



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 04:20 PM UTC

PDB ID : 5Z57 / pdb_00005z57
EMDB ID : EMD-6890
Title : Cryo-EM structure of the human activated spliceosome (late Bact) at 6.5 angstrom
Authors : Zhang, X.; Yan, C.; Zhan, X.; Li, L.; Lei, J.; Shi, Y.
Deposited on : 2018-01-17
Resolution : 6.50 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:

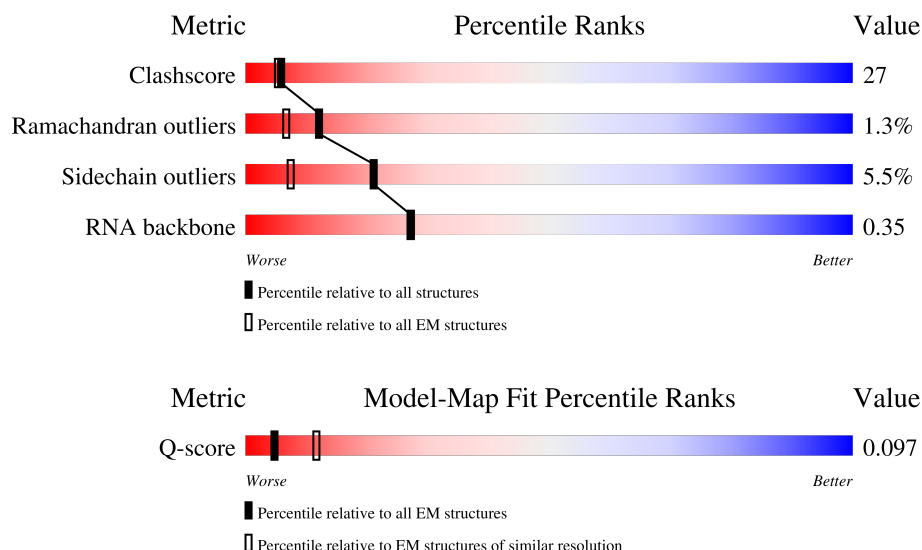
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 6.50 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	556 (6.00 - 7.00)

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	2335	18% 46% 33% 5% 15%
2	B	117	13% 30% 24% 15% 28%
3	C	972	8% 46% 34% 8% 12%

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Mol	Chain	Length	Quality of chain
4	D	2136	
5	E	357	
6	a	126	
6	h	126	
7	b	231	
7	i	231	
8	c	119	
8	j	119	
9	d	118	
9	k	118	
10	f	86	
10	m	86	
11	e	92	
11	l	92	
12	g	76	
12	n	76	
13	F	107	
14	G	274	
15	H	188	
16	o	255	
17	p	225	
18	w	501	
19	u	793	
20	v	464	
21	1	1304	

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Mol	Chain	Length	Quality of chain
22	2	895	
23	3	1217	
24	4	424	
25	5	125	
26	6	110	
27	7	86	
28	J	848	
29	L	802	
30	q	504	
30	r	504	
30	s	504	
30	t	504	
31	K	225	
32	I	855	
33	Q	1485	
34	N	144	
35	O	420	
36	P	229	
37	R	540	
38	S	166	
39	T	514	
40	U	2752	
41	V	908	
42	W	579	
43	X	396	

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Mol	Chain	Length	Quality of chain
44	Y	322	
45	Z	619	
46	x	1041	
47	y	301	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
48	IHP	A	2401	-	-	X	-
50	GTP	C	1500	-	-	X	-

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 113433 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-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1978	Total	C	N	O	S	0	0
			16399	10552	2875	2897	75		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	84	Total	C	N	O	P	0	0
			1768	792	295	597	84		

- Molecule 3 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	860	Total	C	N	O	S	0	0
			6716	4294	1120	1270	32		

- Molecule 4 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	1722	Total	C	N	O		0	0
			8528	5084	1722	1722			

- Molecule 5 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	299	Total	C	N	O	S	0	0
			2338	1470	410	445	13		

- Molecule 6 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	a	81	Total	C	N	O		0	0
			399	237	81	81			

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Mol	Chain	Residues	Atoms				AltConf	Trace
6	h	80	Total	C	N	O	0	0
			393	233	80	80		

- Molecule 7 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	b	82	Total	C	N	O	0	0
			405	241	82	82		
7	i	86	Total	C	N	O	0	0
			422	250	86	86		

- Molecule 8 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	c	82	Total	C	N	O	0	0
			406	242	82	82		
8	j	82	Total	C	N	O	0	0
			406	242	82	82		

- Molecule 9 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	d	97	Total	C	N	O	0	0
			480	286	97	97		
9	k	85	Total	C	N	O	0	0
			422	252	85	85		

- Molecule 10 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	f	74	Total	C	N	O	0	0
			361	213	74	74		
10	m	74	Total	C	N	O	0	0
			361	213	74	74		

- Molecule 11 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	e	79	Total	C	N	O	0	0
			391	233	79	79		
11	l	79	Total	C	N	O	0	0
			391	233	79	79		

- Molecule 12 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	g	74	Total	C	N	O	0	0
			363	215	74	74		
12	n	68	Total	C	N	O	0	0
			334	198	68	68		

- Molecule 13 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	93	Total	C	N	O	P	0	0
			1988	889	363	643	93		

- Molecule 14 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	77	Total	C	N	O	P	0	0
			1545	689	240	539	77		

- Molecule 15 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	136	Total	C	N	O	P	0	0
			2886	1289	499	962	136		

- Molecule 16 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	o	162	Total	C	N	O	0	0
			804	480	162	162		

- Molecule 17 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	p	165	Total	C	N	O	0	0
			813	483	165	165		

- Molecule 18 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	w	438	Total	C	N	O	S	0	0
			2373	1450	461	459	3		

- Molecule 19 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	u	104	Total	C	N	O	0	0
			520	312	104	104		

- Molecule 20 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	v	165	Total	C	N	O	S	0	0
			936	565	191	178	2		

- Molecule 21 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	1	1038	Total	C	N	O	S	0	0
			7702	4900	1347	1415	40		

- Molecule 22 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	2	183	Total	C	N	O	S	0	0
			1252	809	213	226	4		

- Molecule 23 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3	1177	Total	C	N	O	S	0	0
			9195	5834	1561	1755	45		

- Molecule 24 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	4	78	Total	C	N	O	0	0
			527	345	83	99		

- Molecule 25 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	5	108	Total	C	N	O	S	0	0
			807	512	142	150	3		

- Molecule 26 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	6	89	Total	C	N	O	S	0	0
			670	410	119	128	13		

- Molecule 27 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	7	66	Total	C	N	O	S	0	0
			540	343	94	98	5		

- Molecule 28 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	J	522	Total	C	N	O	S	0	0
			3463	2156	653	648	6		

- Molecule 29 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L	342	Total	C	N	O	S	0	0
			2260	1430	406	420	4		

- Molecule 30 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	q	132	Total	C	N	O		0	0
			659	395	132	132			
30	r	131	Total	C	N	O		0	0
			654	392	131	131			
30	s	67	Total	C	N	O		0	0
			335	201	67	67			
30	t	67	Total	C	N	O		0	0
			335	201	67	67			

- Molecule 31 is a protein called Pre-mRNA-splicing factor SPF27.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	K	152	Total	C	N	O	S	0	0
			979	611	177	189	2		

- Molecule 32 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	I	564	Total	C	N	O	0	0
			2778	1650	564	564		

- Molecule 33 is a protein called Intron-binding protein aquarius.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	Q	1317	Total	C	N	O	0	0
			6528	3894	1317	1317		

- Molecule 34 is a protein called Protein BUD31 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	N	143	Total	C	N	O	S	0	0
			1184	746	217	209	12		

- Molecule 35 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	O	285	Total	C	N	O	S	0	0
			2273	1428	401	424	20		

- Molecule 36 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	P	96	Total	C	N	O	S	0	0
			829	508	162	157	2		

- Molecule 37 is a protein called Skip.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	R	288	Total	C	N	O	S	0	0
			2188	1375	392	409	12		

- Molecule 38 is a protein called Peptidyl-prolyl cis-trans isomerase-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	S	159	Total	C	N	O	S	0	0
			1236	787	215	227	7		

- Molecule 39 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	T	313	Total	C	N	O	S	0	0
			2457	1552	447	450	8		

- Molecule 40 is a protein called Serine/arginine repetitive matrix protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	U	26	Total	C	N	O	S	0	0
			193	120	36	36	1		

- Molecule 41 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	V	452	Total	C	N	O		0	0
			2243	1339	452	452			

- Molecule 42 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	W	483	Total	C	N	O		0	0
			2384	1418	483	483			

- Molecule 43 is a protein called Smad nuclear-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	X	158	Total	C	N	O	S	0	0
			1012	645	172	194	1		

- Molecule 44 is a protein called RNA-binding motif protein, X-linked 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Y	105	Total	C	N	O	S	0	0
			743	470	127	144	2		

- Molecule 45 is a protein called BUD13 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Z	113	Total	C	N	O		0	0
			755	474	147	134			

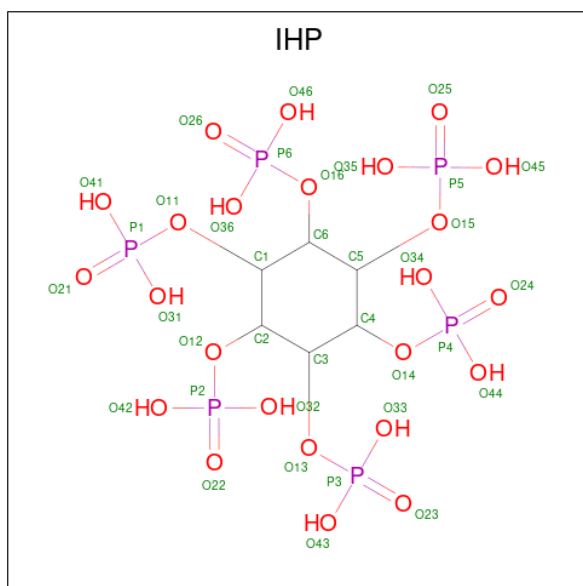
- Molecule 46 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	x	583	Total	C	N	O	0	0
			2882	1715	583	584		

- Molecule 47 is a protein called Peptidyl-prolyl cis-trans isomerase E.

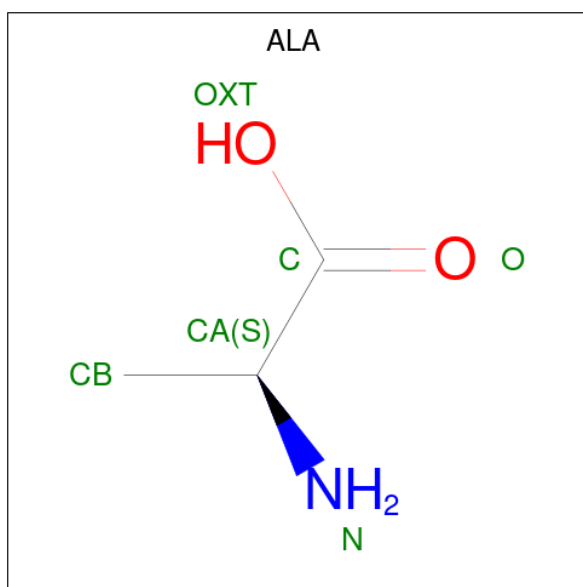
Mol	Chain	Residues	Atoms				AltConf	Trace
47	y	232	Total	C	N	O	0	0
			1133	669	232	232		

- Molecule 48 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: $C_6H_{18}O_{24}P_6$).



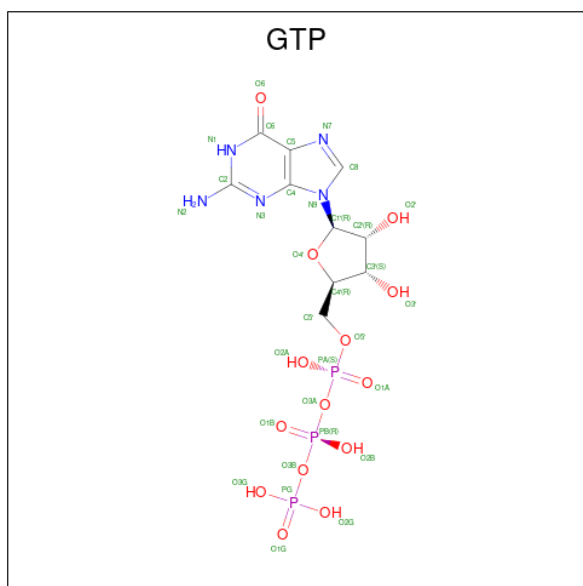
Mol	Chain	Residues	Atoms				AltConf
48	A	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 49 is ALANINE (CCD ID: ALA) (formula: $C_3H_7NO_2$).



Mol	Chain	Residues	Atoms				AltConf
49	A	1	Total	C	N	O	0
			5	3	1	1	

- Molecule 50 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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

- Molecule 51 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
51	C	1	Total 1	Mg 1	0
51	F	5	Total 5	Mg 5	0

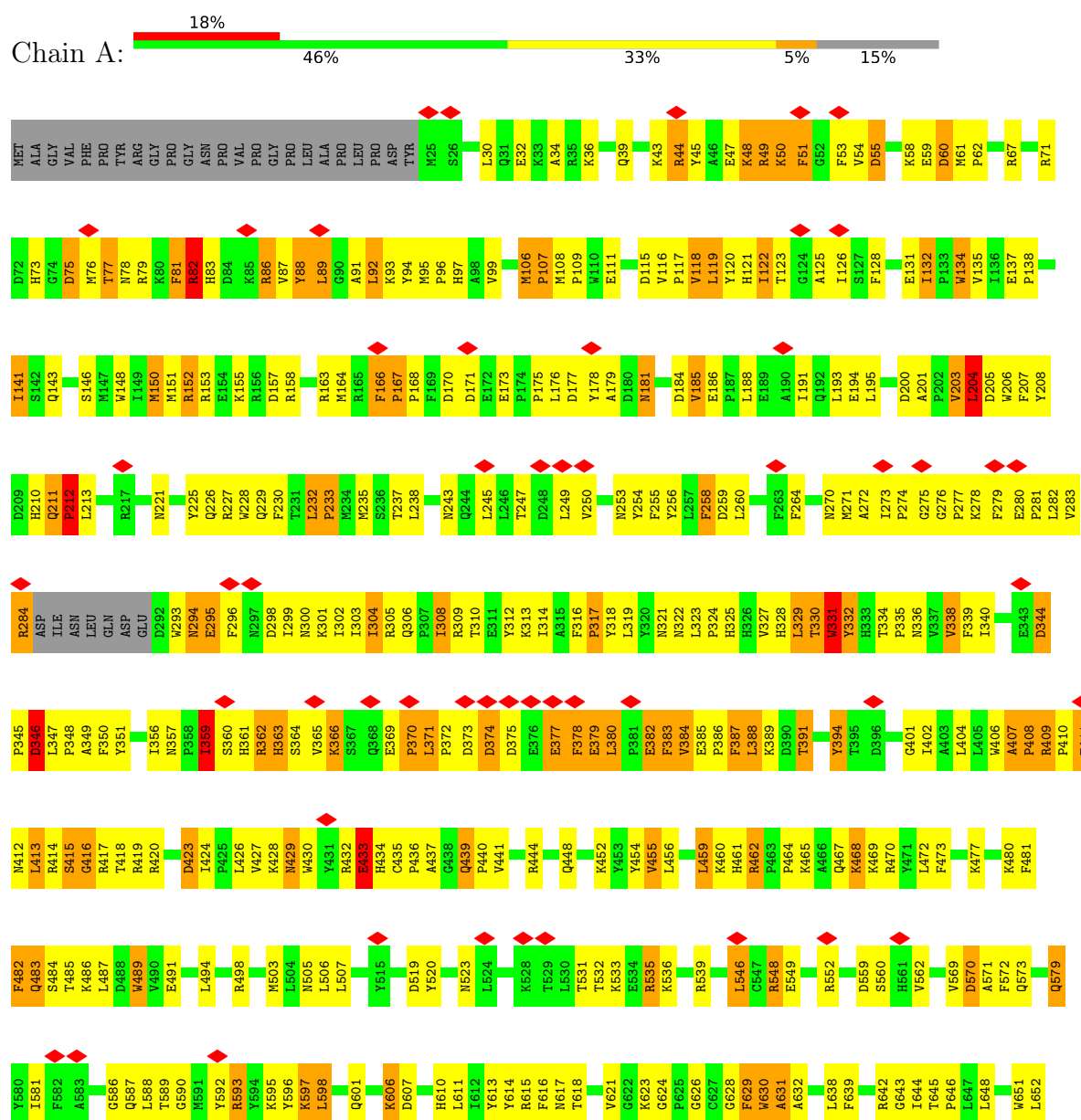
- Molecule 52 is ZINC ION (CCD ID: ZN) (formula: Zn).

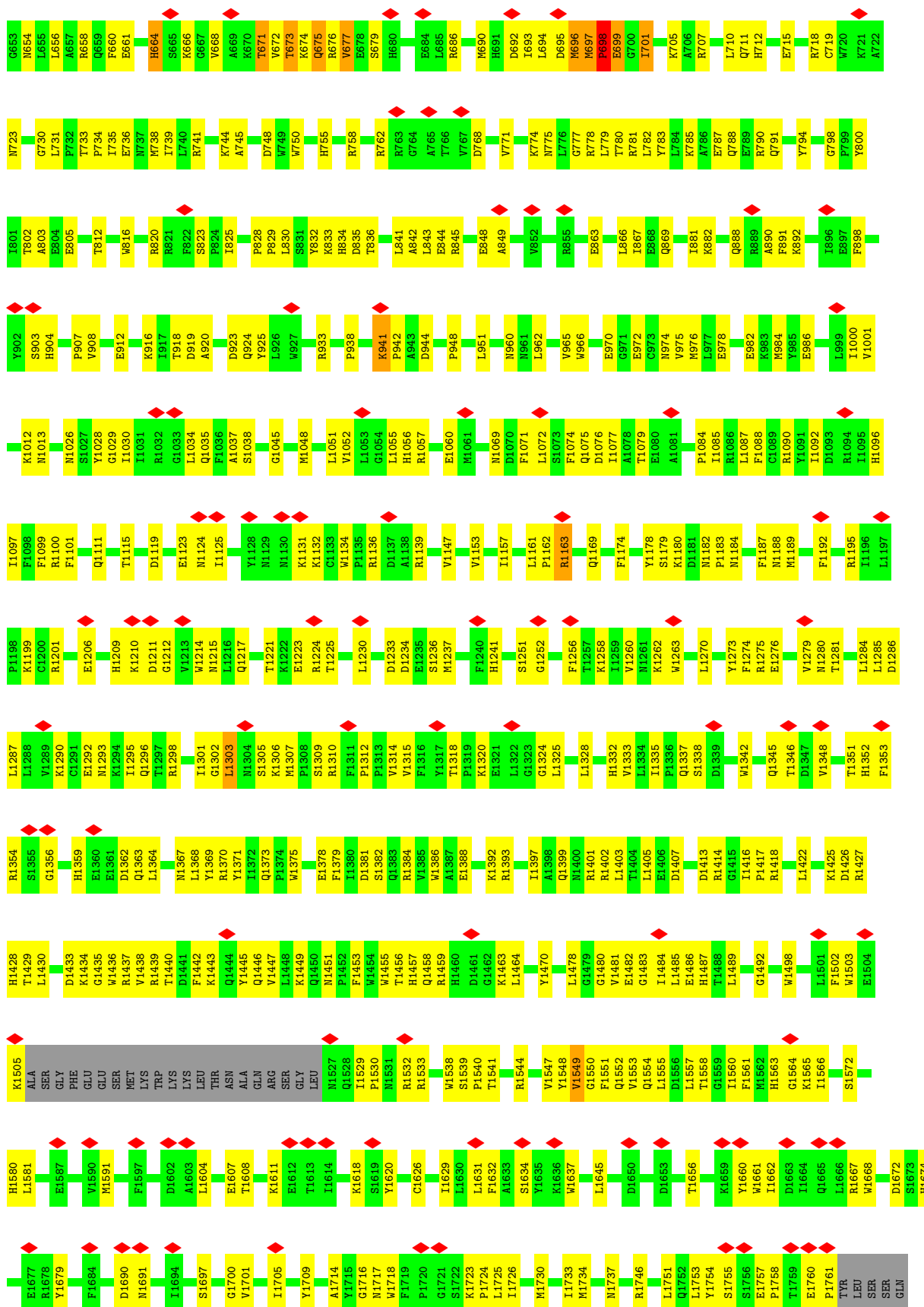
Mol	Chain	Residues	Atoms		AltConf
52	v	1	Total 1	Zn 1	0
52	6	3	Total 3	Zn 3	0
52	N	3	Total 3	Zn 3	0
52	O	3	Total 3	Zn 3	0

3 Residue-property plots [i](#)

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.

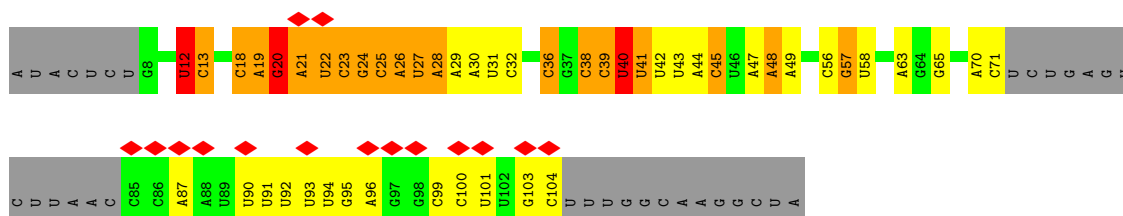
• Molecule 1: Pre-mRNA-processing-splicing factor 8



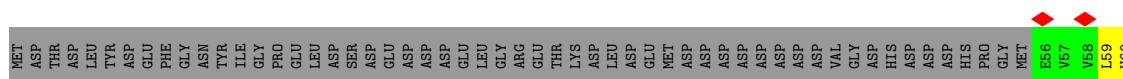


E2307	N2247	Q2187	Y2127	F2067
V2308	P2248	L2188	L2128	S2068
H2309	K2249	S2189	Y2129	S2069
R2310	G2250	P2190	G2130	K2070
P2311	Y2251	Q2191	V2131	T2071
S2312	L2252	D2192	S2132	E2072
H2313	P2253	V2193	P2133	W2073
F2314	S2254	T2194	P2134	R2074
L2315	H2255	T2195	D2135	V2075
M2316	Y2256	H2196	N2136	R2076
F2317	E2257	A2197	P2137	A2077
A2318	R2258	K2198	Q2138	I2078
L2319	V2259	T2199	V2139	S2079
L2320	Q2260	H2200	K2140	A2080
Q2321	M2261	A2201	E2141	A2081
E2322	L2262	D2202	I2142	N2082
G2323	L2263	N2203	R2143	L2083
E2324	S2264	P2204	C2144	H2084
V2325	D2265	S2205	I2145	L2085
Y2326	R2266	W2206	V2146	R2086
S2327	F2267	D2207	M2147	T2087
A2328	L2268	G2208	V2148	N2088
D2329	G2269	E2209	P2149	N2089
R2330	F2270	K2210	Q2150	T2090
E2331	F2271	T2211	W2151	Y2091
D2332	M2272	I2212	G2152	V2092
L2333	P2273	L2213	T2153	S2093
Y2334	V2274	L2214	H2154	S2094
A2335	A2275	T2215	Q2155	D2095
	Q2276	C2216	T2156	D2096
	S2277	S2217	V2157	T2097
	S2278	F2218	H2158	K2098
	W2279	T2219	L2159	E2099
	N2280	P2220	P2160	T2100
	Y2281	G2221	G2161	G2101
	N2282	S2222	Q2162	V2102
	F2283	C2223	L2163	T2103
	M2284	T2224	P2164	V2104
	G2285	L2225	Q2165	L2105
	V2286	T2226	H2166	L2106
	R2287	A2227	E2167	P2107
	H2288	Y2228	Y2168	K2108
	D2289	K2229	L2169	N2109
	P2290	L2230	K2170	W2110
	N2291	T2231	E2171	L2111
	M2292	P2232	M2172	K2112
	K2293	S2233	E2173	K2113
	Y2294	G2234	P2174	F2114
	E2295	Y2235	L2175	L2115
	L2296	F2236	G2176	C2116
	Q2297	W2237	W2177	T2117
	L2298	G2238	L2178	S2118
	A2299	K2239	H2179	D2119
	N2300	Q2240	T2180	L2120
	P2301	N2241	Q2181	A2121
	K2302	T2242	P2182	R2122
	E2303	D2243	N2183	Q2123
	F2304	K2244	E2184	T2124
	Y2305	G2245	S2185	A2125
	H2306	W2246	P2186	Q2126

Chain B: 13% 30% 24% 15% 28%

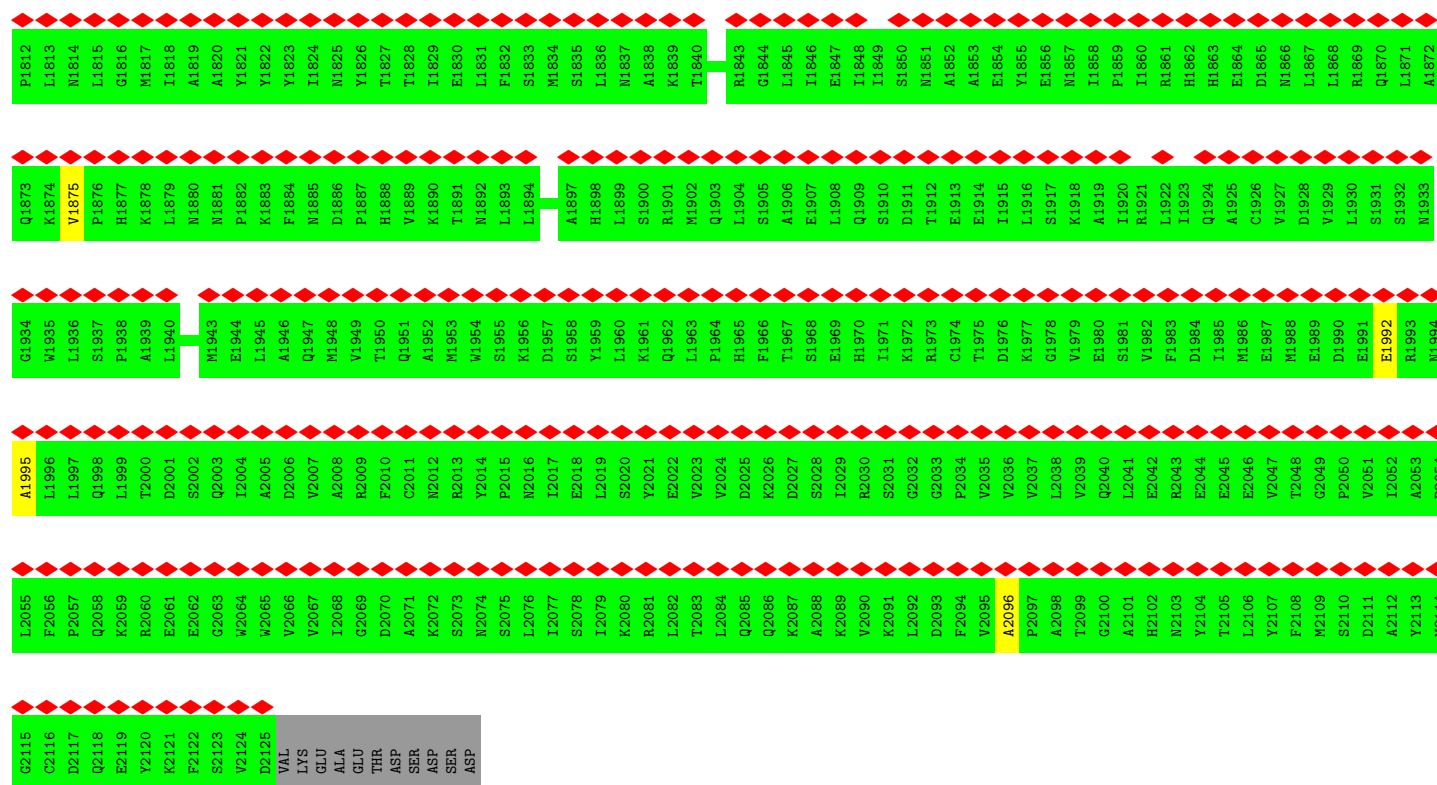


Chain C: 8% 46% 34% 8% 12%

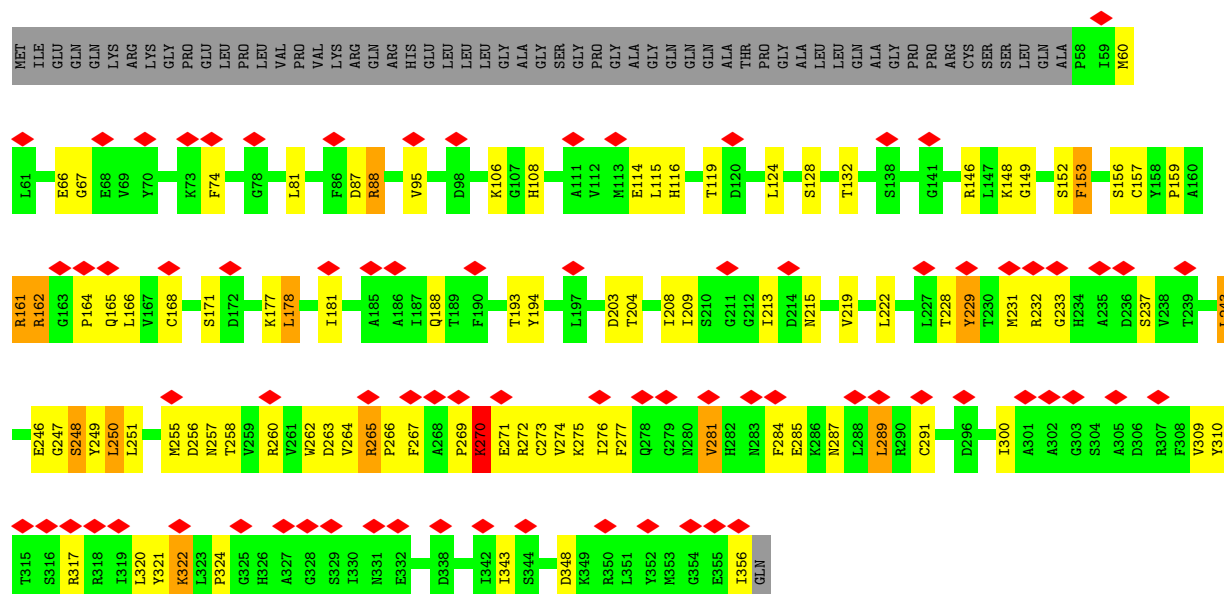




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V1632	E1633	Q1634	L1635	F1636	S1637	S1638	G1639	A1640	I1641	Q1642	V1643	V1644	V1645	A1646	S1647	R1648	S1649	L1650	C1651	M1652	G1653	M1654	N1655	V1656	A1657	A1658	H1659	L1660	V1661	I1662	I1663	M1664	D1665	T1666	Q1667	Y1668	Y1669	N1670	G1671	K1672	I1673	H1674	A1675	V1676	V1677	D1678	Y1679	T1681	Y1682	D1683	V1684	L1685	Q1686	M1687	V1688	G1689	H1690	A1691		
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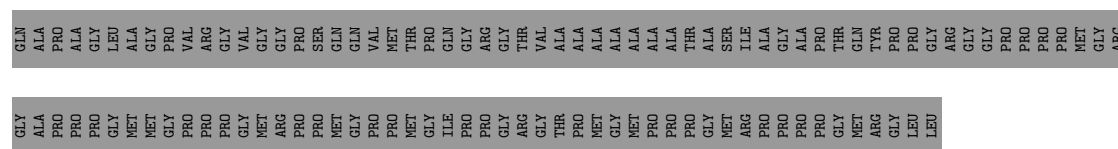


- Molecule 5: U5 small nuclear ribonucleoprotein 40 kDa protein

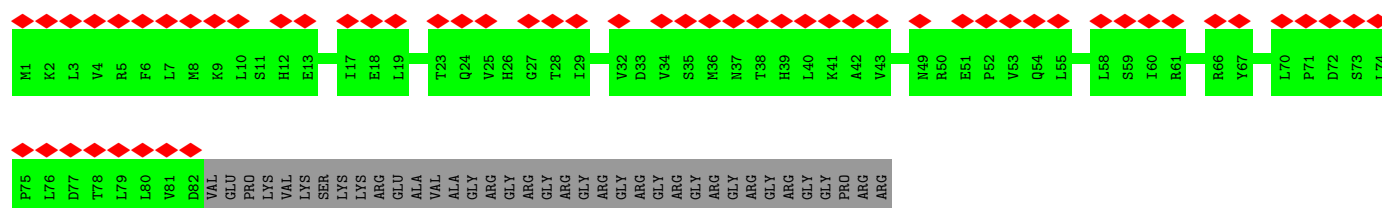


- Molecule 6: Small nuclear ribonucleoprotein Sm D3





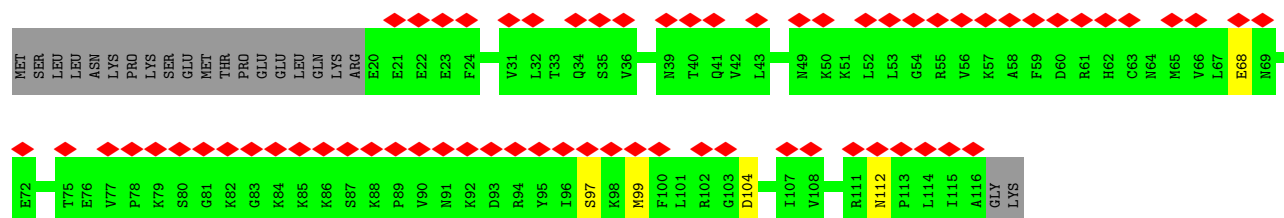
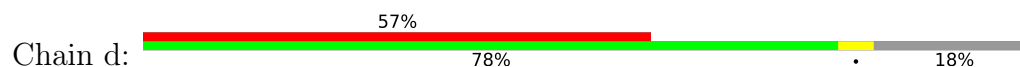
• Molecule 8: Small nuclear ribonucleoprotein Sm D1



• Molecule 8: Small nuclear ribonucleoprotein Sm D1



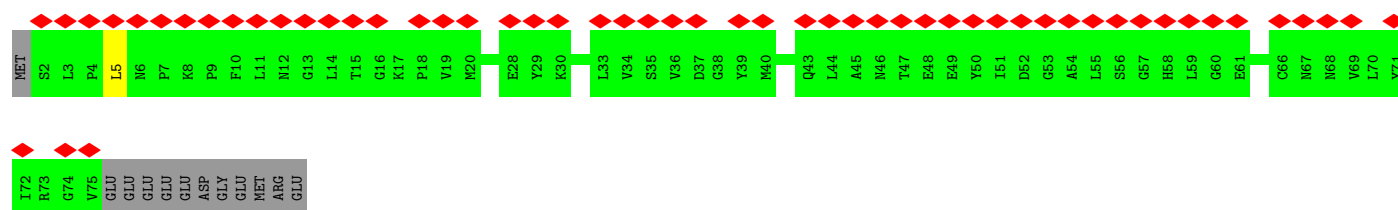
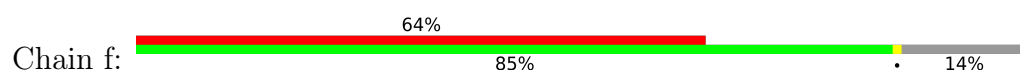
• Molecule 9: Small nuclear ribonucleoprotein Sm D2



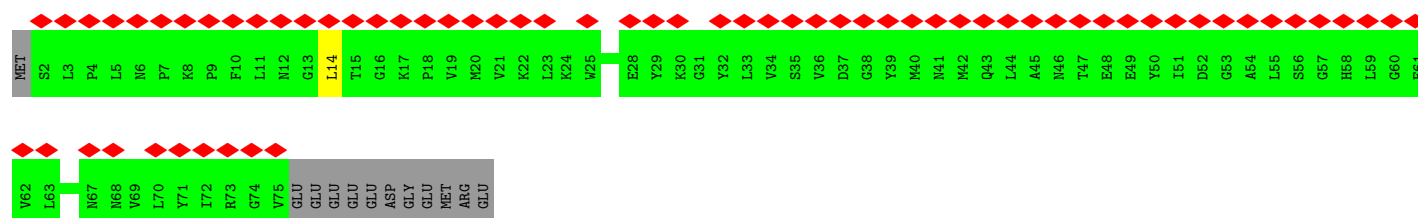
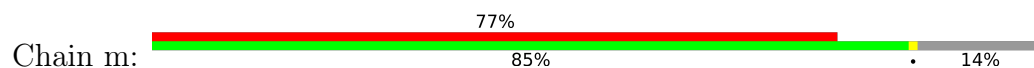
• Molecule 9: Small nuclear ribonucleoprotein Sm D2



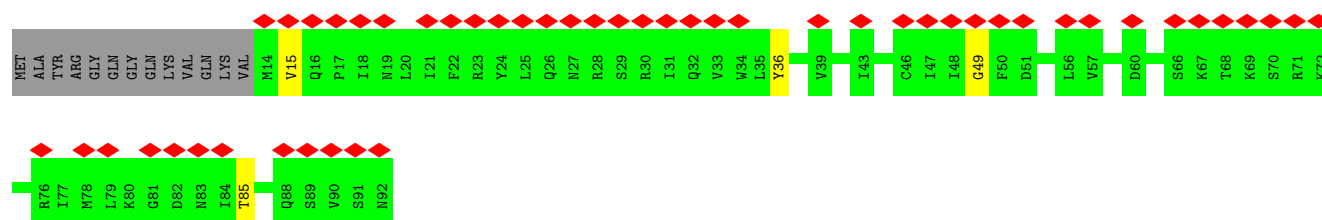
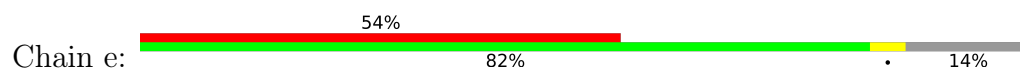
• Molecule 10: Small nuclear ribonucleoprotein F



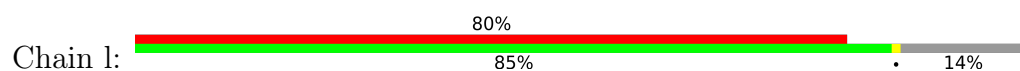
• Molecule 10: Small nuclear ribonucleoprotein F



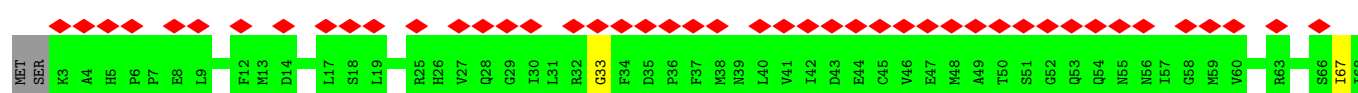
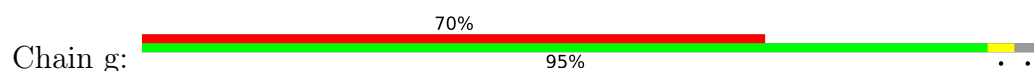
• Molecule 11: Small nuclear ribonucleoprotein E

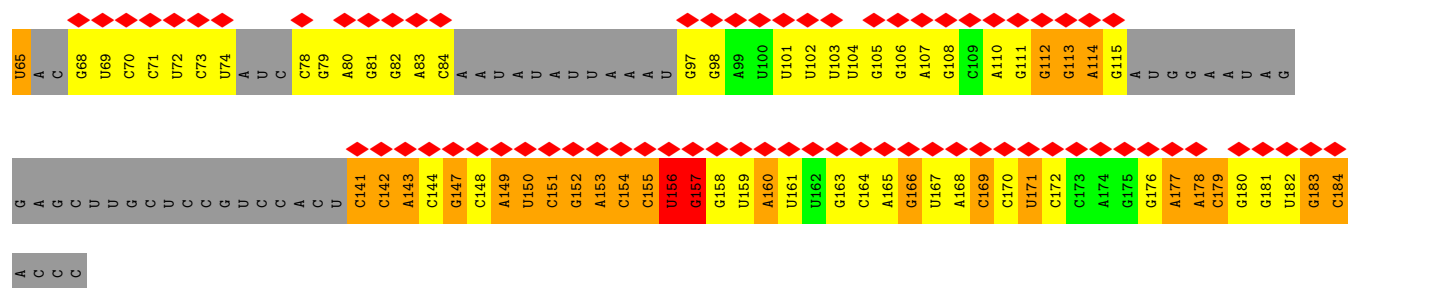


• Molecule 11: Small nuclear ribonucleoprotein E

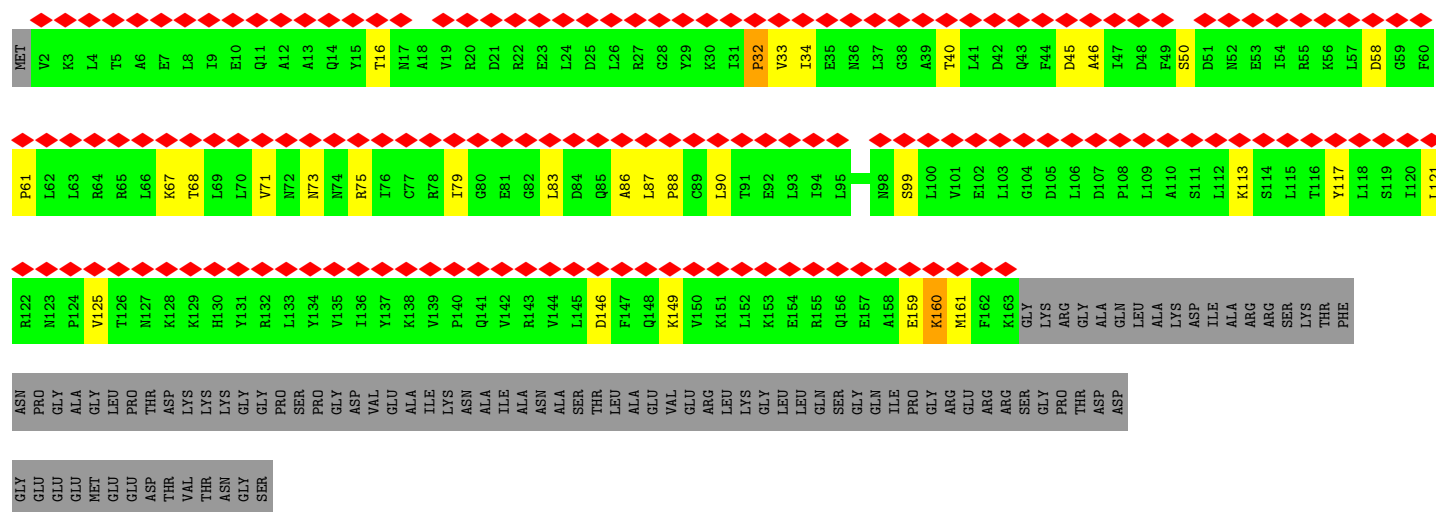


• Molecule 12: Small nuclear ribonucleoprotein G

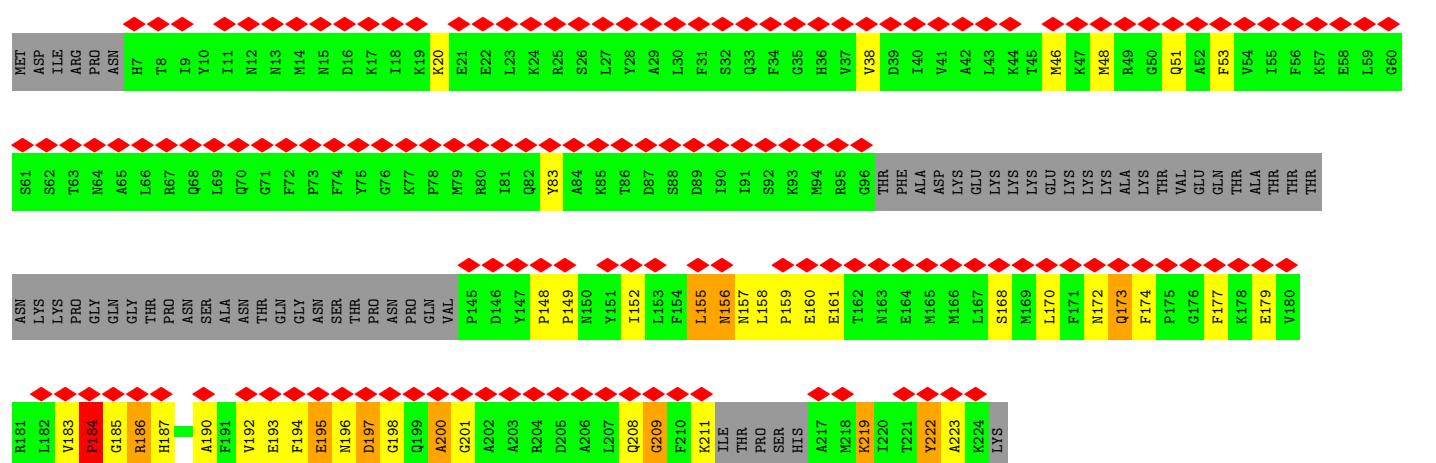




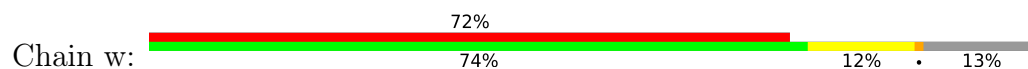
• Molecule 16: U2 small nuclear ribonucleoprotein A'

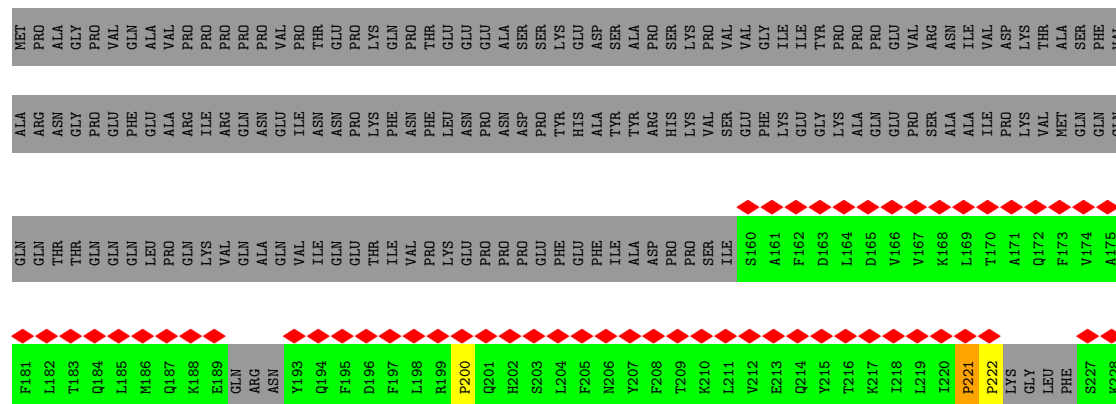


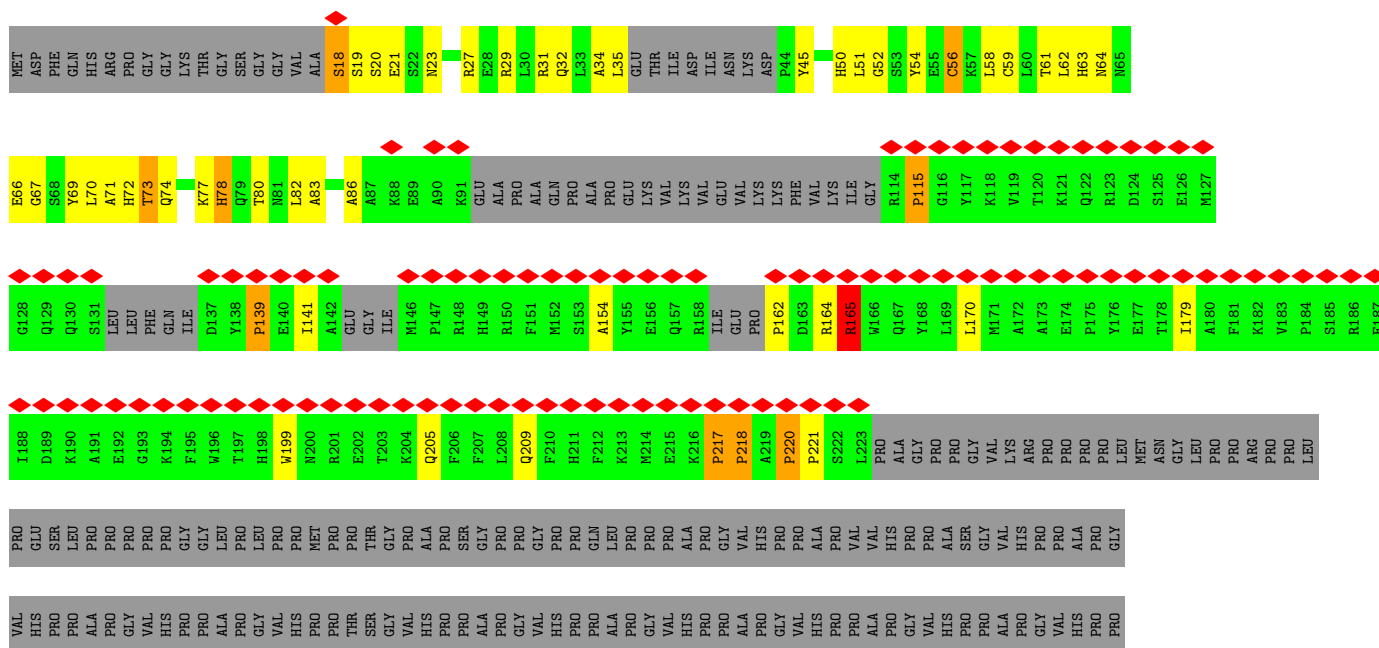
• Molecule 17: U2 small nuclear ribonucleoprotein B''



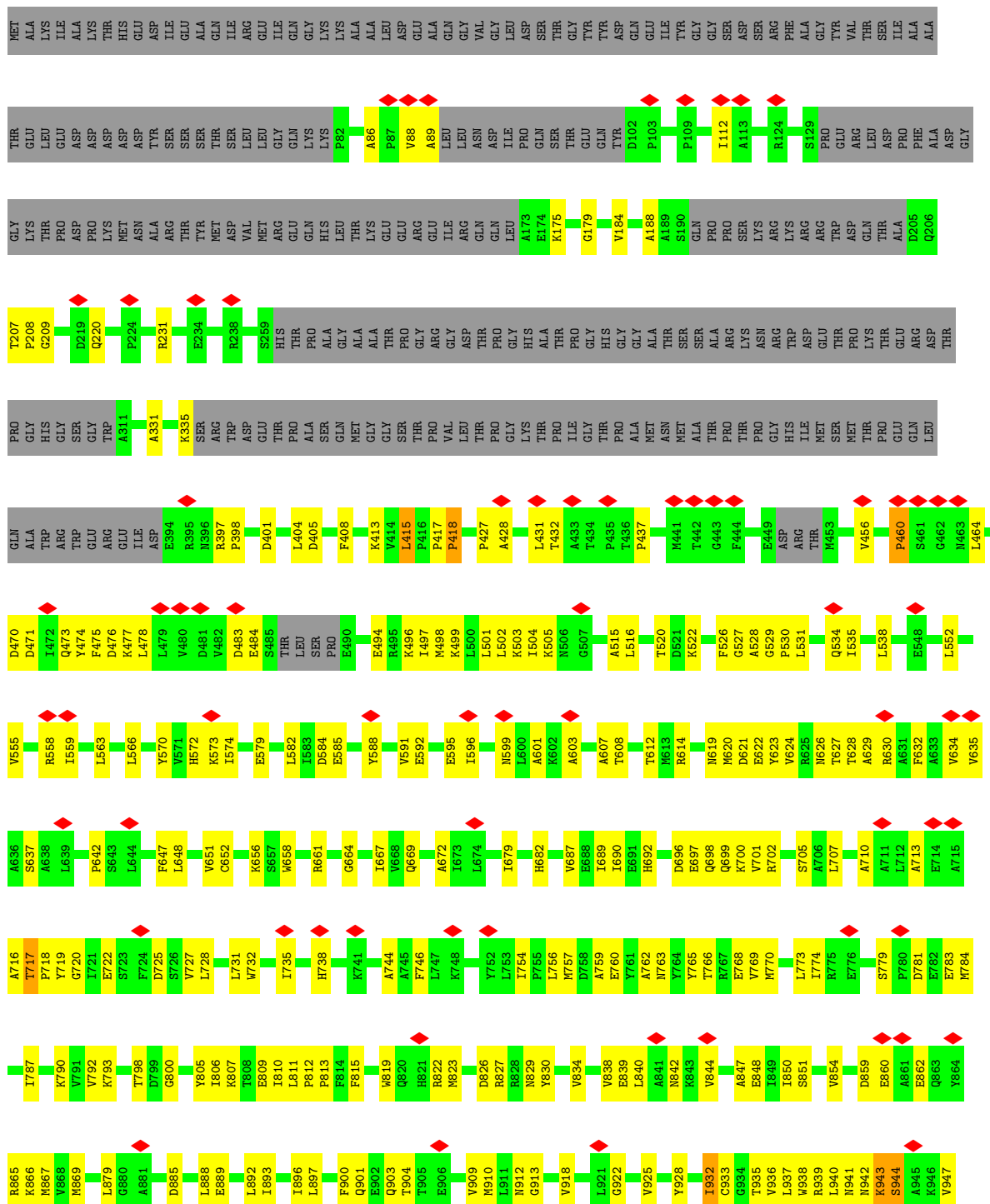
• Molecule 18: Splicing factor 3A subunit 3

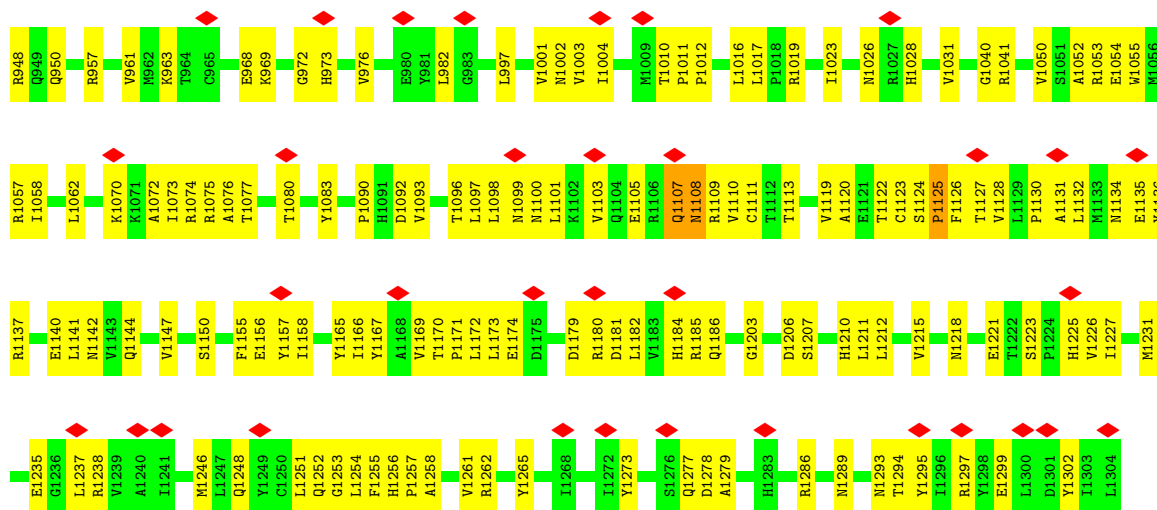




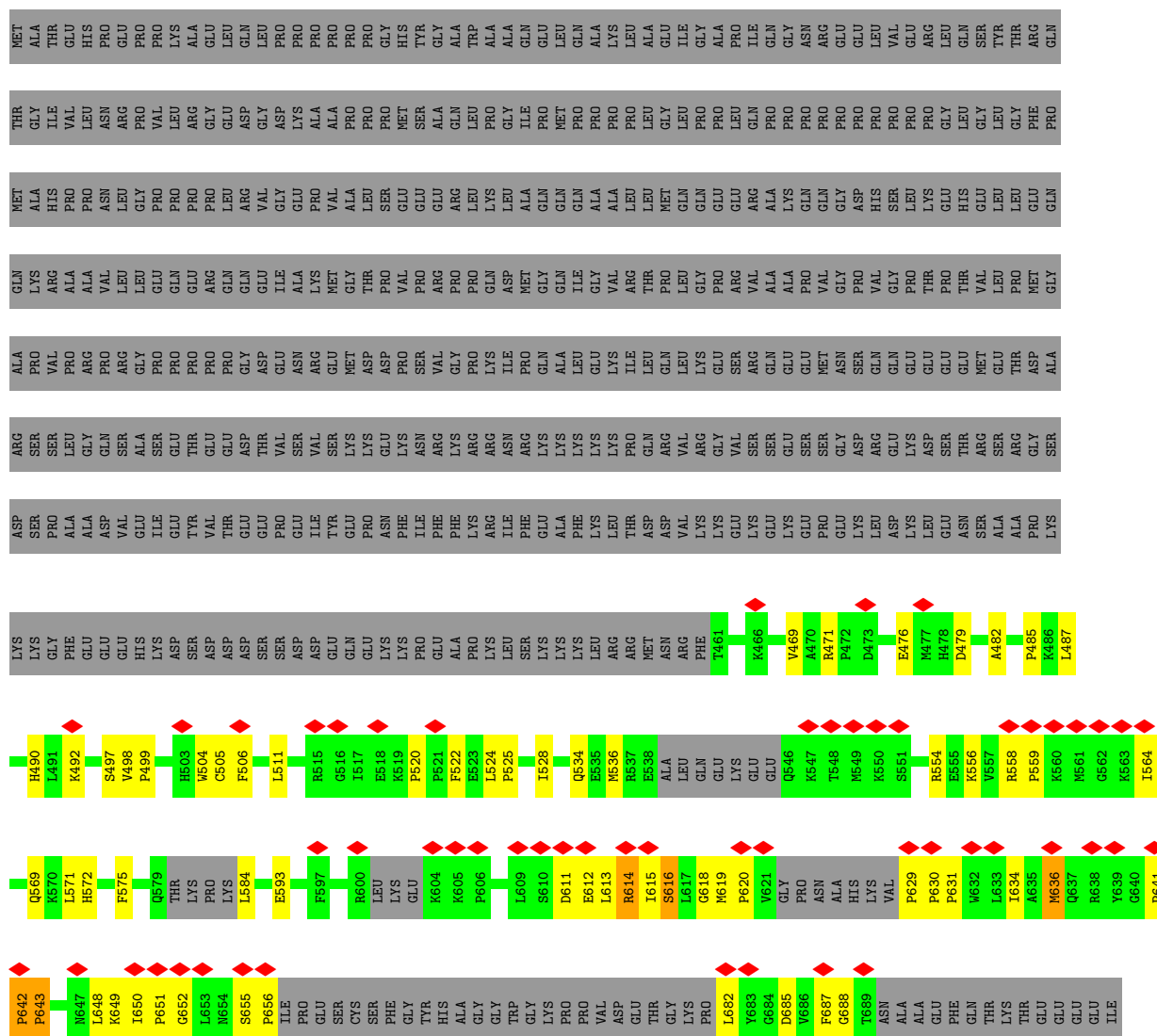


- Molecule 21: Splicing factor 3B subunit 1



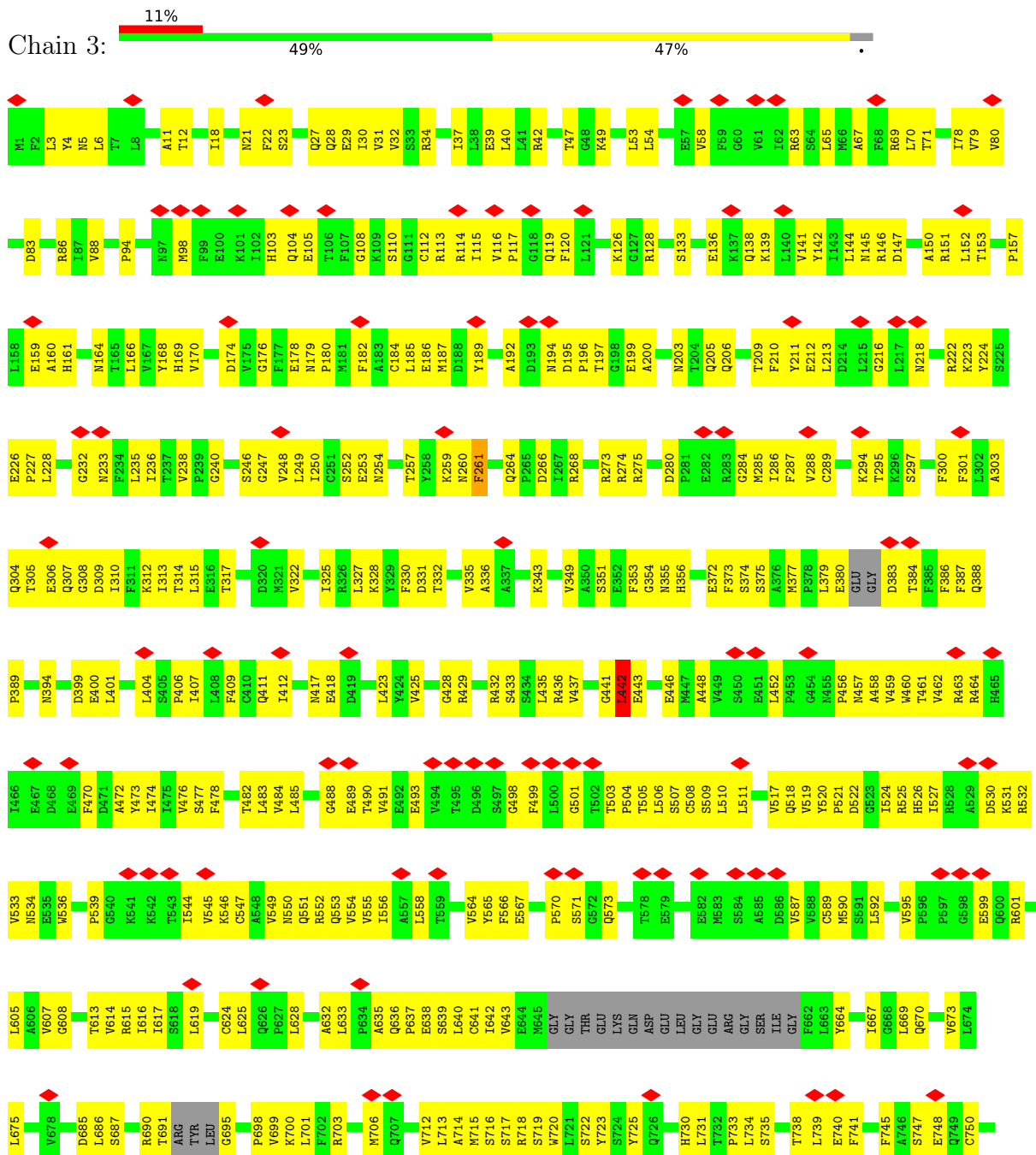


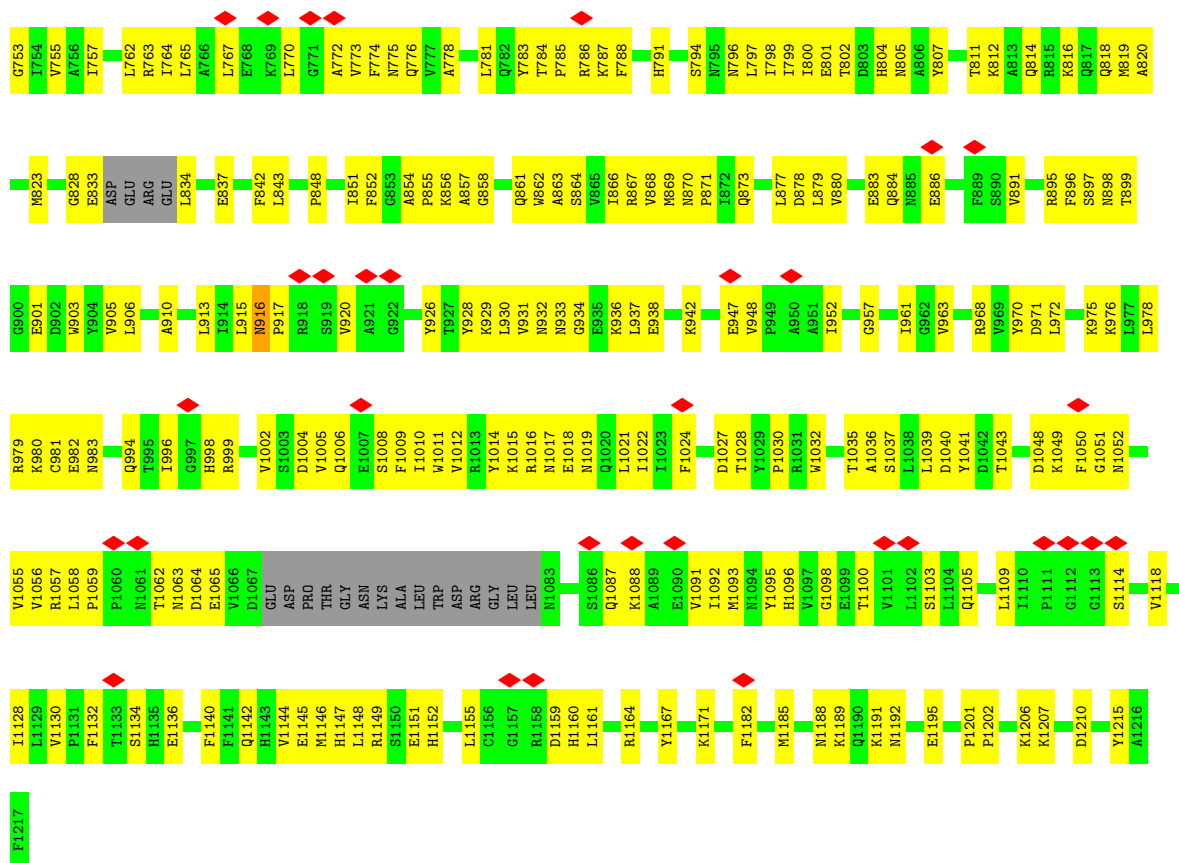
• Molecule 22: Splicing factor 3B subunit 2



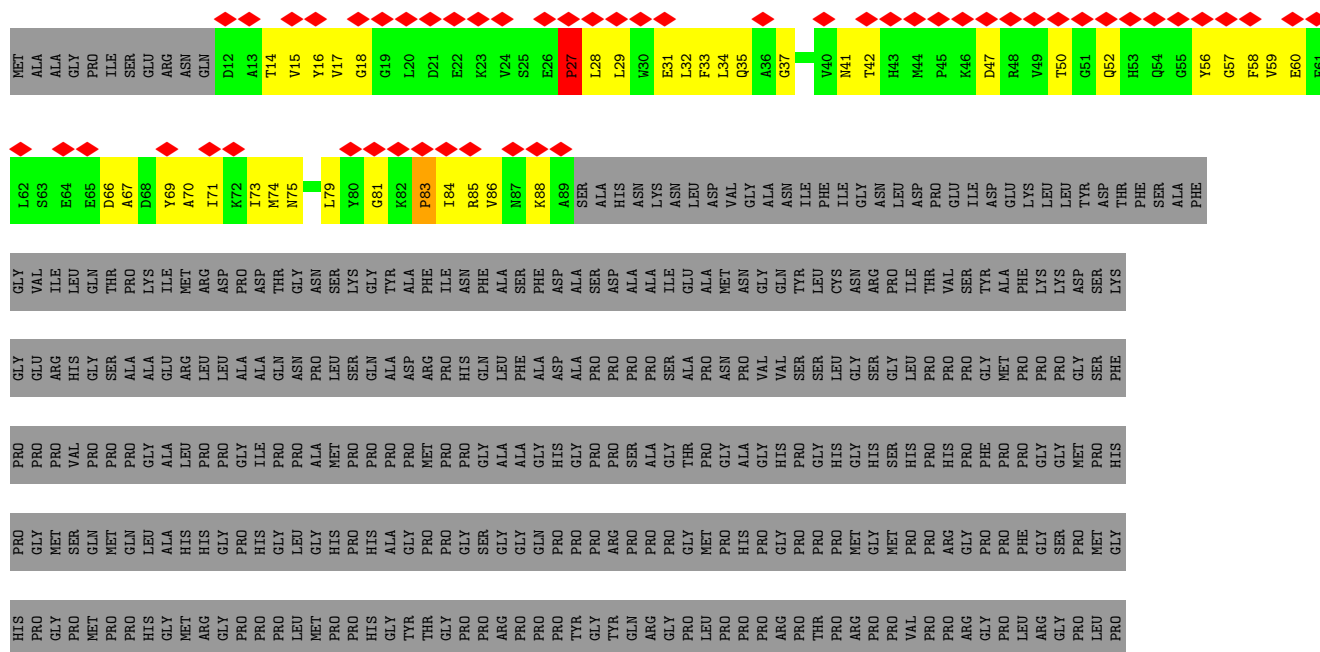
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- Molecule 23: Splicing factor 3B subunit 3





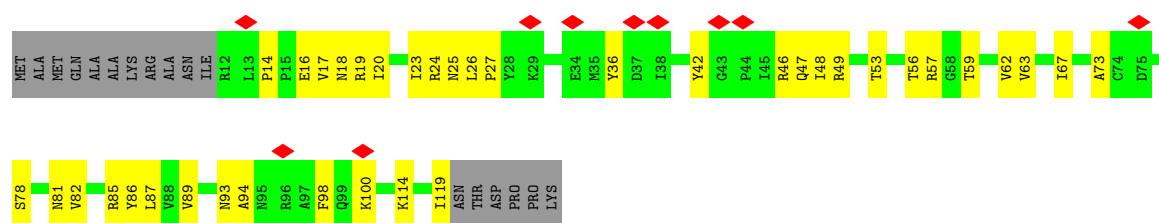
• Molecule 24: Splicing factor 3B subunit 4



GLN

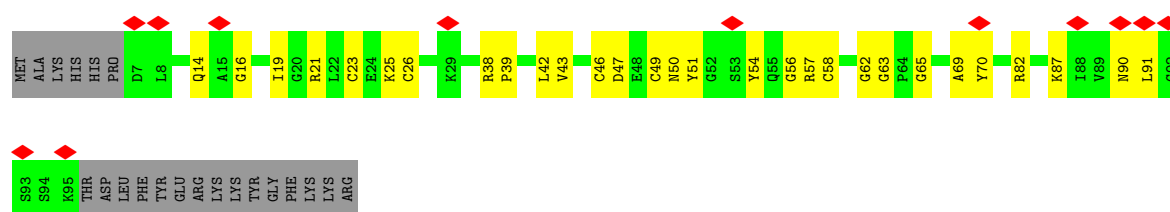
- Molecule 25: Splicing factor 3B subunit 6

Chain 5: 8% 56% 30% 14%



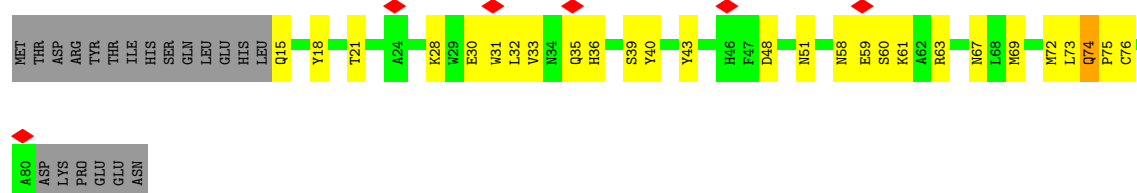
- Molecule 26: PHD finger-like domain-containing protein 5A

Chain 6: 11% 55% 26% 19%



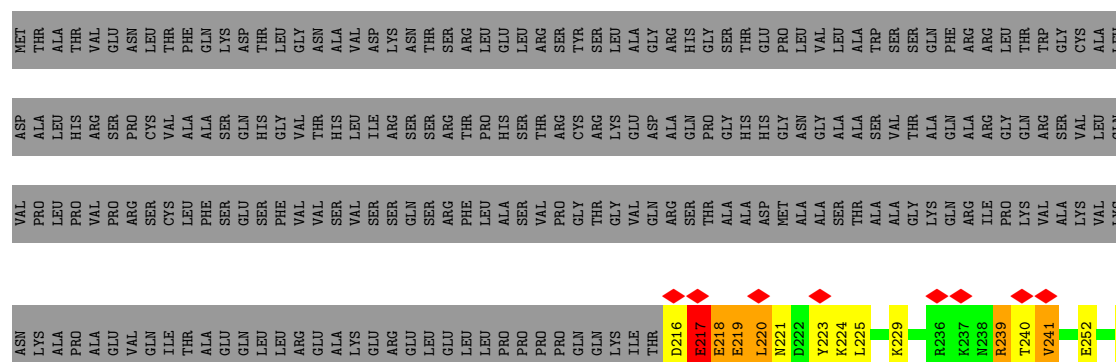
- Molecule 27: Splicing factor 3B subunit 5

