.71
24:u:35:ILE:CD1	27:w:79:LEU:HD11	2.20	0.71
27:h:34:ASN:HB3	27:h:36:THR:HG23	1.72	0.71
6:Q:102:GLU:OE2	12:d:82:ARG:NH2	2.24	0.71
12:d:267:TYR:OH	12:d:287:PHE:HB2	1.90	0.71
27:w:32:LYS:HG3	27:w:33:PHE:CE1	2.25	0.71
7:R:149:LYS:HD2	7:R:211:GLU:OE1	1.90	0.71
11:c:189:ARG:CZ	12:d:38:LEU:HD13	2.20	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
12:d:267:TYR:CE2	12:d:287:PHE:CD2	2.79	0.71
20:v:388:LEU:HA	20:v:391:LEU:HD12	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
28:e:48:LEU:HD22	28:e:52:HIS:NE2	2.05	0.71
1:A:1866:PHE:CB	19:L:51:C:H42	2.02	0.71
24:i:30:TRP:CD2	24:i:38:ARG:CZ	2.73	0.71
1:A:2027:LEU:CD1	28:e:57:ARG:HH21	2.02	0.71
17:D:166:U:O2	28:g:63:ARG:NH1	2.23	0.71
25:m:47:LEU:HD11	25:m:61:ALA:HB3	1.73	0.71
6:Q:299:ALA:HB3	7:R:158:SER:HB2	1.72	0.71
19:L:117:U:C5	25:z:88:ARG:NH1	2.59	0.71
20:v:365:ASP:HA	20:v:399:VAL:HG22	1.72	0.71
1:A:1993:ASP:OD2	1:A:2040:TRP:CG	2.44	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
7:R:142:ILE:HG21	7:R:156:ILE:HG21	1.73	0.70
11:c:181:ARG:HB2	11:c:181:ARG:HH11	1.56	0.70
11:c:253:LEU:HD13	12:d:37:ILE:HB	1.73	0.70
6:Q:104:ALA:HB1	11:c:216:ASP:OD2	1.90	0.70
7:R:147:ASN:C	7:R:148:SER:OG	2.33	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
5:P:34:ILE:HD13	12:d:155:LEU:HD13	1.72	0.70
15:H:49:GLU:O	15:H:52:ARG:HG2	1.91	0.70
24:i:40:LYS:HG3	24:i:60:ILE:HD11	1.74	0.70
30:y:21:LEU:HD23	30:y:72:ILE:HG12	1.73	0.70
19:L:110:A:H61	25:z:35:GLN:CD	1.98	0.70
29:k:52:ARG:NH2	29:k:78:GLU:OE2	2.24	0.70
1:A:431:ILE:H	10:Z:182:GLN:HE21	1.39	0.70
1:A:2032:ILE:HD11	1:A:2043:PHE:CD1	2.26	0.70
2:C:125:SER:OG	30:l:77:LEU:HD13	1.91	0.70
15:H:29:TYR:HE1	15:H:32:TYR:HE2	1.37	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
10:Z:73:ILE:HG22	10:Z:123:ILE:HD12	1.71	0.70
10:Z:199:GLU:O	10:Z:202:GLN:HG3	1.91	0.70
6:Q:104:ALA:CB	11:c:216:ASP:OD2	2.39	0.70
30:l:11:LEU:HD11	30:l:72:ILE:HD12	1.73	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:v:388:LEU:HB3	20:v:392:TYR:OH	1.92	0.69
19:L:1146:G:H3'	19:L:1147:A:H5''	1.74	0.69
10:Z:148:LEU:HD12	10:Z:190:LEU:HD21	1.75	0.69
25:z:39:ILE:HD11	25:z:84:TYR:HE1	1.56	0.69
15:H:34:ARG:NH1	15:H:36:ARG:HB2	2.07	0.69
25:m:20:LYS:HG2	25:m:91:THR:O	1.92	0.69
12:d:267:TYR:HE2	12:d:287:PHE:CB	2.06	0.69
27:w:68:LEU:HD23	27:w:71:ILE:HD11	1.73	0.69
19:L:1137:U:C2'	19:L:1138:G:C1'	2.53	0.69
28:e:59:LYS:HD3	28:e:70:GLU:OE1	1.93	0.69
11:c:226:GLY:HA3	12:d:120:ASN:CG	2.18	0.69
15:H:29:TYR:CD1	15:H:32:TYR:HD2	2.11	0.69
22:b:14:TYR:C	29:s:102:LEU:HD12	2.17	0.69
16:B:16:U:H3'	16:B:17:G:C8	2.28	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
12:d:289:LYS:HE2	20:v:643:HIS:CE1	2.25	0.68
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
1:A:2024:MET:CA	28:e:71:ASN:HD21	2.05	0.68
11:c:252:GLY:O	11:c:253:LEU:HB2	1.93	0.68
12:d:284:LEU:HD13	12:d:284:LEU:C	2.18	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
3:J:24:LEU:H	10:Z:310:HIS:HD2	1.42	0.68
6:Q:109:MET:HE2	6:Q:112:PHE:HB3	1.74	0.68
17:D:174:G:H3'	28:g:49:ARG:HH12	1.58	0.68
28:e:89:ARG:NH2	28:e:91:ILE:HD11	2.07	0.68
24:i:54:ILE:HG13	24:i:57:ALA:HB2	1.73	0.68
1:A:2027:LEU:HB2	28:e:71:ASN:OD1	1.93	0.68
2:C:125:SER:OG	30:l:77:LEU:CD1	2.41	0.68
19:L:1118:U:H2'	19:L:1119:C:C6	2.28	0.68
11:c:227:ILE:O	13:I:152:ILE:CG2	2.42	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
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
25:m:88:ARG:HH11	25:m:90:ASN:ND2	1.92	0.68
15:H:28:ASP:O	15:H:29:TYR:HB2	1.94	0.68
15:H:58:ILE:CD1	15:H:85:LEU:CD2	2.69	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:1093:C:H6	19:L:1093:C:C5'	2.06	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
2:C:827:SER:O	2:C:828:ASP:HB2	1.94	0.68
2:C:830:ASN:OD1	2:C:830:ASN:N	2.27	0.68
24:u:29:ILE:HG22	24:u:90:ILE:HA	1.75	0.68
28:g:50:ASN:ND2	28:g:52:HIS:CE1	2.54	0.68
1:A:1961:LEU:CD2	1:A:2084:LEU:HB2	2.24	0.67
4:O:446:LEU:HD12	12:d:237:ILE:CB	2.24	0.67
9:T:104:CYS:HB3	9:T:153:CYS:SG	2.25	0.67
16:B:9:U:H1'	16:B:10:A:OP1	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
12:d:229:VAL:HG12	12:d:274:TRP:HZ2	1.60	0.67
19:L:114:U:O4'	26:x:64:ARG:NH1	2.26	0.67
19:L:1117:G:O2'	19:L:1118:U:H5'	1.94	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
26:j:27:GLY:CA	26:j:40:LEU:CD1	2.69	0.67
30:l:70:LYS:NZ	30:l:70:LYS:HB2	2.07	0.67
17:D:128:A:H3'	17:D:128:A:N3	2.09	0.67
1:A:1286:TRP:HB2	1:A:1300:ALA:HB3	1.77	0.67
19:L:125:C:OP1	25:z:55:LEU:HD11	1.94	0.67
19:L:1119:C:O5'	19:L:1119:C:H6	1.78	0.67
19:L:1125:U:H2'	19:L:1126:G:C8	2.30	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
29:s:28:ARG:HG2	29:s:52:ARG:HG2	1.75	0.67
4:O:271:GLN:HG2	4:O:314:THR:H	1.59	0.67
29:k:15:LEU:HB2	29:k:18:TYR:CE2	2.29	0.67
1:A:2033:THR:CG2	28:e:43:PRO:CG	2.64	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
16:B:16:U:H3'	16:B:17:G:H8	1.59	0.67
17:D:95:C:O2'	17:D:96:U:OP2	2.11	0.67
19:L:117:U:C5	25:z:88:ARG:CZ	2.78	0.67
19:L:1146:G:H2'	19:L:1147:A:N9	2.10	0.67
20:v:395:TYR:O	20:v:398:ASP:HB3	1.95	0.67
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
15:H:32:TYR:CB	15:H:50:TRP:CZ2	2.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:m:21:ASN:HD21	29:k:93:LEU:HD11	1.60	0.66
29:s:82:LEU:HD13	29:s:85:THR:HG21	1.75	0.66
1:A:424:PHE:CE2	10:Z:178:ARG:HD2	2.29	0.66
6:Q:217:TRP:CZ3	7:R:187:LYS:HE2	2.29	0.66
6:Q:248:CYS:SG	6:Q:316:LEU:HD11	2.34	0.66
11:c:189:ARG:NH2	12:d:38:LEU:CD1	2.59	0.66
12:d:241:MET:CG	12:d:279:LEU:HD11	2.17	0.66
1:A:424:PHE:CD2	10:Z:178:ARG:CD	2.78	0.66
1:A:1999:ILE:HD11	1:A:2045:ASP:OD2	1.95	0.66
28:e:78:GLU:CG	25:z:52:LEU:HD22	2.25	0.66
25:m:17:ILE:CG2	25:m:92:ILE:HG23	2.26	0.66
29:s:44:VAL:HG22	29:s:86:ILE:HG22	1.77	0.66
2:C:286:LEU:CD2	10:Z:182:GLN:CB	2.59	0.66
10:Z:174:TRP:HZ2	10:Z:205:TYR:OH	1.70	0.66
17:D:168:U:C6	24:i:49:PHE:CE1	2.83	0.66
19:L:125:C:H4'	28:e:81:GLY:N	2.09	0.66
28:e:56:ALA:HB3	28:e:69:LEU:CD2	2.14	0.66
10:Z:134:VAL:HB	10:Z:227:TYR:O	1.96	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
1:A:2023:LYS:O	28:e:71:ASN:ND2	2.29	0.66
23:t:111:VAL:O	23:t:114:LEU:N	2.29	0.66
1:A:1286:TRP:NE1	1:A:1348:GLU:OE2	2.27	0.66
1:A:2024:MET:CE	28:e:93:LYS:CE	2.68	0.66
15:H:34:ARG:N	15:H:35:PRO:HA	2.09	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
1:A:996:ASP:OD2	1:A:1511:ARG:NH2	2.29	0.66
19:L:114:U:H1'	26:x:66:ASN:HB2	1.76	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
19:L:1093:C:H6	19:L:1093:C:O5'	1.78	0.66
25:m:3:LEU:HG	28:g:95:PHE:CE1	2.31	0.66
29:s:93:LEU:HD11	25:z:21:ASN:HD21	1.60	0.66
1:A:426:PRO:HG3	10:Z:201:ARG:HH11	1.61	0.65
4:O:111:ILE:HG21	12:d:197:PRO:CD	2.26	0.65
10:Z:204:ASP:O	10:Z:205:TYR:HB2	1.95	0.65
1:A:1987:VAL:HG12	1:A:1989:PHE:CE2	2.31	0.65
19:L:1129:U:H2'	19:L:1130:U:C5'	2.26	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:e:89:ARG:CZ	28:e:91:ILE:HD11	2.26	0.65
12:d:267:TYR:CE2	12:d:287:PHE:CB	2.79	0.65
19:L:121:C:H1'	28:e:49:ARG:CG	2.24	0.65
19:L:1150:U:OP1	29:s:55:LYS:HG3	1.95	0.65
25:m:43:VAL:HG21	25:m:85:ILE:HG21	1.78	0.65
16:B:260:G:H1	19:L:40:U:H3	1.44	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
25:z:51:ARG:O	25:z:54:LYS:N	2.29	0.65
17:D:27:G:H4'	17:D:28:G:OP1	1.97	0.65
6:Q:109:MET:HE1	6:Q:112:PHE:HD2	1.59	0.65
16:B:8:C:H42	18:E:45:A:H61	1.45	0.65
2:C:187:ARG:NH2	2:C:654:CYS:SG	2.70	0.65
28:g:50:ASN:HB3	28:g:52:HIS:CE1	2.32	0.65
11:c:241:PHE:HD1	12:d:79:HIS:O	1.79	0.65
17:D:129:G:H1'	17:D:131:A:H2'	1.79	0.65
17:D:176:A:N3	27:h:33:PHE:HD1	1.94	0.65
19:L:1137:U:C4	21:a:67:LYS:O	2.50	0.65
27:h:71:ILE:HG23	28:g:103:VAL:CG2	2.25	0.65
1:A:2027:LEU:CB	28:e:71:ASN:CB	2.69	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
30:y:34:VAL:HG12	30:y:35:GLU:HG2	1.77	0.65
12:d:141:ILE:HG21	13:I:105:TYR:HD1	1.62	0.65
19:L:121:C:C1'	28:e:49:ARG:HG2	2.24	0.65
24:i:30:TRP:CE2	24:i:38:ARG:CZ	2.80	0.65
11:c:169:ARG:HH11	11:c:169:ARG:CG	2.09	0.64
29:k:30:TYR:CD1	29:k:50:GLU:HB3	2.32	0.64
28:e:48:LEU:HD22	28:e:52:HIS:CE1	2.33	0.64
19:L:114:U:O2	26:x:64:ARG:HG2	1.97	0.64
22:b:110:ARG:CB	22:b:134:VAL:CB	2.74	0.64
29:s:88:ARG:NH1	30:y:40:MET:SD	2.70	0.64
25:z:45:LEU:CD1	25:z:65:LEU:HD13	2.26	0.64
28:e:93:LYS:HB3	25:z:97:LEU:CD1	2.27	0.64
12:d:270:ALA:CB	12:d:280:LEU:HD21	2.27	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
27:w:32:LYS:CG	27:w:33:PHE:CE1	2.81	0.64
12:d:284:LEU:HD13	12:d:285:LEU:N	2.12	0.64
1:A:430:PRO:HG3	10:Z:198:PHE:HD2	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2027:LEU:HD11	28:e:57:ARG:HH21	1.61	0.64
6:Q:217:TRP:CH2	7:R:187:LYS:HE2	2.33	0.64
7:R:142:ILE:HG21	7:R:156:ILE:CG2	2.28	0.64
1:A:1506:ARG:O	1:A:1511:ARG:NH1	2.31	0.64
1:A:2027:LEU:C	28:e:71:ASN:HB3	2.22	0.64
10:Z:74:PRO:HB3	10:Z:123:ILE:HD13	1.78	0.64
16:B:16:U:H5''	16:B:17:G:OP2	1.98	0.64
19:L:1105:C:H1'	19:L:1106:G:H1'	1.78	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
16:B:11:G:N3	16:B:11:G:H2'	2.13	0.64
22:b:110:ARG:N	22:b:134:VAL:CB	2.60	0.64
19:L:1086:U:O5'	19:L:1086:U:H6	1.81	0.64
26:j:69:ILE:HA	30:l:68:GLN:HG3	1.80	0.63
28:e:93:LYS:HD2	25:z:97:LEU:CD1	2.27	0.63
1:A:431:ILE:H	10:Z:182:GLN:NE2	1.96	0.63
19:L:141:A:C2	19:L:1168:U:O2	2.51	0.63
25:m:67:LEU:HB3	29:k:29:VAL:HG21	1.80	0.63
2:C:187:ARG:NH1	2:C:653:ASP:OD2	2.31	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
6:Q:206:PHE:HD2	6:Q:291:ILE:HD11	1.63	0.63
12:d:57:TYR:CE1	18:E:85:C:OP2	2.48	0.63
26:j:63:ILE:HG13	24:i:89:LEU:HD23	1.79	0.63
1:A:1035:LEU:HD12	1:A:1035:LEU:C	2.22	0.63
17:D:167:A:H3'	27:h:48:TYR:OH	1.98	0.63
19:L:69:G:H1	19:L:83:U:H3	1.47	0.63
25:m:83:GLN:NE2	25:m:84:TYR:HB2	2.13	0.63
1:A:1991:ILE:HD12	1:A:1992:TYR:HE1	1.62	0.63
12:d:270:ALA:HB3	12:d:280:LEU:HD21	1.80	0.63
15:H:32:TYR:CB	15:H:50:TRP:CH2	2.73	0.63
24:u:58:VAL:HG12	24:u:76:PRO:HA	1.79	0.63
25:m:89:GLY:O	25:m:92:ILE:HG13	1.99	0.63
29:s:29:VAL:HG21	25:z:67:LEU:HB3	1.80	0.63
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
25:m:17:ILE:HG23	25:m:92:ILE:HG21	1.76	0.63
24:i:30:TRP:CD1	24:i:38:ARG:NE	2.66	0.63
26:x:27:GLY:HA3	26:x:40:LEU:HD13	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:430:PRO:HB3	10:Z:198:PHE:CD2	2.34	0.62
10:Z:174:TRP:CH2	10:Z:201:ARG:CD	2.81	0.62
1:A:1889:LEU:HB2	1:A:1989:PHE:O	1.98	0.62
2:C:133:ILE:HG22	2:C:209:MET:HB3	1.80	0.62
10:Z:133:ILE:HD13	10:Z:136:LEU:HD21	1.81	0.62
12:d:141:ILE:HG21	13:I:105:TYR:CD1	2.34	0.62
17:D:95:C:H1'	17:D:96:U:OP2	1.98	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: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
15:H:42:LYS:H	15:H:42:LYS:CD	2.11	0.62
19:L:1090:A:O2'	19:L:1091:G:H5'	2.00	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:1990:ASN:HD21	1:A:1993:ASP:N	1.98	0.62
4:O:206:VAL:HB	4:O:220:TYR:HB2	1.82	0.62
4:O:229:THR:HG21	4:O:271:GLN:HA	1.81	0.62
1:A:426:PRO:CG	10:Z:201:ARG:NH1	2.63	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
29:s:54:PRO:HG2	29:s:76:LYS:O	1.98	0.62
11:c:214:ASN:HD21	12:d:44:ARG:HD3	1.63	0.62
11:c:249:ASN:OD1	12:d:40:LEU:HB2	1.99	0.62
1:A:2024:MET:HA	28:e:71:ASN:ND2	2.15	0.62
20:v:385:PHE:O	20:v:388:LEU:HB2	2.00	0.62
18:E:49:A:HO2'	18:E:50:G:P	2.22	0.61
19:L:115:U:C2	30:y:39:SER:OG	2.53	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
19:L:1154:U:H2'	19:L:1155:C:H6	1.63	0.61
11:c:160:LEU:HD23	13:I:196:ILE:HG12	1.82	0.61
15:H:67:ASP:O	15:H:70:LEU:HG	2.00	0.61
17:D:130:A:H2'	17:D:130:A:P	2.41	0.61
17:D:173:U:O2	28:g:97:ARG:NE	2.32	0.61
29:s:42:ASN:HB3	29:s:89:GLY:H	1.65	0.61
24:i:30:TRP:HA	24:i:38:ARG:HG3	1.82	0.61
1:A:864:GLN:HE22	1:A:1101:TYR:H	1.48	0.61
4:O:101:ILE:HG21	12:d:224:LEU:CD1	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:l:41:ASN:HB3	30:l:66:GLY:H	1.65	0.61
10:Z:70:GLY:HA2	10:Z:73:ILE:CG1	2.29	0.61
20:v:582:LEU:HD12	20:v:582:LEU:O	2.00	0.61
22:b:65:ILE:HA	22:b:85:ASN:O	2.01	0.61
2:C:129:ILE:HG12	30:l:16:GLY:O	2.01	0.61
2:C:234:LEU:C	2:C:234:LEU:HD12	2.25	0.61
11:c:241:PHE:CD1	12:d:79:HIS:O	2.53	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
19:L:119:G:H2'	19:L:120:G:H5'	1.82	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
2:C:132:ARG:NH2	30:l:13:GLU:O	2.34	0.61
4:O:101:ILE:HG21	12:d:224:LEU:HD11	1.83	0.61
17:D:28:G:O2'	17:D:29:G:OP1	2.19	0.61
19:L:1083:A:H2'	19:L:1084:A:H8	1.65	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
1:A:854:ARG:HH21	19:L:25:A:H5''	1.66	0.61
7:R:146:LEU:O	7:R:147:ASN:HB2	2.01	0.61
7:R:171:ASP:OD2	7:R:185:LYS:HD3	2.01	0.61
12:d:267:TYR:HE2	12:d:287:PHE:CG	2.18	0.61
19:L:1095:U:H2'	19:L:1096:C:C6	2.35	0.61
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
2:C:234:LEU:HD21	2:C:439:ILE:CG2	2.26	0.61
5:P:148:HIS:CB	12:d:131:ARG:HG3	2.25	0.61
5:P:34:ILE:HG21	12:d:155:LEU:HD12	1.82	0.60
11:c:253:LEU:CD1	12:d:37:ILE:HD12	2.30	0.60
16:B:275:G:N3	16:B:275:G:H2'	2.15	0.60
19:L:126:A:P	28:e:80:LYS:CB	2.89	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
1:A:676:GLN:HG2	1:A:714:PHE:HB2	1.83	0.60
2:C:126:MET:SD	2:C:132:ARG:NH1	2.74	0.60
7:R:151:LEU:O	7:R:155:GLN:HB2	2.01	0.60
9:T:150:CYS:SG	9:T:151:ARG:N	2.74	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
16:B:9:U:H1'	16:B:10:A:P	2.41	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:1125:U:H2'	19:L:1126:G:H8	1.64	0.60
19:L:1085:G:N3	19:L:1085:G:H2'	2.16	0.60
28:e:62:ASP:OD1	28:e:63:ARG:N	2.32	0.60
1:A:255:ILE:HG23	1:A:640:ARG:HG2	1.84	0.60
1:A:1990:ASN:ND2	1:A:1993:ASP:N	2.48	0.60
19:L:1107:C:H2'	19:L:1108:A:OP2	2.00	0.60
1:A:744:THR:O	1:A:749:ARG:NH2	2.34	0.60
11:c:189:ARG:CZ	12:d:38:LEU:CD1	2.80	0.60
19:L:1106:G:H4'	19:L:1107:C:OP1	2.00	0.60
25:m:52:LEU:O	25:m:52:LEU:HD12	2.01	0.60
10:Z:174:TRP:CE3	10:Z:201:ARG:NH2	2.69	0.60
25:m:41:THR:O	25:m:83:GLN:HA	2.02	0.60
20:v:680:ILE:O	20:v:680:ILE:HG22	2.00	0.60
26:j:20:ASN:OD1	24:i:32:PHE:CE2	2.55	0.60
2:C:788:LEU:HD11	2:C:823:ILE:HG21	1.84	0.60
6:Q:213:SER:O	6:Q:214:ILE:HG22	2.02	0.60
4:O:259:VAL:HG12	4:O:260:ILE:HG13	1.84	0.59
12:d:342:PHE:O	12:d:346:ILE:N	2.31	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
4:O:343:THR:HB	5:P:47:ARG:HB2	1.82	0.59
7:R:124:MET:HB2	16:B:13:G:O6	2.02	0.59
28:e:46:ILE:HD12	28:e:54:ILE:HD11	1.84	0.59
29:s:12:LEU:HD12	29:s:15:LEU:HD11	1.84	0.59
10:Z:181:LEU:HD11	10:Z:194:LEU:HD12	1.83	0.59
25:m:39:ILE:CD1	25:m:84:TYR:CE1	2.85	0.59
6:Q:251:LEU:HG	6:Q:251:LEU:O	2.02	0.59
10:Z:181:LEU:HG	10:Z:194:LEU:HD12	1.83	0.59
15:H:86:PHE:HE2	15:H:90:LYS:HE3	1.63	0.59
24:u:35:ILE:HD11	27:w:79:LEU:HD13	1.82	0.59
2:C:101:GLN:HE22	17:D:75:A:H61	1.50	0.59
5:P:34:ILE:CD1	12:d:155:LEU:CD1	2.78	0.59
10:Z:178:ARG:HA	10:Z:198:PHE:HZ	1.67	0.59
19:L:1142:G:C2'	19:L:1143:C:H5'	2.32	0.59
27:h:33:PHE:CZ	28:g:49:ARG:CD	2.86	0.59
28:e:78:GLU:HG2	25:z:52:LEU:HD22	1.85	0.59
28:g:46:ILE:HD12	28:g:54:ILE:HD11	1.84	0.59
24:i:40:LYS:CD	24:i:60:ILE:HD13	2.32	0.59
1:A:1368:GLN:NE2	1:A:1389:TYR:OH	2.36	0.59
1:A:2043:PHE:HE2	1:A:2047:GLN:H	1.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
26:j:6:GLU:OE2	30:l:35:GLU:HB3	2.03	0.59
1:A:1808:ALA:HB2	1:A:1947:HIS:CE1	2.32	0.59
4:O:327:CYS:SG	4:O:328:THR:N	2.75	0.59
6:Q:213:SER:C	6:Q:214:ILE:HG22	2.28	0.59
12:d:284:LEU:HD22	12:d:284:LEU:C	2.28	0.59
17:D:167:A:C5	27:h:48:TYR:CE1	2.91	0.59
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:1146:G:C2'	19:L:1147:A:C8	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
28:e:73:LYS:NZ	28:e:75:LEU:HD21	2.17	0.58
28:e:91:ILE:HD13	25:z:96:ILE:HD11	1.84	0.58
1:A:1035:LEU:CD1	1:A:1038:ILE:HG23	2.33	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:1035:LEU:CD1	1:A:1038:ILE:CG2	2.81	0.58
26:j:61:THR:HG22	24:i:91:THR:CG2	2.31	0.58
11:c:230:THR:HG22	12:d:116:ASN:CB	2.34	0.58
1:A:1852:VAL:HB	1:A:1935:VAL:HG22	1.85	0.58
6:Q:304:THR:HG22	7:R:153:PRO:HG3	1.79	0.58
11:c:214:ASN:ND2	12:d:44:ARG:CG	2.55	0.58
19:L:1093:C:C5'	19:L:1093:C:C6	2.85	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:1710:GLU:HG2	1:A:1728:ILE:HG12	1.85	0.58
2:C:804:LYS:HD3	2:C:805:GLU:HG3	1.85	0.58
4:O:145:VAL:HG22	4:O:157:THR:HG22	1.85	0.58
11:c:181:ARG:HH21	12:d:49:ARG:CZ	2.16	0.58
1:A:2023:LYS:O	28:e:71:ASN:OD1	2.21	0.58
1:A:2035:LYS:HB2	1:A:2038:HIS:HB2	1.85	0.58
2:C:220:ASN:HB3	2:C:651:TYR:HB2	1.85	0.58
6:Q:234:ASP:HB3	7:R:3:SER:OG	2.04	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:286:LEU:HD21	10:Z:182:GLN:CB	2.30	0.58
6:Q:109:MET:HE2	6:Q:112:PHE:HD2	1.62	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
1:A:1868:GLY:O	19:L:50:U:O4	2.22	0.57
1:A:1921:VAL:O	1:A:1929:GLN:NE2	2.36	0.57
11:c:13:TRP:CH2	11:c:43:LYS:HG3	2.38	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
12:d:330:ILE:CG2	12:d:339:MET:HA	2.34	0.57
29:k:15:LEU:HD12	29:k:15:LEU:O	2.03	0.57
2:C:183:GLN:HE22	2:C:654:CYS:HA	1.69	0.57
11:c:179:SER:HB3	15:H:68:PRO:HD3	1.83	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:1855:THR:HG22	1:A:1937:ARG:HH21	1.69	0.57
10:Z:402:LEU:HD12	10:Z:405:ILE:HD13	1.85	0.57
17:D:129:G:O3'	17:D:130:A:H3'	2.05	0.57
17:D:173:U:O2'	27:h:74:ARG:NH2	2.37	0.57
11:c:227:ILE:HG12	13:I:152:ILE:HG21	1.87	0.57
19:L:1137:U:O2'	19:L:1138:G:C4'	2.43	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:91:GLN:HG3	30:y:70:LYS:HG3	1.87	0.57
1:A:1073:ILE:HG13	1:A:1074:VAL:HG23	1.86	0.57
1:A:1405:ILE:HD13	10:Z:303:LEU:HB2	1.86	0.57
1:A:1056:GLU:HB2	1:A:1059:GLU:HB3	1.86	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
5:P:34:ILE:HD13	12:d:155:LEU:HA	1.87	0.57
28:e:56:ALA:HB2	28:e:72:VAL:CB	2.32	0.57
29:s:29:VAL:O	29:s:50:GLU:HA	2.05	0.57
4:O:352:ILE:CD1	4:O:369:ASP:OD2	2.53	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
22:b:14:TYR:C	29:s:102:LEU:CD1	2.76	0.57
28:e:46:ILE:HG12	28:e:104:VAL:HG22	1.86	0.57
1:A:1914:ALA:HA	1:A:1944:LEU:HD23	1.87	0.57
4:O:135:ILE:HB	4:O:423:ILE:HB	1.87	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:732:ARG:NH2	18:E:71:G:OP2	2.38	0.56
12:d:142:VAL:HG13	13:I:164:LEU:HD21	1.85	0.56
12:d:289:LYS:CG	20:v:609:GLU:HG2	2.32	0.56
16:B:253:G:H1	19:L:47:U:H3	1.53	0.56
27:h:58:GLU:O	27:h:65:HIS:N	2.38	0.56
4:O:292:LEU:HD12	4:O:302:LYS:HB3	1.87	0.56
10:Z:181:LEU:CG	10:Z:194:LEU:HD12	2.35	0.56
11:c:513:ILE:O	11:c:517:VAL:N	2.38	0.56
19:L:110:A:H61	25:z:35:GLN:HE21	1.50	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:1294:LYS:O	10:Z:429:ASN:ND2	2.38	0.56
2:C:866:ILE:HB	2:C:902:VAL:HB	1.87	0.56
6:Q:299:ALA:O	6:Q:300:ALA:HB3	2.05	0.56
15:H:33:GLN:CB	15:H:35:PRO:HB3	2.35	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
29:s:53:VAL:HG23	25:z:67:LEU:HD11	1.86	0.56
26:x:47:ASN:OD1	26:x:48:GLY:N	2.31	0.56
6:Q:299:ALA:CB	7:R:158:SER:HB2	2.34	0.56
11:c:253:LEU:HD12	12:d:37:ILE:HB	1.87	0.56
20:v:349:PHE:O	20:v:353:CYS:N	2.37	0.56
30:l:17:HIS:HB3	30:l:75:PRO:CG	2.35	0.56
4:O:105:GLU:HG2	4:O:106:VAL:HG23	1.88	0.56
22:b:14:TYR:O	29:s:102:LEU:HD13	2.03	0.56
10:Z:101:MET:O	10:Z:105:GLN:NE2	2.37	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
28:e:54:ILE:HD13	28:e:72:VAL:HG21	1.88	0.56
12:d:267:TYR:CE2	12:d:287:PHE:CG	2.94	0.56
19:L:125:C:H5''	28:e:80:LYS:CA	2.34	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:1663:PHE:HZ	1:A:1902:GLN:HE21	1.50	0.56
1:A:2023:LYS:O	28:e:71:ASN:CG	2.49	0.56
10:Z:10:ASP:OD2	10:Z:244:LYS:NZ	2.37	0.56
10:Z:19:GLU:OE2	10:Z:22:ARG:NH1	2.37	0.56
27:w:58:GLU:O	27:w:65:HIS:N	2.38	0.56
26:x:7:LEU:HD23	26:x:29:LEU:HD11	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:c:226:GLY:O	13:I:151:LYS:NZ	2.30	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
25:z:23:THR:HG22	25:z:47:LEU:CD1	2.34	0.56
6:Q:270:LEU:HD12	6:Q:289:PHE:HE1	1.71	0.56
7:R:153:PRO:HB3	7:R:177:GLU:CD	2.31	0.56
11:c:41:GLN:O	11:c:42:LYS:HB2	2.05	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:768:GLU:HG3	4:O:312:ARG:HH21	1.71	0.55
1:A:1159:ARG:HE	1:A:1173:HIS:HB3	1.71	0.55
30:l:21:LEU:CD2	30:l:69:ILE:HD13	2.36	0.55
1:A:1011:ASN:HB2	1:A:1144:PHE:HA	1.87	0.55
4:O:371:GLY:HA3	4:O:400:ARG:HG2	1.89	0.55
20:v:542:LEU:HD23	20:v:582:LEU:HD12	1.88	0.55
25:z:39:ILE:HD11	25:z:84:TYR:CE1	2.40	0.55
7:R:232:PRO:HA	7:R:235:GLN:HB2	1.88	0.55
11:c:181:ARG:HH21	12:d:49:ARG:HH12	1.53	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:93:LYS:NZ	25:z:103:LEU:HD13	2.21	0.55
5:P:34:ILE:HD13	12:d:155:LEU:HD12	1.87	0.55
6:Q:194:GLU:O	6:Q:291:ILE:HG21	2.05	0.55
19:L:116:U:N3	29:s:40:HIS:CD2	2.74	0.55
20:v:385:PHE:N	20:v:385:PHE:CD1	2.73	0.55
1:A:2040:TRP:HA	1:A:2040:TRP:HE3	1.71	0.55
7:R:153:PRO:HB3	7:R:177:GLU:OE1	2.06	0.55
10:Z:70:GLY:HA2	10:Z:73:ILE:CD1	2.36	0.55
16:B:9:U:C1'	16:B:10:A:P	2.94	0.55
19:L:1129:U:C2'	19:L:1130:U:C5'	2.85	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
28:e:56:ALA:CA	28:e:72:VAL:HG23	2.36	0.55
28:e:97:ARG:NH2	25:z:36:MET:SD	2.79	0.55
28:e:102:ILE:HG13	28:e:103:VAL:H	1.70	0.55
15:H:45:LYS:O	15:H:48:ASN:HB2	2.06	0.55
28:g:37:ALA:CB	28:g:44:VAL:HG11	2.37	0.55
28:e:56:ALA:HB1	28:e:69:LEU:HB3	1.88	0.55
28:e:73:LYS:HG3	28:e:90:PHE:CD2	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:i:30:TRP:O	24:i:88:THR:HB	2.07	0.55
1:A:1382:ARG:NH2	1:A:1635:HIS:O	2.39	0.55
1:A:2056:ARG:O	1:A:2060:LEU:N	2.35	0.55
11:c:60:LEU:HD22	11:c:94:PRO:HG3	1.87	0.55
19:L:120:G:H4'	19:L:121:C:O5'	2.06	0.55
19:L:152:C:N4	19:L:1085:G:H1	1.97	0.55
29:k:49:ILE:HG23	29:k:81:VAL:HG23	1.88	0.55
2:C:141:PRO:O	2:C:146:LYS:NZ	2.40	0.55
14:n:386:GLY:O	14:n:387:ILE:CB	2.54	0.55
