



# Full wwPDB EM Validation Report ⓘ

Jun 26, 2025 – 06:35 AM JST

PDB ID : 8XI2 / pdb\_00008xi2  
EMDB ID : EMD-38362  
Title : Cryo-EM structure of the Chlamydomonas C\* complex  
Authors : Lu, Y.; Zhan, X.  
Deposited on : 2023-12-19  
Resolution : 2.60 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev118  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4-5-2 with Phenix2.0rc1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.44

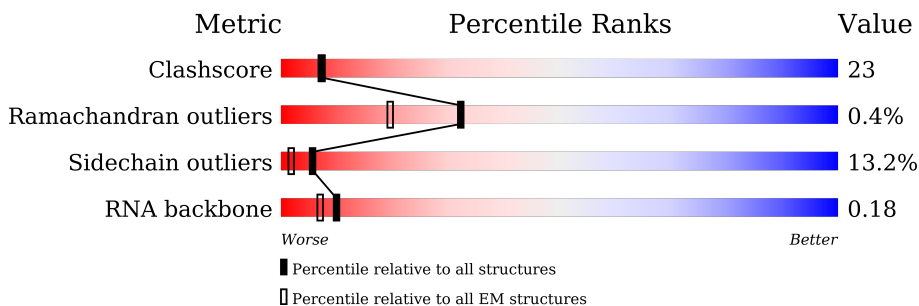
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.60 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	2398	
2	B	111	
3	C	989	
4	E	362	
5	F	101	
6	q	503	
6	r	503	

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Mol	Chain	Length	Quality of chain
6	s	503	
6	t	503	
7	a	127	
8	g	77	
9	e	87	
10	f	85	
11	d	110	
12	c	114	
13	b	265	
14	I	925	
15	J	835	
16	P	235	
17	M	563	
18	T	518	
19	O	417	
20	N	233	
21	R	684	
22	H	192	
23	S	157	
24	W	576	
25	L	833	
26	K	303	
27	U	721	
28	V	928	
29	Q	1844	

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Mol	Chain	Length	Quality of chain
30	5	7	
31	3	173	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
32	GTP	C	1001	-	-	X	-

## 2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 73326 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 MPN domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1931	Total	C	N	O	S	0	0
			15194	9743	2699	2682	70		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	86	Total	C	N	O	P	0	0
			1817	812	307	612	86		

- Molecule 3 is a protein called Elongation factor Tu, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	897	Total	C	N	O	S	0	0
			6973	4431	1203	1297	42		

- Molecule 4 is a protein called U5-40K.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	318	Total	C	N	O	S	0	0
			2441	1524	436	465	16		

- Molecule 5 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	92	Total	C	N	O	P	0	0
			1985	885	369	637	94		

- Molecule 6 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	q	106	Total	C	N	O	S	0	0
			831	522	145	160	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	r	131	Total	C	N	O	S	0	0
			1021	638	183	196	4		
6	s	70	Total	C	N	O	S	0	0
			570	353	108	107	2		
6	t	62	Total	C	N	O	S	0	0
			504	312	95	96	1		

- Molecule 7 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	a	90	Total	C	N	O	S	0	0
			705	444	129	126	6		

- Molecule 8 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	g	65	Total	C	N	O	S	0	0
			512	323	90	96	3		

- Molecule 9 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	e	80	Total	C	N	O	S	0	0
			660	420	117	119	4		

- Molecule 10 is a protein called Sm protein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	f	71	Total	C	N	O	S	0	0
			559	358	91	106	4		

- Molecule 11 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	d	100	Total	C	N	O	S	0	0
			810	505	152	147	6		

- Molecule 12 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	c	88	Total	C	N	O	S	0	0
			684	435	121	124	4		

- Molecule 13 is a protein called Sm domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	b	99	Total	C	N	O	S	0	0
			780	489	149	138	4		

- Molecule 14 is a protein called Syf1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	661	Total	C	N	O	S	0	0
			4629	2900	855	861	13		

- Molecule 15 is a protein called Crooked neck protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	595	Total	C	N	O	S	0	0
			4033	2511	759	753	10		

- Molecule 16 is a protein called Cwf15/Cwc15 cell cycle control protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	P	104	Total	C	N	O	0	0
			867	536	175	156		

- Molecule 17 is a protein called PPIase cyclophilin-type domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	80	Total	C	N	O	S	0	0
			644	402	121	120	1		

- Molecule 18 is a protein called PLRG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	344	Total	C	N	O	S	0	0
			2700	1705	488	490	17		

- Molecule 19 is a protein called Rbm22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	273	Total	C	N	O	S	0	0
			2136	1337	376	405	18		

- Molecule 20 is a protein called G10 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	171	Total	C	N	O	S	0	0
			1412	897	260	248	7		

- Molecule 21 is a protein called SKI-interacting protein SKIP SNW domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	R	260	Total	C	N	O	P	S	0	0
			1994	1251	361	377	2	3		

- Molecule 22 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	H	40	Total	C	N	O	P	0	0
			838	375	134	289	40		

- Molecule 23 is a protein called Peptidyl-prolyl cis-trans isomerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	155	Total	C	N	O	S	0	0
			1198	754	213	225	6		

- Molecule 24 is a protein called Prp17.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	487	Total	C	N	O	S	0	0
			2826	1721	553	549	3		

- Molecule 25 is a protein called Cdc5L.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	L	468	Total	C	N	O	S	0	0
			3795	2349	722	712	12		

- Molecule 26 is a protein called Pre-mRNA-splicing factor SPF27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	K	210	Total	C	N	O	S	0	0
			1688	1045	318	321	4		

- Molecule 27 is a protein called CWF21 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	U	26	Total	C	N	O	S	0	0
			191	119	34	36	2		

- Molecule 28 is a protein called MI domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	V	186	Total	C	N	O	S	0	0
			1020	621	198	200	1		

- Molecule 29 is a protein called Intron-binding protein aquarius.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Q	1299	Total	C	N	O		0	0
			6423	3825	1299	1299			

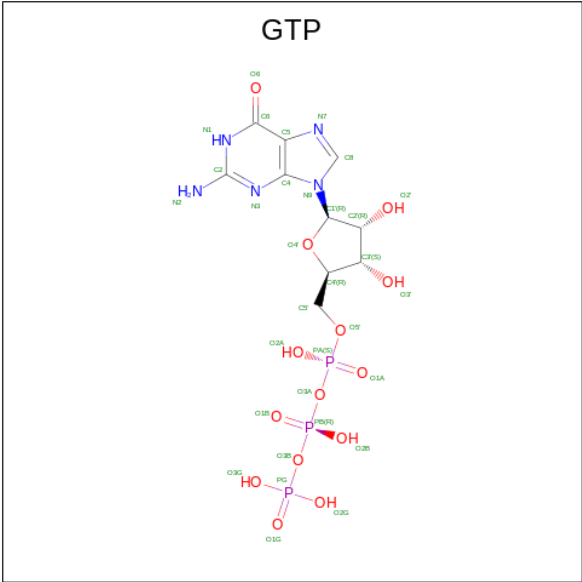
- Molecule 30 is a RNA chain called RNA (5'-R(P\*CP\*CP\*GP\*AP\*AP\*CP\*G)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
30	5	7	Total	C	N	O	P	0	0
			150	67	29	47	7		

- Molecule 31 is a RNA chain called RNA (173-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
31	3	34	Total	C	N	O	P	0	0
			694	311	111	238	34		

- Molecule 32 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>14</sub>P<sub>3</sub>).



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

- Molecule 33 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
33	C	1	Total	Mg	0
			1	1	
33	F	6	Total	Mg	0
			6	6	

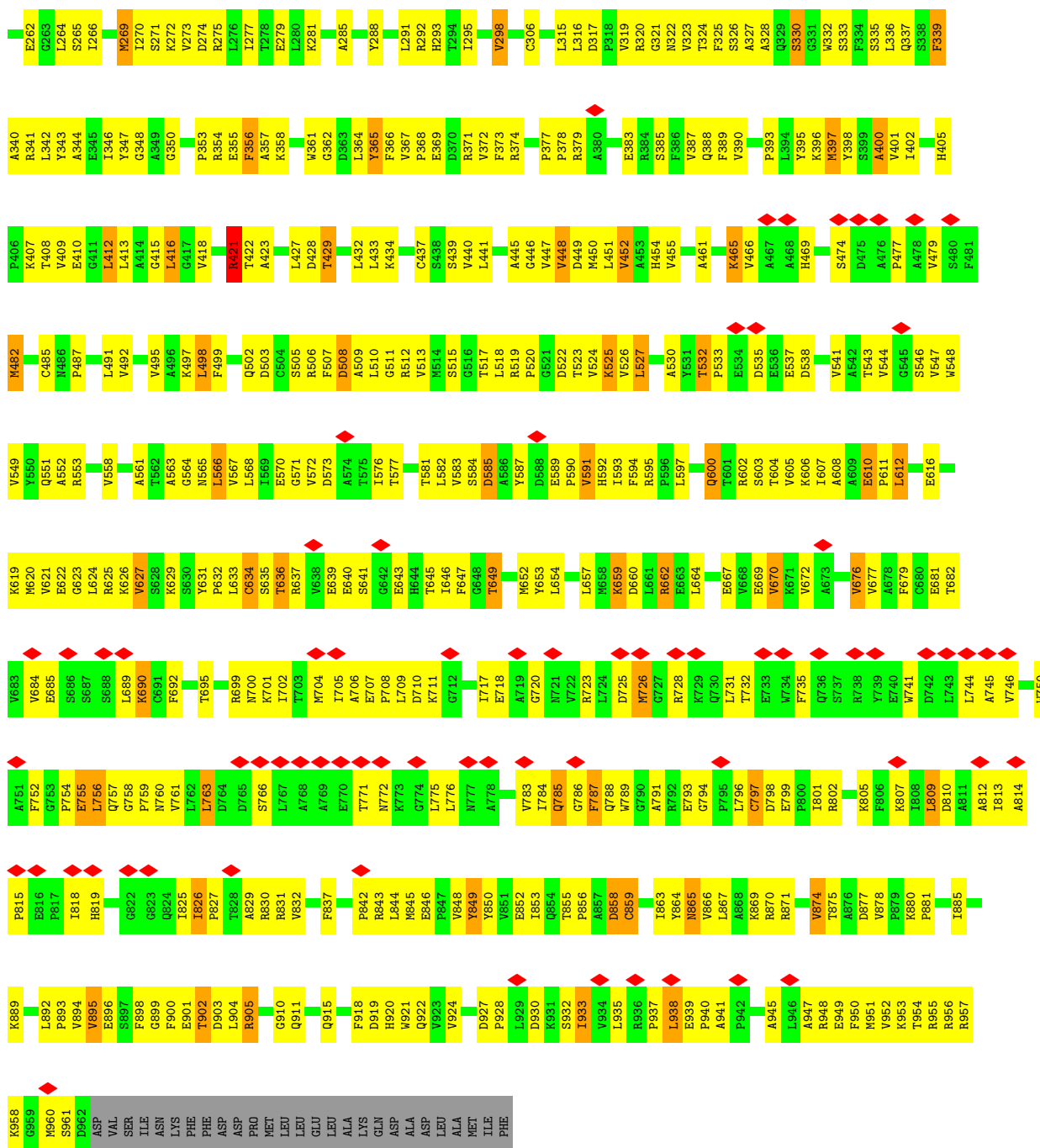
- Molecule 34 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
34	O	2	Total	Zn	0
			2	2	
34	N	1	Total	Zn	0
			1	1	









### • Molecule 4: U5-40K

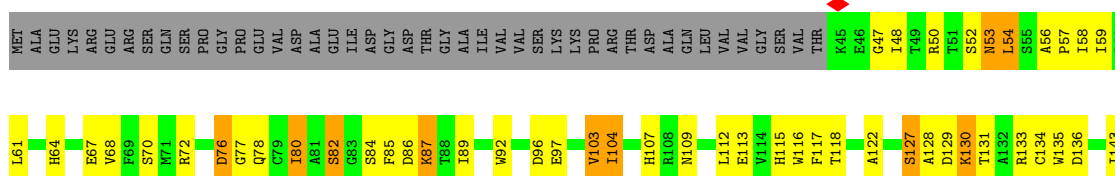
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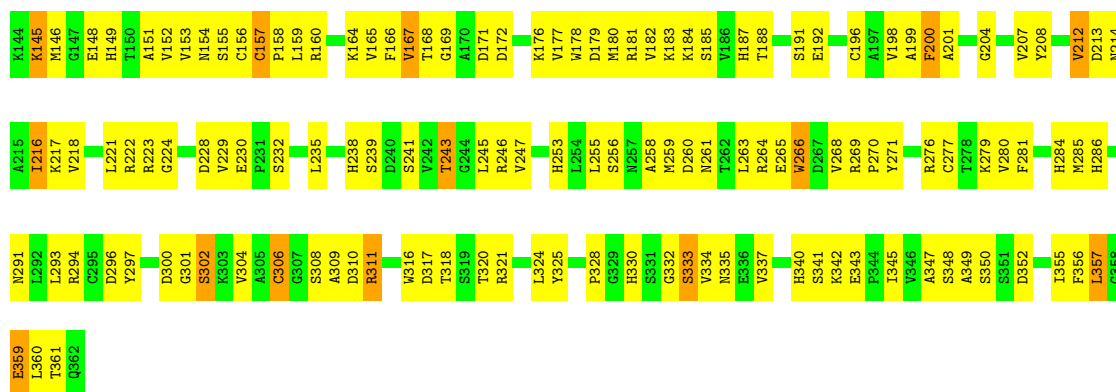
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44%

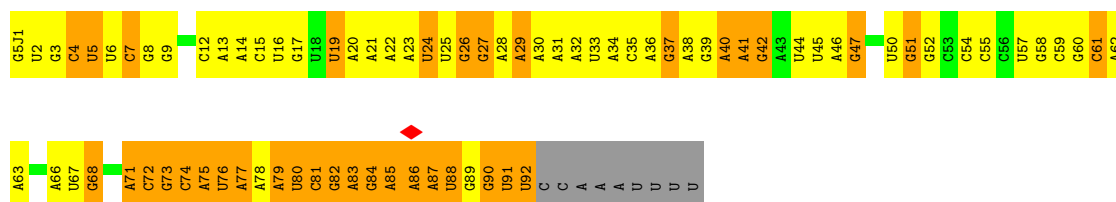
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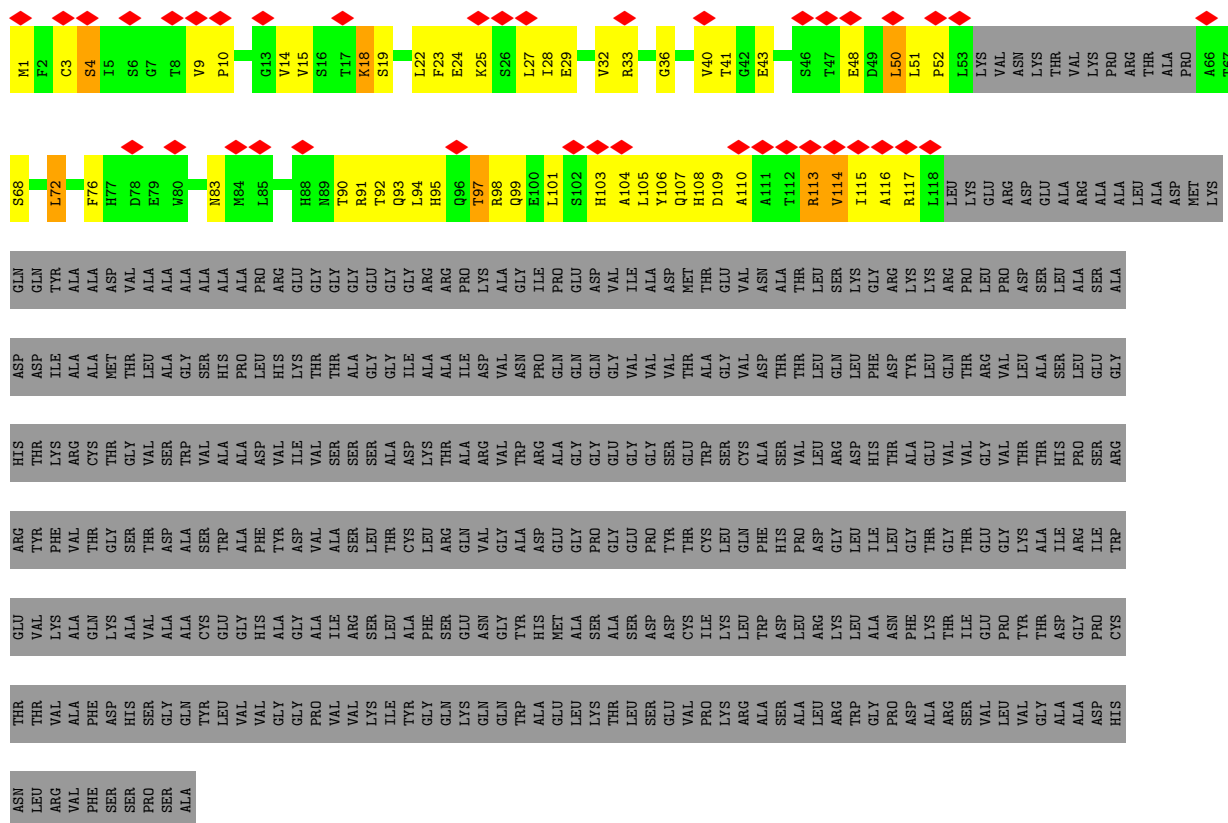




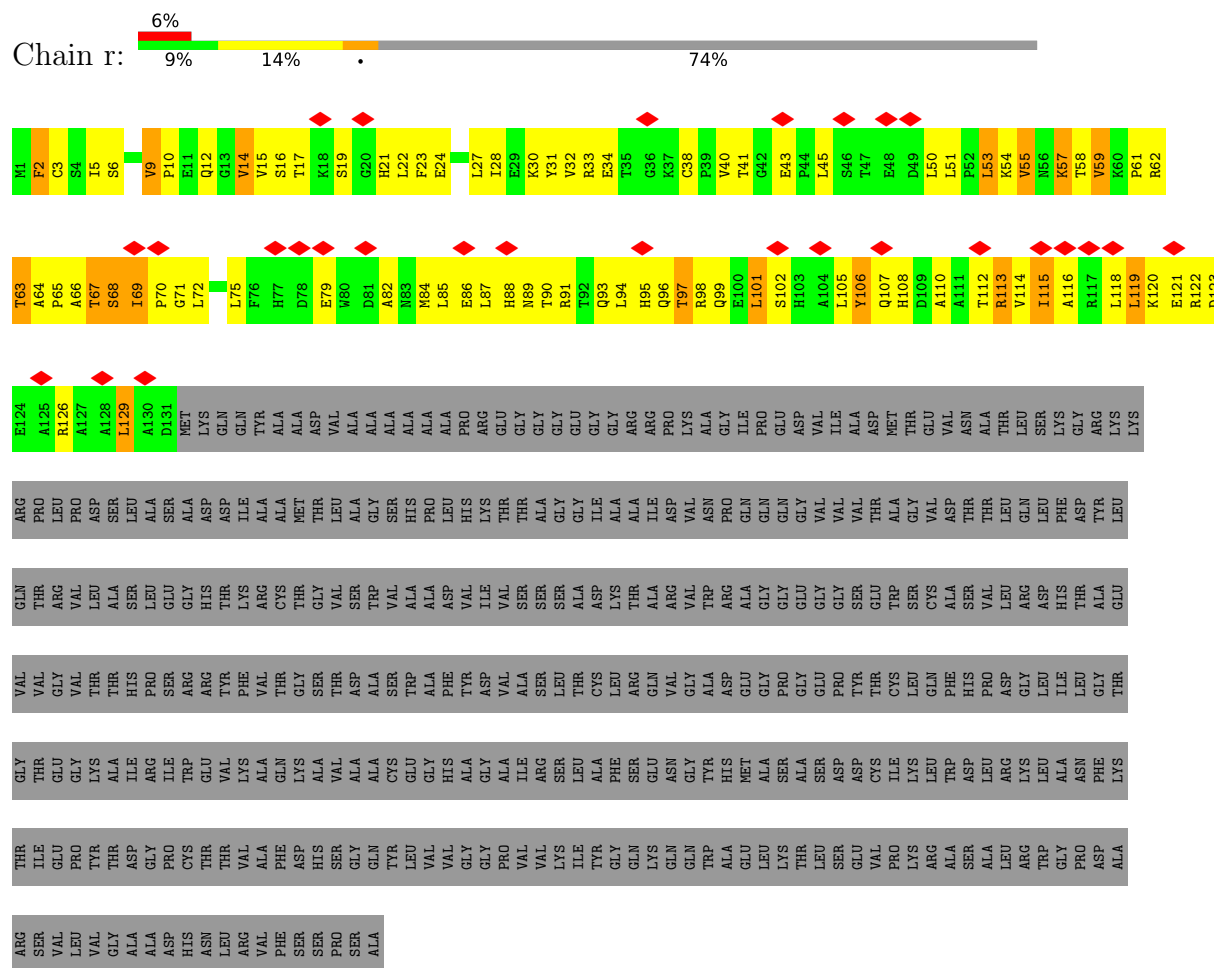
• Molecule 5: U6 snRNA



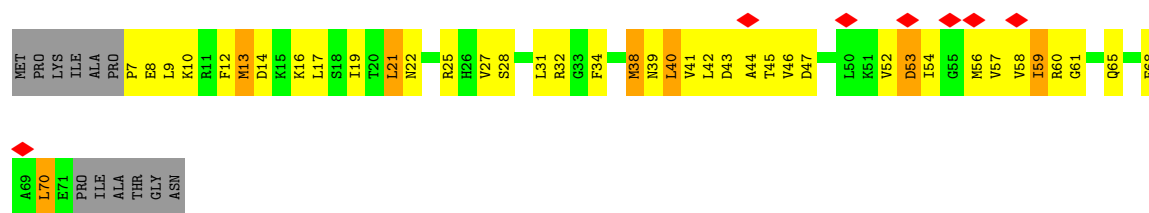
• Molecule 6: Pre-mRNA-processing factor 19



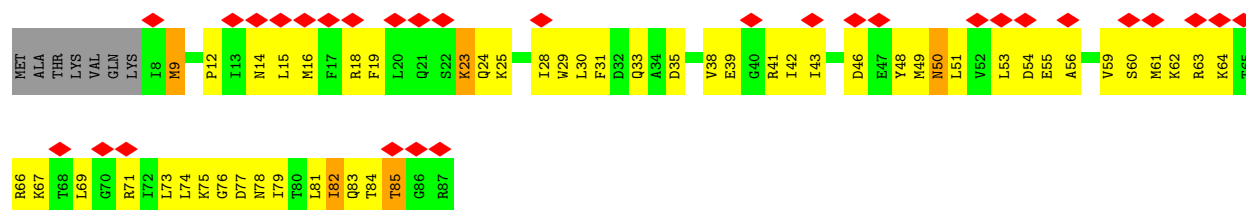
## ● Molecule 6: Pre-mRNA-processing factor 19



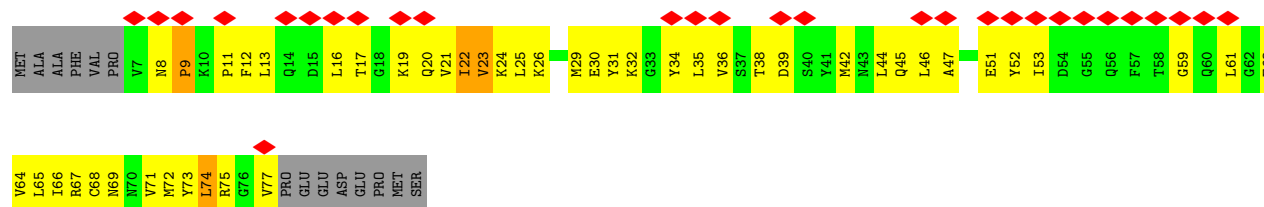




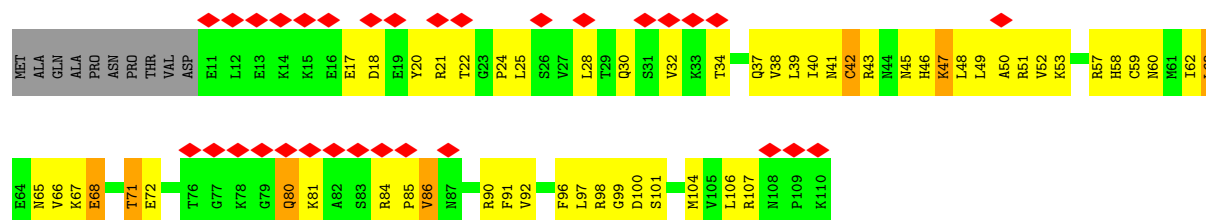
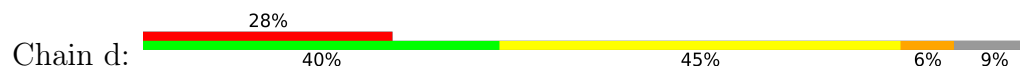
• Molecule 9: Small nuclear ribonucleoprotein E



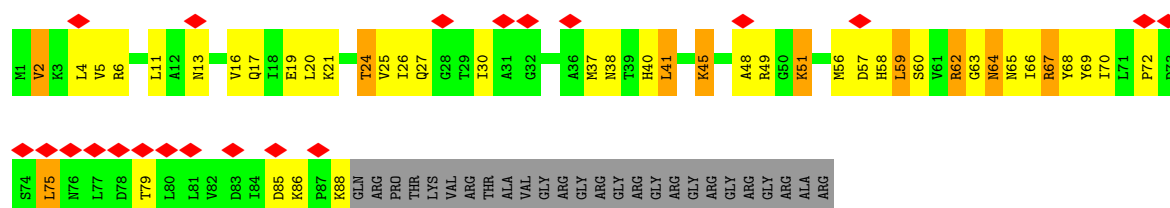
• Molecule 10: Sm protein F



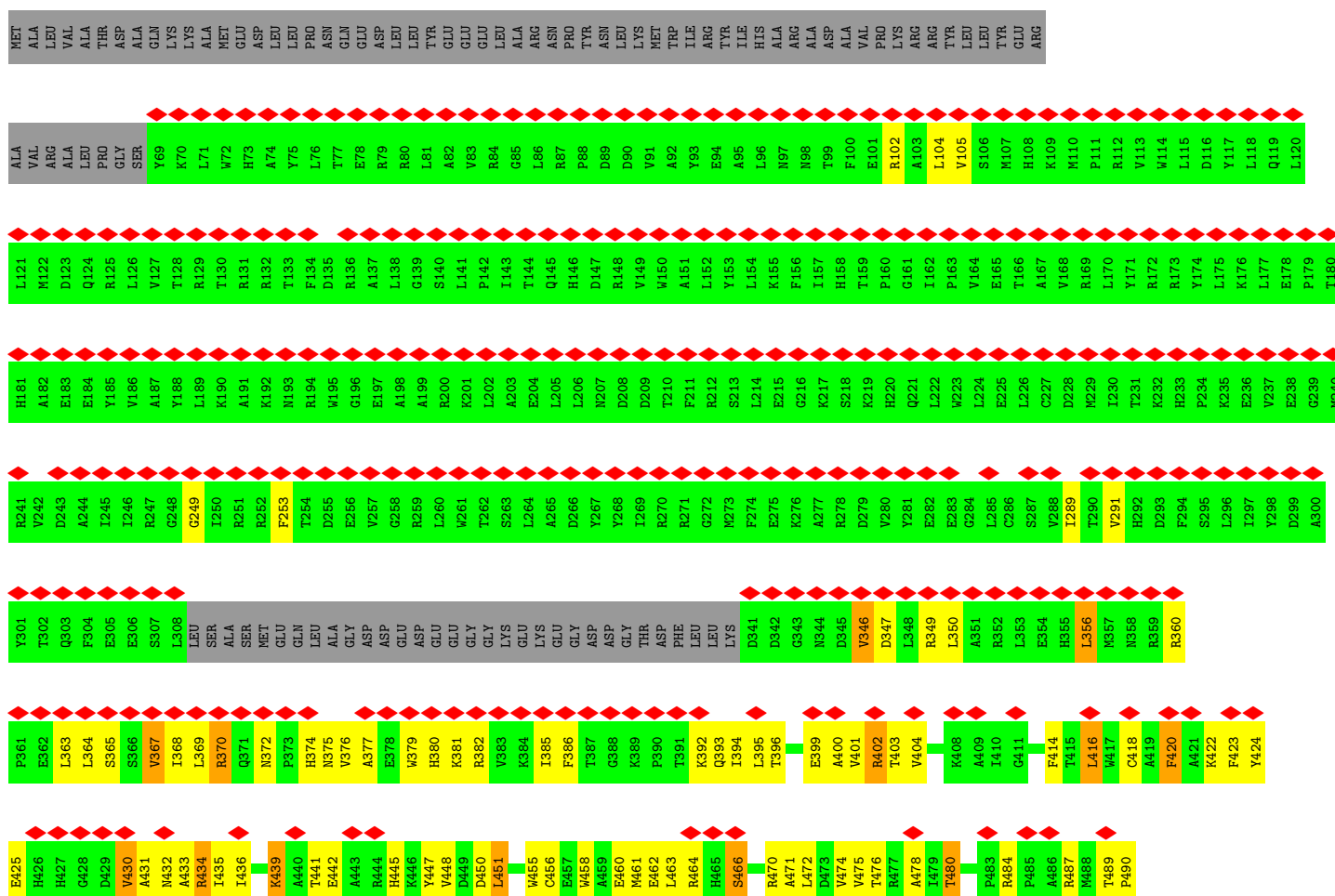
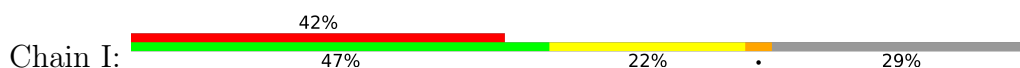
• Molecule 11: Small nuclear ribonucleoprotein Sm D2

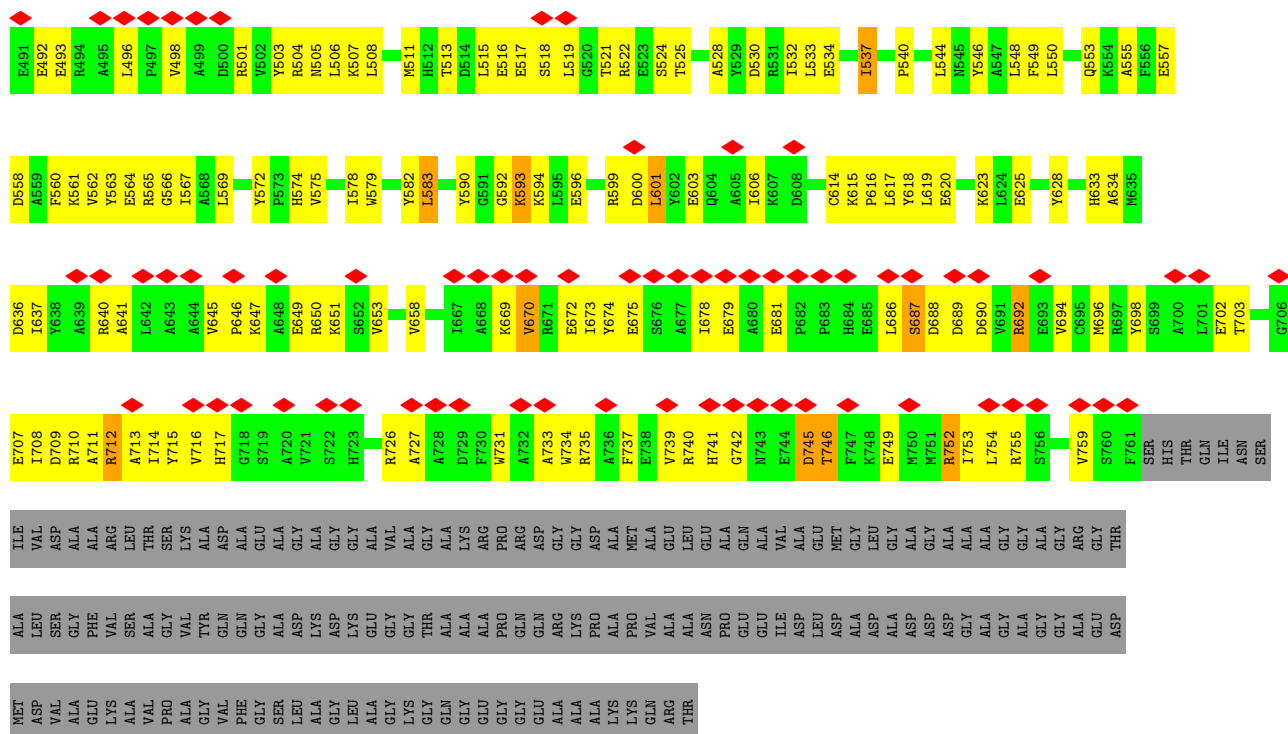


• Molecule 12: Small nuclear ribonucleoprotein Sm D1

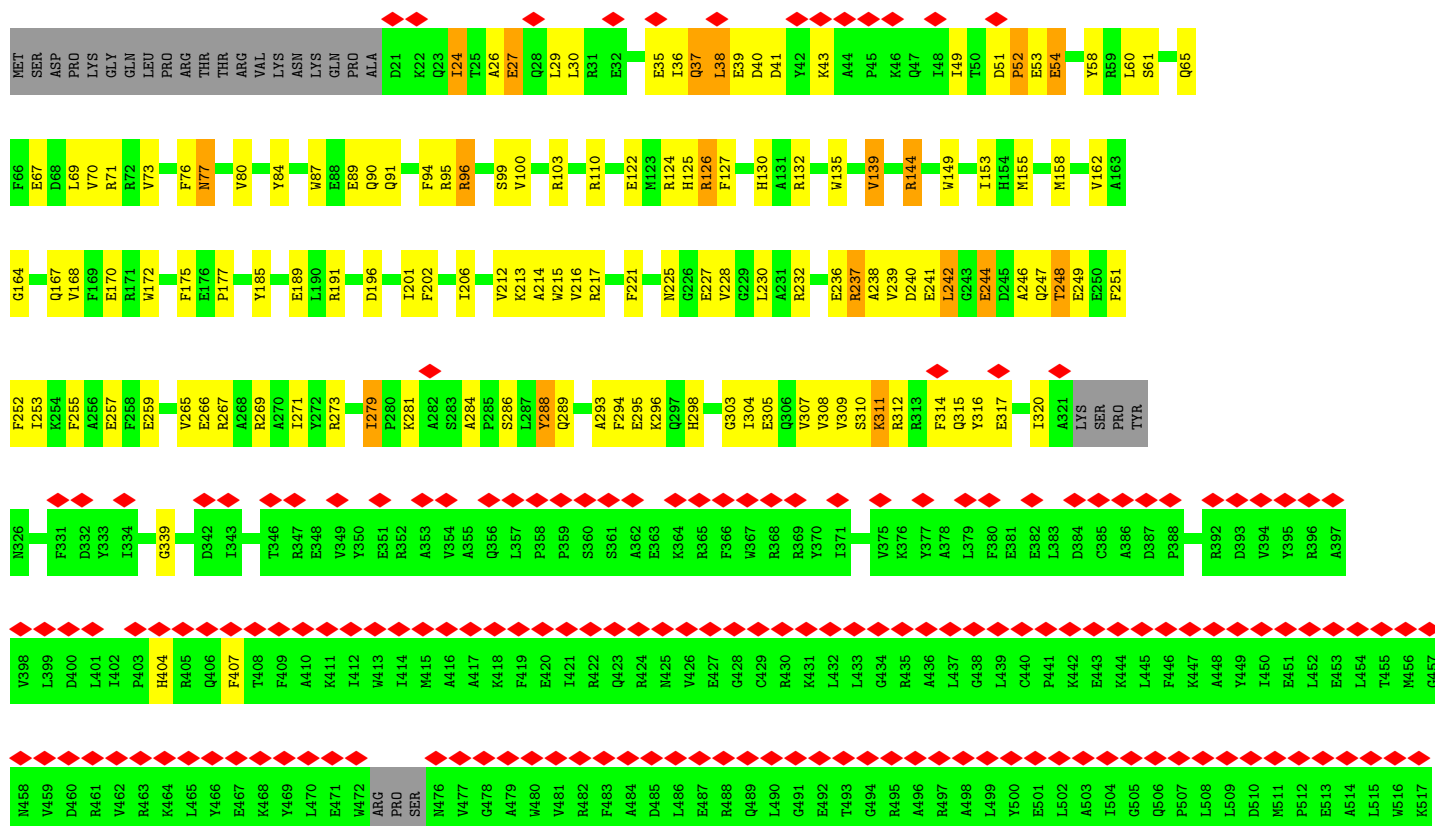


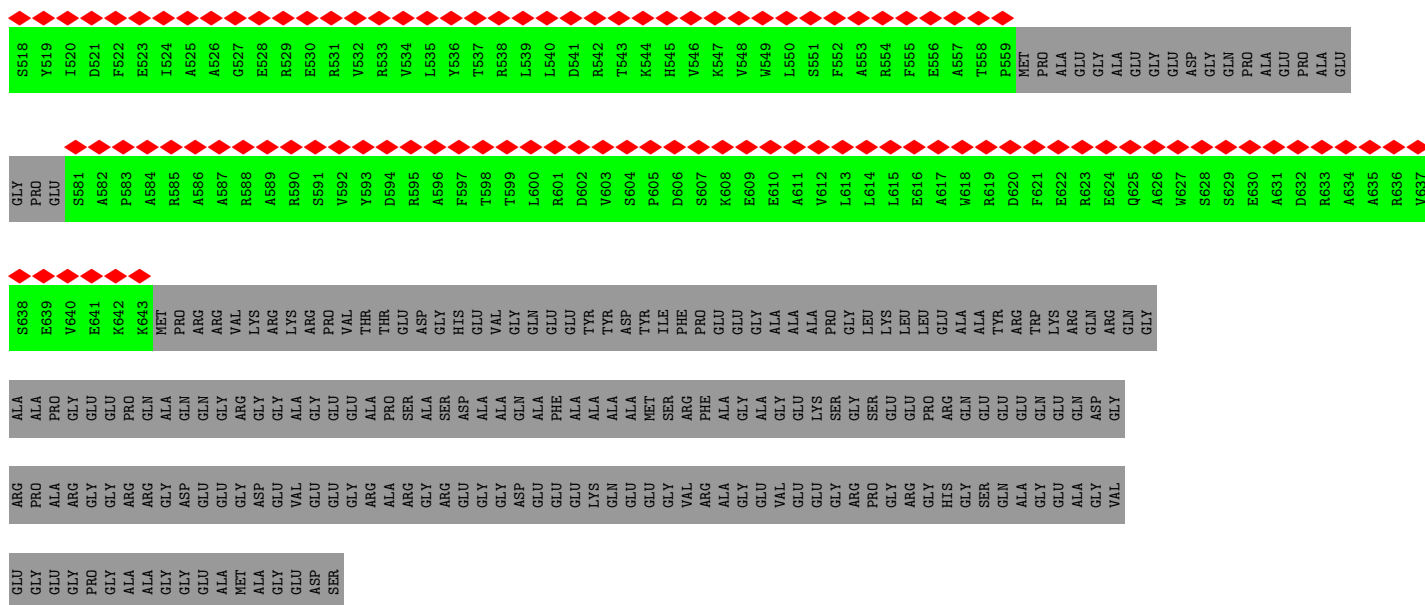
Chain b:



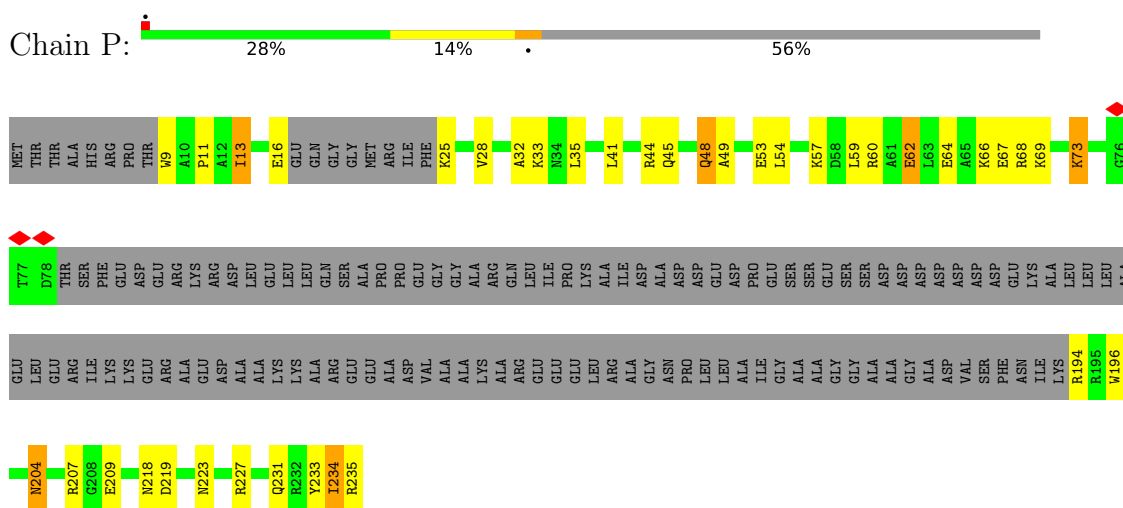


### • Molecule 15: Crooked neck protein

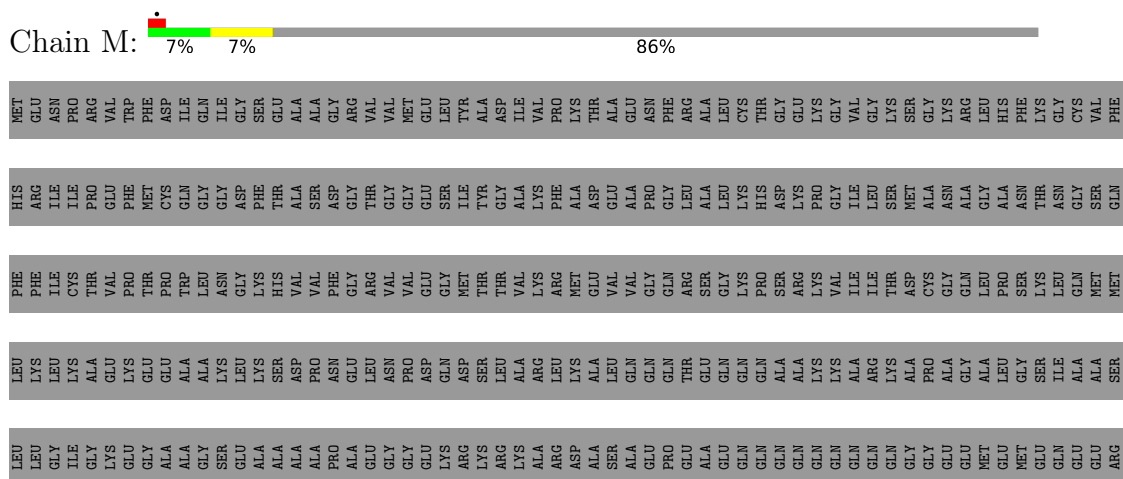


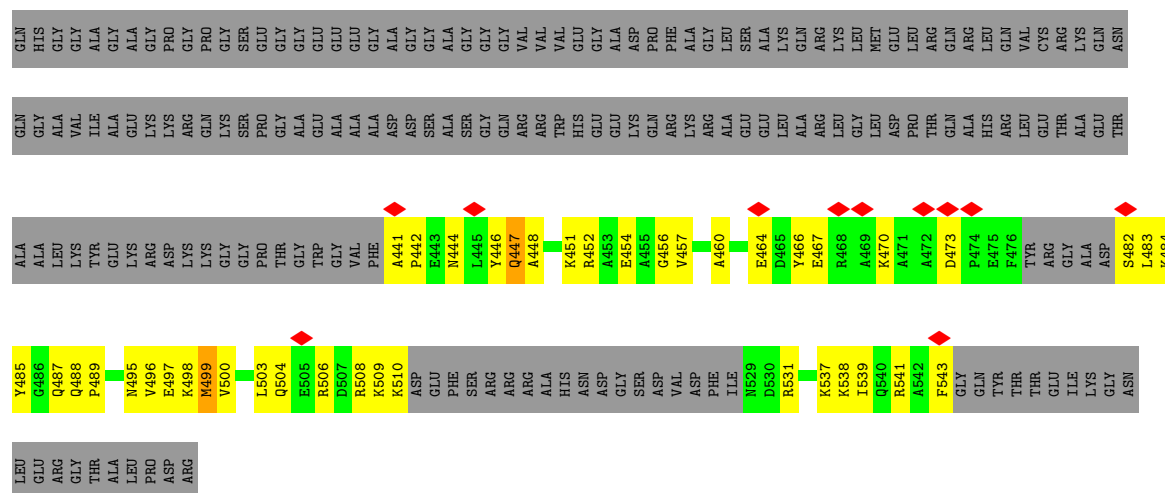


- Molecule 16: Cwf15/Cwc15 cell cycle control protein

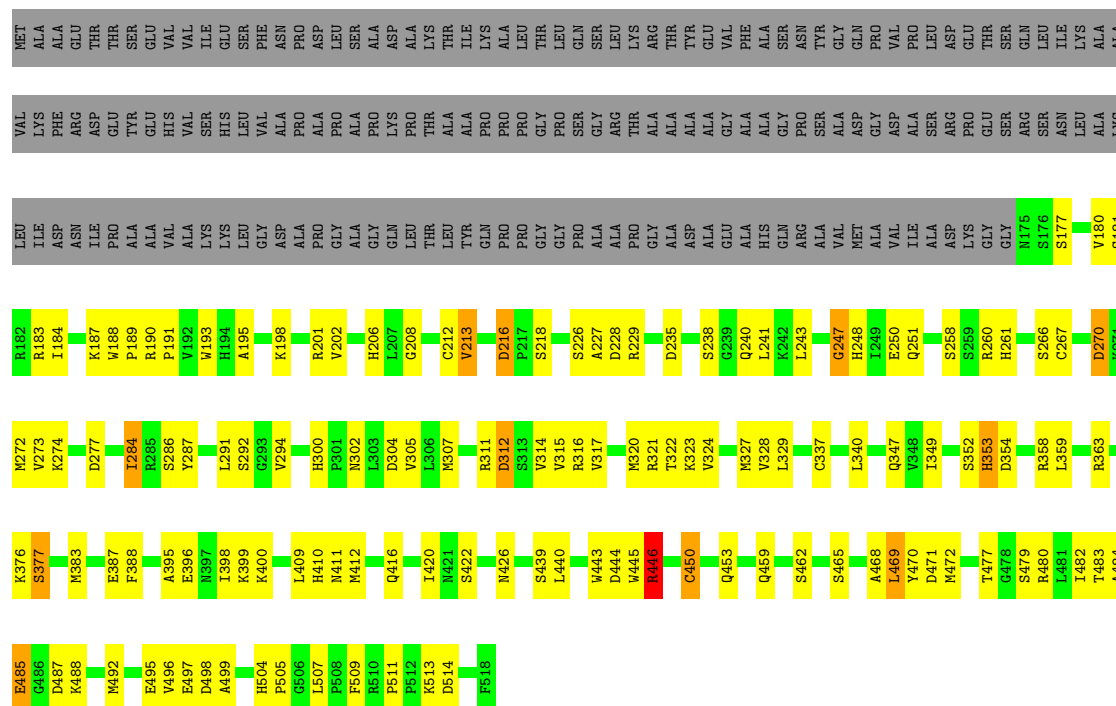


- Molecule 17: PPIase cyclophilin-type domain-containing protein

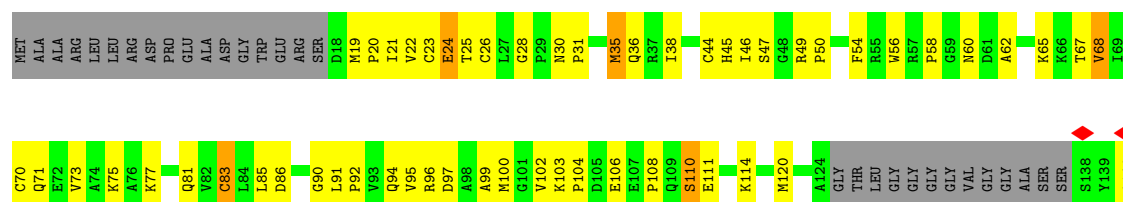




### • Molecule 18: PLRG1



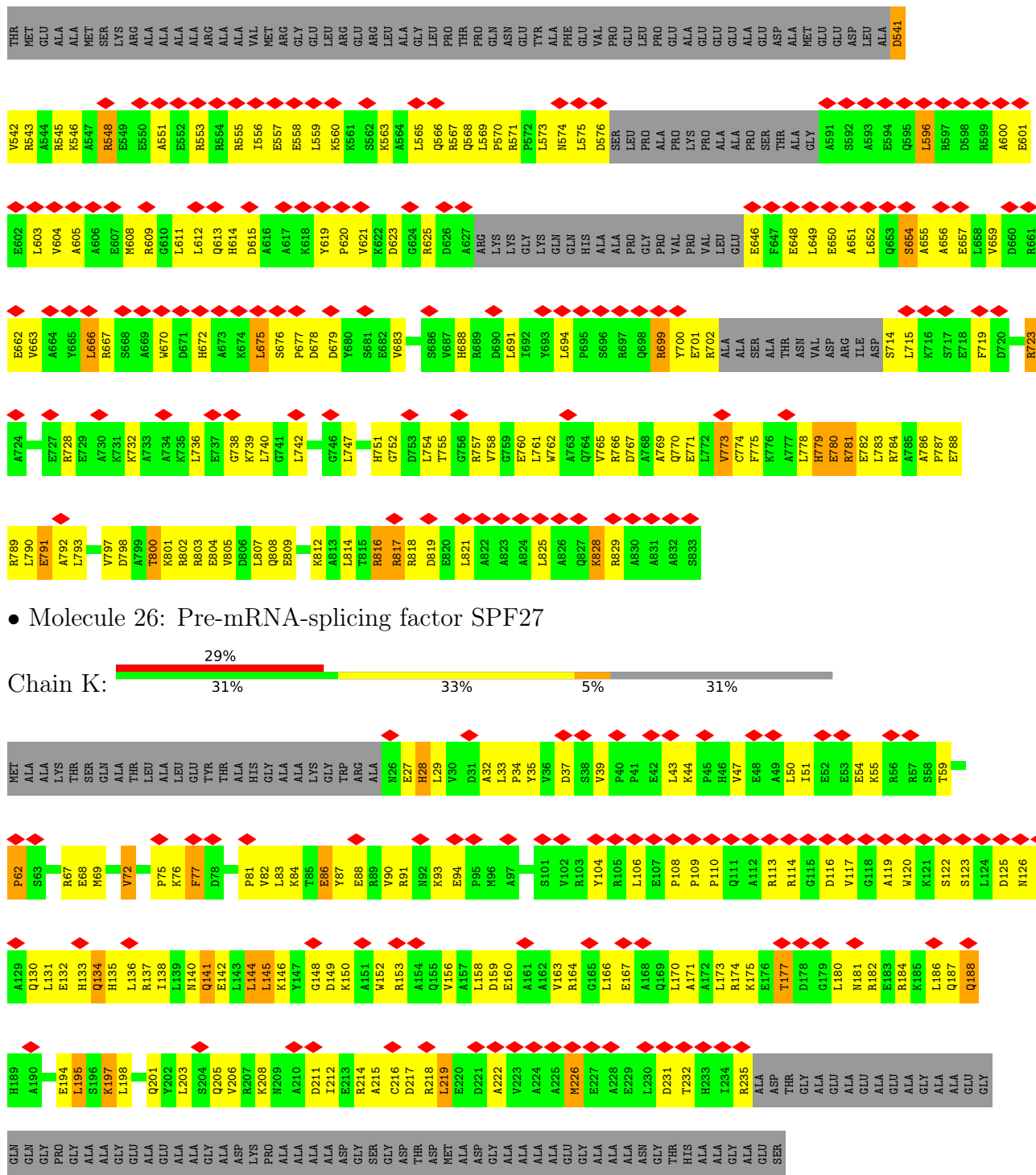
### • Molecule 19: Rbm22





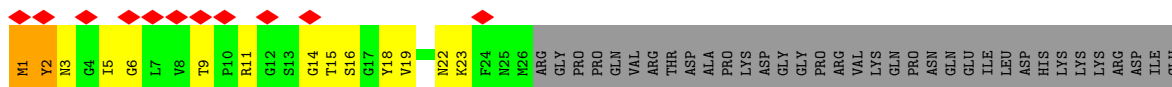






• Molecule 26: Pre-mRNA-splicing factor SPF27

Chain K: 96%

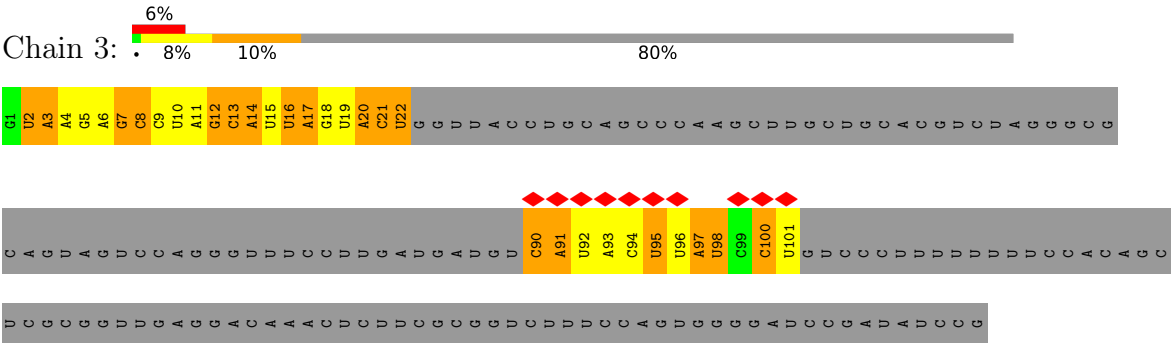












## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	518369	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50.00	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.593	Depositor
Minimum map value	-1.565	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.038	Depositor
Recommended contour level	0.08	Depositor
Map size ( $\text{\AA}$ )	404.80002, 404.80002, 404.80002	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.92, 0.92, 0.92	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, SEP, GTP, G5J, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.80	2/15581 (0.0%)	0.72	5/21167 (0.0%)
2	B	0.62	0/2024	0.55	0/3144
3	C	0.36	0/7126	0.61	5/9683 (0.1%)
4	E	0.31	0/2496	0.61	0/3382
5	F	0.77	0/2188	0.67	0/3409
6	q	0.25	0/847	0.58	0/1148
6	r	0.30	0/1040	0.67	1/1411 (0.1%)
6	s	0.25	0/580	0.60	0/784
6	t	0.28	0/514	0.67	0/698
7	a	0.23	0/716	0.60	0/960
8	g	0.23	0/516	0.54	0/691
9	e	0.23	0/667	0.56	0/891
10	f	0.20	0/567	0.52	0/764
11	d	0.19	0/821	0.51	0/1097
12	c	0.25	0/691	0.57	0/933
13	b	0.25	0/792	0.70	0/1059
14	I	0.21	0/4712	0.50	0/6427
15	J	0.56	0/4092	0.61	0/5574
16	P	0.70	0/882	0.63	0/1173
17	M	0.29	0/654	0.64	0/874
18	T	1.15	2/2773 (0.1%)	0.89	1/3765 (0.0%)
19	O	0.46	0/2179	0.64	0/2944
20	N	0.77	0/1446	0.64	0/1944
21	R	0.61	0/2020	0.66	0/2736
22	H	0.64	0/932	0.64	1/1447 (0.1%)
23	S	0.38	0/1224	0.58	0/1652
24	W	0.47	1/2852 (0.0%)	0.72	5/3908 (0.1%)
25	L	0.42	0/3847	0.63	0/5158
26	K	0.25	0/1717	0.63	1/2320 (0.0%)
27	U	0.26	0/194	0.62	0/259
28	V	0.21	0/1023	0.48	0/1413
29	Q	0.33	0/6411	0.74	9/8913 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
30	5	0.62	0/167	0.56	0/258
31	3	0.33	0/771	0.67	0/1193
All	All	0.57	5/75062 (0.0%)	0.66	28/103179 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	11
3	C	0	1
6	s	0	1
6	t	0	1
25	L	0	1
28	V	0	1
All	All	0	16

