



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 04:16 AM UTC

PDB ID : 5GM6 / pdb_00005gm6
EMDB ID : EMD-9524
Title : Cryo-EM structure of the activated spliceosome (Bact complex) at 3.5 angstrom resolution
Authors : Yan, C.; Wan, R.; Bai, R.; Huang, G.; Shi, Y.
Deposited on : 2016-07-12
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

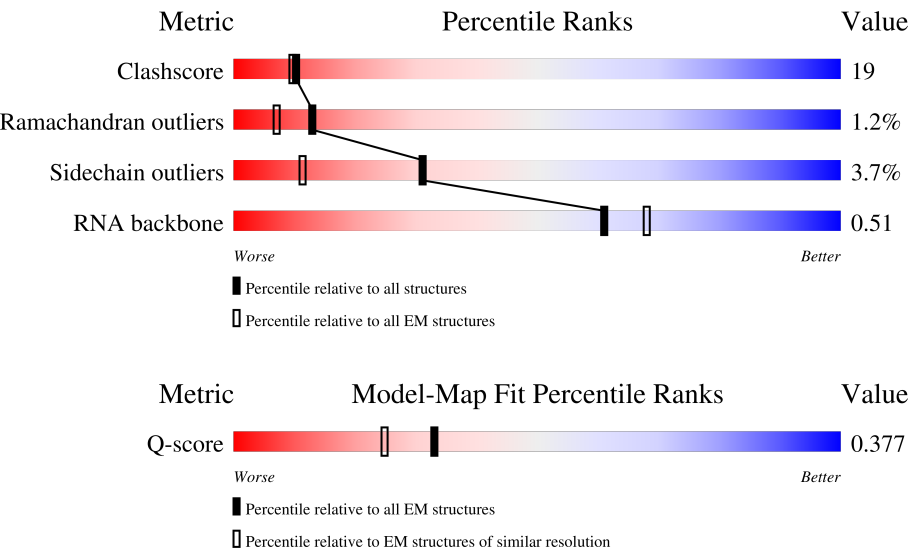
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

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

Mol	Chain	Length	Quality of chain
1	A	2287	8% 62% 30% . .
2	B	2163	45% 56% 27% 16%
3	C	1008	13% 54% 31% . 13%

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Mol	Chain	Length	Quality of chain
4	D	214	
5	E	112	
6	F	1361	
7	H	436	
8	I	266	
9	J	107	
10	K	85	
11	L	1175	
12	N	25	
13	M	61	
14	O	451	
15	P	379	
16	Q	364	
17	R	339	
18	S	175	
19	T	157	
20	U	207	
21	V	148	
22	W	266	
23	Y	876	
24	Z	577	
25	a	259	
26	b	301	
27	c	587	
28	G	971	

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Mol	Chain	Length	Quality of chain
29	d	687	
30	X	135	
31	v	859	
32	e	213	
33	f	215	
34	o	503	
34	p	503	
34	q	503	
34	r	503	
35	t	175	
36	n	455	
37	k	196	
38	i	94	
39	h	86	
40	j	77	
41	l	101	
42	m	146	
43	g	94	

2 Entry composition [i](#)

There are 47 unique types of molecules in this entry. The entry contains 112064 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2200	Total	C	N	O	S	0	0
			18101	11636	3086	3315	64		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	127	ALA	-	insertion	UNP P33334

- Molecule 2 is a protein called Pre-mRNA-splicing helicase BRR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1809	Total	C	N	O	S	0	0
			14504	9283	2414	2750	57		

- Molecule 3 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	878	Total	C	N	O	S	0	0
			7014	4526	1166	1293	29		

- Molecule 4 is a RNA chain called *Saccharomyces cerevisiae* strain CDRDR_sf_H chromosome VII sequence.

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

- Molecule 5 is a RNA chain called *Saccharomyces cerevisiae* strain T.52_2H chromosome XII sequence.

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

- Molecule 6 is a protein called Pre-mRNA-splicing factor RSE1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	1180	Total	C	N	O	S	0	0
			9380	5996	1580	1753	51		

- Molecule 7 is a protein called Cold sensitive U2 snRNA suppressor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	151	Total	C	N	O	S	0	0
			1248	804	217	221	6		

- Molecule 8 is a protein called Pre-mRNA-splicing factor PRP11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	102	Total	C	N	O	S	0	0
			800	495	150	150	5		

- Molecule 9 is a protein called Pre-mRNA-splicing factor RDS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	103	Total	C	N	O	S	0	0
			814	503	154	143	14		

- Molecule 10 is a protein called RDS3 complex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	84	Total	C	N	O	S	0	0
			693	429	130	132	2		

- Molecule 11 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	66	Total	C	N	O	P	0	0
			1388	622	228	472	66		

- Molecule 12 is a RNA chain called Pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	25	Total	C	N	O	P	0	0
			521	234	77	185	25		

- Molecule 13 is a RNA chain called Pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	50	Total	C	N	O	P	0	0
			1057	479	191	338	49		

- Molecule 14 is a protein called Pre-mRNA-splicing factor PRP46.

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

- Molecule 15 is a protein called Pre-mRNA-processing protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	246	Total	C	N	O	S	0	0
			1978	1233	359	380	6		

- Molecule 16 is a protein called Pre-mRNA-splicing factor SLT11.

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

- Molecule 17 is a protein called Pre-mRNA-splicing factor CWC2.

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

- Molecule 18 is a protein called Pre-mRNA-splicing factor CWC15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	71	Total	C	N	O	S	0	0
			578	361	117	99	1		

- Molecule 19 is a protein called Pre-mRNA-splicing factor BUD31.

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

- Molecule 20 is a protein called Pre-mRNA leakage protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	176	Total	C	N	O	S	0	0
			1401	877	237	277	10		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	205	HIS	-	insertion	UNP Q07930
U	206	HIS	-	insertion	UNP Q07930
U	207	HIS	-	insertion	UNP Q07930

- Molecule 21 is a protein called U2 snRNP component IST3.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	128	Total	C	N	O	S	0	0
			1051	662	181	208			

- Molecule 22 is a protein called Pre-mRNA-splicing factor CWC26.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	104	Total	C	N	O	S	0	0
			842	528	145	167	2		

- Molecule 23 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase-like protein PRP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	598	Total	C	N	O	S	0	0
			4047	2590	690	752	15		

- Molecule 24 is a protein called Pre-mRNA-splicing factor CWC22.

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

- Molecule 25 is a protein called Pre-mRNA-splicing factor CWC24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	123	Total	C	N	O	S	0	0
			988	621	171	183	13		

- Molecule 26 is a protein called Peptidyl-prolyl isomerase CWC27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	150	Total	C	N	O	S	0	0
			1224	789	206	223	6		

- Molecule 27 is a protein called Pre-mRNA-splicing factor CEF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	415	Total	C	N	O	S	0	0
			2803	1741	518	537	7		

- Molecule 28 is a protein called U2 snRNP component HSH155.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	G	875	Total	C	N	O	S	0	0
			6970	4467	1196	1265	42		

- Molecule 29 is a protein called Pre-mRNA-splicing factor CLF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	545	Total	C	N	O	S	0	0
			3558	2212	671	667	8		

- Molecule 30 is a protein called Pre-mRNA-splicing factor CWC21.

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

- Molecule 31 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	v	566	Total	C	N	O	S	0	0
			3047	1871	576	599	1		

- Molecule 32 is a protein called Protein HSH49.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	149	Total	C	N	O	S	0	0
			947	617	154	174	2		

- Molecule 33 is a protein called Pre-mRNA-splicing factor SYF2.

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

- Molecule 34 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	o	124	Total	C	N	O	S	0	0
			819	518	132	167	2		
34	p	128	Total	C	N	O	S	0	0
			843	533	136	172	2		
34	q	381	Total	C	N	O	S	0	0
			2315	1456	396	455	8		
34	r	125	Total	C	N	O	S	0	0
			823	521	133	167	2		

- Molecule 35 is a protein called Pre-mRNA-splicing factor SNT309.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	t	155	Total	C	N	O	S	0	0
			921	582	159	179	1		

- Molecule 36 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	n	23	Total	C	N	O	0	0
			195	122	41	32		

- Molecule 37 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	k	80	Total	C	N	O	S	0	0
			631	403	114	111	3		

- Molecule 38 is a protein called Small nuclear ribonucleoprotein E.

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

- Molecule 39 is a protein called Small nuclear ribonucleoprotein F.

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

- Molecule 40 is a protein called Small nuclear ribonucleoprotein G.

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

- Molecule 41 is a protein called Small nuclear ribonucleoprotein Sm D3.

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

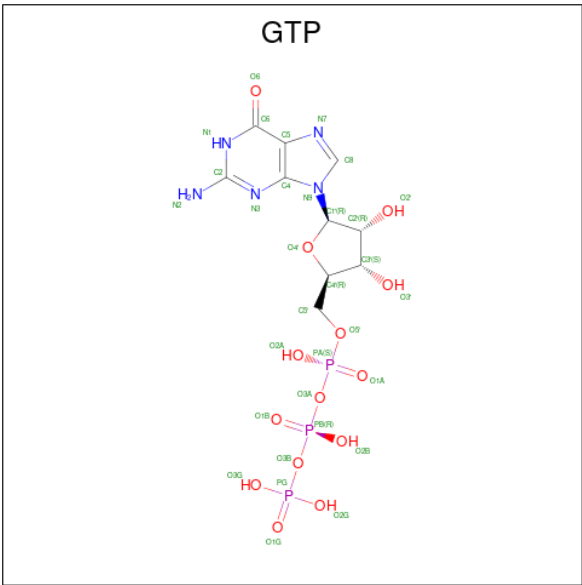
- Molecule 42 is a protein called Small nuclear ribonucleoprotein Sm D1.

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

- Molecule 43 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	g	94	Total	C	N	O	S	0	0
			741	477	141	119	4		

- Molecule 44 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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

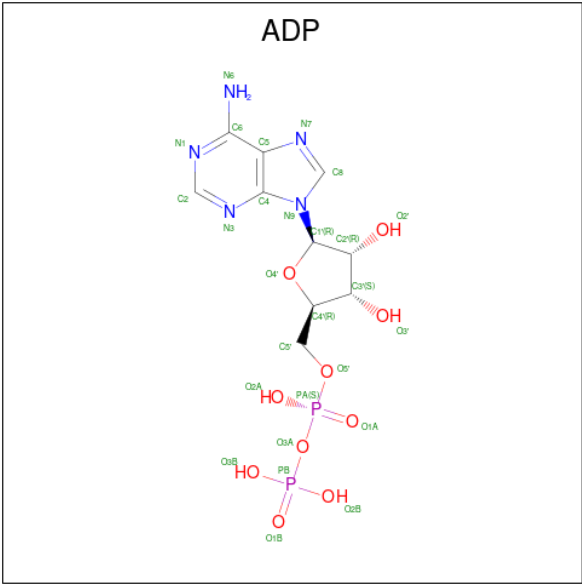
- Molecule 45 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
45	E	4	Total	Mg	0
			4	4	
45	Y	1	Total	Mg	0
			1	1	

- Molecule 46 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
46	I	1	Total	Zn	0
			1	1	
46	J	3	Total	Zn	0
			3	3	
46	Q	2	Total	Zn	0
			2	2	
46	R	1	Total	Zn	0
			1	1	
46	T	3	Total	Zn	0
			3	3	
46	a	3	Total	Zn	0
			3	3	

- Molecule 47 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
47	Y	1	27	10	5	10	2	0

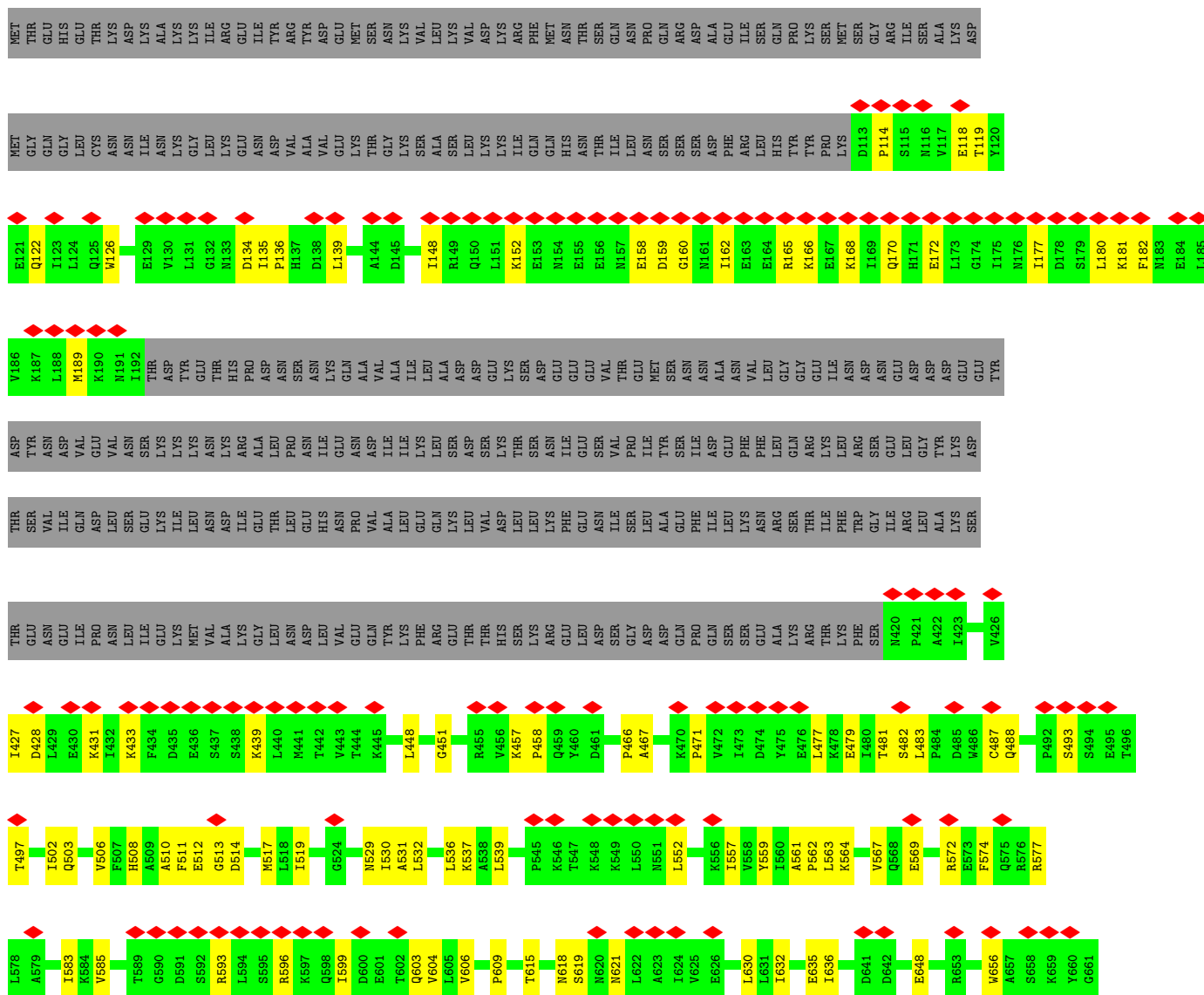
3 Residue-property plots

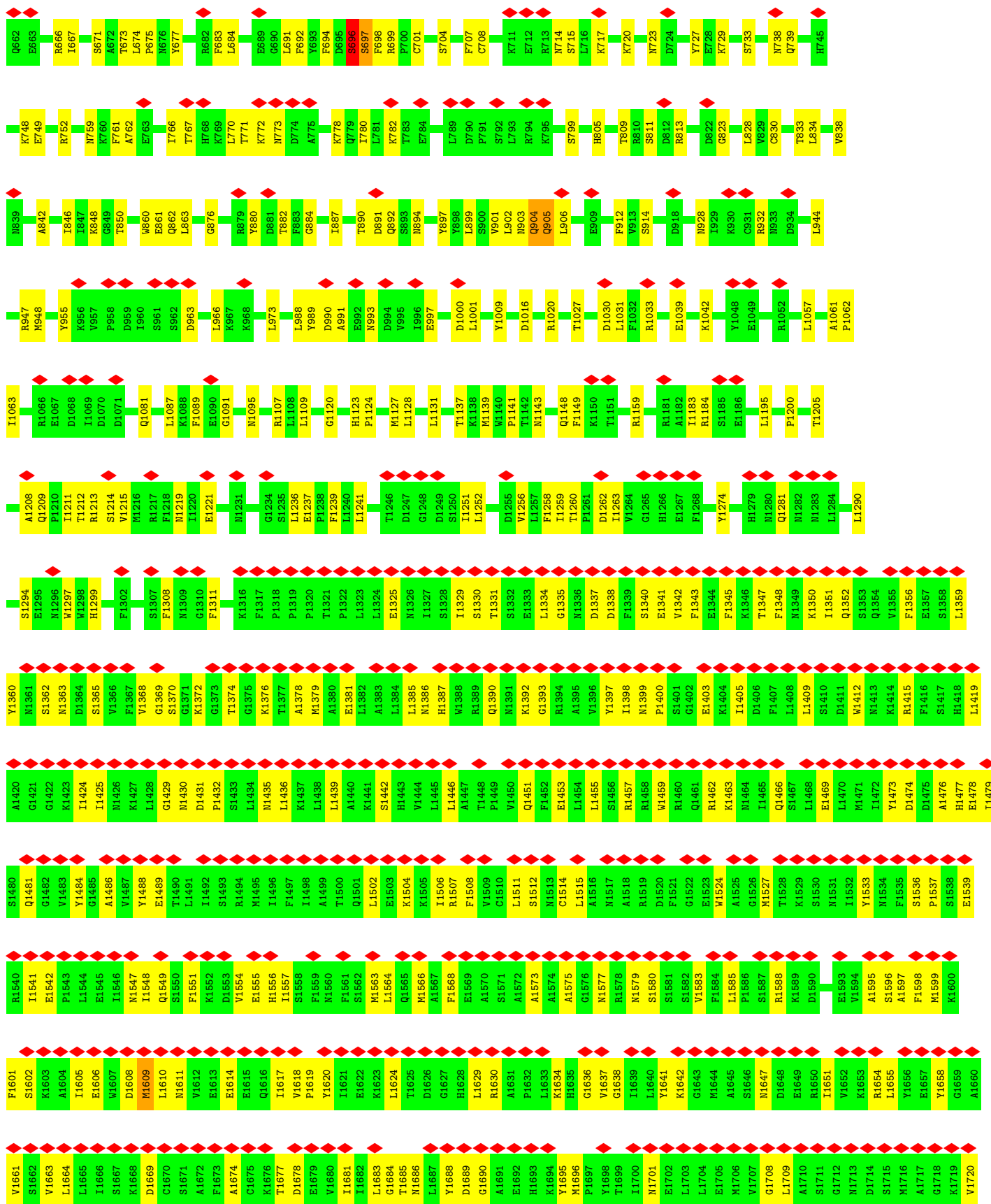
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

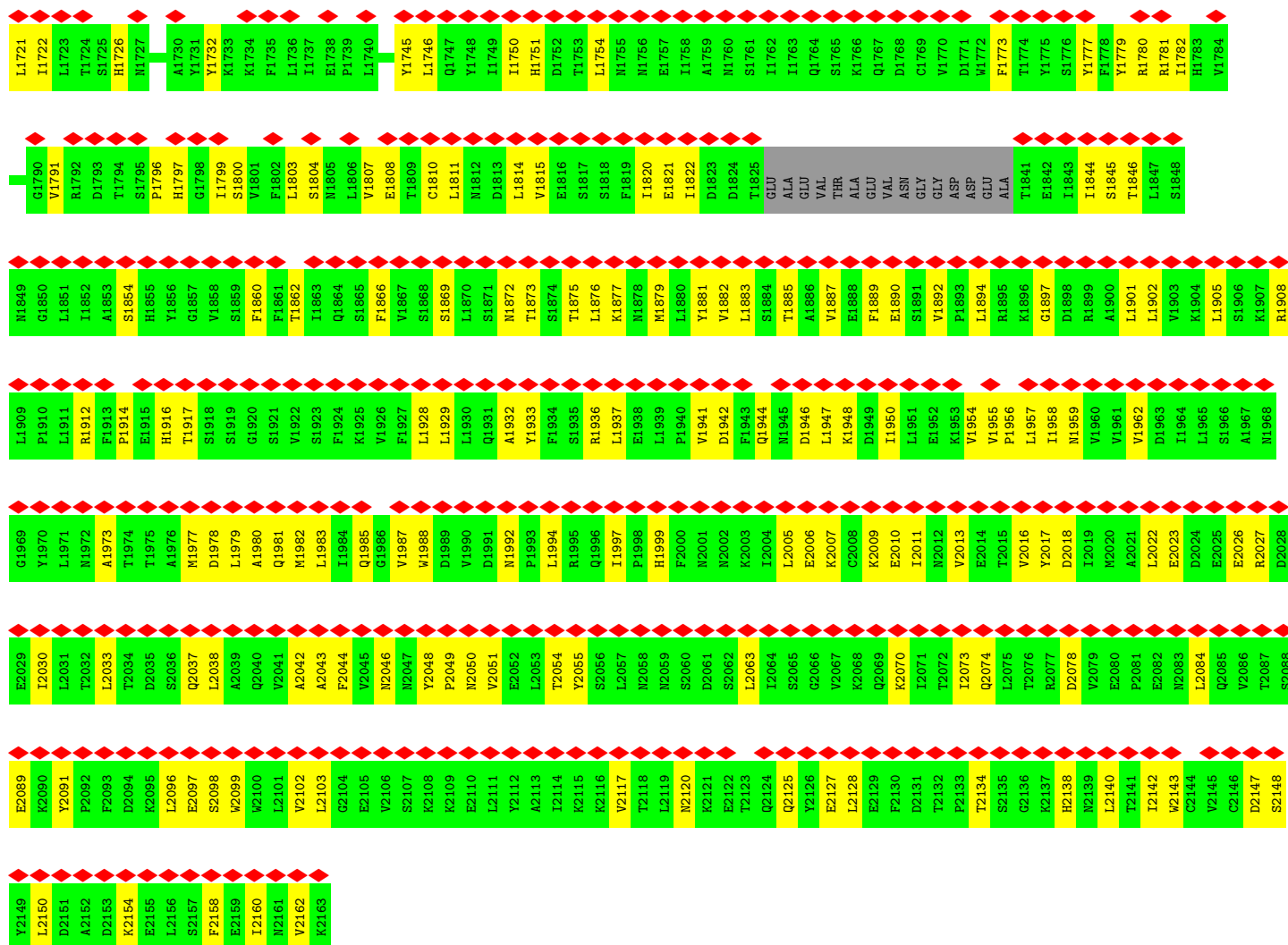
• Molecule 1: Pre-mRNA-splicing factor 8



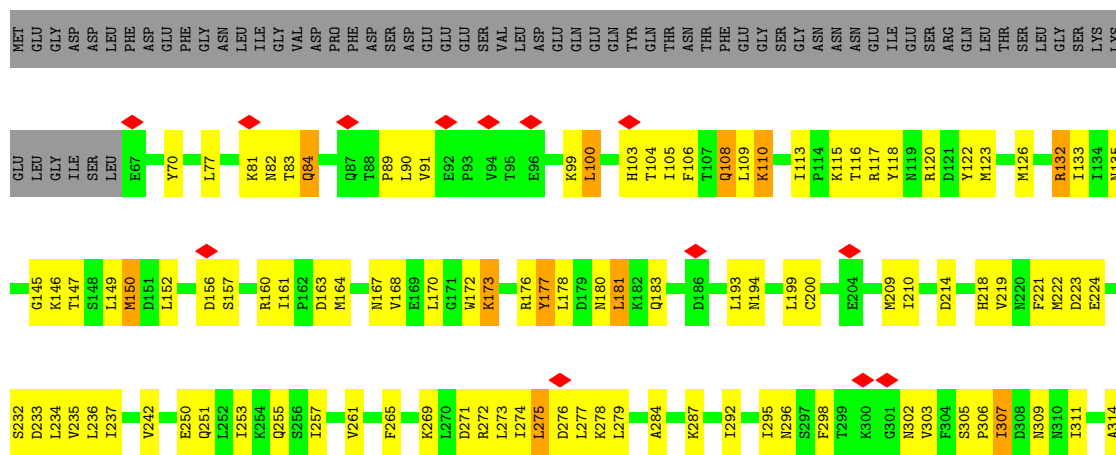


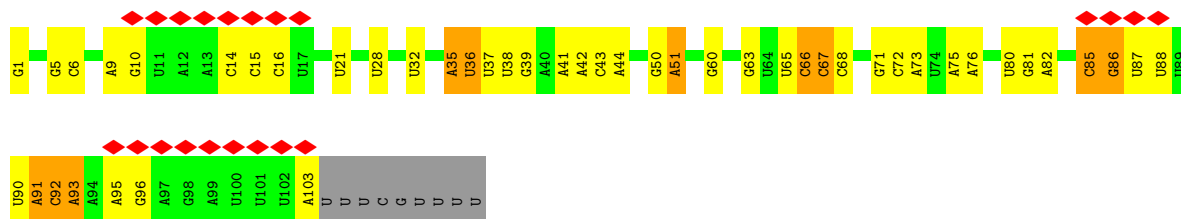




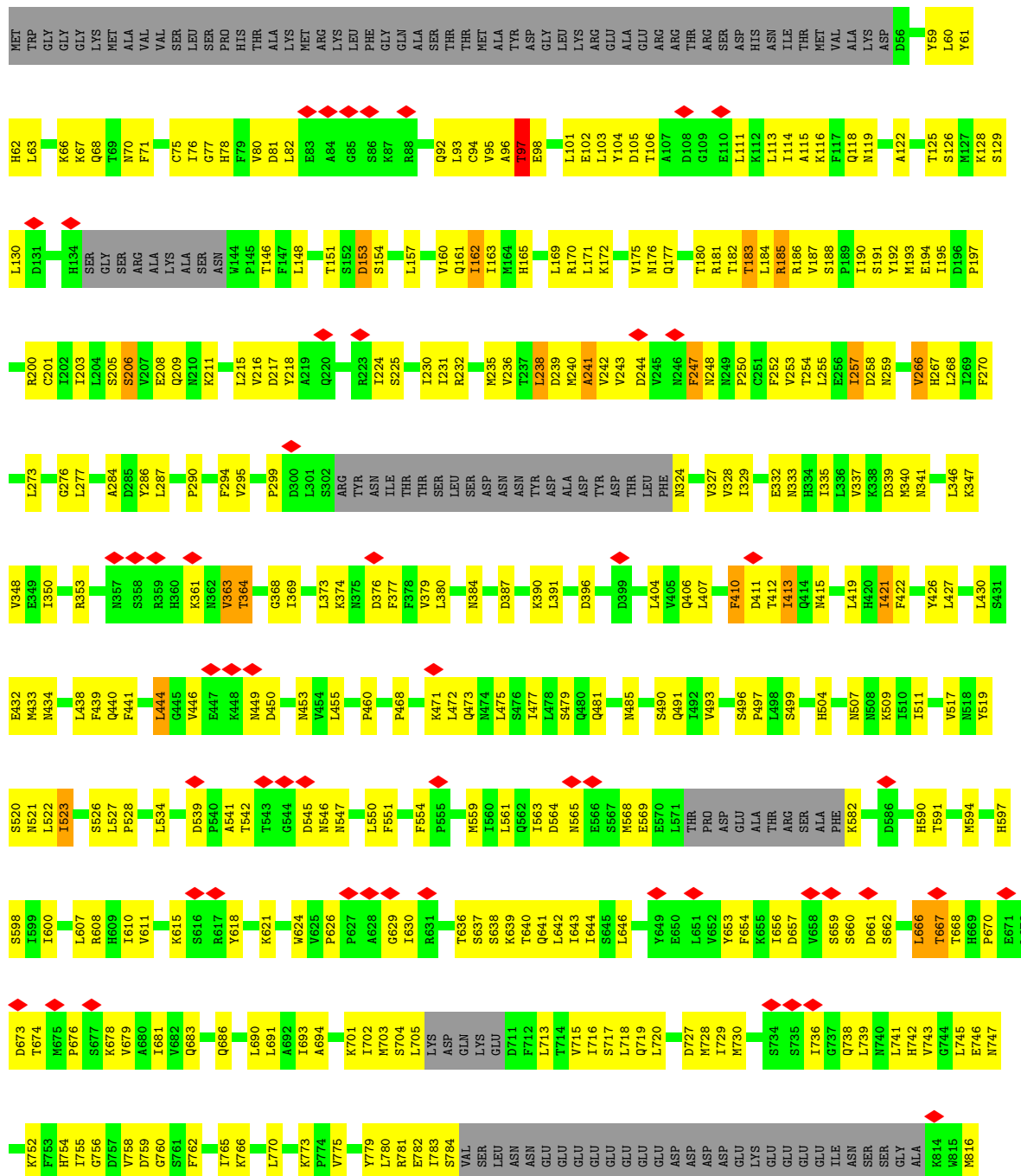


• Molecule 3: Pre-mRNA-splicing factor SNU114





• Molecule 6: Pre-mRNA-splicing factor RSE1





Chain I:

Amino Acid	Frequency (%)
M1	6%
H2	6%
Y3	6%
L4	6%
E5	6%
G13	27%
G14	27%
G15	27%
I16	27%
A17	27%
S18	27%
E19	27%
S20	27%
Q21	27%
L24	27%
K36	27%
Y42	27%
F44	27%
Q45	27%
D46	27%
E47	27%
LYS	27%
ASP	27%
Q51	9%
V52	9%
R53	9%
S54	9%
R55	9%
P56	9%
Y57	9%
I58	9%
V59	9%
H62	9%
S63	9%
L70	9%
G71	9%
M72	9%
S77	9%
S80	9%
I81	9%
R83	9%
K88	9%
I99	62%
S100	62%
T101	62%
E102	62%
K103	62%

Chain J:

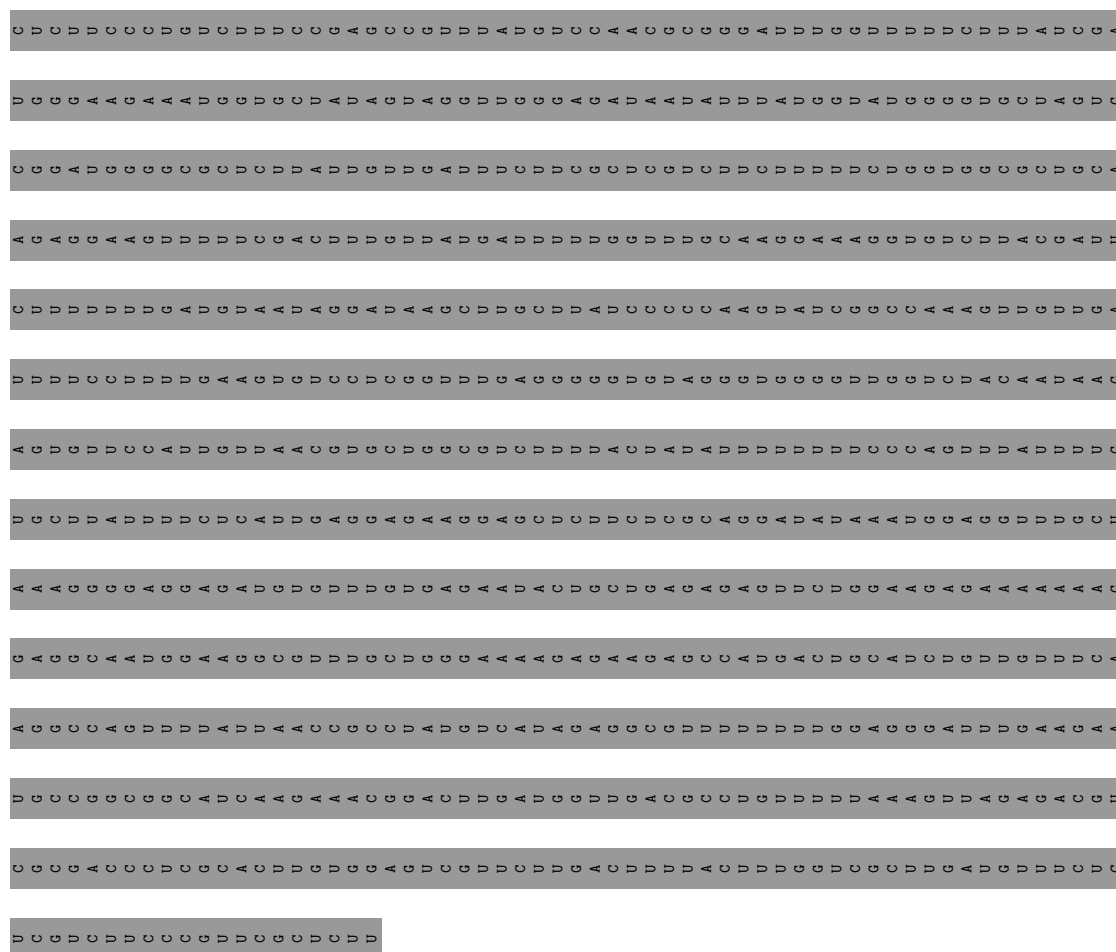
Amino Acid	Count
MET	1
S2	1
R3	1
H4	1
Q5	1
F6	1
D7	1
L8	1
G11	1
V17	1
G20	1
L21	1
L22	1
C26	1
D27	1
G28	1
K29	1
V37	1
R38	1
P39	1
K40	1
R41	1
K42	1
V43	1
S50	1
F51	1
G52	1
K53	1
Q54	1
V67	1
D68	1
N69	1
A70	1
F71	1
L79	1
D82	1
K83	1
D84	1
G85	1
C86	1
I89	1
G93	1
S94	1
N95	1
R96	1
L97	1
D98	1
R99	1

Chain K:

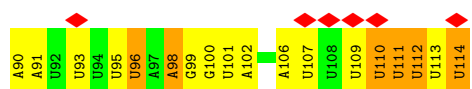
Label	Color	Percentage
M1	Green	
A2	Green	
E3	Green	
K4	Green	
Q5	Green	
R6	Green	
Q7	Green	
L8	Green	
K17	Green	
Y18	Green	
I19	Green	
G20	Green	
L21	Green	
G22	Green	
D23	Green	
D23	Green	
E24	Green	
T27	Red	
R28	Orange	
Q32	Yellow	
D38	Green	
T39	Green	
L40	Green	
N41	Green	
T42	Orange	
L43	Green	
Q44	Green	
A48	Green	
S49	Orange	
L50	Yellow	
S54	Yellow	
R57	Orange	
G58	Green	
D59	Green	
L60	Yellow	
S61	Yellow	
I62	Green	
R63	Green	
D64	Green	
T65	Yellow	
L69	Yellow	
L70	Yellow	
S74	Yellow	
P75	Yellow	
Y80	Yellow	
L81	Green	
R82	Green	
E83	Green	
E84	Green	

Chain L: 94%

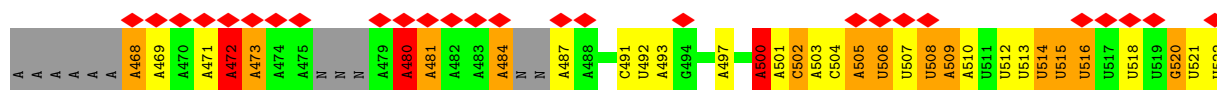
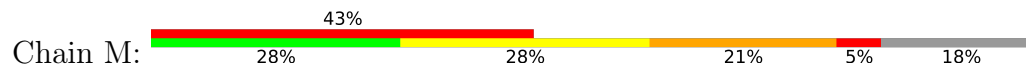
Position	Amino Acid
1	A
2	U
3	G
4	A
5	G
6	G
7	C
8	U
9	U
10	A
11	U
12	C
13	C
14	U
15	U
16	A
17	U
18	U
19	U
20	G
21	A
22	U
23	A
24	G
25	C
26	A
27	A
28	A
29	A
30	A
31	A
32	A
33	U
34	U
35	U
36	U
37	U
38	U
39	U
40	U
41	U
42	U
43	U
44	U
45	U
46	U
47	U
48	U
49	U
50	U
51	U
52	U
53	U
54	U
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60	U
61	U
62	U
63	U
64	U
65	U
66	U



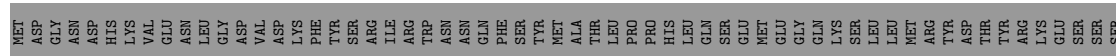
- Molecule 12: Pre-mRNA

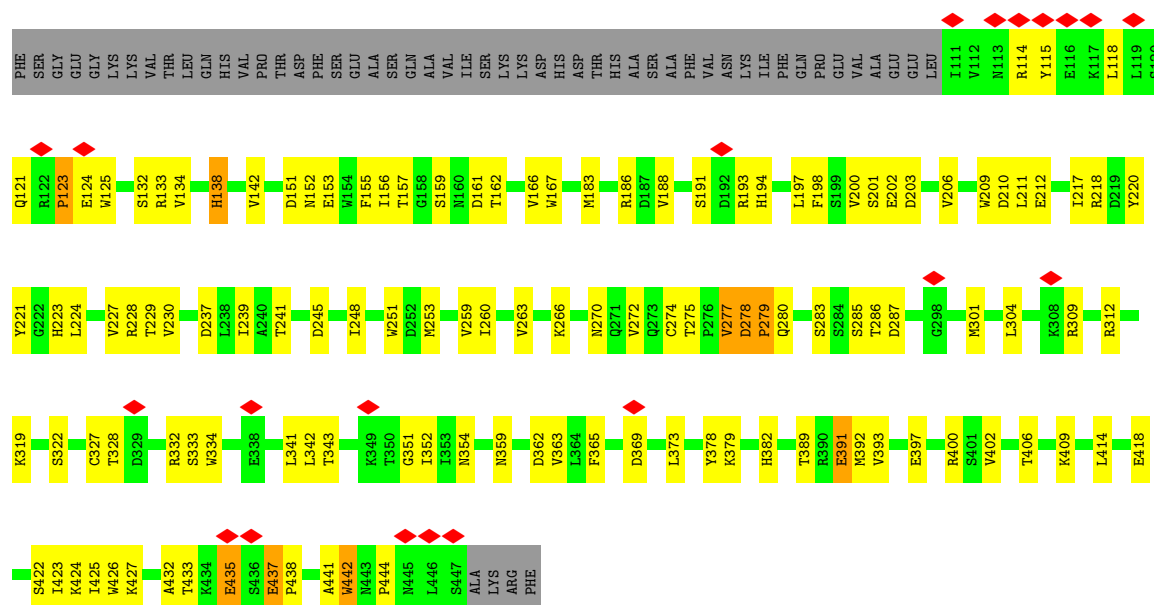


- Molecule 13: Pre-mRNA

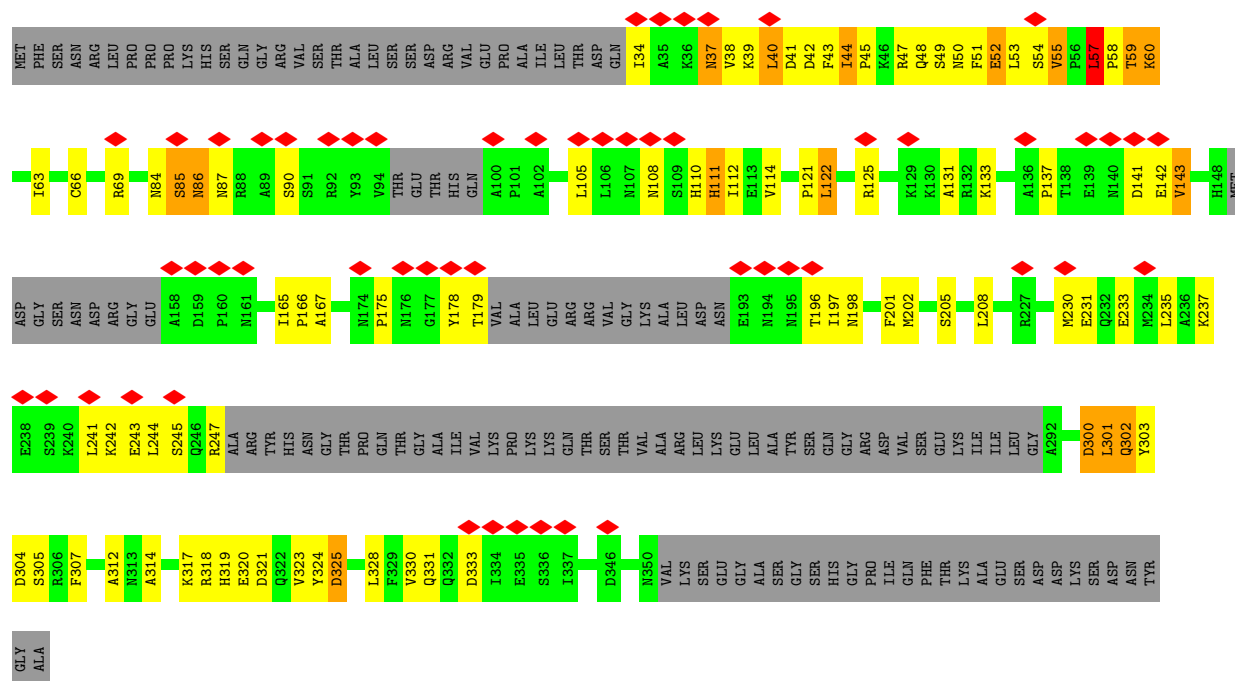


- Molecule 14: Pre-mRNA-splicing factor PRP46

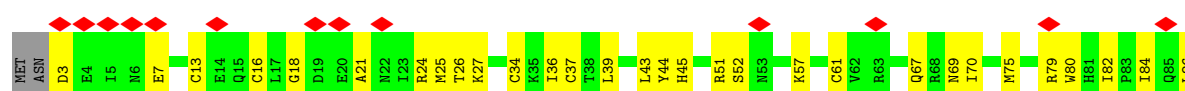


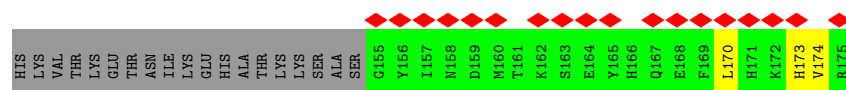


• Molecule 15: Pre-mRNA-processing protein 45

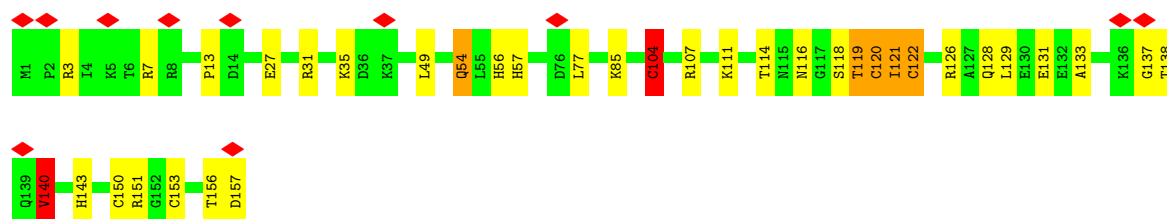
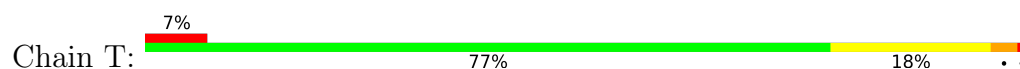


• Molecule 16: Pre-mRNA-splicing factor SLT11

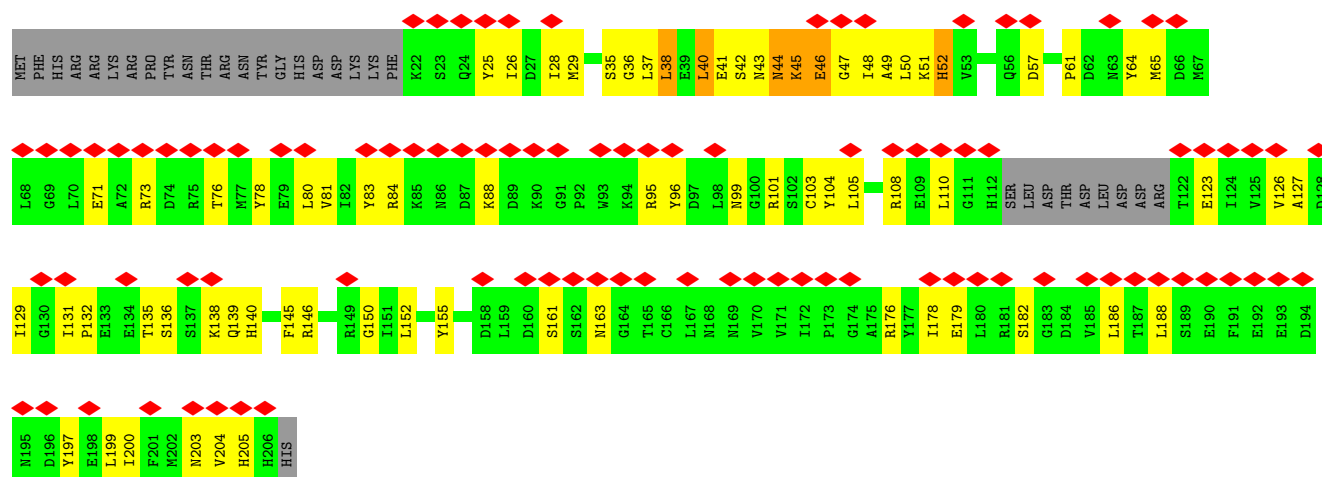




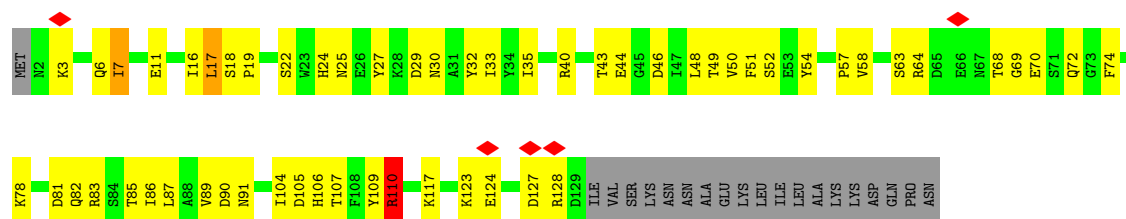
• Molecule 19: Pre-mRNA-splicing factor BUD31



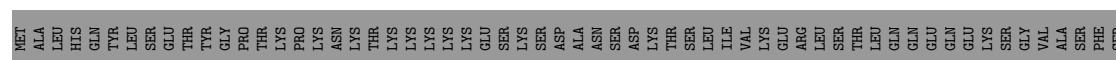
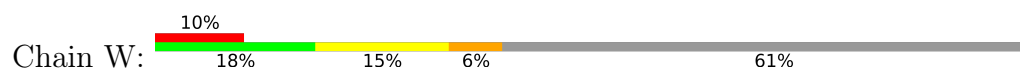
• Molecule 20: Pre-mRNA leakage protein 1



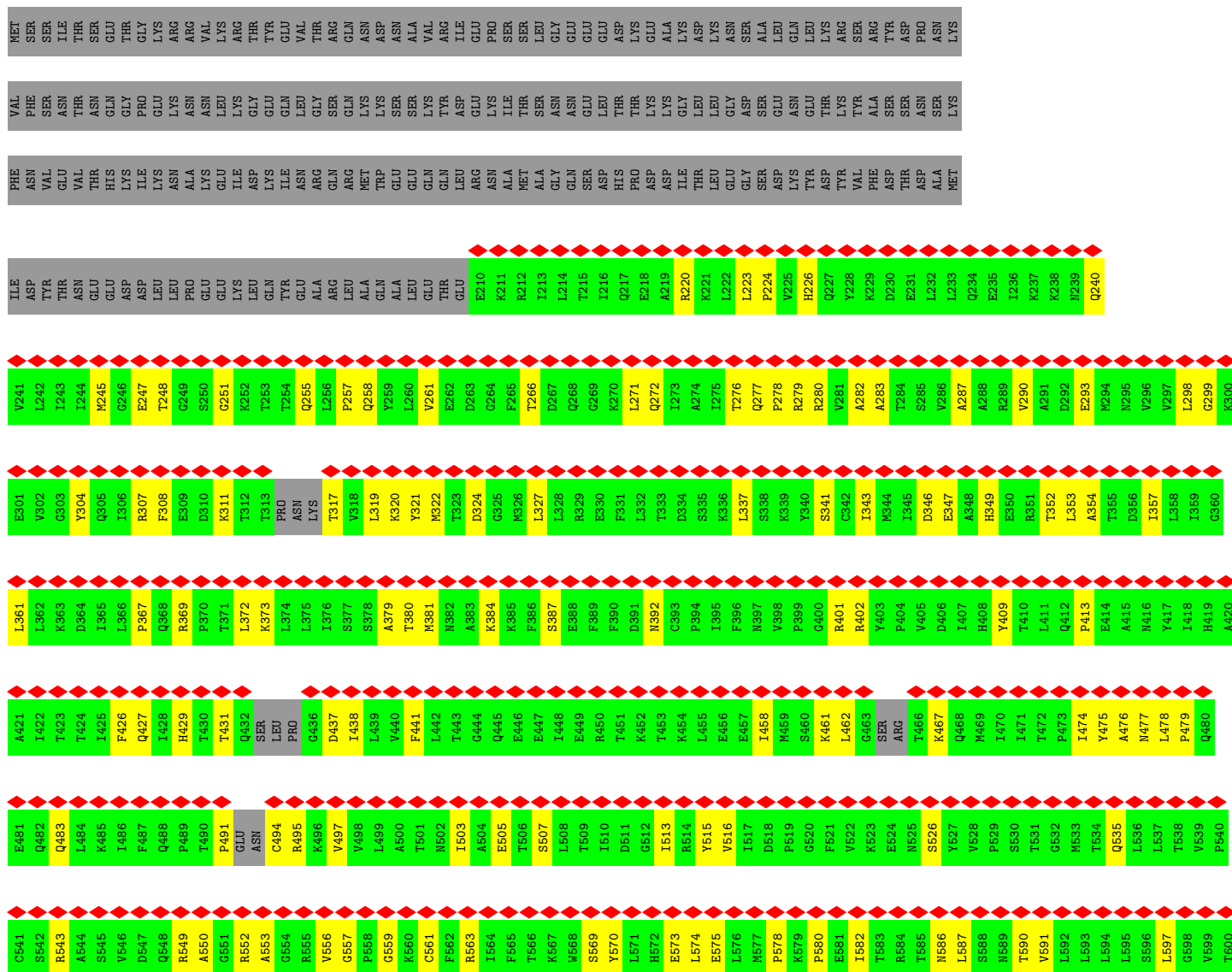
• Molecule 21: U2 snRNP component IST3

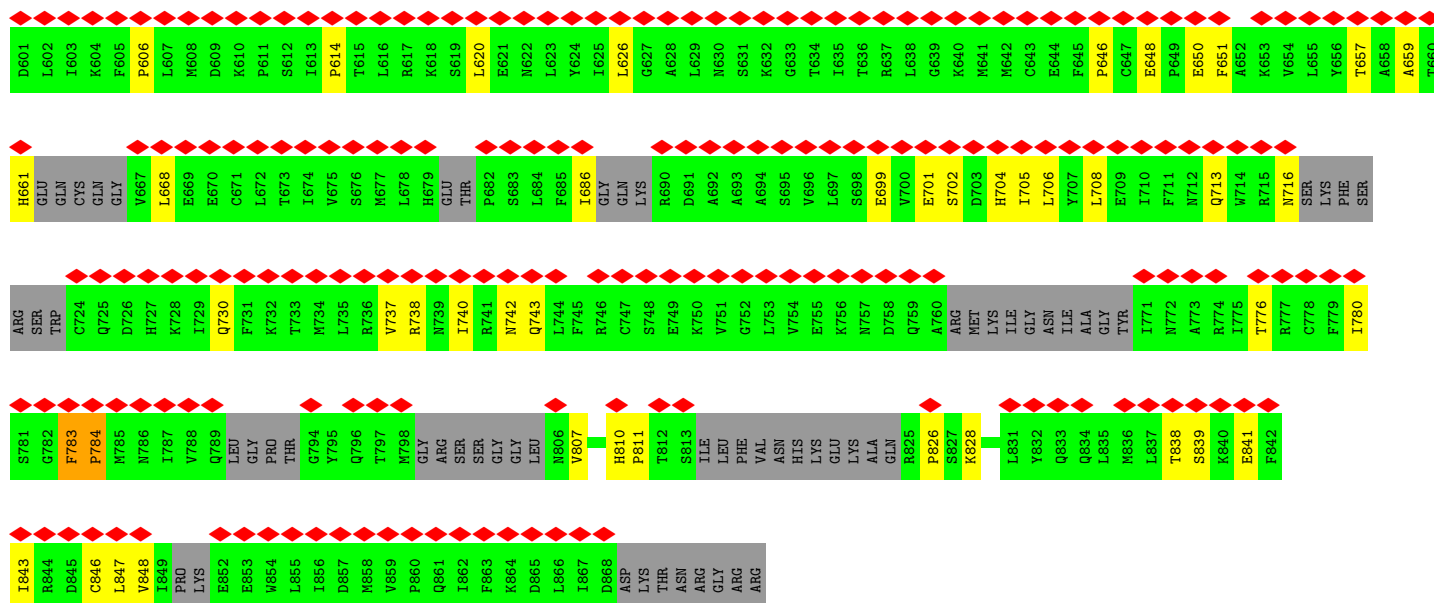


• Molecule 22: Pre-mRNA-splicing factor CWC26

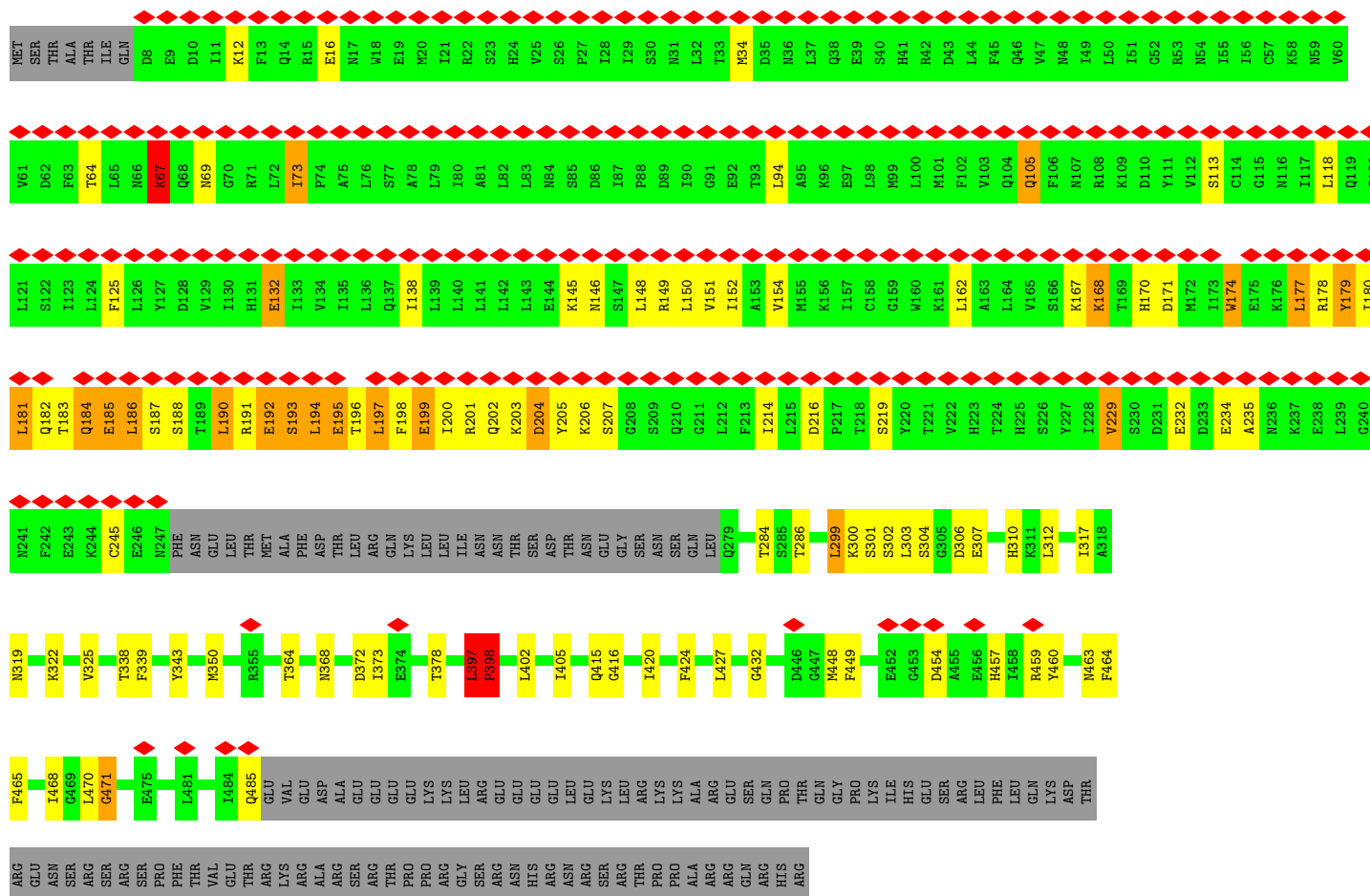
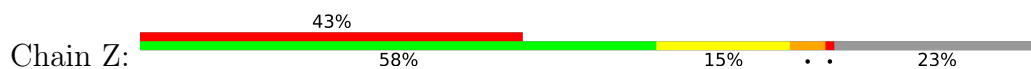


- Molecule 23: Pre-mRNA-splicing factor ATP-dependent RNA helicase-like protein PRP2

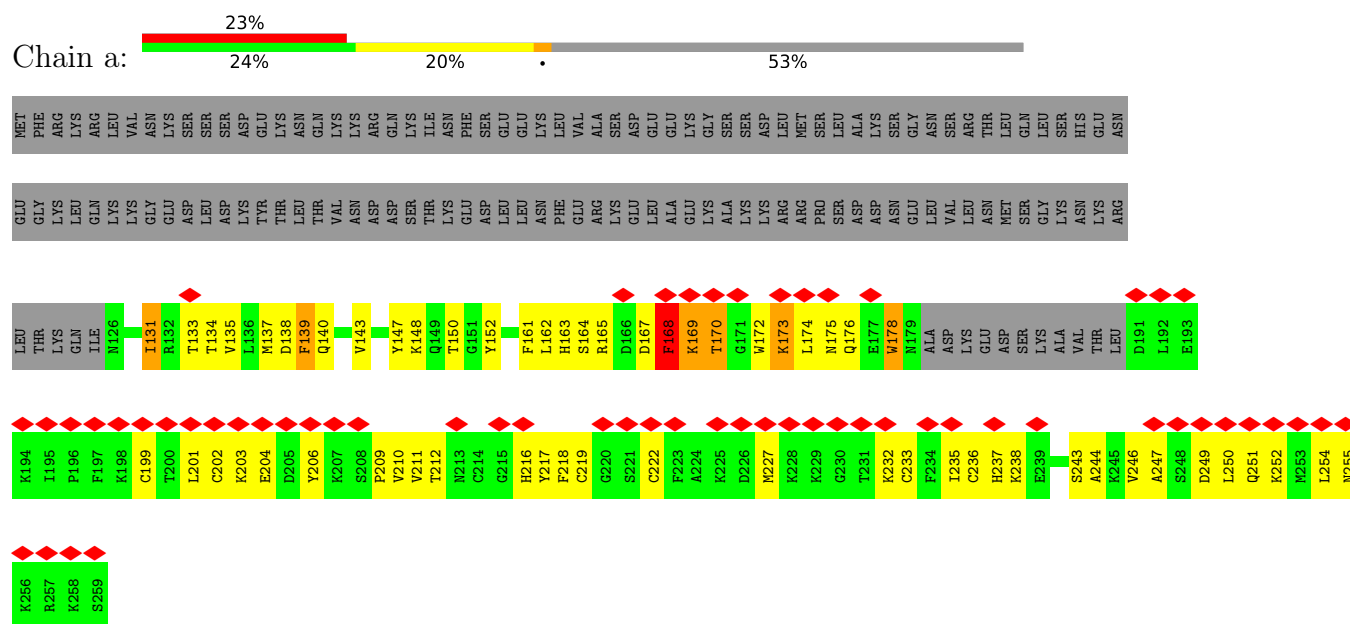




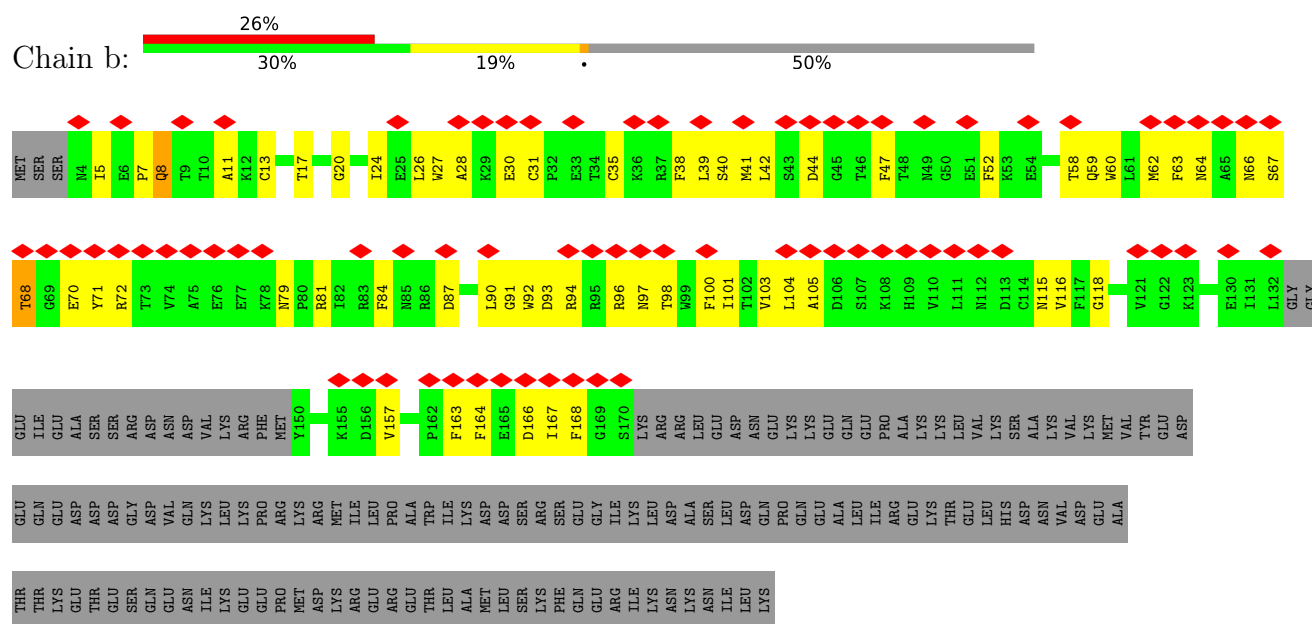
• Molecule 24: Pre-mRNA-splicing factor CWC22



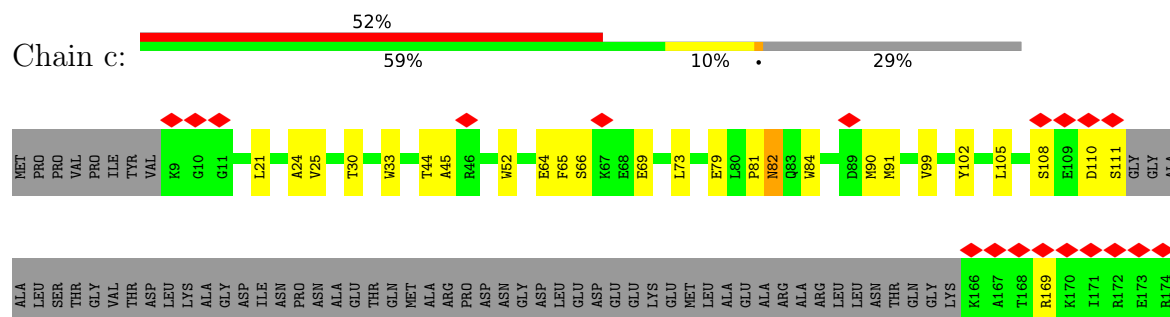
• Molecule 25: Pre-mRNA-splicing factor CWC24