20:v:325:LEU:O	20:v:329:SER:N	2.38	0.55
1:A:1051:GLU:OE1	1:A:1167:ARG:NH2	2.39	0.55
1:A:2024:MET:CE	25:z:99:ASP:O	2.55	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
26:x:74:LEU:O	26:x:74:LEU:HD12	2.07	0.55
29:s:53:VAL:HG23	25:z:67:LEU:CD1	2.37	0.54
1:A:1403:SER:OG	1:A:1429:MET:SD	2.62	0.54
1:A:2018:ASN:ND2	1:A:2058:LEU:HD22	2.22	0.54
2:C:905:GLN:OE1	2:C:938:ARG:NH2	2.39	0.54
14:n:272:ILE:HD11	14:n:310:SER:HB3	1.89	0.54
19:L:113:U:C6	27:w:48:TYR:CE1	2.96	0.54
29:k:49:ILE:HG22	29:k:80:ARG:C	2.32	0.54
20:v:255:GLU:O	20:v:259:LYS:N	2.40	0.54
24:u:44:VAL:HB	24:u:53:VAL:HG23	1.89	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
17:D:172:U:N3	25:m:37:ASN:OD1	2.41	0.54
29:k:39:LYS:HG3	29:k:40:HIS:N	2.23	0.54
1:A:1668:ILE:HD13	1:A:1801:SER:HB2	1.89	0.54
1:A:1934:ILE:HG12	1:A:1957:ARG:HB2	1.89	0.54
5:P:149:MET:C	12:d:131:ARG:HD2	2.32	0.54
12:d:211:ARG:HG2	20:v:520:ILE:CG1	2.38	0.54
14:n:253:VAL:HG21	14:n:298:ALA:HA	1.89	0.54
18:E:11:U:H3	18:E:15:C:H42	1.55	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:1268:ARG:HB3	1:A:1301:TYR:HB2	1.88	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
11:c:237:ILE:HD12	12:d:114:CYS:SG	2.40	0.54
26:x:71:LEU:N	30:y:63:PHE:O	2.28	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:P:35:ALA:H	12:d:123:ASN:HD21	1.54	0.54
12:d:319:ASP:OD1	12:d:319:ASP:N	2.40	0.54
25:m:86:ASN:ND2	29:k:41:MET:CE	2.70	0.54
28:e:56:ALA:CB	28:e:72:VAL:HB	2.37	0.54
1:A:2020:GLU:CG	1:A:2024:MET:HE1	2.38	0.54
7:R:69:GLN:HG3	7:R:71:PHE:H	1.72	0.54
12:d:298:GLU:HA	12:d:301:ILE:HG22	1.88	0.54
17:D:132:A:N6	17:D:146:C:O2	2.41	0.54
18:E:47:A:C2'	18:E:48:C:H5'	2.37	0.54
11:c:165:LYS:HE2	18:E:54:U:O4	2.07	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
12:d:267:TYR:HD2	12:d:284:LEU:HD23	1.70	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
29:k:52:ARG:HB3	29:k:52:ARG:NH1	2.23	0.53
29:s:16:ILE:O	29:s:17:ASP:HB2	2.09	0.53
25:z:27:GLY:HA3	25:z:43:VAL:HG12	1.90	0.53
1:A:460:PRO:HG2	2:C:375:GLU:HG2	1.90	0.53
10:Z:105:GLN:OE1	10:Z:108:ARG:NH2	2.42	0.53
26:j:71:LEU:HB3	30:l:63:PHE:HB3	1.90	0.53
28:e:50:ASN:O	28:e:51:ASN:CB	2.57	0.53
30:l:63:PHE:CD1	30:l:63:PHE:C	2.85	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
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
26:x:63:ILE:HG21	26:x:68:ILE:HD11	1.90	0.53
2:C:88:THR:O	4:O:214:ASN:ND2	2.40	0.53
19:L:3:G:O2'	19:L:4:A:N7	2.42	0.53
19:L:1137:U:H5'	21:a:66:LYS:O	2.09	0.53
30:l:71:PHE:C	30:l:71:PHE:CD1	2.85	0.53
2:C:348:LEU:HD12	2:C:372:THR:HG22	1.90	0.53
24:i:30:TRP:HE1	24:i:38:ARG:HD3	1.62	0.53
1:A:1711:VAL:HA	1:A:1791:PHE:HA	1.90	0.53
1:A:1850:LEU:HD13	1:A:1930:PRO:HG3	1.89	0.53
11:c:230:THR:HG22	12:d:116:ASN:C	2.34	0.53
29:s:58:LEU:HD11	25:z:62:MET:HE3	1.91	0.53
1:A:1843:LEU:HD22	1:A:1851:PHE:HZ	1.74	0.53
2:C:466:GLY:O	2:C:581:LYS:NZ	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:869:HIS:HD2	2:C:899:LEU:HB3	1.73	0.53
5:P:179:THR:H	13:I:200:ASN:HD21	1.57	0.53
11:c:157:ALA:O	11:c:161:ASN:ND2	2.41	0.53
20:v:391:LEU:HB3	20:v:395:TYR:CE2	2.43	0.53
26:x:35:PHE:HB2	26:x:37:ASN:ND2	2.23	0.53
1:A:2057:ASP:HA	1:A:2060:LEU:HB2	1.89	0.53
4:O:102:PHE:HZ	12:d:202:TRP:HH2	1.56	0.53
5:P:129:LYS:NZ	8:S:23:THR:O	2.38	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
1:A:2027:LEU:CB	28:e:71:ASN:OD1	2.52	0.53
12:d:141:ILE:HG23	13:I:105:TYR:HD1	1.49	0.53
20:v:489:LEU:HD22	20:v:547:LYS:HD3	1.89	0.53
26:x:14:LYS:CG	26:x:74:LEU:HD11	2.39	0.53
1:A:742:VAL:HB	4:O:224:LEU:HD23	1.91	0.53
11:c:244:PHE:CD1	12:d:79:HIS:CD2	2.97	0.53
12:d:211:ARG:HG2	20:v:520:ILE:HG13	1.91	0.53
15:H:32:TYR:N	15:H:32:TYR:CD1	2.73	0.53
15:H:58:ILE:CD1	15:H:58:ILE:N	2.72	0.53
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
28:e:54:ILE:HB	28:e:72:VAL:CG2	2.38	0.53
6:Q:109:MET:HE1	6:Q:112:PHE:CD2	2.38	0.52
6:Q:217:TRP:CE3	7:R:187:LYS:HE2	2.43	0.52
12:d:342:PHE:O	12:d:345:ALA:N	2.42	0.52
28:g:35:ASN:HA	28:g:61:PHE:CD2	2.40	0.52
1:A:936:GLU:HG2	1:A:986:PRO:HB3	1.91	0.52
1:A:966:PRO:HB3	1:A:1089:VAL:HB	1.91	0.52
2:C:99:LYS:NZ	17:D:43:G:OP2	2.41	0.52
7:R:155:GLN:HE21	19:L:78:G:P	2.32	0.52
11:c:509:LEU:O	11:c:513:ILE:N	2.39	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
28:e:45:ILE:HB	28:e:105:LEU:HG	1.91	0.52
28:e:93:LYS:NZ	25:z:103:LEU:CD1	2.73	0.52
30:l:10:LEU:O	30:l:13:GLU:HB2	2.09	0.52
1:A:1320:LEU:HD11	1:A:1366:ARG:HB3	1.91	0.52
2:C:608:GLN:HE21	2:C:669:LYS:HD2	1.74	0.52
19:L:1125:U:H6	19:L:1125:U:H5''	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:s:42:ASN:HB3	29:s:89:GLY:N	2.23	0.52
1:A:1296:ARG:NH1	10:Z:430:GLU:OE2	2.43	0.52
4:O:373:LEU:HD12	4:O:373:LEU:C	2.35	0.52
19:L:1101:C:H2'	19:L:1101:C:O2	2.09	0.52
10:Z:136:LEU:CD1	10:Z:137:GLN:HG3	2.39	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
30:l:79:LYS:HG3	30:l:80:ASN:N	2.25	0.52
25:z:52:LEU:HD23	25:z:55:LEU:HD22	1.92	0.52
4:O:259:VAL:HG11	5:P:74:ILE:HG23	1.91	0.52
7:R:211:GLU:O	7:R:214:ASP:N	2.35	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
1:A:1980:LYS:HZ1	28:e:39:VAL:CG1	2.06	0.52
4:O:275:THR:OG1	4:O:279:PRO:O	2.27	0.52
6:Q:306:THR:OG1	7:R:174:ARG:NH2	2.43	0.52
10:Z:317:ILE:HD13	10:Z:325:VAL:HG21	1.91	0.52
28:g:50:ASN:O	28:g:51:ASN:CB	2.57	0.52
30:l:17:HIS:CG	30:l:75:PRO:CG	2.88	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
28:g:32:SER:O	28:g:35:ASN:ND2	2.37	0.52
30:l:44:LEU:HD12	30:l:47:VAL:HG11	1.91	0.52
2:C:360:ARG:HH11	2:C:362:LYS:HE3	1.75	0.52
7:R:10:LYS:NZ	7:R:57:LEU:O	2.42	0.52
17:D:130:A:H5''	17:D:131:A:H3'	1.92	0.52
19:L:1154:U:C2'	19:L:1155:C:C5'	2.88	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
30:l:22:GLU:HB3	30:l:71:PHE:CE1	2.44	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
2:C:231:ALA:O	2:C:487:ARG:NH1	2.43	0.52
6:Q:109:MET:HE3	6:Q:112:PHE:CD2	2.44	0.52
6:Q:213:SER:O	6:Q:214:ILE:CG2	2.58	0.52
10:Z:84:ASN:ND2	10:Z:220:TYR:OH	2.43	0.52
11:c:181:ARG:CB	11:c:181:ARG:CZ	2.88	0.52
11:c:181:ARG:HE	12:d:49:ARG:NH1	2.07	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:w:29:VAL:HG12	27:w:81:ILE:HG12	1.91	0.52
27:w:32:LYS:HA	27:w:79:LEU:HD12	1.92	0.52
1:A:1182:LEU:HD13	1:A:1225:ALA:HB1	1.92	0.51
1:A:1185:GLU:OE1	8:S:128:ARG:NH1	2.43	0.51
1:A:1361:VAL:HG21	1:A:1407:ILE:HD11	1.92	0.51
15:H:72:GLU:O	15:H:76:ALA:HB2	2.10	0.51
19:L:113:U:C6	27:w:48:TYR:CD1	2.96	0.51
27:h:32:LYS:HA	27:h:79:LEU:HD12	1.92	0.51
10:Z:136:LEU:HD12	10:Z:137:GLN:HG3	1.93	0.51
11:c:244:PHE:CE1	12:d:79:HIS:CD2	2.97	0.51
1:A:416:GLU:HB3	1:A:419:THR:HG23	1.91	0.51
1:A:1197:ASN:ND2	1:A:1221:ASN:OD1	2.40	0.51
6:Q:51:ARG:NH1	6:Q:51:ARG:HA	2.25	0.51
17:D:94:C:H2'	17:D:95:C:H5'	1.91	0.51
17:D:128:A:N3	17:D:128:A:C2'	2.74	0.51
28:g:76:TRP:CH2	28:g:87:ARG:CD	2.86	0.51
29:s:18:TYR:CE1	29:s:101:PRO:HD3	2.44	0.51
27:h:23:VAL:HA	27:h:42:LEU:HD22	1.92	0.51
29:s:24:THR:OG1	29:s:26:ASP:OD1	2.25	0.51
17:D:179:U:OP1	28:g:79:LYS:O	2.27	0.51
18:E:47:A:O2'	18:E:48:C:H5'	2.10	0.51
1:A:1270:LEU:HD13	1:A:1275:MET:HG2	1.91	0.51
6:Q:67:GLN:NE2	6:Q:116:LYS:O	2.43	0.51
10:Z:105:GLN:HA	10:Z:108:ARG:HB2	1.92	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
30:y:21:LEU:CD1	30:y:44:LEU:CD1	2.71	0.51
31:r:8:LYS:CG	31:o:88:TRP:HH2	2.24	0.51
1:A:467:GLU:O	2:C:387:TYR:OH	2.28	0.51
2:C:947:LYS:NZ	2:C:984:ASN:O	2.44	0.51
11:c:42:LYS:O	11:c:43:LYS:HD3	2.11	0.51
12:d:269:ILE:O	12:d:273:LYS:HB2	2.11	0.51
28:g:76:TRP:CZ2	28:g:87:ARG:NE	2.79	0.51
28:e:70:GLU:OE2	28:e:71:ASN:OD1	2.28	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:709:ARG:NH2	17:D:82:A:O3'	2.44	0.51
1:A:737:ARG:NH1	18:E:70:U:OP2	2.44	0.51
2:C:286:LEU:HD22	10:Z:182:GLN:HB3	1.77	0.51
2:C:468:LEU:HD21	2:C:493:LEU:HD12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:d:301:ILE:HD11	20:v:646:PHE:CG	2.46	0.51
19:L:1154:U:C2'	19:L:1155:C:O5'	2.58	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:589:THR:OG1	7:R:39:GLN:NE2	2.44	0.51
1:A:2044:THR:O	1:A:2045:ASP:HB2	2.11	0.51
7:R:170:ILE:HD13	7:R:173:ILE:HD11	1.93	0.51
11:c:165:LYS:CE	18:E:54:U:O4	2.59	0.51
15:H:34:ARG:N	15:H:35:PRO:CA	2.74	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
28:e:59:LYS:HG3	28:e:70:GLU:HG2	1.90	0.51
1:A:1011:ASN:ND2	1:A:1143:GLU:O	2.37	0.51
1:A:1991:ILE:O	1:A:2040:TRP:NE1	2.44	0.51
11:c:189:ARG:NE	12:d:38:LEU:HD13	2.25	0.51
1:A:1800:ASN:OD1	1:A:1803:ARG:NH2	2.40	0.50
6:Q:109:MET:SD	11:c:218:VAL:O	2.69	0.50
19:L:1146:G:C6	19:L:1147:A:C6	3.00	0.50
1:A:372:ARG:HB3	2:C:973:ARG:HH11	1.76	0.50
1:A:1093:LYS:NZ	19:L:27:A:OP1	2.41	0.50
19:L:1090:A:C2'	19:L:1091:G:H5'	2.41	0.50
26:j:71:LEU:HD23	26:j:71:LEU:C	2.36	0.50
1:A:1490:ARG:HH11	1:A:1536:LEU:HA	1.76	0.50
2:C:500:ARG:NH1	2:C:536:SER:OG	2.43	0.50
15:H:58:ILE:HD13	15:H:58:ILE:N	2.26	0.50
29:k:38:ASP:OD1	29:k:39:LYS:N	2.41	0.50
28:e:89:ARG:NH2	28:e:91:ILE:CD1	2.72	0.50
30:l:41:ASN:HB3	30:l:66:GLY:N	2.26	0.50
25:z:17:ILE:HD12	25:z:40:LEU:HD11	1.92	0.50
1:A:416:GLU:HG2	1:A:418:ASP:H	1.77	0.50
1:A:2021:SER:O	1:A:2025:ILE:N	2.43	0.50
5:P:170:SER:OG	5:P:173:LYS:O	2.30	0.50
10:Z:77:SER:HA	10:Z:80:ILE:HD12	1.92	0.50
10:Z:136:LEU:HA	10:Z:139:LEU:HD12	1.94	0.50
12:d:175:PHE:HA	12:d:178:ARG:NH2	2.27	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:x:10:TYR:HB3	26:x:15:ILE:HD11	1.94	0.50
1:A:591:LEU:HD11	1:A:613:SER:HB2	1.92	0.50
6:Q:214:ILE:HG23	6:Q:214:ILE:O	2.12	0.50
30:y:33:LEU:HA	30:y:44:LEU:CD2	2.35	0.50
25:z:16:THR:HA	25:z:25:VAL:O	2.11	0.50
1:A:1361:VAL:HG22	1:A:1403:SER:HB2	1.92	0.50
1:A:1716:LEU:O	1:A:1795:LYS:NZ	2.44	0.50
7:R:153:PRO:CB	7:R:177:GLU:OE1	2.59	0.50
19:L:1106:G:C4'	19:L:1107:C:OP1	2.60	0.50
29:s:85:THR:HG22	30:y:73:VAL:HG22	1.93	0.50
1:A:1125:LEU:O	1:A:1233:ARG:NH1	2.44	0.50
1:A:2021:SER:CA	1:A:2024:MET:HB2	2.40	0.50
6:Q:207:LEU:HD22	6:Q:290:ILE:HG22	1.93	0.50
12:d:145:SER:HA	13:I:112:LEU:HD21	1.92	0.50
28:g:41:ARG:HH21	28:g:41:ARG:HG3	1.75	0.50
30:l:61:GLN:HG3	30:l:62:ILE:N	2.25	0.50
1:A:755:ASP:OD2	19:L:21:G:O2'	2.25	0.50
4:O:352:ILE:CD1	4:O:369:ASP:CG	2.85	0.50
6:Q:207:LEU:CD2	6:Q:290:ILE:CG2	2.83	0.50
9:T:40:LYS:HG3	9:T:41:LEU:HD12	1.92	0.50
15:H:65:ILE:HD13	15:H:82:LEU:HD11	1.94	0.50
17:D:175:G:O5'	28:g:49:ARG:NH1	2.45	0.50
19:L:1127:A:H8	19:L:1127:A:O5'	1.95	0.50
22:b:67:ILE:CB	22:b:89:VAL:CB	2.90	0.50
7:R:152:LYS:HG3	7:R:153:PRO:HD3	1.90	0.50
10:Z:88:PRO:HB3	10:Z:223:HIS:CG	2.46	0.50
11:c:62:PHE:HE1	11:c:94:PRO:HG2	1.76	0.50
19:L:1105:C:HI1'	19:L:1106:G:O4'	2.12	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
29:s:38:ASP:OD1	29:s:39:LYS:N	2.39	0.50
24:i:46:PHE:HB3	24:i:52:VAL:HG12	1.94	0.50
25:z:19:LEU:HD22	25:z:91:THR:HG22	1.94	0.50
1:A:430:PRO:HG3	10:Z:198:PHE:CD2	2.46	0.49
4:O:365:PHE:CE1	4:O:373:LEU:HB2	2.47	0.49
6:Q:250:GLY:C	6:Q:297:PHE:CZ	2.90	0.49
28:e:63:ARG:HH11	28:e:64:HIS:HE1	1.59	0.49
1:A:1993:ASP:CG	1:A:2040:TRP:H	2.19	0.49
1:A:2027:LEU:CD1	28:e:57:ARG:NE	2.38	0.49
15:H:34:ARG:HH11	15:H:36:ARG:HB2	1.77	0.49
15:H:71:ASN:O	15:H:75:ILE:HG12	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:1168:U:H2'	19:L:1169:C:C6	2.46	0.49
24:i:54:ILE:CG1	24:i:57:ALA:HB2	2.41	0.49
1:A:834:ILE:HG12	1:A:840:VAL:HG11	1.94	0.49
10:Z:421:LYS:HG3	10:Z:468:ILE:HG23	1.94	0.49
15:H:32:TYR:CB	15:H:50:TRP:HZ2	2.26	0.49
15:H:55:SER:O	15:H:58:ILE:HB	2.12	0.49
20:v:667:ILE:HA	20:v:670:SER:HB3	1.94	0.49
28:e:73:LYS:HE3	28:e:90:PHE:HE2	1.78	0.49
30:y:24:THR:HA	30:y:70:LYS:HE3	1.93	0.49
2:C:248:VAL:HA	2:C:933:TRP:HH2	1.78	0.49
4:O:134:VAL:HG22	4:O:424:LYS:HG2	1.93	0.49
6:Q:12:ILE:HA	6:Q:71:CYS:HB2	1.95	0.49
6:Q:206:PHE:CD2	6:Q:291:ILE:CD1	2.87	0.49
19:L:1084:A:O3'	19:L:1085:G:H8	1.95	0.49
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:144:ASN:HB3	9:T:36:ASP:HB2	1.94	0.49
5:P:112:ILE:HD11	6:Q:17:LEU:HD21	1.95	0.49
6:Q:39:LEU:HD23	6:Q:63:ARG:HH12	1.78	0.49
6:Q:283:ILE:HD12	6:Q:283:ILE:N	2.26	0.49
10:Z:32:LEU:HD23	10:Z:76:LEU:HD23	1.93	0.49
28:e:59:LYS:HG3	25:z:103:LEU:HD22	1.94	0.49
1:A:863:ARG:HH12	1:A:1101:TYR:HD2	1.60	0.49
1:A:1964:PRO:HG2	1:A:2013:ARG:HA	1.93	0.49
2:C:139:ILE:HD12	2:C:252:LEU:HD22	1.95	0.49
2:C:780:PRO:HA	2:C:783:ILE:HB	1.95	0.49
2:C:880:MET:HE3	2:C:886:SER:HB3	1.94	0.49
30:l:44:LEU:HB2	30:l:47:VAL:CG1	2.43	0.49
1:A:782:ILE:HD13	5:P:165:ILE:HD13	1.95	0.49
17:D:176:A:H1'	27:h:33:PHE:CE1	2.43	0.49
19:L:1095:U:H3'	19:L:1096:C:C6	2.48	0.49
19:L:1107:C:H3'	19:L:1107:C:OP2	2.12	0.49
20:v:365:ASP:CB	20:v:399:VAL:HG22	2.42	0.49
26:j:19:ILE:HG22	24:i:88:THR:HG23	1.94	0.49
1:A:1570:TRP:HA	1:A:1573:LEU:HD12	1.94	0.49
17:D:129:G:N3	17:D:129:G:H2'	2.27	0.49
19:L:109:C:OP1	25:z:34:PRO:HG2	2.12	0.49
24:u:35:ILE:HD12	27:w:32:LYS:O	2.12	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
27:w:32:LYS:HD2	27:w:33:PHE:HE1	1.77	0.49
1:A:809:LYS:NZ	1:A:813:GLU:OE2	2.39	0.49
22:b:49:HIS:O	22:b:50:LEU:CB	2.61	0.49
28:e:56:ALA:HB1	28:e:69:LEU:CD2	2.37	0.49
1:A:1283:GLU:OE2	10:Z:341:LYS:N	2.46	0.49
1:A:1329:THR:HG21	1:A:1601:ILE:H	1.78	0.49
2:C:498:THR:HG22	2:C:538:GLU:HG2	1.94	0.49
4:O:256:ARG:NH2	8:S:31:LEU:O	2.46	0.49
4:O:351:GLY:C	4:O:352:ILE:HG12	2.37	0.49
19:L:1114:G:H2'	19:L:1115:G:C1'	2.42	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
4:O:321:PHE:HB2	5:P:57:LEU:HD23	1.94	0.48
6:Q:194:GLU:O	6:Q:291:ILE:CG2	2.61	0.48
6:Q:280:VAL:HG23	6:Q:280:VAL:O	2.13	0.48
19:L:1106:G:N2	21:a:69:ARG:O	2.46	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
25:z:14:GLN:HB3	25:z:26:TRP:CH2	2.48	0.48
1:A:1381:THR:HG21	1:A:1618:ASN:HB3	1.95	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
2:C:110:LYS:HD2	2:C:113:ILE:HD12	1.94	0.48
4:O:159:SER:OG	4:O:160:ASN:N	2.42	0.48
4:O:307:HIS:NE2	4:O:325:SER:OG	2.38	0.48
10:Z:148:LEU:CD1	10:Z:190:LEU:HD21	2.42	0.48
15:H:89:TRP:NE1	15:H:93:GLN:NE2	2.60	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
1:A:1961:LEU:CD2	1:A:2084:LEU:CD1	2.89	0.48
11:c:214:ASN:ND2	12:d:44:ARG:O	2.46	0.48
11:c:233:GLU:CD	12:d:116:ASN:H	2.21	0.48
15:H:34:ARG:NH1	15:H:36:ARG:CB	2.74	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:r:8:LYS:CG	31:o:88:TRP:CH2	2.96	0.48
10:Z:119:GLN:O	10:Z:123:ILE:HG13	2.13	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
28:g:41:ARG:HB2	28:g:57:ARG:HD3	1.95	0.48
1:A:1687:HIS:HB3	1:A:1690:LYS:HB2	1.96	0.48
11:c:152:LEU:HD21	11:c:156:ARG:HH21	1.78	0.48
24:u:35:ILE:HD11	27:w:79:LEU:HD12	1.86	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	1.95	0.48
31:r:14:VAL:HG12	31:r:52:GLU:HA	1.95	0.48
4:O:95:SER:OG	4:O:96:ALA:N	2.45	0.48
8:S:5:HIS:HA	18:E:62:A:H61	1.77	0.48
10:Z:132:GLU:O	10:Z:136:LEU:HD23	2.14	0.48
11:c:169:ARG:CG	11:c:169:ARG:NH1	2.73	0.48
2:C:129:ILE:CG1	30:l:16:GLY:O	2.61	0.48
4:O:289:THR:HG22	4:O:305:THR:HG22	1.95	0.48
17:D:168:U:C4	24:i:49:PHE:CZ	3.02	0.48
20:v:652:LEU:HD11	20:v:666:PHE:CZ	2.49	0.48
28:e:45:ILE:HD12	28:e:55:ILE:HG12	1.96	0.48
30:l:17:HIS:CB	30:l:75:PRO:HG2	2.44	0.48
2:C:218:HIS:HB3	2:C:221:PHE:HD2	1.79	0.48
19:L:31:A:C2'	19:L:31:A:N3	2.76	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:1735:ASP:HB3	1:A:1774:MET:HG3	1.95	0.48
4:O:414:LEU:HB3	4:O:426:TRP:HB2	1.96	0.48
10:Z:166:SER:HG	10:Z:169:THR:HG1	1.62	0.48
10:Z:322:LYS:HE3	10:Z:357:TRP:CE2	2.48	0.48
11:c:181:ARG:HB2	11:c:181:ARG:CZ	2.42	0.48
15:H:37:ASN:ND2	15:H:40:LYS:HD3	2.29	0.48
26:x:35:PHE:O	26:x:36:LEU:HB3	2.14	0.48
6:Q:217:TRP:CE3	7:R:187:LYS:CE	2.97	0.48
27:h:29:VAL:O	27:h:37:GLU:HA	2.14	0.48
1:A:1286:TRP:CE2	1:A:1302:LEU:HD11	2.49	0.47
4:O:446:LEU:CD1	12:d:237:ILE:HB	2.41	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:128:A:O2'	17:D:129:G:O5'	2.31	0.47
18:E:49:A:H8	18:E:49:A:H5''	1.79	0.47
25:z:82:LEU:HD11	25:z:85:ILE:HB	1.96	0.47
1:A:1993:ASP:HB2	1:A:2040:TRP:HB2	1.96	0.47
2:C:129:ILE:HG12	30:l:16:GLY:C	2.40	0.47
12:d:241:MET:CG	12:d:279:LEU:HD12	2.41	0.47
15:H:44:ILE:O	15:H:47:ALA:HB3	2.14	0.47
15:H:72:GLU:HA	15:H:75:ILE:HD11	1.96	0.47
19:L:25:A:H2'	19:L:27:A:OP2	2.14	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:1154:LYS:HA	1:A:1159:ARG:HH12	1.80	0.47
6:Q:70:ILE:HD13	6:Q:84:ILE:HD11	1.95	0.47
6:Q:300:ALA:HB1	7:R:154:ALA:CB	2.38	0.47
15:H:29:TYR:HE1	15:H:32:TYR:CE2	2.18	0.47
16:B:17:G:H8	16:B:17:G:OP2	1.97	0.47
19:L:1107:C:HO2'	19:L:1108:A:P	2.37	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
27:w:29:VAL:O	27:w:37:GLU:HA	2.14	0.47
2:C:708:ILE:HD13	2:C:841:LEU:HD12	1.95	0.47
4:O:351:GLY:C	4:O:352:ILE:CG1	2.87	0.47
19:L:4:A:C1'	20:v:529:HIS:CD2	2.96	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
30:l:77:LEU:O	30:l:79:LYS:N	2.47	0.47
1:A:1992:TYR:N	1:A:1992:TYR:HD1	2.12	0.47
10:Z:194:LEU:O	10:Z:194:LEU:HD13	2.14	0.47
18:E:65:U:O2'	18:E:67:C:OP2	2.26	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:831:ARG:HD2	1:A:852:LEU:HD11	1.97	0.47
1:A:1863:HIS:CD2	1:A:1873:LYS:HD2	2.49	0.47
6:Q:208:TYR:HB2	6:Q:316:LEU:HD13	1.95	0.47
10:Z:148:LEU:HA	10:Z:151:VAL:HG12	1.95	0.47
19:L:120:G:H4'	19:L:121:C:C5'	2.45	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
25:z:25:VAL:HG22	25:z:45:LEU:HB2	1.97	0.47
1:A:1012:TRP:HB2	1:A:1162:THR:HA	1.96	0.47
1:A:1647:GLN:O	1:A:1650:ARG:NH1	2.43	0.47
1:A:1701:ILE:HB	1:A:1734:PHE:HB2	1.96	0.47
1:A:1716:LEU:HD23	1:A:1718:HIS:H	1.79	0.47
1:A:1992:TYR:N	1:A:1992:TYR:CD1	2.83	0.47
2:C:90:LEU:HD23	4:O:211:LEU:HD22	1.97	0.47
2:C:106:PHE:HZ	2:C:550:VAL:HG23	1.79	0.47
2:C:129:ILE:HG22	2:C:132:ARG:H	1.78	0.47
2:C:778:THR:HG23	2:C:781:ASP:H	1.79	0.47
2:C:869:HIS:HA	2:C:899:LEU:HA	1.96	0.47
4:O:290:VAL:HB	4:O:304:LEU:HB2	1.97	0.47
10:Z:403:LYS:HG2	10:Z:445:LEU:HB3	1.96	0.47
22:b:65:ILE:O	22:b:86:ILE:HA	2.14	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
1:A:880:THR:HG23	5:P:211:ALA:HB2	1.95	0.47
19:L:1083:A:H2'	19:L:1084:A:C8	2.47	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
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
2:C:132:ARG:HD3	2:C:132:ARG:HA	1.62	0.47
12:d:70:ARG:NH1	18:E:88:U:C1'	2.74	0.47
28:e:49:ARG:NH2	27:w:76:ASN:CG	2.73	0.47
30:l:42:VAL:HG22	30:l:64:VAL:CG2	2.44	0.47
2:C:468:LEU:HB3	2:C:579:SER:HB3	1.97	0.47
4:O:446:LEU:CD1	12:d:237:ILE:CB	2.91	0.47
6:Q:214:ILE:HD12	6:Q:283:ILE:HG21	1.96	0.47
19:L:1127:A:H2'	19:L:1128:C:O5'	2.14	0.47
20:v:389:ILE:HA	20:v:392:TYR:CD2	2.50	0.47
19:L:118:U:N3	28:e:66:ASN:ND2	2.58	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
25:z:33:SER:HB2	25:z:37:ASN:HB2	1.97	0.46
1:A:1773:VAL:HA	1:A:1788:GLY:HA3	1.97	0.46
2:C:501:ILE:HD13	2:C:567:ILE:HG23	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:228:ARG:NH1	4:O:270:ASN:OD1	2.48	0.46
4:O:343:THR:HA	5:P:45:PRO:HB3	1.96	0.46
5:P:76:ARG:HE	6:Q:5:ILE:HD12	1.79	0.46
12:d:219:ARG:HA	12:d:222:TYR:HB2	1.98	0.46
12:d:269:ILE:HA	12:d:272:GLU:HG2	1.96	0.46
15:H:50:TRP:O	15:H:53:GLN:HB3	2.15	0.46
19:L:113:U:O4	27:w:47:ASN:C	2.58	0.46
24:u:81:LEU:HD22	27:w:19:LEU:HD11	1.97	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
1:A:946:ASN:HB3	1:A:949:ASP:HB2	1.98	0.46
4:O:102:PHE:CZ	12:d:202:TRP:HH2	2.33	0.46
4:O:244:ARG:HA	4:O:268:PRO:HB3	1.98	0.46
7:R:121:ARG:NH1	18:E:39:G:O4'	2.48	0.46
7:R:230:PRO:HD2	16:B:14:C:H2'	1.97	0.46
14:n:60:ARG:HH22	18:E:1:G:H8	1.63	0.46
15:H:42:LYS:H	15:H:42:LYS:HD3	1.80	0.46
15:H:79:ASN:HA	15:H:82:LEU:HD12	1.97	0.46
19:L:1146:G:H5'	19:L:1147:A:OP2	2.15	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
2:C:586:MET:HA	2:C:589:LEU:HD23	1.97	0.46
12:d:281:LYS:O	12:d:284:LEU:HB3	2.15	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:1331:VAL:HG12	1:A:1367:ILE:HG23	1.96	0.46
4:O:446:LEU:HD11	12:d:237:ILE:CG2	2.18	0.46
15:H:66:TYR:CD1	15:H:66:TYR:N	2.84	0.46
29:s:53:VAL:CG2	25:z:67:LEU:HD11	2.45	0.46
30:l:21:LEU:HD21	30:l:72:ILE:CD1	2.45	0.46
30:y:44:LEU:CB	30:y:47:VAL:HG11	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:372:ARG:HD2	2:C:973:ARG:HD2	1.98	0.46
1:A:1035:LEU:C	1:A:1035:LEU:CD1	2.89	0.46
2:C:205:SER:O	30:l:83:LEU:HD23	2.16	0.46
10:Z:174:TRP:CZ3	10:Z:201:ARG:NE	2.83	0.46
28:g:67:MET:HG3	28:g:69:LEU:HD11	1.97	0.46
1:A:1438:PRO:HD2	1:A:1546:VAL:HG22	1.98	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
7:R:155:GLN:NE2	19:L:78:G:P	2.89	0.46
11:c:72:GLN:NE2	11:c:91:MET:SD	2.89	0.46
12:d:60:ARG:O	18:E:64:U:O2'	2.32	0.46
19:L:1117:G:H2'	19:L:1118:U:H5'	1.98	0.46
24:u:51:ASN:HB3	24:u:84:GLY:H	1.81	0.46
28:g:41:ARG:CB	28:g:57:ARG:HD3	2.45	0.46
24:i:51:ASN:HB3	24:i:84:GLY:H	1.81	0.46
4:O:345:PHE:HE2	4:O:364:LEU:HD13	1.79	0.46
10:Z:70:GLY:C	10:Z:73:ILE:HG13	2.41	0.46
10:Z:200:ILE:O	10:Z:204:ASP:N	2.48	0.46
19:L:1105:C:O3'	19:L:1106:G:O4'	2.34	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
21:a:67:LYS:O	21:a:68:GLN:CB	2.64	0.46
1:A:1961:LEU:HD21	1:A:2084:LEU:HD12	1.96	0.46
12:d:320:TYR:CD1	12:d:356:LYS:HA	2.50	0.46
17:D:128:A:C2'	17:D:129:G:O5'	2.64	0.46
17:D:130:A:H4'	17:D:131:A:H5''	1.97	0.46
19:L:121:C:N4	27:w:33:PHE:CG	2.84	0.46
29:k:16:ILE:O	29:k:17:ASP:HB2	2.16	0.46
28:e:93:LYS:CD	25:z:97:LEU:CD1	2.94	0.46
30:l:11:LEU:HD11	30:l:72:ILE:HD13	1.94	0.46
6:Q:245:LYS:HD3	7:R:174:ARG:NH1	2.31	0.46
11:c:21:LEU:HD22	11:c:56:LEU:HD22	1.98	0.46
11:c:223:PRO:HG2	12:d:85:ARG:HD3	1.98	0.46
11:c:230:THR:HG22	12:d:116:ASN:HB2	1.97	0.46
12:d:306:LYS:NZ	12:d:326:TYR:OH	2.40	0.46
18:E:79:A:OP1	18:E:81:G:O2'	2.32	0.46
26:j:23:ARG:NH2	26:j:23:ARG:CG	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
4:O:112:VAL:HG11	12:d:232:LEU:HD13	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:T:120:CYS:SG	9:T:145:CYS:HB2	2.55	0.45