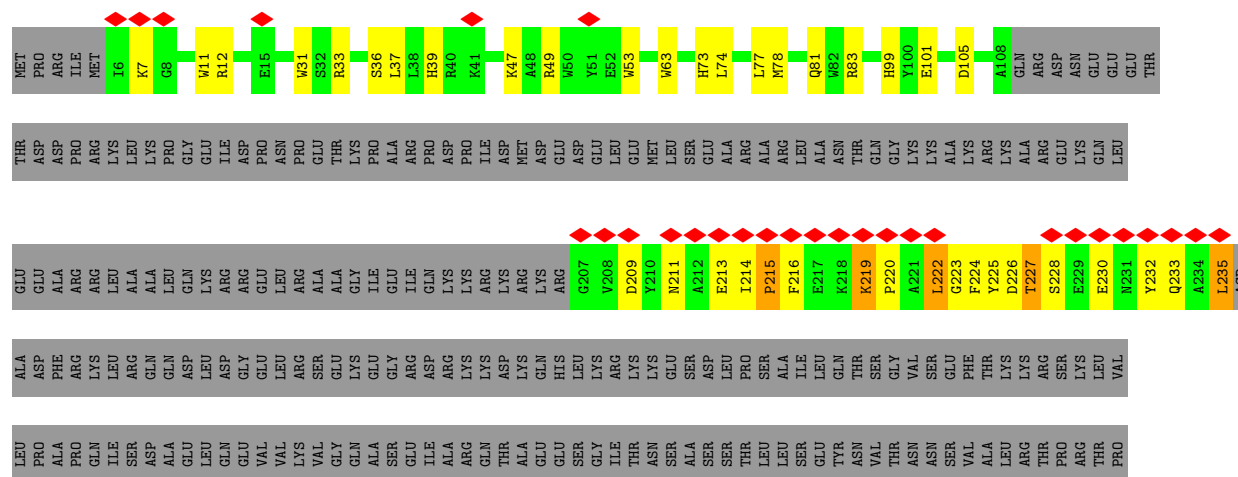
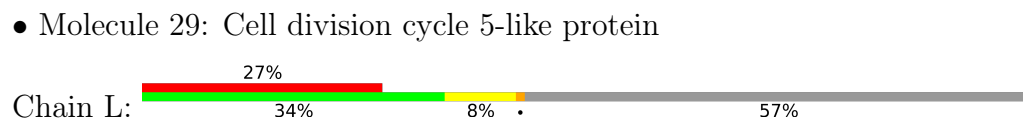
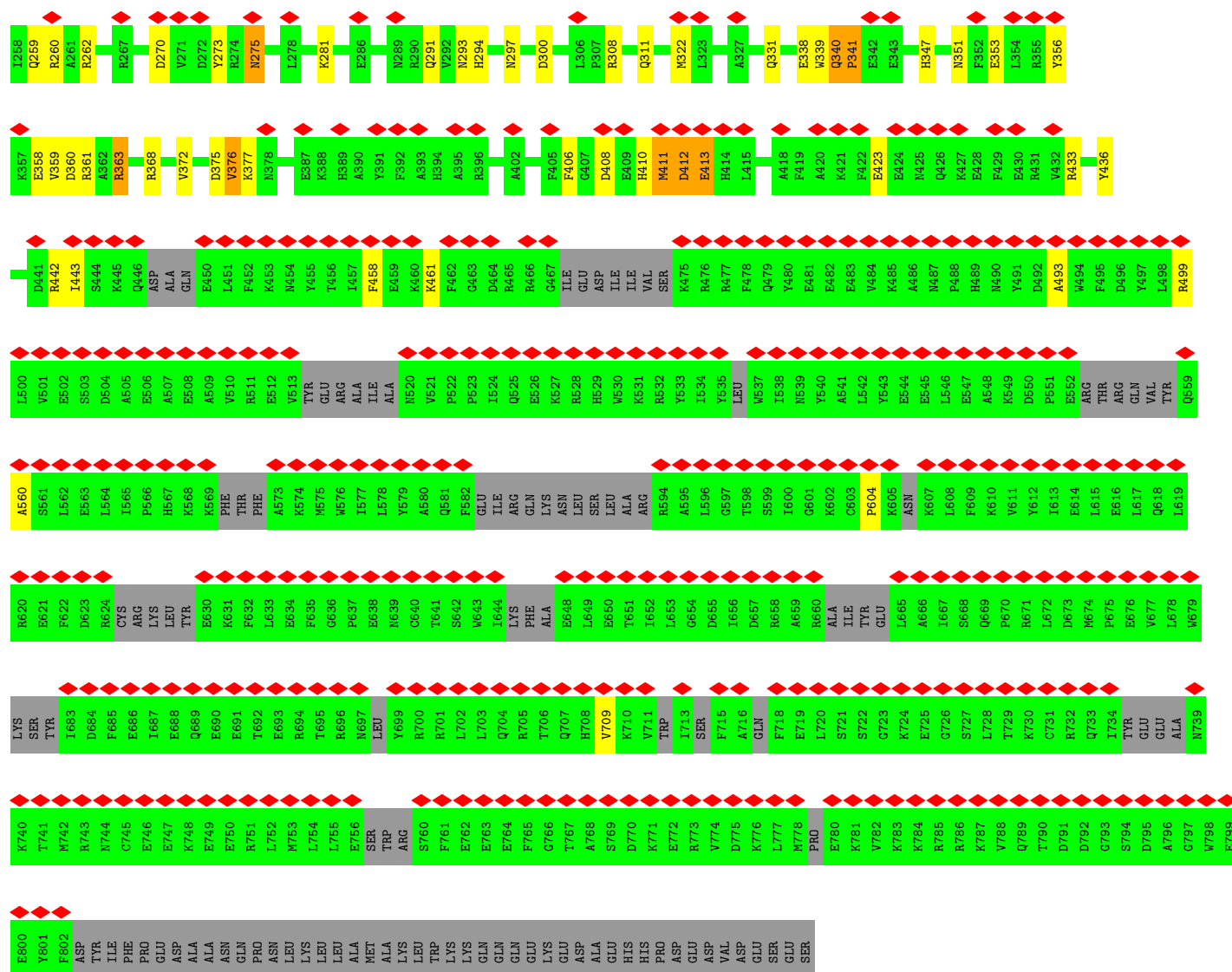
Chain 7: 7% 45% 30% 23%

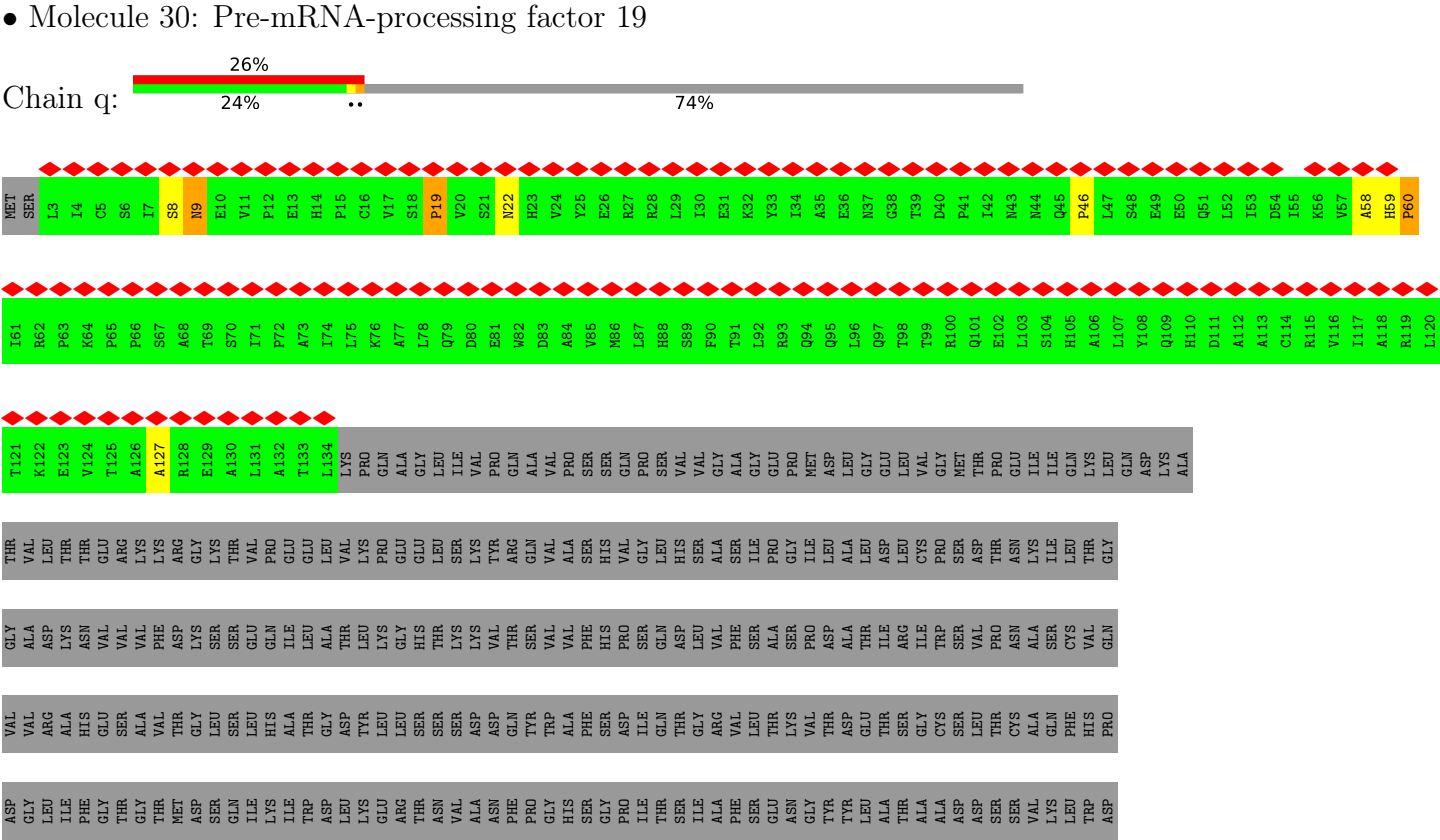
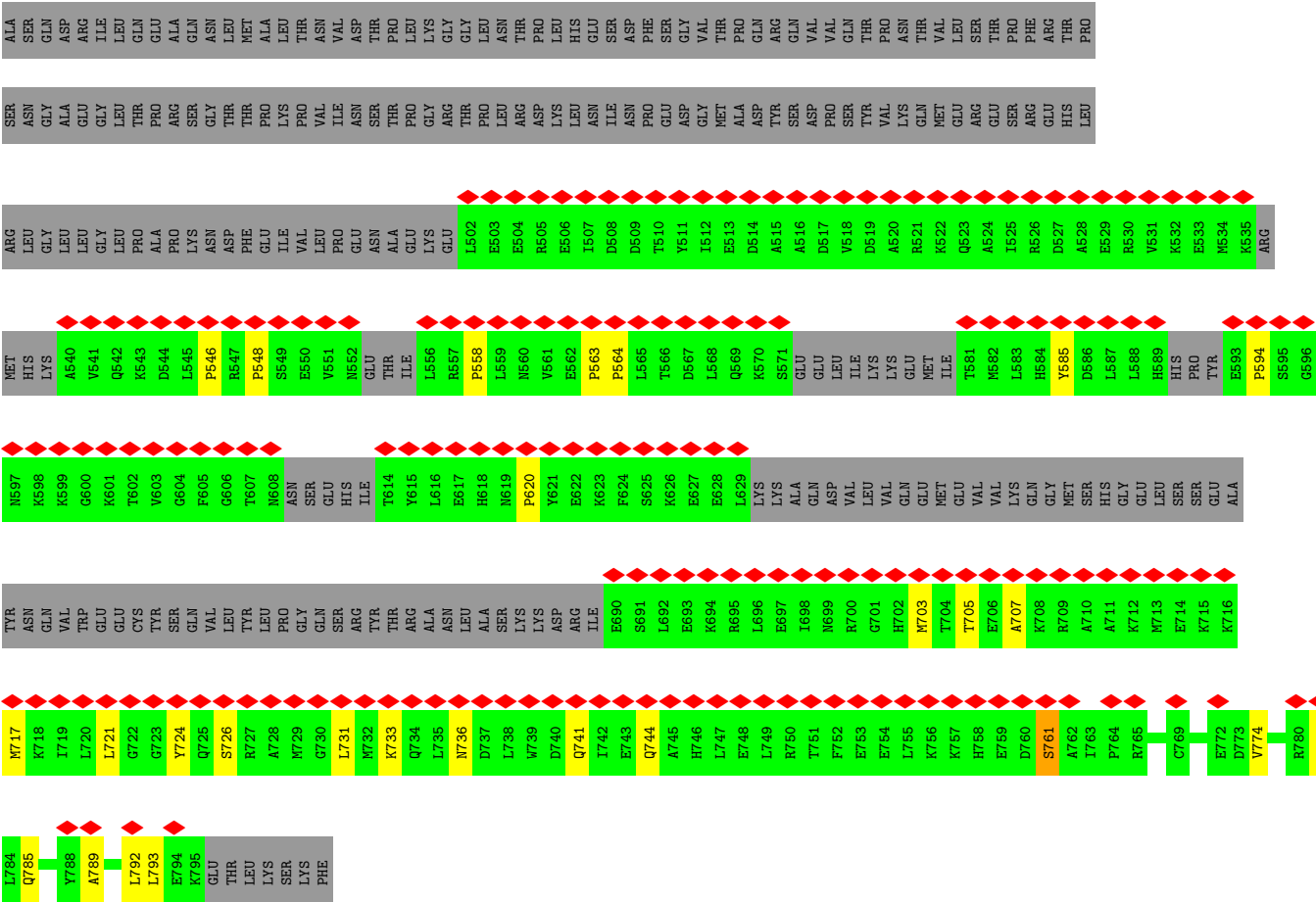


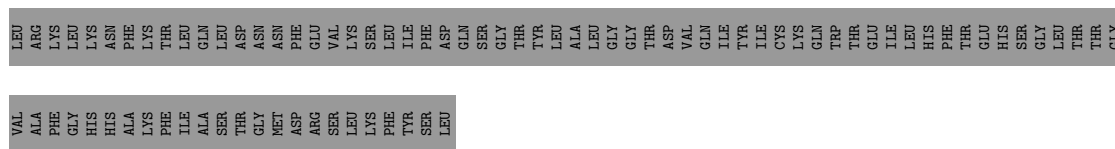
- Molecule 28: Crooked neck-like protein 1

Chain J: 41% 53% 6% 38%

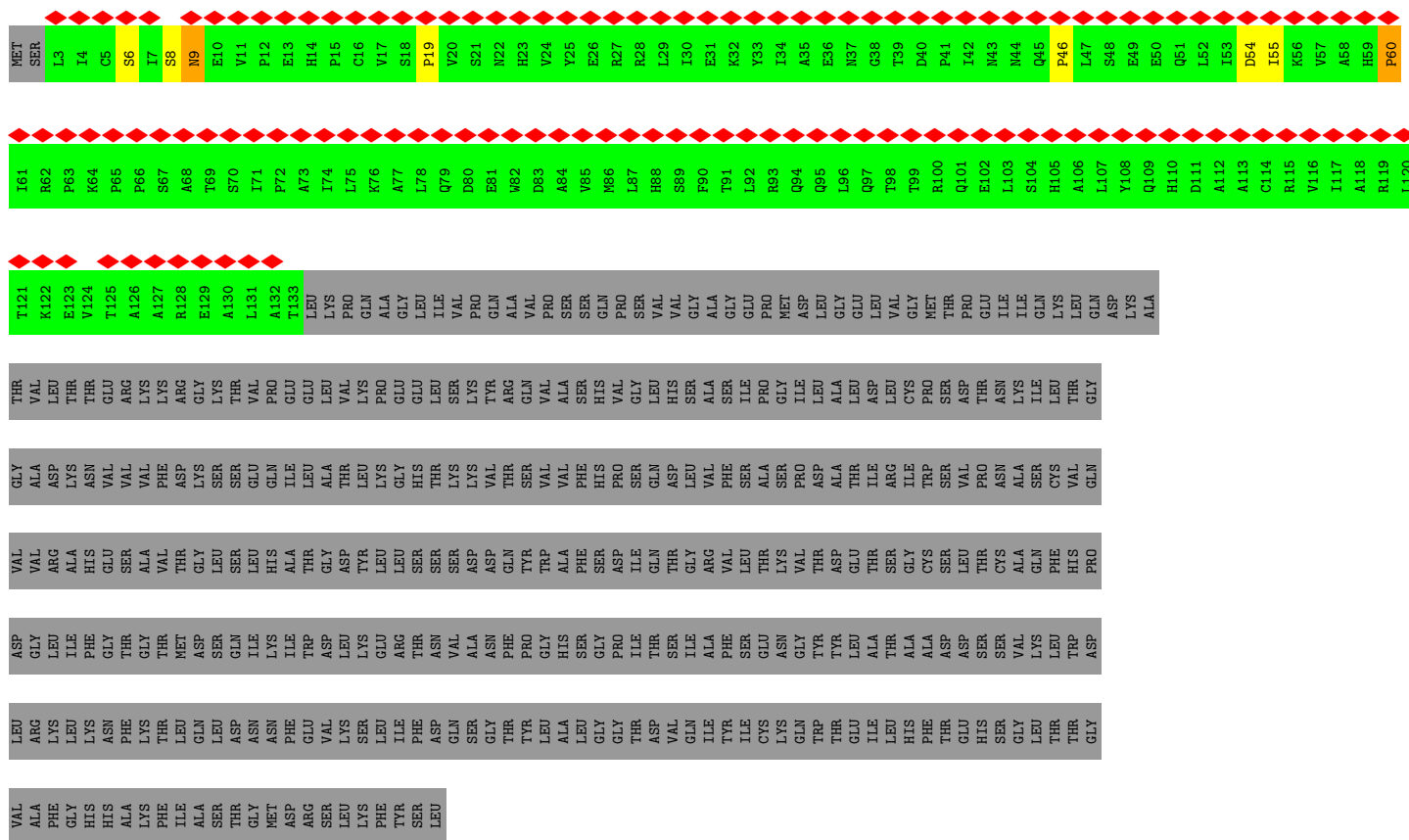




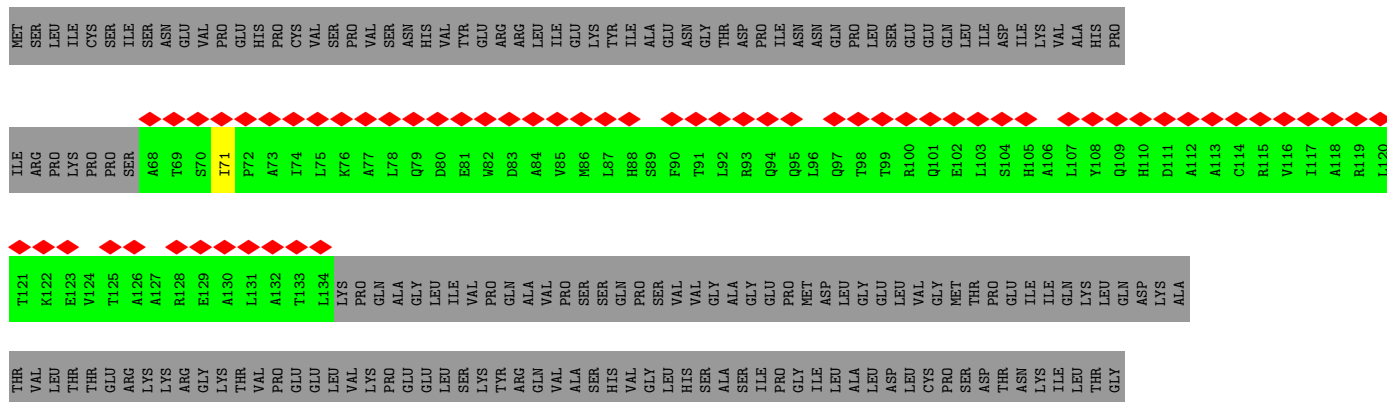




- Molecule 30: Pre-mRNA-processing factor 19



- Molecule 30: Pre-mRNA-processing factor 19



VAL	VAL	LEU	ASP	VAL	GLY
ALA	ALA	ARG	GLY	VAL	ASP
ALA	ALA	ARG	GLY	VAL	ASP
PHE	PHE	LYS	LEU	ALA	LYS
GLY	GLY	LEU	PHE	ILE	ASN
HIS	HIS	LEU	GLY	HIS	VAL
HIS	HIS	ASN	GLY	GLU	VAL
ALA	ALA	PHE	THR	SER	VAL
LYS	LYS	GLY	THR	VAL	PHE
PHE	PHE	THR	THR	VAL	ASP
ILE	ILE	LEU	MET	THR	LYS
ALA	ALA	GLN	ASP	GLY	LYS
SER	SER	LEU	SER	LEU	SER
THR	THR	ASP	GLN	SER	SER
THR	THR	ASN	ILE	LEU	GLN
MET	MET	ASN	LYS	HIS	GLN
ASP	ASP	PHE	ILE	ALA	ILE
ARG	ARG	GLU	TRP	THR	LEU
SER	SER	VAL	ASP	GLY	ALA
LEU	LEU	LYS	LEU	ASP	THR
LYS	LYS	SER	LYS	TYR	THR
PHE	PHE	LEU	GLU	LEU	LYS
TYR	TYR	ILE	ARG	LEU	GLY
SER	SER	PHE	THR	SER	HIS
SER	SER	ASP	ASN	SER	THR
LEU	LEU	ASP	VAL	SER	LYS
		SER	ALA	ASP	LYS
		GLY	ASN	ASP	VAL
		THR	PHE	GLN	THR
		TYR	PRO	TYR	SER
		LEU	GLY	TRP	VAL
		ALA	HIS	ALA	VAL
		LEU	SER	PHE	PHE
		GLY	GLY	SER	HIS
		GLY	PRO	ASP	PRO
		THR	ILE	ILE	SER
		ASP	THR	ILE	SER
		VAL	SER	GLN	GLN
		GLN	SER	THR	ASP
		ILE	ILE	GLY	LEU
		ILE	ALA	ARG	VAL
		TYR	PHE	VAL	PHE
		ILE	SER	LEU	SER
		CYS	GLU	THR	ALA
		LYS	ASN	LYS	SER
		GLN	GLY	VAL	PRO
		TRP	TYR	ASP	ALA
		THR	TYR	THR	THR
		GLU	LEU	GLU	THR
		ILE	ALA	THR	ILE
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		GLY	VAL	ALA	ALA
		LEU	LYS	GLN	SER
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		TYR	TRP	HIS	GLN
		CYS	ASP	ARG	GLN

- Molecule 30: Pre-mRNA-processing factor 19

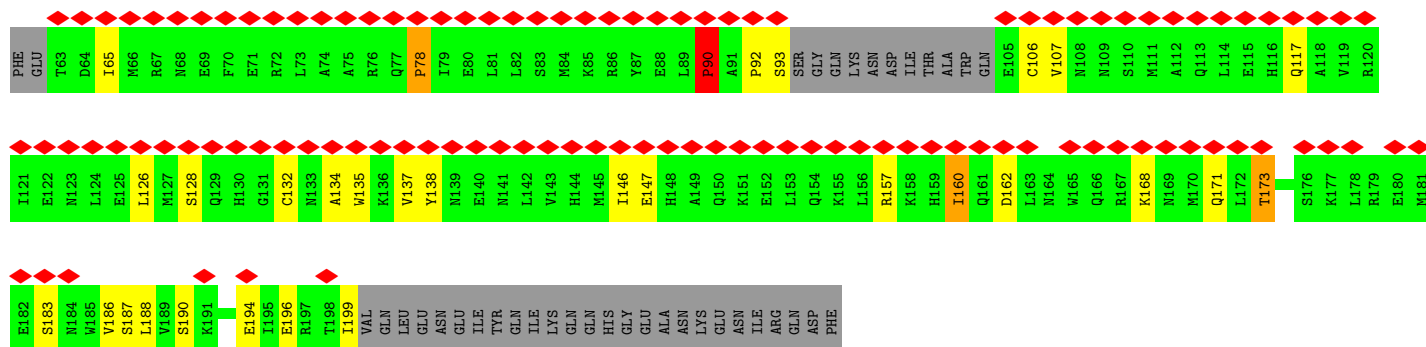


VAL	VAL	ASP	VAL	THR	T121	ILE	MET
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GLY	ALA	LEU	ILE	THR	E124	LYS	ILE
HIS	HIS	PHE	ASN	THR	V124	CYS	CYS
HIS	ASN	GLY	VAL	GLU	T125	PRO	SER
ALA	SER	THR	VAL	ARG	A126	S67	ILE
PHE	ALA	GLY	VAL	LYS	A127	SER	SER
THR	VAL	MET	ASP	ARG	R128	A68	ASN
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ALA	LEU	SER	LEU	LYS	S70	S70	VAL
SER	ASP	SER	THR	LYS	I71	I71	PRO
LEU	GLN	GLN	SER	THR	P72	P72	GLU
LYS	LEU	ILE	LEU	VAL	L131	L131	HIS
MET	ASN	LYS	HIS	PRO	A73	A73	PRO
ASP	PHE	ILE	ALA	ILE	A132	A132	CYS
ARG	GLU	TRP	THR	GLU	T133	I74	VAL
SER	VAL	ASP	GLY	LEU	LEU	L75	SER
LEU	LYS	LEU	THR	VAL	LYS	K76	SER
LYS	TYR	LYS	LEU	VAL	PRO	A77	PRO
PHE	LEU	GLU	LEU	GLN	GLN	I78	VAL
TYR	ILE	ARG	GLY	GLU	ALA	L78	SER
SER	PHE	THR	SER	GLU	GLY	Q79	ASN
ASP	ASN	VAL	THR	LEU	ILE	D80	HIS
GLN	VAL	SER	SER	SER	ILE	E81	VAL
SER	ALA	ALA	ASP	LYS	VAL	W82	TYR
GLY	ASN	ASN	VAL	LYS	PRO	D83	GLU
THR	PHE	THR	GLN	THR	ARG	I83	ARG
TYR	PRO	PRO	TYR	ARG	GLN	A84	LEU
LEU	GLY	GLY	TRP	SER	VAL	V85	ILE
ALA	HIS	HIS	ALA	VAL	PRO	V85	GLU
LEU	SER	PHE	PHE	ALA	SER	H86	LYS
GLY	GLY	GLY	SER	HIS	SER	L87	TYR
GLY	GLY	PRO	PRO	VAL	GLN	H88	ILE
THR	ILE	ILE	ILE	GLY	PRO	ALA	ALA
ASP	THR	THR	GLN	LEU	SER	S89	GLU
VAL	SER	SER	ASP	HIS	VAL	F90	ASN
GLN	ILE	ILE	LEU	SER	VAL	T91	GLY
ILE	ALA	ALA	VAL	ALA	GLY	L92	THR
TYR	VAL	PHE	VAL	SER	ALA	R93	ASP
ILE	SER	SER	LEU	ILE	GLY	Q94	PRO
CYS	GLU	GLU	THR	PRO	GLU	Q94	ILE
LYS	ASN	ASN	LYS	GLY	PRO	Q95	ASN
GLN	GLY	GLY	VAL	ILE	MET	R96	ASN
TRP	TYR	TYR	THR	ILE	ASP	L96	GLN
THR	THR	THR	ASP	LEU	ASP	Q97	LEU
GLU	GLU	GLU	ALA	ALA	LEU	T98	LEU
ILE	ALA	THR	ILE	ASP	GLY	T99	SER
LEU	THR	SER	ARG	LEU	LEU	R100	GLU
HIS	ALA	GLY	ILE	CYS	VAL	Q101	GLU
PHE	ALA	CYS	TRP	PRO	GLY	E102	GLN
THR	THR	SER	SER	THR	MET	L103	LEU
GLU	ASP	ASP	VAL	ASP	THR	E104	ILE
HIS	THR	THR	VAL	THR	PRO	S104	ASP
SER	SER	CYS	ASN	ASN	GLU	H105	ILE
VAL	VAL	ALA	ALA	LYS	ILE	A106	LYS
LYS	LYS	GLN	SER	ILE	ILE	L107	VAL
LEU	LEU	CYS	PHE	GLN	GLN	A108	ALA
THR	THR	HIS	VAL	THR	LYS	I109	HIS
GLY	ASP	TRP	PRO	THR	LEU	Y108	PRO

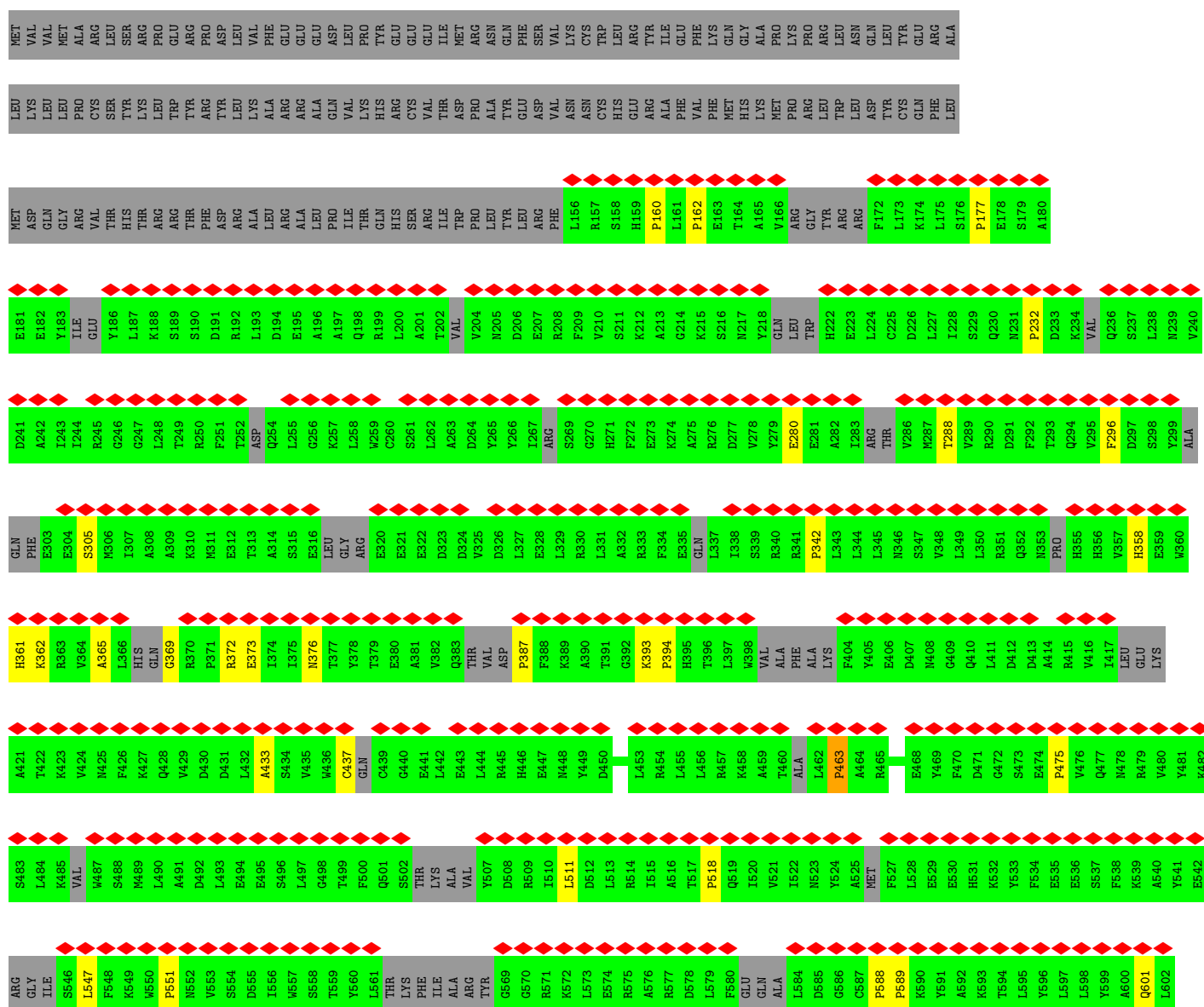
- Molecule 31: Pre-mRNA-splicing factor SPF27



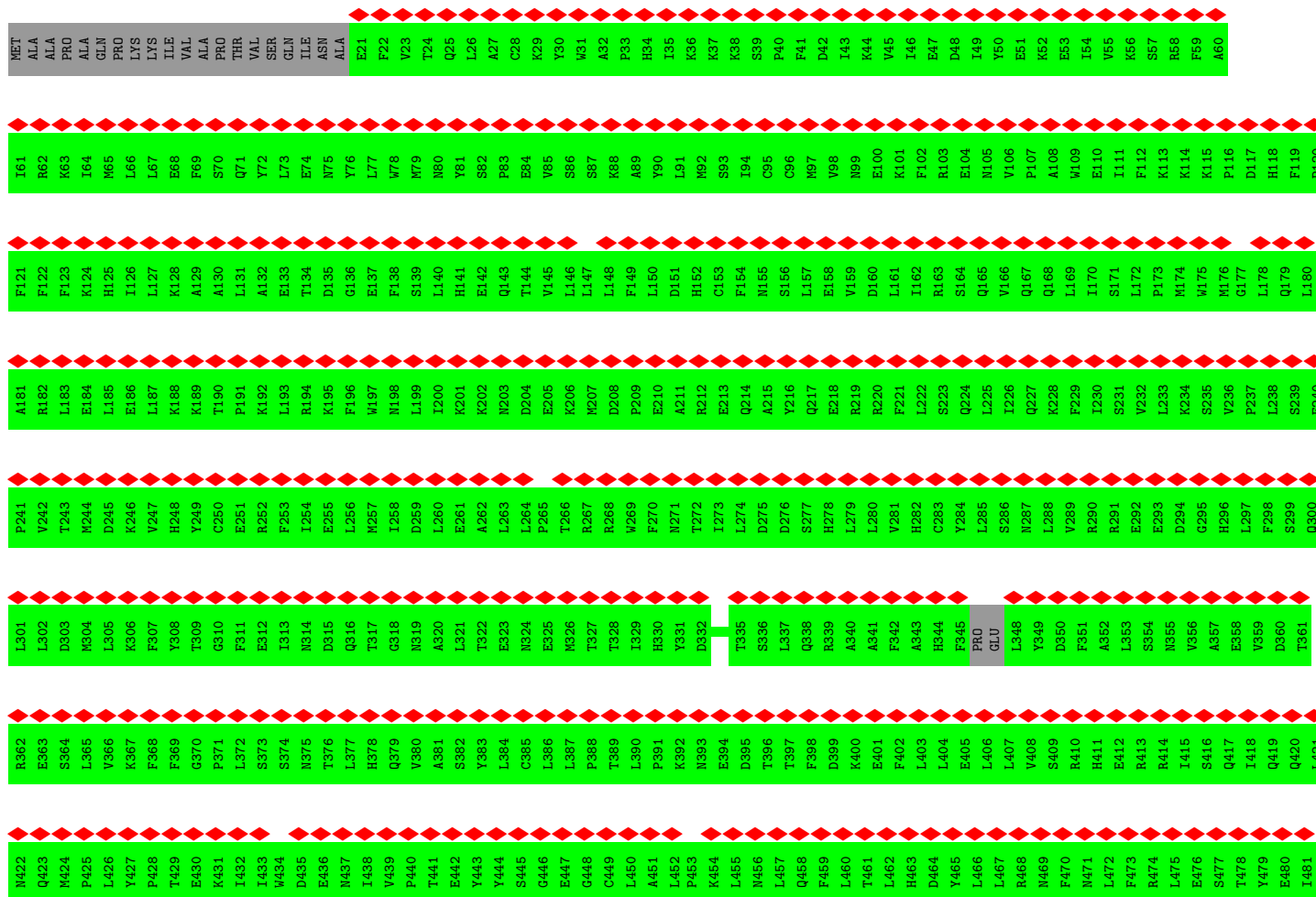
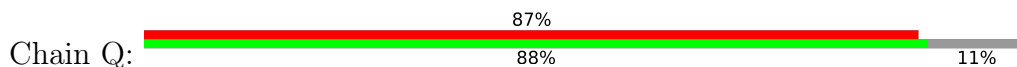
NET	ALA	GLY	THR	GLY	LEU	VAL	ALA	GLY	GLU	VAL	VAL	V13	D14	A15	L16	P17	Y18	F19	D20	Q21	G22	TYR	GLU	ALA	ALA	PRO	GLY	V28	R29	E30	A31	A32	A33	A34	L35	V36	E37	E38	E39	T40	R41	R42	Y43	ARG	PRO	THR	LYS	ASN	TYR	LEU	SER	TYR	THR	ALA	PRO	ASP	TYR	SER
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• Molecule 32: Pre-mRNA-splicing factor SYF1

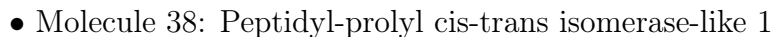


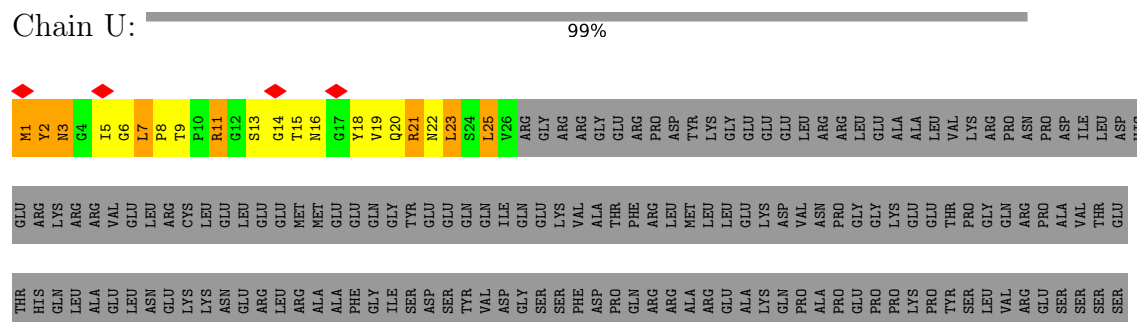
- Molecule 33: Intron-binding protein aquarium



E1203	L1143	D1083	R1023	E963	A903	N843	V783	H723	D603	L543	R482
A1204	C1144	G1084	S1024	V964	R904	F944	I784	L724	K604	N544	I482
E1205	M1145	F1085	K1025	S965	R905	P845	P785	K725	G605	N545	I485
Y1206	L1146	S1086	Y1026	T966	I906	E846	N786	A726	R606	N546	E486
V1207	Y1147	R1087	L1027	F967	E907	Q847	R787	F727	V607	N547	D487
V1208	M1148	L1088	L1028	F968	L908	R848	G788	F728	I608	N548	S488
A1209	R1149	K1089	V1029	P969	L909	T849	F789	F729	GLU	N549	V489
L1210	W1150	R1090	K1030	F970	E910	L850	Y790	G730	ASP	N550	S490
F1211	Y1151	W1091	E1031	H971	E911	I851	P791	H731	GLY	N551	R491
M1212	K1152	I1092	A1032	E972	V912	V852	Y792	N732	GLU	N552	M492
Y1213	M1153	M1093	K1033	F973	R913	T853	N793	V733	P614	N553	K493
M1214	L1154	I1094	I1034	F974	R914	H854	Q794	K734	R615	N554	P494
C1215	G1155	G1095	I1035	A975	L915	S855	P795	V735	P616	N555	W495
L1216	M1156	D1096	A1036	N976	Q916	N856	K796	T736	N617	N556	Q496
L1217	H1097	H1097	M1037	A977	Q917	Q857	R797	V737	M677	N557	S497
G1218	L1158	H1098	T1038	S918	K918	A858	N798	E738	R619	N558	GLU
Y1219	H1159	Q1099	C1039	GLN	L919	L859	T799	D739	G620	N559	TYR
P1220	V1160	L1100	T1040	PRO	G920	N860	I800	P740	E621	N560	G500
A1221	Q1161	P1101	H1041	I981	V921	Q861	Q801	A741	S622	N561	G501
D1222	L1162	P1102	A1042	F982	P922	L862	F802	L742	R623	N562	V502
K1223	L1163	V1103	A1043	K983	G923	F863	T803	Q743	G624	N563	V503
I1224	P1164	I1104	L1044	G984	D924	E864	H804	ILE	T624	N564	F504
S1225	E1165	K1105	K1045	R985	A925	K865	T805	PRO	F625	N565	G505
I1226	F1166	N1106	R1046	S986	A926	I866	Q806	P746	R626	N566	G506
L1227	S1167	M1107	H1047	Y987	S926	M867	Q806	F747	V627	N567	W507
T1228	T1168	A1108	D1048	E988	T927	I807	L887	R748	F628	N568	A508
T1229	A1169	F1109	L1049	E989	T928	A868	E808	I749	L629	N569	S509
Y1230	M1170	Q1110	V1050	D990	C929	L869	A809	T750	D630	N570	M510
M1231	A1171	K1111	K1051	M991	E930	I871	I810	F751	P631	N571	A511
G1232	G1172	Y1112	L1052	E992	T931	D872	R811	P752	N632	N572	Q512
K1233	L1173	S1113	G1053	I993	A932	E873	A812	V753	Q633	N573	P513
Q1234	L1174	N1114	F1054	A994	G933	R874	G813	ARG	Y634	N574	I514
H1235	Y1175	M1115	K1055	E995	Y934	H875	M814	SER	Q635	N575	V515
L1236	D1176	E1116	Y1056	G996	F935	L876	Q815	GLY	Q636	N576	A516
I1237	F1177	Q1117	D1057	C997	F936	L877	P816	GLY	D637	N577	F517
D1238	Q1178	S1118	N1058	F998	L937	R878	L818	LYS	M638	N578	T518
D1239	L1179	L1119	I1059	R999	Y938	L879	T819	LYS	T639	N579	V519
I1240	I1180	F1120	L1060	H1000	Q939	L879	T819	ARG	N640	N580	V520
I1241	M1181	T1121	M1061	I1001	V940	H881	M820	LYS	T641	N581	E521
M1242	V1182	K1122	E1062	K1002	S942	GLY	V821	ALA	I642	N582	V522
R1243	E1183	F1123	E1063	R943	R943	E884	G823	ASP	Q643	N583	A523
C1244	D1184	V1124	A1064	I1004	Y944	E885	P824	GLU	N644	N584	K524
G1245	F1185	R1125	A1065	F1005	E945	E885	P825	ASP	G645	N585	P525
G1246	Q1186	V1126	Q1066	T1006	E945	L886	Q826	GLU	A646	N586	N526
M1247	G1187	G1127	I1067	E946	E946	E887	G826	ASP	E647	N587	I527
N1248	Q1188	L1008	L1068	L1007	Y947	T888	T827	THR	D648	N588	G528
P1249	V1188	V1128	E1069	Q1008	I948	E889	G828	GLU	V649	N589	E529
L1250	G1189	P1129	E1070	E1009	S949	E889	K829	GLU	I709	N590	N530
I1251	E1190	T1130	E1071	K950	K950	D891	T830	A774	E651	N591	A531
G1252	S1191	V1131	T1072	V951	V951	F892	D831	K775	T652	N592	P532
R1253	E1192	D1132	F1073	R1012	K952	F892	V832	T776	F653	N593	T533
P1254	P1193	L1133	I1074	A1013	K952	S993	A833	L777	N654	N594	R534
M1255	M1194	D1134	I1074	S1014	N953	R894	V834	I778	I655	N595	G594
K1256	L1195	E1015	P1075	E1015	LYS	Y895	Q835	V779	N715	N596	C595
V1257	Y1196	L1016	L1076	L1016	GLY	G896	I836	E780	I656	N597	R536
F1197	F1197	L1017	L1077	L1017	SER	R897	I836	P781	M657	N598	A537
T1258	Y1198	G1137	L1078	L1018	THR	V898	I837	H782	R658	N599	D538
T1259	Q1199	R1138	Q1079	R1018	LEU	N899	S838		R659	N600	V539
V1260	L1199	A1139	M1080	S1019	P960	N900	N839		K660	N601	T540
D1261	M1200	R1140	P1081	G1020	V961	V901	I840		P661	N602	I541
R1262	L1201	A1141	Q1082	T962	T962	L902	H842		K662	N602	N542

Chain P:



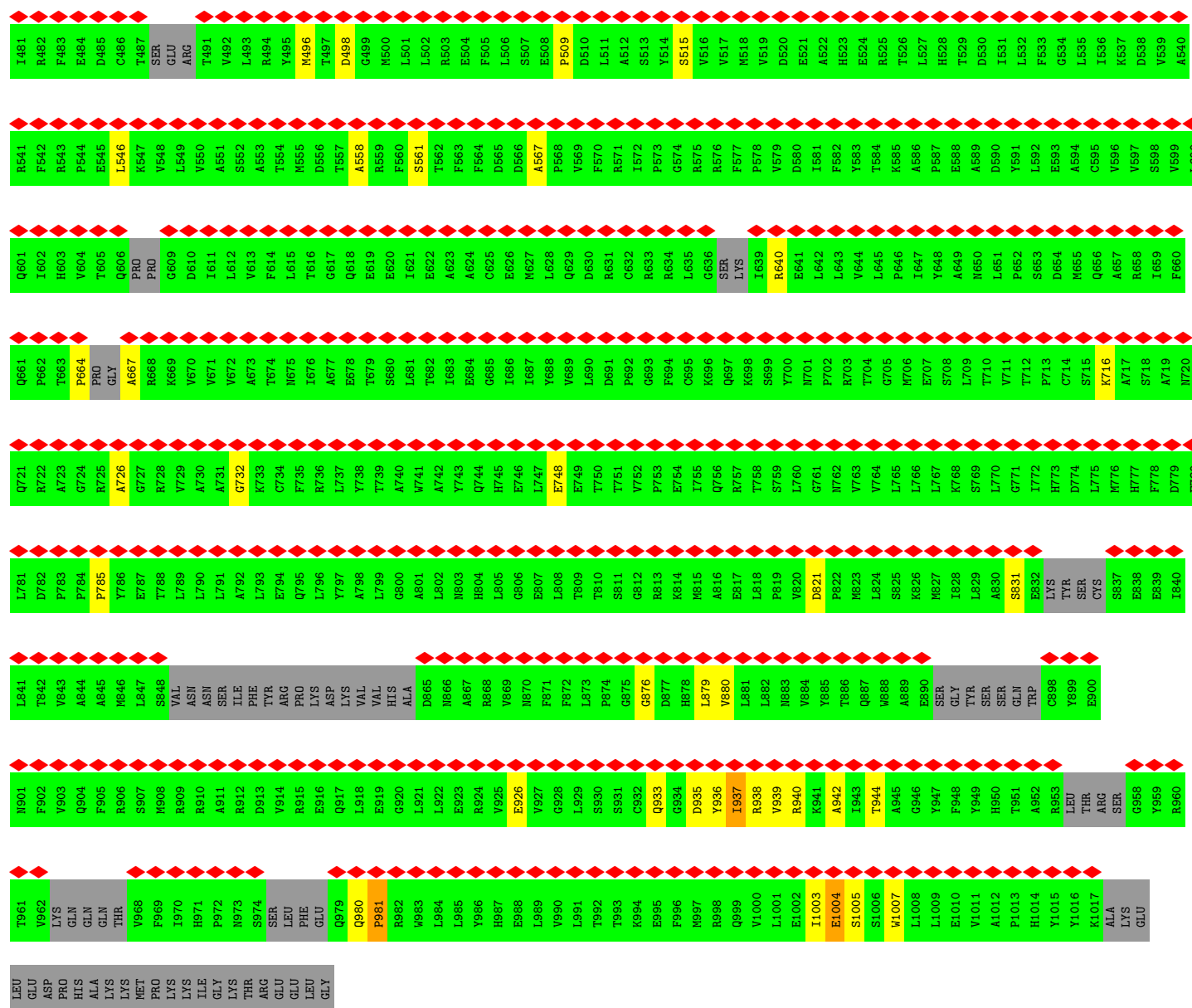




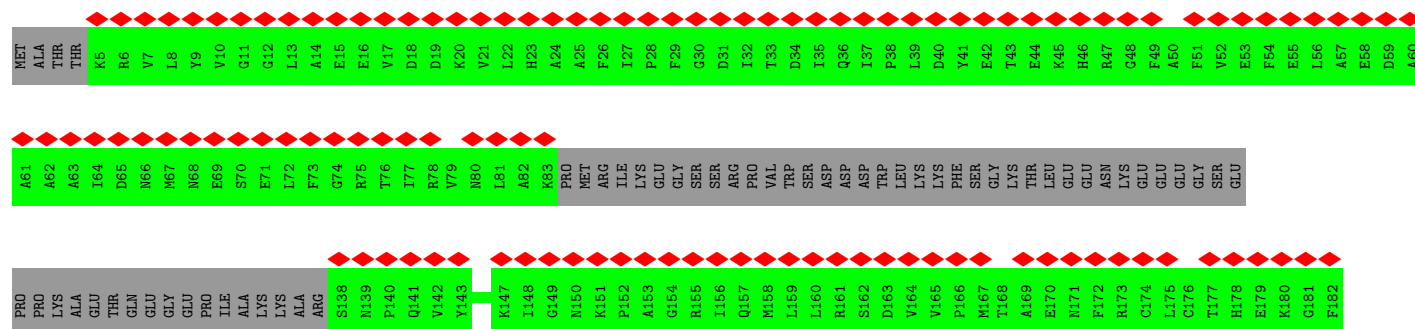
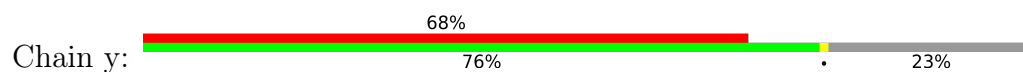


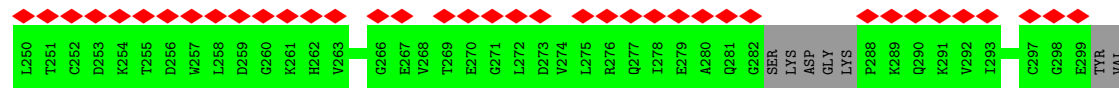
Chain V:





• Molecule 47: Peptidyl-prolyl cis-trans isomerase E





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	14316	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	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	0.142	Depositor
Minimum map value	-0.067	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0323	Depositor
Map size ($\text{\AA}$)	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.338, 1.338, 1.338	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.88	38/16867 (0.2%)	0.99	49/22888 (0.2%)
2	B	0.67	1/1970 (0.1%)	0.95	7/3060 (0.2%)
3	C	1.08	13/6864 (0.2%)	1.27	40/9334 (0.4%)
4	D	0.55	0/8527	1.11	27/11887 (0.2%)
5	E	0.87	0/2392	1.00	6/3242 (0.2%)
6	a	0.77	0/397	0.99	0/549
6	h	0.77	0/391	0.99	0/540
7	b	0.83	0/404	1.12	2/561 (0.4%)
7	i	0.84	0/421	1.15	3/583 (0.5%)
8	c	0.88	0/405	1.11	0/563
8	j	0.87	0/405	1.11	0/563
9	d	1.12	0/479	1.25	1/666 (0.2%)
9	k	1.14	0/420	1.23	1/583 (0.2%)
10	f	1.20	0/360	1.25	0/497
10	m	1.21	1/360 (0.3%)	1.25	0/497
11	e	1.03	0/390	1.24	1/542 (0.2%)
11	l	1.02	0/390	1.23	0/542
12	g	0.86	0/362	1.08	1/501 (0.2%)
12	n	0.85	0/332	1.08	1/458 (0.2%)
13	F	0.35	0/2224	0.66	5/3462 (0.1%)
14	G	0.25	0/1717	0.54	0/2664
15	H	0.51	7/3217 (0.2%)	0.77	8/4997 (0.2%)
16	o	0.93	0/803	2.15	35/1119 (3.1%)
17	p	1.60	3/810 (0.4%)	2.10	25/1122 (2.2%)
18	w	0.62	6/2380 (0.3%)	0.98	14/3274 (0.4%)
19	u	0.36	0/514	0.95	3/710 (0.4%)
20	v	0.88	4/935 (0.4%)	1.08	10/1266 (0.8%)
21	1	0.27	0/7826	0.61	3/10617 (0.0%)
22	2	0.59	4/1277 (0.3%)	0.92	9/1724 (0.5%)
23	3	0.23	0/9381	0.55	5/12732 (0.0%)
24	4	1.08	2/535 (0.4%)	1.28	5/724 (0.7%)
25	5	0.20	0/823	0.53	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	6	0.20	0/678	0.59	0/909
27	7	0.22	0/556	0.49	0/751
28	J	0.80	1/3500 (0.0%)	1.13	3/4750 (0.1%)
29	L	0.58	4/2283 (0.2%)	0.88	8/3088 (0.3%)
30	q	0.62	0/658	0.97	3/919 (0.3%)
30	r	0.58	0/653	0.99	3/912 (0.3%)
30	s	0.49	0/334	0.91	0/466
30	t	0.56	0/334	0.82	0/466
31	K	0.98	11/981 (1.1%)	1.03	6/1317 (0.5%)
32	I	0.54	0/2745	0.91	18/3765 (0.5%)
33	Q	0.37	0/6518	0.85	3/9075 (0.0%)
34	N	1.15	1/1210 (0.1%)	1.17	4/1622 (0.2%)
35	O	1.05	5/2321 (0.2%)	1.11	10/3135 (0.3%)
36	P	0.98	0/841	1.27	4/1117 (0.4%)
37	R	0.87	7/2224 (0.3%)	1.16	10/2992 (0.3%)
38	S	0.81	0/1268	1.14	9/1714 (0.5%)
39	T	1.44	13/2522 (0.5%)	1.42	26/3438 (0.8%)
40	U	1.44	2/196 (1.0%)	1.54	4/265 (1.5%)
41	V	0.89	1/2239 (0.0%)	1.17	3/3118 (0.1%)
42	W	0.88	2/2381 (0.1%)	1.33	27/3310 (0.8%)
43	X	0.21	0/1012	0.57	0/1351
44	Y	0.24	0/753	0.58	0/1014
45	Z	0.65	6/772 (0.8%)	1.11	9/1056 (0.9%)
46	x	0.59	1/2871 (0.0%)	0.82	11/3981 (0.3%)
47	y	0.55	0/1129	0.91	0/1558
All	All	0.75	133/115557 (0.1%)	1.00	422/159679 (0.3%)

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
3	C	0	3
4	D	0	1
9	d	0	1
9	k	0	1
21	1	0	9
22	2	0	1
23	3	0	4
27	7	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
34	N	0	1
37	R	0	1
39	T	0	2
43	X	0	1
All	All	0	32

All (133) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	K	106	CYS	CB-SG	-11.61	1.43	1.81
31	K	132	CYS	CB-SG	-8.70	1.52	1.81
3	C	387	ASP	CA-C	-8.61	1.48	1.52
17	p	156	ASN	C-N	-8.31	1.22	1.33
1	A	316	PHE	C-N	-8.15	1.25	1.34
1	A	483	GLN	CA-C	-7.69	1.43	1.52
39	T	353	THR	CA-C	-7.66	1.43	1.52
15	H	142	C	C1'-N1	7.55	1.59	1.48
42	W	278	LYS	CA-C	-7.47	1.44	1.53
31	K	186	VAL	CA-CB	-7.27	1.44	1.54
1	A	212	PRO	N-CA	-7.26	1.38	1.47
2	B	103	G	C1'-N9	-7.22	1.37	1.48
35	O	224	ASP	C-N	7.17	1.41	1.33
24	4	50	THR	CB-OG1	7.12	1.55	1.43
3	C	319	THR	CA-C	-7.07	1.44	1.52
24	4	42	THR	CB-OG1	7.00	1.54	1.43
15	H	150	U	C1'-N1	6.96	1.58	1.48
35	O	54	VAL	CA-C	-6.95	1.44	1.52
17	p	155	LEU	C-N	-6.93	1.24	1.33
1	A	416	GLY	C-O	6.81	1.31	1.23
15	H	97	G	C1'-N9	-6.78	1.37	1.48
20	v	80	THR	CB-OG1	6.76	1.54	1.43
1	A	472	LEU	CA-C	-6.74	1.45	1.52
18	w	284	ARG	CA-CB	-6.71	1.42	1.53
31	K	40	THR	CB-OG1	6.70	1.54	1.43
1	A	607	ASP	CA-C	-6.68	1.44	1.52
15	H	151	C	C1'-N1	6.64	1.58	1.48
15	H	184	C	C1'-N1	6.57	1.58	1.48
15	H	141	C	C1'-N1	6.51	1.58	1.48
3	C	637	LEU	CA-C	-6.45	1.44	1.52
3	C	876	PRO	N-CA	-6.42	1.39	1.47
34	N	101	CYS	CA-C	-6.37	1.45	1.52
22	2	619	MET	C-N	6.37	1.41	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	321	ASN	N-CA	-6.35	1.38	1.46
1	A	141	ILE	CA-CB	-6.32	1.46	1.54
1	A	581	ILE	CA-CB	-6.31	1.47	1.54
1	A	533	LYS	N-CA	-6.20	1.38	1.46
18	w	415	THR	CB-OG1	6.19	1.53	1.43
3	C	317	CYS	CA-C	-6.19	1.46	1.52
1	A	125	ALA	C-O	-6.18	1.16	1.24
45	Z	570	ALA	C-N	6.17	1.40	1.33
39	T	208	ARG	CA-C	-6.07	1.44	1.52
39	T	333	VAL	N-CA	-6.07	1.39	1.46
1	A	593	ARG	CA-C	-5.99	1.44	1.52
3	C	446	LYS	C-N	5.95	1.41	1.34
29	L	761	SER	CB-OG	5.84	1.53	1.42
39	T	332	ALA	CA-C	-5.80	1.45	1.52
42	W	94	GLY	C-N	5.79	1.41	1.33
18	w	491	THR	CB-OG1	5.76	1.52	1.43
1	A	221	ASN	CA-C	-5.75	1.45	1.52
1	A	135	VAL	CA-C	-5.75	1.45	1.52
18	w	177	ARG	CA-CB	-5.73	1.43	1.53
37	R	252	PRO	C-N	5.70	1.41	1.33
31	K	160	ILE	CB-CG1	-5.68	1.42	1.53
1	A	272	ALA	CA-C	-5.66	1.45	1.52
46	x	926	GLU	CA-CB	-5.66	1.45	1.53
39	T	270	VAL	CA-C	-5.66	1.45	1.52
45	Z	563	ARG	C-N	5.66	1.41	1.33
18	w	448	ASN	CA-CB	-5.62	1.44	1.53
31	K	162	ASP	CA-CB	-5.61	1.44	1.53
1	A	482	PHE	N-CA	-5.60	1.39	1.46
1	A	150	MET	CA-C	-5.58	1.45	1.52
3	C	875	ILE	C-O	-5.57	1.17	1.24
1	A	221	ASN	N-CA	-5.57	1.39	1.46
1	A	106	MET	C-N	-5.55	1.28	1.34
39	T	376	ARG	CA-C	-5.53	1.45	1.52
15	H	110	A	C1'-N9	-5.52	1.39	1.48
20	v	165	ARG	CA-CB	-5.52	1.44	1.53
31	K	128	SER	CB-OG	5.52	1.53	1.42
1	A	317	PRO	N-CA	-5.51	1.40	1.47
45	Z	569	PRO	N-CD	5.50	1.55	1.47
40	U	3	ASN	CA-C	-5.49	1.47	1.53
1	A	415	SER	C-O	-5.48	1.17	1.23
22	2	620	PRO	N-CD	5.48	1.55	1.47
31	K	173	THR	CB-OG1	5.45	1.52	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	K	183	SER	CB-OG	5.43	1.53	1.42
37	R	231	VAL	CA-C	-5.43	1.45	1.52
41	V	505	LYS	C-O	-5.42	1.17	1.24
35	O	225	PRO	N-CD	5.40	1.55	1.47
18	w	457	SER	CB-OG	5.39	1.52	1.42
39	T	218	TRP	CA-C	-5.38	1.46	1.52
3	C	369	PHE	C-O	-5.38	1.17	1.24
39	T	319	THR	CA-C	-5.36	1.45	1.52
29	L	705	THR	CB-OG1	5.35	1.52	1.43
1	A	598	LEU	CA-C	-5.35	1.44	1.52
22	2	643	PRO	N-CD	5.31	1.55	1.47
3	C	899	SER	N-CA	-5.30	1.39	1.46
29	L	726	SER	CB-OG	5.30	1.52	1.42
3	C	659	VAL	C-O	-5.30	1.18	1.23
35	O	226	PRO	N-CD	5.30	1.55	1.47
1	A	335	PRO	N-CA	-5.29	1.40	1.47
17	p	187	HIS	N-CA	5.29	1.53	1.46
29	L	793	LEU	CA-CB	-5.29	1.44	1.53
1	A	505	ASN	CA-C	-5.29	1.46	1.52
35	O	20	PHE	C-O	-5.29	1.17	1.24
1	A	107	PRO	N-CA	-5.27	1.40	1.47
31	K	190	SER	CB-OG	5.26	1.52	1.42
37	R	130	PRO	N-CD	5.25	1.55	1.47
1	A	489	TRP	CA-C	-5.23	1.45	1.52
1	A	610	HIS	CA-C	-5.23	1.46	1.52
31	K	187	SER	CB-OG	5.23	1.52	1.42
1	A	597	LYS	CA-C	5.22	1.59	1.52
45	Z	521	PRO	N-CD	5.22	1.55	1.47
1	A	203	VAL	C-O	-5.22	1.17	1.24
1	A	134	TRP	CA-C	-5.21	1.46	1.52
37	R	222	PRO	N-CD	5.20	1.55	1.47
10	m	14	LEU	CA-C	5.18	1.59	1.52
1	A	411	PHE	CA-C	-5.18	1.45	1.52
3	C	258	ASN	N-CA	-5.17	1.39	1.45
20	v	73	THR	CB-OG1	5.15	1.51	1.43
3	C	311	SER	CA-C	-5.13	1.48	1.53
37	R	253	PRO	N-CD	5.13	1.54	1.47
20	v	154	ALA	CA-CB	-5.12	1.44	1.53
40	U	21	ARG	CA-C	-5.12	1.46	1.53
37	R	252	PRO	N-CD	5.11	1.54	1.47
39	T	216	ASN	CA-C	-5.11	1.46	1.53
39	T	267	ASP	C-O	-5.10	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
37	R	227	PRO	N-CD	5.10	1.54	1.47
1	A	455	VAL	CA-C	-5.10	1.46	1.52
1	A	407	ALA	N-CA	-5.10	1.39	1.45
1	A	531	THR	CA-C	-5.09	1.46	1.53
1	A	116	VAL	CA-C	-5.08	1.47	1.52
1	A	170	ASP	CA-C	5.08	1.59	1.52
39	T	268	LYS	CA-C	-5.07	1.46	1.52
22	2	642	PRO	C-N	5.06	1.40	1.34
3	C	447	PRO	N-CD	5.06	1.54	1.47
45	Z	564	PRO	N-CD	5.06	1.54	1.47
28	J	340	GLN	C-O	-5.05	1.21	1.23
39	T	465	ILE	N-CA	-5.05	1.40	1.46
45	Z	572	PRO	N-CD	5.04	1.54	1.47
1	A	617	ASN	CA-C	-5.03	1.48	1.53
39	T	346	ILE	CA-C	-5.01	1.46	1.52
1	A	654	ASN	CA-C	-5.01	1.46	1.52