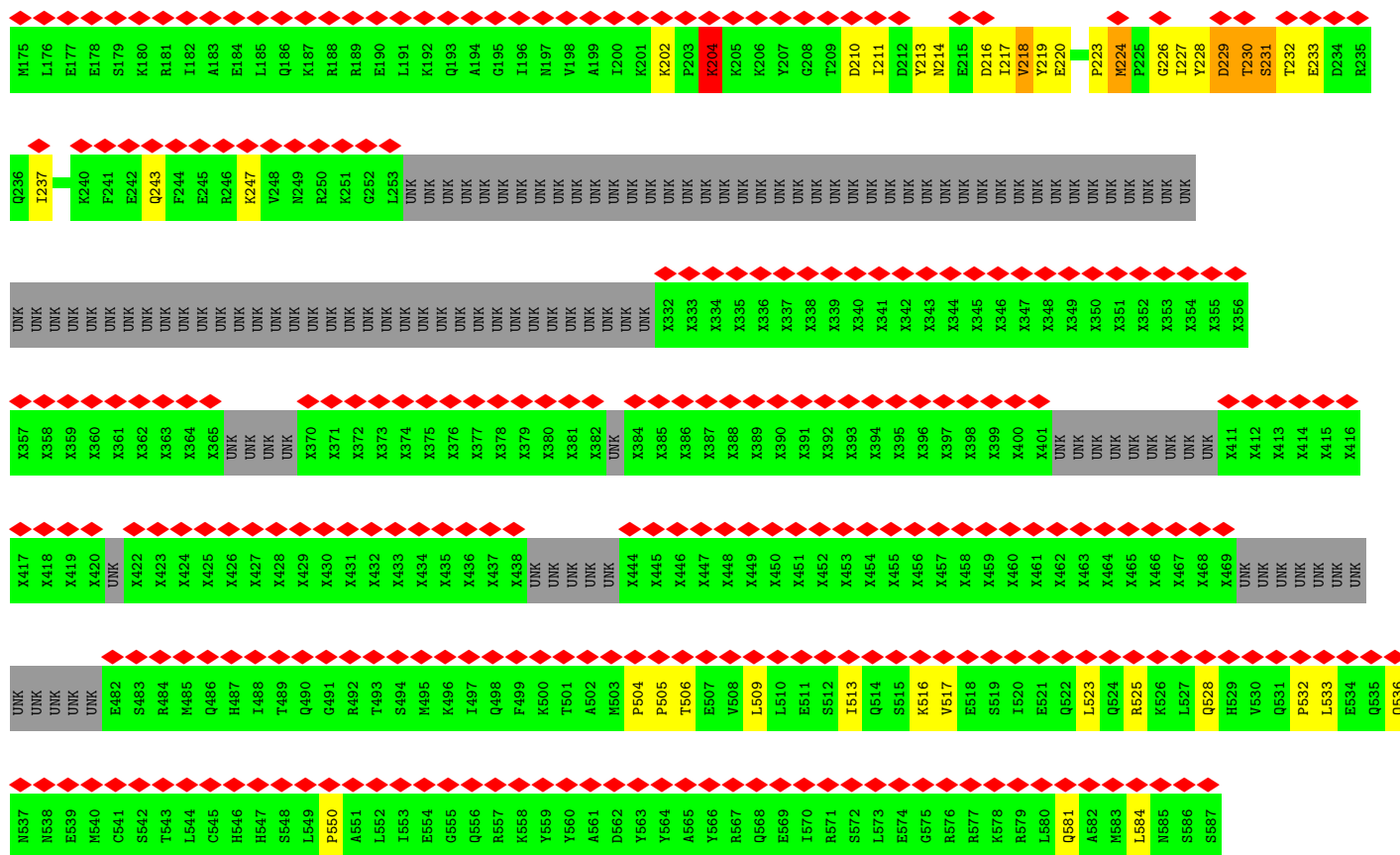


• Molecule 26: Peptidyl-prolyl isomerase CWC27

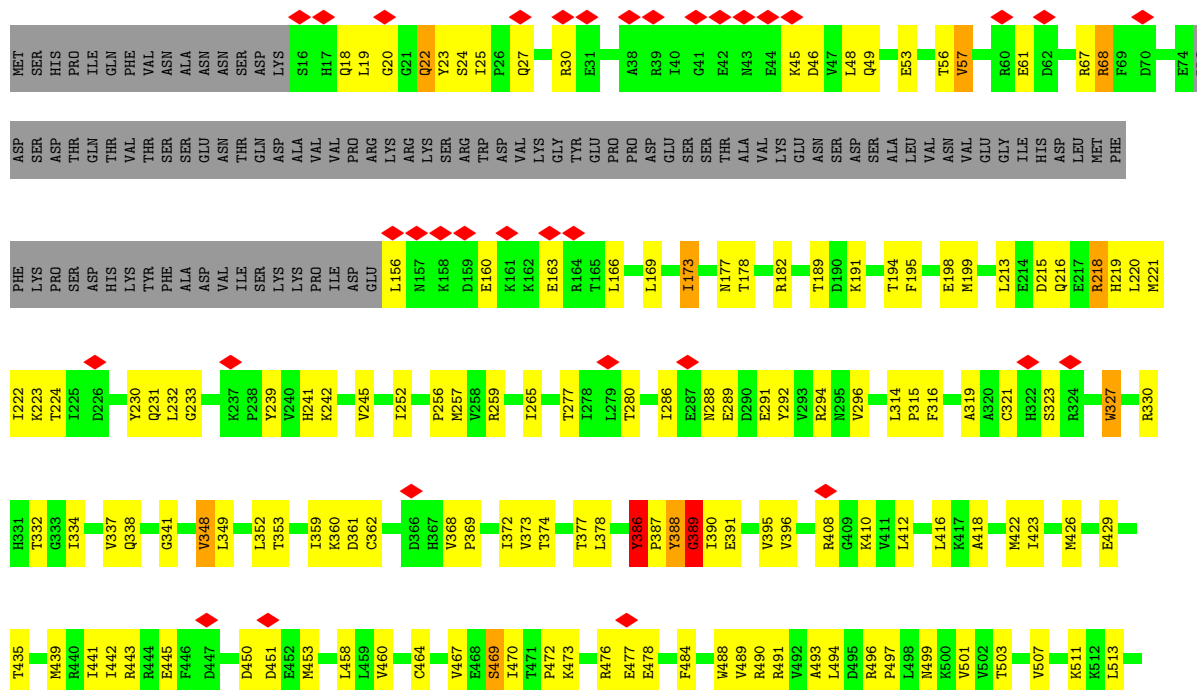


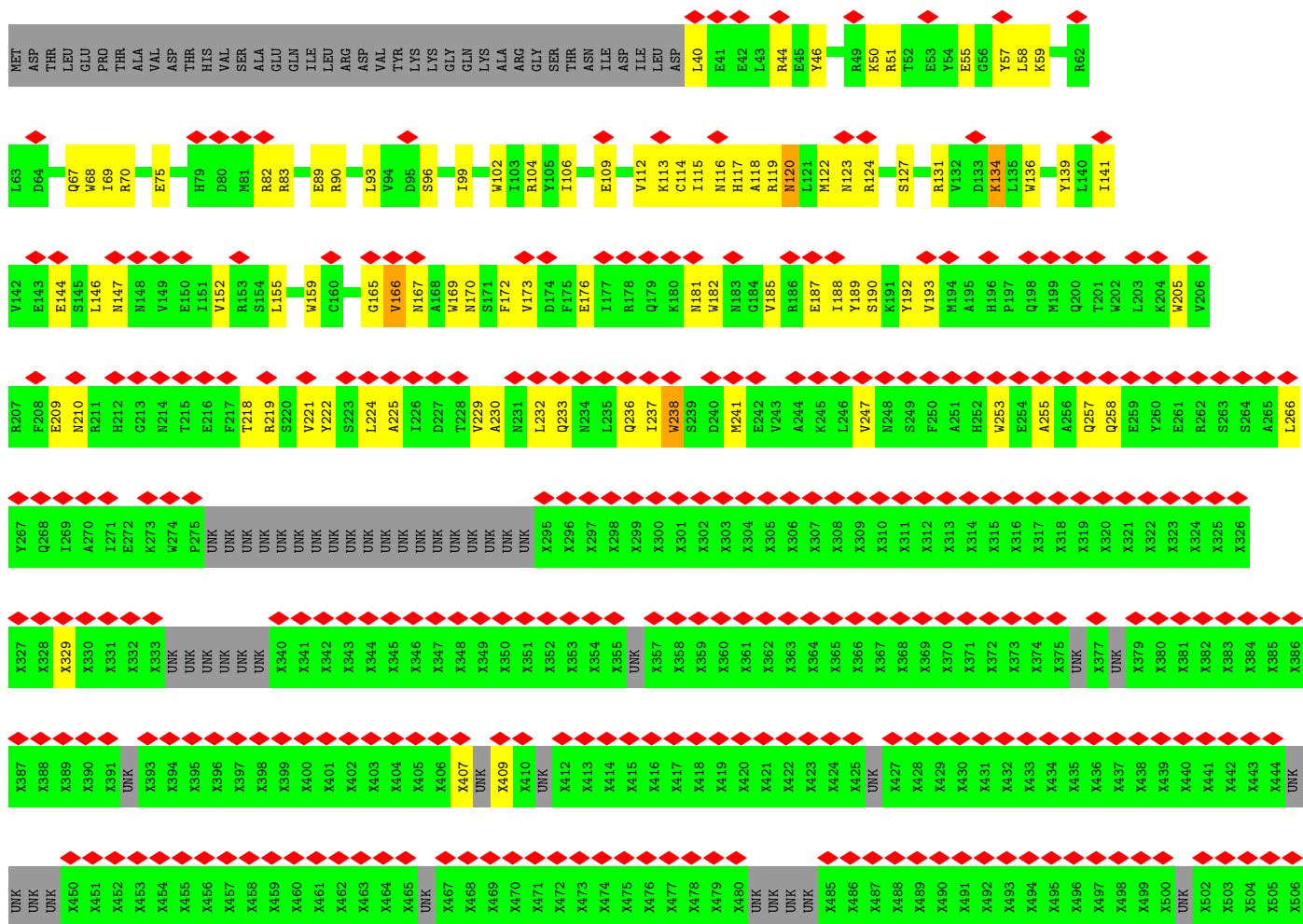
• Molecule 27: Pre-mRNA-splicing factor CEF1

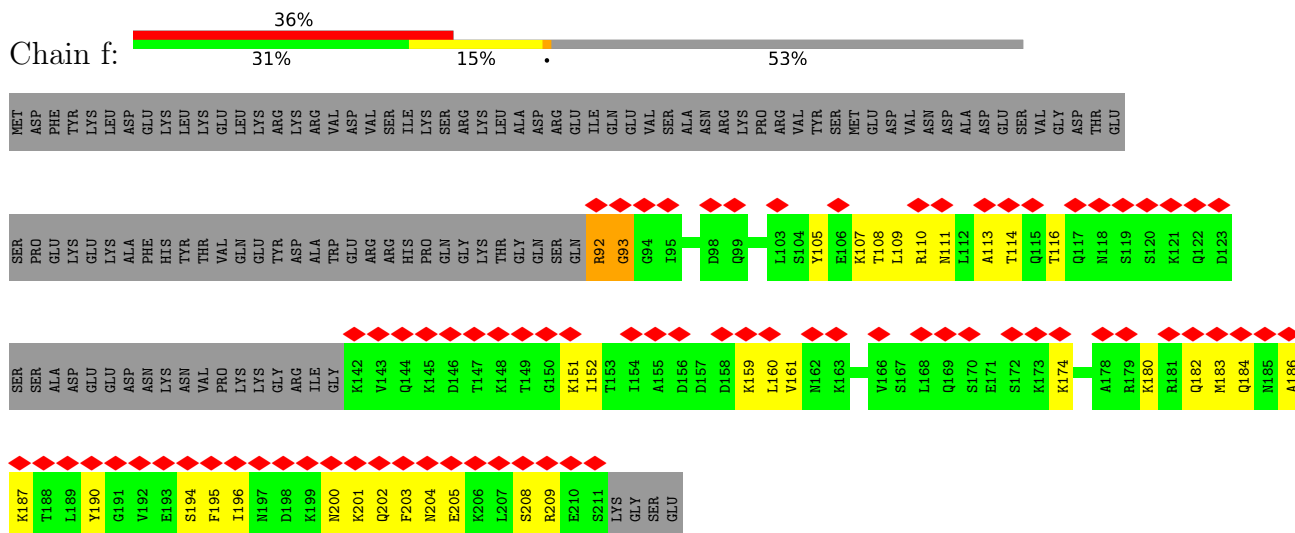




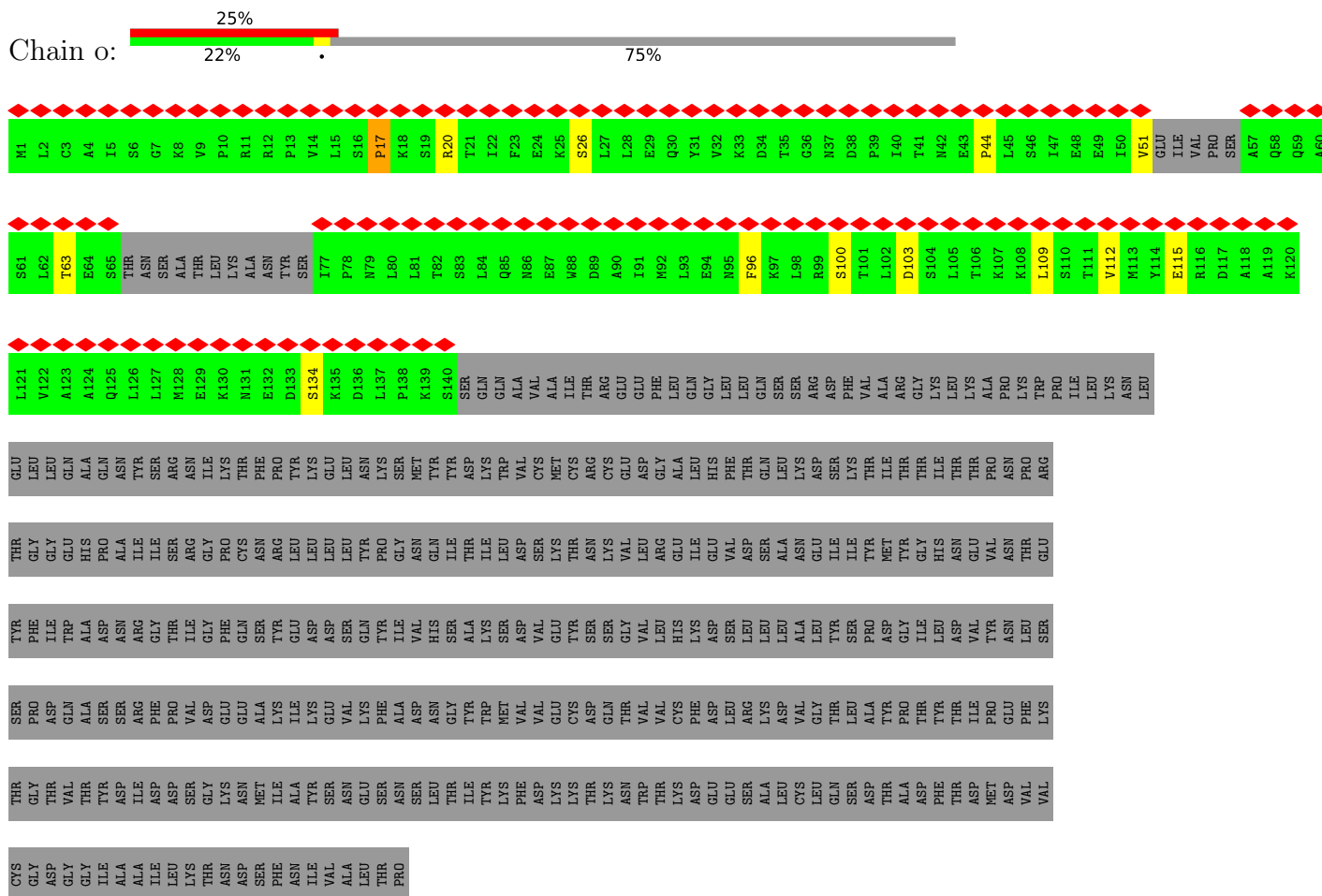
• Molecule 28: U2 snRNP component HSH155





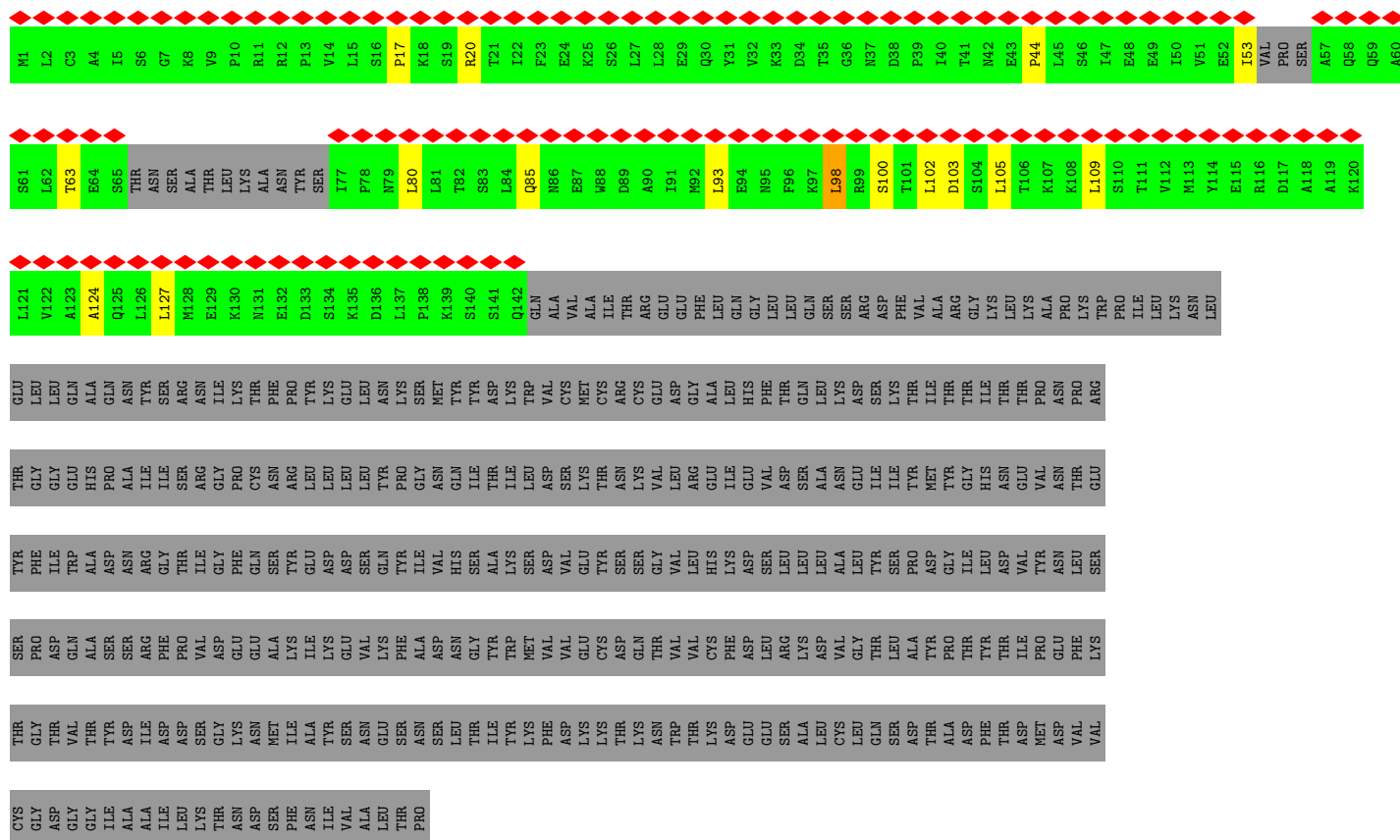


- Molecule 34: Pre-mRNA-processing factor 19

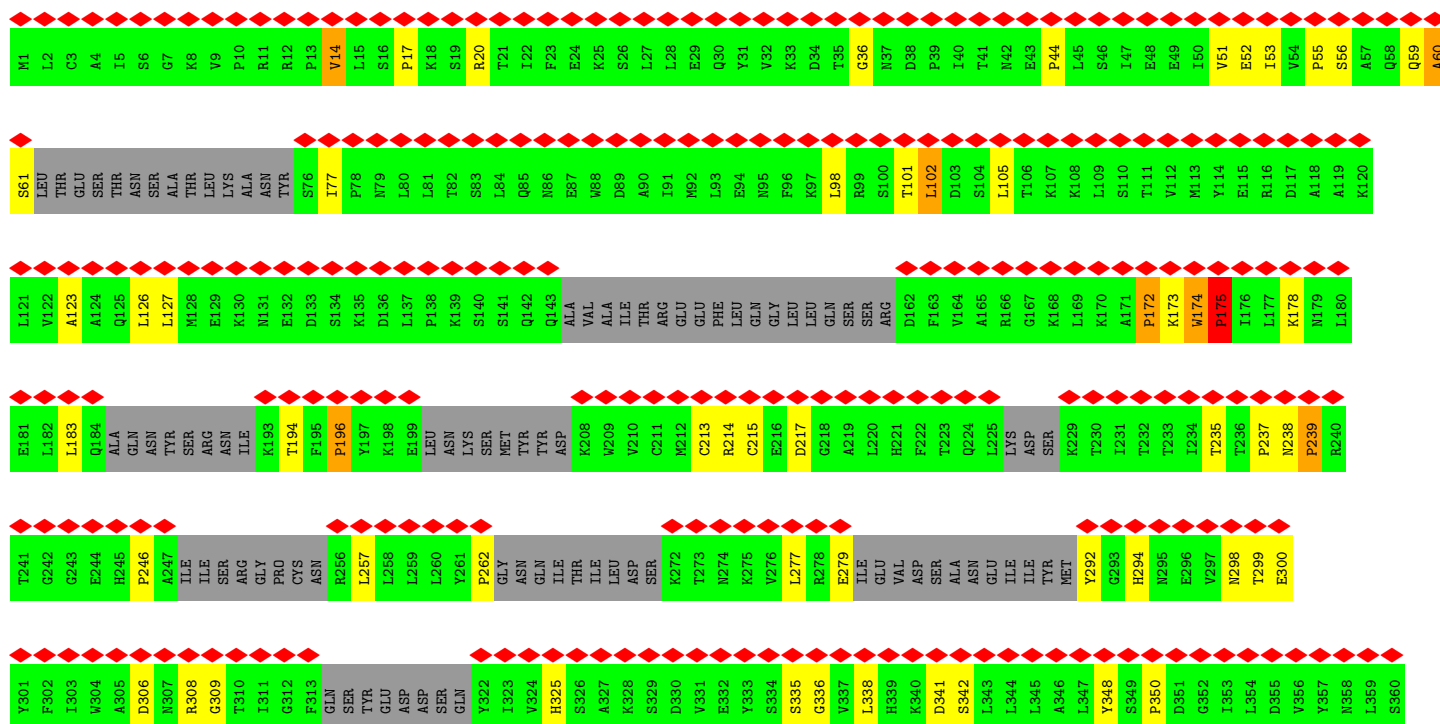
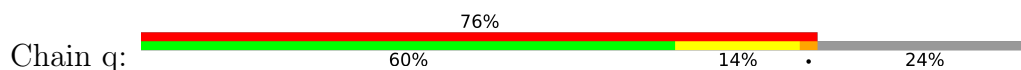


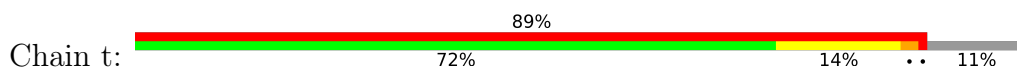
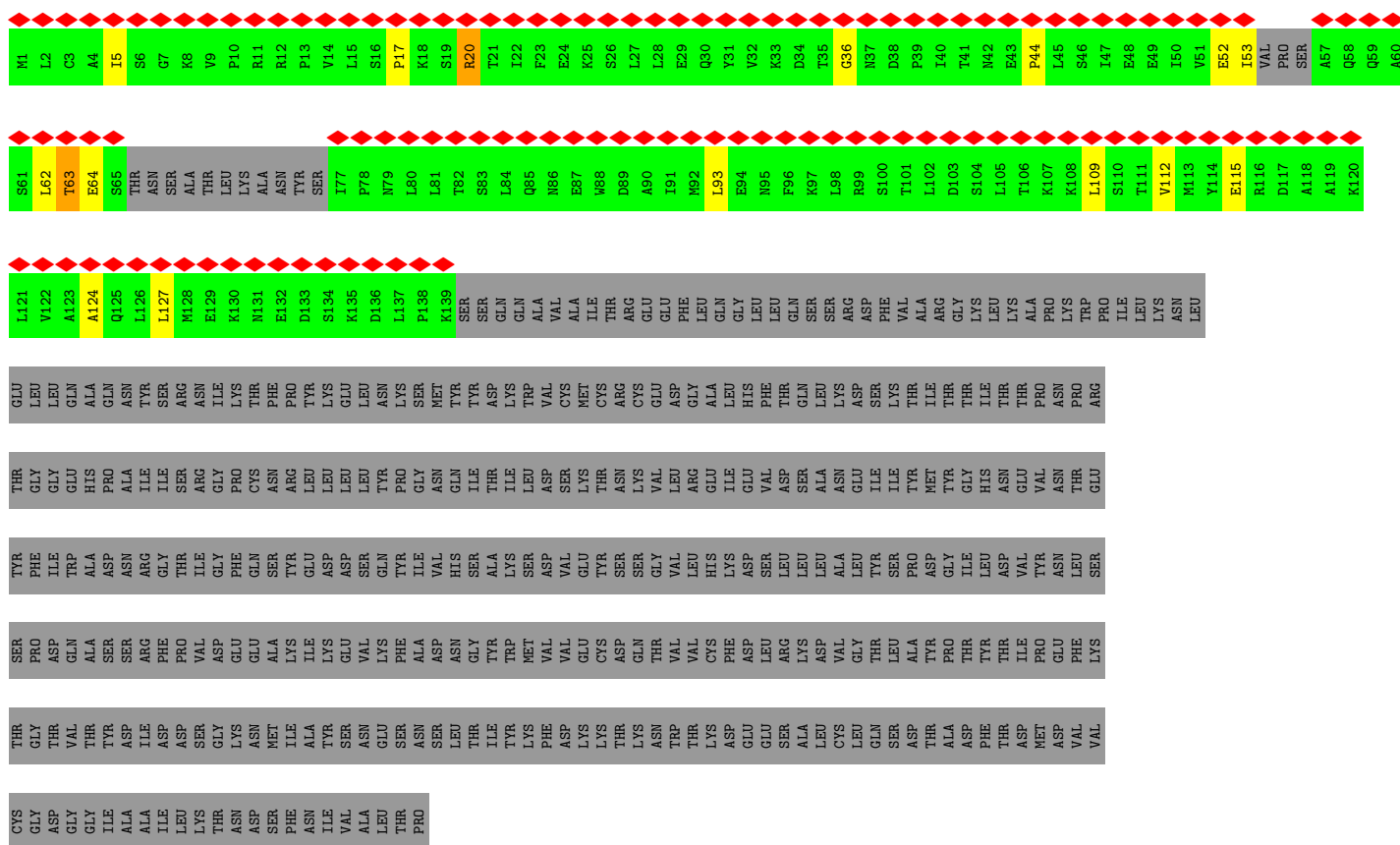
- Molecule 34: Pre-mRNA-processing factor 19

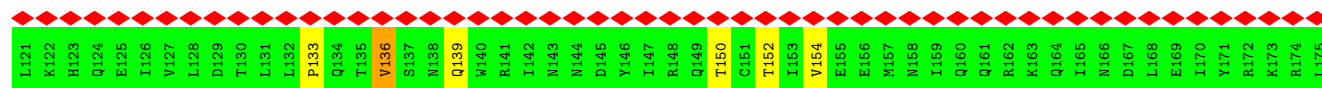




• Molecule 34: Pre-mRNA-processing factor 19

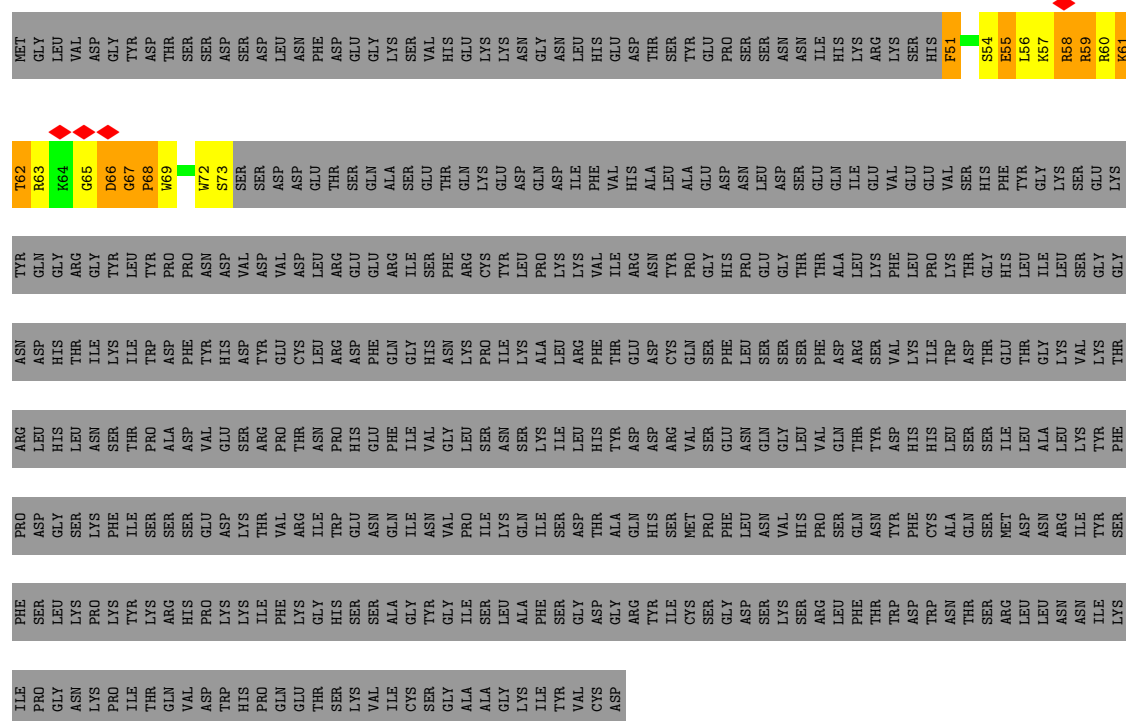






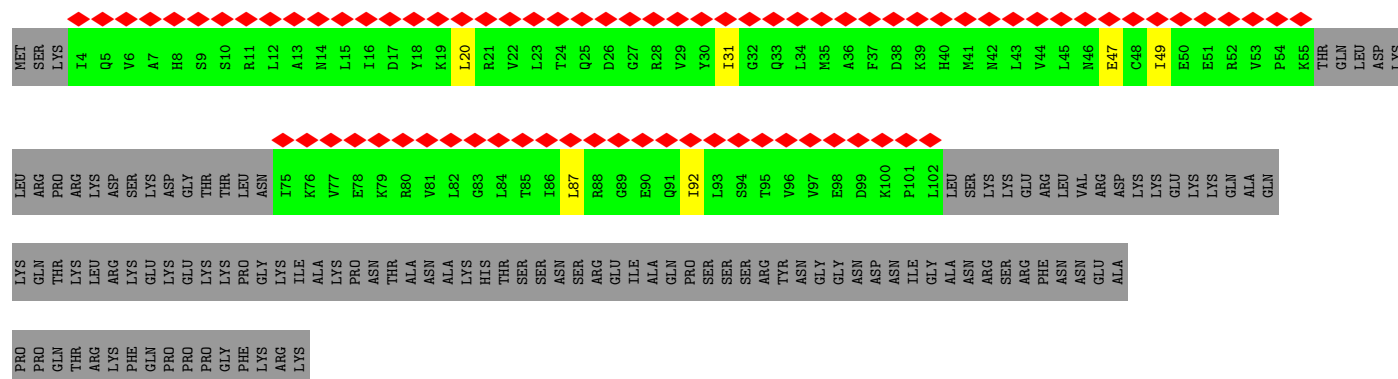
• Molecule 36: Pre-mRNA-processing factor 17

Chain n: 95%



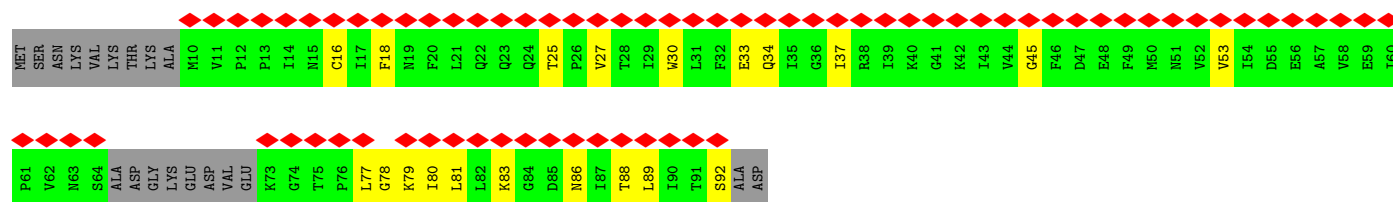
• Molecule 37: Small nuclear ribonucleoprotein-associated protein B

Chain k: 41%
38% 59%

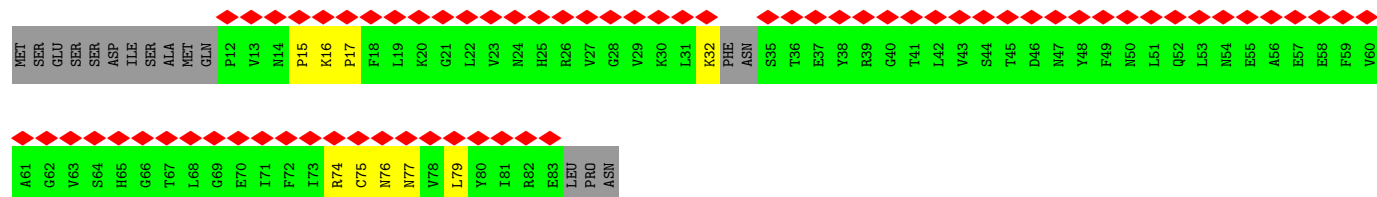
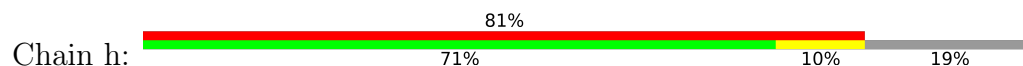


• Molecule 38: Small nuclear ribonucleoprotein E

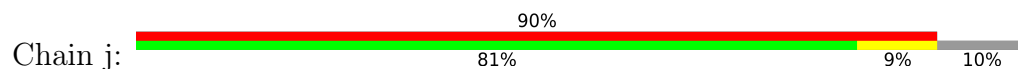
Chain i: 79%
59% 21% 20%



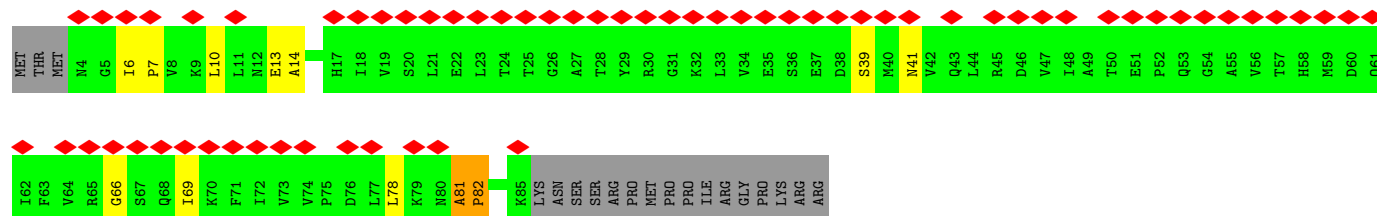
• Molecule 39: Small nuclear ribonucleoprotein F



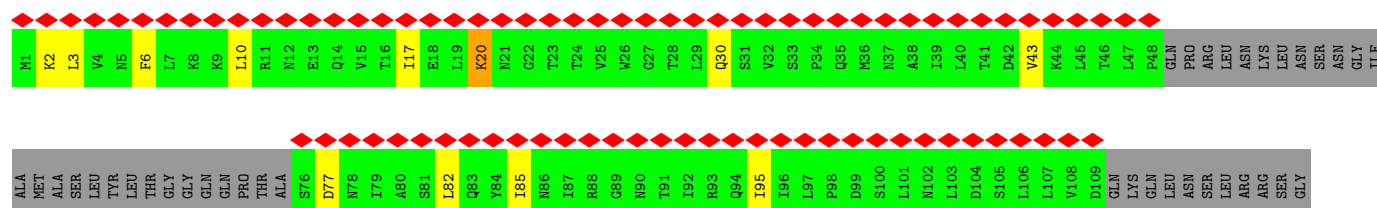
• Molecule 40: Small nuclear ribonucleoprotein G



• Molecule 41: Small nuclear ribonucleoprotein Sm D3

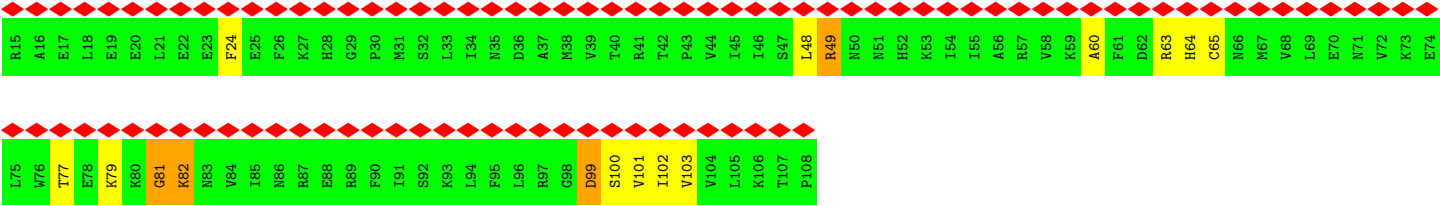
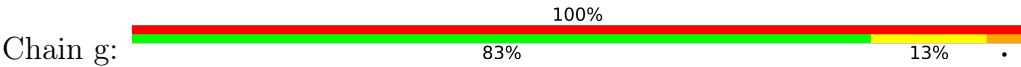


• Molecule 42: Small nuclear ribonucleoprotein Sm D1



GLN	ILE	ALA	ASN	ASP	PRO	SER	LYS	ARG	ARG	ARG	ASP	PHE	GLY	ALA	PRO	ALA	ASN	LYS	ARG	PRO	ARG	ARG	GLY	LEU
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● Molecule 43: Small nuclear ribonucleoprotein Sm D2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	77312	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	4.7	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.285	Depositor
Minimum map value	-0.174	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.0405	Depositor
Map size (Å)	522.4, 522.4, 522.4	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3060001, 1.3060001, 1.3060001	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.94	9/18560 (0.0%)	0.89	19/25158 (0.1%)
2	B	0.45	0/14812	0.57	0/20077
3	C	0.65	1/7162 (0.0%)	0.74	6/9698 (0.1%)
4	D	0.51	0/2747	0.67	0/4267
5	E	0.52	0/2452	0.65	0/3817
6	F	0.99	11/9564 (0.1%)	0.97	7/12963 (0.1%)
7	H	0.92	2/1281 (0.2%)	1.09	6/1727 (0.3%)
8	I	0.97	1/812 (0.1%)	0.95	3/1081 (0.3%)
9	J	1.04	0/827	0.98	1/1105 (0.1%)
10	K	1.09	2/702 (0.3%)	1.00	1/939 (0.1%)
11	L	0.50	0/1547	0.67	0/2404
12	N	0.47	0/579	0.65	0/897
13	M	0.50	1/1183 (0.1%)	0.94	9/1833 (0.5%)
14	O	0.92	0/2704	0.86	3/3676 (0.1%)
15	P	0.64	0/2008	0.84	5/2703 (0.2%)
16	Q	0.56	1/1496 (0.1%)	0.80	4/2014 (0.2%)
17	R	0.63	0/2135	0.83	3/2871 (0.1%)
18	S	0.57	0/592	0.72	0/790
19	T	0.79	1/1315 (0.1%)	0.84	0/1759
20	U	0.40	0/1424	0.63	0/1922
21	V	0.84	0/1071	0.87	2/1445 (0.1%)
22	W	0.76	1/856 (0.1%)	1.01	2/1149 (0.2%)
23	Y	0.49	0/4085	0.67	3/5499 (0.1%)
24	Z	0.79	2/3712 (0.1%)	1.02	5/5004 (0.1%)
25	a	0.76	0/1010	0.83	0/1351
26	b	0.48	0/1252	0.58	0/1692
27	c	0.70	0/2237	0.84	1/2995 (0.0%)
28	G	0.95	1/7104 (0.0%)	0.92	11/9632 (0.1%)
29	d	0.51	0/2075	0.65	2/2808 (0.1%)
30	X	0.77	0/191	1.01	0/254
31	v	0.56	0/899	0.99	0/1206
32	e	0.62	0/954	1.07	5/1285 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.52	0/826	0.68	1/1097 (0.1%)
34	o	0.54	0/824	0.85	0/1111
34	p	0.54	0/848	0.91	0/1143
34	q	0.63	0/2312	0.93	2/3097 (0.1%)
34	r	0.53	0/828	0.86	0/1117
35	t	0.57	0/919	1.06	2/1237 (0.2%)
36	n	0.65	0/200	1.10	1/264 (0.4%)
37	k	0.55	0/636	0.76	0/856
38	i	0.63	0/585	0.86	0/795
39	h	0.60	0/564	0.87	0/761
40	j	0.53	0/532	0.82	1/715 (0.1%)
41	l	0.55	0/634	0.96	2/859 (0.2%)
42	m	0.58	0/649	0.81	0/880
43	g	0.65	0/753	0.96	2/1013 (0.2%)
All	All	0.75	33/110458 (0.0%)	0.83	109/150966 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	6
2	B	0	2
3	C	0	5
6	F	0	13
7	H	0	6
8	I	0	3
14	O	0	6
15	P	0	1
16	Q	0	2
19	T	0	2
20	U	0	2
24	Z	0	4
28	G	0	3
29	d	0	1
33	f	0	1
36	n	0	2
40	j	0	1
41	l	0	2
43	g	0	2
All	All	0	64

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	F	1226	GLY	CA-C	-7.91	1.43	1.51
19	T	121	ILE	C-O	-6.59	1.16	1.24
1	A	1384	PRO	C-O	-6.51	1.19	1.24
13	M	468	A	C3'-O3'	6.38	1.51	1.42
24	Z	299	LEU	C-O	-6.12	1.16	1.24
6	F	97	THR	CA-C	-6.06	1.45	1.52
7	H	231	ALA	C-O	-5.84	1.16	1.24
6	F	826	THR	C-O	-5.82	1.16	1.24
1	A	298	TYR	C-O	-5.67	1.15	1.23
1	A	1051	GLU	N-CA	-5.67	1.39	1.46
6	F	266	VAL	C-O	-5.55	1.18	1.24
7	H	225	LEU	C-O	-5.53	1.17	1.24
10	K	27	THR	N-CA	-5.49	1.39	1.46
10	K	48	ALA	C-O	-5.46	1.17	1.24
1	A	193	TYR	CA-C	-5.43	1.46	1.52
16	Q	215	PRO	N-CD	5.42	1.55	1.47
6	F	1311	TYR	C-O	-5.41	1.17	1.24
8	I	15	GLY	C-O	5.34	1.31	1.23
1	A	402	TRP	N-CA	5.33	1.53	1.46
24	Z	307	GLU	C-O	-5.33	1.16	1.24
6	F	1120	VAL	CA-CB	-5.28	1.49	1.55
6	F	438	LEU	C-O	-5.27	1.17	1.24
6	F	1314	VAL	CA-C	-5.26	1.46	1.52
28	G	863	HIS	CA-C	-5.22	1.45	1.52
1	A	1088	VAL	N-CA	-5.17	1.40	1.46
3	C	870	ALA	N-CA	-5.16	1.42	1.46
1	A	715	LEU	C-O	-5.15	1.18	1.24
6	F	1315	ARG	N-CA	-5.12	1.39	1.46
6	F	1307	TYR	CA-C	-5.08	1.46	1.52
1	A	833	ARG	C-O	-5.07	1.18	1.24
1	A	1014	LYS	CA-C	-5.04	1.46	1.52
6	F	1230	PRO	C-O	-5.01	1.18	1.23
22	W	242	GLU	C-O	-5.00	1.17	1.24

All (109) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	M	468	A	C4'-C3'-O3'	-15.40	89.89	113.00
24	Z	397	LEU	CA-C-N	13.82	137.12	119.84
24	Z	397	LEU	C-N-CA	13.82	137.12	119.84
28	G	680	PRO	CA-C-N	13.19	136.32	119.84
28	G	680	PRO	C-N-CA	13.19	136.32	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	R	217	GLU	N-CA-C	11.40	124.79	111.11
13	M	468	A	C2'-C3'-O3'	10.87	130.00	113.70
7	H	234	GLN	CA-C-N	10.72	133.24	119.84
7	H	234	GLN	C-N-CA	10.72	133.24	119.84
1	A	773	SER	N-CA-C	10.06	122.25	111.28
8	I	55	ASN	C-N-CD	-9.27	86.99	125.00
28	G	680	PRO	N-CA-C	8.91	121.57	110.70
1	A	614	ARG	N-CA-C	-8.31	98.18	110.23
29	d	238	TRP	N-CA-C	8.10	121.94	108.73
34	q	238	ASN	CA-C-N	8.10	129.96	119.84
34	q	238	ASN	C-N-CA	8.10	129.96	119.84
6	F	1015	LEU	N-CA-C	7.65	122.82	109.96
17	R	120	TYR	CB-CA-C	-7.63	107.78	116.63
3	C	464	PRO	N-CA-CB	7.36	109.89	103.27
6	F	856	ASP	N-CA-C	-7.17	98.92	110.32
28	G	423	ILE	CB-CA-C	-7.13	106.93	113.70
32	e	36	LEU	N-CA-C	-6.87	104.53	113.12
3	C	113	ILE	CA-C-N	-6.79	112.77	119.76
3	C	113	ILE	C-N-CA	-6.79	112.77	119.76
13	M	472	A	C2'-C3'-O3'	6.78	119.67	109.50
28	G	389	GLY	N-CA-C	6.78	122.45	113.37
33	f	93	GLY	N-CA-C	6.75	118.90	112.08
17	R	218	GLY	N-CA-C	6.72	129.12	113.18
13	M	480	A	C2'-C3'-O3'	6.65	119.47	109.50
23	Y	648	GLU	CA-C-N	6.56	126.33	119.05
23	Y	648	GLU	C-N-CA	6.56	126.33	119.05
43	g	82	LYS	N-CA-C	6.53	124.71	110.80
28	G	386	TYR	CA-C-N	-6.42	112.21	119.28
28	G	386	TYR	C-N-CA	-6.42	112.21	119.28
8	I	16	ILE	N-CA-C	6.32	117.10	110.72
27	c	229	ASP	N-CA-C	6.22	119.82	111.24
15	P	55	VAL	CA-C-N	-6.19	114.25	120.31
15	P	55	VAL	C-N-CA	-6.19	114.25	120.31
22	W	227	MET	CA-C-N	-6.13	113.65	119.85
22	W	227	MET	C-N-CA	-6.13	113.65	119.85
28	G	388	TYR	N-CA-C	6.13	118.93	111.82
14	O	352	ILE	N-CA-C	-6.10	98.92	108.86
3	C	461	LYS	N-CA-CB	6.04	120.96	110.81
13	M	468	A	C1'-C2'-O2'	5.99	117.38	108.40
23	Y	648	GLU	O-C-N	5.95	127.23	121.28
35	t	105	PRO	CA-CB-CG	5.92	115.75	104.50
1	A	1379	MET	CA-C-N	-5.92	112.92	119.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1379	MET	C-N-CA	-5.92	112.92	119.19
1	A	377	VAL	N-CA-C	5.85	113.99	109.19
6	F	819	VAL	N-CA-C	5.81	115.10	106.85
16	Q	213	SER	N-CA-C	5.80	117.60	111.28
1	A	1745	SER	N-CA-C	5.76	117.56	111.28
6	F	1012	LYS	N-CA-C	5.73	119.01	111.28
9	J	93	GLY	CA-C-O	-5.66	117.71	122.29
1	A	1529	ASN	N-CA-C	-5.54	99.49	108.52
1	A	1589	LYS	N-CA-C	5.51	118.21	111.82
35	t	77	PRO	CA-CB-CG	5.50	114.94	104.50
1	A	721	LEU	N-CA-CB	5.49	117.92	109.91
21	V	110	ARG	CA-C-N	-5.47	114.32	119.85
21	V	110	ARG	C-N-CA	-5.47	114.32	119.85
3	C	172	TRP	N-CA-C	5.46	117.66	111.11
16	Q	121	GLY	N-CA-C	5.45	121.15	111.02
13	M	500	A	C2'-C3'-O3'	-5.44	105.54	113.70
13	M	500	A	C4'-C3'-O3'	-5.44	104.84	113.00
7	H	269	VAL	N-CA-C	-5.44	104.12	110.05
6	F	241	ALA	N-CA-C	5.44	117.96	110.35
14	O	432	ALA	CB-CA-C	-5.43	110.30	116.54
32	e	159	GLU	N-CA-C	-5.43	105.44	111.36
1	A	1794	LEU	N-CA-C	5.43	118.02	111.40
13	M	468	A	N9-C1'-C2'	5.41	120.12	112.00
32	e	45	VAL	N-CA-C	5.41	116.47	111.81
43	g	81	GLY	N-CA-C	5.41	119.50	112.25
8	I	15	GLY	N-CA-C	5.40	125.98	113.18
6	F	76	ILE	N-CA-CB	-5.39	106.28	112.21
1	A	1591	THR	N-CA-CB	-5.38	102.67	110.36
6	F	829	SER	N-CA-C	5.37	118.99	111.74
1	A	331	PHE	N-CA-C	5.34	119.06	112.54
3	C	952	PRO	N-CA-C	5.33	123.45	112.47
28	G	937	VAL	CB-CA-C	-5.33	104.95	112.14
1	A	240	PRO	CA-C-N	-5.32	113.05	118.85
1	A	240	PRO	C-N-CA	-5.32	113.05	118.85
28	G	838	ILE	N-CA-CB	-5.29	104.03	112.07
24	Z	398	PRO	N-CA-C	5.27	123.32	112.47
13	M	468	A	C5'-C4'-C3'	-5.24	108.14	116.00
7	H	196	LEU	CA-C-N	-5.24	114.38	119.78
7	H	196	LEU	C-N-CA	-5.24	114.38	119.78
28	G	681	PRO	N-CA-C	5.21	123.21	112.47
1	A	539	PRO	N-CA-C	5.21	118.67	110.50
29	d	238	TRP	N-CA-CB	-5.20	101.95	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Q	291	ILE	N-CA-C	5.19	120.09	108.88
24	Z	73	ILE	O-C-N	5.19	123.74	120.42
1	A	659	HIS	N-CA-C	5.18	118.62	112.72
15	P	301	LEU	N-CA-C	5.17	116.91	111.28
15	P	57	LEU	CA-C-N	-5.15	113.62	119.28
15	P	57	LEU	C-N-CA	-5.15	113.62	119.28
16	Q	120	LEU	N-CA-C	5.14	117.07	108.99
1	A	776	GLN	N-CA-C	5.13	116.88	111.28
32	e	147	LYS	N-CA-C	5.12	121.72	110.80
1	A	540	THR	N-CA-C	5.08	121.61	110.80
32	e	15	ASN	N-CA-C	-5.08	106.39	112.58
24	Z	397	LEU	C-N-CD	-5.06	104.25	125.00
7	H	234	GLN	O-C-N	5.05	124.97	120.48
40	j	42	ASP	N-CA-C	5.04	117.19	110.53
14	O	123	PRO	N-CA-C	5.04	118.41	110.80
41	l	81	ALA	CA-C-N	5.04	126.13	119.84
41	l	81	ALA	C-N-CA	5.04	126.13	119.84
1	A	1470	GLN	N-CA-C	5.03	116.84	111.36
36	n	68	PRO	N-CA-C	5.02	120.63	114.35
10	K	22	GLY	N-CA-C	-5.02	105.34	112.37

There are no chirality outliers.

All (64) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1014	LYS	Peptide
1	A	1418	THR	Peptide
1	A	239	PHE	Mainchain,Peptide
1	A	539	PRO	Peptide
1	A	772	GLU	Peptide
2	B	696	SER	Peptide
2	B	904	GLN	Peptide
3	C	460	GLY	Mainchain,Peptide
3	C	534	THR	Peptide
3	C	70	TYR	Peptide
3	C	951	ILE	Peptide
6	F	1012	LYS	Mainchain,Peptide
6	F	1014	LYS	Mainchain,Peptide
6	F	1183	CYS	Mainchain,Peptide
6	F	185	ARG	Peptide
6	F	206	SER	Peptide
6	F	666	LEU	Peptide

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Mol	Chain	Res	Type	Group
6	F	667	THR	Mainchain,Peptide
6	F	855	ALA	Mainchain,Peptide
28	G	389	GLY	Peptide
28	G	680	PRO	Mainchain,Peptide
7	H	184	SER	Peptide
7	H	185	GLY	Peptide
7	H	212	LEU	Mainchain,Peptide
7	H	234	GLN	Mainchain,Peptide
8	I	13	GLY	Peptide
8	I	14	GLY	Peptide
8	I	15	GLY	Peptide
14	O	123	PRO	Peptide
14	O	278	ASP	Peptide
14	O	351	GLY	Mainchain,Peptide
14	O	437	GLU	Peptide
14	O	441	ALA	Peptide
15	P	85	SER	Peptide
16	Q	103	GLU	Peptide
16	Q	291	ILE	Peptide
19	T	104	CYS	Peptide
19	T	140	VAL	Peptide
20	U	44	ASN	Peptide
20	U	71	GLU	Peptide
24	Z	219	SER	Peptide
24	Z	232	GLU	Peptide
24	Z	397	LEU	Mainchain,Peptide
29	d	237	ILE	Peptide
33	f	92	ARG	Peptide
43	g	81	GLY	Mainchain,Peptide
40	j	41	ASP	Peptide
41	l	81	ALA	Mainchain,Peptide
36	n	67	GLY	Mainchain,Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	18101	0	18027	790	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	14504	0	14508	420	0
3	C	7014	0	7189	289	0
4	D	2465	0	1251	61	0
5	E	2192	0	1106	58	0
6	F	9380	0	9482	466	0
7	H	1248	0	1263	96	0
8	I	800	0	802	48	0
9	J	814	0	809	54	0
10	K	693	0	705	45	0
11	L	1388	0	701	39	0
12	N	521	0	260	24	0
13	M	1057	0	537	53	0
14	O	2646	0	2639	98	0
15	P	1978	0	1981	130	0
16	Q	1472	0	1485	179	0
17	R	2089	0	2053	171	0
18	S	578	0	565	35	0
19	T	1291	0	1312	44	0
20	U	1401	0	1362	78	0
21	V	1051	0	1015	77	0
22	W	842	0	818	106	0
23	Y	4047	0	3394	125	0
24	Z	3651	0	3707	153	0
25	a	988	0	954	93	0
26	b	1224	0	1217	47	0
27	c	2803	0	2169	74	0
28	G	6970	0	7181	308	0
29	d	3558	0	2329	131	0
30	X	190	0	186	16	0
31	v	3047	0	1177	55	0
32	e	947	0	703	58	0
33	f	822	0	845	66	0
34	o	819	0	657	10	0
34	p	843	0	672	13	0
34	q	2315	0	1626	46	0
34	r	823	0	654	7	0
35	t	921	0	605	14	0
36	n	195	0	198	40	0
37	k	631	0	670	3	0
38	i	575	0	597	21	0
39	h	554	0	556	18	0
40	j	529	0	557	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
41	l	625	0	647	6	0
42	m	644	0	686	14	0
43	g	741	0	778	17	0
44	C	32	0	12	4	0
45	E	4	0	0	0	0
45	Y	1	0	0	0	0
46	I	1	0	0	0	0
46	J	3	0	0	0	0
46	Q	2	0	0	0	0
46	R	1	0	0	0	0
46	T	3	0	0	0	0
46	a	3	0	0	0	0
47	Y	27	0	12	2	0
All	All	112064	0	102659	4093	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 19.

All (4093) 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)
1:A:769:MET:HE1	1:A:811:ILE:CD1	1.28	1.56
7:H:262:HIS:CD2	7:H:283:LYS:HZ1	1.31	1.46
29:d:115:ILE:HD11	29:d:119:ARG:NH2	1.35	1.42
23:Y:699:GLU:HB3	23:Y:702:SER:CB	1.49	1.41
22:W:207:THR:O	22:W:214:LEU:CD1	1.68	1.40
16:Q:212:ALA:HB1	17:R:237:ARG:NH2	1.35	1.39
21:V:63:SER:CB	21:V:74:PHE:CE1	2.06	1.38
3:C:116:THR:CG2	3:C:118:TYR:CE1	2.08	1.36
31:v:729:TYR:CZ	31:v:749:UNK:CB	2.08	1.35
24:Z:192:GLU:CA	24:Z:195:GLU:OE2	1.74	1.34
16:Q:212:ALA:CB	17:R:237:ARG:HH21	1.38	1.34
3:C:265:PHE:HE2	3:C:295:ILE:CG2	1.42	1.33
7:H:262:HIS:CD2	7:H:283:LYS:NZ	1.90	1.32
17:R:48:VAL:CG2	17:R:216:ARG:O	1.77	1.30
24:Z:192:GLU:HA	24:Z:195:GLU:OE2	1.12	1.29
36:n:59:ARG:O	36:n:62:THR:HG23	1.26	1.29
3:C:116:THR:HG21	3:C:118:TYR:CE1	1.63	1.28
31:v:729:TYR:CE1	31:v:749:UNK:CB	2.18	1.26
1:A:1748:ILE:HD11	1:A:1783:MET:CB	1.64	1.25
34:q:422:GLY:O	34:q:442:SER:CB	1.84	1.23