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	W	89	PRO	N-CA	17.32	1.69	1.47
1	A	1002	CYS	CA-C	-8.30	1.41	1.52
1	A	769	LYS	CA-C	-6.62	1.40	1.52
18	T	446	ARG	C-N	-6.53	1.24	1.33
18	T	426	ASN	CB-CG	-5.79	1.37	1.52

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	Q	786	ILE	CA-C-N	18.58	138.90	119.76
29	Q	786	ILE	C-N-CA	18.58	138.90	119.76
24	W	88	GLY	CA-C-N	15.21	138.85	119.84
24	W	88	GLY	C-N-CA	15.21	138.85	119.84
3	C	400	ALA	N-CA-C	-12.27	98.31	113.28
18	T	187	LYS	N-CA-C	9.39	123.43	112.72
29	Q	1110	PHE	CA-C-N	8.18	127.77	118.85
29	Q	1110	PHE	C-N-CA	8.18	127.77	118.85
29	Q	787	PRO	N-CA-C	7.59	122.98	111.14
29	Q	788	ALA	N-CA-C	-7.06	95.76	110.80
24	W	89	PRO	CA-N-CD	-6.95	102.28	112.00
3	C	421	ARG	N-CA-C	6.85	120.95	112.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	Q	1134	PHE	CA-C-N	6.80	126.76	120.03
29	Q	1134	PHE	C-N-CA	6.80	126.76	120.03
26	K	62	PRO	N-CA-CB	6.68	110.26	103.25
22	H	22	C	O5'-P-OP1	-6.31	89.07	108.00
24	W	89	PRO	N-CA-C	-6.03	100.04	112.47
3	C	415	GLY	N-CA-C	-5.76	99.53	113.18
3	C	400	ALA	CA-C-N	-5.70	115.63	122.35
3	C	400	ALA	C-N-CA	-5.70	115.63	122.35
24	W	91	HIS	CB-CA-C	5.50	121.01	110.17
1	A	965	LEU	CA-C-N	5.48	132.01	121.54
1	A	965	LEU	C-N-CA	5.48	132.01	121.54
1	A	1004	VAL	CA-C-N	-5.35	108.75	121.80
1	A	1004	VAL	C-N-CA	-5.35	108.75	121.80
29	Q	758	TYR	N-CA-C	5.22	117.90	107.62
6	r	97	THR	N-CA-C	-5.05	105.86	111.36
1	A	866	THR	CB-CA-C	5.01	117.34	109.27

There are no chirality outliers.

All (16) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1004	VAL	Peptide
1	A	1005	LYS	Peptide
1	A	1045	PHE	Peptide
1	A	1338	TYR	Peptide
1	A	1470	ASP	Peptide
1	A	1480	ILE	Peptide
1	A	1701	TRP	Peptide
1	A	1751	TYR	Peptide
1	A	1783	PHE	Peptide
1	A	532	LYS	Peptide
1	A	686	GLY	Peptide
3	C	69	GLU	Peptide
25	L	670	TRP	Peptide
28	V	703	PHE	Peptide
6	s	67	THR	Peptide
6	t	67	THR	Peptide

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	15194	0	14471	679	0
2	B	1817	0	922	67	0
3	C	6973	0	6995	505	0
4	E	2441	0	2371	154	0
5	F	1985	0	983	93	0
6	q	831	0	826	51	0
6	r	1021	0	1024	116	0
6	s	570	0	554	59	0
6	t	504	0	489	45	0
7	a	705	0	724	58	0
8	g	512	0	536	51	0
9	e	660	0	693	48	0
10	f	559	0	565	46	0
11	d	810	0	843	58	0
12	c	684	0	737	38	0
13	b	780	0	808	50	0
14	I	4629	0	3948	190	0
15	J	4033	0	3189	136	0
16	P	867	0	857	35	0
17	M	644	0	633	44	0
18	T	2700	0	2652	90	0
19	O	2136	0	2104	142	0
20	N	1412	0	1410	53	0
21	R	1994	0	2005	106	0
22	H	838	0	425	37	0
23	S	1198	0	1185	88	0
24	W	2826	0	1876	138	0
25	L	3795	0	3825	298	0
26	K	1688	0	1678	184	0
27	U	191	0	188	19	0
28	V	1020	0	596	27	0
29	Q	6423	0	2986	54	0
30	5	150	0	78	6	0
31	3	694	0	355	53	0
32	C	32	0	12	9	0
33	C	1	0	0	1	0
33	F	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	N	1	0	0	0	0
34	O	2	0	0	0	0
All	All	73326	0	63543	3163	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 23.