All (422) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	T	187	LYS	CA-C-N	13.13	132.89	119.76
39	T	187	LYS	C-N-CA	13.13	132.89	119.76
24	4	83	PRO	CA-CB-CG	10.35	124.17	104.50
35	O	225	PRO	N-CA-C	10.32	123.29	110.70
42	W	278	LYS	CB-CA-C	-9.96	95.82	111.17
2	B	104	C	C2'-C3'-O3'	-9.92	94.61	109.50
36	P	189	ASP	N-CA-C	-9.51	100.67	112.47
39	T	191	HIS	CA-C-N	9.46	126.47	119.66
39	T	191	HIS	C-N-CA	9.46	126.47	119.66
18	w	442	ASN	CA-CB-CG	-9.32	103.28	112.60
18	w	441	PRO	N-CA-CB	9.20	111.89	103.33
42	W	382	ASN	CA-C-N	8.94	128.66	119.19
42	W	382	ASN	C-N-CA	8.94	128.66	119.19
45	Z	569	PRO	CA-N-CD	-8.91	99.52	112.00
31	K	90	PRO	CA-CB-CG	8.82	121.26	104.50
45	Z	573	PRO	CA-N-CD	-8.80	99.67	112.00
1	A	696	MET	CA-C-N	8.76	130.49	120.06
1	A	696	MET	C-N-CA	8.76	130.49	120.06
18	w	227	PRO	N-CA-CB	8.75	111.06	103.36
1	A	332	TYR	N-CA-C	-8.70	95.85	109.07
13	F	36	A	C2'-C3'-O3'	-8.69	100.67	113.70
21	1	1108	ASN	N-CA-C	8.69	124.00	109.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	r	46	PRO	N-CA-CB	8.68	111.08	103.27
3	C	144	CYS	N-CA-CB	8.66	123.56	110.22
3	C	776	GLU	N-CA-C	8.63	125.02	113.97
34	N	101	CYS	CB-CA-C	-8.63	97.58	110.95
15	H	141	C	O3'-P-O5'	-8.57	91.14	104.00
15	H	150	U	O3'-P-O5'	-8.57	91.14	104.00
15	H	113	G	O3'-P-O5'	-8.53	91.21	104.00
35	O	225	PRO	CA-N-CD	-8.52	100.07	112.00
15	H	114	A	O3'-P-O5'	-8.51	91.23	104.00
1	A	211	GLN	CA-C-N	8.49	130.45	119.84
1	A	211	GLN	C-N-CA	8.49	130.45	119.84
30	q	46	PRO	N-CA-CB	8.46	111.21	103.34
35	O	226	PRO	CA-N-CD	-8.42	100.21	112.00
42	W	279	LYS	N-CA-C	-8.24	93.26	110.80
39	T	213	GLU	CA-C-N	8.11	129.97	119.84
39	T	213	GLU	C-N-CA	8.11	129.97	119.84
19	u	222	PRO	N-CA-CB	8.06	111.87	103.00
16	o	16	THR	CA-C-O	-8.06	111.74	120.36
46	x	1004	GLU	N-CA-C	8.01	120.01	111.28
40	U	19	VAL	CB-CA-C	-8.00	101.13	111.53
37	R	101	ILE	CB-CA-C	-7.95	101.53	111.70
16	o	99	SER	N-CA-C	7.94	122.75	112.26
22	2	641	PRO	N-CA-CB	7.92	110.76	103.08
35	O	23	LEU	N-CA-C	7.87	121.43	109.23
18	w	120	PRO	N-CA-CB	7.86	111.06	103.51
19	u	221	PRO	N-CA-CB	7.86	110.70	103.08
1	A	677	VAL	CB-CA-C	-7.81	101.78	112.24
22	2	656	PRO	N-CA-CB	7.78	111.56	103.00
3	C	919	ARG	CA-C-N	7.77	127.48	119.56
3	C	919	ARG	C-N-CA	7.77	127.48	119.56
19	u	200	PRO	N-CA-CB	7.74	110.87	103.52
2	B	12	U	C2'-C3'-O3'	-7.73	102.10	113.70
16	o	117	TYR	CA-C-O	7.68	128.47	120.40
22	2	651	PRO	N-CA-CB	7.67	109.77	103.32
20	v	115	PRO	N-CA-CB	7.65	111.28	103.25
33	Q	1379	TYR	N-CA-C	7.61	122.65	112.30
17	p	187	HIS	N-CA-C	-7.61	103.95	113.23
23	3	916	ASN	CA-C-N	7.57	129.30	119.84
23	3	916	ASN	C-N-CA	7.57	129.30	119.84
31	K	90	PRO	N-CA-CB	7.56	111.19	103.25
37	R	433	ILE	N-CA-C	7.53	118.30	110.62
17	p	219	LYS	O-C-N	7.53	132.07	123.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	v	139	PRO	N-CA-CB	7.52	111.15	103.25
18	w	230	PRO	N-CA-CB	7.52	110.33	103.19
29	L	563	PRO	N-CA-CB	7.52	110.37	103.08
46	x	785	PRO	N-CA-CB	7.49	109.97	103.31
24	4	27	PRO	N-CA-CB	7.48	111.10	103.25
3	C	823	ALA	N-CA-C	7.47	120.75	110.06
20	v	220	PRO	N-CA-CB	7.47	110.33	103.08
30	q	60	PRO	N-CA-CB	7.46	111.08	103.25
20	v	217	PRO	N-CA-CB	7.45	110.31	103.08
1	A	81	PHE	N-CA-C	7.44	119.39	111.28
46	x	933	GLN	N-CA-C	7.40	119.43	111.36
31	K	78	PRO	N-CA-CB	7.38	111.00	103.25
40	U	7	LEU	CA-C-N	7.34	127.69	119.32
40	U	7	LEU	C-N-CA	7.34	127.69	119.32
32	I	588	PRO	N-CA-CB	7.34	110.20	103.08
1	A	167	PRO	CA-C-N	7.32	126.99	119.82
1	A	167	PRO	C-N-CA	7.32	126.99	119.82
17	p	192	VAL	CA-C-O	7.31	128.52	120.48
1	A	276	GLY	CA-C-N	7.30	127.88	120.14
1	A	276	GLY	C-N-CA	7.30	127.88	120.14
20	v	73	THR	CA-CB-OG1	7.27	120.50	109.60
18	w	305	PRO	N-CA-CB	7.24	110.77	102.88
4	D	1044	VAL	CA-C-N	7.23	126.73	118.85
4	D	1044	VAL	C-N-CA	7.23	126.73	118.85
20	v	218	PRO	N-CA-CB	7.22	110.83	103.25
16	o	71	VAL	CA-C-N	7.21	131.63	120.75
16	o	71	VAL	C-N-CA	7.21	131.63	120.75
1	A	423	ASP	N-CA-C	-7.20	104.52	112.72
37	R	252	PRO	CA-C-N	-7.19	112.36	119.76
37	R	252	PRO	C-N-CA	-7.19	112.36	119.76
4	D	1666	THR	N-CA-C	7.16	121.46	112.87
18	w	174	PRO	N-CA-CB	7.14	110.75	103.25
1	A	334	THR	CA-C-N	-7.13	112.64	119.85
1	A	334	THR	C-N-CA	-7.13	112.64	119.85
3	C	215	VAL	CB-CA-C	-7.13	102.52	112.14
23	3	915	LEU	CA-C-N	-7.08	115.06	122.28
23	3	915	LEU	C-N-CA	-7.08	115.06	122.28
18	w	105	PRO	N-CA-CB	7.06	110.79	103.23
46	x	509	PRO	N-CA-CB	7.06	110.66	103.25
17	p	155	LEU	N-CA-CB	7.03	122.37	110.49
17	p	184	PRO	N-CA-CB	7.02	110.62	103.25
39	T	220	VAL	CB-CA-C	-7.02	99.65	110.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	W	269	MET	CA-C-N	-7.02	113.15	120.38
42	W	269	MET	C-N-CA	-7.02	113.15	120.38
45	Z	570	ALA	CA-C-N	-7.00	113.17	120.38
45	Z	570	ALA	C-N-CA	-7.00	113.17	120.38
4	D	533	VAL	N-CA-C	6.97	118.84	112.29
24	4	50	THR	CA-CB-OG1	6.95	120.02	109.60
20	v	221	PRO	N-CA-CB	6.95	110.55	103.25
1	A	1303	LEU	CA-C-N	-6.94	112.33	123.23
1	A	1303	LEU	C-N-CA	-6.94	112.33	123.23
32	I	475	PRO	N-CA-CB	6.93	110.87	103.52
42	W	251	GLY	N-CA-C	-6.86	96.93	113.18
32	I	551	PRO	N-CA-CB	6.85	110.78	103.52
32	I	160	PRO	N-CA-CB	6.85	110.44	103.25
39	T	405	PHE	N-CA-C	6.84	119.75	111.82
32	I	589	PRO	N-CA-CB	6.83	110.77	103.39
35	O	225	PRO	CB-CA-C	6.83	119.26	110.92
32	I	162	PRO	N-CA-CB	6.81	110.73	103.52
16	o	121	LEU	CA-C-O	6.80	128.79	121.44
18	w	399	LEU	CD1-CG-CD2	6.80	125.76	110.80
20	v	162	PRO	N-CA-CB	6.78	110.45	103.00
32	I	232	PRO	N-CA-CB	6.77	110.69	103.52
45	Z	563	ARG	CA-C-N	-6.76	113.00	119.76
45	Z	563	ARG	C-N-CA	-6.76	113.00	119.76
17	p	53	PHE	CA-C-O	-6.75	112.90	120.32
18	w	419	PRO	N-CA-CB	6.73	110.32	103.25
32	I	342	PRO	N-CA-CB	6.72	110.30	103.25
29	L	558	PRO	N-CA-CB	6.71	110.64	103.52
30	q	19	PRO	N-CA-CB	6.71	110.29	103.25
16	o	58	ASP	N-CA-CB	-6.69	100.66	111.24
29	L	594	PRO	N-CA-CB	6.69	110.28	103.25
30	r	19	PRO	N-CA-CB	6.69	110.25	102.76
46	x	403	PRO	N-CA-CB	6.68	110.92	103.44
32	I	387	PRO	N-CA-CB	6.68	110.35	103.00
34	N	37	HIS	N-CA-CB	-6.68	102.07	111.62
3	C	799	GLU	CA-C-N	6.68	126.37	119.56
3	C	799	GLU	C-N-CA	6.68	126.37	119.56
1	A	455	VAL	CB-CA-C	-6.66	103.03	112.22
42	W	94	GLY	CA-C-N	-6.65	113.13	119.85
42	W	94	GLY	C-N-CA	-6.65	113.13	119.85
13	F	33	G	C2'-C3'-O3'	-6.65	103.73	113.70
29	L	620	PRO	N-CA-CB	6.64	110.23	103.25
18	w	202	PRO	N-CA-CB	6.63	110.55	103.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	x	821	ASP	CA-C-N	6.63	126.41	119.05
46	x	821	ASP	C-N-CA	6.63	126.41	119.05
17	p	185	GLY	N-CA-C	-6.63	104.56	113.24
2	B	48	A	C1'-C2'-O2'	6.61	118.31	108.40
32	I	816	PRO	N-CA-CB	6.60	110.51	103.52
3	C	148	CYS	CB-CA-C	6.58	122.04	110.85
42	W	565	LYS	N-CA-C	6.57	118.84	108.79
22	2	629	PRO	N-CA-CB	6.57	110.22	103.00
32	I	722	GLU	N-CA-C	6.52	118.38	111.28
22	2	619	MET	CA-C-N	-6.49	113.60	120.03
22	2	619	MET	C-N-CA	-6.49	113.60	120.03
35	O	224	ASP	CA-C-N	-6.47	113.71	120.38
35	O	224	ASP	C-N-CA	-6.47	113.71	120.38
18	w	99	PRO	N-CA-CB	6.47	110.45	103.33
16	o	87	LEU	CA-C-N	6.45	126.21	119.05
16	o	87	LEU	C-N-CA	6.45	126.21	119.05
1	A	617	ASN	CB-CA-C	-6.44	102.12	111.91
22	2	636	MET	CG-SD-CE	6.43	115.05	100.90
32	I	463	PRO	N-CA-CB	6.43	110.00	103.25
17	p	148	PRO	N-CA-CB	6.41	109.30	103.08
32	I	177	PRO	N-CA-CB	6.41	110.61	103.44
29	L	564	PRO	N-CA-CB	6.40	110.30	103.52
29	L	546	PRO	N-CA-CB	6.40	110.60	103.44
1	A	581	ILE	CB-CA-C	-6.39	103.79	111.97
31	K	40	THR	CA-CB-OG1	6.37	119.16	109.60
32	I	518	PRO	N-CA-CB	6.37	110.28	103.52
39	T	323	VAL	CB-CA-C	-6.36	103.82	111.97
17	p	149	PRO	N-CA-CB	6.35	109.58	102.60
32	I	788	PRO	N-CA-CB	6.34	110.54	103.44
1	A	170	ASP	N-CA-C	6.33	118.97	110.35
2	B	20	G	N9-C1'-C2'	6.32	123.48	114.00
42	W	460	SER	N-CA-C	6.29	118.14	111.28
39	T	192	PRO	O-C-N	6.29	124.11	121.15
30	r	60	PRO	N-CA-CB	6.28	109.85	103.25
16	o	40	THR	CA-C-N	6.27	131.49	122.40
16	o	40	THR	C-N-CA	6.27	131.49	122.40
42	W	106	ALA	CA-C-N	6.26	126.21	119.76
42	W	106	ALA	C-N-CA	6.26	126.21	119.76
32	I	394	PRO	N-CA-CB	6.25	110.44	103.44
39	T	354	ILE	CB-CA-C	-6.23	103.18	110.91
17	p	198	GLY	N-CA-C	-6.23	104.80	112.77
3	C	89	LEU	N-CA-C	6.19	118.82	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	x	1003	ILE	N-CA-C	6.18	119.15	108.95
42	W	116	GLU	CA-C-N	6.17	126.53	119.92
42	W	116	GLU	C-N-CA	6.17	126.53	119.92
39	T	381	HIS	CA-C-N	6.15	127.52	119.84
39	T	381	HIS	C-N-CA	6.15	127.52	119.84
1	A	204	LEU	N-CA-C	6.13	118.93	111.82
13	F	34	G	C2'-C3'-O3'	-6.12	104.52	113.70
3	C	843	VAL	CB-CA-C	-6.11	103.89	112.14
37	R	181	PRO	N-CA-C	6.11	125.06	112.47
32	I	761	PRO	N-CA-CB	6.11	109.99	103.52
35	O	40	LYS	N-CA-C	6.10	117.62	110.97
16	o	73	ASN	N-CA-C	6.10	119.77	111.17
42	W	281	ILE	N-CA-C	6.09	117.45	111.67
4	D	1006	LYS	CA-C-N	6.08	126.25	119.32
4	D	1006	LYS	C-N-CA	6.08	126.25	119.32
29	L	548	PRO	N-CA-CB	6.06	110.22	103.44
28	J	412	ASP	N-CA-C	6.05	117.44	108.60
39	T	327	SER	N-CA-C	-6.03	102.75	110.53
3	C	264	ILE	CB-CA-C	-6.03	105.71	111.44
1	A	132	ILE	CA-C-O	6.00	123.23	119.51
38	S	128	ILE	CA-C-N	5.98	128.58	120.44
38	S	128	ILE	C-N-CA	5.98	128.58	120.44
46	x	821	ASP	O-C-N	5.98	127.26	121.28
16	o	79	ILE	CA-C-N	5.98	125.78	120.10
16	o	79	ILE	C-N-CA	5.98	125.78	120.10
16	o	75	ARG	N-CA-CB	-5.98	102.66	111.51
17	p	200	ALA	N-CA-C	-5.97	104.85	111.36
35	O	223	LEU	N-CA-C	5.97	120.84	113.50
17	p	46	MET	N-CA-C	-5.96	104.69	111.07
12	g	67	ILE	CB-CA-C	-5.96	104.80	111.23
3	C	707	ILE	N-CA-C	5.94	118.52	111.09
12	n	67	ILE	CB-CA-C	-5.94	104.82	111.23
2	B	40	U	N1-C1'-C2'	5.93	120.90	112.00
32	I	625	PRO	N-CA-CB	5.92	109.84	103.33
45	Z	525	TYR	N-CA-C	5.92	118.55	108.67
16	o	50	SER	CA-C-O	5.89	127.80	121.55
42	W	285	SER	CB-CA-C	-5.89	109.79	116.63
39	T	254	VAL	CB-CA-C	-5.87	102.39	110.96
1	A	487	LEU	N-CA-C	5.87	119.12	109.85
3	C	922	GLU	CA-C-N	5.87	125.80	119.76
3	C	922	GLU	C-N-CA	5.87	125.80	119.76
17	p	161	GLU	N-CA-C	-5.85	106.09	113.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	167	PRO	N-CA-C	5.85	117.84	110.70
3	C	358	LYS	N-CA-C	-5.84	101.77	110.23
1	A	387	PHE	N-CA-C	5.83	118.11	111.11
16	o	113	LYS	N-CA-C	5.80	118.36	111.33
24	4	27	PRO	CA-CB-CG	5.79	115.51	104.50
31	K	107	VAL	CA-CB-CG1	5.79	120.25	110.40
42	W	464	MET	CA-C-N	-5.77	113.07	119.19
42	W	464	MET	C-N-CA	-5.77	113.07	119.19
39	T	188	PRO	N-CA-C	5.76	120.24	111.19
3	C	536	ARG	N-CA-C	-5.75	100.92	109.83
1	A	2199	ILE	CB-CA-C	-5.74	104.50	112.02
4	D	1135	LEU	CA-C-N	5.73	125.66	119.76
4	D	1135	LEU	C-N-CA	5.73	125.66	119.76
1	A	698	PRO	CA-C-N	5.72	132.47	121.54
1	A	698	PRO	C-N-CA	5.72	132.47	121.54
39	T	187	LYS	CB-CA-C	5.71	115.25	111.20
4	D	782	PHE	N-CA-C	5.70	118.08	109.41
5	E	309	VAL	CB-CA-C	-5.70	104.06	110.96
1	A	243	ASN	N-CA-C	5.69	118.26	111.71
16	o	149	LYS	CB-CA-C	-5.67	101.99	110.16
1	A	2153	THR	N-CA-C	-5.67	101.79	109.95
2	B	25	C	C1'-C2'-O2'	5.67	120.30	111.80
13	F	33	G	C4'-C3'-O3'	5.67	121.50	113.00
4	D	1291	LEU	CA-C-N	5.65	125.97	119.92
4	D	1291	LEU	C-N-CA	5.65	125.97	119.92
3	C	747	ASP	N-CA-C	5.64	117.98	107.99
3	C	544	VAL	CA-C-N	5.64	125.84	120.31
3	C	544	VAL	C-N-CA	5.64	125.84	120.31
46	x	981	PRO	N-CA-CB	5.62	109.16	103.25
16	o	71	VAL	O-C-N	-5.62	115.55	122.57
3	C	446	LYS	CA-C-N	-5.62	112.73	118.85
3	C	446	LYS	C-N-CA	-5.62	112.73	118.85
7	i	52	LYS	CA-C-N	-5.61	114.15	119.76
7	i	52	LYS	C-N-CA	-5.61	114.15	119.76
1	A	118	VAL	CB-CA-C	-5.61	101.01	110.71
38	S	66	ASP	CA-C-N	5.59	125.26	119.56
38	S	66	ASP	C-N-CA	5.59	125.26	119.56
4	D	1048	VAL	N-CA-C	-5.59	106.35	113.22
1	A	2225	LEU	N-CA-C	5.55	117.84	109.23
1	A	314	ILE	CA-CB-CG1	-5.55	100.96	110.40
23	3	917	PRO	N-CA-C	-5.55	101.04	112.47
37	R	96	ILE	N-CA-C	-5.54	102.38	109.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	b	52	LYS	CA-C-N	-5.53	114.23	119.76
7	b	52	LYS	C-N-CA	-5.53	114.23	119.76
5	E	322	LYS	N-CA-C	-5.53	98.18	108.02
36	P	50	ALA	CA-C-N	5.52	125.36	119.28
36	P	50	ALA	C-N-CA	5.52	125.36	119.28
46	x	443	ASN	N-CA-C	5.52	117.29	111.28
16	o	32	PRO	CA-C-N	5.51	130.65	122.99
16	o	32	PRO	C-N-CA	5.51	130.65	122.99
16	o	34	ILE	CA-C-O	-5.50	114.25	120.74
3	C	281	ILE	CB-CA-C	-5.50	104.94	111.97
42	W	279	LYS	N-CA-CB	5.49	119.77	110.49
1	A	2241	ASN	N-CA-C	5.49	118.27	110.10
39	T	307	SER	N-CA-C	5.48	117.52	109.24
45	Z	520	LYS	CA-C-N	-5.48	112.99	119.84
45	Z	520	LYS	C-N-CA	-5.48	112.99	119.84
1	A	2203	ASN	N-CA-C	5.48	120.78	109.11
42	W	151	LYS	N-CA-C	5.48	118.33	109.40
1	A	664	HIS	N-CA-C	-5.48	100.87	109.25
15	H	157	G	P-O5'-C5'	-5.48	112.69	120.90
16	o	16	THR	O-C-N	5.47	129.46	123.22
5	E	281	VAL	N-CA-C	5.46	116.17	108.36
5	E	284	PHE	N-CA-C	5.46	119.44	112.34
16	o	159	GLU	N-CA-C	-5.46	104.98	111.69
3	C	469	ASP	CA-C-N	-5.45	113.66	119.98
3	C	469	ASP	C-N-CA	-5.45	113.66	119.98
1	A	157	ASP	N-CA-C	5.44	120.03	112.90
7	i	5	LYS	N-CA-C	5.44	118.13	111.82
24	4	81	GLY	N-CA-C	-5.44	108.34	115.47
39	T	421	VAL	N-CA-C	5.44	116.11	108.17
22	2	642	PRO	CA-C-N	-5.44	113.02	119.05
22	2	642	PRO	C-N-CA	-5.44	113.02	119.05
5	E	237	SER	N-CA-C	5.42	117.94	110.35
1	A	487	LEU	N-CA-CB	-5.42	102.42	111.20
4	D	1228	VAL	CB-CA-C	-5.42	104.94	112.04
3	C	907	VAL	CB-CA-C	-5.42	105.04	110.89
1	A	427	VAL	CB-CA-C	-5.40	104.99	111.85
42	W	470	SER	CA-C-N	5.40	125.06	119.56
42	W	470	SER	C-N-CA	5.40	125.06	119.56
3	C	744	ILE	CB-CA-C	-5.40	102.58	110.62
39	T	317	VAL	CB-CA-C	-5.38	104.99	112.04
16	o	125	VAL	CA-C-N	5.37	128.01	120.28
16	o	125	VAL	C-N-CA	5.37	128.01	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	p	158	LEU	CA-C-N	5.37	126.55	119.84
17	p	158	LEU	C-N-CA	5.37	126.55	119.84
3	C	420	CYS	CA-CB-SG	-5.36	102.07	114.40
4	D	749	GLY	N-CA-C	-5.36	108.31	114.69
5	E	156	SER	N-CA-C	5.36	116.67	108.42
16	o	40	THR	N-CA-C	-5.34	106.26	112.89
1	A	2100	THR	N-CA-C	-5.34	106.76	113.28
4	D	811	SER	N-CA-C	5.34	115.18	108.45
36	P	194	PHE	N-CA-C	5.34	117.78	108.76
37	R	231	VAL	CB-CA-C	-5.34	105.08	112.24
3	C	815	VAL	CB-CA-C	-5.34	105.14	111.97
40	U	6	GLY	CA-C-O	5.33	126.61	122.29
16	o	33	VAL	N-CA-CB	-5.33	103.73	111.52
39	T	281	ILE	CB-CA-C	-5.33	106.37	111.06
28	J	356	TYR	N-CA-C	-5.33	102.31	110.14
4	D	1228	VAL	N-CA-C	5.32	116.69	110.62
4	D	1693	ARG	CA-C-N	5.32	125.13	119.28
4	D	1693	ARG	C-N-CA	5.32	125.13	119.28
42	W	462	HIS	N-CA-C	5.31	117.15	111.36
21	l	1125	PRO	CA-C-N	5.31	128.13	120.38
21	l	1125	PRO	C-N-CA	5.31	128.13	120.38
20	v	199	TRP	N-CA-C	5.30	117.28	107.73
18	w	50	TYR	N-CA-CB	-5.29	103.10	110.29
2	B	12	U	C4'-C3'-O3'	5.28	120.92	113.00
35	O	226	PRO	N-CA-C	5.28	123.35	112.47
17	p	20	LYS	N-CA-C	5.27	117.43	111.11
38	S	152	ARG	CA-C-N	5.26	125.18	119.76
38	S	152	ARG	C-N-CA	5.26	125.18	119.76
1	A	132	ILE	CA-C-N	5.26	126.42	119.84
1	A	132	ILE	C-N-CA	5.26	126.42	119.84
16	o	146	ASP	CA-C-N	5.26	130.03	122.40
16	o	146	ASP	C-N-CA	5.26	130.03	122.40
4	D	2096	ALA	CA-C-N	5.26	125.46	120.31
4	D	2096	ALA	C-N-CA	5.26	125.46	120.31
4	D	1127	CYS	CA-C-N	5.25	125.56	119.47
4	D	1127	CYS	C-N-CA	5.25	125.56	119.47
17	p	170	LEU	N-CA-C	-5.25	105.64	111.36
17	p	190	ALA	O-C-N	5.25	129.46	123.27
1	A	166	PHE	N-CA-C	5.25	117.27	110.40
34	N	100	LEU	N-CA-C	5.24	117.63	110.24
16	o	88	PRO	CB-CA-C	-5.24	103.98	112.62
1	A	429	ASN	N-CA-C	5.23	119.41	113.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	K	146	ILE	CA-CB-CG1	5.22	119.28	110.40
37	R	143	ILE	CB-CA-C	-5.22	105.29	111.97
37	R	411	TYR	N-CA-C	5.21	118.22	110.14
42	W	274	CYS	N-CA-C	5.21	117.40	110.53
17	p	48	MET	N-CA-C	5.21	119.63	113.28
3	C	809	ILE	O-C-N	5.20	123.75	120.42
17	p	51	GLN	N-CA-C	5.20	117.59	109.52
39	T	346	ILE	CB-CA-C	-5.20	103.36	110.96
15	H	171	U	C2'-C3'-O3'	-5.19	105.91	113.70
3	C	863	ILE	CA-C-O	5.18	122.21	119.15
29	L	774	VAL	CA-CB-CG2	5.18	119.20	110.40
3	C	97	VAL	N-CA-C	5.17	116.06	110.21
4	D	488	LEU	N-CA-C	5.17	119.68	113.17
41	V	483	GLU	N-CA-C	5.17	116.99	111.36
39	T	414	ALA	N-CA-C	-5.16	100.29	108.14
17	p	83	TYR	CA-C-O	-5.16	115.17	121.05
4	D	572	ASP	N-CA-C	-5.16	103.34	110.35
42	W	399	LYS	N-CA-C	5.14	117.74	110.50
1	A	99	VAL	CB-CA-C	-5.13	105.21	112.14
3	C	308	CYS	CB-CA-C	-5.13	100.73	109.51
3	C	307	VAL	N-CA-C	5.13	115.43	107.78
3	C	552	ILE	CB-CA-C	-5.13	104.32	110.99
3	C	866	SER	CA-C-N	5.13	126.25	119.84
3	C	866	SER	C-N-CA	5.13	126.25	119.84
28	J	275	ASN	N-CA-C	5.12	116.61	108.67
9	k	99	MET	N-CA-C	5.12	116.86	108.76
17	p	38	VAL	O-C-N	5.12	127.11	121.83
9	d	99	MET	N-CA-C	5.12	116.84	108.76
16	o	90	LEU	CA-C-O	-5.12	113.19	120.51
18	w	150	ILE	N-CA-CB	-5.11	102.81	111.50
42	W	176	GLU	N-CA-C	5.11	118.67	111.52
17	p	168	SER	N-CA-C	-5.11	105.90	111.82
38	S	32	ALA	CA-C-N	5.10	124.89	119.28
38	S	32	ALA	C-N-CA	5.10	124.89	119.28
16	o	90	LEU	O-C-N	5.10	129.37	122.59
39	T	401	PRO	N-CA-C	5.09	122.96	112.47
15	H	155	C	P-O3'-C3'	5.09	127.84	120.20
3	C	125	ASN	N-CA-C	5.09	116.51	111.07
1	A	2310	ARG	CG-CD-NE	5.09	123.19	112.00
11	e	85	THR	N-CA-C	-5.09	105.92	112.68
15	H	156	U	C4'-C3'-C2'	5.08	107.68	102.60
1	A	424	ILE	CA-C-N	5.08	126.19	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	424	ILE	C-N-CA	5.08	126.19	119.84
16	o	83	LEU	N-CA-C	5.08	117.47	111.33
37	R	88	ILE	N-CA-C	-5.08	102.54	109.55
4	D	1875	VAL	CA-C-N	5.08	124.52	119.24
4	D	1875	VAL	C-N-CA	5.08	124.52	119.24
17	p	197	ASP	O-C-N	-5.08	115.79	122.39
33	Q	568	ARG	CA-C-N	5.07	125.08	119.90
33	Q	568	ARG	C-N-CA	5.07	125.08	119.90
17	p	201	GLY	N-CA-C	-5.07	106.28	112.77
41	V	459	ILE	CB-CA-C	-5.07	105.48	111.97
34	N	102	CYS	CB-CA-C	-5.07	99.59	111.09
1	A	539	ARG	CB-CA-C	-5.06	101.31	109.72
3	C	243	ILE	CB-CA-C	-5.06	105.50	111.97
4	D	574	GLN	N-CA-C	5.05	117.90	111.69
3	C	310	SER	N-CA-C	5.05	116.66	109.14
39	T	479	THR	N-CA-C	5.05	117.62	109.40
13	F	34	G	C4'-C3'-O3'	5.03	120.55	113.00
39	T	253	ILE	CB-CA-C	-5.03	102.76	110.50
20	v	78	HIS	N-CA-C	-5.01	105.82	111.28
38	S	126	HIS	N-CA-C	5.01	117.28	109.52
41	V	467	LEU	CB-CA-C	-5.01	100.45	110.42
16	o	99	SER	N-CA-CB	-5.00	102.96	111.17

There are no chirality outliers.

All (32) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	1	1028	HIS	Peptide
21	1	1105	GLU	Peptide
21	1	1107	GLN	Peptide
21	1	220	GLN	Peptide
21	1	415	LEU	Peptide
21	1	418	PRO	Peptide
21	1	460	PRO	Peptide
21	1	717	THR	Peptide
21	1	943	LYS	Peptide
22	2	558	ARG	Peptide
23	3	261	PHE	Peptide
23	3	530	ASP	Peptide
23	3	552	ARG	Peptide
23	3	916	ASN	Peptide
27	7	74	GLN	Peptide

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Mol	Chain	Res	Type	Group
1	A	166	PHE	Peptide
1	A	346	ASP	Peptide
1	A	408	PRO	Peptide
1	A	433	GLU	Peptide
1	A	697	MET	Peptide
1	A	941	LYS	Peptide
3	C	622	GLU	Peptide
3	C	736	GLY	Peptide
3	C	823	ALA	Peptide
4	D	430	LEU	Peptide
34	N	36	PRO	Peptide
37	R	94	GLY	Peptide
39	T	400	PHE	Peptide,Mainchain
43	X	193	ASN	Peptide
9	d	112	ASN	Peptide
9	k	112	ASN	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	16399	0	16176	1449	0
2	B	1768	0	897	120	0
3	C	6716	0	6691	916	0
4	D	8528	0	3745	82	0
5	E	2338	0	2272	156	0
6	a	399	0	173	0	0
6	h	393	0	170	0	0
7	b	405	0	170	0	0
7	i	422	0	177	10	0
8	c	406	0	170	0	0
8	j	406	0	170	0	0
9	d	480	0	200	2	0
9	k	422	0	175	2	0
10	f	361	0	158	1	0
10	m	361	0	158	0	0
11	e	391	0	163	3	0
11	l	391	0	163	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	g	363	0	160	1	0
12	n	334	0	143	3	0
13	F	1988	0	1005	185	0
14	G	1545	0	786	208	0
15	H	2886	0	1463	277	0
16	o	804	0	350	9	0
17	p	813	0	366	14	0
18	w	2373	0	1301	97	0
19	u	520	0	214	0	0
20	v	936	0	591	82	0
21	1	7702	0	7389	336	0
22	2	1252	0	1040	61	0
23	3	9195	0	9091	501	0
24	4	527	0	438	41	0
25	5	807	0	729	28	0
26	6	670	0	654	21	0
27	7	540	0	509	24	0
28	J	3463	0	2544	116	0
29	L	2260	0	1776	100	0
30	q	659	0	296	7	0
30	r	654	0	294	6	0
30	s	335	0	168	0	0
30	t	335	0	168	1	0
31	K	979	0	739	12	0
32	I	2778	0	1238	22	0
33	Q	6528	0	2814	6	0
34	N	1184	0	1190	75	0
35	O	2273	0	2244	257	0
36	P	829	0	814	200	0
37	R	2188	0	2102	412	0
38	S	1236	0	1210	140	0
39	T	2457	0	2416	253	0
40	U	193	0	196	44	0
41	V	2243	0	971	50	0
42	W	2384	0	1055	134	0
43	X	1012	0	733	17	0
44	Y	743	0	613	67	0
45	Z	755	0	591	115	0
46	x	2882	0	1308	23	0
47	y	1133	0	519	2	0
48	A	36	0	6	10	0
49	A	5	0	4	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	C	32	0	12	11	0
51	C	1	0	0	0	0
51	F	5	0	0	0	0
52	6	3	0	0	0	0
52	N	3	0	0	0	0
52	O	3	0	0	2	0
52	v	1	0	0	0	0
All	All	113433	0	84078	5291	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 27.

All (5291) 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)
44:Y:37:TRP:CH2	45:Z:498:GLY:HA2	1.23	1.65
1:A:1758:PRO:HA	21:1:938:TRP:CD1	1.28	1.59
1:A:2270:PHE:HB3	4:D:1264:PRO:CB	1.34	1.56
3:C:149:LEU:HD13	3:C:427:PHE:CD2	1.38	1.54
1:A:2270:PHE:CG	4:D:1264:PRO:CB	1.89	1.54
3:C:77:VAL:HG11	39:T:196:LEU:CG	1.39	1.52
20:v:51:LEU:CB	21:1:1141:LEU:HD12	1.40	1.51
44:Y:37:TRP:CH2	45:Z:498:GLY:CA	1.93	1.51
37:R:442:ARG:HH11	37:R:443:GLY:C	1.17	1.50
1:A:2270:PHE:CB	4:D:1264:PRO:CB	1.86	1.49
45:Z:564:PRO:HB2	45:Z:582:TYR:CG	1.45	1.49
20:v:51:LEU:HB3	21:1:1141:LEU:CD1	1.40	1.48
18:w:485:ASN:CA	23:3:978:LEU:HD21	1.42	1.47
36:P:193:VAL:HG23	36:P:194:PHE:CD2	1.46	1.47
1:A:1758:PRO:HA	21:1:938:TRP:NE1	1.16	1.46
1:A:844:GLU:CB	37:R:422:MET:CE	1.94	1.45
36:P:193:VAL:CG2	36:P:194:PHE:HD2	1.28	1.45
35:O:149:LYS:HD2	35:O:290:LYS:CE	1.49	1.43
37:R:414:ARG:NH1	45:Z:598:PHE:CZ	1.86	1.43
38:S:57:ILE:HD13	42:W:97:ASN:CB	1.44	1.42
14:G:21:A:H2	35:O:212:LYS:CB	1.30	1.42
3:C:705:VAL:HG23	3:C:717:PHE:CD2	1.55	1.41
3:C:77:VAL:HG12	39:T:196:LEU:C	1.46	1.41
1:A:384:VAL:HG12	3:C:331:PHE:CE2	1.56	1.40
3:C:79:THR:CG2	39:T:199:VAL:HB	1.51	1.40
35:O:189:PRO:HG3	42:W:223:ARG:CA	1.48	1.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:HIS:HD2	1:A:81:PHE:CE2	1.37	1.40
1:A:2270:PHE:CD1	4:D:1264:PRO:CB	2.03	1.40
28:J:293:ASN:CB	29:L:225:TYR:CB	1.98	1.39
3:C:77:VAL:CG1	39:T:196:LEU:C	1.94	1.39
3:C:79:THR:HG23	39:T:199:VAL:CB	1.49	1.39
5:E:260:ARG:NH1	5:E:273:CYS:SG	1.95	1.39
1:A:299:ILE:CG1	1:A:1342:TRP:HZ3	1.34	1.39
28:J:339:TRP:HA	37:R:116:TYR:CE2	1.58	1.38
3:C:387:ASP:O	3:C:388:VAL:HG12	1.20	1.37
37:R:442:ARG:CD	37:R:443:GLY:H	1.37	1.37
4:D:863:THR:CB	23:3:599:GLU:HA	1.53	1.37
1:A:380:LEU:CB	3:C:354:ARG:HG3	1.54	1.36
37:R:92:SER:CA	38:S:19:SER:HB2	1.55	1.36
1:A:762:ARG:HH22	36:P:226:LYS:NZ	1.19	1.35
29:L:216:PHE:CD1	35:O:113:ASN:CA	2.08	1.35
28:J:339:TRP:HA	37:R:116:TYR:CD2	1.60	1.35
37:R:414:ARG:NH1	45:Z:598:PHE:CE2	1.93	1.35
1:A:844:GLU:CB	37:R:422:MET:HE3	1.51	1.35
1:A:1758:PRO:CA	21:1:938:TRP:NE1	1.89	1.34
3:C:149:LEU:CD1	3:C:427:PHE:CD2	2.08	1.34
37:R:442:ARG:HD3	37:R:443:GLY:N	1.05	1.34
37:R:414:ARG:NE	45:Z:598:PHE:CZ	1.95	1.34
3:C:452:THR:CG2	3:C:577:PHE:HD2	1.40	1.34
38:S:39:PHE:CB	38:S:129:PHE:CZ	2.10	1.34
15:H:45:C:N4	18:w:395:TRP:CD1	1.95	1.34
32:I:280:GLU:C	32:I:288:THR:CB	2.00	1.33
1:A:121:HIS:NE2	1:A:481:PHE:HB3	1.42	1.33
15:H:42:G:OP1	20:v:77:LYS:HB2	1.21	1.32
1:A:1482:GLU:O	1:A:1486:GLU:HG2	1.29	1.32
3:C:145:PHE:CA	3:C:312:SER:HB2	1.57	1.31
38:S:57:ILE:CD1	42:W:97:ASN:CB	2.08	1.31
37:R:414:ARG:CZ	45:Z:598:PHE:CZ	2.14	1.31
3:C:670:SER:HA	3:C:823:ALA:CB	1.60	1.31
23:3:687:SER:OG	23:3:1206:LYS:HD2	1.26	1.31
1:A:73:HIS:CD2	1:A:81:PHE:CZ	2.20	1.30
1:A:299:ILE:HG13	1:A:1342:TRP:CZ3	1.67	1.30
36:P:212:ASN:O	39:T:458:SER:HA	1.30	1.30
1:A:264:PHE:CZ	1:A:459:LEU:HD13	1.66	1.30
1:A:1342:TRP:CD2	3:C:921:LEU:HD13	1.65	1.30
32:I:280:GLU:CB	32:I:288:THR:CB	2.08	1.29
1:A:296:PHE:CG	3:C:656:ALA:HB2	1.66	1.29