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1618:ASN:HB2	1:A:1744:ASP:OD2	1.37	1.23
15:P:57:LEU:CD2	15:P:58:PRO:HD2	1.67	1.22
24:Z:170:HIS:CE1	24:Z:174:TRP:CZ3	2.26	1.22
24:Z:459:ARG:O	24:Z:463:ASN:ND2	1.72	1.21
1:A:1748:ILE:CD1	1:A:1783:MET:HB3	1.70	1.20
3:C:391:MET:CE	3:C:395:LYS:HE2	1.73	1.18
16:Q:215:PRO:HB3	17:R:171:ASP:OD1	1.00	1.17
2:B:880:TYR:O	6:F:686:GLN:NE2	1.77	1.17
1:A:2405:GLU:OE1	2:B:833:THR:OG1	1.59	1.16
29:d:115:ILE:CD1	29:d:119:ARG:HH21	1.58	1.16
3:C:265:PHE:CE2	3:C:295:ILE:HG21	1.81	1.16
1:A:330:LEU:O	1:A:335:SER:OG	1.63	1.15
1:A:769:MET:CE	1:A:811:ILE:CD1	2.24	1.15
16:Q:79:ARG:CD	16:Q:126:THR:HG23	1.77	1.15
16:Q:101:THR:CG2	16:Q:120:LEU:HD21	1.77	1.15
1:A:769:MET:CE	1:A:811:ILE:HD11	1.76	1.14
16:Q:215:PRO:CB	17:R:171:ASP:OD1	1.94	1.14
25:a:216:HIS:HE1	25:a:235:ILE:HB	1.12	1.14
23:Y:699:GLU:CB	23:Y:702:SER:CB	2.25	1.14
3:C:265:PHE:CE2	3:C:295:ILE:CG2	2.29	1.13
16:Q:101:THR:HG21	16:Q:120:LEU:HD21	1.26	1.13
25:a:216:HIS:CE1	25:a:235:ILE:HB	1.83	1.13
7:H:262:HIS:HD2	7:H:283:LYS:NZ	1.31	1.13
15:P:57:LEU:HD23	15:P:58:PRO:HD2	1.27	1.13
1:A:1130:ARG:HH11	1:A:1156:HIS:HB3	0.98	1.12
24:Z:170:HIS:CE1	24:Z:174:TRP:HZ3	1.65	1.12
32:e:140:ILE:HA	32:e:151:ALA:HB2	1.33	1.11
1:A:1130:ARG:NH1	1:A:1156:HIS:HB3	1.66	1.11
35:t:7:VAL:HG11	35:t:154:VAL:CB	1.81	1.10
17:R:48:VAL:HG21	17:R:216:ARG:O	1.49	1.10
16:Q:91:ILE:HG21	16:Q:125:ILE:HD12	1.25	1.09
32:e:139:GLU:O	32:e:151:ALA:HB1	1.51	1.09
1:A:1509:ARG:NH1	1:A:1533:ASP:OD2	1.86	1.08
3:C:116:THR:CG2	3:C:118:TYR:CD1	2.37	1.08
11:L:5:A:H5'	33:f:114:THR:HG21	1.22	1.07
16:Q:79:ARG:HD3	16:Q:126:THR:HG23	1.13	1.07
16:Q:217:TRP:CH2	17:R:187:LYS:HD3	1.89	1.07
1:A:931:ALA:HA	1:A:934:ARG:NH1	1.68	1.06
16:Q:217:TRP:CZ2	17:R:187:LYS:HD3	1.88	1.06
22:W:197:PHE:CE2	24:Z:463:ASN:HB3	1.89	1.06
24:Z:177:LEU:HD22	24:Z:194:LEU:HD21	1.35	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:769:MET:HE1	1:A:811:ILE:HD12	1.30	1.06
22:W:189:THR:O	22:W:195:ILE:HG13	1.53	1.06
1:A:1428:GLY:O	30:X:16:THR:HG22	1.55	1.06
21:V:63:SER:HB2	21:V:74:PHE:CE1	1.78	1.05
3:C:391:MET:HE1	3:C:395:LYS:HE2	1.39	1.05
20:U:45:LYS:HG2	20:U:126:VAL:HG13	1.07	1.05
29:d:117:HIS:O	29:d:120:ASN:ND2	1.90	1.05
31:v:729:TYR:CE2	31:v:749:UNK:CB	2.38	1.05
1:A:1589:LYS:O	8:I:16:ILE:HG13	1.55	1.05
8:I:57:TYR:CE1	8:I:70:LEU:CD1	2.40	1.05
1:A:1122:ASP:OD1	1:A:1161:TYR:OH	1.75	1.04
24:Z:177:LEU:CD2	24:Z:194:LEU:HD21	1.85	1.04
16:Q:79:ARG:HD3	16:Q:126:THR:CG2	1.88	1.04
24:Z:170:HIS:CE1	24:Z:174:TRP:CE3	2.45	1.04
3:C:274:ILE:HG12	3:C:382:TYR:CE1	1.92	1.04
13:M:514:U:H4'	13:M:515:U:H5'	1.38	1.04
24:Z:178:ARG:HG3	24:Z:198:PHE:CE2	1.93	1.03
15:P:319:HIS:HE1	22:W:264:GLU:OE1	1.41	1.03
34:o:51:VAL:HG21	34:p:20:ARG:CB	1.89	1.03
1:A:1325:SER:O	1:A:1331:VAL:CG2	2.07	1.03
4:D:165:A:H4'	4:D:166:U:C5'	1.89	1.02
1:A:931:ALA:HA	1:A:934:ARG:HH12	1.15	1.02
1:A:1842:GLU:O	1:A:1845:ASN:ND2	1.91	1.02
29:d:113:LYS:HG3	33:f:161:VAL:HG11	1.40	1.02
19:T:54:GLN:HG3	36:n:69:TRP:CE2	1.95	1.02
27:c:229:ASP:HB3	33:f:151:LYS:HB3	1.38	1.01
5:E:91:A:C5	29:d:99:ILE:HD11	1.95	1.01
6:F:715:VAL:O	25:a:246:VAL:HG21	1.61	1.01
7:H:288:HIS:O	7:H:289:LYS:HG3	1.60	1.01
1:A:2018:ASN:OD1	1:A:2021:SER:OG	1.77	1.00
16:Q:39:LEU:HD11	16:Q:111:ARG:HG3	1.44	1.00
21:V:48:LEU:O	22:W:231:ARG:NH1	1.95	1.00
24:Z:181:LEU:HG	24:Z:194:LEU:HD13	1.41	1.00
27:c:213:TYR:CE1	29:d:55:GLU:OE1	2.14	1.00
1:A:563:ASP:OD2	1:A:640:ARG:NH2	1.93	1.00
1:A:997:GLN:NE2	1:A:1511:ARG:NH2	2.10	1.00
3:C:150:MET:SD	3:C:178:LEU:HD11	2.01	1.00
29:d:117:HIS:HA	29:d:120:ASN:ND2	1.75	1.00
16:Q:226:LEU:CD1	16:Q:227:LEU:HD23	1.91	1.00
28:G:578:ILE:HG23	28:G:579:ILE:HD12	1.41	1.00
36:n:68:PRO:HD2	36:n:69:TRP:CE3	1.96	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Z:178:ARG:CB	24:Z:198:PHE:HZ	1.74	1.00
17:R:146:LEU:CD2	17:R:211:GLU:OE1	2.09	1.00
15:P:57:LEU:HD23	15:P:58:PRO:CD	1.91	0.99
36:n:59:ARG:O	36:n:62:THR:CG2	2.10	0.99
1:A:893:ARG:HH11	1:A:893:ARG:HG3	1.27	0.99
1:A:1325:SER:O	1:A:1331:VAL:HG23	1.63	0.99
20:U:45:LYS:HG2	20:U:126:VAL:CG1	1.92	0.99
21:V:63:SER:HB3	21:V:74:PHE:CE1	1.99	0.98
4:D:165:A:C4'	4:D:166:U:H5'	1.91	0.98
36:n:55:GLU:OE2	36:n:58:ARG:NE	1.95	0.98
16:Q:216:GLU:OE2	16:Q:240:LEU:HG	1.64	0.98
31:v:730:GLN:HA	31:v:733:ILE:HD11	1.45	0.98
25:a:147:TYR:CD2	25:a:163:HIS:O	2.17	0.98
1:A:143:ILE:CD1	1:A:570:GLN:HG3	1.94	0.97
16:Q:101:THR:HB	16:Q:120:LEU:HD11	1.44	0.97
15:P:37:ASN:OD1	15:P:143:VAL:HG11	1.63	0.97
17:R:48:VAL:HG22	17:R:216:ARG:O	1.64	0.97
3:C:116:THR:HG21	3:C:118:TYR:CZ	1.97	0.97
19:T:54:GLN:NE2	36:n:69:TRP:CD1	2.33	0.97
16:Q:226:LEU:HD21	16:Q:262:PHE:CD1	2.00	0.97
34:q:257:LEU:CD2	34:q:279:GLU:CG	2.42	0.97
10:K:57:ARG:NH1	10:K:59:ASP:OD2	1.97	0.96
22:W:208:SER:HB2	22:W:212:ARG:O	1.65	0.96
18:S:9:LEU:HD21	18:S:11:ALA:HB3	1.45	0.96
32:e:140:ILE:HA	32:e:151:ALA:CB	1.96	0.96
16:Q:91:ILE:HG21	16:Q:125:ILE:CD1	1.96	0.96
1:A:1012:TRP:NE1	1:A:1122:ASP:OD2	2.00	0.95
15:P:57:LEU:HD22	15:P:58:PRO:HD2	1.46	0.95
19:T:104:CYS:SG	19:T:150:CYS:HB2	2.06	0.95
24:Z:170:HIS:HE1	24:Z:174:TRP:CZ3	1.75	0.95
6:F:1113:SER:O	7:H:168:ASN:ND2	1.99	0.95
22:W:207:THR:O	22:W:214:LEU:HD13	0.78	0.95
16:Q:226:LEU:CG	16:Q:227:LEU:HD23	1.97	0.95
3:C:126:MET:SD	3:C:132:ARG:NH1	2.39	0.94
16:Q:226:LEU:HD11	16:Q:227:LEU:HD23	1.49	0.94
22:W:197:PHE:CZ	24:Z:463:ASN:HB3	2.01	0.94
3:C:116:THR:HG23	3:C:118:TYR:CE1	2.01	0.94
6:F:363:VAL:HG12	6:F:364:THR:H	1.32	0.94
8:I:57:TYR:CE1	8:I:70:LEU:HD13	2.02	0.94
16:Q:108:MET:SD	27:c:211:ILE:HD11	2.07	0.94
15:P:319:HIS:CE1	22:W:264:GLU:OE1	2.21	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:W:207:THR:C	22:W:214:LEU:HD13	1.93	0.94
3:C:177:TYR:CE1	3:C:548:ARG:HD3	2.03	0.94
15:P:53:LEU:HD23	15:P:54:SER:N	1.83	0.94
20:U:45:LYS:CG	20:U:126:VAL:HG13	1.97	0.93
10:K:38:ASP:O	10:K:42:THR:HG23	1.67	0.93
16:Q:79:ARG:CD	16:Q:126:THR:CG2	2.45	0.93
20:U:50:LEU:HA	20:U:139:GLN:HE22	1.32	0.93
1:A:143:ILE:HD13	1:A:570:GLN:HG3	1.49	0.93
31:v:718:SER:OG	31:v:725:THR:HG21	1.67	0.93
3:C:116:THR:HG22	3:C:118:TYR:CD1	2.01	0.93
1:A:774:ILE:HD12	1:A:775:ARG:N	1.84	0.93
24:Z:199:GLU:O	24:Z:202:GLN:HG2	1.68	0.93
4:D:165:A:C2	42:m:2:LYS:CE	2.51	0.93
21:V:63:SER:HB2	21:V:74:PHE:HE1	1.24	0.93
24:Z:174:TRP:CZ2	24:Z:197:LEU:HD11	2.04	0.92
32:e:27:GLU:O	32:e:122:ASP:HB3	1.68	0.92
4:D:165:A:H4'	4:D:166:U:H5'	0.95	0.92
1:A:351:LYS:NZ	12:N:91:A:OP1	2.02	0.92
29:d:115:ILE:HD11	29:d:119:ARG:HH21	0.77	0.92
34:q:468:GLN:CB	34:q:481:CYS:SG	2.58	0.92
17:R:206:LEU:HG	17:R:207:PRO:HD2	1.51	0.92
22:W:213:LYS:HB3	22:W:230:SER:OG	1.70	0.92
16:Q:255:SER:OG	16:Q:257:GLU:HG2	1.70	0.91
6:F:656:ILE:HA	6:F:662:SER:O	1.69	0.91
6:F:1111:ASP:OD2	7:H:167:LYS:NZ	2.02	0.91
23:Y:505:GLU:O	23:Y:552:ARG:NH2	2.04	0.91
7:H:262:HIS:CD2	7:H:283:LYS:HZ2	1.87	0.91
34:o:20:ARG:CB	34:p:53:ILE:HA	2.00	0.91
32:e:33:ASN:CB	32:e:62:ASP:CG	2.43	0.91
8:I:53:ARG:HB3	8:I:53:ARG:NH1	1.85	0.91
24:Z:192:GLU:HA	24:Z:195:GLU:CD	1.94	0.91
31:v:682:LYS:O	31:v:685:GLU:CG	2.19	0.91
16:Q:214:ILE:HD11	16:Q:218:LYS:CG	1.99	0.91
1:A:1364:GLU:OE1	1:A:1403:SER:CB	2.19	0.90
6:F:690:LEU:HA	6:F:703:MET:O	1.71	0.90
35:t:81:ASP:CB	35:t:85:THR:CB	2.49	0.90
1:A:769:MET:HE1	1:A:811:ILE:HD11	0.90	0.90
1:A:1130:ARG:HH11	1:A:1156:HIS:CB	1.82	0.90
3:C:117:ARG:NH1	3:C:156:ASP:O	2.05	0.90
6:F:715:VAL:O	25:a:246:VAL:CG2	2.20	0.90
1:A:143:ILE:CD1	1:A:570:GLN:CG	2.49	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:777:LYS:HA	1:A:777:LYS:CE	2.00	0.90
23:Y:626:LEU:CD1	23:Y:650:GLU:HA	2.02	0.90
19:T:120:CYS:HB2	19:T:122:CYS:HB3	1.54	0.90
24:Z:178:ARG:CG	24:Z:198:PHE:CZ	2.54	0.90
4:D:165:A:C2	42:m:2:LYS:HE2	2.07	0.89
15:P:53:LEU:HD23	15:P:54:SER:H	1.36	0.89
15:P:60:LYS:HE3	15:P:63:ILE:HD11	1.51	0.89
31:v:729:TYR:CD1	31:v:749:UNK:CB	2.55	0.89
1:A:997:GLN:HE22	1:A:1511:ARG:NH2	1.69	0.89
1:A:1816:ARG:HG2	1:A:1816:ARG:HH11	1.37	0.89
1:A:1122:ASP:OD1	1:A:1161:TYR:CZ	2.25	0.89
17:R:3:SER:O	17:R:7:LYS:HD3	1.73	0.89
1:A:273:ASP:HA	1:A:310:ASN:HD21	1.38	0.89
1:A:1836:ASN:ND2	1:A:2006:SER:OG	2.04	0.89
3:C:219:VAL:HG11	3:C:931:TYR:HB3	1.53	0.89
22:W:214:LEU:HD21	22:W:227:MET:HB2	1.54	0.89
28:G:675:LEU:HD11	28:G:714:LEU:HB3	1.54	0.89
1:A:322:VAL:HG21	1:A:327:TYR:CE2	2.08	0.88
13:M:514:U:O2'	13:M:515:U:OP2	1.89	0.88
17:R:210:LYS:HZ3	17:R:210:LYS:HA	1.36	0.88
21:V:63:SER:OG	21:V:74:PHE:CE1	2.26	0.88
16:Q:212:ALA:HB3	17:R:237:ARG:HH21	1.36	0.88
21:V:63:SER:OG	21:V:74:PHE:CZ	2.26	0.88
1:A:928:ARG:HD2	1:A:1582:GLU:OE2	1.70	0.88
6:F:161:GLN:HG2	6:F:163:ILE:CG2	2.03	0.88
28:G:830:MET:O	28:G:832:LYS:N	2.06	0.88
25:a:147:TYR:CE2	25:a:163:HIS:O	2.26	0.88
1:A:342:LEU:HD13	1:A:392:ASN:HD21	1.36	0.88
1:A:1364:GLU:OE1	1:A:1403:SER:OG	1.91	0.88
8:I:57:TYR:CD1	8:I:70:LEU:HD13	2.09	0.88
23:Y:491:PRO:O	23:Y:494:CYS:CB	2.22	0.88
32:e:108:ALA:CB	32:e:155:PHE:O	2.22	0.88
1:A:614:ARG:HH11	1:A:614:ARG:HG2	1.39	0.88
1:A:1488:ILE:HG22	1:A:1489:PRO:HD3	1.55	0.88
11:L:41:C:H6	11:L:41:C:H5''	1.39	0.88
22:W:188:LEU:HD21	24:Z:415:GLN:HG2	1.53	0.88
20:U:38:LEU:HD22	21:V:46:ASP:OD1	1.74	0.87
16:Q:212:ALA:CB	17:R:237:ARG:NH2	2.12	0.87
1:A:1571:GLU:HB3	15:P:331:GLN:OE1	1.75	0.87
6:F:1116:ARG:HH22	6:F:1141:LEU:HD21	1.37	0.87
3:C:265:PHE:HE2	3:C:295:ILE:HG23	1.38	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:W:188:LEU:HG	24:Z:378:THR:CG2	2.04	0.87
1:A:1056:GLU:HB3	1:A:1059:GLU:HB2	1.56	0.87
5:E:38:U:O2	17:R:196:LYS:NZ	2.08	0.87
28:G:578:ILE:HG23	28:G:579:ILE:CD1	2.05	0.87
15:P:44:ILE:HD13	15:P:45:PRO:O	1.74	0.87
1:A:1295:GLN:HE21	24:Z:432:GLY:HA3	1.40	0.86
1:A:2412:PHE:O	1:A:2413:SER:OG	1.93	0.86
17:R:138:TYR:CE1	17:R:181:CYS:HB3	2.10	0.86
28:G:641:ASN:HD21	28:G:673:MET:HE1	1.40	0.86
9:J:3:ARG:NH1	28:G:901:GLU:OE2	2.09	0.86
22:W:190:ILE:O	22:W:192:ASP:N	2.07	0.86
1:A:1458:TRP:CD2	28:G:25:ILE:HG22	2.11	0.86
11:L:5:A:C5'	33:f:114:THR:HG21	2.05	0.86
1:A:854:ARG:HG2	1:A:854:ARG:HH21	1.41	0.86
24:Z:459:ARG:O	24:Z:463:ASN:CG	2.18	0.85
28:G:213:LEU:HD13	28:G:218:ARG:HB2	1.58	0.85
25:a:173:LYS:HD3	25:a:175:ASN:HD21	1.41	0.85
25:a:174:LEU:HD21	25:a:176:GLN:HE21	1.41	0.85
1:A:1608:LEU:HD11	1:A:1648:ILE:HD11	1.59	0.85
4:D:165:A:C2	42:m:2:LYS:HE3	2.10	0.85
16:Q:91:ILE:CG2	16:Q:125:ILE:HD12	2.04	0.85
1:A:299:LYS:HA	1:A:493:MET:HG3	1.58	0.85
1:A:610:ARG:NH2	12:N:101:U:OP2	2.10	0.84
3:C:274:ILE:HD13	3:C:385:PHE:CE2	2.11	0.84
1:A:2403:GLU:N	1:A:2403:GLU:OE2	2.09	0.84
1:A:978:ILE:HG22	18:S:174:VAL:HA	1.58	0.84
11:L:5:A:H5'	33:f:114:THR:CG2	2.06	0.84
23:Y:626:LEU:HD13	23:Y:650:GLU:HA	1.57	0.84
24:Z:178:ARG:HG3	24:Z:198:PHE:HE2	1.38	0.84
32:e:169:ASN:O	32:e:170:ASN:CB	2.24	0.84
2:B:2084:LEU:HD11	2:B:2120:ASN:HA	1.57	0.84
6:F:257:ILE:HD11	10:K:74:SER:HB2	1.60	0.84
29:d:117:HIS:CA	29:d:120:ASN:ND2	2.41	0.84
1:A:856:TRP:CD1	18:S:174:VAL:HG11	2.13	0.84
25:a:233:CYS:HB2	25:a:237:HIS:H	1.41	0.84
1:A:1876:ASN:OD1	1:A:1895:HIS:HD2	1.61	0.83
14:O:354:ASN:ND2	14:O:369:ASP:OD1	2.11	0.83
31:v:730:GLN:HA	31:v:733:ILE:CD1	2.07	0.83
3:C:265:PHE:CE2	3:C:295:ILE:HG23	2.12	0.83
29:d:141:ILE:HD11	33:f:105:TYR:HA	1.59	0.83
31:v:726:ARG:NH2	31:v:761:UNK:CB	2.41	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:505:A:O4'	13:M:505:A:OP1	1.96	0.83
27:c:213:TYR:CD1	29:d:55:GLU:OE1	2.31	0.83
35:t:114:LEU:O	35:t:117:VAL:HG12	1.78	0.83
32:e:147:LYS:O	32:e:149:LYS:N	2.11	0.83
34:q:51:VAL:HG13	34:r:20:ARG:CB	2.09	0.83
1:A:770:MET:HE1	15:P:165:ILE:HD11	1.58	0.83
16:Q:209:ASN:ND2	16:Q:288:ILE:O	2.12	0.83
3:C:265:PHE:HE2	3:C:295:ILE:HG21	1.17	0.83
17:R:22:ILE:HG22	17:R:30:PHE:CZ	2.13	0.83
17:R:146:LEU:HD21	17:R:211:GLU:OE1	1.76	0.83
24:Z:149:ARG:NH1	24:Z:193:SER:HB3	1.94	0.83
27:c:228:TYR:O	27:c:229:ASP:OD1	1.97	0.83
5:E:21:U:OP2	36:n:54:SER:OG	1.96	0.83
28:G:904:GLU:CD	28:G:940:ASN:HB3	2.03	0.83
16:Q:217:TRP:CE2	17:R:187:LYS:HD3	2.14	0.82
10:K:22:GLY:HA3	28:G:935:TRP:CZ3	2.14	0.82
23:Y:526:SER:O	23:Y:535:GLN:CG	2.26	0.82
1:A:997:GLN:NE2	1:A:1511:ARG:HH22	1.77	0.82
6:F:185:ARG:HD3	28:G:946:GLN:OE1	1.80	0.82
5:E:87:U:O2	29:d:70:ARG:NH1	2.13	0.82
12:N:110:U:O2'	17:R:141:GLY:HA2	1.78	0.82
15:P:37:ASN:OD1	15:P:143:VAL:CG1	2.27	0.82
17:R:55:PRO:HB3	17:R:93:ILE:HD11	1.59	0.82
1:A:796:ASN:ND2	1:A:861:GLN:OE1	2.12	0.82
7:H:180:LYS:HA	7:H:180:LYS:CE	2.10	0.82
2:B:508:HIS:ND1	2:B:512:GLU:OE1	2.10	0.82
16:Q:226:LEU:HG	16:Q:227:LEU:HD23	1.59	0.82
1:A:1364:GLU:OE1	1:A:1403:SER:HB3	1.80	0.82
1:A:1742:ASP:H	1:A:1745:SER:HB3	1.45	0.82
24:Z:180:ILE:HG22	24:Z:186:LEU:HD21	1.62	0.82
1:A:775:ARG:O	1:A:779:ALA:N	2.12	0.82
24:Z:192:GLU:C	24:Z:195:GLU:OE2	2.22	0.82
31:v:724:VAL:O	31:v:727:GLU:CG	2.28	0.82
5:E:50:G:O2'	5:E:51:A:N7	2.12	0.81
28:G:881:MET:HG2	28:G:885:ILE:HD11	1.62	0.81
3:C:395:LYS:HB2	3:C:395:LYS:NZ	1.95	0.81
8:I:55:ASN:HD22	8:I:56:PRO:N	1.78	0.81
16:Q:209:ASN:ND2	16:Q:288:ILE:HG22	1.95	0.81
22:W:209:LEU:HD12	22:W:209:LEU:O	1.81	0.81
38:i:86:ASN:HD21	39:h:32:LYS:HD3	1.43	0.81
1:A:931:ALA:CA	1:A:934:ARG:HH12	1.92	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:433:LYS:HE2	2:B:914:SER:HA	1.62	0.81
2:B:696:SER:O	2:B:698:PHE:N	2.13	0.81
2:B:773:ASN:ND2	6:F:754:HIS:CE1	2.49	0.81
24:Z:192:GLU:OE1	24:Z:192:GLU:N	2.14	0.81
28:G:835:ILE:O	28:G:837:PHE:N	2.14	0.81
3:C:274:ILE:CG1	3:C:382:TYR:CE1	2.63	0.81
16:Q:256:SER:O	16:Q:259:GLY:N	2.14	0.81
20:U:40:LEU:HG	20:U:49:ALA:HB2	1.63	0.81
23:Y:702:SER:O	23:Y:706:LEU:N	2.14	0.81
16:Q:215:PRO:HG3	16:Q:217:TRP:CZ3	2.16	0.81
22:W:188:LEU:CD2	24:Z:415:GLN:HG2	2.10	0.81
1:A:777:LYS:HA	1:A:777:LYS:HZ2	1.46	0.81
1:A:143:ILE:HD12	1:A:570:GLN:HG2	1.62	0.81
1:A:194:HIS:CD2	15:P:122:LEU:HD22	2.16	0.81
15:P:303:TYR:HB3	15:P:307:PHE:HD2	1.45	0.81
1:A:309:SER:OG	1:A:475:ASP:HB3	1.79	0.81
24:Z:178:ARG:HA	24:Z:198:PHE:CZ	2.15	0.81
13:M:515:U:O2'	28:G:291:GLU:OE2	1.99	0.80
17:R:146:LEU:HD22	17:R:211:GLU:OE1	1.79	0.80
39:h:74:ARG:NH2	43:g:64:HIS:O	2.14	0.80
26:b:67:SER:HB2	26:b:96:ARG:HB3	1.63	0.80
34:o:20:ARG:CB	34:p:53:ILE:CG1	2.59	0.80
3:C:219:VAL:O	3:C:222:MET:HG2	1.80	0.80
28:G:435:THR:HG21	28:G:467:VAL:HG21	1.62	0.80
15:P:41:ASP:O	15:P:44:ILE:HG22	1.81	0.80
24:Z:178:ARG:CB	24:Z:198:PHE:CZ	2.64	0.80
2:B:762:ALA:HA	2:B:766:ILE:HD11	1.64	0.80
8:I:57:TYR:CE1	8:I:70:LEU:HD11	2.15	0.80
15:P:241:LEU:O	15:P:245:SER:CB	2.30	0.80
16:Q:207:LEU:HB2	16:Q:249:GLY:O	1.81	0.80
1:A:342:LEU:HD13	1:A:392:ASN:ND2	1.95	0.80
34:q:257:LEU:HD13	34:q:277:LEU:CG	2.10	0.80
31:v:730:GLN:O	31:v:733:ILE:HD12	1.81	0.80
16:Q:222:THR:HA	16:Q:225:GLN:NE2	1.96	0.80
34:q:369:PHE:O	34:q:370:PRO:CB	2.30	0.80
2:B:2102:VAL:HB	2:B:2143:TRP:HB2	1.62	0.80
6:F:886:PHE:HE2	6:F:1225:VAL:HG21	1.46	0.80
16:Q:209:ASN:ND2	16:Q:209:ASN:O	2.15	0.80
16:Q:217:TRP:CH2	17:R:187:LYS:CD	2.64	0.80
31:v:724:VAL:HA	31:v:727:GLU:CG	2.12	0.80
1:A:1846:ASN:O	1:A:1847:ASP:O	1.99	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:174:G:H5'	43:g:99:ASP:OD2	1.82	0.80
34:q:178:LYS:HB3	34:q:468:GLN:CB	2.12	0.80
16:Q:214:ILE:HD11	16:Q:218:LYS:HG2	1.62	0.79
6:F:590:HIS:HE1	6:F:637:SER:HB3	1.47	0.79
28:G:338:GLN:HG3	28:G:377:THR:HG22	1.63	0.79
32:e:148:LEU:O	32:e:149:LYS:CB	2.26	0.79
1:A:253:GLN:O	1:A:257:ASN:ND2	2.15	0.79
1:A:1668:ILE:HD13	1:A:1801:SER:HB2	1.62	0.79
32:e:108:ALA:HB1	32:e:155:PHE:O	1.82	0.79
6:F:441:PHE:HB3	6:F:475:LEU:HD23	1.63	0.79
22:W:189:THR:HG22	22:W:195:ILE:HD11	1.63	0.79
1:A:777:LYS:HA	1:A:777:LYS:NZ	1.96	0.79
6:F:1125:ASP:HB3	6:F:1128:THR:HG22	1.64	0.79
16:Q:69:ASN:HB2	16:Q:123:ALA:HB1	1.63	0.79
17:R:210:LYS:HA	17:R:210:LYS:NZ	1.96	0.79
24:Z:152:ILE:CD1	24:Z:194:LEU:HA	2.12	0.79
1:A:238:ARG:CB	1:A:238:ARG:HH11	1.96	0.79
19:T:121:ILE:HD11	19:T:129:LEU:HD21	1.65	0.79
20:U:52:HIS:HE1	20:U:103:CYS:SG	2.06	0.79
24:Z:180:ILE:O	24:Z:184:GLN:HB2	1.82	0.79
6:F:364:THR:OG1	6:F:384:ASN:ND2	2.14	0.79
24:Z:460:TYR:HA	24:Z:463:ASN:HD22	1.47	0.79
1:A:147:SER:OG	1:A:573:ARG:NH2	2.15	0.79
8:I:53:ARG:NH2	8:I:58:ILE:O	2.16	0.79
28:G:587:THR:HG22	28:G:594:MET:HE3	1.63	0.79
3:C:265:PHE:CD2	3:C:295:ILE:HG21	2.17	0.78
3:C:391:MET:HE2	3:C:395:LYS:HE2	1.65	0.78
5:E:42:A:N1	17:R:38:SER:O	2.17	0.78
19:T:54:GLN:HG3	36:n:69:TRP:CD2	2.18	0.78
16:Q:226:LEU:HD21	16:Q:262:PHE:CE1	2.19	0.78
17:R:7:LYS:O	17:R:61:LYS:N	2.14	0.78
20:U:36:GLY:O	20:U:40:LEU:HB2	1.83	0.78
25:a:162:LEU:O	25:a:163:HIS:HB2	1.83	0.78
34:q:257:LEU:HD21	34:q:279:GLU:CG	2.14	0.78
17:R:46:ARG:NH2	17:R:220:GLY:O	2.15	0.78
1:A:1041:VAL:HG11	1:A:1253:LYS:HA	1.66	0.78
13:M:500:A:C8	13:M:500:A:H5'	2.19	0.78
24:Z:152:ILE:HD13	24:Z:194:LEU:HA	1.64	0.78
26:b:41:MET:SD	26:b:68:THR:OG1	2.41	0.78
29:d:141:ILE:HD13	33:f:108:THR:OG1	1.84	0.78
32:e:143:LEU:O	32:e:145:ASN:N	2.16	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:P:318:ARG:HA	22:W:261:THR:HG22	1.65	0.78
1:A:1034:ASN:ND2	28:G:20:GLY:HA2	1.98	0.78
1:A:2018:ASN:CG	1:A:2021:SER:HG	1.91	0.78
1:A:525:LEU:HD12	1:A:686:ILE:CD1	2.14	0.78
16:Q:209:ASN:HD22	16:Q:288:ILE:HG22	1.48	0.78
22:W:190:ILE:C	22:W:192:ASP:H	1.92	0.78
24:Z:178:ARG:HG3	24:Z:198:PHE:CZ	2.17	0.78
17:R:15:GLU:O	17:R:18:LEU:HD12	1.84	0.77
20:U:51:LYS:HG3	20:U:52:HIS:N	1.99	0.77
32:e:116:ALA:O	32:e:118:SER:N	2.16	0.77
1:A:1485:ASP:O	1:A:1490:ARG:NH2	2.17	0.77
6:F:676:PRO:HB3	6:F:693:ILE:HD11	1.66	0.77
13:M:514:U:H4'	13:M:515:U:C5'	2.13	0.77
24:Z:197:LEU:HD12	24:Z:197:LEU:O	1.84	0.77
29:d:117:HIS:C	29:d:120:ASN:ND2	2.42	0.77
10:K:44:GLN:NE2	10:K:70:LEU:HD21	1.98	0.77
16:Q:91:ILE:CG2	16:Q:125:ILE:CD1	2.61	0.77
4:D:41:A:N6	4:D:78:A:H2'	2.00	0.77
13:M:500:A:H5'	13:M:500:A:H8	1.48	0.77
17:R:207:PRO:O	17:R:212:TRP:CE2	2.37	0.77
23:Y:299:GLY:HA3	23:Y:311:LYS:HE3	1.67	0.77
3:C:105:ILE:O	3:C:180:ASN:ND2	2.18	0.77
24:Z:170:HIS:NE2	24:Z:174:TRP:CZ3	2.51	0.77
1:A:614:ARG:NH1	12:N:98:A:H5''	2.00	0.77
2:B:656:TRP:HE1	2:B:928:ASN:HB3	1.46	0.77
1:A:525:LEU:HD12	1:A:686:ILE:HD11	1.65	0.77
1:A:1073:ILE:HG23	1:A:1074:VAL:HG23	1.66	0.77
3:C:607:LEU:HD22	3:C:668:ILE:HD12	1.67	0.77
28:G:464:CYS:O	28:G:470:ILE:HD11	1.84	0.77
6:F:719:GLN:HG2	6:F:762:PHE:HD2	1.50	0.77
7:H:176:TRP:O	7:H:177:GLN:HG2	1.83	0.77
11:L:19:U:O2	15:P:175:PRO:HD2	1.84	0.77
2:B:1820:ILE:HG22	2:B:1846:THR:HG22	1.66	0.77
1:A:1509:ARG:HH12	1:A:1533:ASP:CG	1.93	0.76
17:R:3:SER:O	17:R:7:LYS:CD	2.33	0.76
18:S:9:LEU:HD23	18:S:11:ALA:N	1.99	0.76
26:b:11:ALA:HB3	26:b:26:LEU:HB2	1.66	0.76
1:A:1561:LEU:CD1	1:A:1608:LEU:HD22	2.16	0.76
10:K:42:THR:HG21	28:G:950:VAL:HG21	1.67	0.76
17:R:145:ALA:HB2	17:R:204:LEU:HD12	1.65	0.76
28:G:539:HIS:O	28:G:543:ARG:HG3	1.85	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:132:ARG:NH2	41:l:13:GLU:O	2.17	0.76
6:F:324:ASN:OD1	6:F:341:ASN:ND2	2.19	0.76
1:A:742:VAL:CG1	14:O:224:LEU:HD23	2.16	0.76
23:Y:258:GLN:HE21	23:Y:290:VAL:HG13	1.48	0.76
24:Z:168:LYS:NZ	24:Z:171:ASP:HB2	1.99	0.76
29:d:117:HIS:HA	29:d:120:ASN:HD21	1.47	0.76
29:d:141:ILE:HD11	33:f:105:TYR:CD1	2.20	0.76
1:A:1093:LYS:NZ	11:L:27:A:OP1	2.19	0.76
1:A:1403:SER:OG	1:A:1429:MET:SD	2.43	0.76
2:B:1674:ALA:HB3	2:B:1709:LEU:HD13	1.67	0.76
28:G:632:LYS:HD2	28:G:672:VAL:HG13	1.65	0.76
1:A:1057:MET:HE2	1:A:1114:PHE:CE1	2.21	0.76
17:R:206:LEU:HG	17:R:207:PRO:CD	2.16	0.76
28:G:778:ARG:NH1	28:G:811:ASN:OD1	2.18	0.76
1:A:2018:ASN:CG	1:A:2021:SER:OG	2.29	0.76
17:R:8:SER:HA	17:R:61:LYS:O	1.85	0.76
24:Z:181:LEU:HG	24:Z:194:LEU:CD1	2.14	0.76
24:Z:192:GLU:CB	24:Z:195:GLU:OE2	2.33	0.76
16:Q:221:ASP:C	16:Q:225:GLN:HE21	1.93	0.76
18:S:9:LEU:CD2	18:S:11:ALA:HB3	2.14	0.76
20:U:52:HIS:CE1	20:U:103:CYS:SG	2.79	0.76
7:H:180:LYS:HA	7:H:180:LYS:HE3	1.67	0.75
9:J:7:ASP:OD1	9:J:8:LEU:HD23	1.86	0.75
16:Q:217:TRP:CZ3	17:R:187:LYS:HD3	2.20	0.75
22:W:215:TYR:CE2	22:W:232:TRP:HE3	2.04	0.75
24:Z:178:ARG:CG	24:Z:198:PHE:CE2	2.67	0.75
29:d:113:LYS:HG3	33:f:161:VAL:CG1	2.14	0.75
31:v:726:ARG:HH22	31:v:761:UNK:CB	1.98	0.75
6:F:236:VAL:HG13	6:F:257:ILE:HG23	1.65	0.75
10:K:32:GLN:NE2	28:G:960:ASN:HB3	2.02	0.75
15:P:178:TYR:OH	33:f:203:PHE:CZ	2.35	0.75
16:Q:202:THR:HA	16:Q:252:ARG:HG3	1.68	0.75
22:W:214:LEU:HD21	22:W:227:MET:CB	2.16	0.75
1:A:216:GLN:O	1:A:220:THR:HG23	1.86	0.75
1:A:782:ILE:O	1:A:782:ILE:HD12	1.87	0.75
1:A:1325:SER:O	1:A:1331:VAL:HG21	1.86	0.75
1:A:525:LEU:CD1	1:A:686:ILE:HD12	2.17	0.75
23:Y:626:LEU:HD11	23:Y:650:GLU:CB	2.17	0.75
7:H:288:HIS:C	7:H:289:LYS:HG3	2.10	0.75
2:B:2022:LEU:HB2	2:B:2027:ARG:HE	1.52	0.75
6:F:611:VAL:HG21	6:F:621:LYS:HE2	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:e:33:ASN:CB	32:e:62:ASP:OD2	2.35	0.75
1:A:1335:TRP:CH2	1:A:1364:GLU:HG3	2.21	0.75
2:B:1370:SER:HB3	2:B:1376:LYS:HD3	1.68	0.75
1:A:1846:ASN:O	1:A:1847:ASP:C	2.30	0.74
1:A:2408:GLN:HE21	1:A:2408:GLN:HA	1.52	0.74
5:E:67:C:H6	5:E:67:C:H5"	1.51	0.74
6:F:886:PHE:CE2	6:F:1225:VAL:HG21	2.22	0.74
7:H:183:LEU:HD22	7:H:188:LEU:HD11	1.68	0.74
16:Q:215:PRO:HG3	16:Q:217:TRP:CH2	2.21	0.74
1:A:1835:LEU:HD11	1:A:1836:ASN:ND2	2.02	0.74
2:B:766:ILE:HG22	2:B:767:THR:H	1.50	0.74
21:V:63:SER:HB3	21:V:74:PHE:CD1	2.22	0.74
22:W:215:TYR:CE2	22:W:232:TRP:CE3	2.75	0.74
27:c:230:THR:HG21	29:d:117:HIS:CE1	2.21	0.74
27:c:230:THR:HG21	29:d:117:HIS:CG	2.22	0.74
1:A:143:ILE:HD12	1:A:570:GLN:CG	2.17	0.74
3:C:219:VAL:HG21	3:C:929:GLN:HB3	1.68	0.74
6:F:641:GLN:HE21	6:F:653:TYR:HE1	1.35	0.74
24:Z:310:HIS:CD2	30:X:23:SER:HA	2.22	0.74
25:a:216:HIS:HE1	25:a:235:ILE:CB	1.97	0.74
27:c:237:ILE:HD11	29:d:114:CYS:SG	2.28	0.74
6:F:957:ILE:HG22	6:F:962:LEU:HD11	1.69	0.74
11:L:16:U:O4	33:f:202:GLN:HB3	1.87	0.74
1:A:1034:ASN:HD22	28:G:20:GLY:H	1.34	0.74
2:B:901:VAL:HG22	2:B:906:LEU:HD22	1.68	0.74
3:C:395:LYS:HB2	3:C:395:LYS:HZ2	1.51	0.74
31:v:669:TYR:HE2	31:v:686:ILE:HG13	1.53	0.74
1:A:936:GLU:HG2	1:A:986:PRO:HB3	1.69	0.74
17:R:22:ILE:HG22	17:R:30:PHE:CE2	2.22	0.74
24:Z:178:ARG:CA	24:Z:198:PHE:HZ	1.99	0.74
1:A:431:ILE:HG23	24:Z:182:GLN:HG2	1.70	0.74
15:P:319:HIS:HE1	22:W:264:GLU:CD	1.96	0.74
17:R:87:CYS:HB3	17:R:91:HIS:HE1	1.53	0.74
1:A:1034:ASN:HD22	28:G:20:GLY:N	1.84	0.74
1:A:1286:TRP:NE1	1:A:1348:GLU:OE1	2.21	0.74
6:F:161:GLN:HG2	6:F:163:ILE:HG22	1.70	0.74
22:W:188:LEU:HG	24:Z:378:THR:HG22	1.70	0.74
25:a:168:PHE:HA	25:a:169:LYS:NZ	2.03	0.74
1:A:2287:ASP:O	1:A:2288:CYS:O	2.05	0.73
23:Y:247:GLU:OE1	23:Y:402:ARG:CG	2.36	0.73
15:P:196:THR:HA	27:c:90:MET:HE1	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:14:LYS:N	17:R:14:LYS:HE3	2.03	0.73
31:v:729:TYR:CD2	31:v:749:UNK:CB	2.72	0.73
2:B:636:ILE:HG22	2:B:671:SER:HB2	1.68	0.73
3:C:177:TYR:CE1	3:C:548:ARG:CD	2.71	0.73
1:A:930:ASN:O	1:A:934:ARG:NH1	2.22	0.73
2:B:1387:HIS:NE2	2:B:1393:GLY:O	2.20	0.73
6:F:78:HIS:NE2	6:F:81:ASP:OD1	2.21	0.73
34:q:173:LYS:O	34:q:174:TRP:CB	2.36	0.73
15:P:241:LEU:O	15:P:245:SER:HB2	1.88	0.73
29:d:113:LYS:HG2	29:d:113:LYS:O	1.86	0.73
1:A:268:LEU:HD23	1:A:268:LEU:O	1.88	0.73
7:H:198:ASP:OD1	7:H:199:ILE:N	2.21	0.73
20:U:25:TYR:HB3	21:V:117:LYS:HG2	1.71	0.73
21:V:63:SER:CB	21:V:74:PHE:HE1	1.82	0.73
6:F:276:GLY:O	28:G:388:TYR:O	2.07	0.73
13:M:513:U:OP2	28:G:259:ARG:NH1	2.21	0.73
1:A:1163:ARG:HG2	1:A:1163:ARG:HH11	1.53	0.73
24:Z:174:TRP:CH2	24:Z:197:LEU:HD11	2.23	0.73
1:A:1836:ASN:ND2	1:A:2006:SER:HG	1.87	0.72
6:F:105:ASP:HB2	6:F:114:ILE:HD11	1.71	0.72
1:A:1034:ASN:HD22	28:G:20:GLY:CA	2.02	0.72
3:C:100:LEU:HD21	3:C:479:GLY:C	2.14	0.72
6:F:547:ASN:HA	6:F:563:ILE:O	1.90	0.72
2:B:514:ASP:OD1	2:B:537:LYS:NZ	2.20	0.72
6:F:1124:LEU:HB2	6:F:1130:ILE:HD11	1.69	0.72
6:F:1222:GLN:NE2	10:K:48:ALA:CA	2.51	0.72
16:Q:101:THR:CG2	16:Q:120:LEU:CD2	2.65	0.72
16:Q:207:LEU:O	16:Q:248:CYS:HA	1.89	0.72
29:d:144:GLU:OE1	33:f:109:LEU:CD2	2.37	0.72
1:A:854:ARG:NE	11:L:25:A:OP1	2.22	0.72
6:F:379:VAL:HG22	6:F:391:LEU:HB2	1.70	0.72
1:A:2408:GLN:HE21	1:A:2408:GLN:CA	2.03	0.72
1:A:1843:LEU:HA	1:A:1849:LYS:HZ2	1.55	0.72
12:N:111:U:H4'	12:N:112:U:OP2	1.89	0.72
20:U:26:ILE:HB	20:U:29:MET:HE3	1.72	0.72
1:A:1305:SER:OG	1:A:1307:GLU:OE1	2.06	0.72
1:A:1861:THR:HG1	1:A:1863:HIS:HE2	1.36	0.72
3:C:348:LEU:HD12	3:C:372:THR:HG22	1.71	0.72
28:G:222:ILE:HG23	28:G:265:ILE:HD11	1.71	0.72
32:e:82:LYS:O	32:e:83:VAL:CB	2.37	0.72
38:i:86:ASN:HD21	39:h:32:LYS:CD	2.02	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1236:LEU:HD11	2:B:1258:PHE:HB3	1.71	0.72
6:F:186:ARG:NH2	10:K:38:ASP:OD1	2.22	0.72
6:F:396:ASP:HB2	6:F:404:LEU:HG	1.71	0.72
6:F:961:CYS:O	6:F:962:LEU:HD12	1.89	0.72
14:O:210:ASP:HB2	14:O:217:ILE:HG13	1.69	0.72
25:a:173:LYS:HD3	25:a:175:ASN:ND2	2.04	0.72
6:F:335:ILE:HD12	6:F:407:LEU:HD11	1.72	0.72
15:P:241:LEU:O	15:P:245:SER:N	2.21	0.72
22:W:171:GLY:C	22:W:172:ILE:HG12	2.13	0.72
24:Z:186:LEU:HD12	24:Z:186:LEU:N	2.05	0.72
24:Z:454:ASP:HB3	24:Z:457:HIS:HD2	1.53	0.72
23:Y:467:LYS:CB	23:Y:494:CYS:HA	2.19	0.72
28:G:587:THR:HB	28:G:630:VAL:HG21	1.70	0.72
1:A:269:ASP:OD1	1:A:271:GLN:N	2.22	0.71
2:B:699:ARG:NH1	2:B:701:CYS:O	2.22	0.71
2:B:1620:TYR:HD1	2:B:1651:ILE:HG23	1.55	0.71
1:A:238:ARG:HH11	1:A:238:ARG:HB3	1.56	0.71
1:A:1122:ASP:OD1	1:A:1161:TYR:CE2	2.43	0.71
14:O:259:VAL:HG12	14:O:260:ILE:HG13	1.72	0.71
17:R:23:PRO:O	17:R:37:TRP:NE1	2.23	0.71
24:Z:178:ARG:CA	24:Z:198:PHE:CZ	2.73	0.71
1:A:377:VAL:HG12	1:A:378:PRO:HD2	1.73	0.71
6:F:180:THR:HG21	6:F:188:SER:HB2	1.72	0.71
6:F:1222:GLN:HE22	10:K:48:ALA:HB2	1.55	0.71
1:A:570:GLN:O	1:A:574:GLN:HG2	1.89	0.71
3:C:265:PHE:CD2	3:C:295:ILE:HD13	2.26	0.71
6:F:104:TYR:OH	6:F:481:GLN:NE2	2.24	0.71
15:P:197:ILE:HG23	27:c:90:MET:HE2	1.71	0.71
21:V:63:SER:CB	21:V:74:PHE:CD1	2.70	0.71
23:Y:699:GLU:CG	23:Y:702:SER:CB	2.69	0.71
36:n:55:GLU:OE2	36:n:55:GLU:HA	1.91	0.71
36:n:55:GLU:OE2	36:n:58:ARG:CD	2.38	0.71
1:A:324:ASP:OD1	1:A:324:ASP:N	2.23	0.71
1:A:2052:GLU:O	1:A:2056:ARG:HB2	1.91	0.71
24:Z:181:LEU:HD21	24:Z:191:ARG:HG3	1.71	0.71
27:c:214:ASN:HD21	29:d:44:ARG:HD2	1.55	0.71
29:d:144:GLU:OE1	33:f:109:LEU:HD21	1.90	0.71
19:T:54:GLN:HE21	36:n:69:TRP:CD1	2.06	0.71
4:D:174:G:OP1	4:D:174:G:H4'	1.90	0.71
6:F:927:ARG:HG3	6:F:928:THR:HG23	1.72	0.71
6:F:932:PHE:HA	6:F:984:ILE:HD11	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:199:ILE:HG22	7:H:250:VAL:HG13	1.72	0.71
16:Q:226:LEU:C	16:Q:226:LEU:HD12	2.15	0.71
2:B:1583:VAL:HG22	2:B:1681:ILE:HB	1.72	0.71
21:V:48:LEU:O	22:W:231:ARG:CZ	2.39	0.71
23:Y:307:ARG:HE	23:Y:646:PRO:HB2	1.56	0.71
24:Z:170:HIS:CE1	24:Z:174:TRP:HE3	2.08	0.71
7:H:192:ARG:HB3	7:H:192:ARG:CZ	2.19	0.70
36:n:68:PRO:HD2	36:n:69:TRP:HE3	1.53	0.70
1:A:790:TRP:HE1	1:A:794:LYS:HE3	1.56	0.70
3:C:232:SER:OG	3:C:234:LEU:O	2.09	0.70
16:Q:259:GLY:O	16:Q:263:VAL:HG23	1.90	0.70
22:W:170:LEU:O	22:W:172:ILE:HG12	1.90	0.70
16:Q:69:ASN:CB	16:Q:123:ALA:HB1	2.20	0.70
29:d:189:TYR:HA	29:d:192:TYR:HB3	1.74	0.70
1:A:183:TRP:CZ2	1:A:216:GLN:OE1	2.45	0.70
1:A:1405:ILE:HG22	1:A:1406:LEU:H	1.56	0.70
19:T:120:CYS:CB	19:T:122:CYS:HB3	2.21	0.70
20:U:35:SER:OG	21:V:46:ASP:OD2	2.08	0.70
2:B:1605:ILE:HG22	2:B:1606:GLU:H	1.57	0.70
28:G:851:LEU:HD21	28:G:895:ALA:HB2	1.73	0.70
1:A:774:ILE:HG13	1:A:778:LYS:HD2	1.72	0.70
3:C:133:ILE:HG22	3:C:209:MET:HB3	1.73	0.70
3:C:465:GLU:CD	3:C:466:GLY:H	1.99	0.70
3:C:602:VAL:HG21	3:C:932:PHE:CE2	2.27	0.70
6:F:427:LEU:N	6:F:439:PHE:O	2.22	0.70
20:U:43:ASN:C	20:U:44:ASN:HD22	1.99	0.70
23:Y:220:ARG:O	23:Y:226:HIS:NE2	2.25	0.70
24:Z:191:ARG:NH1	24:Z:192:GLU:OE2	2.24	0.70
1:A:518:VAL:HG11	1:A:689:TYR:HD2	1.56	0.70
16:Q:226:LEU:CD2	16:Q:262:PHE:CE1	2.75	0.70
1:A:1362:LYS:NZ	30:X:13:GLY:O	2.24	0.70
9:J:6:PHE:HZ	28:G:897:MET:HE1	1.56	0.70
20:U:40:LEU:O	20:U:43:ASN:O	2.09	0.70
32:e:110:LEU:CG	32:e:153:VAL:HG13	2.21	0.70
9:J:102:GLU:OE1	9:J:103:LYS:N	2.25	0.70
28:G:550:THR:HG23	28:G:553:LEU:CD2	2.22	0.70
1:A:1130:ARG:HD3	1:A:1156:HIS:CD2	2.27	0.70
5:E:67:C:C2	5:E:82:A:C2	2.80	0.70
24:Z:310:HIS:HD2	30:X:23:SER:HA	1.54	0.70
26:b:52:PHE:HA	26:b:63:PHE:HB3	1.74	0.70
1:A:1054:LEU:HD21	1:A:1168:ILE:HD11	1.72	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1337:THR:HG21	15:P:321:ASP:HB3	1.73	0.69
2:B:673:THR:OG1	2:B:904:GLN:NE2	2.24	0.69
3:C:152:LEU:HD13	3:C:432:GLN:HE22	1.56	0.69
6:F:1170:VAL:HG12	6:F:1184:LYS:HD2	1.72	0.69
10:K:44:GLN:HE21	10:K:70:LEU:HD21	1.57	0.69
11:L:19:U:O4'	11:L:19:U:OP2	2.09	0.69
17:R:207:PRO:O	17:R:212:TRP:CD2	2.43	0.69
31:v:611:THR:CB	31:v:623:LEU:HD13	2.22	0.69
2:B:882:THR:HG23	6:F:686:GLN:HE22	1.57	0.69
24:Z:190:LEU:HD23	24:Z:190:LEU:C	2.18	0.69
4:D:173:U:H4'	4:D:174:G:OP1	1.91	0.69
15:P:34:ILE:HG13	29:d:123:ASN:HA	1.72	0.69
23:Y:280:ARG:NH2	23:Y:476:ALA:O	2.23	0.69
29:d:141:ILE:CD1	33:f:105:TYR:HA	2.21	0.69
3:C:780:PRO:HA	3:C:783:ILE:HB	1.74	0.69
7:H:141:VAL:CG1	7:H:165:CYS:SG	2.80	0.69
38:i:86:ASN:HD21	39:h:32:LYS:CE	2.06	0.69
6:F:384:ASN:O	6:F:415:ASN:ND2	2.18	0.69
20:U:50:LEU:CA	20:U:139:GLN:HE22	2.03	0.69
1:A:2014:ALA:HB3	1:A:2055:MET:HE3	1.74	0.69
2:B:1362:SER:O	2:B:1507:ARG:NH1	2.25	0.69
3:C:602:VAL:HG21	3:C:932:PHE:CD2	2.28	0.69
6:F:1073:LYS:HD2	6:F:1090:ILE:HD11	1.74	0.69
7:H:186:ARG:NH2	8:I:70:LEU:O	2.25	0.69
24:Z:174:TRP:CZ2	24:Z:197:LEU:CD1	2.75	0.69
24:Z:178:ARG:CG	24:Z:198:PHE:HZ	2.01	0.69
3:C:132:ARG:HH11	3:C:132:ARG:HG3	1.57	0.69
5:E:91:A:C6	29:d:99:ILE:HD11	2.27	0.69
7:H:180:LYS:HD3	7:H:184:SER:OG	1.92	0.69
20:U:43:ASN:O	20:U:44:ASN:ND2	2.20	0.69
23:Y:553:ALA:HB1	23:Y:559:GLY:HA3	1.75	0.69
23:Y:738:ARG:O	23:Y:742:ASN:CG	2.35	0.69
28:G:386:TYR:CG	28:G:387:PRO:HD3	2.27	0.69
31:v:601:VAL:O	31:v:604:SER:OG	2.09	0.69
2:B:1473:TYR:O	2:B:1511:LEU:N	2.25	0.69
4:D:174:G:N7	42:m:20:LYS:HE2	2.08	0.69
7:H:167:LYS:O	7:H:167:LYS:HD2	1.93	0.69
10:K:3:GLU:OE2	10:K:7:GLN:OE1	2.10	0.69
11:L:41:C:H6	11:L:41:C:C5'	2.05	0.69
14:O:263:VAL:HG13	18:S:11:ALA:HB2	1.74	0.69
15:P:301:LEU:HD11	15:P:303:TYR:CE1	2.27	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Q:209:ASN:ND2	16:Q:288:ILE:CG2	2.56	0.69
17:R:14:LYS:HE3	17:R:14:LYS:CA	2.23	0.69
17:R:142:ILE:HG21	17:R:180:ASN:ND2	2.07	0.69
27:c:229:ASP:CB	33:f:151:LYS:HB3	2.19	0.69
1:A:1057:MET:HG3	1:A:1239:THR:HG21	1.74	0.69
1:A:1843:LEU:N	1:A:1843:LEU:HD23	2.08	0.69
2:B:667:ILE:HG21	2:B:684:LEU:HD22	1.74	0.69
16:Q:34:CYS:SG	16:Q:61:CYS:N	2.65	0.69
18:S:9:LEU:HD21	18:S:11:ALA:CB	2.20	0.69
31:v:616:PRO:CG	31:v:617:PRO:N	2.55	0.69
1:A:1281:ASN:HD21	1:A:1285:VAL:HB	1.57	0.69
2:B:585:VAL:HG12	2:B:604:VAL:HB	1.74	0.69
6:F:97:THR:O	6:F:97:THR:OG1	2.07	0.69
32:e:147:LYS:O	32:e:147:LYS:CG	2.40	0.69
1:A:396:ARG:HH11	1:A:396:ARG:HG3	1.57	0.68
1:A:893:ARG:HG3	1:A:893:ARG:NH1	2.03	0.68
2:B:552:LEU:HB3	2:B:603:GLN:HE21	1.56	0.68
2:B:1139:MET:HE3	2:B:1143:ASN:HB2	1.73	0.68
2:B:1681:ILE:HG12	2:B:1721:LEU:HB3	1.75	0.68
3:C:236:LEU:HD21	3:C:435:LEU:HD11	1.75	0.68
14:O:433:THR:OG1	14:O:435:GLU:OE1	2.10	0.68
2:B:1689:ASP:HB2	2:B:1696:MET:HG2	1.76	0.68
3:C:219:VAL:CG1	3:C:931:TYR:HB3	2.22	0.68
4:D:175:G:C2	38:i:33:GLU:HG3	2.29	0.68
6:F:187:VAL:HG21	10:K:17:LYS:O	1.93	0.68
9:J:51:PHE:HD2	9:J:52:GLY:H	1.40	0.68
23:Y:626:LEU:HD11	23:Y:650:GLU:CA	2.24	0.68
1:A:1015:PRO:HG2	1:A:1510:ILE:HG12	1.76	0.68
2:B:1551:PHE:HE2	2:B:1563:MET:HA	1.57	0.68
6:F:816:MET:HE2	6:F:830:TYR:HB2	1.74	0.68
24:Z:177:LEU:HD21	24:Z:194:LEU:HD21	1.75	0.68
25:a:219:CYS:HB2	25:a:222:CYS:SG	2.33	0.68
28:G:61:GLU:OE2	28:G:68:ARG:NH2	2.21	0.68
1:A:1053:THR:HG22	1:A:1167:ARG:HD2	1.75	0.68
6:F:1222:GLN:NE2	10:K:48:ALA:HA	2.09	0.68
1:A:1935:VAL:HG11	1:A:1940:MET:HB2	1.75	0.68
28:G:22:GLN:OE1	28:G:22:GLN:HA	1.92	0.68
34:q:20:ARG:CB	34:r:53:ILE:HA	2.24	0.68
28:G:348:VAL:HG13	28:G:349:LEU:H	1.58	0.68
1:A:237:MET:HE1	1:A:635:THR:HG22	1.75	0.68
1:A:1056:GLU:OE2	1:A:1059:GLU:OE1	2.12	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:990:ASP:OD2	2:B:993:ASN:ND2	2.26	0.68
3:C:412:ALA:HA	3:C:415:TYR:CE2	2.29	0.68
16:Q:34:CYS:HB3	16:Q:36:ILE:H	1.58	0.68
16:Q:69:ASN:ND2	16:Q:126:THR:HB	2.08	0.68
1:A:1561:LEU:HD11	1:A:1608:LEU:HD22	1.74	0.68
6:F:600:ILE:HD13	6:F:642:LEU:HD13	1.75	0.68
6:F:1096:LEU:HD13	6:F:1187:PHE:HZ	1.58	0.68
7:H:185:GLY:HA3	8:I:72:ASN:HD21	1.59	0.68
1:A:1286:TRP:CD1	1:A:1448:GLU:HG3	2.29	0.68
1:A:1618:ASN:CB	1:A:1744:ASP:OD2	2.30	0.68
16:Q:210:ILE:HG22	16:Q:211:ASP:O	1.93	0.68
20:U:38:LEU:HD23	21:V:49:THR:HG21	1.75	0.68
24:Z:190:LEU:HD23	24:Z:191:ARG:N	2.09	0.68
28:G:464:CYS:O	28:G:470:ILE:CD1	2.41	0.68
1:A:1829:SER:O	1:A:1830:VAL:HG22	1.94	0.68
2:B:1822:ILE:HG12	2:B:1844:ILE:HG12	1.75	0.68
6:F:363:VAL:O	6:F:364:THR:HG23	1.94	0.68
9:J:6:PHE:CZ	28:G:897:MET:HE1	2.29	0.68
14:O:217:ILE:HG22	14:O:218:ARG:HG3	1.75	0.68
1:A:518:VAL:HG12	1:A:685:HIS:HB3	1.76	0.67
1:A:2262:GLN:HG2	1:A:2264:GLU:H	1.60	0.67
2:B:1638:GLY:HA3	2:B:1664:LEU:HD12	1.75	0.67
4:D:174:G:C5'	43:g:99:ASP:HB2	2.25	0.67
5:E:28:U:H1'	16:Q:51:ARG:NH2	2.10	0.67
6:F:728:MET:HE3	6:F:741:LEU:HD11	1.76	0.67
9:J:41:ARG:NH1	9:J:82:ASP:OD2	2.26	0.67
15:P:84:ASN:O	15:P:125:ARG:NH1	2.27	0.67
26:b:67:SER:HB3	26:b:71:TYR:HD1	1.59	0.67
1:A:237:MET:CE	1:A:635:THR:HG22	2.24	0.67
5:E:85:C:O4'	5:E:85:C:OP1	2.12	0.67
6:F:783:ILE:HG13	6:F:784:SER:H	1.58	0.67
7:H:188:LEU:HD13	28:G:849:ARG:HB2	1.74	0.67
26:b:38:PHE:HD2	26:b:39:LEU:HD12	1.60	0.67
5:E:51:A:OP1	27:c:169:ARG:NH2	2.27	0.67
8:I:53:ARG:HB3	8:I:53:ARG:HH11	1.58	0.67
16:Q:79:ARG:HD2	16:Q:126:THR:HG23	1.73	0.67
2:B:1057:LEU:HD21	2:B:1089:PHE:HE1	1.59	0.67
6:F:594:MET:O	6:F:598:SER:OG	2.13	0.67
6:F:884:ASN:OD1	6:F:885:TRP:N	2.26	0.67
12:N:114:U:OP1	17:R:174:ARG:NH2	2.27	0.67
1:A:769:MET:CE	1:A:811:ILE:HD12	2.05	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:343:ASP:O	3:C:347:ARG:HG2	1.93	0.67
6:F:1165:LYS:HE2	32:e:34:PRO:HG3	1.76	0.67
24:Z:364:THR:O	24:Z:368:ASN:ND2	2.26	0.67
31:v:509:UNK:O	31:v:513:UNK:N	2.27	0.67
34:q:306:ASP:CG	34:q:308:ARG:H	2.03	0.67
1:A:1034:ASN:HD22	28:G:20:GLY:HA2	1.59	0.67
1:A:1843:LEU:HA	1:A:1849:LYS:NZ	2.10	0.67
6:F:1116:ARG:NH2	6:F:1141:LEU:HD21	2.10	0.67
14:O:230:VAL:HG22	14:O:241:THR:HG22	1.75	0.67
16:Q:69:ASN:HD21	16:Q:126:THR:HG21	1.59	0.67
17:R:172:ARG:HH22	17:R:237:ARG:NH1	1.92	0.67
24:Z:167:LYS:NZ	24:Z:171:ASP:OD2	2.26	0.67
27:c:73:LEU:HD21	27:c:102:TYR:HB2	1.76	0.67
1:A:1335:TRP:CZ2	1:A:1364:GLU:HG3	2.30	0.67
1:A:1829:SER:C	1:A:1830:VAL:HG13	2.20	0.67
2:B:487:CYS:HB2	2:B:536:LEU:HD13	1.76	0.67
2:B:1455:LEU:O	2:B:1462:ARG:NH1	2.28	0.67
20:U:108:ARG:NH1	20:U:136:SER:O	2.28	0.67
29:d:119:ARG:HH22	29:d:146:LEU:HD13	1.60	0.67
34:o:51:VAL:HG11	34:p:20:ARG:CB	2.25	0.67
42:m:82:LEU:HD12	42:m:85:ILE:HD11	1.77	0.67
1:A:1064:THR:HG22	27:c:81:PRO:HD2	1.77	0.67
2:B:1141:PRO:O	2:B:1299:HIS:NE2	2.27	0.67
3:C:752:ARG:HD3	3:C:759:SER:HA	1.76	0.67
25:a:174:LEU:HD21	25:a:176:GLN:NE2	2.08	0.67
26:b:103:VAL:HG12	26:b:104:LEU:H	1.59	0.67
1:A:1322:ALA:O	1:A:1323:SER:CB	2.41	0.67
3:C:100:LEU:HD21	3:C:480:GLY:N	2.10	0.67
6:F:639:LYS:HB3	6:F:686:GLN:HA	1.77	0.67
7:H:185:GLY:O	7:H:188:LEU:N	2.28	0.67
20:U:76:THR:HG1	20:U:205:HIS:HE2	1.43	0.67
23:Y:626:LEU:CD1	23:Y:650:GLU:CA	2.72	0.67
1:A:525:LEU:CD1	1:A:686:ILE:CD1	2.73	0.67
3:C:100:LEU:HD13	3:C:108:GLN:OE1	1.95	0.67
3:C:135:ASN:ND2	3:C:559:GLY:O	2.26	0.67
11:L:57:A:OP1	28:G:928:LYS:HB3	1.95	0.67
16:Q:214:ILE:CD1	16:Q:218:LYS:HG2	2.25	0.67
32:e:161:ALA:O	32:e:165:ILE:HG12	1.95	0.67
34:o:20:ARG:CB	34:p:53:ILE:CA	2.72	0.67
6:F:180:THR:O	9:J:83:LYS:HD2	1.94	0.66
15:P:202:MET:SD	27:c:79:GLU:HG3	2.35	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:c:218:VAL:HG21	29:d:55:GLU:OE2	1.95	0.66
39:h:74:ARG:NH1	43:g:65:CYS:SG	2.66	0.66
1:A:763:MET:CE	1:A:779:ALA:HB1	2.26	0.66
1:A:1197:ASN:ND2	1:A:1221:ASN:OD1	2.27	0.66
3:C:251:GLN:HE21	3:C:255:GLN:HE21	1.43	0.66
19:T:133:ALA:O	19:T:137:GLY:N	2.29	0.66
24:Z:178:ARG:HB2	24:Z:198:PHE:HZ	1.60	0.66
25:a:138:ASP:O	25:a:140:GLN:N	2.28	0.66
1:A:978:ILE:CG2	18:S:174:VAL:HA	2.26	0.66
2:B:1466:GLN:HB2	2:B:1502:LEU:HD11	1.76	0.66
3:C:365:GLU:HG3	3:C:366:ASN:H	1.60	0.66
17:R:9:ALA:HB1	17:R:58:HIS:O	1.96	0.66
17:R:54:GLN:H	17:R:58:HIS:HD2	1.40	0.66
20:U:83:TYR:HB3	20:U:88:LYS:HG2	1.77	0.66
1:A:763:MET:HE2	1:A:779:ALA:HB1	1.78	0.66
1:A:854:ARG:HH21	1:A:854:ARG:CG	2.09	0.66
13:M:506:U:OP2	28:G:698:ARG:HD3	1.94	0.66
16:Q:101:THR:CB	16:Q:120:LEU:HD11	2.22	0.66
22:W:186:SER:C	22:W:190:ILE:HD12	2.20	0.66
6:F:387:ASP:HA	6:F:412:THR:HG22	1.76	0.66
28:G:359:ILE:HG21	28:G:378:LEU:HD21	1.78	0.66
1:A:1050:LEU:HD23	1:A:1248:VAL:HG22	1.77	0.66
21:V:57:PRO:HG2	22:W:231:ARG:HH21	1.61	0.66
31:v:709:TRP:HA	31:v:712:CYS:SG	2.35	0.66
34:q:20:ARG:CB	34:r:52:GLU:O	2.43	0.66
3:C:803:VAL:HG13	3:C:813:ILE:HB	1.76	0.66
4:D:60:U:H3'	4:D:60:U:O2	1.95	0.66
14:O:134:VAL:HG22	14:O:424:LYS:HG2	1.78	0.66
16:Q:226:LEU:HD21	16:Q:262:PHE:HD1	1.57	0.66
17:R:146:LEU:HD23	17:R:147:ASN:N	2.10	0.66
34:q:257:LEU:HD23	34:q:279:GLU:CG	2.26	0.66
17:R:210:LYS:HA	17:R:210:LYS:CE	2.25	0.66
34:q:348:TYR:CB	34:q:377:ILE:CB	2.74	0.66
2:B:880:TYR:O	6:F:686:GLN:CD	2.38	0.66
2:B:1541:ILE:HG13	2:B:1542:GLU:HG3	1.78	0.66
6:F:71:PHE:HE2	6:F:481:GLN:HE22	1.42	0.66
6:F:184:LEU:O	28:G:947:ASP:OD2	2.13	0.66
15:P:319:HIS:CD2	15:P:320:GLU:H	2.13	0.66
23:Y:251:GLY:HA2	47:Y:902:ADP:H5'2	1.78	0.66
1:A:1172:PHE:HZ	1:A:1230:ILE:HD11	1.60	0.66
1:A:1365:THR:O	1:A:1369:ASN:ND2	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2050:ASN:ND2	2:B:2078:ASP:OD1	2.29	0.66
5:E:67:C:H6	5:E:67:C:C5'	2.07	0.66
24:Z:168:LYS:HZ3	24:Z:171:ASP:HB2	1.61	0.66
1:A:978:ILE:HG22	18:S:173:HIS:O	1.97	0.65
1:A:1067:ASN:O	1:A:1071:ARG:HG2	1.96	0.65
2:B:134:ASP:CG	2:B:752:ARG:HH22	2.04	0.65
2:B:988:LEU:HB2	2:B:997:GLU:HB3	1.78	0.65
3:C:274:ILE:HD13	3:C:385:PHE:HE2	1.60	0.65
6:F:161:GLN:O	6:F:163:ILE:HG23	1.96	0.65
6:F:165:HIS:HB3	6:F:170:ARG:HD3	1.78	0.65
6:F:943:ASP:HB2	6:F:952:ARG:HG2	1.76	0.65
16:Q:69:ASN:HD21	16:Q:126:THR:CG2	2.08	0.65
34:q:463:SER:O	34:q:464:ALA:HB3	1.96	0.65
6:F:290:PRO:HB2	10:K:80:TYR:CE1	2.31	0.65
23:Y:438:ILE:HA	23:Y:515:TYR:HB2	1.78	0.65
32:e:108:ALA:HB3	32:e:155:PHE:O	1.95	0.65
1:A:299:LYS:HA	1:A:493:MET:CG	2.26	0.65
3:C:500:ARG:NH1	3:C:534:THR:OG1	2.29	0.65
6:F:446:VAL:HG21	6:F:453:ASN:HD21	1.61	0.65
8:I:62:HIS:NE2	28:G:848:ASP:OD1	2.28	0.65
1:A:859:ASN:ND2	18:S:170:LEU:HD12	2.11	0.65
6:F:75:CYS:HB2	6:F:129:SER:OG	1.96	0.65
6:F:154:SER:HA	6:F:182:THR:HG22	1.76	0.65
19:T:27:GLU:OE2	19:T:31:ARG:NE	2.30	0.65
1:A:228:LYS:HG2	1:A:695:LEU:HD13	1.79	0.65
1:A:831:ARG:HD3	1:A:848:ASN:HD21	1.60	0.65
1:A:1053:THR:HG22	1:A:1167:ARG:CD	2.26	0.65
6:F:590:HIS:CE1	6:F:637:SER:HB3	2.32	0.65
13:M:469:A:H2	32:e:149:LYS:CB	2.08	0.65
28:G:288:ASN:OD1	28:G:289:GLU:N	2.30	0.65
31:v:718:SER:OG	31:v:725:THR:CG2	2.43	0.65
1:A:745:THR:HG21	14:O:203:ASP:HB2	1.77	0.65
6:F:411:ASP:OD2	6:F:472:LEU:HG	1.95	0.65
16:Q:70:ILE:HG21	16:Q:84:ILE:HD11	1.79	0.65
23:Y:349:HIS:CE1	23:Y:379:ALA:H	2.13	0.65
23:Y:570:TYR:HA	23:Y:574:LEU:HD12	1.77	0.65
27:c:230:THR:HG21	29:d:117:HIS:ND1	2.11	0.65
2:B:1609:MET:HB3	2:B:1611:ASN:H	1.62	0.65
36:n:60:ARG:O	36:n:62:THR:N	2.29	0.65
1:A:777:LYS:HA	1:A:777:LYS:HE3	1.78	0.65
6:F:626:PRO:HB3	6:F:630:ILE:HB	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:57:TYR:O	8:I:59:TYR:CD1	2.50	0.65
15:P:325:ASP:OD1	15:P:325:ASP:N	2.23	0.65
21:V:72:GLN:OE1	21:V:72:GLN:HA	1.97	0.65
24:Z:149:ARG:NH1	24:Z:193:SER:CB	2.60	0.65
1:A:2255:LEU:O	1:A:2285:LYS:NZ	2.30	0.65
6:F:1112:ASP:OD1	6:F:1113:SER:N	2.30	0.65
17:R:172:ARG:HH22	17:R:237:ARG:HH11	1.45	0.65
28:G:334:ILE:HD11	28:G:362:CYS:HB3	1.79	0.65
1:A:2412:PHE:HD1	1:A:2413:SER:N	1.95	0.65
5:E:15:C:H2'	5:E:16:C:C6	2.31	0.65
7:H:141:VAL:HG13	7:H:165:CYS:SG	2.37	0.65
26:b:60:TRP:HZ3	26:b:62:MET:HB2	1.62	0.65
3:C:218:HIS:HB3	3:C:221:PHE:HD2	1.61	0.64
3:C:452:LYS:HZ2	3:C:487:ARG:HH12	1.44	0.64
19:T:150:CYS:SG	19:T:151:ARG:N	2.70	0.64
25:a:168:PHE:HA	25:a:169:LYS:HZ1	1.61	0.64
29:d:141:ILE:CG1	33:f:105:TYR:CD1	2.81	0.64
33:f:195:PHE:HE1	33:f:204:ASN:HD22	1.44	0.64
1:A:322:VAL:HG11	1:A:327:TYR:CD2	2.32	0.64
2:B:180:LEU:HD21	28:G:592:ILE:HD13	1.79	0.64
23:Y:272:GLN:NE2	23:Y:317:THR:OG1	2.30	0.64
23:Y:626:LEU:HD11	23:Y:650:GLU:HB3	1.79	0.64
24:Z:402:LEU:HG	24:Z:405:ILE:HD12	1.79	0.64
39:h:77:ASN:OD1	43:g:49:ARG:HD3	1.97	0.64
18:S:125:ARG:O	18:S:125:ARG:HG2	1.97	0.64
23:Y:474:ILE:HA	23:Y:478:LEU:HD11	1.78	0.64
24:Z:192:GLU:O	24:Z:195:GLU:OE2	2.15	0.64
25:a:147:TYR:HD2	25:a:163:HIS:O	1.76	0.64
8:I:14:GLY:HA2	25:a:152:TYR:CE1	2.33	0.64
17:R:31:ASN:ND2	17:R:38:SER:OG	2.22	0.64
23:Y:838:THR:HG23	23:Y:839:SER:H	1.61	0.64
28:G:904:GLU:OE1	28:G:940:ASN:HB3	1.96	0.64
1:A:227:GLU:OE2	1:A:231:ARG:NH1	2.30	0.64
2:B:675:PRO:HD3	2:B:905:GLN:H	1.62	0.64
6:F:1093:SER:OG	6:F:1114:VAL:O	2.12	0.64
1:A:372:ARG:O	3:C:973:ARG:NH2	2.31	0.64
2:B:503:GLN:NE2	2:B:529:ASN:HB2	2.13	0.64
6:F:1197:ASP:OD2	6:F:1224:THR:OG1	2.10	0.64
20:U:45:LYS:O	20:U:48:ILE:N	2.30	0.64
2:B:1205:THR:HB	2:B:1221:GLU:HB2	1.80	0.64
6:F:924:PHE:HD2	6:F:952:ARG:HD2	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:G:645:ILE:HD11	28:G:679:GLN:HG2	1.78	0.64
31:v:602:MET:HA	31:v:605:PHE:HD2	1.62	0.64
31:v:729:TYR:CG	31:v:749:UNK:CB	2.81	0.64
32:e:117:ASP:HA	32:e:147:LYS:CG	2.27	0.64
3:C:360:ARG:HG2	3:C:362:LYS:HB2	1.79	0.64
23:Y:505:GLU:OE2	23:Y:549:ARG:NE	2.25	0.64
1:A:775:ARG:HG2	1:A:776:GLN:N	2.12	0.64
2:B:882:THR:HG23	6:F:686:GLN:NE2	2.12	0.64
13:M:480:A:O2'	13:M:481:A:H8	1.81	0.64
16:Q:101:THR:HG22	16:Q:120:LEU:HD21	1.74	0.64
16:Q:207:LEU:N	16:Q:249:GLY:O	2.31	0.64
19:T:57:HIS:CD2	36:n:69:TRP:HZ3	2.16	0.64
23:Y:659:ALA:HB1	23:Y:668:LEU:CB	2.27	0.64
28:G:542:THR:O	28:G:546:ASN:ND2	2.30	0.64
1:A:1748:ILE:HG13	1:A:1783:MET:HE3	1.80	0.64
2:B:749:GLU:OE1	2:B:752:ARG:NH1	2.30	0.64
6:F:720:LEU:HD12	25:a:227:MET:HG3	1.79	0.64
10:K:20:GLY:O	28:G:942:TYR:CE2	2.51	0.64
24:Z:184:GLN:CA	24:Z:184:GLN:HE21	2.11	0.64
27:c:229:ASP:OD1	33:f:152:ILE:O	2.15	0.64
1:A:777:LYS:HZ2	1:A:777:LYS:CA	2.11	0.63
35:t:81:ASP:CB	35:t:85:THR:OG1	2.46	0.63
1:A:330:LEU:O	1:A:335:SER:CB	2.46	0.63
1:A:375:PHE:HE2	1:A:1414:TRP:CZ2	2.16	0.63
1:A:1156:HIS:CE1	18:S:127:TRP:HB2	2.33	0.63
3:C:104:THR:HG22	3:C:181:LEU:HD12	1.81	0.63
23:Y:686:ILE:HD11	23:Y:730:GLN:HB2	1.81	0.63
23:Y:704:HIS:HD2	23:Y:847:LEU:CG	2.11	0.63
24:Z:194:LEU:HD22	24:Z:194:LEU:O	1.98	0.63
38:i:77:LEU:HD21	38:i:80:ILE:HD12	1.79	0.63
3:C:287:LYS:NZ	3:C:895:ALA:O	2.26	0.63
6:F:190:ILE:O	6:F:191:SER:OG	2.15	0.63
24:Z:200:ILE:O	24:Z:204:ASP:N	2.28	0.63
28:G:569:PHE:HE1	28:G:580:PHE:HE1	1.46	0.63
9:J:51:PHE:CZ	9:J:54:GLN:HB2	2.33	0.63
12:N:95:U:O2'	12:N:96:U:H5''	1.98	0.63
1:A:774:ILE:HD12	1:A:774:ILE:C	2.22	0.63
1:A:1739:ARG:HD2	1:A:1778:ASP:OD1	1.98	0.63
2:B:596:ARG:HA	2:B:599:ILE:HD12	1.81	0.63
3:C:829:VAL:HA	3:C:832:ASP:HB2	1.81	0.63
5:E:91:A:C4	29:d:99:ILE:HD11	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:212:TRP:O	17:R:215:ARG:HB3	1.98	0.63
2:B:1432:PRO:HA	2:B:1435:ASN:HD22	1.62	0.63
3:C:108:GLN:C	3:C:109:LEU:HD12	2.23	0.63
20:U:45:LYS:HE3	20:U:46:GLU:H	1.63	0.63
21:V:52:SER:HB3	22:W:231:ARG:CZ	2.29	0.63
26:b:60:TRP:CZ3	26:b:62:MET:HB2	2.33	0.63
1:A:1061:ILE:HD12	1:A:1103:LEU:HB2	1.81	0.63
2:B:158:GLU:HG3	2:B:159:ASP:H	1.63	0.63
15:P:317:LYS:HB3	22:W:258:GLN:OE1	1.99	0.63
25:a:249:ASP:HA	25:a:252:LYS:HD2	1.80	0.63
31:v:724:VAL:C	31:v:727:GLU:CG	2.72	0.63
1:A:1876:ASN:OD1	1:A:1895:HIS:CD2	2.49	0.63
2:B:427:ILE:HD11	2:B:973:LEU:HD23	1.80	0.63
2:B:1459:TRP:HA	2:B:1462:ARG:HB2	1.79	0.63
3:C:580:VAL:HG22	3:C:582:SER:H	1.62	0.63
6:F:102:GLU:OE2	6:F:116:LYS:NZ	2.32	0.63
7:H:182:TYR:O	7:H:272:GLU:CD	2.40	0.63
28:G:390:ILE:HD12	28:G:426:MET:HA	1.81	0.63
1:A:609:GLU:OE2	5:E:43:C:O2'	2.09	0.63
1:A:1458:TRP:CE2	28:G:25:ILE:HG22	2.34	0.63
2:B:2013:VAL:HG13	2:B:2018:ASP:HB3	1.80	0.63
3:C:108:GLN:O	3:C:109:LEU:HD12	1.99	0.63
6:F:1060:LEU:HD11	6:F:1062:ARG:HH21	1.64	0.63
13:M:468:A:H3'	13:M:469:A:C8	2.34	0.63
2:B:1430:ASN:ND2	2:B:2091:TYR:OH	2.32	0.62
22:W:189:THR:HG22	22:W:195:ILE:CD1	2.29	0.62
29:d:141:ILE:HD11	33:f:105:TYR:CA	2.27	0.62
29:d:221:VAL:O	29:d:225:ALA:N	2.31	0.62
32:e:165:ILE:O	32:e:166:LYS:HB3	1.98	0.62
1:A:1424:HIS:CD2	30:X:6:ILE:HD13	2.34	0.62
28:G:904:GLU:CD	28:G:940:ASN:CB	2.72	0.62
1:A:168:LEU:HB3	1:A:622:MET:HE2	1.81	0.62
3:C:193:LEU:HD23	3:C:224:GLU:HB3	1.81	0.62
6:F:201:CYS:HB3	6:F:215:LEU:HD12	1.82	0.62
16:Q:87:ARG:HH22	16:Q:123:ALA:HA	1.63	0.62
25:a:201:LEU:HD12	25:a:222:CYS:HB3	1.80	0.62
29:d:115:ILE:CD1	29:d:119:ARG:NH2	2.30	0.62
33:f:196:ILE:HB	33:f:200:ASN:ND2	2.14	0.62
1:A:1831:GLN:O	1:A:1834:PHE:N	2.29	0.62
3:C:510:ARG:NH1	3:C:533:GLU:OE1	2.33	0.62
4:D:174:G:O5'	39:h:76:ASN:ND2	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:1178:PRO:HG2	7:H:146:ILE:HD11	1.81	0.62
1:A:1044:GLY:HA3	1:A:1176:GLU:HG3	1.81	0.62
1:A:1286:TRP:HA	1:A:1448:GLU:OE2	1.99	0.62
4:D:175:G:N7	39:h:32:LYS:HD2	2.15	0.62
6:F:259:ASN:O	10:K:75:PRO:HD3	1.99	0.62
6:F:597:HIS:O	6:F:597:HIS:ND1	2.32	0.62
16:Q:217:TRP:CZ2	17:R:187:LYS:CD	2.77	0.62
17:R:66:ASN:N	17:R:66:ASN:OD1	2.32	0.62
23:Y:282:ALA:HB2	23:Y:507:SER:HB3	1.82	0.62
28:G:531:GLU:OE1	28:G:534:ARG:NH2	2.33	0.62
28:G:925:HIS:O	28:G:931:ARG:NH2	2.32	0.62
31:v:722:PRO:O	31:v:725:THR:OG1	2.17	0.62
13:M:469:A:C2	32:e:149:LYS:CB	2.82	0.62
20:U:135:THR:O	20:U:163:ASN:ND2	2.32	0.62
25:a:174:LEU:HD23	25:a:174:LEU:C	2.24	0.62
25:a:199:CYS:SG	25:a:202:CYS:HB2	2.40	0.62
27:c:216:ASP:OD1	27:c:217:ILE:N	2.33	0.62
36:n:72:TRP:O	36:n:73:SER:OG	2.16	0.62
1:A:1748:ILE:CD1	1:A:1783:MET:C	2.73	0.62
2:B:1031:LEU:HD22	2:B:1128:LEU:HD21	1.82	0.62
3:C:231:ALA:O	3:C:487:ARG:NH1	2.33	0.62
3:C:697:ARG:NH1	3:C:852:THR:OG1	2.33	0.62
6:F:551:PHE:HD2	6:F:591:THR:HG21	1.63	0.62
6:F:736:ILE:HG23	6:F:738:GLN:H	1.63	0.62
6:F:1222:GLN:HE22	10:K:48:ALA:CA	2.11	0.62
14:O:285:SER:OG	14:O:287:ASP:OD1	2.14	0.62
23:Y:278:PRO:HB3	23:Y:352:THR:HG21	1.82	0.62
28:G:445:GLU:HG3	28:G:453:MET:HE2	1.82	0.62
28:G:550:THR:HG23	28:G:553:LEU:HD22	1.81	0.62
1:A:771:PRO:O	14:O:309:ARG:NH2	2.32	0.62
1:A:1846:ASN:OD1	1:A:1847:ASP:N	2.33	0.62
2:B:1588:ARG:HE	2:B:1942:ASP:CG	2.08	0.62
6:F:412:THR:O	6:F:413:ILE:HG23	1.99	0.62
9:J:103:LYS:O	9:J:104:LYS:HB2	1.99	0.62
16:Q:255:SER:HG	16:Q:257:GLU:HG2	1.65	0.62
2:B:1598:PHE:O	2:B:1602:SER:N	2.33	0.62
6:F:1169:ASP:O	6:F:1172:THR:OG1	2.16	0.62
7:H:262:HIS:HD2	7:H:283:LYS:HZ1	0.70	0.62
13:M:472:A:O2'	13:M:473:A:H8	1.81	0.62
23:Y:626:LEU:HD11	23:Y:650:GLU:HA	1.81	0.62
1:A:319:ARG:HD3	1:A:486:PHE:HE2	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1843:LEU:HD13	1:A:1851:PHE:HZ	1.64	0.62
1:A:2412:PHE:C	1:A:2413:SER:HG	2.04	0.62
6:F:71:PHE:HA	6:F:97:THR:HG22	1.82	0.62
34:q:374:GLU:O	34:q:375:ALA:HB3	1.99	0.62
1:A:454:LEU:HD23	3:C:336:ILE:HG21	1.81	0.61
2:B:126:TRP:HH2	2:B:177:ILE:HD11	1.65	0.61
17:R:48:VAL:HG21	17:R:216:ARG:C	2.24	0.61
21:V:11:GLU:HG2	21:V:16:ILE:HG21	1.82	0.61
24:Z:195:GLU:HG2	24:Z:196:THR:N	2.15	0.61
26:b:59:GLN:HB3	26:b:60:TRP:HD1	1.64	0.61
1:A:1275:MET:O	1:A:1276:GLU:HG2	2.00	0.61
6:F:1174:GLN:CD	6:F:1184:LYS:HD3	2.25	0.61
13:M:468:A:H3'	13:M:469:A:H8	1.64	0.61
16:Q:215:PRO:HB2	16:Q:217:TRP:CE3	2.36	0.61
16:Q:226:LEU:HG	16:Q:227:LEU:CD2	2.29	0.61
1:A:396:ARG:HG3	1:A:396:ARG:NH1	2.13	0.61
2:B:1159:ARG:NH1	2:B:1183:ILE:O	2.30	0.61
2:B:1479:ILE:HB	2:B:1489:GLU:HB2	1.83	0.61
6:F:766:LYS:HD3	6:F:836:TRP:NE1	2.14	0.61
17:R:4:TRP:CD1	17:R:92:HIS:HB3	2.34	0.61
24:Z:148:LEU:HD12	24:Z:190:LEU:HD11	1.80	0.61
25:a:173:LYS:CD	25:a:175:ASN:HD21	2.12	0.61
28:G:590:LEU:HD11	28:G:594:MET:HE2	1.82	0.61
1:A:394:ARG:HH11	1:A:394:ARG:CG	2.13	0.61
1:A:1163:ARG:HG2	1:A:1163:ARG:NH1	2.15	0.61
7:H:248:HIS:CE1	7:H:252:PHE:HD2	2.18	0.61
28:G:443:ARG:NE	28:G:478:GLU:OE2	2.33	0.61
31:v:724:VAL:CA	31:v:727:GLU:CG	2.79	0.61
3:C:932:PHE:O	3:C:933:TRP:CD1	2.53	0.61
28:G:61:GLU:CD	28:G:68:ARG:HH21	2.07	0.61
28:G:675:LEU:HD13	28:G:715:ALA:HB2	1.81	0.61
1:A:395:PRO:HB2	1:A:398:VAL:HG21	1.82	0.61
1:A:725:TYR:CD1	5:E:72:C:H1'	2.36	0.61
1:A:911:ILE:HG23	1:A:997:GLN:HB3	1.83	0.61
2:B:593:ARG:NH1	2:B:621:ASN:OD1	2.22	0.61
18:S:9:LEU:HD23	18:S:11:ALA:H	1.63	0.61
21:V:82:GLN:H	22:W:168:GLN:HE21	1.48	0.61
29:d:141:ILE:HD11	33:f:105:TYR:HD1	1.65	0.61
29:d:141:ILE:CD1	33:f:105:TYR:HD1	2.13	0.61
5:E:35:A:O2'	5:E:36:U:O5'	2.18	0.61
6:F:93:LEU:HD23	6:F:422:PHE:HZ	1.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:W:160:LYS:NZ	22:W:160:LYS:HB2	2.14	0.61
25:a:150:THR:HG22	25:a:152:TYR:H	1.65	0.61
26:b:59:GLN:HB3	26:b:60:TRP:CD1	2.35	0.61
1:A:271:GLN:NE2	1:A:271:GLN:O	2.34	0.61
6:F:332:GLU:OE1	6:F:332:GLU:N	2.30	0.61
15:P:53:LEU:CD2	15:P:54:SER:N	2.60	0.61
23:Y:337:LEU:O	23:Y:369:ARG:NH1	2.31	0.61
28:G:360:LYS:HD2	28:G:395:VAL:HG12	1.83	0.61
28:G:641:ASN:ND2	28:G:673:MET:HE1	2.14	0.61
34:q:178:LYS:CB	34:q:468:GLN:CB	2.79	0.61
1:A:143:ILE:CD1	1:A:570:GLN:HG2	2.22	0.61
1:A:375:PHE:CE2	1:A:1414:TRP:CZ2	2.89	0.61
1:A:1474:ARG:NH1	15:P:304:ASP:OD1	2.33	0.61
3:C:701:GLU:HG2	3:C:703:LEU:H	1.65	0.61
4:D:174:G:H5''	43:g:99:ASP:HB2	1.82	0.61
7:H:141:VAL:HG12	7:H:143:TYR:H	1.64	0.61
13:M:480:A:HO2'	13:M:481:A:H8	1.46	0.61
42:m:3:LEU:HD11	43:g:60:ALA:HB1	1.82	0.61
1:A:183:TRP:CE2	1:A:216:GLN:OE1	2.53	0.61
1:A:1672:GLU:HG3	1:A:1797:LEU:HD11	1.81	0.61
3:C:697:ARG:NH1	3:C:848:VAL:O	2.34	0.61
6:F:855:ALA:HA	6:F:856:ASP:C	2.26	0.61
14:O:322:SER:OG	14:O:378:TYR:OH	2.13	0.61
20:U:51:LYS:O	20:U:52:HIS:HB3	1.99	0.61
29:d:141:ILE:CG1	33:f:105:TYR:HD1	2.13	0.61
1:A:273:ASP:HA	1:A:310:ASN:ND2	2.14	0.60
1:A:379:ILE:HG22	1:A:379:ILE:O	2.00	0.60
3:C:223:ASP:HB3	3:C:630:PRO:HG2	1.84	0.60
4:D:174:G:OP2	39:h:76:ASN:CB	2.49	0.60
9:J:51:PHE:CE2	9:J:54:GLN:HB2	2.36	0.60
15:P:241:LEU:HD13	20:U:204:VAL:HA	1.81	0.60
25:a:212:THR:OG1	25:a:216:HIS:HB2	2.01	0.60
2:B:439:LYS:HE2	2:B:862:GLN:HB2	1.83	0.60
2:B:536:LEU:HD23	2:B:539:LEU:HD12	1.82	0.60
3:C:233:ASP:OD1	3:C:487:ARG:NH2	2.32	0.60
4:D:78:A:H4'	4:D:79:C:OP1	2.00	0.60
7:H:262:HIS:CD2	7:H:283:LYS:CE	2.84	0.60
13:M:514:U:H5''	13:M:515:U:H5''	1.82	0.60
15:P:319:HIS:CE1	22:W:264:GLU:CD	2.77	0.60
16:Q:226:LEU:HD11	16:Q:227:LEU:CD2	2.29	0.60
17:R:210:LYS:HD3	17:R:211:GLU:N	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:W:208:SER:HA	22:W:214:LEU:CD1	2.31	0.60
24:Z:317:ILE:HD13	24:Z:325:VAL:HG21	1.82	0.60
36:n:54:SER:O	36:n:58:ARG:HG2	2.01	0.60
6:F:128:LYS:NZ	6:F:193:MET:O	2.30	0.60
21:V:89:VAL:HG22	21:V:104:ILE:HG22	1.83	0.60
28:G:450:ASP:OD1	28:G:451:ASP:N	2.34	0.60
28:G:739:ASN:OD1	28:G:740:LYS:N	2.33	0.60
1:A:194:HIS:NE2	15:P:122:LEU:HD22	2.15	0.60
1:A:1130:ARG:HD3	1:A:1156:HIS:CG	2.36	0.60
2:B:1212:THR:HG22	2:B:1213:ARG:H	1.66	0.60
2:B:2006:GLU:O	2:B:2010:GLU:N	2.21	0.60
3:C:122:TYR:CE2	41:l:82:PRO:HD3	2.35	0.60
6:F:432:GLU:O	6:F:485:ASN:ND2	2.35	0.60
15:P:110:HIS:CE1	16:Q:18:GLY:O	2.54	0.60
17:R:138:TYR:HE1	17:R:181:CYS:HB3	1.66	0.60
24:Z:170:HIS:HE1	24:Z:174:TRP:HZ3	1.15	0.60
1:A:849:LEU:HD12	1:A:973:GLU:HB3	1.84	0.60
1:A:2392:PHE:HE1	2:B:1062:PRO:HB2	1.67	0.60
7:H:198:ASP:OD1	7:H:199:ILE:HG12	2.02	0.60
13:M:505:A:OP1	13:M:505:A:C4'	2.50	0.60
17:R:64:GLY:O	17:R:68:GLY:N	2.35	0.60
21:V:48:LEU:C	22:W:231:ARG:NH1	2.59	0.60
24:Z:170:HIS:NE2	24:Z:174:TRP:CE3	2.69	0.60
24:Z:184:GLN:HE21	24:Z:185:GLU:H	1.48	0.60
38:i:83:LYS:NZ	39:h:75:CYS:O	2.35	0.60
1:A:631:LEU:HD21	1:A:663:LEU:HD13	1.84	0.60
20:U:76:THR:OG1	20:U:205:HIS:NE2	2.34	0.60
22:W:229:GLY:O	22:W:231:ARG:N	2.35	0.60
24:Z:149:ARG:HH11	24:Z:193:SER:CB	2.14	0.60
24:Z:184:GLN:HE21	24:Z:184:GLN:HA	1.66	0.60
29:d:117:HIS:CA	29:d:120:ASN:HD21	2.09	0.60
1:A:514:TYR:HB3	1:A:518:VAL:CG2	2.32	0.60
1:A:1835:LEU:HD12	1:A:1836:ASN:N	2.17	0.60
3:C:147:THR:HG23	3:C:178:LEU:HB2	1.84	0.60
3:C:806:GLY:H	3:C:810:GLU:HA	1.66	0.60
5:E:91:A:C4	29:d:99:ILE:CD1	2.84	0.60
6:F:1065:THR:HG22	6:F:1105:VAL:HG23	1.84	0.60
7:H:235:PRO:O	28:G:722:LYS:NZ	2.35	0.60
9:J:4:HIS:CD2	13:M:502:C:H4'	2.37	0.60
14:O:115:TYR:OH	14:O:444:PRO:O	2.19	0.60
15:P:41:ASP:OD1	15:P:42:ASP:N	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Y:248:THR:OG1	23:Y:552:ARG:NH2	2.32	0.60
1:A:332:ASP:O	1:A:333:LYS:C	2.45	0.60
6:F:1222:GLN:HE22	10:K:48:ALA:CB	2.14	0.60
13:M:468:A:H5''	13:M:469:A:OP2	2.02	0.60
21:V:123:LYS:O	21:V:127:ASP:N	2.34	0.60
24:Z:188:SER:O	24:Z:192:GLU:HG2	2.01	0.60
24:Z:470:LEU:HD12	24:Z:471:GLY:H	1.66	0.60
25:a:209:PRO:HB2	25:a:247:ALA:HB3	1.84	0.60
29:d:176:GLU:OE1	29:d:181:ASN:ND2	2.34	0.60
33:f:180:LYS:O	33:f:183:MET:HB2	2.02	0.60
4:D:165:A:H2	42:m:2:LYS:HE2	1.58	0.60
6:F:347:LYS:HD2	6:F:460:PRO:HB2	1.84	0.60
24:Z:470:LEU:HD12	24:Z:471:GLY:N	2.17	0.60
29:d:144:GLU:CD	33:f:109:LEU:HD21	2.26	0.60
30:X:27:ASN:OD1	30:X:28:ASN:N	2.31	0.60
2:B:1016:ASP:OD2	2:B:1020:ARG:NH1	2.34	0.60
6:F:286:TYR:OH	6:F:340:MET:O	2.18	0.60
7:H:183:LEU:HD23	7:H:272:GLU:HG3	1.83	0.60
16:Q:67:GLN:NE2	16:Q:116:LYS:O	2.34	0.60
17:R:244:LEU:O	17:R:248:ASN:ND2	2.35	0.60
20:U:78:TYR:H	20:U:99:ASN:HD21	1.49	0.60
24:Z:178:ARG:HD3	24:Z:182:GLN:HE22	1.67	0.60
28:G:927:ALA:C	28:G:929:ASN:H	2.10	0.60
1:A:1051:GLU:HB3	1:A:1167:ARG:HH21	1.67	0.59
1:A:1739:ARG:CD	1:A:1778:ASP:OD1	2.50	0.59
2:B:1381:GLU:OE2	2:B:1412:TRP:NE1	2.35	0.59
3:C:234:LEU:HD23	3:C:443:TYR:HB2	1.84	0.59
16:Q:79:ARG:HD2	16:Q:126:THR:CG2	2.28	0.59
16:Q:116:LYS:NZ	27:c:220:GLU:O	2.34	0.59
25:a:209:PRO:HB2	25:a:250:LEU:HD12	1.84	0.59
26:b:7:PRO:O	26:b:8:GLN:HG2	2.02	0.59
1:A:744:THR:O	1:A:749:ARG:NH2	2.35	0.59
1:A:933:GLU:OE1	1:A:933:GLU:N	2.34	0.59
2:B:780:ILE:HD11	6:F:759:ASP:HB3	1.84	0.59
2:B:2098:SER:H	2:B:2147:ASP:CG	2.09	0.59
31:v:557:UNK:O	31:v:561:UNK:N	2.35	0.59
1:A:2287:ASP:O	1:A:2288:CYS:C	2.46	0.59
1:A:2392:PHE:CE1	2:B:1062:PRO:HB2	2.36	0.59
2:B:1690:GLY:HA3	2:B:1894:LEU:HB2	1.82	0.59
6:F:105:ASP:OD1	6:F:106:THR:N	2.36	0.59
6:F:299:PRO:HD2	6:F:377:PHE:CE1	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:433:MET:O	6:F:485:ASN:HB3	2.03	0.59
6:F:718:LEU:HB2	25:a:244:ALA:HB3	1.84	0.59
6:F:1179:ASN:OD1	6:F:1180:THR:N	2.35	0.59
9:J:100:HIS:CE1	28:G:257:MET:HG3	2.37	0.59
17:R:69:GLN:HE21	17:R:71:PHE:HD2	1.49	0.59
22:W:264:GLU:HG3	22:W:265:ASP:H	1.68	0.59
23:Y:409:TYR:OH	23:Y:563:ARG:NH1	2.36	0.59
23:Y:828:LYS:HB2	28:G:429:GLU:OE2	2.03	0.59
1:A:268:LEU:O	1:A:269:ASP:HB3	2.01	0.59
2:B:1325:GLU:HA	2:B:1350:LYS:HE3	1.84	0.59
2:B:1916:HIS:O	2:B:1917:THR:OG1	2.19	0.59
6:F:1222:GLN:NE2	10:K:48:ALA:N	2.51	0.59
7:H:181:GLU:O	7:H:182:TYR:HB3	2.02	0.59
20:U:110:LEU:N	20:U:123:GLU:OE1	2.30	0.59
28:G:538:VAL:O	28:G:542:THR:HG23	2.01	0.59
1:A:610:ARG:HE	1:A:614:ARG:HH21	1.48	0.59
2:B:1369:GLY:N	2:B:1533:TYR:O	2.29	0.59
5:E:28:U:C1'	19:T:121:ILE:HD13	2.31	0.59
6:F:1007:LYS:HE3	6:F:1009:LEU:HD21	1.82	0.59
10:K:50:LEU:HD22	10:K:62:ILE:HG23	1.84	0.59
15:P:301:LEU:H	15:P:301:LEU:CD2	2.16	0.59
16:Q:98:ASN:O	16:Q:99:VAL:HG12	2.01	0.59
27:c:525:ARG:O	27:c:528:GLN:CG	2.51	0.59
28:G:919:ILE:CD1	28:G:937:VAL:HG11	2.32	0.59
32:e:112:ILE:O	32:e:150:CYS:HB2	2.03	0.59
1:A:1054:LEU:HD21	1:A:1168:ILE:CD1	2.31	0.59
1:A:1056:GLU:HB2	1:A:1060:LYS:HG3	1.85	0.59
1:A:1829:SER:O	1:A:1830:VAL:HG13	2.01	0.59
2:B:134:ASP:OD2	2:B:752:ARG:NH2	2.35	0.59
8:I:16:ILE:O	8:I:17:ALA:HB3	2.00	0.59
22:W:173:ASN:O	22:W:174:VAL:HG12	2.02	0.59
1:A:1365:THR:HG22	1:A:1429:MET:HE3	1.82	0.59
3:C:106:PHE:CE1	3:C:548:ARG:O	2.56	0.59
3:C:117:ARG:HG2	3:C:157:SER:O	2.03	0.59
15:P:110:HIS:O	15:P:111:HIS:HB2	2.01	0.59
16:Q:75:MET:HE1	17:R:130:PHE:CE1	2.37	0.59
21:V:40:ARG:NH1	21:V:72:GLN:O	2.36	0.59
36:n:60:ARG:C	36:n:62:THR:N	2.59	0.59
1:A:676:GLN:HG2	1:A:714:PHE:HB2	1.83	0.59
3:C:116:THR:HG23	3:C:118:TYR:HE1	1.64	0.59
3:C:826:PRO:HB2	3:C:832:ASP:HB3	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:266:VAL:HG12	6:F:290:PRO:HA	1.84	0.59
6:F:607:LEU:HB2	6:F:624:TRP:HB3	1.85	0.59
14:O:121:GLN:NE2	15:P:49:SER:O	2.36	0.59
14:O:194:HIS:NE2	14:O:237:ASP:OD1	2.32	0.59
24:Z:187:SER:OG	24:Z:190:LEU:HB3	2.03	0.59
27:c:44:THR:HG22	27:c:45:ALA:H	1.67	0.59
17:R:211:GLU:HG2	17:R:211:GLU:O	2.03	0.59
20:U:45:LYS:HA	20:U:45:LYS:CE	2.31	0.59
27:c:223:PRO:O	29:d:124:ARG:NH1	2.36	0.59
31:v:718:SER:HG	31:v:725:THR:HG21	1.64	0.59
1:A:1410:SER:HB3	1:A:1423:THR:H	1.67	0.59
1:A:1899:TRP:HA	1:A:1899:TRP:CE3	2.38	0.59
2:B:506:VAL:HG12	2:B:692:PHE:CD2	2.38	0.59
4:D:167:A:N7	43:g:63:ARG:NE	2.51	0.59
6:F:411:ASP:OD1	6:F:472:LEU:HA	2.03	0.59
17:R:164:PHE:CD2	17:R:184:VAL:HG21	2.38	0.59
28:G:922:GLY:HA3	28:G:934:PHE:CD2	2.37	0.59
32:e:27:GLU:C	32:e:122:ASP:HB3	2.28	0.59
1:A:1295:GLN:NE2	24:Z:432:GLY:HA3	2.15	0.58
6:F:1097:PHE:HE1	6:F:1108:PRO:HB3	1.68	0.58
14:O:277:VAL:HG13	15:P:63:ILE:HG22	1.85	0.58
15:P:323:VAL:HG23	15:P:324:TYR:CG	2.38	0.58
34:q:194:THR:OG1	34:q:213:CYS:HB3	2.03	0.58
1:A:218:SER:O	1:A:221:TRP:HB3	2.02	0.58
2:B:148:ILE:HG23	2:B:189:MET:HE1	1.85	0.58
2:B:1209:GLN:OE1	2:B:1219:ASN:ND2	2.36	0.58
6:F:96:ALA:HB2	6:F:101:LEU:HD13	1.84	0.58
8:I:53:ARG:HB3	8:I:53:ARG:CZ	2.32	0.58
27:c:230:THR:HG21	29:d:117:HIS:CD2	2.38	0.58
29:d:141:ILE:HG13	33:f:105:TYR:CD1	2.38	0.58
2:B:2051:VAL:O	2:B:2154:LYS:NZ	2.36	0.58
6:F:545:ASP:OD1	6:F:546:ASN:N	2.36	0.58
6:F:582:LYS:O	6:F:608:ARG:NH2	2.35	0.58
29:d:166:VAL:HG23	29:d:167:ASN:H	1.69	0.58
38:i:86:ASN:ND2	39:h:32:LYS:HD3	2.13	0.58
1:A:1229:GLU:OE1	18:S:127:TRP:CH2	2.56	0.58
1:A:2403:GLU:O	1:A:2404:LEU:HB2	2.02	0.58
2:B:2147:ASP:OD1	2:B:2148:SER:N	2.36	0.58
3:C:250:GLU:OE2	3:C:298:PHE:CZ	2.57	0.58
6:F:836:TRP:CZ3	6:F:838:ILE:HG23	2.39	0.58
6:F:1002:ARG:NH2	6:F:1004:LEU:HD11	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:K:57:ARG:HB3	10:K:57:ARG:HH11	1.67	0.58
14:O:156:ILE:CD1	14:O:197:LEU:HD22	2.33	0.58
15:P:59:THR:O	15:P:63:ILE:HG23	2.03	0.58
23:Y:713:GLN:O	23:Y:716:ASN:CG	2.46	0.58
1:A:1748:ILE:HD11	1:A:1783:MET:HB3	0.73	0.58
5:E:86:G:O6	29:d:57:TYR:CE1	2.56	0.58
6:F:153:ASP:O	6:F:154:SER:OG	2.14	0.58
14:O:275:THR:OG1	14:O:279:PRO:O	2.22	0.58
25:a:162:LEU:HG	25:a:164:SER:H	1.68	0.58
28:G:519:ILE:HG21	28:G:561:LEU:HD12	1.85	0.58
31:v:485:UNK:O	31:v:490:UNK:N	2.36	0.58
34:p:98:LEU:HD12	34:q:98:LEU:HD23	1.85	0.58
1:A:790:TRP:NE1	1:A:794:LYS:HE3	2.18	0.58
6:F:369:ILE:HD11	6:F:380:LEU:HB2	1.84	0.58
7:H:159:LEU:HD13	10:K:28:ARG:HG3	1.84	0.58
14:O:155:PHE:CE2	14:O:167:TRP:HB2	2.39	0.58
19:T:3:ARG:NH2	19:T:85:LYS:O	2.34	0.58
24:Z:149:ARG:CZ	24:Z:193:SER:HB3	2.32	0.58
28:G:294:ARG:HB3	28:G:332:THR:HG21	1.84	0.58
2:B:773:ASN:ND2	6:F:754:HIS:HE1	1.99	0.58
3:C:302:ASN:OD1	3:C:303:VAL:N	2.36	0.58
6:F:243:VAL:HG12	6:F:244:ASP:O	2.03	0.58
16:Q:70:ILE:HD13	16:Q:84:ILE:HD11	1.84	0.58
27:c:210:ASP:OD1	27:c:211:ILE:N	2.37	0.58
32:e:32:ILE:O	32:e:33:ASN:CB	2.52	0.58
1:A:2189:LEU:O	1:A:2193:PHE:CB	2.52	0.58
3:C:418:GLN:HB3	3:C:419:PRO:HD3	1.83	0.58
6:F:163:ILE:HD13	6:F:172:LYS:HD3	1.85	0.58
23:Y:843:ILE:HG22	23:Y:846:CYS:SG	2.44	0.58
24:Z:191:ARG:HE	24:Z:192:GLU:CD	2.12	0.58
28:G:386:TYR:HB3	28:G:387:PRO:CD	2.34	0.58
34:q:378:LYS:CG	34:q:423:THR:O	2.51	0.58
1:A:1669:LEU:HD11	1:A:1734:PHE:CE2	2.39	0.58
1:A:1899:TRP:HA	1:A:1899:TRP:HE3	1.68	0.58
2:B:502:ILE:HG23	2:B:694:PHE:HE2	1.69	0.58
6:F:118:GLN:HE21	6:F:1299:ILE:HD13	1.68	0.58
11:L:19:U:C2	15:P:175:PRO:HD2	2.39	0.58
22:W:207:THR:C	22:W:214:LEU:CD1	2.66	0.58
28:G:550:THR:HG21	28:G:590:LEU:HD23	1.84	0.58
1:A:404:ASN:HD21	3:C:927:MET:HE3	1.69	0.58
6:F:1125:ASP:OD1	6:F:1126:GLU:N	2.30	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:U:155:TYR:HD1	20:U:179:GLU:HA	1.68	0.58
25:a:210:VAL:HG13	25:a:244:ALA:HB1	1.85	0.58
1:A:618:SER:OG	1:A:725:TYR:HB3	2.04	0.57
1:A:759:ARG:NH2	1:A:783:LEU:HD23	2.19	0.57
6:F:541:ALA:HB2	6:F:618:TYR:HE1	1.69	0.57
6:F:1111:ASP:HB2	6:F:1183:CYS:SG	2.44	0.57
15:P:318:ARG:HH22	15:P:325:ASP:HB3	1.68	0.57
16:Q:25:MET:HB2	16:Q:45:HIS:O	2.04	0.57
21:V:58:VAL:HG12	22:W:212:ARG:CZ	2.35	0.57
3:C:703:LEU:O	3:C:705:GLY:N	2.37	0.57
5:E:91:A:C5	29:d:99:ILE:CD1	2.81	0.57
6:F:186:ARG:HB3	10:K:41:ASN:ND2	2.19	0.57
17:R:152:LYS:HG2	17:R:153:PRO:HD2	1.85	0.57
28:G:216:GLN:HE21	28:G:220:LEU:HD11	1.68	0.57
29:d:141:ILE:HG13	33:f:105:TYR:HD1	1.69	0.57
31:v:602:MET:HA	31:v:605:PHE:CD2	2.39	0.57
36:n:68:PRO:HD2	36:n:69:TRP:CZ3	2.36	0.57
1:A:309:SER:HG	1:A:475:ASP:HB3	1.68	0.57
1:A:514:TYR:HB3	1:A:518:VAL:HG21	1.85	0.57
3:C:385:PHE:HE1	3:C:425:LEU:HD11	1.70	0.57
5:E:32:U:H5'	16:Q:45:HIS:CE1	2.39	0.57
15:P:110:HIS:O	16:Q:21:ALA:O	2.23	0.57
1:A:140:ARG:HH21	1:A:252:GLU:HB3	1.68	0.57
1:A:1656:LYS:O	1:A:1660:SER:OG	2.11	0.57
2:B:880:TYR:O	6:F:686:GLN:CG	2.53	0.57
3:C:855:PRO:HG2	3:C:944:VAL:HG21	1.87	0.57
10:K:19:ILE:HG22	10:K:20:GLY:N	2.18	0.57
11:L:14:C:OP2	33:f:209:ARG:NH2	2.38	0.57
25:a:236:CYS:HB3	25:a:238:LYS:HG3	1.86	0.57
28:G:728:CYS:SG	28:G:753:ILE:HG21	2.43	0.57
29:d:221:VAL:HA	29:d:224:LEU:HB2	1.86	0.57
34:q:472:ALA:HB2	34:q:477:MET:CG	2.35	0.57
1:A:322:VAL:HG11	1:A:327:TYR:CG	2.39	0.57
3:C:391:MET:CE	3:C:395:LYS:CE	2.67	0.57
4:D:175:G:N1	38:i:33:GLU:O	2.36	0.57
8:I:3:TYR:CD2	12:N:99:G:C6	2.92	0.57
9:J:98:ASP:OD2	28:G:223:LYS:NZ	2.33	0.57
12:N:110:U:O2'	17:R:141:GLY:CA	2.51	0.57
14:O:223:HIS:CD2	14:O:227:VAL:HG21	2.39	0.57
25:a:233:CYS:HB2	25:a:237:HIS:N	2.16	0.57
27:c:214:ASN:ND2	29:d:44:ARG:HD2	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:d:141:ILE:CD1	33:f:105:TYR:CD1	2.86	0.57
41:l:66:GLY:HA2	41:l:69:ILE:HD12	1.85	0.57
1:A:184:GLU:OE2	1:A:283:SER:HA	2.04	0.57
1:A:266:LEU:HG	1:A:267:PRO:HD2	1.85	0.57
1:A:1527:TRP:CE3	1:A:1528:THR:HG23	2.39	0.57
1:A:1762:ASP:OD1	1:A:1763:ASN:N	2.37	0.57
6:F:783:ILE:HG13	6:F:784:SER:N	2.19	0.57
6:F:1142:ARG:HB2	6:F:1190:LEU:HD22	1.87	0.57
7:H:172:VAL:HG23	28:G:934:PHE:CZ	2.40	0.57
9:J:4:HIS:ND1	13:M:500:A:O2'	2.38	0.57
21:V:78:LYS:NZ	22:W:162:LEU:O	2.37	0.57
24:Z:200:ILE:HA	24:Z:203:LYS:HB2	1.86	0.57
42:m:43:VAL:HG11	42:m:85:ILE:HD12	1.87	0.57
1:A:1161:TYR:HD1	1:A:1170:MET:HG2	1.69	0.57
1:A:2409:ILE:HG22	1:A:2411:VAL:HG23	1.86	0.57
2:B:861:GLU:HG2	2:B:862:GLN:H	1.70	0.57
3:C:798:GLY:HA2	3:C:839:ILE:HG23	1.87	0.57