17:D:168:U:C6	24:i:49:PHE:HE1	2.33	0.45
28:e:33:LEU:HD23	27:w:72:PHE:HB2	1.99	0.45
28:e:48:LEU:HD22	28:e:52:HIS:HE2	1.77	0.45
1:A:1771:THR:HA	1:A:1789:ASN:HD21	1.81	0.45
1:A:1961:LEU:CD2	1:A:2084:LEU:HD13	2.37	0.45
7:R:109:LEU:HD13	7:R:113:GLY:HA2	1.98	0.45
10:Z:113:SER:HA	10:Z:116:ASN:HD22	1.81	0.45
26:x:37:ASN:OD1	26:x:64:ARG:HA	2.16	0.45
1:A:1965:PHE:O	1:A:1966:SER:HB3	2.16	0.45
4:O:200:VAL:HG13	4:O:230:VAL:HG22	1.97	0.45
4:O:356:LEU:HD22	4:O:364:LEU:HD21	1.98	0.45
17:D:167:A:C1'	28:g:64:HIS:HE2	2.27	0.45
19:L:117:U:C5	25:z:88:ARG:NH2	2.84	0.45
19:L:1146:G:H3'	19:L:1147:A:C5'	2.44	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
30:l:44:LEU:HB2	30:l:47:VAL:HG13	1.98	0.45
1:A:431:ILE:C	10:Z:182:GLN:HG2	2.37	0.45
2:C:116:THR:HA	2:C:158:HIS:HA	1.98	0.45
7:R:159:ARG:HD3	7:R:204:LEU:O	2.17	0.45
12:d:263:SER:CB	12:d:287:PHE:HZ	2.17	0.45
14:n:57:LYS:NZ	18:E:1:G:OP2	2.49	0.45
17:D:168:U:C4	24:i:49:PHE:HZ	2.35	0.45
19:L:1129:U:H2'	19:L:1130:U:O5'	2.16	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
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:23:LEU:HB3	30:l:25:THR:HG22	1.98	0.45
27:w:33:PHE:CD1	27:w:33:PHE:N	2.84	0.45
1:A:1051:GLU:HB3	1:A:1167:ARG:HH21	1.82	0.45
6:Q:217:TRP:CZ2	7:R:187:LYS:HE2	2.51	0.45
15:H:72:GLU:O	15:H:76:ALA:CB	2.64	0.45
17:D:6:G:C4'	29:k:11:ARG:HH22	2.22	0.45
17:D:73:U:H4'	17:D:79:C:H4'	1.97	0.45
28:g:62:ASP:HB3	28:g:66:ASN:OD1	2.17	0.45
28:e:62:ASP:HB3	28:e:66:ASN:OD1	2.17	0.45
30:l:65:ARG:HH11	30:l:65:ARG:CG	2.14	0.45
26:x:15:ILE:HG23	26:x:72:GLU:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:p:14:VAL:HG12	31:p:52:GLU:HA	1.97	0.45
1:A:376:ARG:HG3	2:C:909:ILE:HG13	1.98	0.45
1:A:1663:PHE:HZ	1:A:1902:GLN:NE2	2.13	0.45
5:P:179:THR:H	13:I:200:ASN:ND2	2.14	0.45
7:R:34:TYR:O	7:R:36:LYS:N	2.49	0.45
28:g:78:GLU:CG	28:g:85:ILE:HG23	2.47	0.45
29:s:54:PRO:CG	29:s:57:GLN:CG	2.94	0.45
1:A:1016:SER:HB3	1:A:1019:GLU:HG2	1.99	0.45
1:A:2032:ILE:HG21	1:A:2041:PRO:HB2	1.97	0.45
2:C:606:VAL:HG22	2:C:643:VAL:HG22	1.98	0.45
4:O:238:LEU:HD21	5:P:74:ILE:HD13	1.99	0.45
4:O:321:PHE:HB2	5:P:57:LEU:HA	1.98	0.45
17:D:173:U:C2	28:g:97:ARG:NE	2.84	0.45
24:u:91:THR:HG21	26:x:57:LEU:HB3	1.99	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
28:e:91:ILE:HG21	25:z:96:ILE:CG1	2.47	0.45
25:z:18:GLU:HG3	25:z:24:THR:HG22	1.98	0.45
10:Z:25:VAL:HG11	10:Z:56:ILE:HA	1.99	0.45
10:Z:228:ILE:C	10:Z:230:SER:H	2.24	0.45
15:H:28:ASP:HB3	15:H:29:TYR:H	1.66	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
29:s:54:PRO:CG	29:s:76:LYS:O	2.65	0.45
30:l:14:ALA:HB1	30:l:19:VAL:HG11	1.98	0.45
1:A:581:LEU:HD12	1:A:581:LEU:HA	1.81	0.45
1:A:831:ARG:HH12	1:A:978:ILE:HD11	1.81	0.45
6:Q:283:ILE:N	6:Q:283:ILE:CD1	2.79	0.45
17:D:128:A:O2'	17:D:129:G:C8	2.69	0.45
17:D:128:A:H2'	17:D:129:G:H5''	1.99	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
30:l:33:LEU:CD2	30:l:35:GLU:O	2.63	0.45
1:A:497:GLN:HG3	1:A:712:LEU:HD23	1.99	0.45
4:O:280:GLN:NE2	5:P:66:CYS:SG	2.87	0.45
10:Z:74:PRO:CA	10:Z:123:ILE:HD13	2.47	0.45
12:d:47:GLN:NE2	12:d:78:GLN:OE1	2.39	0.45
19:L:1095:U:H2'	19:L:1096:C:N1	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
22:b:54:THR:CA	22:b:77:HIS:CB	2.94	0.45
22:b:148:VAL:O	22:b:149:PRO:CB	2.64	0.45
28:e:66:ASN:HB3	28:e:98:GLY:H	1.81	0.45
30:l:21:LEU:CD2	30:l:42:VAL:HG21	2.46	0.45
1:A:860:GLU:OE2	1:A:863:ARG:NH2	2.37	0.44
19:L:116:U:C2	29:s:40:HIS:CD2	3.04	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
28:e:52:HIS:CD2	28:e:52:HIS:O	2.70	0.44
25:z:14:GLN:NE2	25:z:28:THR:OG1	2.50	0.44
1:A:1964:PRO:O	1:A:1965:PHE:HB2	2.17	0.44
6:Q:302:PHE:O	6:Q:312:LEU:HD13	2.18	0.44
11:c:13:TRP:CE2	11:c:43:LYS:HE2	2.52	0.44
11:c:51:ARG:HG3	11:c:56:LEU:HD13	1.99	0.44
12:d:267:TYR:CB	12:d:284:LEU:HD23	2.47	0.44
16:B:17:G:C8	16:B:17:G:OP2	2.71	0.44
17:D:163:C:O2'	17:D:165:A:OP1	2.27	0.44
22:b:97:ASN:O	22:b:98:VAL:CB	2.64	0.44
25:m:39:ILE:CD1	25:m:84:TYR:HE1	2.22	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
6:Q:190:LEU:HD11	6:Q:312:LEU:HD11	1.99	0.44
12:d:293:ASP:OD1	12:d:293:ASP:N	2.46	0.44
15:H:89:TRP:HE1	15:H:93:GLN:NE2	2.16	0.44
19:L:1093:C:C5	19:L:1093:C:OP2	2.70	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: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
25:z:72:GLN:NE2	25:z:75:ALA:HB2	2.33	0.44
4:O:308:LYS:HA	5:P:148:HIS:CE1	2.52	0.44
6:Q:94:VAL:HG11	6:Q:135:ILE:HG23	1.99	0.44
11:c:81:PRO:HA	11:c:82:ASN:HA	1.67	0.44
18:E:49:A:C2'	18:E:50:G:O5'	2.66	0.44
19:L:1107:C:OP2	19:L:1107:C:C6	2.70	0.44
26:j:5:PRO:HA	30:l:37:GLU:OE1	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:1158:ILE:HG12	1:A:1172:PHE:CE1	2.52	0.44
1:A:1365:THR:HG21	3:J:15:SER:HB3	1.99	0.44
7:R:83:LEU:HB2	7:R:87:CYS:HB2	1.99	0.44
7:R:176:VAL:HG12	7:R:179:LYS:H	1.82	0.44
11:c:230:THR:CG2	12:d:116:ASN:C	2.90	0.44
12:d:271:ILE:HD13	12:d:281:LYS:CG	2.08	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:305:LEU:HD12	1:A:472:ASN:HB3	2.00	0.44
1:A:1972:ASP:HB3	28:e:41:ARG:HH21	1.82	0.44
1:A:2019:GLU:HB3	1:A:2020:GLU:OE1	2.18	0.44
2:C:132:ARG:O	2:C:208:ARG:HB2	2.18	0.44
9:T:103:LEU:HD12	9:T:104:CYS:H	1.83	0.44
10:Z:170:HIS:HA	10:Z:173:ILE:HD12	1.99	0.44
17:D:130:A:H4'	17:D:131:A:OP2	2.13	0.44
19:L:114:U:C2	26:x:64:ARG:HG3	2.52	0.44
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
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:1110:ALA:HA	1:A:1113:ILE:HD12	2.00	0.44
2:C:514:GLN:NE2	2:C:587:LYS:O	2.50	0.44
6:Q:79:ARG:HG2	6:Q:80:TRP:CD1	2.53	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	2.00	0.44
19:L:1136:U:OP1	19:L:1136:U:C6	2.70	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
29:s:54:PRO:HG2	29:s:57:GLN:CG	2.48	0.44
27:w:16:LYS:HB3	27:w:17:PRO:HD3	2.00	0.44
1:A:1161:TYR:HD1	1:A:1170:MET:HG2	1.82	0.44
1:A:1995:TRP:O	1:A:1999:ILE:HD12	2.17	0.44
2:C:660:ARG:NH2	2:C:670:ILE:HD12	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:128:A:N3	17:D:128:A:H2'	2.33	0.44
17:D:176:A:N3	27:h:33:PHE:CD1	2.81	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
30:y:44:LEU:HB3	30:y:47:VAL:HG11	2.00	0.44
1:A:236:ARG:NH2	32:A:3000:IHP:O41	2.51	0.44
1:A:1990:ASN:O	1:A:1993:ASP:OD1	2.35	0.44
1:A:2024:MET:HE1	25:z:99:ASP:O	2.17	0.44
12:d:320:TYR:CE1	12:d:356:LYS:HA	2.53	0.44
17:D:169:U:O2	26:j:66:ASN:N	2.51	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
28:e:93:LYS:NZ	25:z:101:LEU:O	2.51	0.44
24:i:31:LEU:HD21	24:i:82:LEU:HD21	2.00	0.44
1:A:1991:ILE:H	1:A:1991:ILE:HG13	1.40	0.43
1:A:2027:LEU:CG	28:e:57:ARG:HE	2.26	0.43
1:A:2043:PHE:CE2	1:A:2047:GLN:HB3	2.53	0.43
2:C:200:CYS:HB2	2:C:210:ILE:HD12	2.00	0.43
6:Q:203:LYS:HE3	19:L:75:A:OP2	2.18	0.43
19:L:116:U:C4	29:s:40:HIS:NE2	2.86	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:971:MET:HE3	1:A:978:ILE:HG22	2.00	0.43
1:A:1020:ILE:HG13	1:A:1023:LEU:H	1.82	0.43
1:A:1995:TRP:CZ3	1:A:2040:TRP:CD1	3.06	0.43
4:O:200:VAL:HG12	4:O:206:VAL:HG22	2.00	0.43
6:Q:51:ARG:HA	6:Q:51:ARG:CZ	2.49	0.43
6:Q:216:GLU:HB3	7:R:170:ILE:O	2.18	0.43
11:c:55:TYR:HD2	11:c:56:LEU:HD12	1.82	0.43
16:B:10:A:C8	16:B:10:A:OP2	2.72	0.43
19:L:1126:G:H8	19:L:1126:G:O5'	2.01	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
1:A:1889:LEU:HD21	1:A:1991:ILE:CD1	2.47	0.43
2:C:625:ILE:HG23	2:C:629:TYR:HD2	1.81	0.43
7:R:152:LYS:HE2	7:R:152:LYS:HB2	1.79	0.43
11:c:244:PHE:CE1	12:d:79:HIS:HD2	2.36	0.43
17:D:167:A:C8	27:h:48:TYR:CZ	3.06	0.43
25:m:47:LEU:CD1	25:m:61:ALA:HB1	2.38	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
28:e:91:ILE:HG21	25:z:96:ILE:CD1	2.48	0.43
30:l:33:LEU:HD23	30:l:33:LEU:C	2.43	0.43
1:A:835:LYS:HG2	1:A:976:GLN:HA	2.00	0.43
1:A:1602:PRO:HD2	1:A:1605:ARG:HD3	2.00	0.43
4:O:102:PHE:CE2	12:d:194:MET:HE3	2.52	0.43
7:R:149:LYS:CD	7:R:211:GLU:OE1	2.64	0.43
10:Z:174:TRP:CE3	10:Z:201:ARG:CZ	3.01	0.43
12:d:139:TYR:CG	12:d:155:LEU:HD21	2.53	0.43
16:B:259:U:H2'	16:B:260:G:H8	1.83	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
25:z:15:VAL:HG11	25:z:29:LEU:HD12	2.00	0.43
1:A:1145:MET:HE3	1:A:1145:MET:HB2	1.74	0.43
11:c:16:VAL:CG1	11:c:152:LEU:HD12	2.45	0.43
15:H:61:LYS:O	15:H:65:ILE:HG13	2.19	0.43
19:L:1146:G:H2'	19:L:1147:A:C1'	2.48	0.43
29:k:104:SER:O	29:k:107:GLU:HB3	2.17	0.43
28:e:79:LYS:HA	28:e:83:ASN:O	2.19	0.43
25:z:26:TRP:O	25:z:43:VAL:HA	2.17	0.43
1:A:1663:PHE:CZ	1:A:1902:GLN:NE2	2.80	0.43
10:Z:74:PRO:HA	10:Z:123:ILE:HG21	2.00	0.43
12:d:364:ILE:O	12:d:368:MET:N	2.48	0.43
19:L:31:A:N3	19:L:31:A:H2'	2.33	0.43
19:L:1086:U:OP2	19:L:1086:U:C6	2.71	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
25:z:31:SER:O	25:z:39:ILE:HG22	2.18	0.43
1:A:1183:THR:HB	1:A:1222:LEU:HD23	2.00	0.43
1:A:1211:SER:HB3	1:A:1268:ARG:HD2	2.00	0.43
2:C:107:THR:HG23	2:C:549:TYR:HB3	2.01	0.43
2:C:352:VAL:O	2:C:372:THR:OG1	2.31	0.43
4:O:121:GLN:NE2	5:P:49:SER:O	2.49	0.43
10:Z:84:ASN:HB3	10:Z:220:TYR:HE1	1.82	0.43
20:v:728:LEU:O	20:v:732:CYS:N	2.48	0.43
22:b:77:HIS:HA	22:b:98:VAL:HA	1.99	0.43
28:e:77:THR:HB	28:e:86:ASN:HD22	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:i:32:PHE:HB3	24:i:34:GLN:OE1	2.18	0.43
4:O:244:ARG:HH12	8:S:8:GLN:NE2	2.16	0.43
16:B:11:G:N3	16:B:11:G:C2'	2.81	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
29:s:21:ARG:HD3	25:z:67:LEU:O	2.19	0.43
30:y:49:ALA:HB2	30:y:59:MET:HE3	2.01	0.43
1:A:1494:LEU:O	1:A:1499:ARG:NH2	2.46	0.43
1:A:1991:ILE:O	1:A:1993:ASP:OD2	2.36	0.43
2:C:136:VAL:HA	2:C:234:LEU:O	2.19	0.43
11:c:218:VAL:HB	11:c:219:TYR:H	1.67	0.43
12:d:203:LEU:HA	12:d:206:VAL:HG22	2.01	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
27:w:80:TYR:HE1	27:w:82:ARG:HD2	1.83	0.43
2:C:613:ARG:NH1	2:C:614:GLU:OE2	2.52	0.43
4:O:224:LEU:HD13	8:S:12:ARG:HG3	2.01	0.43
6:Q:109:MET:HE3	11:c:219:TYR:HA	2.01	0.43
6:Q:119:LYS:O	6:Q:124:GLN:NE2	2.52	0.43
11:c:165:LYS:O	11:c:169:ARG:HB2	2.18	0.43
25:m:33:SER:HB2	25:m:37:ASN:HB2	2.01	0.43
25:m:96:ILE:CD1	28:g:89:ARG:NH2	2.73	0.43
29:s:54:PRO:CB	29:s:57:GLN:CG	2.88	0.43
1:A:1879:ILE:HG12	1:A:1913:THR:HG22	2.00	0.42
6:Q:206:PHE:HB3	6:Q:291:ILE:HD12	2.00	0.42
6:Q:208:TYR:HB2	6:Q:316:LEU:CD1	2.48	0.42
10:Z:105:GLN:HG2	10:Z:113:SER:HB2	2.01	0.42
12:d:289:LYS:HD3	12:d:289:LYS:HA	1.90	0.42
12:d:298:GLU:HA	12:d:301:ILE:CG2	2.49	0.42
17:D:130:A:H4'	17:D:131:A:C5'	2.49	0.42
19:L:119:G:OP2	27:w:76:ASN:ND2	2.39	0.42
19:L:1147:A:O2'	19:L:1148:U:H5'	2.19	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
30:l:21:LEU:HD13	30:l:42:VAL:HG21	2.00	0.42
27:w:67:THR:C	27:w:68:LEU:HD12	2.44	0.42
10:Z:67:LYS:HD3	10:Z:116:ASN:HD21	1.84	0.42
17:D:175:G:P	28:g:49:ARG:HH12	2.42	0.42
19:L:120:G:H4'	19:L:121:C:H5'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:125:C:H4'	28:e:81:GLY:H	1.83	0.42
20:v:385:PHE:CD1	20:v:388:LEU:HD12	2.54	0.42
28:e:91:ILE:HD12	28:e:94:LEU:CD1	2.48	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:135:ASN:O	2:C:233:ASP:N	2.43	0.42
2:C:802:ALA:HB2	2:C:843:LYS:HA	2.01	0.42
17:D:173:U:C1'	28:g:99:ASP:HB3	2.34	0.42
20:v:397:ASN:HD22	20:v:397:ASN:HA	1.66	0.42
20:v:529:HIS:O	20:v:529:HIS:CG	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
25:z:45:LEU:HG	25:z:45:LEU:O	2.20	0.42
2:C:315:SER:HB3	2:C:320:PHE:CE1	2.54	0.42
6:Q:306:THR:CG2	6:Q:307:ALA:N	2.82	0.42
29:s:31:ILE:O	29:s:48:CYS:HA	2.19	0.42
1:A:908:ASP:OD1	1:A:994:TYR:OH	2.32	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
19:L:1084:A:H2'	19:L:1084:A:N3	2.34	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
30:y:41:ASN:HB3	30:y:66:GLY:H	1.83	0.42
1:A:1972:ASP:HB3	28:e:41:ARG:NH2	2.35	0.42
1:A:2024:MET:CE	28:e:93:LYS:HE3	2.35	0.42
4:O:317:HIS:HD2	4:O:318:PRO:HD2	1.85	0.42
5:P:196:THR:HA	11:c:90:MET:HE1	2.02	0.42
10:Z:37:LEU:CD2	10:Z:214:ILE:HG13	2.37	0.42
15:H:34:ARG:H	15:H:34:ARG:HG3	1.60	0.42
15:H:58:ILE:HD13	15:H:58:ILE:H	1.83	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
25:z:103:LEU:HD23	25:z:107:LEU:HD11	2.01	0.42
11:c:180:LYS:HE2	11:c:180:LYS:HB2	1.74	0.42
12:d:241:MET:HG3	12:d:279:LEU:CD1	2.45	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
28:e:54:ILE:HB	28:e:72:VAL:HG22	2.01	0.42
1:A:430:PRO:CB	10:Z:198:PHE:CD2	3.00	0.42
6:Q:109:MET:HE3	11:c:218:VAL:O	2.20	0.42
12:d:334:PHE:O	12:d:335:PRO:C	2.62	0.42
15:H:45:LYS:HG3	15:H:46:GLU:N	2.35	0.42
15:H:62:SER:HA	15:H:65:ILE:CD1	2.50	0.42
19:L:1082:A:C2	19:L:1083:A:C5	3.07	0.42
28:e:91:ILE:CG2	25:z:96:ILE:CG2	2.98	0.42
1:A:593:LEU:HD23	1:A:599:LEU:HD13	2.01	0.42
1:A:1111:SER:HB2	1:A:1510:ILE:HG13	2.01	0.42
1:A:1522:ASN:OD1	1:A:1522:ASN:N	2.53	0.42
1:A:1687:HIS:HD2	1:A:1688:PRO:HD2	1.85	0.42
1:A:1806:MET:O	1:A:1816:ARG:NH2	2.52	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
7:R:206:LEU:O	7:R:208:SER:N	2.53	0.42
11:c:200:ILE:CG2	12:d:45:GLU:HG3	2.30	0.42
12:d:270:ALA:HB1	12:d:280:LEU:HD11	2.02	0.42
12:d:271:ILE:O	12:d:274:TRP:C	2.63	0.42
30:l:41:ASN:ND2	30:l:63:PHE:CZ	2.88	0.42
1:A:1047:ALA:HB3	1:A:1251:TYR:HB3	2.02	0.42
1:A:1125:LEU:HD22	1:A:1230:ILE:HG23	2.01	0.42
1:A:1993:ASP:HB3	1:A:2038:HIS:HB3	2.00	0.42
11:c:181:ARG:NH2	12:d:49:ARG:NH1	2.57	0.42
12:d:269:ILE:O	12:d:273:LYS:CB	2.68	0.42
17:D:94:C:C2'	17:D:95:C:H5'	2.49	0.42
17:D:168:U:H2'	24:i:49:PHE:CE1	2.53	0.42
19:L:1097:G:H21	19:L:1146:G:H1'	1.84	0.42
1:A:1616:ARG:NH2	1:A:1744:ASP:OD1	2.52	0.41
5:P:146:VAL:HG23	12:d:128:THR:O	2.19	0.41
7:R:146:LEU:CD2	7:R:151:LEU:CD2	2.98	0.41
17:D:28:G:O2'	17:D:29:G:P	2.78	0.41
17:D:147:C:H2'	17:D:148:G:C8	2.55	0.41
25:m:104:ASP:OD1	25:m:105:SER:N	2.53	0.41
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:273:ASP:HA	1:A:310:ASN:HD21	1.84	0.41
1:A:426:PRO:HB3	10:Z:201:ARG:NH1	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1896:THR:HA	1:A:1899:TRP:CD1	2.49	0.41
2:C:227:VAL:HG13	2:C:473:LEU:HB3	2.01	0.41
14:n:311:SER:HB2	14:n:339:MET:HB3	2.02	0.41
16:B:9:U:C4'	16:B:10:A:OP2	2.68	0.41
17:D:174:G:H2'	28:g:49:ARG:NH1	2.35	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
28:e:89:ARG:NH1	28:e:91:ILE:HD11	2.35	0.41
12:d:125:ALA:HB1	12:d:135:LEU:HD22	2.02	0.41
15:H:65:ILE:CD1	15:H:82:LEU:HD11	2.50	0.41
19:L:1093:C:O2'	30:y:54:GLY:HA3	2.20	0.41
19:L:1095:U:C2'	19:L:1096:C:C6	3.03	0.41
19:L:1137:U:H6	19:L:1137:U:H3'	1.85	0.41
22:b:84:ASN:O	22:b:106:ASN:HA	2.21	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
1:A:709:ARG:HH22	17:D:83:C:P	2.43	0.41
1:A:1153:GLU:HG2	1:A:1159:ARG:HH11	1.85	0.41
1:A:1288:LEU:HD11	1:A:1300:ALA:HB2	2.03	0.41
2:C:126:MET:CE	2:C:132:ARG:HH12	2.33	0.41
2:C:176:ARG:HH12	2:C:185:ILE:HA	1.85	0.41
2:C:571:TYR:CG	2:C:575:ALA:HB2	2.54	0.41
4:O:365:PHE:HE1	4:O:373:LEU:HB2	1.86	0.41
13:I:206:LYS:HA	13:I:209:ARG:HE	1.86	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
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
1:A:240:PRO:HA	1:A:241:PRO:HD3	1.86	0.41
1:A:1632:ILE:HG21	1:A:1645:LEU:HD13	2.03	0.41
32:A:3000:IHP:P2	32:A:3000:IHP:O31	2.79	0.41
6:Q:316:LEU:O	6:Q:319:LEU:N	2.53	0.41
9:T:98:THR:OG1	18:E:25:C:O2'	2.36	0.41
11:c:544:LEU:HA	11:c:547:HIS:HB2	2.02	0.41
17:D:65:U:H2'	17:D:66:A:H8	1.85	0.41
19:L:1085:G:N2	19:L:1086:U:C6	2.87	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:l:83:LEU:HD12	30:l:84:PHE:N	2.35	0.41
26:x:35:PHE:O	26:x:36:LEU:CB	2.68	0.41
1:A:1320:LEU:HB3	1:A:1370:ARG:HH21	1.84	0.41
2:C:92:GLU:HA	2:C:93:PRO:HD3	1.96	0.41
6:Q:207:LEU:O	6:Q:249:GLY:N	2.50	0.41
7:R:146:LEU:O	7:R:147:ASN:CB	2.68	0.41
7:R:211:GLU:O	7:R:213:ASP:N	2.54	0.41
11:c:253:LEU:HD23	11:c:253:LEU:O	2.21	0.41
15:H:40:LYS:HA	15:H:40:LYS:NZ	2.36	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
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
19:L:1082:A:O2'	19:L:1083:A:H5'	2.21	0.41
29:k:59:ASP:HA	29:k:62:ARG:HH21	1.86	0.41
27:w:30:LYS:HD2	27:w:80:TYR:CE2	2.55	0.41
1:A:1182:LEU:HD13	1:A:1225:ALA:CB	2.50	0.41
1:A:1316:ILE:HD13	1:A:1363:GLY:HA3	2.02	0.41
32:A:3000:IHP:O12	32:A:3000:IHP:P1	2.79	0.41
32:A:3000:IHP:O14	32:A:3000:IHP:P3	2.79	0.41
10:Z:203:LYS:O	10:Z:204:ASP:HB2	2.20	0.41
11:c:174:ARG:O	11:c:178:GLU:HG2	2.21	0.41
11:c:233:GLU:CG	12:d:114:CYS:HA	2.45	0.41
11:c:253:LEU:HD13	12:d:37:ILE:HD12	2.01	0.41
19:L:41:C:H2'	19:L:42:U:C6	2.55	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
28:e:50:ASN:O	28:e:51:ASN:HB3	2.21	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
27:w:79:LEU:HD22	27:w:80:TYR:HD2	1.86	0.41
1:A:275:TYR:HB3	1:A:307:GLU:HG2	2.03	0.41
1:A:856:TRP:CD1	8:S:174:VAL:HG21	2.56	0.41
1:A:1035:LEU:HD12	1:A:1038:ILE:HG12	2.03	0.41
1:A:1287:ASP:HB3	1:A:1296:ARG:HG2	2.03	0.41
2:C:132:ARG:HH22	30:l:13:GLU:HA	1.85	0.41
2:C:743:ASN:HB3	2:C:746:LYS:HB3	2.03	0.41
2:C:968:MET:HE1	2:C:986:GLY:HA2	2.02	0.41
4:O:218:ARG:HA	4:O:256:ARG:HD3	2.03	0.41
4:O:392:MET:HG2	8:S:158:ASN:HB2	2.02	0.41
4:O:446:LEU:HD23	4:O:451:PHE:HZ	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Q:269:THR:HG22	6:Q:279:GLY:HA2	2.02	0.41
7:R:147:ASN:O	7:R:148:SER:CB	2.68	0.41
7:R:208:SER:HB3	19:L:79:A:H5'	2.03	0.41
10:Z:44:LEU:HD21	10:Z:56:ILE:HD11	2.03	0.41
10:Z:312:LEU:HD12	10:Z:346:LEU:HD11	2.03	0.41
11:c:228:TYR:CD2	12:d:119:ARG:HB3	2.56	0.41
17:D:162:G:O2'	17:D:164:C:OP1	2.38	0.41
19:L:114:U:O2'	30:y:65:ARG:NH2	2.53	0.41
19:L:1085:G:N3	19:L:1086:U:H5	2.12	0.41
19:L:1097:G:N2	19:L:1146:G:H1'	2.36	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
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
31:p:98:LEU:HD12	31:q:98:LEU:HG	2.03	0.41
1:A:826:ALA:O	1:A:830:ASN:ND2	2.54	0.41
1:A:1406:LEU:HB3	1:A:1425:PHE:HB3	2.02	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:134:ILE:HD12	2:C:439:ILE:HG22	2.03	0.41
12:d:270:ALA:HB1	12:d:280:LEU:HD21	2.01	0.41
12:d:391:LEU:O	12:d:395:ILE:N	2.53	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:616:GLY:N	18:E:71:G:H5''	2.36	0.40
1:A:1040:ASP:OD2	1:A:1045:GLN:NE2	2.54	0.40
2:C:636:VAL:HG22	2:C:642:HIS:HD1	1.85	0.40
10:Z:104:GLN:HB3	10:Z:108:ARG:NH2	2.36	0.40
10:Z:228:ILE:HD12	10:Z:230:SER:HB2	2.03	0.40
12:d:255:ALA:HB2	12:d:291:PHE:CD2	2.48	0.40
19:L:1129:U:C2'	19:L:1130:U:O5'	2.69	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:k:85:THR:HG22	30:l:73:VAL:HG13	2.03	0.40
25:z:93:ARG:HG2	25:z:94:GLN:HG3	2.03	0.40
7:R:1:MET:HA	7:R:5:ARG:HB2	2.03	0.40
11:c:65:PHE:CD2	11:c:101:ARG:HG2	2.56	0.40
12:d:141:ILE:HG22	13:I:105:TYR:HE1	1.77	0.40
12:d:240:ASP:CG	12:d:277:ASN:HB3	2.46	0.40
19:L:117:U:O2	25:z:35:GLN:O	2.39	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
1:A:583:ILE:HG23	1:A:588:LEU:HB2	2.03	0.40
12:d:51:ARG:NE	12:d:75:GLU:OE2	2.51	0.40
12:d:189:TYR:HA	12:d:192:TYR:HB3	2.03	0.40
17:D:169:U:C6	26:j:35:PHE:CD1	3.10	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
28:e:69:LEU:HD12	28:e:69:LEU:N	2.36	0.40
28:e:70:GLU:HG3	28:e:70:GLU:H	1.73	0.40
28:e:92:SER:CB	25:z:99:ASP:OD1	2.70	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:400:ILE:HG23	2:C:187:ARG:HE	1.87	0.40
1:A:2021:SER:O	1:A:2024:MET:HB2	2.21	0.40
2:C:129:ILE:HB	2:C:132:ARG:HB2	2.03	0.40
6:Q:251:LEU:HD11	6:Q:253:PHE:CZ	2.56	0.40
12:d:288:GLU:HB3	12:d:297:ILE:HG13	2.03	0.40
12:d:330:ILE:HG21	12:d:339:MET:HA	2.02	0.40
15:H:32:TYR:HB3	15:H:50:TRP:CZ2	2.56	0.40
19:L:121:C:N4	27:w:33:PHE:CD1	2.90	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:73:LYS:HE3	28:e:90:PHE:CE2	2.56	0.40
25:z:10:LEU:O	25:z:10:LEU:HD23	2.22	0.40
31:r:19:SER:OG	31:r:38:ASP:OD2	2.34	0.40
1:A:162:LEU:HD12	1:A:162:LEU:HA	1.88	0.40
1:A:173:LEU:HD12	1:A:715:LEU:HB3	2.04	0.40
1:A:194:HIS:CD2	5:P:122:LEU:HD22	2.57	0.40
1:A:1605:ARG:HH21	1:A:1824:GLN:HB2	1.85	0.40
15:H:29:TYR:CE1	15:H:32:TYR:CD2	2.96	0.40
19:L:1106:G:C5'	19:L:1107:C:OP1	2.70	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:v:385:PHE:HD1	20:v:388:LEU:HD12	1.85	0.40
24:u:90:ILE:HB	26:x:62:VAL:CG1	2.52	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
28:g:50:ASN:HB2	28:g:52:HIS:CE1	2.55	0.40
28:e:89:ARG:HH22	28:e:91:ILE:CD1	2.33	0.40
27:w:51:LEU:HB2	27:w:73:ILE:HB	2.04	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	1860/2413 (77%)	1774 (95%)	80 (4%)	6 (0%)	36	68
2	C	914/1008 (91%)	881 (96%)	33 (4%)	0	100	100
3	J	25/135 (18%)	23 (92%)	2 (8%)	0	100	100
4	O	355/451 (79%)	318 (90%)	35 (10%)	2 (1%)	21	56
5	P	197/379 (52%)	190 (96%)	7 (4%)	0	100	100
6	Q	288/364 (79%)	264 (92%)	22 (8%)	2 (1%)	18	52
7	R	259/339 (76%)	246 (95%)	11 (4%)	2 (1%)	16	50
8	S	64/175 (37%)	63 (98%)	1 (2%)	0	100	100
9	T	155/157 (99%)	150 (97%)	5 (3%)	0	100	100
10	Z	443/577 (77%)	425 (96%)	16 (4%)	2 (0%)	24	59
11	c	418/590 (71%)	396 (95%)	20 (5%)	2 (0%)	24	59
12	d	534/687 (78%)	513 (96%)	16 (3%)	5 (1%)	14	47
13	I	98/215 (46%)	96 (98%)	2 (2%)	0	100	100
14	n	279/455 (61%)	265 (95%)	12 (4%)	2 (1%)	18	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	H	68/235 (29%)	64 (94%)	2 (3%)	2 (3%)	3	24
20	v	666/859 (78%)	642 (96%)	22 (3%)	2 (0%)	36	68
21	a	82/111 (74%)	78 (95%)	3 (4%)	1 (1%)	10	42
22	b	165/238 (69%)	138 (84%)	20 (12%)	7 (4%)	2	16
23	t	150/175 (86%)	145 (97%)	4 (3%)	1 (1%)	18	52
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	39
26	x	73/77 (95%)	65 (89%)	7 (10%)	1 (1%)	9	39
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	31
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	27
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	8686/13195 (66%)	8245 (95%)	397 (5%)	44 (0%)	26	59