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:P:211:VAL:HG13	39:T:457:GLY:CA	1.62	1.29
14:G:-9:C:C4	40:U:18:TYR:CE1	2.20	1.29
1:A:73:HIS:CD2	1:A:81:PHE:CE2	2.20	1.28
3:C:77:VAL:CG1	39:T:196:LEU:HG	1.63	1.28
3:C:705:VAL:CG2	3:C:717:PHE:CE2	2.15	1.28
20:v:63:HIS:CB	20:v:69:TYR:CB	2.08	1.28
1:A:1342:TRP:CE3	3:C:921:LEU:HD13	1.69	1.28
1:A:1364:LEU:CD1	41:V:461:LEU:CB	2.11	1.28
37:R:92:SER:HA	38:S:19:SER:CB	1.61	1.28
1:A:1757:GLU:O	21:1:938:TRP:CZ2	1.87	1.26
3:C:78:GLU:O	39:T:198:ARG:HA	1.35	1.26
3:C:145:PHE:HA	3:C:312:SER:CB	1.65	1.26
14:G:-9:C:C5	40:U:18:TYR:CE1	2.23	1.26
36:P:211:VAL:CG1	39:T:457:GLY:HA3	1.65	1.26
36:P:193:VAL:CG2	36:P:194:PHE:CD2	2.09	1.26
5:E:146:ARG:NH1	5:E:148:LYS:CE	1.98	1.25
37:R:414:ARG:CZ	45:Z:598:PHE:HZ	1.47	1.25
1:A:299:ILE:CG1	1:A:1342:TRP:CZ3	2.18	1.25
1:A:2268:LEU:HD23	4:D:1261:PRO:O	1.22	1.25
38:S:131:ARG:HD3	38:S:132:VAL:O	1.09	1.25
38:S:39:PHE:CG	38:S:129:PHE:HE2	1.53	1.25
1:A:2268:LEU:HD22	4:D:1261:PRO:CB	1.65	1.25
1:A:299:ILE:CD1	3:C:921:LEU:HB2	1.67	1.24
1:A:380:LEU:HD22	3:C:354:ARG:O	1.24	1.24
14:G:131:U:OP1	18:w:396:LEU:HD13	1.31	1.24
20:v:21:GLU:CG	21:1:1101:LEU:CB	2.14	1.24
24:4:14:THR:HA	24:4:59:VAL:O	1.32	1.24
38:S:39:PHE:HB2	38:S:129:PHE:CZ	1.66	1.24
1:A:1758:PRO:CA	21:1:938:TRP:CD1	2.16	1.24
3:C:679:PRO:HB2	3:C:807:GLN:OE1	1.25	1.24
3:C:84:GLU:O	39:T:238:LEU:HD23	1.34	1.24
1:A:2113:LYS:HE3	4:D:1229:ASP:O	1.33	1.23
14:G:21:A:C2	35:O:212:LYS:CB	2.21	1.23
30:q:22:ASN:CB	30:r:55:ILE:HA	1.68	1.23
1:A:380:LEU:HB2	3:C:354:ARG:CG	1.67	1.23
1:A:593:ARG:NH1	1:A:1565:LYS:HE2	1.53	1.23
44:Y:37:TRP:CZ3	45:Z:498:GLY:CA	2.20	1.23
44:Y:37:TRP:CZ3	45:Z:498:GLY:HA2	1.73	1.23
1:A:121:HIS:CE1	1:A:481:PHE:HB3	1.73	1.23
3:C:140:HIS:CG	3:C:230:ASP:HB2	1.74	1.22
1:A:1342:TRP:CD2	3:C:921:LEU:CD1	2.22	1.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:w:485:ASN:CB	23:3:978:LEU:HD21	1.68	1.22
1:A:762:ARG:HH22	36:P:226:LYS:CE	1.51	1.22
3:C:78:GLU:HG2	3:C:80:ILE:CD1	1.69	1.22
3:C:145:PHE:CA	3:C:312:SER:CB	2.18	1.22
18:w:284:ARG:CB	18:w:295:SER:O	1.87	1.22
28:J:256:LYS:O	29:L:232:TYR:CD2	1.93	1.22
3:C:77:VAL:HG13	39:T:196:LEU:O	1.40	1.21
3:C:497:LEU:HD13	3:C:577:PHE:CZ	1.76	1.21
13:F:28:A:O2'	34:N:39:GLY:HA2	1.40	1.21
44:Y:18:VAL:CB	45:Z:600:ARG:HH21	1.53	1.21
15:H:42:G:OP2	20:v:77:LYS:HD3	1.38	1.21
35:O:149:LYS:HD2	35:O:290:LYS:NZ	1.53	1.21
1:A:1320:LYS:HE2	37:R:434:TYR:CE1	1.76	1.21
3:C:137:HIS:CD2	3:C:236:MET:HB2	1.75	1.21
1:A:2298:LEU:HB3	4:D:1283:PRO:CB	1.71	1.20
37:R:442:ARG:CD	37:R:443:GLY:N	1.95	1.20
38:S:39:PHE:CB	38:S:129:PHE:HZ	1.46	1.20
1:A:227:ARG:HA	1:A:416:GLY:O	1.39	1.20
15:H:45:C:C4	18:w:395:TRP:CD1	2.29	1.20
1:A:755:HIS:ND1	36:P:223:PHE:CG	2.10	1.19
3:C:705:VAL:HG23	3:C:717:PHE:CE2	1.75	1.19
5:E:146:ARG:NH1	5:E:148:LYS:HE3	1.53	1.19
38:S:39:PHE:CG	38:S:129:PHE:CE2	2.30	1.19
1:A:380:LEU:HB3	3:C:354:ARG:NH1	1.58	1.19
32:I:280:GLU:O	32:I:288:THR:CB	1.90	1.19
1:A:380:LEU:O	3:C:354:ARG:HG2	1.37	1.18
13:F:68:C:N4	36:P:33:ARG:HB3	1.55	1.18
1:A:402:ILE:HG21	3:C:268:LYS:NZ	1.55	1.18
29:L:209:ASP:OD2	35:O:111:ASP:HB2	1.39	1.18
1:A:695:ASP:HB3	39:T:374:SER:OG	1.40	1.18
1:A:2325:VAL:HG13	4:D:788:GLY:O	1.40	1.18
23:3:699:VAL:HA	23:3:715:MET:O	1.40	1.18
37:R:442:ARG:NH1	37:R:443:GLY:C	2.00	1.18
1:A:2268:LEU:CD2	4:D:1261:PRO:O	1.91	1.18
1:A:299:ILE:HD11	3:C:921:LEU:CB	1.75	1.17
1:A:1290:LYS:HE2	40:U:13:SER:CA	1.74	1.17
3:C:149:LEU:HD13	3:C:427:PHE:CG	1.79	1.17
1:A:705:LYS:CB	37:R:251:ILE:HD12	1.72	1.17
2:B:42:U:N3	14:G:-3:A:H2	1.42	1.17
3:C:140:HIS:CG	3:C:230:ASP:CB	2.27	1.17
1:A:696:MET:CB	39:T:415:ILE:CD1	2.22	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:77:VAL:CG1	39:T:196:LEU:O	1.89	1.16
1:A:86:ARG:HH22	37:R:211:ARG:CG	1.57	1.16
1:A:417:ARG:HH22	2:B:58:U:H5"	1.03	1.16
1:A:1290:LYS:CE	40:U:13:SER:HA	1.75	1.16
3:C:78:GLU:CG	3:C:80:ILE:HD11	1.72	1.16
3:C:221:ILE:HD11	3:C:479:THR:OG1	1.46	1.16
1:A:758:ARG:HB3	36:P:227:TYR:CE2	1.79	1.16
29:L:216:PHE:HE1	35:O:112:VAL:C	1.53	1.16
3:C:679:PRO:CB	3:C:807:GLN:OE1	1.95	1.15
1:A:338:VAL:CG2	3:C:867:PRO:HG3	1.74	1.15
1:A:755:HIS:CE1	36:P:223:PHE:CG	2.35	1.14
37:R:92:SER:C	38:S:19:SER:HB2	1.71	1.14
38:S:131:ARG:CD	38:S:132:VAL:O	1.95	1.14
35:O:189:PRO:CG	42:W:223:ARG:HA	1.76	1.14
1:A:1262:LYS:HG2	37:R:431:ASP:CB	1.77	1.14
1:A:2298:LEU:O	4:D:1283:PRO:CB	1.95	1.14
3:C:670:SER:HA	3:C:823:ALA:HB1	1.27	1.14
5:E:74:PHE:CE1	5:E:81:LEU:HD21	1.82	1.14
24:4:28:LEU:O	24:4:32:LEU:HB2	1.48	1.14
32:I:373:GLU:CA	32:I:393:LYS:CB	2.26	1.14
37:R:101:ILE:O	37:R:104:GLN:HG3	1.48	1.14
46:x:664:PRO:O	46:x:667:ALA:HB3	1.46	1.14
1:A:305:ARG:CB	3:C:879:ASP:OD1	1.94	1.14
1:A:1405:LEU:HB3	37:R:415:LEU:HD23	1.29	1.14
15:H:156:U:H6	15:H:156:U:H5"	1.10	1.14
44:Y:18:VAL:CB	45:Z:600:ARG:NH2	2.10	1.14
1:A:1405:LEU:HB3	37:R:415:LEU:CD2	1.78	1.14
3:C:77:VAL:HG12	39:T:197:TYR:N	1.61	1.14
1:A:1342:TRP:CE2	3:C:921:LEU:CD1	2.31	1.13
13:F:27:A:N3	35:O:181:TYR:CE2	2.16	1.13
35:O:185:LYS:HD2	42:W:215:GLU:CB	1.79	1.13
14:G:11:A:C2	14:G:12:G:C8	2.36	1.13
3:C:452:THR:CG2	3:C:577:PHE:CD2	2.31	1.13
3:C:679:PRO:HD2	3:C:807:GLN:HB3	1.16	1.13
1:A:705:LYS:HB2	37:R:251:ILE:HD12	1.28	1.13
1:A:1548:TYR:CD2	1:A:1549:VAL:HG22	1.83	1.13
2:B:42:U:N3	14:G:-3:A:C2	2.15	1.13
1:A:762:ARG:NH2	36:P:226:LYS:NZ	1.95	1.13
1:A:439:GLN:NE2	1:A:614:TYR:CZ	2.18	1.12
1:A:1758:PRO:N	21:1:938:TRP:HE1	1.45	1.12
3:C:216:THR:HG22	3:C:245:HIS:HE1	0.97	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:81:VAL:HG13	39:T:201:SER:CB	1.77	1.12
3:C:140:HIS:CB	3:C:230:ASP:HB2	1.79	1.12
1:A:299:ILE:HD11	3:C:921:LEU:HB2	1.18	1.12
3:C:507:VAL:HG11	3:C:565:ILE:HG23	1.30	1.12
3:C:216:THR:HG22	3:C:245:HIS:CE1	1.85	1.12
13:F:68:C:C4	36:P:33:ARG:HB3	1.85	1.12
1:A:696:MET:CB	39:T:415:ILE:HD11	1.80	1.11
1:A:758:ARG:HB3	36:P:227:TYR:HE2	0.96	1.11
3:C:77:VAL:HG11	39:T:196:LEU:CB	1.79	1.11
14:G:-9:C:C4	40:U:18:TYR:CZ	2.38	1.11
23:3:687:SER:OG	23:3:1206:LYS:CD	1.97	1.11
1:A:762:ARG:NH2	36:P:226:LYS:CE	2.14	1.11
15:H:45:C:N4	18:w:395:TRP:NE1	1.98	1.11
37:R:420:LYS:HE3	37:R:420:LYS:HA	1.18	1.11
3:C:465:MET:HE1	3:C:475:MET:HG3	1.14	1.11
45:Z:566:TYR:CE2	45:Z:584:TRP:CZ3	2.39	1.11
1:A:692:ASP:HA	39:T:376:ARG:NH2	1.65	1.10
18:w:485:ASN:HD22	23:3:976:LYS:HG2	1.01	1.10
1:A:73:HIS:NE2	1:A:81:PHE:CE1	2.20	1.10
1:A:1548:TYR:HD2	1:A:1549:VAL:HG22	1.14	1.10
28:J:225:LEU:HD21	29:L:211:ASN:HB2	1.29	1.10
1:A:1757:GLU:C	21:1:938:TRP:HE1	1.60	1.10
32:I:296:PHE:HA	32:I:305:SER:CB	1.80	1.10
1:A:299:ILE:HG12	3:C:920:PRO:O	1.52	1.10
1:A:402:ILE:HG21	3:C:268:LYS:CE	1.81	1.10
3:C:470:PRO:HB3	3:C:500:THR:HG23	1.34	1.10
35:O:149:LYS:HD2	35:O:290:LYS:HE2	1.12	1.10
1:A:1305:SER:HB2	1:A:1310:ARG:NH1	1.66	1.09
1:A:1757:GLU:O	21:1:938:TRP:CE2	2.04	1.09
1:A:762:ARG:NH2	36:P:226:LYS:HE2	1.66	1.09
1:A:2287:ARG:NH2	4:D:1147:ASN:CB	2.15	1.09
18:w:485:ASN:HA	23:3:978:LEU:HD21	1.35	1.09
1:A:73:HIS:HD2	1:A:81:PHE:CD2	1.69	1.09
3:C:66:TYR:CD2	39:T:457:GLY:HA2	1.87	1.09
14:G:-9:C:N4	40:U:18:TYR:OH	1.86	1.08
44:Y:85:GLU:O	45:Z:502:ALA:N	1.85	1.08
1:A:76:MET:CE	1:A:88:TYR:CD2	2.36	1.08
1:A:1342:TRP:CE2	3:C:921:LEU:HD13	1.86	1.08
3:C:465:MET:CE	3:C:475:MET:HG3	1.82	1.08
35:O:149:LYS:CD	35:O:290:LYS:NZ	2.16	1.08
45:Z:566:TYR:CE2	45:Z:584:TRP:HZ3	1.71	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:299:ILE:HD11	3:C:921:LEU:CA	1.84	1.08
1:A:783:TYR:CE1	36:P:228:ILE:HG21	1.88	1.08
38:S:39:PHE:HB3	38:S:129:PHE:CZ	1.85	1.08
28:J:259:GLN:HE22	29:L:220:PRO:CD	1.66	1.08
3:C:497:LEU:CD1	3:C:577:PHE:CZ	2.36	1.07
32:I:280:GLU:CA	32:I:288:THR:CB	2.32	1.07
35:O:185:LYS:HE3	42:W:215:GLU:O	1.54	1.07
1:A:546:LEU:HD11	1:A:595:LYS:HD2	1.12	1.07
24:4:17:VAL:HA	24:4:85:ARG:O	1.53	1.07
29:L:216:PHE:CE1	35:O:113:ASN:N	2.21	1.07
1:A:264:PHE:HE1	1:A:455:VAL:HG13	1.15	1.07
3:C:670:SER:CB	3:C:823:ALA:HB3	1.85	1.07
15:H:45:C:H2'	18:w:394:TYR:CE2	1.90	1.07
1:A:744:LYS:CE	36:P:213:ASP:HA	1.84	1.06
18:w:485:ASN:O	23:3:978:LEU:CD2	2.03	1.06
13:F:68:C:C4	36:P:33:ARG:CB	2.38	1.06
1:A:587:GLN:CG	1:A:1550:GLY:O	2.04	1.06
1:A:86:ARG:HH22	37:R:211:ARG:HG2	1.15	1.05
1:A:264:PHE:CE1	1:A:455:VAL:HG13	1.90	1.05
35:O:132:ARG:HH11	38:S:149:SER:HB3	1.15	1.05
38:S:39:PHE:CB	38:S:129:PHE:CE2	2.40	1.05
1:A:305:ARG:HB3	3:C:879:ASP:OD1	1.55	1.05
1:A:532:THR:HG23	14:G:2:U:P	1.97	1.05
2:B:39:C:H4'	2:B:40:U:OP1	1.23	1.05
20:v:45:TYR:CE1	20:v:58:LEU:CD1	2.40	1.05
1:A:705:LYS:CG	37:R:251:ILE:HD12	1.86	1.05
1:A:1364:LEU:HD13	41:V:461:LEU:CB	1.86	1.05
1:A:1758:PRO:CA	21:1:938:TRP:HE1	1.60	1.05
3:C:452:THR:HG22	3:C:577:PHE:HD2	1.21	1.05
1:A:1342:TRP:CZ3	3:C:921:LEU:HD13	1.92	1.05
1:A:168:PRO:HG3	1:A:559:ASP:HB3	1.39	1.04
1:A:301:LYS:HE3	3:C:940:ARG:HA	1.38	1.04
39:T:399:LYS:CG	39:T:406:ILE:HD11	1.87	1.04
1:A:369:GLU:O	1:A:371:LEU:N	1.88	1.04
1:A:692:ASP:HA	39:T:376:ARG:HH22	1.18	1.04
3:C:228:PHE:HA	3:C:256:CYS:O	1.57	1.04
4:D:863:THR:CB	23:3:599:GLU:CA	2.35	1.04
37:R:178:ARG:HD3	37:R:194:GLN:HE22	1.17	1.04
1:A:1307:MET:HB3	1:A:1310:ARG:HD2	1.07	1.04
1:A:1449:LYS:HE3	37:R:428:GLY:HA3	1.37	1.04
3:C:78:GLU:HG2	3:C:80:ILE:HD11	1.06	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:755:HIS:ND1	36:P:223:PHE:CD1	2.26	1.04
2:B:43:U:H4'	13:F:67:G:H1	0.93	1.04
3:C:488:VAL:HG13	3:C:609:LYS:HE2	1.39	1.04
13:F:25:C:H4'	13:F:26:U:OP2	1.22	1.04
7:i:88:LYS:CB	18:w:173:ILE:CB	2.34	1.04
37:R:436:VAL:HG23	37:R:437:TYR:CD1	1.93	1.04
1:A:402:ILE:CG2	3:C:268:LYS:NZ	2.19	1.04
1:A:593:ARG:HH12	1:A:1565:LYS:HE2	0.91	1.04
23:3:442:LEU:HD12	23:3:734:LEU:HD23	1.05	1.04
1:A:168:PRO:CG	1:A:559:ASP:HB3	1.87	1.03
1:A:1342:TRP:CE3	3:C:921:LEU:HD22	1.93	1.03
24:4:70:ALA:O	24:4:74:MET:CB	2.04	1.03
1:A:755:HIS:CE1	36:P:223:PHE:CD2	2.46	1.03
29:L:224:PHE:CD1	37:R:86:LEU:HD12	1.93	1.03
1:A:254:TYR:CZ	1:A:434:HIS:HB3	1.93	1.03
1:A:384:VAL:HG12	3:C:331:PHE:CD2	1.94	1.03
1:A:388:LEU:HB2	3:C:379:LYS:HD3	1.33	1.03
18:w:485:ASN:CA	23:3:978:LEU:CD2	2.36	1.03
18:w:485:ASN:C	23:3:978:LEU:HD21	1.82	1.03
37:R:92:SER:HA	38:S:19:SER:HB3	1.35	1.03
1:A:1306:LYS:NZ	2:B:38:C:O2'	1.90	1.03
28:J:273:TYR:CZ	37:R:228:PRO:HB3	1.94	1.03
35:O:116:TYR:OH	37:R:222:PRO:HD3	1.58	1.03
1:A:299:ILE:CD1	1:A:1342:TRP:CZ3	2.42	1.03
1:A:1305:SER:HB2	1:A:1310:ARG:HH11	1.16	1.03
15:H:105:G:H2'	15:H:106:G:H5''	1.37	1.03
23:3:442:LEU:HD12	23:3:734:LEU:CD2	1.87	1.03
1:A:254:TYR:CE2	1:A:434:HIS:HB2	1.94	1.02
1:A:642:ARG:HD3	2:B:28:A:H1'	1.37	1.02
2:B:43:U:H5'	13:F:67:G:H22	1.19	1.02
3:C:452:THR:HG22	3:C:577:PHE:CD2	1.94	1.02
28:J:331:GLN:HG2	37:R:98:TYR:OH	1.59	1.02
45:Z:564:PRO:CB	45:Z:582:TYR:CG	2.41	1.02
1:A:844:GLU:CB	37:R:422:MET:HE1	1.87	1.02
3:C:387:ASP:O	3:C:388:VAL:CG1	2.07	1.02
37:R:420:LYS:HG3	37:R:421:GLY:H	1.20	1.02
1:A:384:VAL:CG1	3:C:331:PHE:CE2	2.42	1.02
2:B:42:U:O2'	13:F:69:A:N3	1.93	1.02
13:F:68:C:C5	36:P:33:ARG:CB	2.42	1.02
37:R:434:TYR:O	37:R:435:ASN:ND2	1.90	1.02
44:Y:37:TRP:CD1	44:Y:83:CYS:HB2	1.92	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:339:PHE:CE1	1:A:406:TRP:CE3	2.46	1.02
13:F:36:A:H3'	13:F:37:C:H5''	1.39	1.02
18:w:411:CYS:SG	18:w:425:HIS:CE1	2.52	1.02
34:N:40:LYS:O	34:N:41:ARG:HG3	1.59	1.02
35:O:132:ARG:NH1	38:S:149:SER:HB3	1.73	1.02
1:A:1307:MET:CB	1:A:1310:ARG:HD2	1.90	1.01
45:Z:525:TYR:CD1	45:Z:526:ILE:HG23	1.95	1.01
3:C:511:GLY:O	3:C:576:ILE:CD1	2.07	1.01
1:A:532:THR:HG21	14:G:2:U:C5'	1.89	1.01
1:A:1457:HIS:HE1	1:A:1459:ARG:CG	1.74	1.01
3:C:132:VAL:HG12	3:C:226:VAL:HG23	1.43	1.01
3:C:349:PHE:CD1	3:C:356:PHE:CE1	2.49	1.01
20:v:50:HIS:NE2	21:1:1180:ARG:CB	2.24	1.01
1:A:1305:SER:CB	1:A:1310:ARG:HH11	1.73	1.00
1:A:2287:ARG:HH21	4:D:1147:ASN:CB	1.72	1.00
35:O:149:LYS:CG	35:O:290:LYS:NZ	2.25	1.00
42:W:420:ALA:O	42:W:438:ASP:N	1.93	1.00
3:C:261:ASP:OD2	50:C:1500:GTP:N1	1.92	1.00
3:C:703:GLU:OE2	3:C:740:THR:HG21	1.61	1.00
15:H:179:C:H2'	15:H:180:G:H8	1.25	1.00
3:C:705:VAL:CG2	3:C:717:PHE:CD2	2.39	1.00
14:G:17:U:O2	35:O:198:ILE:HD11	1.62	1.00
36:P:193:VAL:HG21	36:P:194:PHE:HD2	1.26	1.00
39:T:352:THR:HG22	39:T:373:LYS:C	1.86	1.00
3:C:81:VAL:CG1	39:T:201:SER:HB3	1.90	1.00
23:3:303:ALA:O	23:3:310:ILE:HA	1.61	1.00
1:A:623:LYS:O	48:A:2401:IHP:P4	2.20	1.00
29:L:209:ASP:OD1	35:O:111:ASP:N	1.95	1.00
2:B:43:U:H4'	13:F:67:G:N1	1.75	1.00
3:C:85:ASP:HB3	39:T:238:LEU:HG	1.43	1.00
3:C:129:ILE:HG22	3:C:199:LEU:HB3	1.44	1.00
1:A:1162:PRO:HG2	36:P:194:PHE:CE2	1.97	1.00
45:Z:525:TYR:CE1	45:Z:526:ILE:HG23	1.96	1.00
1:A:779:LEU:HD21	36:P:223:PHE:CE2	1.97	0.99
37:R:414:ARG:NE	45:Z:598:PHE:HZ	1.38	0.99
38:S:11:PRO:HB3	38:S:166:GLY:HA3	1.40	0.99
1:A:783:TYR:HB2	36:P:228:ILE:HG12	1.43	0.99
28:J:270:ASP:OD2	37:R:222:PRO:CG	2.10	0.99
1:A:86:ARG:NH2	37:R:211:ARG:CG	2.24	0.99
23:3:442:LEU:CD1	23:3:734:LEU:HD23	1.90	0.99
38:S:11:PRO:HB3	38:S:165:SER:O	1.62	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:264:PHE:CE1	1:A:459:LEU:HD13	1.96	0.99
13:F:28:A:HO2'	34:N:39:GLY:HA2	1.25	0.99
1:A:696:MET:CB	39:T:415:ILE:HD13	1.89	0.99
39:T:434:GLY:HA2	39:T:464:GLY:HA2	1.41	0.99
1:A:715:GLU:OE2	37:R:258:TRP:HZ3	1.43	0.99
1:A:2328:ALA:HB2	4:D:788:GLY:HA2	1.44	0.99
18:w:411:CYS:SG	18:w:425:HIS:HE1	1.84	0.99
45:Z:600:ARG:HB3	45:Z:600:ARG:HH11	1.24	0.99
1:A:2074:ARG:NH2	4:D:1044:VAL:O	1.96	0.99
3:C:64:LYS:HE3	36:P:206:LYS:HE2	1.45	0.99
3:C:137:HIS:CD2	3:C:236:MET:CB	2.45	0.99
13:F:68:C:C5	36:P:33:ARG:HB2	1.97	0.99
1:A:593:ARG:HH12	1:A:1565:LYS:CE	1.76	0.99
1:A:1457:HIS:NE2	37:R:425:GLY:N	2.09	0.99
18:w:485:ASN:HB3	23:3:978:LEU:CD2	1.92	0.99
35:O:149:LYS:CG	35:O:290:LYS:HZ3	1.75	0.99
37:R:92:SER:CA	38:S:19:SER:CB	2.29	0.99
20:v:54:TYR:CG	20:v:66:GLU:CG	2.45	0.99
29:L:216:PHE:CE1	35:O:113:ASN:CA	2.46	0.99
35:O:149:LYS:HZ3	35:O:290:LYS:HG2	1.23	0.98
3:C:78:GLU:O	39:T:198:ARG:CA	2.11	0.98
42:W:242:HIS:CB	42:W:325:LEU:O	2.10	0.98
1:A:76:MET:HE1	1:A:88:TYR:CD2	1.98	0.98
1:A:1084:PRO:HG2	36:P:188:TRP:HZ2	1.26	0.98
13:F:27:A:C4	35:O:181:TYR:CE2	2.50	0.98
36:P:210:PHE:CD2	39:T:455:GLN:OE1	2.16	0.98
37:R:420:LYS:HB2	45:Z:610:LEU:HD11	1.44	0.98
1:A:1211:ASP:OD1	41:V:505:LYS:CB	2.12	0.98
1:A:1481:VAL:HG11	1:A:1498:TRP:CE2	1.99	0.98
3:C:306:ASN:OD1	3:C:437:HIS:CE1	2.16	0.98
35:O:149:LYS:CD	35:O:290:LYS:HE2	1.94	0.98
36:P:30:TYR:OH	37:R:162:ALA:HA	1.63	0.98
15:H:42:G:OP2	20:v:77:LYS:CD	2.10	0.98
18:w:485:ASN:HB3	23:3:978:LEU:HD21	1.41	0.98
1:A:1307:MET:HB3	1:A:1310:ARG:CD	1.94	0.98
1:A:1757:GLU:O	21:1:938:TRP:HZ2	1.45	0.98
15:H:83:A:H2'	15:H:84:C:O4'	1.64	0.98
38:S:11:PRO:CB	38:S:165:SER:O	2.11	0.98
1:A:461:HIS:NE2	2:B:26:A:N6	2.12	0.97
3:C:84:GLU:O	39:T:238:LEU:CD2	2.12	0.97
3:C:670:SER:CA	3:C:823:ALA:HB3	1.94	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:R:412:ASP:CG	37:R:413:GLN:H	1.69	0.97
38:S:100:MET:HG2	38:S:108:ASN:OD1	1.64	0.97
41:V:548:ALA:CB	41:V:585:ILE:CB	2.42	0.97
3:C:66:TYR:HB3	39:T:456:PRO:O	1.64	0.97
3:C:81:VAL:HG13	39:T:201:SER:HB3	0.99	0.97
44:Y:37:TRP:CZ3	45:Z:498:GLY:HA3	2.00	0.97
29:L:216:PHE:CE1	35:O:112:VAL:C	2.40	0.97
45:Z:566:TYR:HE2	45:Z:584:TRP:HZ3	1.05	0.97
3:C:711:ARG:HD3	3:C:730:ARG:HH11	1.29	0.97
1:A:1348:VAL:HG12	3:C:921:LEU:HD23	1.43	0.97
1:A:1364:LEU:HD12	41:V:461:LEU:CB	1.89	0.97
35:O:149:LYS:CD	35:O:290:LYS:HZ3	1.74	0.97
3:C:500:THR:HG22	3:C:545:PRO:HA	1.47	0.97
29:L:216:PHE:HD1	35:O:113:ASN:CA	1.59	0.97
3:C:670:SER:HA	3:C:823:ALA:HB3	1.43	0.97
1:A:1320:LYS:HE2	37:R:434:TYR:HE1	1.15	0.97
35:O:189:PRO:HG3	42:W:223:ARG:HA	1.01	0.97
3:C:670:SER:CA	3:C:823:ALA:CB	2.43	0.96
28:J:300:ASP:OD2	37:R:101:ILE:HG13	1.65	0.96
34:N:28:LYS:HZ3	42:W:190:ASP:HA	1.28	0.96
1:A:380:LEU:CD2	3:C:354:ARG:O	2.12	0.96
1:A:1293:ASN:HD22	40:U:14:GLY:HA2	1.28	0.96
20:v:58:LEU:CD2	20:v:82:LEU:HB2	1.95	0.96
1:A:296:PHE:CE1	3:C:591:ALA:HB1	2.01	0.96
1:A:546:LEU:HD11	1:A:595:LYS:CD	1.94	0.96
3:C:855:GLY:O	3:C:856:HIS:HB3	1.63	0.96
5:E:321:TYR:CE1	42:W:84:THR:HA	1.99	0.96
32:I:358:HIS:CB	32:I:376:ASN:CB	2.44	0.96
14:G:18:A:H5'	35:O:69:GLU:OE1	1.66	0.96
1:A:380:LEU:CB	3:C:354:ARG:NH1	2.27	0.96
1:A:2335:ALA:O	4:D:570:THR:HA	1.65	0.96
39:T:352:THR:HG22	39:T:373:LYS:O	1.65	0.96
44:Y:37:TRP:HH2	45:Z:498:GLY:CA	1.70	0.96
1:A:303:ILE:HG21	3:C:933:PHE:CE1	2.01	0.96
20:v:70:LEU:O	20:v:74:GLN:N	1.97	0.96
1:A:47:GLU:O	1:A:50:LYS:HB2	1.64	0.96
3:C:135:CYS:SG	3:C:227:LEU:HD12	2.06	0.96
15:H:78:C:H2'	15:H:79:G:H8	1.27	0.96
1:A:121:HIS:NE2	1:A:481:PHE:CB	2.29	0.96
1:A:748:ASP:OD1	36:P:214:THR:HG22	1.64	0.96
1:A:369:GLU:OE2	1:A:369:GLU:N	1.97	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:o:46:ALA:HB1	16:o:68:THR:O	1.64	0.96
1:A:2298:LEU:CB	4:D:1283:PRO:CB	2.44	0.95
3:C:115:GLU:O	3:C:118:PHE:N	1.98	0.95
1:A:587:GLN:HG3	1:A:1550:GLY:O	1.65	0.95
1:A:783:TYR:CD1	36:P:228:ILE:HG21	2.01	0.95
5:E:146:ARG:HH11	5:E:148:LYS:HE2	1.27	0.95
14:G:11:A:N3	14:G:12:G:H8	1.64	0.95
35:O:225:PRO:HB3	35:O:302:TRP:NE1	1.80	0.95
44:Y:37:TRP:CH2	45:Z:498:GLY:HA3	1.96	0.95
14:G:140:A:C1'	20:v:64:ASN:CG	2.40	0.95
37:R:442:ARG:HD3	37:R:443:GLY:CA	1.96	0.95
1:A:171:ASP:O	1:A:520:TYR:CD2	2.20	0.95
15:H:45:C:H42	18:w:395:TRP:CD1	1.83	0.95
15:H:156:U:H5''	15:H:156:U:C6	2.02	0.95
1:A:299:ILE:HD12	1:A:1342:TRP:CZ3	1.99	0.95
1:A:299:ILE:CB	1:A:1342:TRP:HZ3	1.79	0.95
3:C:145:PHE:CB	3:C:312:SER:HB3	1.97	0.95
13:F:22:A:H5''	34:N:116:ASN:O	1.66	0.95
35:O:149:LYS:CD	35:O:290:LYS:CE	2.44	0.95
1:A:388:LEU:O	3:C:379:LYS:NZ	2.00	0.95
3:C:700:ILE:HG23	3:C:735:PHE:CD2	2.01	0.95
1:A:264:PHE:CZ	1:A:459:LEU:CD1	2.50	0.95
1:A:705:LYS:HG2	37:R:251:ILE:HB	1.49	0.95
1:A:253:ASN:HB3	3:C:893:GLY:O	1.67	0.95
1:A:1426:ASP:CG	37:R:421:GLY:HA3	1.91	0.95
14:G:-9:C:N4	40:U:18:TYR:CZ	2.34	0.95
1:A:785:LYS:CE	36:P:215:LEU:HD11	1.97	0.94
14:G:11:A:C2	14:G:12:G:N7	2.34	0.94
1:A:384:VAL:CG1	3:C:331:PHE:CD2	2.50	0.94
1:A:1162:PRO:HG3	36:P:194:PHE:CD2	2.02	0.94
1:A:1457:HIS:CE1	37:R:424:SER:HA	2.01	0.94
28:J:339:TRP:CA	37:R:116:TYR:CE2	2.48	0.94
1:A:151:MET:HE3	1:A:628:GLY:O	1.67	0.94
3:C:711:ARG:NH2	3:C:730:ARG:O	2.00	0.94
1:A:299:ILE:HG13	1:A:1342:TRP:CH2	2.02	0.94
13:F:49:G:N7	29:L:33:ARG:NH1	2.15	0.94
30:q:22:ASN:CB	30:r:55:ILE:CA	2.45	0.94
5:E:119:THR:CG2	5:E:161:ARG:HB3	1.97	0.94
15:H:180:G:H2'	15:H:181:G:H8	1.30	0.94
13:F:27:A:P	34:N:41:ARG:HH21	1.90	0.94
1:A:587:GLN:CB	1:A:1550:GLY:O	2.16	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1405:LEU:CB	37:R:415:LEU:CD2	2.45	0.94
1:A:1459:ARG:HE	37:R:423:ASP:HB2	1.31	0.94
1:A:2268:LEU:CD2	4:D:1261:PRO:CB	2.46	0.94
3:C:145:PHE:HA	3:C:312:SER:HB2	0.95	0.94
3:C:445:ALA:HB3	3:C:466:SER:HA	1.50	0.94
14:G:-9:C:C5	40:U:18:TYR:HE1	1.79	0.94
15:H:79:G:H2'	15:H:80:A:H8	1.33	0.94
24:4:69:TYR:CZ	24:4:73:ILE:HG13	2.03	0.94
3:C:349:PHE:HD1	3:C:356:PHE:CD1	1.85	0.94
15:H:42:G:OP1	20:v:77:LYS:CB	2.15	0.94
2:B:39:C:C4'	2:B:40:U:OP1	2.16	0.94
1:A:158:ARG:NH2	1:A:570:ASP:OD2	2.01	0.93
1:A:2113:LYS:HE2	4:D:1229:ASP:CB	1.98	0.93
13:F:8:C:H6	13:F:8:C:H5''	1.31	0.93
14:G:131:U:OP1	18:w:396:LEU:CD1	2.15	0.93
20:v:56:CYS:HB2	20:v:78:HIS:HE1	1.32	0.93
1:A:461:HIS:CD2	2:B:27:U:O4	2.20	0.93
13:F:25:C:C4'	13:F:26:U:OP2	2.16	0.93
18:w:485:ASN:HD22	23:3:976:LYS:CG	1.81	0.93
37:R:171:LEU:HD12	37:R:201:GLU:OE1	1.67	0.93
3:C:76:GLU:OE1	3:C:76:GLU:N	2.01	0.93
5:E:146:ARG:NH1	5:E:148:LYS:HE2	1.82	0.93
3:C:149:LEU:CD1	3:C:427:PHE:HD2	1.80	0.93
14:G:140:A:H1'	20:v:64:ASN:CG	1.93	0.93
29:L:209:ASP:HA	35:O:110:SER:HB2	1.49	0.93
1:A:73:HIS:CD2	1:A:81:PHE:CE1	2.56	0.93
1:A:151:MET:CE	1:A:628:GLY:O	2.15	0.93
1:A:695:ASP:CB	39:T:374:SER:OG	2.15	0.93
1:A:2113:LYS:CE	4:D:1229:ASP:O	2.16	0.93
3:C:449:ILE:HG21	3:C:457:VAL:CG1	1.99	0.93
28:J:259:GLN:NE2	29:L:220:PRO:CD	2.30	0.93
1:A:67:ARG:HD3	1:A:179:ALA:HB2	1.51	0.93
20:v:45:TYR:CE1	20:v:58:LEU:HD13	2.02	0.93
28:J:294:HIS:CE1	29:L:227:THR:HB	2.04	0.93
1:A:417:ARG:NH2	2:B:58:U:H5''	1.82	0.93
1:A:2314:PHE:CB	4:D:1125:SER:CA	2.47	0.93
3:C:497:LEU:HD13	3:C:577:PHE:HZ	1.17	0.93
13:F:68:C:C4	36:P:33:ARG:CG	2.52	0.93
1:A:548:ARG:NH2	1:A:549:GLU:OE2	2.01	0.92
2:B:43:U:C4'	13:F:67:G:H1	1.80	0.92
35:O:189:PRO:CG	42:W:223:ARG:CA	2.41	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:O:225:PRO:HG3	35:O:302:TRP:HE1	1.29	0.92
36:P:224:MET:HA	36:P:224:MET:HE3	1.51	0.92
37:R:101:ILE:O	37:R:104:GLN:CG	2.16	0.92
1:A:299:ILE:HD12	1:A:1342:TRP:CE3	2.03	0.92
1:A:2328:ALA:CB	4:D:788:GLY:HA2	1.99	0.92
3:C:69:ALA:HA	39:T:456:PRO:HG3	1.49	0.92
3:C:449:ILE:CG2	3:C:457:VAL:CG1	2.46	0.92
3:C:678:THR:HG21	3:C:683:ASN:HD22	1.35	0.92
13:F:28:A:O2'	34:N:39:GLY:CA	2.17	0.92
42:W:258:PRO:O	42:W:260:ASP:N	2.02	0.92
35:O:223:LEU:HD13	35:O:224:ASP:N	1.84	0.92
3:C:140:HIS:CG	3:C:230:ASP:HB3	2.03	0.92
37:R:414:ARG:NH1	45:Z:598:PHE:HE2	1.58	0.92
1:A:523:ASN:OD1	1:A:552:ARG:NH2	2.02	0.92
1:A:532:THR:CG2	14:G:2:U:O5'	2.17	0.92
3:C:445:ALA:O	3:C:449:ILE:N	2.03	0.92
3:C:476:CYS:HB3	3:C:565:ILE:HB	1.51	0.92
28:J:339:TRP:CA	37:R:116:TYR:CD2	2.51	0.92
1:A:228:TRP:O	1:A:415:SER:HA	1.70	0.92
1:A:339:PHE:CE1	1:A:406:TRP:CZ3	2.58	0.92
3:C:670:SER:HB3	3:C:823:ALA:HB3	1.48	0.92
13:F:27:A:P	34:N:41:ARG:NH2	2.43	0.92
15:H:42:G:P	20:v:77:LYS:HB2	2.09	0.92
28:J:259:GLN:HE22	29:L:220:PRO:HD2	1.32	0.92
34:N:128:VAL:HG13	34:N:130:ARG:H	1.35	0.92
1:A:762:ARG:HH22	36:P:226:LYS:HZ1	1.08	0.92
3:C:77:VAL:CG1	39:T:196:LEU:CB	2.45	0.92
1:A:651:TRP:NE1	13:F:66:C:C2	2.38	0.92
1:A:779:LEU:HD21	36:P:223:PHE:CZ	2.05	0.92
3:C:244:LYS:HA	3:C:292:TYR:HD2	1.34	0.91
37:R:106:GLN:HG2	37:R:110:LYS:HE2	1.51	0.91
3:C:483:SER:HA	3:C:490:PHE:HB3	1.52	0.91
3:C:674:CYS:SG	3:C:822:MET:SD	2.67	0.91
1:A:86:ARG:NH2	37:R:211:ARG:HG3	1.84	0.91
1:A:235:MET:CE	1:A:411:PHE:HA	1.99	0.91
1:A:1307:MET:SD	1:A:1547:VAL:HB	2.09	0.91
3:C:86:THR:O	39:T:239:LYS:O	1.88	0.91
3:C:132:VAL:CG1	3:C:226:VAL:HG23	2.00	0.91
38:S:131:ARG:NH1	38:S:133:CYS:HA	1.86	0.91
1:A:171:ASP:HB3	1:A:519:ASP:HB2	1.53	0.91
1:A:305:ARG:HA	1:A:305:ARG:HH11	1.33	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:296:PHE:CE1	3:C:591:ALA:CB	2.54	0.91
35:O:234:LEU:O	35:O:271:PHE:HA	1.70	0.91
1:A:1320:LYS:CE	37:R:434:TYR:CE1	2.54	0.91
1:A:372:PRO:CG	3:C:342:ARG:HE	1.83	0.91
3:C:452:THR:HG22	3:C:577:PHE:HB3	1.52	0.91
29:L:224:PHE:CD1	37:R:86:LEU:CD1	2.53	0.91
3:C:145:PHE:N	3:C:312:SER:HB2	1.85	0.90
1:A:1757:GLU:O	21:1:938:TRP:NE1	2.03	0.90
13:F:35:A:C8	14:G:12:G:C6	2.59	0.90
18:w:485:ASN:CB	23:3:978:LEU:CD2	2.49	0.90
23:3:34:ARG:HB2	23:3:37:ILE:HB	1.51	0.90
1:A:232:LEU:HD22	1:A:404:LEU:HD13	1.53	0.90
3:C:230:ASP:OD2	3:C:233:GLU:HG2	1.70	0.90
1:A:1457:HIS:CE1	37:R:425:GLY:H	1.88	0.90
3:C:678:THR:OG1	3:C:680:ASN:O	1.89	0.90
1:A:1320:LYS:CE	37:R:434:TYR:HE1	1.85	0.90
44:Y:37:TRP:NE1	44:Y:83:CYS:HB2	1.87	0.90
1:A:587:GLN:CA	1:A:1550:GLY:O	2.20	0.90
1:A:623:LYS:HB3	48:A:2401:IHP:O34	1.72	0.90
3:C:221:ILE:CD1	3:C:479:THR:OG1	2.19	0.90
13:F:94:C:P	28:J:351:ASN:HD22	1.95	0.90
37:R:82:MET:HE3	37:R:82:MET:C	1.97	0.90
1:A:782:LEU:HD13	36:P:220:HIS:HE1	1.34	0.90
1:A:1290:LYS:HG2	40:U:13:SER:O	1.71	0.90
3:C:711:ARG:HD3	3:C:730:ARG:NH1	1.86	0.90
13:F:27:A:H1'	35:O:181:TYR:HE2	1.36	0.90
3:C:228:PHE:CA	3:C:256:CYS:O	2.20	0.90
38:S:35:THR:C	38:S:129:PHE:HE1	1.80	0.90
1:A:705:LYS:HG2	37:R:251:ILE:CB	2.01	0.89
39:T:399:LYS:HG3	39:T:406:ILE:HD11	1.54	0.89
18:w:485:ASN:ND2	23:3:976:LYS:HG2	1.87	0.89
23:3:699:VAL:HG22	23:3:716:SER:HB2	1.53	0.89
38:S:34:LYS:HE3	38:S:78:TYR:CE2	2.07	0.89
34:N:124:SER:O	34:N:127:GLU:HG2	1.71	0.89
44:Y:36:ALA:HB2	45:Z:499:LYS:O	1.72	0.89
1:A:227:ARG:CA	1:A:416:GLY:O	2.20	0.89
1:A:744:LYS:HE2	36:P:213:ASP:HA	1.52	0.89
1:A:296:PHE:CB	3:C:656:ALA:HB2	2.02	0.89
36:P:192:VAL:HG12	36:P:194:PHE:H	1.35	0.89
1:A:387:PHE:CE2	3:C:399:LEU:HD23	2.07	0.89
1:A:748:ASP:HA	36:P:214:THR:HG21	1.54	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:TYR:CZ	1:A:434:HIS:CB	2.54	0.89
15:H:80:A:H2'	15:H:81:G:H8	1.36	0.89
37:R:81:LYS:HA	37:R:81:LYS:CE	2.02	0.89
1:A:1342:TRP:CE2	3:C:921:LEU:HD11	2.08	0.89
28:J:220:LEU:HD11	28:J:224:LYS:HE3	1.53	0.89
1:A:532:THR:OG1	14:G:2:U:O5'	1.89	0.89
15:H:81:G:H2'	15:H:82:G:H8	1.35	0.89
15:H:82:G:H2'	15:H:83:A:H8	1.38	0.89
37:R:92:SER:O	38:S:19:SER:HB2	1.73	0.89
36:P:193:VAL:HG21	36:P:194:PHE:CD2	2.02	0.88
1:A:2314:PHE:HB2	4:D:1125:SER:CA	2.03	0.88
14:G:11:A:N3	14:G:12:G:C8	2.38	0.88
37:R:81:LYS:HA	37:R:81:LYS:NZ	1.88	0.88
1:A:785:LYS:HE2	36:P:215:LEU:HD11	1.54	0.88
3:C:78:GLU:O	39:T:199:VAL:N	2.06	0.88
3:C:140:HIS:CE1	3:C:233:GLU:HB2	2.07	0.88
20:v:45:TYR:CD1	20:v:58:LEU:HD13	2.09	0.88
1:A:175:PRO:HG2	1:A:498:ARG:NH2	1.88	0.88
1:A:1314:VAL:HG11	1:A:1487:HIS:CD2	2.07	0.88
3:C:79:THR:C	3:C:80:ILE:HD12	1.98	0.88
3:C:465:MET:HE1	3:C:475:MET:CG	2.01	0.88
3:C:679:PRO:CG	3:C:807:GLN:OE1	2.21	0.88
1:A:419:ARG:NH2	1:A:423:ASP:O	2.06	0.88
3:C:678:THR:CG2	3:C:683:ASN:HB2	2.04	0.88
13:F:68:C:C4	36:P:33:ARG:HG2	2.07	0.88
1:A:384:VAL:HG12	3:C:331:PHE:HE2	1.08	0.88
1:A:587:GLN:HA	1:A:1550:GLY:O	1.74	0.88
1:A:1342:TRP:CD2	3:C:921:LEU:HD11	2.08	0.88
18:w:485:ASN:O	23:3:978:LEU:HD22	1.70	0.88
46:x:664:PRO:O	46:x:667:ALA:CB	2.22	0.88
1:A:715:GLU:OE2	37:R:258:TRP:CZ3	2.25	0.88
1:A:1755:SER:OG	21:1:938:TRP:CH2	2.26	0.88
22:2:614:ARG:HH11	22:2:614:ARG:HG3	1.38	0.88
3:C:261:ASP:OD1	50:C:1500:GTP:O6	1.92	0.88
35:O:189:PRO:HG3	42:W:223:ARG:N	1.88	0.88
38:S:111:GLN:HE22	42:W:93:PHE:CB	1.86	0.88
1:A:1457:HIS:CE1	37:R:425:GLY:N	2.41	0.88
1:A:1459:ARG:HG3	37:R:422:MET:O	1.74	0.88
28:J:270:ASP:CG	37:R:222:PRO:HB3	1.99	0.88
36:P:224:MET:CE	36:P:228:ILE:HD13	2.04	0.88
1:A:76:MET:HE1	1:A:88:TYR:CG	2.08	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:LYS:NZ	14:G:-9:C:OP1	2.06	0.87
1:A:372:PRO:HG3	3:C:342:ARG:HE	1.38	0.87
3:C:97:VAL:CG2	36:P:45:GLN:HG3	2.03	0.87
15:H:179:C:O2'	15:H:180:G:H5'	1.74	0.87
3:C:149:LEU:HD12	3:C:427:PHE:HD2	1.39	0.87
3:C:700:ILE:HG23	3:C:735:PHE:CE2	2.09	0.87
20:v:27:ARG:HG2	29:L:37:LEU:HD21	1.56	0.87
23:3:812:LYS:O	23:3:816:LYS:HB2	1.74	0.87
3:C:64:LYS:HZ1	36:P:206:LYS:HG2	1.39	0.87
14:G:137:C:H42	15:H:40:C:H42	1.22	0.87
24:4:75:ASN:OD1	24:4:86:VAL:HB	1.74	0.87
1:A:329:LEU:HD13	3:C:177:ARG:HE	1.40	0.87
3:C:523:GLN:OE1	3:C:524:ILE:N	2.07	0.87
1:A:433:GLU:OE1	1:A:436:PRO:HB3	1.74	0.87
3:C:705:VAL:HG21	3:C:717:PHE:CE2	2.07	0.87
5:E:243:LEU:CD1	5:E:247:GLY:HA2	2.04	0.87
15:H:68:G:O2'	15:H:69:U:H5'	1.74	0.87
15:H:78:C:H2'	15:H:79:G:C8	2.10	0.87
1:A:1162:PRO:CG	36:P:194:PHE:CE2	2.57	0.87
1:A:1370:ARG:HG2	41:V:464:GLN:HA	1.54	0.87
3:C:488:VAL:HG13	3:C:609:LYS:CE	2.05	0.87
15:H:154:C:O2	15:H:176:G:N2	2.07	0.87
23:3:442:LEU:CD1	23:3:734:LEU:CD2	2.50	0.87
23:3:545:VAL:HG12	23:3:546:LYS:HG2	1.57	0.87
28:J:339:TRP:CD2	37:R:116:TYR:HD2	1.93	0.87
37:R:423:ASP:O	37:R:424:SER:OG	1.92	0.87
15:H:180:G:H2'	15:H:181:G:C8	2.10	0.87
3:C:701:GLU:HA	3:C:740:THR:OG1	1.75	0.87
28:J:255:LEU:HD22	29:L:235:LEU:HD13	1.56	0.87
1:A:232:LEU:HD22	1:A:404:LEU:CD1	2.04	0.86
3:C:216:THR:CG2	3:C:245:HIS:HE1	1.84	0.86
37:R:442:ARG:NH1	37:R:443:GLY:O	2.07	0.86
1:A:2113:LYS:HE3	4:D:1229:ASP:C	2.01	0.86
13:F:27:A:OP2	34:N:41:ARG:NH2	2.09	0.86
1:A:1481:VAL:HG11	1:A:1498:TRP:CD2	2.10	0.86
1:A:318:TYR:CA	3:C:638:ASP:OD1	2.22	0.86
15:H:179:C:H2'	15:H:180:G:C8	2.09	0.86
1:A:86:ARG:NH2	37:R:211:ARG:HG2	1.85	0.86
18:w:485:ASN:HA	23:3:978:LEU:CD2	2.03	0.86
33:Q:500:GLY:N	37:R:51:ILE:HD11	1.89	0.86
34:N:28:LYS:HZ1	42:W:190:ASP:H	1.18	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:O:20:PHE:CD1	37:R:177:ILE:HD11	2.11	0.86
1:A:1342:TRP:HB3	3:C:921:LEU:HD21	1.54	0.86
5:E:267:PHE:CE1	31:K:194:GLU:CB	2.59	0.86
15:H:148:C:O2'	15:H:149:A:H5'	1.75	0.86
21:1:1179:ASP:OD2	21:1:1185:ARG:NH1	2.08	0.86
37:R:125:MET:HE3	37:R:131:ASP:OD1	1.76	0.86
39:T:399:LYS:HG2	39:T:406:ILE:HD11	1.53	0.86
5:E:269:PRO:O	5:E:270:LYS:HB3	1.76	0.86
13:F:26:U:H3'	13:F:27:A:H5''	1.56	0.86
28:J:256:LYS:O	29:L:232:TYR:CE2	2.29	0.86
36:P:210:PHE:HD2	39:T:455:GLN:OE1	1.53	0.86
37:R:147:THR:HG23	39:T:360:VAL:HG12	1.57	0.86
38:S:57:ILE:HD11	42:W:97:ASN:CB	2.03	0.86
1:A:1757:GLU:C	21:1:938:TRP:NE1	2.33	0.86
39:T:417:ASN:OD1	39:T:432:ASP:OD1	1.94	0.86
1:A:299:ILE:CD1	1:A:1342:TRP:HZ3	1.85	0.86
1:A:402:ILE:CG2	3:C:268:LYS:HZ2	1.84	0.86
38:S:35:THR:O	38:S:129:PHE:CE1	2.29	0.86
1:A:296:PHE:HB3	3:C:656:ALA:CB	2.05	0.85
1:A:338:VAL:HG21	3:C:867:PRO:HG3	1.57	0.85
1:A:532:THR:CG2	14:G:2:U:C5'	2.52	0.85
37:R:135:PRO:O	37:R:136:ASP:OD1	1.94	0.85
1:A:299:ILE:CG1	3:C:920:PRO:O	2.24	0.85
20:v:164:ARG:O	20:v:165:ARG:CB	2.24	0.85
37:R:420:LYS:HE3	37:R:420:LYS:CA	1.98	0.85
38:S:39:PHE:HB2	38:S:129:PHE:CE2	2.09	0.85
38:S:9:TRP:O	38:S:11:PRO:HD3	1.76	0.85
3:C:72:VAL:HG22	39:T:453:ALA:HB1	1.58	0.85
3:C:149:LEU:HD12	3:C:427:PHE:CD2	2.07	0.85
15:H:79:G:O2'	15:H:80:A:H5'	1.76	0.85
20:v:51:LEU:CG	21:1:1141:LEU:HD12	2.05	0.85
35:O:225:PRO:CG	35:O:302:TRP:HE1	1.88	0.85
38:S:35:THR:O	38:S:129:PHE:HE1	1.57	0.85
3:C:145:PHE:HB2	3:C:312:SER:HB3	1.57	0.85
15:H:45:C:C4	18:w:395:TRP:HD1	1.93	0.85
21:1:672:ALA:HA	21:1:679:ILE:HD11	1.58	0.85
22:2:634:ILE:CB	47:y:209:THR:CA	2.55	0.85
35:O:185:LYS:HG3	42:W:216:LEU:N	1.92	0.85
2:B:95:G:H4'	2:B:96:A:O4'	1.76	0.85
37:R:414:ARG:NH1	45:Z:598:PHE:HZ	1.44	0.85
5:E:162:ARG:NH2	5:E:203:ASP:O	2.10	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:267:PHE:CE1	31:K:194:GLU:HB3	2.10	0.85
1:A:152:ARG:HB3	1:A:152:ARG:HH11	1.40	0.85
37:R:414:ARG:HB2	37:R:414:ARG:NH2	1.92	0.85
3:C:133:THR:O	3:C:226:VAL:N	2.10	0.85
42:W:137:TYR:HA	42:W:154:GLY:HA3	1.59	0.85
1:A:121:HIS:CG	1:A:481:PHE:O	2.30	0.85
1:A:338:VAL:HG23	3:C:867:PRO:HG3	1.58	0.85
1:A:452:LYS:NZ	2:B:48:A:OP1	2.10	0.84
3:C:94:ILE:HD13	36:P:44:ARG:NH1	1.92	0.84
15:H:156:U:H6	15:H:156:U:C5'	1.88	0.84
20:v:58:LEU:HD21	20:v:82:LEU:CB	2.06	0.84
45:Z:600:ARG:HH11	45:Z:600:ARG:CB	1.90	0.84
2:B:40:U:H3	14:G:-1:G:H1	1.25	0.84
14:G:140:A:O4'	20:v:64:ASN:CG	2.19	0.84
3:C:444:GLY:O	3:C:447:PRO:HD2	1.77	0.84
3:C:516:LEU:HD12	3:C:517:GLU:HG3	1.59	0.84
1:A:595:LYS:HE3	1:A:644:ILE:HD11	1.58	0.84
13:F:36:A:H2'	13:F:38:G:OP2	1.78	0.84
15:H:80:A:O2'	15:H:81:G:H5'	1.78	0.84
15:H:181:G:O2'	15:H:182:U:H5'	1.77	0.84
15:H:182:U:O2'	15:H:183:G:H5'	1.75	0.84
23:3:356:HIS:HB2	23:3:401:LEU:HB2	1.60	0.84
1:A:1348:VAL:CG1	3:C:921:LEU:HD23	2.06	0.84
3:C:80:ILE:O	39:T:200:ILE:HA	1.78	0.84
37:R:415:LEU:O	37:R:417:ASN:N	2.09	0.84
1:A:755:HIS:CE1	36:P:223:PHE:CB	2.60	0.84
3:C:711:ARG:HD3	3:C:730:ARG:HE	1.42	0.84
20:v:23:ASN:HD22	29:L:39:HIS:CE1	1.96	0.84
1:A:588:LEU:O	1:A:1551:PHE:CE1	2.31	0.84
3:C:244:LYS:HA	3:C:292:TYR:CD2	2.13	0.84
3:C:365:SER:OG	3:C:371:GLU:OE2	1.95	0.84
3:C:725:ASP:OD1	3:C:727:LEU:N	2.10	0.84
15:H:78:C:O2'	15:H:79:G:H5'	1.77	0.84
37:R:178:ARG:HD3	37:R:194:GLN:NE2	1.91	0.84
1:A:1426:ASP:CB	37:R:421:GLY:HA3	2.08	0.84
1:A:1457:HIS:CE1	1:A:1459:ARG:CG	2.61	0.84
1:A:1457:HIS:NE2	37:R:424:SER:HA	1.93	0.83
3:C:705:VAL:HG21	3:C:717:PHE:HE2	1.40	0.83
1:A:254:TYR:CE2	1:A:434:HIS:CB	2.61	0.83
1:A:1342:TRP:CZ2	3:C:921:LEU:HD13	2.13	0.83
3:C:348:TYR:CD1	3:C:359:LYS:HB3	2.13	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:71:C:O2'	15:H:72:U:H5'	1.78	0.83
20:v:52:GLY:H	21:1:1141:LEU:HB2	1.42	0.83
45:Z:566:TYR:CE2	45:Z:584:TRP:CE3	2.66	0.83
3:C:488:VAL:CG1	3:C:609:LYS:HE2	2.08	0.83
14:G:22:C:O2'	14:G:23:U:OP1	1.95	0.83
15:H:152:G:N2	15:H:153:A:N7	2.27	0.83
1:A:168:PRO:HG3	1:A:559:ASP:CB	2.07	0.83
5:E:74:PHE:CE1	5:E:81:LEU:CD2	2.62	0.83
44:Y:37:TRP:CZ2	45:Z:498:GLY:HA2	2.08	0.83
3:C:151:GLU:OE1	3:C:417:ARG:NH2	2.11	0.83
15:H:70:C:O2'	15:H:71:C:H5'	1.78	0.83
37:R:117:THR:O	37:R:120:VAL:HG12	1.78	0.83
1:A:365:VAL:HG12	1:A:366:LYS:H	1.44	0.83
3:C:77:VAL:CG1	39:T:196:LEU:CG	2.35	0.83
1:A:1310:ARG:NH2	1:A:1564:GLY:HA3	1.94	0.83
1:A:1342:TRP:CH2	3:C:921:LEU:HD13	2.12	0.83
3:C:80:ILE:N	39:T:199:VAL:O	2.12	0.83
1:A:303:ILE:CG2	3:C:933:PHE:CE1	2.62	0.83
3:C:824:THR:HG23	3:C:824:THR:O	1.77	0.83
37:R:134:ARG:O	37:R:136:ASP:N	2.12	0.83
1:A:1457:HIS:HE1	1:A:1459:ARG:HG2	1.43	0.83
18:w:485:ASN:HD21	23:3:976:LYS:H	1.22	0.83
3:C:145:PHE:CA	3:C:312:SER:HB3	2.04	0.83
15:H:72:U:O2'	15:H:73:C:H5'	1.77	0.83
18:w:485:ASN:HA	23:3:978:LEU:HD11	1.59	0.83
28:J:406:PHE:CD2	28:J:411:MET:HE3	2.13	0.83
3:C:470:PRO:HB3	3:C:500:THR:CG2	2.08	0.82
21:1:1108:ASN:ND2	21:1:1111:CYS:SG	2.52	0.82
42:W:277:PRO:CB	42:W:578:TRP:C	2.51	0.82
15:H:73:C:O2'	15:H:74:U:H5'	1.79	0.82
1:A:1084:PRO:HG2	36:P:188:TRP:CZ2	2.12	0.82
1:A:1293:ASN:ND2	40:U:14:GLY:HA2	1.94	0.82
3:C:220:ARG:NH1	3:C:578:ARG:O	2.12	0.82
3:C:228:PHE:CB	3:C:256:CYS:O	2.27	0.82
3:C:482:TYR:HE2	3:C:493:PHE:CG	1.97	0.82
5:E:165:GLN:O	5:E:166:LEU:HD23	1.79	0.82
28:J:259:GLN:NE2	29:L:220:PRO:HD2	1.94	0.82
3:C:705:VAL:CB	3:C:717:PHE:CE2	2.61	0.82
15:H:45:C:H2'	18:w:394:TYR:HE2	1.39	0.82
14:G:11:A:C4	14:G:12:G:C8	2.67	0.82
15:H:69:U:O2'	15:H:70:C:H5'	1.80	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:o:46:ALA:CB	16:o:68:THR:O	2.27	0.82
37:R:103:ARG:HB3	37:R:103:ARG:HH11	1.44	0.82
1:A:532:THR:HG21	14:G:2:U:H5''	1.62	0.82
15:H:81:G:O2'	15:H:82:G:H5'	1.78	0.82
3:C:140:HIS:ND1	3:C:230:ASP:HB3	1.94	0.82
23:3:304:GLN:HE21	23:3:308:GLY:HA2	1.44	0.82
42:W:209:SER:O	42:W:213:GLN:N	2.12	0.82
1:A:132:ILE:CD1	2:B:57:G:OP1	2.27	0.82
3:C:489:GLN:O	3:C:489:GLN:NE2	2.13	0.82
15:H:105:G:C2'	15:H:106:G:H5''	2.10	0.82
36:P:30:TYR:OH	37:R:162:ALA:CA	2.27	0.82
1:A:615:ARG:O	1:A:618:THR:OG1	1.96	0.82
1:A:1342:TRP:CE3	3:C:921:LEU:CD2	2.62	0.82
1:A:1457:HIS:CE1	1:A:1459:ARG:HG2	2.15	0.82
3:C:259:LYS:HG2	3:C:262:ARG:CD	2.09	0.82
36:P:212:ASN:HB3	39:T:458:SER:HB2	1.61	0.82
1:A:1370:ARG:NH1	41:V:466:SER:O	2.10	0.82
1:A:303:ILE:CG2	3:C:933:PHE:HE1	1.93	0.81
5:E:74:PHE:CE2	5:E:343:ILE:HG12	2.14	0.81
14:G:132:G:O4'	18:w:399:LEU:HD13	1.80	0.81
44:Y:37:TRP:HA	44:Y:82:LEU:O	1.80	0.81
3:C:64:LYS:HE3	36:P:206:LYS:CE	2.10	0.81
3:C:244:LYS:HB2	3:C:292:TYR:CE2	2.15	0.81
3:C:306:ASN:OD1	3:C:437:HIS:ND1	2.14	0.81
3:C:507:VAL:CG1	3:C:565:ILE:HG23	2.10	0.81
22:2:643:PRO:HD2	24:4:69:TYR:CD2	2.16	0.81
23:3:42:ARG:HE	23:3:53:LEU:HD11	1.45	0.81
23:3:210:PHE:HB2	23:3:224:TYR:HB2	1.60	0.81
26:6:49:CYS:HB3	26:6:87:LYS:HD3	1.61	0.81
34:N:111:THR:HG21	34:N:115:THR:O	1.79	0.81
36:P:193:VAL:HG23	36:P:194:PHE:CG	2.15	0.81
1:A:164:MET:HE1	1:A:560:SER:HA	1.63	0.81
39:T:213:GLU:HG3	39:T:218:TRP:CE2	2.16	0.81
1:A:121:HIS:HA	1:A:482:PHE:HA	1.62	0.81
1:A:651:TRP:NE1	13:F:66:C:O2	2.14	0.81
3:C:511:GLY:O	3:C:576:ILE:HD13	1.79	0.81
38:S:39:PHE:CD2	38:S:129:PHE:CE2	2.68	0.81
1:A:247:THR:OG1	1:A:429:ASN:HB3	1.80	0.81
1:A:402:ILE:HG21	3:C:268:LYS:HE3	1.62	0.81
1:A:623:LYS:O	48:A:2401:IHP:O44	1.99	0.81
1:A:1184:ASN:OD1	1:A:1195:ARG:NH1	2.14	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1426:ASP:HB2	37:R:421:GLY:CA	2.11	0.81
3:C:261:ASP:CG	50:C:1500:GTP:HN1	1.88	0.81
3:C:452:THR:HG21	3:C:577:PHE:HD2	1.43	0.81
5:E:74:PHE:CZ	5:E:81:LEU:HD21	2.16	0.81
5:E:281:VAL:CG2	42:W:148:VAL:HA	2.10	0.81
35:O:229:LYS:HG3	35:O:277:ARG:HH12	1.45	0.81
1:A:705:LYS:HB2	37:R:251:ILE:CD1	2.07	0.81
1:A:228:TRP:N	1:A:416:GLY:O	2.14	0.81
1:A:235:MET:HE1	1:A:411:PHE:HA	1.61	0.81
1:A:907:PRO:HD3	36:P:229:LYS:HB2	1.63	0.81
3:C:96:PRO:HA	36:P:48:GLN:HE21	1.44	0.81
3:C:140:HIS:NE2	3:C:233:GLU:HG3	1.95	0.81
38:S:39:PHE:CD1	38:S:129:PHE:HE2	1.97	0.81
1:A:296:PHE:CD1	3:C:656:ALA:HB2	2.16	0.81
3:C:140:HIS:ND1	3:C:230:ASP:N	2.28	0.81
3:C:452:THR:CB	3:C:577:PHE:HD2	1.93	0.81
3:C:507:VAL:HG11	3:C:565:ILE:CG2	2.09	0.81
3:C:711:ARG:HD3	3:C:730:ARG:NE	1.96	0.81
14:G:26:U:C1'	35:O:269:CYS:SG	2.68	0.81
15:H:183:G:H2'	15:H:184:C:H6	1.44	0.80
35:O:220:MET:SD	35:O:222:ARG:CB	2.70	0.80
1:A:461:HIS:CE1	2:B:23:C:C6	2.69	0.80
15:H:83:A:H2'	15:H:84:C:C1'	2.10	0.80
1:A:2314:PHE:HB3	4:D:1125:SER:CA	2.11	0.80
2:B:18:C:O2'	2:B:19:A:O5'	1.98	0.80
13:F:68:C:H41	36:P:33:ARG:HB3	1.45	0.80
28:J:273:TYR:CE1	37:R:228:PRO:HB3	2.17	0.80
1:A:318:TYR:HB2	3:C:638:ASP:OD1	1.80	0.80
14:G:134:U:H3	15:H:42:G:H1	1.24	0.80
23:3:979:ARG:HD2	23:3:982:GLU:HB2	1.63	0.80
35:O:235:TYR:HD2	35:O:301:LYS:HB2	1.45	0.80
37:R:65:PRO:HG2	37:R:66:GLU:OE2	1.79	0.80
1:A:95:MET:HE2	1:A:503:MET:HE1	1.63	0.80
15:H:149:A:H2'	15:H:150:U:H6	1.44	0.80
20:v:34:ALA:O	20:v:35:LEU:C	2.24	0.80
22:2:682:LEU:HD13	22:2:687:PHE:HA	1.63	0.80
23:3:637:PRO:HA	23:3:669:LEU:HA	1.63	0.80
33:Q:500:GLY:N	37:R:51:ILE:CD1	2.44	0.80
1:A:748:ASP:CA	36:P:214:THR:HG21	2.11	0.80
3:C:705:VAL:CG2	3:C:717:PHE:HE2	1.84	0.80
15:H:82:G:O2'	15:H:83:A:H5'	1.81	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:596:TYR:CD2	14:G:-5:G:C6	2.70	0.80
1:A:1482:GLU:O	1:A:1486:GLU:CG	2.23	0.80
3:C:87:GLN:OE1	3:C:91:GLU:HG2	1.82	0.80
3:C:140:HIS:CE1	3:C:230:ASP:HB3	2.16	0.80
3:C:776:GLU:O	3:C:781:ASP:OD1	2.00	0.80
5:E:265:ARG:H	5:E:272:ARG:NH2	1.80	0.80
13:F:68:C:N3	36:P:33:ARG:HG2	1.97	0.80
15:H:152:G:H5''	15:H:153:A:OP2	1.80	0.80
21:1:732:TRP:HE1	21:1:768:GLU:HG2	1.47	0.80
23:3:590:MET:HG2	23:3:607:VAL:HA	1.63	0.80
1:A:439:GLN:O	1:A:444:ARG:NH1	2.14	0.80
2:B:31:U:H5''	36:P:32:SER:OG	1.81	0.80
1:A:245:LEU:HA	1:A:430:TRP:HZ2	1.46	0.80
1:A:264:PHE:HE1	1:A:455:VAL:CG1	1.94	0.80
1:A:293:TRP:CZ3	1:A:295:GLU:OE1	2.35	0.80
1:A:301:LYS:CE	3:C:940:ARG:HA	2.12	0.80
1:A:481:PHE:CE2	37:R:205:ASP:HA	2.17	0.80
1:A:593:ARG:NH1	1:A:1565:LYS:CE	2.40	0.80
3:C:445:ALA:HB1	3:C:449:ILE:HD11	1.63	0.80
3:C:738:ASP:HB2	3:C:740:THR:O	1.82	0.80
35:O:20:PHE:CE1	37:R:177:ILE:HD11	2.17	0.80
5:E:248:SER:HB2	5:E:249:TYR:CD1	2.17	0.80
13:F:22:A:C5'	34:N:116:ASN:O	2.30	0.80
14:G:130:A:N1	18:w:400:HIS:CE1	2.50	0.80
7:i:85:PRO:CA	18:w:187:GLU:CB	2.58	0.80
24:4:28:LEU:O	24:4:32:LEU:CB	2.27	0.80
35:O:225:PRO:HB3	35:O:302:TRP:CE2	2.17	0.80
1:A:374:ASP:HB2	3:C:355:LYS:HD3	1.64	0.79
1:A:387:PHE:CD2	3:C:399:LEU:HD23	2.17	0.79
2:B:90:U:H5''	2:B:91:U:H5'	1.65	0.79
5:E:209:ILE:HG21	5:E:250:LEU:CD1	2.12	0.79
29:L:222:LEU:H	29:L:222:LEU:HD22	1.45	0.79
1:A:825:ILE:HB	1:A:1001:VAL:HG12	1.65	0.79
3:C:145:PHE:N	3:C:312:SER:CB	2.41	0.79
14:G:-8:U:C6	40:U:16:ASN:HA	2.17	0.79
14:G:21:A:OP2	35:O:156:TYR:OH	1.99	0.79
23:3:687:SER:OG	23:3:1206:LYS:CE	2.29	0.79
38:S:11:PRO:CB	38:S:166:GLY:HA3	2.12	0.79
1:A:283:VAL:O	1:A:284:ARG:NE	2.15	0.79
29:L:216:PHE:HE1	35:O:112:VAL:O	1.66	0.79
39:T:292:TYR:CZ	39:T:308:ARG:HG3	2.18	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:546:LEU:CD1	1:A:595:LYS:HD2	2.06	0.79
3:C:77:VAL:HG11	39:T:196:LEU:HG	0.79	0.79
5:E:310:TYR:CE1	5:E:322:LYS:HD2	2.18	0.79
39:T:306:CYS:SG	39:T:336:VAL:HB	2.22	0.79
1:A:596:TYR:CZ	14:G:-5:G:C8	2.71	0.79
20:v:45:TYR:CE1	20:v:58:LEU:HD11	2.15	0.79
23:3:641:CYS:HB2	23:3:701:LEU:HB3	1.64	0.79
42:W:212:GLU:O	42:W:214:LYS:N	2.14	0.79
1:A:318:TYR:C	3:C:638:ASP:OD1	2.25	0.79
1:A:2325:VAL:HG13	4:D:788:GLY:C	2.07	0.79
3:C:244:LYS:HB2	3:C:292:TYR:HE2	1.47	0.79
15:H:153:A:H2'	15:H:154:C:H5'	1.65	0.79
37:R:67:ILE:HG22	37:R:69:VAL:HG23	1.65	0.79
38:S:34:LYS:HE3	38:S:78:TYR:HE2	1.47	0.79
20:v:58:LEU:CD2	20:v:82:LEU:CB	2.59	0.79
36:P:212:ASN:O	39:T:458:SER:CA	2.23	0.79
37:R:420:LYS:HG3	37:R:421:GLY:N	1.97	0.79
39:T:351:ASP:O	39:T:352:THR:OG1	1.98	0.79
3:C:515:THR:O	3:C:517:GLU:N	2.16	0.79
3:C:705:VAL:HB	3:C:717:PHE:CE2	2.18	0.79
1:A:73:HIS:CD2	1:A:81:PHE:CD2	2.57	0.79
3:C:140:HIS:ND1	3:C:230:ASP:CB	2.46	0.79
3:C:259:LYS:HE2	3:C:262:ARG:CD	2.13	0.79
15:H:68:G:H1	15:H:84:C:H42	1.29	0.79
15:H:79:G:H2'	15:H:80:A:C8	2.17	0.79
1:A:596:TYR:CE2	14:G:-5:G:C5	2.71	0.78
13:F:34:G:N7	14:G:12:G:O6	2.16	0.78
15:H:101:U:H5''	15:H:102:U:H5'	1.64	0.78
45:Z:593:PHE:O	45:Z:597:ARG:HB2	1.83	0.78
1:A:1342:TRP:CE3	3:C:921:LEU:CD1	2.53	0.78
13:F:27:A:C4	35:O:181:TYR:CZ	2.71	0.78
29:L:209:ASP:CG	35:O:111:ASP:H	1.91	0.78
38:S:111:GLN:NE2	42:W:93:PHE:CB	2.46	0.78
1:A:718:ARG:NH2	37:R:259:LYS:HE3	1.98	0.78
15:H:82:G:H2'	15:H:83:A:C8	2.17	0.78
23:3:1109:LEU:HD11	23:3:1128:ILE:HG21	1.65	0.78
1:A:695:ASP:OD2	39:T:350:HIS:HB3	1.83	0.78
23:3:477:SER:HA	23:3:482:THR:HG22	1.65	0.78
38:S:39:PHE:HB3	38:S:129:PHE:HZ	1.26	0.78
40:U:1:MET:SD	40:U:1:MET:N	2.54	0.78
1:A:664:HIS:NE2	1:A:666:LYS:HD3	1.98	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:435:LEU:HD22	23:3:799:ILE:HD11	1.66	0.78
1:A:312:TYR:OH	3:C:853:ARG:NH2	2.17	0.78
37:R:132:LEU:HB3	39:T:399:LYS:NZ	1.99	0.78
1:A:299:ILE:HD12	3:C:921:LEU:HB2	1.66	0.78
1:A:705:LYS:HG2	37:R:251:ILE:HD12	1.65	0.78
1:A:758:ARG:CB	36:P:227:TYR:CE2	2.64	0.78
39:T:387:PHE:CE1	39:T:398:TRP:CD1	2.72	0.78
24:4:17:VAL:HG22	24:4:86:VAL:HG22	1.66	0.78
39:T:434:GLY:HA2	39:T:464:GLY:CA	2.14	0.78
1:A:468:LYS:HD3	1:A:469:LYS:N	1.99	0.78
3:C:133:THR:HB	3:C:225:VAL:HG23	1.65	0.78
23:3:295:THR:HG22	23:3:297:SER:H	1.48	0.78
35:O:149:LYS:HZ3	35:O:290:LYS:CG	1.97	0.78
1:A:2166:HIS:CD2	1:A:2272:MET:HE1	2.18	0.78
3:C:452:THR:HG21	3:C:577:PHE:CD2	2.16	0.78
22:2:649:LYS:HB3	22:2:655:SER:HB2	1.65	0.78
23:3:474:ILE:O	23:3:485:LEU:HB2	1.83	0.78
24:4:17:VAL:O	24:4:56:TYR:HA	1.83	0.78
35:O:131:THR:HG23	42:W:111:LEU:H	1.48	0.78
39:T:267:ASP:HB3	39:T:269:GLN:HG2	1.64	0.78
1:A:692:ASP:CA	39:T:376:ARG:HH22	1.97	0.77
1:A:919:ASP:OD2	1:A:1012:LYS:NZ	2.17	0.77
21:1:1053:ARG:NH1	22:2:559:PRO:O	2.17	0.77
23:3:805:ASN:ND2	23:3:858:GLY:O	2.14	0.77
1:A:168:PRO:HG2	1:A:559:ASP:HB3	1.64	0.77
1:A:1290:LYS:HG2	40:U:13:SER:C	2.08	0.77
3:C:449:ILE:HG21	3:C:457:VAL:HG12	1.66	0.77
3:C:677:GLU:OE2	3:C:684:LYS:HG2	1.83	0.77
21:1:941:ASN:HA	21:1:948:ARG:HH22	1.48	0.77
1:A:587:GLN:O	1:A:1551:PHE:HA	1.83	0.77
1:A:666:LYS:HB3	1:A:668:VAL:HG23	1.66	0.77
1:A:1405:LEU:CA	37:R:415:LEU:CD2	2.62	0.77
2:B:43:U:H5'	13:F:67:G:N2	1.98	0.77
3:C:449:ILE:CD1	3:C:466:SER:OG	2.33	0.77
15:H:80:A:H2'	15:H:81:G:C8	2.19	0.77
24:4:69:TYR:CE1	24:4:73:ILE:HG13	2.19	0.77
35:O:189:PRO:HG3	42:W:223:ARG:CB	2.15	0.77
38:S:11:PRO:HB2	38:S:165:SER:O	1.83	0.77
45:Z:595:GLN:O	45:Z:599:ALA:N	2.14	0.77
1:A:456:LEU:O	1:A:460:LYS:HG2	1.84	0.77
1:A:1352:HIS:ND1	40:U:21:ARG:HA	1.98	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:349:PHE:CD1	3:C:356:PHE:CD1	2.68	0.77
5:E:277:PHE:HE2	5:E:300:ILE:CD1	1.98	0.77
13:F:8:C:H5''	13:F:8:C:C6	2.19	0.77
35:O:292:ILE:HG12	35:O:297:ARG:HA	1.66	0.77
1:A:651:TRP:CE2	13:F:66:C:C2	2.72	0.77
3:C:85:ASP:CB	39:T:238:LEU:HG	2.14	0.77
3:C:140:HIS:HA	3:C:259:LYS:HZ3	1.48	0.77
3:C:151:GLU:OE1	3:C:417:ARG:CZ	2.33	0.77
14:G:11:A:H2'	14:G:12:G:O4'	1.84	0.77
35:O:45:CYS:SG	52:O:502:ZN:ZN	1.71	0.77
44:Y:86:ASP:HA	45:Z:502:ALA:HB3	1.65	0.77
1:A:152:ARG:HH11	1:A:152:ARG:CB	1.97	0.77
1:A:362:ARG:O	1:A:362:ARG:NE	2.18	0.77
28:J:291:GLN:NE2	29:L:230:GLU:OE2	2.17	0.77
39:T:318:ARG:HG3	39:T:319:THR:HG23	1.67	0.77
39:T:352:THR:CG2	39:T:373:LYS:C	2.58	0.77
3:C:482:TYR:HE2	3:C:493:PHE:CB	1.98	0.77
45:Z:603:SER:O	45:Z:607:VAL:HG23	1.84	0.77
1:A:43:LYS:HD2	42:W:168:PHE:CB	2.14	0.77
1:A:203:VAL:HG21	1:A:237:THR:CG2	2.14	0.77
1:A:1426:ASP:HB2	37:R:421:GLY:HA3	1.64	0.77
3:C:145:PHE:CZ	3:C:427:PHE:CE1	2.73	0.77
3:C:471:ASP:H	3:C:499:GLY:HA2	1.47	0.77
5:E:74:PHE:CD1	5:E:81:LEU:CD2	2.67	0.77
23:3:785:PRO:HA	23:3:800:ILE:O	1.84	0.77
1:A:623:LYS:CB	48:A:2401:IHP:O34	2.33	0.77
1:A:1314:VAL:HG11	1:A:1487:HIS:CG	2.19	0.77
1:A:1342:TRP:HE3	3:C:921:LEU:HD22	1.49	0.77
3:C:567:GLU:HG2	3:C:572:GLU:OE2	1.85	0.77
15:H:177:A:H5''	15:H:178:A:OP1	1.84	0.77
23:3:981:CYS:SG	23:3:982:GLU:N	2.57	0.77
38:S:11:PRO:HB3	38:S:166:GLY:CA	2.14	0.77
1:A:782:LEU:HD13	36:P:220:HIS:CE1	2.18	0.76
3:C:82:GLN:CB	39:T:231:TRP:HZ3	1.98	0.76
3:C:711:ARG:HD3	3:C:730:ARG:CZ	2.16	0.76
5:E:146:ARG:HH12	5:E:148:LYS:HE3	1.49	0.76
35:O:132:ARG:NH1	38:S:149:SER:CB	2.46	0.76
35:O:149:LYS:NZ	35:O:290:LYS:HG2	1.99	0.76
35:O:177:GLU:OE1	35:O:177:GLU:N	2.18	0.76
1:A:119:LEU:HD12	1:A:484:SER:HB2	1.67	0.76
1:A:630:TRP:O	1:A:632:ALA:N	2.18	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:473:GLN:HE22	25:5:93:ASN:H	1.33	0.76
37:R:420:LYS:HG2	37:R:423:ASP:OD2	1.84	0.76
1:A:43:LYS:CD	42:W:168:PHE:CB	2.63	0.76
1:A:230:PHE:N	1:A:414:ARG:O	2.18	0.76
1:A:705:LYS:CB	37:R:251:ILE:CD1	2.59	0.76
3:C:449:ILE:HD11	3:C:466:SER:N	1.99	0.76
15:H:143:A:H3'	15:H:143:A:N3	2.01	0.76
38:S:9:TRP:CZ2	38:S:44:ARG:HD3	2.20	0.76
38:S:13:ASN:HA	38:S:25:LEU:O	1.85	0.76
5:E:162:ARG:NH2	5:E:204:THR:HA	1.99	0.76
15:H:148:C:H2'	15:H:149:A:H8	1.48	0.76
38:S:9:TRP:HE3	38:S:11:PRO:HD3	1.49	0.76
1:A:1342:TRP:CB	3:C:921:LEU:HD21	2.13	0.76
3:C:471:ASP:OD1	3:C:472:GLY:N	2.19	0.76
22:2:611:ASP:O	22:2:614:ARG:HB3	1.86	0.76
38:S:10:GLN:HA	38:S:29:TRP:CZ2	2.20	0.76
38:S:131:ARG:HD3	38:S:132:VAL:C	2.09	0.76
1:A:755:HIS:HA	36:P:223:PHE:CE1	2.20	0.76
15:H:168:A:H5'	15:H:169:C:OP2	1.86	0.76
18:w:176:GLU:O	18:w:177:ARG:CB	2.33	0.76
20:v:66:GLU:O	20:v:70:LEU:N	2.18	0.76
38:S:20:MET:HE2	38:S:141:ARG:HB3	1.68	0.76
45:Z:566:TYR:HD2	45:Z:580:PRO:HG2	1.50	0.76
3:C:750:LEU:O	3:C:754:VAL:HG23	1.84	0.76
13:F:40:U:H2'	13:F:41:A:C8	2.20	0.76
23:3:328:LYS:HB2	23:3:372:GLU:HG3	1.68	0.76