7:H:192:ARG:HG2	7:H:192:ARG:HH11	1.69	0.57
16:Q:240:LEU:HD12	16:Q:241:ILE:N	2.20	0.57
18:S:9:LEU:CD2	18:S:11:ALA:H	2.18	0.57
28:G:618:GLN:NE2	28:G:657:GLU:HB2	2.19	0.57
1:A:1857:VAL:HG21	1:A:1913:THR:HG21	1.87	0.57
2:B:1866:PHE:HA	2:B:1869:SER:HB2	1.87	0.57
3:C:701:GLU:HB3	3:C:704:PRO:HA	1.86	0.57
3:C:761:ALA:HA	3:C:764:ASN:HB2	1.85	0.57
3:C:788:LEU:HB3	3:C:792:LYS:HE2	1.87	0.57
5:E:67:C:O2	5:E:82:A:C2	2.58	0.57
23:Y:349:HIS:CD2	23:Y:380:THR:HG23	2.39	0.57
24:Z:460:TYR:HA	24:Z:463:ASN:ND2	2.18	0.57
26:b:166:ASP:C	26:b:168:PHE:H	2.13	0.57
1:A:839:HIS:ND1	4:D:95:C:C2	2.73	0.57
1:A:1892:LYS:NZ	1:A:1916:GLU:OE1	2.38	0.57
2:B:1688:TYR:HA	2:B:1695:TYR:HD1	1.69	0.57
14:O:138:HIS:NE2	14:O:159:SER:HB2	2.19	0.57
23:Y:279:ARG:HD3	23:Y:503:ILE:HG12	1.87	0.57
26:b:92:TRP:CZ2	26:b:97:ASN:HA	2.40	0.57
1:A:1890:PHE:HB3	1:A:1986:MET:HE1	1.86	0.57
4:D:78:A:O2'	4:D:79:C:O5'	2.20	0.57
6:F:504:HIS:HD2	6:F:511:ILE:HD11	1.68	0.57
11:L:7:C:OP1	33:f:174:LYS:HE3	2.05	0.57
17:R:93:ILE:HD13	17:R:166:ARG:O	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:U:37:LEU:O	20:U:41:GLU:HG2	2.05	0.57
24:Z:197:LEU:HD12	24:Z:197:LEU:C	2.29	0.57
28:G:239:TYR:HD1	28:G:242:LYS:HD2	1.70	0.57
1:A:472:ASN:HB2	3:C:390:SER:OG	2.05	0.56
1:A:2072:SER:O	28:G:527:ARG:NH2	2.38	0.56
2:B:891:ASP:OD1	2:B:892:GLN:N	2.38	0.56
3:C:883:ARG:NH2	3:C:912:ALA:O	2.35	0.56
4:D:174:G:C5	42:m:20:LYS:HE2	2.39	0.56
6:F:520:SER:O	6:F:874:GLY:HA2	2.04	0.56
15:P:230:MET:SD	20:U:73:ARG:HB3	2.45	0.56
29:d:185:VAL:HA	29:d:188:ILE:HD12	1.87	0.56
29:d:218:THR:HG22	29:d:222:TYR:HE2	1.68	0.56
1:A:416:GLU:HB3	1:A:419:THR:HG23	1.86	0.56
1:A:1405:ILE:CD1	1:A:1439:THR:HG21	2.35	0.56
1:A:1458:TRP:HE1	1:A:1489:PRO:HD2	1.70	0.56
2:B:1345:PHE:HE1	2:B:1348:PHE:HA	1.69	0.56
2:B:1585:LEU:HD21	2:B:1683:LEU:HD23	1.87	0.56
6:F:924:PHE:CD2	6:F:952:ARG:HD2	2.38	0.56
7:H:156:TYR:OH	10:K:27:THR:HG22	2.04	0.56
20:U:131:ILE:HG13	20:U:188:LEU:HD11	1.87	0.56
26:b:7:PRO:HG2	26:b:27:TRP:CD1	2.39	0.56
32:e:27:GLU:C	32:e:122:ASP:CG	2.73	0.56
36:n:60:ARG:C	36:n:62:THR:H	2.11	0.56
1:A:893:ARG:NH2	1:A:1136:GLY:O	2.38	0.56
1:A:1660:SER:HB3	1:A:1809:ASN:OD1	2.05	0.56
1:A:1846:ASN:O	1:A:1885:LYS:NZ	2.32	0.56
1:A:2384:ASN:OD1	1:A:2385:GLU:N	2.38	0.56
3:C:123:MET:HB2	3:C:199:LEU:HD23	1.87	0.56
6:F:541:ALA:HB2	6:F:618:TYR:CE1	2.40	0.56
6:F:642:LEU:HD21	6:F:644:ILE:HG23	1.87	0.56
6:F:1027:ILE:HD12	6:F:1045:MET:HE1	1.86	0.56
15:P:58:PRO:O	15:P:59:THR:HG23	2.05	0.56
15:P:66:CYS:HA	15:P:69:ARG:HG2	1.86	0.56
17:R:207:PRO:O	17:R:212:TRP:CG	2.58	0.56
22:W:186:SER:O	22:W:190:ILE:HD12	2.04	0.56
23:Y:220:ARG:NH1	23:Y:258:GLN:OE1	2.38	0.56
27:c:217:ILE:HD12	29:d:83:ARG:HG2	1.86	0.56
34:o:51:VAL:CG2	34:p:20:ARG:CB	2.77	0.56
1:A:366:GLU:HG3	1:A:372:ARG:HH11	1.69	0.56
1:A:1322:ALA:O	1:A:1323:SER:OG	2.21	0.56
3:C:292:ILE:HG12	3:C:311:ILE:HD13	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:501:ILE:HD13	3:C:567:ILE:HG23	1.87	0.56
5:E:28:U:H1'	19:T:121:ILE:HD13	1.86	0.56
6:F:1085:LEU:HB2	6:F:1097:PHE:HB2	1.88	0.56
6:F:1124:LEU:HB2	6:F:1130:ILE:CD1	2.35	0.56
15:P:242:LYS:NZ	20:U:83:TYR:OH	2.37	0.56
16:Q:215:PRO:CB	16:Q:217:TRP:CE3	2.88	0.56
17:R:9:ALA:CB	17:R:58:HIS:O	2.54	0.56
21:V:27:TYR:HD2	21:V:30:ASN:HD22	1.51	0.56
28:G:189:THR:O	28:G:231:GLN:NE2	2.29	0.56
1:A:805:PRO:HG2	1:A:808:ILE:HD12	1.87	0.56
1:A:1816:ARG:HH11	1:A:1816:ARG:CG	2.14	0.56
1:A:2189:LEU:O	1:A:2193:PHE:HB2	2.06	0.56
7:H:166:THR:HG22	7:H:167:LYS:N	2.21	0.56
15:P:231:GLU:O	15:P:235:LEU:N	2.38	0.56
15:P:303:TYR:HB3	15:P:307:PHE:CD2	2.34	0.56
23:Y:776:THR:O	23:Y:780:ILE:N	2.37	0.56
29:d:205:TRP:CE2	29:d:209:GLU:HG3	2.40	0.56
1:A:2306:ASN:HB2	1:A:2335:THR:HB	1.86	0.56
3:C:706:LEU:HD21	3:C:833:VAL:HG22	1.87	0.56
3:C:769:TYR:OH	3:C:774:LEU:HB2	2.05	0.56
21:V:49:THR:HG23	22:W:233:ASP:HB2	1.87	0.56
23:Y:223:LEU:HD11	47:Y:902:ADP:H4'	1.86	0.56
28:G:827:ILE:O	28:G:827:ILE:HG13	2.04	0.56
29:d:219:ARG:HH21	29:d:257:GLN:HG3	1.71	0.56
3:C:167:ASN:ND2	3:C:173:LYS:HG3	2.21	0.56
3:C:235:VAL:HG13	3:C:261:VAL:HG11	1.88	0.56
6:F:182:THR:O	6:F:183:THR:HG23	2.06	0.56
6:F:493:VAL:HA	6:F:937:LYS:HG2	1.87	0.56
6:F:701:LYS:HG2	6:F:718:LEU:HD23	1.86	0.56
6:F:936:PRO:C	6:F:937:LYS:HD2	2.30	0.56
6:F:1161:ASN:OD1	6:F:1162:GLY:N	2.39	0.56
9:J:8:LEU:HD21	9:J:93:GLY:HA3	1.87	0.56
17:R:13:VAL:CG1	17:R:17:GLU:HB3	2.35	0.56
22:W:170:LEU:N	22:W:170:LEU:HD22	2.20	0.56
1:A:1007:LYS:HD3	1:A:1141:PRO:HG3	1.88	0.56
2:B:901:VAL:HA	2:B:906:LEU:HB2	1.88	0.56
2:B:1474:ASP:HA	2:B:1511:LEU:HB2	1.86	0.56
6:F:527:LEU:HD12	6:F:528:PRO:HD2	1.87	0.56
15:P:167:ALA:HB3	33:f:203:PHE:HZ	1.69	0.56
15:P:300:ASP:OD1	15:P:300:ASP:N	2.38	0.56
24:Z:152:ILE:HD11	24:Z:194:LEU:HA	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:c:226:GLY:O	33:f:151:LYS:NZ	2.30	0.56
28:G:579:ILE:HD12	28:G:579:ILE:N	2.21	0.56
28:G:904:GLU:OE2	28:G:940:ASN:CB	2.54	0.56
36:n:55:GLU:OE2	36:n:58:ARG:HD2	2.05	0.56
1:A:454:LEU:N	3:C:357:GLY:O	2.37	0.56
2:B:448:LEU:HD21	2:B:899:LEU:HD21	1.86	0.56
6:F:200:ARG:HH11	6:F:250:PRO:HD3	1.70	0.56
6:F:944:ASN:HD21	6:F:979:CYS:H	1.54	0.56
6:F:1029:SER:OG	6:F:1045:MET:SD	2.57	0.56
15:P:301:LEU:N	15:P:301:LEU:HD23	2.21	0.56
16:Q:226:LEU:HD12	16:Q:226:LEU:O	2.05	0.56
17:R:142:ILE:CG2	17:R:180:ASN:ND2	2.69	0.56
28:G:163:GLU:HA	28:G:199:MET:HE2	1.87	0.56
29:d:117:HIS:C	29:d:120:ASN:HD22	2.09	0.56
34:q:294:HIS:CG	34:q:338:LEU:H	2.24	0.56
1:A:147:SER:HG	1:A:573:ARG:HH22	1.52	0.56
1:A:228:LYS:HD3	1:A:700:GLY:HA3	1.86	0.56
1:A:934:ARG:NH2	1:A:1587:PHE:CZ	2.73	0.56
2:B:1811:LEU:HD23	2:B:1814:LEU:HD12	1.88	0.56
3:C:90:LEU:HD22	14:O:211:LEU:HD22	1.87	0.56
6:F:181:ARG:NH1	9:J:84:ASP:OD1	2.39	0.56
6:F:534:LEU:HD21	6:F:550:LEU:HD11	1.88	0.56
10:K:23:ASP:OD1	10:K:24:GLU:N	2.35	0.56
11:L:19:U:O2'	15:P:175:PRO:HG2	2.06	0.56
11:L:43:G:N2	13:M:492:U:O2	2.39	0.56
24:Z:179:TYR:C	24:Z:179:TYR:CD1	2.84	0.56
26:b:17:THR:OG1	26:b:20:GLY:O	2.18	0.56
1:A:380:ARG:HH11	1:A:380:ARG:HG2	1.69	0.55
1:A:687:ILE:HD11	1:A:706:PRO:HG2	1.88	0.55
1:A:1094:ASP:OD1	11:L:25:A:N3	2.39	0.55
1:A:1145:MET:HB3	28:G:19:LEU:HB2	1.87	0.55
1:A:1367:ILE:O	1:A:1370:ARG:HB3	2.07	0.55
2:B:2042:ALA:O	2:B:2046:ASN:ND2	2.39	0.55
6:F:104:TYR:HD1	6:F:113:LEU:HA	1.70	0.55
11:L:19:U:OP2	11:L:19:U:C6	2.58	0.55
25:a:150:THR:HG22	25:a:152:TYR:N	2.21	0.55
28:G:386:TYR:CG	28:G:387:PRO:CD	2.88	0.55
29:d:40:LEU:HD21	29:d:44:ARG:HH21	1.71	0.55
31:v:611:THR:CB	31:v:623:LEU:CD1	2.84	0.55
32:e:46:LEU:CG	32:e:48:ALA:H	2.19	0.55
1:A:541:ASN:HD21	4:D:79:C:H5	1.52	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:930:ASN:HB3	1:A:933:GLU:OE1	2.06	0.55
1:A:1233:ARG:CD	18:S:131:THR:HG21	2.36	0.55
2:B:532:LEU:HD13	2:B:577:ARG:HD2	1.88	0.55
3:C:106:PHE:CZ	3:C:548:ARG:O	2.59	0.55
3:C:576:THR:HG22	3:C:592:PHE:HD2	1.71	0.55
6:F:161:GLN:HG2	6:F:163:ILE:HG23	1.87	0.55
6:F:608:ARG:HD3	6:F:610:ILE:HD11	1.87	0.55
6:F:638:SER:HB3	6:F:641:GLN:HB3	1.88	0.55
22:W:197:PHE:CZ	24:Z:463:ASN:CB	2.83	0.55
23:Y:591:VAL:HG11	23:Y:620:LEU:HD23	1.87	0.55
24:Z:184:GLN:HA	24:Z:184:GLN:NE2	2.21	0.55
29:d:69:ILE:HG21	29:d:104:ARG:CD	2.36	0.55
32:e:143:LEU:O	32:e:146:GLY:N	2.39	0.55
1:A:2255:LEU:H	1:A:2255:LEU:HD12	1.71	0.55
1:A:2314:TRP:NE1	1:A:2327:GLU:O	2.38	0.55
7:H:185:GLY:CA	8:I:72:ASN:HD21	2.19	0.55
17:R:150:HIS:HB3	17:R:155:GLN:HB2	1.88	0.55
19:T:156:THR:OG1	36:n:56:LEU:HD13	2.05	0.55
23:Y:699:GLU:C	23:Y:702:SER:CB	2.79	0.55
36:n:59:ARG:NH1	36:n:59:ARG:HG2	2.21	0.55
38:i:77:LEU:HD21	38:i:80:ILE:CD1	2.36	0.55
1:A:268:LEU:O	1:A:273:ASP:OD2	2.25	0.55
1:A:640:ARG:HG2	1:A:640:ARG:NH1	2.20	0.55
1:A:668:ARG:HD2	12:N:96:U:H4'	1.88	0.55
1:A:1405:ILE:HD13	1:A:1439:THR:HG21	1.87	0.55
2:B:1000:ASP:OD1	2:B:1001:LEU:N	2.40	0.55
2:B:1547:ASN:N	2:B:1720:VAL:O	2.39	0.55
2:B:2070:LYS:HD3	2:B:2127:GLU:HB3	1.89	0.55
3:C:715:MET:SD	3:C:772:ASN:HB3	2.46	0.55
6:F:115:ALA:HB2	6:F:169:LEU:HD12	1.88	0.55
9:J:103:LYS:O	9:J:104:LYS:CB	2.55	0.55
17:R:164:PHE:CE1	17:R:199:MET:HG3	2.42	0.55
19:T:111:LYS:HA	19:T:118:SER:HB2	1.88	0.55
20:U:48:ILE:HG22	20:U:49:ALA:N	2.21	0.55
21:V:87:LEU:HD21	22:W:222:ASN:HD21	1.71	0.55
26:b:60:TRP:HA	26:b:103:VAL:HG23	1.89	0.55
28:G:820:MET:HA	28:G:823:MET:HG2	1.88	0.55
3:C:437:ASP:OD1	3:C:441:ARG:NH2	2.40	0.55
3:C:617:LYS:HD2	3:C:666:ILE:HG23	1.87	0.55
3:C:672:ASP:OD1	3:C:673:PRO:HD2	2.06	0.55
4:D:174:G:O6	42:m:20:LYS:HB3	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:177:GLN:OE1	9:J:17:VAL:HG12	2.06	0.55
6:F:1216:CYS:SG	6:F:1228:PHE:HB2	2.46	0.55
7:H:141:VAL:HG11	7:H:165:CYS:SG	2.45	0.55
7:H:185:GLY:HA3	8:I:72:ASN:ND2	2.22	0.55
7:H:192:ARG:HH11	7:H:192:ARG:CG	2.18	0.55
9:J:79:LEU:HD21	28:G:866:LEU:HD21	1.87	0.55
13:M:506:U:OP2	28:G:698:ARG:NH1	2.40	0.55
15:P:87:ASN:HB3	15:P:90:SER:H	1.70	0.55
17:R:146:LEU:CG	17:R:147:ASN:H	2.20	0.55
17:R:207:PRO:O	17:R:212:TRP:CD1	2.59	0.55
24:Z:424:PHE:CE1	24:Z:448:MET:HE1	2.42	0.55
1:A:1012:TRP:CD1	1:A:1013:ILE:N	2.74	0.55
1:A:1588:LYS:HE3	11:L:31:A:OP1	2.06	0.55
1:A:1755:LYS:O	1:A:1759:TYR:HD2	1.89	0.55
2:B:739:GLN:HE22	2:B:823:GLY:HA2	1.71	0.55
2:B:1595:ALA:HB1	2:B:1637:VAL:HG11	1.89	0.55
2:B:1905:LEU:HD12	2:B:1908:ARG:HD3	1.87	0.55
3:C:803:VAL:HG22	3:C:813:ILE:HD12	1.88	0.55
6:F:180:THR:O	9:J:83:LYS:HB3	2.07	0.55
9:J:101:PHE:CE2	28:G:219:HIS:CD2	2.95	0.55
14:O:115:TYR:HD1	14:O:118:LEU:HD12	1.72	0.55
19:T:54:GLN:CG	36:n:69:TRP:CD2	2.89	0.55
22:W:188:LEU:CD2	24:Z:415:GLN:CG	2.85	0.55
24:Z:192:GLU:HB3	24:Z:195:GLU:OE2	2.05	0.55
27:c:202:LYS:O	27:c:204:LYS:N	2.38	0.55
3:C:601:ALA:HB1	3:C:645:LEU:HB3	1.88	0.55
3:C:778:THR:OG1	3:C:780:PRO:HD2	2.07	0.55
6:F:832:TRP:CD1	6:F:833:LYS:H	2.25	0.55
16:Q:257:GLU:HG3	16:Q:258:LEU:N	2.21	0.55
17:R:63:ARG:HH21	19:T:143:HIS:CD2	2.24	0.55
17:R:146:LEU:HG	17:R:147:ASN:H	1.72	0.55
25:a:168:PHE:C	25:a:169:LYS:HE2	2.31	0.55
1:A:1270:LEU:HD13	1:A:1275:MET:HG2	1.89	0.55
1:A:2259:ILE:HD11	1:A:2293:ILE:HD11	1.88	0.55
2:B:739:GLN:NE2	2:B:823:GLY:HA2	2.21	0.55
3:C:309:ASN:HD22	3:C:441:ARG:HH11	1.55	0.55
6:F:496:SER:HB3	6:F:497:PRO:HD3	1.89	0.55
6:F:716:ILE:HG21	6:F:759:ASP:O	2.06	0.55
23:Y:475:TYR:HE2	23:Y:477:ASN:CG	2.15	0.55
24:Z:178:ARG:HA	24:Z:198:PHE:CE1	2.42	0.55
32:e:33:ASN:CB	32:e:62:ASP:CB	2.85	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:q:292:TYR:CB	34:q:335:SER:HA	2.37	0.55
1:A:1335:TRP:HB2	1:A:1367:ILE:HD13	1.89	0.55
2:B:773:ASN:HD22	6:F:754:HIS:CE1	2.22	0.55
2:B:1608:ASP:O	2:B:1609:MET:HG2	2.06	0.55
2:B:1944:GLN:O	2:B:1948:LYS:N	2.29	0.55
5:E:28:U:H5"	19:T:118:SER:O	2.07	0.55
6:F:66:LYS:HB3	6:F:1225:VAL:HG22	1.89	0.55
16:Q:208:TYR:O	16:Q:209:ASN:HB3	2.07	0.55
17:R:31:ASN:HB3	17:R:34:TYR:O	2.07	0.55
17:R:109:LEU:HD13	17:R:113:GLY:HA2	1.88	0.55
19:T:156:THR:HG23	19:T:157:ASP:H	1.72	0.55
24:Z:168:LYS:HZ2	24:Z:171:ASP:HB2	1.71	0.55
33:f:111:ASN:O	33:f:114:THR:OG1	2.23	0.55
1:A:1951:PHE:HB3	1:A:1954:ILE:HD12	1.88	0.55
8:I:63:SER:HB3	28:G:810:THR:CG2	2.37	0.55
14:O:197:LEU:HB3	14:O:209:TRP:HB2	1.88	0.55
15:P:178:TYR:HE1	33:f:203:PHE:CG	2.25	0.55
20:U:45:LYS:O	20:U:46:GLU:C	2.51	0.55
28:G:277:THR:O	28:G:280:THR:OG1	2.24	0.55
28:G:337:VAL:HG11	28:G:359:ILE:HD11	1.87	0.55
31:v:682:LYS:O	31:v:686:ILE:HG12	2.07	0.55
36:n:55:GLU:O	36:n:59:ARG:HB2	2.07	0.55
1:A:2199:VAL:HG13	1:A:2200:LYS:HG3	1.89	0.54
2:B:1362:SER:O	2:B:1386:ASN:ND2	2.40	0.54
2:B:1548:ILE:HG12	2:B:1722:ILE:HD12	1.89	0.54
6:F:547:ASN:ND2	6:F:564:ASP:HB2	2.22	0.54
8:I:57:TYR:CZ	8:I:70:LEU:HD11	2.42	0.54
13:M:506:U:OP2	28:G:698:ARG:CZ	2.55	0.54
15:P:301:LEU:H	15:P:301:LEU:HD23	1.72	0.54
27:c:228:TYR:C	27:c:229:ASP:OD1	2.50	0.54
28:G:442:ILE:HD11	28:G:460:VAL:HB	1.89	0.54
28:G:542:THR:HG22	28:G:582:GLY:HA2	1.89	0.54
28:G:606:LEU:HD22	28:G:646:ILE:HD13	1.89	0.54
29:d:329:UNK:CB	31:v:642:GLU:HG3	2.38	0.54
1:A:354:PRO:O	1:A:355:LEU:HB3	2.08	0.54
1:A:396:ARG:HH11	1:A:396:ARG:CG	2.19	0.54
1:A:2402:GLU:OE1	1:A:2402:GLU:N	2.40	0.54
2:B:944:LEU:HG	2:B:948:MET:HE2	1.89	0.54
7:H:155:ARG:HH21	7:H:155:ARG:HG3	1.72	0.54
16:Q:101:THR:HG22	16:Q:120:LEU:CD2	2.35	0.54
17:R:245:GLU:HG3	17:R:249:MET:HE2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:G:919:ILE:HD11	28:G:937:VAL:HG11	1.89	0.54
32:e:139:GLU:O	32:e:151:ALA:CB	2.40	0.54
1:A:1424:HIS:CD2	30:X:6:ILE:CD1	2.91	0.54
2:B:567:VAL:HG13	2:B:606:VAL:HG12	1.88	0.54
2:B:1200:PRO:HG2	2:B:1297:TRP:CD1	2.42	0.54
6:F:594:MET:HB3	6:F:656:ILE:HG21	1.88	0.54
6:F:640:THR:OG1	6:F:686:GLN:O	2.21	0.54
14:O:206:VAL:HB	14:O:220:TYR:HB2	1.90	0.54
16:Q:217:TRP:CZ3	17:R:187:LYS:CD	2.86	0.54
17:R:206:LEU:HB3	17:R:209:ASP:CG	2.33	0.54
21:V:35:ILE:HD13	21:V:51:PHE:CE2	2.42	0.54
1:A:2314:TRP:CE2	1:A:2329:PHE:HB2	2.43	0.54
2:B:1977:MET:HE1	2:B:2102:VAL:HG21	1.88	0.54
3:C:802:ALA:HB2	3:C:843:LYS:HA	1.89	0.54
11:L:25:A:H3'	11:L:26:G:H5''	1.89	0.54
22:W:214:LEU:N	22:W:230:SER:OG	2.41	0.54
24:Z:179:TYR:C	24:Z:179:TYR:HD1	2.16	0.54
29:d:57:TYR:HD2	29:d:67:GLN:HG2	1.72	0.54
1:A:254:HIS:HD2	26:b:81:ARG:HG3	1.72	0.54
1:A:614:ARG:CZ	12:N:98:A:H5''	2.37	0.54
1:A:1267:VAL:HG22	1:A:1302:LEU:HD23	1.90	0.54
2:B:1620:TYR:CD1	2:B:1651:ILE:HG23	2.41	0.54
2:B:1929:LEU:HB3	2:B:1947:LEU:HD13	1.90	0.54
6:F:369:ILE:HD13	6:F:421:ILE:HD13	1.89	0.54
6:F:629:GLY:O	6:F:630:ILE:HG13	2.07	0.54
6:F:703:MET:HE1	6:F:713:LEU:HD13	1.89	0.54
24:Z:168:LYS:NZ	24:Z:168:LYS:O	2.37	0.54
2:B:1987:VAL:HG22	2:B:1988:TRP:O	2.08	0.54
3:C:772:ASN:HD21	3:C:815:GLY:N	2.06	0.54
6:F:390:LYS:HD2	6:F:410:PHE:HE1	1.73	0.54
8:I:57:TYR:CZ	8:I:70:LEU:CD1	2.89	0.54
11:L:19:U:O2	15:P:175:PRO:CD	2.55	0.54
16:Q:215:PRO:CG	16:Q:217:TRP:CE3	2.91	0.54
28:G:881:MET:O	28:G:885:ILE:HD12	2.07	0.54
1:A:477:MET:HE2	3:C:278:LYS:HE3	1.88	0.54
1:A:572:CYS:SG	1:A:629:MET:HE3	2.47	0.54
1:A:1447:TRP:HB3	1:A:1451:PHE:CE2	2.43	0.54
1:A:2408:GLN:HA	1:A:2408:GLN:NE2	2.21	0.54
2:B:1610:LEU:HD23	2:B:1636:GLY:HA3	1.89	0.54
6:F:368:GLY:HA2	6:F:380:LEU:O	2.08	0.54
6:F:673:ASP:OD1	6:F:674:THR:N	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:P:301:LEU:HG	15:P:302:GLN:O	2.07	0.54
28:G:18:GLN:HG3	28:G:19:LEU:N	2.23	0.54
34:q:467:LEU:CG	34:q:481:CYS:SG	2.96	0.54
1:A:1861:THR:OG1	1:A:1863:HIS:NE2	2.36	0.54
1:A:2262:GLN:HE22	1:A:2266:LEU:HD12	1.73	0.54
2:B:1549:GLN:NE2	2:B:1566:MET:SD	2.81	0.54
3:C:492:LEU:HD22	3:C:557:HIS:ND1	2.22	0.54
6:F:192:TYR:HB2	6:F:205:SER:OG	2.08	0.54
9:J:95:ASN:HD21	13:M:503:A:H1'	1.73	0.54
21:V:64:ARG:NH2	21:V:69:GLY:O	2.41	0.54
27:c:223:PRO:HA	29:d:89:GLU:HG3	1.89	0.54
29:d:181:ASN:O	29:d:185:VAL:N	2.35	0.54
2:B:1815:VAL:HG23	2:B:1821:GLU:HA	1.90	0.54
2:B:1956:PRO:HA	2:B:1959:ASN:HD22	1.73	0.54
2:B:2049:PRO:HG3	2:B:2097:GLU:OE2	2.08	0.54
3:C:697:ARG:CZ	3:C:849:GLY:HA2	2.38	0.54
3:C:769:TYR:HA	3:C:800:TYR:HE1	1.72	0.54
6:F:324:ASN:ND2	6:F:339:ASP:OD2	2.41	0.54
6:F:780:LEU:HD21	6:F:862:VAL:HG21	1.90	0.54
14:O:332:ARG:HD3	14:O:341:LEU:HD11	1.88	0.54
20:U:40:LEU:O	20:U:44:ASN:ND2	2.40	0.54
24:Z:177:LEU:CD2	24:Z:194:LEU:CD2	2.73	0.54
32:e:33:ASN:CB	32:e:62:ASP:HB3	2.38	0.54
1:A:1308:GLU:HG2	1:A:1311:LYS:HD2	1.90	0.54
1:A:1999:ILE:HD11	1:A:2007:ARG:NH2	2.23	0.54
2:B:2017:TYR:OH	2:B:2049:PRO:O	2.24	0.54
12:N:93:U:O2	12:N:93:U:H2'	2.08	0.54
13:M:509:A:N1	28:G:499:ASN:HB3	2.23	0.54
14:O:152:ASN:HD21	14:O:409:LYS:HB3	1.72	0.54
20:U:145:PHE:HB3	20:U:152:LEU:HD11	1.90	0.54
22:W:224:PHE:O	22:W:225:ALA:HB3	2.07	0.54
24:Z:192:GLU:O	24:Z:195:GLU:HG2	2.08	0.54
25:a:168:PHE:O	25:a:169:LYS:HG3	2.07	0.54
28:G:695:ASN:HD22	28:G:700:VAL:HG21	1.73	0.54
2:B:2140:LEU:HD13	2:B:2160:ILE:HG12	1.89	0.53
10:K:44:GLN:O	10:K:50:LEU:HD12	2.08	0.53
16:Q:226:LEU:CD2	16:Q:262:PHE:HE1	2.20	0.53
21:V:90:ASP:OD2	22:W:241:PHE:CD1	2.62	0.53
28:G:618:GLN:HE21	28:G:657:GLU:HB2	1.73	0.53
1:A:2041:PRO:HG2	1:A:2043:PHE:CE2	2.43	0.53
1:A:2149:LYS:HE3	1:A:2151:GLU:HB3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1889:PHE:HE1	2:B:1950:ILE:HG23	1.73	0.53
2:B:1933:TYR:HB2	2:B:1947:LEU:HD21	1.89	0.53
2:B:1987:VAL:HG13	2:B:2150:LEU:HD22	1.89	0.53
3:C:646:GLY:HA3	3:C:652:MET:HE3	1.90	0.53
6:F:719:GLN:OE1	25:a:243:SER:HA	2.08	0.53
6:F:994:LEU:HB2	6:F:1008:ILE:HD11	1.91	0.53
6:F:1173:LEU:HD21	7:H:268:ASP:OD1	2.08	0.53
8:I:80:SER:O	8:I:83:ARG:HB2	2.08	0.53
16:Q:214:ILE:HD11	16:Q:218:LYS:HG3	1.89	0.53
17:R:13:VAL:HG13	17:R:17:GLU:HB3	1.90	0.53
22:W:213:LYS:HB3	22:W:230:SER:CB	2.38	0.53
25:a:172:TRP:CD1	25:a:173:LYS:N	2.76	0.53
31:v:726:ARG:HA	31:v:729:TYR:CD2	2.44	0.53
1:A:404:ASN:OD1	3:C:927:MET:HE1	2.08	0.53
1:A:1881:THR:OG1	1:A:1890:PHE:HB2	2.08	0.53
1:A:2359:TYR:HA	1:A:2362:MET:HB2	1.90	0.53
1:A:2409:ILE:HG22	1:A:2411:VAL:CG2	2.39	0.53
6:F:337:VAL:HG22	6:F:346:LEU:HB2	1.90	0.53
6:F:930:LEU:HD13	6:F:984:ILE:HG23	1.89	0.53
28:G:386:TYR:CB	28:G:387:PRO:CD	2.86	0.53
1:A:1561:LEU:HD12	1:A:1608:LEU:HD22	1.89	0.53
1:A:2189:LEU:HD13	1:A:2224:VAL:HG23	1.89	0.53
2:B:770:LEU:HD22	2:B:799:SER:O	2.08	0.53
2:B:1214:SER:HB3	2:B:1281:GLN:HE21	1.72	0.53
2:B:1486:ALA:HB2	2:B:1745:TYR:HB3	1.89	0.53
2:B:1524:TRP:HB2	2:B:1780:ARG:HG3	1.90	0.53
1:A:1846:ASN:C	1:A:1847:ASP:O	2.51	0.53
5:E:39:G:N1	17:R:120:TYR:O	2.42	0.53
6:F:1091:HIS:CE1	28:G:963:TYR:OH	2.61	0.53
6:F:1233:SER:O	6:F:1234:LYS:HG2	2.08	0.53
16:Q:207:LEU:HB3	16:Q:210:ILE:HD11	1.90	0.53
25:a:251:GLN:O	25:a:255:ASN:N	2.41	0.53
28:G:327:TRP:C	28:G:327:TRP:CD1	2.86	0.53
28:G:372:ILE:HD13	28:G:410:LYS:HE3	1.91	0.53
33:f:196:ILE:HB	33:f:200:ASN:HD21	1.73	0.53
1:A:1851:PHE:O	1:A:1881:THR:HA	2.09	0.53
2:B:162:ILE:HG22	2:B:165:ARG:HH21	1.72	0.53
2:B:1091:GLY:O	2:B:1095:ASN:ND2	2.37	0.53
2:B:1372:LYS:HD3	2:B:1708:GLY:HA3	1.89	0.53
2:B:1457:ARG:NH1	2:B:1854:SER:O	2.39	0.53
13:M:515:U:O2	13:M:515:U:H2'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:P:58:PRO:C	15:P:59:THR:HG23	2.34	0.53
15:P:314:ALA:O	22:W:258:GLN:NE2	2.42	0.53
23:Y:704:HIS:CD2	23:Y:847:LEU:CG	2.91	0.53
25:a:135:VAL:HG12	25:a:137:MET:HE2	1.90	0.53
34:p:102:LEU:O	34:p:105:LEU:CG	2.57	0.53
1:A:428:LEU:HD22	3:C:896:GLY:O	2.09	0.53
1:A:681:LYS:O	1:A:684:LYS:HB3	2.08	0.53
1:A:731:THR:HG21	15:P:86:ASN:HD21	1.74	0.53
1:A:1372:LYS:HG2	1:A:1383:PHE:CD2	2.44	0.53
1:A:2184:VAL:HB	1:A:2220:GLU:HG2	1.91	0.53
2:B:1992:ASN:HD21	2:B:2005:LEU:HD13	1.73	0.53
3:C:132:ARG:NH1	3:C:132:ARG:HG3	2.20	0.53
4:D:174:G:H8	43:g:99:ASP:OD2	1.91	0.53
6:F:1018:ASP:OD1	6:F:1019:ILE:N	2.41	0.53
28:G:945:TYR:HB3	28:G:948:ALA:HB3	1.90	0.53
38:i:27:VAL:HG22	38:i:92:SER:HB2	1.91	0.53
1:A:1348:GLU:HG2	1:A:1446:THR:HB	1.91	0.53
2:B:1547:ASN:O	2:B:1722:ILE:N	2.39	0.53
6:F:641:GLN:HE22	6:F:705:LEU:HD23	1.73	0.53
6:F:642:LEU:HB3	6:F:654:PHE:HB2	1.90	0.53
6:F:1163:ALA:HB1	6:F:1165:LYS:NZ	2.23	0.53
9:J:51:PHE:CE2	9:J:54:GLN:HG2	2.44	0.53
10:K:54:SER:HA	10:K:65:THR:HG21	1.89	0.53
15:P:178:TYR:HE1	33:f:203:PHE:CD2	2.27	0.53
15:P:305:SER:HA	22:W:221:GLU:OE1	2.09	0.53
22:W:209:LEU:HD12	22:W:209:LEU:C	2.34	0.53
24:Z:203:LYS:O	24:Z:204:ASP:CB	2.57	0.53
28:G:885:ILE:HG23	28:G:888:ILE:HD12	1.91	0.53
1:A:401:PRO:O	1:A:402:TRP:HB3	2.09	0.53
1:A:1461:TYR:HD1	1:A:1480:LEU:HD11	1.73	0.53
2:B:483:LEU:HB2	2:B:488:GLN:HG2	1.90	0.53
3:C:183:GLN:HE22	3:C:654:CYS:HA	1.74	0.53
3:C:200:CYS:SG	3:C:210:ILE:HD12	2.49	0.53
6:F:493:VAL:O	6:F:499:SER:OG	2.18	0.53
6:F:831:THR:OG1	6:F:835:VAL:O	2.14	0.53
6:F:1117:HIS:O	6:F:1133:ASP:HA	2.08	0.53
17:R:117:PHE:O	17:R:129:SER:HA	2.08	0.53
21:V:82:GLN:HB3	22:W:168:GLN:NE2	2.24	0.53
23:Y:258:GLN:NE2	23:Y:290:VAL:HG13	2.22	0.53
28:G:489:VAL:HG12	28:G:491:ARG:H	1.74	0.53
28:G:696:LYS:HG2	28:G:697:HIS:H	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1156:HIS:HD2	1:A:1158:ILE:HB	1.74	0.53
1:A:2409:ILE:CG2	1:A:2411:VAL:HG23	2.38	0.53
2:B:618:ASN:HB3	2:B:621:ASN:HD22	1.74	0.53
2:B:1999:HIS:H	2:B:2089:GLU:CD	2.17	0.53
2:B:2006:GLU:HA	2:B:2009:LYS:HB3	1.90	0.53
13:M:516:U:H5'	28:G:291:GLU:OE2	2.09	0.53
16:Q:291:ILE:HG23	16:Q:292:PRO:HA	1.91	0.53
25:a:216:HIS:O	25:a:217:TYR:CD1	2.62	0.53
28:G:894:HIS:O	28:G:898:ARG:HG2	2.09	0.53
34:p:124:ALA:O	34:p:127:LEU:CG	2.57	0.53
1:A:323:THR:O	1:A:323:THR:HG22	2.08	0.52
2:B:1334:LEU:HD22	2:B:1340:SER:HA	1.91	0.52
6:F:75:CYS:SG	6:F:94:CYS:HB3	2.48	0.52
6:F:1031:ILE:HD11	6:F:1045:MET:SD	2.49	0.52
14:O:115:TYR:HA	14:O:118:LEU:HG	1.91	0.52
14:O:132:SER:HB3	14:O:427:LYS:HB2	1.89	0.52
16:Q:108:MET:HG3	16:Q:109:MET:HE2	1.91	0.52
16:Q:209:ASN:HB3	16:Q:288:ILE:O	2.10	0.52
23:Y:361:LEU:HD21	23:Y:597:LEU:HD13	1.91	0.52
29:d:51:ARG:NH2	29:d:75:GLU:OE1	2.39	0.52
37:k:31:ILE:HD11	37:k:49:ILE:HD12	1.90	0.52
1:A:946:ASN:HB3	1:A:949:ASP:HB3	1.91	0.52
1:A:978:ILE:N	18:S:173:HIS:O	2.42	0.52
3:C:234:LEU:HD21	3:C:439:ILE:HG23	1.91	0.52
3:C:271:ASP:HB2	3:C:275:LEU:HD23	1.91	0.52
3:C:758:ASP:HB3	3:C:761:ALA:HB3	1.90	0.52
6:F:97:THR:O	6:F:98:GLU:C	2.51	0.52
6:F:641:GLN:NE2	6:F:705:LEU:HD23	2.23	0.52
16:Q:108:MET:SD	27:c:219:TYR:OH	2.67	0.52
19:T:104:CYS:N	19:T:153:CYS:SG	2.70	0.52
1:A:394:ARG:HH11	1:A:394:ARG:HG3	1.74	0.52
1:A:1831:GLN:O	1:A:1832:GLU:C	2.52	0.52
2:B:596:ARG:HD2	2:B:599:ILE:HD12	1.92	0.52
2:B:2103:LEU:HD11	2:B:2140:LEU:HD23	1.91	0.52
6:F:299:PRO:HD2	6:F:377:PHE:CZ	2.44	0.52
6:F:987:PHE:CD2	6:F:1054:LEU:HB2	2.44	0.52
13:M:506:U:H3'	13:M:506:U:O2	2.10	0.52
14:O:224:LEU:HD11	18:S:10:GLU:HA	1.92	0.52
14:O:229:THR:HG21	14:O:272:VAL:N	2.24	0.52
16:Q:253:PHE:HB3	16:Q:258:LEU:HD12	1.90	0.52
26:b:47:PHE:CD1	26:b:64:ASN:HB3	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:c:223:PRO:O	27:c:224:MET:HG2	2.09	0.52
1:A:1771:THR:HA	1:A:1789:ASN:HD22	1.74	0.52
2:B:805:HIS:O	2:B:813:ARG:HD3	2.10	0.52
2:B:1260:THR:OG1	2:B:1262:ASP:OD1	2.25	0.52
2:B:1431:ASP:OD2	2:B:2096:LEU:HG	2.10	0.52
9:J:101:PHE:CD2	28:G:219:HIS:CG	2.97	0.52
15:P:319:HIS:CD2	15:P:320:GLU:N	2.78	0.52
21:V:17:LEU:HD23	22:W:249:GLN:OE1	2.09	0.52
23:Y:467:LYS:CB	23:Y:494:CYS:CA	2.88	0.52
24:Z:118:LEU:HB3	24:Z:154:VAL:HG22	1.90	0.52
34:q:405:ASP:CB	35:t:30:ASN:CG	2.82	0.52
1:A:749:ARG:HG3	1:A:753:TYR:CE2	2.45	0.52
1:A:1069:LEU:HD23	1:A:1120:VAL:HG21	1.90	0.52
1:A:1465:ARG:HG3	15:P:301:LEU:HD13	1.91	0.52
1:A:2198:ASP:OD1	1:A:2199:VAL:N	2.42	0.52
2:B:1335:GLY:N	2:B:1360:TYR:OH	2.43	0.52
3:C:251:GLN:NE2	3:C:255:GLN:HE21	2.05	0.52
3:C:486:VAL:HG11	3:C:564:ILE:HD11	1.91	0.52
6:F:332:GLU:HG2	6:F:333:ASN:N	2.25	0.52
6:F:504:HIS:CD2	6:F:511:ILE:HD11	2.45	0.52
6:F:1298:SER:C	6:F:1300:LEU:H	2.18	0.52
11:L:6:U:H2'	11:L:7:C:C6	2.44	0.52
12:N:106:A:H2'	12:N:107:U:O4'	2.08	0.52
15:P:301:LEU:O	15:P:302:GLN:HG2	2.10	0.52
15:P:318:ARG:HG2	15:P:319:HIS:O	2.09	0.52
21:V:50:VAL:HG12	22:W:237:ARG:CD	2.40	0.52
28:G:904:GLU:OE2	28:G:940:ASN:HB2	2.10	0.52
34:q:292:TYR:CB	34:q:336:GLY:N	2.72	0.52
1:A:653:ILE:HD11	1:A:704:TRP:CE2	2.45	0.52
1:A:874:ILE:O	1:A:875:THR:OG1	2.24	0.52
1:A:1679:GLU:OE2	1:A:1706:VAL:HA	2.10	0.52
1:A:1790:TRP:HZ3	1:A:1798:ILE:HD12	1.75	0.52
2:B:778:LYS:HG2	2:B:782:LYS:HE3	1.90	0.52
2:B:947:ARG:HB3	2:B:955:TYR:CE2	2.45	0.52
2:B:1343:PHE:HE2	2:B:1385:LEU:HD11	1.75	0.52
14:O:362:ASP:CG	14:O:379:LYS:HZ3	2.17	0.52
16:Q:43:LEU:HD11	16:Q:57:LYS:HG3	1.91	0.52
16:Q:208:TYR:HB2	16:Q:290:ILE:HD12	1.92	0.52
23:Y:240:GLN:HG3	23:Y:373:LYS:HG2	1.92	0.52
23:Y:271:LEU:CG	23:Y:341:SER:OG	2.57	0.52
28:G:786:GLY:HA2	28:G:823:MET:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:e:170:ASN:O	32:e:171:GLN:C	2.52	0.52
1:A:947:PRO:HB3	28:G:48:LEU:HD13	1.92	0.52
1:A:1017:ASP:O	1:A:1509:ARG:NH2	2.43	0.52
1:A:1211:SER:OG	1:A:1268:ARG:NH1	2.43	0.52
1:A:1697:SER:OG	1:A:1767:TYR:OH	2.26	0.52
2:B:828:LEU:HG	2:B:830:CYS:SG	2.50	0.52
3:C:178:LEU:CD1	3:C:214:ASP:HB2	2.40	0.52
3:C:629:TYR:OH	3:C:658:ASP:OD2	2.25	0.52
3:C:681:CYS:HB3	3:C:850:LEU:HD12	1.92	0.52
3:C:869:HIS:HD2	3:C:925:LEU:HB3	1.75	0.52
16:Q:217:TRP:CD2	17:R:187:LYS:HD3	2.44	0.52
28:G:794:PRO:HG2	28:G:827:ILE:HD13	1.90	0.52
28:G:801:ILE:HG22	28:G:816:VAL:HG13	1.92	0.52
1:A:180:PRO:O	1:A:181:HIS:HB2	2.08	0.52
1:A:1831:GLN:C	1:A:1833:PRO:HD2	2.35	0.52
2:B:457:LYS:HB3	2:B:458:PRO:HD2	1.92	0.52
2:B:1400:PRO:HG3	2:B:1478:GLU:HG3	1.91	0.52
7:H:172:VAL:HG23	28:G:934:PHE:CE2	2.45	0.52
8:I:55:ASN:HB2	8:I:56:PRO:CD	2.40	0.52
16:Q:256:SER:O	16:Q:259:GLY:CA	2.58	0.52
18:S:9:LEU:CD2	18:S:11:ALA:N	2.72	0.52
22:W:190:ILE:C	22:W:192:ASP:N	2.57	0.52
24:Z:181:LEU:CD2	24:Z:191:ARG:HG3	2.39	0.52
34:q:341:ASP:O	34:q:342:SER:CB	2.56	0.52
1:A:389:HIS:HB2	3:C:653:ASP:OD1	2.10	0.52
1:A:1285:VAL:HG22	1:A:1301:TYR:HD1	1.75	0.52
1:A:1304:VAL:H	1:A:1353:THR:HG21	1.74	0.52
1:A:1372:LYS:HB3	1:A:1377:SER:O	2.10	0.52
1:A:1751:TYR:O	1:A:1755:LYS:HG2	2.10	0.52
1:A:2071:ILE:HG13	1:A:2074:LEU:HD12	1.92	0.52
2:B:1331:THR:HA	2:B:1334:LEU:HD13	1.91	0.52
2:B:2099:TRP:HB2	2:B:2117:VAL:HG23	1.91	0.52
6:F:71:PHE:O	6:F:430:LEU:HD21	2.10	0.52
6:F:678:LYS:HD2	6:F:727:ASP:HA	1.90	0.52
16:Q:219:ILE:O	16:Q:222:THR:OG1	2.16	0.52
19:T:57:HIS:CD2	36:n:69:TRP:CZ3	2.98	0.52
26:b:67:SER:HA	26:b:97:ASN:HB2	1.91	0.52
31:v:687:LEU:HD23	31:v:713:ILE:HA	1.91	0.52
1:A:2309:ASP:HA	1:A:2312:TYR:HD2	1.74	0.52
2:B:467:ALA:HB2	2:B:704:SER:HB3	1.90	0.52
2:B:1256:VAL:O	2:B:1556:HIS:NE2	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1820:ILE:HA	2:B:1846:THR:HA	1.91	0.52
6:F:180:THR:HG21	6:F:188:SER:CB	2.40	0.52
17:R:143:ASP:O	17:R:146:LEU:N	2.42	0.52
21:V:49:THR:CG2	22:W:233:ASP:HB2	2.40	0.52
22:W:213:LYS:C	22:W:230:SER:OG	2.53	0.52
28:G:894:HIS:O	28:G:898:ARG:CG	2.58	0.52
1:A:380:ARG:HH11	1:A:380:ARG:CG	2.23	0.51
1:A:614:ARG:HG2	1:A:614:ARG:NH1	2.12	0.51
1:A:1755:LYS:HE3	1:A:1759:TYR:CE2	2.45	0.51
1:A:1828:SER:HB3	28:G:612:LYS:HD3	1.92	0.51
2:B:134:ASP:OD2	2:B:748:LYS:HB2	2.11	0.51
2:B:1554:VAL:HG23	2:B:1557:ILE:HD11	1.92	0.51
3:C:253:ILE:O	3:C:257:ILE:HG13	2.09	0.51
3:C:794:GLN:HE21	3:C:835:LYS:HE3	1.75	0.51
7:H:153:ASP:OD2	11:L:58:A:OP1	2.28	0.51
21:V:105:ASP:OD1	21:V:106:HIS:N	2.43	0.51
24:Z:150:LEU:O	24:Z:154:VAL:HG23	2.10	0.51
24:Z:416:GLY:O	24:Z:420:ILE:HD12	2.10	0.51
28:G:539:HIS:O	28:G:543:ARG:CG	2.58	0.51
29:d:144:GLU:OE1	33:f:109:LEU:HD23	2.09	0.51
34:q:309:GLY:O	34:q:325:HIS:CG	2.63	0.51
1:A:218:SER:HB2	1:A:317:PRO:HG2	1.93	0.51
2:B:569:GLU:OE1	2:B:572:ARG:NH2	2.40	0.51
4:D:81:A:H4'	4:D:82:A:OP2	2.10	0.51
6:F:59:TYR:CD2	6:F:1237:VAL:HG21	2.45	0.51
6:F:333:ASN:O	6:F:350:ILE:HG22	2.10	0.51
15:P:85:SER:O	15:P:87:ASN:N	2.43	0.51
15:P:178:TYR:CE1	33:f:203:PHE:CE2	2.98	0.51
17:R:14:LYS:CA	17:R:14:LYS:CE	2.87	0.51
17:R:161:ARG:O	17:R:165:SER:HB3	2.09	0.51
25:a:162:LEU:HG	25:a:164:SER:CB	2.41	0.51
25:a:178:TRP:CE3	28:G:792:CYS:SG	2.98	0.51
27:c:228:TYR:CD1	29:d:119:ARG:HG2	2.46	0.51
1:A:258:ILE:HG22	1:A:259:GLU:O	2.10	0.51
1:A:285:PRO:HD2	1:A:298:TYR:OH	2.10	0.51
1:A:1180:GLU:HA	1:A:1183:THR:HG22	1.93	0.51
1:A:1281:ASN:ND2	1:A:1285:VAL:HB	2.25	0.51
1:A:1496:GLN:NE2	1:A:1531:HIS:O	2.42	0.51
2:B:708:CYS:SG	2:B:729:LYS:HE2	2.51	0.51
2:B:1882:VAL:O	2:B:1885:THR:OG1	2.28	0.51
3:C:277:LEU:HB3	3:C:279:LEU:HD13	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:929:ILE:HG12	6:F:941:PHE:HD1	1.75	0.51
9:J:51:PHE:CZ	9:J:54:GLN:CB	2.93	0.51
9:J:51:PHE:CZ	9:J:54:GLN:CG	2.93	0.51
15:P:40:LEU:HG	15:P:41:ASP:N	2.23	0.51
23:Y:308:PHE:HA	23:Y:743:GLN:HG3	1.91	0.51
24:Z:459:ARG:C	24:Z:463:ASN:ND2	2.63	0.51
36:n:55:GLU:O	36:n:58:ARG:HG3	2.09	0.51
1:A:140:ARG:HH21	1:A:252:GLU:CB	2.24	0.51
1:A:212:VAL:O	1:A:216:GLN:HG3	2.10	0.51
1:A:1038:ILE:HG13	1:A:1039:TRP:N	2.25	0.51
2:B:126:TRP:CH2	2:B:177:ILE:HD11	2.46	0.51
2:B:1342:VAL:HB	2:B:1415:ARG:HH11	1.75	0.51
2:B:1398:ILE:HB	2:B:1473:TYR:HD1	1.74	0.51
3:C:145:GLY:O	3:C:149:LEU:N	2.43	0.51
14:O:156:ILE:HD13	14:O:197:LEU:HD22	1.91	0.51
17:R:212:TRP:O	17:R:215:ARG:HD3	2.10	0.51
24:Z:177:LEU:HD21	24:Z:194:LEU:CD2	2.37	0.51
28:G:476:ARG:HG2	28:G:513:LEU:HD22	1.93	0.51
28:G:542:THR:HG22	28:G:582:GLY:CA	2.39	0.51
1:A:922:VAL:HG22	1:A:1519:LEU:HD21	1.93	0.51
1:A:1739:ARG:HG2	1:A:1740:TYR:N	2.26	0.51
2:B:158:GLU:OE2	2:B:165:ARG:NH2	2.43	0.51
2:B:1580:SER:O	2:B:1677:THR:OG1	2.29	0.51
6:F:328:VAL:HG22	6:F:337:VAL:HG12	1.91	0.51
16:Q:209:ASN:HD21	16:Q:288:ILE:CG2	2.23	0.51
34:q:298:ASN:O	34:q:299:THR:CB	2.57	0.51
1:A:640:ARG:HH11	1:A:640:ARG:CG	2.23	0.51
1:A:1748:ILE:HD13	1:A:1783:MET:C	2.36	0.51
3:C:318:LEU:HB3	3:C:425:LEU:HD12	1.93	0.51
7:H:234:GLN:HB3	7:H:235:PRO:HA	1.93	0.51
12:N:101:U:C4	25:a:161:PHE:CE2	2.97	0.51
13:M:491:C:H2'	13:M:492:U:O4'	2.10	0.51
16:Q:69:ASN:HD22	16:Q:126:THR:HB	1.73	0.51
20:U:40:LEU:CG	20:U:49:ALA:HB2	2.37	0.51
21:V:81:ASP:HB2	22:W:167:VAL:HG21	1.92	0.51
23:Y:651:PHE:HB2	23:Y:783:PHE:HE1	1.76	0.51
24:Z:204:ASP:C	24:Z:205:TYR:CD2	2.88	0.51
28:G:408:ARG:HA	28:G:412:LEU:HB2	1.92	0.51
34:r:124:ALA:O	34:r:127:LEU:CG	2.59	0.51
1:A:1082:ILE:HG23	1:A:1113:ILE:HD11	1.92	0.51
1:A:1268:ARG:HE	1:A:1301:TYR:HD2	1.57	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1466:GLN:O	1:A:1470:GLN:HB2	2.11	0.51
1:A:1843:LEU:HD23	1:A:1843:LEU:H	1.74	0.51
3:C:109:LEU:HD21	4:D:43:G:C6	2.45	0.51
6:F:666:LEU:HA	6:F:667:THR:OG1	2.10	0.51
9:J:95:ASN:HD21	13:M:503:A:C1'	2.24	0.51
10:K:42:THR:HG22	28:G:947:ASP:CG	2.36	0.51
12:N:110:U:O2	12:N:110:U:H2'	2.11	0.51
15:P:179:THR:OG1	33:f:196:ILE:HD12	2.11	0.51
22:W:167:VAL:HG13	22:W:209:LEU:CD2	2.41	0.51
22:W:223:ARG:HG3	22:W:242:GLU:OE2	2.11	0.51
24:Z:312:LEU:HD12	24:Z:350:MET:HE1	1.93	0.51
24:Z:368:ASN:HA	24:Z:372:ASP:HB3	1.93	0.51
25:a:168:PHE:C	25:a:169:LYS:HZ3	2.19	0.51
26:b:26:LEU:HD23	26:b:118:GLY:HA3	1.93	0.51
28:G:925:HIS:CG	28:G:926:PRO:HD2	2.46	0.51
36:n:59:ARG:HH11	36:n:59:ARG:CG	2.24	0.51
1:A:1543:ARG:HD3	15:P:328:LEU:HD13	1.93	0.51
1:A:1711:VAL:HG11	1:A:1789:ASN:HB3	1.93	0.51
2:B:1398:ILE:O	2:B:1474:ASP:N	2.36	0.51
2:B:1958:ILE:HD13	2:B:1979:LEU:HD23	1.92	0.51
3:C:141:PRO:O	3:C:146:LYS:NZ	2.44	0.51
3:C:715:MET:HG2	3:C:817:GLN:HB2	1.92	0.51
3:C:801:TRP:CD1	3:C:843:LYS:HD2	2.46	0.51
6:F:67:LYS:NZ	6:F:119:ASN:HD21	2.09	0.51
6:F:704:SER:O	6:F:705:LEU:HD12	2.11	0.51
15:P:301:LEU:HD11	15:P:303:TYR:CZ	2.45	0.51
16:Q:205:PHE:CD2	16:Q:291:ILE:HD11	2.46	0.51
22:W:208:SER:CB	22:W:214:LEU:HD12	2.41	0.51
1:A:329:TYR:CD2	1:A:330:LEU:HG	2.45	0.51
1:A:380:ARG:CB	1:A:380:ARG:CZ	2.89	0.51
1:A:484:PHE:CD1	4:D:81:A:C6	2.99	0.51
1:A:839:HIS:ND1	4:D:95:C:O2	2.43	0.51
1:A:1008:LEU:CD2	1:A:1073:ILE:HD11	2.41	0.51
1:A:1211:SER:O	1:A:1257:ASN:ND2	2.44	0.51
1:A:2194:ILE:HD11	1:A:2293:ILE:HG21	1.92	0.51
22:W:217:LYS:HB3	22:W:218:PRO:HD2	1.93	0.51
28:G:338:GLN:O	28:G:341:GLY:N	2.44	0.51
28:G:591:ASP:OD1	28:G:592:ILE:HD12	2.09	0.51
28:G:823:MET:O	28:G:827:ILE:HG12	2.10	0.51
29:d:170:ASN:HA	29:d:173:VAL:HG22	1.92	0.51
33:f:196:ILE:H	33:f:200:ASN:HD22	1.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1253:LYS:O	1:A:1274:ARG:NH2	2.44	0.51
1:A:1386:ALA:O	1:A:1390:THR:HG23	2.11	0.51
2:B:1476:ALA:HB3	2:B:1512:SER:HB2	1.92	0.51
3:C:104:THR:HG22	3:C:181:LEU:HA	1.93	0.51
6:F:856:ASP:OD1	6:F:857:VAL:N	2.43	0.51
10:K:39:THR:HG22	28:G:950:VAL:HG13	1.92	0.51
29:d:232:LEU:HD23	29:d:241:MET:HE2	1.93	0.51
33:f:182:GLN:O	33:f:186:ALA:HB2	2.10	0.51
1:A:261:LEU:HD22	1:A:642:GLY:HA2	1.94	0.50
1:A:333:LYS:O	1:A:336:PHE:N	2.44	0.50
1:A:461:LEU:HD11	3:C:380:PRO:HB2	1.92	0.50
1:A:1057:MET:HG3	1:A:1239:THR:CG2	2.41	0.50
1:A:1057:MET:CE	1:A:1114:PHE:CE1	2.92	0.50
1:A:1389:TYR:CE1	1:A:1401:SER:HB3	2.46	0.50
2:B:563:LEU:O	2:B:567:VAL:HG23	2.11	0.50
2:B:675:PRO:HD2	2:B:906:LEU:O	2.11	0.50
2:B:1351:ILE:HD12	2:B:1374:THR:HG21	1.92	0.50
2:B:1686:ASN:HB3	2:B:1695:TYR:HB3	1.93	0.50
3:C:177:TYR:CD1	3:C:548:ARG:CD	2.94	0.50
6:F:493:VAL:HG13	6:F:499:SER:OG	2.10	0.50
14:O:221:TYR:O	14:O:251:TRP:HH2	1.93	0.50
17:R:22:ILE:CG2	17:R:30:PHE:CE2	2.93	0.50
17:R:72:PHE:HD1	17:R:90:LEU:HB2	1.76	0.50
19:T:54:GLN:CD	36:n:69:TRP:CG	2.89	0.50
21:V:19:PRO:HA	21:V:22:SER:OG	2.11	0.50
21:V:33:ILE:HG22	21:V:85:THR:HG23	1.94	0.50
23:Y:353:LEU:HD21	23:Y:582:ILE:HA	1.93	0.50
25:a:211:VAL:HG22	25:a:217:TYR:HE1	1.76	0.50
26:b:70:GLU:OE1	26:b:72:ARG:NE	2.42	0.50
29:d:109:GLU:HB3	29:d:118:ALA:HB2	1.92	0.50
31:v:606:GLN:HA	31:v:609:GLU:CG	2.41	0.50
32:e:27:GLU:O	32:e:122:ASP:CB	2.50	0.50
1:A:228:LYS:HG2	1:A:695:LEU:CD1	2.40	0.50
1:A:763:MET:HE1	1:A:779:ALA:CB	2.42	0.50
1:A:879:ALA:HB1	15:P:208:LEU:HD21	1.94	0.50
1:A:928:ARG:CD	1:A:1582:GLU:OE2	2.51	0.50
1:A:1678:ILE:HD13	1:A:1703:MET:HE1	1.93	0.50
2:B:1877:LYS:HE3	2:B:1912:ARG:O	2.10	0.50
3:C:711:ALA:HB2	3:C:821:LEU:HD11	1.93	0.50
6:F:1323:CYS:HB3	6:F:1353:ILE:HD12	1.93	0.50
8:I:42:TYR:HB2	8:I:45:GLN:HG3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Q:222:THR:HA	16:Q:225:GLN:HE21	1.76	0.50
28:G:624:CYS:O	28:G:628:ILE:HG12	2.11	0.50
28:G:763:LEU:O	28:G:766:LEU:N	2.44	0.50
28:G:922:GLY:C	28:G:934:PHE:HD2	2.19	0.50
39:h:74:ARG:HD3	43:g:101:VAL:O	2.12	0.50
1:A:1458:TRP:CD1	28:G:24:SER:O	2.64	0.50
1:A:1642:LYS:CE	25:a:138:ASP:OD2	2.59	0.50
1:A:1889:LEU:HG	1:A:1991:ILE:HG13	1.94	0.50
3:C:161:ILE:HD12	3:C:164:MET:HE3	1.92	0.50
3:C:667:GLU:OE1	3:C:667:GLU:N	2.44	0.50
3:C:715:MET:HB2	3:C:720:ILE:HD11	1.93	0.50
7:H:192:ARG:CZ	7:H:192:ARG:CB	2.89	0.50
9:J:3:ARG:HH12	28:G:901:GLU:CD	2.19	0.50
17:R:210:LYS:HD3	17:R:210:LYS:C	2.37	0.50
23:Y:699:GLU:H	23:Y:706:LEU:CG	2.24	0.50
2:B:1486:ALA:HB1	2:B:1746:LEU:HA	1.92	0.50
3:C:778:THR:HG23	3:C:781:ASP:H	1.77	0.50
6:F:820:VAL:HA	6:F:828:VAL:HA	1.93	0.50
6:F:1295:GLY:O	6:F:1299:ILE:N	2.43	0.50
7:H:155:ARG:NH2	7:H:156:TYR:HE1	2.08	0.50
7:H:262:HIS:CG	7:H:283:LYS:HZ2	2.28	0.50
8:I:18:SER:O	8:I:21:GLN:N	2.37	0.50
10:K:22:GLY:CA	28:G:935:TRP:CZ3	2.92	0.50
15:P:178:TYR:CE1	33:f:203:PHE:CD2	3.00	0.50
20:U:45:LYS:HD3	20:U:126:VAL:HA	1.92	0.50
24:Z:368:ASN:O	24:Z:373:ILE:HG12	2.11	0.50
1:A:470:LEU:HD13	3:C:391:MET:SD	2.51	0.50
1:A:1690:LYS:HE2	1:A:1700:ASP:OD1	2.11	0.50
1:A:1997:ASP:HB2	1:A:1998:ARG:HD2	1.93	0.50
2:B:761:PHE:HD2	2:B:770:LEU:HD12	1.77	0.50
2:B:1063:ILE:HB	2:B:1081:GLN:NE2	2.26	0.50
2:B:1397:TYR:HD2	2:B:1446:LEU:HG	1.76	0.50
6:F:610:ILE:CG2	6:F:618:TYR:HB3	2.42	0.50
6:F:1136:GLY:HA2	6:F:1197:ASP:O	2.11	0.50
9:J:100:HIS:O	9:J:103:LYS:HG2	2.12	0.50
13:M:508:U:H3'	13:M:508:U:OP2	2.11	0.50
14:O:391:GLU:HG3	14:O:392:MET:H	1.76	0.50
17:R:63:ARG:HD3	17:R:86:LYS:HA	1.94	0.50
17:R:142:ILE:CG2	17:R:180:ASN:HD22	2.25	0.50
23:Y:223:LEU:HD13	23:Y:251:GLY:HA3	1.94	0.50
23:Y:699:GLU:O	23:Y:702:SER:CB	2.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:a:232:LYS:HD3	25:a:237:HIS:O	2.12	0.50
28:G:685:ILE:O	28:G:688:THR:OG1	2.29	0.50
32:e:117:ASP:HA	32:e:147:LYS:CB	2.42	0.50
1:A:487:ASN:OD1	1:A:488:ARG:HG3	2.11	0.50
2:B:1057:LEU:HD21	2:B:1089:PHE:CE1	2.44	0.50
6:F:194:GLU:HG2	6:F:242:VAL:HB	1.93	0.50
6:F:477:ILE:O	6:F:479:SER:N	2.40	0.50
8:I:63:SER:HB3	28:G:810:THR:HG22	1.93	0.50
23:Y:429:HIS:O	23:Y:495:ARG:NH1	2.45	0.50
28:G:894:HIS:HA	28:G:897:MET:HE3	1.93	0.50
1:A:2208:TYR:HB2	1:A:2223:THR:HB	1.94	0.50
2:B:846:ILE:HG12	2:B:887:ILE:HB	1.93	0.50
2:B:1429:GLY:HA3	2:B:1451:GLN:NE2	2.26	0.50
3:C:660:ARG:HH22	3:C:670:ILE:HD12	1.75	0.50
6:F:1042:LEU:HD21	6:F:1085:LEU:HD11	1.94	0.50
16:Q:205:PHE:O	16:Q:250:GLY:HA2	2.11	0.50
16:Q:209:ASN:CG	16:Q:288:ILE:O	2.54	0.50
22:W:167:VAL:CG1	22:W:209:LEU:HD23	2.42	0.50
28:G:177:ASN:OD1	28:G:178:THR:N	2.44	0.50
28:G:835:ILE:C	28:G:837:PHE:H	2.20	0.50
28:G:855:GLN:HG3	28:G:895:ALA:HA	1.92	0.50
36:n:51:PHE:HE1	36:n:55:GLU:HG3	1.75	0.50
1:A:653:ILE:HD11	1:A:704:TRP:NE1	2.27	0.50
1:A:665:GLY:HA2	1:A:667:TYR:CE2	2.47	0.50
1:A:1144:PHE:CE2	1:A:1145:MET:HE2	2.47	0.50
1:A:1156:HIS:CD2	1:A:1158:ILE:HB	2.47	0.50
1:A:1368:GLN:NE2	1:A:1389:TYR:OH	2.45	0.50
1:A:2409:ILE:CG2	1:A:2411:VAL:CG2	2.90	0.50
2:B:772:LYS:NZ	6:F:758:VAL:HG23	2.27	0.50
2:B:1994:LEU:HA	2:B:1997:ILE:HD12	1.94	0.50
6:F:717:SER:HA	25:a:244:ALA:O	2.11	0.50
7:H:155:ARG:HH22	7:H:156:TYR:HE1	1.58	0.50
7:H:166:THR:CG2	7:H:167:LYS:N	2.73	0.50
14:O:304:LEU:HD13	14:O:334:TRP:CD2	2.47	0.50
14:O:342:LEU:O	15:P:45:PRO:HB2	2.12	0.50
15:P:105:LEU:O	15:P:108:ASN:N	2.38	0.50
17:R:72:PHE:CE2	17:R:94:PRO:HG3	2.46	0.50
17:R:164:PHE:HE1	17:R:199:MET:HG3	1.77	0.50
17:R:210:LYS:CG	17:R:211:GLU:N	2.75	0.50
23:Y:277:GLN:O	23:Y:324:ASP:N	2.44	0.50
28:G:232:LEU:HD12	28:G:233:GLY:N	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:G:922:GLY:HA3	28:G:934:PHE:CE2	2.47	0.50
28:G:958:ASP:OD1	28:G:959:ASN:N	2.45	0.50
1:A:209:ILE:HG13	1:A:493:MET:HE1	1.93	0.50
1:A:1490:ARG:HE	1:A:1536:LEU:HD23	1.76	0.50
2:B:479:GLU:O	2:B:482:SER:OG	2.22	0.50
2:B:1241:LEU:HD11	2:B:1290:LEU:HD11	1.92	0.50
2:B:1262:ASP:OD1	2:B:1263:ILE:N	2.44	0.50
6:F:1065:THR:HG21	6:F:1106:PHE:H	1.77	0.50
7:H:268:ASP:O	28:G:882:ASN:HB3	2.12	0.50
14:O:319:LYS:O	15:P:57:LEU:HG	2.12	0.50
16:Q:108:MET:CE	27:c:211:ILE:HD11	2.42	0.50
16:Q:215:PRO:CG	16:Q:217:TRP:CZ3	2.91	0.50
20:U:38:LEU:HD22	21:V:49:THR:HB	1.94	0.50
20:U:45:LYS:HE3	20:U:46:GLU:N	2.27	0.50
23:Y:437:ASP:HB2	23:Y:513:ILE:HD13	1.94	0.50
27:c:21:LEU:O	27:c:24:ALA:N	2.44	0.50
28:G:887:ASN:HB3	28:G:899:ILE:HD13	1.93	0.50
32:e:147:LYS:C	32:e:149:LYS:H	2.15	0.50
34:o:20:ARG:CB	34:p:53:ILE:CB	2.90	0.50
34:o:100:SER:O	34:o:103:ASP:CG	2.55	0.50
38:i:86:ASN:HD21	39:h:32:LYS:NZ	2.09	0.50
1:A:1458:TRP:NE1	1:A:1489:PRO:HD2	2.27	0.49
1:A:1831:GLN:O	1:A:1833:PRO:N	2.45	0.49
2:B:477:LEU:HD12	6:F:660:SER:HB2	1.94	0.49
3:C:218:HIS:HB3	3:C:221:PHE:CD2	2.46	0.49
3:C:864:VAL:HG12	3:C:866:ILE:HG13	1.94	0.49
6:F:68:GLN:HA	6:F:1223:GLY:O	2.11	0.49
6:F:929:ILE:HG12	6:F:941:PHE:CD1	2.47	0.49
6:F:1224:THR:HG22	6:F:1225:VAL:N	2.27	0.49
14:O:188:VAL:HG13	14:O:197:LEU:HD11	1.93	0.49
17:R:143:ASP:C	17:R:146:LEU:H	2.19	0.49
24:Z:179:TYR:HD1	24:Z:179:TYR:O	1.95	0.49
24:Z:184:GLN:HE21	24:Z:185:GLU:N	2.09	0.49
25:a:202:CYS:HB3	25:a:204:GLU:HB2	1.92	0.49
26:b:40:SER:O	26:b:44:ASP:N	2.39	0.49
28:G:166:LEU:HD21	28:G:195:PHE:CD2	2.47	0.49
31:v:574:TYR:CZ	31:v:591:PHE:HB2	2.47	0.49
34:q:175:PRO:O	34:q:467:LEU:CG	2.59	0.49
1:A:284:ARG:NH1	4:D:33:U:O4	2.46	0.49
1:A:319:ARG:HD3	1:A:486:PHE:CE2	2.46	0.49
1:A:849:LEU:CD1	1:A:973:GLU:HB3	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1589:LYS:O	8:I:16:ILE:CG1	2.45	0.49
1:A:2412:PHE:HD1	1:A:2413:SER:H	1.58	0.49
2:B:517:MET:SD	2:B:666:ARG:NH2	2.85	0.49
2:B:1331:THR:OG1	2:B:1345:PHE:O	2.19	0.49
4:D:96:U:H3	12:N:99:G:H1	1.58	0.49
4:D:174:G:OP2	39:h:76:ASN:HB2	2.12	0.49
6:F:157:LEU:O	6:F:176:ASN:HA	2.11	0.49
6:F:369:ILE:HG23	6:F:419:LEU:HB2	1.93	0.49
6:F:779:TYR:C	6:F:780:LEU:HD12	2.37	0.49
6:F:1097:PHE:CE1	6:F:1108:PRO:HB3	2.46	0.49
11:L:25:A:H3'	11:L:26:G:C5'	2.41	0.49
16:Q:209:ASN:HD21	16:Q:288:ILE:HG23	1.78	0.49
17:R:46:ARG:HH12	17:R:222:LEU:HG	1.77	0.49
20:U:57:ASP:CG	20:U:146:ARG:HE	2.20	0.49
24:Z:299:LEU:HD21	24:Z:343:TYR:HE1	1.77	0.49
28:G:830:MET:C	28:G:832:LYS:H	2.10	0.49
1:A:1632:ILE:HD11	1:A:1649:PHE:CE2	2.48	0.49
1:A:1711:VAL:CG1	1:A:1789:ASN:HB3	2.43	0.49
1:A:1816:ARG:HG2	1:A:1816:ARG:NH1	2.15	0.49
1:A:2412:PHE:CD1	1:A:2413:SER:N	2.78	0.49
2:B:1936:ARG:NH2	2:B:1985:GLN:O	2.40	0.49
3:C:292:ILE:O	3:C:296:ASN:ND2	2.45	0.49
5:E:91:A:H1'	29:d:134:LYS:HG2	1.94	0.49
6:F:217:ASP:OD1	6:F:218:TYR:N	2.45	0.49
6:F:391:LEU:HA	6:F:406:GLN:O	2.12	0.49
7:H:153:ASP:OD2	11:L:57:A:O3'	2.29	0.49
14:O:197:LEU:O	14:O:209:TRP:N	2.44	0.49
17:R:15:GLU:HA	17:R:18:LEU:HD11	1.92	0.49
20:U:101:ARG:N	20:U:104:TYR:OH	2.38	0.49
23:Y:441:PHE:HE2	23:Y:516:VAL:HG13	1.76	0.49
25:a:218:PHE:HB3	25:a:222:CYS:HB2	1.94	0.49
2:B:177:ILE:HD13	2:B:182:PHE:HD1	1.76	0.49
2:B:1580:SER:N	2:B:1678:ASP:OD2	2.44	0.49
3:C:727:THR:H	3:C:736:ASP:HB2	1.78	0.49
3:C:918:LEU:HD23	3:C:928:CYS:HB2	1.93	0.49
6:F:238:LEU:O	6:F:255:LEU:HB2	2.12	0.49
6:F:962:LEU:HD23	6:F:1016:SER:C	2.37	0.49
6:F:1042:LEU:HD13	6:F:1051:LEU:HD13	1.93	0.49
6:F:1305:GLN:O	6:F:1309:SER:HB3	2.12	0.49
15:P:205:SER:OG	27:c:79:GLU:OE1	2.30	0.49
17:R:210:LYS:CE	17:R:210:LYS:CA	2.90	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Y:224:PRO:HG3	23:Y:401:ARG:HD2	1.95	0.49
23:Y:346:ASP:OD1	23:Y:347:GLU:N	2.45	0.49
28:G:334:ILE:HG22	28:G:377:THR:HG21	1.94	0.49
28:G:386:TYR:HB3	28:G:387:PRO:HD2	1.95	0.49
1:A:777:LYS:HB3	11:L:18:U:C4	2.48	0.49
1:A:854:ARG:HG2	1:A:854:ARG:NH2	2.20	0.49
1:A:1475:LEU:HD13	15:P:301:LEU:HD12	1.93	0.49
1:A:1511:ARG:O	1:A:1515:LYS:HG2	2.12	0.49
1:A:1664:ASP:OD2	1:A:1809:ASN:ND2	2.45	0.49
2:B:714:ASN:HD22	2:B:717:LYS:HE2	1.78	0.49
2:B:1750:ILE:HD11	2:B:1773:PHE:HE1	1.76	0.49
3:C:736:ASP:OD1	3:C:737:ILE:N	2.45	0.49
6:F:59:TYR:CE2	6:F:1316:LYS:HD2	2.48	0.49
6:F:71:PHE:CD2	6:F:95:VAL:HG11	2.48	0.49
16:Q:227:LEU:HD21	16:Q:262:PHE:HD1	1.78	0.49
20:U:38:LEU:HD23	21:V:49:THR:CG2	2.41	0.49
20:U:176:ARG:HH21	20:U:178:ILE:HD13	1.76	0.49
21:V:91:ASN:O	22:W:239:ASN:CB	2.60	0.49
22:W:167:VAL:HG11	22:W:209:LEU:HD23	1.94	0.49
27:c:513:ILE:HA	27:c:516:LYS:CG	2.43	0.49
28:G:166:LEU:HD11	28:G:195:PHE:HB3	1.94	0.49
29:d:255:ALA:O	29:d:258:GLN:NE2	2.45	0.49
1:A:589:THR:HG21	17:R:31:ASN:ND2	2.27	0.49
1:A:1932:GLN:HG2	1:A:1955:ALA:HB3	1.95	0.49
2:B:493:SER:O	2:B:497:THR:N	2.45	0.49
2:B:618:ASN:OD1	2:B:619:SER:N	2.46	0.49
3:C:706:LEU:HD23	3:C:826:PRO:HD3	1.94	0.49
9:J:8:LEU:HD13	9:J:89:ILE:HG21	1.95	0.49
16:Q:220:THR:HG23	16:Q:240:LEU:HD23	1.94	0.49
17:R:152:LYS:CG	17:R:153:PRO:HD2	2.43	0.49
22:W:167:VAL:CG1	22:W:209:LEU:CD2	2.91	0.49
25:a:216:HIS:NE2	25:a:233:CYS:HB3	2.27	0.49
3:C:271:ASP:CG	44:C:1500:GTP:HN1	2.20	0.49
3:C:968:MET:O	3:C:972:ARG:NH1	2.46	0.49
5:E:93:A:H5"	33:f:107:LYS:HD2	1.94	0.49
19:T:114:THR:OG1	19:T:118:SER:HA	2.13	0.49
28:G:488:TRP:CE3	28:G:536:MET:HE3	2.48	0.49
33:f:184:GLN:HA	33:f:187:LYS:NZ	2.27	0.49
1:A:394:ARG:CG	1:A:394:ARG:NH1	2.73	0.49
1:A:839:HIS:CE1	4:D:95:C:O2	2.65	0.49
1:A:2410:ASP:OD1	1:A:2412:PHE:HE1	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:159:ASP:HB3	2:B:165:ARG:NH1	2.28	0.49
3:C:618:LEU:HD13	3:C:666:ILE:HD11	1.94	0.49
7:H:155:ARG:HH21	7:H:155:ARG:CG	2.26	0.49
13:M:506:U:OP2	28:G:698:ARG:CD	2.61	0.49
16:Q:69:ASN:ND2	16:Q:126:THR:CB	2.73	0.49
17:R:206:LEU:HD12	17:R:207:PRO:HD3	1.94	0.49
21:V:91:ASN:O	22:W:239:ASN:HB3	2.12	0.49
22:W:229:GLY:C	22:W:231:ARG:H	2.21	0.49
28:G:361:ASP:OD1	28:G:362:CYS:N	2.46	0.49
28:G:368:VAL:N	28:G:369:PRO:HD2	2.28	0.49
29:d:69:ILE:CG2	29:d:104:ARG:CD	2.90	0.49
34:q:405:ASP:HB2	35:t:30:ASN:CG	2.38	0.49
1:A:2204:ALA:HA	1:A:2260:HIS:HA	1.95	0.49
2:B:727:TYR:HE1	2:B:761:PHE:CE1	2.31	0.49
3:C:539:VAL:HG13	3:C:564:ILE:HG23	1.94	0.49
6:F:977:ILE:HG12	6:F:1004:LEU:HD22	1.94	0.49
9:J:7:ASP:OD1	9:J:8:LEU:N	2.46	0.49
13:M:484:A:H8	13:M:484:A:H3'	1.78	0.49
16:Q:84:ILE:HA	16:Q:87:ARG:HG2	1.94	0.49
17:R:22:ILE:HG13	17:R:22:ILE:O	2.13	0.49
17:R:232:PRO:HA	17:R:235:GLN:HB3	1.94	0.49
20:U:50:LEU:CB	20:U:139:GLN:HE22	2.26	0.49
23:Y:277:GLN:N	23:Y:322:MET:O	2.45	0.49
28:G:790:LYS:HD2	28:G:826:TYR:HB3	1.94	0.49
29:d:122:MET:HG3	29:d:139:TYR:CD1	2.47	0.49
1:A:831:ARG:HH11	1:A:848:ASN:ND2	2.11	0.49
1:A:869:LYS:C	15:P:198:ASN:HD21	2.19	0.49
3:C:272:ARG:HG3	3:C:276:ASP:OD2	2.13	0.49
6:F:759:ASP:OD1	6:F:760:GLY:N	2.44	0.49
7:H:192:ARG:CB	7:H:192:ARG:NH1	2.76	0.49
9:J:8:LEU:CD2	9:J:93:GLY:HA3	2.43	0.49
14:O:229:THR:HG21	14:O:272:VAL:H	1.78	0.49
15:P:167:ALA:CB	33:f:203:PHE:HZ	2.26	0.49
15:P:197:ILE:HG23	27:c:90:MET:CE	2.41	0.49
16:Q:217:TRP:CE3	17:R:187:LYS:HD3	2.47	0.49
22:W:167:VAL:O	22:W:171:GLY:N	2.45	0.49
25:a:211:VAL:HG22	25:a:217:TYR:CE1	2.48	0.49
28:G:674:ASP:OD1	28:G:675:LEU:N	2.46	0.49
1:A:1747:ASP:OD1	1:A:1747:ASP:N	2.29	0.48
3:C:567:ILE:HG22	3:C:571:TYR:HE1	1.78	0.48
3:C:772:ASN:HD21	3:C:815:GLY:H	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:41:A:C8	17:R:34:TYR:CD2	3.01	0.48
6:F:819:VAL:HG23	6:F:819:VAL:O	2.13	0.48
6:F:1227:CYS:SG	6:F:1229:ILE:HD11	2.53	0.48
6:F:1233:SER:CB	6:F:1236:ASN:H	2.26	0.48
1:A:194:HIS:CD2	15:P:122:LEU:CD2	2.93	0.48
1:A:309:SER:OG	1:A:475:ASP:CB	2.56	0.48
1:A:1755:LYS:HE3	1:A:1759:TYR:HE2	1.79	0.48
1:A:2390:VAL:O	1:A:2394:GLN:HG2	2.13	0.48
2:B:1365:SER:HB3	2:B:1527:MET:HE2	1.95	0.48
2:B:1405:ILE:O	2:B:1409:LEU:N	2.45	0.48
2:B:1875:THR:O	2:B:1879:MET:N	2.38	0.48
5:E:66:C:O2	5:E:66:C:H2'	2.10	0.48
5:E:92:C:OP1	5:E:92:C:H4'	2.13	0.48
6:F:1051:LEU:HB3	6:F:1063:SER:HB3	1.95	0.48
8:I:55:ASN:O	8:I:56:PRO:CB	2.61	0.48
19:T:143:HIS:O	19:T:151:ARG:HG2	2.13	0.48
24:Z:148:LEU:HD12	24:Z:190:LEU:HD21	1.95	0.48
25:a:217:TYR:CD1	25:a:250:LEU:HD11	2.48	0.48
26:b:58:THR:O	26:b:105:ALA:HB3	2.13	0.48
1:A:909:THR:OG1	28:G:48:LEU:HB2	2.13	0.48
1:A:1999:ILE:CD1	1:A:2007:ARG:NH2	2.76	0.48
2:B:1239:PHE:CE1	2:B:1294:SER:HB2	2.48	0.48
2:B:1337:ASP:O	2:B:1341:GLU:N	2.40	0.48
3:C:488:ILE:HD11	3:C:493:LEU:HD12	1.95	0.48
6:F:832:TRP:CG	6:F:833:LYS:H	2.31	0.48
9:J:67:VAL:HG23	9:J:68:ASN:H	1.78	0.48
14:O:389:THR:HG22	14:O:426:TRP:HZ2	1.78	0.48
16:Q:91:ILE:HB	16:Q:99:VAL:HG21	1.95	0.48
17:R:255:ASN:O	17:R:259:ASN:N	2.40	0.48
35:t:86:LEU:O	35:t:89:GLU:CG	2.61	0.48
36:n:59:ARG:HG2	36:n:59:ARG:HH11	1.79	0.48
1:A:388:PRO:O	1:A:392:ASN:HB2	2.12	0.48
1:A:997:GLN:HE21	1:A:1511:ARG:HH22	1.54	0.48
1:A:1839:ASN:HA	1:A:1842:GLU:HG2	1.96	0.48
1:A:1889:LEU:HD21	1:A:1991:ILE:HD11	1.95	0.48
2:B:1641:TYR:HE1	2:B:1941:VAL:HG11	1.79	0.48
6:F:746:GLU:O	6:F:747:ASN:CG	2.57	0.48
6:F:965:GLY:N	6:F:1016:SER:OG	2.46	0.48
26:b:87:ASP:HB3	26:b:104:LEU:HA	1.95	0.48
27:c:226:GLY:HA3	29:d:120:ASN:HB2	1.95	0.48
29:d:117:HIS:CA	29:d:120:ASN:HD22	2.21	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:563:ASP:OD1	1:A:564:TRP:N	2.47	0.48
1:A:732:ARG:NH1	5:E:73:A:OP2	2.45	0.48
1:A:1070:LEU:HA	1:A:1073:ILE:HG22	1.94	0.48
1:A:1222:LEU:O	1:A:1225:ALA:N	2.47	0.48
1:A:1440:ILE:O	1:A:1442:ARG:N	2.46	0.48
1:A:1911:TRP:NE1	1:A:2324:VAL:HG21	2.29	0.48
3:C:328:VAL:HG13	3:C:332:TYR:HB2	1.95	0.48
3:C:635:LYS:HB2	3:C:643:VAL:HB	1.95	0.48
5:E:41:A:C8	17:R:34:TYR:CE2	3.01	0.48
6:F:693:ILE:CG2	6:F:701:LYS:HB2	2.43	0.48
7:H:180:LYS:O	7:H:181:GLU:HB2	2.12	0.48
7:H:203:THR:HG22	7:H:250:VAL:HG21	1.95	0.48
13:M:520:G:N2	21:V:107:THR:OG1	2.45	0.48
15:P:43:PHE:HE2	29:d:131:ARG:NE	2.11	0.48
16:Q:220:THR:HG23	16:Q:240:LEU:CD2	2.43	0.48
17:R:12:GLN:HG2	17:R:79:GLY:O	2.13	0.48
23:Y:550:ALA:HB2	23:Y:563:ARG:HH21	1.78	0.48
28:G:389:GLY:O	28:G:391:GLU:N	2.46	0.48
34:q:214:ARG:HB3	34:q:217:ASP:CG	2.38	0.48
1:A:701:CYS:SG	1:A:702:GLY:N	2.81	0.48
1:A:1458:TRP:CE3	28:G:25:ILE:HG22	2.46	0.48
2:B:574:PHE:HB3	2:B:585:VAL:HG11	1.96	0.48
2:B:674:LEU:HD22	2:B:906:LEU:HB3	1.96	0.48
2:B:766:ILE:C	2:B:767:THR:HG1	2.19	0.48
2:B:1642:LYS:HZ1	2:B:1948:LYS:HD3	1.77	0.48
3:C:679:GLU:OE1	3:C:807:PRO:HD2	2.14	0.48
3:C:705:GLY:C	3:C:826:PRO:HG3	2.38	0.48
6:F:471:LYS:HE3	6:F:473:GLN:HB3	1.94	0.48
6:F:1048:THR:OG1	6:F:1065:THR:O	2.22	0.48
7:H:154:ALA:O	7:H:157:PRO:HD3	2.13	0.48
14:O:389:THR:O	14:O:400:ARG:HD2	2.14	0.48
14:O:392:MET:HG3	14:O:393:VAL:H	1.77	0.48
16:Q:291:ILE:HG23	16:Q:292:PRO:N	2.29	0.48
17:R:145:ALA:O	17:R:146:LEU:HB3	2.14	0.48
19:T:54:GLN:CD	36:n:69:TRP:CD1	2.90	0.48
20:U:50:LEU:HA	20:U:139:GLN:NE2	2.14	0.48
21:V:83:ARG:HH12	22:W:224:PHE:HB3	1.78	0.48
21:V:124:GLU:O	21:V:128:ARG:HG2	2.14	0.48
27:c:227:ILE:HG22	29:d:123:ASN:HD21	1.78	0.48
30:X:9:LYS:O	30:X:10:SER:OG	2.26	0.48
30:X:12:LYS:C	30:X:14:SER:H	2.22	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:e:33:ASN:CB	32:e:34:PRO:HD2	2.44	0.48
33:f:92:ARG:N	33:f:93:GLY:HA3	2.28	0.48
1:A:254:HIS:CD2	26:b:81:ARG:HG3	2.48	0.48
1:A:1212:ARG:HG2	1:A:1213:MET:H	1.78	0.48
1:A:1714:PRO:HA	1:A:1788:GLY:O	2.13	0.48
2:B:677:TYR:HD2	2:B:691:LEU:HD11	1.79	0.48
2:B:1039:GLU:OE2	2:B:1042:LYS:HD2	2.13	0.48
2:B:1208:ALA:HB3	2:B:1311:PHE:CE2	2.49	0.48
2:B:1481:GLN:CD	2:B:1701:ASN:HD22	2.21	0.48
3:C:362:LYS:CG	3:C:363:PRO:HD2	2.43	0.48
6:F:130:LEU:HB3	6:F:195:ILE:HD13	1.96	0.48
6:F:175:VAL:HG11	6:F:224:ILE:HD12	1.95	0.48
6:F:240:MET:HA	6:F:254:THR:HG22	1.94	0.48
6:F:719:GLN:CG	6:F:762:PHE:HD2	2.23	0.48
9:J:20:GLY:H	9:J:43:VAL:HG23	1.79	0.48
10:K:23:ASP:O	28:G:935:TRP:CB	2.61	0.48
12:N:112:U:H3	17:R:226:ALA:HA	1.79	0.48
15:P:142:GLU:N	15:P:142:GLU:OE1	2.46	0.48
22:W:185:ALA:O	22:W:189:THR:OG1	2.29	0.48
24:Z:459:ARG:HH21	24:Z:485:GLN:HG2	1.77	0.48
25:a:199:CYS:HB2	25:a:203:LYS:H	1.78	0.48
26:b:90:LEU:N	26:b:118:GLY:O	2.46	0.48
27:c:69:GLU:O	27:c:73:LEU:N	2.34	0.48
27:c:243:GLN:O	27:c:247:LYS:HG2	2.14	0.48
28:G:45:LYS:NZ	28:G:53:GLU:OE2	2.47	0.48
1:A:834:ILE:HG12	1:A:840:VAL:HG11	1.95	0.48
1:A:2238:ILE:HG22	1:A:2239:SER:O	2.14	0.48
2:B:767:THR:HA	2:B:771:THR:HG22	1.94	0.48
6:F:197:PRO:HG2	6:F:244:ASP:HA	1.95	0.48
8:I:57:TYR:O	8:I:59:TYR:HD1	1.97	0.48
20:U:78:TYR:H	20:U:99:ASN:ND2	2.12	0.48
23:Y:702:SER:CB	23:Y:705:ILE:HB	2.43	0.48
26:b:103:VAL:HG12	26:b:104:LEU:N	2.27	0.48
28:G:565:LEU:O	28:G:569:PHE:N	2.46	0.48
33:f:190:TYR:HE2	33:f:195:PHE:HZ	1.61	0.48
1:A:377:VAL:CG1	1:A:378:PRO:HD2	2.43	0.48
1:A:402:TRP:CG	1:A:402:TRP:O	2.66	0.48
1:A:757:GLU:HG3	1:A:758:LEU:N	2.29	0.48
1:A:909:THR:HG21	28:G:49:GLN:HG3	1.95	0.48
7:H:182:TYR:O	7:H:272:GLU:OE1	2.31	0.48
11:L:16:U:C5	11:L:18:U:OP1	2.67	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Q:88:ASP:OD1	16:Q:89:HIS:N	2.46	0.48
16:Q:215:PRO:HG3	16:Q:217:TRP:CE3	2.47	0.48
23:Y:369:ARG:NE	23:Y:372:LEU:HB2	2.29	0.48
28:G:191:LYS:HE3	28:G:194:THR:HG21	1.96	0.48
28:G:851:LEU:HD21	28:G:895:ALA:CB	2.44	0.48
29:d:144:GLU:OE2	33:f:109:LEU:HD21	2.14	0.48
31:v:712:CYS:O	31:v:713:ILE:C	2.57	0.48
36:n:60:ARG:O	36:n:63:ARG:HG2	2.14	0.48
1:A:742:VAL:HG11	14:O:224:LEU:HD23	1.94	0.48
2:B:1212:THR:HG22	2:B:1213:ARG:N	2.28	0.48
6:F:339:ASP:OD1	6:F:340:MET:N	2.47	0.48
6:F:839:ARG:HG3	6:F:880:PRO:HG2	1.96	0.48
9:J:101:PHE:HE2	28:G:219:HIS:CD2	2.31	0.48
16:Q:256:SER:O	16:Q:260:GLU:OE1	2.32	0.48
17:R:206:LEU:CG	17:R:207:PRO:CD	2.90	0.48
23:Y:220:ARG:HD2	23:Y:255:GLN:HE22	1.78	0.48
23:Y:737:VAL:HA	23:Y:740:ILE:HB	1.96	0.48
27:c:84:TRP:CD2	27:c:99:VAL:HG22	2.49	0.48
38:i:34:GLN:HE21	38:i:37:ILE:HD12	1.79	0.48
1:A:1456:ARG:HH22	1:A:1486:ARG:NH1	2.12	0.47
2:B:510:ALA:HB2	2:B:517:MET:HE1	1.96	0.47
5:E:37:U:C4	17:R:47:PHE:CZ	3.02	0.47
6:F:829:SER:HB2	6:F:838:ILE:HG22	1.95	0.47
8:I:55:ASN:ND2	8:I:56:PRO:N	2.56	0.47
16:Q:36:ILE:O	16:Q:110:LYS:HD3	2.14	0.47
17:R:65:ASP:OD1	17:R:90:LEU:HD22	2.14	0.47
17:R:146:LEU:HD23	17:R:147:ASN:H	1.78	0.47
17:R:164:PHE:CE2	17:R:184:VAL:HG21	2.48	0.47
28:G:686:LEU:HD12	28:G:711:ILE:HG21	1.96	0.47
28:G:805:TYR:HB2	28:G:816:VAL:HG11	1.95	0.47
1:A:266:LEU:HD23	1:A:268:LEU:HA	1.96	0.47
1:A:640:ARG:NH1	1:A:640:ARG:CG	2.77	0.47
2:B:160:GLY:HA3	28:G:511:LYS:O	2.15	0.47
2:B:1563:MET:HE1	2:B:1684:GLY:HA2	1.95	0.47
2:B:2134:THR:O	2:B:2138:HIS:NE2	2.46	0.47
3:C:90:LEU:HD11	14:O:166:VAL:HG21	1.95	0.47
3:C:787:LEU:HD12	3:C:790:LYS:HD2	1.96	0.47
6:F:205:SER:HB3	6:F:240:MET:HE3	1.96	0.47
6:F:1090:ILE:O	6:F:1117:HIS:HA	2.13	0.47
6:F:1213:ARG:HD2	6:F:1360:TYR:CD1	2.48	0.47
6:F:1299:ILE:C	6:F:1300:LEU:HD12	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:141:VAL:HG12	7:H:143:TYR:N	2.29	0.47
8:I:16:ILE:O	8:I:17:ALA:CB	2.62	0.47
9:J:54:GLN:OE1	9:J:54:GLN:HA	2.14	0.47
20:U:48:ILE:CG2	20:U:49:ALA:N	2.77	0.47
23:Y:298:LEU:HD21	23:Y:304:TYR:HE1	1.79	0.47
25:a:217:TYR:CD2	25:a:250:LEU:HD21	2.49	0.47
27:c:228:TYR:CE1	29:d:119:ARG:HG2	2.50	0.47
27:c:230:THR:O	27:c:232:THR:N	2.38	0.47
1:A:264:ILE:O	1:A:265:ASN:C	2.56	0.47
1:A:872:PRO:HD3	15:P:201:PHE:CE1	2.48	0.47
1:A:936:GLU:O	1:A:940:ILE:HD12	2.13	0.47
1:A:1208:PRO:HB2	1:A:1417:GLN:O	2.14	0.47
1:A:2007:ARG:HG3	1:A:2008:LEU:N	2.28	0.47
3:C:106:PHE:O	4:D:44:A:H3'	2.13	0.47
6:F:406:GLN:HA	6:F:455:LEU:O	2.14	0.47
10:K:32:GLN:HE22	28:G:960:ASN:HB3	1.79	0.47
43:g:49:ARG:HD2	43:g:49:ARG:HA	1.64	0.47
1:A:244:ASP:OD1	1:A:596:ASN:ND2	2.45	0.47
1:A:1041:VAL:O	1:A:1041:VAL:HG12	2.14	0.47
1:A:1233:ARG:HD3	18:S:131:THR:HG21	1.95	0.47
1:A:1475:LEU:O	15:P:304:ASP:HB2	2.14	0.47
1:A:1646:ILE:HG22	25:a:162:LEU:HD22	1.95	0.47
1:A:1899:TRP:O	1:A:1901:GLY:N	2.47	0.47
2:B:114:PRO:O	2:B:118:GLU:N	2.34	0.47
7:H:134:LEU:HD13	7:H:138:LYS:HE2	1.96	0.47
9:J:51:PHE:HE2	9:J:54:GLN:HG2	1.78	0.47
16:Q:118:VAL:O	16:Q:119:LYS:CB	2.63	0.47
16:Q:214:ILE:HD11	16:Q:218:LYS:CB	2.44	0.47
17:R:146:LEU:CD1	17:R:211:GLU:OE1	2.62	0.47
20:U:45:LYS:HE3	20:U:45:LYS:HA	1.96	0.47
20:U:146:ARG:HD3	20:U:155:TYR:CE2	2.49	0.47
28:G:493:ALA:HA	28:G:499:ASN:OD1	2.15	0.47
28:G:924:PHE:O	28:G:931:ARG:HD3	2.13	0.47
29:d:96:SER:O	29:d:102:TRP:NE1	2.39	0.47
1:A:291:LYS:HE2	1:A:292:LYS:HD3	1.96	0.47
1:A:893:ARG:NH1	1:A:893:ARG:CG	2.74	0.47
1:A:1268:ARG:NE	1:A:1301:TYR:HD2	2.12	0.47
2:B:1555:GLU:OE2	2:B:1726:HIS:N	2.47	0.47
2:B:1642:LYS:HB2	2:B:1669:ASP:HB3	1.95	0.47
2:B:1685:THR:HG21	2:B:1732:TYR:HE2	1.79	0.47
3:C:81:LYS:O	3:C:82:ASN:ND2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:347:ARG:O	3:C:352:VAL:HG11	2.15	0.47
5:E:28:U:H1'	16:Q:51:ARG:HH22	1.79	0.47
6:F:153:ASP:O	6:F:154:SER:CB	2.62	0.47
13:M:505:A:O3'	13:M:506:U:O4'	2.32	0.47
17:R:146:LEU:CD2	17:R:147:ASN:H	2.27	0.47
17:R:207:PRO:O	17:R:212:TRP:NE1	2.47	0.47
20:U:186:LEU:HB2	20:U:199:LEU:HB2	1.96	0.47
23:Y:699:GLU:CA	23:Y:702:SER:CB	2.92	0.47
24:Z:184:GLN:CA	24:Z:184:GLN:NE2	2.77	0.47
28:G:579:ILE:CD1	28:G:579:ILE:N	2.77	0.47
28:G:835:ILE:C	28:G:837:PHE:N	2.72	0.47
1:A:2247:LEU:HB2	1:A:2250:THR:HG21	1.96	0.47
1:A:2402:GLU:N	1:A:2402:GLU:CD	2.73	0.47
3:C:697:ARG:HH11	3:C:848:VAL:HG12	1.79	0.47
5:E:91:A:C4	29:d:99:ILE:HD12	2.49	0.47
6:F:101:LEU:HD12	6:F:102:GLU:H	1.80	0.47
6:F:205:SER:HB2	6:F:211:LYS:HG2	1.97	0.47
6:F:836:TRP:HZ3	6:F:838:ILE:HG23	1.79	0.47
7:H:271:TYR:CZ	7:H:274:ARG:HB2	2.49	0.47
14:O:125:TRP:HE1	14:O:437:GLU:HB3	1.80	0.47
14:O:133:ARG:HH11	14:O:425:ILE:HD12	1.78	0.47
28:G:550:THR:CG2	28:G:553:LEU:HD22	2.45	0.47
29:d:69:ILE:CG2	29:d:104:ARG:HD2	2.44	0.47
29:d:136:TRP:CZ3	29:d:159:TRP:HB2	2.49	0.47
32:e:27:GLU:HB3	32:e:122:ASP:CB	2.44	0.47
33:f:187:LYS:HA	33:f:201:LYS:NZ	2.29	0.47
1:A:134:MET:CE	19:T:107:ARG:HD2	2.45	0.47
1:A:263:PRO:HD2	19:T:7:ARG:NH2	2.29	0.47
1:A:377:VAL:HG12	1:A:378:PRO:CD	2.44	0.47
1:A:421:ALA:HB3	1:A:469:ILE:HD12	1.97	0.47
1:A:672:LYS:N	4:D:101:C:OP1	2.43	0.47
1:A:716:ARG:HD3	4:D:111:C:O2	2.15	0.47
1:A:878:GLU:HG2	18:S:133:PHE:HE1	1.80	0.47
1:A:1424:HIS:NE2	30:X:6:ILE:HD13	2.29	0.47
1:A:1449:ASN:HB3	24:Z:338:THR:HG21	1.96	0.47
1:A:1797:LEU:O	1:A:1800:ASN:N	2.48	0.47
2:B:1061:ALA:HB1	2:B:1081:GLN:OE1	2.15	0.47
2:B:1123:HIS:HB3	2:B:1124:PRO:HD3	1.96	0.47
2:B:1536:SER:HB3	2:B:1539:GLU:HG2	1.95	0.47
2:B:1876:LEU:HA	2:B:1879:MET:HB2	1.96	0.47
3:C:104:THR:CG2	3:C:181:LEU:HD12	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:273:LEU:HD21	3:C:284:ALA:HB1	1.95	0.47
6:F:78:HIS:O	6:F:146:THR:HG22	2.14	0.47
6:F:528:PRO:HG3	6:F:559:MET:HE1	1.97	0.47
6:F:1096:LEU:HD13	6:F:1187:PHE:CZ	2.44	0.47
6:F:1302:ARG:HG2	6:F:1307:TYR:HB2	1.97	0.47
7:H:192:ARG:CG	7:H:192:ARG:NH1	2.77	0.47
11:L:4:A:H2'	11:L:5:A:C8	2.50	0.47
14:O:191:SER:O	18:S:40:ARG:NH2	2.43	0.47
14:O:437:GLU:N	14:O:438:PRO:HD3	2.30	0.47
15:P:167:ALA:CB	33:f:203:PHE:CZ	2.98	0.47
15:P:301:LEU:CD1	15:P:303:TYR:CE1	2.96	0.47
16:Q:24:ARG:CD	19:T:116:ASN:HD22	2.27	0.47
16:Q:37:CYS:SG	16:Q:39:LEU:HB2	2.55	0.47
17:R:12:GLN:HB3	17:R:79:GLY:O	2.14	0.47
19:T:128:GLN:O	19:T:131:GLU:N	2.41	0.47
20:U:51:LYS:HG3	20:U:52:HIS:H	1.78	0.47
20:U:96:TYR:CE2	20:U:129:ILE:HG23	2.50	0.47
21:V:83:ARG:NH1	22:W:224:PHE:HB3	2.30	0.47
25:a:174:LEU:C	25:a:174:LEU:CD2	2.88	0.47
28:G:458:LEU:HD13	28:G:501:VAL:HG12	1.96	0.47
28:G:472:PRO:O	28:G:476:ARG:HG3	2.14	0.47
28:G:637:PHE:O	28:G:641:ASN:ND2	2.48	0.47
31:v:726:ARG:HA	31:v:729:TYR:CE2	2.50	0.47
1:A:264:ILE:O	1:A:265:ASN:O	2.33	0.47
1:A:1227:PHE:CD2	1:A:1243:TRP:HE3	2.33	0.47
1:A:1999:ILE:HG23	1:A:2003:THR:OG1	2.15	0.47
1:A:2395:PHE:HB2	2:B:1087:LEU:HD21	1.97	0.47
2:B:1009:TYR:O	2:B:1107:ARG:NH1	2.44	0.47
2:B:1978:ASP:O	2:B:1982:MET:HG3	2.15	0.47
3:C:233:ASP:HB3	3:C:443:TYR:CE1	2.50	0.47
9:J:4:HIS:HB3	13:M:500:A:O2'	2.14	0.47
15:P:114:VAL:CG1	16:Q:27:LYS:HB2	2.45	0.47
17:R:13:VAL:HG12	17:R:14:LYS:O	2.14	0.47
20:U:84:ARG:HG2	20:U:197:TYR:CE2	2.50	0.47
25:a:216:HIS:CE1	25:a:235:ILE:HD12	2.50	0.47
28:G:962:GLU:HG2	28:G:963:TYR:N	2.29	0.47
29:d:173:VAL:HG12	29:d:188:ILE:HG21	1.96	0.47
32:e:150:CYS:O	32:e:151:ALA:HB2	2.14	0.47
1:A:745:THR:CG2	14:O:203:ASP:HB2	2.45	0.47
1:A:749:ARG:NH1	5:E:76:A:OP2	2.44	0.47
1:A:1066:LEU:O	1:A:1067:ASN:C	2.58	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2032:ILE:HD13	1:A:2043:PHE:CD1	2.50	0.47
2:B:899:LEU:HD12	2:B:903:ASN:HD21	1.80	0.47
2:B:1237:GLU:HB2	2:B:1259:ILE:HB	1.97	0.47
2:B:1387:HIS:CE1	2:B:1392:LYS:HB2	2.49	0.47
2:B:1641:TYR:CE1	2:B:1941:VAL:HG11	2.50	0.47
2:B:2055:TYR:HB2	2:B:2073:ILE:HG12	1.96	0.47
4:D:124:C:H2'	4:D:125:C:O4'	2.15	0.47
6:F:361:LYS:C	6:F:363:VAL:H	2.23	0.47
16:Q:245:LYS:HA	16:Q:245:LYS:HZ2	1.80	0.47
20:U:81:VAL:HG22	20:U:95:ARG:HG2	1.96	0.47
25:a:199:CYS:HB2	25:a:203:LYS:N	2.29	0.47
26:b:7:PRO:HG3	26:b:30:GLU:HG3	1.97	0.47
28:G:496:ARG:N	28:G:497:PRO:HD2	2.29	0.47
1:A:1424:HIS:ND1	30:X:22:ARG:HA	2.29	0.47
1:A:1748:ILE:CG1	1:A:1783:MET:HE3	2.43	0.47
2:B:180:LEU:CD2	28:G:592:ILE:HD13	2.45	0.47
2:B:1630:ARG:O	2:B:1634:LYS:N	2.47	0.47
2:B:2063:LEU:HD12	2:B:2162:VAL:HG13	1.97	0.47
3:C:625:ILE:HD12	3:C:659:LEU:HD13	1.96	0.47
5:E:87:U:O2	29:d:70:ARG:CZ	2.63	0.47
6:F:71:PHE:CD1	6:F:97:THR:CG2	2.98	0.47
11:L:18:U:C2'	11:L:19:U:OP1	2.63	0.47
15:P:112:ILE:HD13	16:Q:25:MET:HE3	1.97	0.47
15:P:137:PRO:HG3	16:Q:112:PHE:CE1	2.50	0.47
16:Q:222:THR:CA	16:Q:225:GLN:NE2	2.75	0.47
17:R:27:GLY:CA	17:R:37:TRP:HB3	2.45	0.47
26:b:28:ALA:HA	26:b:35:CYS:SG	2.55	0.47
26:b:93:ASP:OD1	26:b:94:ARG:N	2.48	0.47
28:G:583:PHE:HZ	28:G:601:ILE:HD13	1.80	0.47
34:o:96:PHE:HD2	34:r:5:ILE:HG23	1.80	0.47
1:A:322:VAL:HG21	1:A:327:TYR:CD2	2.49	0.46
1:A:1468:ALA:HA	1:A:1473:ARG:HG2	1.97	0.46
1:A:1707:HIS:C	2:B:1184:ARG:HH21	2.23	0.46
1:A:1857:VAL:HG13	1:A:1894:ILE:HD12	1.97	0.46
2:B:2011:ILE:HG13	2:B:2013:VAL:HG23	1.97	0.46
6:F:98:GLU:OE1	6:F:1196:ASN:ND2	2.48	0.46
6:F:564:ASP:OD1	6:F:565:ASN:N	2.45	0.46
6:F:975:ASP:O	6:F:977:ILE:HD12	2.15	0.46
13:M:509:A:C2	28:G:503:THR:HG21	2.50	0.46
20:U:38:LEU:CD2	21:V:49:THR:HB	2.45	0.46
24:Z:168:LYS:HZ3	24:Z:171:ASP:CB	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:b:42:LEU:HB3	26:b:157:VAL:HG11	1.97	0.46
36:n:51:PHE:HE1	36:n:55:GLU:CG	2.27	0.46
1:A:266:LEU:HG	1:A:267:PRO:CD	2.44	0.46
1:A:737:ARG:NH2	5:E:71:G:N7	2.62	0.46
1:A:909:THR:O	1:A:913:VAL:HG23	2.16	0.46
2:B:159:ASP:HB3	2:B:165:ARG:HH12	1.80	0.46
2:B:162:ILE:HG22	2:B:165:ARG:NH2	2.31	0.46
2:B:673:THR:HG21	2:B:694:PHE:O	2.15	0.46
2:B:932:ARG:NH1	2:B:991:ALA:O	2.36	0.46
2:B:2070:LYS:HA	2:B:2128:LEU:O	2.15	0.46
3:C:269:LYS:HG2	44:C:1500:GTP:C5	2.51	0.46
3:C:406:VAL:HG13	3:C:427:LEU:HG	1.97	0.46
4:D:167:A:N7	43:g:63:ARG:CZ	2.78	0.46
4:D:175:G:H4'	4:D:176:A:O4'	2.15	0.46
6:F:60:LEU:HB2	6:F:1317:VAL:HG22	1.95	0.46
6:F:379:VAL:O	6:F:390:LYS:HA	2.15	0.46
6:F:1165:LYS:CE	32:e:34:PRO:HG3	2.45	0.46
6:F:1233:SER:OG	6:F:1236:ASN:ND2	2.33	0.46
7:H:196:LEU:HD22	7:H:200:ILE:HG21	1.97	0.46
11:L:18:U:H2'	11:L:19:U:OP1	2.16	0.46
14:O:114:ARG:O	14:O:118:LEU:HG	2.16	0.46
16:Q:86:LEU:O	16:Q:89:HIS:N	2.48	0.46
17:R:196:LYS:HA	17:R:223:VAL:HG11	1.98	0.46
23:Y:220:ARG:HH11	23:Y:255:GLN:HE22	1.62	0.46
25:a:168:PHE:CD1	25:a:168:PHE:N	2.83	0.46
27:c:581:GLN:O	27:c:584:LEU:CG	2.63	0.46
28:G:334:ILE:HD13	28:G:374:THR:CG2	2.45	0.46
34:q:472:ALA:CB	34:q:477:MET:CG	2.93	0.46
1:A:769:MET:HB2	1:A:769:MET:HE2	1.70	0.46
1:A:1161:TYR:CD1	1:A:1170:MET:HG2	2.48	0.46
1:A:1877:GLY:O	1:A:1894:ILE:N	2.41	0.46
2:B:593:ARG:HH11	2:B:596:ARG:HD3	1.80	0.46
2:B:897:TYR:O	2:B:901:VAL:HG23	2.16	0.46
2:B:1551:PHE:CD2	2:B:1563:MET:HG2	2.51	0.46
2:B:1973:ALA:O	2:B:1977:MET:HG3	2.16	0.46
6:F:683:GLN:N	6:F:683:GLN:OE1	2.48	0.46
9:J:50:SER:O	9:J:51:PHE:CD1	2.69	0.46
11:L:41:C:C5'	11:L:41:C:C6	2.92	0.46
13:M:472:A:O2'	13:M:473:A:H2'	2.16	0.46
14:O:151:ASP:HB3	14:O:153:GLU:HG2	1.97	0.46
17:R:147:ASN:O	17:R:148:SER:C	2.59	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:G:25:ILE:HD11	28:G:30:ARG:HG3	1.98	0.46
28:G:922:GLY:HA3	28:G:934:PHE:HD2	1.79	0.46
29:d:136:TRP:CE2	29:d:159:TRP:CE3	3.03	0.46
32:e:23:GLU:O	32:e:27:GLU:HG3	2.14	0.46
39:h:16:LYS:N	39:h:17:PRO:CD	2.79	0.46
3:C:471:HIS:HB2	3:C:592:PHE:CZ	2.50	0.46
6:F:701:LYS:HG2	6:F:718:LEU:CD2	2.45	0.46
6:F:745:LEU:O	6:F:775:VAL:HG23	2.15	0.46
6:F:1014:LYS:HB2	6:F:1015:LEU:HA	1.96	0.46
11:L:36:A:C2	13:M:500:A:C2	3.03	0.46
11:L:37:G:N7	28:G:182:ARG:NH2	2.63	0.46
17:R:126:GLY:HA2	17:R:196:LYS:NZ	2.31	0.46
18:S:6:ARG:O	18:S:7:PRO:O	2.33	0.46
21:V:90:ASP:OD2	22:W:241:PHE:CE1	2.68	0.46
22:W:220:PRO:HG3	22:W:236:HIS:CE1	2.51	0.46
23:Y:276:THR:O	23:Y:346:ASP:HB3	2.15	0.46
23:Y:357:ILE:HD11	23:Y:590:THR:HG23	1.98	0.46
23:Y:429:HIS:HD2	23:Y:495:ARG:HH11	1.62	0.46
28:G:686:LEU:HD11	28:G:724:TRP:CH2	2.50	0.46
28:G:919:ILE:HD13	28:G:937:VAL:CG1	2.45	0.46
29:d:147:ASN:HD21	33:f:160:LEU:CD2	2.29	0.46
31:v:565:UNK:HA	31:v:570:THR:HG21	1.98	0.46
33:f:205:GLU:O	33:f:208:SER:OG	2.21	0.46
34:q:463:SER:O	34:q:464:ALA:CB	2.62	0.46
1:A:909:THR:HG21	28:G:49:GLN:CG	2.45	0.46
1:A:1364:GLU:OE2	1:A:1401:SER:HA	2.16	0.46
1:A:2015:LEU:O	1:A:2019:GLU:HG2	2.16	0.46
2:B:135:ILE:HD12	2:B:139:LEU:HD22	1.98	0.46
2:B:517:MET:HE2	2:B:519:ILE:HD11	1.98	0.46
2:B:1597:ALA:O	2:B:1601:PHE:N	2.48	0.46
6:F:779:TYR:O	6:F:780:LEU:HD12	2.16	0.46
8:I:57:TYR:CD1	8:I:70:LEU:CD1	2.80	0.46
21:V:32:TYR:CE1	21:V:78:LYS:HD3	2.51	0.46
21:V:48:LEU:C	22:W:231:ARG:CZ	2.88	0.46
23:Y:307:ARG:NE	23:Y:646:PRO:HB2	2.27	0.46
24:Z:191:ARG:HB3	24:Z:192:GLU:OE1	2.15	0.46
28:G:740:LYS:O	28:G:741:GLU:C	2.59	0.46
29:d:58:LEU:HD22	29:d:68:TRP:CE2	2.51	0.46