All (3163) 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)
29:Q:787:PRO:CB	29:Q:790:SER:CB	1.89	1.51
24:W:57:LYS:HD3	26:K:186:LEU:CD1	1.39	1.50
29:Q:1103:ALA:CB	29:Q:1126:PRO:CB	1.91	1.47
24:W:54:ASN:HD21	26:K:182:ARG:CZ	1.28	1.44
24:W:89:PRO:N	24:W:89:PRO:CA	1.69	1.43
1:A:290:LEU:CD2	1:A:468:LEU:HD12	1.58	1.33
19:O:143:ARG:CZ	23:S:113:TRP:HZ3	1.41	1.32
19:O:103:LYS:CE	25:L:234:ARG:HH11	1.41	1.31
24:W:57:LYS:CD	26:K:186:LEU:HD11	1.58	1.31
24:W:54:ASN:HD21	26:K:182:ARG:NH2	1.29	1.30
1:A:449:GLU:HB2	1:A:450:PRO:CD	1.61	1.29
19:O:103:LYS:CD	25:L:234:ARG:NH1	1.94	1.28
29:Q:1103:ALA:HB2	29:Q:1126:PRO:CB	1.53	1.28
6:t:68:SER:O	6:t:72:LEU:HB2	1.28	1.27
26:K:173:LEU:O	26:K:177:THR:HG22	1.19	1.26
24:W:54:ASN:ND2	26:K:182:ARG:NH2	1.84	1.26
19:O:103:LYS:HD3	25:L:234:ARG:NH1	1.48	1.25
19:O:143:ARG:CZ	23:S:113:TRP:CZ3	2.19	1.24
1:A:290:LEU:HD22	1:A:468:LEU:CD1	1.68	1.23
14:I:105:VAL:O	29:Q:1329:TYR:CB	1.87	1.23
24:W:51:LEU:HD11	26:K:181:ASN:ND2	1.52	1.22
19:O:99:ALA:HB1	19:O:145:ASN:ND2	1.56	1.19
19:O:143:ARG:NH2	23:S:112:PRO:HD2	1.58	1.19
19:O:143:ARG:NH2	23:S:110:PRO:O	1.77	1.18
25:L:167:LYS:HA	25:L:171:ARG:NH2	1.60	1.17
26:K:173:LEU:O	26:K:177:THR:CG2	1.91	1.17
25:L:167:LYS:CA	25:L:171:ARG:HH21	1.61	1.13
29:Q:1103:ALA:HB3	29:Q:1126:PRO:CB	1.66	1.13
3:C:465:LYS:O	3:C:469:HIS:HB2	1.49	1.12
25:L:167:LYS:CA	25:L:171:ARG:NH2	2.13	1.11
19:O:140:ALA:O	24:W:93:TYR:HA	1.48	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:I:105:VAL:C	29:Q:1329:TYR:CB	2.24	1.10
1:A:449:GLU:CB	1:A:450:PRO:CD	2.29	1.09
19:O:143:ARG:HH22	23:S:112:PRO:HD2	0.99	1.09
24:W:54:ASN:ND2	26:K:182:ARG:CZ	2.11	1.07
19:O:151:LEU:HD12	19:O:217:VAL:HG11	1.37	1.06
1:A:449:GLU:CB	1:A:450:PRO:HD3	1.83	1.05
14:I:105:VAL:HA	29:Q:1330:THR:N	1.70	1.05
15:J:94:PHE:HB2	25:L:233:THR:HG23	1.40	1.04
19:O:103:LYS:CD	25:L:234:ARG:HH11	1.65	1.03
1:A:290:LEU:HD22	1:A:468:LEU:HD12	1.25	1.03
29:Q:790:SER:O	29:Q:1510:ALA:HB2	1.58	1.03
15:J:35:GLU:O	15:J:37:GLN:HG2	1.58	1.02
6:r:98:ARG:NH1	26:K:72:VAL:HB	1.73	1.02
5:F:3:G:N7	24:W:171:ARG:NH2	2.07	1.02
1:A:290:LEU:HD21	1:A:468:LEU:HD12	1.39	1.02
6:r:93:GLN:O	6:r:97:THR:HG23	1.61	1.00
19:O:151:LEU:CD1	19:O:217:VAL:HG11	1.91	1.00
19:O:103:LYS:CE	25:L:234:ARG:NH1	2.22	1.00
6:s:106:TYR:HD1	24:W:49:LEU:CD1	1.74	0.99
24:W:91:HIS:CD2	24:W:92:PRO:HD2	1.97	0.99
3:C:418:VAL:HG21	3:C:439:SER:HB2	1.44	0.99
1:A:447:GLY:N	3:C:371:ARG:NH1	2.10	0.98
26:K:170:LEU:O	26:K:174:ARG:HG2	1.62	0.98
3:C:147:HIS:C	32:C:1001:GTP:O1B	2.07	0.98
1:A:447:GLY:CA	3:C:371:ARG:NH1	2.26	0.97
15:J:238:ALA:O	15:J:242:LEU:HB2	1.64	0.97
18:T:353:HIS:HA	18:T:377:SER:HB2	1.46	0.97
2:B:40:C:H42	2:B:46:A:H61	1.12	0.97
15:J:130:HIS:CE1	25:L:229:GLU:HB2	1.98	0.97
24:W:57:LYS:CD	26:K:186:LEU:CD1	2.26	0.96
3:C:732:THR:HG22	3:C:746:VAL:HG11	1.48	0.96
3:C:339:PHE:HE1	3:C:390:VAL:HA	1.31	0.95
3:C:626:LYS:O	3:C:629:LYS:HB2	1.65	0.95
19:O:143:ARG:NH2	23:S:113:TRP:CZ3	2.35	0.94
19:O:143:ARG:HH22	23:S:112:PRO:CD	1.78	0.94
19:O:143:ARG:NE	23:S:113:TRP:CZ3	2.35	0.94
1:A:852:GLN:HG2	1:A:1088:HIS:HB3	1.47	0.94
19:O:103:LYS:HE2	25:L:234:ARG:HH11	1.29	0.94
6:s:106:TYR:HD1	24:W:49:LEU:HD11	1.31	0.93
14:I:105:VAL:HA	29:Q:1330:THR:CB	1.98	0.93
1:A:533:LYS:NZ	2:B:59:G:N7	2.16	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:L:814:LEU:HD21	26:K:218:ARG:HB2	1.51	0.92
1:A:1655:MET:HG3	1:A:1675:LYS:HD2	1.50	0.92
1:A:448:VAL:O	3:C:347:TYR:CZ	2.23	0.91
1:A:449:GLU:CG	1:A:450:PRO:HD2	2.01	0.91
29:Q:1120:LYS:H	29:Q:1181:ALA:HB3	1.33	0.91
19:O:103:LYS:CD	25:L:234:ARG:HH12	1.81	0.91
1:A:526:ARG:NH1	2:B:54:G:N7	2.19	0.91
1:A:448:VAL:O	3:C:347:TYR:CE2	2.24	0.91
1:A:447:GLY:HA2	3:C:371:ARG:NH1	1.86	0.91
6:r:106:TYR:CE2	26:K:55:LYS:HD2	2.06	0.91
25:L:167:LYS:CB	25:L:171:ARG:HH21	1.83	0.91
24:W:51:LEU:HD11	25:L:775:PHE:CE1	1.97	0.90
6:s:106:TYR:CD1	24:W:49:LEU:CD1	2.55	0.90
15:J:90:GLN:OE1	25:L:248:LEU:O	1.89	0.90
6:s:115:ILE:HD11	26:K:47:VAL:HG13	1.53	0.90
1:A:449:GLU:HB2	1:A:450:PRO:HD3	0.92	0.90
3:C:793:GLU:OE1	3:C:830:ARG:NH2	2.05	0.90
16:P:204:ASN:HB3	16:P:207:ARG:HD3	1.55	0.89
3:C:546:SER:H	3:C:570:GLU:HB2	1.39	0.87
1:A:290:LEU:CD2	1:A:468:LEU:CD1	2.37	0.87
6:t:68:SER:O	6:t:72:LEU:CB	2.20	0.87
15:J:158:MET:HE1	17:M:456:GLY:HA3	1.57	0.87
25:L:779:HIS:O	25:L:783:LEU:HB2	1.73	0.87
14:I:647:LYS:HG3	14:I:686:LEU:HA	1.55	0.86
24:W:57:LYS:HD3	26:K:186:LEU:HD12	1.56	0.86
3:C:491:LEU:HA	3:C:515:SER:O	1.74	0.86
19:O:99:ALA:HB1	19:O:145:ASN:HD21	1.40	0.86
11:d:48:LEU:HG	11:d:68:GLU:HB3	1.56	0.86
19:O:99:ALA:HB1	19:O:145:ASN:HD22	1.35	0.86
8:g:41:VAL:HG12	8:g:58:VAL:HG22	1.56	0.86
1:A:735:THR:O	1:A:740:ARG:NH1	2.08	0.86
6:r:102:SER:HA	26:K:69:MET:CE	2.05	0.86
19:O:60:ASN:ND2	24:W:128:HIS:O	2.09	0.86
14:I:346:VAL:HA	14:I:349:ARG:HD2	1.58	0.85
1:A:219:HIS:NE2	1:A:1750:ASP:OD1	2.09	0.85
1:A:727:ARG:NH2	5:F:57:U:OP2	2.09	0.85
1:A:1521:HIS:HD2	1:A:1524:HIS:CD2	1.94	0.85
27:U:23:LYS:H	28:V:674:HIS:HD2	1.22	0.85
1:A:1346:GLN:HE21	1:A:1399:ILE:HG23	1.41	0.85
6:t:69:ILE:HG13	6:t:70:PRO:HD3	1.58	0.85
18:T:312:ASP:OD2	18:T:316:ARG:NH1	2.10	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:448:VAL:HG23	3:C:347:TYR:CD2	2.12	0.84
3:C:193:SER:OG	33:C:1002:MG:MG	1.17	0.84
19:O:140:ALA:O	24:W:92:PRO:O	1.95	0.84
5:F:73:G:H4'	5:F:74:C:H5'	1.60	0.84
19:O:143:ARG:NE	23:S:113:TRP:CH2	2.46	0.84
23:S:30:ASN:HD22	23:S:69:ILE:HG12	1.40	0.84
19:O:91:LEU:HD21	19:O:151:LEU:O	1.76	0.84
5:F:42:G:N7	25:L:32:ARG:NE	2.26	0.84
3:C:397:MET:HA	3:C:397:MET:HE3	1.60	0.83
3:C:870:ARG:NH2	3:C:898:PHE:O	2.09	0.83
6:r:102:SER:OG	26:K:69:MET:HE2	1.79	0.83
13:b:55:LYS:H	13:b:55:LYS:HD2	1.41	0.83
1:A:822:ARG:NH1	1:A:964:ASP:OD2	2.11	0.83
5:F:29:A:H61	31:3:11:A:H2'	1.43	0.83
13:b:39:ASN:HA	13:b:73:LEU:O	1.77	0.83
8:g:16:LYS:HD3	8:g:70:LEU:HD13	1.61	0.83
29:Q:790:SER:C	29:Q:1510:ALA:HB2	2.04	0.83
15:J:94:PHE:HB2	25:L:233:THR:CG2	2.07	0.83
1:A:1227:ARG:NH2	16:P:209:GLU:OE1	2.11	0.83
1:A:471:ALA:O	1:A:476:ASN:ND2	2.10	0.83
5:F:72:C:H4'	5:F:73:G:H5''	1.59	0.83
4:E:154:ASN:ND2	4:E:171:ASP:OD1	2.11	0.82
6:r:112:THR:HG21	26:K:27:GLU:CD	2.04	0.82
3:C:241:VAL:HG12	3:C:269:MET:HG2	1.60	0.82
4:E:243:THR:O	4:E:294:ARG:NH1	2.12	0.82
15:J:58:TYR:CE1	25:L:248:LEU:HD22	2.14	0.82
17:M:541:ARG:NH1	22:H:14:C:O2'	2.11	0.82
19:O:151:LEU:CD1	19:O:217:VAL:CG1	2.57	0.82
1:A:1301:LEU:HD22	1:A:1348:LEU:HG	1.61	0.82
25:L:167:LYS:C	25:L:171:ARG:HH21	1.87	0.82
15:J:24:ILE:HG22	15:J:29:LEU:HD11	1.60	0.82
18:T:216:ASP:OD2	18:T:218:SER:OG	1.98	0.82
24:W:54:ASN:OD1	26:K:182:ARG:NE	2.13	0.81
1:A:957:GLU:OE2	25:L:46:LYS:NZ	2.13	0.81
1:A:290:LEU:HD22	1:A:468:LEU:HD11	1.61	0.81
3:C:621:VAL:O	3:C:625:ARG:N	2.13	0.81
6:r:98:ARG:NH1	26:K:72:VAL:CB	2.43	0.81
19:O:140:ALA:O	24:W:93:TYR:CA	2.29	0.81
25:L:167:LYS:CB	25:L:171:ARG:NH2	2.41	0.81
25:L:165:LYS:HD2	25:L:168:ARG:HD2	1.62	0.81
19:O:262:ARG:HB2	19:O:271:PHE:HB3	1.63	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:447:GLY:CA	3:C:371:ARG:HH12	1.92	0.80
1:A:1702:ASN:ND2	1:A:1716:TYR:O	2.13	0.80
1:A:469:LEU:HD11	3:C:402:ILE:HD13	1.62	0.80
25:L:167:LYS:HB3	25:L:171:ARG:NH2	1.96	0.80
1:A:145:ARG:HH22	21:R:205:LYS:HA	1.46	0.80
8:g:60:ARG:HD2	9:e:79:ILE:HB	1.62	0.80
25:L:167:LYS:HB3	25:L:171:ARG:HH21	1.45	0.80
31:3:5:G:H2'	31:3:6:A:C8	2.17	0.80
19:O:103:LYS:HE3	25:L:234:ARG:HD3	1.64	0.80
1:A:947:ARG:NH2	25:L:126:GLU:OE2	2.14	0.80
17:M:483:LEU:HG	21:R:85:VAL:HG21	1.61	0.80
1:A:1725:TRP:CZ3	1:A:1727:ASP:HB2	2.16	0.80
12:c:6:ARG:NH2	12:c:86:LYS:O	2.15	0.80
1:A:315:LEU:HD13	1:A:369:GLU:HG3	1.64	0.79
14:I:369:LEU:HD11	14:I:382:ARG:HG2	1.63	0.79
4:E:238:HIS:NE2	4:E:256:SER:OG	2.15	0.79
21:R:86:ASN:HB3	21:R:88:LYS:HE3	1.65	0.79
2:B:12:G:H22	2:B:67:U:H3	1.29	0.79
1:A:449:GLU:HG3	1:A:450:PRO:HD2	1.65	0.79
16:P:49:ALA:HB2	18:T:218:SER:HB3	1.65	0.79
1:A:371:LYS:HB3	1:A:379:ASN:HD21	1.47	0.79
6:s:106:TYR:CD1	24:W:49:LEU:HD11	2.16	0.79
19:O:26:CYS:SG	19:O:65:LYS:NZ	2.56	0.79
3:C:699:ARG:HB3	3:C:814:ALA:HB2	1.65	0.79
1:A:552:ASP:OD2	1:A:629:ARG:NH1	2.16	0.78
3:C:74:TYR:OH	16:P:219:ASP:OD2	2.00	0.78
25:L:575:LEU:HD11	25:L:612:LEU:HB3	1.65	0.78
6:r:106:TYR:CE2	26:K:55:LYS:CD	2.66	0.78
16:P:28:VAL:HB	21:R:158:PRO:HB3	1.65	0.78
17:M:539:ILE:O	17:M:543:PHE:N	2.13	0.78
1:A:1275:ASP:HB3	1:A:1343:LEU:HD11	1.66	0.78
3:C:532:THR:OG1	3:C:535:ASP:O	1.99	0.78
6:s:87:LEU:O	6:s:90:THR:OG1	2.02	0.78
1:A:1188:ASN:O	1:A:1215:ARG:NH1	2.17	0.78
1:A:1702:ASN:ND2	1:A:1717:ASP:O	2.17	0.78
4:E:89:ILE:HB	4:E:104:ILE:HG12	1.66	0.78
19:O:151:LEU:HD11	19:O:217:VAL:CG1	2.14	0.78
25:L:175:LEU:H	25:L:175:LEU:HD12	1.49	0.78
16:P:219:ASP:O	16:P:223:ASN:ND2	2.17	0.78
24:W:51:LEU:CD1	26:K:181:ASN:ND2	2.42	0.78
2:B:42:U:H3	30:5:-1:G:H22	1.31	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:r:30:LYS:O	6:r:34:GLU:HB2	1.84	0.77
9:e:16:MET:HG3	9:e:49:MET:HE1	1.64	0.77
3:C:446:GLY:O	3:C:450:MET:HB2	1.84	0.77
6:t:107:GLN:HE21	25:L:608:MET:HE1	1.49	0.77
1:A:279:ASN:ND2	1:A:284:LYS:O	2.16	0.77
6:r:102:SER:CB	26:K:69:MET:HE2	2.14	0.77
21:R:257:LEU:HD13	25:L:23:MET:HG2	1.66	0.77
31:3:90:C:O2'	31:3:91:A:OP1	2.01	0.77
3:C:635:SER:HB2	3:C:647:PHE:HB2	1.67	0.77
15:J:94:PHE:HE2	25:L:236:MET:SD	2.08	0.77
1:A:262:VAL:HG11	1:A:296:LEU:HD13	1.67	0.77
14:I:599:ARG:NH1	14:I:600:ASP:OD2	2.18	0.77
6:s:106:TYR:CD1	24:W:49:LEU:HD13	2.19	0.77
3:C:148:HIS:N	32:C:1001:GTP:O1B	2.17	0.77
11:d:45:ASN:HA	11:d:47:LYS:HZ3	1.50	0.77
15:J:24:ILE:CG2	15:J:29:LEU:HD11	2.14	0.76
3:C:145:HIS:O	3:C:150:LYS:NZ	2.17	0.76
14:I:105:VAL:HA	29:Q:1330:THR:CA	2.16	0.76
25:L:167:LYS:O	25:L:171:ARG:NE	2.19	0.76
3:C:863:ILE:HD13	3:C:904:LEU:HD11	1.68	0.76
12:c:40:HIS:HE1	12:c:58:HIS:HB3	1.49	0.76
14:I:711:ALA:HA	14:I:714:ILE:HD12	1.65	0.76
19:O:103:LYS:HD3	25:L:234:ARG:HH12	1.39	0.76
25:L:54:ASP:HB3	25:L:57:ILE:HG13	1.64	0.76
10:f:21:VAL:HG21	10:f:35:LEU:HB2	1.68	0.76
1:A:1619:LEU:HD21	1:A:1626:MET:HG3	1.66	0.76
2:B:38:C:O2	27:U:11:ARG:NH2	2.19	0.76
10:f:45:GLN:HG3	11:d:24:PRO:HA	1.68	0.76
1:A:1244:ARG:O	1:A:1265:ARG:NH2	2.16	0.76
6:r:102:SER:HA	26:K:69:MET:HE2	1.65	0.76
23:S:53:MET:HE1	23:S:55:GLN:HB2	1.66	0.76
1:A:1205:ARG:H	1:A:1246:ASN:HD21	1.34	0.76
3:C:649:THR:O	3:C:849:TYR:OH	2.04	0.76
15:J:94:PHE:CE2	25:L:236:MET:SD	2.79	0.75
23:S:19:LEU:HD21	23:S:31:PHE:HB3	1.66	0.75
1:A:1084:LYS:NZ	22:H:27:A:OP1	2.17	0.75
6:r:38:CYS:N	6:r:43:GLU:O	2.19	0.75
1:A:921:ASN:OD1	1:A:924:GLN:NE2	2.19	0.75
1:A:185:ILE:HD11	21:R:201:LEU:HD11	1.69	0.75
3:C:265:SER:OG	3:C:454:HIS:O	2.05	0.75
6:q:94:LEU:HD13	6:t:94:LEU:HA	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:707:GLU:HB2	3:C:805:LYS:HB2	1.68	0.75
3:C:339:PHE:CE1	3:C:390:VAL:HA	2.19	0.75
3:C:254:ARG:NH1	3:C:600:GLN:OE1	2.20	0.74
5:F:15:C:H5''	20:N:116:THR:HB	1.69	0.74
6:s:67:THR:O	6:s:71:GLY:N	2.19	0.74
14:I:105:VAL:O	29:Q:1329:TYR:C	2.30	0.74
22:H:20:G:N2	22:H:21:G:O6	2.19	0.74
1:A:1665:LEU:HA	1:A:1670:ILE:HD11	1.68	0.74
15:J:293:ALA:HA	15:J:296:LYS:HG2	1.69	0.74
19:O:235:TYR:OH	19:O:269:CYS:SG	2.40	0.74
1:A:259:ASP:OD1	1:A:298:ARG:NH1	2.15	0.74
4:E:263:LEU:HB3	4:E:281:PHE:HB2	1.70	0.74
4:E:265:GLU:OE2	4:E:297:TYR:OH	2.06	0.74
15:J:130:HIS:HE1	25:L:229:GLU:HB2	1.50	0.74
19:O:83:CYS:O	19:O:201:ARG:NH2	2.21	0.74
1:A:1521:HIS:HD2	1:A:1524:HIS:HD2	1.33	0.74
3:C:147:HIS:HA	32:C:1001:GTP:O3B	1.87	0.74
14:I:522:ARG:O	14:I:525:THR:OG1	2.06	0.74
3:C:482:MET:SD	3:C:515:SER:OG	2.46	0.74
1:A:1102:SER:HB3	1:A:1506:MET:HG3	1.67	0.74
1:A:1725:TRP:HZ3	1:A:1727:ASP:HB2	1.53	0.74
3:C:605:VAL:HA	3:C:677:VAL:HG12	1.67	0.74
4:E:216:ILE:HG23	4:E:235:LEU:HB2	1.67	0.74
22:H:12:G:H1'	22:H:13:G:H5'	1.70	0.74
1:A:1702:ASN:HA	1:A:1719:LYS:HB3	1.68	0.74
6:r:115:ILE:HD11	6:s:118:LEU:CD1	2.18	0.74
19:O:28:GLY:O	21:R:189:ARG:NH1	2.20	0.74
21:R:69:ASP:OD1	21:R:72:LYS:NZ	2.21	0.74
2:B:90:C:H42	10:f:42:MET:HB2	1.52	0.74
1:A:580:LEU:HD11	1:A:602:SER:HB2	1.70	0.73
10:f:67:ARG:NH1	11:d:59:CYS:SG	2.61	0.73
29:Q:807:GLN:CB	29:Q:1052:LEU:O	2.36	0.73
19:O:141:ALA:HA	24:W:92:PRO:HG2	1.69	0.73
1:A:96:TRP:O	1:A:100:ASN:ND2	2.21	0.73
1:A:1058:ASN:OD1	1:A:1059:ARG:NH1	2.22	0.73
25:L:167:LYS:HA	25:L:171:ARG:HH22	1.53	0.73
1:A:290:LEU:HD11	1:A:464:SER:OG	1.87	0.73
4:E:270:PRO:HG2	25:L:812:LYS:HD3	1.69	0.73
4:E:128:ALA:HA	4:E:152:VAL:HG13	1.69	0.73
18:T:469:LEU:HD21	18:T:483:THR:HB	1.70	0.73
19:O:144:PRO:HB2	19:O:149:GLN:NE2	2.03	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:190:ARG:HD2	3:C:652:MET:HE1	1.71	0.73
3:C:421:ARG:C	3:C:423:ALA:H	1.97	0.73
15:J:227:GLU:HB3	15:J:230:LEU:HB2	1.71	0.73
24:W:124:TYR:O	24:W:128:HIS:CB	2.36	0.73
1:A:824:ARG:NH1	1:A:830:THR:O	2.22	0.73
3:C:518:LEU:HD22	3:C:547:VAL:HG21	1.71	0.73
6:r:3:CYS:HB3	6:r:6:SER:HB2	1.71	0.73
29:Q:782:ASP:O	29:Q:786:ILE:O	2.07	0.73
4:E:115:HIS:NE2	4:E:156:CYS:O	2.21	0.73
3:C:146:LEU:HD11	3:C:192:MET:HE2	1.69	0.73
6:r:24:GLU:HB3	6:r:27:LEU:HB2	1.71	0.72
19:O:143:ARG:NE	23:S:113:TRP:HZ3	1.79	0.72
10:f:46:LEU:HD11	10:f:66:ILE:HG12	1.70	0.72
1:A:1342:VAL:HG13	1:A:1348:LEU:HD13	1.70	0.72
20:N:36:GLU:OE2	20:N:49:LYS:NZ	2.20	0.72
24:W:89:PRO:N	24:W:89:PRO:C	2.47	0.72
1:A:1448:ARG:HH11	1:A:1478:ARG:HH21	1.37	0.72
4:E:136:ASP:HB2	4:E:143:ILE:HD11	1.71	0.72
15:J:127:PHE:HA	25:L:229:GLU:OE2	1.90	0.72
25:L:557:GLU:HG2	25:L:560:LYS:HD2	1.69	0.72
1:A:145:ARG:NH2	21:R:205:LYS:HA	2.04	0.72
1:A:823:GLU:OE2	16:P:233:TYR:OH	2.07	0.72
10:f:16:LEU:HA	10:f:19:LYS:HE2	1.70	0.72
19:O:143:ARG:HE	23:S:113:TRP:HH2	1.36	0.72
1:A:97:ALA:HA	1:A:100:ASN:HD21	1.54	0.72
1:A:779:GLU:OE1	1:A:782:ARG:NH1	2.22	0.72
15:J:130:HIS:ND1	25:L:229:GLU:CB	2.53	0.72
17:M:539:ILE:HG21	21:R:259:LYS:HD3	1.71	0.72
26:K:33:LEU:HB3	26:K:188:GLN:HG3	1.70	0.72
1:A:855:GLN:NE2	1:A:1091:SER:H	1.88	0.72
1:A:1400:PRO:HA	1:A:1417:PHE:HB3	1.72	0.72
3:C:388:GLN:O	3:C:393:PRO:HD2	1.90	0.72
9:e:28:ILE:HD12	9:e:82:ILE:HD13	1.72	0.72
6:r:106:TYR:CZ	26:K:55:LYS:HD2	2.25	0.72
20:N:176:TRP:O	24:W:195:GLN:NE2	2.22	0.72
3:C:735:PHE:HB3	3:C:741:TRP:HB2	1.72	0.71
1:A:1475:SER:HA	1:A:1478:ARG:HD3	1.71	0.71
6:r:94:LEU:HD11	6:s:90:THR:HA	1.71	0.71
6:r:115:ILE:HG13	6:s:114:VAL:CG1	2.20	0.71
3:C:505:SER:O	3:C:626:LYS:NZ	2.21	0.71
3:C:846:GLU:OE1	3:C:922:GLN:NE2	2.22	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:f:20:GLN:HB3	10:f:77:VAL:HB	1.72	0.71
18:T:445:TRP:O	18:T:446:ARG:HB3	1.91	0.71
3:C:487:PRO:O	3:C:517:THR:OG1	2.07	0.71
1:A:1343:LEU:HA	28:V:667:PHE:CE1	2.25	0.71
25:L:58:LYS:O	25:L:90:ARG:NH1	2.24	0.71
6:r:115:ILE:O	6:r:115:ILE:HD13	1.90	0.71
12:c:63:GLY:HA2	12:c:66:ILE:HD12	1.73	0.71
1:A:368:THR:HB	27:U:1:MET:HE2	1.72	0.71
3:C:221:HIS:CE1	3:C:915:GLN:HE22	2.09	0.71
5:F:36:A:H2'	5:F:37:G:H8	1.55	0.71
3:C:342:LEU:HD23	3:C:342:LEU:C	2.16	0.70
3:C:684:VAL:HG21	3:C:843:ARG:HH11	1.56	0.70
3:C:794:GLY:HA3	3:C:801:ILE:HD11	1.73	0.70
8:g:16:LYS:HZ1	8:g:28:SER:HB3	1.56	0.70
24:W:86:VAL:HG23	24:W:87:LEU:H	1.57	0.70
31:3:12:G:O2'	31:3:13:C:OP1	2.08	0.70
3:C:418:VAL:CG2	3:C:439:SER:HB2	2.20	0.70
14:I:522:ARG:HD2	14:I:553:GLN:HE22	1.56	0.70
15:J:130:HIS:CE1	25:L:229:GLU:CB	2.73	0.70
1:A:1430:PRO:HD2	1:A:1538:VAL:HG23	1.72	0.70
26:K:109:PRO:O	26:K:114:ARG:NH1	2.25	0.70
29:Q:1571:ALA:HB2	29:Q:1746:GLN:HA	1.72	0.70
22:H:29:C:HO2'	22:H:30:A:H8	1.37	0.70
4:E:279:LYS:HG3	4:E:321:ARG:HD3	1.73	0.70
6:r:102:SER:CA	26:K:69:MET:HE2	2.22	0.70
15:J:91:GLN:HE22	25:L:248:LEU:HG	1.56	0.70
1:A:290:LEU:CD1	1:A:464:SER:OG	2.38	0.70
1:A:1425:GLU:C	1:A:1427:GLN:H	2.00	0.70
16:P:67:GLU:OE2	18:T:480:ARG:NH1	2.18	0.70
24:W:57:LYS:HD3	26:K:186:LEU:HD11	0.72	0.70
1:A:858:TYR:OH	1:A:1053:ASP:OD1	2.08	0.70
3:C:324:THR:HG22	3:C:335:SER:HB3	1.72	0.70
3:C:935:LEU:HD12	3:C:948:ARG:HH21	1.56	0.70
16:P:45:GLN:H	16:P:48:GLN:HG3	1.57	0.70
22:H:25:A:H5'	22:H:26:G:H5''	1.73	0.70
1:A:1665:LEU:HD11	1:A:1672:THR:HG22	1.73	0.70
3:C:611:PRO:HB3	3:C:620:MET:HG3	1.73	0.70
6:r:116:ALA:O	6:r:120:LYS:HD2	1.91	0.70
15:J:191:ARG:HD2	17:M:457:VAL:HG11	1.74	0.70
1:A:390:TYR:HB3	3:C:190:ARG:HG2	1.72	0.70
7:a:27:LEU:HG	7:a:29:SER:H	1.55	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:O:186:LEU:HD22	24:W:218:ILE:HG21	1.73	0.70
25:L:751:HIS:HB2	26:K:156:VAL:HG22	1.74	0.70
1:A:1354:LYS:NZ	1:A:1355:CYS:SG	2.64	0.69
14:I:414:PHE:HB3	14:I:450:ASP:HB3	1.73	0.69
15:J:247:GLN:HE22	15:J:279:ILE:HG13	1.57	0.69
3:C:723:ARG:HB2	3:C:726:MET:HG2	1.74	0.69
5:F:35:C:H3'	5:F:36:A:C8	2.27	0.69
24:W:57:LYS:CE	26:K:186:LEU:HD12	2.23	0.69
1:A:301:GLY:O	1:A:305:THR:N	2.24	0.69
1:A:855:GLN:HE22	1:A:1092:TYR:H	1.40	0.69
1:A:1147:HIS:HD2	1:A:1149:ILE:H	1.39	0.69
8:g:25:ARG:HH11	9:e:29:TRP:HE3	1.40	0.69
8:g:42:LEU:O	8:g:56:MET:HA	1.92	0.69
3:C:398:TYR:O	3:C:402:ILE:HG13	1.91	0.69
6:s:106:TYR:CE1	24:W:49:LEU:HD13	2.26	0.69
19:O:143:ARG:CZ	23:S:113:TRP:CH2	2.75	0.69
1:A:400:THR:OG1	3:C:281:LYS:NZ	2.22	0.69
1:A:1786:ILE:O	1:A:1790:VAL:N	2.21	0.69
6:r:19:SER:HB2	6:r:21:HIS:CD2	2.27	0.69
1:A:1287:GLU:HG3	28:V:795:GLY:HA2	1.75	0.69
1:A:1346:GLN:NE2	1:A:1399:ILE:HG23	2.07	0.69
15:J:58:TYR:HE1	25:L:248:LEU:HD22	1.56	0.69
1:A:1019:TRP:CD1	1:A:1253:MET:HE1	2.28	0.69
18:T:227:ALA:HA	18:T:251:GLN:HG2	1.73	0.69
21:R:99:GLN:HE22	23:S:138:GLN:HE22	1.41	0.69
25:L:172:GLU:CA	25:L:175:LEU:HD13	2.23	0.69
1:A:92:LYS:NZ	4:E:212:VAL:O	2.25	0.69
1:A:1198:TRP:HB3	1:A:1259:ARG:HH21	1.58	0.69
1:A:1417:PHE:HZ	28:V:674:HIS:CG	2.10	0.69
6:t:95:HIS:HA	6:t:98:ARG:HD3	1.75	0.69
21:R:274:ASN:HD22	21:R:276:LYS:H	1.40	0.69
24:W:57:LYS:CE	26:K:186:LEU:CD1	2.71	0.69
25:L:10:TRP:HB2	25:L:48:ARG:HH21	1.58	0.69
1:A:1787:LYS:O	1:A:1791:ILE:HB	1.93	0.69
6:r:63:THR:O	6:r:67:THR:OG1	2.10	0.69
7:a:69:ARG:HD3	7:a:72:ARG:HG2	1.73	0.69
1:A:1776:HIS:ND1	1:A:1798:MET:HG3	2.07	0.69
3:C:269:MET:HE2	3:C:326:SER:HB2	1.74	0.69
3:C:513:VAL:O	3:C:564:GLY:N	2.26	0.69
14:I:105:VAL:CA	29:Q:1330:THR:N	2.54	0.69
25:L:172:GLU:HA	25:L:175:LEU:HD13	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:363:ARG:HE	3:C:950:PHE:HZ	1.41	0.68
6:s:102:SER:HB2	25:L:774:CYS:HB3	1.74	0.68
18:T:292:SER:HB2	18:T:311:ARG:HB2	1.75	0.68
20:N:31:LYS:O	20:N:35:ASN:ND2	2.26	0.68
24:W:73:VAL:HG11	24:W:82:MET:HE2	1.74	0.68
25:L:179:ARG:HD2	25:L:179:ARG:C	2.18	0.68
1:A:899:ASP:OD1	1:A:985:TYR:OH	2.09	0.68
19:O:77:LYS:HZ2	19:O:203:TYR:HD1	1.42	0.68
1:A:171:GLN:NE2	1:A:247:LEU:O	2.27	0.68
1:A:1374:ARG:NH1	1:A:1627:HIS:O	2.24	0.68
3:C:285:ALA:HA	3:C:387:VAL:HG11	1.73	0.68
3:C:760:ASN:HD22	3:C:791:ALA:HB1	1.57	0.68
9:e:53:LEU:O	9:e:71:ARG:HA	1.93	0.68
24:W:49:LEU:HD22	24:W:49:LEU:N	2.07	0.68
25:L:175:LEU:HD12	25:L:175:LEU:N	2.07	0.68
1:A:1006:PRO:HD2	1:A:1106:GLN:HE22	1.59	0.68
2:B:15:G:H3'	2:B:16:A:H5''	1.75	0.68
3:C:871:ARG:HH22	3:C:893:PRO:HG2	1.58	0.68
6:r:75:LEU:O	6:r:79:GLU:HB2	1.92	0.68
19:O:91:LEU:HD23	19:O:213:MET:HE1	1.76	0.68
24:W:124:TYR:O	24:W:128:HIS:HB3	1.93	0.68
25:L:807:LEU:HB3	26:K:212:ILE:HG21	1.76	0.68
1:A:1147:HIS:O	1:A:1150:ARG:NH1	2.26	0.68
1:A:1682:LYS:NZ	1:A:1692:ASP:OD1	2.27	0.68
4:E:265:GLU:HB2	4:E:279:LYS:HB3	1.74	0.68
6:q:22:LEU:HD12	6:r:53:LEU:HD11	1.75	0.68
11:d:98:ARG:NE	11:d:100:ASP:OD2	2.24	0.68
10:f:30:GLU:HG2	10:f:52:TYR:HB2	1.76	0.68
22:H:39:A:N6	31:3:91:A:N1	2.42	0.68
6:q:1:MET:HA	6:r:55:VAL:HG23	1.76	0.68
6:r:110:ALA:C	26:K:54:GLU:CD	2.62	0.68
18:T:226:SER:HB3	18:T:228:ASP:OD1	1.94	0.68
24:W:106:PHE:HD2	24:W:107:VAL:HG22	1.58	0.68
3:C:383:GLU:HB3	3:C:387:VAL:HG21	1.76	0.68
23:S:58:ASP:OD2	23:S:61:GLY:N	2.27	0.68
1:A:449:GLU:CG	1:A:450:PRO:CD	2.67	0.68
22:H:16:U:H1'	22:H:17:U:H5'	1.75	0.68
1:A:1485:THR:HA	1:A:1488:GLN:HG3	1.76	0.67
3:C:66:VAL:HG22	21:R:276:LYS:HE2	1.75	0.67
11:d:18:ASP:HA	11:d:21:ARG:HB2	1.76	0.67
3:C:797:CYS:HB3	3:C:954:THR:HG21	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:S:153:ARG:HH21	23:S:155:ARG:HB3	1.58	0.67
15:J:242:LEU:HB3	15:J:246:ALA:HB2	1.76	0.67
25:L:779:HIS:CG	26:K:184:ARG:HG3	2.30	0.67
1:A:1416:HIS:HB2	27:U:5:ILE:HD13	1.75	0.67
3:C:649:THR:H	3:C:653:TYR:HD1	1.41	0.67
25:L:145:GLU:O	25:L:149:GLU:HB2	1.95	0.67
1:A:85:GLN:HG3	1:A:87:LYS:HD2	1.75	0.67
1:A:1367:LEU:HD12	1:A:1375:PHE:CZ	2.30	0.67
3:C:611:PRO:HD3	3:C:620:MET:HE3	1.75	0.67
3:C:798:ASP:OD2	3:C:955:ARG:NH2	2.28	0.67
25:L:175:LEU:H	25:L:175:LEU:CD1	2.07	0.67
1:A:447:GLY:N	3:C:371:ARG:HH11	1.88	0.67
1:A:1423:HIS:HB3	1:A:1427:GLN:HB3	1.76	0.67
12:c:64:ASN:OD1	12:c:65:ASN:ND2	2.27	0.67
2:B:65:U:H2'	2:B:66:U:O4'	1.95	0.67
6:t:67:THR:O	6:t:71:GLY:N	2.25	0.67
12:c:57:ASP:O	12:c:58:HIS:ND1	2.27	0.67
20:N:42:ARG:HB2	20:N:45:GLU:HG3	1.77	0.67
23:S:78:ILE:HG21	23:S:116:GLY:HA2	1.77	0.67
1:A:1265:ARG:O	1:A:1267:ALA:N	2.24	0.67
14:I:490:PRO:HA	14:I:493:GLU:HB2	1.77	0.67
1:A:1661:PHE:HE1	1:A:1789:LEU:HD21	1.59	0.67
3:C:240:LEU:HD11	3:C:252:THR:HG23	1.77	0.67
6:r:115:ILE:HG13	6:s:114:VAL:HG11	1.75	0.67
14:I:374:HIS:HA	14:I:404:VAL:HG22	1.76	0.67
16:P:60:ARG:O	16:P:64:GLU:HG2	1.95	0.67
18:T:422:SER:HB2	18:T:472:MET:HG2	1.76	0.67
25:L:779:HIS:CE1	26:K:184:ARG:HG3	2.30	0.67
6:q:24:GLU:HB3	6:q:27:LEU:HB2	1.77	0.67
6:r:67:THR:HG22	26:K:140:ASN:HB3	1.77	0.67
4:E:68:VAL:O	4:E:335:ASN:ND2	2.25	0.66
24:W:49:LEU:HD22	24:W:49:LEU:H	1.60	0.66
1:A:1765:VAL:HG22	1:A:1781:ASN:H	1.61	0.66
3:C:152:THR:OG1	32:C:1001:GTP:O1A	2.14	0.66
1:A:308:PRO:HB3	1:A:496:GLN:HB3	1.77	0.66
1:A:992:PHE:HA	1:A:1498:ARG:HG3	1.76	0.66
1:A:1729:GLN:NE2	1:A:1766:MET:SD	2.66	0.66
3:C:258:GLN:HG2	3:C:600:GLN:HG3	1.77	0.66
19:O:103:LYS:HE3	25:L:234:ARG:HH11	1.54	0.66
15:J:69:LEU:O	15:J:73:VAL:HG12	1.95	0.66
25:L:543:ARG:HA	25:L:546:LYS:HE2	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1797:ILE:HG23	1:A:1801:ASN:HD21	1.58	0.66
3:C:520:PRO:HB3	3:C:546:SER:HA	1.77	0.66
3:C:625:ARG:HH22	3:C:629:LYS:HE2	1.61	0.66
6:t:68:SER:OG	26:K:82:VAL:HA	1.95	0.66
7:a:66:LEU:HG	7:a:68:ILE:HG12	1.78	0.66
4:E:67:GLU:O	4:E:85:PHE:N	2.26	0.66
14:I:422:LYS:HE3	14:I:464:ARG:HH22	1.60	0.66
19:O:143:ARG:NH2	23:S:113:TRP:CH2	2.64	0.66
13:b:30:ARG:NH2	13:b:32:MET:SD	2.69	0.66
14:I:400:ALA:HB1	14:I:416:LEU:HD11	1.78	0.66
18:T:213:VAL:HG23	18:T:471:ASP:HB3	1.77	0.66
20:N:22:VAL:HG13	24:W:194:LEU:HD13	1.77	0.66
24:W:91:HIS:HD2	24:W:92:PRO:HD2	1.53	0.66
24:W:376:PHE:HA	24:W:386:PHE:HA	1.77	0.66
1:A:1210:ASP:OD2	1:A:1243:SER:OG	2.13	0.66
3:C:233:ARG:HD3	3:C:597:LEU:HD23	1.77	0.66
3:C:447:VAL:O	3:C:451:LEU:HD12	1.96	0.66
7:a:44:MET:HE1	13:b:74:ARG:HB2	1.78	0.66
28:V:658:THR:O	28:V:662:THR:OG1	2.13	0.66
3:C:492:VAL:H	3:C:515:SER:HB2	1.61	0.65
1:A:1695:LEU:HD21	1:A:1725:TRP:HD1	1.60	0.65
6:r:12:GLN:HA	6:r:54:LYS:HZ3	1.61	0.65
8:g:70:LEU:H	8:g:70:LEU:HD12	1.61	0.65
26:K:75:PRO:HG3	26:K:87:TYR:HD1	1.62	0.65
29:Q:790:SER:CA	29:Q:1510:ALA:HB2	2.26	0.65
14:I:105:VAL:CA	29:Q:1330:THR:CB	2.73	0.65
1:A:465:GLY:HA3	3:C:402:ILE:O	1.95	0.65
19:O:95:VAL:HG21	19:O:213:MET:HE2	1.77	0.65
1:A:1601:TRP:CD1	1:A:1815:LEU:HD13	2.31	0.65
10:f:17:THR:HA	10:f:35:LEU:HD23	1.77	0.65
25:L:817:ARG:O	25:L:821:LEU:HG	1.96	0.65
1:A:1501:ARG:NH1	1:A:1519:TRP:O	2.29	0.65
3:C:397:MET:HA	3:C:397:MET:CE	2.27	0.65
6:t:86:GLU:O	6:t:90:THR:OG1	2.11	0.65
3:C:927:ASP:HB3	3:C:930:ASP:HB2	1.77	0.65
4:E:53:ASN:N	4:E:53:ASN:OD1	2.29	0.65
5:F:76:U:H4'	5:F:76:U:OP2	1.95	0.65
6:r:108:HIS:HE1	26:K:27:GLU:OE1	1.79	0.65
6:s:110:ALA:O	6:s:114:VAL:HG23	1.96	0.65
31:3:7:G:H2'	31:3:8:C:C6	2.31	0.65
1:A:1765:VAL:HG13	1:A:1780:GLY:HA3	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:N:28:GLN:O	20:N:32:GLU:HG3	1.96	0.65
25:L:563:LYS:HA	25:L:566:GLN:HB2	1.78	0.65
1:A:117:LYS:NZ	1:A:546:PHE:O	2.29	0.65
1:A:1002:CYS:O	1:A:1005:LYS:NZ	2.27	0.65
1:A:1659:GLN:HG3	1:A:1675:LYS:HE3	1.77	0.65
14:I:575:VAL:HG12	14:I:579:TRP:HD1	1.61	0.65
15:J:91:GLN:OE1	25:L:248:LEU:HD11	1.98	0.65
24:W:562:LYS:HA	24:W:575:TRP:O	1.96	0.65
3:C:495:VAL:HA	3:C:511:GLY:HA3	1.78	0.64
20:N:25:ASP:O	20:N:29:GLN:HG3	1.97	0.64
25:L:173:LYS:O	25:L:177:GLU:HG2	1.97	0.64
3:C:446:GLY:O	3:C:450:MET:CB	2.45	0.64
4:E:285:MET:HE2	4:E:310:ASP:HB3	1.78	0.64
23:S:47:ARG:HB3	23:S:55:GLN:HB3	1.80	0.64
26:K:117:VAL:HA	26:K:120:TRP:HD1	1.62	0.64
3:C:146:LEU:HG	3:C:147:HIS:CD2	2.33	0.64
8:g:38:MET:HG3	8:g:61:GLY:HA2	1.78	0.64
23:S:76:ASP:H	23:S:98:ASN:HD22	1.45	0.64
25:L:761:LEU:HD11	26:K:167:GLU:HB3	1.79	0.64
1:A:1133:ASN:ND2	1:A:1137:THR:O	2.31	0.64
3:C:119:ARG:NH2	3:C:120:THR:O	2.31	0.64
8:g:13:MET:HE3	9:e:9:MET:HE3	1.77	0.64
3:C:948:ARG:NH1	3:C:952:VAL:HG21	2.12	0.64
4:E:56:ALA:HB3	4:E:59:ILE:HD11	1.79	0.64
4:E:59:ILE:O	4:E:357:LEU:N	2.30	0.64
6:q:9:VAL:HG11	26:K:158:LEU:HD13	1.78	0.64
6:r:99:GLN:OE1	6:r:99:GLN:N	2.30	0.64
19:O:103:LYS:HZ3	19:O:104:PRO:HD2	1.63	0.64
23:S:94:ASN:ND2	23:S:117:LYS:O	2.24	0.64
1:A:359:LYS:HE2	3:C:957:ARG:HA	1.79	0.64
19:O:172:GLY:HA2	24:W:215:LYS:HZ2	1.62	0.64
20:N:127:ARG:HD2	20:N:131:GLN:O	1.98	0.64
24:W:66:GLN:NE2	24:W:72:LYS:O	2.30	0.64
8:g:16:LYS:NZ	8:g:28:SER:HB3	2.12	0.64
8:g:41:VAL:HA	8:g:57:VAL:O	1.98	0.64
14:I:372:ASN:HB3	14:I:375:ASN:HB2	1.80	0.64
26:K:171:ALA:O	26:K:175:LYS:HG3	1.97	0.64
1:A:1312:LEU:HD11	1:A:1358:LYS:HB3	1.80	0.64
1:A:1376:PRO:HG2	1:A:1378:VAL:HG12	1.80	0.64
2:B:42:U:H3	30:5:-1:G:H1	1.46	0.64
3:C:354:ARG:NH1	3:C:354:ARG:O	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:s:117:ARG:HH22	6:s:120:LYS:HD2	1.63	0.64
3:C:139:ASN:OD1	3:C:214:ASN:ND2	2.30	0.64
3:C:250:VAL:HG23	3:C:852:GLU:OE1	1.98	0.64
24:W:57:LYS:CG	26:K:186:LEU:HD11	2.28	0.64
25:L:807:LEU:HB3	26:K:212:ILE:HG13	1.79	0.64
1:A:367:ARG:NH1	3:C:903:ASP:OD1	2.30	0.63
3:C:257:ARG:HB2	3:C:600:GLN:NE2	2.13	0.63
3:C:756:LEU:H	3:C:756:LEU:HD22	1.64	0.63
1:A:339:PRO:O	2:B:50:A:O2'	2.16	0.63
1:A:1045:PHE:HB3	1:A:1230:THR:HG21	1.80	0.63
1:A:1493:THR:O	1:A:1493:THR:OG1	2.11	0.63
3:C:248:ILE:HD11	3:C:298:VAL:HG23	1.80	0.63
13:b:18:ARG:NH1	13:b:26:GLN:OE1	2.31	0.63
18:T:180:VAL:HG11	21:R:115:VAL:HG13	1.80	0.63
19:O:103:LYS:HD2	25:L:234:ARG:HH12	1.64	0.63
25:L:543:ARG:H	25:L:543:ARG:HD2	1.62	0.63
25:L:779:HIS:HA	26:K:184:ARG:HG2	1.80	0.63
31:3:8:C:H2'	31:3:9:C:C6	2.33	0.63
1:A:832:ASP:OD2	1:A:833:LYS:N	2.31	0.63
19:O:103:LYS:HD2	25:L:234:ARG:NH1	2.09	0.63
25:L:779:HIS:CG	26:K:184:ARG:CG	2.81	0.63
1:A:866:THR:HG22	1:A:869:GLU:H	1.62	0.63
4:E:311:ARG:HH12	21:R:172:LYS:HZ1	1.46	0.63
1:A:1600:LEU:HG	1:A:1636:SER:HB3	1.80	0.63
10:f:22:ILE:HG23	10:f:32:LYS:HG2	1.81	0.63
19:O:36:GLN:HB3	21:R:196:LEU:HG	1.81	0.63
26:K:84:LYS:O	26:K:88:GLU:HG2	1.99	0.63
1:A:852:GLN:HG2	1:A:1088:HIS:CB	2.25	0.63
3:C:760:ASN:HD21	3:C:801:ILE:HB	1.63	0.63
7:a:24:THR:HB	7:a:77:ILE:HB	1.79	0.63
1:A:1404:LEU:HD21	27:U:6:GLY:H	1.64	0.63
2:B:42:U:H3	30:5:-1:G:N2	1.96	0.63
10:f:23:VAL:HG13	10:f:74:LEU:HB3	1.81	0.63
18:T:446:ARG:CZ	18:T:446:ARG:HB2	2.24	0.63
25:L:70:LEU:HD21	25:L:99:TYR:HB2	1.81	0.63
31:3:5:G:H2'	31:3:6:A:H8	1.62	0.63
1:A:1605:THR:HG22	1:A:1608:ARG:HH21	1.64	0.63
3:C:113:LEU:HD21	3:C:502:GLN:HE21	1.63	0.63
6:r:12:GLN:O	6:r:14:VAL:HG12	1.99	0.63
7:a:74:ARG:HG3	7:a:75:PHE:CD2	2.34	0.63
10:f:8:ASN:HB2	10:f:11:PRO:HD2	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:d:41:ASN:HB2	11:d:104:MET:HB3	1.81	0.63
23:S:68:SER:OG	23:S:101:GLY:O	2.17	0.63
1:A:331:ILE:HA	27:U:1:MET:HE3	1.81	0.62
1:A:1205:ARG:HG2	1:A:1206:LEU:H	1.63	0.62
14:I:521:THR:HG22	14:I:522:ARG:H	1.64	0.62
14:I:707:GLU:OE2	14:I:710:ARG:NH1	2.31	0.62
19:O:103:LYS:HE2	25:L:234:ARG:NH1	2.05	0.62
19:O:277:ARG:NE	19:O:281:GLU:OE1	2.32	0.62
27:U:23:LYS:H	28:V:674:HIS:CD2	2.10	0.62
3:C:354:ARG:HH12	3:C:357:ALA:HB3	1.62	0.62
7:a:45:ASN:HD21	8:g:38:MET:HE2	1.64	0.62
11:d:58:HIS:CD2	12:c:2:VAL:HG11	2.33	0.62
15:J:35:GLU:C	15:J:37:GLN:H	2.07	0.62
19:O:259:ALA:N	19:O:273:THR:O	2.32	0.62
24:W:285:GLY:HA2	24:W:570:GLY:H	1.64	0.62
1:A:104:TYR:HB3	4:E:109:ASN:ND2	2.15	0.62
1:A:359:LYS:HE2	3:C:957:ARG:HD3	1.82	0.62
5:F:36:A:H2	31:3:4:A:H61	1.46	0.62
6:r:30:LYS:NZ	6:r:34:GLU:OE2	2.29	0.62
19:O:264:MET:HE2	19:O:267:LYS:H	1.63	0.62
1:A:368:THR:O	1:A:372:VAL:HB	2.00	0.62
1:A:1026:VAL:HG22	1:A:1029:VAL:HB	1.81	0.62
2:B:92:U:O4	7:a:45:ASN:ND2	2.33	0.62
3:C:254:ARG:O	3:C:600:GLN:NE2	2.32	0.62
5:F:31:A:H2'	5:F:32:A:C8	2.35	0.62
6:r:105:LEU:O	6:r:105:LEU:HD23	1.99	0.62
13:b:73:LEU:HB3	13:b:78:ILE:HD11	1.81	0.62
15:J:35:GLU:O	15:J:37:GLN:CG	2.41	0.62
1:A:1706:PRO:HA	1:A:1780:GLY:O	1.99	0.62
3:C:766:SER:HB3	3:C:771:THR:HG21	1.80	0.62
6:q:94:LEU:HB2	6:t:94:LEU:HD12	1.82	0.62
25:L:574:ASN:ND2	25:L:576:ASP:OD1	2.31	0.62
1:A:614:ILE:O	1:A:618:THR:HG23	2.00	0.62
12:c:16:VAL:HG12	12:c:72:PRO:HD3	1.82	0.62
18:T:398:ILE:HB	18:T:412:MET:HG2	1.82	0.62
22:H:32:G:H22	31:3:100:C:H42	1.46	0.62
1:A:338:GLU:OE1	2:B:49:A:H1'	1.99	0.62
1:A:450:PRO:O	3:C:347:TYR:OH	2.17	0.62
3:C:138:ARG:HB2	3:C:213:LEU:HD12	1.80	0.62
7:a:44:MET:HB3	7:a:70:GLY:HA3	1.81	0.62
18:T:499:ALA:HB1	18:T:504:HIS:HB2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:L:184:LEU:C	25:L:184:LEU:HD12	2.24	0.62
25:L:563:LYS:O	25:L:567:ARG:HG2	2.00	0.62
26:K:75:PRO:HB2	26:K:77:PHE:CZ	2.33	0.62
6:r:115:ILE:HD11	6:s:118:LEU:HD12	1.81	0.62
12:c:27:GLN:HB3	12:c:45:LYS:HE3	1.81	0.62
12:c:60:SER:HB2	13:b:81:LEU:HB2	1.82	0.62
14:I:544:LEU:HD21	14:I:578:ILE:HA	1.82	0.62
14:I:603:GLU:HA	14:I:606:ILE:HD12	1.81	0.62
25:L:765:VAL:HA	26:K:170:LEU:HD23	1.81	0.62
3:C:466:VAL:HG11	3:C:482:MET:HG2	1.80	0.62
6:t:85:LEU:HD13	26:K:125:ASP:HA	1.81	0.62
25:L:779:HIS:CD2	26:K:184:ARG:HG3	2.35	0.62
1:A:355:ASN:O	1:A:1409:GLN:NE2	2.33	0.62
1:A:543:THR:O	1:A:544:LYS:HB3	2.00	0.62
1:A:1554:PHE:O	1:A:1555:LYS:HB2	1.99	0.62
3:C:685:GLU:HA	3:C:708:PRO:HG3	1.82	0.62
4:E:127:SER:H	4:E:153:VAL:HG23	1.64	0.62
6:r:115:ILE:CD1	6:s:118:LEU:HD12	2.29	0.62
14:I:430:VAL:HG12	14:I:434:ARG:HH21	1.65	0.62
25:L:557:GLU:O	25:L:560:LYS:HB2	1.99	0.62
25:L:694:LEU:HD22	25:L:701:GLU:HG3	1.81	0.62
1:A:956:LYS:HD2	1:A:976:GLU:HG2	1.82	0.61
3:C:849:TYR:CE2	3:C:894:VAL:HG13	2.34	0.61
5:F:1:G5J:PB	20:N:149:GLY:O	2.57	0.61
14:I:399:GLU:O	14:I:403:THR:OG1	2.07	0.61
14:I:572:TYR:HH	14:I:579:TRP:CD1	2.18	0.61
14:I:674:TYR:O	14:I:678:ILE:HG13	2.00	0.61
24:W:375:LYS:O	24:W:387:MET:N	2.32	0.61
25:L:48:ARG:NH1	25:L:134:LYS:O	2.30	0.61
1:A:151:LEU:O	1:A:154:VAL:HG12	2.00	0.61
1:A:457:LEU:HD11	3:C:395:TYR:HB2	1.81	0.61
3:C:935:LEU:HD11	3:C:945:ALA:HB1	1.81	0.61
5:F:87:A:HI'	5:F:88:U:C6	2.35	0.61
19:O:256:GLY:HA3	19:O:279:ALA:HB1	1.81	0.61
1:A:212:ARG:NH1	1:A:253:GLU:OE2	2.33	0.61
3:C:126:PHE:CZ	7:a:86:PRO:HD3	2.35	0.61
1:A:447:GLY:N	3:C:371:ARG:HH12	1.90	0.61
1:A:1480:ILE:HG22	1:A:1481:PRO:HD3	1.83	0.61
1:A:2010:ASN:O	1:A:2013:LYS:N	2.21	0.61
17:M:495:ASN:O	17:M:498:LYS:HB2	2.00	0.61
1:A:1474:ASP:OD2	1:A:1474:ASP:N	2.31	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:84:GLU:OE1	3:C:84:GLU:N	2.30	0.61
3:C:400:ALA:O	3:C:409:VAL:HG22	2.00	0.61
14:I:434:ARG:NH1	14:I:462:GLU:OE1	2.34	0.61
21:R:278:ALA:HA	25:L:76:LEU:HD22	1.81	0.61
1:A:727:ARG:HD3	5:F:58:G:O6	2.01	0.61
2:B:68:G:N2	2:B:69:C:O4'	2.33	0.61
3:C:679:PHE:N	3:C:799:GLU:OE1	2.34	0.61
5:F:25:U:H2'	5:F:26:G:C8	2.35	0.61
14:I:735:ARG:O	14:I:739:VAL:HG23	2.00	0.61
1:A:965:LEU:HD12	1:A:968:HIS:CE1	2.35	0.61
1:A:1295:ARG:NH1	1:A:1347:GLU:OE1	2.34	0.61
6:r:86:GLU:O	6:r:90:THR:HG23	2.00	0.61
14:I:582:TYR:CZ	14:I:601:LEU:HD11	2.35	0.61
26:K:144:LEU:O	26:K:148:GLY:N	2.32	0.61
6:q:23:PHE:HB3	6:q:28:ILE:HB	1.82	0.61
6:r:115:ILE:HD11	6:s:118:LEU:HD11	1.80	0.61
14:I:367:VAL:HA	14:I:370:ARG:HB2	1.81	0.61
14:I:516:GLU:OE1	14:I:524:SER:OG	2.17	0.61
24:W:211:THR:HG23	24:W:214:GLN:H	1.65	0.61
1:A:1398:LEU:HD12	28:V:671:GLU:HG3	1.81	0.61
14:I:291:VAL:HA	14:I:367:VAL:HB	1.82	0.61
1:A:451:LEU:HD11	3:C:346:ILE:HG21	1.83	0.61
3:C:208:GLY:HA3	7:a:13:LYS:HG2	1.82	0.61
4:E:70:SER:OG	4:E:112:LEU:O	2.17	0.61
5:F:80:U:H4'	5:F:81:C:OP1	2.00	0.61
6:t:106:TYR:OH	25:L:615:ASP:OD2	2.15	0.61
25:L:167:LYS:C	25:L:171:ARG:NH2	2.54	0.61
3:C:549:VAL:HG13	3:C:558:VAL:HG21	1.82	0.60
4:E:309:ALA:HA	4:E:333:SER:HB2	1.83	0.60
5:F:2:U:H2'	5:F:3:G:C8	2.36	0.60
18:T:248:HIS:NE2	18:T:266:SER:OG	2.21	0.60
24:W:49:LEU:H	24:W:49:LEU:CD2	2.14	0.60
25:L:62:TRP:CZ2	25:L:90:ARG:HG3	2.36	0.60
1:A:383:ARG:CZ	1:A:384:LYS:H	2.14	0.60
2:B:16:A:OP1	2:B:16:A:H4'	2.00	0.60
3:C:853:ILE:HG21	3:C:863:ILE:HD12	1.84	0.60
6:t:114:VAL:HG13	6:t:117:ARG:HH21	1.66	0.60
9:e:76:GLY:HA2	9:e:79:ILE:HG13	1.83	0.60
10:f:26:LYS:NZ	10:f:71:VAL:O	2.26	0.60
1:A:667:ARG:HG2	1:A:1612:TYR:OH	2.01	0.60
1:A:787:ASN:HD22	1:A:852:GLN:NE2	1.99	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1198:TRP:CB	1:A:1259:ARG:HH21	2.14	0.60
1:A:1521:HIS:CD2	1:A:1524:HIS:HD2	2.17	0.60
3:C:418:VAL:HG21	3:C:439:SER:CB	2.25	0.60
3:C:421:ARG:O	3:C:423:ALA:N	2.33	0.60
3:C:654:LEU:HA	3:C:657:LEU:HG	1.84	0.60
3:C:955:ARG:HA	3:C:955:ARG:HE	1.65	0.60
6:t:92:THR:HA	6:t:95:HIS:CE1	2.36	0.60
24:W:126:ASN:HA	24:W:130:LEU:HD12	1.83	0.60
24:W:126:ASN:O	24:W:130:LEU:HB2	2.01	0.60
25:L:739:LYS:HD2	25:L:742:LEU:HD12	1.82	0.60
31:3:4:A:H2'	31:3:5:G:C8	2.35	0.60
1:A:1059:ARG:NE	21:R:288:GLU:OE2	2.33	0.60
1:A:1367:LEU:HD12	1:A:1375:PHE:CE1	2.36	0.60
3:C:507:PHE:CD2	3:C:629:LYS:HD2	2.35	0.60
4:E:223:ARG:HH21	4:E:229:VAL:HG13	1.66	0.60
11:d:67:LYS:HG2	11:d:91:PHE:HD2	1.67	0.60
11:d:37:GLN:HG2	11:d:51:ARG:HH12	1.66	0.60
20:N:56:GLU:OE1	24:W:200:TRP:NE1	2.34	0.60
20:N:118:SER:OG	20:N:120:CYS:SG	2.59	0.60
30:5:-2:C:H2'	30:5:-1:G:C8	2.37	0.60
1:A:241:LEU:HD11	1:A:626:VAL:HG13	1.84	0.60
1:A:1656:ASP:O	1:A:1660:VAL:HG23	2.01	0.60
4:E:86:ASP:O	4:E:87:LYS:HG2	2.01	0.60
4:E:184:LYS:HZ3	4:E:185:SER:H	1.50	0.60
4:E:330:HIS:HD2	4:E:334:VAL:HG22	1.67	0.60
9:e:19:PHE:HE1	9:e:84:THR:HG22	1.67	0.60
12:c:40:HIS:CE1	12:c:58:HIS:HB3	2.35	0.60
29:Q:1109:ALA:O	29:Q:1204:PRO:CB	2.50	0.60
3:C:315:LEU:O	3:C:320:ARG:NH2	2.28	0.60
3:C:495:VAL:HG21	3:C:509:ALA:HB1	1.84	0.60
3:C:955:ARG:HB3	3:C:960:MET:HB3	1.83	0.60
4:E:285:MET:N	4:E:308:SER:OG	2.33	0.60
6:r:106:TYR:HE2	26:K:55:LYS:CD	2.14	0.60
7:a:27:LEU:HA	7:a:74:ARG:H	1.66	0.60
14:I:636:ASP:HB2	14:I:640:ARG:HH22	1.66	0.60
18:T:477:THR:OG1	18:T:479:SER:OG	2.17	0.60
19:O:46:ILE:HG12	19:O:202:TYR:CD1	2.37	0.60
1:A:394:MET:SD	1:A:395:SER:N	2.75	0.60
1:A:1474:ASP:O	1:A:1478:ARG:NH1	2.34	0.60
3:C:954:THR:O	3:C:958:LYS:HG2	2.00	0.60
18:T:459:GLN:NE2	18:T:487:ASP:O	2.27	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:S:67:GLU:O	23:S:102:SER:HB3	2.02	0.60
31:3:3:A:H2'	31:3:4:A:H8	1.67	0.60
1:A:1398:LEU:HB2	28:V:671:GLU:HG3	1.82	0.60
3:C:126:PHE:O	3:C:130:LEU:HD12	2.02	0.60
3:C:526:VAL:HG11	3:C:576:ILE:HD11	1.83	0.60
6:q:18:LYS:HE2	6:q:43:GLU:HB3	1.84	0.60
14:I:434:ARG:NH1	14:I:458:TRP:HE1	2.00	0.60
3:C:939:GLU:HG2	3:C:940:PRO:HD2	1.83	0.60
6:q:94:LEU:O	6:q:98:ARG:HG2	2.01	0.60
8:g:45:THR:O	8:g:54:ILE:N	2.31	0.60
13:b:51:LEU:HB3	13:b:62:ARG:NH2	2.17	0.60
18:T:177:SER:O	18:T:181:SER:OG	2.12	0.60
25:L:789:ARG:HD2	26:K:195:LEU:HD11	1.82	0.60
1:A:262:VAL:HG23	1:A:262:VAL:O	2.02	0.59
1:A:1804:LEU:HB3	1:A:1808:ARG:HH11	1.66	0.59
2:B:91:U:O4'	8:g:60:ARG:NH2	2.35	0.59
6:r:105:LEU:HD23	6:r:105:LEU:C	2.26	0.59
11:d:96:PHE:HB3	12:c:69:TYR:HB2	1.83	0.59
15:J:132:ARG:HG3	15:J:155:MET:HE1	1.84	0.59
18:T:358:ARG:NH2	21:R:217:SEP:O1P	2.23	0.59
1:A:1202:ALA:O	1:A:1259:ARG:NH1	2.31	0.59
14:I:755:ARG:O	14:I:759:VAL:HG23	2.01	0.59
24:W:125:HIS:HA	24:W:128:HIS:HB3	1.83	0.59
1:A:338:GLU:HB2	27:U:9:THR:HB	1.83	0.59
6:t:105:LEU:HD11	25:L:563:LYS:HB2	1.84	0.59
23:S:55:GLN:HE22	24:W:87:LEU:HB3	1.67	0.59
5:F:33:U:H2'	5:F:34:A:C8	2.38	0.59