41:V:548:ALA:HB1	41:V:586:PHE:N	2.00	0.76
1:A:779:LEU:CD2	36:P:223:PHE:CE2	2.69	0.76
1:A:1301:ILE:HD11	1:A:1306:LYS:HE2	1.68	0.76
5:E:231:MET:HB3	5:E:262:TRP:CZ3	2.21	0.76
18:w:283:GLN:O	18:w:284:ARG:CB	2.32	0.76
18:w:485:ASN:C	23:3:978:LEU:CD2	2.48	0.76
23:3:442:LEU:O	23:3:735:SER:N	2.18	0.76
29:L:209:ASP:CG	35:O:111:ASP:HB2	2.11	0.76
1:A:1162:PRO:CG	36:P:194:PHE:CD2	2.69	0.75
23:3:11:ALA:O	23:3:34:ARG:NH1	2.17	0.75
35:O:149:LYS:HG2	35:O:290:LYS:HZ3	1.49	0.75
45:Z:594:GLU:O	45:Z:598:PHE:HB2	1.86	0.75
1:A:318:TYR:N	3:C:638:ASP:OD1	2.19	0.75
30:q:8:SER:O	30:q:9:ASN:CB	2.34	0.75
32:I:720:ILE:O	32:I:721:LYS:CB	2.34	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:GLN:HG2	1:A:415:SER:HB2	1.68	0.75
1:A:532:THR:OG1	14:G:2:U:C5'	2.34	0.75
3:C:149:LEU:CD1	3:C:427:PHE:CG	2.53	0.75
3:C:593:GLU:HG3	3:C:594:PRO:HD2	1.67	0.75
14:G:132:G:H1	15:H:44:U:H3	1.34	0.75
23:3:784:THR:O	23:3:786:ARG:NH1	2.18	0.75
34:N:28:LYS:NZ	42:W:190:ASP:HA	2.01	0.75
37:R:66:GLU:OE2	37:R:66:GLU:N	2.19	0.75
37:R:181:PRO:O	37:R:182:SER:HB2	1.84	0.75
38:S:119:THR:OG1	38:S:122:LEU:HD12	1.87	0.75
1:A:318:TYR:CB	3:C:638:ASP:OD1	2.35	0.75
4:D:452:PRO:CB	23:3:570:PRO:HB2	2.16	0.75
14:G:11:A:C4	14:G:12:G:H8	2.04	0.75
15:H:81:G:H2'	15:H:82:G:C8	2.19	0.75
23:3:905:VAL:HB	23:3:928:TYR:HB2	1.68	0.75
1:A:402:ILE:CG2	3:C:268:LYS:HZ1	1.97	0.75
18:w:485:ASN:ND2	23:3:976:LYS:H	1.83	0.75
35:O:20:PHE:CD1	37:R:177:ILE:CD1	2.70	0.75
46:x:876:GLY:O	46:x:880:VAL:N	2.14	0.75
3:C:470:PRO:HA	3:C:499:GLY:HA2	1.67	0.75
3:C:711:ARG:CD	3:C:730:ARG:HE	1.99	0.75
15:H:10:C:H2'	15:H:11:G:H8	1.52	0.75
16:o:45:ASP:O	16:o:67:LYS:N	2.18	0.75
23:3:1105:GLN:O	23:3:1118:VAL:HB	1.87	0.75
13:F:36:A:C3'	13:F:37:C:H5''	2.16	0.75
15:H:45:C:C2'	18:w:394:TYR:CE2	2.69	0.75
28:J:339:TRP:CE3	37:R:116:TYR:HD2	2.04	0.75
41:V:515:CYS:HA	41:V:521:TYR:CB	2.17	0.75
1:A:76:MET:HE2	1:A:88:TYR:CD2	2.21	0.75
3:C:82:GLN:HB2	39:T:231:TRP:HZ3	1.50	0.75
15:H:71:C:H2'	15:H:72:U:C6	2.21	0.75
37:R:412:ASP:CG	37:R:413:GLN:N	2.39	0.75
42:W:101:THR:O	42:W:102:GLN:C	2.30	0.75
15:H:153:A:C2'	15:H:154:C:H5'	2.17	0.75
3:C:348:TYR:CE1	3:C:359:LYS:HB3	2.22	0.74
3:C:510:LEU:HD22	3:C:514:TYR:CE2	2.22	0.74
28:J:256:LYS:O	29:L:232:TYR:HD2	1.66	0.74
28:J:273:TYR:CG	37:R:228:PRO:HG2	2.21	0.74
1:A:1405:LEU:CA	37:R:415:LEU:HD21	2.15	0.74
3:C:449:ILE:CG2	3:C:457:VAL:HG12	2.17	0.74
35:O:225:PRO:CB	35:O:302:TRP:HE1	2.00	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:339:PHE:HE1	1:A:406:TRP:CZ3	2.01	0.74
1:A:532:THR:CG2	14:G:2:U:P	2.75	0.74
1:A:783:TYR:CB	36:P:228:ILE:HG12	2.17	0.74
20:v:56:CYS:HB2	20:v:78:HIS:CE1	2.22	0.74
35:O:185:LYS:CE	42:W:215:GLU:O	2.33	0.74
45:Z:525:TYR:HD1	45:Z:526:ILE:HG23	1.52	0.74
1:A:666:LYS:CB	1:A:668:VAL:HG23	2.17	0.74
1:A:2073:TRP:CD1	1:A:2074:ARG:HD2	2.22	0.74
23:3:437:VAL:O	23:3:776:GLN:HA	1.87	0.74
42:W:198:LYS:O	42:W:199:TYR:O	2.04	0.74
1:A:380:LEU:O	3:C:354:ARG:CG	2.30	0.74
1:A:1457:HIS:CD2	37:R:425:GLY:H	2.04	0.74
3:C:137:HIS:CG	3:C:236:MET:HB2	2.22	0.74
15:H:180:G:O2'	15:H:181:G:H5'	1.88	0.74
18:w:476:GLU:CB	23:3:978:LEU:HD22	2.17	0.74
28:J:406:PHE:CD2	28:J:411:MET:CE	2.70	0.74
37:R:70:ALA:O	37:R:71:GLN:O	2.05	0.74
1:A:73:HIS:NE2	1:A:81:PHE:CZ	2.51	0.74
1:A:203:VAL:CG2	1:A:237:THR:CG2	2.66	0.74
1:A:305:ARG:HB2	3:C:879:ASP:OD1	1.88	0.74
1:A:1405:LEU:HA	37:R:415:LEU:CD2	2.17	0.74
20:v:29:ARG:O	20:v:32:GLN:CG	2.36	0.74
23:3:294:LYS:O	23:3:343:LYS:NZ	2.21	0.74
23:3:931:VAL:HG12	23:3:932:ASN:H	1.53	0.74
28:J:270:ASP:OD2	37:R:222:PRO:HG2	1.88	0.74
38:S:131:ARG:NH1	38:S:132:VAL:O	2.20	0.74
1:A:132:ILE:HD11	2:B:57:G:OP1	1.88	0.74
5:E:258:THR:HG22	5:E:260:ARG:HG2	1.68	0.74
15:H:41:U:OP1	20:v:72:HIS:CE1	2.40	0.74
37:R:132:LEU:HB3	39:T:399:LYS:HZ2	1.52	0.74
1:A:744:LYS:HE3	36:P:213:ASP:HA	1.70	0.74
3:C:140:HIS:CA	3:C:230:ASP:HB2	2.17	0.74
13:F:34:G:H5''	13:F:34:G:N3	2.03	0.74
29:L:209:ASP:OD1	35:O:111:ASP:CG	2.31	0.74
35:O:225:PRO:CB	35:O:302:TRP:NE1	2.50	0.74
37:R:422:MET:O	37:R:424:SER:N	2.17	0.74
39:T:385:TYR:O	39:T:400:PHE:HB2	1.88	0.74
1:A:260:LEU:HD23	1:A:455:VAL:HG22	1.70	0.74
1:A:2270:PHE:HD1	4:D:1264:PRO:CB	1.96	0.74
3:C:445:ALA:HB1	3:C:449:ILE:CD1	2.17	0.74
13:F:1:G:O2'	34:N:99:ASN:ND2	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:45:C:N3	18:w:395:TRP:CD1	2.55	0.74
1:A:380:LEU:CA	3:C:354:ARG:HG3	2.16	0.73
1:A:748:ASP:OD1	36:P:214:THR:CG2	2.36	0.73
5:E:243:LEU:HD11	5:E:247:GLY:HA2	1.68	0.73
20:v:58:LEU:HD21	20:v:82:LEU:HA	1.68	0.73
1:A:176:LEU:HD13	1:A:181:ASN:HD22	1.52	0.73
3:C:89:LEU:HD23	3:C:89:LEU:C	2.14	0.73
18:w:482:SER:CB	23:3:975:LYS:CB	2.65	0.73
1:A:312:TYR:CE2	3:C:882:GLY:HA3	2.23	0.73
1:A:593:ARG:HD3	14:G:-4:A:H4'	1.70	0.73
5:E:119:THR:HG21	5:E:161:ARG:CB	2.17	0.73
1:A:380:LEU:CB	3:C:354:ARG:CG	2.45	0.73
3:C:97:VAL:HG21	36:P:45:GLN:HG3	1.69	0.73
15:H:45:C:C2'	18:w:394:TYR:HE2	2.01	0.73
21:1:563:LEU:HD22	21:1:566:LEU:HD22	1.70	0.73
42:W:137:TYR:CB	42:W:159:ALA:HB2	2.17	0.73
1:A:2078:ILE:CG2	4:D:1047:PRO:CB	2.66	0.73
2:B:42:U:C4'	13:F:70:A:H4'	2.18	0.73
3:C:94:ILE:HD11	36:P:44:ARG:NH2	2.03	0.73
1:A:294:ASN:OD1	3:C:654:LYS:HD3	1.89	0.73
3:C:516:LEU:CD1	3:C:517:GLU:HG3	2.18	0.73
3:C:671:SER:O	3:C:672:LEU:HD13	1.89	0.73
15:H:69:U:H2'	15:H:70:C:C6	2.23	0.73
15:H:165:A:O2'	15:H:166:G:H5'	1.88	0.73
35:O:149:LYS:HG3	35:O:290:LYS:HZ1	1.54	0.73
35:O:247:ASP:OD2	35:O:294:ASN:ND2	2.21	0.73
38:S:131:ARG:NH1	38:S:133:CYS:CA	2.51	0.73
5:E:287:ASN:O	5:E:289:LEU:HD23	1.88	0.73
15:H:39:U:O2'	20:v:62:LEU:O	2.07	0.73
26:6:51:TYR:H	26:6:54:TYR:HB2	1.53	0.73
35:O:149:LYS:CG	35:O:290:LYS:HZ1	2.02	0.73
37:R:67:ILE:HG22	37:R:69:VAL:CG2	2.18	0.73
37:R:420:LYS:HG2	37:R:423:ASP:CG	2.13	0.73
38:S:9:TRP:HZ2	38:S:44:ARG:HD3	1.52	0.73
38:S:100:MET:CG	38:S:108:ASN:OD1	2.36	0.73
1:A:1301:ILE:O	1:A:1303:LEU:O	2.06	0.73
38:S:81:GLN:HA	38:S:108:ASN:O	1.88	0.73
2:B:42:U:C2	14:G:-3:A:H2	2.07	0.73
15:H:106:G:H4'	15:H:107:A:O4'	1.89	0.73
7:i:85:PRO:N	18:w:184:ARG:O	2.22	0.73
23:3:555:VAL:HG23	23:3:592:LEU:HD22	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:1145:GLU:OE2	23:3:1149:ARG:NH2	2.21	0.73
28:J:339:TRP:CE3	37:R:116:TYR:CD2	2.76	0.73
42:W:101:THR:O	42:W:104:MET:N	2.22	0.73
3:C:711:ARG:CD	3:C:730:ARG:HH11	2.01	0.73
20:v:23:ASN:ND2	29:L:39:HIS:CE1	2.55	0.73
28:J:259:GLN:NE2	29:L:220:PRO:HD3	2.02	0.73
42:W:212:GLU:C	42:W:214:LYS:H	1.97	0.73
1:A:380:LEU:C	3:C:354:ARG:HG2	2.14	0.72
3:C:449:ILE:HG22	3:C:457:VAL:CG1	2.18	0.72
5:E:146:ARG:HH12	5:E:148:LYS:CE	1.99	0.72
5:E:250:LEU:HD23	5:E:250:LEU:O	1.88	0.72
15:H:70:C:H2'	15:H:71:C:C6	2.24	0.72
20:v:51:LEU:CG	21:1:1141:LEU:CD1	2.66	0.72
41:V:548:ALA:HB3	41:V:585:ILE:CB	2.19	0.72
1:A:1342:TRP:CZ2	3:C:921:LEU:CD1	2.71	0.72
3:C:508:LYS:HE3	3:C:566:THR:HG21	1.70	0.72
15:H:42:G:OP2	20:v:77:LYS:CE	2.37	0.72
39:T:434:GLY:CA	39:T:464:GLY:HA2	2.19	0.72
2:B:40:U:H4'	2:B:41:U:OP2	1.89	0.72
3:C:93:ILE:HD13	39:T:230:ILE:HD13	1.72	0.72
15:H:106:G:H21	15:H:107:A:N6	1.87	0.72
15:H:182:U:H2'	15:H:183:G:H8	1.53	0.72
21:1:428:ALA:O	21:1:432:THR:N	2.21	0.72
23:3:547:CYS:HA	23:3:555:VAL:O	1.89	0.72
1:A:675:GLN:OE1	13:F:70:A:OP1	2.08	0.72
3:C:519:GLU:N	3:C:519:GLU:OE2	2.21	0.72
13:F:34:G:N3	13:F:34:G:H3'	2.05	0.72
38:S:11:PRO:HB3	38:S:165:SER:C	2.15	0.72
1:A:549:GLU:OE1	1:A:552:ARG:NH1	2.23	0.72
1:A:1457:HIS:HE2	37:R:424:SER:CA	2.02	0.72
1:A:1755:SER:CB	21:1:938:TRP:CH2	2.72	0.72
3:C:125:ASN:O	3:C:126:SER:OG	2.04	0.72
3:C:726:LEU:HD12	3:C:726:LEU:O	1.89	0.72
14:G:20:A:H1'	35:O:193:LEU:CD2	2.19	0.72
1:A:150:MET:SD	1:A:153:ARG:NH2	2.62	0.72
1:A:303:ILE:HD13	3:C:933:PHE:CD1	2.25	0.72
1:A:712:HIS:CE1	37:R:254:CYS:HB2	2.24	0.72
3:C:77:VAL:CG1	39:T:196:LEU:CA	2.68	0.72
3:C:449:ILE:HG21	3:C:457:VAL:HG11	1.70	0.72
13:F:5:U:H3'	13:F:7:G:H5''	1.71	0.72
1:A:1413:ASP:O	1:A:1418:ARG:NH1	2.21	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:250:ARG:HE	3:C:451:HIS:CD2	2.07	0.72
23:3:720:TRP:HB3	23:3:731:LEU:HD11	1.69	0.72
1:A:107:PRO:O	1:A:111:GLU:OE1	2.08	0.72
1:A:193:LEU:HD12	1:A:194:GLU:H	1.55	0.72
1:A:1338:SER:OG	1:A:1351:THR:N	2.16	0.72
13:F:39:A:H61	14:G:8:C:H42	1.36	0.72
22:2:614:ARG:HG3	22:2:614:ARG:NH1	1.98	0.72
34:N:40:LYS:C	34:N:41:ARG:HG3	2.13	0.72
35:O:240:GLY:HA3	35:O:296:ARG:HH12	1.55	0.72
1:A:718:ARG:CZ	37:R:259:LYS:HE3	2.20	0.72
5:E:264:VAL:HA	5:E:272:ARG:HH21	1.55	0.72
13:F:28:A:O4'	34:N:41:ARG:HA	1.90	0.72
23:3:783:TYR:HB2	23:3:801:GLU:HB3	1.72	0.72
37:R:92:SER:C	38:S:19:SER:CB	2.56	0.72
42:W:491:GLN:O	42:W:493:ARG:N	2.23	0.72
1:A:785:LYS:HE3	36:P:215:LEU:HD11	1.71	0.72
1:A:1481:VAL:HG21	1:A:1498:TRP:CH2	2.25	0.72
1:A:2324:GLU:HG2	1:A:2330:ARG:HH12	1.54	0.72
2:B:42:U:O4'	13:F:70:A:H4'	1.89	0.72
15:H:165:A:C2'	15:H:166:G:H5'	2.20	0.72
1:A:228:TRP:O	1:A:415:SER:CA	2.38	0.71
3:C:64:LYS:NZ	36:P:206:LYS:HG2	2.05	0.71
3:C:129:ILE:HA	3:C:199:LEU:O	1.90	0.71
1:A:203:VAL:HG23	1:A:237:THR:HG21	1.72	0.71
1:A:696:MET:C	1:A:698:PRO:HD3	2.15	0.71
2:B:31:U:C5'	36:P:32:SER:OG	2.38	0.71
28:J:273:TYR:CE1	37:R:228:PRO:CB	2.72	0.71
29:L:224:PHE:CE1	37:R:86:LEU:CD1	2.73	0.71
36:P:66:ARG:HB2	36:P:66:ARG:HH11	1.55	0.71
1:A:168:PRO:CG	1:A:559:ASP:CB	2.64	0.71
1:A:730:GLY:O	37:R:252:PRO:HG2	1.90	0.71
1:A:1402:ARG:HH22	45:Z:572:PRO:HA	1.53	0.71
1:A:1481:VAL:HG21	1:A:1498:TRP:CZ2	2.25	0.71
21:1:1206:ASP:OD1	21:1:1207:SER:N	2.21	0.71
1:A:434:HIS:ND1	1:A:435:CYS:SG	2.62	0.71
1:A:462:ARG:HD2	1:A:462:ARG:N	2.05	0.71
15:H:153:A:H2'	15:H:154:C:C5'	2.19	0.71
21:1:405:ASP:HA	25:5:49:ARG:HH22	1.55	0.71
37:R:135:PRO:O	37:R:136:ASP:CG	2.33	0.71
46:x:640:ARG:CB	46:x:667:ALA:HA	2.19	0.71
1:A:299:ILE:HD13	1:A:1346:THR:HG21	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:461:HIS:HD2	2:B:27:U:O4	1.71	0.71
3:C:706:GLN:HE21	3:C:708:THR:H	1.38	0.71
5:E:74:PHE:CE2	5:E:343:ILE:CG1	2.73	0.71
18:w:485:ASN:HA	23:3:978:LEU:CD1	2.20	0.71
36:P:224:MET:HA	36:P:224:MET:CE	2.21	0.71
37:R:414:ARG:CZ	37:R:414:ARG:HB2	2.18	0.71
1:A:76:MET:CE	1:A:88:TYR:CG	2.70	0.71
1:A:81:PHE:O	1:A:83:HIS:N	2.24	0.71
1:A:1529:ILE:O	1:A:1532:ARG:N	2.24	0.71
1:A:2328:ALA:HB3	4:D:788:GLY:N	2.05	0.71
3:C:700:ILE:HA	3:C:705:VAL:CG1	2.21	0.71
3:C:705:VAL:HG23	3:C:717:PHE:HD2	1.48	0.71
15:H:72:U:H2'	15:H:73:C:C6	2.26	0.71
35:O:185:LYS:HG3	42:W:216:LEU:CA	2.20	0.71
1:A:76:MET:CE	1:A:506:LEU:HD11	2.21	0.71
1:A:264:PHE:CE2	1:A:459:LEU:CD1	2.73	0.71
1:A:2325:VAL:CG1	4:D:789:MET:HA	2.20	0.71
3:C:80:ILE:HD12	3:C:80:ILE:N	2.05	0.71
3:C:94:ILE:HD13	36:P:44:ARG:CZ	2.20	0.71
3:C:441:PRO:O	3:C:444:GLY:HA3	1.90	0.71
3:C:490:PHE:CZ	3:C:612:LYS:HD2	2.26	0.71
35:O:235:TYR:HD1	35:O:271:PHE:HE1	1.37	0.71
36:P:191:ASP:N	36:P:191:ASP:OD1	2.23	0.71
42:W:277:PRO:CB	42:W:578:TRP:O	2.39	0.71
45:Z:612:TYR:O	45:Z:614:TRP:N	2.23	0.71
1:A:1290:LYS:CG	40:U:13:SER:O	2.38	0.71
2:B:40:U:C4'	2:B:41:U:OP2	2.39	0.71
20:v:51:LEU:CB	21:1:1141:LEU:CD1	2.26	0.71
41:V:549:LYS:O	41:V:552:ALA:HB3	1.91	0.71
1:A:402:ILE:HG21	3:C:268:LYS:HZ1	1.51	0.71
1:A:1459:ARG:CG	37:R:422:MET:O	2.39	0.71
3:C:679:PRO:HG2	3:C:807:GLN:OE1	1.91	0.71
28:J:270:ASP:OD2	37:R:222:PRO:HG3	1.88	0.71
29:L:209:ASP:OD2	35:O:111:ASP:CB	2.30	0.71
37:R:422:MET:HG2	37:R:423:ASP:N	2.05	0.71
38:S:71:GLY:O	42:W:93:PHE:CB	2.39	0.71
1:A:705:LYS:HG2	37:R:251:ILE:CD1	2.21	0.71
1:A:1085:ILE:HG12	1:A:1099:PHE:HE1	1.56	0.71
1:A:1552:GLN:HB3	49:A:2402:ALA:CB	2.21	0.71
1:A:2078:ILE:HG21	4:D:1047:PRO:CB	2.20	0.71
3:C:474:LEU:HD23	3:C:474:LEU:C	2.16	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:1221:GLU:HG3	21:1:1223:SER:H	1.56	0.71
28:J:353:GLU:OE1	28:J:358:GLU:HB3	1.91	0.71
36:P:189:ASP:OD2	36:P:192:VAL:HG21	1.91	0.71
39:T:366:VAL:HG21	39:T:402:ASP:HA	1.72	0.71
1:A:719:CYS:SG	37:R:258:TRP:CH2	2.84	0.70
3:C:259:LYS:HG3	50:C:1500:GTP:C6	2.26	0.70
14:G:20:A:H1'	35:O:193:LEU:HD21	1.72	0.70
1:A:1342:TRP:CG	3:C:921:LEU:HD21	2.25	0.70
15:H:160:A:O2'	15:H:161:U:H5'	1.90	0.70
35:O:197:ASN:OD1	35:O:198:ILE:N	2.24	0.70
35:O:262:THR:HB	35:O:271:PHE:HB2	1.73	0.70
1:A:1549:VAL:CG2	14:G:-6:C:O2'	2.39	0.70
14:G:11:A:N3	14:G:11:A:H5''	2.05	0.70
15:H:168:A:N3	15:H:168:A:H2'	2.06	0.70
23:3:722:SER:HA	23:3:730:HIS:O	1.92	0.70
38:S:88:PRO:O	38:S:91:LYS:HE3	1.90	0.70
1:A:593:ARG:O	14:G:-4:A:H1'	1.91	0.70
13:F:24:A:H2	13:F:26:U:C2	2.09	0.70
7:i:85:PRO:CA	18:w:184:ARG:HA	2.22	0.70
23:3:446:GLU:OE1	23:3:763:ARG:NH1	2.24	0.70
35:O:144:SER:HA	35:O:148:LEU:HD13	1.73	0.70
37:R:189:ASN:HD21	37:R:195:ARG:NH2	1.90	0.70
39:T:267:ASP:O	39:T:268:LYS:HG3	1.91	0.70
1:A:171:ASP:O	1:A:520:TYR:CG	2.44	0.70
1:A:181:ASN:O	1:A:185:VAL:HG22	1.90	0.70
3:C:449:ILE:HD13	3:C:466:SER:OG	1.92	0.70
13:F:94:C:OP1	28:J:351:ASN:ND2	2.25	0.70
15:H:181:G:H2'	15:H:182:U:C6	2.26	0.70
20:v:58:LEU:HD21	20:v:82:LEU:CA	2.22	0.70
21:1:901:GLN:HA	21:1:939:ARG:NH2	2.07	0.70
29:L:216:PHE:CE1	35:O:112:VAL:HG12	2.25	0.70
37:R:103:ARG:HH11	37:R:103:ARG:CB	2.04	0.70
1:A:338:VAL:HG21	3:C:867:PRO:CG	2.22	0.70
1:A:2156:THR:OG1	1:A:2157:VAL:N	2.21	0.70
3:C:457:VAL:CB	3:C:462:GLY:HA3	2.22	0.70
13:F:38:G:P	13:F:38:G:H8	2.14	0.70
13:F:68:C:C2	36:P:33:ARG:HG2	2.27	0.70
14:G:12:G:N3	14:G:12:G:H2'	2.07	0.70
21:1:1108:ASN:OD1	21:1:1110:VAL:N	2.25	0.70
41:V:536:ILE:O	41:V:578:SER:CB	2.39	0.70
1:A:296:PHE:HE1	3:C:591:ALA:HB1	1.52	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:ARG:CG	3:C:879:ASP:OD1	2.39	0.70
3:C:132:VAL:CG1	3:C:226:VAL:CG2	2.70	0.70
3:C:135:CYS:SG	3:C:227:LEU:CD1	2.80	0.70
13:F:27:A:H1'	35:O:181:TYR:CE2	2.23	0.70
14:G:-9:C:C6	40:U:18:TYR:CD1	2.80	0.70
35:O:189:PRO:CG	42:W:223:ARG:N	2.54	0.70
37:R:220:ARG:NH1	37:R:220:ARG:HB2	2.06	0.70
38:S:10:GLN:HB3	38:S:29:TRP:CE3	2.27	0.70
38:S:39:PHE:HB2	38:S:129:PHE:HZ	1.10	0.70
46:x:831:SER:CB	46:x:942:ALA:CA	2.70	0.70
1:A:76:MET:SD	1:A:88:TYR:CG	2.85	0.70
1:A:377:GLU:O	1:A:378:PHE:HB3	1.91	0.70
1:A:596:TYR:CD2	14:G:-5:G:C5	2.79	0.70
1:A:675:GLN:O	13:F:55:C:O2'	2.10	0.70
1:A:1318:THR:HB	1:A:1324:GLY:HA3	1.73	0.70
15:H:154:C:H2'	15:H:155:C:C6	2.27	0.70
21:1:1155:PHE:HA	21:1:1158:ILE:HG12	1.73	0.70
37:R:80:LYS:O	37:R:81:LYS:NZ	2.25	0.70
1:A:132:ILE:HD13	2:B:57:G:OP1	1.92	0.70
1:A:719:CYS:SG	37:R:258:TRP:HH2	2.13	0.70
2:B:42:U:H4'	13:F:70:A:H5'	1.73	0.70
3:C:137:HIS:CE1	3:C:236:MET:SD	2.85	0.70
35:O:149:LYS:NZ	35:O:290:LYS:CG	2.55	0.70
1:A:318:TYR:HB2	3:C:638:ASP:CG	2.16	0.69
1:A:481:PHE:CD2	37:R:205:ASP:HA	2.27	0.69
1:A:718:ARG:NE	37:R:259:LYS:HE3	2.06	0.69
3:C:452:THR:HB	3:C:577:PHE:CD2	2.26	0.69
23:3:524:ILE:HD11	23:3:556:ILE:HG21	1.74	0.69
1:A:461:HIS:CD2	2:B:26:A:N6	2.60	0.69
35:O:223:LEU:HD13	35:O:223:LEU:C	2.15	0.69
1:A:76:MET:HE1	1:A:88:TYR:CB	2.22	0.69
1:A:673:THR:O	1:A:677:VAL:HG23	1.91	0.69
3:C:64:LYS:NZ	36:P:206:LYS:CG	2.55	0.69
3:C:452:THR:O	3:C:577:PHE:HA	1.92	0.69
5:E:74:PHE:HE2	5:E:343:ILE:HG12	1.54	0.69
5:E:264:VAL:HA	5:E:272:ARG:NH2	2.07	0.69
35:O:48:CYS:SG	35:O:71:CYS:SG	2.91	0.69
1:A:974:ASN:HB2	1:A:1178:TYR:HB3	1.73	0.69
1:A:71:ARG:HD2	1:A:177:ASP:OD2	1.92	0.69
1:A:338:VAL:CB	3:C:867:PRO:HG3	2.21	0.69
1:A:805:GLU:CB	36:P:194:PHE:HZ	2.04	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:709:TRP:HB3	3:C:713:LYS:HD2	1.73	0.69
23:3:280:ASP:H	23:3:857:ALA:HB3	1.58	0.69
36:P:30:TYR:OH	37:R:161:ALA:O	2.10	0.69
37:R:436:VAL:HG23	37:R:437:TYR:CE1	2.26	0.69
1:A:755:HIS:HE1	36:P:223:PHE:CD2	2.06	0.69
14:G:19:G:H5''	35:O:159:ARG:HD2	1.74	0.69
15:H:149:A:H2'	15:H:150:U:C6	2.27	0.69
15:H:153:A:N6	15:H:177:A:C2	2.60	0.69
15:H:183:G:H2'	15:H:184:C:C6	2.26	0.69
37:R:408:GLU:CG	37:R:409:VAL:H	2.04	0.69
1:A:1180:LYS:HA	1:A:1201:ARG:HH12	1.58	0.69
3:C:141:GLY:C	3:C:258:ASN:HD22	2.01	0.69
16:o:46:ALA:HB2	16:o:68:THR:CB	2.23	0.69
23:3:428:GLY:HA3	23:3:433:SER:HA	1.73	0.69
34:N:51:ARG:NH2	42:W:192:PHE:O	2.26	0.69
1:A:229:GLN:CG	1:A:415:SER:HB2	2.21	0.69
1:A:296:PHE:HB3	3:C:656:ALA:HB2	1.66	0.69
1:A:762:ARG:NH2	36:P:226:LYS:HZ3	1.87	0.69
1:A:1342:TRP:HB3	3:C:921:LEU:CD2	2.22	0.69
3:C:482:TYR:CE2	3:C:493:PHE:HB2	2.28	0.69
5:E:178:LEU:CD1	5:E:222:LEU:CD2	2.71	0.69
15:H:83:A:C2'	15:H:84:C:O4'	2.39	0.69
25:5:18:ASN:OD1	25:5:19:ARG:N	2.25	0.69
43:X:185:ARG:O	43:X:189:HIS:HB2	1.93	0.69
1:A:76:MET:HE3	1:A:506:LEU:HD11	1.74	0.69
1:A:1348:VAL:CG1	3:C:921:LEU:CD2	2.71	0.69
1:A:1459:ARG:HG3	37:R:424:SER:H	1.57	0.69
3:C:93:ILE:CG2	39:T:218:TRP:CE2	2.76	0.69
3:C:736:GLY:CA	3:C:770:PHE:CE2	2.75	0.69
15:H:152:G:O3'	15:H:153:A:O4'	2.11	0.69
23:3:236:ILE:HB	23:3:249:LEU:HB2	1.75	0.69
28:J:353:GLU:OE1	28:J:358:GLU:CB	2.41	0.69
36:P:30:TYR:CZ	37:R:162:ALA:HA	2.28	0.69
36:P:224:MET:CE	36:P:228:ILE:CD1	2.71	0.69
42:W:474:LYS:HA	42:W:490:ALA:HB3	1.75	0.69
46:x:726:ALA:HB1	46:x:732:GLY:HA3	1.75	0.69
1:A:2113:LYS:CE	4:D:1229:ASP:CB	2.71	0.69
3:C:72:VAL:HG22	39:T:453:ALA:CB	2.23	0.69
3:C:256:CYS:SG	3:C:308:CYS:HB2	2.33	0.69
5:E:74:PHE:CD1	5:E:81:LEU:HD23	2.28	0.69
35:O:26:THR:OG1	35:O:159:ARG:NH2	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:338:VAL:CG2	3:C:867:PRO:CG	2.64	0.68
1:A:755:HIS:CE1	36:P:223:PHE:HB3	2.28	0.68
1:A:1076:ASP:O	1:A:1079:THR:OG1	2.11	0.68
4:D:455:PHE:CB	23:3:573:GLN:CD	2.66	0.68
13:F:37:C:H4'	13:F:38:G:OP2	1.91	0.68
22:2:487:LEU:O	22:2:490:HIS:N	2.26	0.68
1:A:299:ILE:CD1	3:C:921:LEU:CB	2.50	0.68
1:A:1307:MET:HE1	1:A:1549:VAL:O	1.93	0.68
3:C:140:HIS:CD2	3:C:230:ASP:HB3	2.28	0.68
3:C:445:ALA:CB	3:C:466:SER:HA	2.20	0.68
3:C:725:ASP:OD1	3:C:728:ALA:N	2.25	0.68
23:3:452:LEU:HD11	23:3:762:LEU:HB2	1.74	0.68
37:R:434:TYR:HE2	37:R:436:VAL:HG22	1.57	0.68
1:A:73:HIS:NE2	1:A:81:PHE:CD1	2.59	0.68
1:A:203:VAL:CG2	1:A:237:THR:HG21	2.23	0.68
18:w:478:GLU:CB	23:3:978:LEU:HD12	2.23	0.68
20:v:58:LEU:CD2	20:v:82:LEU:HA	2.24	0.68
22:2:643:PRO:HD2	24:4:69:TYR:CG	2.27	0.68
36:P:72:ARG:NH1	36:P:72:ARG:HB2	2.08	0.68
37:R:106:GLN:CG	37:R:110:LYS:HE2	2.22	0.68
44:Y:33:LYS:HA	44:Y:87:GLN:HE22	1.59	0.68
1:A:32:GLU:HG3	1:A:36:LYS:HE3	1.74	0.68
1:A:126:ILE:HG21	37:R:207:MET:HE2	1.74	0.68
1:A:245:LEU:HA	1:A:430:TRP:CZ2	2.28	0.68
1:A:2267:PHE:HA	4:D:1261:PRO:CB	2.23	0.68
3:C:453:TYR:CZ	3:C:575:GLN:HB2	2.28	0.68
23:3:718:ARG:NH2	23:3:734:LEU:O	2.26	0.68
38:S:102:ASN:ND2	38:S:104:GLY:O	2.25	0.68
44:Y:86:ASP:HB2	45:Z:502:ALA:CB	2.23	0.68
1:A:44:ARG:HD2	1:A:45:TYR:CE2	2.28	0.68
1:A:121:HIS:HE2	1:A:481:PHE:HB3	1.51	0.68
1:A:171:ASP:OD2	1:A:519:ASP:OD2	2.12	0.68
3:C:482:TYR:CE2	3:C:493:PHE:CB	2.77	0.68
3:C:678:THR:HG21	3:C:683:ASN:ND2	2.06	0.68
14:G:-2:C:H2'	14:G:-1:G:C8	2.28	0.68
15:H:29:A:C6	20:v:19:SER:HB3	2.28	0.68
23:3:687:SER:HG	23:3:1206:LYS:HD2	1.55	0.68
23:3:868:VAL:O	23:3:877:LEU:N	2.27	0.68
42:W:466:ALA:CB	42:W:512:CYS:O	2.41	0.68
1:A:296:PHE:CE1	3:C:591:ALA:HB3	2.27	0.68
1:A:384:VAL:HG11	3:C:331:PHE:CD2	2.28	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:108:HIS:CE1	5:E:128:SER:CB	2.77	0.68
15:H:147:G:O2'	15:H:148:C:H5'	1.94	0.68
29:L:216:PHE:CZ	35:O:112:VAL:HG12	2.29	0.68
35:O:116:TYR:HH	37:R:222:PRO:HD3	1.56	0.68
35:O:137:LEU:HD12	35:O:140:ALA:HB3	1.76	0.68
36:P:63:LEU:O	36:P:63:LEU:HD23	1.94	0.68
37:R:414:ARG:NE	45:Z:598:PHE:CE1	2.47	0.68
1:A:91:ALA:O	1:A:93:LYS:N	2.27	0.68
1:A:779:LEU:CD2	36:P:223:PHE:HE2	2.06	0.68
1:A:1457:HIS:HE2	37:R:424:SER:HA	1.55	0.68
13:F:68:C:C5	36:P:33:ARG:HB3	2.20	0.68
37:R:88:ILE:CG2	37:R:96:ILE:CG2	2.71	0.68
1:A:299:ILE:HD11	3:C:921:LEU:HA	1.73	0.68
1:A:779:LEU:HD22	36:P:224:MET:HE1	1.75	0.68
1:A:1705:ILE:HD11	1:A:1730:MET:HE1	1.75	0.68
1:A:2146:VAL:HG22	1:A:2272:MET:HB2	1.74	0.68
2:B:32:C:OP1	36:P:33:ARG:CZ	2.41	0.68
3:C:79:THR:HG23	39:T:199:VAL:CG2	2.24	0.68
3:C:350:ASN:CG	3:C:353:THR:HG23	2.19	0.68
3:C:452:THR:HG22	3:C:577:PHE:CB	2.23	0.68
5:E:74:PHE:CD1	5:E:81:LEU:HD21	2.29	0.68
23:3:546:LYS:O	23:3:556:ILE:HA	1.94	0.68
37:R:92:SER:O	38:S:19:SER:O	2.11	0.68
45:Z:597:ARG:NH1	45:Z:601:LEU:CD1	2.57	0.68
1:A:228:TRP:O	1:A:416:GLY:N	2.26	0.68
1:A:758:ARG:HG3	1:A:779:LEU:HD11	1.75	0.68
1:A:1210:LYS:NZ	1:A:1369:TYR:OH	2.27	0.68
2:B:21:A:O3'	2:B:22:U:H4'	1.94	0.68
3:C:141:GLY:O	3:C:258:ASN:ND2	2.27	0.68
20:v:83:ALA:O	20:v:86:ALA:HB3	1.93	0.68
22:2:614:ARG:NH2	22:2:685:ASP:OD1	2.26	0.68
23:3:301:PHE:HB2	23:3:313:ILE:HB	1.76	0.68
27:7:48:ASP:O	27:7:51:ASN:N	2.27	0.68
28:J:360:ASP:O	28:J:363:ARG:HG3	1.93	0.68
44:Y:86:ASP:CA	45:Z:502:ALA:HB3	2.23	0.68
1:A:645:THR:HB	1:A:646:PRO:HD3	1.74	0.68
1:A:2300:ASN:OD1	4:D:1228:VAL:O	2.12	0.68
3:C:94:ILE:CD1	36:P:44:ARG:NH1	2.57	0.68
13:F:35:A:H5''	13:F:35:A:N3	2.09	0.68
15:H:159:U:O2'	15:H:160:A:H5'	1.94	0.68
23:3:374:SER:HB3	23:3:377:MET:HG3	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:753:GLY:HA3	23:3:765:LEU:O	1.93	0.68
28:J:353:GLU:OE2	28:J:361:ARG:NH2	2.27	0.68
3:C:94:ILE:CD1	36:P:44:ARG:CZ	2.72	0.67
3:C:360:ALA:H	3:C:361:PRO:HD3	1.59	0.67
3:C:534:VAL:HG12	3:C:535:ALA:H	1.59	0.67
37:R:420:LYS:HB2	45:Z:610:LEU:CD1	2.22	0.67
41:V:547:VAL:O	41:V:550:MET:N	2.27	0.67
1:A:75:ASP:OD1	1:A:75:ASP:N	2.26	0.67
3:C:140:HIS:HB3	3:C:230:ASP:HB2	1.71	0.67
21:1:498:MET:HE1	21:1:530:PRO:HB2	1.76	0.67
23:3:18:ILE:HD12	23:3:67:ALA:HB2	1.77	0.67
37:R:147:THR:CG2	39:T:360:VAL:HG12	2.23	0.67
1:A:122:ILE:CD1	1:A:483:GLN:HG3	2.24	0.67
1:A:2314:PHE:HD2	4:D:1123:TRP:CB	2.05	0.67
3:C:140:HIS:CD2	3:C:230:ASP:CB	2.77	0.67
3:C:737:PRO:HG3	3:C:774:THR:OG1	1.93	0.67
21:1:437:PRO:O	43:X:262:TYR:HA	1.94	0.67
1:A:89:LEU:HD22	1:A:656:LEU:HD22	1.76	0.67
1:A:255:PHE:HE1	1:A:432:ARG:O	1.75	0.67
1:A:630:TRP:O	1:A:631:ALA:C	2.37	0.67
1:A:1072:LEU:HD22	1:A:1087:LEU:HD22	1.76	0.67
1:A:1661:TRP:CE2	1:A:1700:GLY:HA3	2.30	0.67
3:C:259:LYS:HE2	3:C:262:ARG:HD2	1.74	0.67
18:w:434:GLY:O	18:w:438:LEU:HB2	1.94	0.67
21:1:1097:LEU:O	21:1:1100:ASN:ND2	2.24	0.67
23:3:412:ILE:HG12	23:3:423:LEU:HG	1.76	0.67
35:O:131:THR:HG23	42:W:111:LEU:N	2.10	0.67
1:A:380:LEU:CA	3:C:354:ARG:CG	2.72	0.67
1:A:1422:LEU:HD22	21:1:88:VAL:CB	2.25	0.67
3:C:389:ASP:OD1	3:C:389:ASP:N	2.26	0.67
5:E:66:GLU:HB2	5:E:87:ASP:OD2	1.94	0.67
21:1:474:TYR:OH	25:5:93:ASN:ND2	2.27	0.67
21:1:798:THR:HG22	21:1:800:GLY:H	1.60	0.67
37:R:119:LEU:CB	37:R:232:MET:HG3	2.24	0.67
37:R:285:ASN:OD1	37:R:286:GLU:N	2.27	0.67
39:T:185:MET:CB	39:T:186:PRO:HD3	2.24	0.67
1:A:76:MET:SD	1:A:88:TYR:CD1	2.88	0.67
1:A:298:ASP:O	1:A:302:ILE:HG12	1.95	0.67
1:A:1281:THR:HG22	1:A:1284:LEU:H	1.59	0.67
3:C:94:ILE:HD11	36:P:44:ARG:HH22	1.60	0.67
3:C:132:VAL:HG12	3:C:226:VAL:CG2	2.23	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:246:GLU:HB2	5:E:248:SER:OG	1.94	0.67
39:T:455:GLN:HG3	39:T:485:THR:HG21	1.76	0.67
1:A:229:GLN:HA	1:A:414:ARG:O	1.94	0.67
1:A:299:ILE:CB	1:A:1342:TRP:CZ3	2.66	0.67
1:A:1258:LYS:HE2	37:R:432:GLU:HA	1.77	0.67
1:A:1758:PRO:CB	21:1:938:TRP:CD1	2.77	0.67
3:C:736:GLY:CA	3:C:770:PHE:HE2	2.07	0.67
35:O:131:THR:HG23	42:W:111:LEU:HA	1.77	0.67
44:Y:62:ILE:HA	44:Y:84:TYR:HA	1.75	0.67
44:Y:100:ILE:O	44:Y:106:THR:HA	1.94	0.67
45:Z:597:ARG:NH1	45:Z:601:LEU:HD12	2.08	0.67
1:A:296:PHE:CG	3:C:656:ALA:CB	2.62	0.67
3:C:572:GLU:HG3	3:C:573:GLU:H	1.60	0.67
15:H:151:C:C2	15:H:152:G:C8	2.83	0.67
37:R:81:LYS:HA	37:R:81:LYS:HZ1	1.59	0.67
37:R:119:LEU:HA	37:R:232:MET:SD	2.34	0.67
39:T:272:CYS:HB3	39:T:282:ARG:HG3	1.76	0.67
1:A:134:TRP:HB3	1:A:418:THR:CG2	2.25	0.67
1:A:380:LEU:N	3:C:354:ARG:HB3	2.09	0.67
2:B:40:U:C5'	2:B:41:U:OP2	2.43	0.67
3:C:452:THR:CB	3:C:577:PHE:CD2	2.73	0.67
5:E:243:LEU:HD12	5:E:247:GLY:HA2	1.76	0.67
14:G:10:U:O5'	14:G:10:U:H6	1.78	0.67
15:H:40:C:OP1	20:v:61:THR:HA	1.95	0.67
15:H:169:C:O2'	15:H:170:C:H5'	1.95	0.67
23:3:63:ARG:NH2	23:3:119:GLN:OE1	2.22	0.67
23:3:802:THR:HA	23:3:863:ALA:O	1.95	0.67
38:S:20:MET:HE2	38:S:141:ARG:CB	2.25	0.67
1:A:282:LEU:C	1:A:282:LEU:HD23	2.20	0.67
1:A:2306:HIS:CD2	1:A:2308:VAL:H	2.13	0.67
3:C:149:LEU:HD13	3:C:427:PHE:CE2	2.22	0.67
3:C:510:LEU:HD22	3:C:514:TYR:CD2	2.30	0.67
13:F:27:A:N3	35:O:181:TYR:CD2	2.62	0.67
15:H:153:A:C3'	15:H:154:C:H5'	2.25	0.67
21:1:1126:PHE:HA	21:1:1165:TYR:OH	1.94	0.67
42:W:420:ALA:N	42:W:438:ASP:CB	2.57	0.67
1:A:1111:GLN:O	1:A:1115:THR:OG1	2.11	0.66
1:A:1309:SER:O	1:A:1544:ARG:HD3	1.94	0.66
3:C:77:VAL:CG1	39:T:196:LEU:HB3	2.24	0.66
3:C:129:ILE:HG22	3:C:199:LEU:CB	2.23	0.66
23:3:470:PHE:HB3	23:3:747:SER:HA	1.75	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:1035:THR:HG21	23:3:1103:SER:HA	1.75	0.66
24:4:17:VAL:HG13	24:4:84:ILE:HG23	1.77	0.66
1:A:2328:ALA:CB	4:D:788:GLY:CA	2.74	0.66
3:C:230:ASP:OD1	3:C:259:LYS:CB	2.43	0.66
15:H:143:A:H2'	15:H:144:C:H6	1.59	0.66
15:H:151:C:O2	15:H:152:G:C8	2.48	0.66
20:v:51:LEU:CG	21:1:1180:ARG:CB	2.73	0.66
35:O:185:LYS:HG3	42:W:215:GLU:C	2.21	0.66
38:S:34:LYS:CE	38:S:78:TYR:CE2	2.77	0.66
38:S:77:ILE:HG13	38:S:78:TYR:HD1	1.58	0.66
1:A:439:GLN:NE2	1:A:614:TYR:OH	2.27	0.66
1:A:676:ARG:NE	13:F:56:A:OP1	2.28	0.66
3:C:62:ASP:OD1	3:C:62:ASP:N	2.28	0.66
3:C:244:LYS:CB	3:C:292:TYR:CE2	2.79	0.66
15:H:151:C:H2'	15:H:152:G:H8	1.59	0.66
23:3:147:ASP:OD1	23:3:151:ARG:N	2.25	0.66
23:3:687:SER:HA	23:3:1206:LYS:HE3	1.76	0.66
23:3:947:GLU:HB3	23:3:963:VAL:HG22	1.75	0.66
1:A:532:THR:HG23	14:G:2:U:O5'	1.89	0.66
1:A:748:ASP:OD2	39:T:204:LEU:O	2.13	0.66
1:A:1386:TRP:HE1	1:A:1417:PRO:HD2	1.61	0.66
1:A:1457:HIS:CE1	1:A:1459:ARG:HB2	2.30	0.66
2:B:19:A:O2'	2:B:20:G:OP1	2.12	0.66
3:C:141:GLY:C	3:C:258:ASN:ND2	2.53	0.66
5:E:146:ARG:HH11	5:E:148:LYS:CE	1.83	0.66
15:H:73:C:H2'	15:H:74:U:C6	2.30	0.66
15:H:114:A:H61	15:H:142:C:H42	1.44	0.66
21:1:397:ARG:HD3	21:1:398:PRO:HD2	1.78	0.66
23:3:187:MET:HE3	23:3:206:GLN:HB3	1.78	0.66
26:6:25:LYS:NZ	26:6:26:CYS:SG	2.68	0.66
1:A:254:TYR:OH	1:A:434:HIS:HB3	1.95	0.66
1:A:420:ARG:NH1	2:B:56:C:O2'	2.28	0.66
35:O:28:LEU:HD23	37:R:195:ARG:HE	1.61	0.66
36:P:224:MET:HE3	36:P:228:ILE:HD13	1.74	0.66
1:A:532:THR:CB	14:G:2:U:O5'	2.42	0.66
3:C:473:PRO:O	3:C:474:LEU:HB3	1.96	0.66
15:H:47:U:H1'	15:H:48:A:H8	1.61	0.66
23:3:1017:ASN:OD1	23:3:1018:GLU:N	2.29	0.66
35:O:147:LEU:O	35:O:151:ALA:N	2.29	0.66
35:O:243:ILE:HG12	35:O:294:ASN:HD22	1.61	0.66
36:P:212:ASN:OD1	39:T:483:ASP:HA	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:T:314:ILE:HD12	39:T:324:HIS:HB2	1.75	0.66
44:Y:39:PHE:O	44:Y:109:VAL:HA	1.95	0.66
44:Y:98:ASN:OD1	44:Y:99:GLY:N	2.25	0.66
45:Z:525:TYR:HE1	45:Z:526:ILE:HG23	1.57	0.66
1:A:365:VAL:HG12	1:A:366:LYS:N	2.06	0.66
1:A:377:GLU:O	1:A:378:PHE:CB	2.44	0.66
3:C:145:PHE:CE1	3:C:427:PHE:HE1	2.14	0.66
3:C:221:ILE:CG1	3:C:479:THR:OG1	2.43	0.66
39:T:342:GLU:HB3	39:T:343:PRO:CD	2.26	0.66
1:A:380:LEU:HB2	3:C:354:ARG:HG3	0.72	0.66
1:A:718:ARG:HH21	37:R:259:LYS:HE3	1.58	0.66
1:A:785:LYS:HE3	36:P:215:LEU:CD1	2.26	0.66
3:C:140:HIS:HA	3:C:259:LYS:NZ	2.10	0.66
5:E:116:HIS:O	5:E:124:LEU:HD12	1.95	0.66
5:E:281:VAL:HG22	42:W:148:VAL:HA	1.76	0.66
23:3:355:ASN:OD1	23:3:436:ARG:NH2	2.26	0.66
35:O:196:GLN:HE21	35:O:208:PRO:HG2	1.61	0.66
38:S:10:GLN:HB3	38:S:29:TRP:CD2	2.30	0.66
39:T:355:ARG:C	39:T:356:LEU:HD12	2.21	0.66
1:A:304:ILE:HD11	1:A:1342:TRP:CZ2	2.30	0.66
14:G:146:C:H41	21:1:1107:GLN:HG3	1.60	0.66
23:3:670:GLN:HA	23:3:698:PRO:HA	1.78	0.66
23:3:952:ILE:HG12	23:3:961:ILE:HG12	1.78	0.66
27:7:63:ARG:O	27:7:67:ASN:ND2	2.29	0.66
28:J:300:ASP:OD2	37:R:101:ILE:CG1	2.44	0.66
41:V:548:ALA:HB1	41:V:585:ILE:CB	2.25	0.66
1:A:406:TRP:HH2	3:C:265:LEU:O	1.79	0.66
1:A:755:HIS:HE1	36:P:223:PHE:HB3	1.61	0.66
1:A:829:PRO:O	1:A:882:LYS:NZ	2.27	0.66
1:A:1457:HIS:NE2	37:R:424:SER:CA	2.59	0.66
3:C:87:GLN:HE21	39:T:239:LYS:HD3	1.61	0.66
3:C:750:LEU:C	3:C:750:LEU:HD12	2.21	0.66
5:E:320:LEU:O	42:W:85:TYR:CB	2.44	0.66
23:3:330:PHE:O	23:3:394:ASN:ND2	2.29	0.66
34:N:28:LYS:HZ1	42:W:190:ASP:N	1.91	0.66
2:B:42:U:O4	14:G:-3:A:N1	2.29	0.65
3:C:77:VAL:HG12	39:T:197:TYR:CA	2.25	0.65
3:C:136:GLY:HA2	3:C:239:THR:HG22	1.77	0.65
5:E:178:LEU:HD11	5:E:222:LEU:CD2	2.26	0.65
37:R:124:VAL:HG13	37:R:125:MET:H	1.60	0.65
1:A:271:MET:HE1	1:A:313:LYS:HD2	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:293:TRP:HZ3	1:A:295:GLU:OE1	1.76	0.65
1:A:651:TRP:CD1	13:F:66:C:H1'	2.31	0.65
1:A:1459:ARG:HE	37:R:423:ASP:CB	2.06	0.65
14:G:-12:G:H2'	14:G:-11:G:C8	2.30	0.65
39:T:439:TRP:CZ3	39:T:446:ASN:HB2	2.32	0.65
1:A:339:PHE:CD1	1:A:406:TRP:CE3	2.84	0.65
2:B:43:U:H3	14:G:-4:A:H2	1.37	0.65
2:B:43:U:O4	14:G:-4:A:N1	2.30	0.65
21:1:1171:PRO:O	21:1:1174:GLU:HB2	1.96	0.65
36:P:210:PHE:HB3	39:T:455:GLN:HE22	1.61	0.65
1:A:97:HIS:HD2	1:A:473:PHE:CZ	2.15	0.65
1:A:344:ASP:N	1:A:344:ASP:OD1	2.28	0.65
1:A:468:LYS:HD3	1:A:469:LYS:H	1.61	0.65
1:A:639:PHE:O	2:B:28:A:O2'	2.12	0.65
1:A:1356:GLY:O	40:U:15:THR:HG22	1.96	0.65
1:A:1459:ARG:CD	37:R:422:MET:O	2.45	0.65
2:B:63:A:H4'	5:E:106:LYS:NZ	2.12	0.65
21:1:713:ALA:HA	21:1:716:ALA:HB3	1.77	0.65
36:P:66:ARG:HH11	36:P:66:ARG:CB	2.09	0.65
37:R:92:SER:O	38:S:19:SER:C	2.39	0.65
1:A:301:LYS:HG2	3:C:940:ARG:N	2.12	0.65
3:C:457:VAL:HB	3:C:462:GLY:HA3	1.78	0.65
15:H:45:C:N3	18:w:395:TRP:HB3	2.11	0.65
23:3:714:ALA:O	23:3:720:TRP:HB2	1.97	0.65
39:T:327:SER:O	39:T:357:TRP:HH2	1.79	0.65
3:C:700:ILE:HG21	3:C:741:GLY:O	1.97	0.65
14:G:137:C:H42	15:H:40:C:N4	1.95	0.65
21:1:584:ASP:OD1	21:1:585:GLU:N	2.29	0.65
22:2:487:LEU:HD12	27:7:28:LYS:HE3	1.78	0.65
22:2:511:LEU:HD23	22:2:593:GLU:HG3	1.79	0.65
35:O:31:ASN:OD1	35:O:33:TYR:N	2.27	0.65
39:T:459:LEU:HD12	39:T:460:ASP:H	1.61	0.65
1:A:375:ASP:H	3:C:355:LYS:HZ2	1.44	0.65
5:E:108:HIS:CE1	5:E:128:SER:HB3	2.31	0.65
13:F:24:A:H2	13:F:26:U:N3	1.94	0.65
23:3:525:ARG:HG3	23:3:533:VAL:HG13	1.78	0.65
35:O:185:LYS:HG3	42:W:216:LEU:HA	1.79	0.65
37:R:171:LEU:CD1	37:R:201:GLU:CD	2.70	0.65
1:A:155:LYS:NZ	1:A:624:GLY:O	2.29	0.65
1:A:225:TYR:O	1:A:418:THR:OG1	2.11	0.65
1:A:338:VAL:HG11	3:C:267:LEU:CD2	2.27	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:378:PHE:CD1	1:A:379:GLU:N	2.65	0.65
1:A:2314:PHE:CD2	4:D:1123:TRP:CB	2.80	0.65
3:C:572:GLU:HG3	3:C:573:GLU:N	2.12	0.65
23:3:866:ILE:HB	23:3:880:VAL:HB	1.79	0.65
29:L:11:TRP:CG	29:L:49:ARG:HE	2.15	0.65
32:I:296:PHE:CA	32:I:305:SER:CB	2.66	0.65
35:O:68:THR:HA	35:O:83:THR:HG22	1.77	0.65
38:S:9:TRP:HE3	38:S:11:PRO:CD	2.10	0.65
39:T:458:SER:OG	39:T:459:LEU:N	2.30	0.65
1:A:151:MET:SD	1:A:628:GLY:C	2.80	0.65
1:A:661:GLU:CD	37:R:214:ILE:HD11	2.22	0.65
1:A:2319:LEU:HG	1:A:2320:LEU:N	2.11	0.65
14:G:130:A:H5''	18:w:396:LEU:HD21	1.78	0.65
20:v:58:LEU:CD2	20:v:82:LEU:CA	2.74	0.65
23:3:687:SER:CB	23:3:1206:LYS:HE2	2.27	0.65
23:3:791:HIS:HE1	23:3:934:GLY:HA3	1.62	0.65
24:4:75:ASN:OD1	24:4:86:VAL:CB	2.45	0.65
34:N:28:LYS:NZ	42:W:190:ASP:H	1.95	0.65
2:B:44:A:C2	14:G:-5:G:N1	2.62	0.65
3:C:749:THR:O	3:C:753:GLU:N	2.27	0.65
13:F:33:G:OP2	13:F:33:G:H8	1.80	0.65
15:H:153:A:H3'	15:H:154:C:H5'	1.79	0.65
15:H:156:U:C6	15:H:156:U:C5'	2.72	0.65
21:1:1026:ASN:HD22	21:1:1031:VAL:HG11	1.60	0.65
35:O:253:TYR:OH	38:S:120:GLN:HG2	1.97	0.65
36:P:210:PHE:CE2	39:T:455:GLN:OE1	2.50	0.65
3:C:97:VAL:CG1	36:P:47:THR:OG1	2.45	0.64
3:C:463:GLU:OE1	3:C:463:GLU:N	2.29	0.64
3:C:488:VAL:HG13	3:C:609:LYS:NZ	2.12	0.64
5:E:277:PHE:HE2	5:E:300:ILE:HD13	1.61	0.64
21:1:912:ASN:OD1	21:1:957:ARG:NH1	2.30	0.64
37:R:171:LEU:CD1	37:R:201:GLU:OE1	2.44	0.64
2:B:19:A:H2'	2:B:20:G:H5''	1.78	0.64
3:C:72:VAL:CG2	39:T:453:ALA:HB1	2.26	0.64
14:G:11:A:N3	14:G:11:A:H3'	2.12	0.64
15:H:148:C:H2'	15:H:149:A:C8	2.30	0.64
23:3:458:ALA:HA	23:3:741:PHE:HB3	1.78	0.64
5:E:153:PHE:O	5:E:171:SER:HB2	1.97	0.64
7:i:84:GLY:HA2	18:w:188:MET:CB	2.27	0.64
23:3:429:ARG:HH12	27:7:58:ASN:HA	1.62	0.64
1:A:95:MET:HE2	1:A:503:MET:CE	2.26	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:779:LEU:HD21	36:P:223:PHE:HE2	1.59	0.64
1:A:1051:LEU:CD2	36:P:193:VAL:HG11	2.27	0.64
3:C:256:CYS:SG	3:C:308:CYS:CB	2.86	0.64
23:3:206:GLN:HG3	23:3:228:LEU:HD12	1.78	0.64
37:R:88:ILE:H	37:R:88:ILE:HD12	1.61	0.64
44:Y:24:ASP:O	44:Y:27:SER:N	2.30	0.64
45:Z:594:GLU:O	45:Z:598:PHE:N	2.25	0.64
1:A:299:ILE:HB	1:A:1342:TRP:CZ3	2.33	0.64
1:A:976:MET:HG2	1:A:1187:PHE:HB3	1.78	0.64
1:A:1069:ASN:OD1	1:A:1075:GLN:NE2	2.31	0.64
2:B:40:U:H5'	2:B:41:U:OP2	1.97	0.64
3:C:97:VAL:HG22	36:P:45:GLN:HG3	1.77	0.64
3:C:482:TYR:HE2	3:C:493:PHE:CD2	2.14	0.64
23:3:687:SER:CB	23:3:1206:LYS:CE	2.76	0.64
45:Z:574:ASN:O	45:Z:575:ARG:C	2.40	0.64
1:A:176:LEU:HD13	1:A:181:ASN:ND2	2.12	0.64
15:H:68:G:H1	15:H:84:C:N4	1.95	0.64
23:3:184:CYS:SG	23:3:209:THR:OG1	2.56	0.64
35:O:223:LEU:O	35:O:223:LEU:HD22	1.98	0.64
35:O:225:PRO:HB2	35:O:226:PRO:HD2	1.80	0.64
37:R:419:SER:O	37:R:420:LYS:O	2.16	0.64
3:C:350:ASN:ND2	3:C:353:THR:HG23	2.13	0.64
3:C:705:VAL:HB	3:C:717:PHE:CZ	2.33	0.64
14:G:149:G:C2	14:G:150:U:H2'	2.32	0.64
21:1:847:ALA:O	21:1:851:SER:CB	2.46	0.64
37:R:433:ILE:HD12	37:R:435:ASN:ND2	2.12	0.64
38:S:10:GLN:OE1	38:S:10:GLN:N	2.31	0.64
1:A:380:LEU:CB	3:C:354:ARG:HH11	2.08	0.64
1:A:1342:TRP:CD2	3:C:921:LEU:CD2	2.80	0.64
3:C:824:THR:O	3:C:824:THR:CG2	2.45	0.64
13:F:38:G:H8	13:F:38:G:O5'	1.79	0.64
21:1:599:ASN:O	21:1:603:ALA:HB2	1.98	0.64
21:1:702:ARG:O	21:1:705:SER:OG	2.13	0.64
24:4:15:VAL:O	24:4:58:PHE:HA	1.97	0.64
29:L:224:PHE:HD1	37:R:86:LEU:HD12	1.54	0.64
1:A:175:PRO:HG2	1:A:498:ARG:CZ	2.27	0.64
1:A:481:PHE:CE2	37:R:205:ASP:CA	2.81	0.64
1:A:1134:TRP:O	1:A:1139:ARG:NH1	2.31	0.64
1:A:1252:GLY:HA2	1:A:1298:ARG:NH2	2.13	0.64
3:C:363:SER:O	3:C:364:SER:OG	2.11	0.64
14:G:-9:C:C6	40:U:18:TYR:CE1	2.84	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:25:G:H2'	15:H:26:A:H8	1.62	0.64
20:v:23:ASN:HD22	29:L:39:HIS:HE1	1.45	0.64
23:3:635:ALA:HB3	23:3:669:LEU:HD23	1.79	0.64
28:J:294:HIS:CE1	29:L:227:THR:CB	2.80	0.64
37:R:110:LYS:HD2	37:R:110:LYS:C	2.23	0.64
42:W:264:ASN:O	42:W:267:SER:CB	2.46	0.64
46:x:936:TYR:O	46:x:939:VAL:N	2.30	0.64
1:A:1215:ASN:HB3	1:A:1224:ARG:HD2	1.79	0.64
1:A:1457:HIS:CE1	37:R:424:SER:CA	2.79	0.64
2:B:12:U:O2'	2:B:13:C:O5'	2.14	0.64
3:C:678:THR:HG21	3:C:683:ASN:HB2	1.76	0.64
14:G:155:U:H4'	14:G:156:U:H5'	1.79	0.64
18:w:445:HIS:CG	18:w:446:PHE:CD2	2.86	0.64
35:O:276:THR:HG23	35:O:279:ALA:H	1.62	0.64
38:S:13:ASN:HD22	38:S:24:VAL:HG11	1.62	0.64
1:A:134:TRP:HB3	1:A:418:THR:HG21	1.79	0.63
1:A:1337:GLN:O	1:A:1352:HIS:HB2	1.98	0.63
3:C:482:TYR:CE2	3:C:493:PHE:CD2	2.86	0.63
28:J:406:PHE:CG	28:J:411:MET:HE2	2.33	0.63
1:A:461:HIS:CE1	2:B:23:C:C5	2.86	0.63
1:A:643:GLY:HA3	2:B:29:A:O4'	1.99	0.63
3:C:481:MET:SD	3:C:492:ALA:HB2	2.37	0.63
3:C:596:ASN:HD22	3:C:596:ASN:N	1.96	0.63
13:F:94:C:OP1	28:J:351:ASN:HB2	1.98	0.63
14:G:-9:C:C5	40:U:18:TYR:CD1	2.84	0.63
14:G:26:U:C1'	35:O:269:CYS:HB3	2.28	0.63
15:H:152:G:C2	15:H:153:A:C5	2.87	0.63
24:4:75:ASN:OD1	24:4:86:VAL:N	2.31	0.63
37:R:415:LEU:C	37:R:417:ASN:H	2.05	0.63
3:C:77:VAL:HG12	39:T:196:LEU:O	1.70	0.63
5:E:119:THR:HG23	5:E:161:ARG:HB3	1.80	0.63
13:F:35:A:H2'	13:F:36:A:C5'	2.28	0.63
23:3:553:GLN:NE2	23:3:565:TYR:OH	2.31	0.63
23:3:931:VAL:N	23:3:936:LYS:O	2.29	0.63
25:5:20:ILE:HG12	25:5:63:VAL:HG22	1.78	0.63
1:A:695:ASP:CG	39:T:374:SER:OG	2.41	0.63
1:A:755:HIS:CD2	36:P:219:PHE:HE2	2.15	0.63
3:C:78:GLU:CD	39:T:198:ARG:HE	2.07	0.63
13:F:27:A:OP1	34:N:41:ARG:NH2	2.30	0.63
13:F:58:G:H2'	13:F:59:G:C8	2.32	0.63
7:i:85:PRO:C	18:w:184:ARG:HA	2.24	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:86:ARG:HA	23:3:105:GLU:O	1.98	0.63
23:3:174:ASP:OD2	23:3:240:GLY:N	2.31	0.63
23:3:489:GLU:HG2	23:3:748:GLU:HB3	1.80	0.63
35:O:78:LYS:O	35:O:97:ARG:NH2	2.32	0.63
42:W:97:ASN:C	42:W:99:PHE:H	2.06	0.63
42:W:463:SER:O	42:W:480:SER:HA	1.98	0.63
43:X:241:GLY:N	43:X:262:TYR:O	2.31	0.63
1:A:44:ARG:HD2	1:A:45:TYR:CZ	2.34	0.63
1:A:380:LEU:HB3	3:C:354:ARG:HH11	1.60	0.63
1:A:596:TYR:CE2	14:G:-5:G:N7	2.66	0.63
3:C:129:ILE:CG2	3:C:199:LEU:HB3	2.27	0.63
3:C:295:ASP:OD1	3:C:297:ASN:N	2.32	0.63
3:C:456:GLY:O	3:C:457:VAL:HG22	1.99	0.63
13:F:36:A:C5'	13:F:36:A:H8	2.12	0.63
36:P:210:PHE:HD2	39:T:455:GLN:CD	2.05	0.63
37:R:132:LEU:HD23	37:R:132:LEU:H	1.63	0.63
3:C:137:HIS:NE2	3:C:236:MET:HE2	2.14	0.63
4:D:1992:GLU:HA	4:D:1995:ALA:HB3	1.80	0.63
13:F:28:A:H1'	34:N:39:GLY:O	1.98	0.63
23:3:673:VAL:HA	23:3:691:THR:H	1.63	0.63
23:3:794:SER:OG	23:3:796:ASN:OD1	2.15	0.63
37:R:123:GLU:OE1	37:R:124:VAL:N	2.30	0.63
1:A:43:LYS:NZ	42:W:168:PHE:O	2.30	0.63
1:A:460:LYS:NZ	2:B:49:A:OP2	2.29	0.63
1:A:1260:VAL:HG21	1:A:1325:LEU:HB3	1.80	0.63
1:A:1309:SER:O	1:A:1544:ARG:CD	2.47	0.63
5:E:178:LEU:HD21	5:E:208:ILE:CD1	2.28	0.63
15:H:47:U:H1'	15:H:48:A:C8	2.34	0.63
21:1:812:PRO:HB2	21:1:813:PRO:HD3	1.81	0.63
23:3:1182:PHE:HA	23:3:1185:MET:HE2	1.81	0.63
25:5:23:ILE:HD12	25:5:89:VAL:HG12	1.81	0.63
35:O:115:GLU:HB3	37:R:218:ILE:HG21	1.80	0.63
1:A:319:LEU:N	3:C:638:ASP:OD1	2.31	0.63
1:A:693:ILE:HG13	1:A:738:MET:SD	2.38	0.63
1:A:1000:ILE:HG22	1:A:1001:VAL:HG13	1.81	0.63
3:C:93:ILE:CD1	39:T:230:ILE:HD13	2.29	0.63
3:C:476:CYS:CB	3:C:565:ILE:HB	2.27	0.63
7:i:85:PRO:CA	18:w:184:ARG:O	2.47	0.63
21:1:698:GLN:O	21:1:702:ARG:NH1	2.32	0.63
23:3:399:ASP:OD1	23:3:400:GLU:N	2.32	0.63
30:r:8:SER:O	30:r:9:ASN:CB	2.47	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:R:67:ILE:HD13	37:R:67:ILE:N	2.13	0.63
1:A:109:PRO:HD3	1:A:630:TRP:CZ2	2.33	0.63
3:C:259:LYS:HE2	3:C:262:ARG:HD3	1.79	0.63
13:F:26:U:C3'	13:F:27:A:H5''	2.29	0.63
13:F:40:U:H2'	13:F:41:A:H8	1.61	0.63
37:R:418:GLN:O	45:Z:606:ALA:HB2	1.97	0.63
1:A:595:LYS:HA	2:B:44:A:O3'	1.98	0.62
1:A:768:ASP:HB2	1:A:771:VAL:HG12	1.79	0.62
3:C:250:ARG:NE	3:C:451:HIS:NE2	2.47	0.62
5:E:265:ARG:H	5:E:272:ARG:HH21	1.47	0.62
15:H:179:C:C2	15:H:180:G:N7	2.67	0.62
20:v:58:LEU:HD22	20:v:82:LEU:HB2	1.80	0.62
23:3:524:ILE:HD11	23:3:556:ILE:HD13	1.80	0.62
37:R:250:LYS:HD3	37:R:251:ILE:N	2.13	0.62
41:V:549:LYS:O	41:V:552:ALA:N	2.32	0.62
45:Z:566:TYR:HB2	45:Z:581:GLY:O	1.98	0.62
1:A:1085:ILE:HG12	1:A:1099:PHE:CE1	2.34	0.62
5:E:251:LEU:HG	5:E:291:CYS:SG	2.39	0.62
34:N:116:ASN:OD1	34:N:116:ASN:N	2.32	0.62
35:O:219:THR:O	35:O:221:PRO:HD3	1.99	0.62
1:A:365:VAL:CG1	1:A:366:LYS:H	2.13	0.62
1:A:2068:SER:HB2	1:A:2072:GLU:HB2	1.82	0.62
3:C:64:LYS:HZ2	36:P:206:LYS:HG3	1.62	0.62
3:C:79:THR:HG23	39:T:199:VAL:HB	0.68	0.62
21:1:1010:THR:OG1	21:1:1011:PRO:HD3	1.98	0.62
1:A:141:ILE:HG12	1:A:426:LEU:CD2	2.30	0.62
1:A:283:VAL:HG13	1:A:284:ARG:H	1.64	0.62
1:A:755:HIS:ND1	36:P:223:PHE:CD2	2.60	0.62
3:C:360:ALA:N	3:C:361:PRO:HD3	2.14	0.62
15:H:45:C:H42	18:w:395:TRP:NE1	1.81	0.62
21:1:1257:PRO:HG3	22:2:482:ALA:HB2	1.81	0.62
45:Z:566:TYR:CD2	45:Z:584:TRP:CE3	2.88	0.62
1:A:121:HIS:CE1	1:A:481:PHE:CB	2.68	0.62
1:A:203:VAL:HG21	1:A:237:THR:HG22	1.81	0.62
1:A:1306:LYS:NZ	2:B:38:C:C2'	2.62	0.62
1:A:2105:ILE:HD13	1:A:2266:ARG:HH22	1.64	0.62
2:B:43:U:N3	14:G:-4:A:C2	2.60	0.62
3:C:132:VAL:HG11	3:C:434:CYS:SG	2.39	0.62
23:3:27:GLN:OE1	23:3:42:ARG:NH1	2.32	0.62
23:3:380:GLU:O	23:3:383:ASP:N	2.32	0.62
35:O:19:ASP:OD1	35:O:20:PHE:N	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:P:188:TRP:O	36:P:189:ASP:C	2.42	0.62
36:P:188:TRP:C	36:P:190:ASP:N	2.52	0.62
37:R:250:LYS:HA	37:R:250:LYS:HE3	1.81	0.62
39:T:185:MET:HB3	39:T:186:PRO:HD3	1.81	0.62
42:W:280:GLN:HA	42:W:577:LEU:O	2.00	0.62
1:A:97:HIS:CD2	1:A:473:PHE:CZ	2.87	0.62
1:A:305:ARG:HA	1:A:305:ARG:NH1	2.09	0.62
1:A:312:TYR:CD2	3:C:882:GLY:HA3	2.34	0.62
1:A:402:ILE:HG22	3:C:268:LYS:NZ	2.10	0.62
1:A:755:HIS:HE1	36:P:223:PHE:CG	2.11	0.62
3:C:259:LYS:HG2	3:C:262:ARG:HD2	1.81	0.62
15:H:182:U:H2'	15:H:183:G:C8	2.34	0.62
23:3:273:ARG:O	23:3:386:PHE:HA	2.00	0.62
1:A:253:ASN:CB	3:C:893:GLY:O	2.46	0.62
1:A:800:TYR:CG	3:C:59:LEU:HD13	2.34	0.62
1:A:1548:TYR:CG	14:G:-6:C:C6	2.87	0.62
5:E:119:THR:HG21	5:E:161:ARG:HB3	1.72	0.62
23:3:505:THR:HG21	23:3:508:CYS:SG	2.40	0.62
23:3:567:GLU:OE2	23:3:601:ARG:NE	2.29	0.62
36:P:211:VAL:HG13	39:T:457:GLY:HA3	0.75	0.62
37:R:171:LEU:HD12	37:R:201:GLU:CD	2.25	0.62
39:T:351:ASP:C	39:T:352:THR:HG1	2.05	0.62
39:T:356:LEU:HD12	39:T:356:LEU:N	2.15	0.62
1:A:50:LYS:O	1:A:51:PHE:C	2.43	0.62
5:E:146:ARG:CZ	5:E:148:LYS:HE3	2.27	0.62
21:1:847:ALA:O	21:1:851:SER:HB3	1.99	0.62
23:3:642:ILE:O	23:3:703:ARG:NH2	2.32	0.62
33:Q:500:GLY:N	37:R:51:ILE:HG13	2.14	0.62
45:Z:600:ARG:HH11	45:Z:600:ARG:CG	2.13	0.62
1:A:155:LYS:HD2	1:A:626:GLY:O	2.00	0.62
1:A:762:ARG:NH2	36:P:226:LYS:HZ1	1.79	0.62
1:A:2325:VAL:CG1	4:D:788:GLY:O	2.33	0.62
15:H:154:C:H2'	15:H:155:C:H6	1.63	0.62
15:H:161:U:H6	15:H:161:U:O5'	1.83	0.62
21:1:664:GLY:HA2	21:1:667:ILE:HD12	1.80	0.62
21:1:696:ASP:OD1	21:1:697:GLU:N	2.33	0.62
21:1:1052:ALA:HA	21:1:1055:TRP:HD1	1.64	0.62
22:2:612:GLU:O	22:2:615:ILE:N	2.33	0.62
23:3:521:PRO:HA	23:3:544:ILE:HG22	1.81	0.62
28:J:406:PHE:CE2	28:J:411:MET:CE	2.83	0.62
35:O:81:CYS:SG	52:O:501:ZN:ZN	1.88	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:S:9:TRP:CE3	38:S:11:PRO:CG	2.83	0.62
1:A:1217:GLN:NE2	41:V:592:GLU:O	2.32	0.62
1:A:2328:ALA:HB3	4:D:788:GLY:CA	2.30	0.62
3:C:230:ASP:OD1	3:C:259:LYS:HB3	2.00	0.62
1:A:338:VAL:HG11	3:C:267:LEU:HD21	1.81	0.61
1:A:835:ASP:OD1	1:A:836:THR:N	2.32	0.61
5:E:277:PHE:HE2	5:E:300:ILE:HD12	1.63	0.61
17:p:194:PHE:O	17:p:196:ASN:N	2.33	0.61
23:3:811:THR:OG1	23:3:884:GLN:OE1	2.14	0.61
23:3:1004:ASP:OD1	23:3:1005:VAL:N	2.33	0.61
30:q:22:ASN:CB	30:r:55:ILE:CB	2.78	0.61
1:A:587:GLN:HA	1:A:1550:GLY:C	2.25	0.61
13:F:24:A:C2	13:F:26:U:C2	2.88	0.61
14:G:13:C:H2'	14:G:14:A:C8	2.36	0.61
21:1:624:VAL:O	21:1:628:THR:OG1	2.14	0.61
23:3:786:ARG:NH1	23:3:802:THR:O	2.33	0.61
28:J:262:ARG:HD3	29:L:220:PRO:HG2	1.82	0.61
45:Z:597:ARG:HH12	45:Z:601:LEU:HD12	1.66	0.61
1:A:344:ASP:OD1	1:A:347:LEU:CD1	2.49	0.61
1:A:783:TYR:HB2	36:P:228:ILE:CG1	2.26	0.61
1:A:2106:LEU:HD12	1:A:2107:PRO:HD2	1.83	0.61
3:C:619:THR:C	3:C:620:LYS:HG3	2.25	0.61
13:F:38:G:P	13:F:38:G:C8	2.94	0.61
14:G:26:U:H5''	35:O:235:TYR:OH	2.00	0.61
21:1:866:LYS:HG3	21:1:909:VAL:HG11	1.82	0.61
23:3:317:THR:HA	23:3:322:VAL:HA	1.81	0.61
1:A:588:LEU:O	1:A:1551:PHE:HE1	1.78	0.61
1:A:1754:TYR:CD1	21:1:941:ASN:OD1	2.53	0.61
1:A:1754:TYR:HD1	21:1:941:ASN:OD1	1.82	0.61
14:G:146:C:H1'	15:H:33:G:N2	2.15	0.61
15:H:165:A:H8	15:H:165:A:O5'	1.84	0.61
37:R:55:LEU:O	37:R:73:PRO:O	2.19	0.61
37:R:92:SER:N	38:S:19:SER:HB2	2.15	0.61
45:Z:566:TYR:CD1	45:Z:567:SER:N	2.69	0.61
1:A:203:VAL:CG2	1:A:237:THR:HB	2.30	0.61
1:A:305:ARG:HG3	3:C:879:ASP:OD1	1.99	0.61
1:A:344:ASP:OD1	1:A:347:LEU:HD12	2.00	0.61
3:C:679:PRO:HD3	3:C:811:THR:OG1	1.99	0.61
15:H:56:A:H61	22:2:505:CYS:HA	1.66	0.61
15:H:68:G:H2'	15:H:69:U:C6	2.35	0.61
21:1:648:LEU:O	21:1:651:VAL:N	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:288:VAL:HG23	23:3:289:CYS:H	1.65	0.61
23:3:994:GLN:NE2	23:3:1036:ALA:O	2.33	0.61
39:T:327:SER:O	39:T:357:TRP:CH2	2.53	0.61
1:A:299:ILE:CD1	3:C:920:PRO:O	2.48	0.61
1:A:1755:SER:OG	21:1:938:TRP:CZ2	2.50	0.61
3:C:97:VAL:HG13	36:P:47:THR:OG1	2.00	0.61
3:C:140:HIS:CG	3:C:230:ASP:H	2.18	0.61
3:C:809:ILE:HB	3:C:810:PRO:HD3	1.82	0.61
15:H:42:G:P	20:v:77:LYS:CB	2.87	0.61
23:3:1191:LYS:NZ	23:3:1195:GLU:OE2	2.33	0.61
34:N:28:LYS:NZ	42:W:190:ASP:CA	2.64	0.61
41:V:537:HIS:HA	41:V:578:SER:CB	2.31	0.61
1:A:299:ILE:HD11	3:C:921:LEU:N	2.16	0.61
1:A:623:LYS:HD3	48:A:2401:IHP:O43	2.01	0.61
3:C:471:ASP:N	3:C:499:GLY:HA2	2.15	0.61
3:C:495:ARG:HD2	3:C:497:LEU:HD23	1.81	0.61
21:1:720:GLY:N	23:3:216:GLY:O	2.29	0.61
29:L:209:ASP:CG	35:O:111:ASP:CB	2.73	0.61
32:I:361:HIS:O	32:I:372:ARG:CB	2.48	0.61
34:N:38:GLU:C	34:N:40:LYS:H	2.08	0.61
35:O:283:ALA:O	35:O:287:SER:OG	2.18	0.61
37:R:185:GLY:O	37:R:186:VAL:HG22	2.00	0.61
39:T:339:GLN:NE2	39:T:342:GLU:O	2.34	0.61
42:W:290:GLY:CA	42:W:571:TRP:O	2.49	0.61
1:A:260:LEU:CD2	1:A:455:VAL:HG22	2.30	0.61
1:A:375:ASP:N	3:C:355:LYS:HZ2	1.99	0.61
1:A:461:HIS:NE2	2:B:23:C:C6	2.69	0.61
1:A:593:ARG:CZ	1:A:1565:LYS:HE2	2.26	0.61
1:A:1286:ASP:OD1	1:A:1354:ARG:NH2	2.33	0.61
1:A:1548:TYR:CD1	14:G:-6:C:C5	2.89	0.61
3:C:151:GLU:OE1	3:C:417:ARG:NH1	2.34	0.61
3:C:470:PRO:HA	3:C:499:GLY:CA	2.29	0.61
3:C:675:PHE:HD1	3:C:675:PHE:H	1.47	0.61
3:C:701:GLU:HA	3:C:740:THR:HG1	1.65	0.61
14:G:8:C:H2'	14:G:9:C:C6	2.35	0.61
15:H:106:G:N2	15:H:107:A:C6	2.67	0.61
15:H:142:C:C2'	15:H:143:A:H5'	2.30	0.61
15:H:157:G:H5''	15:H:157:G:H8	1.65	0.61
28:J:408:ASP:OD1	28:J:442:ARG:HG2	2.01	0.61
3:C:478:THR:OG1	3:C:563:ALA:O	2.14	0.61
3:C:705:VAL:HG22	3:C:705:VAL:O	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:153:A:N6	15:H:177:A:H2	1.98	0.61
21:1:608:THR:O	21:1:612:THR:OG1	2.15	0.61
23:3:740:GLU:HB2	23:3:757:ILE:HD12	1.83	0.61
29:L:74:LEU:HD23	29:L:77:LEU:HD12	1.83	0.61
35:O:196:GLN:NE2	35:O:209:VAL:HG23	2.14	0.61
44:Y:87:GLN:O	44:Y:90:THR:N	2.33	0.61
1:A:73:HIS:CD2	1:A:81:PHE:CG	2.89	0.61
1:A:73:HIS:CD2	1:A:81:PHE:CD1	2.88	0.61
1:A:256:TYR:CE1	3:C:888:ARG:CZ	2.83	0.61
1:A:1481:VAL:HG12	1:A:1485:LEU:CD1	2.31	0.61
5:E:108:HIS:CE1	5:E:128:SER:HB2	2.35	0.61
13:F:6:C:OP2	13:F:6:C:H4'	1.99	0.61
21:1:1203:GLY:O	23:3:1171:LYS:NZ	2.34	0.61
23:3:226:GLU:HG3	23:3:261:PHE:HZ	1.65	0.61
23:3:452:LEU:HB3	23:3:478:PHE:HE1	1.66	0.61
24:4:71:ILE:HD11	24:4:88:LYS:HB3	1.83	0.61
37:R:92:SER:O	38:S:19:SER:CB	2.48	0.61
37:R:241:MET:HE2	37:R:241:MET:HA	1.82	0.61