29:d:247:VAL:HG13	29:d:266:LEU:HD11	1.97	0.46
31:v:645:ARG:NE	31:v:669:TYR:OH	2.48	0.46
34:r:62:LEU:O	34:r:63:THR:C	2.59	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:l:39:SER:O	41:l:41:ASN:N	2.48	0.46
1:A:725:TYR:CD1	5:E:72:C:C1'	2.98	0.46
2:B:531:ALA:HB1	2:B:632:ILE:HD13	1.98	0.46
2:B:1751:HIS:HB3	2:B:1860:PHE:CD1	2.51	0.46
6:F:93:LEU:O	6:F:103:LEU:HD12	2.16	0.46
6:F:267:HIS:HB3	6:F:287:LEU:HA	1.96	0.46
9:J:51:PHE:CE2	9:J:54:GLN:CG	2.99	0.46
15:P:48:GLN:HG3	15:P:49:SER:N	2.29	0.46
16:Q:105:LYS:O	16:Q:109:MET:HB2	2.15	0.46
16:Q:108:MET:HE3	27:c:211:ILE:CG1	2.46	0.46
23:Y:287:ALA:HB2	23:Y:321:TYR:HB2	1.96	0.46
23:Y:807:VAL:HG12	23:Y:841:GLU:HB3	1.97	0.46
28:G:919:ILE:HD13	28:G:937:VAL:HG11	1.97	0.46
33:f:184:GLN:HA	33:f:187:LYS:HZ3	1.81	0.46
1:A:1642:LYS:HE2	25:a:138:ASP:OD2	2.16	0.46
2:B:618:ASN:HB3	2:B:621:ASN:ND2	2.30	0.46
2:B:733:SER:HB3	2:B:738:ASN:HB2	1.98	0.46
2:B:1405:ILE:HG23	2:B:1446:LEU:HB3	1.97	0.46
14:O:161:ASP:O	14:O:162:THR:OG1	2.23	0.46
20:U:140:HIS:CE1	20:U:161:SER:HG	2.33	0.46
22:W:170:LEU:N	22:W:170:LEU:CD2	2.78	0.46
27:c:110:ASP:OD1	27:c:111:SER:N	2.46	0.46
2:B:513:GLY:O	2:B:666:ARG:NH1	2.49	0.46
2:B:562:PRO:HG3	2:B:635:GLU:OE1	2.16	0.46
2:B:1568:PHE:HB2	2:B:1598:PHE:CE1	2.51	0.46
2:B:1782:ILE:HD11	2:B:1791:VAL:HG21	1.98	0.46
2:B:1981:GLN:HA	2:B:2147:ASP:O	2.16	0.46
3:C:307:ILE:HA	3:C:324:ILE:HD11	1.98	0.46
3:C:722:ASP:OD2	3:C:755:TYR:OH	2.25	0.46
3:C:869:HIS:CD2	3:C:925:LEU:HD22	2.50	0.46
8:I:36:LYS:HG2	33:f:194:SER:HB3	1.98	0.46
27:c:230:THR:OG1	27:c:231:SER:N	2.48	0.46
29:d:219:ARG:HA	29:d:222:TYR:HD2	1.81	0.46
31:v:730:GLN:HA	31:v:733:ILE:HD12	1.97	0.46
38:i:86:ASN:ND2	39:h:32:LYS:NZ	2.64	0.46
1:A:899:PRO:HD3	1:A:1006:ARG:HH12	1.81	0.46
1:A:905:TYR:CE2	1:A:907:ASN:HB2	2.51	0.46
1:A:1080:ASP:HB3	27:c:82:ASN:HD22	1.81	0.46
1:A:1354:GLU:N	1:A:1355:PRO:HD2	2.31	0.46
1:A:1703:MET:HB2	1:A:1732:MET:H	1.81	0.46
1:A:2262:GLN:OE1	1:A:2292:SER:OG	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:899:LEU:O	2:B:903:ASN:ND2	2.21	0.46
2:B:1120:GLY:HA2	2:B:1251:ILE:HB	1.96	0.46
2:B:1368:VAL:HB	2:B:1511:LEU:HD23	1.98	0.46
2:B:2055:TYR:HA	2:B:2073:ILE:HA	1.98	0.46
3:C:502:LEU:HB3	3:C:576:THR:OG1	2.15	0.46
3:C:539:VAL:HG13	3:C:564:ILE:CG2	2.46	0.46
4:D:174:G:C8	43:g:99:ASP:OD2	2.69	0.46
7:H:166:THR:CG2	7:H:167:LYS:H	2.29	0.46
9:J:37:VAL:HG13	9:J:38:ARG:HG2	1.98	0.46
10:K:24:GLU:C	10:K:24:GLU:CD	2.83	0.46
15:P:57:LEU:HD23	15:P:58:PRO:HD3	1.91	0.46
26:b:90:LEU:HD23	26:b:101:ILE:HD12	1.97	0.46
27:c:227:ILE:HG22	29:d:123:ASN:ND2	2.31	0.46
27:c:233:GLU:OE2	29:d:115:ILE:CG2	2.63	0.46
28:G:467:VAL:HG12	28:G:469:SER:H	1.81	0.46
31:v:712:CYS:O	31:v:715:LYS:N	2.48	0.46
35:t:7:VAL:CG1	35:t:154:VAL:CB	2.72	0.46
42:m:6:PHE:CZ	42:m:10:LEU:HD11	2.51	0.46
1:A:997:GLN:HE22	1:A:1511:ARG:HH21	1.58	0.46
2:B:1796:PRO:HA	2:B:1799:ILE:HD12	1.96	0.46
3:C:110:LYS:HB2	3:C:110:LYS:HE3	1.66	0.46
6:F:111:LEU:HD12	6:F:111:LEU:O	2.17	0.46
6:F:1180:THR:HG23	7:H:168:ASN:OD1	2.15	0.46
8:I:18:SER:O	8:I:19:GLU:C	2.58	0.46
14:O:132:SER:HB3	14:O:427:LYS:CB	2.46	0.46
14:O:365:PHE:CZ	14:O:373:LEU:HD22	2.50	0.46
16:Q:118:VAL:O	16:Q:119:LYS:HB2	2.16	0.46
16:Q:217:TRP:CD1	16:Q:217:TRP:C	2.93	0.46
18:S:174:VAL:O	18:S:174:VAL:HG12	2.16	0.46
21:V:89:VAL:HG21	21:V:106:HIS:CD2	2.52	0.46
23:Y:327:LEU:HD11	23:Y:343:ILE:HD13	1.98	0.46
24:Z:301:SER:O	24:Z:302:SER:OG	2.30	0.46
25:a:178:TRP:CD1	25:a:178:TRP:H	2.33	0.46
31:v:670:SER:CB	31:v:687:LEU:HD11	2.46	0.46
32:e:57:PHE:CD2	32:e:63:ALA:HA	2.52	0.46
1:A:134:MET:HB3	1:A:135:PRO:CD	2.45	0.45
1:A:346:ILE:HD11	1:A:385:VAL:HG11	1.98	0.45
1:A:930:ASN:C	1:A:934:ARG:NH1	2.74	0.45
1:A:1710:GLU:HB3	1:A:1724:PHE:O	2.16	0.45
1:A:2050:THR:O	1:A:2053:SER:OG	2.28	0.45
2:B:1476:ALA:H	2:B:1512:SER:HB2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1862:THR:OG1	2:B:1887:VAL:HB	2.17	0.45
3:C:274:ILE:CG1	3:C:382:TYR:HE1	2.21	0.45
3:C:670:ILE:HG22	3:C:671:SER:O	2.15	0.45
4:D:167:A:N7	43:g:63:ARG:NH1	2.65	0.45
5:E:95:A:H2'	5:E:96:G:O4'	2.15	0.45
6:F:284:ALA:HB1	6:F:286:TYR:CZ	2.51	0.45
6:F:363:VAL:CG1	6:F:364:THR:H	2.13	0.45
6:F:1198:ILE:HG13	10:K:48:ALA:HB1	1.98	0.45
6:F:1308:ARG:HD3	6:F:1308:ARG:HA	1.70	0.45
9:J:43:VAL:CG2	9:J:70:ALA:HB3	2.47	0.45
13:M:480:A:O2'	13:M:481:A:H2'	2.16	0.45
14:O:327:CYS:SG	14:O:328:THR:N	2.89	0.45
15:P:301:LEU:CD2	15:P:301:LEU:N	2.78	0.45
17:R:4:TRP:NE1	17:R:92:HIS:HB3	2.31	0.45
17:R:187:LYS:O	17:R:187:LYS:HD2	2.16	0.45
22:W:229:GLY:C	22:W:231:ARG:N	2.73	0.45
23:Y:467:LYS:CB	23:Y:494:CYS:N	2.78	0.45
23:Y:702:SER:O	23:Y:705:ILE:N	2.49	0.45
28:G:156:LEU:O	28:G:160:GLU:N	2.43	0.45
32:e:153:VAL:O	32:e:153:VAL:HG22	2.17	0.45
34:q:14:VAL:HG12	34:q:52:GLU:HA	1.98	0.45
1:A:742:VAL:CG1	14:O:224:LEU:HA	2.46	0.45
1:A:1163:ARG:NH1	1:A:1163:ARG:CG	2.78	0.45
1:A:1454:SER:OG	28:G:23:TYR:O	2.32	0.45
1:A:2060:LEU:HD22	1:A:2071:ILE:HD11	1.98	0.45
2:B:497:THR:HG22	6:F:657:ASP:OD2	2.16	0.45
2:B:557:ILE:HG22	2:B:630:LEU:HB3	1.98	0.45
2:B:809:THR:HG23	2:B:811:SER:HB3	1.98	0.45
2:B:1365:SER:HB3	2:B:1508:PHE:HB2	1.97	0.45
2:B:1663:VAL:HG12	2:B:1664:LEU:H	1.80	0.45
2:B:1803:LEU:O	2:B:1807:VAL:HG23	2.16	0.45
3:C:468:LEU:O	3:C:578:TYR:HA	2.16	0.45
4:D:174:G:N7	42:m:20:LYS:CE	2.77	0.45
5:E:39:G:N1	17:R:117:PHE:HB2	2.31	0.45
6:F:118:GLN:HB2	6:F:1325:ASN:OD1	2.16	0.45
7:H:248:HIS:CE1	7:H:252:PHE:CD2	3.02	0.45
10:K:22:GLY:HA3	28:G:935:TRP:CH2	2.50	0.45
16:Q:91:ILE:HD13	16:Q:125:ILE:HD12	1.98	0.45
17:R:143:ASP:O	17:R:146:LEU:HA	2.16	0.45
23:Y:426:PHE:HB3	23:Y:462:LEU:HD11	1.98	0.45
23:Y:807:VAL:CG2	23:Y:843:ILE:HD11	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Z:319:ASN:HA	24:Z:322:LYS:HD3	1.97	0.45
26:b:41:MET:HE1	26:b:66:ASN:O	2.17	0.45
26:b:79:ASN:HD21	26:b:81:ARG:HH21	1.63	0.45
28:G:689:LEU:HD21	28:G:707:PHE:CD1	2.52	0.45
28:G:698:ARG:HE	28:G:739:ASN:HD22	1.64	0.45
29:d:165:GLY:O	29:d:169:TRP:HD1	1.99	0.45
29:d:182:TRP:HA	29:d:185:VAL:HG12	1.98	0.45
1:A:695:LEU:HD12	1:A:695:LEU:O	2.16	0.45
1:A:2208:TYR:HD1	1:A:2255:LEU:HA	1.81	0.45
3:C:178:LEU:HD12	3:C:214:ASP:HB2	1.97	0.45
3:C:237:ILE:HD13	3:C:253:ILE:HG22	1.99	0.45
3:C:644:ILE:HG22	3:C:652:MET:HE1	1.98	0.45
4:D:179:U:OP1	43:g:79:LYS:HG2	2.15	0.45
6:F:71:PHE:CD1	6:F:97:THR:HG21	2.52	0.45
6:F:187:VAL:O	6:F:206:SER:OG	2.25	0.45
6:F:509:LYS:HE3	6:F:890:GLU:OE2	2.16	0.45
6:F:643:ILE:HG21	6:F:691:LEU:HD11	1.99	0.45
6:F:1191:ASN:ND2	6:F:1316:LYS:HB2	2.31	0.45
7:H:285:MET:HG2	32:e:26:TYR:CD2	2.51	0.45
11:L:60:A:H2'	11:L:61:A:O4'	2.17	0.45
12:N:113:U:O4'	17:R:183:PHE:CE2	2.69	0.45
21:V:63:SER:HB2	21:V:74:PHE:CD1	2.39	0.45
22:W:215:TYR:CE2	22:W:232:TRP:CZ3	3.04	0.45
23:Y:324:ASP:CG	23:Y:354:ALA:HB3	2.42	0.45
25:a:216:HIS:ND1	25:a:235:ILE:HD12	2.32	0.45
28:G:334:ILE:HD11	28:G:362:CYS:CB	2.46	0.45
31:v:624:TRP:HE1	31:v:651:ALA:CB	2.29	0.45
32:e:143:LEU:O	32:e:144:SER:C	2.60	0.45
33:f:113:ALA:O	33:f:116:THR:OG1	2.32	0.45
1:A:296:THR:CG2	4:D:33:U:OP2	2.64	0.45
1:A:774:ILE:HD12	1:A:775:ARG:H	1.74	0.45
1:A:1561:LEU:HD11	1:A:1608:LEU:CD2	2.44	0.45
1:A:1852:VAL:HG22	1:A:1881:THR:HG22	1.97	0.45
2:B:162:ILE:O	2:B:166:LYS:N	2.48	0.45
2:B:593:ARG:HD2	2:B:596:ARG:HD3	1.99	0.45
6:F:1122:LYS:O	6:F:1129:VAL:HG13	2.16	0.45
14:O:201:SER:OG	14:O:202:GLU:N	2.50	0.45
17:R:31:ASN:O	17:R:34:TYR:O	2.33	0.45
22:W:208:SER:CA	22:W:214:LEU:HD12	2.47	0.45
25:a:168:PHE:C	25:a:169:LYS:CE	2.90	0.45
28:G:67:ARG:HD2	28:G:292:TYR:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:G:198:GLU:HG2	28:G:239:TYR:OH	2.16	0.45
31:v:606:GLN:HA	31:v:609:GLU:HG2	1.99	0.45
32:e:165:ILE:HG23	32:e:180:VAL:O	2.17	0.45
1:A:271:GLN:NE2	1:A:271:GLN:C	2.74	0.45
1:A:334:LYS:HD3	1:A:400:ILE:O	2.17	0.45
1:A:366:GLU:O	1:A:372:ARG:NH1	2.50	0.45
1:A:379:ILE:HA	1:A:383:TYR:HD2	1.82	0.45
1:A:782:ILE:HD12	1:A:782:ILE:C	2.36	0.45
1:A:1379:MET:HE2	1:A:1379:MET:HB3	1.76	0.45
1:A:1889:LEU:O	1:A:1988:LEU:HD23	2.16	0.45
2:B:717:LYS:HA	2:B:720:LYS:HB3	1.97	0.45
2:B:1797:HIS:O	2:B:1800:SER:OG	2.24	0.45
3:C:861:ILE:HG21	3:C:905:GLN:HB3	1.98	0.45
4:D:79:C:O2	4:D:79:C:H3'	2.16	0.45
6:F:630:ILE:HG21	6:F:646:LEU:HB2	1.99	0.45
6:F:643:ILE:HG13	6:F:691:LEU:HD12	1.98	0.45
6:F:676:PRO:HA	6:F:694:ALA:O	2.17	0.45
6:F:1221:LEU:C	6:F:1223:GLY:H	2.25	0.45
9:J:11:CYS:HB3	9:J:86:CYS:HB3	1.98	0.45
17:R:76:PHE:HB2	17:R:91:HIS:CD2	2.51	0.45
17:R:256:ASN:HA	17:R:259:ASN:HD22	1.82	0.45
21:V:11:GLU:HG2	21:V:16:ILE:CG2	2.45	0.45
23:Y:308:PHE:CD2	23:Y:740:ILE:HG12	2.51	0.45
23:Y:543:ARG:N	23:Y:575:GLU:O	2.47	0.45
23:Y:556:VAL:HG23	23:Y:557:GLY:N	2.32	0.45
27:c:66:SER:OG	27:c:69:GLU:HG2	2.15	0.45
27:c:220:GLU:OE2	29:d:82:ARG:NE	2.46	0.45
28:G:256:PRO:HA	28:G:259:ARG:HB2	1.98	0.45
28:G:881:MET:HG2	28:G:885:ILE:CD1	2.41	0.45
34:p:100:SER:O	34:p:103:ASP:CG	2.60	0.45
36:n:67:GLY:HA2	36:n:68:PRO:HA	1.76	0.45
1:A:380:ARG:CG	1:A:380:ARG:NH1	2.79	0.45
1:A:978:ILE:CG2	18:S:174:VAL:HG22	2.46	0.45
1:A:1008:LEU:HD21	1:A:1073:ILE:HD11	1.98	0.45
1:A:1998:ARG:HD3	1:A:1998:ARG:H	1.82	0.45
1:A:2015:LEU:HD23	1:A:2022:ALA:HB3	1.99	0.45
2:B:1027:THR:HA	2:B:1127:MET:HE1	1.97	0.45
3:C:109:LEU:HD21	4:D:43:G:N1	2.31	0.45
3:C:194:ASN:OD1	3:C:478:TYR:OH	2.33	0.45
6:F:70:ASN:O	6:F:97:THR:HB	2.17	0.45
6:F:703:MET:SD	6:F:715:VAL:HG22	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:1088:GLY:HA3	6:F:1118:VAL:HG21	1.99	0.45
6:F:1122:LYS:NZ	6:F:1202:PHE:O	2.48	0.45
28:G:558:GLU:HG2	28:G:597:PHE:HE2	1.82	0.45
36:n:59:ARG:NH1	36:n:59:ARG:CG	2.80	0.45
1:A:763:MET:CE	1:A:779:ALA:CB	2.95	0.45
1:A:854:ARG:CG	1:A:854:ARG:NH2	2.72	0.45
1:A:856:TRP:CG	18:S:174:VAL:HG11	2.50	0.45
1:A:867:ILE:HG21	1:A:1101:TYR:CD1	2.52	0.45
1:A:1835:LEU:CD1	1:A:1836:ASN:CG	2.90	0.45
6:F:551:PHE:CD2	6:F:591:THR:HG21	2.49	0.45
6:F:1012:LYS:HA	6:F:1013:ASP:HA	1.62	0.45
6:F:1036:LYS:NZ	6:F:1082:TYR:OH	2.50	0.45
13:M:506:U:OP1	13:M:506:U:H4'	2.16	0.45
15:P:53:LEU:CD2	15:P:53:LEU:C	2.89	0.45
32:e:27:GLU:C	32:e:122:ASP:CB	2.90	0.45
34:p:98:LEU:HD21	34:q:102:LEU:HD12	1.99	0.45
1:A:1051:GLU:HA	1:A:1168:ILE:O	2.17	0.45
1:A:1882:LEU:HB3	1:A:1889:LEU:HD23	1.99	0.45
2:B:1754:LEU:HD12	2:B:1810:CYS:SG	2.57	0.45
3:C:501:ILE:O	3:C:535:PRO:HG2	2.16	0.45
6:F:71:PHE:HD1	6:F:97:THR:CG2	2.30	0.45
6:F:258:ASP:OD1	6:F:259:ASN:N	2.50	0.45
6:F:490:SER:OG	6:F:491:GLN:N	2.50	0.45
6:F:1222:GLN:HE22	10:K:48:ALA:N	2.13	0.45
14:O:186:ARG:NH1	14:O:202:GLU:OE2	2.49	0.45
16:Q:205:PHE:CD1	16:Q:205:PHE:N	2.85	0.45
21:V:16:ILE:CG2	21:V:17:LEU:N	2.79	0.45
21:V:19:PRO:O	21:V:25:ASN:HB2	2.17	0.45
21:V:58:VAL:HG12	22:W:212:ARG:NH1	2.31	0.45
22:W:188:LEU:C	22:W:190:ILE:N	2.73	0.45
23:Y:223:LEU:HB2	23:Y:226:HIS:CD2	2.52	0.45
27:c:30:THR:O	27:c:33:TRP:NE1	2.50	0.45
28:G:241:HIS:O	28:G:245:VAL:HG23	2.17	0.45
28:G:286:ILE:HD12	28:G:316:PHE:HZ	1.81	0.45
28:G:916:MET:HE3	28:G:941:MET:HG3	1.99	0.45
28:G:927:ALA:HB3	28:G:930:VAL:HB	1.99	0.45
1:A:645:ASP:OD1	1:A:646:ALA:N	2.48	0.45
3:C:343:ASP:O	3:C:347:ARG:CG	2.63	0.45
3:C:883:ARG:NH2	3:C:910:GLU:O	2.50	0.45
6:F:255:LEU:HG	6:F:295:VAL:CG2	2.47	0.45
6:F:542:THR:HG22	6:F:615:LYS:NZ	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:638:SER:OG	6:F:639:LYS:N	2.50	0.45
7:H:248:HIS:NE2	7:H:252:PHE:CD2	2.85	0.45
14:O:266:LYS:NZ	29:d:93:LEU:O	2.33	0.45
16:Q:120:LEU:HG	16:Q:121:GLY:N	2.32	0.45
17:R:142:ILE:HG22	17:R:180:ASN:HD22	1.82	0.45
21:V:68:THR:HG23	21:V:70:GLU:HG2	1.99	0.45
29:d:69:ILE:HG21	29:d:104:ARG:NE	2.32	0.45
33:f:159:LYS:O	33:f:160:LEU:HB2	2.17	0.45
37:k:20:LEU:O	37:k:31:ILE:HA	2.16	0.45
38:i:30:TRP:CE2	38:i:89:LEU:HD22	2.51	0.45
1:A:236:ARG:CG	1:A:651:ASP:OD2	2.65	0.45
1:A:296:THR:HB	4:D:33:U:OP2	2.17	0.45
1:A:742:VAL:HG11	14:O:224:LEU:HA	1.99	0.45
1:A:801:VAL:HG11	1:A:804:MET:HE3	1.99	0.45
1:A:2407:GLU:C	1:A:2407:GLU:CD	2.85	0.45
2:B:1330:SER:HA	2:B:1347:THR:HA	1.99	0.45
2:B:1338:ASP:HB3	2:B:1419:LEU:HD11	1.99	0.45
2:B:1502:LEU:HD13	2:B:1504:LYS:HD2	1.98	0.45
3:C:163:ASP:OD2	3:C:548:ARG:NH1	2.46	0.45
3:C:315:SER:HB3	3:C:320:PHE:CE1	2.52	0.45
3:C:788:LEU:O	3:C:792:LYS:HG2	2.17	0.45
3:C:867:THR:O	3:C:926:GLY:HA2	2.17	0.45
3:C:932:PHE:O	3:C:933:TRP:HD1	1.96	0.45
6:F:822:HIS:ND1	6:F:846:MET:O	2.50	0.45
6:F:1073:LYS:HB2	6:F:1090:ILE:HG13	1.98	0.45
6:F:1093:SER:HB2	6:F:1112:ASP:HB3	1.98	0.45
14:O:157:THR:HG21	14:O:423:ILE:HD11	1.99	0.45
15:P:47:ARG:O	15:P:50:ASN:O	2.34	0.45
16:Q:108:MET:HE3	27:c:211:ILE:HG13	2.00	0.45
17:R:1:MET:HA	17:R:5:ARG:HB2	1.98	0.45
17:R:62:THR:HG23	17:R:64:GLY:H	1.81	0.45
21:V:48:LEU:O	22:W:231:ARG:HD2	2.16	0.45
24:Z:174:TRP:CZ2	24:Z:201:ARG:HB2	2.51	0.45
1:A:840:VAL:O	1:A:840:VAL:HG22	2.17	0.44
1:A:843:THR:O	1:A:847:LYS:HB2	2.17	0.44
1:A:939:LEU:HD12	1:A:986:PRO:HB2	1.99	0.44
1:A:1048:VAL:HG22	1:A:1250:VAL:HG22	1.98	0.44
2:B:1030:ASP:OD1	2:B:1033:ARG:NH1	2.40	0.44
2:B:1555:GLU:O	2:B:1686:ASN:ND2	2.50	0.44
3:C:746:LYS:O	3:C:750:ILE:HG12	2.17	0.44
6:F:660:SER:OG	6:F:661:ASP:N	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:208:MET:HE2	7:H:240:LEU:O	2.16	0.44
9:J:26:CYS:O	9:J:29:LYS:HG3	2.17	0.44
10:K:42:THR:CG2	28:G:950:VAL:HG21	2.41	0.44
17:R:236:LYS:O	17:R:240:GLU:N	2.47	0.44
21:V:110:ARG:HE	21:V:110:ARG:HB3	1.56	0.44
22:W:167:VAL:O	22:W:171:GLY:HA2	2.17	0.44
23:Y:319:LEU:HD12	23:Y:320:LYS:H	1.82	0.44
24:Z:192:GLU:N	24:Z:192:GLU:CD	2.75	0.44
25:a:135:VAL:CG1	25:a:137:MET:CE	2.96	0.44
28:G:221:MET:O	28:G:224:THR:OG1	2.25	0.44
28:G:927:ALA:C	28:G:929:ASN:N	2.75	0.44
1:A:195:THR:HG23	1:A:556:TYR:O	2.17	0.44
1:A:1755:LYS:HB3	1:A:1759:TYR:HE2	1.81	0.44
1:A:2281:PHE:HB3	1:A:2285:LYS:O	2.17	0.44
2:B:136:PRO:HA	2:B:860:TRP:CE2	2.52	0.44
2:B:511:PHE:O	2:B:537:LYS:HD3	2.17	0.44
2:B:1137:THR:HG21	2:B:1148:GLN:HE21	1.83	0.44
2:B:1329:ILE:HG21	2:B:1356:PHE:CE1	2.52	0.44
2:B:1329:ILE:HG13	2:B:1356:PHE:CG	2.52	0.44
2:B:1403:GLU:OE1	2:B:1403:GLU:N	2.50	0.44
2:B:1514:CYS:HB2	2:B:1537:PRO:HG3	1.99	0.44
3:C:103:HIS:CD2	3:C:104:THR:HG23	2.52	0.44
6:F:859:ILE:C	6:F:861:GLY:H	2.25	0.44
8:I:3:TYR:CE2	12:N:99:G:C5	3.05	0.44
14:O:151:ASP:CB	14:O:153:GLU:HG2	2.47	0.44
17:R:15:GLU:HA	17:R:18:LEU:CD1	2.47	0.44
17:R:176:VAL:O	17:R:179:LYS:O	2.34	0.44
21:V:32:TYR:OH	22:W:162:LEU:HD11	2.18	0.44
22:W:170:LEU:O	22:W:172:ILE:CG1	2.62	0.44
22:W:222:ASN:OD1	22:W:223:ARG:N	2.50	0.44
23:Y:290:VAL:HA	23:Y:293:GLU:HB2	1.99	0.44
25:a:210:VAL:O	25:a:217:TYR:HA	2.17	0.44
25:a:211:VAL:HG23	25:a:247:ALA:CB	2.47	0.44
1:A:1814:VAL:HG21	28:G:645:ILE:HG21	1.99	0.44
1:A:2385:GLU:HB3	1:A:2392:PHE:HE2	1.81	0.44
2:B:830:CYS:SG	2:B:834:LEU:HD22	2.57	0.44
2:B:850:THR:O	2:B:863:LEU:N	2.49	0.44
2:B:1345:PHE:HE1	2:B:1348:PHE:HD1	1.65	0.44
2:B:1469:GLU:C	2:B:1506:ILE:HG23	2.42	0.44
2:B:1564:LEU:HG	2:B:1601:PHE:HE2	1.81	0.44
3:C:799:PHE:CZ	3:C:803:VAL:HG21	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:O:406:THR:O	14:O:414:LEU:HD12	2.17	0.44
15:P:323:VAL:CG2	15:P:324:TYR:CD2	3.00	0.44
16:Q:13:CYS:SG	16:Q:16:CYS:N	2.84	0.44
17:R:146:LEU:CD2	17:R:147:ASN:N	2.80	0.44
19:T:138:THR:HG22	19:T:138:THR:O	2.16	0.44
21:V:33:ILE:CG2	21:V:85:THR:HG23	2.48	0.44
23:Y:438:ILE:HB	23:Y:497:VAL:HG22	1.99	0.44
24:Z:194:LEU:HD22	24:Z:194:LEU:C	2.42	0.44
25:a:250:LEU:O	25:a:254:LEU:N	2.44	0.44
28:G:473:LYS:O	28:G:477:GLU:HG2	2.17	0.44
28:G:569:PHE:HE1	28:G:580:PHE:CE1	2.31	0.44
28:G:583:PHE:HE2	28:G:627:LEU:HD21	1.83	0.44
31:v:730:GLN:C	31:v:733:ILE:HD12	2.41	0.44
32:e:117:ASP:C	32:e:119:ILE:H	2.24	0.44
33:f:110:ARG:O	33:f:114:THR:HG23	2.18	0.44
1:A:765:ASP:OD1	14:O:312:ARG:NH2	2.44	0.44
1:A:913:VAL:HG21	28:G:46:ASP:OD2	2.17	0.44
1:A:1835:LEU:CD1	1:A:1836:ASN:ND2	2.78	0.44
2:B:648:GLU:OE1	2:B:912:PHE:HB2	2.18	0.44
2:B:932:ARG:HD3	2:B:989:TYR:OH	2.17	0.44
2:B:1397:TYR:CD2	2:B:1446:LEU:HG	2.52	0.44
2:B:1881:TYR:CG	2:B:1914:PRO:HG2	2.52	0.44
2:B:2033:LEU:HD13	2:B:2037:GLN:HB3	1.99	0.44
6:F:71:PHE:HD1	6:F:97:THR:HG21	1.82	0.44
6:F:782:GLU:HB3	6:F:783:ILE:H	1.67	0.44
11:L:2:C:H2'	11:L:3:G:C8	2.52	0.44
13:M:484:A:C8	13:M:484:A:C3'	3.00	0.44
13:M:487:A:OP2	13:M:487:A:H4'	2.17	0.44
20:U:101:ARG:HB2	20:U:104:TYR:CZ	2.53	0.44
25:a:135:VAL:HG11	25:a:137:MET:CE	2.48	0.44
26:b:42:LEU:HD22	26:b:157:VAL:HG21	1.99	0.44
28:G:855:GLN:HG2	28:G:898:ARG:HG3	2.00	0.44
33:f:184:GLN:OE1	33:f:187:LYS:NZ	2.50	0.44
1:A:185:GLN:HE21	1:A:263:PRO:HD3	1.81	0.44
1:A:251:TYR:CE2	1:A:256:GLU:HG2	2.52	0.44
1:A:379:ILE:HA	1:A:383:TYR:CD2	2.52	0.44
1:A:1578:ALA:HB3	22:W:265:ASP:C	2.42	0.44
1:A:1860:VAL:HG13	1:A:1872:THR:HB	1.99	0.44
2:B:170:GLN:CD	2:B:177:ILE:HG22	2.42	0.44
2:B:714:ASN:HB3	2:B:717:LYS:HB2	2.00	0.44
2:B:1618:VAL:N	2:B:1619:PRO:HD2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1997:ILE:HG12	2:B:2044:PHE:CE2	2.52	0.44
3:C:320:PHE:HB2	3:C:429:PHE:HD2	1.81	0.44
3:C:633:ILE:HB	3:C:645:LEU:HB2	2.00	0.44
6:F:162:ILE:O	6:F:162:ILE:HG13	2.17	0.44
6:F:250:PRO:HG2	6:F:273:LEU:HB3	2.00	0.44
6:F:521:ASN:OD1	6:F:522:LEU:N	2.50	0.44
7:H:212:LEU:HD11	28:G:806:THR:CG2	2.48	0.44
14:O:237:ASP:OD2	18:S:39:TYR:OH	2.34	0.44
16:Q:69:ASN:HB3	16:Q:123:ALA:CB	2.48	0.44
24:Z:464:PHE:CE2	24:Z:468:ILE:HD11	2.53	0.44
25:a:162:LEU:HG	25:a:164:SER:HB3	1.99	0.44
28:G:286:ILE:HD12	28:G:316:PHE:CZ	2.51	0.44
29:d:236:GLN:O	29:d:238:TRP:HA	2.18	0.44
36:n:65:GLY:C	36:n:66:ASP:CG	2.86	0.44
1:A:1735:ASP:OD2	1:A:1767:TYR:OH	2.22	0.44
1:A:2182:VAL:HA	1:A:2338:GLN:HB2	2.00	0.44
2:B:477:LEU:HD11	6:F:659:SER:O	2.17	0.44
2:B:1429:GLY:C	2:B:1431:ASP:H	2.25	0.44
3:C:274:ILE:HG12	3:C:382:TYR:CD1	2.45	0.44
4:D:60:U:O2	4:D:60:U:C3'	2.65	0.44
5:E:5:G:O2'	5:E:6:C:H5'	2.18	0.44
5:E:90:U:OP2	29:d:104:ARG:NH2	2.51	0.44
6:F:253:VAL:HG22	6:F:270:PHE:CD2	2.53	0.44
6:F:348:VAL:HG12	6:F:407:LEU:HD12	2.00	0.44
6:F:747:ASN:C	6:F:747:ASN:OD1	2.61	0.44
16:Q:124:GLN:CD	16:Q:124:GLN:C	2.86	0.44
16:Q:290:ILE:HG22	16:Q:292:PRO:HD2	2.00	0.44
21:V:54:TYR:HB3	21:V:87:LEU:HD23	2.00	0.44
21:V:87:LEU:HD21	22:W:222:ASN:ND2	2.31	0.44
23:Y:580:PRO:HB2	23:Y:582:ILE:HG22	1.99	0.44
24:Z:178:ARG:HG2	24:Z:198:PHE:CZ	2.50	0.44
38:i:30:TRP:CD2	38:i:89:LEU:HD22	2.52	0.44
38:i:45:GLY:HA3	38:i:53:VAL:HG12	2.00	0.44
1:A:518:VAL:O	1:A:521:SER:N	2.50	0.44
1:A:1082:ILE:CG2	1:A:1113:ILE:HD11	2.48	0.44
1:A:1565:THR:O	1:A:1816:ARG:HG3	2.17	0.44
1:A:1681:VAL:HG22	1:A:1703:MET:SD	2.58	0.44
3:C:807:PRO:HG3	3:C:850:LEU:HD23	1.99	0.44
6:F:924:PHE:HD2	6:F:952:ARG:CD	2.28	0.44
6:F:996:ILE:O	6:F:1003:LEU:HD12	2.18	0.44
6:F:1188:GLN:HG3	6:F:1188:GLN:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:242:LEU:HD12	7:H:242:LEU:HA	1.77	0.44
11:L:7:C:O5'	11:L:7:C:H6	2.01	0.44
12:N:113:U:C6	17:R:183:PHE:CZ	3.05	0.44
14:O:248:ILE:HD11	14:O:283:SER:HB3	2.00	0.44
16:Q:106:ASN:HB2	16:Q:109:MET:HG2	1.99	0.44
20:U:64:TYR:OH	20:U:150:GLY:O	2.27	0.44
20:U:108:ARG:NH2	20:U:138:LYS:HE3	2.33	0.44
20:U:182:SER:HB2	20:U:203:ASN:ND2	2.32	0.44
23:Y:475:TYR:CE2	23:Y:477:ASN:CG	2.94	0.44
23:Y:807:VAL:HG23	23:Y:843:ILE:HD11	1.99	0.44
29:d:117:HIS:C	29:d:120:ASN:HD21	2.19	0.44
1:A:644:VAL:O	1:A:645:ASP:HB2	2.17	0.44
1:A:1400:ILE:HG23	1:A:1542:TYR:CE2	2.52	0.44
1:A:1456:ARG:HG3	1:A:1457:VAL:N	2.32	0.44
2:B:593:ARG:NH2	2:B:615:THR:HA	2.32	0.44
2:B:1958:ILE:HG21	2:B:1980:ALA:HA	2.00	0.44
2:B:2054:THR:O	2:B:2074:GLN:N	2.40	0.44
6:F:374:LYS:C	6:F:376:ASP:H	2.26	0.44
7:H:175:HIS:CD2	7:H:182:TYR:HB2	2.53	0.44
10:K:23:ASP:CG	10:K:24:GLU:H	2.23	0.44
12:N:93:U:O2	12:N:93:U:C2'	2.64	0.44
15:P:196:THR:CA	27:c:90:MET:HE1	2.44	0.44
16:Q:69:ASN:ND2	16:Q:126:THR:CG2	2.79	0.44
16:Q:88:ASP:O	16:Q:99:VAL:HG11	2.18	0.44
16:Q:205:PHE:HB3	16:Q:291:ILE:O	2.17	0.44
19:T:119:THR:O	19:T:120:CYS:C	2.60	0.44
20:U:47:GLY:C	20:U:48:ILE:HG13	2.42	0.44
20:U:80:LEU:HD12	20:U:200:ILE:O	2.18	0.44
23:Y:657:THR:O	23:Y:661:HIS:CG	2.71	0.44
24:Z:170:HIS:NE2	24:Z:174:TRP:HZ3	1.99	0.44
27:c:230:THR:C	27:c:232:THR:H	2.24	0.44
27:c:509:LEU:O	27:c:513:ILE:N	2.48	0.44
28:G:314:LEU:N	28:G:315:PRO:HD2	2.33	0.44
28:G:378:LEU:HD11	28:G:396:VAL:HG11	2.00	0.44
35:t:81:ASP:C	35:t:82:ASP:CG	2.86	0.44
1:A:1626:GLN:OE1	25:a:137:MET:HE1	2.18	0.44
2:B:428:ASP:HB3	2:B:431:LYS:HG2	1.99	0.44
2:B:842:ALA:O	2:B:876:GLY:N	2.49	0.44
2:B:1477:HIS:ND1	2:B:1512:SER:OG	2.35	0.44
3:C:100:LEU:CD2	3:C:479:GLY:CA	2.96	0.44
3:C:766:TRP:HB2	3:C:776:ASN:HD22	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:216:VAL:HG12	6:F:217:ASP:N	2.31	0.44
14:O:263:VAL:CG1	18:S:11:ALA:HB2	2.44	0.44
16:Q:206:PHE:HB3	16:Q:208:TYR:OH	2.17	0.44
17:R:187:LYS:HG3	17:R:188:TYR:CD1	2.52	0.44
21:V:82:GLN:H	22:W:168:GLN:NE2	2.12	0.44
22:W:208:SER:CA	22:W:214:LEU:CD1	2.95	0.44
24:Z:300:LYS:HA	24:Z:300:LYS:HD3	1.88	0.44
28:G:517:TYR:OH	28:G:521:LYS:NZ	2.50	0.44
34:q:102:LEU:O	34:q:105:LEU:CG	2.66	0.44
34:q:405:ASP:HB3	35:t:30:ASN:CG	2.43	0.44
1:A:168:LEU:N	1:A:169:PRO:HD2	2.32	0.43
1:A:1843:LEU:HD13	1:A:1851:PHE:CZ	2.50	0.43
1:A:2061:THR:O	1:A:2065:ARG:HG2	2.18	0.43
2:B:714:ASN:OD1	2:B:715:SER:N	2.50	0.43
2:B:1308:PHE:HA	2:B:1311:PHE:CE2	2.53	0.43
3:C:799:PHE:O	3:C:802:ALA:N	2.49	0.43
5:E:65:U:O2'	29:d:59:LYS:HE2	2.18	0.43
6:F:224:ILE:HG22	6:F:225:SER:O	2.17	0.43
6:F:493:VAL:HG23	6:F:937:LYS:HG2	1.99	0.43
6:F:1305:GLN:O	6:F:1309:SER:CB	2.66	0.43
7:H:180:LYS:CE	7:H:180:LYS:CA	2.90	0.43
7:H:244:TYR:HB3	25:a:178:TRP:HA	1.99	0.43
13:M:484:A:H3'	13:M:484:A:C8	2.53	0.43
16:Q:242:VAL:O	17:R:161:ARG:NH2	2.50	0.43
17:R:14:LYS:HE3	17:R:14:LYS:HA	1.99	0.43
23:Y:516:VAL:HB	23:Y:561:CYS:HA	2.01	0.43
23:Y:569:SER:HA	23:Y:573:GLU:HB2	1.99	0.43
24:Z:203:LYS:O	24:Z:204:ASP:HB2	2.18	0.43
27:c:105:LEU:O	27:c:108:SER:OG	2.24	0.43
28:G:963:TYR:CG	28:G:964:ILE:N	2.86	0.43
29:d:187:GLU:O	29:d:190:SER:HB3	2.18	0.43
1:A:371:ASP:O	3:C:969:LYS:HD3	2.18	0.43
1:A:1214:ARG:HB2	1:A:1255:ASN:OD1	2.19	0.43
2:B:168:LYS:O	2:B:172:GLU:N	2.46	0.43
2:B:1352:GLN:HE22	2:B:1378:ALA:HB3	1.83	0.43
3:C:77:LEU:HD21	14:O:133:ARG:HD3	2.00	0.43
3:C:242:VAL:HG21	3:C:272:ARG:HG2	1.99	0.43
3:C:743:ASN:O	3:C:746:LYS:HB3	2.18	0.43
5:E:67:C:H5''	5:E:67:C:C6	2.41	0.43
6:F:927:ARG:HG2	6:F:979:CYS:SG	2.58	0.43
8:I:55:ASN:O	8:I:56:PRO:HB3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:K:65:THR:O	10:K:69:LEU:HG	2.18	0.43
12:N:90:A:C2	30:X:2:SER:O	2.71	0.43
16:Q:203:LYS:HG3	16:Q:256:SER:OG	2.18	0.43
20:U:80:LEU:HD21	20:U:199:LEU:HD23	1.99	0.43
21:V:27:TYR:O	21:V:29:ASP:N	2.47	0.43
22:W:223:ARG:CG	22:W:242:GLU:OE2	2.65	0.43
24:Z:181:LEU:HD21	24:Z:191:ARG:CG	2.44	0.43
24:Z:306:ASP:OD1	30:X:25:ALA:HB3	2.18	0.43
28:G:941:MET:HE3	28:G:941:MET:HB3	1.79	0.43
29:d:147:ASN:ND2	33:f:160:LEU:HD22	2.33	0.43
41:l:14:ALA:HA	41:l:78:LEU:HD21	2.01	0.43
1:A:762:VAL:HG21	1:A:786:LEU:CD1	2.48	0.43
1:A:928:ARG:NH1	1:A:1582:GLU:OE2	2.51	0.43
1:A:1233:ARG:NE	18:S:131:THR:HG21	2.33	0.43
1:A:1419:ASP:OD1	1:A:1419:ASP:O	2.35	0.43
1:A:1488:ILE:HD12	1:A:1488:ILE:HA	1.85	0.43
1:A:1705:SER:O	2:B:1184:ARG:NH2	2.48	0.43
1:A:2318:ASN:ND2	1:A:2327:GLU:OE2	2.51	0.43
2:B:890:THR:HG1	2:B:894:ASN:HD22	1.58	0.43
3:C:135:ASN:O	3:C:233:ASP:N	2.39	0.43
3:C:362:LYS:HG3	3:C:363:PRO:HD2	2.00	0.43
3:C:544:LEU:HG	3:C:553:VAL:HG21	1.99	0.43
4:D:175:G:C2	38:i:33:GLU:O	2.71	0.43
6:F:82:LEU:HD22	6:F:114:ILE:HD13	2.01	0.43
6:F:756:GLY:HA3	6:F:759:ASP:OD1	2.17	0.43
7:H:248:HIS:NE2	7:H:252:PHE:HD2	2.16	0.43
8:I:57:TYR:O	8:I:59:TYR:CE1	2.72	0.43
15:P:233:GLU:O	15:P:237:LYS:HB2	2.18	0.43
16:Q:246:ALA:O	16:Q:247:LYS:HB2	2.18	0.43
22:W:193:PRO:HG3	24:Z:464:PHE:CE1	2.53	0.43
23:Y:479:PRO:O	23:Y:483:GLN:HG3	2.19	0.43
24:Z:397:LEU:HD12	24:Z:397:LEU:HA	1.85	0.43
29:d:189:TYR:CB	29:d:205:TRP:HD1	2.31	0.43
1:A:140:ARG:O	1:A:143:ILE:HG22	2.19	0.43
1:A:173:LEU:HD13	1:A:715:LEU:HB3	2.01	0.43
1:A:571:LEU:HD23	1:A:629:MET:SD	2.58	0.43
1:A:978:ILE:HG21	18:S:174:VAL:HG22	2.00	0.43
1:A:1229:GLU:O	1:A:1232:SER:OG	2.33	0.43
2:B:1575:ALA:HA	2:B:1579:ASN:O	2.18	0.43
2:B:1663:VAL:HG12	2:B:1664:LEU:N	2.33	0.43
2:B:1932:ALA:O	2:B:1937:LEU:N	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1932:ALA:HB1	2:B:1937:LEU:HB2	1.99	0.43
5:E:86:G:O6	29:d:57:TYR:CD1	2.72	0.43
6:F:636:THR:HB	6:F:679:VAL:HG23	2.00	0.43
16:Q:203:LYS:O	16:Q:251:LEU:O	2.37	0.43
16:Q:207:LEU:HB2	16:Q:249:GLY:C	2.42	0.43
20:U:26:ILE:HG22	20:U:28:ILE:H	1.83	0.43
20:U:45:LYS:HG2	20:U:126:VAL:CB	2.44	0.43
20:U:50:LEU:CB	20:U:139:GLN:NE2	2.81	0.43
24:Z:205:TYR:C	24:Z:207:SER:H	2.26	0.43
26:b:62:MET:HG3	26:b:98:THR:HG23	2.00	0.43
28:G:25:ILE:HD11	28:G:30:ARG:CG	2.49	0.43
28:G:484:PHE:O	28:G:488:TRP:HB2	2.18	0.43
28:G:927:ALA:O	28:G:929:ASN:N	2.50	0.43
29:d:407:UNK:C	29:d:409:UNK:H2	2.30	0.43
31:v:438:UNK:O	31:v:442:UNK:N	2.51	0.43
1:A:268:LEU:HD23	1:A:273:ASP:CB	2.48	0.43
1:A:268:LEU:HD23	1:A:273:ASP:OD2	2.18	0.43
1:A:855:LEU:HD23	1:A:855:LEU:HA	1.82	0.43
1:A:931:ALA:CA	1:A:934:ARG:NH1	2.55	0.43
1:A:1012:TRP:CD1	1:A:1012:TRP:C	2.96	0.43
2:B:766:ILE:HG22	2:B:767:THR:N	2.26	0.43
2:B:1436:LEU:HD12	2:B:1439:LEU:HD23	1.99	0.43
2:B:1954:VAL:HG13	2:B:1983:LEU:HD13	1.98	0.43
2:B:2048:TYR:CD1	2:B:2049:PRO:HD2	2.53	0.43
3:C:733:ASN:OD1	3:C:734:CYS:N	2.51	0.43
3:C:945:LEU:HD12	3:C:945:LEU:O	2.19	0.43
6:F:353:ARG:NH1	6:F:468:PRO:HG3	2.33	0.43
6:F:730:MET:SD	6:F:739:LEU:HD21	2.58	0.43
6:F:957:ILE:HG22	6:F:962:LEU:CD1	2.45	0.43
14:O:198:PHE:HE2	14:O:253:MET:HE2	1.84	0.43
17:R:73:CYS:HB2	17:R:89:TYR:HB2	2.01	0.43
22:W:215:TYR:HE2	22:W:232:TRP:CZ3	2.36	0.43
23:Y:387:SER:O	23:Y:392:ASN:N	2.42	0.43
38:i:88:THR:HG23	40:j:67:SER:CB	2.49	0.43
2:B:479:GLU:HG3	2:B:481:THR:H	1.83	0.43
2:B:1651:ILE:O	2:B:1655:LEU:HG	2.17	0.43
2:B:2023:GLU:HB2	2:B:2026:GLU:OE1	2.18	0.43
3:C:491:GLY:O	3:C:492:LEU:HD23	2.17	0.43
6:F:208:GLU:HA	6:F:235:MET:O	2.19	0.43
6:F:449:ASN:OD1	6:F:450:ASP:N	2.51	0.43
6:F:1037:PHE:HB2	6:F:1042:LEU:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:160:LEU:HD12	28:G:925:HIS:H	1.83	0.43
14:O:115:TYR:HA	14:O:118:LEU:CG	2.48	0.43
14:O:162:THR:HG22	14:O:183:MET:C	2.44	0.43
14:O:198:PHE:CZ	14:O:239:ILE:HD11	2.54	0.43
14:O:359:ASN:HB3	14:O:363:VAL:HB	1.99	0.43
15:P:38:VAL:HG22	15:P:39:LYS:N	2.33	0.43
15:P:323:VAL:HG23	15:P:324:TYR:CD2	2.53	0.43
16:Q:239:SER:O	16:Q:251:LEU:HD12	2.18	0.43
19:T:54:GLN:HG3	36:n:69:TRP:NE1	2.27	0.43
21:V:109:TYR:CD1	21:V:109:TYR:C	2.96	0.43
23:Y:257:PRO:O	23:Y:261:VAL:HG23	2.18	0.43
23:Y:279:ARG:HD2	23:Y:507:SER:OG	2.18	0.43
24:Z:191:ARG:NE	24:Z:192:GLU:OE1	2.49	0.43
25:a:247:ALA:O	25:a:249:ASP:N	2.51	0.43
28:G:418:ALA:O	28:G:422:MET:HG2	2.17	0.43
28:G:922:GLY:CA	28:G:934:PHE:HD2	2.32	0.43
38:i:88:THR:HG22	38:i:89:LEU:HD12	2.01	0.43
1:A:589:THR:CG2	17:R:31:ASN:ND2	2.82	0.43
1:A:640:ARG:HG2	1:A:640:ARG:HH11	1.83	0.43
1:A:769:MET:SD	1:A:811:ILE:HD11	2.55	0.43
1:A:912:LEU:O	1:A:913:VAL:C	2.62	0.43
1:A:1223:GLY:HA2	1:A:1248:VAL:HG11	2.00	0.43
1:A:1699:ALA:HB1	1:A:1733:TRP:HB2	2.00	0.43
1:A:1781:TYR:N	1:A:1781:TYR:CD1	2.87	0.43
1:A:1910:LYS:HB2	1:A:1940:MET:SD	2.59	0.43
2:B:767:THR:O	2:B:770:LEU:N	2.51	0.43
2:B:1624:LEU:HD21	2:B:1629:LEU:HB2	1.99	0.43
2:B:1932:ALA:HA	2:B:1937:LEU:HD13	2.00	0.43
3:C:126:MET:HE1	3:C:132:ARG:HH12	1.83	0.43
6:F:520:SER:O	6:F:874:GLY:CA	2.66	0.43
6:F:1041:LEU:O	6:F:1051:LEU:HD12	2.19	0.43
15:P:319:HIS:CE1	22:W:264:GLU:HB2	2.53	0.43
16:Q:251:LEU:HD12	16:Q:252:ARG:N	2.33	0.43
20:U:45:LYS:HE3	20:U:45:LYS:CA	2.48	0.43
21:V:74:PHE:CD1	21:V:74:PHE:C	2.97	0.43
23:Y:586:ASN:OD1	23:Y:587:LEU:N	2.51	0.43
26:b:31:CYS:SG	26:b:115:ASN:ND2	2.90	0.43
28:G:599:ALA:HA	28:G:639:MET:HE1	2.01	0.43
30:X:2:SER:OG	30:X:4:ASN:ND2	2.43	0.43
36:n:72:TRP:O	36:n:73:SER:CB	2.67	0.43
1:A:375:PHE:HE2	1:A:1414:TRP:HZ2	1.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:460:PRO:HB2	1:A:463:ALA:HB2	2.01	0.43
1:A:950:THR:OG1	1:A:953:ARG:NH2	2.52	0.43
1:A:1350:ILE:HG23	1:A:1356:LEU:HD22	2.00	0.43
2:B:503:GLN:HE22	2:B:529:ASN:HB2	1.82	0.43
2:B:770:LEU:HD23	2:B:770:LEU:O	2.17	0.43
2:B:948:MET:HA	2:B:955:TYR:HD2	1.84	0.43
2:B:1352:GLN:HA	2:B:1379:MET:HE2	2.01	0.43
2:B:1997:ILE:HD11	2:B:2016:VAL:HG22	2.00	0.43
5:E:32:U:H5'	16:Q:45:HIS:NE2	2.34	0.43
6:F:208:GLU:H	6:F:236:VAL:HA	1.83	0.43
6:F:742:HIS:HE2	6:F:752:LYS:HE2	1.83	0.43
6:F:780:LEU:HD23	6:F:782:GLU:OE2	2.18	0.43
6:F:1133:ASP:OD2	6:F:1137:ASN:HB2	2.18	0.43
10:K:5:GLN:HB3	28:G:230:TYR:OH	2.19	0.43
14:O:224:LEU:N	14:O:245:ASP:OD2	2.51	0.43
17:R:187:LYS:HG3	17:R:188:TYR:CE1	2.54	0.43
24:Z:203:LYS:HD3	24:Z:203:LYS:HA	1.66	0.43
25:a:172:TRP:CD1	25:a:173:LYS:O	2.72	0.43
27:c:219:TYR:O	29:d:90:ARG:HD2	2.18	0.43
28:G:27:GLN:HE22	28:G:30:ARG:HH21	1.66	0.43
28:G:698:ARG:HG3	28:G:699:LYS:N	2.34	0.43
39:h:16:LYS:CG	39:h:17:PRO:HD3	2.49	0.43
1:A:806:ALA:N	1:A:807:PRO:HD2	2.33	0.43
1:A:878:GLU:HG2	18:S:133:PHE:CE1	2.54	0.43
1:A:1057:MET:CE	1:A:1114:PHE:CZ	3.02	0.43
1:A:1322:ALA:O	1:A:1323:SER:HB3	2.16	0.43
1:A:1447:TRP:HB3	1:A:1451:PHE:HE2	1.84	0.43
1:A:1711:VAL:HG12	1:A:1712:SER:N	2.33	0.43
1:A:1895:HIS:CD2	1:A:1896:THR:H	2.37	0.43
2:B:471:PRO:HD3	2:B:697:SER:O	2.19	0.43
2:B:648:GLU:HA	2:B:683:PHE:HZ	1.82	0.43
2:B:723:ASN:OD1	2:B:848:LYS:NZ	2.41	0.43
2:B:1359:LEU:HA	2:B:1507:ARG:HH22	1.84	0.43
2:B:1484:TYR:O	2:B:1488:TYR:N	2.49	0.43
2:B:1821:GLU:HG2	2:B:1845:SER:O	2.19	0.43
3:C:99:LYS:NZ	4:D:43:G:OP2	2.41	0.43
3:C:766:TRP:HZ2	3:C:792:LYS:HB3	1.84	0.43
4:D:96:U:O5'	4:D:96:U:H6	2.01	0.43
6:F:277:LEU:HD21	28:G:353:THR:HG23	2.01	0.43
6:F:327:VAL:O	6:F:337:VAL:HA	2.19	0.43
6:F:363:VAL:HG12	6:F:364:THR:N	2.13	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:526:SER:HA	6:F:870:ARG:HG3	2.00	0.43
6:F:561:LEU:HG	6:F:569:GLU:O	2.19	0.43
6:F:1221:LEU:C	6:F:1223:GLY:N	2.76	0.43
9:J:50:SER:O	9:J:51:PHE:CG	2.72	0.43
13:M:468:A:H5''	13:M:469:A:P	2.59	0.43
14:O:152:ASN:ND2	14:O:409:LYS:HB3	2.33	0.43
14:O:382:HIS:CE1	14:O:442:TRP:H	2.36	0.43
15:P:37:ASN:CB	29:d:127:SER:HB2	2.49	0.43
15:P:50:ASN:ND2	15:P:53:LEU:N	2.67	0.43
16:Q:26:THR:O	16:Q:44:TYR:HA	2.18	0.43
16:Q:217:TRP:CE3	17:R:187:LYS:HB2	2.54	0.43
17:R:15:GLU:H	17:R:15:GLU:HG3	1.57	0.43
22:W:208:SER:HB3	22:W:212:ARG:N	2.34	0.43
23:Y:290:VAL:HG21	23:Y:321:TYR:OH	2.18	0.43
24:Z:205:TYR:O	24:Z:207:SER:N	2.52	0.43
25:a:165:ARG:NH2	28:G:723:GLU:OE2	2.52	0.43
28:G:534:ARG:O	28:G:538:VAL:HG23	2.18	0.43
31:v:606:GLN:HA	31:v:609:GLU:HG3	2.00	0.43
34:q:257:LEU:HD22	34:q:277:LEU:CG	2.48	0.43
36:n:60:ARG:O	36:n:61:LYS:C	2.61	0.43
1:A:135:PRO:HG3	19:T:56:HIS:CD2	2.54	0.43
1:A:936:GLU:O	1:A:939:LEU:N	2.52	0.43
1:A:1032:ILE:HG12	1:A:1171:LEU:HD22	2.01	0.43
1:A:1043:ARG:HB2	1:A:1044:GLY:H	1.71	0.43
1:A:1308:GLU:OE1	1:A:1346:PHE:HZ	2.01	0.43
1:A:1376:ASN:O	1:A:1377:SER:OG	2.31	0.43
1:A:1828:SER:O	1:A:1829:SER:CB	2.66	0.43
1:A:1891:LEU:HD11	1:A:1974:LEU:HD22	2.00	0.43
2:B:1109:LEU:HD13	2:B:1131:LEU:HB3	2.00	0.43
2:B:1148:GLN:HE22	2:B:1297:TRP:HA	1.83	0.43
3:C:576:THR:HG21	3:C:592:PHE:H	1.83	0.43
3:C:888:ILE:O	3:C:888:ILE:HG13	2.18	0.43
4:D:78:A:O2'	4:D:79:C:P	2.77	0.43
4:D:167:A:N7	43:g:63:ARG:HB3	2.34	0.43
6:F:257:ILE:HD13	6:F:257:ILE:HG21	1.79	0.43
6:F:755:ILE:HD12	6:F:762:PHE:CE1	2.54	0.43
6:F:779:TYR:HD1	6:F:819:VAL:HG12	1.84	0.43
6:F:1081:ASN:C	6:F:1083:GLU:H	2.27	0.43
6:F:1085:LEU:HD23	6:F:1085:LEU:HA	1.84	0.43
16:Q:206:PHE:C	16:Q:207:LEU:HD12	2.44	0.43
21:V:35:ILE:O	21:V:74:PHE:HA	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Y:245:MET:CG	23:Y:381:MET:HA	2.49	0.43
23:Y:341:SER:O	23:Y:372:LEU:HA	2.19	0.43
24:Z:67:LYS:HE2	24:Z:67:LYS:HA	2.00	0.43
24:Z:168:LYS:NZ	24:Z:171:ASP:CB	2.76	0.43
27:c:230:THR:HG22	29:d:116:ASN:HB2	2.01	0.43
28:G:169:LEU:O	28:G:173:ILE:HD12	2.19	0.43
29:d:115:ILE:HG23	29:d:116:ASN:H	1.84	0.43
1:A:134:MET:HB3	1:A:135:PRO:HD2	2.01	0.42
1:A:499:VAL:HG12	1:A:501:LEU:HD12	2.01	0.42
1:A:770:MET:HE2	1:A:808:ILE:HD11	2.01	0.42
1:A:978:ILE:HG23	18:S:174:VAL:HG13	2.01	0.42
1:A:1739:ARG:HD3	1:A:1778:ASP:OD1	2.19	0.42
1:A:2208:TYR:CD1	1:A:2255:LEU:HA	2.53	0.42
2:B:1453:GLU:O	2:B:1457:ARG:HG3	2.19	0.42
2:B:1804:SER:O	2:B:1808:GLU:HG2	2.19	0.42
2:B:2033:LEU:HB3	2:B:2037:GLN:HB2	2.01	0.42
6:F:242:VAL:HG22	6:F:252:PHE:CB	2.49	0.42
6:F:426:TYR:HD1	6:F:440:GLN:HB3	1.84	0.42
6:F:827:TRP:N	6:F:827:TRP:CD1	2.87	0.42
14:O:138:HIS:CD2	14:O:159:SER:HB2	2.53	0.42
14:O:397:GLU:HG3	14:O:400:ARG:HH12	1.83	0.42
15:P:44:ILE:HG12	15:P:45:PRO:HD2	2.00	0.42
15:P:51:PHE:N	15:P:51:PHE:CD1	2.86	0.42
15:P:52:GLU:OE1	15:P:52:GLU:HA	2.19	0.42
17:R:222:LEU:HD13	17:R:224:LYS:HE2	2.00	0.42
20:U:48:ILE:HG22	20:U:49:ALA:O	2.18	0.42
22:W:208:SER:CB	22:W:212:ARG:O	2.51	0.42
24:Z:64:THR:HG23	24:Z:73:ILE:HG12	2.01	0.42
26:b:8:GLN:O	26:b:27:TRP:CD1	2.72	0.42
26:b:67:SER:HB3	26:b:71:TYR:HA	2.01	0.42
27:c:217:ILE:HD12	29:d:83:ARG:CG	2.48	0.42
28:G:56:THR:O	28:G:57:VAL:HB	2.19	0.42
28:G:349:LEU:HA	28:G:349:LEU:HD23	1.83	0.42
28:G:386:TYR:CD2	28:G:387:PRO:HD3	2.53	0.42
28:G:390:ILE:CD1	28:G:426:MET:HA	2.49	0.42
28:G:435:THR:O	28:G:439:MET:N	2.33	0.42
28:G:789:ALA:HA	28:G:797:VAL:HG21	2.00	0.42
28:G:862:THR:HG22	28:G:902:GLY:HA2	2.01	0.42
35:t:136:VAL:O	35:t:139:GLN:CG	2.67	0.42
41:l:6:ILE:N	41:l:7:PRO:CD	2.82	0.42
1:A:744:THR:HG22	5:E:75:A:OP1	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1050:LEU:CD2	1:A:1248:VAL:HG22	2.47	0.42
1:A:1286:TRP:HB2	1:A:1300:ALA:HB3	2.00	0.42
2:B:559:TYR:HB3	2:B:606:VAL:HG22	2.01	0.42
2:B:759:ASN:O	2:B:762:ALA:N	2.52	0.42
2:B:1887:VAL:HG13	2:B:1890:GLU:CD	2.44	0.42
3:C:545:LEU:HD12	3:C:545:LEU:O	2.19	0.42
4:D:103:A:O2'	4:D:104:G:H5''	2.19	0.42
6:F:637:SER:OG	6:F:638:SER:N	2.52	0.42
6:F:1336:PHE:O	6:F:1339:LYS:HG2	2.20	0.42
9:J:100:HIS:C	9:J:100:HIS:CD2	2.96	0.42
22:W:169:LYS:HB2	22:W:169:LYS:HE3	1.88	0.42
23:Y:277:GLN:HB2	23:Y:283:ALA:HB2	2.01	0.42
23:Y:503:ILE:O	23:Y:507:SER:HB2	2.19	0.42
24:Z:105:GLN:HG3	24:Z:113:SER:HB2	2.01	0.42
26:b:91:GLY:HA3	26:b:100:PHE:HB3	2.01	0.42
28:G:319:ALA:O	28:G:323:SER:HB2	2.19	0.42
28:G:581:LYS:O	28:G:585:ALA:N	2.52	0.42
29:d:230:ALA:HA	29:d:233:GLN:HG2	2.01	0.42
34:o:112:VAL:O	34:o:115:GLU:CG	2.66	0.42
34:q:123:ALA:O	34:q:127:LEU:CG	2.67	0.42
1:A:589:THR:HG21	17:R:38:SER:OG	2.19	0.42
1:A:803:GLY:O	15:P:166:PRO:HG3	2.19	0.42
1:A:992:ASP:OD1	1:A:1085:LYS:NZ	2.52	0.42
1:A:1808:ALA:O	1:A:1809:ASN:C	2.63	0.42
2:B:904:GLN:O	2:B:905:GLN:HG3	2.19	0.42
2:B:1214:SER:HB3	2:B:1281:GLN:NE2	2.33	0.42
2:B:1564:LEU:HD21	2:B:1597:ALA:HB1	2.01	0.42
2:B:1779:TYR:O	2:B:1782:ILE:HG22	2.19	0.42
2:B:1883:LEU:HG	2:B:1957:LEU:HD13	2.00	0.42
3:C:393:LYS:HB3	3:C:413:LEU:HD22	2.01	0.42
6:F:702:ILE:HG22	6:F:717:SER:N	2.34	0.42
6:F:729:ILE:O	6:F:741:LEU:HD12	2.19	0.42
6:F:780:LEU:HB3	6:F:782:GLU:OE2	2.19	0.42
6:F:1029:SER:OG	6:F:1045:MET:HA	2.18	0.42
6:F:1299:ILE:HG22	6:F:1300:LEU:HD12	2.01	0.42
13:M:514:U:HO2'	13:M:515:U:P	2.30	0.42
14:O:193:ARG:HH22	14:O:237:ASP:H	1.67	0.42
14:O:274:CYS:HA	14:O:280:GLN:O	2.19	0.42
14:O:304:LEU:HD22	14:O:334:TRP:CZ3	2.55	0.42
17:R:83:LEU:HB2	17:R:87:CYS:HB2	2.01	0.42
17:R:255:ASN:O	17:R:259:ASN:ND2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Z:338:THR:HG22	24:Z:339:PHE:N	2.34	0.42
25:a:143:VAL:HG11	25:a:148:LYS:HD3	2.01	0.42
26:b:163:PHE:CG	26:b:164:PHE:N	2.87	0.42
28:G:386:TYR:CD1	28:G:386:TYR:C	2.96	0.42
28:G:580:PHE:O	28:G:626:ILE:HD13	2.20	0.42
28:G:873:HIS:O	28:G:875:ASP:N	2.46	0.42
31:v:673:GLU:CB	31:v:683:SER:HB3	2.48	0.42
1:A:1115:GLN:HE22	1:A:1165:LEU:HD23	1.84	0.42
2:B:2043:ALA:HA	2:B:2046:ASN:HD22	1.84	0.42
3:C:317:LYS:HB2	44:C:1500:GTP:C5	2.55	0.42
6:F:741:LEU:HG	6:F:743:VAL:HG23	2.01	0.42
6:F:1080:TRP:NE1	6:F:1126:GLU:HB2	2.34	0.42
6:F:1223:GLY:O	6:F:1224:THR:OG1	2.37	0.42
6:F:1247:MET:HE3	6:F:1247:MET:HB3	1.90	0.42
7:H:213:PRO:HB2	8:I:42:TYR:CE2	2.55	0.42
7:H:233:VAL:HG13	25:a:150:THR:OG1	2.20	0.42
13:M:514:U:O4'	13:M:515:U:C5	2.73	0.42
16:Q:205:PHE:CE1	16:Q:293:TRP:HD1	2.37	0.42
17:R:4:TRP:NE1	17:R:91:HIS:O	2.51	0.42
19:T:133:ALA:HB1	19:T:140:VAL:H	1.84	0.42
24:Z:174:TRP:HZ2	24:Z:197:LEU:CD1	2.28	0.42
28:G:386:TYR:CD1	28:G:387:PRO:N	2.88	0.42
28:G:667:TYR:HE1	28:G:710:LEU:HB2	1.85	0.42
32:e:49:TYR:CG	32:e:50:GLN:N	2.87	0.42
37:k:87:LEU:HG	37:k:92:ILE:HD11	2.00	0.42
1:A:134:MET:CE	19:T:107:ARG:CD	2.97	0.42
1:A:271:GLN:C	1:A:271:GLN:CD	2.86	0.42
1:A:869:LYS:O	15:P:198:ASN:ND2	2.40	0.42
1:A:1158:ILE:HG12	1:A:1172:PHE:CE2	2.55	0.42
1:A:1567:PHE:CZ	1:A:1820:ARG:HD2	2.55	0.42
2:B:583:ILE:HG23	2:B:603:GLN:HB2	2.02	0.42
2:B:1363:ASN:HD21	2:B:1390:GLN:HE22	1.66	0.42
2:B:1412:TRP:HB3	2:B:1424:ILE:HD13	2.00	0.42
3:C:287:LYS:HD2	3:C:896:GLY:HA3	2.01	0.42
3:C:576:THR:HG22	3:C:592:PHE:HB2	2.01	0.42
3:C:864:VAL:HG22	3:C:930:LEU:CD2	2.49	0.42
4:D:176:A:O2'	42:m:20:LYS:HE3	2.19	0.42
6:F:105:ASP:HB2	6:F:114:ILE:CD1	2.47	0.42
6:F:997:CYS:SG	6:F:1034:MET:HE1	2.60	0.42
7:H:189:LEU:O	8:I:43:THR:HG21	2.18	0.42
20:U:40:LEU:HA	20:U:49:ALA:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:V:24:HIS:HB3	21:V:86:ILE:HG12	2.01	0.42
25:a:131:ILE:HG22	25:a:133:THR:HG23	2.01	0.42
25:a:178:TRP:HH2	28:G:755:GLU:O	2.02	0.42
28:G:494:LEU:HD21	28:G:532:PRO:HG3	2.02	0.42
1:A:557:PHE:HE1	15:P:121:PRO:HG2	1.84	0.42
1:A:712:LEU:HD12	1:A:712:LEU:HA	1.78	0.42
1:A:900:PHE:N	1:A:1075:ASP:OD2	2.52	0.42
1:A:1011:ASN:HB2	1:A:1144:PHE:HA	2.02	0.42
1:A:1320:LEU:HA	1:A:1320:LEU:HD23	1.81	0.42
1:A:1364:GLU:OE2	1:A:1401:SER:CB	2.67	0.42
1:A:1369:ASN:OD1	1:A:1378:LYS:HE2	2.19	0.42
1:A:1935:VAL:HG11	1:A:1940:MET:CB	2.48	0.42
1:A:1944:LEU:HB3	1:A:1956:ILE:HD13	2.02	0.42
1:A:1969:MET:HE1	1:A:1978:VAL:HB	2.01	0.42
1:A:2352:PRO:HA	1:A:2374:PHE:HD1	1.85	0.42
2:B:1211:ILE:HD12	2:B:1215:VAL:HG12	2.02	0.42
2:B:1477:HIS:HB3	2:B:1515:LEU:HD21	2.02	0.42
2:B:1902:LEU:HB3	2:B:1928:LEU:HD12	2.00	0.42
3:C:305:SER:OG	3:C:307:ILE:HG12	2.19	0.42
6:F:232:ARG:NH1	6:F:235:MET:HE3	2.34	0.42
6:F:636:THR:OG1	6:F:681:ILE:HG22	2.19	0.42
6:F:1027:ILE:HG23	6:F:1045:MET:HE1	2.01	0.42
16:Q:208:TYR:HB2	16:Q:290:ILE:HB	2.02	0.42
17:R:72:PHE:HE1	17:R:90:LEU:HD12	1.84	0.42
17:R:251:VAL:HG12	17:R:255:ASN:ND2	2.34	0.42
21:V:27:TYR:C	21:V:29:ASP:H	2.27	0.42
23:Y:427:GLN:O	23:Y:431:THR:OG1	2.33	0.42
25:a:169:LYS:HE2	25:a:169:LYS:N	2.34	0.42
26:b:166:ASP:C	26:b:168:PHE:N	2.78	0.42
28:G:682:ILE:H	28:G:682:ILE:HD12	1.85	0.42
31:v:729:TYR:O	31:v:733:ILE:HG13	2.19	0.42
1:A:316:THR:N	1:A:317:PRO:HD2	2.35	0.42
1:A:367:PHE:CD1	3:C:608:GLN:OE1	2.72	0.42
1:A:744:THR:HG23	1:A:746:THR:HG23	2.01	0.42
1:A:835:LYS:HD2	18:S:173:HIS:CE1	2.54	0.42
1:A:932:SER:O	1:A:936:GLU:HG3	2.20	0.42
1:A:1057:MET:HE2	1:A:1114:PHE:CZ	2.53	0.42
1:A:1411:ASP:H	30:X:6:ILE:HG22	1.84	0.42
1:A:1461:TYR:CD1	1:A:1480:LEU:HD11	2.53	0.42
1:A:1477:PHE:O	1:A:1481:GLU:HB2	2.20	0.42
1:A:2329:PHE:HA	1:A:2333:PHE:CE2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:850:THR:OG1	2:B:862:GLN:NE2	2.53	0.42
3:C:100:LEU:CD2	3:C:479:GLY:HA3	2.50	0.42
3:C:150:MET:SD	3:C:178:LEU:CD1	2.91	0.42
6:F:1002:ARG:NH2	6:F:1024:GLN:OE1	2.48	0.42
6:F:1239:MET:HE2	6:F:1239:MET:HB3	1.98	0.42
7:H:153:ASP:OD2	11:L:58:A:P	2.77	0.42
7:H:252:PHE:O	7:H:256:ALA:HB2	2.19	0.42
12:N:90:A:N1	30:X:6:ILE:HD11	2.34	0.42
20:U:110:LEU:HA	20:U:132:PRO:HA	2.02	0.42
24:Z:195:GLU:O	24:Z:198:PHE:HB2	2.19	0.42
33:f:190:TYR:CE2	33:f:195:PHE:HZ	2.37	0.42
38:i:77:LEU:HD23	38:i:78:GLY:N	2.35	0.42
42:m:17:ILE:HG12	42:m:95:ILE:HG23	2.00	0.42
1:A:378:PRO:HB2	1:A:380:ARG:HG3	2.02	0.42
1:A:1316:ILE:O	1:A:1317:ARG:C	2.63	0.42
1:A:1458:TRP:CH2	1:A:1491:ILE:HD13	2.55	0.42
1:A:1590:LEU:N	1:A:1590:LEU:HD13	2.35	0.42
2:B:561:ALA:O	2:B:609:PRO:HD3	2.20	0.42
2:B:707:PHE:HZ	2:B:902:LEU:HD12	1.85	0.42
2:B:2142:ILE:HG13	2:B:2158:PHE:HE1	1.84	0.42
3:C:106:PHE:CD1	3:C:548:ARG:O	2.73	0.42
3:C:168:VAL:HG12	3:C:173:LYS:HB2	2.02	0.42
3:C:885:GLY:HA2	3:C:907:PRO:HD3	2.01	0.42
6:F:116:LYS:HD3	6:F:883:ASP:OD1	2.20	0.42
6:F:240:MET:O	6:F:241:ALA:C	2.63	0.42
6:F:332:GLU:CG	6:F:333:ASN:N	2.82	0.42
6:F:666:LEU:HB3	6:F:668:THR:N	2.35	0.42
6:F:780:LEU:C	6:F:781:ARG:HG3	2.44	0.42
6:F:1115:LYS:HD2	28:G:951:PRO:O	2.20	0.42
14:O:132:SER:OG	14:O:425:ILE:O	2.24	0.42
15:P:241:LEU:CD1	20:U:204:VAL:HA	2.49	0.42
15:P:323:VAL:HG23	15:P:324:TYR:CD1	2.55	0.42
17:R:72:PHE:CD1	17:R:90:LEU:HB2	2.53	0.42
17:R:146:LEU:CG	17:R:147:ASN:N	2.80	0.42
17:R:210:LYS:CG	17:R:211:GLU:H	2.32	0.42
26:b:41:MET:HA	26:b:44:ASP:HB2	2.02	0.42
27:c:533:LEU:O	27:c:536:GLN:CG	2.68	0.42
28:G:213:LEU:O	28:G:213:LEU:HD12	2.19	0.42
28:G:682:ILE:O	28:G:685:ILE:N	2.47	0.42
29:d:210:ASN:OD1	29:d:218:THR:HG21	2.20	0.42
31:v:669:TYR:CE2	31:v:686:ILE:HG13	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:q:374:GLU:O	34:q:375:ALA:CB	2.66	0.42
1:A:220:THR:O	1:A:221:TRP:C	2.62	0.42
1:A:282:ASP:HB2	1:A:285:PRO:HA	2.01	0.42
1:A:388:PRO:HB2	1:A:398:VAL:HG11	2.02	0.42
1:A:1687:HIS:CG	1:A:1688:PRO:HD2	2.55	0.42
1:A:2228:PRO:HB3	1:A:2359:TYR:CE1	2.54	0.42
2:B:1661:VAL:HG12	2:B:1663:VAL:O	2.18	0.42
2:B:2074:GLN:HA	2:B:2125:GLN:HB3	2.02	0.42
3:C:391:MET:HE1	3:C:395:LYS:CE	2.28	0.42
3:C:675:THR:OG1	3:C:676:VAL:N	2.51	0.42
3:C:834:MET:HB2	3:C:837:GLN:HG2	2.01	0.42
5:E:1:G:OP1	36:n:60:ARG:NH2	2.51	0.42
6:F:496:SER:O	6:F:1209:SER:OG	2.27	0.42
6:F:590:HIS:CD2	6:F:591:THR:N	2.88	0.42
6:F:1356:VAL:HA	6:F:1360:TYR:CD2	2.55	0.42
8:I:3:TYR:CE2	12:N:99:G:C6	3.07	0.42
14:O:118:LEU:CD2	15:P:49:SER:O	2.68	0.42
14:O:142:VAL:HG13	14:O:157:THR:CG2	2.49	0.42
25:a:168:PHE:C	25:a:169:LYS:NZ	2.78	0.42
25:a:170:THR:HG22	28:G:718:TYR:CD1	2.55	0.42
26:b:13:CYS:O	26:b:24:ILE:HB	2.19	0.42
28:G:606:LEU:HD21	28:G:643:LEU:HD23	2.01	0.42
34:q:59:GLN:O	34:q:60:ALA:HB3	2.20	0.42
35:t:109:SER:O	35:t:110:GLU:CB	2.67	0.42
1:A:1156:HIS:CG	1:A:1157:PRO:HD2	2.55	0.42
1:A:1340:ILE:O	1:A:1344:THR:OG1	2.34	0.42
2:B:1614:GLU:O	2:B:1618:VAL:HG23	2.20	0.42
3:C:269:LYS:HG2	44:C:1500:GTP:C6	2.55	0.42
6:F:77:GLY:HA3	6:F:146:THR:HG21	2.00	0.42
6:F:738:GLN:HG3	6:F:754:HIS:CD2	2.55	0.42
6:F:924:PHE:HD1	6:F:945:HIS:HA	1.85	0.42
10:K:23:ASP:O	28:G:935:TRP:HB3	2.20	0.42
11:L:41:C:H5"	11:L:41:C:C6	2.32	0.42
14:O:270:ASN:HD21	14:O:286:THR:HG22	1.85	0.42
22:W:232:TRP:CZ3	22:W:234:GLY:HA2	2.54	0.42
31:v:468:UNK:O	31:v:472:UNK:N	2.53	0.42
32:e:27:GLU:HB3	32:e:122:ASP:HB2	2.01	0.42
32:e:139:GLU:C	32:e:151:ALA:HB1	2.34	0.42
1:A:639:PHE:CB	1:A:649:LEU:HD22	2.50	0.41
1:A:1275:MET:C	1:A:1277:GLU:H	2.28	0.41
1:A:1835:LEU:HD11	1:A:2006:SER:OG	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1399:ASN:HB2	2:B:1474:ASP:HB3	2.02	0.41
2:B:1614:GLU:HA	2:B:1617:ILE:HG22	2.02	0.41
2:B:1655:LEU:HB3	2:B:1661:VAL:HG23	2.02	0.41
3:C:150:MET:HB3	3:C:150:MET:HE2	1.69	0.41
3:C:325:LYS:HD3	3:C:441:ARG:HH12	1.85	0.41
3:C:547:GLY:O	3:C:548:ARG:C	2.63	0.41
6:F:239:ASP:OD2	6:F:295:VAL:N	2.26	0.41
6:F:441:PHE:HB3	6:F:475:LEU:CD2	2.42	0.41
6:F:507:ASN:ND2	6:F:509:LYS:HE2	2.34	0.41
6:F:517:VAL:HG21	6:F:828:VAL:HG21	2.01	0.41
6:F:1096:LEU:HB3	6:F:1109:TYR:CE1	2.55	0.41
6:F:1178:PRO:HB3	7:H:145:GLN:NE2	2.34	0.41
7:H:185:GLY:O	7:H:186:ARG:C	2.61	0.41
7:H:193:PRO:O	7:H:194:PHE:HB2	2.20	0.41
7:H:203:THR:CG2	7:H:250:VAL:HG21	2.50	0.41
8:I:20:SER:HB2	28:G:772:VAL:HG13	2.01	0.41
17:R:54:GLN:H	17:R:58:HIS:CD2	2.29	0.41
17:R:164:PHE:HD2	17:R:184:VAL:HG21	1.83	0.41
17:R:251:VAL:HA	17:R:254:ILE:HG12	2.02	0.41
20:U:105:LEU:HD23	20:U:127:ALA:HA	2.02	0.41
21:V:43:THR:OG1	21:V:44:GLU:OE1	2.37	0.41
23:Y:780:ILE:O	23:Y:784:PRO:HB3	2.18	0.41
24:Z:179:TYR:CD1	24:Z:179:TYR:O	2.72	0.41
28:G:772:VAL:HG11	28:G:777:LEU:HD12	2.02	0.41
29:d:225:ALA:O	29:d:229:VAL:HB	2.20	0.41
32:e:40:TYR:HA	32:e:53:ALA:HB2	2.01	0.41
35:t:31:ILE:O	35:t:32:LYS:CB	2.68	0.41
1:A:304:ASP:OD1	1:A:305:LEU:N	2.48	0.41
1:A:614:ARG:HD3	1:A:614:ARG:HA	1.69	0.41
1:A:995:LEU:HD11	1:A:1078:ILE:HG23	2.02	0.41
1:A:1591:THR:O	1:A:1594:GLN:HB3	2.20	0.41
2:B:126:TRP:NE1	2:B:181:LYS:O	2.52	0.41
2:B:707:PHE:CZ	2:B:902:LEU:HD12	2.54	0.41
2:B:963:ASP:CG	2:B:966:LEU:HA	2.46	0.41
2:B:1252:LEU:HD22	2:B:1274:TYR:CZ	2.54	0.41
2:B:1897:GLY:O	2:B:1901:LEU:HD13	2.20	0.41
2:B:1946:ASP:O	2:B:1950:ILE:N	2.50	0.41
3:C:369:LYS:HG3	3:C:369:LYS:O	2.19	0.41
6:F:94:CYS:SG	6:F:101:LEU:HD11	2.59	0.41
6:F:126:SER:HB2	6:F:151:THR:HG22	2.01	0.41
6:F:268:LEU:HD13	6:F:329:ILE:CD1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:950:GLN:HE21	6:F:973:ILE:HG21	1.85	0.41
11:L:64:G:H2'	11:L:65:A:C8	2.55	0.41
16:Q:3:ASP:HB3	16:Q:7:GLU:OE2	2.20	0.41
17:R:162:PHE:O	17:R:165:SER:OG	2.27	0.41
19:T:120:CYS:C	19:T:122:CYS:N	2.77	0.41
25:a:216:HIS:HB3	25:a:218:PHE:CE2	2.55	0.41
27:c:91:MET:HE3	27:c:91:MET:HB3	1.97	0.41
28:G:252:ILE:HD13	28:G:296:VAL:HG22	2.01	0.41
28:G:580:PHE:HB3	28:G:626:ILE:HD11	2.02	0.41
29:d:46:TYR:O	29:d:50:LYS:HG2	2.21	0.41
31:v:730:GLN:CA	31:v:733:ILE:CD1	2.91	0.41
1:A:520:VAL:O	1:A:524:LYS:HG2	2.20	0.41
1:A:861:GLN:HE21	1:A:1097:HIS:HB3	1.85	0.41
1:A:1034:ASN:ND2	28:G:20:GLY:CA	2.66	0.41
2:B:451:GLY:HA3	2:B:466:PRO:HG3	2.01	0.41
2:B:1889:PHE:HA	2:B:1892:VAL:HG23	2.02	0.41
7:H:233:VAL:HG13	25:a:150:THR:CG2	2.49	0.41
16:Q:13:CYS:SG	16:Q:16:CYS:HB3	2.60	0.41
16:Q:261:ARG:O	16:Q:264:SER:HB2	2.19	0.41
20:U:61:PRO:O	20:U:65:MET:HG2	2.20	0.41
23:Y:713:GLN:HA	23:Y:716:ASN:HB3	2.01	0.41
24:Z:152:ILE:HD13	24:Z:194:LEU:CA	2.42	0.41
25:a:209:PRO:HG3	25:a:251:GLN:HG3	2.02	0.41
27:c:227:ILE:O	33:f:151:LYS:HA	2.20	0.41
39:h:32:LYS:HG3	39:h:77:ASN:HA	2.03	0.41
1:A:141:LYS:HG2	19:T:49:LEU:HD23	2.02	0.41
1:A:1051:GLU:HB3	1:A:1167:ARG:NH2	2.34	0.41
1:A:1145:MET:SD	1:A:1160:LEU:HD22	2.61	0.41
1:A:1348:GLU:CG	1:A:1446:THR:HB	2.49	0.41
1:A:1611:SER:OG	1:A:1612:PRO:HD3	2.21	0.41
1:A:1738:LEU:HD22	1:A:1779:LEU:HD21	2.02	0.41
1:A:2411:VAL:HG11	2:B:564:LYS:NZ	2.35	0.41
2:B:503:GLN:HG2	2:B:530:ILE:HG13	2.02	0.41
2:B:1596:SER:HA	2:B:1599:MET:HE3	2.01	0.41
3:C:323:THR:O	3:C:326:GLU:N	2.53	0.41
6:F:118:GLN:HE21	6:F:1299:ILE:CD1	2.34	0.41
6:F:539:ASP:OD2	6:F:541:ALA:HB3	2.21	0.41
6:F:864:SER:OG	6:F:865:ILE:N	2.54	0.41
6:F:889:HIS:CG	6:F:890:GLU:N	2.88	0.41
6:F:1096:LEU:HD23	6:F:1109:TYR:OH	2.20	0.41
7:H:185:GLY:N	8:I:72:ASN:HD21	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:39:PRO:HB2	9:J:71:PHE:HD2	1.85	0.41
14:O:433:THR:O	14:O:437:GLU:HB2	2.20	0.41
15:P:50:ASN:HD21	15:P:53:LEU:N	2.17	0.41
15:P:141:ASP:OD1	15:P:142:GLU:N	2.51	0.41
16:Q:75:MET:HE1	17:R:130:PHE:HE1	1.84	0.41
17:R:152:LYS:HG2	17:R:153:PRO:CD	2.50	0.41
17:R:210:LYS:C	17:R:210:LYS:CD	2.94	0.41
21:V:25:ASN:HD22	28:G:490:ARG:HH22	1.68	0.41
21:V:50:VAL:HG12	22:W:237:ARG:HD2	2.01	0.41
23:Y:650:GLU:CG	23:Y:651:PHE:N	2.83	0.41
23:Y:705:ILE:O	23:Y:708:LEU:HB3	2.20	0.41
23:Y:807:VAL:HA	23:Y:841:GLU:HB2	2.03	0.41
28:G:900:LEU:O	28:G:904:GLU:HG2	2.20	0.41
29:d:109:GLU:CB	29:d:118:ALA:HB2	2.51	0.41
1:A:426:PRO:HB3	24:Z:201:ARG:HG3	2.02	0.41
1:A:934:ARG:NH2	1:A:1587:PHE:CE1	2.88	0.41
1:A:1999:ILE:HD13	1:A:1999:ILE:HG21	1.89	0.41
2:B:704:SER:N	2:B:884:GLY:O	2.52	0.41
3:C:237:ILE:HD12	3:C:265:PHE:HE1	1.84	0.41
3:C:460:GLY:HA3	3:C:461:LYS:HA	1.80	0.41
3:C:477:ASP:HB2	3:C:628:TYR:CE1	2.55	0.41
3:C:951:ILE:HB	3:C:952:PRO:HD3	2.03	0.41
6:F:70:ASN:O	6:F:70:ASN:OD1	2.39	0.41
6:F:242:VAL:HG22	6:F:252:PHE:HB3	2.01	0.41
6:F:826:THR:HG23	6:F:845:ASN:HA	2.03	0.41
6:F:1113:SER:C	7:H:168:ASN:ND2	2.74	0.41
9:J:27:ASP:CG	9:J:68:ASN:HD22	2.29	0.41
14:O:402:VAL:HG22	14:O:418:GLU:HG2	2.01	0.41
25:a:147:TYR:HE2	25:a:163:HIS:O	1.96	0.41
28:G:801:ILE:CG2	28:G:816:VAL:HG13	2.49	0.41
29:d:69:ILE:HG21	29:d:104:ARG:HD2	2.03	0.41
29:d:120:ASN:HD22	29:d:120:ASN:H	1.69	0.41
29:d:147:ASN:HD21	33:f:160:LEU:HD22	1.85	0.41
33:f:109:LEU:HD23	33:f:109:LEU:HA	1.79	0.41
43:g:102:ILE:HG22	43:g:103:VAL:HG23	2.01	0.41
1:A:561:THR:O	1:A:562:ILE:HB	2.19	0.41
1:A:1440:ILE:HD13	1:A:1440:ILE:HG21	1.80	0.41
1:A:1628:ASP:OD1	25:a:139:PHE:HA	2.21	0.41
1:A:1693:LYS:HB2	1:A:1693:LYS:HE3	1.89	0.41
1:A:1865:THR:HG21	1:A:1869:ASN:HD22	1.86	0.41
1:A:1948:MET:HG3	1:A:1956:ILE:HD11	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1991:ILE:HD13	1:A:1991:ILE:HG21	1.88	0.41
3:C:89:PRO:HA	14:O:212:GLU:O	2.20	0.41
3:C:758:ASP:OD1	3:C:759:SER:N	2.54	0.41
6:F:160:VAL:HG11	6:F:171:LEU:HG	2.03	0.41
6:F:594:MET:HE1	6:F:641:GLN:O	2.20	0.41
6:F:765:ILE:H	6:F:765:ILE:HD12	1.85	0.41
6:F:1165:LYS:HE2	32:e:34:PRO:CG	2.48	0.41
6:F:1315:ARG:HG2	6:F:1316:LYS:HG2	2.03	0.41
7:H:180:LYS:O	7:H:181:GLU:CB	2.67	0.41
13:M:468:A:C8	13:M:469:A:N7	2.89	0.41
16:Q:69:ASN:CB	16:Q:123:ALA:CB	2.96	0.41
16:Q:263:VAL:O	16:Q:263:VAL:HG12	2.20	0.41
19:T:156:THR:HG23	19:T:157:ASP:N	2.36	0.41
28:G:525:PRO:HB3	28:G:533:PHE:CZ	2.56	0.41
38:i:34:GLN:NE2	38:i:37:ILE:HD12	2.34	0.41
1:A:288:GLU:O	1:A:288:GLU:HG2	2.21	0.41
1:A:460:PRO:HG3	3:C:375:GLU:HG3	2.03	0.41
1:A:1196:GLU:HB3	1:A:1199:ILE:HD12	2.03	0.41
1:A:1854:ASP:HA	1:A:1857:VAL:HG23	2.02	0.41
2:B:428:ASP:OD2	2:B:431:LYS:NZ	2.54	0.41
2:B:1548:ILE:HA	2:B:1722:ILE:HB	2.03	0.41
2:B:1554:VAL:HG21	2:B:1563:MET:SD	2.61	0.41
2:B:1573:ALA:O	2:B:1577:ASN:N	2.53	0.41
2:B:1654:ARG:HG2	2:B:1658:TYR:CE2	2.56	0.41
6:F:104:TYR:HE1	6:F:113:LEU:HD12	1.86	0.41
6:F:561:LEU:HD21	6:F:568:MET:HG3	2.02	0.41
6:F:1002:ARG:HH22	6:F:1004:LEU:HD11	1.85	0.41
21:V:3:LYS:O	21:V:7:ILE:HD12	2.20	0.41
22:W:167:VAL:HG13	22:W:209:LEU:HD21	2.02	0.41
26:b:164:PHE:CE1	26:b:166:ASP:HB3	2.55	0.41
28:G:840:PRO:O	28:G:843:GLU:HB3	2.21	0.41
31:v:616:PRO:O	31:v:618:GLU:N	2.54	0.41
32:e:117:ASP:C	32:e:119:ILE:N	2.79	0.41
34:q:298:ASN:CG	34:q:300:GLU:H	2.29	0.41
34:r:112:VAL:O	34:r:115:GLU:CG	2.68	0.41
1:A:1080:ASP:HB3	27:c:82:ASN:ND2	2.36	0.41
1:A:1568:ASN:HB2	1:A:1832:GLU:OE2	2.21	0.41
1:A:2060:LEU:HB3	1:A:2071:ILE:CD1	2.50	0.41
2:B:119:THR:HA	2:B:122:GLN:HG2	2.03	0.41
2:B:834:LEU:HD12	2:B:838:VAL:HB	2.03	0.41
2:B:1777:TYR:OH	2:B:1781:ARG:HD3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1962:VAL:HG13	2:B:1973:ALA:HB1	2.02	0.41
2:B:2033:LEU:HB2	2:B:2038:LEU:HG	2.03	0.41
3:C:306:PRO:HG2	3:C:349:TRP:CE3	2.55	0.41
3:C:348:LEU:O	3:C:372:THR:HB	2.20	0.41
6:F:347:LYS:HB3	6:F:460:PRO:HB3	2.01	0.41
6:F:444:LEU:HD23	6:F:444:LEU:O	2.21	0.41
6:F:473:GLN:H	6:F:473:GLN:CD	2.29	0.41
6:F:679:VAL:HG12	6:F:693:ILE:HD12	2.03	0.41
6:F:766:LYS:HD3	6:F:836:TRP:CE2	2.55	0.41
6:F:995:ILE:HG13	6:F:1041:LEU:HD21	2.03	0.41
6:F:1173:LEU:HA	6:F:1173:LEU:HD23	1.76	0.41
6:F:1315:ARG:NH2	28:G:872:GLY:O	2.54	0.41
8:I:55:ASN:HD22	8:I:55:ASN:C	2.28	0.41
15:P:178:TYR:HE1	33:f:203:PHE:CE2	2.38	0.41
17:R:251:VAL:HG12	17:R:255:ASN:HD21	1.85	0.41
27:c:217:ILE:HD13	29:d:83:ARG:CZ	2.51	0.41
28:G:321:CYS:O	28:G:330:ARG:HG2	2.21	0.41
28:G:373:VAL:O	28:G:377:THR:HG23	2.21	0.41
28:G:378:LEU:CD1	28:G:396:VAL:HG11	2.51	0.41
28:G:583:PHE:CE2	28:G:627:LEU:HD21	2.56	0.41
29:d:102:TRP:O	29:d:106:ILE:HG13	2.21	0.41
35:t:113:LEU:O	35:t:116:ILE:CG1	2.69	0.41
1:A:244:ASP:CG	1:A:594:ASP:OD2	2.64	0.41
1:A:775:ARG:O	1:A:778:LYS:HB2	2.21	0.41
1:A:923:TYR:CD1	1:A:926:LYS:HD3	2.56	0.41
1:A:1018:SER:OG	1:A:1019:GLU:HG3	2.21	0.41
1:A:1169:TYR:CE2	1:A:1262:MET:HG2	2.55	0.41
1:A:1212:ARG:HG2	1:A:1213:MET:N	2.35	0.41
1:A:1585:MET:HG3	1:A:1586:GLN:OE1	2.21	0.41
1:A:1890:PHE:CE1	1:A:1988:LEU:HD21	2.56	0.41
1:A:2177:VAL:HG12	1:A:2179:GLU:H	1.85	0.41
1:A:2185:LEU:O	1:A:2341:LEU:HD12	2.20	0.41
1:A:2215:HIS:HB2	1:A:2218:VAL:HG23	2.03	0.41
1:A:2380:LEU:HD22	1:A:2384:ASN:ND2	2.36	0.41
2:B:1345:PHE:CE1	2:B:1348:PHE:HD1	2.39	0.41
2:B:1481:GLN:OE1	2:B:1701:ASN:ND2	2.54	0.41
2:B:1641:TYR:HD1	2:B:1642:LYS:O	2.04	0.41
2:B:2007:LYS:HB3	2:B:2030:ILE:HG12	2.03	0.41
3:C:89:PRO:C	3:C:91:VAL:H	2.28	0.41
3:C:314:ALA:CB	3:C:321:THR:HG22	2.51	0.41
5:E:39:G:C6	17:R:117:PHE:CD2	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:91:A:C6	29:d:99:ILE:CD1	3.02	0.41
6:F:61:TYR:CE2	6:F:63:LEU:HD11	2.56	0.41
6:F:62:HIS:HD2	6:F:1228:PHE:CE1	2.39	0.41
6:F:104:TYR:CD1	6:F:113:LEU:HA	2.54	0.41
6:F:122:ALA:HB3	6:F:1300:LEU:HD22	2.03	0.41
6:F:125:THR:HG22	6:F:191:SER:HA	2.03	0.41
6:F:200:ARG:NH2	6:F:247:PHE:HA	2.36	0.41
6:F:1353:ILE:O	6:F:1356:VAL:HG22	2.21	0.41
7:H:222:GLU:OE1	7:H:223:LYS:N	2.53	0.41
8:I:19:GLU:C	8:I:19:GLU:CD	2.88	0.41
9:J:8:LEU:HB3	9:J:89:ILE:HG23	2.03	0.41
9:J:67:VAL:HG23	9:J:68:ASN:N	2.36	0.41
14:O:200:VAL:HG21	14:O:227:VAL:HG12	2.03	0.41
14:O:422:SER:OG	14:O:424:LYS:NZ	2.53	0.41
15:P:241:LEU:O	15:P:245:SER:HB3	2.18	0.41
16:Q:69:ASN:HB3	16:Q:123:ALA:HB1	2.01	0.41
19:T:129:LEU:HD23	19:T:129:LEU:HA	1.93	0.41
23:Y:290:VAL:HG11	23:Y:319:LEU:HD23	2.01	0.41
25:a:135:VAL:HG11	25:a:137:MET:HE1	2.03	0.41
25:a:206:TYR:HD2	25:a:254:LEU:HD11	1.86	0.41
26:b:84:PHE:CZ	26:b:116:VAL:HG22	2.55	0.41
27:c:25:VAL:HG11	27:c:52:TRP:CZ2	2.56	0.41
27:c:81:PRO:O	27:c:82:ASN:C	2.64	0.41
28:G:25:ILE:HG21	28:G:25:ILE:HD13	1.85	0.41
28:G:503:THR:O	28:G:507:VAL:HG23	2.20	0.41
28:G:839:THR:N	28:G:840:PRO:HD2	2.36	0.41
28:G:843:GLU:OE1	28:G:879:HIS:NE2	2.54	0.41
28:G:850:ASP:OD1	28:G:853:HIS:CD2	2.73	0.41
28:G:908:GLN:HG2	28:G:945:TYR:OH	2.20	0.41
29:d:172:PHE:CE2	29:d:188:ILE:HG12	2.56	0.41
29:d:189:TYR:O	29:d:193:VAL:HG22	2.21	0.41
32:e:115:LEU:HB2	32:e:149:LYS:O	2.21	0.41
32:e:169:ASN:HA	32:e:180:VAL:HG23	2.03	0.41
34:p:98:LEU:HD12	34:q:98:LEU:CD2	2.49	0.41
34:q:101:THR:O	34:q:105:LEU:CG	2.69	0.41
34:q:183:LEU:CG	34:q:237:PRO:O	2.69	0.41
40:j:26:ALA:C	40:j:43:ALA:HB3	2.46	0.41
1:A:173:LEU:HD22	1:A:719:ILE:HD11	2.01	0.41
1:A:404:ASN:OD1	1:A:405:ASN:N	2.54	0.41
1:A:1506:ARG:O	1:A:1511:ARG:NH1	2.53	0.41
2:B:1463:LYS:HG3	2:B:1466:GLN:NE2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:596:ASP:OD1	3:C:597:TYR:N	2.54	0.41
3:C:795:ILE:HG23	3:C:842:MET:HE3	2.04	0.41
4:D:114:G:O2'	4:D:115:G:H5'	2.21	0.41
6:F:215:LEU:HB3	6:F:225:SER:HB3	2.02	0.41
6:F:839:ARG:HG3	6:F:880:PRO:CG	2.50	0.41
13:M:504:C:N4	28:G:776:GLN:NE2	2.69	0.41
14:O:279:PRO:HG3	14:O:301:MET:SD	2.60	0.41
16:Q:103:GLU:HG2	16:Q:104:ALA:HB3	2.02	0.41
16:Q:291:ILE:HG23	16:Q:292:PRO:CA	2.50	0.41
19:T:13:PRO:HG2	19:T:77:LEU:HA	2.02	0.41
28:G:416:LEU:HD11	28:G:441:ILE:HG21	2.02	0.41
28:G:538:VAL:CG1	28:G:578:ILE:HG13	2.51	0.41
29:d:152:VAL:HA	29:d:155:LEU:HB2	2.02	0.41
1:A:254:HIS:O	1:A:258:ILE:HD12	2.21	0.40
1:A:1144:PHE:CD2	1:A:1145:MET:HG2	2.56	0.40
1:A:1774:MET:O	1:A:1786:ALA:HA	2.21	0.40
1:A:2410:ASP:OD1	1:A:2412:PHE:CE1	2.74	0.40
2:B:1647:ASN:O	2:B:1651:ILE:HG12	2.20	0.40
3:C:501:ILE:HD11	3:C:567:ILE:HD12	2.03	0.40
4:D:43:G:H2'	4:D:45:A:H5'	2.02	0.40
5:E:65:U:OP1	18:S:12:ARG:NH1	2.54	0.40
6:F:838:ILE:H	6:F:838:ILE:HG13	1.58	0.40
8:I:88:LYS:HE2	8:I:88:LYS:HB3	1.92	0.40
13:M:509:A:H2	28:G:503:THR:CG2	2.34	0.40
14:O:333:SER:HB3	14:O:343:THR:HG22	2.02	0.40
14:O:373:LEU:HD21	14:O:402:VAL:HG21	2.02	0.40
23:Y:308:PHE:CE2	23:Y:740:ILE:HG12	2.56	0.40
23:Y:384:LYS:O	23:Y:387:SER:N	2.54	0.40
24:Z:204:ASP:O	24:Z:205:TYR:CD2	2.73	0.40
24:Z:449:PHE:CE1	24:Z:465:PHE:HE2	2.39	0.40
28:G:928:LYS:O	28:G:928:LYS:HG3	2.21	0.40
1:A:330:LEU:HD23	1:A:330:LEU:HA	1.87	0.40
1:A:503:LYS:HE3	4:D:82:A:OP1	2.21	0.40
1:A:722:LEU:HD23	1:A:722:LEU:HA	1.84	0.40
1:A:1087:ASN:ND2	1:A:1099:ASN:O	2.54	0.40
1:A:1755:LYS:HB3	1:A:1759:TYR:CE2	2.55	0.40
2:B:557:ILE:HD11	2:B:604:VAL:HG22	2.02	0.40
2:B:1149:PHE:CD2	2:B:1195:LEU:HB3	2.56	0.40
2:B:1425:ILE:HB	2:B:1442:SER:OG	2.21	0.40
2:B:1872:ASN:OD1	2:B:1873:THR:HG23	2.21	0.40
3:C:274:ILE:HD13	3:C:385:PHE:CD2	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:365:GLU:CG	3:C:366:ASN:H	2.32	0.40
3:C:624:LYS:HB3	3:C:628:TYR:HE2	1.86	0.40
3:C:769:TYR:OH	3:C:774:LEU:HD22	2.22	0.40
5:E:67:C:C6	5:E:67:C:C4'	3.05	0.40
6:F:153:ASP:OD1	6:F:183:THR:C	2.64	0.40
6:F:161:GLN:HE21	6:F:163:ILE:HG22	1.87	0.40
6:F:186:ARG:N	10:K:41:ASN:ND2	2.70	0.40
6:F:831:THR:O	6:F:831:THR:HG23	2.22	0.40
7:H:196:LEU:HD22	7:H:200:ILE:CG2	2.51	0.40
7:H:288:HIS:ND1	7:H:288:HIS:N	2.69	0.40
8:I:36:LYS:O	33:f:195:PHE:O	2.38	0.40
14:O:198:PHE:CE2	14:O:253:MET:HE2	2.56	0.40
15:P:58:PRO:O	15:P:59:THR:CB	2.70	0.40
16:Q:80:TRP:HE3	16:Q:82:ILE:HD12	1.85	0.40
16:Q:82:ILE:HG23	16:Q:86:LEU:HD23	2.03	0.40
24:Z:284:THR:HB	24:Z:286:THR:HG23	2.02	0.40
25:a:168:PHE:CA	25:a:169:LYS:NZ	2.79	0.40
28:G:349:LEU:O	28:G:352:LEU:HB2	2.21	0.40
28:G:555:GLU:C	28:G:555:GLU:CD	2.89	0.40
1:A:505:TRP:CE3	1:A:690:LYS:HD3	2.57	0.40
1:A:1447:TRP:O	1:A:1448:GLU:C	2.64	0.40
1:A:1790:TRP:HE3	1:A:1794:LEU:HB3	1.85	0.40
1:A:1849:LYS:HG2	1:A:1932:GLN:HB2	2.03	0.40
5:E:9:A:H2'	5:E:10:G:C8	2.56	0.40
6:F:163:ILE:HD13	6:F:172:LYS:CD	2.49	0.40
6:F:373:LEU:O	6:F:376:ASP:HB3	2.21	0.40
6:F:519:TYR:CE1	6:F:874:GLY:HA3	2.56	0.40
6:F:528:PRO:HG2	6:F:554:PHE:CZ	2.56	0.40
6:F:703:MET:HE3	6:F:713:LEU:HB2	2.02	0.40
6:F:715:VAL:O	25:a:246:VAL:CB	2.69	0.40
7:H:151:ASP:OD2	7:H:164:LYS:NZ	2.53	0.40
8:I:24:LEU:HD23	8:I:24:LEU:HA	1.94	0.40
13:M:481:A:H5'	32:e:52:TYR:CD1	2.57	0.40
13:M:500:A:OP2	28:G:775:ARG:NH2	2.46	0.40
14:O:210:ASP:HB2	14:O:217:ILE:CG1	2.46	0.40
20:U:80:LEU:HD23	20:U:129:ILE:HD13	2.02	0.40
23:Y:810:HIS:CG	23:Y:811:PRO:HD2	2.56	0.40
24:Z:125:PHE:CZ	24:Z:132:GLU:HB2	2.57	0.40
27:c:64:GLU:HG2	27:c:65:PHE:H	1.86	0.40
28:G:215:ASP:OD1	28:G:215:ASP:N	2.54	0.40
29:d:189:TYR:HB3	29:d:205:TRP:HD1	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:e:174:ALA:C	32:e:176:ASN:H	2.30	0.40
1:A:138:HIS:O	1:A:142:ILE:HG12	2.22	0.40
1:A:271:GLN:O	1:A:272:ASP:C	2.63	0.40
1:A:756:LEU:HD11	5:E:63:G:H4'	2.04	0.40
1:A:1222:LEU:O	1:A:1223:GLY:C	2.65	0.40
1:A:1375:LEU:O	1:A:1376:ASN:CB	2.69	0.40
1:A:1689:ARG:HG2	1:A:1692:TYR:OH	2.20	0.40
1:A:2060:LEU:HB3	1:A:2071:ILE:HD13	2.03	0.40
2:B:1469:GLU:HA	2:B:1506:ILE:HG12	2.02	0.40
3:C:83:THR:O	3:C:84:GLN:C	2.64	0.40
3:C:89:PRO:O	3:C:91:VAL:N	2.52	0.40
3:C:120:ARG:O	3:C:123:MET:HB3	2.21	0.40
3:C:606:VAL:HB	3:C:671:SER:HB2	2.03	0.40
6:F:208:GLU:CG	6:F:209:GLN:H	2.35	0.40
6:F:716:ILE:O	6:F:716:ILE:HG22	2.21	0.40
6:F:832:TRP:CG	6:F:833:LYS:N	2.89	0.40
6:F:1249:GLU:O	6:F:1250:ALA:C	2.63	0.40
9:J:22:LEU:HG	9:J:70:ALA:HB2	2.03	0.40
9:J:51:PHE:CD2	9:J:52:GLY:N	2.74	0.40
10:K:44:GLN:HB3	10:K:69:LEU:HD12	2.03	0.40
15:P:131:ALA:HA	18:S:18:ALA:HA	2.02	0.40
19:T:31:ARG:O	19:T:35:LYS:HG3	2.22	0.40
23:Y:357:ILE:O	23:Y:361:LEU:HG	2.21	0.40
24:Z:449:PHE:CE1	24:Z:465:PHE:CE2	3.09	0.40
27:c:230:THR:HG21	29:d:117:HIS:NE2	2.35	0.40
28:G:396:VAL:O	28:G:396:VAL:HG12	2.20	0.40
28:G:740:LYS:O	28:G:743:ARG:N	2.55	0.40
29:d:112:VAL:O	29:d:113:LYS:HB3	2.21	0.40
1:A:375:PHE:O	3:C:956:PRO:HA	2.22	0.40
1:A:404:ASN:HD21	3:C:927:MET:CE	2.33	0.40
1:A:470:LEU:O	1:A:473:THR:HG22	2.22	0.40
1:A:609:GLU:OE2	5:E:44:A:H5'	2.22	0.40
1:A:1288:LEU:HB2	1:A:1298:ALA:HB3	2.04	0.40
1:A:1346:PHE:O	1:A:1347:ARG:C	2.64	0.40
1:A:1740:TYR:CE1	1:A:1780:ALA:HB2	2.57	0.40
2:B:152:LYS:HB2	2:B:189:MET:HE3	2.02	0.40
2:B:1955:VAL:HG12	2:B:1959:ASN:HD21	1.86	0.40
2:B:2011:ILE:HD11	2:B:2030:ILE:HD11	2.02	0.40
3:C:362:LYS:O	3:C:364:PHE:N	2.55	0.40
3:C:368:GLU:OE2	3:C:370:TYR:N	2.54	0.40
3:C:701:GLU:OE1	3:C:706:LEU:N	2.48	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:840:PRO:O	3:C:843:LYS:HB3	2.20	0.40
6:F:670:PRO:HB3	6:F:713:LEU:HD21	2.04	0.40
7:H:200:ILE:O	7:H:203:THR:OG1	2.31	0.40
9:J:7:ASP:OD1	9:J:7:ASP:C	2.64	0.40
15:P:178:TYR:HE1	33:f:203:PHE:CD1	2.39	0.40
15:P:330:VAL:O	15:P:333:ASP:N	2.54	0.40
16:Q:24:ARG:HD2	19:T:116:ASN:HD22	1.87	0.40
16:Q:240:LEU:HD12	16:Q:241:ILE:H	1.85	0.40
17:R:153:PRO:HD3	17:R:177:GLU:OE1	2.22	0.40
21:V:11:GLU:OE2	21:V:22:SER:HA	2.20	0.40
23:Y:458:ILE:HA	23:Y:461:LYS:HB2	2.03	0.40
23:Y:701:GLU:HB3	23:Y:848:VAL:HG12	2.04	0.40
28:G:894:HIS:O	28:G:898:ARG:HG3	2.22	0.40
29:d:219:ARG:HB2	29:d:253:TRP:HZ2	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	2192/2287 (96%)	2037 (93%)	134 (6%)	21 (1%)	12	44
2	B	1803/2163 (83%)	1687 (94%)	112 (6%)	4 (0%)	43	74
3	C	872/1008 (86%)	800 (92%)	62 (7%)	10 (1%)	11	43
6	F	1164/1361 (86%)	1042 (90%)	110 (10%)	12 (1%)	12	44
7	H	147/436 (34%)	139 (95%)	6 (4%)	2 (1%)	9	38
8	I	98/266 (37%)	87 (89%)	9 (9%)	2 (2%)	6	32
9	J	101/107 (94%)	87 (86%)	14 (14%)	0	100	100
10	K	82/85 (96%)	78 (95%)	3 (4%)	1 (1%)	10	41
14	O	335/451 (74%)	302 (90%)	26 (8%)	7 (2%)	5	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	P	236/379 (62%)	209 (89%)	23 (10%)	4 (2%)	7	35
16	Q	177/364 (49%)	157 (89%)	16 (9%)	4 (2%)	5	30
17	R	259/339 (76%)	238 (92%)	18 (7%)	3 (1%)	10	41
18	S	65/175 (37%)	53 (82%)	9 (14%)	3 (5%)	2	17
19	T	155/157 (99%)	139 (90%)	13 (8%)	3 (2%)	6	33
20	U	172/207 (83%)	162 (94%)	9 (5%)	1 (1%)	21	54
21	V	126/148 (85%)	118 (94%)	6 (5%)	2 (2%)	7	36
22	W	98/266 (37%)	89 (91%)	6 (6%)	3 (3%)	3	25
23	Y	570/876 (65%)	548 (96%)	21 (4%)	1 (0%)	43	74
24	Z	443/577 (77%)	399 (90%)	32 (7%)	12 (3%)	4	27
25	a	119/259 (46%)	104 (87%)	13 (11%)	2 (2%)	7	35
26	b	146/301 (48%)	134 (92%)	9 (6%)	3 (2%)	5	31
27	c	291/587 (50%)	276 (95%)	9 (3%)	6 (2%)	5	31
28	G	871/971 (90%)	820 (94%)	41 (5%)	10 (1%)	11	43
29	d	234/687 (34%)	214 (92%)	19 (8%)	1 (0%)	30	62
30	X	25/135 (18%)	20 (80%)	5 (20%)	0	100	100
31	v	120/859 (14%)	110 (92%)	5 (4%)	5 (4%)	2	19
32	e	141/213 (66%)	114 (81%)	16 (11%)	11 (8%)	1	8
33	f	98/215 (46%)	95 (97%)	3 (3%)	0	100	100
34	o	118/503 (24%)	113 (96%)	4 (3%)	1 (1%)	16	49
34	p	122/503 (24%)	116 (95%)	6 (5%)	0	100	100
34	q	349/503 (69%)	321 (92%)	16 (5%)	12 (3%)	3	23
34	r	119/503 (24%)	111 (93%)	5 (4%)	3 (2%)	4	28
35	t	149/175 (85%)	133 (89%)	13 (9%)	3 (2%)	6	32
36	n	21/455 (5%)	19 (90%)	1 (5%)	1 (5%)	2	16
37	k	76/196 (39%)	69 (91%)	7 (9%)	0	100	100
38	i	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
39	h	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	8	37
40	j	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
41	l	80/101 (79%)	70 (88%)	9 (11%)	1 (1%)	9	39
42	m	78/146 (53%)	74 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	g	92/94 (98%)	85 (92%)	6 (6%)	1 (1%)	11	43
All	All	12546/19315 (65%)	11559 (92%)	831 (7%)	156 (1%)	13	41