9:e:30:LEU:HD22	9:e:78:ASN:HD22	1.68	0.59
10:f:22:ILE:O	10:f:74:LEU:HA	2.02	0.59
14:I:575:VAL:HG12	14:I:579:TRP:CD1	2.36	0.59
19:O:103:LYS:HG3	19:O:104:PRO:HD2	1.84	0.59
25:L:553:ARG:O	25:L:557:GLU:HB2	2.02	0.59
1:A:1176:ARG:HG2	1:A:1219:TRP:HH2	1.68	0.59
1:A:1194:ASN:HD21	1:A:1203:ARG:HB3	1.66	0.59
3:C:272:LYS:HD3	3:C:275:ARG:HD2	1.83	0.59
4:E:58:ILE:HD13	13:b:111:ARG:HG3	1.85	0.59
17:M:487:GLN:OE1	23:S:133:ARG:HD3	2.01	0.59
24:W:124:TYR:O	24:W:128:HIS:HB2	2.02	0.59
1:A:744:HIS:HD2	18:T:250:GLU:OE1	1.86	0.59
1:A:2010:ASN:O	1:A:2012:GLU:N	2.35	0.59
2:B:16:A:H2'	2:B:17:A:C5	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:95:U:H4'	2:B:96:G:H5''	1.85	0.59
3:C:418:VAL:O	3:C:418:VAL:HG13	2.02	0.59
3:C:639:GLU:HB3	3:C:641:SER:H	1.68	0.59
4:E:61:LEU:HB2	4:E:355:ILE:HB	1.83	0.59
13:b:26:GLN:HB2	13:b:48:PHE:O	2.01	0.59
14:I:105:VAL:O	29:Q:1329:TYR:CA	2.50	0.59
21:R:114:LEU:HD11	21:R:223:LEU:HB3	1.85	0.59
23:S:88:GLY:N	23:S:107:THR:O	2.34	0.59
1:A:973:TYR:HB2	1:A:1097:GLY:HA3	1.85	0.59
3:C:179:ARG:HB3	3:C:182:ASP:HB2	1.84	0.59
3:C:259:ALA:HA	3:C:264:LEU:HD12	1.84	0.59
4:E:68:VAL:HG11	4:E:355:ILE:HD11	1.85	0.59
6:q:109:ASP:OD2	6:q:110:ALA:N	2.35	0.59
6:r:108:HIS:CE1	26:K:27:GLU:OE1	2.55	0.59
10:f:46:LEU:HD13	10:f:64:VAL:HG13	1.84	0.59
25:L:714:SER:OG	25:L:715:LEU:N	2.28	0.59
1:A:709:VAL:O	1:A:713:GLU:HG3	2.02	0.59
5:F:25:U:H2'	5:F:26:G:N9	2.17	0.59
15:J:189:GLU:HG3	15:J:201:ILE:CD1	2.32	0.59
1:A:952:GLN:NE2	1:A:954:SER:O	2.36	0.59
1:A:969:LEU:HD12	16:P:234:ILE:HD13	1.84	0.59
1:A:1147:HIS:CD2	1:A:1149:ILE:H	2.19	0.59
6:q:76:PHE:CE2	6:r:72:LEU:HB3	2.38	0.59
18:T:322:THR:HG21	21:R:153:LEU:HD11	1.83	0.59
1:A:1058:ASN:HB2	1:A:1074:THR:HG21	1.84	0.59
3:C:150:LYS:HG2	3:C:241:VAL:HG21	1.83	0.59
5:F:54:C:H2'	5:F:55:C:O4'	2.01	0.59
15:J:99:SER:O	15:J:103:ARG:HG3	2.03	0.59
21:R:38:TYR:OH	23:S:23:HIS:ND1	2.30	0.59
1:A:1174:ILE:HG23	1:A:1212:ASN:HB3	1.85	0.58
3:C:147:HIS:CA	32:C:1001:GTP:O1B	2.50	0.58
4:E:271:TYR:CE1	26:K:211:ASP:HB3	2.38	0.58
7:a:38:CYS:HB2	7:a:49:LYS:HE3	1.85	0.58
11:d:39:LEU:HB2	11:d:49:LEU:HD12	1.85	0.58
15:J:304:ILE:O	15:J:308:VAL:HG22	2.03	0.58
25:L:623:ASP:HB3	25:L:625:ARG:HG2	1.85	0.58
31:3:21:C:H4'	31:3:22:U:OP2	2.03	0.58
1:A:309:ASP:HB3	1:A:311:ASN:H	1.68	0.58
3:C:181:THR:OG1	3:C:217:ASP:OD2	2.18	0.58
3:C:625:ARG:HH12	3:C:629:LYS:HZ3	1.51	0.58
4:E:191:SER:OG	4:E:192:GLU:N	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:f:61:LEU:HD13	11:d:106:LEU:HD22	1.85	0.58
25:L:167:LYS:O	25:L:171:ARG:CZ	2.50	0.58
1:A:1634:LYS:O	1:A:1638:ILE:HB	2.03	0.58
3:C:118:LEU:HD23	3:C:119:ARG:H	1.66	0.58
14:I:448:VAL:HG22	14:I:498:VAL:HG22	1.85	0.58
16:P:25:LYS:NZ	21:R:205:LYS:H	2.01	0.58
26:K:130:GLN:HA	26:K:133:HIS:CD2	2.39	0.58
1:A:1012:PRO:HB3	1:A:1254:LEU:HD13	1.84	0.58
3:C:699:ARG:HH12	3:C:815:PRO:HD2	1.68	0.58
6:r:5:ILE:HD12	6:s:88:HIS:CD2	2.39	0.58
6:r:106:TYR:OH	26:K:55:LYS:CG	2.51	0.58
14:I:712:ARG:NH2	14:I:741:HIS:O	2.34	0.58
18:T:387:GLU:OE2	18:T:446:ARG:NH1	2.36	0.58
1:A:740:ARG:NH2	5:F:63:A:OP2	2.37	0.58
3:C:167:MET:HA	3:C:167:MET:HE3	1.85	0.58
3:C:636:THR:C	3:C:637:ARG:HD2	2.28	0.58
3:C:677:VAL:HG22	3:C:895:VAL:HG13	1.86	0.58
8:g:57:VAL:HB	9:e:81:LEU:HD11	1.85	0.58
15:J:130:HIS:CE1	25:L:226:THR:HB	2.39	0.58
25:L:600:ALA:O	25:L:604:VAL:HG23	2.03	0.58
25:L:814:LEU:HG	25:L:818:ARG:HH11	1.69	0.58
1:A:1786:ILE:CD1	1:A:1787:LYS:H	2.17	0.58
2:B:48:U:O2'	27:U:11:ARG:HD2	2.02	0.58
3:C:194:ILE:HD12	3:C:224:PHE:HE2	1.69	0.58
3:C:316:LEU:HD23	3:C:322:ASN:HB2	1.84	0.58
3:C:775:LEU:HD21	3:C:815:PRO:HA	1.85	0.58
6:s:117:ARG:NH2	6:s:120:LYS:HD2	2.19	0.58
23:S:84:HIS:N	23:S:115:ASP:OD1	2.28	0.58
31:3:13:C:H2'	31:3:14:A:C8	2.38	0.58
3:C:292:ARG:HH22	3:C:362:GLY:HA2	1.68	0.58
6:q:110:ALA:O	6:q:114:VAL:HB	2.03	0.58
6:r:123:ASP:HA	6:r:126:ARG:NH1	2.19	0.58
12:c:30:ILE:HA	12:c:41:LEU:HD12	1.86	0.58
15:J:303:GLY:O	15:J:307:VAL:HG23	2.04	0.58
18:T:440:LEU:HD13	18:T:472:MET:HE1	1.85	0.58
1:A:268:ASP:HB2	1:A:271:PRO:HA	1.86	0.58
1:A:663:MET:HE1	1:A:1613:VAL:HG21	1.85	0.58
3:C:196:MET:HG3	3:C:227:GLU:HB3	1.85	0.58
4:E:201:ALA:HB2	4:E:208:TYR:HE2	1.67	0.58
14:I:394:ILE:HG13	14:I:423:PHE:HE2	1.69	0.58
18:T:347:GLN:HE22	21:R:141:THR:HG21	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:447:GLY:HA2	3:C:371:ARG:CZ	2.34	0.58
1:A:1461:LYS:HE3	1:A:1466:ARG:HD2	1.84	0.58
3:C:474:SER:HA	3:C:479:VAL:HG21	1.85	0.58
19:O:75:LYS:HB2	24:W:106:PHE:CE1	2.39	0.58
19:O:151:LEU:HD12	19:O:217:VAL:CG1	2.21	0.58
1:A:279:ASN:HD21	1:A:284:LYS:H	1.52	0.58
1:A:455:SER:OG	3:C:412:LEU:HD11	2.03	0.58
1:A:1121:ARG:NH1	1:A:1149:ILE:O	2.33	0.58
1:A:1723:LYS:HB3	1:A:1761:SER:HB2	1.84	0.58
7:a:73:VAL:HG11	7:a:76:PHE:CE2	2.38	0.58
15:J:91:GLN:HE22	25:L:248:LEU:CG	2.16	0.58
18:T:337:CYS:SG	18:T:353:HIS:HD2	2.27	0.58
18:T:483:THR:OG1	18:T:485:GLU:OE2	2.18	0.58
25:L:73:LEU:HB3	25:L:84:ILE:HG12	1.86	0.58
1:A:1227:ARG:CZ	1:A:1231:THR:HG21	2.34	0.57
3:C:218:CYS:SG	3:C:228:VAL:HA	2.44	0.57
19:O:120:MET:HG2	21:R:215:PRO:HD2	1.85	0.57
19:O:164:ARG:NH2	31:3:17:A:OP2	2.36	0.57
21:R:55:GLY:HA3	23:S:128:MET:HB2	1.85	0.57
21:R:274:ASN:ND2	21:R:276:LYS:H	2.00	0.57
1:A:165:MET:HE3	1:A:642:LEU:HD13	1.86	0.57
3:C:796:LEU:HD11	3:C:842:PRO:HB2	1.86	0.57
5:F:31:A:H61	31:3:9:C:H42	1.52	0.57
6:r:93:GLN:O	6:r:97:THR:CG2	2.44	0.57
8:g:32:ARG:HE	8:g:43:ASP:HB2	1.69	0.57
15:J:189:GLU:HG3	15:J:201:ILE:HD11	1.86	0.57
18:T:443:TRP:HA	18:T:450:CYS:HA	1.84	0.57
19:O:60:ASN:OD1	24:W:128:HIS:NE2	2.37	0.57
25:L:19:LYS:O	25:L:23:MET:HG3	2.04	0.57
25:L:31:ALA:HA	25:L:34:SER:HB3	1.85	0.57
6:q:109:ASP:HB2	25:L:666:LEU:HD12	1.86	0.57
23:S:55:GLN:NE2	23:S:103:GLN:OE1	2.38	0.57
25:L:740:LEU:HD23	26:K:145:LEU:HD13	1.85	0.57
1:A:1200:ARG:HG2	1:A:1409:GLN:HA	1.86	0.57
3:C:508:ASP:HB3	3:C:568:LEU:HG	1.86	0.57
3:C:933:ILE:HG13	3:C:935:LEU:HG	1.84	0.57
5:F:74:C:H4'	25:L:162:ARG:NH1	2.19	0.57
25:L:775:PHE:HA	26:K:184:ARG:NH1	2.18	0.57
29:Q:1097:GLY:HA2	29:Q:1129:PRO:CB	2.33	0.57
1:A:1412:LEU:HB3	3:C:938:LEU:HD11	1.87	0.57
1:A:1782:TRP:CD1	1:A:1787:LYS:HE3	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:r:15:VAL:O	6:r:51:LEU:N	2.31	0.57
6:t:113:ARG:NH1	25:L:611:LEU:HB3	2.20	0.57
12:c:72:PRO:HD2	12:c:75:LEU:HD22	1.85	0.57
14:I:712:ARG:HH21	14:I:742:GLY:HA2	1.69	0.57
21:R:192:LYS:HB2	24:W:120:PHE:CZ	2.39	0.57
23:S:17:VAL:HG11	23:S:90:LEU:HD23	1.87	0.57
24:W:91:HIS:CD2	24:W:92:PRO:CD	2.82	0.57
25:L:738:GLY:O	25:L:742:LEU:HG	2.04	0.57
29:Q:790:SER:CB	29:Q:1510:ALA:CB	2.82	0.57
1:A:391:HIS:HE1	3:C:147:HIS:CD2	2.22	0.57
1:A:574:ARG:HH11	1:A:574:ARG:HG3	1.68	0.57
3:C:145:HIS:CG	3:C:146:LEU:H	2.21	0.57
3:C:681:GLU:HB3	3:C:796:LEU:HD12	1.87	0.57
4:E:347:ALA:HB2	4:E:357:LEU:HD23	1.87	0.57
14:I:470:ARG:O	14:I:474:VAL:HG23	2.04	0.57
14:I:557:GLU:O	14:I:561:LYS:HG3	2.05	0.57
14:I:690:ASP:O	14:I:694:VAL:HG23	2.04	0.57
16:P:218:ASN:OD1	18:T:488:LYS:HD2	2.04	0.57
19:O:209:VAL:O	19:O:213:MET:HG3	2.03	0.57
1:A:540:LEU:O	1:A:543:THR:OG1	2.22	0.57
3:C:97:LEU:HD12	18:T:243:LEU:HD21	1.86	0.57
4:E:107:HIS:CD2	4:E:135:TRP:HZ2	2.23	0.57
10:f:51:GLU:HB2	10:f:59:GLY:O	2.05	0.57
14:I:382:ARG:HH21	14:I:386:PHE:HE2	1.52	0.57
14:I:441:THR:HA	14:I:451:LEU:HD11	1.87	0.57
20:N:170:GLU:O	24:W:196:GLU:HG3	2.04	0.57
3:C:524:VAL:HG12	3:C:584:SER:HA	1.85	0.57
1:A:371:LYS:HB3	1:A:379:ASN:ND2	2.19	0.57
1:A:376:TYR:CZ	3:C:659:LYS:HE2	2.40	0.57
3:C:573:ASP:HB2	3:C:629:LYS:HE3	1.87	0.57
6:r:107:GLN:OE1	6:s:108:HIS:CG	2.28	0.57
15:J:58:TYR:CZ	25:L:248:LEU:HD22	2.40	0.57
22:H:34:G:H22	31:3:98:U:H3	1.52	0.57
25:L:167:LYS:O	25:L:171:ARG:NH2	2.38	0.57
25:L:789:ARG:HA	25:L:792:ALA:HB3	1.85	0.57
1:A:1208:LYS:O	1:A:1212:ASN:HB2	2.04	0.57
2:B:61:G:H2'	2:B:62:A:C8	2.40	0.57
13:b:12:TYR:HB3	13:b:17:MET:HE1	1.86	0.57
19:O:160:ARG:HD2	31:3:18:G:H5''	1.87	0.57
21:R:56:GLY:N	23:S:128:MET:SD	2.77	0.57
21:R:245:SER:O	21:R:260:ARG:NH1	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:L:605:ALA:O	25:L:609:ARG:HG2	2.04	0.57
25:L:620:PRO:O	25:L:621:VAL:HG23	2.04	0.57
1:A:1339:ARG:NH2	1:A:1437:GLN:O	2.38	0.56
4:E:107:HIS:CD2	4:E:133:ARG:HD2	2.39	0.56
5:F:75:A:H8	22:H:18:U:H5'	1.69	0.56
6:q:99:GLN:NE2	25:L:677:PRO:HB2	2.20	0.56
15:J:240:ASP:OD2	15:J:241:GLU:N	2.37	0.56
1:A:262:VAL:HG12	1:A:265:TRP:CZ2	2.39	0.56
1:A:494:TRP:HE3	1:A:675:LEU:HD13	1.70	0.56
6:r:14:VAL:O	6:r:23:PHE:N	2.33	0.56
1:A:338:GLU:CB	27:U:9:THR:HB	2.35	0.56
1:A:1412:LEU:HB2	3:C:938:LEU:HD21	1.88	0.56
1:A:1601:TRP:HD1	1:A:1815:LEU:HD22	1.70	0.56
1:A:1709:MET:HB2	1:A:1778:ALA:HB3	1.87	0.56
2:B:13:C:H2'	2:B:14:U:C6	2.40	0.56
3:C:413:LEU:O	3:C:416:LEU:O	2.22	0.56
3:C:465:LYS:O	3:C:469:HIS:CB	2.38	0.56
3:C:859:CYS:O	3:C:863:ILE:HG12	2.05	0.56
4:E:64:HIS:ND1	4:E:84:SER:HB2	2.20	0.56
6:q:114:VAL:HG23	25:L:662:GLU:CD	2.30	0.56
6:r:28:ILE:O	6:r:32:VAL:HG23	2.06	0.56
6:r:118:LEU:HG	6:s:122:ARG:HD2	1.88	0.56
10:f:34:TYR:HB2	10:f:47:ALA:HB3	1.88	0.56
22:H:29:C:H4'	22:H:30:A:C8	2.39	0.56
24:W:50:VAL:HA	26:K:35:TYR:CE1	2.40	0.56
24:W:484:MET:O	24:W:490:PHE:HA	2.05	0.56
25:L:648:GLU:OE1	25:L:651:ALA:N	2.35	0.56
25:L:783:LEU:HG	26:K:187:GLN:HE22	1.68	0.56
1:A:1365:ILE:HG12	1:A:1370:LYS:NZ	2.21	0.56
3:C:221:HIS:HD2	3:C:652:MET:HG2	1.70	0.56
3:C:750:TRP:HH2	3:C:776:LEU:HG	1.70	0.56
4:E:159:LEU:HD11	4:E:204:GLY:HA2	1.86	0.56
12:c:24:THR:OG1	12:c:48:ALA:HA	2.06	0.56
14:I:249:GLY:O	14:I:253:PHE:N	2.38	0.56
14:I:379:TRP:HA	14:I:382:ARG:HG3	1.87	0.56
14:I:530:ASP:OD1	14:I:565:ARG:NH1	2.38	0.56
15:J:35:GLU:C	15:J:37:GLN:N	2.63	0.56
19:O:77:LYS:HG3	19:O:202:TYR:CZ	2.41	0.56
1:A:866:THR:HG22	1:A:869:GLU:N	2.20	0.56
3:C:354:ARG:HH11	3:C:354:ARG:HA	1.71	0.56
5:F:83:A:O2'	5:F:84:G:OP2	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:J:286:SER:O	15:J:289:GLN:NE2	2.38	0.56
17:M:441:ALA:HB3	17:M:444:ASN:HB2	1.86	0.56
17:M:541:ARG:NH1	22:H:14:C:HO2'	2.02	0.56
21:R:157:ASN:OD1	21:R:159:THR:HG22	2.05	0.56
1:A:1301:LEU:CD2	1:A:1348:LEU:HG	2.34	0.56
3:C:196:MET:HE3	3:C:231:ALA:HB2	1.88	0.56
4:E:224:GLY:HA3	4:E:229:VAL:HG21	1.87	0.56
7:a:37:LEU:HD13	7:a:46:CYS:HB2	1.88	0.56
25:L:208:ASP:OD2	25:L:211:SER:OG	2.23	0.56
1:A:120:MET:CG	1:A:547:GLN:HG2	2.35	0.56
1:A:1263:LYS:HD2	1:A:1288:ARG:O	2.06	0.56
1:A:1369:SER:HB2	1:A:1374:ARG:HD2	1.88	0.56
1:A:1456:LYS:HG2	1:A:1467:LEU:HD21	1.88	0.56
3:C:397:MET:HE3	3:C:397:MET:CA	2.32	0.56
5:F:77:A:OP1	5:F:77:A:H4'	2.05	0.56
6:t:110:ALA:O	6:t:114:VAL:HG23	2.05	0.56
8:g:41:VAL:HG11	9:e:12:PRO:HA	1.87	0.56
23:S:76:ASP:H	23:S:98:ASN:ND2	2.03	0.56
1:A:481:HIS:HD2	2:B:26:G:N1	2.04	0.56
3:C:275:ARG:HA	3:C:279:GLU:HG3	1.88	0.56
3:C:699:ARG:HH11	3:C:814:ALA:HB1	1.71	0.56
6:r:57:LYS:O	6:r:59:VAL:N	2.38	0.56
6:r:106:TYR:OH	26:K:55:LYS:HG2	2.06	0.56
6:t:113:ARG:HH12	25:L:611:LEU:HB3	1.71	0.56
18:T:305:VAL:HG21	21:R:145:LEU:HD13	1.88	0.56
18:T:315:VAL:HB	18:T:329:LEU:HB2	1.88	0.56
23:S:134:LEU:HD11	23:S:149:VAL:HG11	1.88	0.56
1:A:840:LEU:O	1:A:844:THR:HG22	2.06	0.56
6:s:72:LEU:HD13	6:t:76:PHE:HD1	1.71	0.56
14:I:513:THR:O	14:I:517:GLU:HG2	2.05	0.56
25:L:672:HIS:HA	25:L:675:LEU:HD21	1.88	0.56
31:3:3:A:H2'	31:3:4:A:C8	2.41	0.56
1:A:819:HIS:O	1:A:823:GLU:HG2	2.06	0.56
1:A:855:GLN:HE22	1:A:1092:TYR:N	2.04	0.56
3:C:103:ALA:O	16:P:48:GLN:NE2	2.39	0.56
6:q:29:GLU:O	6:q:33:ARG:HG2	2.05	0.56
15:J:126:ARG:HG3	17:M:500:VAL:HG21	1.88	0.56
25:L:185:GLN:HA	25:L:185:GLN:OE1	2.06	0.56
1:A:359:LYS:HB2	3:C:957:ARG:CZ	2.36	0.55
1:A:1454:ALA:O	1:A:1458:GLU:HB2	2.06	0.55
3:C:84:GLU:H	3:C:84:GLU:CD	2.13	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:d:28:LEU:O	11:d:32:VAL:HG23	2.05	0.55
11:d:38:VAL:HA	11:d:106:LEU:O	2.06	0.55
15:J:238:ALA:O	15:J:242:LEU:CB	2.48	0.55
19:O:21:ILE:HG23	24:W:107:VAL:HG21	1.88	0.55
25:L:800:THR:O	25:L:804:GLU:HG2	2.06	0.55
1:A:1147:HIS:HD2	1:A:1149:ILE:N	2.03	0.55
5:F:74:C:H2'	5:F:76:U:OP1	2.06	0.55
1:A:1278:TRP:CD1	1:A:1440:GLU:HB2	2.41	0.55
3:C:214:ASN:HB3	3:C:566:LEU:HD11	1.87	0.55
4:E:87:LYS:HB3	4:E:109:ASN:C	2.31	0.55
6:q:107:GLN:HB2	25:L:663:VAL:HG21	1.87	0.55
6:s:109:ASP:O	6:s:112:THR:OG1	2.23	0.55
19:O:213:MET:SD	31:3:20:A:N6	2.79	0.55
25:L:809:GLU:HA	25:L:812:LYS:HG3	1.87	0.55
26:K:87:TYR:CE2	26:K:91:ARG:HG2	2.41	0.55
1:A:1278:TRP:CE2	1:A:1294:LEU:HD11	2.41	0.55
3:C:397:MET:HE1	3:C:413:LEU:HD11	1.88	0.55
5:F:1:G5J:N2	5:F:12:C:O2	2.39	0.55
5:F:40:A:H2'	5:F:41:A:C5	2.42	0.55
5:F:71:A:H2'	5:F:72:C:H2'	1.87	0.55
5:F:90:G:N2	22:H:4:C:O2	2.39	0.55
6:q:113:ARG:HD2	25:L:666:LEU:HG	1.88	0.55
6:s:82:ALA:HA	6:s:85:LEU:HD23	1.89	0.55
12:c:17:GLN:HB2	12:c:70:ILE:HB	1.87	0.55
15:J:96:ARG:O	15:J:100:VAL:HG23	2.06	0.55
15:J:130:HIS:ND1	25:L:229:GLU:HB2	2.18	0.55
20:N:41:LYS:HZ1	20:N:46:LEU:HD23	1.71	0.55
20:N:52:ARG:HG2	24:W:200:TRP:CZ2	2.41	0.55
24:W:57:LYS:CD	26:K:186:LEU:HD12	2.19	0.55
1:A:1765:VAL:CG2	1:A:1781:ASN:H	2.19	0.55
7:a:74:ARG:HH12	13:b:78:ILE:HG12	1.72	0.55
9:e:16:MET:HE1	9:e:82:ILE:HG13	1.87	0.55
14:I:436:ILE:HD13	14:I:439:LYS:NZ	2.22	0.55
15:J:265:VAL:O	15:J:269:ARG:HG3	2.06	0.55
15:J:281:LYS:HA	15:J:284:ALA:HB2	1.89	0.55
18:T:363:ARG:HH21	21:R:137:THR:HG23	1.71	0.55
19:O:172:GLY:HA2	24:W:215:LYS:NZ	2.22	0.55
24:W:54:ASN:ND2	26:K:182:ARG:HH21	1.96	0.55
1:A:309:ASP:HB2	1:A:312:TYR:CE2	2.41	0.55
1:A:387:LEU:HD22	3:C:189:ALA:HB3	1.88	0.55
1:A:628:PHE:HA	1:A:633:VAL:HG12	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1670:ILE:HA	1:A:1697:ALA:HB1	1.88	0.55
4:E:77:GLY:O	4:E:340:HIS:NE2	2.38	0.55
6:s:75:LEU:O	6:s:79:GLU:HG2	2.06	0.55
17:M:504:GLN:O	17:M:508:ARG:HD2	2.07	0.55
17:M:537:LYS:O	17:M:541:ARG:NE	2.31	0.55
18:T:273:VAL:HB	18:T:287:TYR:HB2	1.89	0.55
19:O:211:ALA:O	19:O:215:LYS:HG2	2.06	0.55
25:L:567:ARG:HG3	25:L:569:LEU:HG	1.88	0.55
1:A:198:VAL:HG11	1:A:271:PRO:HG2	1.87	0.55
1:A:538:ARG:NH1	2:B:14:U:OP1	2.37	0.55
4:E:317:ASP:OD2	4:E:320:THR:OG1	2.24	0.55
6:q:25:LYS:O	6:q:29:GLU:HB2	2.06	0.55
7:a:51:VAL:HB	7:a:63:LEU:HB2	1.88	0.55
10:f:29:MET:HG3	10:f:53:ILE:HG13	1.89	0.55
10:f:36:VAL:HB	10:f:45:GLN:HB3	1.87	0.55
24:W:55:GLU:HA	24:W:55:GLU:OE2	2.06	0.55
24:W:550:CYS:HA	24:W:567:GLY:HA2	1.87	0.55
1:A:285:ARG:HA	1:A:480:GLY:O	2.07	0.55
1:A:329:MET:HE1	1:A:371:LYS:HB2	1.88	0.55
1:A:469:LEU:HD21	3:C:429:THR:OG1	2.06	0.55
3:C:745:ALA:O	3:C:763:LEU:HD11	2.07	0.55
19:O:213:MET:O	19:O:217:VAL:HG13	2.06	0.55
20:N:143:SER:OG	20:N:148:ASP:OD2	2.23	0.55
23:S:46:HIS:CE1	23:S:55:GLN:HG2	2.42	0.55
26:K:75:PRO:HG3	26:K:87:TYR:CD1	2.41	0.55
1:A:855:GLN:HE21	1:A:1091:SER:H	1.52	0.55
1:A:1652:SER:HA	1:A:1655:MET:HE2	1.89	0.55
2:B:67:U:H2'	2:B:68:G:H8	1.72	0.55
3:C:119:ARG:HB3	3:C:163:GLU:HG3	1.89	0.55
11:d:96:PHE:O	12:c:68:TYR:HB2	2.06	0.55
25:L:575:LEU:HG	25:L:613:GLN:HA	1.87	0.55
1:A:242:LEU:HD23	20:N:31:LYS:HD2	1.89	0.55
1:A:1720:PRO:HG2	1:A:1723:LYS:HB2	1.88	0.55
1:A:1786:ILE:H	1:A:1786:ILE:HD12	1.72	0.55
3:C:626:LYS:HA	3:C:629:LYS:HG3	1.88	0.55
3:C:660:ASP:O	3:C:664:LEU:HB2	2.06	0.55
3:C:875:THR:HB	3:C:889:LYS:HB2	1.89	0.55
15:J:73:VAL:HG23	15:J:76:PHE:CZ	2.42	0.55
15:J:89:GLU:OE2	15:J:125:HIS:NE2	2.37	0.55
24:W:196:GLU:HB3	24:W:199:PRO:HD3	1.89	0.55
1:A:676:ILE:O	1:A:680:PHE:HB2	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1709:MET:HA	1:A:1787:LYS:HE2	1.89	0.54
3:C:340:ALA:HB1	3:C:356:PHE:HB3	1.88	0.54
4:E:72:ARG:HG2	4:E:115:HIS:HA	1.88	0.54
5:F:87:A:H4'	5:F:88:U:H5'	1.88	0.54
6:q:103:HIS:O	6:q:106:TYR:HB2	2.07	0.54
6:r:119:LEU:HD12	6:r:122:ARG:HH12	1.72	0.54
25:L:63:THR:HG22	25:L:64:ARG:H	1.72	0.54
1:A:1265:ARG:HH12	1:A:1266:MET:HE3	1.72	0.54
1:A:1711:ASP:O	1:A:1787:LYS:HD3	2.07	0.54
3:C:796:LEU:O	3:C:955:ARG:HD3	2.07	0.54
11:d:34:THR:OG1	11:d:107:ARG:NH2	2.40	0.54
11:d:39:LEU:HD11	11:d:47:LYS:HB3	1.89	0.54
14:I:596:GLU:HG3	15:J:312:ARG:HG3	1.88	0.54
25:L:563:LYS:H	25:L:563:LYS:HD2	1.71	0.54
25:L:571:ARG:HH22	25:L:620:PRO:HA	1.72	0.54
26:K:69:MET:N	26:K:69:MET:SD	2.80	0.54
1:A:150:ALA:HB2	21:R:201:LEU:HD13	1.90	0.54
1:A:376:TYR:CE2	3:C:659:LYS:HE2	2.42	0.54
1:A:449:GLU:O	3:C:389:PHE:CE1	2.61	0.54
1:A:1503:ARG:O	1:A:1507:LYS:HG2	2.07	0.54
4:E:177:VAL:HB	4:E:187:HIS:HB2	1.89	0.54
5:F:36:A:H2'	5:F:37:G:C8	2.40	0.54
5:F:72:C:H3'	5:F:72:C:OP2	2.08	0.54
6:s:84:MET:SD	6:s:87:LEU:HB3	2.47	0.54
14:I:472:LEU:HA	14:I:475:VAL:HG12	1.89	0.54
29:Q:154:GLN:C	29:Q:156:LEU:H	2.16	0.54
1:A:1786:ILE:HD12	1:A:1787:LYS:H	1.73	0.54
4:E:160:ARG:HH22	4:E:247:VAL:HB	1.73	0.54
14:I:522:ARG:HD2	14:I:553:GLN:NE2	2.21	0.54
25:L:814:LEU:HD22	26:K:219:LEU:HD22	1.88	0.54
26:K:47:VAL:O	26:K:51:ILE:HG12	2.06	0.54
3:C:140:VAL:HG11	3:C:451:LEU:HD22	1.90	0.54
3:C:506:ARG:HH12	3:C:571:GLY:HA2	1.73	0.54
6:q:83:ASN:HD21	6:t:87:LEU:HD12	1.72	0.54
6:t:96:GLN:O	6:t:100:GLU:HG2	2.08	0.54
14:I:689:ASP:OD1	14:I:726:ARG:NH2	2.41	0.54
17:M:503:LEU:O	17:M:506:ARG:HB3	2.07	0.54
1:A:236:ASP:HB3	1:A:239:ASP:HB2	1.90	0.54
1:A:1349:LEU:HD21	28:V:667:PHE:CE1	2.43	0.54
1:A:1692:ASP:HB2	1:A:1726:VAL:O	2.07	0.54
11:d:98:ARG:NH1	12:c:37:MET:SD	2.81	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:J:206:ILE:HD13	15:J:215:TRP:CZ2	2.42	0.54
17:M:442:PRO:O	17:M:446:TYR:CB	2.55	0.54
29:Q:918:ARG:O	29:Q:942:GLY:HA3	2.08	0.54
1:A:1331:LEU:HD13	1:A:1432:LEU:HD22	1.88	0.54
2:B:96:G:OP2	11:d:43:ARG:NH2	2.40	0.54
3:C:469:HIS:HA	3:C:595:ARG:HD3	1.89	0.54
12:c:58:HIS:HB2	13:b:83:ILE:HD11	1.90	0.54
14:I:641:ALA:O	14:I:645:VAL:HG22	2.07	0.54
15:J:232:ARG:NH2	15:J:259:GLU:OE2	2.40	0.54
1:A:968:HIS:HB2	16:P:235:ARG:HG3	1.90	0.54
6:t:88:HIS:HD2	26:K:128:ALA:HA	1.72	0.54
10:f:65:LEU:HD22	11:d:25:LEU:HA	1.89	0.54
18:T:340:LEU:HD13	18:T:383:MET:HG2	1.90	0.54
24:W:286:VAL:HA	24:W:303:GLY:HA2	1.90	0.54
1:A:391:HIS:HE1	3:C:147:HIS:HD2	1.55	0.54
3:C:342:LEU:HD23	3:C:342:LEU:O	2.06	0.54
11:d:41:ASN:HA	11:d:47:LYS:HD2	1.89	0.54
16:P:59:LEU:HA	16:P:62:GLU:HG3	1.90	0.54
18:T:352:SER:HB3	18:T:354:ASP:OD1	2.07	0.54
19:O:236:VAL:HB	19:O:270:ALA:HB3	1.88	0.54
25:L:104:ASP:HA	25:L:107:VAL:HG12	1.90	0.54
1:A:163:GLU:O	1:A:192:PRO:HG3	2.08	0.54
1:A:330:CYS:O	27:U:1:MET:HB2	2.08	0.54
1:A:728:GLN:OE1	21:R:208:HIS:ND1	2.41	0.54
1:A:1731:ARG:HG3	1:A:1731:ARG:HH21	1.72	0.54
3:C:271:SER:HA	3:C:326:SER:HB3	1.90	0.54
7:a:38:CYS:N	7:a:47:GLN:O	2.25	0.54
14:I:583:LEU:HD12	14:I:601:LEU:HD23	1.90	0.54
14:I:649:GLU:O	14:I:653:VAL:HG23	2.07	0.54
23:S:9:ASP:HB3	23:S:14:SER:HB2	1.89	0.54
3:C:226:ASP:HB2	3:C:632:PRO:HB2	1.89	0.53
3:C:695:THR:HG21	3:C:700:ASN:HB2	1.88	0.53
3:C:700:ASN:HA	3:C:812:ALA:O	2.08	0.53
3:C:870:ARG:NH1	3:C:896:GLU:O	2.41	0.53
5:F:91:U:H4'	5:F:92:U:OP1	2.07	0.53
11:d:92:VAL:HG11	12:c:70:ILE:HG23	1.89	0.53
15:J:284:ALA:O	15:J:288:TYR:HB2	2.07	0.53
1:A:325:LYS:HE2	1:A:337:PHE:CE2	2.43	0.53
3:C:123:SER:H	7:a:89:LYS:HZ2	1.55	0.53
14:I:363:LEU:O	14:I:367:VAL:HG22	2.08	0.53
14:I:530:ASP:HA	14:I:533:LEU:HD12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:J:52:PRO:C	15:J:54:GLU:H	2.17	0.53
19:O:264:MET:HE2	19:O:267:LYS:HB2	1.90	0.53
26:K:83:LEU:HA	26:K:86:GLU:HB2	1.89	0.53
1:A:606:ASN:O	1:A:610:LEU:HB2	2.07	0.53
1:A:1703:MET:HG2	1:A:1783:PHE:HB3	1.90	0.53
3:C:850:TYR:HB2	3:C:919:ASP:HB2	1.91	0.53
3:C:902:THR:OG1	3:C:903:ASP:N	2.41	0.53
15:J:89:GLU:OE2	15:J:124:ARG:NH1	2.40	0.53
18:T:300:HIS:HD1	18:T:302:ASN:H	1.55	0.53
25:L:793:LEU:HB3	26:K:198:LEU:HD13	1.90	0.53
1:A:622:VAL:O	1:A:626:VAL:HG23	2.08	0.53
1:A:927:GLU:HG3	1:A:977:PRO:HB3	1.90	0.53
1:A:972:VAL:HG21	1:A:1512:THR:HG23	1.90	0.53
2:B:69:C:H4'	2:B:70:U:C4	2.43	0.53
6:r:64:ALA:HB3	6:r:65:PRO:HD3	1.90	0.53
18:T:183:ARG:NH1	21:R:119:ASP:OD2	2.29	0.53
1:A:1371:MET:HG3	30:5:-6:C:H1'	1.91	0.53
3:C:848:VAL:HA	3:C:893:PRO:HA	1.90	0.53
14:I:463:LEU:HD21	14:I:515:LEU:HD21	1.90	0.53
18:T:307:MET:HG3	18:T:317:VAL:HG22	1.90	0.53
25:L:35:SER:HB3	25:L:157:ARG:HH12	1.74	0.53
25:L:238:GLN:O	25:L:240:PHE:CD2	2.61	0.53
25:L:801:LYS:HB3	26:K:205:GLN:HE21	1.72	0.53
1:A:939:HIS:O	1:A:943:GLN:HG2	2.09	0.53
1:A:1793:ALA:O	1:A:1797:ILE:HG13	2.09	0.53
2:B:13:C:H2'	2:B:14:U:H6	1.72	0.53
4:E:148:GLU:HB2	4:E:178:TRP:CH2	2.44	0.53
15:J:91:GLN:HE22	25:L:248:LEU:CD2	2.21	0.53
29:Q:152:TYR:C	29:Q:154:GLN:H	2.16	0.53
4:E:255:LEU:HD13	4:E:265:GLU:HG2	1.91	0.53
5:F:73:G:O2'	5:F:74:C:O2	2.25	0.53
7:a:11:PRO:O	7:a:14:LEU:HB3	2.09	0.53
7:a:86:PRO:O	7:a:90:ARG:HB3	2.08	0.53
14:I:564:GLU:HG3	15:J:296:LYS:C	2.34	0.53
15:J:95:ARG:HH22	19:O:106:GLU:HB3	1.74	0.53
19:O:47:SER:HB3	19:O:73:VAL:HG21	1.89	0.53
25:L:793:LEU:HG	26:K:198:LEU:HB3	1.91	0.53
26:K:67:ARG:HG3	26:K:67:ARG:HH11	1.74	0.53
1:A:457:LEU:HD11	3:C:395:TYR:CB	2.39	0.53
1:A:478:ARG:HD2	3:C:428:ASP:HA	1.89	0.53
1:A:1357:ASN:O	1:A:1361:THR:HG23	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1360:GLN:NE2	1:A:1381:TYR:OH	2.42	0.53
6:r:98:ARG:HH12	26:K:72:VAL:N	2.06	0.53
6:t:76:PHE:O	6:t:80:TRP:HB2	2.08	0.53
11:d:60:ASN:OD1	11:d:99:GLY:N	2.40	0.53
22:H:29:C:O2'	22:H:30:A:H8	1.91	0.53
24:W:51:LEU:HD12	24:W:52:ARG:H	1.73	0.53
1:A:313:PHE:HB2	1:A:317:GLU:HG3	1.91	0.53
1:A:1016:VAL:HG21	1:A:1256:PHE:CD2	2.44	0.53
1:A:1245:ASP:OD1	1:A:1245:ASP:N	2.36	0.53
1:A:1398:LEU:O	1:A:1400:PRO:HD3	2.09	0.53
1:A:1406:TYR:HB3	3:C:938:LEU:HD12	1.90	0.53
1:A:1754:ASP:OD2	1:A:1756:MET:N	2.41	0.53
3:C:273:VAL:HG23	3:C:326:SER:O	2.08	0.53
3:C:662:ARG:HD2	3:C:669:GLU:HA	1.91	0.53
3:C:775:LEU:HB3	3:C:813:ILE:HD12	1.90	0.53
4:E:164:LYS:HE3	4:E:180:MET:HG2	1.89	0.53
5:F:1:G5J:O1B	20:N:149:GLY:O	2.27	0.53
13:b:18:ARG:HB2	13:b:84:GLU:HG2	1.91	0.53
14:I:566:GLY:HA2	14:I:569:LEU:HB2	1.91	0.53
15:J:135:TRP:O	15:J:139:VAL:HB	2.09	0.53
18:T:193:TRP:NE1	18:T:504:HIS:O	2.38	0.53
23:S:12:MET:O	23:S:133:ARG:NH1	2.42	0.53
25:L:565:LEU:HD23	25:L:619:TYR:HE2	1.74	0.53
26:K:135:HIS:O	26:K:138:ILE:HG22	2.08	0.53
3:C:150:LYS:HZ1	3:C:220:GLY:HA3	1.73	0.53
4:E:156:CYS:HB3	4:E:168:THR:HG22	1.89	0.53
6:q:10:PRO:HG2	6:q:22:LEU:HD22	1.91	0.53
6:q:93:GLN:O	6:q:97:THR:OG1	2.26	0.53
15:J:49:ILE:HD12	25:L:245:VAL:CG2	2.38	0.53
15:J:239:VAL:HG13	15:J:251:PHE:CZ	2.43	0.53
19:O:169:PHE:O	24:W:215:LYS:NZ	2.33	0.53
1:A:1430:PRO:HA	28:V:665:SER:HA	1.90	0.52
1:A:1708:LEU:HG	1:A:1779:TYR:HD2	1.75	0.52
1:A:1796:LYS:O	1:A:1800:SER:OG	2.17	0.52
6:t:119:LEU:HA	6:t:122:ARG:HB2	1.91	0.52
14:I:105:VAL:CB	29:Q:1329:TYR:CB	2.87	0.52
18:T:317:VAL:HB	18:T:327:MET:HB3	1.91	0.52
25:L:769:ALA:O	25:L:773:VAL:HG23	2.09	0.52
1:A:110:PHE:HB3	4:E:87:LYS:HE3	1.90	0.52
1:A:327:LEU:HD13	1:A:379:ASN:ND2	2.24	0.52
1:A:332:PRO:HD3	27:U:1:MET:SD	2.49	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1783:PHE:HD2	1:A:1786:ILE:HG21	1.73	0.52
6:r:23:PHE:CD2	6:r:28:ILE:HG12	2.44	0.52
7:a:86:PRO:HA	7:a:89:LYS:HE2	1.91	0.52
9:e:25:LYS:O	9:e:85:THR:OG1	2.27	0.52
15:J:58:TYR:HE1	25:L:248:LEU:CD2	2.23	0.52
15:J:58:TYR:OH	25:L:248:LEU:HD22	2.09	0.52
17:M:509:LYS:O	17:M:510:LYS:HB3	2.09	0.52
18:T:235:ASP:OD2	18:T:238:SER:OG	2.27	0.52
20:N:176:TRP:HB3	24:W:194:LEU:HD12	1.91	0.52
24:W:519:VAL:O	24:W:530:PHE:HA	2.09	0.52
25:L:605:ALA:HA	25:L:608:MET:HE3	1.91	0.52
26:K:28:HIS:N	26:K:28:HIS:CD2	2.77	0.52
1:A:764:GLY:H	21:R:230:LEU:CD2	2.22	0.52
1:A:896:TYR:OH	1:A:993:GLU:OE2	2.27	0.52
1:A:1704:SER:HB2	1:A:1714:ASP:O	2.08	0.52
2:B:88:A:O3'	11:d:57:ARG:NH2	2.42	0.52
6:r:28:ILE:HG23	6:r:50:LEU:HD21	1.92	0.52
14:I:625:GLU:HB3	14:I:633:HIS:HE1	1.75	0.52
14:I:713:ALA:O	14:I:717:HIS:ND1	2.42	0.52
15:J:247:GLN:HE21	15:J:252:PHE:HE2	1.57	0.52
19:O:23:CYS:SG	19:O:25:THR:HB	2.49	0.52
19:O:103:LYS:HE3	25:L:234:ARG:CD	2.37	0.52
1:A:587:ASN:HB2	1:A:589:LYS:HE3	1.92	0.52
1:A:1357:ASN:ND2	27:U:14:GLY:O	2.43	0.52
2:B:90:C:O2'	2:B:91:U:OP2	2.23	0.52
3:C:401:VAL:HG13	3:C:432:LEU:HD23	1.90	0.52
3:C:864:TYR:CZ	3:C:874:VAL:HG11	2.44	0.52
4:E:80:ILE:HB	4:E:92:TRP:HB2	1.92	0.52
5:F:38:A:N6	31:3:3:A:H1'	2.25	0.52
6:q:28:ILE:O	6:q:32:VAL:HG22	2.09	0.52
6:s:122:ARG:HB3	6:s:126:ARG:HH21	1.75	0.52
20:N:41:LYS:NZ	20:N:46:LEU:HD23	2.23	0.52
21:R:69:ASP:O	21:R:72:LYS:HG2	2.10	0.52
26:K:214:ARG:O	26:K:218:ARG:HG2	2.09	0.52
29:Q:718:LEU:O	29:Q:720:SER:N	2.42	0.52
1:A:663:MET:O	1:A:667:ARG:HG3	2.09	0.52
3:C:625:ARG:HH22	3:C:629:LYS:CE	2.23	0.52
9:e:73:LEU:HD11	10:f:9:PRO:HB3	1.90	0.52
14:I:672:GLU:HA	14:I:675:GLU:HG2	1.92	0.52
15:J:124:ARG:HB2	17:M:503:LEU:HD11	1.92	0.52
1:A:167:MET:HE3	1:A:694:TRP:CH2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1176:ARG:HG2	1:A:1219:TRP:CH2	2.44	0.52
3:C:187:GLU:HB2	3:C:194:ILE:HG12	1.91	0.52
3:C:277:ILE:HG12	3:C:395:TYR:CE2	2.45	0.52
3:C:320:ARG:HG3	3:C:322:ASN:ND2	2.25	0.52
3:C:919:ASP:OD2	3:C:920:HIS:ND1	2.37	0.52
4:E:84:SER:HB3	4:E:86:ASP:OD1	2.10	0.52
14:I:420:PHE:CE2	14:I:424:TYR:HE2	2.28	0.52
14:I:461:MET:HA	14:I:464:ARG:HE	1.75	0.52
19:O:54:PHE:CE1	21:R:193:MET:HE1	2.45	0.52
19:O:245:GLU:HB2	19:O:263:LYS:HD3	1.92	0.52
1:A:163:GLU:HA	1:A:702:LEU:HD11	1.92	0.52
21:R:286:THR:O	21:R:290:LYS:HG3	2.09	0.52
1:A:321:PHE:CD1	1:A:519:VAL:HG21	2.45	0.52
1:A:363:ARG:NH1	3:C:871:ARG:HH21	2.08	0.52
1:A:368:THR:N	27:U:3:ASN:OD1	2.43	0.52
1:A:387:LEU:HD23	3:C:190:ARG:HG3	1.90	0.52
3:C:339:PHE:CD1	3:C:390:VAL:HG22	2.45	0.52
3:C:367:VAL:HG12	3:C:378:PRO:HB3	1.92	0.52
3:C:513:VAL:HG12	3:C:563:ALA:HA	1.92	0.52
4:E:61:LEU:N	4:E:355:ILE:O	2.36	0.52
6:t:68:SER:HB3	26:K:82:VAL:HG13	1.91	0.52
6:t:92:THR:HA	6:t:95:HIS:NE2	2.25	0.52
13:b:113:MET:HG3	24:W:73:VAL:HG23	1.91	0.52
1:A:826:ARG:HG3	1:A:967:SER:HA	1.92	0.52
1:A:1425:GLU:C	1:A:1427:GLN:N	2.68	0.52
1:A:1603:SER:HB3	1:A:1633:LEU:HD21	1.91	0.52
14:I:712:ARG:NH2	14:I:742:GLY:HA2	2.24	0.52
1:A:314:TYR:CE2	3:C:910:GLY:HA3	2.45	0.52
1:A:838:LYS:O	1:A:842:ARG:HG3	2.10	0.52
3:C:682:THR:HG22	3:C:802:ARG:O	2.10	0.52
9:e:46:ASP:HB3	10:f:9:PRO:HD2	1.91	0.52
11:d:38:VAL:HG12	11:d:107:ARG:HA	1.92	0.52
14:I:456:CYS:HB2	14:I:511:MET:HE2	1.91	0.52
19:O:299:LYS:N	19:O:299:LYS:HD2	2.24	0.52
25:L:35:SER:CB	25:L:157:ARG:HH12	2.23	0.52
25:L:780:GLU:O	25:L:784:ARG:HD2	2.10	0.52
1:A:534:LYS:HD2	21:R:161:LEU:HD13	1.92	0.51
1:A:963:MET:HG3	1:A:1512:THR:HG22	1.92	0.51
1:A:1390:GLY:HA2	1:A:1535:ARG:NH2	2.25	0.51
1:A:1445:ASP:O	1:A:1449:VAL:HG13	2.10	0.51
3:C:587:TYR:CE1	3:C:589:GLU:HB3	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:r:14:VAL:HG21	6:r:50:LEU:HG	1.91	0.51
7:a:27:LEU:CD2	7:a:31:GLU:HG2	2.40	0.51
8:g:44:ALA:H	8:g:56:MET:HE3	1.75	0.51
15:J:293:ALA:O	15:J:296:LYS:HB2	2.09	0.51
17:M:483:LEU:HD11	21:R:85:VAL:HG11	1.91	0.51
20:N:178:GLN:NE2	24:W:190:ALA:O	2.39	0.51
29:Q:1542:ARG:O	29:Q:1546:ALA:N	2.41	0.51
1:A:1558:TYR:HB2	1:A:1808:ARG:HH21	1.75	0.51
2:B:15:G:H3'	2:B:16:A:C5'	2.38	0.51
3:C:243:ASP:CG	3:C:272:LYS:HD2	2.35	0.51
4:E:58:ILE:O	4:E:59:ILE:HD13	2.11	0.51
10:f:46:LEU:O	10:f:63:GLU:HA	2.10	0.51
11:d:50:ALA:HB2	11:d:66:VAL:HA	1.90	0.51
24:W:125:HIS:HD2	24:W:128:HIS:ND1	2.08	0.51
1:A:323:THR:HG23	1:A:375:PRO:HB3	1.92	0.51
1:A:1052:ILE:O	1:A:1092:TYR:O	2.28	0.51
3:C:621:VAL:HA	3:C:624:LEU:HB2	1.92	0.51
3:C:941:ALA:HB1	3:C:945:ALA:HB3	1.90	0.51
6:r:66:ALA:O	6:r:72:LEU:HG	2.09	0.51
16:P:69:LYS:O	16:P:73:LYS:HB2	2.10	0.51
16:P:196:TRP:CD1	16:P:196:TRP:H	2.29	0.51
19:O:30:ASN:ND2	24:W:127:PHE:HB3	2.25	0.51
22:H:11:C:O2'	22:H:12:G:C8	2.63	0.51
25:L:786:ALA:O	25:L:790:LEU:HG	2.10	0.51
26:K:77:PHE:CG	26:K:83:LEU:HB2	2.45	0.51
1:A:1314:SER:OG	1:A:1362:ARG:NH1	2.36	0.51
1:A:1407:SER:HA	1:A:1412:LEU:HD22	1.92	0.51
2:B:40:C:H5'	2:B:41:C:OP2	2.09	0.51
4:E:72:ARG:HB3	4:E:116:TRP:CD1	2.45	0.51
4:E:350:SER:HB3	4:E:352:ASP:OD1	2.10	0.51
7:a:28:LYS:HG2	13:b:77:GLU:CD	2.35	0.51
8:g:40:LEU:O	8:g:58:VAL:HA	2.09	0.51
14:I:712:ARG:HE	14:I:746:THR:HG21	1.76	0.51
15:J:95:ARG:NH2	19:O:106:GLU:HB3	2.25	0.51
3:C:728:ARG:HH11	3:C:731:LEU:HD22	1.75	0.51
12:c:56:MET:HE2	13:b:82:THR:OG1	2.10	0.51
14:I:360:ARG:O	14:I:364:LEU:HD23	2.11	0.51
14:I:712:ARG:O	14:I:716:VAL:HG23	2.10	0.51
29:Q:1363:ALA:C	29:Q:1365:VAL:N	2.67	0.51
1:A:1346:GLN:HG2	1:A:1401:GLN:HE21	1.73	0.51
3:C:122:TYR:CE1	3:C:202:VAL:HB	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:718:GLU:OE1	3:C:758:GLY:HA2	2.11	0.51
3:C:949:GLU:O	3:C:953:LYS:HG2	2.10	0.51
6:r:122:ARG:O	6:r:126:ARG:HG3	2.11	0.51
6:s:96:GLN:O	6:s:100:GLU:HG2	2.10	0.51
13:b:31:PHE:CZ	13:b:40:LEU:HD22	2.46	0.51
17:M:444:ASN:HA	17:M:447:GLN:NE2	2.26	0.51
17:M:460:ALA:HB1	17:M:498:LYS:HD3	1.92	0.51
19:O:141:ALA:HA	24:W:92:PRO:O	2.10	0.51
21:R:257:LEU:HG	25:L:49:TRP:HH2	1.76	0.51
23:S:27:THR:HG22	23:S:74:PHE:HE2	1.75	0.51
25:L:25:TYR:CE1	25:L:32:ARG:HD3	2.44	0.51
25:L:144:ASP:O	25:L:148:LYS:N	2.43	0.51
25:L:655:ALA:O	25:L:659:VAL:HG23	2.10	0.51
1:A:1320:PHE:HE1	1:A:1366:GLY:HA3	1.75	0.51
1:A:1327:TRP:CZ2	1:A:1331:LEU:HG	2.46	0.51
3:C:518:LEU:HB3	3:C:561:ALA:HB3	1.92	0.51
3:C:843:ARG:HA	3:C:928:PRO:HG3	1.92	0.51
6:r:9:VAL:HB	6:r:57:LYS:HE2	1.93	0.51
6:t:116:ALA:O	6:t:119:LEU:HD23	2.10	0.51
15:J:316:TYR:O	15:J:320:ILE:HG12	2.10	0.51
19:O:92:PRO:HG2	19:O:210:ALA:HB2	1.92	0.51
26:K:231:ASP:O	26:K:235:ARG:HG3	2.11	0.51
1:A:388:SER:O	1:A:390:TYR:N	2.40	0.51
3:C:512:ARG:HA	3:C:566:LEU:HA	1.93	0.51
3:C:625:ARG:HH12	3:C:629:LYS:NZ	2.09	0.51
5:F:44:U:H2'	5:F:45:U:O4'	2.10	0.51
8:g:32:ARG:NE	8:g:43:ASP:HB2	2.25	0.51
19:O:164:ARG:HH21	31:3:16:U:H1'	1.75	0.51
23:S:58:ASP:OD1	23:S:60:THR:OG1	2.28	0.51
23:S:153:ARG:HG2	23:S:155:ARG:HH21	1.75	0.51
23:S:153:ARG:NH2	23:S:155:ARG:HB3	2.24	0.51
24:W:111:GLU:HG2	24:W:112:ASP:O	2.11	0.51
1:A:1378:VAL:O	1:A:1382:SER:OG	2.11	0.51
2:B:14:U:H2'	2:B:15:G:O4'	2.11	0.51
3:C:127:LEU:HD11	3:C:549:VAL:HG21	1.93	0.51
3:C:150:LYS:HG2	3:C:241:VAL:CG2	2.40	0.51
3:C:367:VAL:HG22	3:C:372:VAL:O	2.11	0.51
4:E:238:HIS:CE1	4:E:264:ARG:HB2	2.46	0.51
9:e:30:LEU:HB3	9:e:78:ASN:ND2	2.26	0.51
14:I:379:TRP:CE3	14:I:400:ALA:HB2	2.45	0.51
18:T:292:SER:CB	18:T:311:ARG:HB2	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:O:20:PRO:HB2	19:O:22:VAL:HG13	1.93	0.51
1:A:310:ARG:NE	1:A:310:ARG:HA	2.26	0.51
1:A:404:ASP:OD2	1:A:404:ASP:N	2.43	0.51
3:C:154:MET:HE1	3:C:201:LEU:HD11	1.92	0.51
4:E:52:SER:OG	4:E:53:ASN:N	2.44	0.51
8:g:9:LEU:HA	8:g:12:PHE:HD2	1.76	0.51
11:d:37:GLN:HG2	11:d:51:ARG:NH1	2.26	0.51
11:d:80:GLN:HE21	11:d:81:LYS:HE2	1.75	0.51
15:J:212:VAL:O	15:J:216:VAL:HG13	2.10	0.51
15:J:314:PHE:HA	15:J:317:GLU:HB2	1.92	0.51
19:O:176:ARG:HG2	19:O:180:CYS:HA	1.93	0.51
1:A:314:TYR:CD2	3:C:910:GLY:HA3	2.46	0.50
1:A:461:ASN:HD22	1:A:461:ASN:N	2.08	0.50
1:A:959:ALA:HB3	1:A:974:GLU:HB3	1.93	0.50
1:A:1396:HIS:HE1	1:A:1422:SER:O	1.94	0.50
2:B:66:U:H2'	2:B:67:U:C6	2.45	0.50
3:C:77:ALA:HB3	3:C:87:THR:HG21	1.93	0.50
3:C:354:ARG:NH1	3:C:357:ALA:HB3	2.24	0.50
5:F:73:G:C8	22:H:18:U:H4'	2.46	0.50
9:e:31:PHE:N	9:e:78:ASN:O	2.43	0.50
14:I:489:THR:OG1	14:I:492:GLU:HB2	2.11	0.50
15:J:39:GLU:C	15:J:41:ASP:H	2.18	0.50
20:N:61:ILE:HD13	20:N:85:ALA:HB2	1.93	0.50
24:W:57:LYS:NZ	26:K:186:LEU:CD1	2.73	0.50
25:L:793:LEU:O	25:L:797:VAL:HG23	2.11	0.50
25:L:807:LEU:HD22	26:K:212:ILE:HG21	1.92	0.50
1:A:134:ASP:OD2	1:A:134:ASP:N	2.37	0.50
1:A:1410:THR:HG21	3:C:937:PRO:HB2	1.93	0.50
3:C:157:PHE:HZ	3:C:447:VAL:HG11	1.76	0.50
3:C:518:LEU:HD23	3:C:519:ARG:N	2.26	0.50
3:C:631:TYR:HD1	3:C:653:TYR:HE2	1.59	0.50
6:s:105:LEU:HD12	24:W:47:THR:OG1	2.10	0.50
9:e:23:LYS:HG3	9:e:41:ARG:HB3	1.91	0.50
25:L:13:THR:HG21	25:L:147:GLU:HG3	1.92	0.50
31:3:3:A:OP2	31:3:3:A:H8	1.95	0.50
1:A:1448:ARG:HH11	1:A:1478:ARG:NH2	2.08	0.50
3:C:623:GLY:O	3:C:627:VAL:N	2.39	0.50
3:C:865:ASN:O	3:C:869:LYS:HG3	2.11	0.50
6:q:32:VAL:O	6:q:36:GLY:N	2.37	0.50
7:a:76:PHE:O	13:b:71:VAL:HA	2.11	0.50
8:g:59:ILE:HG12	9:e:81:LEU:HD13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:453:GLN:HG3	18:T:507:LEU:HD11	1.93	0.50
19:O:140:ALA:O	24:W:92:PRO:C	2.53	0.50
21:R:180:ALA:HA	21:R:185:GLY:HA2	1.92	0.50
23:S:37:LYS:HE3	23:S:69:ILE:HG22	1.94	0.50
23:S:54:CYS:SG	23:S:108:LEU:HD21	2.51	0.50
25:L:787:PRO:HA	25:L:790:LEU:HD12	1.93	0.50
1:A:659:LYS:HB3	1:A:662:LEU:HD23	1.93	0.50
1:A:1725:TRP:HB3	1:A:1764:GLY:HA2	1.94	0.50
2:B:95:U:H1'	11:d:100:ASP:HB3	1.93	0.50
3:C:145:HIS:CG	3:C:146:LEU:N	2.78	0.50
4:E:58:ILE:HG21	13:b:111:ARG:HG3	1.93	0.50
6:s:87:LEU:O	6:s:91:ARG:HG3	2.11	0.50
7:a:16:HIS:O	7:a:19:GLU:HB2	2.12	0.50
10:f:25:LEU:HD11	10:f:31:TYR:HE2	1.76	0.50
11:d:37:GLN:OE1	11:d:49:LEU:HG	2.11	0.50
23:S:6:VAL:HA	23:S:156:PRO:HA	1.92	0.50
1:A:318:PRO:HB2	1:A:523:LEU:HD13	1.93	0.50
1:A:899:ASP:OD2	1:A:946:LYS:NZ	2.25	0.50
1:A:948:HIS:HE1	25:L:129:PRO:HG3	1.76	0.50
3:C:116:GLU:HG2	3:C:117:PRO:HD2	1.93	0.50
3:C:667:GLU:HG2	3:C:667:GLU:O	2.11	0.50
5:F:39:G:O2'	5:F:40:A:H5'	2.10	0.50
14:I:669:LYS:O	14:I:673:ILE:HG13	2.12	0.50
15:J:206:ILE:HG22	15:J:214:ALA:HB1	1.94	0.50
21:R:107:VAL:HG13	21:R:220:VAL:HG22	1.93	0.50
21:R:256:PRO:HA	25:L:23:MET:HE3	1.94	0.50
25:L:747:LEU:HD11	26:K:153:ARG:HH22	1.76	0.50
4:E:76:ASP:OD2	4:E:78:GLN:NE2	2.40	0.50
9:e:15:LEU:HD13	9:e:18:ARG:NH1	2.26	0.50
10:f:23:VAL:HG12	10:f:71:VAL:HG13	1.93	0.50
18:T:270:ASP:OD1	18:T:272:MET:HB2	2.12	0.50
23:S:49:ILE:HD12	24:W:91:HIS:HB2	1.93	0.50
24:W:306:GLY:HA2	24:W:329:GLY:HA2	1.93	0.50
1:A:391:HIS:ND1	1:A:391:HIS:O	2.44	0.50
1:A:391:HIS:CE1	3:C:147:HIS:CD2	3.00	0.50
1:A:568:LEU:HD13	1:A:612:ARG:HB3	1.93	0.50
3:C:548:TRP:HD1	3:C:568:LEU:HB3	1.77	0.50
6:r:5:ILE:HG23	6:s:88:HIS:CD2	2.47	0.50
7:a:27:LEU:HD21	7:a:29:SER:HB3	1.94	0.50
15:J:237:ARG:HA	15:J:240:ASP:OD1	2.11	0.50
16:P:62:GLU:O	16:P:66:LYS:HE2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1205:ARG:H	1:A:1246:ASN:ND2	2.07	0.50
1:A:1343:LEU:HD23	28:V:667:PHE:CE1	2.47	0.50
3:C:155:ASP:OD2	3:C:180:PHE:N	2.44	0.50
3:C:165:ARG:O	3:C:168:THR:OG1	2.25	0.50
5:F:31:A:H2'	5:F:32:A:H8	1.75	0.50
14:I:681:GLU:CD	14:I:681:GLU:H	2.19	0.50
23:S:6:VAL:HG21	23:S:19:LEU:HD22	1.92	0.50
23:S:30:ASN:ND2	23:S:69:ILE:HG12	2.17	0.50
1:A:288:LEU:HG	1:A:292:VAL:HG11	1.94	0.50
1:A:1600:LEU:HD11	1:A:1640:ILE:HD11	1.94	0.50
1:A:1650:HIS:O	1:A:1654:VAL:HG12	2.12	0.50
1:A:1691:ALA:N	1:A:1725:TRP:HZ2	2.10	0.50
3:C:786:GLY:HA3	3:C:829:ALA:HB3	1.94	0.50
5:F:76:U:H3	15:J:43:LYS:HB2	1.76	0.50
6:r:65:PRO:O	6:r:68:SER:OG	2.30	0.50
11:d:20:TYR:CD1	11:d:25:LEU:HD11	2.47	0.50
19:O:159:LYS:HB3	19:O:159:LYS:NZ	2.27	0.50
25:L:818:ARG:HH21	25:L:818:ARG:HG2	1.75	0.50
1:A:179:TYR:CZ	1:A:547:GLN:HB3	2.46	0.49
3:C:126:PHE:CZ	3:C:130:LEU:HD11	2.47	0.49
3:C:499:PHE:HE2	3:C:510:LEU:HD22	1.76	0.49
5:F:80:U:O2'	17:M:510:LYS:HD2	2.12	0.49
6:q:110:ALA:HB3	25:L:663:VAL:HG23	1.94	0.49
6:r:88:HIS:CD2	6:r:89:ASN:H	2.30	0.49
14:I:558:ASP:O	14:I:562:VAL:HG23	2.12	0.49
25:L:779:HIS:ND1	26:K:184:ARG:HG3	2.26	0.49
26:K:130:GLN:HA	26:K:133:HIS:HD2	1.77	0.49
29:Q:868:VAL:HA	29:Q:886:ALA:HA	1.92	0.49
1:A:325:LYS:HE2	1:A:337:PHE:CZ	2.47	0.49
14:I:289:ILE:O	14:I:370:ARG:HB3	2.12	0.49
14:I:726:ARG:HH12	14:I:727:ALA:HB2	1.76	0.49
19:O:22:VAL:HG11	19:O:56:TRP:CH2	2.48	0.49
19:O:100:MET:HB3	19:O:102:VAL:HG23	1.92	0.49
20:N:13:PRO:HB3	20:N:74:GLU:OE2	2.12	0.49
23:S:83:LYS:HG2	23:S:115:ASP:CG	2.37	0.49
1:A:389:VAL:HB	3:C:905:ARG:NH1	2.27	0.49
1:A:1332:ILE:O	1:A:1336:THR:HB	2.12	0.49
1:A:1763:THR:O	1:A:1765:VAL:HG23	2.11	0.49
3:C:327:ALA:HB3	3:C:332:TRP:CE2	2.47	0.49
4:E:332:GLY:O	4:E:350:SER:OG	2.30	0.49
4:E:349:ALA:HA	4:E:355:ILE:HG12	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:85:A:H1'	5:F:86:A:H5'	1.94	0.49
6:r:2:PHE:HA	6:r:10:PRO:HD3	1.92	0.49
6:s:114:VAL:HG22	26:K:32:ALA:N	2.26	0.49
6:t:84:MET:HG3	26:K:132:GLU:HB2	1.94	0.49
9:e:39:GLU:O	9:e:56:ALA:HA	2.13	0.49
10:f:26:LYS:HA	10:f:72:MET:HE3	1.95	0.49