All (44) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	260	PRO
1	A	1965	PHE
7	R	152	LYS
7	R	153	PRO
12	d	181	ASN
12	d	353	GLU

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Mol	Chain	Res	Type
14	n	387	ILE
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	1964	PRO
4	O	351	GLY
4	O	352	ILE
11	c	218	VAL
15	H	33	GLN
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	510	PRO
1	A	511	ASP
10	Z	235	ALA
12	d	63	LEU
12	d	336	LYS
14	n	427	LYS
20	v	515	PRO
22	b	67	ILE
22	b	94	LEU
30	l	40	MET
26	x	75	ASP
1	A	1157	PRO
6	Q	256	SER
10	Z	229	VAL
6	Q	191	PRO
11	c	418	PRO
12	d	334	PHE
15	H	35	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%)	1724 (99%)	13 (1%)	76	83
2	C	830/910 (91%)	821 (99%)	9 (1%)	65	79
3	J	21/121 (17%)	21 (100%)	0	100	100
4	O	312/397 (79%)	308 (99%)	4 (1%)	61	78
5	P	175/328 (53%)	174 (99%)	1 (1%)	78	84
6	Q	265/332 (80%)	259 (98%)	6 (2%)	44	70
7	R	224/296 (76%)	218 (97%)	6 (3%)	39	68
8	S	57/151 (38%)	55 (96%)	2 (4%)	32	64
9	T	141/141 (100%)	140 (99%)	1 (1%)	76	83
10	Z	417/538 (78%)	413 (99%)	4 (1%)	68	80
11	c	214/525 (41%)	195 (91%)	19 (9%)	9	34
12	d	274/633 (43%)	267 (97%)	7 (3%)	40	69
13	I	92/193 (48%)	92 (100%)	0	100	100
14	n	121/412 (29%)	107 (88%)	14 (12%)	5	24
15	H	68/216 (32%)	46 (68%)	22 (32%)	0	1
20	v	294/786 (37%)	278 (95%)	16 (5%)	20	53
23	t	39/165 (24%)	26 (67%)	13 (33%)	0	1
24	i	55/83 (66%)	52 (94%)	3 (6%)	19	52
24	u	52/83 (63%)	51 (98%)	1 (2%)	50	73
25	m	106/129 (82%)	93 (88%)	13 (12%)	4	22
25	z	95/129 (74%)	92 (97%)	3 (3%)	34	65
26	j	56/66 (85%)	47 (84%)	9 (16%)	2	13
26	x	56/66 (85%)	55 (98%)	1 (2%)	51	74
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%)	76 (93%)	6 (7%)	13	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	g	82/103 (80%)	75 (92%)	7 (8%)	10	37
29	k	92/176 (52%)	80 (87%)	12 (13%)	4	20
29	s	85/176 (48%)	82 (96%)	3 (4%)	32	64
30	l	72/89 (81%)	54 (75%)	18 (25%)	0	3
30	y	68/89 (76%)	68 (100%)	0	100	100
31	o	60/451 (13%)	57 (95%)	3 (5%)	22	55
31	p	62/451 (14%)	58 (94%)	4 (6%)	15	47
31	q	62/451 (14%)	59 (95%)	3 (5%)	23	56
31	r	60/451 (13%)	57 (95%)	3 (5%)	22	55
All	All	6528/11576 (56%)	6302 (96%)	226 (4%)	32	64