All (156) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	265	ASN
1	A	1376	ASN
1	A	1405	ILE
1	A	1829	SER
1	A	1830	VAL
1	A	1847	ASP
1	A	2288	CYS
2	B	696	SER
2	B	697	SER
2	B	905	GLN
3	C	364	PHE
3	C	602	VAL
6	F	363	VAL
6	F	413	ILE
6	F	1299	ILE
8	I	55	ASN
8	I	56	PRO
16	Q	99	VAL
18	S	7	PRO
19	T	140	VAL
21	V	17	LEU
22	W	172	ILE
22	W	191	GLU
25	a	139	PHE
26	b	167	ILE
27	c	204	LYS
28	G	57	VAL
28	G	386	TYR
28	G	681	PRO
28	G	830	MET
28	G	831	SER
28	G	835	ILE
28	G	836	TYR
31	v	616	PRO
32	e	83	VAL
32	e	117	ASP

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Mol	Chain	Res	Type
32	e	144	SER
32	e	148	LEU
32	e	170	ASN
34	q	53	ILE
34	q	77	ILE
34	q	172	PRO
34	q	174	TRP
34	q	239	PRO
34	q	246	PRO
34	q	362	PRO
34	q	442	SER
34	r	64	GLU
35	t	77	PRO
1	A	1323	SER
1	A	1746	HIS
3	C	460	GLY
6	F	961	CYS
16	Q	255	SER
17	R	44	ASN
17	R	146	LEU
17	R	218	GLY
20	U	52	HIS
22	W	230	SER
24	Z	69	ASN
24	Z	206	LYS
24	Z	234	GLU
24	Z	235	ALA
24	Z	398	PRO
25	a	168	PHE
27	c	230	THR
31	v	601	VAL
31	v	618	GLU
31	v	634	HIS
32	e	147	LYS
32	e	149	LYS
32	e	171	GLN
34	q	196	PRO
35	t	110	GLU
36	n	61	LYS
1	A	645	ASP
1	A	1585	MET
3	C	952	PRO