39:T:349:SER:OG	39:T:351:ASP:OD1	2.18	0.61
1:A:296:PHE:CD2	3:C:656:ALA:HB2	2.30	0.60
1:A:1405:LEU:HA	37:R:415:LEU:HD21	1.78	0.60
3:C:133:THR:O	3:C:226:VAL:HB	2.01	0.60
3:C:135:CYS:O	3:C:228:PHE:N	2.28	0.60
3:C:449:ILE:HD11	3:C:466:SER:CA	2.31	0.60
3:C:710:ASN:O	3:C:713:LYS:N	2.31	0.60
13:F:27:A:C1'	35:O:181:TYR:HE2	2.11	0.60
15:H:143:A:H2'	15:H:144:C:C6	2.35	0.60
21:1:1293:ASN:HB3	27:7:76:CYS:HB3	1.83	0.60
35:O:235:TYR:CD2	35:O:301:LYS:HB2	2.33	0.60
45:Z:524:ARG:NE	45:Z:524:ARG:O	2.34	0.60
1:A:800:TYR:CD2	3:C:59:LEU:HD13	2.36	0.60
1:A:1457:HIS:CE1	1:A:1459:ARG:CB	2.83	0.60
21:1:918:VAL:HG12	21:1:961:VAL:HG21	1.83	0.60
28:J:338:GLU:O	37:R:116:TYR:CD1	2.54	0.60
45:Z:491:ASP:O	45:Z:495:ALA:CB	2.48	0.60
1:A:158:ARG:HH12	1:A:573:GLN:HE21	1.48	0.60
1:A:1310:ARG:HH22	1:A:1564:GLY:HA3	1.64	0.60
1:A:2073:TRP:CZ3	1:A:2310:ARG:HG2	2.36	0.60
28:J:291:GLN:OE1	29:L:230:GLU:HG3	2.01	0.60
39:T:339:GLN:HG2	39:T:340:ALA:N	2.16	0.60
45:Z:491:ASP:O	45:Z:495:ALA:HB2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:Z:612:TYR:O	45:Z:613:LYS:C	2.43	0.60
1:A:82:ARG:HB3	1:A:83:HIS:ND1	2.17	0.60
1:A:532:THR:CG2	14:G:2:U:H5''	2.27	0.60
14:G:13:C:H2'	14:G:14:A:H8	1.66	0.60
24:4:31:GLU:O	24:4:35:GLN:HG2	2.02	0.60
39:T:292:TYR:CE2	39:T:308:ARG:HG3	2.36	0.60
1:A:48:LYS:O	1:A:53:PHE:CG	2.54	0.60
1:A:339:PHE:CE1	1:A:406:TRP:HE3	2.12	0.60
1:A:378:PHE:C	1:A:379:GLU:HG2	2.25	0.60
3:C:779:LEU:HB3	3:C:934:MET:HE1	1.83	0.60
5:E:178:LEU:HD21	5:E:208:ILE:HD13	1.82	0.60
5:E:266:PRO:HG3	29:L:785:GLN:NE2	2.16	0.60
23:3:673:VAL:HG12	23:3:690:ARG:HA	1.84	0.60
23:3:833:GLU:HA	23:3:834:LEU:HB2	1.84	0.60
29:L:233:GLN:OE1	29:L:233:GLN:HA	2.01	0.60
42:W:531:LYS:CB	42:W:546:PHE:O	2.50	0.60
45:Z:573:PRO:HD2	45:Z:573:PRO:O	1.99	0.60
1:A:623:LYS:CD	48:A:2401:IHP:O43	2.49	0.60
1:A:1447:VAL:HG11	1:A:1449:LYS:HE2	1.82	0.60
1:A:1548:TYR:HD2	14:G:-6:C:O2'	1.85	0.60
1:A:2298:LEU:CD1	4:D:1265:GLN:CB	2.79	0.60
3:C:86:THR:HG22	39:T:238:LEU:O	2.01	0.60
3:C:452:THR:HG22	3:C:577:PHE:CG	2.37	0.60
3:C:706:GLN:NE2	3:C:708:THR:OG1	2.35	0.60
5:E:267:PHE:HE1	31:K:194:GLU:HB3	1.63	0.60
18:w:422:PHE:HZ	18:w:450:THR:HG22	1.67	0.60
1:A:924:GLN:HE22	1:A:1439:ARG:CZ	2.14	0.60
3:C:221:ILE:HD11	3:C:479:THR:HG1	1.65	0.60
3:C:456:GLY:C	3:C:457:VAL:HG13	2.25	0.60
14:G:130:A:H5''	18:w:396:LEU:CD2	2.32	0.60
23:3:613:THR:HG22	23:3:632:ALA:HA	1.84	0.60
23:3:898:ASN:OD1	23:3:899:THR:N	2.34	0.60
41:V:483:GLU:O	41:V:486:THR:CB	2.49	0.60
1:A:705:LYS:HE2	37:R:251:ILE:HB	1.82	0.60
1:A:960:ASN:ND2	1:A:1225:THR:OG1	2.32	0.60
3:C:77:VAL:HG21	39:T:196:LEU:HD23	1.83	0.60
3:C:148:CYS:HA	3:C:417:ARG:NH2	2.16	0.60
23:3:325:ILE:O	23:3:375:SER:N	2.35	0.60
39:T:267:ASP:O	39:T:268:LYS:CB	2.47	0.60
39:T:455:GLN:HG2	39:T:456:PRO:HD3	1.83	0.60
1:A:151:MET:CE	1:A:628:GLY:C	2.75	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1364:LEU:HD13	41:V:461:LEU:C	2.27	0.60
2:B:42:U:C4'	13:F:70:A:C4'	2.80	0.60
3:C:140:HIS:HA	3:C:230:ASP:HB2	1.83	0.60
3:C:567:GLU:OE2	3:C:570:GLY:HA3	2.02	0.60
13:F:7:G:H5'	13:F:7:G:H8	1.66	0.60
13:F:37:C:H41	14:G:5:G:P	2.24	0.60
15:H:83:A:C2	15:H:84:C:C2	2.90	0.60
29:L:77:LEU:HD22	37:R:289:ALA:HA	1.84	0.60
35:O:132:ARG:HG3	35:O:137:LEU:HD23	1.84	0.60
39:T:342:GLU:HB3	39:T:343:PRO:HD3	1.83	0.60
45:Z:563:ARG:HH21	45:Z:563:ARG:CG	2.14	0.60
1:A:1384:ARG:HH21	1:A:1414:ARG:HH12	1.50	0.60
1:A:1426:ASP:OD2	37:R:421:GLY:HA3	2.01	0.60
3:C:79:THR:CG2	39:T:199:VAL:CB	2.37	0.60
3:C:82:GLN:HB2	39:T:231:TRP:CZ3	2.36	0.60
3:C:94:ILE:CD1	36:P:44:ARG:NH2	2.65	0.60
3:C:443:VAL:O	3:C:447:PRO:HD3	2.02	0.60
3:C:516:LEU:HD13	3:C:516:LEU:C	2.26	0.60
3:C:678:THR:CG2	3:C:683:ASN:CB	2.79	0.60
14:G:26:U:C5'	35:O:235:TYR:OH	2.50	0.60
18:w:411:CYS:HG	18:w:425:HIS:CE1	2.19	0.60
21:1:862:GLU:OE1	21:1:904:THR:OG1	2.19	0.60
33:Q:500:GLY:N	37:R:51:ILE:CG1	2.65	0.60
33:Q:500:GLY:CA	37:R:51:ILE:HD11	2.32	0.60
37:R:106:GLN:HG2	37:R:110:LYS:CE	2.28	0.60
39:T:185:MET:SD	39:T:442:ARG:NH1	2.71	0.60
1:A:122:ILE:HD13	1:A:483:GLN:CG	2.32	0.59
1:A:306:GLN:HG3	3:C:853:ARG:HG2	1.83	0.59
1:A:372:PRO:CG	3:C:342:ARG:NE	2.62	0.59
23:3:772:ALA:O	23:3:774:PHE:N	2.35	0.59
23:3:968:ARG:HD3	23:3:979:ARG:HD3	1.84	0.59
1:A:715:GLU:CD	37:R:258:TRP:CZ3	2.79	0.59
3:C:73:TYR:CD2	39:T:199:VAL:HG21	2.36	0.59
3:C:73:TYR:CZ	39:T:487:LYS:HE3	2.37	0.59
3:C:669:THR:HG22	3:C:690:GLU:HB3	1.84	0.59
23:3:687:SER:HB3	23:3:1206:LYS:HE2	1.83	0.59
29:L:216:PHE:CE1	35:O:112:VAL:O	2.52	0.59
36:P:72:ARG:HB2	36:P:72:ARG:HH11	1.66	0.59
39:T:455:GLN:HG2	39:T:456:PRO:CD	2.32	0.59
1:A:122:ILE:N	1:A:481:PHE:O	2.34	0.59
1:A:532:THR:HG23	14:G:2:U:OP1	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:718:ARG:HE	37:R:259:LYS:HE3	1.67	0.59
3:C:186:VAL:HG22	3:C:535:ALA:HA	1.85	0.59
5:E:114:GLU:CD	5:E:116:HIS:HE2	2.09	0.59
23:3:883:GLU:HG3	23:3:884:GLN:H	1.66	0.59
35:O:133:PRO:HD2	35:O:137:LEU:HD22	1.84	0.59
37:R:104:GLN:NE2	37:R:105:GLY:N	2.50	0.59
1:A:181:ASN:N	1:A:181:ASN:OD1	2.35	0.59
2:B:43:U:C4	14:G:-4:A:N1	2.71	0.59
5:E:233:GLY:O	5:E:260:ARG:NH2	2.35	0.59
13:F:27:A:C1'	35:O:181:TYR:CE2	2.86	0.59
14:G:22:C:O2'	14:G:23:U:P	2.60	0.59
28:J:493:ALA:HB1	28:J:499:ARG:CB	2.32	0.59
34:N:117:CYS:SG	34:N:119:CYS:HB3	2.42	0.59
36:P:228:ILE:O	36:P:229:LYS:C	2.45	0.59
37:R:74:LEU:HD23	37:R:74:LEU:C	2.27	0.59
37:R:124:VAL:HG22	37:R:125:MET:N	2.16	0.59
37:R:420:LYS:HA	37:R:420:LYS:CE	2.12	0.59
1:A:86:ARG:HG3	1:A:87:VAL:N	2.17	0.59
1:A:944:ASP:OD2	1:A:1435:GLY:N	2.34	0.59
1:A:1262:LYS:CG	37:R:431:ASP:CB	2.69	0.59
1:A:1405:LEU:HA	37:R:415:LEU:HD22	1.84	0.59
3:C:298:LEU:HD13	3:C:298:LEU:N	2.18	0.59
15:H:56:A:H2'	15:H:57:A:C8	2.38	0.59
18:w:485:ASN:HB3	23:3:978:LEU:HD23	1.83	0.59
23:3:895:ARG:NH2	23:3:901:GLU:OE1	2.34	0.59
23:3:1040:ASP:OD1	23:3:1043:THR:N	2.35	0.59
29:L:209:ASP:OD1	35:O:111:ASP:CB	2.51	0.59
1:A:692:ASP:O	1:A:696:MET:CB	2.50	0.59
1:A:942:PRO:HB2	1:A:1438:VAL:HG12	1.84	0.59
1:A:1076:ASP:OD1	1:A:1077:ILE:N	2.35	0.59
1:A:1363:GLN:HG2	1:A:1364:LEU:H	1.66	0.59
3:C:66:TYR:HE2	36:P:211:VAL:HG11	1.67	0.59
3:C:91:GLU:OE1	3:C:91:GLU:HA	2.01	0.59
3:C:145:PHE:CB	3:C:312:SER:CB	2.65	0.59
13:F:36:A:C5'	13:F:36:A:C8	2.85	0.59
15:H:112:G:H2'	15:H:113:G:H8	1.65	0.59
21:1:936:VAL:O	21:1:940:LEU:HB2	2.03	0.59
21:1:1125:PRO:HA	21:1:1128:VAL:HG22	1.84	0.59
35:O:132:ARG:HH11	38:S:149:SER:CB	2.00	0.59
35:O:155:PRO:HD3	37:R:188:PHE:CD1	2.38	0.59
39:T:345:ILE:HB	39:T:357:TRP:HB2	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:V:514:PHE:O	41:V:521:TYR:CB	2.51	0.59
1:A:338:VAL:HG21	3:C:867:PRO:CD	2.33	0.59
1:A:387:PHE:HE2	3:C:399:LEU:HD23	1.63	0.59
1:A:569:VAL:O	1:A:570:ASP:CB	2.50	0.59
1:A:1405:LEU:CB	37:R:415:LEU:HD22	2.33	0.59
1:A:1758:PRO:CB	21:1:938:TRP:HD1	2.16	0.59
3:C:149:LEU:CD1	3:C:427:PHE:CB	2.80	0.59
23:3:224:TYR:HB3	23:3:261:PHE:HE2	1.66	0.59
23:3:461:THR:HA	23:3:473:TYR:O	2.03	0.59
23:3:1015:LYS:HE2	23:3:1065:GLU:HG2	1.85	0.59
28:J:225:LEU:CD2	29:L:211:ASN:HB2	2.20	0.59
37:R:90:VAL:CG1	37:R:94:GLY:O	2.50	0.59
38:S:10:GLN:HA	38:S:29:TRP:CH2	2.38	0.59
42:W:198:LYS:O	42:W:199:TYR:C	2.45	0.59
42:W:290:GLY:HA3	42:W:571:TRP:HA	1.84	0.59
44:Y:88:ARG:HH11	45:Z:576:PHE:HB3	1.68	0.59
1:A:44:ARG:CG	1:A:45:TYR:CD2	2.85	0.59
1:A:305:ARG:HH21	3:C:854:ARG:HD3	1.68	0.59
1:A:888:GLN:NE2	1:A:890:ALA:O	2.19	0.59
1:A:1199:LYS:NZ	1:A:1206:GLU:OE2	2.32	0.59
3:C:227:LEU:O	3:C:255:VAL:HA	2.03	0.59
23:3:457:ASN:ND2	23:3:478:PHE:O	2.35	0.59
23:3:784:THR:HB	23:3:786:ARG:HH12	1.67	0.59
23:3:1027:ASP:OD1	23:3:1028:THR:N	2.35	0.59
26:6:56:GLY:O	26:6:65:GLY:N	2.21	0.59
35:O:233:THR:HA	35:O:272:ILE:O	2.03	0.59
36:P:63:LEU:HD23	36:P:63:LEU:C	2.28	0.59
37:R:420:LYS:HG2	37:R:423:ASP:OD1	2.02	0.59
37:R:421:GLY:O	37:R:423:ASP:N	2.35	0.59
38:S:71:GLY:O	42:W:93:PHE:N	2.31	0.59
1:A:43:LYS:HD3	42:W:168:PHE:CB	2.32	0.59
3:C:137:HIS:CD2	3:C:236:MET:HB3	2.35	0.59
3:C:497:LEU:HD11	3:C:577:PHE:CZ	2.32	0.59
5:E:321:TYR:CD1	42:W:84:THR:HA	2.38	0.59
21:1:1223:SER:HB2	21:1:1226:VAL:HG12	1.83	0.59
23:3:638:GLU:H	23:3:669:LEU:HA	1.68	0.59
1:A:232:LEU:HD13	1:A:401:GLY:HA2	1.85	0.59
1:A:1310:ARG:NH2	1:A:1563:HIS:O	2.32	0.59
2:B:44:A:H2	14:G:-5:G:H1	1.48	0.59
3:C:145:PHE:CE1	3:C:427:PHE:CE1	2.91	0.59
3:C:230:ASP:CG	3:C:259:LYS:NZ	2.61	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:465:MET:CE	3:C:475:MET:CG	2.70	0.59
3:C:736:GLY:HA2	3:C:770:PHE:CE2	2.38	0.59
13:F:45:A:H1'	13:F:73:A:C2	2.38	0.59
21:1:522:LYS:HD3	21:1:526:PHE:CZ	2.38	0.59
23:3:22:PHE:HD2	23:3:29:GLU:HB2	1.68	0.59
23:3:753:GLY:CA	23:3:765:LEU:O	2.51	0.59
28:J:259:GLN:HE22	29:L:220:PRO:CG	2.15	0.59
34:N:28:LYS:HZ3	42:W:190:ASP:CA	2.08	0.59
37:R:125:MET:CE	37:R:131:ASP:OD1	2.51	0.59
37:R:148:ARG:HG3	37:R:148:ARG:HH11	1.68	0.59
38:S:77:ILE:HG13	38:S:78:TYR:CD1	2.38	0.59
1:A:44:ARG:HG3	1:A:45:TYR:CD2	2.37	0.58
1:A:723:ASN:HB2	1:A:785:LYS:HG2	1.83	0.58
3:C:69:ALA:CA	39:T:456:PRO:HG3	2.28	0.58
3:C:359:LYS:HE3	3:C:359:LYS:O	2.02	0.58
13:F:35:A:O2'	13:F:36:A:OP1	2.21	0.58
21:1:1278:ASP:OD2	23:3:112:CYS:N	2.36	0.58
22:2:648:LEU:HD11	22:2:650:ILE:HG13	1.85	0.58
23:3:336:ALA:HA	23:3:351:SER:HA	1.85	0.58
28:J:339:TRP:CG	37:R:116:TYR:HD2	2.21	0.58
39:T:185:MET:SD	39:T:442:ARG:NH2	2.75	0.58
44:Y:52:ILE:HA	44:Y:55:VAL:HG22	1.84	0.58
1:A:76:MET:SD	1:A:88:TYR:CD2	2.95	0.58
1:A:1306:LYS:HZ3	2:B:38:C:C2'	2.16	0.58
1:A:1352:HIS:CD2	40:U:5:ILE:CD1	2.86	0.58
1:A:1354:ARG:HH11	40:U:7:LEU:HG	1.68	0.58
1:A:2325:VAL:O	4:D:788:GLY:HA2	2.03	0.58
2:B:42:U:C4	14:G:-3:A:N1	2.71	0.58
3:C:474:LEU:HD11	3:C:501:ILE:HG12	1.85	0.58
21:1:982:LEU:HD11	21:1:997:LEU:HD11	1.83	0.58
21:1:1147:VAL:O	21:1:1150:SER:OG	2.17	0.58
23:3:417:ASN:OD1	23:3:418:GLU:N	2.36	0.58
23:3:797:LEU:HG	23:3:871:PRO:HG3	1.85	0.58
23:3:903:TRP:HB3	23:3:930:LEU:HD23	1.84	0.58
35:O:84:CYS:O	35:O:85:LEU:HB2	2.03	0.58
37:R:433:ILE:CD1	37:R:435:ASN:ND2	2.67	0.58
44:Y:86:ASP:CB	45:Z:502:ALA:HB3	2.33	0.58
46:x:418:LEU:HA	46:x:567:ALA:HB1	1.84	0.58
1:A:32:GLU:OE2	1:A:36:LYS:HE3	2.03	0.58
1:A:229:GLN:HA	1:A:415:SER:HA	1.85	0.58
3:C:133:THR:O	3:C:226:VAL:CA	2.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:87:ASP:O	5:E:88:ARG:HG3	2.04	0.58
18:w:444:ALA:O	18:w:445:HIS:C	2.45	0.58
21:1:773:LEU:HD21	21:1:792:VAL:HG22	1.84	0.58
23:3:304:GLN:NE2	23:3:335:VAL:HA	2.18	0.58
35:O:57:TRP:CD1	35:O:57:TRP:C	2.81	0.58
37:R:233:HIS:CD2	37:R:233:HIS:H	2.22	0.58
1:A:849:ALA:O	1:A:1449:LYS:NZ	2.36	0.58
1:A:1180:LYS:HA	1:A:1201:ARG:NH1	2.18	0.58
3:C:679:PRO:HD2	3:C:807:GLN:CB	2.10	0.58
20:v:52:GLY:N	21:1:1141:LEU:HB2	2.17	0.58
23:3:442:LEU:HD13	23:3:734:LEU:CD2	2.33	0.58
28:J:338:GLU:O	37:R:116:TYR:CG	2.57	0.58
35:O:245:GLU:O	35:O:248:LEU:N	2.37	0.58
1:A:299:ILE:CD1	1:A:1346:THR:HG21	2.32	0.58
1:A:1367:ASN:OD1	1:A:1368:LEU:N	2.37	0.58
1:A:1481:VAL:HG12	1:A:1485:LEU:HD12	1.85	0.58
3:C:750:LEU:O	3:C:750:LEU:HD12	2.03	0.58
5:E:263:ASP:HB3	5:E:274:VAL:HG21	1.84	0.58
20:v:23:ASN:ND2	29:L:39:HIS:HE1	1.97	0.58
23:3:587:VAL:HG11	23:3:590:MET:HG3	1.85	0.58
45:Z:566:TYR:CD2	45:Z:584:TRP:HE3	2.20	0.58
5:E:87:ASP:O	5:E:88:ARG:CB	2.51	0.58
23:3:224:TYR:HB3	23:3:261:PHE:CE2	2.39	0.58
24:4:18:GLY:H	24:4:85:ARG:HB2	1.67	0.58
36:P:35:LEU:HB3	36:P:36:PRO:HD2	1.86	0.58
36:P:224:MET:HE2	36:P:228:ILE:HD13	1.85	0.58
37:R:82:MET:HE3	37:R:82:MET:O	2.04	0.58
41:V:497:CYS:CB	41:V:507:PHE:CB	2.81	0.58
1:A:388:LEU:HD13	3:C:379:LYS:HB3	1.85	0.58
1:A:798:GLY:HA2	37:R:288:PHE:CE2	2.39	0.58
1:A:2095:ASP:OD2	1:A:2258:ARG:NE	2.36	0.58
3:C:509:VAL:O	3:C:510:LEU:HD23	2.04	0.58
15:H:147:G:H2'	15:H:148:C:C6	2.38	0.58
1:A:121:HIS:ND1	1:A:481:PHE:O	2.36	0.58
1:A:152:ARG:HH11	1:A:152:ARG:CG	2.16	0.58
1:A:264:PHE:CE1	1:A:455:VAL:CG1	2.75	0.58
1:A:535:ARG:CZ	1:A:535:ARG:HB3	2.33	0.58
3:C:140:HIS:NE2	3:C:233:GLU:CG	2.66	0.58
15:H:80:A:C2	15:H:81:G:C5	2.92	0.58
25:5:24:ARG:HG2	25:5:59:THR:HG22	1.86	0.58
41:V:609:GLN:O	41:V:612:PHE:N	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2073:TRP:HD1	1:A:2074:ARG:HD2	1.67	0.58
1:A:2310:ARG:NH1	1:A:2314:PHE:HE1	2.02	0.58
3:C:77:VAL:HG13	39:T:196:LEU:C	1.90	0.58
3:C:140:HIS:NE2	3:C:233:GLU:CB	2.67	0.58
14:G:141:C:H2'	14:G:142:U:H6	1.69	0.58
21:1:415:LEU:O	25:5:36:TYR:OH	2.21	0.58
21:1:1109:ARG:NH2	21:1:1142:ASN:HB2	2.19	0.58
21:1:1165:TYR:HE1	22:2:575:PHE:CD1	2.21	0.58
23:3:878:ASP:OD1	23:3:879:LEU:N	2.37	0.58
37:R:124:VAL:HG22	37:R:126:ASN:H	1.68	0.58
45:Z:566:TYR:HE2	45:Z:584:TRP:CZ3	1.92	0.58
1:A:249:LEU:HD22	1:A:254:TYR:HB2	1.86	0.58
1:A:280:GLU:OE2	1:A:281:PRO:HD2	2.03	0.58
1:A:2073:TRP:CD1	1:A:2074:ARG:N	2.72	0.58
3:C:115:GLU:O	3:C:116:MET:C	2.43	0.58
3:C:573:GLU:N	3:C:573:GLU:OE1	2.37	0.58
14:G:18:A:C5'	35:O:69:GLU:OE1	2.46	0.58
17:p:152:ILE:O	17:p:223:ALA:N	2.36	0.58
37:R:171:LEU:HD23	37:R:171:LEU:O	2.03	0.58
46:x:442:THR:O	46:x:446:MET:N	2.37	0.58
1:A:232:LEU:HD22	1:A:404:LEU:HD12	1.86	0.57
2:B:44:A:H2	14:G:-5:G:N1	2.02	0.57
3:C:145:PHE:CD1	3:C:312:SER:HB3	2.39	0.57
5:E:165:GLN:HG3	5:E:181:ILE:HD11	1.85	0.57
37:R:189:ASN:HD21	37:R:195:ARG:HH22	1.50	0.57
39:T:399:LYS:HG2	39:T:406:ILE:CD1	2.31	0.57
1:A:48:LYS:O	1:A:53:PHE:CD2	2.57	0.57
5:E:277:PHE:CE2	5:E:300:ILE:CD1	2.85	0.57
13:F:39:A:N6	14:G:8:C:H42	2.02	0.57
14:G:12:G:N2	14:G:13:C:O4'	2.38	0.57
18:w:478:GLU:N	23:3:978:LEU:CD1	2.66	0.57
23:3:781:LEU:HB3	23:3:801:GLU:OE2	2.04	0.57
1:A:60:ASP:OD1	1:A:60:ASP:N	2.36	0.57
3:C:749:THR:OG1	3:C:752:SER:HB2	2.04	0.57
4:D:454:PRO:HA	23:3:571:SER:O	2.04	0.57
23:3:463:ARG:HB2	23:3:510:LEU:HD22	1.85	0.57
35:O:131:THR:HG23	42:W:111:LEU:CA	2.34	0.57
43:X:285:ARG:NH1	43:X:304:ALA:O	2.35	0.57
1:A:439:GLN:NE2	1:A:614:TYR:CE2	2.49	0.57
1:A:800:TYR:HB3	3:C:59:LEU:CD1	2.34	0.57
2:B:41:U:C4	14:G:-1:G:N1	2.73	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:42:U:H3	14:G:-3:A:H2	0.70	0.57
3:C:617:LEU:HD11	3:C:629:ILE:HG23	1.87	0.57
23:3:306:GLU:OE2	27:7:63:ARG:HG3	2.03	0.57
23:3:478:PHE:O	23:3:504:PRO:HB3	2.05	0.57
23:3:1050:PHE:HB3	23:3:1167:TYR:CE2	2.38	0.57
29:L:73:HIS:O	29:L:77:LEU:HG	2.04	0.57
3:C:79:THR:HG23	39:T:199:VAL:CG1	2.27	0.57
3:C:671:SER:C	3:C:672:LEU:HD22	2.30	0.57
21:1:850:ILE:O	21:1:854:VAL:HG23	2.04	0.57
23:3:136:GLU:OE2	23:3:189:TYR:OH	2.10	0.57
23:3:520:TYR:HB2	23:3:521:PRO:HD2	1.87	0.57
23:3:791:HIS:CE1	23:3:934:GLY:HA3	2.39	0.57
37:R:55:LEU:CB	37:R:73:PRO:O	2.53	0.57
37:R:442:ARG:CD	37:R:443:GLY:C	2.77	0.57
1:A:785:LYS:CE	36:P:215:LEU:CD1	2.78	0.57
1:A:1548:TYR:CD2	1:A:1549:VAL:CG2	2.75	0.57
2:B:20:G:O6	2:B:24:G:OP1	2.21	0.57
3:C:93:ILE:O	3:C:94:ILE:HB	2.04	0.57
3:C:572:GLU:O	3:C:573:GLU:HB2	2.04	0.57
3:C:669:THR:CG2	3:C:690:GLU:OE1	2.52	0.57
5:E:267:PHE:CE1	31:K:194:GLU:HB2	2.40	0.57
14:G:137:C:N4	15:H:40:C:H42	1.99	0.57
23:3:211:TYR:CE1	23:3:222:ARG:HG2	2.40	0.57
23:3:429:ARG:NH1	27:7:58:ASN:OD1	2.38	0.57
36:P:73:GLU:O	36:P:76:ARG:HG2	2.04	0.57
36:P:188:TRP:N	36:P:188:TRP:CE3	2.73	0.57
1:A:623:LYS:O	48:A:2401:IHP:O24	2.22	0.57
1:A:745:ALA:HB2	39:T:206:TRP:CZ2	2.40	0.57
1:A:783:TYR:CG	36:P:228:ILE:HG12	2.39	0.57
3:C:140:HIS:HE2	3:C:233:GLU:HG3	1.68	0.57
15:H:42:G:OP2	20:v:77:LYS:HE2	2.04	0.57
15:H:166:G:OP2	15:H:166:G:N2	2.27	0.57
29:L:33:ARG:O	29:L:36:SER:OG	2.20	0.57
29:L:215:PRO:O	35:O:113:ASN:CA	2.53	0.57
34:N:28:LYS:NZ	42:W:190:ASP:N	2.52	0.57
35:O:240:GLY:HA3	35:O:296:ARG:HH22	1.68	0.57
36:P:31:SER:N	36:P:34:ASP:OD2	2.37	0.57
1:A:293:TRP:HB2	1:A:1136:ARG:NH2	2.19	0.57
1:A:705:LYS:CG	37:R:251:ILE:HB	2.27	0.57
3:C:78:GLU:CD	3:C:80:ILE:HD11	2.30	0.57
3:C:140:HIS:CE1	3:C:233:GLU:CB	2.83	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:487:GLY:HA3	3:C:489:GLN:OE1	2.05	0.57
3:C:490:PHE:HZ	3:C:612:LYS:HD2	1.69	0.57
3:C:511:GLY:O	3:C:576:ILE:HD12	2.02	0.57
15:H:148:C:O5'	15:H:148:C:H6	1.87	0.57
21:1:1109:ARG:HH22	21:1:1142:ASN:HB2	1.69	0.57
21:1:1258:ALA:HB3	21:1:1261:VAL:HG12	1.86	0.57
23:3:275:ARG:HE	23:3:386:PHE:HD2	1.51	0.57
37:R:434:TYR:CD2	37:R:435:ASN:N	2.73	0.57
1:A:91:ALA:O	1:A:92:LEU:C	2.45	0.57
1:A:387:PHE:CD2	3:C:399:LEU:CD2	2.87	0.57
1:A:569:VAL:O	1:A:570:ASP:HB2	2.04	0.57
1:A:692:ASP:CA	39:T:376:ARG:NH2	2.53	0.57
1:A:705:LYS:CG	37:R:251:ILE:CD1	2.70	0.57
5:E:310:TYR:CE1	5:E:322:LYS:CD	2.86	0.57
15:H:45:C:H2'	18:w:394:TYR:CD2	2.40	0.57
15:H:152:G:N2	15:H:153:A:C5	2.73	0.57
21:1:1098:LEU:HD13	21:1:1135:GLU:HG3	1.85	0.57
21:1:1126:PHE:CE2	22:2:572:HIS:HA	2.39	0.57
28:J:224:LYS:HE2	28:J:255:LEU:HD13	1.85	0.57
38:S:131:ARG:NH1	38:S:133:CYS:CB	2.68	0.57
45:Z:525:TYR:CD1	45:Z:526:ILE:N	2.73	0.57
46:x:940:ARG:O	46:x:944:THR:N	2.37	0.57
1:A:107:PRO:O	1:A:111:GLU:CD	2.48	0.57
1:A:532:THR:CB	14:G:2:U:C5'	2.83	0.57
1:A:832:TYR:CE2	1:A:834:HIS:HB2	2.40	0.57
3:C:78:GLU:O	39:T:198:ARG:C	2.47	0.57
3:C:508:LYS:HE3	3:C:566:THR:CG2	2.34	0.57
21:1:807:LYS:HA	21:1:811:LEU:HD12	1.87	0.57
21:1:942:ASN:HD22	21:1:947:VAL:HG11	1.70	0.57
23:3:635:ALA:H	23:3:669:LEU:HD21	1.70	0.57
37:R:181:PRO:O	42:W:112:SER:O	2.21	0.57
39:T:347:THR:CG2	39:T:357:TRP:HE1	2.18	0.57
41:V:489:LEU:O	41:V:492:MET:CB	2.53	0.57
42:W:420:ALA:H	42:W:438:ASP:CB	2.17	0.57
45:Z:611:ALA:O	45:Z:614:TRP:HB3	2.05	0.57
1:A:32:GLU:CG	1:A:36:LYS:HE3	2.35	0.56
1:A:844:GLU:CB	37:R:422:MET:HE2	2.22	0.56
2:B:27:U:O2'	2:B:28:A:O5'	2.23	0.56
3:C:261:ASP:OD1	50:C:1500:GTP:C6	2.57	0.56
28:J:270:ASP:OD2	37:R:222:PRO:CB	2.52	0.56
38:S:10:GLN:CB	38:S:29:TRP:CD2	2.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:T:306:CYS:SG	39:T:336:VAL:CG1	2.93	0.56
1:A:299:ILE:HD11	3:C:920:PRO:C	2.29	0.56
1:A:790:ARG:NE	1:A:986:GLU:OE2	2.38	0.56
1:A:1233:ASP:OD1	1:A:1234:ASP:N	2.37	0.56
1:A:1252:GLY:HA2	1:A:1298:ARG:HH21	1.69	0.56
13:F:57:U:H2'	13:F:58:G:H8	1.69	0.56
14:G:7:G:H2'	14:G:8:C:C6	2.40	0.56
15:H:78:C:HO2'	15:H:79:G:H5'	1.70	0.56
15:H:141:C:C2	15:H:142:C:C5	2.94	0.56
23:3:327:LEU:O	23:3:373:PHE:HB2	2.05	0.56
28:J:273:TYR:CG	37:R:228:PRO:CG	2.88	0.56
37:R:409:VAL:O	37:R:410:GLN:HG2	2.05	0.56
41:V:483:GLU:O	41:V:486:THR:N	2.33	0.56
45:Z:524:ARG:HB3	45:Z:524:ARG:CZ	2.35	0.56
1:A:36:LYS:NZ	42:W:163:GLN:CB	2.69	0.56
1:A:178:TYR:CD2	1:A:491:GLU:HB2	2.40	0.56
1:A:356:ILE:HG22	1:A:357:ASN:N	2.20	0.56
1:A:434:HIS:CE1	1:A:435:CYS:SG	2.98	0.56
1:A:532:THR:CB	14:G:2:U:H5''	2.35	0.56
1:A:587:GLN:O	1:A:587:GLN:HG2	2.04	0.56
1:A:1301:ILE:HD11	1:A:1306:LYS:CE	2.35	0.56
1:A:1386:TRP:HZ2	1:A:1417:PRO:HB2	1.69	0.56
3:C:426:GLU:O	3:C:427:PHE:HB2	2.05	0.56
3:C:449:ILE:CG2	3:C:457:VAL:HG11	2.30	0.56
5:E:250:LEU:CD2	5:E:262:TRP:HB2	2.35	0.56
15:H:152:G:N2	15:H:153:A:C8	2.73	0.56
21:1:847:ALA:O	21:1:851:SER:OG	2.24	0.56
22:2:643:PRO:CD	24:4:69:TYR:CG	2.88	0.56
30:q:58:ALA:HB1	30:r:6:SER:HA	1.87	0.56
36:P:76:ARG:HG3	36:P:77:ASP:N	2.19	0.56
37:R:70:ALA:O	37:R:71:GLN:C	2.48	0.56
37:R:89:GLN:OE1	38:S:146:GLU:N	2.38	0.56
38:S:131:ARG:HH12	38:S:133:CYS:HA	1.68	0.56
1:A:120:TYR:N	1:A:483:GLN:O	2.33	0.56
1:A:226:GLN:HA	1:A:418:THR:OG1	2.06	0.56
1:A:570:ASP:OD1	1:A:571:ALA:N	2.38	0.56
1:A:1425:LYS:C	1:A:1425:LYS:HD3	2.31	0.56
1:A:2113:LYS:CE	4:D:1229:ASP:CA	2.84	0.56
3:C:223:ASP:OD1	3:C:495:ARG:NH2	2.38	0.56
3:C:457:VAL:HA	3:C:462:GLY:HA3	1.88	0.56
3:C:673:LYS:HG3	3:C:686:THR:CG2	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:G:22:C:O2	14:G:22:C:H2'	2.06	0.56
20:v:18:SER:O	20:v:21:GLU:N	2.37	0.56
21:1:944:SER:O	21:1:948:ARG:HG3	2.04	0.56
21:1:1279:ALA:HA	23:3:1167:TYR:CE1	2.41	0.56
24:4:75:ASN:ND2	24:4:86:VAL:O	2.38	0.56
1:A:226:GLN:OE1	1:A:417:ARG:NE	2.31	0.56
1:A:692:ASP:OD1	39:T:376:ARG:NH2	2.38	0.56
1:A:1163:ARG:NH2	3:C:61:GLU:OE2	2.35	0.56
5:E:267:PHE:CZ	31:K:194:GLU:CG	2.88	0.56
13:F:26:U:O2'	13:F:27:A:OP1	2.18	0.56
27:7:32:LEU:O	27:7:36:HIS:ND1	2.23	0.56
28:J:311:GLN:OE1	28:J:311:GLN:N	2.33	0.56
1:A:282:LEU:HD23	1:A:282:LEU:O	2.05	0.56
1:A:301:LYS:HG2	3:C:940:ARG:CA	2.35	0.56
1:A:339:PHE:C	1:A:340:ILE:HD13	2.31	0.56
3:C:301:SER:O	3:C:304:LEU:N	2.30	0.56
13:F:50:A:O2'	13:F:51:U:OP1	2.23	0.56
18:w:411:CYS:SG	18:w:431:HIS:CD2	2.99	0.56
28:J:406:PHE:CE2	28:J:411:MET:HE3	2.41	0.56
1:A:283:VAL:HG22	1:A:284:ARG:HG2	1.88	0.56
1:A:651:TRP:CZ2	13:F:66:C:N3	2.73	0.56
1:A:812:THR:HG23	1:A:1055:LEU:HD11	1.88	0.56
1:A:2320:LEU:HD23	1:A:2322:GLU:H	1.71	0.56
3:C:140:HIS:CB	3:C:230:ASP:CB	2.66	0.56
15:H:168:A:C5	12:n:54:GLN:CB	2.88	0.56
18:w:477:GLU:HA	23:3:980:LYS:NZ	2.21	0.56
24:4:79:LEU:HB2	24:4:84:ILE:HD11	1.88	0.56
29:L:721:LEU:HA	29:L:724:TYR:CG	2.41	0.56
34:N:128:VAL:HG13	34:N:130:ARG:N	2.14	0.56
1:A:44:ARG:NH2	5:E:285:GLU:O	2.38	0.56
1:A:229:GLN:HG2	1:A:415:SER:CB	2.36	0.56
1:A:579:GLN:NE2	1:A:613:TYR:CE1	2.74	0.56
1:A:2153:THR:HG22	1:A:2154:HIS:H	1.70	0.56
3:C:85:ASP:HB3	39:T:238:LEU:CG	2.27	0.56
3:C:677:GLU:HA	3:C:683:ASN:O	2.05	0.56
4:D:455:PHE:CB	23:3:573:GLN:NE2	2.68	0.56
5:E:277:PHE:CE2	5:E:300:ILE:HD13	2.40	0.56
14:G:20:A:C1'	35:O:193:LEU:HD21	2.35	0.56
21:1:1026:ASN:ND2	21:1:1031:VAL:HG11	2.21	0.56
2:B:40:U:H3'	2:B:40:U:O2	2.05	0.56
3:C:385:VAL:HG23	3:C:386:GLY:N	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:153:PHE:HD1	5:E:153:PHE:H	1.54	0.56
15:H:150:U:C2	15:H:151:C:C5	2.94	0.56
21:1:689:ILE:O	21:1:692:HIS:ND1	2.39	0.56
21:1:718:PRO:HA	21:1:756:LEU:HG	1.88	0.56
25:5:93:ASN:OD1	25:5:94:ALA:N	2.34	0.56
28:J:433:ARG:HH12	28:J:461:LYS:CB	2.19	0.56
35:O:236:VAL:O	35:O:269:CYS:HA	2.06	0.56
37:R:442:ARG:HD2	37:R:443:GLY:C	2.31	0.56
39:T:342:GLU:CB	39:T:343:PRO:CD	2.83	0.56
1:A:89:LEU:HD13	1:A:660:PHE:CZ	2.41	0.56
1:A:339:PHE:CD1	1:A:406:TRP:CZ3	2.93	0.56
1:A:978:GLU:CD	1:A:1188:ASN:H	2.14	0.56
1:A:1305:SER:OG	1:A:1310:ARG:HD3	2.06	0.56
1:A:1451:ASN:OD1	1:A:1453:PHE:N	2.39	0.56
1:A:1552:GLN:HB3	49:A:2402:ALA:HB1	1.86	0.56
1:A:1607:GLU:N	1:A:1632:PHE:O	2.38	0.56
3:C:631:GLY:HA3	3:C:637:LEU:HD21	1.88	0.56
15:H:42:G:P	20:v:77:LYS:HD3	2.42	0.56
15:H:83:A:N1	15:H:84:C:C4	2.74	0.56
18:w:478:GLU:CB	23:3:978:LEU:CD1	2.84	0.56
21:1:1293:ASN:HA	27:7:76:CYS:O	2.05	0.56
21:1:1295:TYR:CE2	27:7:28:LYS:HE2	2.41	0.56
23:3:29:GLU:HB3	23:3:40:LEU:HD11	1.87	0.56
23:3:804:HIS:HD2	23:3:862:TRP:CZ2	2.24	0.56
23:3:1028:THR:HG22	23:3:1088:LYS:HD3	1.86	0.56
34:N:59:TYR:CE1	42:W:187:SER:HA	2.41	0.56
1:A:295:GLU:OE2	3:C:593:GLU:OE2	2.23	0.55
1:A:783:TYR:CD1	36:P:228:ILE:HG12	2.41	0.55
14:G:16:G:H4'	14:G:17:U:O5'	2.04	0.55
15:H:154:C:O2'	15:H:155:C:H5'	2.04	0.55
21:1:570:TYR:HD1	21:1:573:LYS:HD2	1.71	0.55
23:3:633:LEU:HD13	23:3:667:ILE:HG21	1.87	0.55
38:S:131:ARG:HH11	38:S:133:CYS:HA	1.69	0.55
1:A:417:ARG:HH12	2:B:58:U:H4'	1.70	0.55
1:A:744:LYS:HZ1	36:P:212:ASN:C	2.14	0.55
15:H:141:C:H2'	15:H:142:C:H6	1.71	0.55
15:H:149:A:C4	15:H:150:U:C5	2.95	0.55
15:H:180:G:C2	15:H:181:G:C5	2.94	0.55
35:O:225:PRO:HG3	35:O:302:TRP:NE1	2.12	0.55
38:S:131:ARG:HH11	38:S:132:VAL:C	2.12	0.55
39:T:351:ASP:C	39:T:352:THR:OG1	2.48	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:LEU:HD13	1:A:660:PHE:HZ	1.71	0.55
1:A:296:PHE:HB3	3:C:656:ALA:HB1	1.86	0.55
1:A:331:TRP:C	1:A:331:TRP:HE3	2.14	0.55
1:A:1418:ARG:HE	1:A:1464:LEU:HD23	1.72	0.55
1:A:1690:ASP:OD1	1:A:1691:ASN:N	2.39	0.55
3:C:674:CYS:HG	3:C:822:MET:CE	2.16	0.55
5:E:250:LEU:HD22	5:E:262:TRP:HB2	1.88	0.55
21:1:1137:ARG:HH21	22:2:524:LEU:HD13	1.72	0.55
42:W:101:THR:O	42:W:103:GLN:N	2.38	0.55
1:A:184:ASP:OD1	34:N:1:MET:N	2.35	0.55
1:A:227:ARG:C	1:A:416:GLY:O	2.48	0.55
3:C:706:GLN:NE2	3:C:708:THR:H	2.02	0.55
22:2:650:ILE:HG12	22:2:688:GLY:HA3	1.89	0.55
23:3:745:PHE:HE2	23:3:750:CYS:HB3	1.71	0.55
28:J:270:ASP:CG	37:R:222:PRO:CB	2.77	0.55
28:J:406:PHE:CD1	28:J:411:MET:HE2	2.41	0.55
42:W:474:LYS:C	42:W:490:ALA:CB	2.80	0.55
1:A:587:GLN:HB2	1:A:1550:GLY:H	1.71	0.55
1:A:1035:GLN:HA	1:A:1446:GLN:NE2	2.21	0.55
1:A:1370:ARG:HH22	41:V:506:PHE:CB	2.19	0.55
2:B:47:A:O2'	2:B:48:A:H5''	2.06	0.55
2:B:94:U:H2'	2:B:95:G:H5''	1.89	0.55
3:C:185:PRO:HG3	3:C:482:TYR:CZ	2.41	0.55
3:C:439:PRO:HB2	3:C:443:VAL:HB	1.88	0.55
3:C:674:CYS:SG	3:C:822:MET:HE1	2.45	0.55
21:1:1166:ILE:O	21:1:1170:THR:HG23	2.07	0.55
24:4:29:LEU:HD22	24:4:33:PHE:HE2	1.72	0.55
38:S:13:ASN:HD22	38:S:24:VAL:CG1	2.19	0.55
45:Z:566:TYR:CD2	45:Z:580:PRO:HG2	2.36	0.55
1:A:89:LEU:O	1:A:89:LEU:HD23	2.05	0.55
1:A:1364:LEU:HD11	41:V:461:LEU:CB	2.29	0.55
1:A:1645:LEU:HB2	1:A:1714:ALA:HB3	1.88	0.55
3:C:702:ASN:O	3:C:703:GLU:HB2	2.07	0.55
5:E:162:ARG:CZ	5:E:203:ASP:O	2.55	0.55
15:H:165:A:H2'	15:H:166:G:H5'	1.88	0.55
18:w:478:GLU:CA	23:3:978:LEU:HD11	2.36	0.55
23:3:996:ILE:HG23	23:3:999:ARG:H	1.72	0.55
37:R:422:MET:C	37:R:424:SER:H	2.12	0.55
1:A:1233:ASP:O	1:A:1236:SER:OG	2.23	0.55
1:A:2306:HIS:HD2	1:A:2308:VAL:H	1.54	0.55
3:C:78:GLU:OE1	39:T:198:ARG:NE	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:79:THR:CG2	39:T:199:VAL:CG1	2.84	0.55
3:C:567:GLU:OE1	3:C:572:GLU:HB3	2.06	0.55
5:E:260:ARG:NH1	5:E:276:ILE:HD11	2.22	0.55
14:G:23:U:O2	14:G:23:U:H2'	2.07	0.55
18:w:485:ASN:ND2	23:3:976:LYS:O	2.39	0.55
21:1:1255:PHE:CD2	22:2:487:LEU:HD22	2.42	0.55
36:P:33:ARG:HG3	36:P:33:ARG:HH11	1.72	0.55
39:T:233:LEU:HD23	39:T:233:LEU:C	2.32	0.55
44:Y:22:VAL:HG22	44:Y:26:VAL:HG13	1.88	0.55
45:Z:600:ARG:HB3	45:Z:600:ARG:NH1	2.08	0.55
1:A:283:VAL:HG13	1:A:284:ARG:N	2.22	0.55
1:A:464:PRO:O	1:A:465:LYS:HB3	2.05	0.55
1:A:848:GLU:CD	37:R:424:SER:OG	2.50	0.55
1:A:1099:PHE:HE2	1:A:1153:VAL:HG13	1.72	0.55
1:A:1457:HIS:HE1	1:A:1459:ARG:HG3	1.68	0.55
21:1:1017:LEU:HD13	21:1:1050:VAL:HG21	1.89	0.55
21:1:1076:ALA:O	21:1:1080:THR:HG23	2.07	0.55
31:K:135:TRP:O	31:K:138:TYR:CG	2.60	0.55
35:O:106:ASP:CG	35:O:107:MET:H	2.15	0.55
37:R:74:LEU:HD23	37:R:75:ASP:OD1	2.06	0.55
37:R:436:VAL:CG2	37:R:437:TYR:CE1	2.89	0.55
41:V:641:ASP:O	41:V:644:ARG:N	2.39	0.55
44:Y:85:GLU:O	45:Z:502:ALA:CB	2.55	0.55
1:A:623:LYS:CG	48:A:2401:IHP:O34	2.55	0.55
1:A:1305:SER:CB	1:A:1310:ARG:NH1	2.44	0.55
3:C:149:LEU:HA	3:C:427:PHE:CD2	2.41	0.55
14:G:142:U:H2'	14:G:143:U:C6	2.42	0.55
15:H:40:C:O2'	20:v:72:HIS:HB2	2.06	0.55
15:H:150:U:H2'	15:H:151:C:H6	1.71	0.55
16:o:46:ALA:CB	16:o:68:THR:CB	2.85	0.55
25:5:17:VAL:HG23	25:5:67:ILE:HD11	1.89	0.55
41:V:484:SER:C	41:V:486:THR:H	2.15	0.55
44:Y:37:TRP:HZ3	45:Z:498:GLY:HA3	1.66	0.55
1:A:119:LEU:HD11	1:A:477:LYS:HG3	1.88	0.55
1:A:168:PRO:HG2	1:A:559:ASP:CB	2.36	0.55
1:A:1457:HIS:HE2	37:R:425:GLY:H	1.46	0.55
3:C:220:ARG:HG2	3:C:479:THR:HG21	1.89	0.55
15:H:168:A:C6	12:n:54:GLN:CB	2.90	0.55
21:1:1174:GLU:OE2	21:1:1210:HIS:NE2	2.35	0.55
27:7:60:SER:HG	27:7:63:ARG:H	1.54	0.55
29:L:224:PHE:CD1	37:R:86:LEU:O	2.59	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:N:139:CYS:SG	34:N:140:ARG:N	2.80	0.55
38:S:131:ARG:HH11	38:S:133:CYS:CA	2.17	0.55
45:Z:574:ASN:O	45:Z:577:ASN:N	2.33	0.55
1:A:148:TRP:CH2	1:A:616:PHE:HB2	2.42	0.54
1:A:356:ILE:HG22	1:A:357:ASN:H	1.72	0.54
1:A:2325:VAL:HG13	4:D:789:MET:HA	1.88	0.54
1:A:2325:VAL:O	4:D:788:GLY:CA	2.56	0.54
23:3:309:ASP:HA	23:3:332:THR:HG22	1.88	0.54
23:3:550:ASN:HD21	23:3:595:VAL:H	1.53	0.54
23:3:848:PRO:HB2	23:3:851:ILE:HG22	1.89	0.54
24:4:14:THR:CA	24:4:59:VAL:O	2.28	0.54
26:6:39:PRO:HB3	26:6:70:TYR:HB2	1.88	0.54
28:J:294:HIS:HE1	29:L:227:THR:HB	1.70	0.54
35:O:166:SER:HA	35:O:169:VAL:HG12	1.89	0.54
35:O:232:THR:HG22	35:O:277:ARG:HA	1.89	0.54
36:P:224:MET:HE2	36:P:228:ILE:CD1	2.36	0.54
37:R:86:LEU:HD12	37:R:86:LEU:O	2.06	0.54
42:W:185:ASP:O	42:W:186:ALA:HB3	2.06	0.54
1:A:2073:TRP:HD1	1:A:2074:ARG:N	2.04	0.54
2:B:36:C:H2'	40:U:11:ARG:HH12	1.71	0.54
5:E:119:THR:HG21	5:E:161:ARG:HB2	1.87	0.54
15:H:153:A:C3'	15:H:154:C:C5'	2.86	0.54
20:v:45:TYR:CZ	20:v:58:LEU:HD11	2.42	0.54
20:v:58:LEU:HD21	20:v:82:LEU:CG	2.37	0.54
21:1:1179:ASP:HB3	22:2:511:LEU:CD1	2.37	0.54
21:1:1279:ALA:HA	23:3:1167:TYR:HE1	1.70	0.54
34:N:38:GLU:O	34:N:40:LYS:N	2.38	0.54
43:X:312:GLU:O	43:X:327:TYR:HB2	2.07	0.54
1:A:592:TYR:HA	1:A:595:LYS:O	2.08	0.54
1:A:738:MET:HE3	1:A:739:ILE:HG13	1.89	0.54
1:A:1132:LYS:HA	1:A:1139:ARG:HD3	1.90	0.54
3:C:140:HIS:CD2	3:C:233:GLU:HG3	2.41	0.54
3:C:144:CYS:C	3:C:312:SER:HB2	2.33	0.54
3:C:510:LEU:HB3	3:C:576:ILE:HD11	1.89	0.54
3:C:559:ILE:C	3:C:559:ILE:HD12	2.31	0.54
13:F:27:A:N9	35:O:181:TYR:OH	2.37	0.54
13:F:36:A:H2'	13:F:37:C:H4'	1.89	0.54
13:F:38:G:H2'	13:F:39:A:C8	2.42	0.54
13:F:56:A:C2	15:H:20:G:C2	2.96	0.54
23:3:553:GLN:HA	23:3:566:PHE:O	2.07	0.54
23:3:1014:TYR:OH	23:3:1019:ASN:OD1	2.24	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:J:218:GLU:HG3	28:J:219:GLU:OE2	2.07	0.54
35:O:123:ARG:O	35:O:126:SER:OG	2.16	0.54
35:O:196:GLN:HE22	35:O:209:VAL:HG23	1.71	0.54
45:Z:612:TYR:C	45:Z:614:TRP:N	2.63	0.54
45:Z:614:TRP:CD1	45:Z:614:TRP:C	2.85	0.54
1:A:151:MET:SD	1:A:628:GLY:O	2.65	0.54
1:A:596:TYR:CZ	14:G:-5:G:N7	2.75	0.54
1:A:676:ARG:HG3	13:F:56:A:P	2.48	0.54
1:A:2117:ILE:O	1:A:2304:PHE:HB2	2.08	0.54
3:C:749:THR:HG1	3:C:752:SER:HB2	1.72	0.54
28:J:220:LEU:HD13	28:J:220:LEU:C	2.32	0.54
35:O:102:SER:OG	35:O:139:LYS:NZ	2.25	0.54
37:R:241:MET:SD	37:R:245:GLU:CD	2.91	0.54
37:R:402:ASN:HB3	43:X:191:GLN:HB2	1.90	0.54
38:S:110:SER:O	38:S:111:GLN:C	2.50	0.54
44:Y:10:ILE:HD13	44:Y:98:ASN:HD21	1.73	0.54
1:A:173:GLU:O	1:A:520:TYR:CD2	2.61	0.54
1:A:329:LEU:HD13	3:C:177:ARG:NE	2.17	0.54
1:A:699:GLU:O	1:A:701:ILE:HD12	2.07	0.54
1:A:1459:ARG:HG3	37:R:424:SER:N	2.22	0.54
3:C:145:PHE:CZ	3:C:427:PHE:HE1	2.21	0.54
5:E:161:ARG:NH1	5:E:203:ASP:OD1	2.40	0.54
18:w:145:CYS:HA	18:w:155:SER:O	2.08	0.54
23:3:913:LEU:HD23	23:3:920:VAL:HG12	1.89	0.54
28:J:262:ARG:HD3	29:L:220:PRO:CG	2.38	0.54
29:L:224:PHE:HD1	37:R:86:LEU:O	1.91	0.54
39:T:455:GLN:NE2	39:T:456:PRO:HD2	2.22	0.54
42:W:474:LYS:C	42:W:490:ALA:HB3	2.33	0.54
1:A:588:LEU:C	1:A:1551:PHE:CD1	2.86	0.54
1:A:705:LYS:HG2	37:R:251:ILE:CG1	2.38	0.54
1:A:1285:LEU:HB3	1:A:1335:ILE:HD12	1.90	0.54
1:A:1333:VAL:HG11	1:A:1367:ASN:HD22	1.73	0.54
1:A:1351:THR:HG22	40:U:25:LEU:HD21	1.88	0.54
2:B:42:U:H4'	13:F:70:A:C4'	2.37	0.54
5:E:108:HIS:ND1	5:E:128:SER:CB	2.70	0.54
5:E:310:TYR:CZ	5:E:322:LYS:HD2	2.42	0.54
23:3:138:GLN:HG2	23:3:161:HIS:CE1	2.43	0.54
23:3:336:ALA:HB2	23:3:349:VAL:HG13	1.90	0.54
23:3:547:CYS:HB3	23:3:556:ILE:HG22	1.90	0.54
37:R:131:ASP:OD2	37:R:132:LEU:HD23	2.07	0.54
1:A:978:GLU:OE2	1:A:1187:PHE:HB2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1328:LEU:HD22	1:A:1368:LEU:HD21	1.89	0.54
1:A:1342:TRP:CG	3:C:921:LEU:HD11	2.42	0.54
3:C:259:LYS:CE	3:C:262:ARG:HD2	2.36	0.54
3:C:482:TYR:CD2	3:C:493:PHE:HB2	2.42	0.54
3:C:700:ILE:CG2	3:C:735:PHE:CD2	2.83	0.54
4:D:1048:VAL:O	4:D:1050:GLU:N	2.40	0.54
21:1:470:ASP:OD1	21:1:471:ASP:N	2.41	0.54
21:1:632:PHE:HA	21:1:635:VAL:HG22	1.90	0.54
23:3:144:LEU:HB3	23:3:152:LEU:HD11	1.89	0.54
23:3:253:GLU:OE2	23:3:254:ASN:ND2	2.41	0.54
28:J:408:ASP:OD1	28:J:443:ILE:HG22	2.07	0.54
15:H:183:G:C4	15:H:184:C:C5	2.95	0.54
17:p:194:PHE:CB	17:p:200:ALA:HB2	2.38	0.54
20:v:45:TYR:CZ	20:v:58:LEU:CD1	2.89	0.54
21:1:331:ALA:O	21:1:335:LYS:N	2.34	0.54
23:3:526:HIS:HB3	23:3:534:ASN:HB2	1.88	0.54
23:3:669:LEU:HB2	23:3:673:VAL:HG22	1.88	0.54
36:P:228:ILE:HD12	36:P:228:ILE:N	2.23	0.54
38:S:55:ARG:CZ	42:W:95:PRO:O	2.56	0.54
39:T:356:LEU:N	39:T:356:LEU:CD1	2.70	0.54
45:Z:612:TYR:O	45:Z:615:SER:N	2.29	0.54
1:A:375:ASP:N	3:C:355:LYS:NZ	2.56	0.54
1:A:628:GLY:O	1:A:629:PHE:HB2	2.08	0.54
1:A:2287:ARG:HH22	4:D:1147:ASN:CB	2.15	0.54
3:C:135:CYS:SG	3:C:227:LEU:HB2	2.47	0.54
15:H:45:C:N3	18:w:395:TRP:CG	2.76	0.54
21:1:893:ILE:HG13	21:1:928:TYR:CD2	2.43	0.54
22:2:476:GLU:N	22:2:479:ASP:OD2	2.41	0.54
23:3:452:LEU:HB3	23:3:478:PHE:CE1	2.42	0.54
27:7:15:GLN:O	27:7:21:THR:OG1	2.22	0.54
28:J:255:LEU:HD22	29:L:235:LEU:CD1	2.35	0.54
34:N:40:LYS:C	34:N:41:ARG:CG	2.81	0.54
36:P:30:TYR:OH	37:R:162:ALA:C	2.50	0.54
37:R:232:MET:O	37:R:232:MET:HG2	2.07	0.54
1:A:339:PHE:HE1	1:A:406:TRP:HZ3	1.54	0.54
1:A:623:LYS:HG2	48:A:2401:IHP:O34	2.07	0.54
1:A:2310:ARG:HH12	1:A:2314:PHE:HE1	1.56	0.54
3:C:79:THR:HA	39:T:199:VAL:H	1.73	0.54
14:G:137:C:H2'	14:G:138:A:O4'	2.07	0.54
15:H:3:C:H2'	15:H:4:G:H8	1.73	0.54
21:1:826:ASP:OD1	21:1:827:ARG:N	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:1010:THR:O	21:1:1012:PRO:HD3	2.08	0.54
23:3:605:LEU:O	23:3:616:ILE:HA	2.08	0.54
35:O:50:ARG:NH1	35:O:122:GLU:OE1	2.41	0.54
35:O:235:TYR:HD1	35:O:271:PHE:CE1	2.24	0.54
36:P:188:TRP:O	36:P:190:ASP:N	2.39	0.54
37:R:135:PRO:HD2	39:T:341:ALA:HB1	1.90	0.54
37:R:442:ARG:CD	37:R:443:GLY:CA	2.70	0.54
42:W:474:LYS:CA	42:W:490:ALA:HB3	2.37	0.54
1:A:148:TRP:CZ2	1:A:616:PHE:HA	2.43	0.53
1:A:436:PRO:O	1:A:437:ALA:HB3	2.07	0.53
1:A:2067:PHE:CE2	1:A:2069:SER:HA	2.43	0.53
3:C:700:ILE:HA	3:C:705:VAL:HG12	1.89	0.53
3:C:742:PRO:HB2	3:C:786:ASN:H	1.72	0.53
5:E:178:LEU:CD1	5:E:222:LEU:HD22	2.37	0.53
14:G:-8:U:C6	40:U:16:ASN:CA	2.90	0.53
39:T:287:HIS:CE1	39:T:313:ARG:HG3	2.43	0.53
42:W:212:GLU:C	42:W:214:LYS:N	2.61	0.53
42:W:481:MET:O	42:W:483:ASN:N	2.41	0.53
42:W:531:LYS:HA	42:W:546:PHE:O	2.07	0.53
45:Z:485:GLU:O	45:Z:489:GLU:CB	2.56	0.53
1:A:71:ARG:NH1	1:A:177:ASP:OD2	2.32	0.53
1:A:254:TYR:O	1:A:434:HIS:HD2	1.91	0.53
1:A:705:LYS:HG2	37:R:251:ILE:CG2	2.38	0.53
1:A:1403:LEU:O	37:R:412:ASP:HB2	2.08	0.53
14:G:135:G:H1	15:H:41:U:H3	1.56	0.53
15:H:84:C:O2	15:H:84:C:H2'	2.09	0.53
23:3:166:LEU:O	23:3:186:GLU:HA	2.08	0.53
23:3:550:ASN:HB3	23:3:553:GLN:HB2	1.90	0.53
34:N:55:GLN:CD	42:W:192:PHE:CB	2.81	0.53
39:T:454:VAL:HG12	39:T:455:GLN:N	2.24	0.53
1:A:2298:LEU:C	4:D:1283:PRO:CB	2.78	0.53
5:E:87:ASP:O	5:E:88:ARG:HB2	2.07	0.53
13:F:53:A:H2'	13:F:54:G:O4'	2.09	0.53
21:1:626:ASN:ND2	21:1:630:ARG:HH12	2.06	0.53
21:1:1299:GLU:HA	21:1:1302:TYR:CE2	2.44	0.53
23:3:639:SER:OG	23:3:701:LEU:N	2.42	0.53
34:N:27:GLN:NE2	34:N:31:GLU:OE2	2.41	0.53
35:O:165:CYS:HB2	35:O:181:TYR:HB2	1.90	0.53
39:T:384:HIS:O	39:T:385:TYR:CB	2.55	0.53
41:V:525:PHE:O	41:V:528:ILE:N	2.41	0.53
43:X:181:PHE:HA	44:Y:50:GLY:H	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:Y:32:TYR:C	44:Y:34:ASP:H	2.15	0.53
1:A:1352:HIS:CD2	40:U:5:ILE:HD13	2.44	0.53
1:A:2129:TYR:HB3	1:A:2172:MET:HE3	1.90	0.53
3:C:78:GLU:C	39:T:198:ARG:HA	2.25	0.53
3:C:449:ILE:CD1	3:C:466:SER:N	2.71	0.53
15:H:82:G:HO2'	15:H:83:A:H5'	1.71	0.53
21:1:822:ARG:HH11	44:Y:31:GLU:HG2	1.74	0.53
21:1:1077:THR:O	21:1:1080:THR:OG1	2.22	0.53
21:1:1127:THR:HA	22:2:571:LEU:HB3	1.88	0.53
23:3:3:LEU:HD12	23:3:1093:MET:SD	2.48	0.53
23:3:476:VAL:HG22	23:3:762:LEU:HD22	1.91	0.53
28:J:218:GLU:HG3	28:J:219:GLU:N	2.23	0.53
37:R:103:ARG:HH11	37:R:103:ARG:CG	2.21	0.53
1:A:122:ILE:HD13	1:A:483:GLN:HG3	1.90	0.53
1:A:151:MET:HE1	1:A:629:PHE:HA	1.91	0.53
1:A:348:PRO:HB3	1:A:394:TYR:CE2	2.43	0.53
3:C:481:MET:SD	3:C:559:ILE:HD11	2.48	0.53
18:w:445:HIS:CG	18:w:446:PHE:CE2	2.97	0.53
20:v:61:THR:HG21	20:v:72:HIS:NE2	2.24	0.53
37:R:171:LEU:HD11	37:R:201:GLU:CD	2.32	0.53
44:Y:24:ASP:CG	44:Y:25:LYS:H	2.14	0.53
1:A:881:ILE:HG23	1:A:918:THR:HG23	1.88	0.53
1:A:1457:HIS:HE2	37:R:425:GLY:N	2.04	0.53
1:A:2073:TRP:CH2	1:A:2310:ARG:HG2	2.44	0.53
1:A:2113:LYS:HE3	4:D:1229:ASP:CA	2.38	0.53
3:C:220:ARG:O	3:C:448:LYS:HE2	2.08	0.53
3:C:360:ALA:N	3:C:361:PRO:CD	2.71	0.53
15:H:147:G:C2	15:H:148:C:C2	2.97	0.53
15:H:153:A:H3'	15:H:154:C:C5'	2.38	0.53
20:v:32:GLN:O	20:v:35:LEU:HB3	2.09	0.53
21:1:1157:TYR:O	26:6:38:ARG:NH2	2.40	0.53
23:3:195:ASP:OD1	23:3:197:THR:OG1	2.23	0.53
23:3:250:ILE:HD13	23:3:259:LYS:HB3	1.91	0.53
36:P:41:ILE:HD11	39:T:318:ARG:HB2	1.90	0.53
1:A:36:LYS:NZ	42:W:163:GLN:O	2.32	0.53
1:A:465:LYS:HG3	1:A:465:LYS:O	2.08	0.53
3:C:449:ILE:HG22	3:C:457:VAL:HG13	1.88	0.53
5:E:108:HIS:ND1	5:E:128:SER:HB2	2.24	0.53
5:E:178:LEU:CD2	5:E:208:ILE:CD1	2.87	0.53
15:H:68:G:C2'	15:H:69:U:H5'	2.37	0.53
23:3:141:VAL:HG11	23:3:213:LEU:HD12	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:L:733:LYS:O	29:L:736:ASN:CG	2.52	0.53
1:A:309:ARG:HH21	40:U:1:MET:HE2	1.74	0.53
1:A:642:ARG:CD	2:B:28:A:H1'	2.24	0.53
2:B:18:C:C2'	2:B:19:A:O5'	2.56	0.53
2:B:32:C:H5''	36:P:33:ARG:NH1	2.24	0.53
3:C:82:GLN:CG	39:T:237:LYS:HA	2.38	0.53
15:H:79:G:C2	15:H:80:A:C5	2.97	0.53
21:1:642:PRO:HB3	21:1:682:HIS:HE2	1.74	0.53
21:1:944:SER:HA	21:1:948:ARG:NE	2.23	0.53
23:3:519:VAL:HG22	23:3:524:ILE:HG12	1.89	0.53
23:3:712:VAL:HG23	23:3:722:SER:HB3	1.91	0.53
23:3:719:SER:OG	23:3:739:LEU:HD11	2.09	0.53
28:J:359:VAL:O	28:J:363:ARG:HG2	2.08	0.53
34:N:55:GLN:NE2	42:W:192:PHE:CB	2.71	0.53
34:N:128:VAL:CG1	34:N:130:ARG:HB3	2.38	0.53
39:T:318:ARG:HH11	39:T:318:ARG:CG	2.22	0.53
40:U:23:LEU:O	40:U:23:LEU:HD13	2.08	0.53
45:Z:571:PRO:HD3	45:Z:579:TRP:CH2	2.43	0.53
1:A:372:PRO:CB	3:C:342:ARG:HH21	2.22	0.53
1:A:595:LYS:NZ	2:B:45:C:OP1	2.31	0.53
3:C:259:LYS:HG2	3:C:262:ARG:HG3	1.90	0.53
5:E:232:ARG:O	5:E:262:TRP:HH2	1.91	0.53
21:1:516:LEU:O	21:1:520:THR:HG23	2.08	0.53
24:4:47:ASP:HB3	24:4:52:GLN:O	2.08	0.53
32:I:362:LYS:HA	32:I:372:ARG:CB	2.39	0.53
35:O:223:LEU:C	35:O:223:LEU:HD22	2.34	0.53
39:T:387:PHE:CD1	39:T:387:PHE:C	2.87	0.53
42:W:97:ASN:C	42:W:99:PHE:N	2.66	0.53
1:A:204:LEU:HD23	1:A:205:ASP:OD1	2.09	0.53
1:A:596:TYR:O	1:A:597:LYS:C	2.50	0.53
1:A:723:ASN:ND2	1:A:788:GLN:OE1	2.41	0.53
1:A:748:ASP:HA	36:P:214:THR:CG2	2.34	0.53
1:A:1275:ARG:HD2	1:A:1375:TRP:CD1	2.44	0.53
1:A:1425:LYS:CG	37:R:417:ASN:OD1	2.56	0.53
2:B:42:U:H4'	13:F:70:A:C5'	2.37	0.53
3:C:250:ARG:NE	3:C:451:HIS:CD2	2.76	0.53
3:C:516:LEU:HB2	3:C:575:GLN:HE22	1.73	0.53
13:F:50:A:H2'	13:F:51:U:C6	2.44	0.53
13:F:56:A:C6	15:H:20:G:C6	2.96	0.53
22:2:614:ARG:HH11	22:2:614:ARG:CG	2.14	0.53
23:3:211:TYR:HE1	23:3:222:ARG:HG2	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:S:34:LYS:CE	38:S:78:TYR:CD2	2.92	0.53
1:A:606:LYS:HD2	1:A:1548:TYR:CE1	2.44	0.52
1:A:891:PHE:O	29:L:83:ARG:NH1	2.42	0.52
21:1:599:ASN:O	21:1:603:ALA:CB	2.57	0.52
22:2:504:TRP:C	22:2:506:PHE:H	2.17	0.52
23:3:1148:LEU:O	23:3:1152:HIS:N	2.39	0.52
37:R:95:LYS:HD3	37:R:95:LYS:N	2.25	0.52
1:A:191:ILE:HG23	1:A:572:PHE:CZ	2.44	0.52
1:A:245:LEU:HD22	1:A:430:TRP:CH2	2.44	0.52
1:A:596:TYR:HB2	14:G:-5:G:C2	2.43	0.52
1:A:2298:LEU:HD13	4:D:1265:GLN:CB	2.39	0.52
3:C:301:SER:C	3:C:303:LEU:N	2.68	0.52
3:C:943:LEU:HD23	3:C:943:LEU:N	2.24	0.52
13:F:48:A:N3	29:L:33:ARG:NH2	2.57	0.52
13:F:94:C:OP1	28:J:351:ASN:CB	2.57	0.52
14:G:153:C:H4'	14:G:154:U:OP1	2.10	0.52
15:H:81:G:C2	15:H:82:G:C5	2.97	0.52
30:q:22:ASN:CB	30:r:54:ASP:O	2.56	0.52
41:V:530:LYS:O	41:V:532:GLN:N	2.42	0.52
1:A:94:TYR:HB2	37:R:207:MET:HE1	1.91	0.52
1:A:296:PHE:CZ	3:C:591:ALA:C	2.88	0.52
1:A:299:ILE:CD1	3:C:920:PRO:C	2.82	0.52
3:C:97:VAL:HG12	36:P:47:THR:OG1	2.10	0.52
13:F:34:G:H2'	13:F:35:A:O5'	2.10	0.52
14:G:-4:A:H2'	14:G:-3:A:C8	2.44	0.52
15:H:148:C:C2'	15:H:149:A:H5'	2.39	0.52
21:1:516:LEU:HD11	21:1:558:ARG:HD3	1.91	0.52
21:1:1090:PRO:HG3	21:1:1123:CYS:HB2	1.91	0.52
23:3:128:ARG:HH21	23:3:180:PRO:HG3	1.73	0.52
23:3:159:GLU:OE2	26:6:14:GLN:HB2	2.09	0.52
35:O:229:LYS:HA	35:O:277:ARG:NH2	2.24	0.52
36:P:189:ASP:O	36:P:191:ASP:N	2.43	0.52
37:R:233:HIS:H	37:R:233:HIS:HD2	1.56	0.52
38:S:39:PHE:CD2	38:S:129:PHE:HE2	2.10	0.52
40:U:9:THR:HG23	40:U:9:THR:O	2.09	0.52
41:V:484:SER:C	41:V:486:THR:N	2.67	0.52
42:W:531:LYS:CA	42:W:546:PHE:O	2.58	0.52
1:A:171:ASP:CG	1:A:519:ASP:OD2	2.53	0.52
1:A:1211:ASP:CG	41:V:505:LYS:CB	2.82	0.52
1:A:1214:TRP:CE2	1:A:1230:LEU:HD11	2.45	0.52
1:A:2133:PRO:HD2	1:A:2139:VAL:HG13	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:178:LEU:N	5:E:178:LEU:HD23	2.25	0.52
14:G:-12:G:H4'	14:G:-11:G:OP1	2.09	0.52
21:1:1108:ASN:OD1	21:1:1109:ARG:N	2.43	0.52
23:3:114:ARG:NE	23:3:136:GLU:OE1	2.32	0.52
35:O:75:SER:O	35:O:79:ASN:N	2.42	0.52
35:O:80:VAL:HG11	35:O:94:ILE:HD11	1.90	0.52
35:O:243:ILE:HG22	35:O:244:THR:O	2.08	0.52
37:R:52:PRO:O	37:R:53:ARG:HB2	2.09	0.52
37:R:81:LYS:HA	37:R:81:LYS:HE3	1.87	0.52
1:A:1275:ARG:NH1	1:A:1378:GLU:OE1	2.43	0.52
1:A:1306:LYS:HB2	14:G:-6:C:H4'	1.92	0.52
1:A:1631:LEU:HD12	1:A:1660:TYR:HD2	1.74	0.52
3:C:80:ILE:CD1	3:C:80:ILE:N	2.73	0.52
3:C:143:THR:HB	50:C:1500:GTP:O1A	2.09	0.52
3:C:700:ILE:CG2	3:C:741:GLY:O	2.57	0.52
13:F:36:A:C8	13:F:36:A:C4'	2.93	0.52
13:F:57:U:H2'	13:F:58:G:C8	2.45	0.52
21:1:717:THR:HG22	21:1:718:PRO:CD	2.39	0.52
21:1:762:ALA:O	21:1:766:THR:OG1	2.19	0.52
23:3:159:GLU:HB3	23:3:161:HIS:CD2	2.44	0.52
34:N:40:LYS:O	34:N:41:ARG:CG	2.47	0.52
45:Z:524:ARG:HD2	45:Z:525:TYR:HB3	1.92	0.52
1:A:115:ASP:HB3	1:A:486:LYS:HE2	1.91	0.52
1:A:121:HIS:HE2	1:A:481:PHE:CB	2.14	0.52
1:A:121:HIS:CD2	1:A:481:PHE:HB3	2.36	0.52
1:A:380:LEU:HD22	3:C:354:ARG:C	2.21	0.52
2:B:42:U:O2'	13:F:69:A:C2	2.58	0.52
2:B:43:U:C5'	13:F:67:G:H22	2.08	0.52
3:C:78:GLU:CG	3:C:80:ILE:CD1	2.54	0.52
3:C:139:HIS:O	3:C:259:LYS:NZ	2.36	0.52
3:C:449:ILE:HD11	3:C:466:SER:HA	1.91	0.52
3:C:508:LYS:HB3	3:C:566:THR:CG2	2.39	0.52
3:C:710:ASN:O	3:C:712:LYS:N	2.42	0.52
18:w:478:GLU:CA	23:3:978:LEU:CD1	2.87	0.52
21:1:1254:LEU:O	21:1:1262:ARG:HG2	2.09	0.52
23:3:755:VAL:HG22	23:3:764:ILE:HD12	1.90	0.52
23:3:1059:PRO:O	23:3:1062:THR:HG23	2.08	0.52
35:O:72:GLN:O	35:O:75:SER:OG	2.19	0.52
39:T:267:ASP:O	39:T:268:LYS:CG	2.56	0.52
45:Z:597:ARG:NH1	45:Z:601:LEU:HD13	2.24	0.52
1:A:1131:LYS:HE3	1:A:1174:PHE:CD1	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1162:PRO:HG3	36:P:194:PHE:CG	2.44	0.52
1:A:1459:ARG:HD2	37:R:422:MET:O	2.09	0.52
14:G:11:A:N1	14:G:12:G:C8	2.77	0.52
20:v:61:THR:OG1	20:v:72:HIS:CD2	2.62	0.52
23:3:285:MET:SD	23:3:305:THR:HB	2.49	0.52
23:3:304:GLN:HE22	23:3:335:VAL:HA	1.73	0.52
24:4:41:ASN:HB2	24:4:60:GLU:HB3	1.92	0.52
39:T:318:ARG:HH11	39:T:319:THR:HG23	1.74	0.52
1:A:47:GLU:OE1	1:A:47:GLU:N	2.35	0.52
1:A:206:TRP:CD1	1:A:213:LEU:HD21	2.45	0.52
1:A:651:TRP:CZ2	13:F:66:C:C4	2.97	0.52
1:A:1502:PHE:CZ	1:A:1505:LYS:HB3	2.45	0.52
1:A:2147:MET:O	1:A:2274:PRO:HD3	2.10	0.52
1:A:2268:LEU:HD22	4:D:1261:PRO:O	1.96	0.52
3:C:710:ASN:O	3:C:711:ARG:C	2.53	0.52
3:C:711:ARG:CZ	3:C:730:ARG:O	2.57	0.52
3:C:902:HIS:ND1	3:C:903:HIS:HB2	2.25	0.52
21:1:1289:ASN:HB3	21:1:1295:TYR:H	1.75	0.52
23:3:108:GLY:O	26:6:82:ARG:HD3	2.09	0.52
23:3:232:GLY:HA2	23:3:252:SER:HA	1.90	0.52
24:4:34:LEU:HA	24:4:37:GLY:O	2.10	0.52
35:O:24:CYS:HB2	35:O:27:CYS:SG	2.49	0.52
37:R:135:PRO:O	37:R:136:ASP:CB	2.58	0.52
1:A:380:LEU:HB2	3:C:354:ARG:NH1	2.18	0.52
1:A:1136:ARG:H	1:A:1345:GLN:HA	1.75	0.52
3:C:259:LYS:HG2	3:C:262:ARG:CG	2.39	0.52
3:C:510:LEU:HD22	3:C:514:TYR:HE2	1.75	0.52
15:H:45:C:H41	18:w:395:TRP:NE1	2.02	0.52
21:1:901:GLN:HA	21:1:939:ARG:HH22	1.72	0.52
28:J:406:PHE:CD2	28:J:411:MET:HE2	2.45	0.52
35:O:97:ARG:NH1	35:O:136:MET:HE2	2.25	0.52
36:P:193:VAL:HG23	36:P:194:PHE:N	2.25	0.52
38:S:9:TRP:CE3	38:S:11:PRO:HG2	2.45	0.52
39:T:347:THR:O	39:T:354:ILE:HG23	2.10	0.52
1:A:666:LYS:HB2	1:A:668:VAL:HG23	1.92	0.52
1:A:676:ARG:HG3	13:F:55:C:O3'	2.09	0.52
3:C:449:ILE:CD1	3:C:466:SER:CA	2.88	0.52
3:C:600:LEU:N	3:C:601:PRO:HD2	2.25	0.52
13:F:27:A:N9	35:O:181:TYR:CZ	2.77	0.52
15:H:45:C:C2	18:w:395:TRP:HB3	2.45	0.52
21:1:661:ARG:NH1	21:1:696:ASP:OD2	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:1070:LYS:HB3	21:1:1073:ILE:HD12	1.91	0.52
21:1:1096:THR:HA	21:1:1099:ASN:ND2	2.25	0.52
23:3:259:LYS:HG3	23:3:266:ASP:OD1	2.09	0.52
23:3:1048:ASP:HB3	23:3:1052:ASN:H	1.75	0.52
30:q:127:ALA:HB1	30:t:127:ALA:HB1	1.92	0.52
35:O:113:ASN:O	35:O:116:TYR:N	2.43	0.52
36:P:189:ASP:OD2	36:P:192:VAL:CG2	2.59	0.52
44:Y:69:ARG:NH2	44:Y:74:GLY:O	2.34	0.52
1:A:128:PHE:CD1	1:A:473:PHE:CZ	2.98	0.51
1:A:941:LYS:HG3	1:A:1071:PHE:CE1	2.46	0.51
1:A:1275:ARG:HD2	1:A:1375:TRP:NE1	2.25	0.51
1:A:1701:VAL:HA	1:A:1716:GLY:HA3	1.91	0.51
1:A:2081:ALA:HB1	4:D:1010:SER:CB	2.40	0.51
3:C:64:LYS:NZ	36:P:206:LYS:HG3	2.22	0.51
3:C:89:LEU:O	3:C:91:GLU:N	2.43	0.51
20:v:45:TYR:CD1	20:v:58:LEU:CD1	2.80	0.51
21:1:1256:HIS:ND1	21:1:1261:VAL:HG11	2.24	0.51
23:3:1134:SER:HB2	23:3:1136:GLU:OE1	2.09	0.51
34:N:43:VAL:O	34:N:47:TRP:NE1	2.44	0.51
36:P:32:SER:O	36:P:35:LEU:HD12	2.09	0.51
1:A:203:VAL:CG2	1:A:237:THR:CB	2.88	0.51
1:A:672:VAL:HG21	39:T:267:ASP:OD1	2.10	0.51
1:A:805:GLU:CB	36:P:194:PHE:CZ	2.89	0.51
1:A:2090:ILE:HA	1:A:2223:CYS:O	2.10	0.51
3:C:77:VAL:HG13	39:T:196:LEU:HB3	1.91	0.51
13:F:36:A:H3'	13:F:37:C:C5'	2.26	0.51
21:1:1185:ARG:HD2	21:1:1218:ASN:CG	2.35	0.51
21:1:1253:GLY:HA3	21:1:1265:TYR:CG	2.45	0.51
26:6:54:TYR:HA	26:6:57:ARG:HB2	1.92	0.51
29:L:224:PHE:CE1	37:R:86:LEU:HD13	2.44	0.51
39:T:392:PRO:HA	39:T:414:ALA:O	2.09	0.51
42:W:425:VAL:O	42:W:433:PHE:CB	2.59	0.51
42:W:518:PRO:O	42:W:519:ASP:CB	2.57	0.51
1:A:461:HIS:HD2	2:B:27:U:C4	2.28	0.51
1:A:750:TRP:CZ2	1:A:778:ARG:HG2	2.45	0.51
1:A:1179:SER:O	1:A:1182:ASN:N	2.44	0.51
3:C:674:CYS:SG	3:C:822:MET:CE	2.99	0.51
13:F:45:A:N1	22:2:554:ARG:NH2	2.53	0.51
20:v:61:THR:HG1	20:v:72:HIS:CD2	2.28	0.51
21:1:1179:ASP:HB2	21:1:1185:ARG:HD3	1.93	0.51
23:3:331:ASP:OD2	23:3:394:ASN:HB2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:I:729:SER:O	32:I:732:ALA:HB3	2.09	0.51
39:T:267:ASP:O	39:T:268:LYS:HB2	2.09	0.51
39:T:454:VAL:CG2	39:T:463:SER:OG	2.58	0.51
1:A:308:ILE:HG22	1:A:308:ILE:O	2.09	0.51