All (226) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	255	ILE
1	A	261	LEU
1	A	396	ARG
1	A	621	LEU
1	A	742	VAL
1	A	1222	LEU
1	A	1608	LEU
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	132	ARG
2	C	234	LEU
2	C	267	ILE
2	C	352	VAL
2	C	430	ARG
2	C	545	LEU
2	C	561	ILE
2	C	726	ASN
2	C	830	ASN
4	O	230	VAL
4	O	236	LEU
4	O	352	ILE

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Mol	Chain	Res	Type
4	O	353	ILE
5	P	30	LEU
6	Q	51	ARG
6	Q	105	LYS
6	Q	109	MET
6	Q	251	LEU
6	Q	282	LEU
6	Q	291	ILE
7	R	143	ASP
7	R	148	SER
7	R	152	LYS
7	R	159	ARG
7	R	210	LYS
7	R	211	GLU
8	S	35	THR
8	S	36	THR
9	T	153	CYS
10	Z	67	LYS
10	Z	177	LEU
10	Z	194	LEU
10	Z	470	LEU
11	c	169	ARG
11	c	170	LYS
11	c	174	ARG
11	c	175	MET
11	c	176	LEU
11	c	177	GLU
11	c	180	LYS
11	c	186	GLN
11	c	187	LYS
11	c	215	GLU
11	c	218	VAL
11	c	223	PRO
11	c	227	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	62	ARG
12	d	155	LEU