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Mol	Chain	Res	Type
6	F	364	THR
10	K	19	ILE
14	O	124	GLU
14	O	391	GLU
14	O	442	TRP
15	P	59	THR
18	S	131	THR
24	Z	67	LYS
24	Z	204	ASP
26	b	68	THR
27	c	82	ASN
32	e	82	LYS
34	o	17	PRO
34	r	20	ARG
35	t	80	ASN
1	A	540	THR
1	A	562	ILE
2	B	1609	MET
3	C	84	GLN
14	O	278	ASP
14	O	279	PRO
14	O	435	GLU
15	P	86	ASN
19	T	119	THR
24	Z	304	SER
26	b	8	GLN
27	c	224	MET
27	c	231	SER
32	e	33	ASN
41	l	82	PRO
43	g	82	LYS
1	A	1015	PRO
1	A	1490	ARG
3	C	366	ASN
3	C	854	ILE
6	F	92	GLN
6	F	247	PHE
6	F	248	ASN
6	F	434	ASN
6	F	773	LYS
7	H	194	PHE
7	H	235	PRO

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Mol	Chain	Res	Type
15	P	312	ALA
16	Q	52	SER
16	Q	119	LYS
21	V	18	SER
24	Z	229	VAL
28	G	873	HIS
34	q	60	ALA
3	C	363	PRO
18	S	22	PRO
19	T	104	CYS
23	Y	783	PHE
24	Z	146	ASN
28	G	348	VAL
28	G	892	SER
1	A	1964	PRO
29	d	166	VAL
34	q	36	GLY
39	h	15	PRO
1	A	407	VAL
1	A	741	ILE
1	A	802	PRO
3	C	704	PRO
3	C	829	VAL
24	Z	471	GLY
31	v	617	PRO
34	q	175	PRO
6	F	523	ILE
24	Z	214	ILE
32	e	18	PRO
1	A	644	VAL
1	A	771	PRO
6	F	1031	ILE
14	O	277	VAL
15	P	143	VAL
27	c	218	VAL
34	r	36	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1994/2066 (96%)	1912 (96%)	82 (4%)	27	53
2	B	1632/1955 (84%)	1632 (100%)	0	100	100
3	C	791/910 (87%)	774 (98%)	17 (2%)	47	66
6	F	1088/1244 (88%)	1063 (98%)	25 (2%)	44	64
7	H	139/392 (36%)	127 (91%)	12 (9%)	10	33
8	I	89/236 (38%)	84 (94%)	5 (6%)	19	46
9	J	93/97 (96%)	88 (95%)	5 (5%)	20	46
10	K	76/77 (99%)	68 (90%)	8 (10%)	6	27
14	O	295/397 (74%)	293 (99%)	2 (1%)	76	78
15	P	218/328 (66%)	202 (93%)	16 (7%)	13	38
16	Q	171/332 (52%)	161 (94%)	10 (6%)	18	44
17	R	224/296 (76%)	208 (93%)	16 (7%)	13	38
18	S	58/151 (38%)	58 (100%)	0	100	100
19	T	141/141 (100%)	137 (97%)	4 (3%)	38	61
20	U	157/189 (83%)	152 (97%)	5 (3%)	34	59
21	V	114/132 (86%)	111 (97%)	3 (3%)	40	62
22	W	91/240 (38%)	73 (80%)	18 (20%)	1	7
23	Y	299/789 (38%)	291 (97%)	8 (3%)	39	62
24	Z	417/538 (78%)	384 (92%)	33 (8%)	11	36
25	a	112/237 (47%)	104 (93%)	8 (7%)	13	38
26	b	134/273 (49%)	133 (99%)	1 (1%)	76	78
27	c	196/316 (62%)	188 (96%)	8 (4%)	27	53
28	G	778/867 (90%)	766 (98%)	12 (2%)	57	71
29	d	215/249 (86%)	213 (99%)	2 (1%)	70	76
30	X	21/121 (17%)	21 (100%)	0	100	100
31	v	59/152 (39%)	49 (83%)	10 (17%)	2	13
32	e	48/189 (25%)	42 (88%)	6 (12%)	4	22
33	f	92/193 (48%)	92 (100%)	0	100	100
34	o	61/451 (14%)	55 (90%)	6 (10%)	7	30
34	p	62/451 (14%)	54 (87%)	8 (13%)	4	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	q	121/451 (27%)	104 (86%)	17 (14%)	3	19
34	r	59/451 (13%)	54 (92%)	5 (8%)	10	34
35	t	39/165 (24%)	27 (69%)	12 (31%)	0	2
36	n	20/413 (5%)	13 (65%)	7 (35%)	0	1
37	k	70/176 (40%)	69 (99%)	1 (1%)	59	71
38	i	65/83 (78%)	60 (92%)	5 (8%)	12	37
39	h	61/77 (79%)	60 (98%)	1 (2%)	55	70
40	j	58/66 (88%)	56 (97%)	2 (3%)	32	57
41	l	69/89 (78%)	68 (99%)	1 (1%)	59	71
42	m	77/129 (60%)	74 (96%)	3 (4%)	28	54
43	g	79/87 (91%)	73 (92%)	6 (8%)	12	37
All	All	10583/16196 (65%)	10193 (96%)	390 (4%)	31	56