14:I:590:TYR:HB3	14:I:594:LYS:HB2	1.94	0.49
14:I:625:GLU:HB3	14:I:633:HIS:CE1	2.48	0.49
19:O:31:PRO:HB2	24:W:136:PRO:HG3	1.93	0.49
19:O:217:VAL:O	19:O:221:ASN:HB2	2.12	0.49
25:L:120:ARG:HB2	25:L:120:ARG:HH11	1.77	0.49
28:V:656:ARG:HH21	28:V:692:MET:HA	1.77	0.49
1:A:375:PRO:HG2	1:A:376:TYR:CE2	2.47	0.49
1:A:1535:ARG:O	1:A:1539:ILE:HG13	2.13	0.49
3:C:610:GLU:C	3:C:670:VAL:HG23	2.38	0.49
4:E:271:TYR:HE1	26:K:211:ASP:HB3	1.76	0.49
17:M:484:LYS:O	17:M:487:GLN:HG2	2.12	0.49
19:O:188:THR:O	19:O:188:THR:OG1	2.27	0.49
24:W:49:LEU:HB3	26:K:184:ARG:HH22	1.75	0.49
25:L:688:HIS:CG	25:L:691:LEU:HD12	2.47	0.49
29:Q:783:GLU:HA	29:Q:787:PRO:HA	1.94	0.49
29:Q:790:SER:O	29:Q:1510:ALA:CB	2.47	0.49
1:A:840:LEU:HD13	1:A:964:ASP:HB2	1.94	0.49
1:A:1366:GLY:O	1:A:1367:LEU:HD23	2.13	0.49
1:A:1412:LEU:HG	1:A:1413:GLY:O	2.13	0.49
3:C:364:LEU:O	3:C:385:SER:N	2.45	0.49
3:C:720:GLY:HA2	3:C:757:GLN:NE2	2.28	0.49
10:f:39:ASP:CG	11:d:24:PRO:HD2	2.36	0.49
18:T:312:ASP:OD1	18:T:312:ASP:N	2.45	0.49
24:W:54:ASN:CG	26:K:182:ARG:CZ	2.83	0.49
25:L:754:LEU:HD13	26:K:160:GLU:HG3	1.95	0.49
26:K:33:LEU:H	26:K:33:LEU:HD12	1.77	0.49
1:A:496:GLN:NE2	1:A:518:TYR:OH	2.45	0.49
1:A:771:ARG:HH22	22:H:19:U:H2'	1.78	0.49
3:C:400:ALA:CB	3:C:412:LEU:HD22	2.43	0.49
3:C:875:THR:N	3:C:889:LYS:O	2.41	0.49
3:C:880:LYS:HB2	3:C:885:ILE:O	2.12	0.49
4:E:148:GLU:HB2	4:E:178:TRP:HH2	1.78	0.49
5:F:26:G:O2'	5:F:27:G:OP1	2.21	0.49
11:d:58:HIS:O	11:d:99:GLY:HA3	2.12	0.49
15:J:295:GLU:OE1	15:J:307:VAL:HG21	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:863:PRO:HD2	21:R:276:LYS:HB2	1.93	0.49
1:A:873:ILE:HD13	1:A:1229:LEU:HD11	1.94	0.49
1:A:1200:ARG:HA	1:A:1203:ARG:NH1	2.26	0.49
3:C:153:ILE:HG12	3:C:328:ALA:HB2	1.94	0.49
4:E:293:LEU:HD22	4:E:334:VAL:O	2.13	0.49
6:r:85:LEU:HD12	6:r:88:HIS:NE2	2.28	0.49
6:r:126:ARG:HA	6:r:129:LEU:HD23	1.95	0.49
6:t:115:ILE:HB	25:L:655:ALA:HB1	1.94	0.49
14:I:432:ASN:O	14:I:436:ILE:HG12	2.13	0.49
14:I:503:TYR:OH	14:I:504:ARG:NH2	2.46	0.49
15:J:36:ILE:O	15:J:36:ILE:HG22	2.12	0.49
19:O:259:ALA:HB3	19:O:273:THR:HG23	1.95	0.49
25:L:728:ARG:O	25:L:732:LYS:HG3	2.13	0.49
31:3:17:A:H2'	31:3:18:G:C8	2.48	0.49
1:A:705:LEU:O	1:A:709:VAL:HG23	2.13	0.49
1:A:1782:TRP:CZ3	1:A:1790:VAL:HG11	2.47	0.49
3:C:660:ASP:HB3	3:C:664:LEU:HD12	1.94	0.49
3:C:877:ASP:OD1	3:C:877:ASP:N	2.46	0.49
4:E:158:PRO:HA	4:E:166:PHE:HB3	1.95	0.49
14:I:445:HIS:HB3	14:I:498:VAL:HG11	1.95	0.49
18:T:267:CYS:HB2	18:T:294:VAL:HB	1.94	0.49
20:N:151:PHE:HB3	20:N:173:ARG:HD3	1.94	0.49
20:N:168:LYS:HD3	20:N:169:LEU:H	1.76	0.49
22:H:32:G:N2	31:3:100:C:H42	2.10	0.49
23:S:64:ARG:HD3	24:W:86:VAL:HG12	1.95	0.49
24:W:54:ASN:CG	26:K:182:ARG:NE	2.70	0.49
25:L:798:ASP:O	25:L:802:ARG:HG2	2.13	0.49
1:A:764:GLY:H	21:R:230:LEU:HD23	1.78	0.49
2:B:88:A:O2'	11:d:57:ARG:NH2	2.37	0.49
3:C:858:ASP:OD1	3:C:858:ASP:N	2.39	0.49
5:F:50:U:H2'	5:F:51:G:C8	2.48	0.49
17:M:487:GLN:OE1	23:S:133:ARG:NH2	2.39	0.49
19:O:176:ARG:NH1	19:O:181:PRO:HD3	2.27	0.49
22:H:30:A:H1'	22:H:31:U:OP1	2.13	0.49
24:W:170:GLU:N	24:W:170:GLU:OE2	2.46	0.49
25:L:174:GLN:HA	25:L:174:GLN:OE1	2.13	0.49
28:V:659:ILE:HG23	28:V:676:LEU:HD21	1.95	0.49
1:A:1178:LEU:HD11	1:A:1212:ASN:ND2	2.27	0.49
6:t:108:HIS:O	6:t:112:THR:HG23	2.13	0.49
9:e:30:LEU:HB2	9:e:33:GLN:HB2	1.94	0.49
14:I:688:ASP:O	14:I:692:ARG:HB2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:L:13:THR:HB	25:L:139:ASP:OD2	2.13	0.49
25:L:573:LEU:HD21	25:L:625:ARG:HH12	1.78	0.49
25:L:801:LYS:HB3	26:K:205:GLN:NE2	2.27	0.49
1:A:148:LEU:HD21	1:A:571:LEU:HB2	1.95	0.48
3:C:222:VAL:HG13	3:C:223:ASN:OD1	2.12	0.48
3:C:413:LEU:HG	3:C:418:VAL:HG11	1.94	0.48
4:E:182:VAL:HG22	4:E:184:LYS:H	1.78	0.48
4:E:325:TYR:CZ	4:E:360:LEU:HB3	2.48	0.48
5:F:24:U:H2'	5:F:25:U:O4'	2.12	0.48
6:r:15:VAL:HA	6:r:22:LEU:HA	1.95	0.48
14:I:540:PRO:HG3	14:I:574:HIS:O	2.12	0.48
14:I:745:ASP:OD2	14:I:745:ASP:N	2.44	0.48
17:M:482:SER:OG	17:M:483:LEU:N	2.46	0.48
21:R:79:GLN:HE21	23:S:50:ARG:HD3	1.78	0.48
25:L:779:HIS:ND1	26:K:184:ARG:CG	2.76	0.48
26:K:134:GLN:HE22	26:K:137:ARG:HD3	1.78	0.48
1:A:451:LEU:CD1	3:C:346:ILE:HG21	2.42	0.48
1:A:1615:PHE:O	1:A:1615:PHE:CD1	2.66	0.48
3:C:71:LYS:HD3	3:C:73:TYR:CE1	2.48	0.48
3:C:101:ILE:HD11	18:T:243:LEU:HD23	1.95	0.48
3:C:387:VAL:HG23	3:C:388:GLN:H	1.77	0.48
10:f:25:LEU:C	10:f:72:MET:HB2	2.38	0.48
15:J:170:GLU:OE1	15:J:185:TYR:OH	2.25	0.48
17:M:483:LEU:O	23:S:133:ARG:NH1	2.45	0.48
24:W:520:MET:HA	24:W:529:PHE:O	2.13	0.48
25:L:179:ARG:C	25:L:179:ARG:CD	2.86	0.48
1:A:200:LEU:HD23	1:A:490:LEU:HD23	1.95	0.48
1:A:213:GLU:HG3	1:A:636:TYR:CE1	2.49	0.48
1:A:377:LEU:HD13	1:A:378:TYR:CE2	2.48	0.48
1:A:948:HIS:CE1	25:L:129:PRO:HG3	2.48	0.48
1:A:1039:VAL:HG13	1:A:1241:VAL:HG22	1.94	0.48
1:A:1329:THR:HG22	1:A:1516:PRO:HG2	1.96	0.48
2:B:48:U:C2'	2:B:49:A:H5'	2.44	0.48
2:B:66:U:H2'	2:B:67:U:H6	1.79	0.48
3:C:123:SER:HB3	7:a:89:LYS:HD2	1.94	0.48
3:C:262:GLU:HB2	3:C:264:LEU:HD11	1.95	0.48
4:E:54:LEU:HD21	4:E:345:ILE:HD13	1.95	0.48
4:E:256:SER:HB3	4:E:266:TRP:HE1	1.78	0.48
9:e:60:SER:HB2	9:e:63:ARG:NH2	2.28	0.48
11:d:20:TYR:HA	11:d:25:LEU:HD11	1.94	0.48
12:c:13:ASN:N	12:c:30:ILE:O	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:J:269:ARG:HG2	15:J:294:PHE:HE2	1.78	0.48
29:Q:788:ALA:C	29:Q:790:SER:H	2.21	0.48
31:3:93:A:H2'	31:3:94:C:C6	2.48	0.48
1:A:1340:GLU:O	1:A:1343:LEU:HB2	2.13	0.48
1:A:1782:TRP:HB3	1:A:1786:ILE:CD1	2.43	0.48
2:B:92:U:O5'	7:a:69:ARG:NH2	2.47	0.48
3:C:157:PHE:CZ	3:C:447:VAL:HG11	2.48	0.48
3:C:421:ARG:C	3:C:423:ALA:N	2.64	0.48
3:C:625:ARG:HH21	3:C:626:LYS:HG3	1.79	0.48
6:r:91:ARG:NH2	6:s:86:GLU:HB3	2.28	0.48
6:s:106:TYR:CD1	24:W:49:LEU:CD2	2.96	0.48
7:a:69:ARG:NH1	8:g:38:MET:HE3	2.28	0.48
15:J:265:VAL:HG11	15:J:298:HIS:CD2	2.48	0.48
19:O:264:MET:O	19:O:264:MET:HG3	2.13	0.48
20:N:121:ARG:NH1	20:N:144:CYS:O	2.46	0.48
25:L:816:ARG:HA	25:L:816:ARG:NH2	2.29	0.48
29:Q:1325:GLU:O	29:Q:1329:TYR:CB	2.62	0.48
1:A:534:LYS:HG3	1:A:535:TYR:N	2.27	0.48
1:A:1170:ALA:O	1:A:1174:ILE:HG13	2.14	0.48
2:B:91:U:O2	8:g:60:ARG:HG2	2.14	0.48
3:C:226:ASP:O	3:C:229:THR:HG22	2.14	0.48
3:C:690:LYS:HA	3:C:705:ILE:HG22	1.96	0.48
4:E:302:SER:O	4:E:318:THR:HG22	2.13	0.48
7:a:66:LEU:HD12	7:a:67:PHE:N	2.29	0.48
12:c:56:MET:HA	12:c:56:MET:HE3	1.95	0.48
12:c:56:MET:HG3	12:c:59:LEU:HD23	1.95	0.48
15:J:126:ARG:HD3	17:M:497:GLU:OE1	2.14	0.48
17:M:448:ALA:HA	17:M:451:LYS:HB2	1.96	0.48
20:N:8:LYS:O	20:N:10:LYS:HE2	2.12	0.48
21:R:230:LEU:HB3	21:R:235:GLN:HE21	1.79	0.48
22:H:2:U:O2'	22:H:3:A:C8	2.66	0.48
24:W:116:HIS:ND1	24:W:118:ILE:HG12	2.28	0.48
25:L:679:ASP:O	25:L:683:VAL:HG23	2.13	0.48
26:K:126:ASN:OD1	26:K:127:ALA:N	2.47	0.48
28:V:657:ARG:O	28:V:661:LEU:HB2	2.14	0.48
31:3:17:A:OP2	31:3:17:A:H8	1.96	0.48
1:A:160:LYS:HD3	1:A:188:VAL:O	2.14	0.48
1:A:539:ALA:O	1:A:543:THR:HG23	2.14	0.48
1:A:1713:ASN:HB3	1:A:1714:ASP:OD1	2.12	0.48
2:B:45:U:H4'	5:F:60:G:H22	1.78	0.48
3:C:955:ARG:HA	3:C:955:ARG:NE	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:q:4:SER:HB2	6:q:23:PHE:CE1	2.49	0.48
6:r:87:LEU:HA	6:s:87:LEU:HD13	1.94	0.48
7:a:39:ASP:HB3	8:g:8:GLU:OE2	2.14	0.48
8:g:21:LEU:HD22	8:g:59:ILE:HG21	1.96	0.48
11:d:53:LYS:HB2	11:d:62:ILE:HB	1.95	0.48
14:I:692:ARG:NH1	14:I:727:ALA:HB1	2.28	0.48
19:O:261:VAL:HG22	19:O:272:VAL:HG13	1.95	0.48
1:A:276:LYS:HE3	1:A:276:LYS:HB2	1.47	0.48
1:A:331:ILE:HG22	1:A:332:PRO:HD2	1.95	0.48
1:A:732:ILE:HG13	1:A:733:ALA:N	2.29	0.48
1:A:1435:TYR:OH	28:V:664:MET:HB3	2.14	0.48
1:A:1701:TRP:CZ3	1:A:1783:PHE:HB2	2.49	0.48
2:B:13:C:H42	2:B:66:U:H3	1.61	0.48
3:C:140:VAL:HA	3:C:237:GLY:O	2.12	0.48
3:C:269:MET:HE3	3:C:324:THR:OG1	2.13	0.48
6:r:98:ARG:HH12	26:K:72:VAL:CA	2.26	0.48
6:r:98:ARG:CZ	26:K:72:VAL:HB	2.38	0.48
23:S:12:MET:HE1	23:S:133:ARG:HG2	1.96	0.48
25:L:719:PHE:HE2	26:K:120:TRP:HB3	1.79	0.48
1:A:84:LEU:C	1:A:85:GLN:HG2	2.39	0.48
1:A:634:ASP:HB2	1:A:637:GLN:HG3	1.96	0.48
1:A:1040:MET:HB2	1:A:1249:LEU:HD11	1.96	0.48
1:A:1402:SER:HB2	1:A:1412:LEU:HD21	1.96	0.48
3:C:871:ARG:HH12	3:C:893:PRO:HG2	1.77	0.48
5:F:32:A:N6	31:3:8:C:H42	2.12	0.48
6:r:114:VAL:HG21	26:K:50:LEU:HG	1.94	0.48
6:s:113:ARG:HD2	26:K:34:PRO:HB3	1.94	0.48
9:e:78:ASN:OD1	10:f:26:LYS:HG2	2.13	0.48
13:b:74:ARG:HE	13:b:76:GLU:CD	2.22	0.48
14:I:422:LYS:HA	14:I:425:GLU:HG3	1.95	0.48
14:I:546:TYR:CD1	14:I:562:VAL:HG11	2.49	0.48
15:J:130:HIS:ND1	25:L:229:GLU:HB3	2.29	0.48
17:M:485:TYR:HE2	25:L:223:PHE:CD2	2.31	0.48
20:N:175:THR:OG1	24:W:196:GLU:HG2	2.13	0.48
25:L:762:TRP:CZ2	25:L:766:ARG:HG3	2.49	0.48
1:A:1491:ARG:NH2	1:A:1523:LYS:O	2.46	0.48
1:A:1616:GLN:HA	1:A:1626:MET:O	2.14	0.48
1:A:1786:ILE:O	1:A:1790:VAL:HG12	2.14	0.48
3:C:634:CYS:N	3:C:653:TYR:OH	2.47	0.48
4:E:64:HIS:CE1	4:E:84:SER:HB2	2.49	0.48
4:E:96:ASP:O	4:E:97:GLU:HG2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:73:G:H2'	22:H:18:U:H4'	1.95	0.48
6:q:114:VAL:HA	6:q:117:ARG:HB2	1.95	0.48
6:r:101:LEU:HD12	6:r:101:LEU:O	2.13	0.48
8:g:52:VAL:HG12	8:g:54:ILE:HG22	1.96	0.48
13:b:49:ARG:HG3	13:b:64:GLU:HB3	1.95	0.48
24:W:167:THR:OG1	24:W:170:GLU:HB2	2.14	0.48
1:A:1491:ARG:HA	1:A:1491:ARG:HD2	1.48	0.48
3:C:337:GLN:HE21	3:C:337:GLN:HA	1.77	0.48
3:C:704:MET:HE2	3:C:832:VAL:HG13	1.95	0.48
4:E:103:VAL:HG21	13:b:103:PRO:HD3	1.94	0.48
4:E:151:ALA:HB3	4:E:171:ASP:HB2	1.95	0.48
4:E:201:ALA:HB2	4:E:208:TYR:CE2	2.47	0.48
11:d:20:TYR:HD1	11:d:25:LEU:HD11	1.79	0.48
14:I:645:VAL:HG21	14:I:653:VAL:HG21	1.96	0.48
15:J:122:GLU:HG2	15:J:130:HIS:HB3	1.96	0.48
15:J:122:GLU:HG3	15:J:127:PHE:HB2	1.94	0.48
15:J:267:ARG:O	15:J:271:ILE:HG12	2.14	0.48
17:M:447:GLN:O	17:M:451:LYS:HD3	2.14	0.48
18:T:400:LYS:HZ1	18:T:446:ARG:H	1.61	0.48
19:O:244:THR:HG22	19:O:245:GLU:H	1.78	0.48
20:N:62:TYR:HD2	20:N:90:ILE:HG23	1.78	0.48
24:W:74:MET:HE3	24:W:74:MET:HB3	1.75	0.48
25:L:782:GLU:CG	26:K:188:GLN:NE2	2.77	0.48
1:A:313:PHE:HE1	1:A:496:GLN:O	1.97	0.47
1:A:1032:THR:HG21	1:A:1243:SER:C	2.39	0.47
2:B:91:U:O2	8:g:61:GLY:N	2.36	0.47
3:C:466:VAL:HG12	3:C:594:PHE:HE1	1.79	0.47
3:C:692:PHE:HA	3:C:702:ILE:O	2.14	0.47
3:C:775:LEU:HD23	3:C:813:ILE:HB	1.95	0.47
3:C:949:GLU:HA	3:C:952:VAL:HB	1.96	0.47
5:F:66:A:OP1	5:F:68:G:O2'	2.32	0.47
7:a:24:THR:HG23	7:a:34:ARG:HG2	1.95	0.47
14:I:456:CYS:O	14:I:460:GLU:HB2	2.14	0.47
15:J:404:HIS:HA	15:J:407:PHE:O	2.14	0.47
18:T:399:LYS:HG2	18:T:411:ASN:OD1	2.14	0.47
25:L:57:ILE:HD13	25:L:91:THR:HG21	1.96	0.47
25:L:787:PRO:O	25:L:791:GLU:HG2	2.14	0.47
31:3:8:C:C4	31:3:9:C:N4	2.81	0.47
1:A:181:ILE:HD11	1:A:547:GLN:OE1	2.14	0.47
1:A:484:ARG:HH12	1:A:706:ARG:HH21	1.62	0.47
1:A:1121:ARG:CZ	1:A:1147:HIS:HB3	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:90:MET:HB3	18:T:241:LEU:HB2	1.96	0.47
3:C:147:HIS:HA	32:C:1001:GTP:PB	2.54	0.47
3:C:342:LEU:C	3:C:342:LEU:CD2	2.86	0.47
3:C:355:GLU:O	3:C:358:LYS:HB3	2.13	0.47
3:C:583:VAL:HG11	3:C:591:VAL:HG11	1.96	0.47
4:E:72:ARG:HD3	4:E:72:ARG:HA	1.54	0.47
4:E:127:SER:OG	4:E:131:THR:O	2.32	0.47
6:r:5:ILE:O	6:s:84:MET:HE3	2.14	0.47
10:f:24:LYS:HA	10:f:30:GLU:HA	1.95	0.47
14:I:425:GLU:OE2	14:I:464:ARG:NH2	2.47	0.47
14:I:646:PRO:O	14:I:650:ARG:HG3	2.14	0.47
15:J:49:ILE:HG23	15:J:54:GLU:HG3	1.96	0.47
16:P:16:GLU:HB2	18:T:328:VAL:HB	1.94	0.47
26:K:113:ARG:HG3	26:K:119:ALA:CB	2.44	0.47
1:A:89:LEU:HD21	4:E:213:ASP:HA	1.95	0.47
1:A:335:PRO:HG3	1:A:516:LYS:HB2	1.97	0.47
1:A:1037:CYS:SG	1:A:1209:HIS:NE2	2.77	0.47
1:A:1671:GLU:CD	1:A:1672:THR:H	2.22	0.47
3:C:157:PHE:HE1	3:C:447:VAL:HG21	1.79	0.47
3:C:530:ALA:N	3:C:538:ASP:OD1	2.46	0.47
3:C:603:SER:OG	3:C:647:PHE:HB3	2.14	0.47
3:C:845:MET:SD	3:C:921:TRP:HB3	2.54	0.47
3:C:937:PRO:O	3:C:938:LEU:HB3	2.14	0.47
4:E:239:SER:HB2	4:E:260:ASP:CG	2.39	0.47
5:F:23:A:H2'	5:F:24:U:O4'	2.14	0.47
6:q:113:ARG:HG3	25:L:662:GLU:OE2	2.14	0.47
6:r:62:ARG:HB2	26:K:144:LEU:HD21	1.96	0.47
10:f:30:GLU:HG3	10:f:32:LYS:NZ	2.30	0.47
11:d:40:ILE:HA	11:d:104:MET:O	2.15	0.47
17:M:454:GLU:HA	17:M:457:VAL:HG12	1.95	0.47
19:O:155:GLN:HA	21:R:181:GLN:OE1	2.14	0.47
1:A:214:LYS:HD3	1:A:685:VAL:CG1	2.45	0.47
1:A:470:TRP:HZ2	3:C:279:GLU:HG2	1.79	0.47
3:C:96:PRO:HG2	3:C:99:VAL:HG23	1.97	0.47
3:C:322:ASN:OD1	3:C:323:VAL:HG23	2.13	0.47
3:C:402:ILE:O	3:C:402:ILE:HG22	2.15	0.47
3:C:846:GLU:CG	3:C:924:VAL:HG22	2.44	0.47
8:g:10:LYS:HG2	8:g:34:PHE:HZ	1.79	0.47
9:e:73:LEU:HB2	10:f:12:PHE:CD2	2.49	0.47
14:I:651:LYS:HE3	14:I:690:ASP:HB3	1.96	0.47
14:I:692:ARG:O	14:I:696:MET:HG2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:J:38:LEU:HD22	17:M:531:ARG:HH21	1.80	0.47
21:R:58:PHE:N	21:R:65:GLN:OE1	2.29	0.47
21:R:88:LYS:HE3	21:R:88:LYS:H	1.79	0.47
21:R:176:ALA:N	24:W:107:VAL:O	2.46	0.47
25:L:64:ARG:HB3	25:L:64:ARG:CZ	2.44	0.47
26:K:113:ARG:HG3	26:K:119:ALA:HB1	1.96	0.47
29:Q:232:LEU:O	29:Q:236:ASP:N	2.46	0.47
1:A:670:LYS:HD2	1:A:1612:TYR:HE1	1.79	0.47
1:A:1080:VAL:HG23	25:L:82:ARG:HD2	1.97	0.47
4:E:151:ALA:CB	4:E:171:ASP:HB2	2.45	0.47
4:E:169:GLY:HA3	4:E:198:VAL:HG11	1.96	0.47
12:c:19:GLU:OE1	12:c:20:LEU:N	2.48	0.47
14:I:382:ARG:HA	14:I:385:ILE:HG13	1.96	0.47
15:J:60:LEU:HD11	25:L:209:TYR:H	1.79	0.47
16:P:49:ALA:HB1	16:P:54:LEU:HD11	1.96	0.47
26:K:145:LEU:HD12	26:K:145:LEU:HA	1.64	0.47
28:V:666:SER:OG	28:V:672:ALA:HB2	2.15	0.47
1:A:203:TRP:CZ2	1:A:695:ALA:HB2	2.50	0.47
1:A:322:VAL:HG22	1:A:523:LEU:HD21	1.97	0.47
1:A:551:LEU:HD12	1:A:556:VAL:HG22	1.96	0.47
1:A:1783:PHE:O	1:A:1786:ILE:HG13	2.14	0.47
3:C:387:VAL:HG23	3:C:388:GLN:N	2.29	0.47
3:C:507:PHE:CE1	3:C:629:LYS:HB3	2.49	0.47
6:r:28:ILE:HD12	6:r:31:TYR:HB3	1.95	0.47
11:d:81:LYS:HE3	11:d:81:LYS:HB2	1.80	0.47
13:b:44:ASP:OD1	13:b:44:ASP:N	2.48	0.47
14:I:424:TYR:CE1	14:I:432:ASN:HB3	2.49	0.47
18:T:376:LYS:HG3	18:T:395:ALA:HB3	1.96	0.47
19:O:94:GLN:O	19:O:97:ASP:N	2.47	0.47
20:N:92:LYS:HD3	20:N:92:LYS:HA	1.67	0.47
21:R:131:GLU:O	21:R:135:GLU:HG2	2.15	0.47
21:R:151:GLY:O	21:R:155:SER:HB2	2.14	0.47
1:A:253:GLU:H	1:A:253:GLU:CD	2.23	0.47
1:A:1005:LYS:O	1:A:1155:TYR:CD2	2.68	0.47
1:A:1078:ASN:HD21	25:L:83:THR:H	1.63	0.47
2:B:7:G:OP1	2:B:7:G:H3'	2.14	0.47
3:C:139:ASN:HA	3:C:214:ASN:HB2	1.95	0.47
3:C:368:PRO:HD2	3:C:379:ARG:NH1	2.29	0.47
5:F:75:A:H5'	5:F:76:U:OP2	2.15	0.47
6:r:63:THR:HA	26:K:152:TRP:HZ2	1.79	0.47
6:r:115:ILE:CG1	6:s:114:VAL:HG12	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:g:25:ARG:NH2	9:e:30:LEU:O	2.33	0.47
9:e:48:TYR:HB2	9:e:50:ASN:HD21	1.79	0.47
9:e:83:GLN:HG2	9:e:84:THR:N	2.30	0.47
12:c:48:ALA:HB3	12:c:51:LYS:HB2	1.97	0.47
14:I:599:ARG:NH1	15:J:312:ARG:HH21	2.13	0.47
14:I:726:ARG:NH1	14:I:727:ALA:HB2	2.29	0.47
14:I:731:TRP:CD2	14:I:754:LEU:HD13	2.49	0.47
16:P:11:PRO:HG3	18:T:311:ARG:NH1	2.30	0.47
17:M:531:ARG:HG2	22:H:18:U:O2	2.14	0.47
18:T:247:GLY:O	18:T:274:LYS:NZ	2.47	0.47
19:O:24:GLU:OE1	21:R:175:PRO:HG3	2.15	0.47
22:H:31:U:H4'	22:H:32:G:OP1	2.15	0.47
24:W:118:ILE:HG12	24:W:118:ILE:H	1.44	0.47
25:L:758:VAL:HG22	26:K:166:LEU:HD12	1.96	0.47
25:L:828:LYS:HE2	25:L:829:ARG:HG2	1.96	0.47
29:Q:1097:GLY:O	29:Q:1129:PRO:HA	2.15	0.47
3:C:846:GLU:HG2	3:C:924:VAL:HG22	1.96	0.47
3:C:948:ARG:HH11	3:C:952:VAL:HG21	1.78	0.47
4:E:134:CYS:O	4:E:143:ILE:N	2.36	0.47
4:E:176:LYS:HG2	4:E:188:THR:HG23	1.96	0.47
4:E:311:ARG:NH1	21:R:172:LYS:HZ1	2.12	0.47
6:q:98:ARG:HA	6:q:101:LEU:HB3	1.95	0.47
7:a:24:THR:OG1	7:a:34:ARG:NE	2.47	0.47
25:L:166:ALA:O	25:L:169:LYS:HB3	2.14	0.47
25:L:825:LEU:HA	25:L:828:LYS:HG2	1.97	0.47
3:C:193:SER:HB2	3:C:219:PRO:HA	1.97	0.47
3:C:699:ARG:NH1	3:C:815:PRO:HD2	2.28	0.47
4:E:103:VAL:HG22	13:b:102:GLY:HA3	1.97	0.47
4:E:259:MET:C	4:E:261:ASN:H	2.23	0.47
4:E:279:LYS:NZ	4:E:318:THR:O	2.39	0.47
6:s:88:HIS:O	6:s:92:THR:OG1	2.25	0.47
14:I:740:ARG:HG2	14:I:740:ARG:HH11	1.80	0.47
16:P:25:LYS:HZ3	21:R:205:LYS:H	1.62	0.47
24:W:87:LEU:HD12	24:W:88:GLY:H	1.80	0.47
25:L:179:ARG:HD2	25:L:179:ARG:O	2.14	0.47
25:L:804:GLU:CD	26:K:208:LYS:HB3	2.40	0.47
1:A:309:ASP:HB3	1:A:311:ASN:HB2	1.97	0.47
1:A:1440:GLU:O	1:A:1444:MET:HG2	2.15	0.47
2:B:90:C:N4	10:f:42:MET:HB2	2.25	0.47
3:C:138:ARG:HD2	3:C:455:VAL:HG12	1.97	0.47
7:a:45:ASN:HB3	7:a:67:PHE:CZ	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:a:85:ALA:HB3	7:a:88:PHE:CD2	2.50	0.47
10:f:32:LYS:HG3	10:f:52:TYR:CE2	2.50	0.47
14:I:462:GLU:HB2	14:I:471:ALA:HB2	1.96	0.47
15:J:249:GLU:O	15:J:253:ILE:HG12	2.15	0.47
18:T:208:GLY:HA2	18:T:488:LYS:HE3	1.96	0.47
22:H:2:U:O2'	22:H:3:A:N7	2.47	0.47
24:W:212:GLU:HA	24:W:215:LYS:HG2	1.97	0.47
25:L:761:LEU:HD22	26:K:166:LEU:HB3	1.96	0.47
1:A:449:GLU:CD	1:A:450:PRO:HD2	2.39	0.46
1:A:552:ASP:O	1:A:556:VAL:HG23	2.15	0.46
1:A:738:LYS:HE2	1:A:738:LYS:HB3	1.47	0.46
1:A:986:LEU:HD22	1:A:990:LEU:HG	1.96	0.46
4:E:306:CYS:HB2	4:E:316:TRP:HZ3	1.79	0.46
6:q:14:VAL:CG1	6:q:25:LYS:HB3	2.45	0.46
9:e:43:ILE:HD13	9:e:54:ASP:OD2	2.15	0.46
14:I:647:LYS:HE3	14:I:687:SER:HB2	1.97	0.46
15:J:51:ASP:N	15:J:52:PRO:CD	2.78	0.46
15:J:52:PRO:O	15:J:54:GLU:N	2.47	0.46
17:M:537:LYS:C	17:M:541:ARG:HH21	2.22	0.46
19:O:200:ASP:OD2	19:O:200:ASP:N	2.46	0.46
23:S:46:HIS:HE1	23:S:55:GLN:HG2	1.78	0.46
24:W:49:LEU:N	24:W:49:LEU:CD2	2.73	0.46
25:L:666:LEU:HD23	25:L:666:LEU:HA	1.77	0.46
25:L:676:SER:OG	25:L:678:ASP:OD2	2.22	0.46
31:3:100:C:H2'	31:3:101:U:H6	1.80	0.46
1:A:1711:ASP:OD1	1:A:1712:THR:N	2.31	0.46
3:C:750:TRP:CH2	3:C:776:LEU:HG	2.49	0.46
3:C:856:PRO:HG2	3:C:911:GLN:HB3	1.97	0.46
6:q:104:ALA:O	6:q:107:GLN:HG3	2.15	0.46
10:f:13:LEU:HD22	10:f:42:MET:HE3	1.98	0.46
14:I:472:LEU:HD11	14:I:515:LEU:HD22	1.96	0.46
15:J:58:TYR:OH	25:L:248:LEU:CD2	2.63	0.46
25:L:32:ARG:O	25:L:157:ARG:NH2	2.41	0.46
26:K:212:ILE:O	26:K:215:ALA:HB3	2.15	0.46
1:A:132:HIS:HB3	1:A:135:MET:SD	2.56	0.46
1:A:227:PRO:HB2	1:A:623:ASP:HB3	1.97	0.46
1:A:570:LEU:O	1:A:574:ARG:HB2	2.15	0.46
1:A:832:ASP:HB3	1:A:835:VAL:HG23	1.97	0.46
3:C:348:GLY:O	3:C:350:GLY:N	2.48	0.46
4:E:152:VAL:HB	4:E:171:ASP:OD2	2.15	0.46
4:E:286:HIS:CD2	4:E:293:LEU:HD12	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:b:25:ARG:HG3	13:b:49:ARG:HB3	1.98	0.46
20:N:67:GLN:HG2	24:W:178:ARG:HH12	1.81	0.46
24:W:277:HIS:O	24:W:574:TYR:N	2.32	0.46
26:K:67:ARG:HG3	26:K:67:ARG:NH1	2.29	0.46
1:A:84:LEU:O	1:A:85:GLN:HG2	2.15	0.46
1:A:167:MET:HG2	1:A:169:TRP:CH2	2.50	0.46
1:A:1657:LEU:HA	1:A:1657:LEU:HD23	1.56	0.46
1:A:1695:LEU:CD2	1:A:1725:TRP:HD1	2.25	0.46
3:C:325:PHE:O	3:C:333:SER:OG	2.23	0.46
3:C:421:ARG:HD3	3:C:421:ARG:H	1.80	0.46
3:C:783:VAL:O	3:C:787:PHE:HB3	2.15	0.46
5:F:75:A:C8	22:H:18:U:H5'	2.49	0.46
6:t:80:TRP:HA	6:t:80:TRP:CE3	2.50	0.46
7:a:39:ASP:OD2	7:a:40:ALA:N	2.45	0.46
12:c:4:LEU:HD12	12:c:4:LEU:HA	1.56	0.46
15:J:76:PHE:CD2	15:J:77:ASN:HB2	2.51	0.46
17:M:442:PRO:O	17:M:446:TYR:HB2	2.14	0.46
19:O:215:LYS:HE2	19:O:215:LYS:N	2.31	0.46
22:H:36:A:H2'	22:H:37:G:C8	2.50	0.46
25:L:656:ALA:O	25:L:659:VAL:HB	2.15	0.46
1:A:97:ALA:HA	1:A:100:ASN:ND2	2.25	0.46
1:A:191:ILE:CG2	1:A:484:ARG:HG2	2.46	0.46
1:A:791:LYS:H	21:R:264:ASP:HA	1.81	0.46
1:A:1367:LEU:HD12	1:A:1375:PHE:HZ	1.76	0.46
3:C:149:GLY:O	3:C:153:ILE:HG13	2.16	0.46
3:C:200:SER:HA	3:C:213:LEU:O	2.15	0.46
6:r:82:ALA:HA	6:r:85:LEU:HB3	1.97	0.46
15:J:60:LEU:HD12	15:J:60:LEU:HA	1.66	0.46
16:P:57:LYS:HE2	16:P:57:LYS:HB3	1.74	0.46
21:R:114:LEU:HD13	21:R:223:LEU:HD13	1.97	0.46
23:S:58:ASP:HB2	23:S:103:GLN:NE2	2.30	0.46
23:S:75:GLU:H	23:S:75:GLU:CD	2.24	0.46
25:L:755:THR:HA	25:L:758:VAL:HG12	1.97	0.46
1:A:180:HIS:HB2	1:A:185:ILE:HD12	1.98	0.46
1:A:357:ILE:HD11	3:C:938:LEU:H	1.80	0.46
1:A:1189:ILE:HG12	1:A:1211:VAL:HG11	1.98	0.46
3:C:274:ASP:HB3	3:C:398:TYR:OH	2.15	0.46
3:C:330:SER:O	3:C:434:LYS:HA	2.15	0.46
3:C:603:SER:HB2	3:C:647:PHE:C	2.41	0.46
6:q:76:PHE:HE2	6:r:72:LEU:HB3	1.80	0.46
8:g:14:ASP:CG	8:g:32:ARG:HH12	2.24	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:I:418:CYS:O	14:I:422:LYS:HD3	2.16	0.46
14:I:484:ARG:CZ	14:I:496:LEU:HD22	2.46	0.46
14:I:675:GLU:HB2	14:I:679:GLU:OE1	2.16	0.46
17:M:470:LYS:O	17:M:473:ASP:N	2.42	0.46
21:R:61:ILE:HG22	21:R:63:VAL:H	1.81	0.46
21:R:144:ALA:O	21:R:148:VAL:HG23	2.16	0.46
26:K:170:LEU:HD13	26:K:174:ARG:CG	2.45	0.46
31:3:13:C:H2'	31:3:14:A:H8	1.79	0.46
1:A:338:GLU:HB2	1:A:339:PRO:HD2	1.96	0.46
1:A:368:THR:OG1	27:U:3:ASN:OD1	2.22	0.46
3:C:366:PHE:HB2	3:C:373:PHE:CE1	2.51	0.46
3:C:606:LYS:NZ	3:C:676:VAL:HG23	2.31	0.46
4:E:109:ASN:HB2	4:E:129:ASP:HB3	1.97	0.46
5:F:16:U:H2'	5:F:17:G:O4'	2.16	0.46
6:r:91:ARG:HE	26:K:75:PRO:HB3	1.80	0.46
6:r:98:ARG:HH11	26:K:72:VAL:HG12	1.80	0.46
7:a:14:LEU:HD13	7:a:88:PHE:CE2	2.51	0.46
14:I:105:VAL:N	29:Q:1330:THR:CB	2.78	0.46
14:I:436:ILE:HA	14:I:439:LYS:HE3	1.98	0.46
14:I:560:PHE:CE2	14:I:590:TYR:HE2	2.34	0.46
14:I:601:LEU:HD12	15:J:296:LYS:NZ	2.31	0.46
15:J:255:PHE:CG	15:J:271:ILE:HD12	2.51	0.46
18:T:511:PRO:O	18:T:513:LYS:N	2.48	0.46
1:A:85:GLN:C	1:A:87:LYS:H	2.24	0.46
1:A:256:GLU:O	1:A:257:GLU:HB2	2.16	0.46
1:A:1340:GLU:OE1	1:A:1439:TRP:HB2	2.15	0.46
1:A:1534:TYR:HE1	1:A:1535:ARG:HH11	1.63	0.46
3:C:397:MET:SD	3:C:440:VAL:HG21	2.56	0.46
3:C:607:ILE:O	3:C:645:THR:HA	2.15	0.46
4:E:296:ASP:OD1	4:E:297:TYR:N	2.49	0.46
6:r:12:GLN:HA	6:r:54:LYS:NZ	2.27	0.46
7:a:45:ASN:HA	7:a:68:ILE:O	2.15	0.46
7:a:80:ASP:O	7:a:83:LYS:HG2	2.15	0.46
12:c:59:LEU:HD13	12:c:60:SER:N	2.30	0.46
15:J:91:GLN:OE1	25:L:248:LEU:HD21	2.16	0.46
17:M:488:GLN:HG3	17:M:489:PRO:HD2	1.97	0.46
18:T:340:LEU:HB2	18:T:349:ILE:HB	1.96	0.46
25:L:779:HIS:NE2	26:K:180:LEU:O	2.48	0.46
1:A:368:THR:HB	27:U:1:MET:CE	2.45	0.46
1:A:1439:TRP:HZ3	1:A:1480:ILE:HD11	1.80	0.46
1:A:1461:LYS:HD2	1:A:1461:LYS:HA	1.53	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:88:A:HO2'	11:d:57:ARG:HH22	1.60	0.46
3:C:341:ARG:HA	3:C:353:PRO:CG	2.46	0.46
3:C:845:MET:HE2	3:C:922:GLN:HA	1.98	0.46
4:E:217:LYS:HD3	4:E:217:LYS:N	2.31	0.46
14:I:424:TYR:HB3	14:I:433:ALA:HB2	1.98	0.46
14:I:579:TRP:O	14:I:583:LEU:HB2	2.16	0.46
14:I:658:VAL:HG13	14:I:670:VAL:HG22	1.98	0.46
15:J:58:TYR:CE1	25:L:248:LEU:CD2	2.95	0.46
18:T:191:PRO:HG3	18:T:509:PHE:HB2	1.97	0.46
19:O:19:MET:SD	19:O:20:PRO:HD2	2.56	0.46
19:O:25:THR:OG1	19:O:156:PRO:HB3	2.16	0.46
25:L:541:ASP:OD1	25:L:543:ARG:NH1	2.49	0.46
25:L:740:LEU:HD23	26:K:145:LEU:CD1	2.46	0.46
25:L:752:GLY:HA2	25:L:755:THR:HG22	1.97	0.46
1:A:100:ASN:O	1:A:104:TYR:HD2	1.99	0.46
1:A:209:MET:SD	1:A:252:MET:HG3	2.56	0.46
1:A:213:GLU:HG3	1:A:636:TYR:CZ	2.51	0.46
1:A:215:ARG:HB2	1:A:685:VAL:HG22	1.98	0.46
1:A:223:MET:HG2	1:A:633:VAL:HG21	1.98	0.46
1:A:250:ILE:O	1:A:251:GLU:HG3	2.16	0.46
1:A:643:GLN:HG2	1:A:691:VAL:O	2.16	0.46
1:A:1019:TRP:CZ3	1:A:1040:MET:HE1	2.51	0.46
1:A:1721:GLY:O	1:A:1723:LYS:HG2	2.16	0.46
3:C:321:GLY:O	3:C:450:MET:HG2	2.16	0.46
3:C:522:ASP:OD2	3:C:523:THR:N	2.49	0.46
4:E:208:TYR:CE1	4:E:268:VAL:HG11	2.50	0.46
4:E:269:ARG:O	4:E:276:ARG:NH1	2.40	0.46
6:s:86:GLU:O	6:s:90:THR:HG23	2.16	0.46
9:e:28:ILE:HD11	9:e:79:ILE:HG23	1.97	0.46
10:f:30:GLU:CG	10:f:52:TYR:HB2	2.44	0.46
12:c:20:LEU:HD21	13:b:79:VAL:HG21	1.98	0.46
14:I:530:ASP:O	14:I:534:GLU:HB2	2.16	0.46
15:J:39:GLU:O	15:J:41:ASP:N	2.49	0.46
23:S:92:MET:HB2	23:S:119:THR:HG23	1.97	0.46
24:W:80:GLU:H	24:W:80:GLU:CD	2.24	0.46
29:Q:233:SER:O	29:Q:237:GLY:N	2.49	0.46
1:A:1183:ASP:OD2	1:A:1187:GLU:HB2	2.16	0.45
1:A:1786:ILE:O	1:A:1789:LEU:N	2.49	0.45
3:C:143:VAL:HG11	3:C:228:VAL:HG13	1.98	0.45
3:C:413:LEU:HG	3:C:418:VAL:CG1	2.46	0.45
3:C:662:ARG:CZ	3:C:662:ARG:HB3	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:863:ILE:O	3:C:867:LEU:HG	2.16	0.45
6:q:91:ARG:HG3	6:q:95:HIS:CE1	2.51	0.45
14:I:462:GLU:CB	14:I:471:ALA:HB2	2.46	0.45
15:J:67:GLU:OE1	15:J:84:TYR:OH	2.22	0.45
15:J:172:TRP:O	15:J:177:PRO:HD3	2.16	0.45
15:J:244:GLU:H	15:J:244:GLU:HG3	1.59	0.45
18:T:198:LYS:HG2	18:T:496:VAL:HG22	1.99	0.45
20:N:128:ALA:HB2	24:W:129:ALA:HA	1.97	0.45
21:R:251:LYS:HB3	21:R:253:TYR:CE2	2.50	0.45
25:L:723:ARG:HE	26:K:106:LEU:HD11	1.81	0.45
29:Q:1363:ALA:C	29:Q:1365:VAL:H	2.23	0.45
29:Q:1644:GLU:HA	29:Q:1648:ALA:HB2	1.98	0.45
1:A:1265:ARG:HH12	1:A:1266:MET:HB2	1.81	0.45
3:C:158:VAL:HG11	3:C:180:PHE:CD2	2.51	0.45
3:C:421:ARG:HD3	3:C:421:ARG:N	2.31	0.45
5:F:30:A:H2'	5:F:31:A:H8	1.81	0.45
14:I:102:ARG:O	29:Q:1326:SER:CB	2.65	0.45
14:I:564:GLU:CD	15:J:296:LYS:HB3	2.40	0.45
14:I:633:HIS:O	14:I:637:ILE:HG12	2.16	0.45
15:J:232:ARG:O	15:J:236:GLU:HG2	2.16	0.45
16:P:223:ASN:O	16:P:227:ARG:HG3	2.16	0.45
19:O:24:GLU:OE2	21:R:182:TYR:HB3	2.16	0.45
19:O:30:ASN:HD21	24:W:127:PHE:HB3	1.80	0.45
25:L:702:ARG:N	25:L:702:ARG:HD2	2.31	0.45
25:L:800:THR:O	25:L:803:ARG:HB3	2.17	0.45
1:A:389:VAL:O	1:A:390:TYR:C	2.59	0.45
1:A:754:MET:SD	1:A:770:ALA:HB1	2.56	0.45
1:A:1433:TYR:C	1:A:1433:TYR:CD2	2.95	0.45
1:A:1480:ILE:HD12	1:A:1480:ILE:HA	1.70	0.45
1:A:1702:ASN:O	1:A:1784:PRO:HD3	2.16	0.45
1:A:1703:MET:HA	1:A:1783:PHE:HA	1.98	0.45
1:A:1782:TRP:HB3	1:A:1786:ILE:HD13	1.97	0.45
3:C:619:LYS:HA	3:C:619:LYS:HD3	1.71	0.45
4:E:361:THR:OG1	24:W:76:ASN:O	2.22	0.45
5:F:23:A:H2'	5:F:24:U:C1'	2.46	0.45
6:s:133:LYS:HA	6:s:133:LYS:HD2	1.53	0.45
8:g:9:LEU:H	8:g:9:LEU:HD22	1.80	0.45
14:I:633:HIS:HA	14:I:636:ASP:OD2	2.16	0.45
21:R:39:LEU:HD21	23:S:22:LYS:HG3	1.97	0.45
21:R:174:THR:HG23	21:R:188:GLN:HG2	1.97	0.45
29:Q:227:PHE:O	29:Q:231:VAL:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1281:GLN:OE1	1:A:1288:ARG:HG3	2.16	0.45
2:B:28:A:H2'	2:B:29:U:H5'	1.98	0.45
3:C:195:LYS:HA	3:C:227:GLU:HG3	1.97	0.45
3:C:447:VAL:HG23	3:C:448:VAL:H	1.82	0.45
3:C:477:PRO:HD2	3:C:589:GLU:OE2	2.17	0.45
5:F:92:U:H2'	14:I:447:TYR:CD1	2.52	0.45
13:b:75:GLY:HA2	13:b:78:ILE:HG13	1.98	0.45
15:J:255:PHE:HB3	15:J:271:ILE:HG21	1.99	0.45
21:R:134:VAL:O	21:R:138:VAL:HG23	2.16	0.45
22:H:11:C:O2'	22:H:12:G:H8	1.99	0.45
23:S:53:MET:CE	23:S:55:GLN:HB2	2.41	0.45
1:A:230:ASP:HB3	1:A:583:ASP:OD2	2.17	0.45
1:A:331:ILE:H	1:A:331:ILE:HG12	1.35	0.45
1:A:568:LEU:CD1	1:A:612:ARG:HB3	2.46	0.45
1:A:920:LEU:HB2	1:A:925:ARG:HG3	1.97	0.45
1:A:1372:PRO:C	1:A:1374:ARG:H	2.24	0.45
2:B:10:G:O2'	2:B:11:A:OP2	2.32	0.45
3:C:339:PHE:HD1	3:C:390:VAL:HG22	1.80	0.45
3:C:429:THR:O	3:C:433:LEU:HB2	2.16	0.45
4:E:348:SER:O	4:E:355:ILE:HG23	2.15	0.45
5:F:61:C:C2	16:P:33:LYS:HD2	2.52	0.45
19:O:108:PRO:HG2	19:O:114:LYS:HA	1.99	0.45
20:N:12:PRO:HB3	20:N:78:TRP:CZ2	2.51	0.45
21:R:55:GLY:HA3	23:S:128:MET:CB	2.47	0.45
21:R:79:GLN:NE2	23:S:50:ARG:HD3	2.30	0.45
21:R:114:LEU:HD12	21:R:114:LEU:HA	1.70	0.45
23:S:12:MET:HE3	23:S:12:MET:HB3	1.58	0.45
28:V:771:THR:O	28:V:775:THR:N	2.50	0.45
31:3:4:A:H2'	31:3:5:G:O4'	2.16	0.45
1:A:120:MET:HG3	1:A:547:GLN:HG2	1.98	0.45
1:A:1162:MET:HE2	1:A:1162:MET:HB3	1.90	0.45
1:A:1697:ALA:HB3	1:A:1724:TYR:CE2	2.51	0.45
1:A:1716:TYR:HB3	1:A:1717:ASP:H	1.57	0.45
2:B:92:U:H4'	2:B:93:U:H5'	1.97	0.45
3:C:139:ASN:HB3	3:C:235:ALA:HA	1.99	0.45
3:C:157:PHE:CE1	3:C:447:VAL:HG21	2.51	0.45
3:C:451:LEU:O	3:C:455:VAL:N	2.49	0.45
4:E:167:VAL:HG21	4:E:207:VAL:HG22	1.98	0.45
4:E:330:HIS:CD2	4:E:334:VAL:HG22	2.48	0.45
6:q:115:ILE:HG23	6:t:118:LEU:HD11	1.98	0.45
6:r:122:ARG:HH11	6:s:118:LEU:HD22	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:g:34:PHE:HA	8:g:39:ASN:O	2.16	0.45
12:c:66:ILE:HG21	12:c:69:TYR:HE2	1.80	0.45
12:c:86:LYS:HZ1	12:c:88:LYS:HB2	1.81	0.45
14:I:420:PHE:HB3	14:I:436:ILE:HG21	1.99	0.45
17:M:466:TYR:O	17:M:470:LYS:HG2	2.17	0.45
18:T:195:ALA:HB3	18:T:495:GLU:HG2	1.98	0.45
22:H:6:U:H4'	22:H:7:U:OP1	2.16	0.45
25:L:147:GLU:O	25:L:147:GLU:HG2	2.17	0.45
1:A:388:SER:O	1:A:390:TYR:HD1	1.99	0.45
1:A:1042:GLN:O	1:A:1042:GLN:HG2	2.17	0.45
3:C:366:PHE:CZ	3:C:371:ARG:HA	2.51	0.45
3:C:527:LEU:HD23	3:C:581:THR:HB	1.98	0.45
4:E:256:SER:O	4:E:263:LEU:HD12	2.17	0.45
5:F:19:U:H6	5:F:19:U:H2'	1.41	0.45
5:F:37:G:H2'	5:F:37:G:N3	2.32	0.45
6:t:80:TRP:HA	6:t:80:TRP:HE3	1.82	0.45
9:e:77:ASP:OD2	9:e:77:ASP:N	2.49	0.45
11:d:68:GLU:H	11:d:68:GLU:HG3	1.68	0.45
19:O:99:ALA:CB	19:O:145:ASN:HD22	2.18	0.45
19:O:146:GLU:OE1	19:O:146:GLU:HA	2.16	0.45
21:R:199:ASP:HB3	21:R:202:GLU:HB2	1.97	0.45
24:W:219:ALA:HA	24:W:222:GLU:HG3	1.98	0.45
25:L:757:ARG:O	25:L:760:GLU:HG3	2.17	0.45
1:A:311:ASN:HD22	1:A:311:ASN:N	2.14	0.45
1:A:318:PRO:O	1:A:322:VAL:HG23	2.17	0.45
1:A:1025:ASN:N	1:A:1025:ASN:HD22	2.15	0.45
1:A:1642:ARG:HB3	1:A:1810:ARG:NH2	2.32	0.45
1:A:1703:MET:HE3	1:A:1703:MET:HB2	1.60	0.45
3:C:518:LEU:HD21	3:C:544:VAL:HG11	1.99	0.45
3:C:602:ARG:HD3	3:C:918:PHE:CE1	2.51	0.45
6:r:98:ARG:HH12	26:K:72:VAL:CB	2.26	0.45
7:a:77:ILE:HG13	13:b:71:VAL:HG22	1.99	0.45
13:b:12:TYR:CB	13:b:17:MET:HE1	2.47	0.45
19:O:83:CYS:HB2	19:O:85:LEU:HG	1.97	0.45
24:W:79:VAL:O	24:W:83:HIS:HB2	2.17	0.45
25:L:551:ALA:O	25:L:555:ARG:HG3	2.17	0.45
25:L:761:LEU:O	25:L:765:VAL:HG23	2.16	0.45
25:L:762:TRP:HB2	26:K:166:LEU:HD11	1.99	0.45
26:K:142:GLU:O	26:K:146:LYS:HB2	2.17	0.45
1:A:457:LEU:CD1	3:C:395:TYR:HB2	2.47	0.45
1:A:1410:THR:OG1	3:C:938:LEU:HD13	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:t:75:LEU:HD22	6:t:79:GLU:OE1	2.17	0.45
20:N:150:LYS:HA	20:N:150:LYS:HD3	1.74	0.45
21:R:55:GLY:O	23:S:123:ARG:NH2	2.40	0.45
23:S:90:LEU:HG	23:S:121:PHE:CZ	2.51	0.45
25:L:767:ASP:O	25:L:771:GLU:HG2	2.16	0.45
25:L:802:ARG:NE	25:L:802:ARG:HA	2.31	0.45
26:K:110:PRO:O	26:K:114:ARG:N	2.50	0.45
26:K:214:ARG:O	26:K:217:ASP:HB3	2.16	0.45
28:V:661:LEU:O	28:V:665:SER:OG	2.21	0.45
1:A:94:LYS:HD2	1:A:94:LYS:O	2.17	0.45
1:A:165:MET:HE2	1:A:694:TRP:CH2	2.52	0.45
1:A:310:ARG:HA	1:A:310:ARG:CZ	2.46	0.45
1:A:544:LYS:O	1:A:544:LYS:HG2	2.17	0.45
1:A:574:ARG:HG3	1:A:574:ARG:NH1	2.31	0.45
1:A:1427:GLN:C	1:A:1428:LEU:HG	2.41	0.45
1:A:1449:VAL:O	1:A:1452:GLU:HG3	2.17	0.45
1:A:1691:ALA:H	1:A:1725:TRP:HZ2	1.64	0.45
3:C:192:MET:SD	3:C:652:MET:HE2	2.57	0.45
4:E:127:SER:O	4:E:153:VAL:HG23	2.17	0.45
4:E:239:SER:HB2	4:E:260:ASP:OD1	2.16	0.45
4:E:330:HIS:CE1	4:E:356:PHE:HD2	2.34	0.45
6:q:90:THR:HG22	6:t:94:LEU:HD13	1.99	0.45
6:r:105:LEU:C	6:r:105:LEU:CD2	2.90	0.45
6:s:94:LEU:O	6:s:98:ARG:HG3	2.17	0.45
14:I:455:TRP:CD2	14:I:478:ALA:HB2	2.52	0.45
14:I:501:ARG:NE	14:I:501:ARG:HA	2.32	0.45
19:O:179:GLU:HA	20:N:133:ILE:HD12	1.99	0.45
24:W:59:LEU:HD22	24:W:59:LEU:N	2.32	0.45
24:W:59:LEU:O	24:W:62:VAL:HG12	2.17	0.45
1:A:259:ASP:O	1:A:263:TYR:HB2	2.16	0.44
1:A:1210:ASP:CG	1:A:1243:SER:HG	2.22	0.44
1:A:1213:LEU:O	1:A:1217:VAL:HG13	2.17	0.44
1:A:1502:VAL:O	1:A:1503:ARG:C	2.60	0.44
3:C:123:SER:HB3	7:a:89:LYS:CE	2.47	0.44
3:C:482:MET:HB2	3:C:482:MET:HE2	1.69	0.44
6:r:16:SER:HB3	6:r:19:SER:OG	2.17	0.44
6:r:23:PHE:HZ	6:r:40:VAL:HG23	1.82	0.44
6:r:33:ARG:HH11	6:r:33:ARG:HB2	1.83	0.44
14:I:105:VAL:CA	29:Q:1329:TYR:CB	2.92	0.44
14:I:370:ARG:HD3	14:I:370:ARG:HA	1.71	0.44
14:I:393:GLN:HB2	14:I:423:PHE:CZ	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:J:27:GLU:HA	15:J:30:LEU:HD12	1.98	0.44
19:O:45:HIS:CD2	19:O:68:VAL:HG22	2.52	0.44
20:N:11:LYS:HG2	20:N:12:PRO:HD2	2.00	0.44
25:L:162:ARG:HG3	25:L:163:GLY:N	2.31	0.44
25:L:568:GLN:HE21	25:L:568:GLN:HB3	1.62	0.44
25:L:688:HIS:CD2	25:L:691:LEU:HD12	2.52	0.44
25:L:770:GLN:NE2	25:L:771:GLU:HG2	2.32	0.44
25:L:775:PHE:HA	26:K:184:ARG:HH12	1.81	0.44
1:A:168:PRO:HB2	1:A:206:MET:SD	2.57	0.44
3:C:606:LYS:HG3	3:C:647:PHE:CE2	2.52	0.44
3:C:789:TRP:CE3	3:C:830:ARG:HD2	2.52	0.44
4:E:146:MET:HB3	4:E:178:TRP:HZ3	1.82	0.44
15:J:213:LYS:HZ1	15:J:217:ARG:NH2	2.15	0.44
19:O:22:VAL:HG11	19:O:56:TRP:HH2	1.83	0.44
19:O:35:MET:HB2	19:O:56:TRP:HB3	1.98	0.44
19:O:75:LYS:HB2	24:W:106:PHE:CZ	2.52	0.44
25:L:767:ASP:O	25:L:770:GLN:HG3	2.17	0.44
29:Q:790:SER:CB	29:Q:1510:ALA:HB2	2.47	0.44
1:A:150:ALA:HA	21:R:201:LEU:HD22	1.99	0.44
1:A:388:SER:O	1:A:390:TYR:CD1	2.71	0.44
1:A:457:LEU:HA	3:C:396:LYS:HG3	1.99	0.44
1:A:540:LEU:HG	1:A:546:PHE:CE2	2.53	0.44
1:A:889:ILE:HB	1:A:1065:VAL:HG12	1.99	0.44
1:A:1247:PRO:HB3	1:A:1265:ARG:NH1	2.32	0.44
1:A:1351:LEU:HD22	1:A:1354:LYS:HE3	1.99	0.44
1:A:1398:LEU:HD13	1:A:1417:PHE:CZ	2.52	0.44
1:A:1516:PRO:O	1:A:1519:TRP:HZ3	2.01	0.44
3:C:131:MET:HB3	3:C:565:ASN:OD1	2.17	0.44
3:C:293:HIS:CE1	3:C:881:PRO:HG2	2.52	0.44
5:F:34:A:C6	5:F:35:C:C4	3.05	0.44
9:e:48:TYR:HB2	9:e:50:ASN:ND2	2.32	0.44
10:f:65:LEU:HD13	11:d:24:PRO:HB2	1.98	0.44
14:I:617:LEU:HD12	14:I:618:TYR:N	2.31	0.44
23:S:153:ARG:HE	23:S:155:ARG:HB3	1.83	0.44
25:L:723:ARG:HH12	26:K:108:PRO:HB3	1.82	0.44
28:V:678:LYS:O	28:V:678:LYS:HG2	2.17	0.44
1:A:319:GLN:OE1	1:A:386:ARG:HB3	2.17	0.44
1:A:359:LYS:HB3	3:C:957:ARG:HB2	1.98	0.44
1:A:746:ASP:OD1	1:A:810:LYS:NZ	2.47	0.44
1:A:1639:GLN:HB2	1:A:1642:ARG:HH21	1.82	0.44
3:C:659:LYS:HD3	3:C:659:LYS:HA	1.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:705:ILE:HG23	3:C:809:LEU:HD11	1.98	0.44
3:C:849:TYR:HB2	3:C:892:LEU:O	2.17	0.44
3:C:900:PHE:CZ	3:C:904:LEU:HD22	2.52	0.44
4:E:222:ARG:HD2	4:E:222:ARG:HA	1.63	0.44
4:E:269:ARG:HB3	25:L:808:GLN:NE2	2.33	0.44
5:F:28:A:H2'	5:F:29:A:C8	2.52	0.44
5:F:73:G:H5'	5:F:74:C:OP1	2.17	0.44
6:t:68:SER:CB	26:K:82:VAL:HA	2.48	0.44
8:g:32:ARG:HD3	8:g:32:ARG:HA	1.78	0.44
9:e:15:LEU:O	9:e:18:ARG:HB2	2.17	0.44
14:I:546:TYR:CZ	14:I:562:VAL:HG21	2.52	0.44
18:T:387:GLU:CD	18:T:446:ARG:HH12	2.25	0.44
18:T:443:TRP:CE3	18:T:450:CYS:HB3	2.53	0.44
21:R:54:ASP:CG	23:S:127:GLY:H	2.24	0.44
22:H:37:G:H2'	22:H:38:U:O4'	2.17	0.44
25:L:654:SER:O	25:L:657:GLU:HG2	2.17	0.44
31:3:92:U:C4	31:3:93:A:N7	2.86	0.44
1:A:394:MET:HE3	3:C:911:GLN:O	2.18	0.44
1:A:532:LYS:HA	1:A:532:LYS:HD2	1.80	0.44
1:A:1339:ARG:H	1:A:1339:ARG:HG3	1.51	0.44
1:A:1340:GLU:OE1	1:A:1439:TRP:N	2.50	0.44
3:C:124:ASN:HA	3:C:127:LEU:HD23	1.98	0.44
3:C:179:ARG:NH2	32:C:1001:GTP:O3'	2.51	0.44
3:C:344:ALA:CB	3:C:353:PRO:HG3	2.48	0.44
3:C:639:GLU:HB3	3:C:641:SER:N	2.32	0.44
4:E:107:HIS:HA	4:E:133:ARG:NH1	2.32	0.44
4:E:129:ASP:OD1	4:E:131:THR:HB	2.17	0.44
4:E:301:GLY:O	4:E:318:THR:HG21	2.17	0.44
7:a:83:LYS:HB3	13:b:70:LEU:HD22	1.99	0.44
8:g:46:VAL:HA	8:g:53:ASP:HA	1.99	0.44
12:c:19:GLU:O	12:c:67:ARG:HB3	2.18	0.44
13:b:9:LEU:HA	13:b:12:TYR:CD2	2.52	0.44
1:A:373:ALA:HB1	1:A:389:VAL:HG21	2.00	0.44
1:A:538:ARG:HD3	2:B:14:U:H5''	1.99	0.44
1:A:747:LEU:HD11	5:F:50:U:H5'	2.00	0.44
1:A:1681:ARG:HH22	1:A:1685:LYS:NZ	2.16	0.44
1:A:1715:VAL:HG21	1:A:1784:PRO:HB3	1.99	0.44
3:C:461:ALA:O	3:C:465:LYS:HB2	2.17	0.44
3:C:827:PRO:O	3:C:831:ARG:HG3	2.18	0.44
4:E:270:PRO:HD2	25:L:812:LYS:HZ2	1.82	0.44
5:F:2:U:H2'	5:F:3:G:H8	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:38:A:N6	31:3:3:A:O2'	2.50	0.44
9:e:15:LEU:HD13	9:e:18:ARG:HH11	1.83	0.44
12:c:62:ARG:HE	13:b:38:MET:CE	2.30	0.44
13:b:13:ILE:HA	13:b:31:PHE:HB3	2.00	0.44
14:I:436:ILE:HD13	14:I:439:LYS:HZ3	1.82	0.44
16:P:13:ILE:HB	21:R:213:ARG:HH12	1.83	0.44
19:O:50:PRO:HG3	21:R:206:PHE:CG	2.53	0.44
31:3:94:C:H2'	31:3:95:U:C6	2.53	0.44
1:A:138:ARG:HG3	1:A:141:ARG:HD3	1.99	0.44
1:A:597:LYS:HB2	31:3:4:A:OP1	2.18	0.44
1:A:1247:PRO:HA	1:A:1265:ARG:HD3	2.00	0.44
1:A:1610:ASN:HB2	1:A:1736:ASP:OD1	2.17	0.44
1:A:2015:ARG:O	1:A:2019:ARG:N	2.51	0.44
2:B:17:A:N1	2:B:62:A:C6	2.86	0.44
5:F:79:A:H2	5:F:80:U:N3	2.16	0.44
6:s:117:ARG:NE	26:K:37:ASP:OD1	2.50	0.44
7:a:37:LEU:HA	7:a:48:LEU:HA	1.99	0.44
9:e:14:ASN:O	9:e:18:ARG:HG3	2.18	0.44
12:c:25:VAL:C	12:c:26:ILE:HG13	2.43	0.44
14:I:394:ILE:HG13	14:I:423:PHE:CE2	2.50	0.44
1:A:330:CYS:H	27:U:2:TYR:HB2	1.82	0.44
1:A:665:GLN:HG2	1:A:704:PHE:HB2	1.98	0.44
1:A:1120:THR:HA	1:A:1123:THR:HG22	1.98	0.44
2:B:40:C:C3'	2:B:41:C:H5'	2.47	0.44
3:C:108:LYS:HE2	3:C:503:ASP:HA	2.00	0.44
3:C:166:LYS:HD2	3:C:166:LYS:HA	1.51	0.44
3:C:364:LEU:HA	3:C:374:ARG:O	2.16	0.44
3:C:755:GLU:O	3:C:758:GLY:N	2.50	0.44
8:g:22:ASN:HA	8:g:65:GLN:NE2	2.33	0.44