1:A:384:VAL:CG1	3:C:331:PHE:HD2	2.16	0.51
1:A:782:LEU:HB3	36:P:224:MET:SD	2.50	0.51
3:C:65:TYR:C	3:C:66:TYR:CG	2.86	0.51
3:C:300:LEU:HD13	3:C:300:LEU:N	2.25	0.51
3:C:449:ILE:HD11	3:C:465:MET:C	2.35	0.51
15:H:55:U:H1'	15:H:58:U:H5	1.74	0.51
15:H:107:A:C6	15:H:108:G:C5	2.99	0.51
23:3:667:ILE:HB	23:3:675:LEU:HB2	1.91	0.51
42:W:481:MET:C	42:W:483:ASN:H	2.18	0.51
45:Z:593:PHE:O	45:Z:597:ARG:CB	2.57	0.51
1:A:122:ILE:CD1	1:A:483:GLN:CG	2.89	0.51
1:A:519:ASP:C	1:A:519:ASP:OD1	2.54	0.51
1:A:593:ARG:NE	14:G:-4:A:O5'	2.43	0.51
1:A:830:LEU:HA	1:A:882:LYS:HZ2	1.75	0.51
1:A:1758:PRO:HB3	21:1:938:TRP:HD1	1.74	0.51
3:C:678:THR:HG23	3:C:683:ASN:H	1.75	0.51
5:E:231:MET:SD	5:E:262:TRP:CE3	3.04	0.51
13:F:68:C:N4	36:P:33:ARG:CB	2.45	0.51
14:G:20:A:P	35:O:159:ARG:HD3	2.50	0.51
21:1:1054:GLU:OE1	21:1:1057:ARG:NH1	2.36	0.51
23:3:460:TRP:CZ2	23:3:507:SER:HA	2.46	0.51
23:3:854:ALA:HB1	23:3:856:LYS:HD2	1.93	0.51
23:3:1002:VAL:HB	23:3:1010:ILE:HB	1.93	0.51
1:A:1447:VAL:HG12	1:A:1449:LYS:HG2	1.92	0.51
13:F:28:A:O2'	34:N:39:GLY:C	2.53	0.51
13:F:43:A:O2'	13:F:44:G:H5'	2.11	0.51
14:G:26:U:C1'	35:O:269:CYS:CB	2.88	0.51
7:i:89:ASP:CB	18:w:171:PHE:CB	2.89	0.51
18:w:411:CYS:O	18:w:414:TYR:N	2.37	0.51
21:1:231:ARG:HA	21:1:607:ALA:HB2	1.92	0.51
23:3:264:GLN:HE22	23:3:322:VAL:H	1.58	0.51
38:S:36:CYS:HA	38:S:129:PHE:CE1	2.45	0.51
39:T:318:ARG:HG3	39:T:318:ARG:HH11	1.76	0.51
44:Y:37:TRP:CZ3	45:Z:498:GLY:C	2.86	0.51
1:A:203:VAL:HG23	1:A:237:THR:CG2	2.35	0.51
1:A:468:LYS:HD3	1:A:468:LYS:C	2.35	0.51
1:A:589:THR:OG1	1:A:590:GLY:N	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1320:LYS:NZ	37:R:434:TYR:CD1	2.77	0.51
1:A:1629:ILE:HB	1:A:1662:ILE:HB	1.92	0.51
3:C:220:ARG:O	3:C:448:LYS:CE	2.58	0.51
13:F:34:G:N3	13:F:34:G:C3'	2.72	0.51
13:F:94:C:H5''	28:J:347:HIS:HB3	1.92	0.51
22:2:469:VAL:HG12	22:2:471:ARG:H	1.76	0.51
23:3:113:ARG:HB2	23:3:116:VAL:HB	1.91	0.51
23:3:971:ASP:OD1	23:3:972:LEU:N	2.43	0.51
35:O:20:PHE:CE1	37:R:197:ILE:HD13	2.46	0.51
35:O:75:SER:OG	35:O:76:LYS:N	2.44	0.51
38:S:35:THR:O	38:S:129:PHE:CZ	2.63	0.51
39:T:459:LEU:HD12	39:T:460:ASP:N	2.25	0.51
44:Y:37:TRP:CH2	45:Z:498:GLY:N	2.74	0.51
1:A:95:MET:N	1:A:96:PRO:HD2	2.26	0.51
1:A:595:LYS:HB3	2:B:45:C:OP1	2.11	0.51
2:B:94:U:H5	9:d:104:ASP:O	1.94	0.51
3:C:133:THR:O	3:C:226:VAL:O	2.29	0.51
13:F:34:G:N3	13:F:34:G:C5'	2.73	0.51
13:F:35:A:N3	13:F:35:A:C5'	2.73	0.51
18:w:485:ASN:ND2	23:3:976:LYS:CG	2.62	0.51
23:3:354:GLY:HA3	23:3:432:ARG:HH12	1.76	0.51
24:4:16:TYR:HA	24:4:57:GLY:O	2.10	0.51
24:4:16:TYR:HD1	24:4:58:PHE:CE2	2.28	0.51
28:J:257:GLU:HA	29:L:232:TYR:CE2	2.46	0.51
28:J:273:TYR:CD2	37:R:228:PRO:CG	2.94	0.51
37:R:134:ARG:O	37:R:135:PRO:C	2.54	0.51
38:S:11:PRO:CA	38:S:166:GLY:HA3	2.41	0.51
1:A:975:VAL:HB	1:A:1099:PHE:HB2	1.93	0.51
1:A:1373:GLN:HB3	1:A:1378:GLU:OE2	2.11	0.51
1:A:1549:VAL:HG22	14:G:-6:C:O2'	2.08	0.51
1:A:2073:TRP:HH2	1:A:2310:ARG:NH1	2.09	0.51
1:A:2095:ASP:OD1	1:A:2095:ASP:N	2.41	0.51
3:C:131:ASN:ND2	3:C:223:ASP:OD2	2.44	0.51
3:C:388:VAL:O	3:C:388:VAL:HG22	2.10	0.51
14:G:11:A:N3	14:G:11:A:C5'	2.73	0.51
14:G:11:A:N1	14:G:12:G:N7	2.59	0.51
14:G:20:A:OP2	35:O:159:ARG:CD	2.58	0.51
18:w:478:GLU:HA	23:3:978:LEU:HD11	1.91	0.51
21:1:669:GLN:O	21:1:672:ALA:N	2.44	0.51
23:3:246:SER:O	23:3:260:ASN:ND2	2.44	0.51
23:3:404:LEU:HD23	23:3:407:ILE:HD11	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:520:TYR:CE1	23:3:522:ASP:HB2	2.46	0.51
23:3:896:PHE:HB2	23:3:899:THR:HG22	1.93	0.51
28:J:273:TYR:CD1	37:R:228:PRO:HG2	2.46	0.51
39:T:300:ILE:O	39:T:301:ASP:HB2	2.11	0.51
1:A:338:VAL:CG1	3:C:267:LEU:HD23	2.41	0.51
1:A:823:SER:OG	1:A:933:ARG:NH1	2.44	0.51
1:A:1276:GLU:O	1:A:1279:VAL:HG12	2.11	0.51
3:C:93:ILE:CD1	39:T:230:ILE:CD1	2.89	0.51
5:E:276:ILE:C	5:E:277:PHE:HD1	2.19	0.51
15:H:111:G:O3'	15:H:112:G:O4'	2.29	0.51
21:1:475:PHE:CE1	21:1:502:LEU:HB2	2.46	0.51
21:1:582:LEU:HD23	21:1:630:ARG:HB3	1.93	0.51
23:3:757:ILE:HG23	23:3:762:LEU:HD13	1.93	0.51
23:3:1144:VAL:O	23:3:1148:LEU:HB2	2.11	0.51
35:O:283:ALA:O	35:O:287:SER:CB	2.58	0.51
39:T:385:TYR:CE2	39:T:400:PHE:HB3	2.46	0.51
1:A:86:ARG:HH21	37:R:211:ARG:HG3	1.74	0.50
1:A:1435:GLY:O	1:A:1438:VAL:HG22	2.10	0.50
3:C:215:VAL:HG11	3:C:242:LEU:HD22	1.93	0.50
23:3:28:GLN:HE22	23:3:343:LYS:HG2	1.77	0.50
23:3:80:VAL:HB	23:3:88:VAL:HG23	1.93	0.50
23:3:110:SER:HB3	26:6:82:ARG:HH12	1.75	0.50
23:3:556:ILE:HD11	23:3:564:VAL:HB	1.93	0.50
28:J:252:GLU:OE1	28:J:260:ARG:HB3	2.12	0.50
28:J:360:ASP:HA	28:J:363:ARG:HD2	1.91	0.50
37:R:185:GLY:C	37:R:186:VAL:HG13	2.35	0.50
37:R:220:ARG:CB	37:R:220:ARG:HH11	2.24	0.50
1:A:863:GLU:OE2	1:A:916:LYS:NZ	2.36	0.50
2:B:20:G:HI1'	2:B:21:A:OP1	2.12	0.50
2:B:44:A:P	13:F:66:C:H42	2.33	0.50
3:C:452:THR:O	3:C:578:ARG:N	2.43	0.50
3:C:457:VAL:HG12	3:C:462:GLY:CA	2.41	0.50
3:C:619:THR:O	3:C:620:LYS:HG3	2.11	0.50
3:C:753:GLU:C	3:C:755:ASP:H	2.19	0.50
5:E:229:TYR:CE2	5:E:272:ARG:NH1	2.77	0.50
5:E:276:ILE:C	5:E:277:PHE:CD1	2.89	0.50
15:H:51:A:N6	15:H:63:G:O6	2.44	0.50
35:O:149:LYS:NZ	35:O:290:LYS:HG3	2.26	0.50
38:S:10:GLN:HA	38:S:29:TRP:CE2	2.46	0.50
45:Z:574:ASN:O	45:Z:576:PHE:N	2.44	0.50
1:A:227:ARG:H	1:A:417:ARG:HA	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:264:PHE:CE1	1:A:459:LEU:CD1	2.81	0.50
1:A:1700:GLY:O	1:A:1717:ASN:N	2.41	0.50
3:C:94:ILE:HG21	39:T:259:PRO:HB3	1.92	0.50
3:C:387:ASP:O	3:C:389:ASP:OD1	2.30	0.50
14:G:-12:G:O2'	14:G:-11:G:O5'	2.30	0.50
15:H:153:A:C2'	15:H:154:C:C5'	2.86	0.50
15:H:182:U:C2'	15:H:183:G:H5'	2.41	0.50
21:1:1156:GLU:O	26:6:38:ARG:NH1	2.45	0.50
23:3:506:LEU:HB3	23:3:547:CYS:SG	2.52	0.50
27:7:32:LEU:HA	27:7:35:GLN:HG2	1.93	0.50
35:O:44:GLU:HA	35:O:50:ARG:O	2.10	0.50
37:R:178:ARG:CD	37:R:194:GLN:HE22	2.07	0.50
37:R:434:TYR:CD1	45:Z:616:VAL:CB	2.95	0.50
39:T:329:HIS:CE1	39:T:355:ARG:HG3	2.46	0.50
41:V:576:THR:O	41:V:580:ARG:N	2.36	0.50
1:A:305:ARG:HE	3:C:854:ARG:NH1	2.10	0.50
1:A:338:VAL:HB	3:C:867:PRO:HG3	1.93	0.50
1:A:1379:PHE:O	1:A:1382:SER:OG	2.17	0.50
3:C:134:LEU:HD23	3:C:226:VAL:HB	1.94	0.50
3:C:140:HIS:HB3	3:C:230:ASP:N	2.26	0.50
3:C:456:GLY:O	3:C:457:VAL:HG13	2.11	0.50
3:C:659:VAL:HG12	3:C:660:VAL:N	2.26	0.50
5:E:277:PHE:CE2	5:E:300:ILE:HD12	2.46	0.50
13:F:35:A:C8	14:G:12:G:N1	2.80	0.50
13:F:37:C:N4	14:G:5:G:OP1	2.44	0.50
14:G:-4:A:H2'	14:G:-3:A:H8	1.76	0.50
21:1:897:LEU:HD11	21:1:932:ILE:HD13	1.93	0.50
23:3:996:ILE:HD13	23:3:1041:TYR:HD1	1.75	0.50
35:O:253:TYR:OH	38:S:120:GLN:HA	2.12	0.50
37:R:125:MET:O	37:R:126:ASN:HB3	2.11	0.50
37:R:434:TYR:CE2	37:R:436:VAL:HG22	2.43	0.50
38:S:35:THR:C	38:S:129:PHE:CE1	2.73	0.50
39:T:306:CYS:SG	39:T:336:VAL:CB	2.97	0.50
44:Y:86:ASP:HB2	45:Z:502:ALA:HB3	1.93	0.50
1:A:693:ILE:O	1:A:697:MET:N	2.42	0.50
1:A:1591:MET:SD	1:A:1611:LYS:NZ	2.75	0.50
1:A:2298:LEU:CD1	4:D:1285:SER:CA	2.89	0.50
3:C:93:ILE:HG21	39:T:218:TRP:CE2	2.46	0.50
3:C:499:GLY:C	3:C:500:THR:HG23	2.36	0.50
3:C:846:VAL:HG22	3:C:887:LEU:HD11	1.94	0.50
14:G:-11:G:OP1	40:U:21:ARG:NE	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:G:132:G:H2'	14:G:133:A:C8	2.46	0.50
20:v:51:LEU:HB3	21:1:1141:LEU:HD12	0.59	0.50
21:1:822:ARG:HD3	44:Y:32:TYR:OH	2.12	0.50
23:3:488:GLY:C	23:3:490:THR:H	2.19	0.50
23:3:685:ASP:OD1	23:3:686:LEU:N	2.44	0.50
23:3:807:TYR:HE1	23:3:861:GLN:HG3	1.76	0.50
29:L:216:PHE:CZ	35:O:112:VAL:CG1	2.95	0.50
31:K:196:GLU:O	31:K:199:ILE:CG1	2.59	0.50
37:R:101:ILE:O	37:R:104:GLN:HG2	2.08	0.50
39:T:297:HIS:HD2	39:T:338:CYS:SG	2.34	0.50
1:A:117:PRO:HG2	1:A:131:GLU:HB2	1.94	0.50
1:A:331:TRP:C	1:A:331:TRP:CE3	2.90	0.50
2:B:100:C:H2'	2:B:101:U:C6	2.47	0.50
3:C:336:TYR:CD1	3:C:336:TYR:C	2.89	0.50
13:F:36:A:C3'	13:F:37:C:C5'	2.85	0.50
15:H:25:G:H2'	15:H:26:A:C8	2.45	0.50
15:H:46:U:O2'	15:H:47:U:OP2	2.25	0.50
15:H:70:C:O5'	15:H:70:C:H6	1.94	0.50
15:H:147:G:N2	15:H:148:C:C2	2.80	0.50
21:1:1003:VAL:HG23	21:1:1004:ILE:H	1.77	0.50
21:1:1132:LEU:O	21:1:1135:GLU:N	2.45	0.50
23:3:300:PHE:CG	23:3:312:LYS:HE2	2.46	0.50
31:K:188:LEU:C	31:K:188:LEU:HD13	2.36	0.50
34:N:105:CYS:SG	34:N:119:CYS:SG	3.10	0.50
36:P:41:ILE:HD11	39:T:318:ARG:HA	1.92	0.50
36:P:210:PHE:CG	39:T:201:SER:OG	2.64	0.50
46:x:443:ASN:HA	46:x:446:MET:O	2.10	0.50
46:x:452:GLN:O	46:x:498:ASP:N	2.44	0.50
1:A:121:HIS:HA	1:A:481:PHE:O	2.12	0.50
1:A:402:ILE:HD13	3:C:268:LYS:HE3	1.94	0.50
1:A:434:HIS:C	1:A:434:HIS:HD1	2.19	0.50
1:A:588:LEU:O	1:A:1551:PHE:CD1	2.65	0.50
1:A:1209:HIS:CG	1:A:1210:LYS:H	2.30	0.50
1:A:1667:ARG:HD2	1:A:1679:TYR:CE2	2.46	0.50
3:C:62:ASP:HB3	36:P:206:LYS:HZ3	1.76	0.50
18:w:150:ILE:CB	18:w:154:ALA:HB3	2.41	0.50
35:O:222:ARG:HA	35:O:288:PHE:HD2	1.76	0.50
1:A:89:LEU:CD2	1:A:656:LEU:HD22	2.42	0.50
1:A:259:ASP:C	1:A:259:ASP:OD1	2.55	0.50
1:A:948:PRO:O	1:A:951:LEU:HB2	2.12	0.50
1:A:1700:GLY:H	1:A:1717:ASN:HD22	1.60	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2113:LYS:HE2	4:D:1229:ASP:CA	2.41	0.50
3:C:66:TYR:CD2	39:T:457:GLY:CA	2.79	0.50
3:C:244:LYS:CA	3:C:292:TYR:CD2	2.92	0.50
23:3:550:ASN:HD21	23:3:595:VAL:N	2.10	0.50
23:3:1050:PHE:HB3	23:3:1167:TYR:HE2	1.75	0.50
23:3:1147:HIS:O	23:3:1151:GLU:HB2	2.10	0.50
39:T:281:ILE:HD12	39:T:282:ARG:HG2	1.92	0.50
42:W:290:GLY:HA2	42:W:573:GLY:HA2	1.94	0.50
1:A:36:LYS:HZ1	42:W:163:GLN:CB	2.25	0.50
1:A:1402:ARG:HH21	45:Z:573:PRO:HG3	1.77	0.50
3:C:259:LYS:HE2	3:C:262:ARG:HH11	1.77	0.50
5:E:228:THR:HG22	5:E:229:TYR:HD1	1.77	0.50
13:F:41:A:H2'	13:F:42:C:C6	2.47	0.50
15:H:74:U:O5'	15:H:74:U:H6	1.95	0.50
21:1:595:GLU:O	21:1:599:ASN:ND2	2.45	0.50
23:3:12:THR:HA	23:3:34:ARG:NH1	2.27	0.50
23:3:441:GLY:HA2	23:3:733:PRO:O	2.11	0.50
23:3:458:ALA:HB3	23:3:477:SER:HB3	1.94	0.50
23:3:527:ILE:HA	23:3:532:ARG:O	2.12	0.50
23:3:745:PHE:CZ	23:3:747:SER:HB3	2.46	0.50
23:3:819:MET:O	23:3:823:MET:HG3	2.12	0.50
43:X:282:LEU:HD23	43:X:295:ASP:HA	1.94	0.50
1:A:55:ASP:OD1	1:A:55:ASP:N	2.45	0.49
1:A:686:ARG:HH11	1:A:710:LEU:HD13	1.77	0.49
2:B:63:A:H4'	5:E:106:LYS:HZ2	1.76	0.49
3:C:499:GLY:O	3:C:500:THR:CG2	2.60	0.49
14:G:132:G:O4'	18:w:399:LEU:CD1	2.57	0.49
21:1:1040:GLY:HA2	21:1:1080:THR:HG22	1.94	0.49
23:3:4:TYR:HB2	23:3:1132:PHE:CZ	2.47	0.49
23:3:734:LEU:HD13	23:3:767:LEU:HD21	1.94	0.49
23:3:1188:ASN:O	23:3:1192:ASN:ND2	2.31	0.49
35:O:186:PRO:HD2	42:W:216:LEU:HA	1.93	0.49
36:P:66:ARG:HH11	36:P:66:ARG:CG	2.24	0.49
1:A:348:PRO:O	1:A:350:PHE:N	2.45	0.49
1:A:965:VAL:HG13	1:A:966:TRP:CD1	2.47	0.49
1:A:1403:LEU:O	37:R:412:ASP:CB	2.60	0.49
2:B:40:U:H3	14:G:-1:G:H22	1.59	0.49
3:C:116:MET:O	3:C:119:LEU:HB3	2.12	0.49
3:C:854:ARG:NH1	3:C:879:ASP:OD2	2.45	0.49
5:E:265:ARG:N	5:E:272:ARG:HH21	2.10	0.49
13:F:27:A:N9	35:O:181:TYR:CE2	2.80	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:181:G:N2	15:H:182:U:C2	2.80	0.49
21:1:717:THR:HG22	21:1:718:PRO:HD3	1.93	0.49
23:3:274:ARG:HG2	23:3:387:PHE:CE1	2.47	0.49
35:O:36:MET:HE2	35:O:57:TRP:CE3	2.46	0.49
38:S:34:LYS:HE3	38:S:78:TYR:CD2	2.47	0.49
42:W:430:ASN:O	42:W:447:TRP:CB	2.59	0.49
44:Y:48:THR:OG1	44:Y:49:GLU:OE1	2.30	0.49
1:A:152:ARG:CG	1:A:152:ARG:NH1	2.73	0.49
1:A:296:PHE:CD1	3:C:591:ALA:HB3	2.47	0.49
1:A:380:LEU:CB	3:C:354:ARG:CZ	2.88	0.49
1:A:409:ARG:N	1:A:410:PRO:HD2	2.26	0.49
1:A:596:TYR:CD1	14:G:-5:G:C4	3.01	0.49
3:C:78:GLU:OE1	39:T:198:ARG:NH2	2.45	0.49
3:C:297:ASN:HB3	3:C:298:LEU:HD13	1.95	0.49
3:C:493:PHE:HD2	3:C:551:LEU:HD21	1.76	0.49
3:C:715:GLY:HA2	3:C:729:ALA:HB1	1.93	0.49
5:E:164:PRO:O	5:E:166:LEU:HG	2.13	0.49
21:1:499:LYS:HD3	21:1:534:GLN:NE2	2.27	0.49
21:1:652:CYS:HB3	21:1:692:HIS:CE1	2.46	0.49
21:1:827:ARG:O	21:1:830:TYR:HB3	2.12	0.49
23:3:235:LEU:HG	23:3:250:ILE:HG13	1.93	0.49
23:3:1008:SER:OG	23:3:1009:PHE:N	2.45	0.49
34:N:59:TYR:CD1	42:W:187:SER:HA	2.48	0.49
35:O:225:PRO:CB	35:O:226:PRO:HD2	2.42	0.49
1:A:76:MET:SD	1:A:88:TYR:CE1	3.05	0.49
1:A:630:TRP:CD1	1:A:630:TRP:H	2.30	0.49
1:A:800:TYR:CB	3:C:59:LEU:HD13	2.43	0.49
1:A:1056:HIS:NE2	1:A:1060:GLU:OE2	2.44	0.49
3:C:62:ASP:HB3	36:P:206:LYS:NZ	2.27	0.49
3:C:66:TYR:CE2	36:P:211:VAL:HG11	2.45	0.49
3:C:349:PHE:CD1	3:C:356:PHE:HE1	2.22	0.49
15:H:37:U:H2'	15:H:38:A:H8	1.77	0.49
23:3:253:GLU:OE2	23:3:284:GLY:HA3	2.12	0.49
34:N:1:MET:HB3	34:N:2:PRO:HD3	1.94	0.49
35:O:147:LEU:HA	35:O:150:LEU:HG	1.94	0.49
37:R:433:ILE:HG13	37:R:434:TYR:O	2.12	0.49
45:Z:524:ARG:CD	45:Z:524:ARG:C	2.85	0.49
46:x:640:ARG:CB	46:x:667:ALA:CA	2.88	0.49
1:A:115:ASP:CB	1:A:486:LYS:HE2	2.43	0.49
1:A:1405:LEU:N	37:R:415:LEU:HD21	2.27	0.49
3:C:133:THR:O	3:C:226:VAL:CB	2.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:335:ASN:OD1	3:C:336:TYR:N	2.45	0.49
3:C:709:TRP:N	3:C:709:TRP:CD1	2.79	0.49
11:l:15:VAL:O	12:n:33:GLY:HA3	2.12	0.49
23:3:994:GLN:HE22	23:3:1037:SER:HA	1.78	0.49
32:I:511:LEU:CB	32:I:547:LEU:CA	2.91	0.49
35:O:106:ASP:OD1	35:O:107:MET:N	2.42	0.49
35:O:161:ARG:NH2	35:O:182:ARG:HD2	2.27	0.49
37:R:231:VAL:HG23	37:R:232:MET:N	2.26	0.49
45:Z:563:ARG:CG	45:Z:563:ARG:NH2	2.73	0.49
1:A:380:LEU:CD2	3:C:354:ARG:C	2.84	0.49
1:A:690:MET:HG3	1:A:694:LEU:HD12	1.95	0.49
1:A:1618:LYS:HD2	1:A:1626:CYS:H	1.78	0.49
1:A:1718:TRP:HZ3	1:A:1726:ILE:HD12	1.77	0.49
2:B:42:U:O4'	13:F:70:A:C4'	2.58	0.49
3:C:709:TRP:CD1	3:C:709:TRP:H	2.30	0.49
5:E:67:GLY:H	5:E:87:ASP:CG	2.20	0.49
5:E:266:PRO:HB3	29:L:785:GLN:HB2	1.95	0.49
13:F:36:A:C8	13:F:36:A:H5'	2.48	0.49
16:o:46:ALA:HB1	16:o:68:THR:C	2.34	0.49
21:1:805:TYR:CE1	21:1:809:GLU:HG3	2.46	0.49
23:3:23:SER:HA	23:3:94:PRO:HG3	1.95	0.49
23:3:483:LEU:HD11	23:3:493:GLU:HG3	1.94	0.49
23:3:755:VAL:HG13	23:3:762:LEU:HD11	1.93	0.49
23:3:794:SER:HB2	23:3:933:ASN:O	2.12	0.49
23:3:1048:ASP:OD1	23:3:1049:LYS:N	2.45	0.49
28:J:331:GLN:CG	37:R:98:TYR:OH	2.47	0.49
29:L:209:ASP:CG	35:O:111:ASP:N	2.63	0.49
35:O:55:PHE:CE1	37:R:199:MET:HE1	2.48	0.49
35:O:240:GLY:HA3	35:O:296:ARG:NH1	2.24	0.49
45:Z:526:ILE:N	45:Z:526:ILE:HD12	2.27	0.49
1:A:365:VAL:CG1	1:A:366:LYS:N	2.73	0.49
1:A:461:HIS:NE2	2:B:23:C:C5	2.80	0.49
1:A:800:TYR:HB3	3:C:59:LEU:HD13	1.95	0.49
1:A:1760:GLU:HB2	1:A:1761:PRO:HD2	1.93	0.49
3:C:140:HIS:O	3:C:258:ASN:HB3	2.13	0.49
3:C:363:SER:O	3:C:364:SER:CB	2.60	0.49
4:D:455:PHE:CB	23:3:573:GLN:HG2	2.43	0.49
14:G:-9:C:N3	40:U:18:TYR:CZ	2.77	0.49
18:w:485:ASN:ND2	23:3:976:LYS:N	2.57	0.49
21:1:1017:LEU:HD21	21:1:1058:ILE:HD11	1.93	0.49
21:1:1273:TYR:OH	21:1:1277:GLN:NE2	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:31:VAL:HG21	23:3:78:ILE:HD11	1.95	0.49
42:W:210:GLU:HA	42:W:213:GLN:CB	2.42	0.49
45:Z:597:ARG:HH12	45:Z:601:LEU:CD1	2.22	0.49
1:A:380:LEU:HB3	3:C:354:ARG:HH12	1.64	0.49
1:A:532:THR:HG21	14:G:2:U:H5'	1.88	0.49
2:B:20:G:OP1	2:B:20:G:H4'	2.12	0.49
3:C:73:TYR:CZ	39:T:487:LYS:CE	2.95	0.49
3:C:137:HIS:NE2	3:C:236:MET:CE	2.75	0.49
3:C:705:VAL:HG21	3:C:718:PHE:CZ	2.47	0.49
5:E:74:PHE:HE1	5:E:95:VAL:CG2	2.25	0.49
11:e:15:VAL:O	12:g:33:GLY:HA3	2.12	0.49
13:F:53:A:C6	13:F:54:G:C5	3.00	0.49
14:G:5:G:H2'	14:G:5:G:N3	2.28	0.49
14:G:155:U:H4'	14:G:156:U:OP2	2.13	0.49
15:H:107:A:C2	15:H:108:G:C4	3.01	0.49
15:H:143:A:N3	15:H:143:A:C3'	2.73	0.49
21:1:175:LYS:O	21:1:179:GLY:HA3	2.11	0.49
21:1:1134:ASN:ND2	22:2:534:GLN:HA	2.28	0.49
23:3:47:THR:HG23	23:3:49:LYS:H	1.77	0.49
23:3:700:LYS:NZ	23:3:740:GLU:O	2.41	0.49
23:3:785:PRO:HA	23:3:801:GLU:HA	1.95	0.49
24:4:32:LEU:HD21	24:4:79:LEU:HD21	1.94	0.49
35:O:189:PRO:CB	42:W:223:ARG:HA	2.40	0.49
36:P:189:ASP:C	36:P:191:ASP:N	2.68	0.49
37:R:55:LEU:CA	37:R:73:PRO:O	2.61	0.49
1:A:258:PHE:HZ	1:A:275:GLY:O	1.96	0.49
1:A:331:TRP:CZ2	3:C:896:PHE:CE1	3.01	0.49
1:A:347:LEU:HD13	1:A:351:TYR:OH	2.12	0.49
1:A:1393:ARG:O	1:A:1397:ILE:HG13	2.12	0.49
3:C:301:SER:O	3:C:303:LEU:N	2.44	0.49
3:C:499:GLY:O	3:C:500:THR:HG23	2.13	0.49
5:E:219:VAL:HB	5:E:229:TYR:HB2	1.95	0.49
20:v:56:CYS:SG	20:v:59:CYS:N	2.86	0.49
26:6:43:VAL:HG21	26:6:69:ALA:HB3	1.94	0.49
28:J:560:ALA:H	32:I:766:MET:CB	2.26	0.49
35:O:235:TYR:CD1	35:O:271:PHE:HE1	2.24	0.49
37:R:131:ASP:OD2	37:R:132:LEU:CD2	2.60	0.49
39:T:442:ARG:HB3	39:T:443:THR:HG23	1.95	0.49
44:Y:38:ILE:HG22	44:Y:90:THR:HG23	1.95	0.49
1:A:304:ILE:HD11	1:A:1342:TRP:HZ2	1.77	0.49
1:A:494:LEU:HD21	1:A:562:VAL:HG21	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:623:LYS:HG2	48:A:2401:IHP:O43	2.13	0.49
1:A:2073:TRP:CH2	1:A:2310:ARG:NH1	2.80	0.49
3:C:381:LEU:CD2	3:C:416:LEU:HD22	2.42	0.49
5:E:74:PHE:HE1	5:E:95:VAL:HG22	1.77	0.49
15:H:71:C:H2'	15:H:72:U:H6	1.75	0.49
35:O:155:PRO:HG3	37:R:188:PHE:HA	1.94	0.49
37:R:433:ILE:O	37:R:434:TYR:HB3	2.13	0.49
41:V:525:PHE:O	41:V:526:GLU:C	2.55	0.49
42:W:536:ASP:O	42:W:540:THR:N	2.42	0.49
1:A:44:ARG:CG	1:A:45:TYR:CE2	2.95	0.48
1:A:322:ASN:OD1	3:C:655:VAL:HB	2.12	0.48
1:A:380:LEU:N	3:C:354:ARG:CB	2.75	0.48
1:A:433:GLU:OE1	1:A:436:PRO:CB	2.54	0.48
1:A:2298:LEU:HD11	4:D:1265:GLN:CB	2.44	0.48
1:A:2303:GLU:CD	1:A:2303:GLU:H	2.19	0.48
3:C:82:GLN:HG3	39:T:237:LYS:HA	1.94	0.48
3:C:334:ILE:HD12	3:C:334:ILE:O	2.13	0.48
4:D:441:GLY:O	4:D:693:THR:N	2.36	0.48
5:E:153:PHE:N	5:E:153:PHE:CD1	2.78	0.48
13:F:26:U:H3'	13:F:27:A:C5'	2.37	0.48
15:H:45:C:N3	18:w:395:TRP:CB	2.75	0.48
21:1:408:PHE:HB2	25:5:49:ARG:NH1	2.28	0.48
23:3:669:LEU:HD22	23:3:673:VAL:HG21	1.93	0.48
37:R:118:ASP:OD1	37:R:232:MET:HE1	2.13	0.48
39:T:342:GLU:O	39:T:343:PRO:C	2.56	0.48
1:A:595:LYS:CE	1:A:644:ILE:HD11	2.38	0.48
1:A:794:TYR:CD2	1:A:1028:TYR:HB2	2.47	0.48
1:A:1457:HIS:CE1	37:R:424:SER:C	2.90	0.48
1:A:2149:PRO:O	1:A:2160:PRO:HD3	2.13	0.48
2:B:40:U:H3	14:G:-1:G:N2	2.11	0.48
3:C:508:LYS:HB3	3:C:566:THR:HG23	1.95	0.48
3:C:855:GLY:O	3:C:856:HIS:CB	2.44	0.48
5:E:162:ARG:HH22	5:E:204:THR:HA	1.74	0.48
13:F:54:G:N2	15:H:22:U:C2	2.81	0.48
14:G:11:A:N3	14:G:11:A:C3'	2.76	0.48
15:H:5:C:H2'	15:H:6:U:H6	1.78	0.48
21:1:483:ASP:OD1	21:1:484:GLU:N	2.46	0.48
28:J:360:ASP:HA	28:J:363:ARG:CG	2.44	0.48
38:S:131:ARG:HH12	38:S:133:CYS:CB	2.26	0.48
1:A:122:ILE:HD12	1:A:483:GLN:HG3	1.94	0.48
1:A:828:PRO:HG3	1:A:925:TYR:CZ	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1214:TRP:CZ2	1:A:1230:LEU:HD11	2.48	0.48
1:A:2097:ILE:HD12	1:A:2099:GLU:HB2	1.93	0.48
1:A:2268:LEU:CD2	4:D:1261:PRO:C	2.81	0.48
3:C:73:TYR:CE1	39:T:453:ALA:O	2.67	0.48
3:C:230:ASP:CG	3:C:259:LYS:HZ1	2.20	0.48
3:C:297:ASN:HD22	3:C:298:LEU:CD1	2.26	0.48
3:C:333:ASP:OD1	3:C:333:ASP:N	2.42	0.48
3:C:401:ILE:HD11	3:C:423:PHE:HB2	1.96	0.48
13:F:49:G:H2'	13:F:50:A:H8	1.78	0.48
14:G:-8:U:C5	40:U:16:ASN:HB3	2.48	0.48
14:G:138:A:H5''	29:L:12:ARG:NE	2.28	0.48
15:H:10:C:H2'	15:H:11:G:C8	2.40	0.48
23:3:157:PRO:HD2	26:6:16:GLY:HA2	1.95	0.48
23:3:870:ASN:ND2	23:3:873:GLN:H	2.10	0.48
34:N:65:TYR:OH	34:N:93:LYS:HE2	2.13	0.48
39:T:302:VAL:HG23	39:T:315:TRP:O	2.14	0.48
45:Z:604:LYS:HA	45:Z:607:VAL:HG23	1.94	0.48
1:A:273:ILE:CG2	1:A:274:PRO:HD2	2.43	0.48
1:A:296:PHE:CD2	3:C:656:ALA:N	2.81	0.48
1:A:2298:LEU:HD11	4:D:1285:SER:CA	2.43	0.48
3:C:291:MET:CG	3:C:292:TYR:CE1	2.96	0.48
3:C:443:VAL:O	3:C:447:PRO:CD	2.62	0.48
3:C:452:THR:O	3:C:577:PHE:CA	2.60	0.48
13:F:8:C:H6	13:F:8:C:C5'	2.15	0.48
13:F:66:C:H2'	13:F:67:G:O4'	2.12	0.48
14:G:-8:U:H2'	14:G:-7:C:O4'	2.13	0.48
14:G:9:C:H2'	14:G:10:U:C6	2.48	0.48
14:G:19:G:C5'	35:O:159:ARG:HD2	2.40	0.48
15:H:25:G:N3	15:H:26:A:C8	2.82	0.48
23:3:886:GLU:OE1	23:3:926:TYR:OH	2.24	0.48
23:3:1149:ARG:HH12	23:3:1161:LEU:HD13	1.79	0.48
28:J:339:TRP:C	37:R:116:TYR:CE2	2.92	0.48
28:J:406:PHE:HB3	28:J:411:MET:HG2	1.96	0.48
37:R:433:ILE:HG13	37:R:434:TYR:N	2.27	0.48
43:X:212:ASN:H	43:X:307:GLN:HE22	1.60	0.48
1:A:774:LYS:HG2	15:H:23:A:C8	2.48	0.48
1:A:1214:TRP:NE1	1:A:1276:GLU:OE1	2.23	0.48
1:A:2328:ALA:HB3	4:D:787:ALA:C	2.38	0.48
3:C:911:PRO:HB2	3:C:934:MET:HE3	1.95	0.48
13:F:45:A:H4'	13:F:46:G:OP2	2.14	0.48
13:F:53:A:C6	15:H:25:G:C4	3.02	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:1167:TYR:O	21:1:1170:THR:OG1	2.25	0.48
23:3:930:LEU:HA	23:3:937:LEU:HD23	1.95	0.48
27:7:40:TYR:HA	27:7:43:TYR:CD2	2.49	0.48
35:O:229:LYS:HA	35:O:277:ARG:HH22	1.78	0.48
37:R:103:ARG:CG	37:R:103:ARG:NH1	2.75	0.48
37:R:419:SER:C	37:R:420:LYS:O	2.55	0.48
39:T:185:MET:CB	39:T:186:PRO:CD	2.90	0.48
39:T:213:GLU:HB2	39:T:218:TRP:O	2.14	0.48
1:A:279:PHE:CZ	1:A:452:LYS:HG3	2.49	0.48
1:A:593:ARG:HE	14:G:-4:A:P	2.37	0.48
1:A:718:ARG:HH21	37:R:259:LYS:CE	2.25	0.48
2:B:63:A:H5"	5:E:106:LYS:HZ3	1.77	0.48
3:C:350:ASN:HB3	3:C:353:THR:HG23	1.94	0.48
3:C:445:ALA:O	3:C:449:ILE:HG13	2.12	0.48
3:C:678:THR:HG23	3:C:683:ASN:CA	2.43	0.48
3:C:736:GLY:N	3:C:770:PHE:HE2	2.10	0.48
21:1:1212:LEU:HD13	21:1:1237:LEU:HD13	1.96	0.48
23:3:142:TYR:CE1	23:3:157:PRO:HB3	2.48	0.48
23:3:565:TYR:CG	23:3:619:LEU:HD13	2.48	0.48
23:3:1055:VAL:HG23	23:3:1093:MET:HE2	1.95	0.48
35:O:27:CYS:O	35:O:28:LEU:C	2.56	0.48
37:R:215:ASN:HD22	37:R:216:LYS:N	2.11	0.48
41:V:549:LYS:O	41:V:552:ALA:CB	2.60	0.48
1:A:247:THR:HG1	1:A:429:ASN:HB3	1.76	0.48
1:A:279:PHE:CE1	1:A:452:LYS:HE3	2.48	0.48
1:A:330:THR:O	1:A:331:TRP:CB	2.62	0.48
1:A:409:ARG:HD2	1:A:409:ARG:O	2.14	0.48
1:A:1295:ILE:HG13	1:A:1296:GLN:N	2.29	0.48
1:A:2328:ALA:CB	4:D:787:ALA:C	2.87	0.48
3:C:135:CYS:SG	3:C:227:LEU:HA	2.54	0.48
3:C:149:LEU:CA	3:C:427:PHE:CE2	2.97	0.48
3:C:349:PHE:HB2	3:C:356:PHE:CE1	2.48	0.48
3:C:514:TYR:CD1	3:C:515:THR:N	2.82	0.48
15:H:83:A:C2	15:H:84:C:N3	2.82	0.48
17:p:152:ILE:O	17:p:222:TYR:HA	2.13	0.48
21:1:634:VAL:O	21:1:637:SER:OG	2.27	0.48
23:3:457:ASN:HD21	23:3:504:PRO:HB3	1.79	0.48
23:3:842:PHE:HD2	23:3:843:LEU:HD12	1.78	0.48
23:3:926:TYR:HE1	23:3:942:LYS:HG3	1.77	0.48
28:J:273:TYR:CZ	37:R:228:PRO:CB	2.82	0.48
37:R:55:LEU:C	37:R:73:PRO:O	2.56	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:HIS:O	1:A:123:THR:N	2.47	0.48
1:A:1119:ASP:OD2	1:A:1124:ASN:N	2.44	0.48
1:A:1332:HIS:HB3	1:A:1359:HIS:HE1	1.78	0.48
1:A:2073:TRP:CD1	1:A:2073:TRP:C	2.91	0.48
3:C:82:GLN:O	39:T:202:GLY:HA3	2.13	0.48
3:C:457:VAL:HG12	3:C:462:GLY:HA3	1.96	0.48
3:C:477:HIS:HD1	3:C:478:THR:N	2.12	0.48
5:E:243:LEU:HD11	5:E:247:GLY:CA	2.41	0.48
14:G:17:U:H2'	14:G:18:A:C8	2.49	0.48
15:H:83:A:C2	15:H:84:C:C4	3.01	0.48
18:w:444:ALA:O	18:w:446:PHE:N	2.47	0.48
21:1:1297:ARG:NH1	27:7:39:SER:OG	2.46	0.48
23:3:462:VAL:O	23:3:472:ALA:N	2.46	0.48
23:3:476:VAL:O	23:3:482:THR:HA	2.14	0.48
39:T:384:HIS:O	39:T:385:TYR:HB3	2.13	0.48
41:V:576:THR:O	41:V:579:SER:N	2.47	0.48
42:W:528:GLY:O	42:W:552:VAL:CB	2.62	0.48
1:A:369:GLU:C	1:A:371:LEU:N	2.65	0.48
1:A:592:TYR:O	1:A:595:LYS:O	2.32	0.48
1:A:1315:VAL:HG12	1:A:1538:TRP:CE3	2.49	0.48
3:C:128:LEU:O	3:C:199:LEU:N	2.37	0.48
3:C:690:GLU:HB2	3:C:691:PRO:HD2	1.95	0.48
13:F:44:G:H2'	22:2:554:ARG:HG2	1.96	0.48
14:G:20:A:OP2	35:O:159:ARG:HD3	2.14	0.48
15:H:37:U:H2'	15:H:38:A:C8	2.49	0.48
15:H:73:C:HO2'	15:H:74:U:H5'	1.77	0.48
18:w:479:TYR:H	18:w:484:GLY:HA3	1.79	0.48
22:2:636:MET:HE1	24:4:35:GLN:O	2.14	0.48
22:2:652:GLY:N	22:2:655:SER:O	2.45	0.48
23:3:21:ASN:HD21	23:3:28:GLN:HG2	1.77	0.48
23:3:58:VAL:HG12	23:3:1155:LEU:HB3	1.95	0.48
23:3:891:VAL:HA	23:3:906:LEU:O	2.13	0.48
23:3:1057:ARG:HG2	23:3:1058:LEU:O	2.13	0.48
37:R:184:GLN:O	37:R:188:PHE:HB2	2.13	0.48
44:Y:110:ASP:OD1	44:Y:111:HIS:N	2.43	0.48
1:A:232:LEU:HD13	1:A:404:LEU:HD12	1.95	0.48
1:A:238:LEU:HB3	1:A:411:PHE:HE2	1.79	0.48
1:A:380:LEU:HB2	3:C:354:ARG:CZ	2.44	0.48
1:A:380:LEU:N	3:C:354:ARG:CG	2.77	0.48
1:A:412:ASN:OD1	1:A:413:LEU:HD23	2.13	0.48
1:A:731:LEU:HD23	1:A:736:GLU:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1551:PHE:O	1:A:1553:VAL:HG23	2.14	0.48
1:A:1607:GLU:HB2	1:A:1634:SER:HA	1.96	0.48
1:A:1723:LYS:HB3	1:A:1724:PRO:HD3	1.95	0.48
3:C:93:ILE:O	3:C:94:ILE:CB	2.62	0.48
3:C:145:PHE:HB2	3:C:312:SER:CB	2.32	0.48
13:F:27:A:N3	35:O:181:TYR:HE2	1.98	0.48
16:o:46:ALA:CA	16:o:68:THR:O	2.61	0.48
21:1:208:PRO:N	21:1:656:LYS:HE3	2.29	0.48
23:3:981:CYS:SG	23:3:1021:LEU:HG	2.54	0.48
37:R:402:ASN:HB2	43:X:192:ARG:CG	2.43	0.48
37:R:415:LEU:C	37:R:417:ASN:N	2.67	0.48
1:A:203:VAL:HG12	1:A:207:PHE:CD1	2.49	0.47
1:A:758:ARG:HD2	1:A:775:ASN:ND2	2.28	0.47
1:A:1183:PRO:HA	1:A:1201:ARG:HE	1.78	0.47
1:A:1548:TYR:CG	14:G:-6:C:C5	3.02	0.47
1:A:2325:VAL:HG11	4:D:789:MET:HA	1.94	0.47
3:C:557:GLN:N	3:C:558:PRO:HD2	2.29	0.47
5:E:263:ASP:OD1	5:E:272:ARG:HB3	2.13	0.47
13:F:44:G:N2	14:G:3:A:C8	2.82	0.47
21:1:209:GLY:HA3	21:1:614:ARG:NH1	2.29	0.47
21:1:823:MET:HE3	21:1:829:ASN:HB3	1.95	0.47
23:3:353:PHE:HB3	23:3:406:PRO:HD3	1.96	0.47
23:3:550:ASN:OD1	23:3:551:GLN:N	2.41	0.47
23:3:814:GLN:O	23:3:818:GLN:HB2	2.13	0.47
26:6:19:ILE:HD12	26:6:42:LEU:HD21	1.96	0.47
28:J:273:TYR:CD2	37:R:228:PRO:HG3	2.49	0.47
37:R:120:VAL:CG2	37:R:121:PRO:HD2	2.44	0.47
43:X:246:TYR:H	43:X:386:ASP:HA	1.79	0.47
1:A:312:TYR:N	1:A:312:TYR:CD1	2.78	0.47
1:A:1045:GLY:HA3	1:A:1090:ARG:NH2	2.29	0.47
1:A:1270:LEU:HD12	1:A:1274:PHE:CD2	2.49	0.47
3:C:753:GLU:O	3:C:755:ASP:N	2.45	0.47
5:E:269:PRO:O	5:E:270:LYS:CB	2.54	0.47
13:F:12:G:H2'	13:F:13:G:O4'	2.14	0.47
15:H:151:C:C2	15:H:152:G:N7	2.82	0.47
21:1:1124:SER:O	21:1:1127:THR:OG1	2.28	0.47
21:1:1212:LEU:HD22	21:1:1246:MET:HE1	1.96	0.47
23:3:1095:TYR:CZ	23:3:1164:ARG:HD2	2.49	0.47
26:6:23:CYS:HB3	26:6:58:CYS:HB2	1.97	0.47
27:7:69:MET:HA	27:7:72:MET:HG2	1.96	0.47
28:J:436:TYR:OH	28:J:458:PHE:HA	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:O:253:TYR:OH	38:S:120:GLN:CG	2.62	0.47
39:T:416:ILE:O	39:T:416:ILE:HD13	2.14	0.47
41:V:527:GLY:O	41:V:530:LYS:N	2.47	0.47
41:V:625:ARG:O	41:V:629:ASN:CB	2.62	0.47
1:A:210:HIS:C	1:A:210:HIS:CD2	2.92	0.47
1:A:385:GLU:OE1	1:A:386:PRO:HD2	2.14	0.47
1:A:388:LEU:CD1	3:C:379:LYS:HB3	2.45	0.47
1:A:1258:LYS:HE2	37:R:432:GLU:CA	2.44	0.47
3:C:66:TYR:OH	36:P:216:ARG:HD2	2.13	0.47
3:C:73:TYR:HE1	39:T:453:ALA:O	1.97	0.47
3:C:441:PRO:O	3:C:444:GLY:CA	2.61	0.47
3:C:449:ILE:HD12	3:C:466:SER:OG	2.13	0.47
3:C:673:LYS:HB3	3:C:688:ILE:HG22	1.96	0.47
5:E:178:LEU:CD2	5:E:208:ILE:HD13	2.44	0.47
14:G:138:A:H2'	14:G:139:U:C6	2.49	0.47
21:1:1252:GLN:HG2	22:2:492:LYS:HA	1.96	0.47
23:3:240:GLY:HA3	23:3:246:SER:HB2	1.95	0.47
23:3:867:ARG:HD3	23:3:869:MET:HE3	1.95	0.47
27:7:33:VAL:HG23	27:7:75:PRO:HG2	1.96	0.47
37:R:73:PRO:HG2	37:R:74:LEU:H	1.79	0.47
37:R:189:ASN:HD21	37:R:195:ARG:CZ	2.26	0.47
37:R:250:LYS:HD3	37:R:250:LYS:C	2.39	0.47
38:S:9:TRP:CE3	38:S:11:PRO:CD	2.95	0.47
44:Y:63:VAL:HG23	44:Y:64:ASN:H	1.78	0.47
1:A:1192:PHE:HE1	1:A:1274:PHE:CD1	2.32	0.47
1:A:1439:ARG:O	1:A:1443:LYS:HG2	2.15	0.47
3:C:240:GLU:OE2	3:C:292:TYR:OH	2.18	0.47
3:C:438:ILE:CD1	3:C:438:ILE:N	2.76	0.47
14:G:17:U:H2'	14:G:18:A:H8	1.79	0.47
14:G:149:G:N2	14:G:150:U:H2'	2.29	0.47
21:1:464:LEU:HD23	21:1:478:LEU:HD21	1.95	0.47
21:1:781:ASP:HB3	21:1:784:MET:HB2	1.95	0.47
23:3:54:LEU:HD22	23:3:98:MET:HA	1.97	0.47
23:3:120:PHE:HB2	23:3:133:SER:OG	2.15	0.47
26:6:21:ARG:HG3	26:6:56:GLY:HA2	1.96	0.47
26:6:57:ARG:HD2	26:6:62:GLY:C	2.40	0.47
36:P:228:ILE:CD1	36:P:228:ILE:N	2.78	0.47
41:V:585:ILE:O	41:V:586:PHE:C	2.58	0.47
42:W:491:GLN:O	42:W:492:ASN:C	2.57	0.47
1:A:277:PRO:HA	1:A:448:GLN:HG3	1.96	0.47
1:A:332:TYR:C	1:A:332:TYR:CD1	2.92	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:340:ILE:HD13	1:A:340:ILE:N	2.29	0.47
1:A:546:LEU:HD11	1:A:595:LYS:CG	2.43	0.47
1:A:1353:PHE:HE2	40:U:22:ASN:CG	2.23	0.47
1:A:1548:TYR:CD2	14:G:-6:C:O2'	2.64	0.47
1:A:2252:LEU:HD23	1:A:2253:PRO:HD2	1.96	0.47
3:C:73:TYR:OH	39:T:487:LYS:CE	2.62	0.47
3:C:185:PRO:HD3	3:C:482:TYR:CE1	2.50	0.47
5:E:161:ARG:HH11	5:E:161:ARG:CG	2.26	0.47
13:F:22:A:H3'	34:N:115:THR:HG21	1.96	0.47
21:1:869:MET:HE3	21:1:913:GLY:HA3	1.96	0.47
21:1:1172:LEU:HA	22:2:522:PHE:HE1	1.79	0.47
23:3:354:GLY:HA3	23:3:432:ARG:NH1	2.30	0.47
23:3:539:PRO:HD2	23:3:558:LEU:HD21	1.95	0.47
36:P:192:VAL:HG12	36:P:193:VAL:N	2.29	0.47
37:R:103:ARG:NH2	37:R:110:LYS:O	2.40	0.47
37:R:178:ARG:CD	37:R:194:GLN:NE2	2.72	0.47
1:A:323:LEU:N	1:A:324:PRO:CD	2.77	0.47
1:A:338:VAL:HB	3:C:867:PRO:CG	2.45	0.47
1:A:380:LEU:H	3:C:354:ARG:HB3	1.79	0.47
1:A:2148:VAL:O	1:A:2150:GLN:HG2	2.14	0.47
1:A:2310:ARG:HH11	1:A:2310:ARG:CG	2.27	0.47
2:B:42:U:H2'	2:B:43:U:O4'	2.13	0.47
3:C:507:VAL:HG12	3:C:508:LYS:N	2.29	0.47
14:G:-5:G:O2'	14:G:-4:A:H8	1.98	0.47
15:H:57:A:H2'	15:H:58:U:O4'	2.14	0.47
20:v:58:LEU:HD23	20:v:82:LEU:CA	2.44	0.47
21:1:404:LEU:HD23	25:5:47:GLN:CD	2.39	0.47
21:1:754:ILE:HA	21:1:757:MET:HE2	1.96	0.47
21:1:1140:GLU:O	21:1:1144:GLN:HG3	2.15	0.47
28:J:216:ASP:O	28:J:219:GLU:N	2.47	0.47
28:J:375:ASP:O	28:J:376:VAL:C	2.58	0.47
37:R:51:ILE:N	37:R:52:PRO:CD	2.77	0.47
37:R:90:VAL:HB	38:S:20:MET:SD	2.55	0.47
38:S:34:LYS:HE2	38:S:78:TYR:CD2	2.48	0.47
39:T:318:ARG:HH11	39:T:319:THR:CG2	2.28	0.47
1:A:32:GLU:CD	1:A:36:LYS:HE3	2.39	0.47
1:A:549:GLU:CD	1:A:552:ARG:NH1	2.72	0.47
1:A:735:ILE:O	1:A:738:MET:HB3	2.15	0.47
1:A:1241:HIS:ND1	1:A:1287:LEU:HD11	2.29	0.47
3:C:749:THR:O	3:C:753:GLU:HB2	2.14	0.47
4:D:863:THR:CB	23:3:599:GLU:C	2.88	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:255:MET:C	5:E:257:ASN:H	2.22	0.47
18:w:485:ASN:HA	23:3:978:LEU:CG	2.44	0.47
21:1:903:GLN:HE22	21:1:910:MET:HG3	1.80	0.47
23:3:18:ILE:HD13	23:3:65:LEU:HG	1.96	0.47
23:3:446:GLU:CD	23:3:763:ARG:HD3	2.38	0.47
23:3:458:ALA:C	23:3:757:ILE:HG12	2.39	0.47
23:3:498:GLY:HA3	23:3:531:LYS:NZ	2.30	0.47
23:3:554:VAL:HB	23:3:566:PHE:HB2	1.97	0.47
23:3:624:CYS:SG	23:3:625:LEU:HD13	2.54	0.47
23:3:675:LEU:HD23	23:3:686:LEU:HD11	1.96	0.47
23:3:931:VAL:O	23:3:936:LYS:N	2.40	0.47
23:3:1032:TRP:O	23:3:1048:ASP:HA	2.15	0.47
28:J:273:TYR:CE2	37:R:228:PRO:HB3	2.46	0.47
34:N:27:GLN:HE21	34:N:31:GLU:HG2	1.79	0.47
35:O:236:VAL:HB	35:O:270:ALA:O	2.15	0.47
36:P:227:TYR:N	36:P:227:TYR:CD1	2.81	0.47
37:R:129:ASP:HB3	37:R:131:ASP:CG	2.40	0.47
38:S:125:LYS:HE3	38:S:125:LYS:N	2.30	0.47
39:T:257:ARG:HD3	39:T:301:ASP:OD1	2.14	0.47
41:V:467:LEU:O	41:V:468:ASP:CB	2.62	0.47
44:Y:40:LEU:HB2	44:Y:43:LEU:HD11	1.96	0.47
1:A:195:LEU:H	1:A:195:LEU:HD12	1.80	0.47
1:A:229:GLN:CB	1:A:415:SER:HB2	2.45	0.47
1:A:1455:TRP:CE3	1:A:1456:THR:HB	2.50	0.47
1:A:2314:PHE:HB3	4:D:1125:SER:N	2.29	0.47
3:C:115:GLU:O	3:C:118:PHE:CA	2.61	0.47
3:C:457:VAL:CA	3:C:462:GLY:HA3	2.44	0.47
7:i:57:LYS:CA	18:w:316:ARG:O	2.63	0.47
21:1:207:THR:HA	21:1:656:LYS:NZ	2.28	0.47
21:1:699:GLN:HA	21:1:702:ARG:CZ	2.45	0.47
23:3:164:ASN:ND2	23:3:189:TYR:OH	2.34	0.47
23:3:304:GLN:HA	23:3:309:ASP:O	2.15	0.47
23:3:931:VAL:HG12	23:3:932:ASN:N	2.26	0.47
25:5:14:PRO:HB2	25:5:16:GLU:OE1	2.15	0.47
32:I:712:VAL:O	32:I:713:ARG:C	2.57	0.47
39:T:246:ILE:HB	39:T:267:ASP:OD1	2.15	0.47
41:V:547:VAL:O	41:V:548:ALA:C	2.58	0.47
1:A:134:TRP:HB3	1:A:418:THR:HG22	1.95	0.47
1:A:596:TYR:CZ	14:G:-5:G:C5	3.03	0.47
1:A:695:ASP:HB3	39:T:374:SER:CB	2.38	0.47
1:A:1608:THR:HG22	1:A:1632:PHE:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:42:U:O5'	2:B:42:U:H6	1.97	0.47
21:1:535:ILE:O	21:1:538:LEU:N	2.47	0.47
21:1:760:GLU:N	21:1:760:GLU:OE1	2.47	0.47
21:1:1132:LEU:HD11	21:1:1150:SER:OG	2.14	0.47
23:3:5:ASN:OD1	23:3:6:LEU:N	2.47	0.47
23:3:212:GLU:OE1	23:3:223:LYS:HD2	2.15	0.47
35:O:219:THR:O	35:O:220:MET:C	2.58	0.47
37:R:67:ILE:HG22	37:R:69:VAL:HG21	1.97	0.47
46:x:452:GLN:N	46:x:496:MET:O	2.45	0.47
1:A:91:ALA:O	1:A:94:TYR:N	2.43	0.47
1:A:331:TRP:CZ2	3:C:896:PHE:HE1	2.33	0.47
1:A:596:TYR:CE1	14:G:-5:G:C4	3.03	0.47
2:B:29:A:O2'	2:B:30:A:H5'	2.15	0.47
3:C:470:PRO:CA	3:C:499:GLY:HA2	2.42	0.47
3:C:490:PHE:CE1	3:C:612:LYS:HD2	2.49	0.47
13:F:49:G:H2'	13:F:50:A:C8	2.50	0.47
14:G:156:U:P	14:G:156:U:H3'	2.54	0.47
15:H:6:U:H2'	15:H:7:U:H6	1.80	0.47
15:H:47:U:H4'	15:H:48:A:OP1	2.15	0.47
15:H:153:A:C8	15:H:154:C:H5'	2.50	0.47
20:v:18:SER:O	20:v:19:SER:C	2.58	0.47
22:2:642:PRO:HG3	22:2:648:LEU:HD22	1.97	0.47
23:3:182:PHE:O	23:3:210:PHE:HA	2.15	0.47
23:3:482:THR:HG23	23:3:503:THR:O	2.15	0.47
28:J:255:LEU:CD2	29:L:235:LEU:HD13	2.38	0.47
1:A:434:HIS:ND1	1:A:434:HIS:C	2.73	0.46
1:A:748:ASP:OD2	39:T:484:LYS:NZ	2.43	0.46
1:A:755:HIS:HE1	36:P:223:PHE:CB	2.14	0.46
1:A:1256:PHE:CZ	1:A:1302:GLY:HA3	2.51	0.46
1:A:2121:ARG:HA	1:A:2121:ARG:HD2	1.55	0.46
3:C:82:GLN:HG3	39:T:238:LEU:N	2.30	0.46
3:C:244:LYS:HG3	3:C:292:TYR:CD2	2.50	0.46
3:C:571:ASN:O	3:C:572:GLU:HB3	2.16	0.46
17:p:179:GLU:CB	17:p:193:GLU:CB	2.93	0.46
21:1:815:PHE:HA	21:1:819:TRP:HD1	1.81	0.46
21:1:1058:ILE:O	21:1:1062:LEU:HG	2.16	0.46
23:3:145:ASN:O	23:3:153:THR:OG1	2.26	0.46
23:3:248:VAL:HG23	23:3:250:ILE:HD11	1.96	0.46
23:3:536:TRP:CG	23:3:566:PHE:HZ	2.33	0.46
35:O:292:ILE:HG23	35:O:296:ARG:C	2.40	0.46
36:P:64:GLU:OE2	36:P:68:ARG:NE	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:299:ILE:HD12	3:C:921:LEU:HD22	1.97	0.46
1:A:1209:HIS:CG	1:A:1210:LYS:N	2.83	0.46
1:A:1212:GLY:HA3	1:A:1280:ASN:ND2	2.31	0.46
1:A:1399:GLN:C	1:A:1401:ARG:H	2.24	0.46
2:B:41:U:H2'	2:B:42:U:C6	2.49	0.46
3:C:262:ARG:HG2	50:C:1500:GTP:N2	2.30	0.46
3:C:350:ASN:CB	3:C:353:THR:HG23	2.45	0.46
5:E:274:VAL:C	5:E:275:LYS:HG3	2.40	0.46
13:F:78:A:H8	13:F:78:A:OP2	1.98	0.46
15:H:150:U:H2'	15:H:151:C:C6	2.50	0.46
21:1:732:TRP:HB2	21:1:765:TYR:HE1	1.79	0.46
21:1:738:HIS:CE1	21:1:746:PHE:HE2	2.32	0.46
21:1:1169:VAL:HG12	21:1:1173:LEU:HG	1.97	0.46
23:3:28:GLN:NE2	23:3:343:LYS:HG2	2.31	0.46
23:3:1005:VAL:O	23:3:1032:TRP:HA	2.15	0.46
28:J:239:ARG:C	28:J:239:ARG:HD3	2.40	0.46
34:N:128:VAL:HG11	34:N:130:ARG:HB3	1.96	0.46
36:P:188:TRP:C	36:P:190:ASP:H	2.21	0.46
38:S:13:ASN:ND2	38:S:24:VAL:CG1	2.79	0.46
38:S:101:ALA:HB1	42:W:94:GLY:HA3	1.96	0.46
1:A:232:LEU:O	1:A:404:LEU:HD11	2.16	0.46
1:A:298:ASP:OD1	1:A:300:ASN:N	2.48	0.46
1:A:437:ALA:O	1:A:439:GLN:HG2	2.15	0.46
1:A:532:THR:CG2	14:G:2:U:OP1	2.63	0.46
1:A:844:GLU:O	1:A:848:GLU:HG2	2.15	0.46
1:A:982:GLU:HG3	1:A:1169:GLN:HG3	1.97	0.46
3:C:221:ILE:HG23	3:C:495:ARG:HB3	1.96	0.46
5:E:87:ASP:O	5:E:88:ARG:CG	2.63	0.46
21:1:728:LEU:O	21:1:731:LEU:N	2.48	0.46
23:3:274:ARG:NH2	23:3:307:GLN:OE1	2.48	0.46
35:O:185:LYS:CD	42:W:215:GLU:CB	2.72	0.46
37:R:195:ARG:HB3	37:R:195:ARG:HH11	1.80	0.46
46:x:716:LYS:N	46:x:748:GLU:O	2.47	0.46
1:A:97:HIS:HD2	1:A:473:PHE:HZ	1.59	0.46
1:A:338:VAL:HG21	3:C:867:PRO:HD3	1.97	0.46
1:A:1305:SER:HB2	1:A:1310:ARG:HH12	1.71	0.46
1:A:1370:ARG:NH2	41:V:506:PHE:CB	2.78	0.46
1:A:1428:HIS:O	1:A:1429:THR:C	2.59	0.46
1:A:1478:LEU:HD12	1:A:1484:ILE:HD11	1.97	0.46
1:A:1718:TRP:CZ3	1:A:1723:LYS:HA	2.51	0.46
3:C:66:TYR:CG	39:T:457:GLY:HA2	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:80:ILE:HD13	39:T:198:ARG:HG3	1.98	0.46
3:C:89:LEU:C	3:C:89:LEU:CD2	2.82	0.46
3:C:678:THR:HG21	3:C:683:ASN:CB	2.43	0.46
5:E:177:LYS:C	5:E:178:LEU:HD23	2.41	0.46
5:E:260:ARG:CZ	5:E:276:ILE:HD11	2.46	0.46
13:F:27:A:C2	35:O:181:TYR:CD2	3.03	0.46
13:F:37:C:O2	13:F:37:C:H2'	2.15	0.46
14:G:149:G:H2'	14:G:150:U:C6	2.50	0.46
15:H:71:C:O5'	15:H:71:C:H6	1.98	0.46
15:H:79:G:N3	15:H:80:A:C8	2.83	0.46
15:H:142:C:H2'	15:H:143:A:H5'	1.98	0.46
21:1:572:HIS:HB2	21:1:612:THR:HG23	1.96	0.46
21:1:722:GLU:O	21:1:725:ASP:HB2	2.14	0.46
21:1:819:TRP:CZ3	21:1:867:MET:HE3	2.50	0.46
21:1:842:ASN:HA	21:1:879:LEU:HD11	1.96	0.46
21:1:1210:HIS:CD2	22:2:584:LEU:HD22	2.51	0.46
23:3:30:ILE:HG22	23:3:32:VAL:HG13	1.98	0.46
23:3:228:LEU:HD23	23:3:259:LYS:NZ	2.30	0.46
23:3:238:VAL:HB	23:3:247:GLY:O	2.16	0.46
23:3:509:SER:CB	23:3:549:VAL:HG21	2.45	0.46
23:3:616:ILE:O	23:3:628:LEU:HB2	2.16	0.46
23:3:801:GLU:O	23:3:864:SER:HA	2.16	0.46
35:O:146:MET:O	35:O:149:LYS:N	2.40	0.46
38:S:81:GLN:HB3	38:S:108:ASN:N	2.31	0.46
39:T:213:GLU:HG3	39:T:218:TRP:NE1	2.29	0.46
42:W:458:GLU:O	42:W:459:PRO:C	2.58	0.46
1:A:67:ARG:HD3	1:A:179:ALA:CB	2.34	0.46
1:A:1096:HIS:CD2	1:A:1189:MET:HE2	2.51	0.46
1:A:1354:ARG:NH1	40:U:7:LEU:CD2	2.79	0.46
1:A:1718:TRP:CZ3	1:A:1726:ILE:HD12	2.51	0.46
3:C:385:VAL:CG2	3:C:386:GLY:N	2.78	0.46
15:H:80:A:N3	15:H:81:G:C8	2.84	0.46
21:1:478:LEU:HA	21:1:496:LYS:HE3	1.97	0.46
21:1:579:GLU:HB3	21:1:627:THR:OG1	2.16	0.46
21:1:903:GLN:HG3	21:1:950:GLN:HE22	1.81	0.46
21:1:1186:GLN:HE22	21:1:1225:HIS:HB3	1.79	0.46
21:1:1253:GLY:HA3	21:1:1265:TYR:CD1	2.51	0.46
23:3:195:ASP:OD2	23:3:200:ALA:N	2.43	0.46
23:3:701:LEU:HA	23:3:713:LEU:O	2.16	0.46
23:3:787:LYS:HB3	23:3:800:ILE:HD11	1.96	0.46
23:3:828:GLY:O	23:3:834:LEU:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:851:ILE:HG23	23:3:852:PHE:CD2	2.50	0.46
25:5:78:SER:HA	25:5:89:VAL:HG21	1.97	0.46
35:O:193:LEU:HD23	35:O:193:LEU:O	2.15	0.46
1:A:270:ASN:HD21	40:U:8:PRO:HA	1.81	0.46
1:A:596:TYR:OH	14:G:-5:G:C8	2.68	0.46
1:A:715:GLU:CD	37:R:258:TRP:HZ3	2.16	0.46
1:A:748:ASP:CB	36:P:214:THR:HG21	2.46	0.46
1:A:1397:ILE:HG12	37:R:408:GLU:CG	2.45	0.46
1:A:1631:LEU:HD12	1:A:1660:TYR:CD2	2.51	0.46
3:C:145:PHE:CG	3:C:312:SER:HB3	2.49	0.46
3:C:149:LEU:N	3:C:427:PHE:HE2	2.14	0.46
3:C:261:ASP:CG	50:C:1500:GTP:N1	2.61	0.46
5:E:281:VAL:HG21	42:W:148:VAL:HA	1.95	0.46
21:1:862:GLU:O	21:1:865:ARG:N	2.48	0.46
21:1:972:GLY:O	21:1:976:VAL:HG22	2.15	0.46
23:3:253:GLU:HG3	23:3:254:ASN:HD22	1.81	0.46
23:3:459:VAL:HB	23:3:757:ILE:HG23	1.97	0.46
25:5:81:ASN:OD1	25:5:82:VAL:N	2.48	0.46
35:O:78:LYS:HG3	35:O:202:TYR:CZ	2.51	0.46
36:P:189:ASP:O	36:P:190:ASP:C	2.58	0.46
39:T:185:MET:HB2	39:T:186:PRO:HD3	1.98	0.46
46:x:640:ARG:CB	46:x:667:ALA:N	2.78	0.46
1:A:75:ASP:HB2	1:A:77:THR:OG1	2.16	0.46
1:A:201:ALA:HA	1:A:204:LEU:HB3	1.98	0.46
1:A:388:LEU:HB3	1:A:391:THR:OG1	2.16	0.46
1:A:2196:HIS:HB3	1:A:2230:LEU:HD11	1.98	0.46
2:B:12:U:H3	2:B:65:G:H1	1.62	0.46
3:C:66:TYR:N	3:C:66:TYR:CD1	2.81	0.46
3:C:507:VAL:HG13	3:C:566:THR:O	2.16	0.46
3:C:559:ILE:HD12	3:C:559:ILE:O	2.15	0.46
3:C:569:ARG:O	3:C:569:ARG:HG2	2.16	0.46
3:C:671:SER:OG	3:C:672:LEU:HD22	2.15	0.46
3:C:853:ARG:O	3:C:854:ARG:CB	2.62	0.46
14:G:135:G:O6	14:G:137:C:N4	2.48	0.46
15:H:29:A:N6	20:v:19:SER:HB3	2.30	0.46
15:H:30:A:C8	29:L:7:LYS:HD3	2.51	0.46
15:H:107:A:C6	15:H:108:G:C6	3.04	0.46
21:1:859:ASP:OD1	21:1:860:GLU:N	2.47	0.46
29:L:78:MET:HB3	29:L:81:GLN:OE1	2.16	0.46
35:O:20:PHE:CG	35:O:21:PRO:HD2	2.51	0.46
45:Z:604:LYS:HA	45:Z:607:VAL:CG2	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:780:THR:HG22	1:A:898:PHE:CD2	2.50	0.46
1:A:802:THR:HG22	1:A:803:ALA:H	1.80	0.46
1:A:1237:MET:HG2	1:A:1284:LEU:HD21	1.98	0.46
1:A:1312:PRO:O	1:A:1315:VAL:HG22	2.14	0.46
1:A:1399:GLN:HB3	1:A:1401:ARG:HG2	1.98	0.46
1:A:1489:LEU:O	1:A:1492:GLY:N	2.45	0.46
1:A:1529:ILE:O	1:A:1530:PRO:C	2.59	0.46
4:D:1349:GLY:HA2	4:D:1491:SER:O	2.16	0.46
13:F:56:A:N1	15:H:20:G:C6	2.84	0.46
15:H:78:C:O5'	15:H:78:C:H6	1.98	0.46
21:1:588:TYR:HA	21:1:591:VAL:HG12	1.98	0.46
21:1:759:ALA:O	21:1:763:ASN:HB2	2.16	0.46
23:3:69:ARG:HG2	23:3:70:LEU:O	2.16	0.46
34:N:5:LYS:HD2	34:N:77:TYR:OH	2.16	0.46
34:N:17:LEU:HD12	34:N:18:ILE:HG23	1.98	0.46
37:R:88:ILE:HG22	37:R:96:ILE:HG23	1.98	0.46
37:R:92:SER:O	38:S:19:SER:CA	2.64	0.46
37:R:220:ARG:NH1	37:R:220:ARG:CB	2.76	0.46
38:S:9:TRP:C	38:S:11:PRO:HD3	2.39	0.46
1:A:378:PHE:CD1	1:A:378:PHE:C	2.93	0.46
1:A:532:THR:OG1	14:G:2:U:H5''	2.12	0.46
1:A:841:LEU:HD13	1:A:1433:ASP:HB2	1.98	0.46
1:A:1306:LYS:NZ	2:B:38:C:H2'	2.30	0.46
1:A:1388:GLU:O	1:A:1392:LYS:HG2	2.16	0.46
3:C:725:ASP:OD1	3:C:727:LEU:CA	2.64	0.46
5:E:266:PRO:HB3	29:L:785:GLN:CB	2.46	0.46
13:F:43:A:H2	14:G:4:A:H61	1.64	0.46
15:H:45:C:H42	18:w:395:TRP:CG	2.29	0.46
15:H:114:A:H2'	15:H:115:G:H8	1.81	0.46
16:o:61:PRO:O	16:o:86:ALA:HB1	2.16	0.46
17:p:194:PHE:O	17:p:195:GLU:C	2.59	0.46
18:w:394:TYR:HA	18:w:397:TYR:CE2	2.51	0.46
21:1:647:PHE:O	21:1:651:VAL:HG23	2.16	0.46
21:1:1125:PRO:O	21:1:1128:VAL:N	2.49	0.46
21:1:1181:ASP:H	21:1:1184:HIS:HD2	1.64	0.46
23:3:71:THR:HG23	23:3:126:LYS:HD2	1.98	0.46
23:3:718:ARG:HG2	23:3:719:SER:N	2.30	0.46
24:4:29:LEU:HD22	24:4:33:PHE:CE2	2.49	0.46
24:4:32:LEU:CD2	24:4:79:LEU:HD21	2.46	0.46
25:5:46:ARG:HB3	25:5:63:VAL:HG12	1.97	0.46
35:O:63:MET:SD	35:O:160:ASN:HB2	2.56	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:P:54:VAL:HG13	36:P:59:PHE:HZ	1.80	0.46
1:A:34:ALA:HA	5:E:213:ILE:CD1	2.46	0.46
1:A:296:PHE:CB	3:C:656:ALA:CB	2.71	0.46
1:A:331:TRP:NE1	3:C:884:GLU:OE2	2.49	0.46
1:A:362:ARG:C	1:A:362:ARG:CD	2.88	0.46
1:A:586:GLY:O	1:A:592:TYR:CE2	2.69	0.46
1:A:1328:LEU:HD23	1:A:1470:TYR:CE2	2.51	0.46
3:C:678:THR:HG23	3:C:683:ASN:N	2.31	0.46
5:E:248:SER:HB2	5:E:249:TYR:HD1	1.75	0.46
21:1:888:LEU:O	21:1:892:LEU:HG	2.15	0.46
23:3:287:PHE:CD1	23:3:303:ALA:HB1	2.50	0.46
31:K:134:ALA:C	31:K:137:VAL:HG12	2.40	0.46
35:O:84:CYS:HB3	35:O:86:LEU:HG	1.98	0.46
35:O:97:ARG:HH12	35:O:136:MET:HE2	1.81	0.46
36:P:48:GLN:O	36:P:49:ASP:CB	2.64	0.46
37:R:129:ASP:C	37:R:131:ASP:N	2.73	0.46
37:R:148:ARG:HG3	37:R:148:ARG:NH1	2.31	0.46
38:S:66:ASP:C	38:S:66:ASP:OD1	2.59	0.46
45:Z:522:LEU:HD13	45:Z:522:LEU:C	2.41	0.46
1:A:121:HIS:HD2	1:A:482:PHE:CE1	2.35	0.45
1:A:735:ILE:O	1:A:738:MET:HE2	2.16	0.45
1:A:892:LYS:HD2	1:A:912:GLU:OE1	2.16	0.45
1:A:903:SER:OG	1:A:904:HIS:N	2.48	0.45
1:A:1026:ASN:ND2	1:A:1029:GLY:O	2.45	0.45
1:A:1348:VAL:HG11	3:C:921:LEU:HD21	1.98	0.45
1:A:2121:ARG:O	1:A:2154:HIS:HA	2.15	0.45
1:A:2169:LEU:HD21	1:A:2272:MET:HG3	1.99	0.45
5:E:232:ARG:O	5:E:262:TRP:CH2	2.69	0.45
20:v:70:LEU:O	20:v:73:THR:C	2.56	0.45
21:1:744:ALA:O	21:1:787:ILE:HG21	2.16	0.45
21:1:1165:TYR:HE1	22:2:575:PHE:CG	2.33	0.45
23:3:58:VAL:HG12	23:3:1155:LEU:HD23	1.98	0.45
23:3:233:ASN:ND2	23:3:286:ILE:HD12	2.31	0.45
23:3:448:ALA:HB3	23:3:764:ILE:HB	1.97	0.45
23:3:1012:VAL:HA	23:3:1022:ILE:O	2.17	0.45
37:R:65:PRO:HA	38:S:93:THR:O	2.16	0.45
1:A:303:ILE:HG23	3:C:933:PHE:CE1	2.50	0.45
1:A:671:THR:OG1	13:F:69:A:OP1	2.34	0.45
1:A:1084:PRO:HB3	1:A:1101:PHE:CE1	2.51	0.45
1:A:1318:THR:CG2	1:A:1484:ILE:HG21	2.46	0.45
1:A:1667:ARG:HD2	1:A:1679:TYR:CD2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:136:GLY:HA3	3:C:228:PHE:O	2.16	0.45
13:F:57:U:C2	13:F:58:G:N7	2.84	0.45
14:G:10:U:O2'	14:G:11:A:OP1	2.28	0.45
21:1:701:VAL:O	21:1:705:SER:HB3	2.16	0.45
38:S:39:PHE:CD1	38:S:129:PHE:CE2	2.88	0.45
38:S:82:PHE:H	38:S:108:ASN:H	1.64	0.45
40:U:1:MET:O	40:U:3:ASN:N	2.48	0.45
1:A:293:TRP:CE3	1:A:293:TRP:C	2.94	0.45
1:A:359:ILE:O	1:A:360:SER:HB3	2.16	0.45
1:A:907:PRO:CD	36:P:229:LYS:HB2	2.39	0.45
1:A:1301:ILE:CD1	1:A:1306:LYS:HE2	2.41	0.45
1:A:2070:LYS:HA	1:A:2070:LYS:HD3	1.67	0.45
1:A:2074:ARG:O	1:A:2078:ILE:HD13	2.17	0.45
1:A:2117:ILE:H	1:A:2117:ILE:HG12	1.64	0.45
5:E:146:ARG:NH1	5:E:148:LYS:NZ	2.62	0.45
15:H:60:U:H2'	15:H:61:C:H6	1.81	0.45
20:v:20:SER:OG	21:1:1103:VAL:CB	2.65	0.45
21:1:1074:ARG:HD2	21:1:1111:CYS:SG	2.55	0.45
23:3:169:HIS:CD2	23:3:170:VAL:H	2.34	0.45
23:3:526:HIS:HB3	23:3:534:ASN:O	2.17	0.45
23:3:805:ASN:O	23:3:856:LYS:HB3	2.16	0.45
35:O:71:CYS:SG	35:O:74:CYS:SG	3.05	0.45
36:P:227:TYR:N	36:P:227:TYR:HD1	2.14	0.45
39:T:306:CYS:SG	39:T:336:VAL:HG12	2.56	0.45
42:W:426:PHE:HA	42:W:433:PHE:HA	1.99	0.45
1:A:121:HIS:C	1:A:123:THR:H	2.23	0.45
1:A:374:ASP:O	1:A:375:ASP:HB3	2.16	0.45
1:A:592:TYR:CE1	14:G:-5:G:H4'	2.51	0.45
1:A:651:TRP:CD1	13:F:66:C:C1'	2.98	0.45
1:A:1434:LYS:O	1:A:1439:ARG:NH1	2.45	0.45
1:A:2279:TRP:CD1	1:A:2279:TRP:H	2.35	0.45
3:C:193:THR:HG22	3:C:428:THR:HG21	1.97	0.45
3:C:482:TYR:CE2	3:C:493:PHE:CG	2.89	0.45
5:E:119:THR:CG2	5:E:161:ARG:CB	2.73	0.45
5:E:157:CYS:HA	5:E:168:CYS:O	2.16	0.45
15:H:181:G:C2	15:H:182:U:N3	2.84	0.45
21:1:427:PRO:O	21:1:431:LEU:N	2.45	0.45
21:1:834:VAL:O	21:1:838:VAL:HG23	2.16	0.45
21:1:1181:ASP:OD1	21:1:1182:LEU:N	2.46	0.45
23:3:257:THR:OG1	23:3:268:ARG:HG2	2.16	0.45
23:3:897:SER:HB2	23:3:957:GLY:HA3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:905:VAL:HG23	23:3:930:LEU:HB2	1.98	0.45
27:7:73:LEU:HD12	27:7:74:GLN:N	2.32	0.45
32:I:712:VAL:O	32:I:715:GLY:N	2.49	0.45
34:N:47:TRP:HB2	34:N:48:PRO:HD3	1.99	0.45
34:N:125:LYS:HD2	42:W:167:VAL:O	2.17	0.45
35:O:234:LEU:HB2	35:O:272:ILE:HB	1.98	0.45
36:P:193:VAL:CG2	36:P:194:PHE:N	2.79	0.45
37:R:88:ILE:HD12	37:R:88:ILE:N	2.29	0.45
37:R:181:PRO:O	37:R:182:SER:CB	2.58	0.45
39:T:309:ASP:OD1	39:T:309:ASP:C	2.59	0.45
1:A:535:ARG:NH1	14:G:2:U:OP2	2.50	0.45
1:A:658:ARG:N	36:P:29:GLN:OE1	2.49	0.45
1:A:966:TRP:HE3	1:A:1178:TYR:CZ	2.35	0.45
1:A:1426:ASP:OD2	37:R:421:GLY:CA	2.64	0.45
1:A:1604:LEU:HD11	1:A:1725:LEU:HD22	1.99	0.45
3:C:183:SER:OG	3:C:480:LYS:NZ	2.50	0.45
5:E:243:LEU:CD1	5:E:247:GLY:CA	2.84	0.45
14:G:26:U:C2'	35:O:269:CYS:SG	3.04	0.45
15:H:25:G:C2	15:H:26:A:C5	3.04	0.45
15:H:150:U:H3	15:H:181:G:H1	1.62	0.45
15:H:152:G:O2'	15:H:153:A:H1'	2.16	0.45
23:3:259:LYS:HG3	23:3:266:ASP:CG	2.42	0.45
23:3:636:GLN:O	23:3:670:GLN:HG2	2.17	0.45
23:3:796:ASN:HA	23:3:871:PRO:HD3	1.98	0.45
28:J:360:ASP:HA	28:J:363:ARG:CD	2.46	0.45
29:L:789:ALA:O	29:L:792:LEU:CG	2.64	0.45
35:O:33:TYR:OH	42:W:139:LEU:O	2.30	0.45
38:S:34:LYS:HG3	38:S:78:TYR:CE2	2.52	0.45
39:T:409:LEU:HD12	39:T:409:LEU:N	2.31	0.45
41:V:512:GLY:O	41:V:513:ARG:C	2.60	0.45
42:W:266:ARG:O	42:W:267:SER:O	2.35	0.45
1:A:61:MET:HB3	1:A:62:PRO:HD2	1.98	0.45
1:A:730:GLY:O	1:A:731:LEU:HB2	2.16	0.45
1:A:1413:ASP:OD1	1:A:1414:ARG:HG3	2.17	0.45
3:C:66:TYR:CB	39:T:456:PRO:O	2.51	0.45
3:C:495:ARG:HG3	3:C:495:ARG:O	2.16	0.45
3:C:497:LEU:CD1	3:C:577:PHE:CE1	2.94	0.45