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Mol	Chain	Res	Type
12	d	263	SER
12	d	271	ILE
12	d	284	LEU
12	d	285	LEU
12	d	334	PHE
14	n	159	PRO
14	n	162	PRO
14	n	165	THR
14	n	208	PRO
14	n	257	PRO
14	n	258	THR
14	n	260	PRO
14	n	327	PRO
14	n	340	PRO
14	n	373	PRO
14	n	424	PRO
14	n	428	PRO
14	n	430	THR
14	n	436	PRO
15	H	27	LYS
15	H	28	ASP
15	H	30	SER
15	H	32	TYR
15	H	33	GLN
15	H	34	ARG
15	H	36	ARG
15	H	40	LYS
15	H	41	VAL
15	H	42	LYS
15	H	43	SER
15	H	44	ILE
15	H	55	SER
15	H	57	GLU
15	H	58	ILE
15	H	66	TYR
15	H	67	ASP
15	H	69	SER
15	H	70	LEU
15	H	72	GLU
15	H	77	GLU
15	H	81	GLU
20	v	385	PHE

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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	70	GLU
28	e	88	GLU
28	e	91	ILE
28	e	92	SER
28	e	94	LEU
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

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Mol	Chain	Res	Type
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
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 (145) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	170	HIS
1	A	181	HIS
1	A	265	ASN
1	A	310	ASN
1	A	429	ASN

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Mol	Chain	Res	Type
1	A	509	HIS
1	A	532	ASN
1	A	580	ASN
1	A	658	ASN
1	A	685	HIS
1	A	705	GLN
1	A	713	ASN
1	A	748	GLN
1	A	830	ASN
1	A	848	ASN
1	A	864	GLN
1	A	961	GLN
1	A	1034	ASN
1	A	1045	GLN
1	A	1067	ASN
1	A	1091	ASN
1	A	1097	HIS
1	A	1128	GLN
1	A	1368	GLN
1	A	1449	ASN
1	A	1466	GLN
1	A	1496	GLN
1	A	1500	HIS
1	A	1529	ASN
1	A	1531	HIS
1	A	1538	ASN
1	A	1540	ASN
1	A	1618	ASN
1	A	1677	GLN
1	A	1687	HIS
1	A	1737	GLN
1	A	1863	HIS
1	A	1947	HIS
1	A	1990	ASN
1	A	2068	ASN
2	C	84	GLN
2	C	101	GLN
2	C	183	GLN
2	C	255	GLN
2	C	289	ASN
2	C	294	ASN
2	C	355	HIS

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Mol	Chain	Res	Type
2	C	431	GLN
2	C	444	GLN
2	C	560	GLN
2	C	608	GLN
2	C	647	ASN
2	C	726	ASN
2	C	869	HIS
2	C	929	GLN
4	O	99	ASN
4	O	121	GLN
4	O	136	ASN
4	O	271	GLN
5	P	84	ASN
5	P	87	ASN
5	P	140	ASN
6	Q	6	ASN
6	Q	85	GLN
6	Q	244	HIS
7	R	91	HIS
7	R	150	HIS
7	R	155	GLN
7	R	227	ASN
7	R	255	ASN
7	R	257	ASN
8	S	171	HIS
8	S	173	HIS
9	T	48	GLN
9	T	57	HIS
9	T	58	GLN
9	T	143	HIS
10	Z	54	ASN
10	Z	69	ASN
10	Z	84	ASN
10	Z	116	ASN
10	Z	131	HIS
10	Z	182	GLN
10	Z	202	GLN
10	Z	310	HIS
10	Z	354	HIS
11	c	26	GLN
11	c	31	HIS
11	c	72	GLN

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Mol	Chain	Res	Type
11	c	103	ASN
11	c	161	ASN
11	c	214	ASN
12	d	79	HIS
12	d	123	ASN
12	d	147	ASN
12	d	248	ASN
12	d	315	ASN
12	d	316	ASN
13	I	99	GLN
13	I	111	ASN
13	I	115	GLN
13	I	144	GLN
13	I	204	ASN
15	H	53	GLN
15	H	93	GLN
20	v	397	ASN
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	71	ASN
28	e	86	ASN

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Mol	Chain	Res	Type
29	s	8	HIS
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	12	ASN
25	z	14	GLN
25	z	21	ASN
31	r	85	GLN
31	q	85	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	B	58/679 (8%)	24 (41%)	2 (3%)
17	D	177/214 (82%)	54 (30%)	7 (3%)
18	E	102/112 (91%)	35 (34%)	1 (0%)
19	L	197/1175 (16%)	64 (32%)	7 (3%)
All	All	534/2180 (24%)	177 (33%)	17 (3%)

All (177) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
16	B	-11	C
16	B	-10	A
16	B	-9	A
16	B	-5	A
16	B	-3	U
16	B	0	G
16	B	1	G
16	B	2	U
16	B	3	A
16	B	9	U
16	B	10	A
16	B	11	G
16	B	12	C
16	B	16	U

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Mol	Chain	Res	Type
16	B	17	G
16	B	248	A
16	B	249	C
16	B	250	U
16	B	251	A
16	B	252	A
16	B	266	A
16	B	270	C
16	B	272	A
16	B	276	C
17	D	12	C
17	D	13	A
17	D	14	G
17	D	18	A
17	D	20	U
17	D	27	G
17	D	28	G
17	D	29	G
17	D	31	G
17	D	33	U
17	D	41	A
17	D	42	A
17	D	43	G
17	D	44	A
17	D	45	A
17	D	75	A
17	D	76	U
17	D	77	A
17	D	79	C
17	D	80	G
17	D	84	A
17	D	95	C
17	D	96	U
17	D	97	U
17	D	101	C
17	D	103	A
17	D	104	G
17	D	109	A
17	D	113	G
17	D	126	A
17	D	127	U
17	D	128	A

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Mol	Chain	Res	Type
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
17	D	146	C
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	19	C
18	E	23	G
18	E	27	U
18	E	31	G
18	E	35	A
18	E	36	U
18	E	42	A
18	E	43	C
18	E	48	C
18	E	49	A
18	E	50	G
18	E	51	A
18	E	52	G
18	E	54	U
18	E	56	A

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Mol	Chain	Res	Type
18	E	59	A
18	E	60	G
18	E	62	A
18	E	63	G
18	E	66	C
18	E	67	C
18	E	68	C
18	E	80	U
18	E	85	C
18	E	86	G
18	E	92	C
18	E	95	A
18	E	98	G
18	E	99	A
18	E	101	U
19	L	3	G
19	L	4	A
19	L	5	A
19	L	6	U
19	L	18	U
19	L	19	U
19	L	21	G
19	L	23	U
19	L	26	G
19	L	30	A
19	L	31	A
19	L	32	G
19	L	50	U
19	L	51	C
19	L	108	A
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

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Mol	Chain	Res	Type
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
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 (17) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	B	9	U

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Mol	Chain	Res	Type
16	B	248	A
17	D	17	C
17	D	27	G
17	D	28	G
17	D	95	C
17	D	130	A
17	D	150	U
17	D	163	C
18	E	49	A
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	1.58	1 (12%)	7,12,14	1.13	1 (14%)

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	-	3/6/8/10	-

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

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	n	73	SEP	OG-CB-CA	2.26	110.34	108.14

There are no chirality outliers.

All (3) torsion outliers are listed below:

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

There are no ring outliers.

No monomer is involved in short contacts.

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	0.91	1 (3%)	50,54,54	1.65	10 (20%)
32	IHP	A	3000	-	36,36,36	0.75	0	60,60,60	0.54	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	-	2/22/38/38	0/3/3/3
32	IHP	A	3000	-	-	10/30/54/54	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	C	1500	GTP	C5-N7	-2.03	1.35	1.39

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	C	1500	GTP	C5-C4-N3	-4.92	120.56	128.39
33	C	1500	GTP	C2-N3-C4	4.55	120.14	112.30
33	C	1500	GTP	N9-C4-N3	3.20	132.34	125.95
33	C	1500	GTP	C2-N1-C6	-2.95	119.76	125.11
33	C	1500	GTP	N9-C8-N7	-2.66	108.48	113.40
33	C	1500	GTP	C5-C6-N1	2.59	119.85	113.25
33	C	1500	GTP	O6-C6-C5	-2.48	120.00	126.53
33	C	1500	GTP	C8-N7-C5	2.44	108.61	104.26
33	C	1500	GTP	O2A-PA-O3A	2.19	113.20	107.27
33	C	1500	GTP	C3'-C2'-C1'	2.13	105.49	101.46

There are no chirality outliers.