14:I:377:ALA:O	14:I:380:HIS:HB2	2.18	0.44
14:I:455:TRP:CB	14:I:508:LEU:HD21	2.47	0.44
14:I:560:PHE:HE2	14:I:590:TYR:HE2	1.65	0.44
14:I:707:GLU:HG3	14:I:707:GLU:O	2.17	0.44
15:J:91:GLN:NE2	25:L:248:LEU:HD21	2.33	0.44
19:O:301:MET:HE2	19:O:301:MET:HB3	1.78	0.44
21:R:293:GLU:O	21:R:297:MET:HG3	2.18	0.44
24:W:54:ASN:OD1	24:W:54:ASN:N	2.50	0.44
24:W:125:HIS:CD2	24:W:128:HIS:ND1	2.86	0.44
25:L:21:ALA:HB1	25:L:33:ILE:HG12	2.00	0.44
26:K:113:ARG:HD2	26:K:113:ARG:HA	1.79	0.44
26:K:170:LEU:HD13	26:K:174:ARG:HG2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:165:MET:CE	1:A:642:LEU:HD13	2.48	0.44
1:A:544:LYS:HB2	20:N:110:GLY:O	2.18	0.44
1:A:1138:TYR:OH	1:A:1150:ARG:O	2.15	0.44
1:A:1350:ASP:OD1	1:A:1399:ILE:HD13	2.18	0.44
2:B:49:A:O2'	2:B:50:A:H8	2.00	0.44
3:C:336:LEU:HD21	3:C:361:TRP:HB2	1.98	0.44
3:C:368:PRO:HD2	3:C:379:ARG:HH12	1.83	0.44
3:C:582:LEU:HA	3:C:582:LEU:HD12	1.68	0.44
5:F:29:A:H2'	5:F:30:A:O4'	2.18	0.44
5:F:86:A:H4'	5:F:87:A:OP1	2.17	0.44
6:r:98:ARG:NH1	26:K:72:VAL:CG1	2.80	0.44
6:r:108:HIS:CD2	6:s:107:GLN:HB3	2.53	0.44
6:s:119:LEU:HD11	26:K:43:LEU:HD21	2.00	0.44
10:f:13:LEU:HD23	10:f:38:THR:HG21	2.00	0.44
10:f:72:MET:HG2	10:f:73:TYR:HD1	1.82	0.44
14:I:392:LYS:O	14:I:396:THR:HG23	2.18	0.44
14:I:504:ARG:HA	14:I:537:ILE:HD13	1.99	0.44
14:I:715:TYR:HB3	14:I:734:TRP:CE2	2.53	0.44
20:N:52:ARG:HD3	20:N:156:TRP:CE2	2.53	0.44
23:S:88:GLY:CA	23:S:128:MET:HE1	2.47	0.44
31:3:5:G:C2	31:3:6:A:C5	3.05	0.44
3:C:194:ILE:HG23	3:C:224:PHE:CZ	2.53	0.43
6:q:3:CYS:HB2	6:q:10:PRO:HG3	1.99	0.43
6:q:116:ALA:HA	25:L:596:LEU:HD23	1.99	0.43
11:d:45:ASN:HA	11:d:47:LYS:NZ	2.28	0.43
13:b:66:ARG:CD	13:b:68:LEU:HG	2.47	0.43
15:J:91:GLN:CD	25:L:248:LEU:HD21	2.43	0.43
19:O:54:PHE:CD1	21:R:193:MET:HE1	2.53	0.43
20:N:12:PRO:HB3	20:N:78:TRP:CH2	2.53	0.43
24:W:93:TYR:O	24:W:93:TYR:CG	2.70	0.43
25:L:548:ARG:HE	25:L:548:ARG:HB3	1.57	0.43
25:L:817:ARG:HH21	26:K:226:MET:HE3	1.83	0.43
1:A:290:LEU:HD21	1:A:465:GLY:HA2	1.99	0.43
1:A:461:ASN:N	1:A:461:ASN:ND2	2.66	0.43
1:A:1267:ALA:C	1:A:1269:GLU:H	2.25	0.43
1:A:1601:TRP:CD1	1:A:1815:LEU:HD22	2.50	0.43
3:C:150:LYS:NZ	3:C:220:GLY:HA3	2.32	0.43
3:C:524:VAL:O	3:C:541:VAL:HA	2.18	0.43
3:C:752:PHE:HA	3:C:760:ASN:O	2.18	0.43
3:C:754:PRO:HD2	3:C:759:PRO:HD2	2.01	0.43
3:C:825:ILE:O	3:C:829:ALA:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:36:A:H2	31:3:4:A:N6	2.14	0.43
6:r:61:PRO:HB2	26:K:152:TRP:CE2	2.53	0.43
6:s:113:ARG:HE	26:K:39:VAL:HG23	1.83	0.43
7:a:21:HIS:O	7:a:36:GLU:HA	2.19	0.43
8:g:42:LEU:HB2	8:g:57:VAL:HG22	2.00	0.43
13:b:52:PRO:O	13:b:62:ARG:NH2	2.43	0.43
14:I:422:LYS:O	14:I:425:GLU:HB2	2.18	0.43
15:J:38:LEU:CD2	17:M:531:ARG:NH2	2.81	0.43
16:P:28:VAL:O	21:R:158:PRO:HG3	2.18	0.43
18:T:206:HIS:ND1	18:T:226:SER:HB2	2.33	0.43
21:R:37:PRO:HG2	21:R:40:ARG:HD3	1.99	0.43
23:S:134:LEU:CD1	23:S:149:VAL:HG11	2.47	0.43
24:W:49:LEU:C	24:W:51:LEU:H	2.26	0.43
25:L:782:GLU:CD	26:K:188:GLN:NE2	2.76	0.43
26:K:81:PRO:O	26:K:84:LYS:HB2	2.18	0.43
31:3:2:U:H5''	31:3:3:A:C8	2.54	0.43
31:3:12:G:HO2'	31:3:13:C:P	2.35	0.43
31:3:90:C:HO2'	31:3:91:A:P	2.34	0.43
1:A:1026:VAL:HG11	1:A:1162:MET:HE1	2.00	0.43
1:A:1041:MET:HG3	1:A:1239:VAL:HG22	1.99	0.43
1:A:1200:ARG:HA	1:A:1203:ARG:HH11	1.83	0.43
1:A:1350:ASP:OD1	1:A:1418:ARG:NH2	2.51	0.43
3:C:161:THR:HG21	3:C:203:MET:HG2	2.00	0.43
6:r:21:HIS:CG	6:r:40:VAL:HG21	2.53	0.43
6:s:82:ALA:O	6:s:86:GLU:HG2	2.18	0.43
11:d:71:THR:HG22	11:d:85:PRO:HB2	1.99	0.43
14:I:434:ARG:NH1	14:I:434:ARG:HB3	2.33	0.43
14:I:634:ALA:O	14:I:637:ILE:HB	2.18	0.43
14:I:749:GLU:OE1	14:I:753:ILE:HG13	2.18	0.43
18:T:213:VAL:HG22	18:T:484:ALA:HB2	2.00	0.43
28:V:677:LEU:HD23	28:V:677:LEU:HA	1.65	0.43
31:3:16:U:H6	31:3:16:U:H2'	1.63	0.43
1:A:1006:PRO:HG2	1:A:1156:LEU:HG	2.01	0.43
1:A:1275:ASP:HB3	1:A:1343:LEU:CD1	2.42	0.43
1:A:1433:TYR:O	1:A:1435:TYR:N	2.52	0.43
3:C:257:ARG:HD2	3:C:600:GLN:HE22	1.83	0.43
3:C:269:MET:HE3	3:C:324:THR:HG1	1.84	0.43
3:C:524:VAL:HG21	3:C:582:LEU:HD11	1.99	0.43
6:r:112:THR:HG21	26:K:27:GLU:OE1	2.16	0.43
6:t:99:GLN:HA	25:L:570:PRO:HG2	2.00	0.43
8:g:54:ILE:HB	9:e:83:GLN:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:f:26:LYS:N	10:f:72:MET:HB2	2.33	0.43
14:I:703:THR:HG22	14:I:708:ILE:HG23	2.00	0.43
15:J:164:GLY:O	15:J:168:VAL:HG23	2.18	0.43
18:T:261:HIS:CD2	18:T:320:MET:HE1	2.53	0.43
21:R:36:PRO:O	21:R:41:ARG:NE	2.51	0.43
21:R:79:GLN:HE21	21:R:79:GLN:HB3	1.59	0.43
25:L:605:ALA:HA	25:L:608:MET:HG2	2.01	0.43
25:L:758:VAL:HG23	26:K:163:VAL:HA	2.00	0.43
25:L:828:LYS:HG3	25:L:829:ARG:N	2.33	0.43
29:Q:1249:THR:O	29:Q:1436:ILE:HA	2.19	0.43
1:A:120:MET:HE1	20:N:51:HIS:HE1	1.83	0.43
1:A:321:PHE:N	1:A:321:PHE:CD2	2.87	0.43
1:A:329:MET:HB3	1:A:368:THR:CG2	2.48	0.43
1:A:469:LEU:CD1	3:C:402:ILE:HG21	2.48	0.43
1:A:1541:ALA:HA	28:V:661:LEU:HD21	2.00	0.43
3:C:199:MET:HE3	3:C:551:GLN:O	2.18	0.43
3:C:288:TYR:HB2	3:C:387:VAL:CG1	2.49	0.43
3:C:720:GLY:HA2	3:C:757:GLN:HE22	1.84	0.43
3:C:952:VAL:O	3:C:956:ARG:HG3	2.17	0.43
5:F:31:A:H61	31:3:9:C:N4	2.14	0.43
7:a:27:LEU:HB2	7:a:72:ARG:O	2.18	0.43
7:a:44:MET:HE3	13:b:74:ARG:HH11	1.82	0.43
7:a:88:PHE:CE1	13:b:32:MET:HB3	2.54	0.43
11:d:50:ALA:HB2	11:d:66:VAL:HG13	2.01	0.43
14:I:466:SER:O	14:I:466:SER:OG	2.27	0.43
19:O:103:LYS:NZ	19:O:104:PRO:HD2	2.32	0.43
19:O:110:SER:O	19:O:114:LYS:HB2	2.19	0.43
25:L:143:MET:HB2	25:L:148:LYS:HG2	1.99	0.43
1:A:863:PRO:HG3	21:R:277:PHE:CD1	2.54	0.43
1:A:1046:GLU:HG2	1:A:1233:GLU:HG3	1.99	0.43
1:A:1520:THR:OG1	1:A:1525:ASP:OD2	2.31	0.43
4:E:57:PRO:HG3	24:W:75:TYR:CD2	2.54	0.43
5:F:38:A:O2'	5:F:39:G:OP2	2.32	0.43
15:J:67:GLU:HG3	25:L:209:TYR:CE2	2.54	0.43
15:J:73:VAL:HG13	15:J:80:VAL:HG21	1.99	0.43
15:J:221:PHE:O	15:J:225:ASN:HB2	2.18	0.43
18:T:349:ILE:HG12	18:T:359:LEU:HD22	2.01	0.43
19:O:261:VAL:HG13	19:O:272:VAL:HG22	2.00	0.43
20:N:52:ARG:O	20:N:56:GLU:HG3	2.18	0.43
21:R:36:PRO:HD2	21:R:44:TRP:CH2	2.53	0.43
23:S:79:THR:OG1	23:S:82:LEU:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:L:699:ARG:HE	25:L:700:TYR:H	1.65	0.43
30:5:-7:C:O2'	30:5:-6:C:O5'	2.32	0.43
1:A:265:TRP:HE3	1:A:271:PRO:HB3	1.83	0.43
1:A:328:ASN:OD1	1:A:339:PRO:HA	2.19	0.43
1:A:1208:LYS:HE2	1:A:1208:LYS:HB3	1.79	0.43
1:A:1562:TRP:HZ3	1:A:1817:LEU:HD11	1.83	0.43
1:A:1649:ILE:HD11	1:A:1807:LEU:HG	2.00	0.43
2:B:20:C:H5	2:B:59:G:H1	1.67	0.43
3:C:140:VAL:O	3:C:215:LEU:HA	2.19	0.43
3:C:842:PRO:O	3:C:843:ARG:HD2	2.19	0.43
4:E:130:LYS:HG3	4:E:151:ALA:O	2.18	0.43
5:F:4:C:C2	5:F:5:U:H1'	2.53	0.43
6:q:113:ARG:CD	25:L:666:LEU:HG	2.49	0.43
8:g:45:THR:HB	8:g:54:ILE:HG12	2.00	0.43
14:I:347:ASP:HA	14:I:350:LEU:HD12	1.99	0.43
14:I:356:LEU:O	14:I:360:ARG:HG2	2.19	0.43
14:I:461:MET:HB2	14:I:464:ARG:HH21	1.83	0.43
14:I:560:PHE:O	14:I:564:GLU:HG2	2.18	0.43
15:J:87:TRP:HE1	25:L:248:LEU:HD23	1.84	0.43
18:T:201:ARG:HB3	18:T:492:MET:HB2	2.01	0.43
18:T:258:SER:OG	18:T:261:HIS:HD2	2.02	0.43
20:N:169:LEU:HD13	20:N:170:GLU:HG2	2.00	0.43
21:R:170:LEU:HA	21:R:170:LEU:HD23	1.72	0.43
25:L:97:ASP:OD2	25:L:98:ARG:N	2.52	0.43
25:L:659:VAL:O	25:L:663:VAL:HG23	2.19	0.43
1:A:766:LYS:NZ	1:A:768:ASN:HB2	2.34	0.43
1:A:1546:GLU:HG2	1:A:1547:GLY:H	1.84	0.43
3:C:123:SER:HB3	7:a:89:LYS:CD	2.49	0.43
3:C:140:VAL:HG11	3:C:451:LEU:CD2	2.49	0.43
3:C:337:GLN:HE22	3:C:354:ARG:HD2	1.83	0.43
3:C:498:LEU:CD1	3:C:629:LYS:HD3	2.49	0.43
3:C:525:LYS:HE2	3:C:585:ASP:HA	2.01	0.43
3:C:612:LEU:HD23	3:C:612:LEU:HA	1.85	0.43
4:E:184:LYS:NZ	4:E:185:SER:H	2.14	0.43
5:F:85:A:HO2'	5:F:86:A:H8	1.61	0.43
15:J:244:GLU:C	15:J:246:ALA:H	2.26	0.43
15:J:288:TYR:CZ	15:J:311:LYS:HD2	2.54	0.43
21:R:146:GLU:O	21:R:150:GLN:HG2	2.19	0.43
23:S:33:GLU:O	23:S:37:LYS:HG3	2.17	0.43
24:W:106:PHE:CD2	24:W:107:VAL:HG22	2.46	0.43
25:L:779:HIS:NE2	26:K:184:ARG:HG3	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:V:675:LYS:O	28:V:679:ILE:HG12	2.19	0.43
1:A:370:TYR:CD1	3:C:899:GLY:HA3	2.53	0.43
1:A:505:VAL:O	1:A:509:VAL:HG23	2.19	0.43
1:A:1340:GLU:H	1:A:1340:GLU:HG3	1.47	0.43
1:A:1562:TRP:HA	1:A:1565:LEU:HD12	1.99	0.43
3:C:140:VAL:O	3:C:216:LEU:HG	2.18	0.43
3:C:604:THR:HG23	3:C:894:VAL:HG11	2.00	0.43
3:C:608:ALA:O	3:C:672:VAL:HG23	2.18	0.43
3:C:865:ASN:HD22	3:C:865:ASN:HA	1.62	0.43
5:F:37:G:N3	31:3:3:A:N1	2.67	0.43
6:r:106:TYR:CD2	6:r:106:TYR:C	2.96	0.43
11:d:72:GLU:OE2	11:d:86:VAL:HB	2.19	0.43
20:N:103:SER:HB3	20:N:139:THR:HG21	2.01	0.43
21:R:59:PRO:HG2	23:S:20:TYR:HE1	1.83	0.43
22:H:29:C:O2'	22:H:30:A:H5''	2.19	0.43
26:K:117:VAL:O	26:K:120:TRP:N	2.52	0.43
1:A:607:ALA:HB2	1:A:715:TRP:HB3	2.01	0.43
1:A:719:LEU:HD13	5:F:59:C:OP2	2.18	0.43
1:A:914:TYR:CD2	1:A:928:LEU:HG	2.54	0.43
1:A:1394:MET:HE1	28:V:667:PHE:CE2	2.53	0.43
2:B:43:U:H2'	2:B:44:U:C6	2.54	0.43
3:C:226:ASP:HB3	3:C:633:LEU:HB2	2.01	0.43
3:C:871:ARG:NH2	3:C:893:PRO:HG2	2.28	0.43
4:E:146:MET:HE2	4:E:146:MET:HB2	1.86	0.43
5:F:5:U:C5	5:F:7:C:H1'	2.53	0.43
5:F:29:A:N6	31:3:11:A:H2'	2.23	0.43
6:r:121:GLU:HB3	6:s:122:ARG:HE	1.83	0.43
6:s:114:VAL:HG22	26:K:32:ALA:H	1.84	0.43
8:g:16:LYS:C	8:g:17:LEU:HD23	2.44	0.43
8:g:31:LEU:HA	8:g:42:LEU:HD13	2.00	0.43
10:f:22:ILE:CG2	10:f:32:LYS:HZ2	2.31	0.43
13:b:113:MET:HG3	24:W:73:VAL:CG2	2.48	0.43
14:I:507:LYS:O	14:I:511:MET:HG2	2.19	0.43
14:I:733:ALA:O	14:I:737:PHE:HB3	2.19	0.43
18:T:260:ARG:NH2	18:T:304:ASP:OD1	2.52	0.43
23:S:80:ARG:HA	23:S:80:ARG:HD2	1.75	0.43
25:L:73:LEU:HD23	25:L:73:LEU:HA	1.82	0.43
25:L:804:GLU:HA	25:L:807:LEU:HD12	2.00	0.43
1:A:178:ILE:HA	1:A:547:GLN:O	2.19	0.42
1:A:1278:TRP:CZ2	1:A:1294:LEU:HD11	2.53	0.42
1:A:1521:HIS:CD2	1:A:1524:HIS:CD2	2.86	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:935:LEU:HD13	3:C:949:GLU:HB3	2.01	0.42
4:E:131:THR:HG21	4:E:133:ARG:CZ	2.50	0.42
4:E:216:ILE:HD12	4:E:245:LEU:HD21	2.00	0.42
4:E:258:ALA:C	4:E:260:ASP:N	2.77	0.42
5:F:1:G5J:O3A	20:N:149:GLY:O	2.37	0.42
5:F:24:U:H3'	5:F:25:U:C6	2.54	0.42
6:r:84:MET:HG3	26:K:90:VAL:HG11	2.01	0.42
11:d:101:SER:HB2	12:c:67:ARG:HH21	1.83	0.42
13:b:32:MET:HA	13:b:32:MET:HE3	2.01	0.42
14:I:379:TRP:HH2	14:I:399:GLU:HG2	1.83	0.42
14:I:431:ALA:O	14:I:435:ILE:HG13	2.19	0.42
14:I:593:LYS:HE3	14:I:593:LYS:HB2	1.79	0.42
17:M:531:ARG:HB3	22:H:18:U:N3	2.34	0.42
23:S:9:ASP:HA	23:S:14:SER:HA	2.01	0.42
24:W:120:PHE:CD1	24:W:120:PHE:C	2.96	0.42
1:A:308:PRO:HD2	1:A:472:PRO:HG3	2.00	0.42
1:A:1085:ASP:OD1	1:A:1085:ASP:N	2.43	0.42
1:A:1265:ARG:HB3	1:A:1265:ARG:HH11	1.83	0.42
1:A:1346:GLN:CG	1:A:1401:GLN:HE21	2.31	0.42
1:A:1608:ARG:O	1:A:1611:VAL:HG13	2.19	0.42
3:C:238:VAL:HG12	3:C:266:ILE:HA	2.01	0.42
3:C:343:TYR:O	3:C:347:TYR:HB2	2.19	0.42
3:C:785:GLN:O	3:C:788:GLN:HG3	2.19	0.42
3:C:935:LEU:HD12	3:C:948:ARG:NH2	2.29	0.42
4:E:308:SER:O	4:E:334:VAL:N	2.47	0.42
6:t:67:THR:OG1	6:t:71:GLY:HA3	2.20	0.42
9:e:46:ASP:OD1	9:e:46:ASP:N	2.51	0.42
14:I:582:TYR:CE1	14:I:601:LEU:HD11	2.53	0.42
15:J:49:ILE:HG23	15:J:54:GLU:CG	2.49	0.42
15:J:49:ILE:CD1	25:L:245:VAL:CG2	2.97	0.42
18:T:206:HIS:CE1	18:T:226:SER:HB2	2.54	0.42
19:O:287:LEU:HB3	19:O:291:PRO:HG3	2.01	0.42
22:H:5:C:H4'	22:H:6:U:OP1	2.18	0.42
24:W:459:MET:HA	24:W:474:GLN:O	2.18	0.42
25:L:118:ASP:OD2	25:L:119:PRO:HD2	2.19	0.42
25:L:747:LEU:HD11	26:K:153:ARG:HH12	1.84	0.42
25:L:778:LEU:HA	25:L:781:ARG:HB2	2.01	0.42
25:L:779:HIS:CA	26:K:184:ARG:HD2	2.49	0.42
29:Q:1628:ILE:O	29:Q:1659:ILE:HA	2.19	0.42
1:A:327:LEU:O	1:A:329:MET:HG3	2.20	0.42
1:A:813:TRP:O	1:A:817:VAL:HG23	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:864:TYR:HA	3:C:66:VAL:HG11	2.01	0.42
1:A:1019:TRP:NE1	1:A:1253:MET:HE1	2.35	0.42
1:A:1401:GLN:HG3	1:A:1418:ARG:HH11	1.85	0.42
3:C:291:LEU:HD13	3:C:325:PHE:CE1	2.53	0.42
3:C:402:ILE:HD11	3:C:433:LEU:HD22	2.01	0.42
3:C:619:LYS:O	3:C:623:GLY:N	2.26	0.42
3:C:797:CYS:HA	3:C:955:ARG:CD	2.49	0.42
4:E:159:LEU:HD13	4:E:200:PHE:CG	2.54	0.42
4:E:281:PHE:CE1	4:E:304:VAL:HG21	2.54	0.42
5:F:28:A:H5'	5:F:29:A:OP1	2.19	0.42
6:r:113:ARG:HA	6:r:113:ARG:HD3	1.62	0.42
6:t:109:ASP:O	6:t:112:THR:OG1	2.31	0.42
6:t:113:ARG:HA	25:L:652:LEU:HD22	1.99	0.42
14:I:528:ALA:O	14:I:532:ILE:HG13	2.19	0.42
14:I:563:TYR:O	14:I:567:ILE:HG23	2.19	0.42
14:I:708:ILE:HG21	14:I:741:HIS:HB3	2.01	0.42
20:N:19:ILE:HD13	20:N:75:LEU:HD21	2.00	0.42
21:R:62:HIS:CE1	23:S:83:LYS:HB2	2.54	0.42
25:L:88:VAL:HG12	25:L:90:ARG:HG2	2.01	0.42
25:L:217:LEU:HD12	25:L:217:LEU:HA	1.56	0.42
25:L:736:LEU:HD12	26:K:138:ILE:HG13	2.00	0.42
25:L:782:GLU:OE1	26:K:188:GLN:NE2	2.52	0.42
31:3:10:U:H2'	31:3:11:A:O4'	2.19	0.42
1:A:181:ILE:HD12	1:A:181:ILE:HA	1.69	0.42
1:A:325:LYS:HG2	1:A:337:PHE:CG	2.53	0.42
1:A:1147:HIS:NE2	16:P:196:TRP:HE3	2.17	0.42
1:A:1645:LEU:HD21	1:A:1807:LEU:HD23	2.01	0.42
3:C:179:ARG:HH12	32:C:1001:GTP:PA	2.41	0.42
4:E:149:HIS:ND1	4:E:172:ASP:OD2	2.40	0.42
4:E:246:ARG:HD2	4:E:246:ARG:HA	1.76	0.42
4:E:270:PRO:HD2	25:L:812:LYS:NZ	2.35	0.42
6:q:14:VAL:HG21	6:q:28:ILE:HG21	2.02	0.42
6:r:88:HIS:CD2	6:r:89:ASN:N	2.88	0.42
8:g:19:ILE:HD13	8:g:40:LEU:HD12	2.01	0.42
11:d:51:ARG:HE	11:d:65:ASN:HB2	1.84	0.42
14:I:592:GLY:O	15:J:339:GLY:HA3	2.19	0.42
14:I:715:TYR:HB3	14:I:734:TRP:CD2	2.55	0.42
15:J:310:SER:O	15:J:314:PHE:HD1	2.03	0.42
15:J:312:ARG:HD3	15:J:312:ARG:HA	1.74	0.42
18:T:416:GLN:NE2	18:T:439:SER:OG	2.38	0.42
19:O:214:LEU:HA	19:O:217:VAL:HG22	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:O:296:ALA:O	19:O:298:VAL:HG23	2.19	0.42
20:N:55:TRP:CZ2	20:N:154:PRO:HD3	2.54	0.42
20:N:96:PRO:HA	20:N:99:GLU:OE1	2.18	0.42
23:S:41:ASP:OD1	23:S:153:ARG:HA	2.20	0.42
23:S:112:PRO:HA	23:S:115:ASP:OD2	2.20	0.42
25:L:557:GLU:HG2	25:L:560:LYS:CD	2.46	0.42
1:A:86:GLN:O	1:A:90:GLU:HG2	2.19	0.42
1:A:1671:GLU:OE2	1:A:1672:THR:OG1	2.34	0.42
3:C:137:VAL:O	3:C:138:ARG:HD3	2.19	0.42
3:C:506:ARG:HB3	3:C:573:ASP:OD2	2.19	0.42
5:F:79:A:N3	5:F:79:A:H2'	2.34	0.42
7:a:89:LYS:O	7:a:92:ASP:HB2	2.19	0.42
9:e:51:LEU:HG	9:e:79:ILE:HD11	2.00	0.42
9:e:67:LYS:HE3	9:e:67:LYS:HB3	1.59	0.42
11:d:63:LEU:HB3	11:d:66:VAL:HG22	2.02	0.42
14:I:518:SER:OG	14:I:519:LEU:HG	2.19	0.42
16:P:11:PRO:HG3	18:T:311:ARG:HH12	1.85	0.42
25:L:47:ALA:HB3	25:L:132:GLU:HG2	2.00	0.42
25:L:766:ARG:O	25:L:769:ALA:HB3	2.20	0.42
26:K:44:LYS:HA	26:K:44:LYS:HD2	1.80	0.42
26:K:130:GLN:HA	26:K:133:HIS:HB2	2.01	0.42
1:A:728:GLN:NE2	1:A:728:GLN:HA	2.34	0.42
1:A:1783:PHE:N	1:A:1786:ILE:HG12	2.34	0.42
2:B:74:G:OP2	2:B:74:G:H8	2.03	0.42
2:B:87:C:H42	13:b:36:ARG:HB2	1.83	0.42
4:E:253:HIS:HB3	4:E:265:GLU:OE2	2.19	0.42
10:f:45:GLN:HG3	11:d:24:PRO:CA	2.45	0.42
11:d:42:CYS:HB2	11:d:46:HIS:O	2.19	0.42
13:b:13:ILE:O	13:b:14:ASN:HB2	2.19	0.42
14:I:709:ASP:HA	14:I:712:ARG:HB2	2.02	0.42
15:J:139:VAL:HG13	15:J:149:TRP:CH2	2.54	0.42
26:K:197:LYS:HA	26:K:197:LYS:HD2	1.59	0.42
31:3:97:A:H4'	31:3:98:U:H5''	2.00	0.42
1:A:223:MET:CE	1:A:633:VAL:HG11	2.49	0.42
1:A:1327:TRP:HB2	1:A:1359:ILE:HG13	2.00	0.42
1:A:1532:ASN:O	1:A:1536:THR:HG23	2.19	0.42
1:A:1632:THR:O	1:A:1635:ILE:HG22	2.19	0.42
1:A:1804:LEU:HD13	1:A:1808:ARG:HH11	1.85	0.42
3:C:206:HIS:HB2	3:C:449:ASP:OD2	2.20	0.42
3:C:240:LEU:HD21	3:C:252:THR:HG23	2.01	0.42
3:C:677:VAL:CG2	3:C:895:VAL:HG13	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:752:PHE:HE2	3:C:761:VAL:HG22	1.83	0.42
4:E:117:PHE:HB2	4:E:122:ALA:O	2.20	0.42
6:q:14:VAL:HG13	6:q:25:LYS:HB3	2.01	0.42
12:c:40:HIS:ND1	12:c:59:LEU:O	2.53	0.42
14:I:381:LYS:O	14:I:385:ILE:HG12	2.20	0.42
14:I:550:LEU:O	14:I:555:ALA:N	2.52	0.42
20:N:119:HIS:HE1	20:N:134:THR:O	2.02	0.42
25:L:818:ARG:HD3	26:K:222:ALA:HB2	2.01	0.42
26:K:120:TRP:HA	26:K:123:SER:HB3	2.01	0.42
26:K:164:ARG:HA	26:K:167:GLU:CG	2.50	0.42
27:U:16:SER:HG	27:U:18:TYR:HD2	1.66	0.42
1:A:802:MET:HE2	1:A:802:MET:HB3	1.73	0.42
1:A:1014:LEU:HD22	1:A:1480:ILE:HG21	2.02	0.42
1:A:1415:THR:O	27:U:22:ASN:HB2	2.20	0.42
1:A:1695:LEU:HD21	1:A:1725:TRP:CD1	2.47	0.42
1:A:1706:PRO:HA	1:A:1780:GLY:C	2.45	0.42
2:B:12:G:N2	2:B:67:U:H3	2.07	0.42
3:C:80:ILE:HD13	3:C:80:ILE:HA	1.87	0.42
3:C:243:ASP:OD1	3:C:272:LYS:HB2	2.18	0.42
3:C:405:HIS:CE1	3:C:407:LYS:HG2	2.55	0.42
3:C:482:MET:SD	3:C:492:VAL:HB	2.60	0.42
3:C:497:LYS:HB3	3:C:510:LEU:HD23	2.02	0.42
3:C:568:LEU:HD12	3:C:568:LEU:HA	1.82	0.42
4:E:155:SER:HB2	4:E:196:CYS:O	2.20	0.42
6:s:79:GLU:HG3	26:K:82:VAL:HG11	2.01	0.42
6:s:118:LEU:O	6:s:122:ARG:HG3	2.20	0.42
6:t:114:VAL:HG21	25:L:604:VAL:HA	2.01	0.42
7:a:74:ARG:NH1	13:b:78:ILE:HG12	2.33	0.42
9:e:19:PHE:CE1	9:e:84:THR:HG22	2.51	0.42
9:e:59:VAL:HG22	9:e:66:ARG:HD3	2.02	0.42
10:f:22:ILE:HD11	10:f:77:VAL:HG22	2.02	0.42
14:I:692:ARG:HH11	14:I:727:ALA:HB1	1.84	0.42
17:M:483:LEU:CD1	21:R:85:VAL:HG11	2.49	0.42
17:M:510:LYS:HB3	17:M:510:LYS:HE3	1.72	0.42
24:W:422:ILE:N	24:W:427:GLN:O	2.38	0.42
25:L:790:LEU:HD22	26:K:194:GLU:HB3	2.01	0.42
25:L:818:ARG:HG2	25:L:818:ARG:NH2	2.35	0.42
26:K:163:VAL:O	26:K:167:GLU:HG2	2.20	0.42
1:A:1163:PHE:CD2	1:A:1163:PHE:N	2.87	0.42
1:A:1282:ASN:ND2	1:A:1289:THR:OG1	2.50	0.42
1:A:1343:LEU:HA	28:V:667:PHE:HE1	1.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:491:LEU:HA	3:C:515:SER:C	2.43	0.42
3:C:760:ASN:HD21	3:C:801:ILE:CB	2.32	0.42
4:E:70:SER:CB	4:E:113:GLU:HA	2.50	0.42
5:F:33:U:C4	5:F:34:A:C6	3.08	0.42
6:r:110:ALA:O	26:K:54:GLU:HG3	2.20	0.42
6:r:122:ARG:HD2	6:r:126:ARG:HD3	2.02	0.42
7:a:66:LEU:HD13	8:g:68:GLU:OE1	2.20	0.42
9:e:75:LYS:HB2	10:f:72:MET:O	2.20	0.42
15:J:110:ARG:HG2	21:R:222:VAL:HG21	2.02	0.42
15:J:130:HIS:ND1	25:L:229:GLU:HG3	2.35	0.42
15:J:149:TRP:O	15:J:153:ILE:HD12	2.19	0.42
16:P:9:TRP:HA	16:P:9:TRP:CE3	2.55	0.42
18:T:468:ALA:HB3	18:T:470:TYR:CZ	2.54	0.42
19:O:95:VAL:HG23	19:O:210:ALA:HB1	2.01	0.42
19:O:216:ARG:HD3	19:O:216:ARG:HA	1.74	0.42
21:R:136:LYS:HD3	21:R:136:LYS:HA	1.61	0.42
26:K:76:LYS:HD3	26:K:76:LYS:HA	1.87	0.42
1:A:335:PRO:CB	1:A:516:LYS:HB2	2.50	0.42
1:A:363:ARG:HD2	3:C:896:GLU:OE1	2.19	0.42
1:A:1134:GLU:O	1:A:1135:PHE:C	2.62	0.42
1:A:1397:ILE:HG22	28:V:666:SER:HA	2.01	0.42
1:A:1559:PHE:HA	1:A:1560:PRO:HD3	1.94	0.42
2:B:66:U:C2	2:B:67:U:C5	3.07	0.42
2:B:96:G:N2	2:B:97:U:O3'	2.53	0.42
3:C:184:ARG:O	3:C:187:GLU:HG2	2.20	0.42
3:C:292:ARG:NH2	3:C:362:GLY:HA2	2.34	0.42
3:C:945:ALA:O	3:C:949:GLU:HG3	2.20	0.42
4:E:50:ARG:HH21	4:E:52:SER:C	2.28	0.42
4:E:243:THR:HG21	4:E:293:LEU:H	1.84	0.42
4:E:328:PRO:O	13:b:111:ARG:HD3	2.20	0.42
6:q:4:SER:OG	6:q:22:LEU:N	2.53	0.42
7:a:72:ARG:HG3	8:g:65:GLN:HA	2.02	0.42
9:e:60:SER:O	9:e:64:LYS:N	2.53	0.42
13:b:26:GLN:HB2	13:b:48:PHE:HB2	2.00	0.42
19:O:86:ASP:OD2	19:O:90:GLY:N	2.53	0.42
19:O:143:ARG:NH1	23:S:113:TRP:HZ3	2.02	0.42
19:O:212:LYS:HB3	19:O:212:LYS:HE2	1.67	0.42
24:W:50:VAL:CG1	26:K:34:PRO:O	2.67	0.42
25:L:803:ARG:O	25:L:807:LEU:HG	2.19	0.42
1:A:120:MET:HG2	1:A:547:GLN:HG2	2.01	0.41
1:A:279:ASN:ND2	1:A:284:LYS:H	2.15	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:469:LEU:HD11	3:C:402:ILE:HG21	2.02	0.41
1:A:506:LYS:HG3	1:A:507:VAL:N	2.34	0.41
1:A:1702:ASN:HD21	1:A:1717:ASP:C	2.27	0.41
3:C:711:LYS:HE2	3:C:711:LYS:HB2	1.88	0.41
4:E:178:TRP:CD1	4:E:178:TRP:N	2.87	0.41
4:E:311:ARG:HB3	4:E:330:HIS:O	2.20	0.41
5:F:82:G:O2'	5:F:83:A:C8	2.68	0.41
5:F:85:A:H4'	5:F:86:A:OP1	2.19	0.41
6:q:51:LEU:HA	6:q:52:PRO:HD3	1.79	0.41
15:J:73:VAL:CG1	15:J:80:VAL:HG21	2.50	0.41
19:O:67:THR:HB	19:O:81:GLN:HB3	2.01	0.41
21:R:153:LEU:HD23	21:R:153:LEU:HA	1.79	0.41
23:S:44:ILE:HG22	23:S:150:LYS:HG2	2.02	0.41
24:W:132:PHE:CD1	24:W:145:PRO:HB3	2.55	0.41
25:L:621:VAL:HG12	25:L:623:ASP:H	1.84	0.41
1:A:1385:GLU:O	1:A:1567:TRP:NE1	2.51	0.41
3:C:523:THR:HG23	3:C:585:ASP:HB2	2.02	0.41
3:C:866:VAL:HG23	3:C:900:PHE:HE2	1.85	0.41
3:C:927:ASP:O	3:C:930:ASP:HB2	2.21	0.41
4:E:149:HIS:NE2	4:E:176:LYS:HD2	2.35	0.41
6:q:48:GLU:CD	6:q:48:GLU:H	2.29	0.41
6:q:83:ASN:HD21	6:t:87:LEU:CD1	2.33	0.41
11:d:104:MET:HB3	11:d:104:MET:HE2	1.73	0.41
13:b:65:ARG:NH1	13:b:67:VAL:HG23	2.35	0.41
19:O:249:ARG:HG3	19:O:258:LEU:HD12	2.02	0.41
20:N:124:LEU:O	20:N:132:ARG:HD3	2.19	0.41
22:H:32:G:H22	31:3:100:C:N4	2.14	0.41
24:W:167:THR:HB	24:W:168:THR:H	1.75	0.41
25:L:213:VAL:HG11	25:L:216:GLU:HG3	2.01	0.41
25:L:600:ALA:HA	25:L:603:LEU:HB2	2.02	0.41
25:L:740:LEU:HD11	26:K:141:GLN:HG3	2.01	0.41
29:Q:1188:GLY:HA2	29:Q:1398:GLY:C	2.45	0.41
1:A:669:CYS:SG	1:A:697:MET:HG2	2.61	0.41
1:A:1287:GLU:HG3	28:V:795:GLY:CA	2.46	0.41
3:C:94:ALA:HB2	18:T:240:GLN:OE1	2.19	0.41
3:C:153:ILE:HD12	3:C:241:VAL:HG11	2.03	0.41
3:C:807:LYS:HB2	3:C:807:LYS:HE3	1.74	0.41
4:E:230:GLU:N	4:E:230:GLU:OE2	2.53	0.41
6:q:4:SER:H	6:q:4:SER:HG	1.64	0.41
6:t:88:HIS:HB3	26:K:128:ALA:HB1	2.01	0.41
8:g:7:PRO:O	8:g:10:LYS:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:c:11:LEU:HB3	12:c:30:ILE:HD12	2.02	0.41
13:b:31:PHE:CZ	13:b:34:PHE:HB3	2.55	0.41
20:N:41:LYS:HB3	20:N:41:LYS:HE3	1.88	0.41
20:N:49:LYS:HG3	24:W:200:TRP:CH2	2.55	0.41
25:L:774:CYS:SG	25:L:775:PHE:HD2	2.43	0.41
31:3:13:C:H6	31:3:13:C:H5''	1.85	0.41
1:A:92:LYS:NZ	4:E:212:VAL:HG12	2.36	0.41
1:A:367:ARG:HB2	1:A:370:TYR:CD2	2.55	0.41
1:A:874:TYR:O	1:A:878:VAL:HG23	2.20	0.41
1:A:952:GLN:O	1:A:953:ARG:NH1	2.47	0.41
1:A:976:GLU:OE2	25:L:43:LYS:NZ	2.42	0.41
1:A:1006:PRO:HD2	1:A:1106:GLN:NE2	2.30	0.41
1:A:1374:ARG:NH2	1:A:1606:ILE:O	2.48	0.41
2:B:29:U:H1'	2:B:30:A:C8	2.55	0.41
3:C:139:ASN:C	3:C:235:ALA:HB1	2.45	0.41
3:C:317:ASP:N	3:C:322:ASN:OD1	2.53	0.41
3:C:533:PRO:HG3	3:C:592:HIS:CD2	2.55	0.41
3:C:602:ARG:HD3	3:C:918:PHE:CZ	2.55	0.41
3:C:744:LEU:HD23	3:C:744:LEU:H	1.85	0.41
4:E:359:GLU:O	24:W:76:ASN:ND2	2.52	0.41
5:F:32:A:C5	5:F:33:U:C5	3.08	0.41
6:q:19:SER:HB3	6:q:41:THR:HG21	2.02	0.41
6:r:69:ILE:N	6:r:70:PRO:HD2	2.35	0.41
6:r:82:ALA:O	6:r:86:GLU:HG3	2.20	0.41
6:t:69:ILE:O	6:t:73:LEU:HB2	2.21	0.41
14:I:707:GLU:OE1	14:I:710:ARG:HD2	2.21	0.41
17:M:452:ARG:HD3	17:M:452:ARG:HA	1.69	0.41
18:T:363:ARG:NH2	21:R:137:THR:HG23	2.34	0.41
18:T:409:LEU:O	18:T:410:HIS:HB3	2.20	0.41
19:O:96:ARG:O	19:O:100:MET:HG2	2.20	0.41
25:L:162:ARG:HG3	25:L:163:GLY:H	1.86	0.41
26:K:75:PRO:HB2	26:K:77:PHE:CE1	2.55	0.41
26:K:197:LYS:O	26:K:201:GLN:HG2	2.19	0.41
1:A:85:GLN:HG3	1:A:87:LYS:CD	2.47	0.41
1:A:129:ILE:HD12	1:A:559:GLN:HG2	2.03	0.41
1:A:367:ARG:O	1:A:370:TYR:HB2	2.20	0.41
1:A:1396:HIS:CE1	1:A:1429:ILE:HD13	2.55	0.41
3:C:253:GLU:HA	3:C:256:VAL:HB	2.03	0.41
3:C:717:ILE:HG22	3:C:757:GLN:HB2	2.03	0.41
3:C:928:PRO:HA	3:C:947:ALA:C	2.45	0.41
3:C:947:ALA:O	3:C:951:MET:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:46:A:H2'	5:F:47:G:O4'	2.19	0.41
6:r:115:ILE:HG13	6:s:114:VAL:HG12	2.01	0.41
11:d:30:GLN:O	11:d:34:THR:OG1	2.38	0.41
14:I:647:LYS:HA	14:I:650:ARG:HD2	2.02	0.41
15:J:144:ARG:NH2	21:R:226:PRO:HD3	2.36	0.41
16:P:41:LEU:HG	18:T:321:ARG:HG3	2.02	0.41
18:T:184:ILE:HD11	21:R:116:PRO:HB2	2.01	0.41
18:T:229:ARG:HE	18:T:229:ARG:HB2	1.56	0.41
18:T:277:ASP:HB2	18:T:284:ILE:HG12	2.02	0.41
21:R:257:LEU:HD12	21:R:257:LEU:HA	1.73	0.41
23:S:69:ILE:HG13	23:S:70:TYR:CD1	2.56	0.41
25:L:559:LEU:HD12	25:L:559:LEU:HA	1.82	0.41
25:L:747:LEU:HD11	26:K:153:ARG:NH2	2.35	0.41
26:K:109:PRO:HB3	26:K:113:ARG:HB3	2.01	0.41
1:A:399:LYS:HD2	1:A:399:LYS:HA	1.86	0.41
1:A:481:HIS:CD2	2:B:26:G:N1	2.86	0.41
1:A:497:GLU:O	1:A:497:GLU:HG2	2.21	0.41
1:A:1207:MET:HA	1:A:1207:MET:HE3	2.03	0.41
3:C:148:HIS:ND1	3:C:243:ASP:HB3	2.35	0.41
3:C:194:ILE:HG23	3:C:224:PHE:CE2	2.55	0.41
3:C:369:GLU:OE1	3:C:379:ARG:NH2	2.54	0.41
3:C:397:MET:CE	3:C:397:MET:CA	2.96	0.41
3:C:413:LEU:HB3	3:C:418:VAL:HG13	2.03	0.41
3:C:607:ILE:HD11	3:C:646:ILE:HB	2.02	0.41
4:E:72:ARG:NH1	4:E:246:ARG:HH12	2.18	0.41
4:E:216:ILE:CG2	4:E:235:LEU:HB2	2.43	0.41
6:q:105:LEU:HD23	6:q:108:HIS:ND1	2.36	0.41
6:t:68:SER:HB2	26:K:86:GLU:OE2	2.20	0.41
7:a:74:ARG:HE	13:b:21:LEU:HD22	1.86	0.41
8:g:47:ASP:N	8:g:52:VAL:O	2.49	0.41
14:I:104:LEU:C	29:Q:1330:THR:CB	2.93	0.41
16:P:44:ARG:HB3	16:P:48:GLN:O	2.21	0.41
18:T:188:TRP:HA	18:T:189:PRO:HD2	1.89	0.41
19:O:44:CYS:SG	19:O:70:CYS:HB2	2.61	0.41
22:H:16:U:C1'	22:H:17:U:H5'	2.49	0.41
24:W:215:LYS:HB3	24:W:215:LYS:HE2	1.71	0.41
25:L:542:VAL:O	25:L:546:LYS:HG3	2.21	0.41
25:L:798:ASP:HA	25:L:801:LYS:HG2	2.03	0.41
26:K:203:LEU:O	26:K:206:VAL:HB	2.19	0.41
1:A:309:ASP:HB2	1:A:312:TYR:CD2	2.56	0.41
1:A:387:LEU:HA	1:A:387:LEU:HD12	1.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1202:ALA:HB1	1:A:1259:ARG:CZ	2.50	0.41
2:B:71:C:H2'	2:B:72:A:O4'	2.20	0.41
3:C:113:LEU:HB2	3:C:553:ARG:O	2.21	0.41
3:C:589:GLU:HG3	3:C:590:PRO:N	2.34	0.41
5:F:51:G:O2'	5:F:52:G:H5'	2.20	0.41
11:d:60:ASN:HA	11:d:97:LEU:O	2.20	0.41
14:I:105:VAL:HA	29:Q:1330:THR:H	1.70	0.41
14:I:533:LEU:HB2	14:I:565:ARG:NH2	2.36	0.41
15:J:240:ASP:OD2	15:J:241:GLU:HG2	2.20	0.41
18:T:193:TRP:HE1	18:T:505:PRO:HA	1.85	0.41
19:O:86:ASP:OD2	19:O:91:LEU:N	2.36	0.41
21:R:97:VAL:HG21	21:R:221:PRO:HG3	2.02	0.41
23:S:17:VAL:HG13	23:S:123:ARG:C	2.46	0.41
25:L:558:GLU:HA	25:L:558:GLU:OE1	2.21	0.41
25:L:762:TRP:HB2	26:K:166:LEU:CD1	2.51	0.41
25:L:788:GLU:O	25:L:792:ALA:HB2	2.21	0.41
1:A:363:ARG:NH2	3:C:895:VAL:HG21	2.36	0.41
1:A:838:LYS:HA	22:H:24:C:O4'	2.20	0.41
1:A:1110:LEU:O	1:A:1114:LEU:HG	2.20	0.41
1:A:1558:TYR:CG	1:A:1808:ARG:NH2	2.89	0.41
3:C:128:ALA:HA	3:C:131:MET:HE3	2.03	0.41
3:C:288:TYR:HE1	3:C:361:TRP:CZ3	2.39	0.41
3:C:330:SER:C	3:C:434:LYS:HG3	2.46	0.41
3:C:706:ALA:HA	3:C:805:LYS:O	2.21	0.41
3:C:796:LEU:HD11	3:C:837:PHE:HE1	1.86	0.41
4:E:291:ASN:ND2	4:E:335:ASN:OD1	2.48	0.41
5:F:73:G:C4'	5:F:74:C:H5'	2.42	0.41
6:q:114:VAL:N	25:L:662:GLU:OE2	2.54	0.41
6:r:115:ILE:CD1	6:s:118:LEU:CD1	2.88	0.41
16:P:32:ALA:O	16:P:35:LEU:HD12	2.21	0.41
17:M:442:PRO:O	17:M:446:TYR:HB3	2.19	0.41
20:N:71:MET:HE3	20:N:71:MET:HB2	1.96	0.41
24:W:103:LYS:HE2	24:W:106:PHE:O	2.20	0.41
25:L:170:ALA:HA	25:L:173:LYS:HE3	2.02	0.41
25:L:780:GLU:HG2	25:L:784:ARG:NE	2.36	0.41
26:K:203:LEU:HD23	26:K:203:LEU:HA	1.92	0.41
1:A:484:ARG:O	1:A:487:ASP:HB2	2.20	0.41
1:A:1402:SER:CB	1:A:1412:LEU:HD21	2.51	0.41
1:A:1517:PHE:HA	1:A:1519:TRP:CZ3	2.56	0.41
1:A:1657:LEU:HD21	1:A:1793:ALA:HB1	2.03	0.41
1:A:1807:LEU:HD23	1:A:1807:LEU:HA	1.81	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:226:ASP:O	3:C:227:GLU:C	2.64	0.41
3:C:258:GLN:O	3:C:262:GLU:HG2	2.21	0.41
3:C:437:CYS:O	3:C:441:LEU:N	2.54	0.41
3:C:547:VAL:HA	3:C:568:LEU:O	2.20	0.41
3:C:829:ALA:O	3:C:832:VAL:HG12	2.21	0.41
4:E:50:ARG:HE	4:E:50:ARG:HB3	1.60	0.41
4:E:164:LYS:HB2	4:E:180:MET:HB2	2.03	0.41
4:E:179:ASP:OD2	4:E:180:MET:N	2.54	0.41
5:F:85:A:C1'	5:F:86:A:H5'	2.50	0.41
6:r:54:LYS:HE3	6:r:54:LYS:HB3	1.69	0.41
6:s:71:GLY:O	6:s:75:LEU:HG	2.21	0.41
8:g:58:VAL:HB	9:e:82:ILE:HG13	2.03	0.41
9:e:74:LEU:HD21	9:e:79:ILE:HG12	2.03	0.41
11:d:41:ASN:HB2	11:d:104:MET:CB	2.51	0.41
11:d:68:GLU:OE2	11:d:90:ARG:HB2	2.21	0.41
13:b:33:ALA:H	13:b:41:VAL:HB	1.86	0.41
14:I:553:GLN:OE1	14:I:555:ALA:HB2	2.21	0.41
15:J:103:ARG:HG2	25:L:217:LEU:HD22	2.02	0.41
18:T:191:PRO:HA	18:T:444:ASP:OD2	2.21	0.41
18:T:412:MET:HB3	18:T:443:TRP:CZ3	2.56	0.41
18:T:472:MET:HA	18:T:482:ILE:O	2.20	0.41
19:O:141:ALA:CA	24:W:92:PRO:HG2	2.44	0.41
19:O:255:PHE:HD2	19:O:283:ALA:HA	1.86	0.41
20:N:65:MET:HA	20:N:71:MET:HB3	2.03	0.41
21:R:97:VAL:HG13	21:R:107:VAL:HG11	2.01	0.41
24:W:201:ALA:C	24:W:203:LYS:H	2.29	0.41
25:L:122:LEU:HD21	25:L:128:ASP:HA	2.02	0.41
25:L:166:ALA:HB3	25:L:167:LYS:HE2	2.03	0.41
25:L:789:ARG:HG2	26:K:195:LEU:HD21	2.03	0.41
28:V:704:LYS:C	28:V:706:PHE:H	2.28	0.41
29:Q:154:GLN:C	29:Q:156:LEU:N	2.79	0.41
31:3:97:A:H4'	31:3:98:U:O5'	2.21	0.41
1:A:316:PHE:HA	1:A:321:PHE:HE2	1.86	0.41
1:A:724:PHE:HB3	21:R:204:PRO:O	2.21	0.41
1:A:760:MET:HE1	1:A:802:MET:HG3	2.03	0.41
1:A:1396:HIS:CD2	1:A:1429:ILE:HD13	2.56	0.41
1:A:1665:LEU:HD11	1:A:1672:THR:CG2	2.47	0.41
1:A:1673:VAL:HB	1:A:1694:LEU:HB3	2.03	0.41
3:C:123:SER:HB3	7:a:89:LYS:HE3	2.03	0.41
3:C:197:MET:HE2	3:C:552:ALA:HA	2.03	0.41
3:C:270:ILE:HD11	3:C:295:ILE:CG2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:682:THR:HG21	3:C:845:MET:SD	2.61	0.41
3:C:818:ILE:HD12	3:C:819:HIS:N	2.36	0.41
4:E:64:HIS:NE2	4:E:82:SER:HB2	2.36	0.41
4:E:113:GLU:OE1	4:E:294:ARG:NH2	2.44	0.41
4:E:157:CYS:CB	4:E:199:ALA:HA	2.51	0.41
6:r:88:HIS:HE1	26:K:93:LYS:HD3	1.86	0.41
9:e:69:LEU:O	10:f:75:ARG:NE	2.54	0.41
13:b:26:GLN:O	13:b:27:ILE:HD13	2.21	0.41
14:I:480:THR:O	14:I:503:TYR:HB3	2.20	0.41
14:I:698:TYR:HB3	14:I:714:ILE:HG21	2.02	0.41
15:J:286:SER:HA	15:J:289:GLN:HG3	2.02	0.41
21:R:161:LEU:HA	21:R:162:PRO:HD3	1.92	0.41
23:S:12:MET:CE	23:S:133:ARG:HG2	2.51	0.41
23:S:33:GLU:HB3	23:S:37:LYS:NZ	2.35	0.41
23:S:54:CYS:SG	23:S:134:LEU:HD23	2.60	0.41
23:S:92:MET:HE3	23:S:92:MET:HB3	1.85	0.41
24:W:469:ASN:HA	24:W:485:VAL:O	2.21	0.41
25:L:130:ASN:HD22	25:L:130:ASN:HA	1.63	0.41
25:L:667:ARG:HD2	25:L:667:ARG:HA	1.83	0.41
26:K:150:LYS:HA	26:K:153:ARG:HB2	2.04	0.41
1:A:643:GLN:HG3	1:A:644:TYR:N	2.35	0.40
1:A:1174:ILE:HD13	1:A:1212:ASN:HB3	2.02	0.40
1:A:1619:LEU:HA	1:A:1619:LEU:HD23	1.65	0.40
1:A:1681:ARG:HG3	1:A:1684:TYR:CE2	2.56	0.40
2:B:68:G:H2'	2:B:68:G:N3	2.36	0.40
3:C:211:PHE:CD1	3:C:452:VAL:HB	2.56	0.40
3:C:272:LYS:HG2	32:C:1001:GTP:C5	2.56	0.40
3:C:445:ALA:O	3:C:449:ASP:HB2	2.21	0.40
3:C:785:GLN:CD	3:C:826:ILE:HG12	2.45	0.40
3:C:844:LEU:C	3:C:924:VAL:HG23	2.46	0.40
3:C:848:VAL:HG21	3:C:922:GLN:HG3	2.03	0.40
4:E:145:LYS:O	4:E:145:LYS:HG3	2.21	0.40
6:q:15:VAL:O	6:q:50:LEU:HA	2.21	0.40
6:q:68:SER:O	6:q:72:LEU:HB2	2.21	0.40
12:c:16:VAL:HB	12:c:70:ILE:O	2.20	0.40
15:J:296:LYS:HD2	15:J:296:LYS:HA	1.88	0.40
16:P:62:GLU:H	16:P:62:GLU:HG2	1.57	0.40
19:O:244:THR:HG22	19:O:245:GLU:N	2.36	0.40
19:O:264:MET:HE3	19:O:264:MET:HB2	1.95	0.40
21:R:233:LYS:HE3	21:R:234:ASP:N	2.36	0.40
26:K:55:LYS:HE3	26:K:55:LYS:HB2	1.75	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:K:134:GLN:NE2	26:K:137:ARG:HD3	2.36	0.40
29:Q:788:ALA:C	29:Q:790:SER:N	2.79	0.40
31:3:7:G:C6	31:3:8:C:N4	2.89	0.40
1:A:371:LYS:HA	1:A:378:TYR:HB2	2.02	0.40
1:A:1016:VAL:HG22	1:A:1253:MET:HB3	2.03	0.40
1:A:1279:ALA:HB1	1:A:1288:ARG:HG2	2.03	0.40
1:A:1395:GLY:HA3	1:A:1421:MET:HE3	2.02	0.40
1:A:1462:ALA:O	1:A:1464:ASN:ND2	2.54	0.40
1:A:1661:PHE:CE1	1:A:1789:LEU:HD21	2.48	0.40
1:A:1671:GLU:N	1:A:1697:ALA:HA	2.35	0.40
1:A:1732:TRP:CD2	1:A:1772:ALA:HB2	2.56	0.40
1:A:1804:LEU:HD13	1:A:1808:ARG:NH1	2.36	0.40
2:B:11:A:C6	2:B:12:G:C6	3.09	0.40
3:C:793:GLU:C	3:C:798:ASP:HA	2.46	0.40
14:I:549:PHE:CD1	14:I:550:LEU:HD12	2.56	0.40
14:I:594:LYS:HA	15:J:305:GLU:OE2	2.21	0.40
14:I:616:PRO:HA	14:I:619:LEU:HD12	2.04	0.40
14:I:749:GLU:OE1	14:I:752:ARG:HB3	2.21	0.40
15:J:202:PHE:O	15:J:206:ILE:HG13	2.20	0.40
15:J:281:LYS:HA	15:J:281:LYS:HD2	1.85	0.40
23:S:3:ALA:N	23:S:19:LEU:O	2.54	0.40
25:L:213:VAL:CG1	25:L:216:GLU:HG3	2.51	0.40
25:L:605:ALA:O	25:L:608:MET:HG2	2.21	0.40
25:L:761:LEU:CD2	26:K:166:LEU:HB3	2.51	0.40
26:K:43:LEU:HD12	26:K:43:LEU:HA	1.86	0.40
31:3:14:A:C6	31:3:15:U:C4	3.08	0.40
1:A:214:LYS:NZ	1:A:689:PRO:O	2.51	0.40
1:A:217:ARG:HD2	1:A:220:PHE:CD2	2.56	0.40
1:A:654:GLY:HA2	1:A:656:TYR:CE1	2.56	0.40
1:A:786:ALA:HA	1:A:1086:MET:HG2	2.04	0.40
1:A:873:ILE:CD1	1:A:1229:LEU:HD11	2.51	0.40
1:A:1252:SER:HA	1:A:1256:PHE:O	2.21	0.40
1:A:1363:ILE:HD13	1:A:1389:LEU:HD13	2.03	0.40
1:A:1546:GLU:HG2	1:A:1547:GLY:N	2.37	0.40
1:A:1557:THR:HG22	1:A:1812:ARG:HG3	2.02	0.40
3:C:184:ARG:HE	3:C:184:ARG:HB3	1.79	0.40
3:C:187:GLU:CB	3:C:194:ILE:HG12	2.52	0.40
3:C:772:ASN:HB3	3:C:775:LEU:HB2	2.04	0.40
3:C:935:LEU:HD12	3:C:948:ARG:HE	1.87	0.40
4:E:134:CYS:SG	4:E:143:ILE:HB	2.62	0.40
4:E:134:CYS:SG	4:E:180:MET:HE1	2.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:157:CYS:HB2	4:E:199:ALA:HA	2.04	0.40
6:r:24:GLU:O	6:r:28:ILE:HG22	2.21	0.40
6:r:71:GLY:O	6:r:75:LEU:HG	2.22	0.40
6:r:115:ILE:CG1	6:s:114:VAL:CG1	2.93	0.40
7:a:36:GLU:O	7:a:48:LEU:HA	2.21	0.40
8:g:38:MET:HG3	8:g:61:GLY:CA	2.47	0.40
8:g:43:ASP:HA	8:g:56:MET:HG3	2.03	0.40
14:I:381:LYS:HE2	14:I:381:LYS:HB2	1.91	0.40
14:I:456:CYS:HB2	14:I:511:MET:CE	2.51	0.40
14:I:505:ASN:HB3	14:I:508:LEU:HD12	2.03	0.40
15:J:212:VAL:HG11	15:J:248:THR:HG21	2.03	0.40
17:M:499:MET:HE2	17:M:499:MET:HB3	1.78	0.40
18:T:188:TRP:CE3	21:R:118:VAL:HG13	2.56	0.40
21:R:171:ILE:HG12	21:R:191:ILE:HB	2.03	0.40
24:W:49:LEU:HB3	26:K:184:ARG:NH2	2.35	0.40
25:L:565:LEU:HA	25:L:565:LEU:HD12	1.73	0.40
25:L:828:LYS:HD2	26:K:232:THR:HG21	2.03	0.40
29:Q:917:ILE:HA	29:Q:943:LEU:HA	2.03	0.40
29:Q:1459:ASP:O	29:Q:1490:LEU:HA	2.21	0.40
31:3:91:A:H8	31:3:91:A:O5'	2.04	0.40
1:A:286:TRP:CD1	1:A:286:TRP:H	2.38	0.40
1:A:359:LYS:HG2	3:C:956:ARG:C	2.47	0.40
1:A:845:ARG:O	1:A:849:LYS:HG3	2.21	0.40
1:A:1005:LYS:HA	1:A:1005:LYS:HD3	1.76	0.40
1:A:1923:LYS:O	1:A:1947:VAL:N	2.36	0.40
2:B:7:G:H5''	2:B:8:A:OP1	2.22	0.40
2:B:12:G:C2	2:B:13:C:C5	3.10	0.40
3:C:129:THR:HG23	7:a:81:MET:HB3	2.03	0.40
6:r:14:VAL:HA	6:r:51:LEU:O	2.22	0.40
6:r:94:LEU:HD11	6:s:90:THR:CA	2.47	0.40
11:d:50:ALA:HB3	11:d:63:LEU:HG	2.02	0.40
14:I:402:ARG:HE	14:I:402:ARG:HB2	1.64	0.40
18:T:229:ARG:HG2	18:T:250:GLU:C	2.46	0.40
19:O:58:PRO:HD2	19:O:62:ALA:HB1	2.03	0.40
23:S:9:ASP:OD1	23:S:153:ARG:HB3	2.22	0.40
24:W:285:GLY:HA2	24:W:570:GLY:N	2.34	0.40
1:A:1014:LEU:HB2	1:A:1443:PHE:CE1	2.57	0.40
3:C:365:TYR:CD1	3:C:377:PRO:HA	2.56	0.40
3:C:522:ASP:O	3:C:543:THR:HA	2.22	0.40
3:C:635:SER:O	3:C:646:ILE:HA	2.21	0.40
4:E:86:ASP:C	4:E:87:LYS:HG2	2.45	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:r:115:ILE:HD13	6:r:115:ILE:C	2.47	0.40
7:a:27:LEU:HA	7:a:74:ARG:N	2.35	0.40
8:g:28:SER:O	8:g:45:THR:HA	2.22	0.40
8:g:58:VAL:HG11	9:e:16:MET:HE2	2.02	0.40
9:e:50:ASN:ND2	9:e:50:ASN:H	2.18	0.40
12:c:66:ILE:HG21	12:c:69:TYR:CE2	2.57	0.40
14:I:445:HIS:CE1	14:I:451:LEU:HD13	2.57	0.40
14:I:461:MET:HA	14:I:464:ARG:HB2	2.03	0.40
14:I:672:GLU:HA	14:I:675:GLU:CG	2.51	0.40
15:J:52:PRO:C	15:J:54:GLU:N	2.79	0.40
18:T:180:VAL:HG21	21:R:115:VAL:HG11	2.03	0.40
21:R:181:GLN:HG3	21:R:182:TYR:CD1	2.56	0.40
22:H:16:U:O2'	22:H:17:U:H5'	2.21	0.40
24:W:222:GLU:O	24:W:226:LEU:HB2	2.21	0.40
25:L:801:LYS:HE3	25:L:801:LYS:HB2	1.79	0.40
25:L:816:ARG:HH12	25:L:819:ASP:HB3	1.86	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	1923/2398 (80%)	1730 (90%)	182 (10%)	11 (1%)	22	43
3	C	895/989 (90%)	816 (91%)	78 (9%)	1 (0%)	48	71
4	E	316/362 (87%)	289 (92%)	26 (8%)	1 (0%)	37	59
6	q	102/503 (20%)	102 (100%)	0	0	100	100
6	r	129/503 (26%)	120 (93%)	8 (6%)	1 (1%)	16	34
6	s	68/503 (14%)	65 (96%)	3 (4%)	0	100	100
6	t	60/503 (12%)	56 (93%)	4 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	a	88/127 (69%)	86 (98%)	2 (2%)	0	100	100
8	g	63/77 (82%)	60 (95%)	3 (5%)	0	100	100
9	e	78/87 (90%)	74 (95%)	4 (5%)	0	100	100
10	f	69/85 (81%)	68 (99%)	1 (1%)	0	100	100
11	d	98/110 (89%)	97 (99%)	1 (1%)	0	100	100
12	c	86/114 (75%)	82 (95%)	4 (5%)	0	100	100
13	b	95/265 (36%)	89 (94%)	6 (6%)	0	100	100
14	I	657/925 (71%)	641 (98%)	16 (2%)	0	100	100
15	J	587/835 (70%)	551 (94%)	30 (5%)	6 (1%)	13	29
16	P	98/235 (42%)	90 (92%)	8 (8%)	0	100	100
17	M	74/563 (13%)	68 (92%)	6 (8%)	0	100	100
18	T	342/518 (66%)	326 (95%)	15 (4%)	1 (0%)	37	59
19	O	269/417 (64%)	245 (91%)	24 (9%)	0	100	100
20	N	167/233 (72%)	154 (92%)	13 (8%)	0	100	100
21	R	254/684 (37%)	240 (94%)	14 (6%)	0	100	100
23	S	153/157 (98%)	137 (90%)	16 (10%)	0	100	100
24	W	475/576 (82%)	431 (91%)	38 (8%)	6 (1%)	10	21
25	L	454/833 (54%)	429 (94%)	25 (6%)	0	100	100
26	K	208/303 (69%)	191 (92%)	16 (8%)	1 (0%)	25	47
27	U	24/721 (3%)	23 (96%)	1 (4%)	0	100	100
28	V	184/928 (20%)	177 (96%)	7 (4%)	0	100	100
29	Q	1275/1844 (69%)	1217 (96%)	49 (4%)	9 (1%)	19	38
All	All	9291/16398 (57%)	8654 (93%)	600 (6%)	37 (0%)	32	52