All (390) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	180	PRO
1	A	220	THR
1	A	228	LYS
1	A	236	ARG
1	A	238	ARG
1	A	256	GLU
1	A	261	LEU
1	A	263	PRO
1	A	266	LEU
1	A	268	LEU
1	A	270	SER
1	A	309	SER
1	A	324	ASP
1	A	377	VAL
1	A	380	ARG
1	A	394	ARG
1	A	396	ARG
1	A	451	ASP
1	A	452	PHE
1	A	461	LEU
1	A	479	LEU
1	A	497	GLN

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Mol	Chain	Res	Type
1	A	570	GLN
1	A	614	ARG
1	A	625	LEU
1	A	640	ARG
1	A	712	LEU
1	A	715	LEU
1	A	716	ARG
1	A	737	ARG
1	A	750	LEU
1	A	769	MET
1	A	773	SER
1	A	774	ILE
1	A	775	ARG
1	A	777	LYS
1	A	782	ILE
1	A	854	ARG
1	A	893	ARG
1	A	928	ARG
1	A	934	ARG
1	A	978	ILE
1	A	1043	ARG
1	A	1325	SER
1	A	1370	ARG
1	A	1376	ASN
1	A	1378	LYS
1	A	1379	MET
1	A	1440	ILE
1	A	1470	GLN
1	A	1499	ARG
1	A	1509	ARG
1	A	1521	ARG
1	A	1588	LYS
1	A	1590	LEU
1	A	1591	THR
1	A	1605	ARG
1	A	1608	LEU
1	A	1629	LEU
1	A	1661	ILE
1	A	1739	ARG
1	A	1747	ASP
1	A	1748	ILE
1	A	1749	SER

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Mol	Chain	Res	Type
1	A	1783	MET
1	A	1794	LEU
1	A	1809	ASN
1	A	1816	ARG
1	A	1830	VAL
1	A	1831	GLN
1	A	1843	LEU
1	A	1998	ARG
1	A	2006	SER
1	A	2018	ASN
1	A	2079	ILE
1	A	2255	LEU
1	A	2402	GLU
1	A	2403	GLU
1	A	2404	LEU
1	A	2408	GLN
1	A	2409	ILE
1	A	2412	PHE
3	C	100	LEU
3	C	108	GLN
3	C	110	LYS
3	C	115	LYS
3	C	132	ARG
3	C	150	MET
3	C	160	ARG
3	C	170	LEU
3	C	173	LYS
3	C	176	ARG
3	C	177	TYR
3	C	181	LEU
3	C	275	LEU
3	C	307	ILE
3	C	395	LYS
3	C	548	ARG
3	C	945	LEU
6	F	80	VAL
6	F	97	THR
6	F	148	LEU
6	F	153	ASP
6	F	162	ILE
6	F	183	THR
6	F	203	ILE

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Mol	Chain	Res	Type
6	F	230	ILE
6	F	231	ILE
6	F	238	LEU
6	F	257	ILE
6	F	294	PHE
6	F	410	PHE
6	F	421	ILE
6	F	444	LEU
6	F	523	ILE
6	F	770	LEU
6	F	838	ILE
6	F	885	TRP
6	F	1008	ILE
6	F	1060	LEU
6	F	1195	VAL
6	F	1231	LEU
6	F	1239	MET
6	F	1318	ILE
7	H	155	ARG
7	H	179	LYS
7	H	180	LYS
7	H	181	GLU
7	H	192	ARG
7	H	195	GLU
7	H	196	LEU
7	H	205	ILE
7	H	233	VAL
7	H	242	LEU
7	H	246	LYS
7	H	288	HIS
8	I	18	SER
8	I	51	GLN
8	I	53	ARG
8	I	55	ASN
8	I	77	SER
9	J	2	SER
9	J	4	HIS
9	J	97	LEU
9	J	99	ARG
9	J	102	GLU
10	K	8	LEU
10	K	27	THR

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Mol	Chain	Res	Type
10	K	28	ARG
10	K	42	THR
10	K	44	GLN
10	K	57	ARG
10	K	60	LEU
10	K	63	ARG
14	O	138	HIS
14	O	228	ARG
15	P	37	ASN
15	P	40	LEU
15	P	44	ILE
15	P	52	GLU
15	P	55	VAL
15	P	57	LEU
15	P	60	LYS
15	P	111	HIS
15	P	122	LEU
15	P	133	LYS
15	P	243	GLU
15	P	244	LEU
15	P	247	ARG
15	P	300	ASP
15	P	302	GLN
15	P	325	ASP
16	Q	119	LYS
16	Q	120	LEU
16	Q	213	SER
16	Q	217	TRP
16	Q	220	THR
16	Q	222	THR
16	Q	226	LEU
16	Q	227	LEU
16	Q	245	LYS
16	Q	248	CYS
17	R	7	LYS
17	R	10	LYS
17	R	12	GLN
17	R	14	LYS
17	R	15	GLU
17	R	17	GLU
17	R	18	LEU
17	R	31	ASN

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Mol	Chain	Res	Type
17	R	66	ASN
17	R	67	ASP
17	R	69	GLN
17	R	121	ARG
17	R	179	LYS
17	R	181	CYS
17	R	210	LYS
17	R	215	ARG
19	T	54	GLN
19	T	120	CYS
19	T	122	CYS
19	T	126	ARG
20	U	38	LEU
20	U	40	LEU
20	U	42	SER
20	U	45	LYS
20	U	46	GLU
21	V	6	GLN
21	V	7	ILE
21	V	110	ARG
22	W	160	LYS
22	W	162	LEU
22	W	168	GLN
22	W	169	LYS
22	W	172	ILE
22	W	174	VAL
22	W	187	SER
22	W	188	LEU
22	W	189	THR
22	W	191	GLU
22	W	196	THR
22	W	207	THR
22	W	208	SER
22	W	209	LEU
22	W	210	LEU
22	W	213	LYS
22	W	214	LEU
22	W	262	LEU
23	Y	266	THR
23	Y	367	PRO
23	Y	413	PRO
23	Y	578	PRO

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Mol	Chain	Res	Type
23	Y	606	PRO
23	Y	614	PRO
23	Y	784	PRO
23	Y	826	PRO
24	Z	12	LYS
24	Z	16	GLU
24	Z	34	MET
24	Z	67	LYS
24	Z	94	LEU
24	Z	105	GLN
24	Z	132	GLU
24	Z	138	ILE
24	Z	145	LYS
24	Z	151	VAL
24	Z	162	LEU
24	Z	168	LYS
24	Z	174	TRP
24	Z	177	LEU
24	Z	179	TYR
24	Z	181	LEU
24	Z	183	THR
24	Z	184	GLN
24	Z	185	GLU
24	Z	186	LEU
24	Z	190	LEU
24	Z	192	GLU
24	Z	193	SER
24	Z	194	LEU
24	Z	195	GLU
24	Z	197	LEU
24	Z	199	GLU
24	Z	216	ASP
24	Z	229	VAL
24	Z	245	CYS
24	Z	303	LEU
24	Z	398	PRO
24	Z	427	LEU
25	a	131	ILE
25	a	134	THR
25	a	167	ASP
25	a	168	PHE
25	a	169	LYS

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Mol	Chain	Res	Type
25	a	170	THR
25	a	173	LYS
25	a	178	TRP
26	b	5	ILE
27	c	204	LYS
27	c	504	PRO
27	c	505	PRO
27	c	506	THR
27	c	517	VAL
27	c	523	LEU
27	c	532	PRO
27	c	550	PRO
28	G	22	GLN
28	G	68	ARG
28	G	173	ILE
28	G	218	ARG
28	G	327	TRP
28	G	469	SER
28	G	543	ARG
28	G	553	LEU
28	G	681	PRO
28	G	740	LYS
28	G	849	ARG
28	G	936	ARG
29	d	120	ASN
29	d	134	LYS
31	v	616	PRO
31	v	617	PRO
31	v	641	PRO
31	v	706	LEU
31	v	712	CYS
31	v	722	PRO
31	v	723	SER
31	v	725	THR
31	v	726	ARG
31	v	733	ILE
32	e	10	THR
32	e	13	VAL
32	e	87	THR
32	e	153	VAL
32	e	165	ILE
32	e	179	THR

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Mol	Chain	Res	Type
34	o	17	PRO
34	o	26	SER
34	o	44	PRO
34	o	63	THR
34	o	109	LEU
34	o	134	SER
34	p	17	PRO
34	p	44	PRO
34	p	63	THR
34	p	80	LEU
34	p	85	GLN
34	p	93	LEU
34	p	98	LEU
34	p	109	LEU
34	q	14	VAL
34	q	17	PRO
34	q	44	PRO
34	q	55	PRO
34	q	56	SER
34	q	61	SER
34	q	102	LEU
34	q	126	LEU
34	q	172	PRO
34	q	175	PRO
34	q	196	PRO
34	q	215	CYS
34	q	235	THR
34	q	239	PRO
34	q	262	PRO
34	q	350	PRO
34	q	412	PRO
34	r	17	PRO
34	r	44	PRO
34	r	63	THR
34	r	93	LEU
34	r	109	LEU
35	t	5	SER
35	t	7	VAL
35	t	13	PRO
35	t	77	PRO
35	t	96	PRO
35	t	100	THR

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Mol	Chain	Res	Type
35	t	105	PRO
35	t	108	SER
35	t	133	PRO
35	t	136	VAL
35	t	150	THR
35	t	152	THR
36	n	51	PHE
36	n	55	GLU
36	n	57	LYS
36	n	58	ARG
36	n	59	ARG
36	n	62	THR
36	n	66	ASP
37	k	47	GLU
38	i	16	CYS
38	i	18	PHE
38	i	25	THR
38	i	79	LYS
38	i	81	LEU
39	h	79	LEU
40	j	18	ASN
40	j	71	LEU
41	l	10	LEU
42	m	20	LYS
42	m	30	GLN
42	m	77	ASP
43	g	24	PHE
43	g	48	LEU
43	g	49	ARG
43	g	77	THR
43	g	99	ASP
43	g	100	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (238) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	181	HIS
1	A	254	HIS
1	A	271	GLN
1	A	392	ASN
1	A	429	ASN
1	A	481	HIS

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Mol	Chain	Res	Type
1	A	541	ASN
1	A	542	HIS
1	A	559	GLN
1	A	574	GLN
1	A	654	HIS
1	A	658	ASN
1	A	685	HIS
1	A	785	HIS
1	A	848	ASN
1	A	868	GLN
1	A	948	HIS
1	A	997	GLN
1	A	1034	ASN
1	A	1115	GLN
1	A	1156	HIS
1	A	1231	GLN
1	A	1295	GLN
1	A	1368	GLN
1	A	1376	ASN
1	A	1496	GLN
1	A	1600	GLN
1	A	1782	ASN
1	A	1789	ASN
1	A	1836	ASN
1	A	1845	ASN
1	A	1895	HIS
1	A	2180	GLN
1	A	2232	HIS
1	A	2355	ASN
1	A	2408	GLN
2	B	116	ASN
2	B	137	HIS
2	B	170	GLN
2	B	676	ASN
2	B	706	GLN
2	B	738	ASN
2	B	739	GLN
2	B	773	ASN
2	B	862	GLN
2	B	904	GLN
2	B	919	ASN
2	B	1003	ASN

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Mol	Chain	Res	Type
2	B	1123	HIS
2	B	1148	GLN
2	B	1191	GLN
2	B	1219	ASN
2	B	1352	GLN
2	B	1361	ASN
2	B	1390	GLN
2	B	1430	ASN
2	B	1435	ASN
2	B	1451	GLN
2	B	1531	ASN
2	B	1549	GLN
2	B	1693	HIS
2	B	1701	ASN
2	B	1760	ASN
2	B	1764	GLN
2	B	1959	ASN
2	B	2046	ASN
2	B	2139	ASN
3	C	68	HIS
3	C	82	ASN
3	C	103	HIS
3	C	112	ASN
3	C	167	ASN
3	C	183	GLN
3	C	255	GLN
3	C	289	ASN
3	C	309	ASN
3	C	423	HIS
3	C	432	GLN
3	C	444	GLN
3	C	772	ASN
3	C	776	ASN
3	C	794	GLN
3	C	869	HIS
3	C	960	ASN
6	F	62	HIS
6	F	119	ASN
6	F	156	ASN
6	F	161	GLN
6	F	248	ASN
6	F	382	GLN

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Mol	Chain	Res	Type
6	F	384	ASN
6	F	420	HIS
6	F	481	GLN
6	F	504	HIS
6	F	547	ASN
6	F	590	HIS
6	F	609	HIS
6	F	641	GLN
6	F	686	GLN
6	F	687	HIS
6	F	738	GLN
6	F	740	ASN
6	F	754	HIS
6	F	840	GLN
6	F	878	ASN
6	F	944	ASN
6	F	950	GLN
6	F	969	HIS
6	F	1039	ASN
6	F	1091	HIS
6	F	1117	HIS
6	F	1191	ASN
6	F	1192	HIS
6	F	1203	HIS
6	F	1210	ASN
6	F	1222	GLN
6	F	1236	ASN
6	F	1304	HIS
6	F	1332	ASN
6	F	1359	ASN
7	H	145	GLN
7	H	175	HIS
7	H	262	HIS
8	I	2	ASN
8	I	25	GLN
8	I	39	ASN
8	I	55	ASN
8	I	72	ASN
8	I	90	HIS
9	J	14	GLN
9	J	95	ASN
9	J	100	HIS

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Mol	Chain	Res	Type
10	K	5	GLN
10	K	32	GLN
10	K	37	ASN
10	K	41	ASN
10	K	44	GLN
10	K	46	HIS
14	O	138	HIS
14	O	215	GLN
14	O	270	ASN
14	O	271	GLN
14	O	273	GLN
14	O	382	HIS
15	P	48	GLN
15	P	50	ASN
15	P	86	ASN
15	P	111	HIS
15	P	302	GLN
15	P	319	HIS
15	P	322	GLN
16	Q	67	GLN
16	Q	69	ASN
16	Q	106	ASN
16	Q	209	ASN
16	Q	225	GLN
16	Q	244	HIS
17	R	31	ASN
17	R	58	HIS
17	R	69	GLN
17	R	91	HIS
17	R	201	ASN
17	R	259	ASN
18	S	27	HIS
18	S	173	HIS
19	T	54	GLN
19	T	57	HIS
19	T	116	ASN
19	T	139	GLN
19	T	143	HIS
20	U	43	ASN
20	U	44	ASN
20	U	52	HIS
20	U	99	ASN

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Mol	Chain	Res	Type
20	U	139	GLN
21	V	5	GLN
21	V	30	ASN
21	V	106	HIS
22	W	168	GLN
22	W	173	ASN
22	W	236	HIS
23	Y	272	GLN
23	Y	349	HIS
23	Y	429	HIS
23	Y	743	GLN
24	Z	48	ASN
24	Z	54	ASN
24	Z	170	HIS
24	Z	182	GLN
24	Z	184	GLN
24	Z	236	ASN
24	Z	319	ASN
24	Z	354	HIS
24	Z	457	HIS
24	Z	463	ASN
25	a	140	GLN
25	a	175	ASN
25	a	176	GLN
27	c	83	GLN
27	c	214	ASN
28	G	17	HIS
28	G	59	ASN
28	G	65	HIS
28	G	216	GLN
28	G	219	HIS
28	G	295	ASN
28	G	311	ASN
28	G	407	HIS
28	G	618	GLN
28	G	641	ASN
28	G	695	ASN
28	G	697	HIS
28	G	760	HIS
28	G	853	HIS
28	G	882	ASN
29	d	67	GLN

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Mol	Chain	Res	Type
29	d	79	HIS
29	d	120	ASN
29	d	147	ASN
29	d	179	GLN
29	d	196	HIS
29	d	252	HIS
29	d	257	GLN
29	d	258	GLN
32	e	114	ASN
33	f	200	ASN
37	k	8	HIS
37	k	91	GLN
38	i	34	GLN
38	i	86	ASN
39	h	25	HIS
39	h	52	GLN
39	h	54	ASN
40	j	66	ASN
41	l	17	HIS
41	l	41	ASN
42	m	30	GLN
42	m	86	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	L	65/1175 (5%)	12 (18%)	0
12	N	24/25 (96%)	9 (37%)	0
13	M	47/61 (77%)	23 (48%)	5 (10%)
4	D	114/214 (53%)	24 (21%)	2 (1%)
5	E	102/112 (91%)	17 (16%)	0
All	All	352/1587 (22%)	85 (24%)	7 (1%)

All (85) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	D	29	G
4	D	31	G
4	D	42	A
4	D	43	G
4	D	45	A

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Mol	Chain	Res	Type
4	D	46	C
4	D	74	U
4	D	75	A
4	D	77	A
4	D	79	C
4	D	81	A
4	D	84	A
4	D	92	U
4	D	101	C
4	D	127	U
4	D	164	C
4	D	165	A
4	D	166	U
4	D	170	U
4	D	171	U
4	D	172	U
4	D	173	U
4	D	174	G
4	D	175	G
5	E	14	C
5	E	35	A
5	E	36	U
5	E	51	A
5	E	60	G
5	E	66	C
5	E	67	C
5	E	68	C
5	E	80	U
5	E	81	G
5	E	85	C
5	E	86	G
5	E	88	U
5	E	91	A
5	E	92	C
5	E	93	A
5	E	103	A
11	L	15	C
11	L	17	U
11	L	18	U
11	L	19	U
11	L	26	G
11	L	32	G

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Mol	Chain	Res	Type
11	L	38	U
11	L	41	C
11	L	46	C
11	L	48	U
11	L	52	A
11	L	66	A
12	N	96	U
12	N	98	A
12	N	100	G
12	N	102	A
12	N	109	U
12	N	110	U
12	N	111	U
12	N	112	U
12	N	114	U
13	M	471	A
13	M	472	A
13	M	473	A
13	M	480	A
13	M	481	A
13	M	484	A
13	M	493	A
13	M	497	A
13	M	501	A
13	M	502	C
13	M	505	A
13	M	506	U
13	M	507	U
13	M	508	U
13	M	509	A
13	M	510	A
13	M	512	U
13	M	515	U
13	M	516	U
13	M	518	U
13	M	520	G
13	M	521	U
13	M	522	U

All (7) RNA pucker outliers are listed below:

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Mol	Chain	Res	Type
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Mol	Chain	Res	Type
4	D	78	A
4	D	172	U
13	M	472	A
13	M	480	A
13	M	500	A
13	M	514	U
13	M	515	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 18 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
47	ADP	Y	902	45	28,29,29	1.49	5 (17%)	43,45,45	1.93	10 (23%)
44	GTP	C	1500	-	33,34,34	1.27	4 (12%)	50,54,54	1.92	7 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
47	ADP	Y	902	45	-	4/16/32/32	0/3/3/3
44	GTP	C	1500	-	-	8/22/38/38	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	Y	902	ADP	C5-C4	4.87	1.47	1.39
44	C	1500	GTP	C5-N7	-3.12	1.32	1.39
44	C	1500	GTP	C6-N1	-3.07	1.33	1.38
47	Y	902	ADP	C5-C6	2.93	1.49	1.41
44	C	1500	GTP	PA-O3A	2.79	1.62	1.59
47	Y	902	ADP	C8-N7	2.45	1.36	1.31
47	Y	902	ADP	PA-O3A	2.35	1.62	1.59
47	Y	902	ADP	C5-N7	-2.22	1.35	1.39
44	C	1500	GTP	C8-N9	-2.03	1.33	1.37

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C	1500	GTP	C5-C4-N3	-6.51	118.04	128.39
47	Y	902	ADP	C5-C4-N3	-6.15	118.25	126.72
44	C	1500	GTP	C2-N3-C4	5.59	121.93	112.30
44	C	1500	GTP	N9-C4-N3	5.47	136.88	125.95
47	Y	902	ADP	N3-C4-N9	4.91	135.52	127.17
47	Y	902	ADP	C2-N3-C4	3.91	121.38	111.83
44	C	1500	GTP	O6-C6-C5	-3.72	116.71	126.53
47	Y	902	ADP	C4-C5-N7	-3.66	106.40	110.58
47	Y	902	ADP	N3-C2-N1	-3.53	123.24	128.58
44	C	1500	GTP	C5-C6-N1	2.94	120.74	113.25
47	Y	902	ADP	C5-N7-C8	2.84	107.91	103.45
47	Y	902	ADP	C4-N9-C8	2.79	108.67	105.74
44	C	1500	GTP	C6-C5-N7	2.63	135.08	130.29
44	C	1500	GTP	C2-N1-C6	-2.41	120.75	125.11
47	Y	902	ADP	C3'-C2'-C1'	2.24	105.70	101.46
47	Y	902	ADP	N9-C8-N7	-2.22	110.78	113.94
47	Y	902	ADP	C6-C5-N7	2.09	136.12	132.09

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
44	C	1500	GTP	C5'-O5'-PA-O3A

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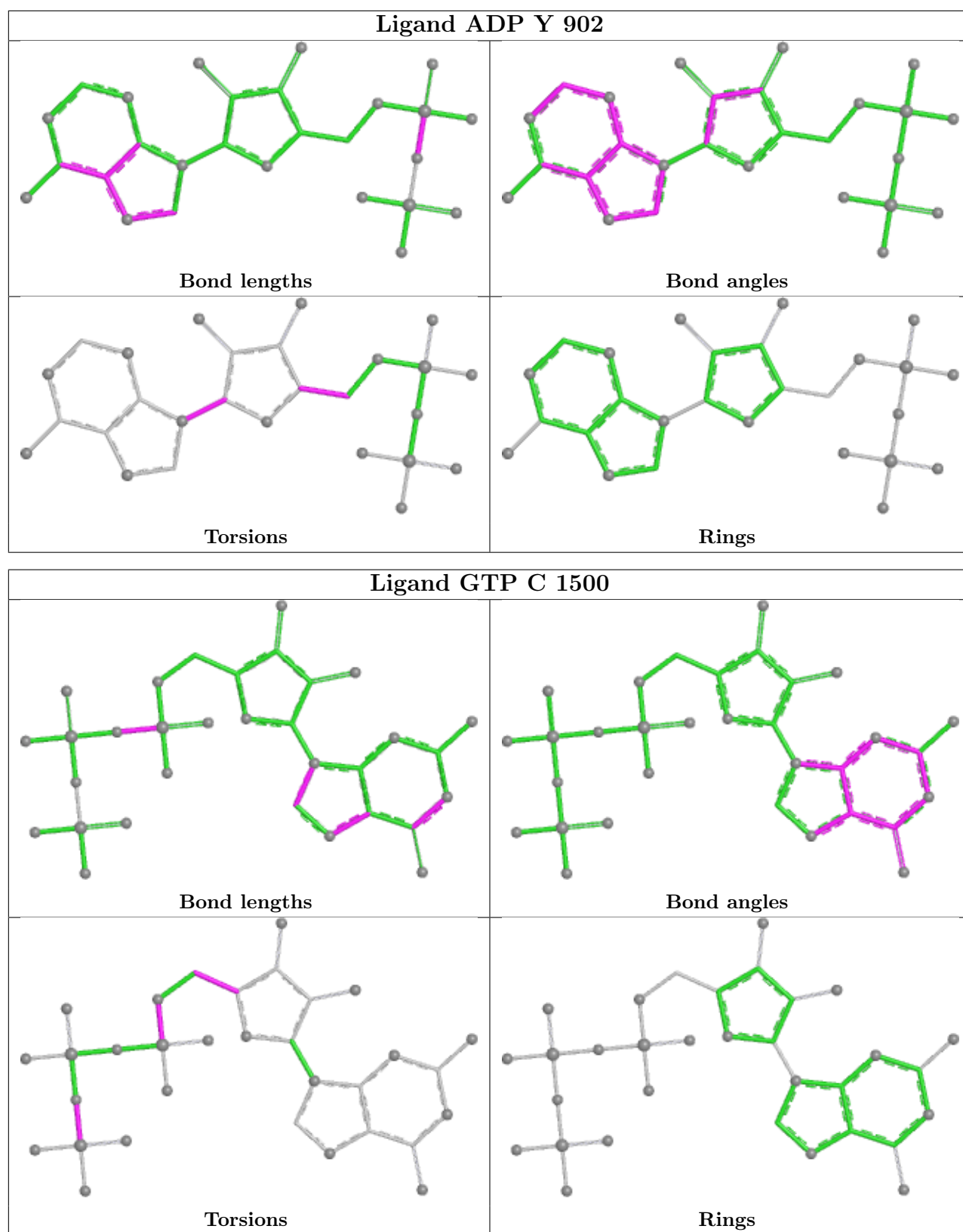
Mol	Chain	Res	Type	Atoms
44	C	1500	GTP	C5'-O5'-PA-O1A
44	C	1500	GTP	C5'-O5'-PA-O2A
44	C	1500	GTP	O4'-C4'-C5'-O5'
44	C	1500	GTP	C3'-C4'-C5'-O5'
47	Y	902	ADP	O4'-C4'-C5'-O5'
47	Y	902	ADP	C3'-C4'-C5'-O5'
47	Y	902	ADP	O4'-C1'-N9-C4
47	Y	902	ADP	O4'-C1'-N9-C8
44	C	1500	GTP	PB-O3B-PG-O1G
44	C	1500	GTP	PB-O3B-PG-O2G
44	C	1500	GTP	PB-O3B-PG-O3G

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
47	Y	902	ADP	2	0
44	C	1500	GTP	4	0

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



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

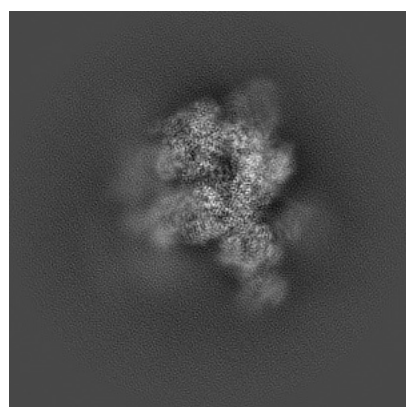
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9524. These allow visual inspection of the internal detail of the map and identification of artifacts.

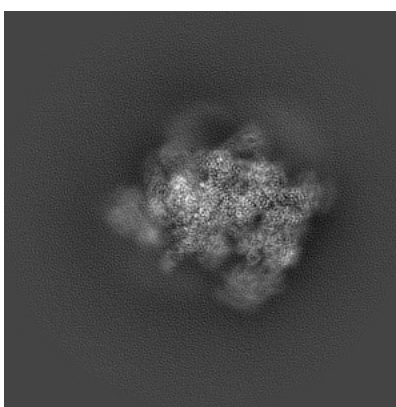
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

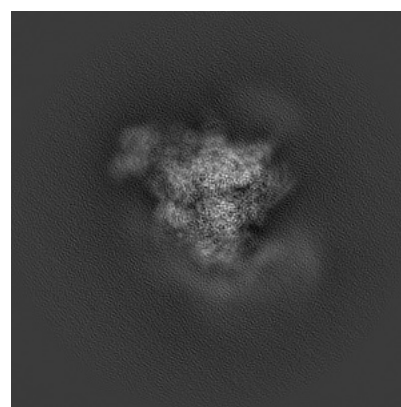
6.1.1 Primary map



X



Y

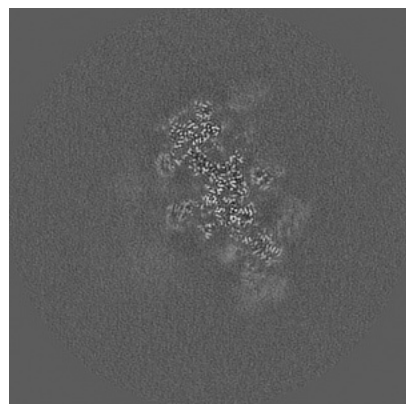


Z

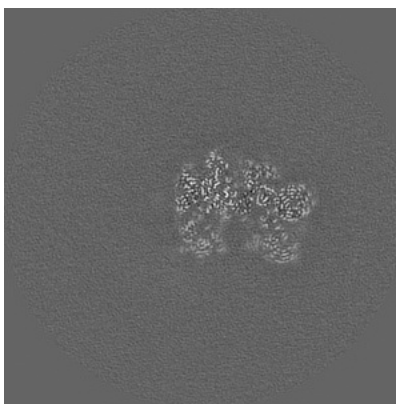
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

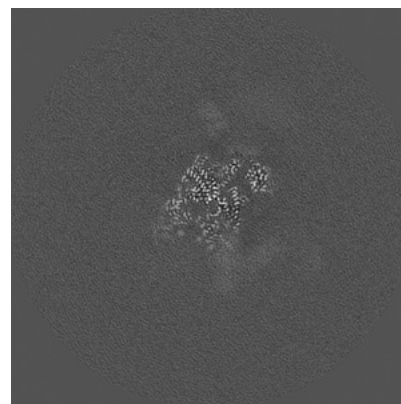
6.2.1 Primary map



X Index: 200



Y Index: 200

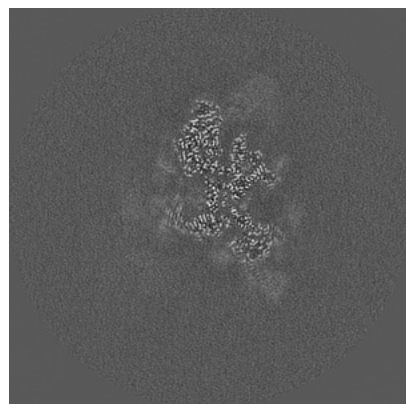


Z Index: 200

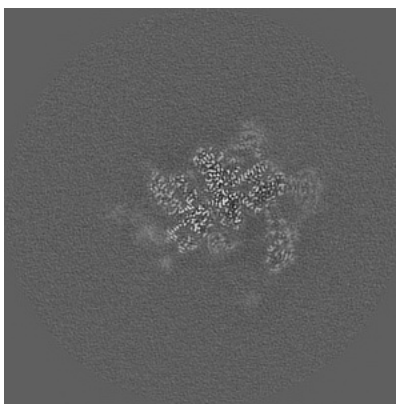
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

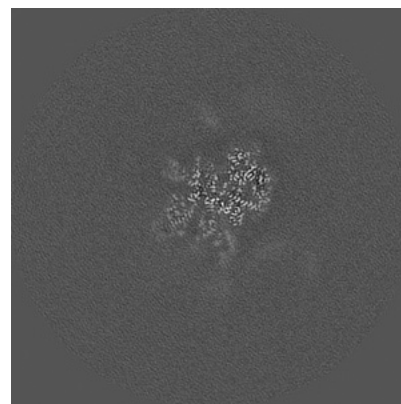
6.3.1 Primary map



X Index: 210



Y Index: 230

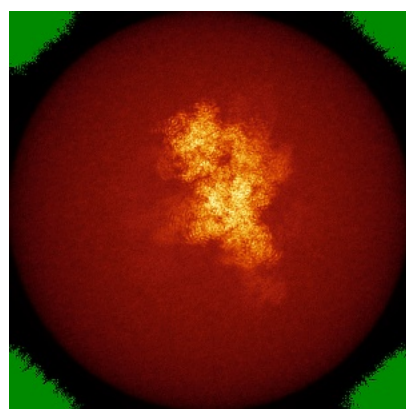


Z Index: 205

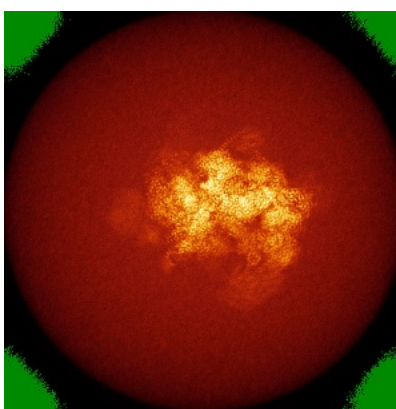
The images above show the largest variance slices of the map in three orthogonal directions.

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

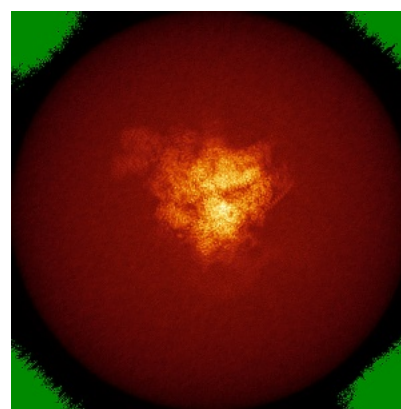
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0405. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

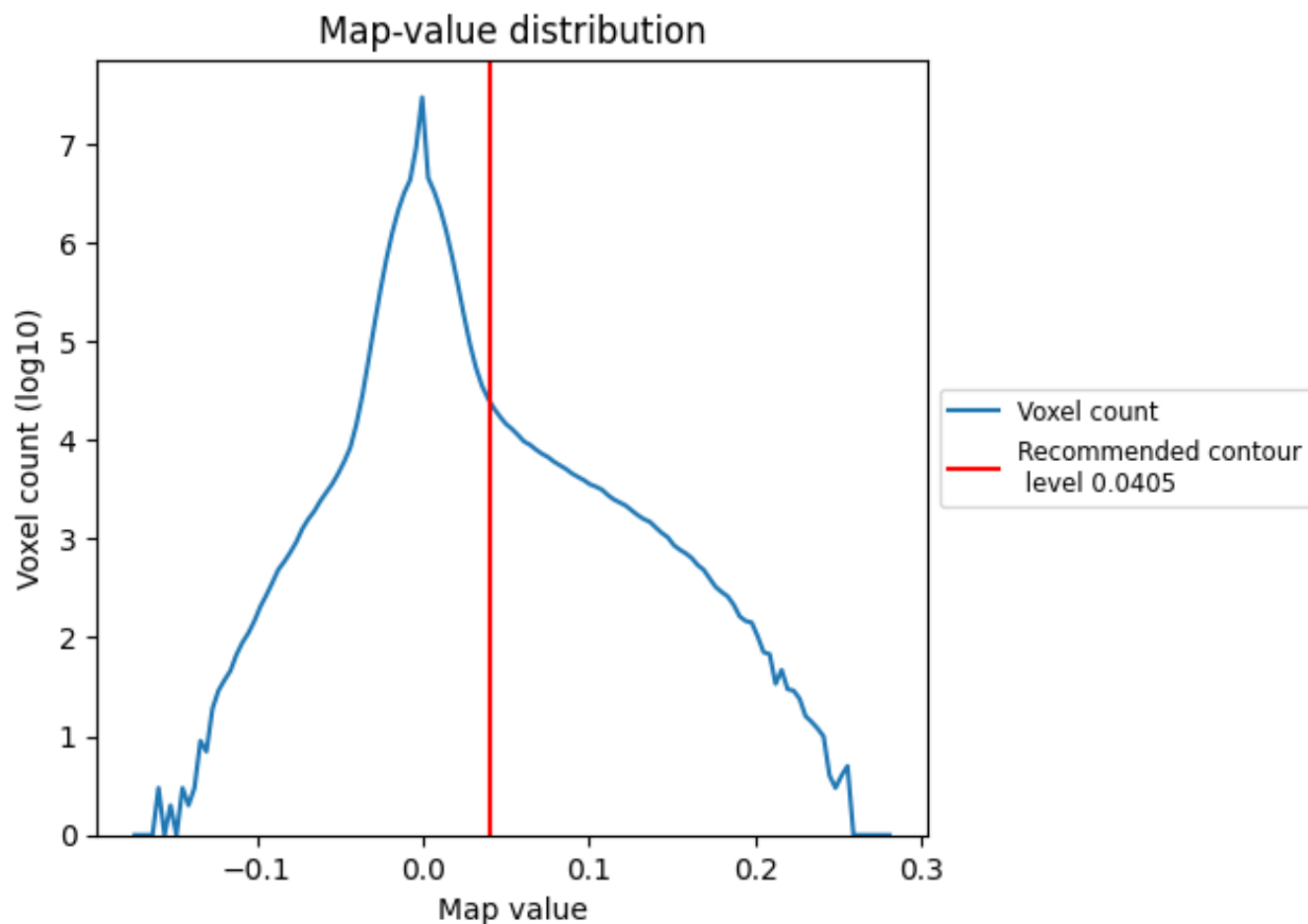
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

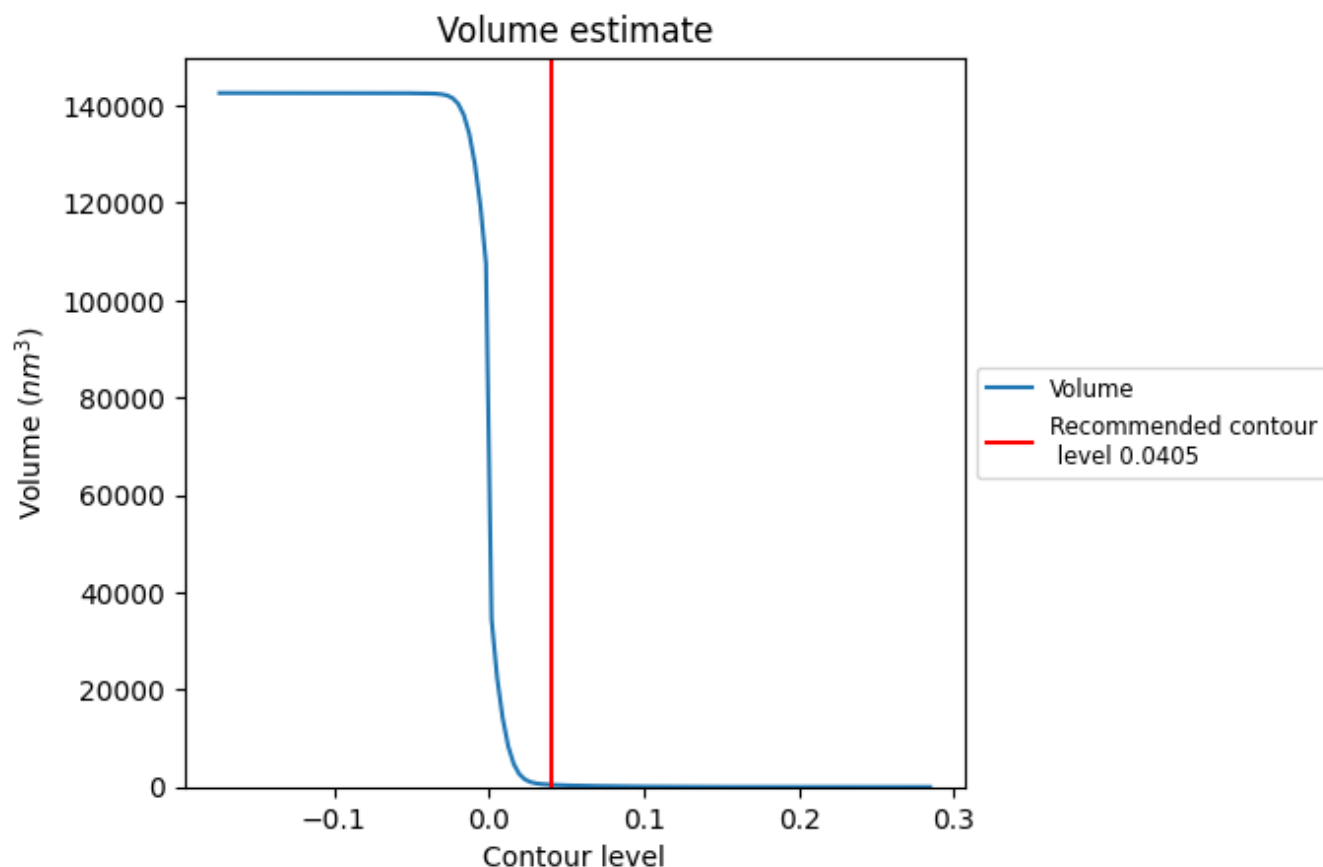
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

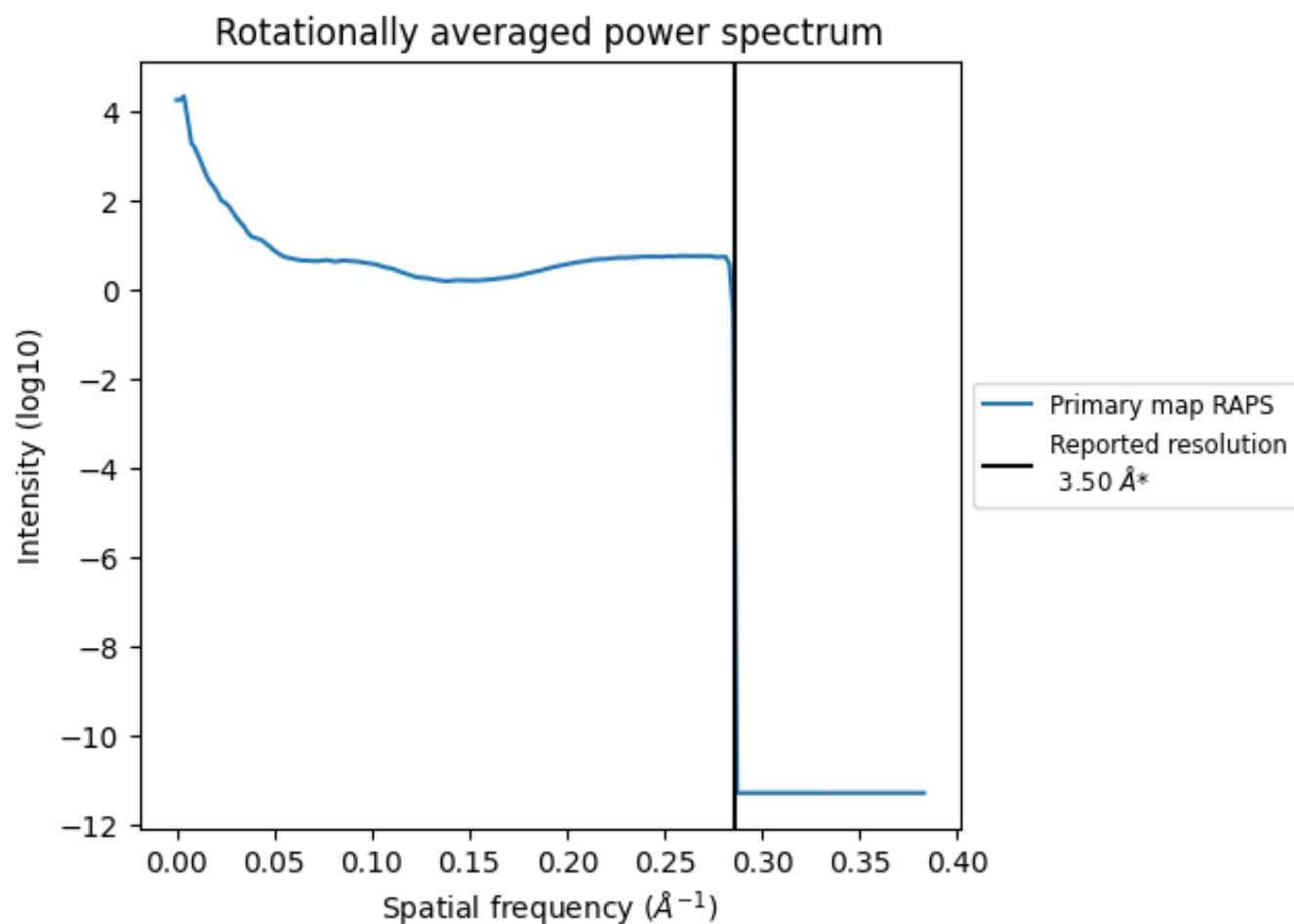
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 444 nm^3 ; this corresponds to an approximate mass of 401 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 0.286 Å⁻¹

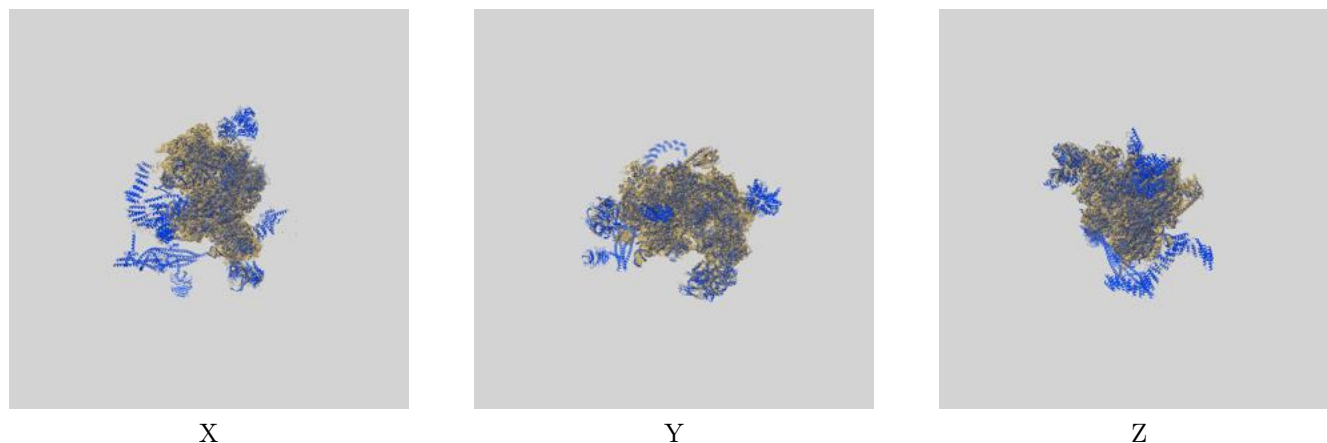
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

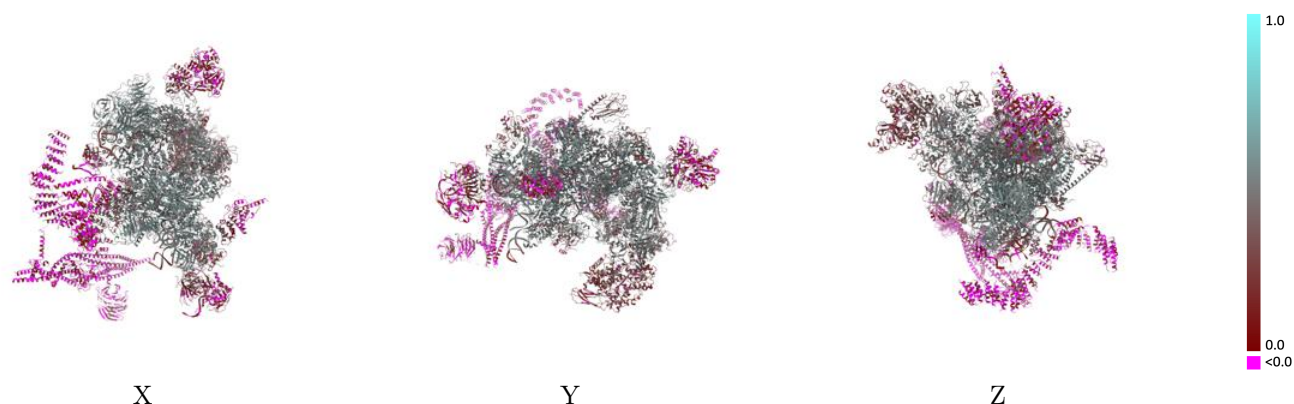
This section contains information regarding the fit between EMDB map EMD-9524 and PDB model 5GM6. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



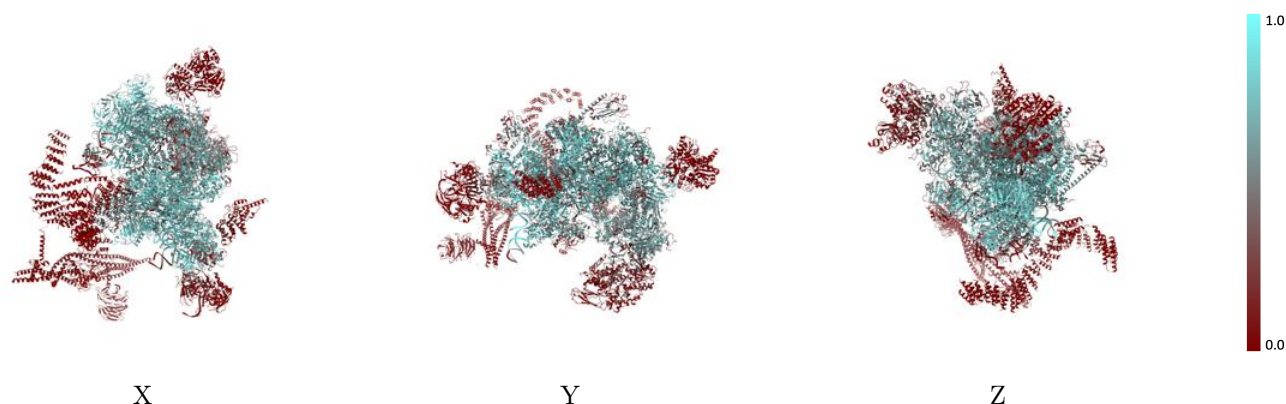
The images above show the 3D surface view of the map at the recommended contour level 0.0405 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



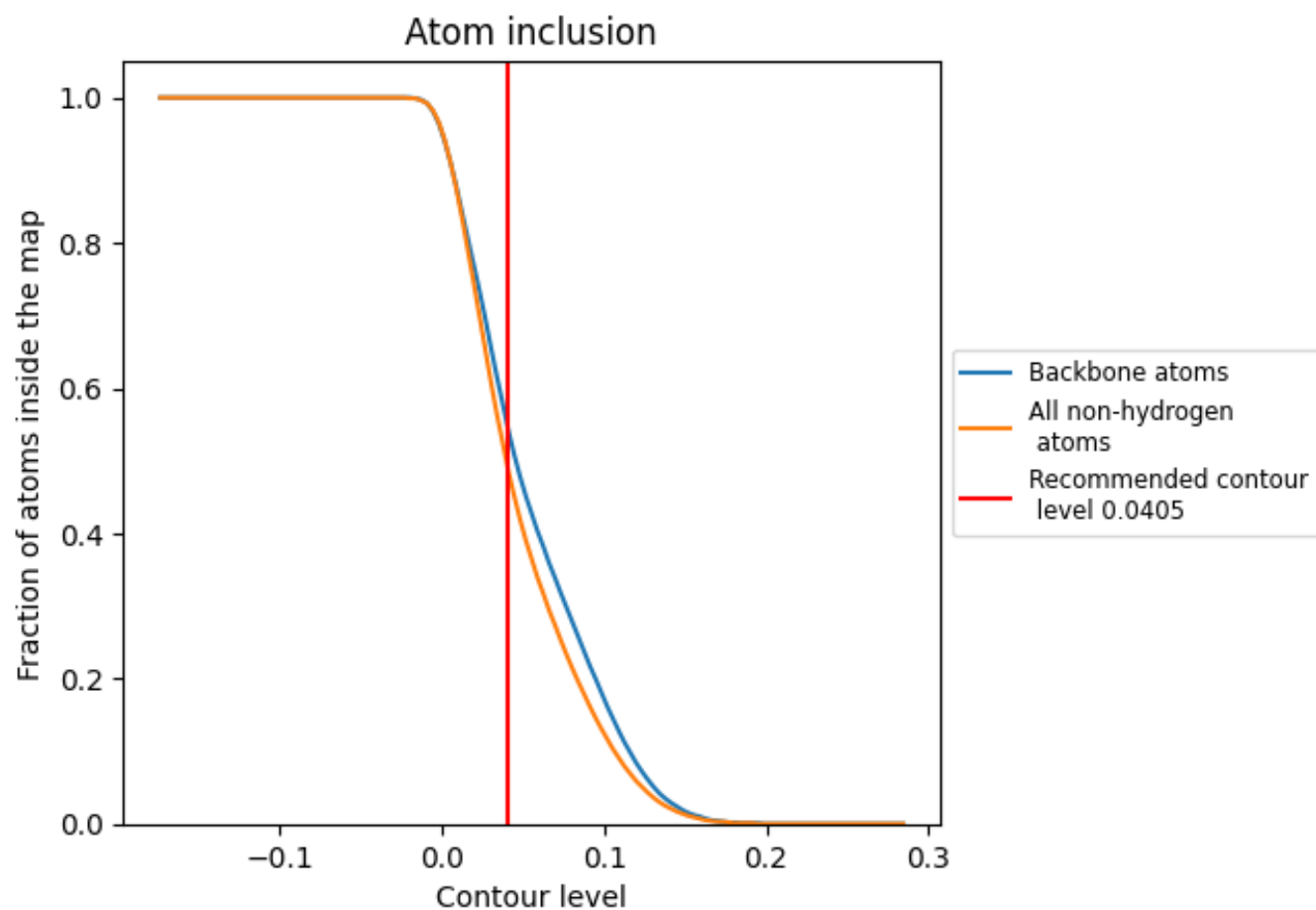
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0405).

9.4 Atom inclusion [i](#)



At the recommended contour level, 55% of all backbone atoms, 49% 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 (0.0405) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4900	 0.3770
A	 0.7180	 0.5060
B	 0.3690	 0.3670
C	 0.6530	 0.4590
D	 0.6510	 0.4110
E	 0.7100	 0.4250
F	 0.7260	 0.4990
G	 0.7370	 0.5160
H	 0.7320	 0.5150
I	 0.7080	 0.5150
J	 0.7820	 0.5380
K	 0.7560	 0.5180
L	 0.5520	 0.3720
M	 0.4310	 0.2930
N	 0.6830	 0.4730
O	 0.7490	 0.5090
P	 0.5780	 0.4550
Q	 0.4370	 0.3720
R	 0.6050	 0.4360
S	 0.3680	 0.4690
T	 0.7270	 0.5000
U	 0.3670	 0.3550
V	 0.7040	 0.4770
W	 0.5710	 0.4320
X	 0.6150	 0.5320
Y	 0.0380	 0.1520
Z	 0.3500	 0.2870
a	 0.4190	 0.4020
b	 0.3770	 0.4070
c	 0.2530	 0.2320
d	 0.2480	 0.2260
e	 0.2340	 0.1550
f	 0.2130	 0.1990
g	 0.0370	 0.0960
h	 0.0310	 0.0760



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Chain	Atom inclusion	Q-score
i	 0.0230	 0.1060
j	 0.0540	 0.1780
k	 0.0870	 0.2060
l	 0.2220	 0.3230
m	 0.0280	 0.1040
n	 0.6810	 0.4770
o	 0.0000	 0.0280
p	 0.0000	 0.0060
q	 0.0000	 0.0160
r	 0.0000	 0.0140
t	 0.0000	 0.0420
v	 0.0000	 0.0180