All (12) torsion outliers are listed below:

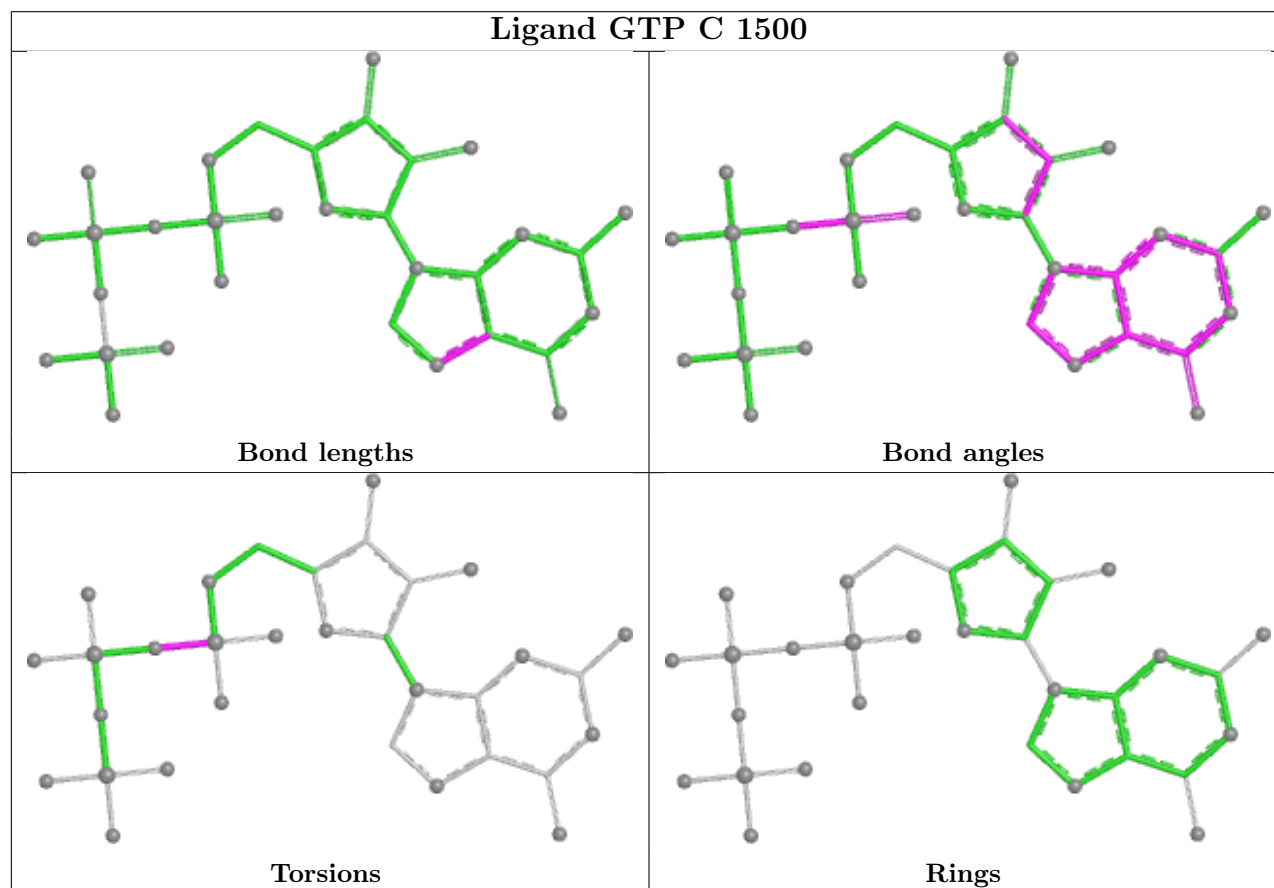
Mol	Chain	Res	Type	Atoms
32	A	3000	IHP	C2-C1-O11-P1
32	A	3000	IHP	C6-C1-O11-P1
32	A	3000	IHP	C5-O15-P5-O25
32	A	3000	IHP	C6-O16-P6-O26
32	A	3000	IHP	C2-C3-O13-P3
32	A	3000	IHP	C4-C3-O13-P3
32	A	3000	IHP	C3-O13-P3-O23
33	C	1500	GTP	PB-O3A-PA-O2A
32	A	3000	IHP	C1-O11-P1-O31
32	A	3000	IHP	C2-O12-P2-O32
32	A	3000	IHP	C2-O12-P2-O22
33	C	1500	GTP	PB-O3A-PA-O1A

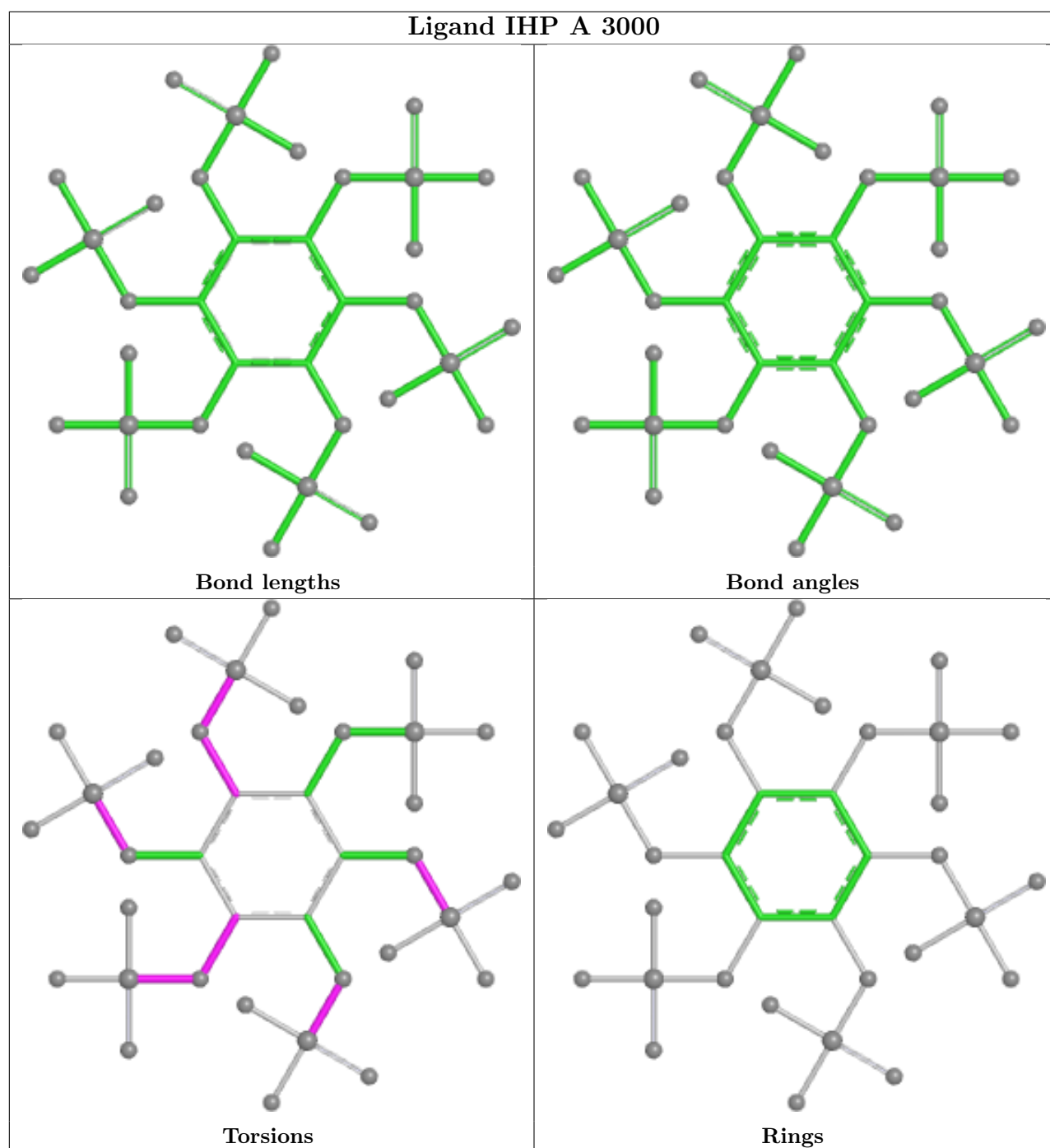
There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	A	3000	IHP	4	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.

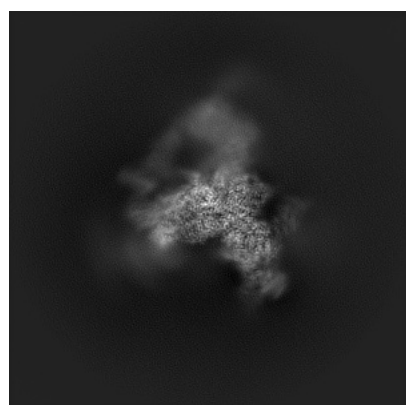
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0686. These allow visual inspection of the internal detail of the map and identification of artifacts.

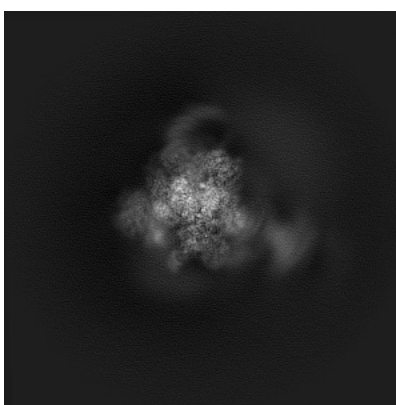
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

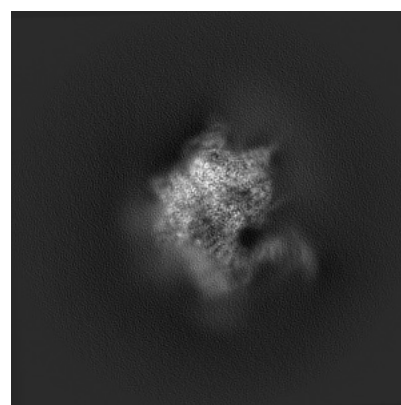
6.1.1 Primary map



X



Y

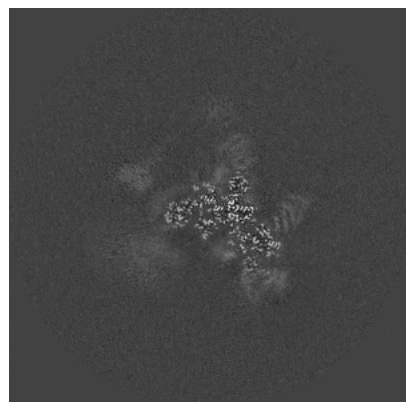


Z

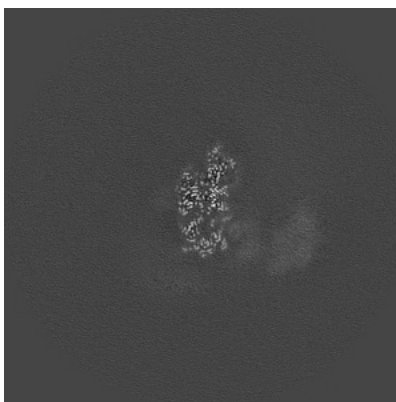
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

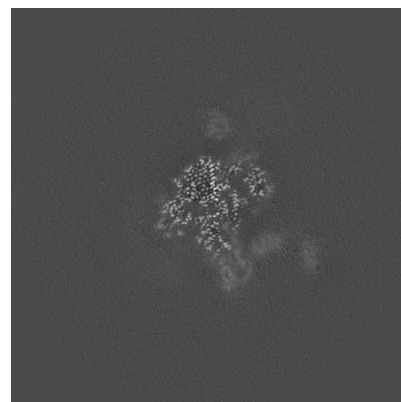
6.2.1 Primary map



X Index: 200



Y Index: 200

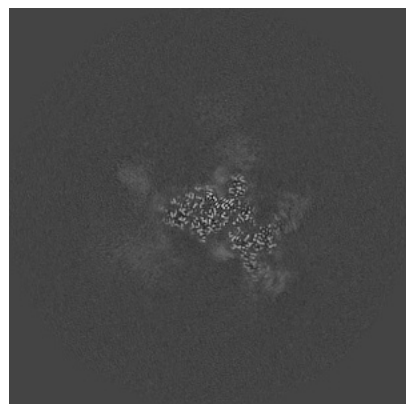


Z Index: 200

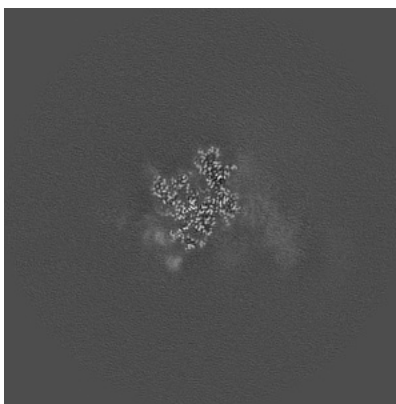
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

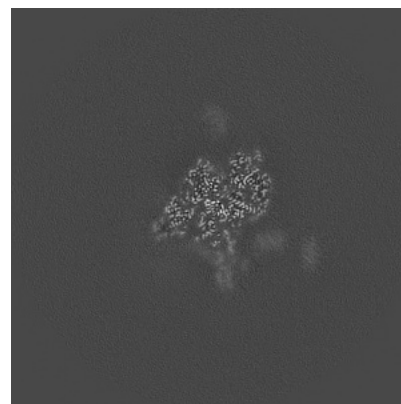
6.3.1 Primary map



X Index: 204



Y Index: 228

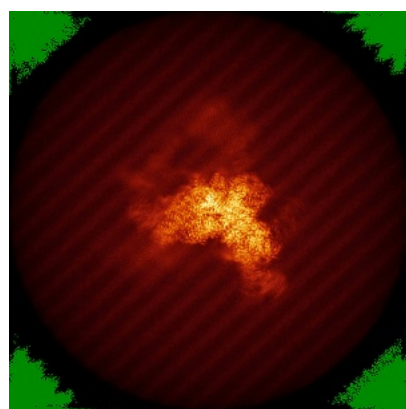


Z Index: 206

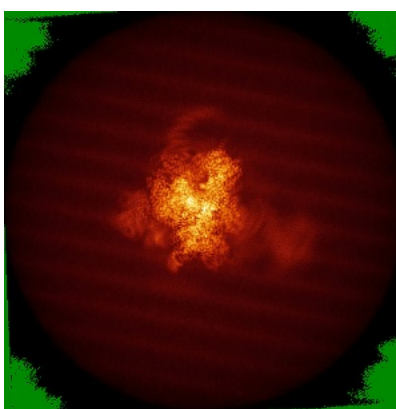
The images above show the largest variance slices of the map in three orthogonal directions.

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

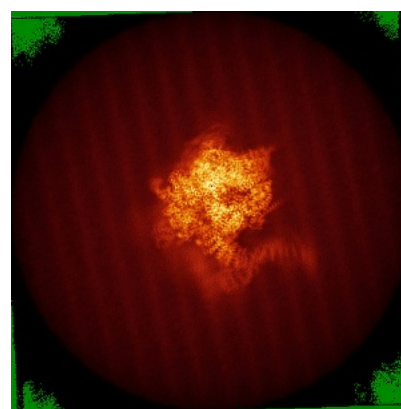
6.4.1 Primary map



X



Y

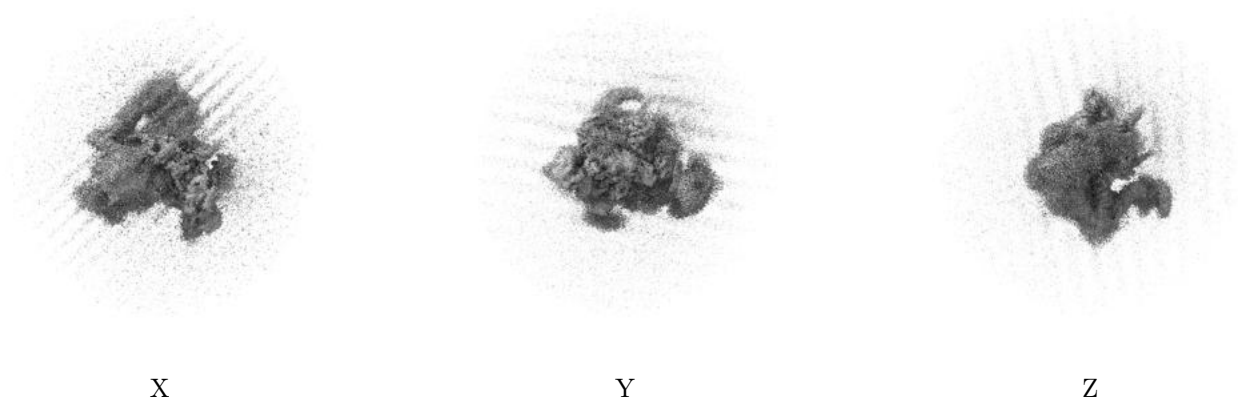


Z

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

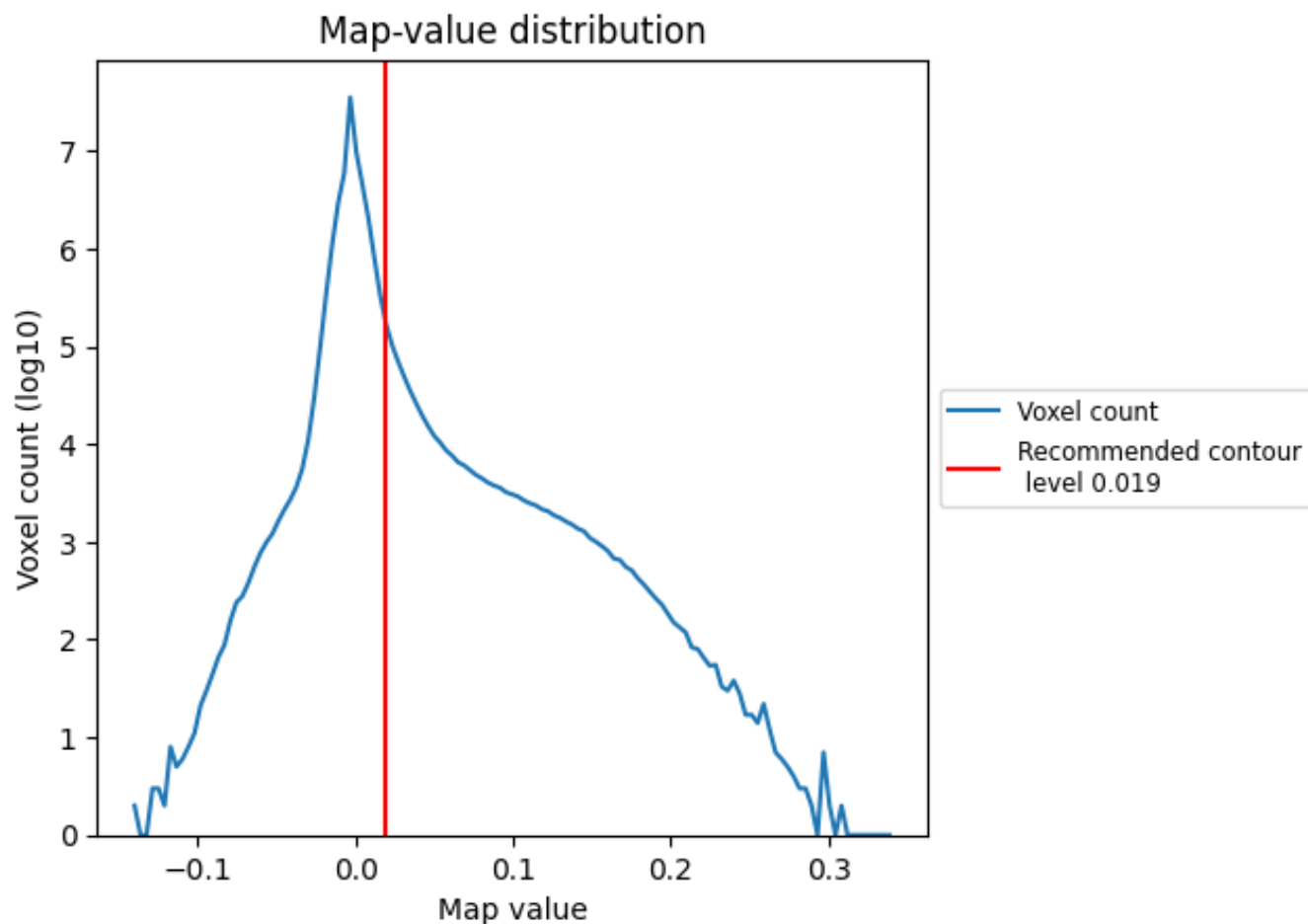
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