All (37) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	389	VAL
1	A	449	GLU
15	J	26	ALA
15	J	27	GLU
29	Q	893	ARG
1	A	246	PRO
3	C	422	THR

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Mol	Chain	Res	Type
6	r	58	THR
15	J	37	GLN
15	J	40	ASP
15	J	53	GLU
26	K	62	PRO
29	Q	155	GLU
29	Q	158	GLY
29	Q	719	ALA
29	Q	789	SER
1	A	247	LEU
1	A	528	PRO
4	E	47	GLY
24	W	86	VAL
29	Q	154	GLN
1	A	1266	MET
1	A	1717	ASP
1	A	2011	PRO
29	Q	153	LYS
1	A	1426	ASP
1	A	1718	GLN
24	W	87	LEU
24	W	92	PRO
24	W	91	HIS
29	Q	898	ASP
29	Q	1365	VAL
1	A	1822	PRO
15	J	52	PRO
24	W	84	ALA
24	W	198	GLN
18	T	247	GLY

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	1505/2124 (71%)	1302 (86%)	203 (14%)	<b>3</b> <b>6</b>

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	753/825 (91%)	645 (86%)	108 (14%)	2	5
4	E	264/300 (88%)	220 (83%)	44 (17%)	2	3
6	q	94/398 (24%)	85 (90%)	9 (10%)	7	14
6	r	113/398 (28%)	91 (80%)	22 (20%)	1	2
6	s	59/398 (15%)	54 (92%)	5 (8%)	8	18
6	t	54/398 (14%)	44 (82%)	10 (18%)	1	2
7	a	76/97 (78%)	64 (84%)	12 (16%)	2	3
8	g	58/67 (87%)	50 (86%)	8 (14%)	3	5
9	e	73/79 (92%)	61 (84%)	12 (16%)	2	3
10	f	62/75 (83%)	55 (89%)	7 (11%)	4	9
11	d	92/100 (92%)	81 (88%)	11 (12%)	4	8
12	c	78/95 (82%)	62 (80%)	16 (20%)	1	1
13	b	84/211 (40%)	76 (90%)	8 (10%)	7	14
14	I	357/743 (48%)	317 (89%)	40 (11%)	5	9
15	J	260/676 (38%)	231 (89%)	29 (11%)	5	9
16	P	88/188 (47%)	78 (89%)	10 (11%)	4	9
17	M	63/424 (15%)	57 (90%)	6 (10%)	7	14
18	T	291/416 (70%)	264 (91%)	27 (9%)	7	15
19	O	228/318 (72%)	208 (91%)	20 (9%)	8	17
20	N	148/193 (77%)	134 (90%)	14 (10%)	7	14
21	R	209/507 (41%)	172 (82%)	37 (18%)	1	2
23	S	128/130 (98%)	111 (87%)	17 (13%)	3	6
24	W	118/474 (25%)	93 (79%)	25 (21%)	1	1
25	L	388/648 (60%)	347 (89%)	41 (11%)	5	11
26	K	177/221 (80%)	151 (85%)	26 (15%)	2	4
27	U	20/572 (4%)	16 (80%)	4 (20%)	1	2
28	V	28/746 (4%)	26 (93%)	2 (7%)	12	26
All	All	5868/11821 (50%)	5095 (87%)	773 (13%)	6	6

All (773) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	GLN

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Mol	Chain	Res	Type
1	A	96	TRP
1	A	102	LYS
1	A	114	GLU
1	A	127	LYS
1	A	129	ILE
1	A	145	ARG
1	A	146	VAL
1	A	148	LEU
1	A	167	MET
1	A	175	VAL
1	A	177	VAL
1	A	181	ILE
1	A	185	ILE
1	A	213	GLU
1	A	276	LYS
1	A	279	ASN
1	A	288	LEU
1	A	296	LEU
1	A	299	LEU
1	A	303	LEU
1	A	305	THR
1	A	310	ARG
1	A	311	ASN
1	A	331	ILE
1	A	362	ILE
1	A	368	THR
1	A	372	VAL
1	A	380	ASN
1	A	384	LYS
1	A	385	VAL
1	A	386	ARG
1	A	387	LEU
1	A	391	HIS
1	A	396	LEU
1	A	398	ILE
1	A	478	ARG
1	A	492	ASN
1	A	493	CYS
1	A	497	GLU
1	A	498	HIS
1	A	502	THR
1	A	503	TYR

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Mol	Chain	Res	Type
1	A	516	LYS
1	A	520	LEU
1	A	522	LEU
1	A	530	SER
1	A	540	LEU
1	A	543	THR
1	A	544	LYS
1	A	547	GLN
1	A	548	SER
1	A	549	THR
1	A	587	ASN
1	A	589	LYS
1	A	593	THR
1	A	595	THR
1	A	596	THR
1	A	610	LEU
1	A	618	THR
1	A	619	LYS
1	A	633	VAL
1	A	634	ASP
1	A	640	ASP
1	A	643	GLN
1	A	675	LEU
1	A	691	VAL
1	A	706	ARG
1	A	708	ILE
1	A	712	LEU
1	A	714	ARG
1	A	722	ARG
1	A	729	SER
1	A	732	ILE
1	A	738	LYS
1	A	741	ILE
1	A	809	GLN
1	A	834	THR
1	A	843	LEU
1	A	861	ASP
1	A	866	THR
1	A	899	ASP
1	A	909	ARG
1	A	919	ARG
1	A	923	SER

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Mol	Chain	Res	Type
1	A	952	GLN
1	A	954	SER
1	A	975	ILE
1	A	978	LEU
1	A	980	LYS
1	A	986	LEU
1	A	987	ASP
1	A	993	GLU
1	A	999	LEU
1	A	1004	VAL
1	A	1005	LYS
1	A	1009	SER
1	A	1015	LEU
1	A	1024	ASN
1	A	1026	VAL
1	A	1027	THR
1	A	1032	THR
1	A	1038	VAL
1	A	1039	VAL
1	A	1042	GLN
1	A	1043	SER
1	A	1059	ARG
1	A	1087	SER
1	A	1091	SER
1	A	1094	LEU
1	A	1120	THR
1	A	1131	CYS
1	A	1133	ASN
1	A	1137	THR
1	A	1142	LYS
1	A	1153	SER
1	A	1157	ASN
1	A	1159	VAL
1	A	1161	ILE
1	A	1163	PHE
1	A	1164	ARG
1	A	1190	VAL
1	A	1201	ASP
1	A	1213	LEU
1	A	1224	ARG
1	A	1230	THR
1	A	1231	THR

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Mol	Chain	Res	Type
1	A	1240	SER
1	A	1245	ASP
1	A	1248	ASN
1	A	1265	ARG
1	A	1283	VAL
1	A	1285	THR
1	A	1289	THR
1	A	1302	LYS
1	A	1319	THR
1	A	1321	THR
1	A	1331	LEU
1	A	1336	THR
1	A	1340	GLU
1	A	1348	LEU
1	A	1351	LEU
1	A	1362	ARG
1	A	1365	ILE
1	A	1397	ILE
1	A	1402	SER
1	A	1417	PHE
1	A	1428	LEU
1	A	1441	SER
1	A	1447	GLU
1	A	1456	LYS
1	A	1457	LYS
1	A	1459	GLU
1	A	1461	LYS
1	A	1468	THR
1	A	1470	ASP
1	A	1474	ASP
1	A	1480	ILE
1	A	1483	ILE
1	A	1491	ARG
1	A	1493	THR
1	A	1502	VAL
1	A	1512	THR
1	A	1513	LYS
1	A	1514	MET
1	A	1527	LYS
1	A	1538	VAL
1	A	1545	VAL
1	A	1557	THR

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Mol	Chain	Res	Type
1	A	1558	TYR
1	A	1590	LEU
1	A	1592	GLN
1	A	1593	ILE
1	A	1600	LEU
1	A	1601	TRP
1	A	1605	THR
1	A	1626	MET
1	A	1630	ILE
1	A	1632	THR
1	A	1633	LEU
1	A	1635	ILE
1	A	1638	ILE
1	A	1658	CYS
1	A	1665	LEU
1	A	1679	HIS
1	A	1683	SER
1	A	1701	TRP
1	A	1712	THR
1	A	1713	ASN
1	A	1725	TRP
1	A	1726	VAL
1	A	1728	VAL
1	A	1729	GLN
1	A	1732	TRP
1	A	1747	LYS
1	A	1757	SER
1	A	1783	PHE
1	A	1786	ILE
1	A	1791	ILE
1	A	1807	LEU
1	A	1813	LYS
1	A	1817	LEU
1	A	1819	SER
3	C	69	GLU
3	C	76	SER
3	C	87	THR
3	C	92	GLU
3	C	93	ASP
3	C	109	LYS
3	C	111	GLU
3	C	112	THR

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Mol	Chain	Res	Type
3	C	114	GLU
3	C	116	GLU
3	C	118	LEU
3	C	119	ARG
3	C	127	LEU
3	C	135	GLU
3	C	140	VAL
3	C	150	LYS
3	C	166	LYS
3	C	171	GLN
3	C	184	ARG
3	C	200	SER
3	C	204	GLU
3	C	210	SER
3	C	216	LEU
3	C	218	CYS
3	C	222	VAL
3	C	243	ASP
3	C	246	GLU
3	C	269	MET
3	C	298	VAL
3	C	306	CYS
3	C	319	VAL
3	C	330	SER
3	C	339	PHE
3	C	356	PHE
3	C	365	TYR
3	C	397	MET
3	C	408	THR
3	C	410	GLU
3	C	412	LEU
3	C	416	LEU
3	C	421	ARG
3	C	427	LEU
3	C	429	THR
3	C	448	VAL
3	C	452	VAL
3	C	465	LYS
3	C	482	MET
3	C	485	CYS
3	C	498	LEU
3	C	508	ASP

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Mol	Chain	Res	Type
3	C	525	LYS
3	C	527	LEU
3	C	532	THR
3	C	537	GLU
3	C	566	LEU
3	C	567	VAL
3	C	572	VAL
3	C	577	THR
3	C	585	ASP
3	C	591	VAL
3	C	593	ILE
3	C	600	GLN
3	C	610	GLU
3	C	612	LEU
3	C	616	GLU
3	C	622	GLU
3	C	627	VAL
3	C	634	CYS
3	C	636	THR
3	C	640	GLU
3	C	643	GLU
3	C	649	THR
3	C	659	LYS
3	C	662	ARG
3	C	670	VAL
3	C	676	VAL
3	C	689	LEU
3	C	690	LYS
3	C	701	LYS
3	C	709	LEU
3	C	710	ASP
3	C	725	ASP
3	C	726	MET
3	C	755	GLU
3	C	756	LEU
3	C	763	LEU
3	C	784	ILE
3	C	785	GLN
3	C	787	PHE
3	C	797	CYS
3	C	809	LEU
3	C	810	ASP

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Mol	Chain	Res	Type
3	C	826	ILE
3	C	849	TYR
3	C	855	THR
3	C	858	ASP
3	C	859	CYS
3	C	865	ASN
3	C	874	VAL
3	C	878	VAL
3	C	895	VAL
3	C	901	GLU
3	C	902	THR
3	C	905	ARG
3	C	932	SER
3	C	933	ILE
3	C	938	LEU
3	C	961	SER
4	E	48	ILE
4	E	53	ASN
4	E	54	LEU
4	E	76	ASP
4	E	80	ILE
4	E	82	SER
4	E	87	LYS
4	E	103	VAL
4	E	104	ILE
4	E	118	THR
4	E	127	SER
4	E	130	LYS
4	E	145	LYS
4	E	157	CYS
4	E	165	VAL
4	E	167	VAL
4	E	181	ARG
4	E	183	LYS
4	E	200	PHE
4	E	212	VAL
4	E	214	ASN
4	E	216	ILE
4	E	218	VAL
4	E	221	LEU
4	E	228	ASP
4	E	232	SER

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Mol	Chain	Res	Type
4	E	241	SER
4	E	243	THR
4	E	266	TRP
4	E	277	CYS
4	E	280	VAL
4	E	284	HIS
4	E	300	ASP
4	E	302	SER
4	E	306	CYS
4	E	311	ARG
4	E	324	LEU
4	E	333	SER
4	E	337	VAL
4	E	341	SER
4	E	342	LYS
4	E	343	GLU
4	E	357	LEU
4	E	359	GLU
6	q	4	SER
6	q	18	LYS
6	q	40	VAL
6	q	50	LEU
6	q	72	LEU
6	q	92	THR
6	q	97	THR
6	q	113	ARG
6	q	114	VAL
6	r	2	PHE
6	r	9	VAL
6	r	14	VAL
6	r	17	THR
6	r	41	THR
6	r	45	LEU
6	r	53	LEU
6	r	55	VAL
6	r	57	LYS
6	r	59	VAL
6	r	63	THR
6	r	67	THR
6	r	68	SER
6	r	69	ILE
6	r	95	HIS

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Mol	Chain	Res	Type
6	r	96	GLN
6	r	101	LEU
6	r	106	TYR
6	r	113	ARG
6	r	115	ILE
6	r	119	LEU
6	r	129	LEU
6	s	74	SER
6	s	75	LEU
6	s	85	LEU
6	s	124	GLU
6	s	131	ASP
6	t	69	ILE
6	t	74	SER
6	t	75	LEU
6	t	80	TRP
6	t	84	MET
6	t	85	LEU
6	t	90	THR
6	t	105	LEU
6	t	119	LEU
6	t	123	ASP
7	a	15	LEU
7	a	19	GLU
7	a	47	GLN
7	a	56	ARG
7	a	57	ASP
7	a	61	THR
7	a	66	LEU
7	a	68	ILE
7	a	82	LEU
7	a	87	MET
7	a	89	LYS
7	a	90	ARG
8	g	13	MET
8	g	21	LEU
8	g	27	VAL
8	g	38	MET
8	g	40	LEU
8	g	53	ASP
8	g	59	ILE
8	g	70	LEU

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Mol	Chain	Res	Type
9	e	9	MET
9	e	23	LYS
9	e	24	GLN
9	e	35	ASP
9	e	38	VAL
9	e	42	ILE
9	e	50	ASN
9	e	55	GLU
9	e	61	MET
9	e	62	LYS
9	e	82	ILE
9	e	85	THR
10	f	9	PRO
10	f	22	ILE
10	f	23	VAL
10	f	44	LEU
10	f	68	CYS
10	f	69	ASN
10	f	74	LEU
11	d	17	GLU
11	d	22	THR
11	d	42	CYS
11	d	47	LYS
11	d	52	VAL
11	d	63	LEU
11	d	68	GLU
11	d	71	THR
11	d	80	GLN
11	d	84	ARG
11	d	86	VAL
12	c	2	VAL
12	c	5	VAL
12	c	21	LYS
12	c	24	THR
12	c	38	ASN
12	c	41	LEU
12	c	45	LYS
12	c	49	ARG
12	c	51	LYS
12	c	59	LEU
12	c	62	ARG
12	c	64	ASN

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Mol	Chain	Res	Type
12	c	67	ARG
12	c	75	LEU
12	c	79	THR
12	c	85	ASP
13	b	9	LEU
13	b	20	THR
13	b	36	ARG
13	b	44	ASP
13	b	61	GLU
13	b	78	ILE
13	b	105	ILE
13	b	113	MET
14	I	346	VAL
14	I	356	LEU
14	I	365	SER
14	I	367	VAL
14	I	368	ILE
14	I	370	ARG
14	I	376	VAL
14	I	395	LEU
14	I	401	VAL
14	I	402	ARG
14	I	416	LEU
14	I	420	PHE
14	I	430	VAL
14	I	434	ARG
14	I	439	LYS
14	I	442	GLU
14	I	451	LEU
14	I	466	SER
14	I	476	THR
14	I	480	THR
14	I	487	ARG
14	I	506	LEU
14	I	537	ILE
14	I	548	LEU
14	I	583	LEU
14	I	593	LYS
14	I	601	LEU
14	I	614	CYS
14	I	615	LYS
14	I	620	GLU

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Mol	Chain	Res	Type
14	I	623	LYS
14	I	628	TYR
14	I	670	VAL
14	I	687	SER
14	I	692	ARG
14	I	702	GLU
14	I	712	ARG
14	I	745	ASP
14	I	746	THR
14	I	752	ARG
15	J	24	ILE
15	J	38	LEU
15	J	54	GLU
15	J	61	SER
15	J	65	GLN
15	J	70	VAL
15	J	71	ARG
15	J	77	ASN
15	J	96	ARG
15	J	126	ARG
15	J	139	VAL
15	J	144	ARG
15	J	162	VAL
15	J	167	GLN
15	J	175	PHE
15	J	196	ASP
15	J	228	VAL
15	J	237	ARG
15	J	242	LEU
15	J	244	GLU
15	J	248	THR
15	J	257	GLU
15	J	266	GLU
15	J	273	ARG
15	J	279	ILE
15	J	288	TYR
15	J	309	VAL
15	J	311	LYS
15	J	315	GLN
16	P	13	ILE
16	P	48	GLN
16	P	53	GLU

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Mol	Chain	Res	Type
16	P	62	GLU
16	P	68	ARG
16	P	73	LYS
16	P	194	ARG
16	P	204	ASN
16	P	231	GLN
16	P	234	ILE
17	M	447	GLN
17	M	464	GLU
17	M	467	GLU
17	M	496	VAL
17	M	499	MET
17	M	538	LYS
18	T	190	ARG
18	T	202	VAL
18	T	212	CYS
18	T	213	VAL
18	T	216	ASP
18	T	270	ASP
18	T	284	ILE
18	T	286	SER
18	T	291	LEU
18	T	312	ASP
18	T	314	VAL
18	T	323	LYS
18	T	324	VAL
18	T	353	HIS
18	T	377	SER
18	T	388	PHE
18	T	396	GLU
18	T	420	ILE
18	T	446	ARG
18	T	450	CYS
18	T	462	SER
18	T	465	SER
18	T	469	LEU
18	T	485	GLU
18	T	497	GLU
18	T	498	ASP
18	T	514	ASP
19	O	24	GLU
19	O	35	MET

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Mol	Chain	Res	Type
19	O	38	ILE
19	O	49	ARG
19	O	68	VAL
19	O	71	GLN
19	O	83	CYS
19	O	110	SER
19	O	111	GLU
19	O	151	LEU
19	O	155	GLN
19	O	165	VAL
19	O	180	CYS
19	O	206	ASN
19	O	217	VAL
19	O	224	THR
19	O	233	THR
19	O	239	VAL
19	O	266	VAL
19	O	282	LYS
20	N	21	GLU
20	N	23	ILE
20	N	37	GLU
20	N	41	LYS
20	N	47	THR
20	N	50	ILE
20	N	52	ARG
20	N	72	SER
20	N	82	GLU
20	N	109	LYS
20	N	118	SER
20	N	134	THR
20	N	146	SER
20	N	169	LEU
21	R	39	LEU
21	R	42	LYS
21	R	61	ILE
21	R	75	THR
21	R	80	GLN
21	R	83	ILE
21	R	88	LYS
21	R	97	VAL
21	R	105	ARG
21	R	110	ASP

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Mol	Chain	Res	Type
21	R	114	LEU
21	R	115	VAL
21	R	117	LYS
21	R	118	VAL
21	R	119	ASP
21	R	128	ARG
21	R	136	LYS
21	R	146	GLU
21	R	152	LYS
21	R	154	SER
21	R	155	SER
21	R	161	LEU
21	R	168	SER
21	R	174	THR
21	R	191	ILE
21	R	195	ASP
21	R	211	VAL
21	R	220	VAL
21	R	223	LEU
21	R	230	LEU
21	R	231	THR
21	R	240	ILE
21	R	254	THR
21	R	255	ILE
21	R	257	LEU
21	R	264	ASP
21	R	286	THR
23	S	5	LEU
23	S	6	VAL
23	S	8	ILE
23	S	9	ASP
23	S	16	THR
23	S	19	LEU
23	S	28	CYS
23	S	49	ILE
23	S	50	ARG
23	S	78	ILE
23	S	80	ARG
23	S	82	LEU
23	S	85	THR
23	S	133	ARG
23	S	134	LEU

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Mol	Chain	Res	Type
23	S	146	VAL
23	S	152	ILE
24	W	47	THR
24	W	49	LEU
24	W	50	VAL
24	W	51	LEU
24	W	65	LEU
24	W	72	LYS
24	W	77	LEU
24	W	87	LEU
24	W	89	PRO
24	W	91	HIS
24	W	107	VAL
24	W	112	ASP
24	W	118	ILE
24	W	121	GLU
24	W	122	GLN
24	W	134	GLU
24	W	139	ILE
24	W	166	LYS
24	W	167	THR
24	W	168	THR
24	W	171	ARG
24	W	180	GLU
24	W	202	SER
24	W	212	GLU
24	W	215	LYS
25	L	24	LYS
25	L	38	VAL
25	L	61	GLU
25	L	68	GLU
25	L	76	LEU
25	L	103	LEU
25	L	122	LEU
25	L	130	ASN
25	L	152	SER
25	L	160	ASN
25	L	161	THR
25	L	175	LEU
25	L	183	GLN
25	L	184	LEU
25	L	217	LEU

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Mol	Chain	Res	Type
25	L	237	GLN
25	L	541	ASP
25	L	545	ARG
25	L	548	ARG
25	L	556	ILE
25	L	596	LEU
25	L	601	GLU
25	L	614	HIS
25	L	646	GLU
25	L	649	LEU
25	L	650	GLU
25	L	654	SER
25	L	666	LEU
25	L	675	LEU
25	L	699	ARG
25	L	723	ARG
25	L	773	VAL
25	L	779	HIS
25	L	780	GLU
25	L	781	ARG
25	L	791	GLU
25	L	800	THR
25	L	805	VAL
25	L	816	ARG
25	L	817	ARG
25	L	828	LYS
26	K	28	HIS
26	K	29	LEU
26	K	59	THR
26	K	68	GLU
26	K	72	VAL
26	K	77	PHE
26	K	86	GLU
26	K	94	GLU
26	K	104	TYR
26	K	116	ASP
26	K	122	SER
26	K	131	LEU
26	K	134	GLN
26	K	136	LEU
26	K	141	GLN
26	K	144	LEU

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Mol	Chain	Res	Type
26	K	145	LEU
26	K	149	ASP
26	K	159	ASP
26	K	177	THR
26	K	188	GLN
26	K	195	LEU
26	K	197	LYS
26	K	216	CYS
26	K	219	LEU
26	K	226	MET
27	U	1	MET
27	U	2	TYR
27	U	15	THR
27	U	19	VAL
28	V	658	THR
28	V	668	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (176) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	GLN
1	A	100	ASN
1	A	124	HIS
1	A	132	HIS
1	A	142	HIS
1	A	156	HIS
1	A	240	ASN
1	A	269	HIS
1	A	279	ASN
1	A	311	ASN
1	A	379	ASN
1	A	461	ASN
1	A	481	HIS
1	A	492	ASN
1	A	496	GLN
1	A	512	GLN
1	A	521	ASN
1	A	559	GLN
1	A	581	HIS
1	A	627	GLN
1	A	643	GLN
1	A	648	HIS

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Mol	Chain	Res	Type
1	A	674	HIS
1	A	681	ASN
1	A	739	GLN
1	A	744	HIS
1	A	755	HIS
1	A	809	GLN
1	A	852	GLN
1	A	855	GLN
1	A	895	ASN
1	A	948	HIS
1	A	952	GLN
1	A	968	HIS
1	A	1024	ASN
1	A	1025	ASN
1	A	1033	ASN
1	A	1078	ASN
1	A	1133	ASN
1	A	1147	HIS
1	A	1157	ASN
1	A	1160	HIS
1	A	1175	GLN
1	A	1188	ASN
1	A	1194	ASN
1	A	1212	ASN
1	A	1223	ASN
1	A	1246	ASN
1	A	1282	ASN
1	A	1284	HIS
1	A	1291	GLN
1	A	1306	ASN
1	A	1310	GLN
1	A	1325	ASN
1	A	1346	GLN
1	A	1360	GLN
1	A	1401	GLN
1	A	1437	GLN
1	A	1488	GLN
1	A	1521	HIS
1	A	1524	HIS
1	A	1610	ASN
1	A	1616	GLN
1	A	1639	GLN

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Mol	Chain	Res	Type
1	A	1702	ASN
1	A	1729	GLN
1	A	1755	ASN
1	A	1792	GLN
1	A	1801	ASN
3	C	68	HIS
3	C	124	ASN
3	C	133	ASN
3	C	145	HIS
3	C	147	HIS
3	C	214	ASN
3	C	221	HIS
3	C	293	HIS
3	C	337	GLN
3	C	388	GLN
3	C	502	GLN
3	C	700	ASN
3	C	757	GLN
3	C	760	ASN
3	C	865	ASN
3	C	915	GLN
3	C	944	GLN
4	E	100	ASN
4	E	214	ASN
4	E	275	ASN
4	E	330	HIS
6	q	83	ASN
6	q	95	HIS
6	q	99	GLN
6	q	107	GLN
6	r	21	HIS
6	r	56	ASN
6	r	88	HIS
6	r	108	HIS
6	s	88	HIS
6	s	134	GLN
6	t	88	HIS
6	t	107	GLN
7	a	16	HIS
7	a	47	GLN
7	a	84	ASN
9	e	14	ASN

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Mol	Chain	Res	Type
9	e	21	GLN
9	e	27	GLN
9	e	50	ASN
9	e	78	ASN
10	f	14	GLN
11	d	30	GLN
11	d	44	ASN
11	d	58	HIS
11	d	80	GLN
12	c	52	ASN
12	c	65	ASN
12	c	76	ASN
14	I	374	HIS
14	I	426	HIS
14	I	427	HIS
14	I	432	ASN
14	I	445	HIS
14	I	453	HIS
14	I	465	HIS
14	I	512	HIS
14	I	545	ASN
14	I	553	GLN
14	I	743	ASN
15	J	154	HIS
15	J	207	GLN
15	J	224	GLN
15	J	247	GLN
16	P	29	GLN
16	P	38	HIS
17	M	540	GLN
18	T	261	HIS
18	T	325	GLN
18	T	347	GLN
18	T	353	HIS
19	O	45	HIS
19	O	60	ASN
19	O	71	GLN
19	O	119	GLN
19	O	149	GLN
19	O	155	GLN
20	N	51	HIS
20	N	111	ASN

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Mol	Chain	Res	Type
20	N	119	HIS
20	N	138	GLN
20	N	172	ASN
21	R	79	GLN
21	R	150	GLN
21	R	235	GLN
21	R	246	ASN
21	R	274	ASN
23	S	30	ASN
23	S	98	ASN
23	S	118	HIS
23	S	138	GLN
24	W	91	HIS
24	W	114	HIS
24	W	125	HIS
24	W	195	GLN
25	L	29	GLN
25	L	568	GLN
25	L	595	GLN
25	L	688	HIS
25	L	770	GLN
26	K	26	ASN
26	K	28	HIS
26	K	134	GLN
26	K	169	GLN
26	K	187	GLN
26	K	233	HIS
28	V	674	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	83/111 (74%)	48 (57%)	2 (2%)
22	H	39/192 (20%)	28 (71%)	3 (7%)
30	5	6/7 (85%)	1 (16%)	0
31	3	33/173 (19%)	16 (48%)	6 (18%)
5	F	90/101 (89%)	48 (53%)	5 (5%)
All	All	251/584 (42%)	141 (56%)	16 (6%)

All (141) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	8	A
2	B	9	C
2	B	10	G
2	B	11	A
2	B	15	G
2	B	16	A
2	B	17	A
2	B	20	C
2	B	27	A
2	B	28	A
2	B	35	U
2	B	39	G
2	B	40	C
2	B	41	C
2	B	42	U
2	B	48	U
2	B	49	A
2	B	52	G
2	B	53	A
2	B	58	C
2	B	59	G
2	B	62	A
2	B	63	G
2	B	64	U
2	B	65	U
2	B	66	U
2	B	68	G
2	B	69	C
2	B	70	U
2	B	71	C
2	B	72	A
2	B	73	C
2	B	74	G
2	B	75	C
2	B	76	A
2	B	77	G
2	B	79	C
2	B	80	G
2	B	88	A
2	B	89	U
2	B	90	C
2	B	91	U
2	B	92	U

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Mol	Chain	Res	Type
2	B	94	U
2	B	95	U
2	B	96	G
2	B	97	U
2	B	98	G
5	F	4	C
5	F	5	U
5	F	6	U
5	F	7	C
5	F	8	G
5	F	9	G
5	F	13	A
5	F	14	A
5	F	19	U
5	F	20	A
5	F	21	A
5	F	22	A
5	F	24	U
5	F	26	G
5	F	27	G
5	F	29	A
5	F	37	G
5	F	40	A
5	F	41	A
5	F	42	G
5	F	47	G
5	F	51	G
5	F	61	C
5	F	62	A
5	F	67	U
5	F	68	G
5	F	71	A
5	F	72	C
5	F	73	G
5	F	74	C
5	F	75	A
5	F	76	U
5	F	77	A
5	F	78	A
5	F	79	A
5	F	80	U
5	F	81	C

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Mol	Chain	Res	Type
5	F	82	G
5	F	83	A
5	F	84	G
5	F	85	A
5	F	86	A
5	F	87	A
5	F	88	U
5	F	89	G
5	F	90	G
5	F	91	U
5	F	92	U
22	H	2	U
22	H	3	A
22	H	4	C
22	H	5	C
22	H	6	U
22	H	7	U
22	H	8	U
22	H	9	C
22	H	10	U
22	H	11	C
22	H	12	G
22	H	13	G
22	H	14	C
22	H	16	U
22	H	17	U
22	H	18	U
22	H	19	U
22	H	20	G
22	H	21	G
22	H	24	C
22	H	25	A
22	H	26	G
22	H	30	A
22	H	31	U
22	H	32	G
22	H	34	G
22	H	38	U
22	H	40	U
30	5	-6	C
31	3	2	U
31	3	3	A

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Mol	Chain	Res	Type
31	3	7	G
31	3	8	C
31	3	12	G
31	3	13	C
31	3	14	A
31	3	17	A
31	3	19	U
31	3	20	A
31	3	21	C
31	3	22	U
31	3	91	A
31	3	96	U
31	3	98	U
31	3	100	C

All (16) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	16	A
2	B	97	U
5	F	19	U
5	F	26	G
5	F	76	U
5	F	78	A
5	F	80	U
22	H	6	U
22	H	30	A
22	H	31	U
31	3	16	U
31	3	20	A
31	3	21	C
31	3	90	C
31	3	95	U
31	3	97	A

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

2 non-standard protein/DNA/RNA residues are 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
21	SEP	R	217	21	8,9,10	1.16	1 (12%)	8,12,14	1.38	1 (12%)
21	SEP	R	225	21	8,9,10	1.19	1 (12%)	8,12,14	1.31	2 (25%)

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
21	SEP	R	217	21	-	1/5/8/10	-
21	SEP	R	225	21	-	0/5/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	R	217	SEP	P-O1P	2.38	1.58	1.50
21	R	225	SEP	P-O1P	2.18	1.57	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	R	217	SEP	O2P-P-OG	3.08	114.92	106.73
21	R	225	SEP	OG-CB-CA	2.72	110.79	108.14
21	R	225	SEP	O3P-P-OG	2.09	112.30	106.73

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
21	R	217	SEP	CA-CB-OG-P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
21	R	217	SEP	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 10 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
32	GTP	C	1001	33	26,34,34	1.11	3 (11%)	32,54,54	0.89	1 (3%)

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
32	GTP	C	1001	33	-	5/18/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	C	1001	GTP	C5-C6	-2.67	1.42	1.47
32	C	1001	GTP	C8-N7	-2.23	1.31	1.35
32	C	1001	GTP	C5-C4	-2.16	1.37	1.43

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	C	1001	GTP	C3'-C2'-C1'	2.08	104.11	100.98

There are no chirality outliers.

All (5) torsion outliers are listed below:

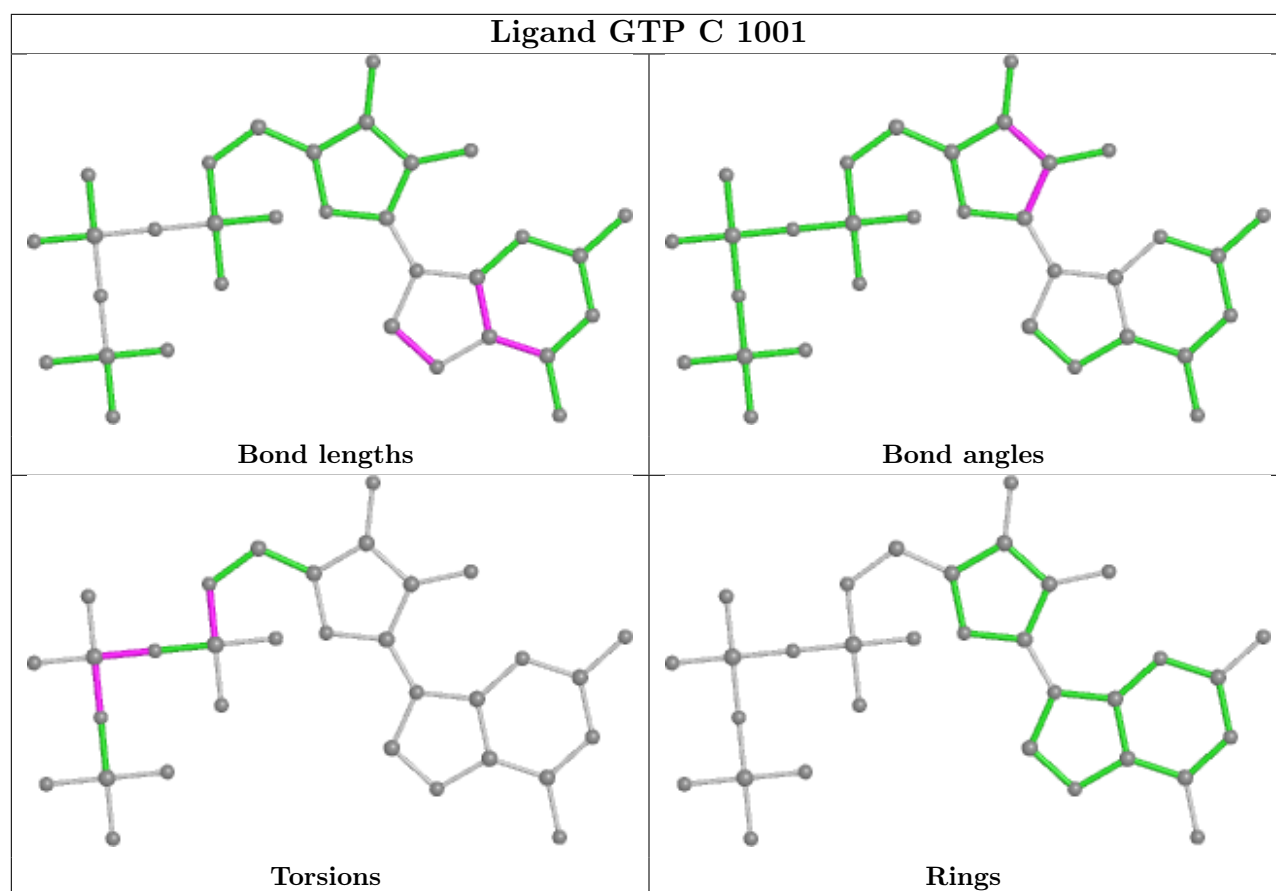
Mol	Chain	Res	Type	Atoms
32	C	1001	GTP	C5'-O5'-PA-O1A
32	C	1001	GTP	C5'-O5'-PA-O2A
32	C	1001	GTP	PA-O3A-PB-O3B
32	C	1001	GTP	PG-O3B-PB-O2B
32	C	1001	GTP	C5'-O5'-PA-O3A

There are no ring outliers.

1 monomer is involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	C	1001	GTP	9	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.

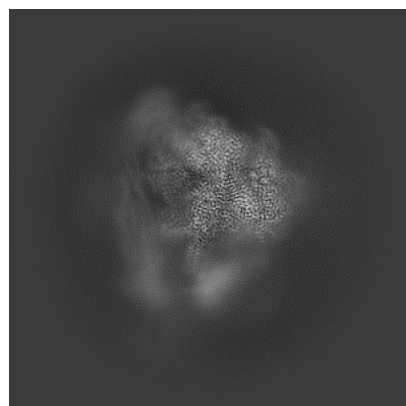
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38362. These allow visual inspection of the internal detail of the map and identification of artifacts.

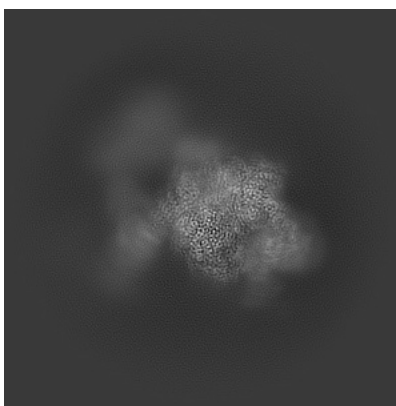
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

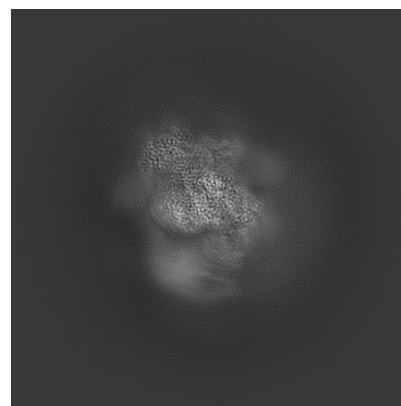
#### 6.1.1 Primary map



X

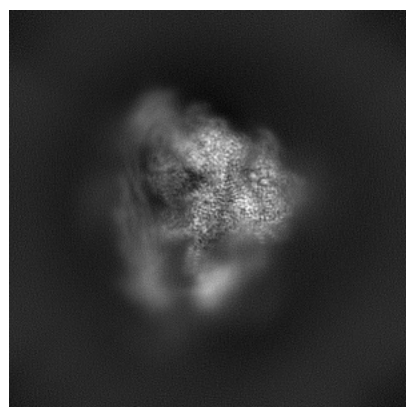


Y

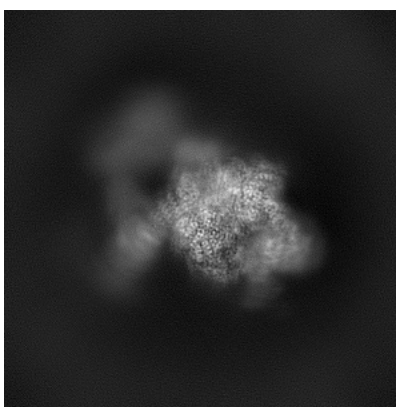


Z

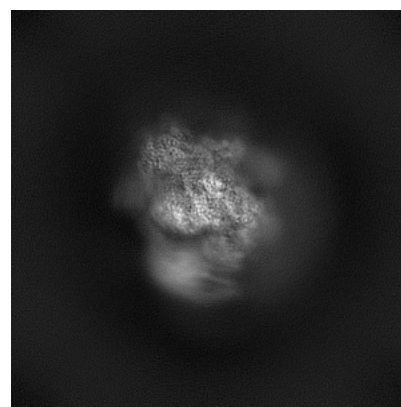
#### 6.1.2 Raw map



X



Y

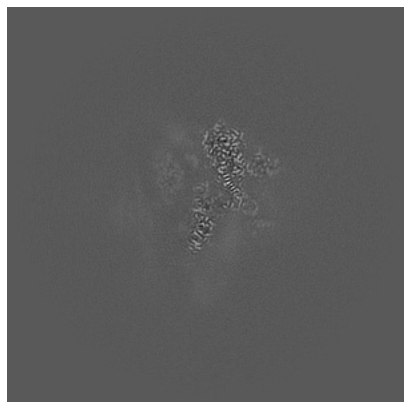


Z

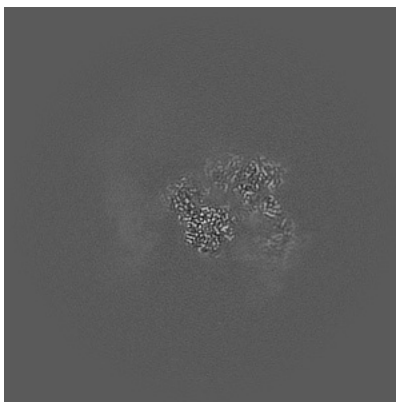
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

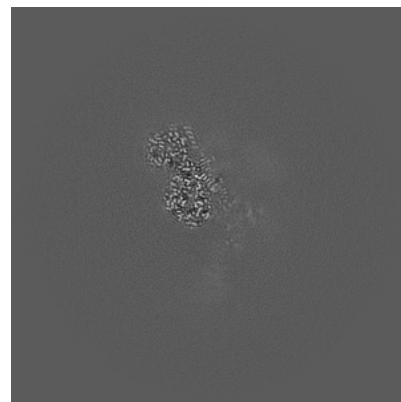
### 6.2.1 Primary map



X Index: 220



Y Index: 220

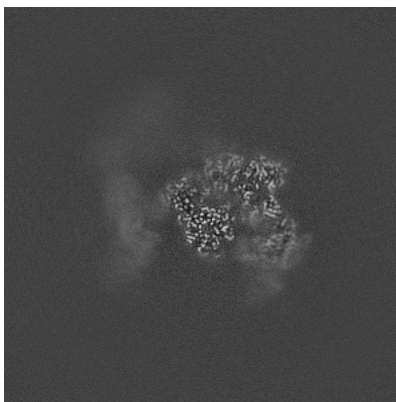


Z Index: 220

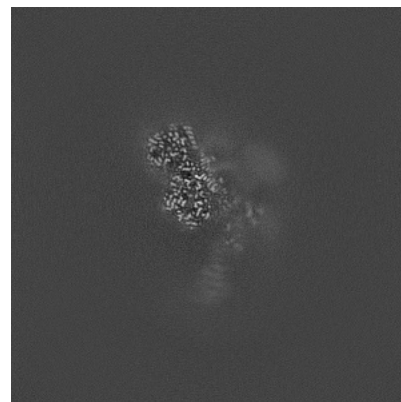
### 6.2.2 Raw map



X Index: 220



Y Index: 220

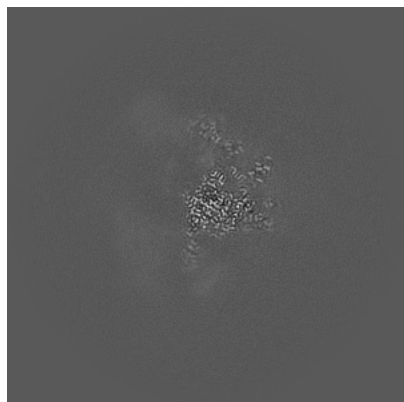


Z Index: 220

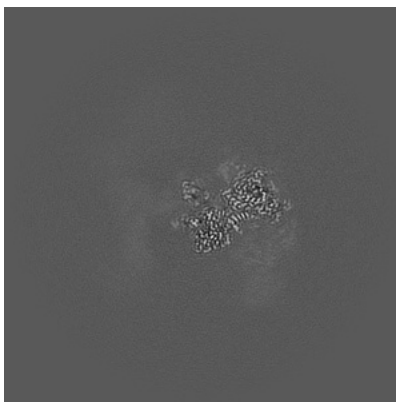
The images above show central slices of the map in three orthogonal directions.

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

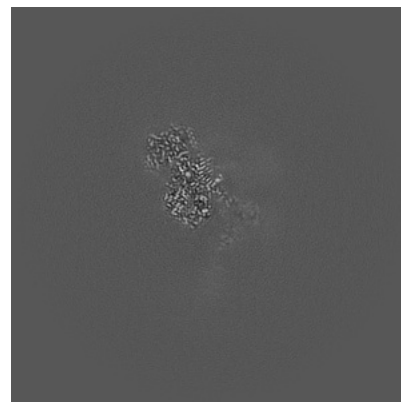
### 6.3.1 Primary map



X Index: 203

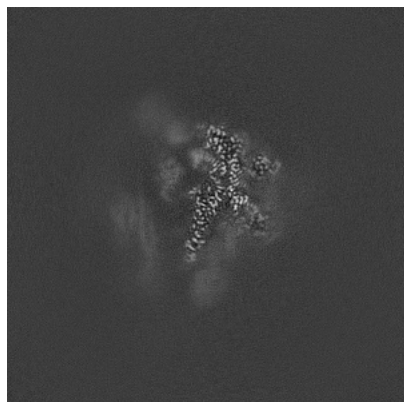


Y Index: 234

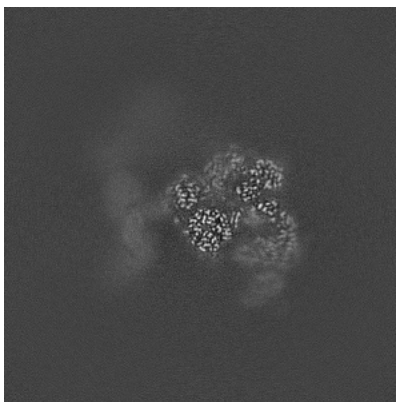


Z Index: 222

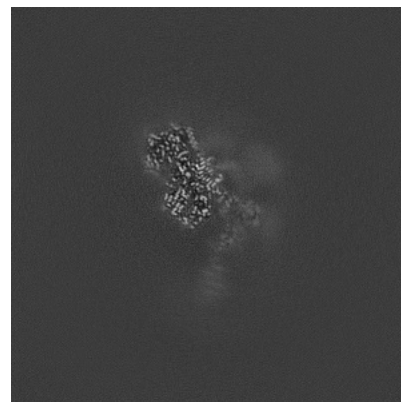
### 6.3.2 Raw map



X Index: 213



Y Index: 224

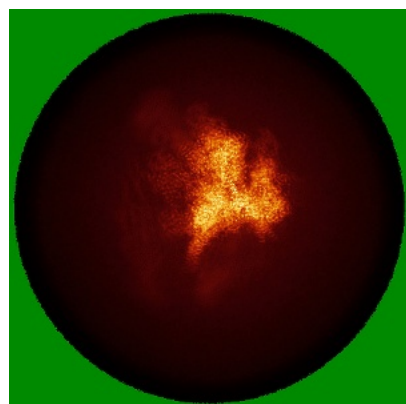


Z Index: 222

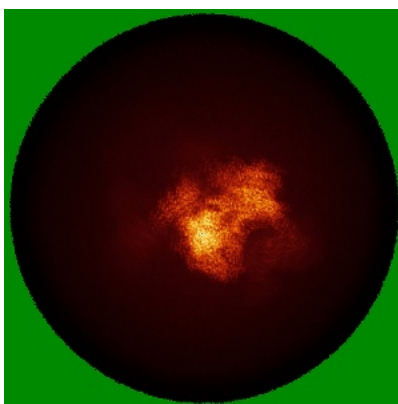
The images above show the largest variance slices of the map in three orthogonal directions.

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

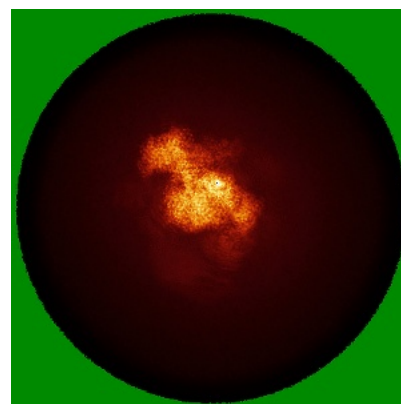
### 6.4.1 Primary map



X

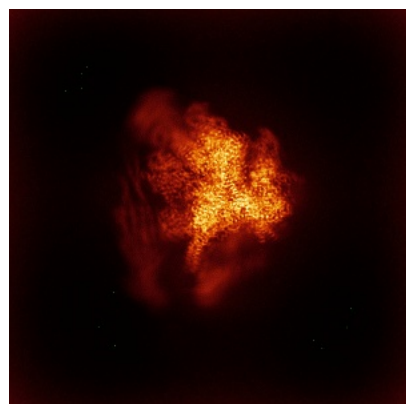


Y

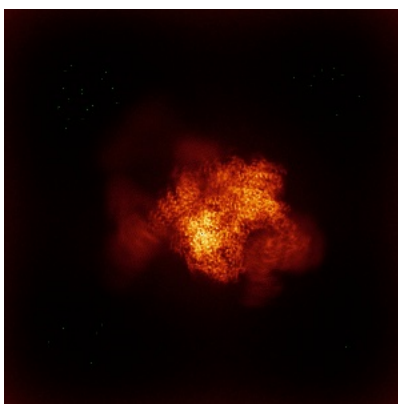


Z

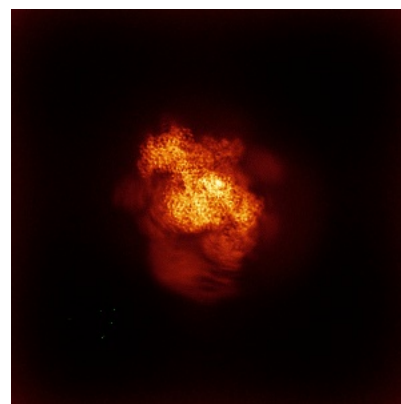
### 6.4.2 Raw map



X



Y

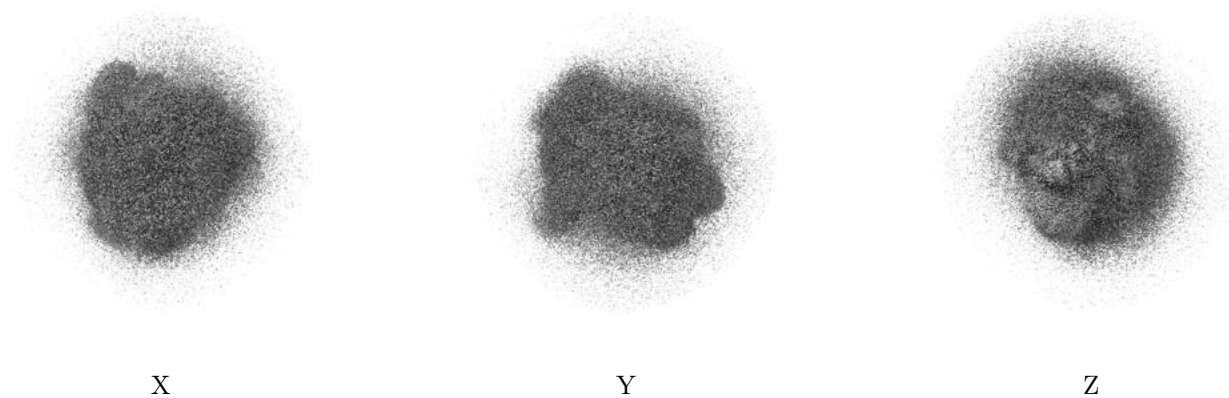


Z

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.

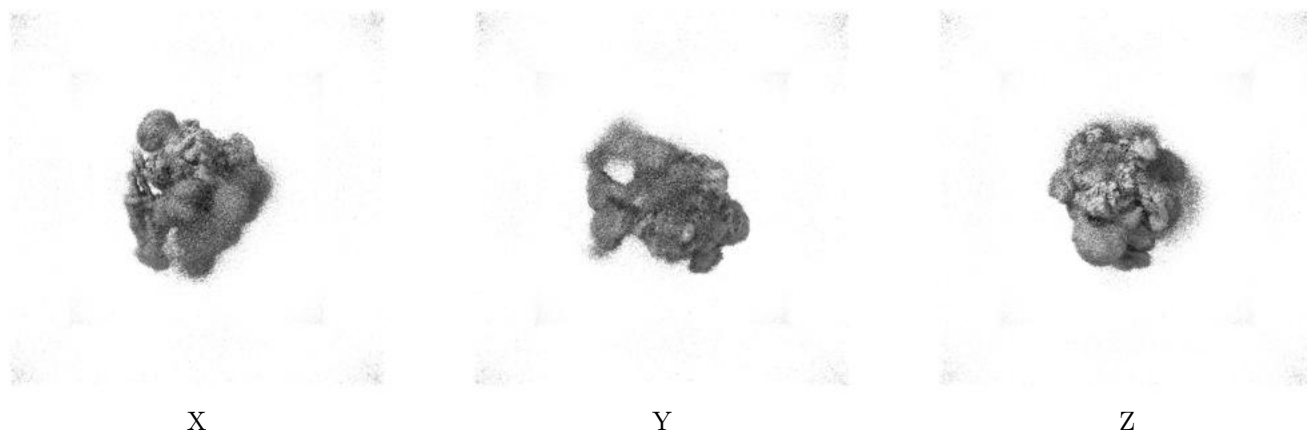
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

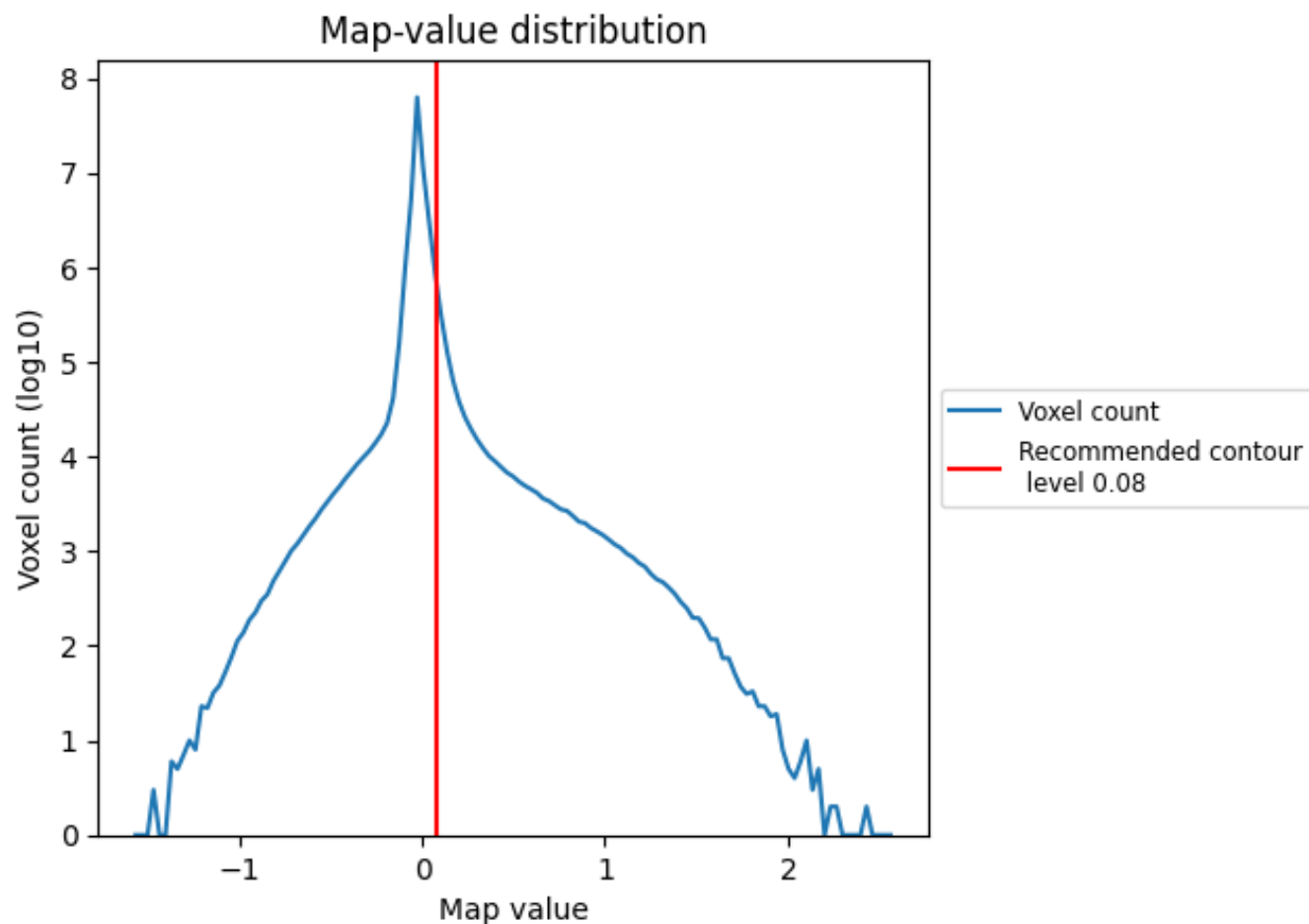
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

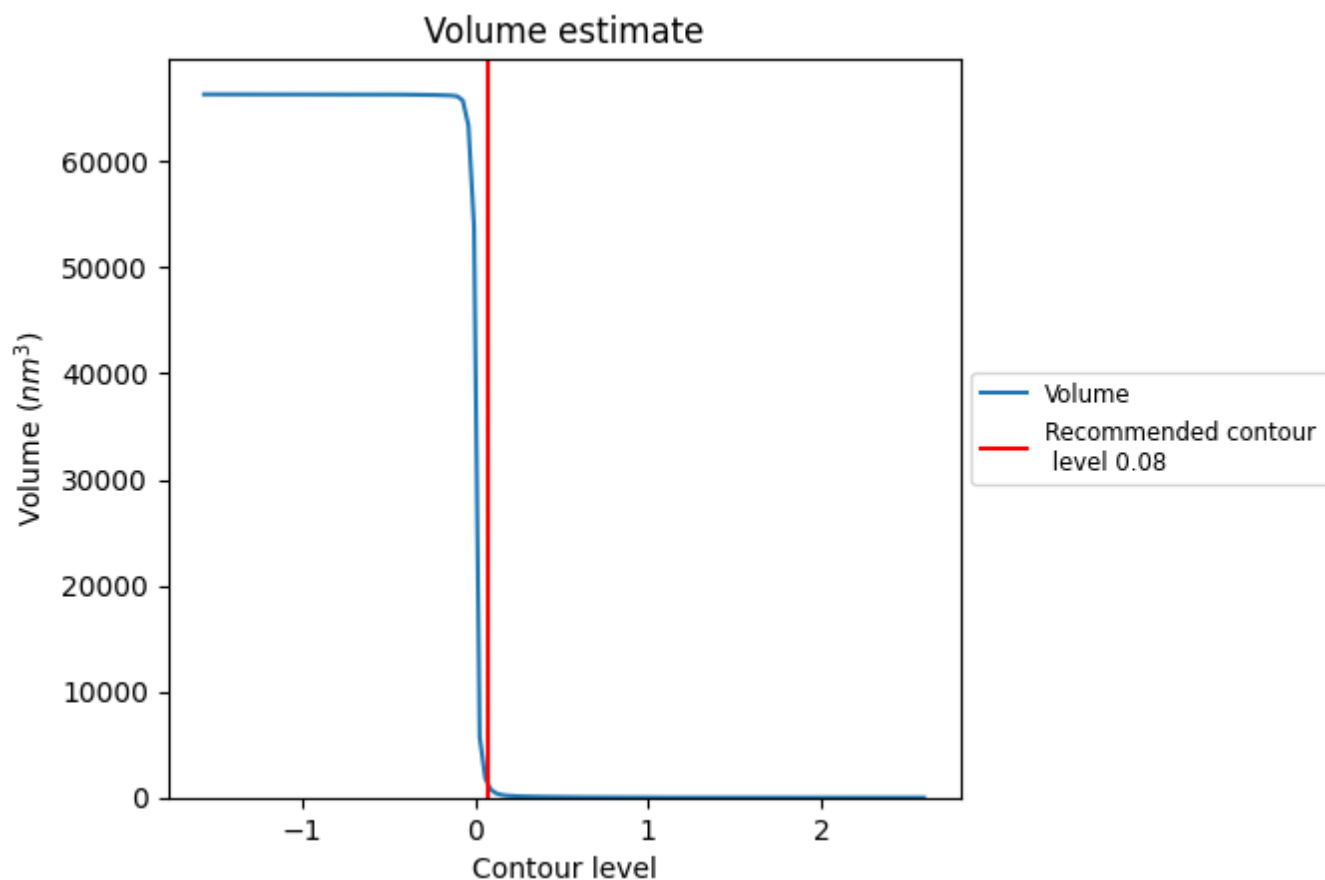
This section contains the results of statistical analysis of the map.

### 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.

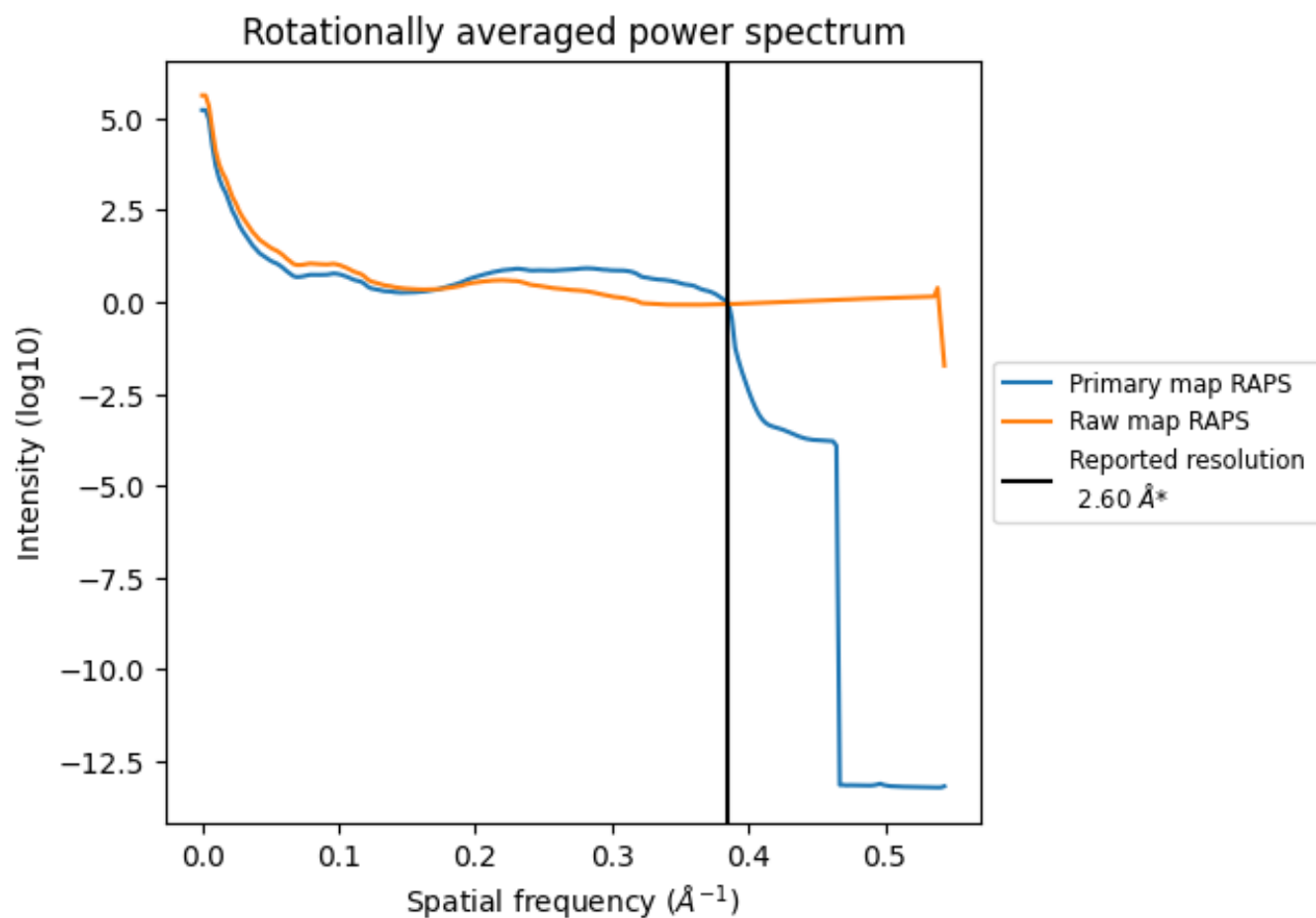
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1131 nm<sup>3</sup>; this corresponds to an approximate mass of 1022 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 ⓘ

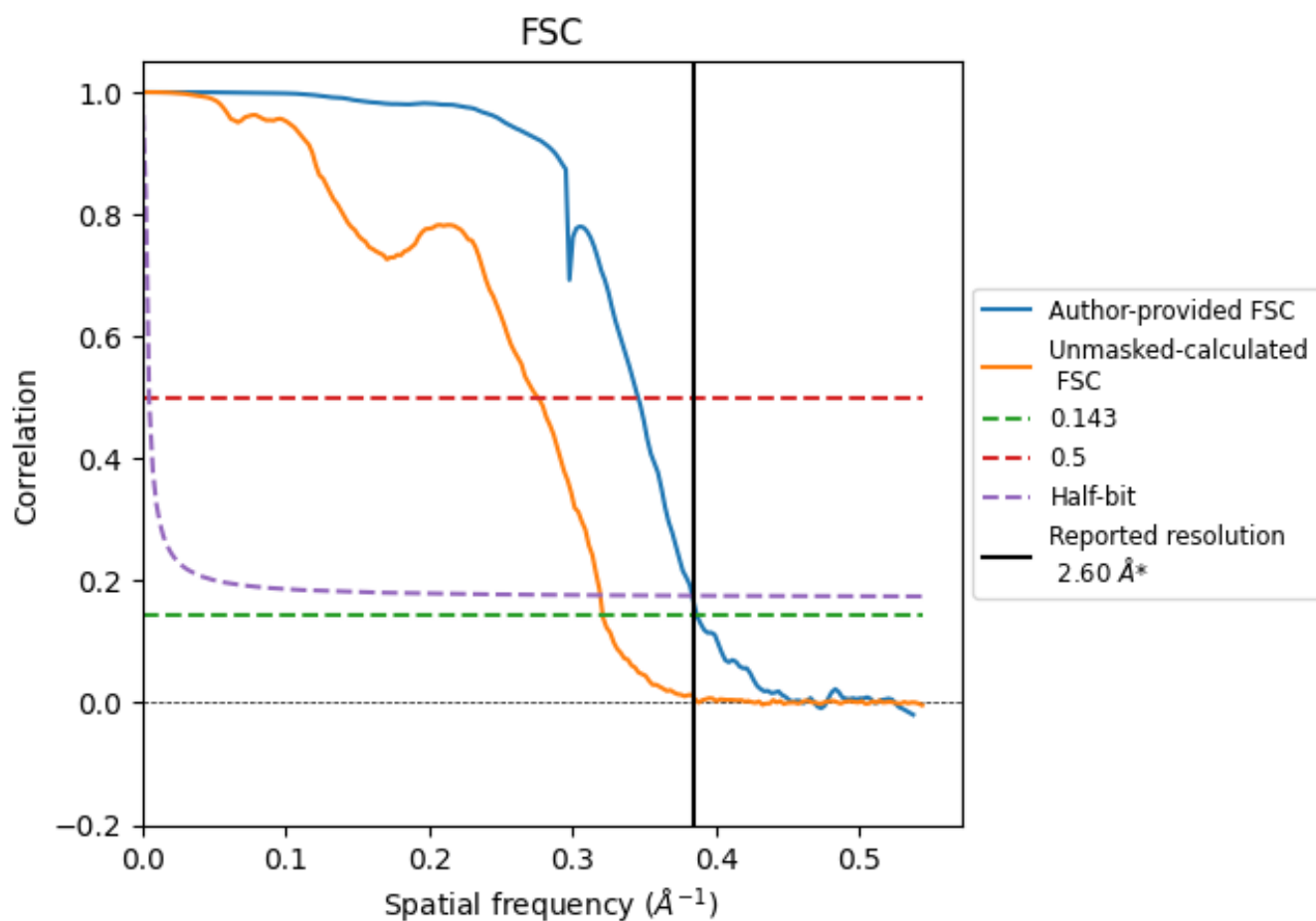


\*Reported resolution corresponds to spatial frequency of 0.385 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.385  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

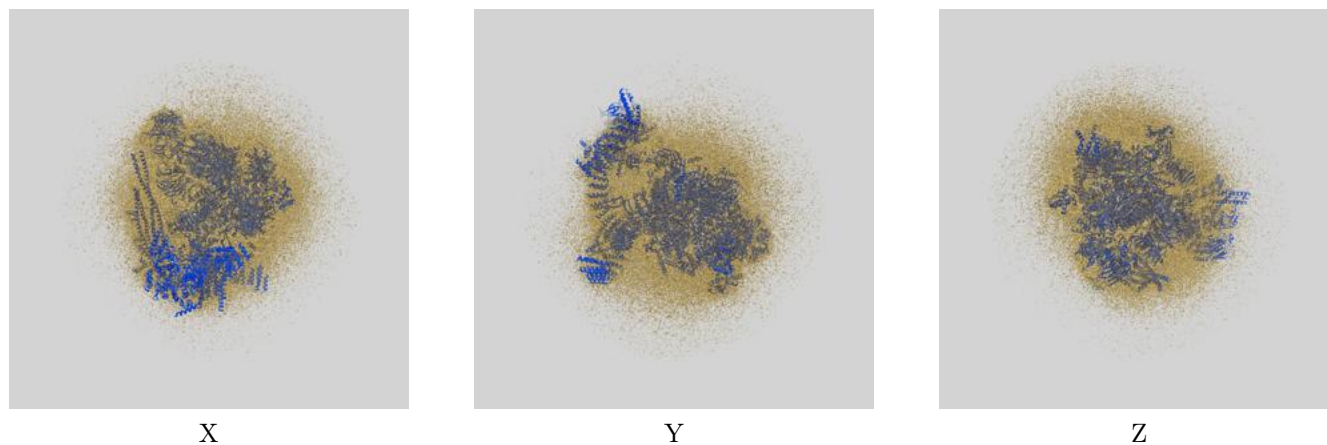
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.59	2.89	2.61
Unmasked-calculated*	3.12	3.63	3.13

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.12 differs from the reported value 2.6 by more than 10 %

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

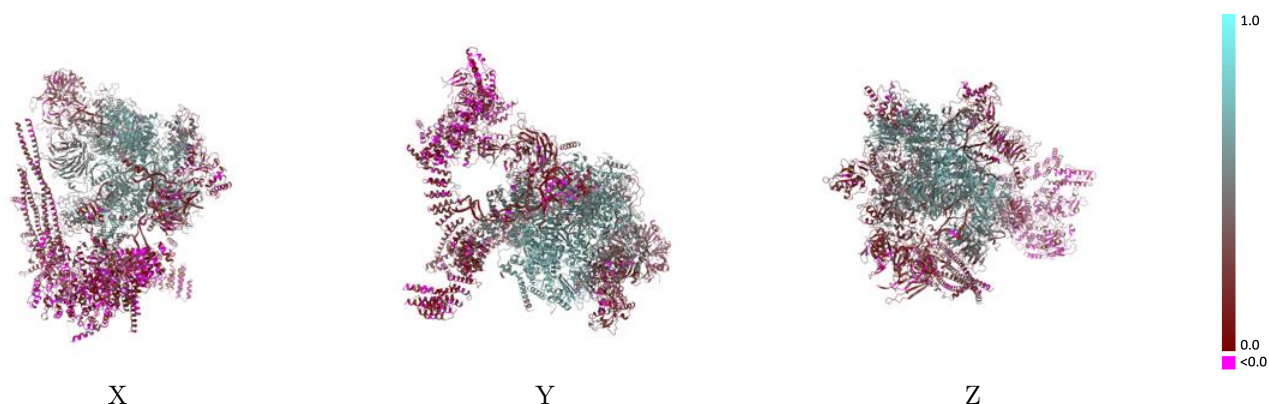
This section contains information regarding the fit between EMDB map EMD-38362 and PDB model 8XI2. Per-residue inclusion information can be found in section 3 on page 11.

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



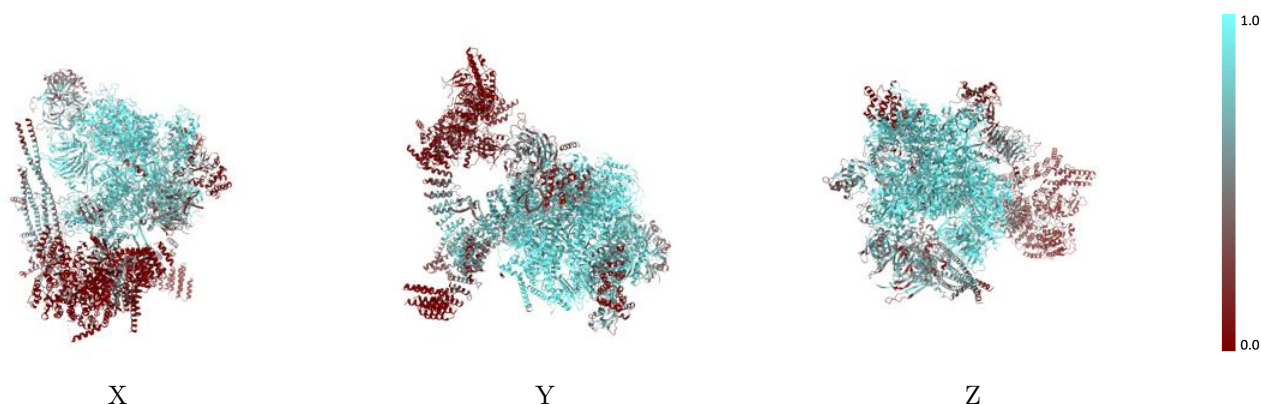
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



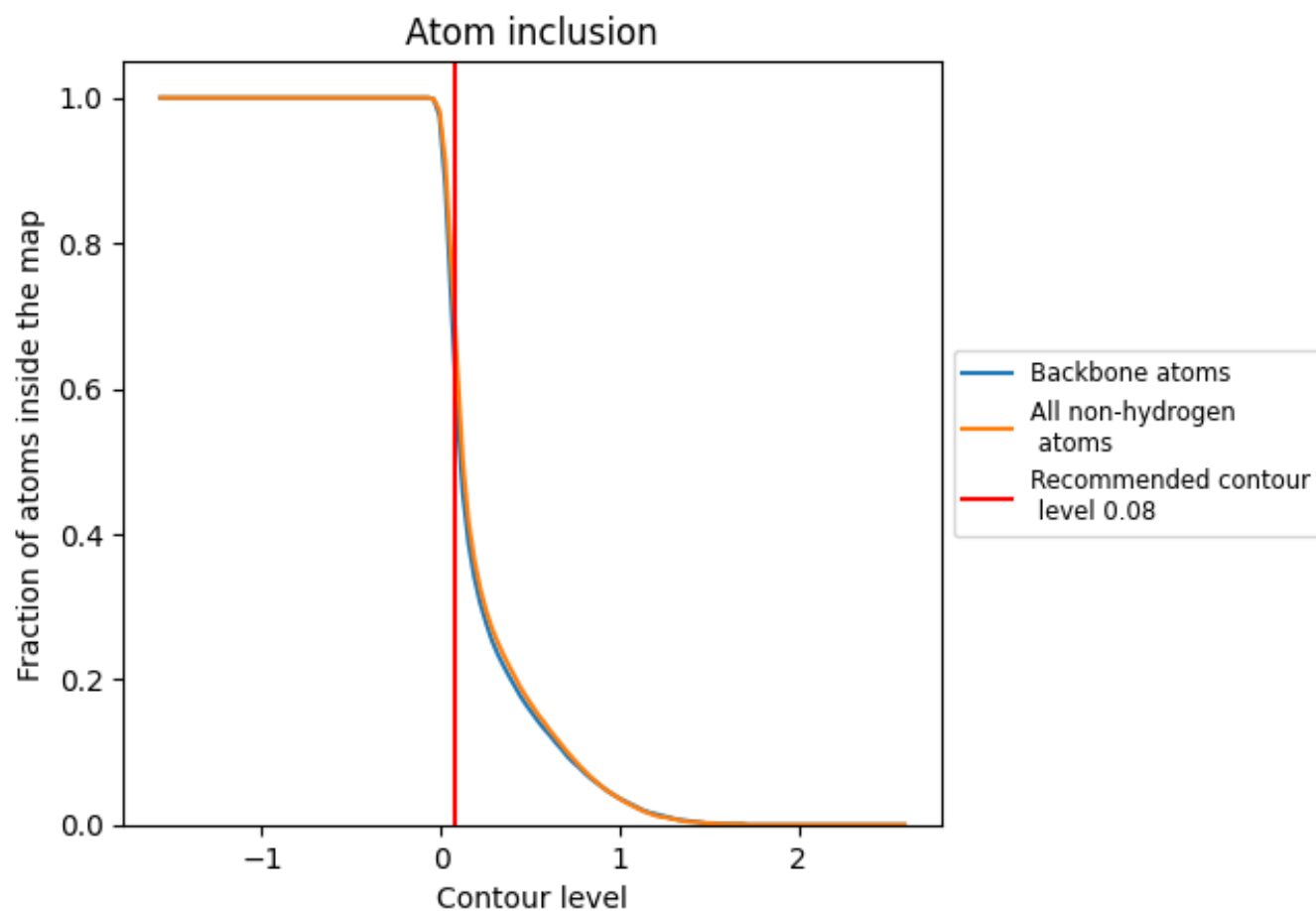
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).







































































## 9.4 Atom inclusion ⓘ



At the recommended contour level, 62% of all backbone atoms, 68% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6850	 0.3810
3	 0.7060	 0.2340
5	 0.9530	 0.6210
A	 0.8830	 0.5470
B	 0.8690	 0.3780
C	 0.7990	 0.3620
E	 0.9280	 0.4580
F	 0.9130	 0.4530
H	 0.6630	 0.2840
I	 0.4210	 0.1850
J	 0.6150	 0.3610
K	 0.4830	 0.2310
L	 0.6460	 0.3640
M	 0.7050	 0.3600
N	 0.9860	 0.6290
O	 0.7890	 0.4460
P	 0.9320	 0.5920
Q	 0.0410	 0.1050
R	 0.9330	 0.5620
S	 0.9540	 0.5290
T	 0.9960	 0.6770
U	 0.4390	 0.3290
V	 0.2680	 0.2470
W	 0.5890	 0.3040
a	 0.7190	 0.2760
b	 0.6710	 0.2880
c	 0.5790	 0.2130
d	 0.5490	 0.2310
e	 0.5280	 0.2160
f	 0.4730	 0.2010
g	 0.6610	 0.2630
q	 0.4630	 0.2050
r	 0.5790	 0.2140
s	 0.6220	 0.2370
t	 0.5040	 0.2050