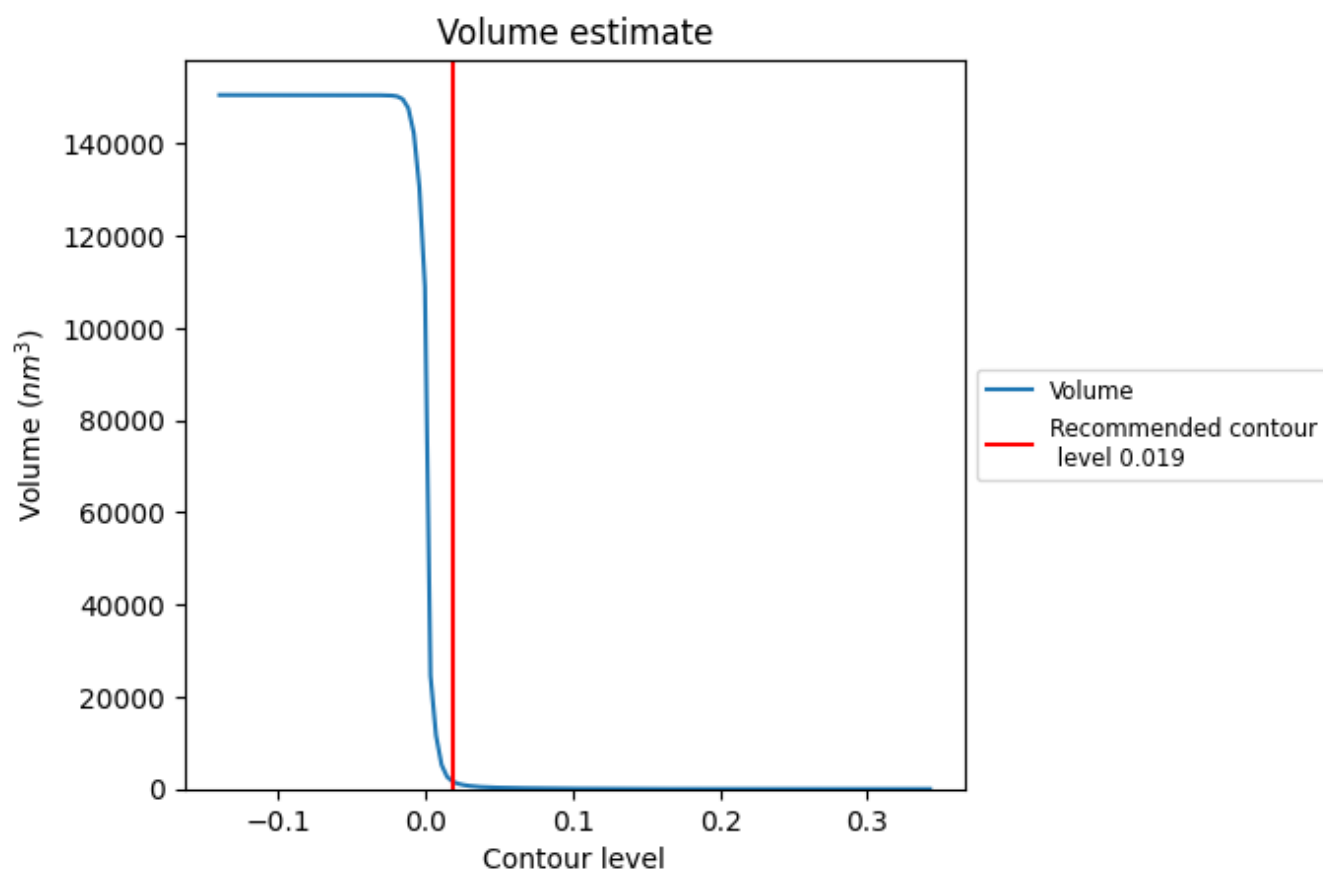
This section contains the results of statistical analysis of the map.

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.

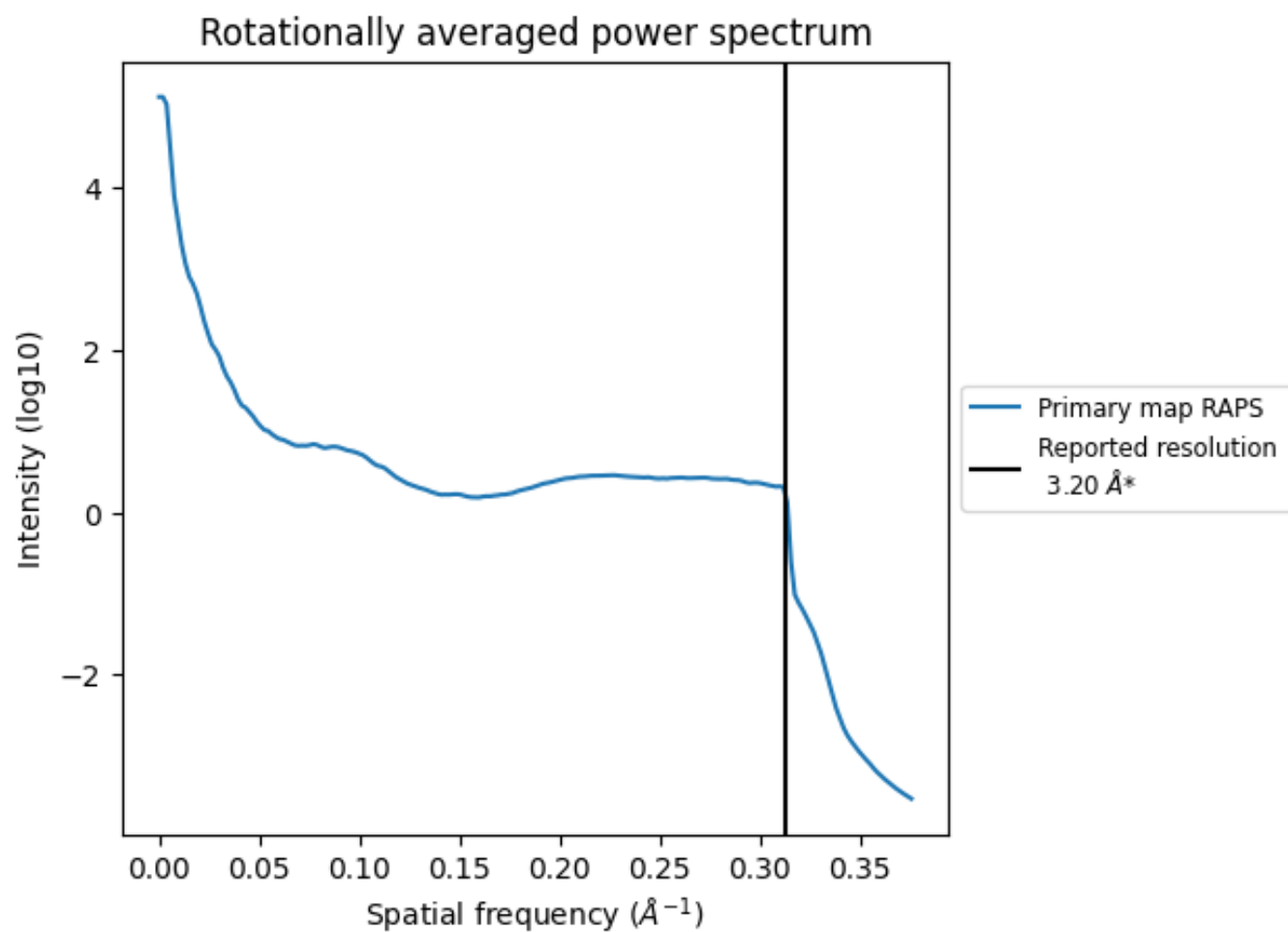
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1533 nm^3 ; this corresponds to an approximate mass of 1385 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 0.312 Å⁻¹

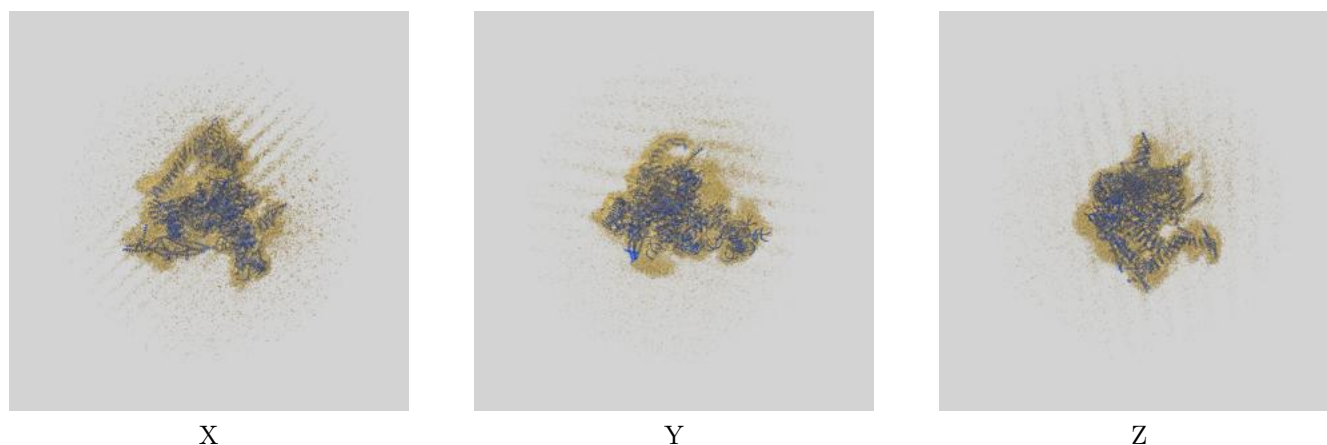
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

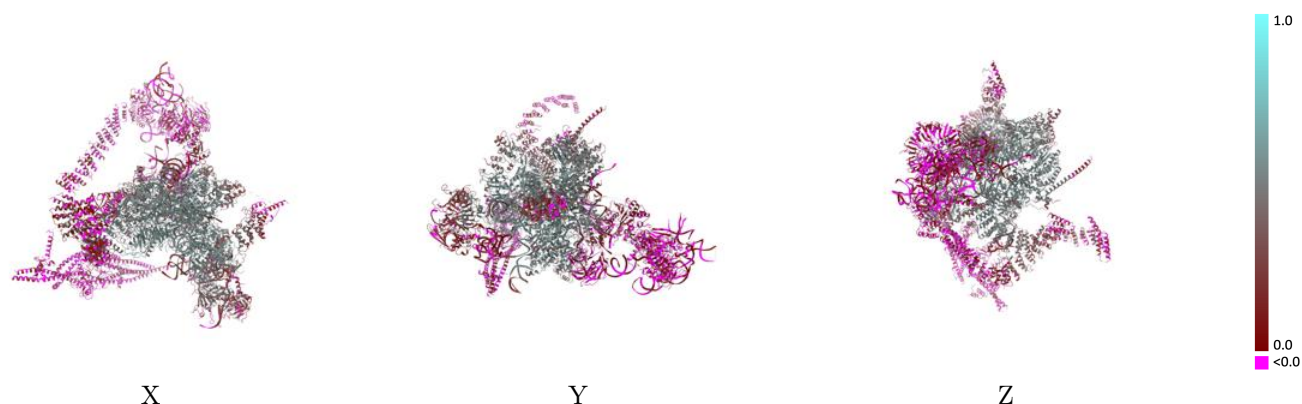
This section contains information regarding the fit between EMDB map EMD-0686 and PDB model 6J6G. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



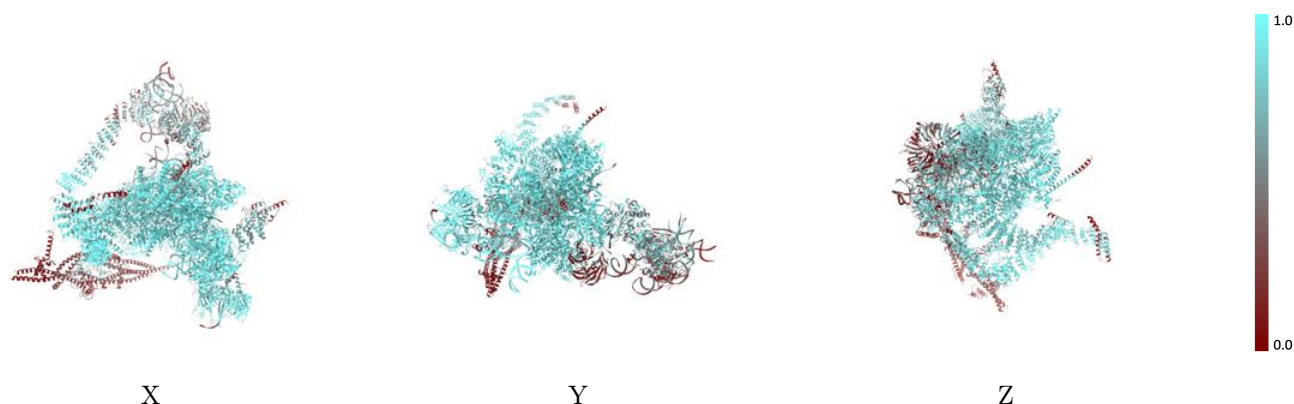
The images above show the 3D surface view of the map at the recommended contour level 0.019 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



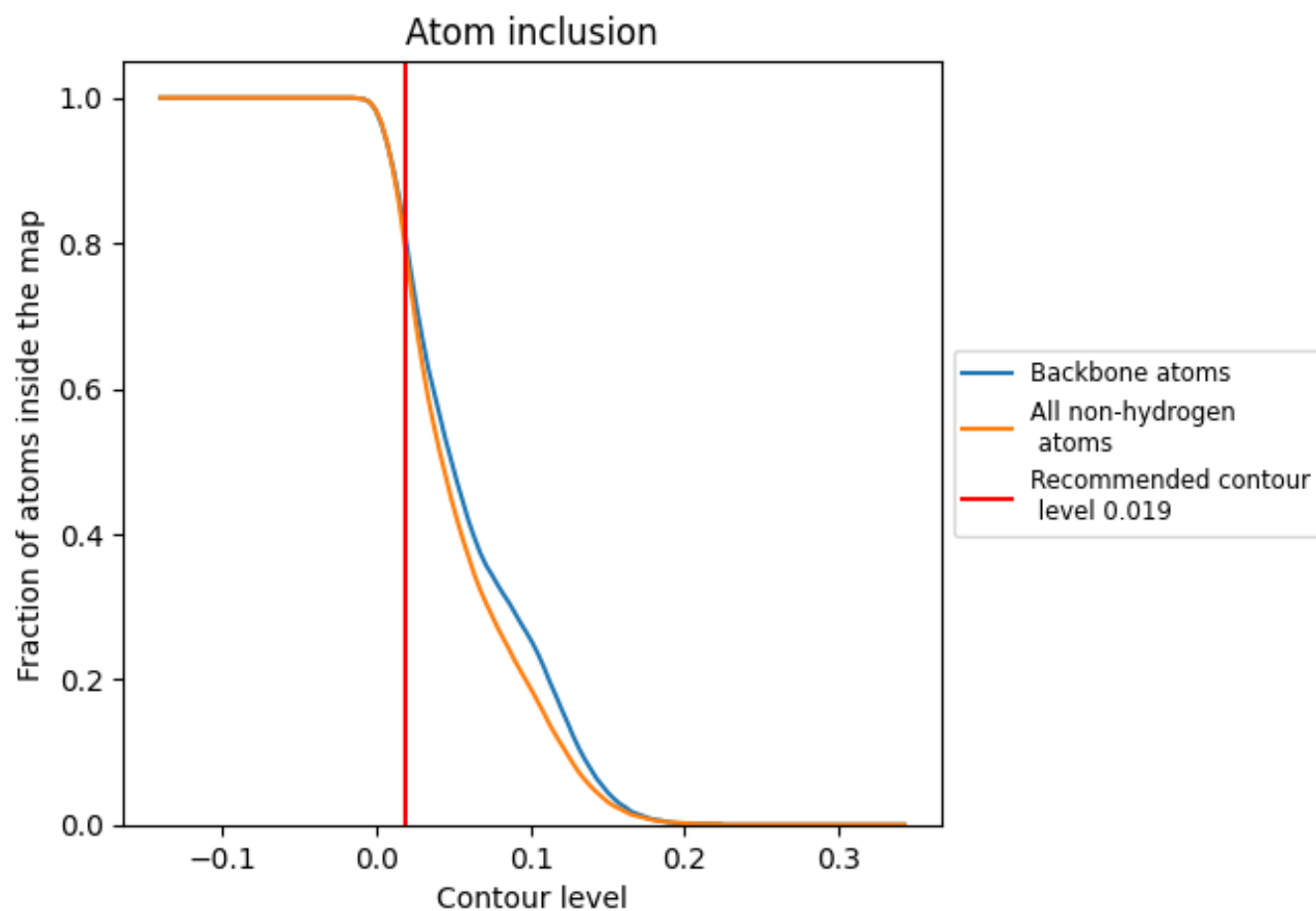
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.019).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 79% 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 (0.019) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7910	 0.3170
A	 0.9170	 0.4650
B	 0.8390	 0.2280
C	 0.9560	 0.4980
D	 0.9520	 0.3350
E	 0.9940	 0.4850
H	 0.7880	 0.1160
I	 0.9170	 0.4460
J	 0.9470	 0.5140
L	 0.6160	 0.0890
O	 0.9680	 0.5330
P	 0.8610	 0.4420
Q	 0.9270	 0.4400
R	 0.9480	 0.4880
S	 0.8520	 0.4900
T	 0.9600	 0.5230
Z	 0.7220	 0.3010
a	 0.5940	 0.0290
b	 0.6400	 0.0370
c	 0.5730	 0.2700
d	 0.8870	 0.3180
e	 0.5610	 0.0280
g	 0.8350	 0.1540
h	 0.9130	 0.1340
i	 0.9160	 0.2180
j	 0.8820	 0.2820
k	 0.8230	 0.2940
l	 0.8960	 0.4280
m	 0.8030	 0.2240
n	 0.2200	 0.0850
o	 0.2680	 0.0010
p	 0.2220	 0.0180
q	 0.1170	 0.0040
r	 0.2400	 -0.0030
s	 0.6120	 -0.0010



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Chain	Atom inclusion	Q-score
t	 0.1330	 -0.0220
u	 0.3870	 0.0270
v	 0.8390	 0.1440
w	 0.5560	 0.0120
x	 0.2760	 0.0440
y	 0.4070	 -0.0060
z	 0.6340	 0.0060