3:C:852:ARG:NH2	14:G:-12:G:OP1	2.50	0.45
5:E:260:ARG:CD	5:E:276:ILE:HG12	2.47	0.45
13:F:94:C:H2'	13:F:95:G:H8	1.82	0.45
14:G:-12:G:HO2'	14:G:-11:G:C5'	2.29	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:v:51:LEU:HB3	21:1:1141:LEU:HD13	1.72	0.45
23:3:115:ILE:HD11	27:7:18:TYR:CE1	2.51	0.45
23:3:482:THR:HG21	23:3:505:THR:OG1	2.17	0.45
37:R:179:TYR:CE2	37:R:181:PRO:HG3	2.52	0.45
39:T:297:HIS:CD2	39:T:338:CYS:SG	3.09	0.45
42:W:516:PHE:HA	42:W:522:TYR:O	2.16	0.45
45:Z:525:TYR:CE1	45:Z:526:ILE:CG2	2.86	0.45
1:A:121:HIS:C	1:A:123:THR:N	2.74	0.45
1:A:317:PRO:HB2	1:A:327:VAL:HG11	1.98	0.45
1:A:536:LYS:HD3	13:F:72:G:O2'	2.16	0.45
1:A:1457:HIS:NE2	37:R:424:SER:C	2.75	0.45
1:A:1733:ILE:HG23	1:A:1737:ASN:HB2	1.98	0.45
2:B:57:G:H2'	2:B:58:U:H5'	1.99	0.45
3:C:926:ALA:N	3:C:927:PRO:HD2	2.32	0.45
5:E:178:LEU:HG	5:E:188:GLN:HB2	1.98	0.45
5:E:277:PHE:CD1	5:E:277:PHE:N	2.83	0.45
13:F:22:A:P	34:N:115:THR:OG1	2.74	0.45
15:H:148:C:HO2'	15:H:149:A:H5'	1.76	0.45
21:1:86:ALA:O	21:1:89:ALA:HB3	2.17	0.45
21:1:476:ASP:OD1	21:1:477:LYS:N	2.49	0.45
21:1:1110:VAL:O	21:1:1113:THR:HB	2.17	0.45
21:1:1251:LEU:HD12	22:2:497:SER:OG	2.16	0.45
23:3:223:LYS:HE2	23:3:224:TYR:CZ	2.52	0.45
23:3:429:ARG:HH12	27:7:59:GLU:H	1.65	0.45
23:3:1114:SER:HB2	23:3:1215:TYR:CE1	2.51	0.45
28:J:338:GLU:O	37:R:116:TYR:CE1	2.69	0.45
35:O:225:PRO:HB3	35:O:302:TRP:CZ2	2.51	0.45
37:R:128:ASP:OD2	37:R:133:GLN:OE1	2.34	0.45
39:T:393:ASP:O	39:T:413:ASN:ND2	2.49	0.45
45:Z:564:PRO:O	45:Z:582:TYR:CG	2.69	0.45
45:Z:600:ARG:CG	45:Z:600:ARG:NH1	2.73	0.45
46:x:876:GLY:O	46:x:879:LEU:N	2.49	0.45
1:A:76:MET:SD	1:A:88:TYR:CE2	3.10	0.45
1:A:402:ILE:HG22	3:C:268:LYS:HZ1	1.77	0.45
1:A:755:HIS:CG	36:P:219:PHE:HE2	2.35	0.45
1:A:833:LYS:HG3	1:A:834:HIS:CD2	2.52	0.45
1:A:975:VAL:HG11	1:A:1153:VAL:HG21	1.98	0.45
1:A:1342:TRP:CE3	3:C:921:LEU:CG	3.00	0.45
1:A:2073:TRP:CZ3	1:A:2313:HIS:CE1	3.05	0.45
2:B:22:U:O2	2:B:22:U:H2'	2.15	0.45
4:D:419:GLY:C	4:D:421:HIS:H	2.25	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:F:38:G:OP2	13:F:38:G:C8	2.70	0.45
14:G:6:A:H2'	14:G:7:G:H8	1.82	0.45
21:1:501:LEU:O	21:1:504:ILE:N	2.48	0.45
21:1:592:GLU:O	21:1:596:ILE:HG23	2.16	0.45
21:1:629:ALA:HA	21:1:667:ILE:HG12	1.99	0.45
23:3:383:ASP:OD1	23:3:384:THR:N	2.50	0.45
23:3:587:VAL:HG11	23:3:590:MET:HE2	1.99	0.45
23:3:607:VAL:HB	23:3:615:ARG:O	2.17	0.45
23:3:1057:ARG:HB2	23:3:1092:ILE:HD13	1.98	0.45
37:R:123:GLU:C	37:R:124:VAL:HG12	2.41	0.45
39:T:316:ASP:C	39:T:316:ASP:OD1	2.58	0.45
42:W:466:ALA:HB2	42:W:512:CYS:O	2.17	0.45
44:Y:41:GLY:HA2	44:Y:79:PHE:HB3	1.99	0.45
1:A:733:THR:OG1	1:A:734:PRO:HD3	2.16	0.45
1:A:1013:ASN:OD1	1:A:1030:ILE:HG13	2.16	0.45
1:A:1125:ILE:HG22	1:A:1147:VAL:HG21	1.99	0.45
1:A:2334:TYR:CE1	4:D:591:GLU:CB	3.00	0.45
2:B:40:U:OP2	2:B:40:U:C6	2.70	0.45
3:C:137:HIS:HD2	3:C:236:MET:HB2	1.61	0.45
3:C:191:PRO:HG2	3:C:426:GLU:OE1	2.17	0.45
3:C:445:ALA:HB1	3:C:449:ILE:CG1	2.45	0.45
3:C:726:LEU:HD12	3:C:726:LEU:C	2.42	0.45
5:E:162:ARG:HH21	5:E:204:THR:HA	1.78	0.45
13:F:51:U:H2'	13:F:52:U:O4'	2.17	0.45
14:G:20:A:OP2	35:O:159:ARG:HG3	2.16	0.45
21:1:552:LEU:HA	21:1:555:VAL:HG12	1.98	0.45
21:1:822:ARG:NH1	44:Y:31:GLU:HG2	2.32	0.45
21:1:897:LEU:O	21:1:901:GLN:HG3	2.17	0.45
21:1:1186:GLN:NE2	21:1:1225:HIS:HB3	2.31	0.45
25:5:48:ILE:HG12	25:5:62:VAL:HG23	1.99	0.45
25:5:53:THR:OG1	25:5:56:THR:OG1	2.14	0.45
28:J:406:PHE:CB	28:J:411:MET:HG2	2.47	0.45
35:O:205:ILE:O	35:O:207:ASP:N	2.50	0.45
35:O:259:ARG:HD2	35:O:273:GLN:HG2	1.99	0.45
39:T:342:GLU:CB	39:T:343:PRO:HD2	2.47	0.45
39:T:454:VAL:HG22	39:T:463:SER:OG	2.16	0.45
39:T:455:GLN:CG	39:T:456:PRO:CD	2.94	0.45
1:A:44:ARG:CD	1:A:45:TYR:CE2	2.99	0.45
1:A:81:PHE:O	1:A:82:ARG:C	2.59	0.45
1:A:380:LEU:C	3:C:354:ARG:CG	2.85	0.45
1:A:845:ARG:NH2	1:A:1439:ARG:HE	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1258:LYS:HE2	37:R:432:GLU:CB	2.47	0.45
1:A:2320:LEU:HD21	1:A:2322:GLU:CD	2.41	0.45
3:C:65:TYR:O	3:C:66:TYR:CB	2.65	0.45
3:C:230:ASP:OD2	3:C:233:GLU:CG	2.55	0.45
3:C:502:HIS:ND1	3:C:543:ARG:HB3	2.32	0.45
3:C:926:ALA:HA	3:C:929:LEU:HG	1.98	0.45
13:F:50:A:H2'	13:F:51:U:H6	1.82	0.45
14:G:6:A:H2'	14:G:7:G:C8	2.52	0.45
14:G:12:G:N3	14:G:12:G:C2'	2.79	0.45
14:G:157:U:H5'	21:1:622:GLU:OE1	2.17	0.45
15:H:113:G:H2'	15:H:114:A:H8	1.82	0.45
21:1:942:ASN:CG	21:1:943:LYS:H	2.24	0.45
21:1:1002:ASN:OD1	21:1:1041:ARG:NH2	2.50	0.45
22:2:611:ASP:O	22:2:614:ARG:CB	2.60	0.45
23:3:883:GLU:HG3	23:3:884:GLN:N	2.32	0.45
23:3:1051:GLY:HA2	23:3:1100:THR:HA	1.99	0.45
25:5:25:ASN:HD22	25:5:86:TYR:C	2.25	0.45
25:5:26:LEU:HD12	25:5:87:LEU:HD22	1.98	0.45
27:7:31:TRP:HE3	27:7:32:LEU:HD12	1.82	0.45
29:L:226:ASP:OD1	37:R:83:SER:HB2	2.16	0.45
32:I:433:ALA:O	32:I:437:CYS:N	2.50	0.45
34:N:91:LYS:HD3	34:N:91:LYS:HA	1.81	0.45
35:O:197:ASN:O	35:O:201:ARG:HG3	2.17	0.45
37:R:88:ILE:HG21	37:R:96:ILE:CG2	2.46	0.45
37:R:89:GLN:OE1	38:S:145:VAL:HG13	2.17	0.45
37:R:408:GLU:CG	37:R:409:VAL:N	2.78	0.45
45:Z:524:ARG:HD2	45:Z:525:TYR:CB	2.46	0.45
1:A:1348:VAL:HG11	3:C:921:LEU:CD2	2.47	0.44
3:C:93:ILE:CG2	39:T:218:TRP:NE1	2.80	0.44
5:E:276:ILE:O	5:E:277:PHE:HD1	2.00	0.44
13:F:68:C:C5	36:P:33:ARG:HG2	2.52	0.44
13:F:94:C:H2'	13:F:95:G:C8	2.52	0.44
15:H:7:U:H2'	15:H:8:C:C6	2.52	0.44
15:H:81:G:N3	15:H:82:G:C8	2.85	0.44
15:H:141:C:H2'	15:H:142:C:C6	2.50	0.44
20:v:71:ALA:C	20:v:74:GLN:H	2.25	0.44
21:1:810:ILE:O	21:1:813:PRO:HD2	2.17	0.44
23:3:544:ILE:HD11	23:3:556:ILE:HG21	1.98	0.44
23:3:1140:PHE:O	23:3:1144:VAL:HG23	2.17	0.44
28:J:406:PHE:CG	28:J:411:MET:CE	2.97	0.44
35:O:56:ARG:HG2	35:O:67:LYS:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:O:131:THR:O	35:O:132:ARG:HB2	2.17	0.44
35:O:294:ASN:O	35:O:296:ARG:HG3	2.17	0.44
37:R:147:THR:HG23	39:T:360:VAL:CG1	2.40	0.44
37:R:416:PHE:O	37:R:416:PHE:CG	2.70	0.44
41:V:530:LYS:C	41:V:532:GLN:N	2.74	0.44
41:V:548:ALA:HB1	41:V:585:ILE:C	2.42	0.44
41:V:548:ALA:HB2	41:V:585:ILE:CB	2.42	0.44
1:A:280:GLU:OE1	40:U:9:THR:HG21	2.17	0.44
1:A:1088:PHE:HD1	1:A:1097:ILE:HG12	1.82	0.44
1:A:1310:ARG:NH1	1:A:1566:ILE:HD11	2.32	0.44
1:A:1430:LEU:HD11	37:R:422:MET:HA	1.98	0.44
1:A:1557:LEU:HD13	1:A:1580:HIS:CE1	2.53	0.44
1:A:2280:ASN:HB3	1:A:2309:HIS:CD2	2.53	0.44
2:B:44:A:OP1	13:F:66:C:N4	2.30	0.44
3:C:93:ILE:CG2	39:T:218:TRP:CZ2	3.00	0.44
3:C:388:VAL:HA	3:C:392:LEU:HB2	1.99	0.44
5:E:132:THR:HG21	5:E:146:ARG:HG2	1.98	0.44
5:E:274:VAL:C	5:E:275:LYS:CG	2.91	0.44
13:F:58:G:O2'	13:F:59:G:OP1	2.31	0.44
15:H:143:A:OP2	15:H:143:A:C2	2.71	0.44
15:H:157:G:H5''	15:H:157:G:C8	2.50	0.44
21:1:762:ALA:O	21:1:766:THR:CB	2.64	0.44
21:1:1252:GLN:NE2	22:2:492:LYS:O	2.51	0.44
22:2:613:LEU:HD21	24:4:32:LEU:HD13	1.99	0.44
23:3:404:LEU:HB3	23:3:407:ILE:HD11	1.99	0.44
23:3:1142:GLN:HG2	23:3:1146:MET:HE3	1.98	0.44
23:3:1159:ASP:OD1	23:3:1160:HIS:N	2.49	0.44
28:J:297:ASN:OD1	29:L:223:GLY:O	2.34	0.44
29:L:213:GLU:CB	35:O:110:SER:HB3	2.47	0.44
35:O:113:ASN:O	35:O:114:LYS:C	2.58	0.44
35:O:230:THR:H	35:O:277:ARG:NH1	2.15	0.44
38:S:38:ASN:HD22	38:S:100:MET:CE	2.31	0.44
1:A:193:LEU:HD12	1:A:194:GLU:N	2.29	0.44
1:A:1136:ARG:CZ	1:A:1139:ARG:HH21	2.30	0.44
1:A:1136:ARG:NE	1:A:1139:ARG:HH21	2.16	0.44
1:A:1459:ARG:HD3	1:A:1459:ARG:HA	1.75	0.44
2:B:63:A:H5''	5:E:106:LYS:NZ	2.32	0.44
3:C:140:HIS:HB3	3:C:230:ASP:CB	2.43	0.44
3:C:671:SER:CB	3:C:672:LEU:HD22	2.46	0.44
5:E:209:ILE:HG21	5:E:250:LEU:HD11	1.94	0.44
13:F:39:A:H2'	13:F:40:U:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:G:20:A:OP2	35:O:159:ARG:CG	2.64	0.44
21:1:529:GLY:HA2	21:1:570:TYR:CZ	2.51	0.44
23:3:205:GLN:HB2	23:3:228:LEU:O	2.17	0.44
23:3:462:VAL:HG21	23:3:508:CYS:HB3	1.98	0.44
23:3:484:VAL:HG21	23:3:499:PHE:HB2	1.99	0.44
23:3:536:TRP:CD1	23:3:566:PHE:HZ	2.35	0.44
23:3:723:TYR:CD1	23:3:725:TYR:HB2	2.53	0.44
25:5:98:PHE:O	25:5:100:LYS:N	2.50	0.44
36:P:188:TRP:N	36:P:188:TRP:CD2	2.86	0.44
37:R:416:PHE:O	37:R:416:PHE:CD1	2.70	0.44
39:T:387:PHE:CZ	39:T:398:TRP:CD1	3.04	0.44
45:Z:500:GLY:O	45:Z:503:GLN:N	2.50	0.44
45:Z:573:PRO:O	45:Z:573:PRO:CD	2.65	0.44
45:Z:597:ARG:CZ	45:Z:601:LEU:HD13	2.47	0.44
1:A:121:HIS:CA	1:A:481:PHE:O	2.66	0.44
1:A:394:TYR:CD1	1:A:394:TYR:N	2.86	0.44
1:A:532:THR:OG1	14:G:2:U:H3'	2.17	0.44
1:A:661:GLU:HA	37:R:213:LYS:HA	2.00	0.44
1:A:777:GLY:O	1:A:780:THR:OG1	2.25	0.44
1:A:1074:PHE:HB3	1:A:1079:THR:OG1	2.17	0.44
1:A:1354:ARG:NH1	40:U:7:LEU:HD21	2.32	0.44
1:A:2125:ALA:O	1:A:2150:GLN:NE2	2.50	0.44
1:A:2328:ALA:CB	4:D:788:GLY:N	2.79	0.44
3:C:334:ILE:HD12	3:C:334:ILE:C	2.42	0.44
4:D:721:VAL:HA	4:D:825:THR:O	2.17	0.44
13:F:5:U:H5'	13:F:6:C:OP2	2.17	0.44
15:H:159:U:H2'	15:H:160:A:C8	2.52	0.44
15:H:165:A:C6	15:H:166:G:O6	2.71	0.44
18:w:438:LEU:HD22	18:w:440:ILE:HD12	1.99	0.44
20:v:29:ARG:HA	20:v:32:GLN:CG	2.48	0.44
20:v:45:TYR:CZ	20:v:58:LEU:HD13	2.51	0.44
21:1:869:MET:HE1	21:1:896:ILE:HG23	2.00	0.44
21:1:937:LEU:O	21:1:940:LEU:HB3	2.18	0.44
22:2:611:ASP:O	22:2:614:ARG:N	2.50	0.44
23:3:643:VAL:HG12	23:3:664:TYR:O	2.17	0.44
23:3:1063:ASN:H	23:3:1087:GLN:HE22	1.65	0.44
23:3:1096:HIS:NE2	23:3:1098:GLY:HA2	2.33	0.44
38:S:38:ASN:HD22	38:S:100:MET:HE1	1.82	0.44
39:T:439:TRP:CE3	39:T:446:ASN:HB2	2.52	0.44
44:Y:36:ALA:CB	45:Z:499:LYS:O	2.54	0.44
46:x:936:TYR:O	46:x:938:ARG:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:ILE:HG12	1:A:426:LEU:HD23	1.99	0.44
1:A:507:LEU:HD12	1:A:507:LEU:HA	1.79	0.44
1:A:1402:ARG:HD2	37:R:412:ASP:HA	1.98	0.44
3:C:135:CYS:SG	3:C:227:LEU:CB	3.06	0.44
3:C:259:LYS:HD2	50:C:1500:GTP:C5	2.52	0.44
3:C:474:LEU:C	3:C:474:LEU:CD2	2.87	0.44
3:C:673:LYS:HG3	3:C:686:THR:HG23	2.00	0.44
14:G:21:A:O3'	14:G:22:C:C6	2.71	0.44
15:H:60:U:H2'	15:H:61:C:C6	2.52	0.44
17:p:172:ASN:C	17:p:174:PHE:N	2.75	0.44
21:1:1211:LEU:O	21:1:1215:VAL:HG23	2.17	0.44
23:3:460:TRP:CE2	23:3:507:SER:HA	2.53	0.44
23:3:511:LEU:HB2	23:3:517:VAL:HG23	1.99	0.44
26:6:58:CYS:N	26:6:63:GLY:O	2.46	0.44
35:O:258:ILE:HG22	35:O:260:THR:N	2.32	0.44
44:Y:58:GLN:HB2	45:Z:584:TRP:NE1	2.33	0.44
1:A:79:ARG:HD2	1:A:79:ARG:O	2.18	0.44
1:A:305:ARG:NH2	3:C:854:ARG:HD3	2.32	0.44
1:A:611:LEU:HA	1:A:611:LEU:HD12	1.85	0.44
1:A:707:ARG:O	1:A:711:GLN:HG3	2.17	0.44
1:A:978:GLU:OE2	1:A:1188:ASN:N	2.36	0.44
1:A:1134:TRP:CZ2	1:A:1195:ARG:HB2	2.53	0.44
3:C:89:LEU:C	3:C:91:GLU:N	2.76	0.44
3:C:301:SER:C	3:C:303:LEU:H	2.25	0.44
3:C:457:VAL:CG1	3:C:462:GLY:HA3	2.46	0.44
15:H:34:U:C4	15:H:35:A:N7	2.85	0.44
15:H:73:C:O5'	15:H:73:C:H6	2.01	0.44
15:H:142:C:O2'	15:H:143:A:H5'	2.18	0.44
15:H:147:G:C6	15:H:148:C:N4	2.86	0.44
20:v:170:LEU:HA	20:v:179:ILE:O	2.18	0.44
20:v:205:GLN:O	20:v:209:GLN:CB	2.65	0.44
21:1:1108:ASN:OD1	21:1:1110:VAL:HG12	2.17	0.44
22:2:569:GLN:CB	42:W:460:SER:CB	2.95	0.44
23:3:589:CYS:O	23:3:608:GLY:N	2.41	0.44
23:3:812:LYS:O	23:3:816:LYS:CB	2.57	0.44
35:O:68:THR:HA	35:O:83:THR:CG2	2.45	0.44
36:P:193:VAL:HG23	36:P:194:PHE:CB	2.47	0.44
38:S:9:TRP:HE3	38:S:11:PRO:CG	2.29	0.44
44:Y:63:VAL:HG23	44:Y:64:ASN:N	2.33	0.44
46:x:936:TYR:C	46:x:938:ARG:N	2.73	0.44
1:A:67:ARG:HE	1:A:67:ARG:HB2	1.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:GLU:C	1:A:520:TYR:CD2	2.96	0.44
1:A:193:LEU:HB3	1:A:208:TYR:OH	2.17	0.44
1:A:373:ASP:OD1	1:A:374:ASP:N	2.51	0.44
1:A:460:LYS:NZ	2:B:49:A:P	2.91	0.44
1:A:1481:VAL:CG1	1:A:1498:TRP:CE2	2.88	0.44
1:A:2237:TRP:HZ2	1:A:2248:PRO:HB2	1.81	0.44
1:A:2310:ARG:HH11	1:A:2310:ARG:HB3	1.83	0.44
3:C:145:PHE:HD1	3:C:312:SER:HB3	1.83	0.44
5:E:266:PRO:CG	29:L:785:GLN:HB3	2.48	0.44
13:F:9:U:H2'	13:F:10:U:C6	2.52	0.44
13:F:68:C:C5	36:P:33:ARG:CG	2.95	0.44
15:H:26:A:C6	15:H:27:U:C4	3.05	0.44
17:p:155:LEU:CB	17:p:219:LYS:O	2.66	0.44
21:1:1072:ALA:O	21:1:1075:ARG:HB3	2.18	0.44
23:3:607:VAL:HG21	23:3:617:ILE:HD12	1.99	0.44
23:3:929:LYS:HD3	23:3:938:GLU:OE2	2.17	0.44
29:L:224:PHE:CE1	37:R:86:LEU:HD12	2.43	0.44
42:W:476:LEU:O	42:W:487:ILE:HA	2.16	0.44
45:Z:584:TRP:CZ3	45:Z:586:GLY:HA2	2.53	0.44
1:A:148:TRP:HE3	1:A:629:PHE:CD1	2.35	0.44
1:A:402:ILE:HG21	3:C:268:LYS:HZ2	1.47	0.44
1:A:1034:LEU:HB2	1:A:1037:ALA:HB2	1.98	0.44
1:A:1533:ARG:HD2	1:A:1751:LEU:O	2.18	0.44
14:G:21:A:P	35:O:156:TYR:HH	2.35	0.44
14:G:26:U:H5'	35:O:235:TYR:OH	2.18	0.44
18:w:485:ASN:HB2	23:3:976:LYS:HE3	2.00	0.44
21:1:601:ALA:HB2	21:1:635:VAL:HG12	2.00	0.44
21:1:969:LYS:O	21:1:973:HIS:ND1	2.36	0.44
23:3:353:PHE:CD1	23:3:406:PRO:HD3	2.53	0.44
23:3:930:LEU:HG	23:3:934:GLY:HA2	1.98	0.44
24:4:79:LEU:HG	24:4:84:ILE:HG13	2.00	0.44
36:P:66:ARG:HB2	36:P:66:ARG:NH1	2.30	0.44
37:R:124:VAL:HG22	37:R:125:MET:H	1.83	0.44
37:R:132:LEU:HD23	37:R:132:LEU:N	2.31	0.44
37:R:208:GLU:OE2	37:R:211:ARG:NH1	2.51	0.44
37:R:415:LEU:H	37:R:415:LEU:HG	1.56	0.44
39:T:358:ASP:HB2	39:T:365:ARG:HD2	2.00	0.44
1:A:82:ARG:NH1	14:G:16:G:O6	2.49	0.44
1:A:106:MET:HG2	1:A:489:TRP:CZ2	2.53	0.44
1:A:300:ASN:O	3:C:936:LYS:CB	2.66	0.44
1:A:382:GLU:O	1:A:383:PHE:CD2	2.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:941:LYS:HE3	1:A:951:LEU:HD21	2.00	0.44
1:A:1038:SER:HA	1:A:1442:PHE:HE2	1.83	0.44
1:A:2072:GLU:O	1:A:2076:ARG:HG3	2.18	0.44
1:A:2222:SER:OG	1:A:2223:CYS:N	2.50	0.44
3:C:439:PRO:O	3:C:440:SER:CB	2.66	0.44
3:C:779:LEU:HD11	3:C:825:PRO:HB2	1.99	0.44
14:G:-8:U:C2	40:U:15:THR:O	2.71	0.44
14:G:11:A:C5	14:G:12:G:C8	3.06	0.44
14:G:21:A:O3'	14:G:22:C:H6	2.00	0.44
15:H:6:U:H2'	15:H:7:U:C6	2.53	0.44
21:1:503:LYS:HD2	21:1:515:ALA:HB2	2.00	0.44
21:1:779:SER:HB3	21:1:784:MET:HG2	2.00	0.44
21:1:1131:ALA:O	21:1:1135:GLU:HG2	2.17	0.44
23:3:411:GLN:HA	23:3:1105:GLN:OE1	2.18	0.44
23:3:798:ILE:HA	23:3:867:ARG:O	2.18	0.44
25:5:46:ARG:N	25:5:63:VAL:O	2.50	0.44
34:N:125:LYS:HA	34:N:125:LYS:HD3	1.74	0.44
35:O:28:LEU:CD2	37:R:195:ARG:HE	2.29	0.44
38:S:81:GLN:HB3	38:S:108:ASN:H	1.82	0.44
42:W:420:ALA:HB3	42:W:438:ASP:CB	2.48	0.44
47:y:218:LYS:HA	47:y:244:ASN:O	2.18	0.44
1:A:44:ARG:HG2	1:A:45:TYR:CD2	2.53	0.43
1:A:330:THR:O	1:A:331:TRP:HB2	2.17	0.43
1:A:402:ILE:HD13	3:C:268:LYS:CE	2.47	0.43
1:A:1532:ARG:HG2	1:A:1572:SER:OG	2.18	0.43
3:C:229:ILE:CG2	3:C:234:GLY:O	2.66	0.43
4:D:1583:ASP:C	4:D:1585:GLN:H	2.26	0.43
5:E:248:SER:HB2	5:E:249:TYR:CE1	2.53	0.43
13:F:35:A:C8	14:G:12:G:O6	2.71	0.43
13:F:68:C:H42	39:T:283:HIS:CE1	2.35	0.43
21:1:903:GLN:HG3	21:1:950:GLN:NE2	2.33	0.43
23:3:176:GLY:O	23:3:178:GLU:HG2	2.17	0.43
23:3:747:SER:N	23:3:750:CYS:O	2.51	0.43
23:3:998:HIS:HE1	23:3:1064:ASP:OD2	2.00	0.43
23:3:1207:LYS:HA	23:3:1210:ASP:OD2	2.18	0.43
25:5:53:THR:O	25:5:57:ARG:HG3	2.18	0.43
37:R:109:ASP:OD1	37:R:110:LYS:N	2.51	0.43
39:T:454:VAL:CG1	39:T:455:GLN:N	2.81	0.43
1:A:73:HIS:HA	1:A:81:PHE:CE2	2.53	0.43
1:A:89:LEU:CD2	1:A:656:LEU:CD2	2.95	0.43
1:A:331:TRP:HE3	1:A:332:TYR:CA	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:664:HIS:CE1	1:A:666:LYS:HD3	2.53	0.43
1:A:694:LEU:O	1:A:698:PRO:HG3	2.18	0.43
1:A:970:GLU:HB2	1:A:972:GLU:OE2	2.17	0.43
1:A:1553:VAL:O	1:A:1561:PHE:HA	2.18	0.43
3:C:135:CYS:N	3:C:226:VAL:O	2.50	0.43
3:C:392:LEU:HD12	3:C:392:LEU:O	2.18	0.43
3:C:508:LYS:O	3:C:566:THR:HG22	2.18	0.43
3:C:674:CYS:HB2	3:C:818:SER:HB3	2.00	0.43
3:C:703:GLU:OE2	3:C:740:THR:CG2	2.50	0.43
5:E:251:LEU:CG	5:E:291:CYS:SG	3.05	0.43
15:H:159:U:H2'	15:H:160:A:H8	1.83	0.43
15:H:182:U:H6	15:H:182:U:O5'	2.01	0.43
21:1:528:ALA:HB2	21:1:563:LEU:HD13	2.00	0.43
21:1:732:TRP:O	21:1:735:ILE:HB	2.19	0.43
22:2:556:LYS:O	22:2:559:PRO:HD3	2.18	0.43
23:3:409:PHE:HD2	23:3:788:PHE:CE2	2.36	0.43
23:3:633:LEU:HD12	23:3:637:PRO:HG2	2.00	0.43
23:3:791:HIS:ND1	23:3:794:SER:HB3	2.33	0.43
23:3:837:GLU:O	23:3:837:GLU:HG2	2.17	0.43
1:A:370:PRO:O	1:A:371:LEU:C	2.60	0.43
1:A:908:VAL:HA	1:A:1445:TYR:O	2.18	0.43
1:A:1071:PHE:CD2	1:A:1072:LEU:HG	2.53	0.43
3:C:131:ASN:HB3	3:C:549:TRP:CZ2	2.52	0.43
3:C:514:TYR:CD1	3:C:514:TYR:C	2.94	0.43
3:C:524:ILE:O	3:C:525:CYS:SG	2.74	0.43
15:H:64:A:H2'	15:H:65:U:C6	2.53	0.43
15:H:153:A:H2'	15:H:154:C:H5''	1.99	0.43
20:v:31:ARG:CG	20:v:67:GLY:HA2	2.47	0.43
21:1:840:LEU:O	21:1:844:VAL:HG12	2.19	0.43
22:2:482:ALA:O	22:2:485:PRO:HD3	2.18	0.43
23:3:88:VAL:HA	23:3:103:HIS:O	2.18	0.43
23:3:1056:VAL:HG22	23:3:1091:VAL:HG22	2.01	0.43
24:4:67:ALA:HA	24:4:70:ALA:HB3	2.00	0.43
31:K:134:ALA:O	31:K:137:VAL:HG12	2.17	0.43
35:O:185:LYS:CG	42:W:216:LEU:HA	2.46	0.43
37:R:88:ILE:HG22	37:R:96:ILE:CG2	2.49	0.43
37:R:423:ASP:C	37:R:424:SER:HG	2.03	0.43
39:T:406:ILE:HG22	39:T:407:GLN:N	2.33	0.43
42:W:309:MET:HA	42:W:334:ALA:HB1	2.00	0.43
1:A:338:VAL:CB	3:C:867:PRO:CG	2.96	0.43
1:A:406:TRP:CH2	3:C:265:LEU:O	2.64	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:741:ARG:NH2	39:T:432:ASP:O	2.41	0.43
1:A:1263:TRP:CE3	1:A:1295:ILE:HD13	2.53	0.43
1:A:1307:MET:SD	1:A:1547:VAL:CB	2.96	0.43
1:A:1480:GLY:O	1:A:1483:GLY:N	2.51	0.43
1:A:1674:HIS:HB3	1:A:1709:TYR:CE2	2.53	0.43
2:B:99:C:H2'	2:B:100:C:C6	2.53	0.43
3:C:133:THR:CB	3:C:225:VAL:HG23	2.43	0.43
3:C:297:ASN:HD22	3:C:298:LEU:HD12	1.83	0.43
3:C:350:ASN:HB3	3:C:353:THR:CG2	2.49	0.43
3:C:505:GLN:HG2	3:C:506:PRO:HD2	2.00	0.43
3:C:776:GLU:O	3:C:781:ASP:HA	2.18	0.43
13:F:42:C:H2'	13:F:43:A:C8	2.53	0.43
21:1:885:ASP:OD1	21:1:888:LEU:HB3	2.18	0.43
21:1:1119:VAL:O	21:1:1122:THR:HG22	2.17	0.43
21:1:1120:ALA:HB1	21:1:1125:PRO:HB3	2.01	0.43
21:1:1179:ASP:HB3	22:2:511:LEU:HD12	2.00	0.43
22:2:630:PRO:HA	22:2:631:PRO:HD3	1.77	0.43
23:3:521:PRO:HA	23:3:544:ILE:CG2	2.49	0.43
23:3:745:PHE:HB2	23:3:755:VAL:HG23	2.00	0.43
29:L:63:TRP:CH2	29:L:99:HIS:HB2	2.54	0.43
29:L:101:GLU:O	29:L:105:ASP:HB2	2.18	0.43
35:O:90:TYR:HB3	35:O:92:LEU:HD12	1.98	0.43
37:R:54:LEU:HD12	37:R:54:LEU:HA	1.86	0.43
39:T:399:LYS:HG3	39:T:406:ILE:CD1	2.37	0.43
44:Y:36:ALA:HB3	45:Z:498:GLY:O	2.18	0.43
1:A:459:LEU:HD12	1:A:459:LEU:HA	1.75	0.43
1:A:2073:TRP:CH2	1:A:2313:HIS:CG	3.06	0.43
3:C:145:PHE:N	3:C:312:SER:OG	2.50	0.43
3:C:736:GLY:HA3	3:C:770:PHE:CE2	2.53	0.43
5:E:67:GLY:N	5:E:87:ASP:OD1	2.42	0.43
14:G:-5:G:O2'	14:G:-4:A:H5''	2.18	0.43
15:H:83:A:C4	15:H:84:C:C6	3.07	0.43
15:H:98:G:H5'	15:H:104:U:OP2	2.18	0.43
15:H:154:C:O2'	15:H:155:C:C5'	2.66	0.43
15:H:181:G:C2	15:H:182:U:C4	3.07	0.43
20:v:51:LEU:CG	21:1:1141:LEU:HD11	2.45	0.43
21:1:897:LEU:HD21	21:1:932:ILE:HD13	2.00	0.43
21:1:1235:GLU:O	21:1:1238:ARG:HB3	2.18	0.43
23:3:139:LYS:HB2	23:3:160:ALA:HB3	2.00	0.43
23:3:868:VAL:HG12	23:3:877:LEU:HB2	1.99	0.43
35:O:58:CYS:HB2	35:O:65:PHE:CE1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:O:230:THR:H	35:O:277:ARG:CZ	2.32	0.43
37:R:126:ASN:HD22	37:R:128:ASP:H	1.66	0.43
44:Y:29:HIS:CG	44:Y:91:ILE:HG23	2.53	0.43
1:A:648:LEU:HA	1:A:648:LEU:HD23	1.79	0.43
1:A:671:THR:O	1:A:672:VAL:C	2.59	0.43
1:A:1382:SER:HB3	1:A:1416:ILE:HG12	2.00	0.43
1:A:1555:LEU:HD12	1:A:1560:ILE:HB	2.00	0.43
1:A:2172:MET:HE3	1:A:2172:MET:HB2	1.89	0.43
2:B:27:U:HO2'	2:B:28:A:P	2.41	0.43
2:B:95:G:C6	11:e:36:TYR:O	2.72	0.43
3:C:60:HIS:ND1	3:C:60:HIS:O	2.51	0.43
13:F:36:A:C3'	13:F:36:A:C8	3.01	0.43
15:H:157:G:H2'	15:H:158:G:O4'	2.19	0.43
7:i:85:PRO:CA	18:w:184:ARG:CA	2.94	0.43
21:1:889:GLU:HA	21:1:892:LEU:HD12	2.00	0.43
22:2:613:LEU:HD11	24:4:32:LEU:HD13	1.99	0.43
23:3:32:VAL:HG23	23:3:39:GLU:HB3	1.99	0.43
23:3:640:LEU:HD22	23:3:667:ILE:HG12	2.01	0.43
25:5:114:LYS:HA	25:5:119:ILE:O	2.19	0.43
29:L:73:HIS:CD2	29:L:77:LEU:HD11	2.53	0.43
35:O:45:CYS:SG	35:O:48:CYS:N	2.92	0.43
35:O:45:CYS:O	35:O:49:ALA:HA	2.18	0.43
35:O:147:LEU:HD12	35:O:148:LEU:N	2.34	0.43
37:R:52:PRO:HB3	37:R:57:ASP:OD2	2.17	0.43
37:R:119:LEU:HA	37:R:232:MET:CE	2.49	0.43
37:R:120:VAL:HG23	37:R:121:PRO:HD2	2.01	0.43
38:S:10:GLN:CA	38:S:29:TRP:CE2	3.01	0.43
39:T:459:LEU:HG	39:T:461:SER:OG	2.18	0.43
39:T:495:ALA:O	39:T:496:THR:C	2.62	0.43
1:A:298:ASP:OD1	1:A:298:ASP:C	2.62	0.43
1:A:345:PRO:O	1:A:346:ASP:O	2.35	0.43
1:A:372:PRO:HB2	3:C:342:ARG:HH21	1.84	0.43
1:A:790:ARG:HG3	3:C:60:HIS:HD2	1.82	0.43
2:B:87:A:H5'	2:B:93:U:OP2	2.19	0.43
3:C:61:GLU:OE1	3:C:62:ASP:N	2.51	0.43
3:C:295:ASP:OD1	3:C:297:ASN:HB2	2.19	0.43
3:C:461:LEU:HD23	3:C:461:LEU:HA	1.78	0.43
21:1:471:ASP:OD2	21:1:505:LYS:NZ	2.34	0.43
29:L:216:PHE:HZ	35:O:112:VAL:CG1	2.31	0.43
34:N:59:TYR:CZ	34:N:63:LEU:HD11	2.53	0.43
37:R:242:THR:HG22	37:R:244:LYS:H	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:S:56:ILE:HD12	38:S:153:PRO:HG3	2.00	0.43
38:S:131:ARG:HH12	38:S:133:CYS:HB2	1.83	0.43
1:A:48:LYS:C	1:A:50:LYS:H	2.24	0.43
1:A:293:TRP:HB2	1:A:1136:ARG:HH22	1.83	0.43
1:A:470:ARG:CZ	1:A:470:ARG:HB2	2.49	0.43
1:A:643:GLY:O	1:A:646:PRO:HD2	2.19	0.43
1:A:781:ARG:NH2	15:H:24:A:H5'	2.34	0.43
1:A:1433:ASP:O	1:A:1434:LYS:HD3	2.19	0.43
1:A:1437:ARG:O	1:A:1440:THR:OG1	2.36	0.43
3:C:73:TYR:CE1	39:T:487:LYS:HE2	2.52	0.43
3:C:137:HIS:HD2	3:C:236:MET:CB	2.22	0.43
3:C:275:TYR:OH	3:C:345:GLY:HA2	2.19	0.43
3:C:349:PHE:CG	3:C:356:PHE:HE1	2.36	0.43
3:C:481:MET:HE2	3:C:559:ILE:HD11	2.00	0.43
3:C:941:LYS:HG2	3:C:942:GLY:N	2.34	0.43
13:F:28:A:C4'	34:N:41:ARG:HA	2.48	0.43
13:F:46:G:H2'	13:F:47:A:C8	2.54	0.43
15:H:166:G:N3	15:H:166:G:H2'	2.33	0.43
15:H:180:G:N3	15:H:181:G:C8	2.87	0.43
21:1:892:LEU:HD23	21:1:892:LEU:HA	1.91	0.43
23:3:458:ALA:HA	23:3:741:PHE:CB	2.45	0.43
23:3:482:THR:OG1	23:3:501:GLY:HA3	2.19	0.43
27:7:51:ASN:OD1	27:7:61:LYS:HE2	2.18	0.43
34:N:46:LEU:HD23	34:N:46:LEU:HA	1.92	0.43
34:N:128:VAL:HG13	34:N:130:ARG:CB	2.48	0.43
35:O:185:LYS:CD	42:W:215:GLU:C	2.91	0.43
36:P:191:ASP:O	36:P:192:VAL:HG23	2.18	0.43
37:R:116:TYR:CD1	37:R:116:TYR:C	2.97	0.43
38:S:55:ARG:NH2	42:W:95:PRO:O	2.52	0.43
39:T:225:ASP:O	39:T:226:ARG:HB2	2.18	0.43
1:A:235:MET:CE	1:A:411:PHE:CA	2.85	0.43
1:A:283:VAL:O	1:A:284:ARG:CZ	2.67	0.43
1:A:284:ARG:HE	1:A:284:ARG:HB3	1.70	0.43
1:A:371:LEU:HD12	1:A:372:PRO:HD2	2.00	0.43
1:A:380:LEU:HD22	1:A:380:LEU:H	1.84	0.43
1:A:843:LEU:HD22	1:A:867:ILE:HG23	2.01	0.43
1:A:1314:VAL:HG11	1:A:1487:HIS:NE2	2.34	0.43
1:A:1539:SER:OG	1:A:1540:PRO:HD3	2.19	0.43
3:C:67:PRO:O	3:C:68:THR:C	2.61	0.43
3:C:70:GLU:C	3:C:70:GLU:CD	2.87	0.43
3:C:289:ILE:CD1	3:C:300:LEU:HD21	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:381:LEU:HD23	3:C:416:LEU:HD22	1.99	0.43
13:F:39:A:H61	14:G:8:C:N4	2.11	0.43
14:G:12:G:C2	14:G:13:C:O4'	2.71	0.43
18:w:477:GLU:HA	23:3:980:LYS:HZ3	1.84	0.43
21:1:184:VAL:O	21:1:188:ALA:CB	2.66	0.43
28:J:339:TRP:CG	37:R:116:TYR:CD2	3.06	0.43
34:N:117:CYS:C	34:N:119:CYS:N	2.73	0.43
35:O:259:ARG:HG3	35:O:274:PHE:C	2.44	0.43
39:T:347:THR:HG21	39:T:357:TRP:HE1	1.82	0.43
43:X:307:GLN:HB3	43:X:331:LEU:HD13	2.01	0.43
1:A:30:LEU:HB3	5:E:194:TYR:CZ	2.53	0.43
1:A:151:MET:SD	1:A:628:GLY:HA3	2.59	0.43
1:A:344:ASP:OD1	1:A:347:LEU:HD11	2.19	0.43
2:B:12:U:O2'	2:B:13:C:P	2.77	0.43
3:C:669:THR:HG22	3:C:690:GLU:CB	2.48	0.43
5:E:178:LEU:CD1	5:E:222:LEU:HD21	2.46	0.43
5:E:321:TYR:OH	5:E:356:ILE:HG23	2.19	0.43
15:H:29:A:N1	20:v:19:SER:HB3	2.33	0.43
15:H:68:G:C6	15:H:84:C:N4	2.85	0.43
20:v:63:HIS:CB	20:v:69:TYR:CA	2.92	0.43
21:1:900:PHE:HA	21:1:903:GLN:HE21	1.83	0.43
21:1:968:GLU:OE1	21:1:968:GLU:N	2.51	0.43
23:3:253:GLU:HA	23:3:286:ILE:HG22	2.01	0.43
23:3:820:ALA:HB2	23:3:843:LEU:HD11	2.00	0.43
23:3:1055:VAL:HB	23:3:1093:MET:HB3	2.00	0.43
26:6:14:GLN:O	26:6:46:CYS:HB3	2.18	0.43
29:L:209:ASP:HA	35:O:110:SER:CB	2.34	0.43
37:R:113:TYR:CG	37:R:118:ASP:OD2	2.72	0.43
39:T:399:LYS:CG	39:T:406:ILE:CD1	2.78	0.43
44:Y:37:TRP:CE2	44:Y:83:CYS:SG	3.11	0.43
44:Y:85:GLU:O	45:Z:502:ALA:CA	2.65	0.43
1:A:76:MET:CE	1:A:88:TYR:CE2	2.99	0.42
1:A:369:GLU:HB2	1:A:370:PRO:HD2	2.00	0.42
1:A:1373:GLN:NE2	1:A:1381:ASP:OD2	2.52	0.42
1:A:2284:MET:HE1	1:A:2311:PRO:HG3	1.99	0.42
3:C:77:VAL:CB	39:T:196:LEU:HG	2.41	0.42
3:C:366:GLN:O	3:C:367:ARG:C	2.58	0.42
3:C:457:VAL:O	3:C:458:ASP:CB	2.67	0.42
13:F:55:C:OP2	13:F:74:U:O2'	2.36	0.42
14:G:132:G:H5'	18:w:399:LEU:HD11	2.01	0.42
21:1:1108:ASN:CG	21:1:1111:CYS:H	2.26	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:169:HIS:H	23:3:185:LEU:HB2	1.83	0.42
23:3:226:GLU:HG3	23:3:261:PHE:CZ	2.51	0.42
23:3:587:VAL:CG1	23:3:590:MET:HG3	2.49	0.42
23:3:1188:ASN:OD1	23:3:1189:LYS:N	2.51	0.42
34:N:2:PRO:HG2	34:N:4:VAL:H	1.84	0.42
34:N:60:ILE:HD13	34:N:78:CYS:HB3	2.00	0.42
35:O:77:LEU:HD12	35:O:77:LEU:HA	1.89	0.42
35:O:278:GLN:O	35:O:282:VAL:HG23	2.19	0.42
37:R:124:VAL:HG22	37:R:126:ASN:N	2.34	0.42
39:T:284:TYR:N	39:T:284:TYR:CD1	2.87	0.42
42:W:474:LYS:C	42:W:490:ALA:HB2	2.43	0.42
44:Y:92:LEU:O	44:Y:96:ASN:CB	2.67	0.42
1:A:39:GLN:OE1	42:W:169:GLU:CB	2.67	0.42
1:A:328:HIS:C	1:A:329:LEU:HD23	2.43	0.42
1:A:412:ASN:OD1	1:A:412:ASN:C	2.62	0.42
1:A:1425:LYS:HG2	37:R:417:ASN:OD1	2.18	0.42
1:A:1427:ARG:O	1:A:1428:HIS:C	2.60	0.42
1:A:1560:ILE:HG12	1:A:1668:TRP:CB	2.49	0.42
1:A:1730:MET:O	1:A:1734:MET:HG2	2.19	0.42
3:C:93:ILE:HG21	39:T:218:TRP:CZ2	2.54	0.42
3:C:115:GLU:C	3:C:117:ASP:N	2.77	0.42
3:C:481:MET:SD	3:C:492:ALA:CB	3.06	0.42
15:H:168:A:N3	15:H:168:A:C2'	2.77	0.42
21:1:460:PRO:C	21:1:464:LEU:HD22	2.44	0.42
21:1:744:ALA:HB2	21:1:784:MET:SD	2.59	0.42
21:1:1289:ASN:HB2	21:1:1294:THR:HA	2.00	0.42
23:3:274:ARG:NH2	23:3:309:ASP:OD2	2.50	0.42
23:3:520:TYR:HE1	23:3:522:ASP:HB2	1.83	0.42
33:Q:500:GLY:HA2	37:R:51:ILE:HD11	2.00	0.42
37:R:220:ARG:HB2	37:R:220:ARG:CZ	2.49	0.42
44:Y:37:TRP:NE1	44:Y:83:CYS:CB	2.70	0.42
1:A:32:GLU:OE2	1:A:36:LYS:CE	2.68	0.42
1:A:75:ASP:C	1:A:77:THR:H	2.27	0.42
1:A:407:ALA:HA	1:A:408:PRO:HD3	1.87	0.42
1:A:962:LEU:HB2	1:A:965:VAL:HB	1.99	0.42
1:A:1052:VAL:HG22	1:A:1161:LEU:HD21	2.01	0.42
1:A:1099:PHE:HZ	1:A:1157:ILE:HD11	1.85	0.42
1:A:1457:HIS:HE2	37:R:424:SER:CB	2.32	0.42
1:A:2067:PHE:HB2	1:A:2072:GLU:HG2	2.00	0.42
3:C:242:LEU:HD23	3:C:242:LEU:HA	1.84	0.42
3:C:413:ARG:HB2	3:C:414:PRO:HD3	1.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:444:GLY:C	3:C:447:PRO:HD2	2.43	0.42
3:C:641:MET:HE2	3:C:655:VAL:HG21	2.01	0.42
15:H:3:C:H2'	15:H:4:G:C8	2.53	0.42
15:H:178:A:N3	15:H:178:A:H2'	2.34	0.42
21:1:707:LEU:O	21:1:710:ALA:HB3	2.20	0.42
21:1:811:LEU:HB2	21:1:812:PRO:HD3	2.00	0.42
21:1:1040:GLY:CA	21:1:1080:THR:HG22	2.48	0.42
22:2:613:LEU:HA	22:2:616:SER:OG	2.20	0.42
23:3:310:ILE:O	23:3:330:PHE:HB3	2.19	0.42
23:3:961:ILE:HB	23:3:970:TYR:CD2	2.54	0.42
34:N:15:TRP:HE3	34:N:74:LEU:HD11	1.83	0.42
35:O:185:LYS:HG2	35:O:186:PRO:HD2	2.00	0.42
42:W:155:SER:O	42:W:156:VAL:CB	2.67	0.42
1:A:173:GLU:O	1:A:520:TYR:HD2	2.02	0.42
1:A:232:LEU:N	1:A:233:PRO:CD	2.83	0.42
1:A:588:LEU:C	1:A:1551:PHE:HD1	2.27	0.42
1:A:1354:ARG:NH1	40:U:7:LEU:HG	2.34	0.42
2:B:94:U:O2'	2:B:95:G:H3'	2.18	0.42
3:C:323:PHE:CE1	3:C:424:PHE:HE1	2.37	0.42
3:C:706:GLN:HE21	3:C:708:THR:N	2.12	0.42
3:C:863:ILE:HA	3:C:864:PRO:HD3	1.88	0.42
15:H:5:C:H2'	15:H:6:U:C6	2.54	0.42
18:w:403:ASN:N	18:w:417:ARG:O	2.53	0.42
18:w:404:ILE:N	18:w:417:ARG:O	2.47	0.42
21:1:413:LYS:HG3	21:1:415:LEU:HD11	2.01	0.42
21:1:619:ASN:ND2	21:1:624:VAL:HG21	2.34	0.42
21:1:619:ASN:OD1	21:1:620:MET:N	2.52	0.42
21:1:722:GLU:O	21:1:725:ASP:CB	2.67	0.42
21:1:903:GLN:HE22	21:1:910:MET:HE2	1.85	0.42
23:3:185:LEU:HD11	23:3:235:LEU:HD13	2.01	0.42
23:3:287:PHE:HA	23:3:304:GLN:O	2.19	0.42
23:3:1014:TYR:CE2	23:3:1016:ARG:HA	2.55	0.42
23:3:1052:ASN:OD1	23:3:1096:HIS:ND1	2.39	0.42
23:3:1201:PRO:HB2	23:3:1202:PRO:HD3	2.02	0.42
26:6:47:ASP:HA	26:6:50:ASN:O	2.20	0.42
28:J:339:TRP:CD2	37:R:116:TYR:CD2	2.85	0.42
29:L:63:TRP:CZ2	29:L:99:HIS:HB2	2.54	0.42
34:N:12:PRO:HG2	34:N:74:LEU:HA	2.02	0.42
35:O:240:GLY:HA3	35:O:296:ARG:NH2	2.34	0.42
37:R:183:GLN:HB3	37:R:188:PHE:CD2	2.54	0.42
38:S:125:LYS:HB3	38:S:126:HIS:CE1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:W:528:GLY:HA2	42:W:552:VAL:CB	2.49	0.42
42:W:571:TRP:C	42:W:573:GLY:N	2.77	0.42
44:Y:69:ARG:HA	44:Y:76:SER:HA	2.02	0.42
46:x:515:SER:O	46:x:546:LEU:HA	2.19	0.42
1:A:61:MET:CE	34:N:104:ARG:HD2	2.49	0.42
1:A:89:LEU:CD2	1:A:89:LEU:C	2.93	0.42
1:A:120:TYR:HE1	1:A:485:THR:HB	1.84	0.42
1:A:596:TYR:CE1	14:G:-5:G:N9	2.88	0.42
1:A:718:ARG:NH2	37:R:259:LYS:CE	2.78	0.42
1:A:1263:TRP:CD2	1:A:1295:ILE:HD13	2.54	0.42
1:A:1363:GLN:O	1:A:1364:LEU:HG	2.18	0.42
1:A:1555:LEU:HB2	1:A:1558:THR:OG1	2.19	0.42
3:C:669:THR:HG22	3:C:690:GLU:OE1	2.19	0.42
3:C:712:LYS:O	3:C:716:GLU:HG3	2.18	0.42
5:E:277:PHE:CE1	5:E:317:ARG:HG2	2.53	0.42
14:G:5:G:C2	14:G:6:A:C5	3.08	0.42
14:G:136:U:O4	21:1:515:ALA:HA	2.19	0.42
21:1:494:GLU:HA	21:1:497:ILE:HG22	2.01	0.42
21:1:940:LEU:O	21:1:948:ARG:NH2	2.51	0.42
21:1:1255:PHE:HD2	22:2:487:LEU:HD22	1.81	0.42
22:2:536:MET:HE2	22:2:564:ILE:O	2.19	0.42
23:3:508:CYS:SG	23:3:518:GLN:NE2	2.92	0.42
23:3:673:VAL:HA	23:3:690:ARG:HA	2.02	0.42
23:3:784:THR:HB	23:3:786:ARG:NH1	2.32	0.42
35:O:104:LYS:HG3	35:O:139:LYS:HZ1	1.84	0.42
35:O:133:PRO:HG2	35:O:137:LEU:HB2	2.01	0.42
35:O:248:LEU:O	35:O:252:PHE:HD2	2.03	0.42
38:S:55:ARG:HH22	42:W:96:GLU:C	2.26	0.42
39:T:318:ARG:CG	39:T:318:ARG:NH1	2.82	0.42
46:x:1004:GLU:CB	46:x:1007:TRP:CB	2.97	0.42
1:A:385:GLU:HB3	1:A:386:PRO:HD2	2.00	0.42
1:A:494:LEU:HD23	1:A:494:LEU:HA	1.84	0.42
1:A:715:GLU:OE1	37:R:258:TRP:CE3	2.73	0.42
1:A:791:GLN:NE2	1:A:1026:ASN:OD1	2.52	0.42
1:A:1362:ASP:OD1	1:A:1362:ASP:N	2.51	0.42
3:C:85:ASP:OD2	39:T:240:LEU:HA	2.20	0.42
3:C:90:THR:O	3:C:92:PRO:HD3	2.19	0.42
15:H:107:A:N1	15:H:108:G:C5	2.88	0.42
18:w:410:ILE:HG13	18:w:452:ILE:HG22	2.02	0.42
21:1:1075:ARG:HE	21:1:1075:ARG:HB2	1.64	0.42
23:3:146:ARG:HB2	23:3:150:ALA:HA	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:353:PHE:O	23:3:432:ARG:NH1	2.44	0.42
27:7:30:GLU:HA	27:7:33:VAL:HG12	2.02	0.42
29:L:219:LYS:NZ	35:O:105:ASP:O	2.53	0.42
35:O:224:ASP:N	35:O:225:PRO:HD2	2.34	0.42
35:O:241:ASP:CG	35:O:268:GLN:HE21	2.28	0.42
37:R:71:GLN:HE21	37:R:71:GLN:HB2	1.61	0.42
38:S:98:LEU:HD21	38:S:129:PHE:HD2	1.84	0.42
38:S:102:ASN:OD1	38:S:107:THR:O	2.37	0.42
39:T:188:PRO:HG3	39:T:443:THR:HG21	2.01	0.42
42:W:381:PHE:O	42:W:382:ASN:C	2.61	0.42
44:Y:38:ILE:HG12	44:Y:82:LEU:HB3	2.02	0.42
1:A:309:ARG:NH2	40:U:1:MET:HE2	2.34	0.42
1:A:384:VAL:O	1:A:385:GLU:HG2	2.20	0.42
1:A:651:TRP:CD1	13:F:66:C:C2	3.07	0.42
2:B:19:A:H2'	2:B:20:G:C5'	2.49	0.42
2:B:32:C:OP1	36:P:33:ARG:NE	2.53	0.42
3:C:140:HIS:CB	3:C:230:ASP:H	2.33	0.42
3:C:259:LYS:HD2	50:C:1500:GTP:C4	2.55	0.42
3:C:452:THR:HB	3:C:577:PHE:CE2	2.55	0.42
5:E:114:GLU:CD	5:E:116:HIS:NE2	2.76	0.42
5:E:152:SER:OG	5:E:153:PHE:HD1	2.03	0.42
13:F:58:G:O2'	13:F:59:G:P	2.78	0.42
14:G:141:C:H2'	14:G:142:U:C6	2.52	0.42
15:H:179:C:C2	15:H:180:G:C8	3.07	0.42
16:o:160:LYS:O	16:o:161:MET:C	2.63	0.42
21:1:401:ASP:HA	21:1:404:LEU:HB2	2.00	0.42
21:1:848:GLU:O	21:1:851:SER:OG	2.32	0.42
21:1:1179:ASP:OD1	21:1:1181:ASP:N	2.52	0.42
23:3:3:LEU:HA	23:3:1130:VAL:O	2.20	0.42
23:3:456:PRO:HB2	23:3:757:ILE:HD13	2.02	0.42
25:5:25:ASN:HB3	25:5:87:LEU:HA	2.02	0.42
28:J:294:HIS:HE1	29:L:227:THR:CB	2.26	0.42
29:L:703:MET:O	29:L:707:ALA:HB3	2.18	0.42
31:K:157:ARG:O	31:K:160:ILE:CG1	2.68	0.42
36:P:226:LYS:HD3	36:P:227:TYR:HE1	1.83	0.42
37:R:67:ILE:CG1	37:R:71:GLN:OE1	2.68	0.42
39:T:471:ASP:C	39:T:471:ASP:OD1	2.62	0.42
41:V:484:SER:O	41:V:486:THR:N	2.53	0.42
42:W:571:TRP:O	42:W:573:GLY:N	2.52	0.42
1:A:120:TYR:CE1	1:A:485:THR:HG22	2.54	0.42
1:A:372:PRO:HB2	3:C:342:ARG:NH2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:382:GLU:O	1:A:383:PHE:CG	2.73	0.42
1:A:651:TRP:CE2	13:F:66:C:N3	2.88	0.42
1:A:816:TRP:CE2	1:A:820:ARG:HG3	2.55	0.42
1:A:1436:TRP:HA	1:A:1439:ARG:CZ	2.50	0.42
1:A:2272:MET:HE3	1:A:2296:LEU:HB3	2.01	0.42
1:A:2302:LYS:HD2	1:A:2306:HIS:CE1	2.54	0.42
3:C:149:LEU:HA	3:C:427:PHE:HD2	1.82	0.42
3:C:465:MET:HE1	3:C:475:MET:CE	2.50	0.42
13:F:28:A:O4'	34:N:41:ARG:CA	2.64	0.42
14:G:-3:A:H2'	14:G:-2:C:C6	2.55	0.42
15:H:82:G:C2	15:H:83:A:C5	3.08	0.42
17:p:197:ASP:HA	17:p:200:ALA:HB3	2.02	0.42
21:1:527:GLY:O	21:1:531:LEU:HD13	2.20	0.42
22:2:525:PRO:HD2	22:2:528:ILE:HD12	2.00	0.42
23:3:412:ILE:HD12	23:3:1118:VAL:HG11	2.01	0.42
23:3:519:VAL:HG22	23:3:524:ILE:HG23	2.02	0.42
23:3:691:THR:HG22	23:3:716:SER:HB3	2.02	0.42
35:O:24:CYS:HB3	35:O:26:THR:H	1.85	0.42
39:T:187:LYS:N	39:T:188:PRO:CD	2.83	0.42
39:T:233:LEU:HD23	39:T:233:LEU:O	2.20	0.42
42:W:431:ARG:O	42:W:446:GLU:HA	2.19	0.42
44:Y:37:TRP:HH2	45:Z:498:GLY:N	2.15	0.42
44:Y:59:TYR:HB3	44:Y:92:LEU:HD23	2.01	0.42
1:A:137:GLU:N	1:A:138:PRO:HD2	2.35	0.42
1:A:228:TRP:CD1	1:A:228:TRP:H	2.38	0.42
1:A:303:ILE:CG2	3:C:933:PHE:CD1	3.03	0.42
1:A:629:PHE:CD2	1:A:629:PHE:O	2.73	0.42
1:A:697:MET:N	1:A:698:PRO:HD3	2.34	0.42
1:A:833:LYS:HE3	1:A:834:HIS:NE2	2.35	0.42
1:A:1416:ILE:HB	1:A:1417:PRO:HD3	2.01	0.42
1:A:1457:HIS:HE1	37:R:424:SER:HA	1.74	0.42
1:A:1554:GLN:NE2	1:A:1620:TYR:O	2.49	0.42
2:B:92:U:C3'	2:B:93:U:H5'	2.50	0.42
3:C:140:HIS:HB3	3:C:230:ASP:H	1.85	0.42
3:C:149:LEU:HA	3:C:427:PHE:CE2	2.54	0.42
3:C:710:ASN:C	3:C:712:LYS:N	2.77	0.42
14:G:139:U:H2'	14:G:140:A:C8	2.55	0.42
15:H:26:A:C5	15:H:27:U:C5	3.08	0.42
17:p:209:GLY:O	17:p:211:LYS:N	2.52	0.42
21:1:687:VAL:HA	21:1:690:ILE:HG22	2.01	0.42
21:1:727:VAL:HG12	21:1:731:LEU:HD11	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:790:LYS:O	21:1:793:LYS:HB3	2.19	0.42
23:3:1039:LEU:HB2	23:3:1043:THR:OG1	2.20	0.42
28:J:240:THR:O	28:J:241:VAL:HB	2.19	0.42
28:J:259:GLN:HE21	29:L:220:PRO:HD3	1.82	0.42
35:O:253:TYR:CZ	38:S:120:GLN:CG	3.02	0.42
36:P:58:ASP:OD2	36:P:61:ARG:HB2	2.19	0.42
45:Z:564:PRO:C	45:Z:582:TYR:CG	2.98	0.42
1:A:48:LYS:HG2	1:A:49:ARG:N	2.35	0.42
1:A:86:ARG:HH22	37:R:211:ARG:HA	1.85	0.42
1:A:1188:ASN:ND2	1:A:1233:ASP:OD2	2.47	0.42
1:A:1371:TYR:OH	41:V:464:GLN:CB	2.67	0.42
1:A:1544:ARG:HB3	1:A:1672:ASP:OD2	2.19	0.42
1:A:2120:LEU:HD12	1:A:2120:LEU:N	2.35	0.42
3:C:220:ARG:HD3	3:C:477:HIS:NE2	2.34	0.42
3:C:474:LEU:HD12	3:C:500:THR:O	2.20	0.42
3:C:489:GLN:N	3:C:489:GLN:CD	2.78	0.42
15:H:147:G:C2	15:H:148:C:N3	2.87	0.42
15:H:155:C:H2'	15:H:156:U:H5''	2.02	0.42
15:H:179:C:O2	15:H:180:G:C8	2.72	0.42
21:1:555:VAL:O	21:1:559:ILE:HG12	2.19	0.42
22:2:643:PRO:HG2	24:4:66:ASP:HA	2.01	0.42
23:3:259:LYS:HE3	23:3:266:ASP:OD2	2.20	0.42
23:3:261:PHE:HD1	23:3:261:PHE:HA	1.72	0.42
23:3:288:VAL:HG23	23:3:289:CYS:N	2.33	0.42
23:3:706:MET:CE	23:3:770:LEU:CB	2.98	0.42
23:3:968:ARG:CZ	23:3:979:ARG:HH11	2.33	0.42
23:3:1011:TRP:HB3	23:3:1024:PHE:CZ	2.55	0.42
28:J:216:ASP:O	28:J:218:GLU:N	2.53	0.42
34:N:56:LYS:HE2	34:N:83:TYR:O	2.20	0.42
38:S:155:ASP:C	38:S:155:ASP:OD1	2.62	0.42
39:T:281:ILE:CD1	39:T:282:ARG:HG2	2.50	0.42
1:A:592:TYR:O	1:A:593:ARG:C	2.59	0.41
1:A:1320:LYS:NZ	37:R:434:TYR:CE1	2.88	0.41
1:A:1402:ARG:CD	37:R:412:ASP:HA	2.50	0.41
1:A:2272:MET:HE3	1:A:2272:MET:HB3	1.74	0.41
3:C:291:MET:HG2	3:C:292:TYR:CE1	2.54	0.41
3:C:445:ALA:HB1	3:C:449:ILE:HG13	2.02	0.41
3:C:829:GLU:HG3	3:C:830:PRO:HD2	2.01	0.41
9:d:68:GLU:HA	9:d:97:SER:O	2.19	0.41
13:F:8:C:C6	13:F:8:C:C5'	2.98	0.41
13:F:31:U:H2'	13:F:32:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:68:G:H2'	15:H:69:U:H6	1.82	0.41
9:k:68:GLU:HA	9:k:97:SER:O	2.19	0.41
21:1:699:GLN:O	21:1:700:LYS:C	2.63	0.41
21:1:783:GLU:O	21:1:787:ILE:HG12	2.20	0.41
23:3:812:LYS:NZ	23:3:855:PRO:HG2	2.35	0.41
28:J:262:ARG:HB3	29:L:220:PRO:HG3	2.02	0.41
28:J:297:ASN:CG	29:L:223:GLY:HA3	2.45	0.41
28:J:368:ARG:O	28:J:372:VAL:HG23	2.20	0.41
37:R:131:ASP:OD2	37:R:132:LEU:N	2.53	0.41
38:S:15:TYR:HB2	38:S:163:TYR:HB2	2.02	0.41
38:S:131:ARG:CD	38:S:131:ARG:C	2.93	0.41
1:A:61:MET:HB3	1:A:62:PRO:CD	2.51	0.41
1:A:121:HIS:CD2	1:A:481:PHE:O	2.70	0.41
1:A:151:MET:SD	1:A:628:GLY:CA	3.08	0.41
1:A:155:LYS:CE	1:A:624:GLY:O	2.68	0.41
1:A:372:PRO:HG2	3:C:342:ARG:HE	1.80	0.41
1:A:1051:LEU:HD22	36:P:193:VAL:HG11	2.00	0.41
1:A:1503:TRP:CZ2	1:A:1753:LEU:HD21	2.55	0.41
1:A:1661:TRP:NE1	1:A:1697:SER:O	2.53	0.41
3:C:73:TYR:HB3	3:C:77:VAL:HG21	2.02	0.41
3:C:259:LYS:HG2	3:C:262:ARG:HD3	1.99	0.41
3:C:449:ILE:CD1	3:C:466:SER:HA	2.50	0.41
4:D:452:PRO:CB	23:3:570:PRO:CB	2.92	0.41
4:D:863:THR:CB	23:3:599:GLU:CB	2.96	0.41
14:G:-8:U:H5	40:U:16:ASN:HB3	1.85	0.41
15:H:80:A:C2	15:H:81:G:N7	2.88	0.41
15:H:153:A:H62	15:H:177:A:H2	1.67	0.41
21:1:1185:ARG:HD2	21:1:1218:ASN:OD1	2.20	0.41
23:3:425:VAL:O	23:3:435:LEU:HD12	2.20	0.41
23:3:436:ARG:HG2	23:3:778:ALA:HA	2.01	0.41
29:L:31:TRP:CH2	29:L:47:LYS:HA	2.55	0.41
34:N:37:HIS:CD2	34:N:37:HIS:O	2.74	0.41
34:N:75:TYR:CZ	34:N:79:ILE:HD11	2.55	0.41
35:O:62:ARG:C	35:O:63:MET:HE2	2.45	0.41
35:O:132:ARG:HG3	35:O:137:LEU:CD2	2.50	0.41
35:O:164:ILE:HD12	35:O:164:ILE:HA	1.91	0.41
35:O:219:THR:O	35:O:221:PRO:CD	2.66	0.41
37:R:82:MET:HE3	37:R:82:MET:CA	2.48	0.41
37:R:88:ILE:CG2	37:R:96:ILE:HG23	2.48	0.41
37:R:418:GLN:HE21	37:R:418:GLN:HB2	1.64	0.41
37:R:442:ARG:NH1	37:R:443:GLY:CA	2.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:W:371:THR:O	42:W:372:ASN:CB	2.68	0.41
44:Y:64:ASN:O	44:Y:83:CYS:HB3	2.19	0.41
45:Z:572:PRO:CG	45:Z:588:ASP:OD2	2.67	0.41
1:A:206:TRP:CE3	1:A:212:PRO:HB3	2.55	0.41
1:A:211:GLN:HA	1:A:212:PRO:HD3	1.82	0.41
1:A:428:LYS:HE3	1:A:454:TYR:CE1	2.55	0.41
1:A:434:HIS:CG	3:C:892:GLN:OE1	2.74	0.41
1:A:638:LEU:HA	1:A:638:LEU:HD23	1.70	0.41
1:A:2216:CYS:HA	1:A:2225:LEU:HB3	2.01	0.41
3:C:148:CYS:SG	3:C:312:SER:O	2.78	0.41
3:C:512:GLU:HG3	3:C:562:THR:O	2.19	0.41
4:D:1481:ILE:C	4:D:1483:ARG:H	2.28	0.41
5:E:263:ASP:O	5:E:272:ARG:NE	2.32	0.41
21:1:520:THR:HG21	21:1:558:ARG:HE	1.85	0.41
29:L:219:LYS:NZ	35:O:104:LYS:O	2.51	0.41
29:L:741:GLN:O	29:L:744:GLN:CG	2.69	0.41
35:O:214:LEU:HD23	35:O:214:LEU:HA	1.82	0.41
39:T:225:ASP:O	39:T:226:ARG:CB	2.67	0.41
1:A:54:VAL:O	1:A:54:VAL:HG23	2.20	0.41
1:A:258:PHE:CD2	1:A:434:HIS:HA	2.55	0.41
1:A:800:TYR:HB3	3:C:59:LEU:HD11	2.02	0.41
1:A:1581:LEU:HD22	1:A:1746:ARG:NH1	2.36	0.41
3:C:70:GLU:CD	3:C:71:GLU:N	2.79	0.41
3:C:445:ALA:CB	3:C:449:ILE:HD11	2.43	0.41
3:C:853:ARG:O	3:C:854:ARG:HB3	2.20	0.41
15:H:152:G:H2'	15:H:152:G:N3	2.36	0.41
15:H:154:C:N3	15:H:176:G:N1	2.61	0.41
18:w:422:PHE:HZ	18:w:450:THR:CG2	2.31	0.41
21:1:1136:TYR:CE1	21:1:1144:GLN:HB3	2.55	0.41
23:3:199:GLU:HB3	23:3:203:ASN:HD21	1.85	0.41
28:J:220:LEU:O	28:J:223:TYR:HB3	2.21	0.41
28:J:412:ASP:O	28:J:413:GLU:C	2.63	0.41
37:R:155:VAL:O	37:R:159:VAL:HG23	2.20	0.41
42:W:97:ASN:O	42:W:99:PHE:N	2.53	0.41
1:A:331:TRP:HE3	1:A:332:TYR:N	2.18	0.41
1:A:346:ASP:O	1:A:347:LEU:C	2.64	0.41
1:A:2112:LYS:HE2	1:A:2112:LYS:HB3	1.67	0.41
3:C:589:LYS:HB3	3:C:659:VAL:O	2.20	0.41
3:C:704:VAL:O	3:C:709:TRP:CZ2	2.74	0.41
3:C:707:ILE:HD11	3:C:735:PHE:HB2	2.01	0.41
5:E:348:ASP:OD1	5:E:348:ASP:C	2.62	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:F:40:U:O4	13:F:41:A:N6	2.54	0.41
15:H:103:U:C3'	15:H:104:U:H5'	2.51	0.41
21:1:621:ASP:OD2	21:1:623:TYR:HB3	2.19	0.41
21:1:719:TYR:CD1	23:3:218:ASN:HB2	2.56	0.41
23:3:116:VAL:HA	23:3:117:PRO:HD3	1.95	0.41
23:3:554:VAL:HG12	23:3:556:ILE:HG23	2.02	0.41
23:3:896:PHE:CZ	23:3:972:LEU:HB2	2.55	0.41
24:4:69:TYR:OH	24:4:73:ILE:HG13	2.20	0.41
28:J:340:GLN:N	28:J:341:PRO:HD3	2.35	0.41
28:J:360:ASP:C	28:J:363:ARG:HG3	2.45	0.41
29:L:717:MET:O	29:L:721:LEU:N	2.48	0.41
34:N:38:GLU:C	34:N:40:LYS:N	2.75	0.41
36:P:192:VAL:CG1	36:P:193:VAL:N	2.83	0.41
39:T:223:SER:OG	39:T:224:ALA:N	2.53	0.41
43:X:173:GLN:NE2	43:X:176:GLU:HA	2.36	0.41
1:A:107:PRO:O	1:A:108:MET:HB2	2.21	0.41
1:A:118:VAL:HG12	1:A:119:LEU:N	2.36	0.41
1:A:1315:VAL:HG12	1:A:1538:TRP:CD2	2.56	0.41
1:A:1325:LEU:HD23	1:A:1325:LEU:HA	1.86	0.41
1:A:2111:LEU:HD21	1:A:2225:LEU:HD21	2.03	0.41
3:C:97:VAL:HG21	36:P:45:GLN:CG	2.46	0.41
3:C:137:HIS:NE2	3:C:236:MET:SD	2.93	0.41
13:F:39:A:H2'	13:F:40:U:O4'	2.21	0.41
14:G:-2:C:H2'	14:G:-1:G:H8	1.82	0.41
15:H:72:U:H6	15:H:72:U:O5'	2.03	0.41
15:H:171:U:H2'	15:H:172:C:O4'	2.21	0.41
18:w:34:ARG:O	18:w:35:ASP:C	2.62	0.41
20:v:56:CYS:SG	20:v:56:CYS:O	2.79	0.41
21:1:815:PHE:HA	21:1:819:TRP:CD1	2.56	0.41
22:2:487:LEU:HD23	22:2:487:LEU:C	2.46	0.41
23:3:168:TYR:CE1	27:7:69:MET:HB3	2.55	0.41
32:I:296:PHE:CB	32:I:305:SER:O	2.68	0.41
39:T:297:HIS:CE1	39:T:300:ILE:HD12	2.56	0.41
39:T:455:GLN:CG	39:T:456:PRO:HD2	2.51	0.41
44:Y:24:ASP:O	44:Y:26:VAL:N	2.54	0.41
46:x:936:TYR:O	46:x:937:ILE:C	2.63	0.41
1:A:148:TRP:CZ2	1:A:616:PHE:CA	3.02	0.41
1:A:175:PRO:CG	1:A:498:ARG:NH2	2.73	0.41
1:A:280:GLU:CD	1:A:281:PRO:HD2	2.46	0.41
1:A:294:ASN:OD1	3:C:654:LYS:CD	2.66	0.41
1:A:596:TYR:O	1:A:598:LEU:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:866:LEU:O	1:A:869:GLN:HB3	2.21	0.41
1:A:984:MET:SD	1:A:1048:MET:HE1	2.60	0.41
1:A:1035:GLN:HA	1:A:1446:GLN:HE22	1.84	0.41
1:A:1099:PHE:CE2	1:A:1153:VAL:HG13	2.53	0.41
1:A:1221:THR:O	1:A:1223:GLU:HG3	2.20	0.41
1:A:1342:TRP:CG	3:C:921:LEU:CD2	2.99	0.41
1:A:1430:LEU:HD21	37:R:422:MET:HA	2.03	0.41
1:A:1458:GLN:HE21	1:A:1463:LYS:HG3	1.86	0.41
1:A:2332:ASP:C	1:A:2334:TYR:H	2.28	0.41
2:B:23:C:H6	2:B:26:A:H62	1.67	0.41
2:B:40:U:O2	2:B:40:U:C2'	2.69	0.41
2:B:63:A:C4'	5:E:106:LYS:NZ	2.81	0.41
3:C:230:ASP:OD1	3:C:259:LYS:HB2	2.17	0.41
3:C:270:PRO:HA	3:C:271:PRO:HD3	1.87	0.41
3:C:457:VAL:C	3:C:458:ASP:CG	2.88	0.41
14:G:26:U:H2'	35:O:269:CYS:SG	2.61	0.41
14:G:155:U:C4'	14:G:156:U:H5'	2.49	0.41
15:H:4:G:H2'	15:H:5:C:C6	2.55	0.41
15:H:83:A:H2'	15:H:84:C:H1'	2.00	0.41
20:v:50:HIS:CE1	21:1:1180:ARG:CB	3.01	0.41
21:1:1127:THR:O	22:2:571:LEU:HD13	2.21	0.41
23:3:314:THR:HG22	23:3:315:LEU:N	2.36	0.41
24:4:67:ALA:O	24:4:70:ALA:HB3	2.21	0.41
28:J:273:TYR:CD1	37:R:228:PRO:CB	3.04	0.41
29:L:214:ILE:O	29:L:215:PRO:C	2.63	0.41
35:O:149:LYS:CE	35:O:290:LYS:HE2	2.48	0.41
35:O:157:TYR:C	35:O:159:ARG:N	2.77	0.41
36:P:189:ASP:C	36:P:191:ASP:H	2.29	0.41
36:P:189:ASP:CG	36:P:192:VAL:CG2	2.94	0.41
37:R:103:ARG:O	37:R:104:GLN:C	2.64	0.41
38:S:11:PRO:HB3	38:S:166:GLY:N	2.34	0.41
1:A:143:GLN:O	1:A:146:SER:HB3	2.20	0.41
1:A:642:ARG:CZ	2:B:28:A:C4	3.04	0.41
1:A:1342:TRP:CD1	3:C:921:LEU:HD11	2.55	0.41
1:A:2310:ARG:HG2	1:A:2310:ARG:HH11	1.84	0.41
2:B:41:U:C4	2:B:42:U:O4	2.73	0.41
3:C:300:LEU:N	3:C:300:LEU:CD1	2.84	0.41
4:D:538:ILE:O	4:D:585:ILE:HA	2.21	0.41
13:F:60:C:H5''	37:R:219:PRO:HB3	2.01	0.41
14:G:21:A:OP1	35:O:156:TYR:CE2	2.73	0.41
15:H:160:A:H2'	15:H:161:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:k:62:HIS:O	9:k:103:GLY:HA3	2.21	0.41
17:p:184:PRO:C	17:p:186:ARG:N	2.75	0.41
21:1:719:TYR:HB3	23:3:216:GLY:O	2.20	0.41
21:1:1016:LEU:O	21:1:1019:ARG:HB3	2.20	0.41
21:1:1055:TRP:O	21:1:1058:ILE:HB	2.20	0.41
21:1:1092:ASP:OD1	21:1:1092:ASP:N	2.53	0.41
23:3:86:ARG:CD	23:3:104:GLN:HE21	2.33	0.41
23:3:205:GLN:HE21	23:3:227:PRO:HB3	1.85	0.41
23:3:718:ARG:HG2	23:3:719:SER:H	1.84	0.41
26:6:90:ASN:OD1	26:6:91:LEU:N	2.54	0.41
34:N:68:LYS:HD3	34:N:68:LYS:HA	1.91	0.41
35:O:104:LYS:H	35:O:104:LYS:HG2	1.71	0.41
36:P:73:GLU:C	36:P:73:GLU:CD	2.88	0.41
42:W:290:GLY:HA2	42:W:571:TRP:O	2.19	0.41
45:Z:525:TYR:HD1	45:Z:526:ILE:CG2	2.29	0.41
1:A:128:PHE:CD1	1:A:473:PHE:CE1	3.09	0.41
1:A:225:TYR:O	1:A:418:THR:CB	2.68	0.41
1:A:293:TRP:HD1	1:A:1136:ARG:NH2	2.19	0.41
1:A:440:PRO:O	1:A:441:VAL:C	2.64	0.41
1:A:965:VAL:O	1:A:1100:ARG:NH1	2.54	0.41
1:A:1052:VAL:CG2	1:A:1161:LEU:HD21	2.51	0.41
1:A:1407:ASP:OD1	1:A:1407:ASP:N	2.51	0.41
1:A:2090:ILE:H	1:A:2090:ILE:HD13	1.86	0.41
3:C:64:LYS:HE2	3:C:64:LYS:HA	2.02	0.41
3:C:65:TYR:O	3:C:66:TYR:CG	2.73	0.41
3:C:79:THR:HA	39:T:199:VAL:O	2.20	0.41
3:C:132:VAL:HG11	3:C:226:VAL:CG2	2.49	0.41
3:C:133:THR:HB	3:C:225:VAL:HA	2.02	0.41
3:C:513:ASN:O	3:C:513:ASN:ND2	2.54	0.41
3:C:518:ASP:N	3:C:519:GLU:OE2	2.54	0.41
5:E:115:LEU:O	5:E:116:HIS:CD2	2.74	0.41
5:E:243:LEU:HD22	5:E:243:LEU:HA	1.80	0.41
5:E:266:PRO:CB	29:L:785:GLN:HB3	2.51	0.41
14:G:132:G:C4'	18:w:399:LEU:HD13	2.51	0.41
15:H:152:G:H2'	15:H:153:A:C1'	2.51	0.41
17:p:156:ASN:O	17:p:219:LYS:O	2.39	0.41
21:1:184:VAL:O	21:1:188:ALA:HB2	2.21	0.41
21:1:642:PRO:HB3	21:1:682:HIS:NE2	2.36	0.41
21:1:664:GLY:O	21:1:667:ILE:HB	2.21	0.41
21:1:770:MET:O	21:1:774:ILE:HG12	2.21	0.41
21:1:963:LYS:HG2	21:1:1003:VAL:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:1080:THR:HA	21:1:1083:TYR:CD2	2.56	0.41
21:1:1092:ASP:OD1	21:1:1093:VAL:N	2.54	0.41
21:1:1227:ILE:O	21:1:1231:MET:HG2	2.20	0.41
21:1:1252:GLN:OE1	22:2:499:PRO:HA	2.20	0.41
23:3:65:LEU:HD12	23:3:79:VAL:O	2.21	0.41
23:3:464:ARG:NH1	23:3:473:TYR:OH	2.53	0.41
23:3:633:LEU:HD13	23:3:667:ILE:CG2	2.51	0.41
23:3:910:ALA:HB2	23:3:948:VAL:HG23	2.02	0.41
28:J:376:VAL:HB	28:J:411:MET:HE1	2.01	0.41
32:I:606:TRP:O	32:I:609:ALA:HB3	2.21	0.41
32:I:616:TYR:O	32:I:618:ARG:N	2.54	0.41
35:O:157:TYR:C	35:O:159:ARG:H	2.27	0.41
36:P:188:TRP:C	36:P:188:TRP:HE3	2.29	0.41
37:R:69:VAL:HG12	37:R:70:ALA:N	2.36	0.41
37:R:106:GLN:N	37:R:106:GLN:CD	2.79	0.41
37:R:132:LEU:HD13	39:T:399:LYS:HE3	2.02	0.41
37:R:414:ARG:NH2	37:R:414:ARG:CB	2.73	0.41
39:T:209:CYS:O	39:T:221:THR:HA	2.21	0.41
39:T:210:ILE:HG12	39:T:221:THR:HG22	2.03	0.41
39:T:294:LEU:N	39:T:294:LEU:HD23	2.36	0.41
39:T:400:PHE:HD1	39:T:401:PRO:HA	1.86	0.41
42:W:298:PRO:O	42:W:299:LEU:CB	2.68	0.41
42:W:517:SER:O	42:W:518:PRO:C	2.60	0.41
43:X:303:HIS:CB	43:X:383:ASP:HB3	2.51	0.41
44:Y:10:ILE:O	44:Y:13:LEU:N	2.53	0.41
44:Y:67:LEU:HA	44:Y:80:CYS:HA	2.02	0.41
45:Z:566:TYR:CE2	45:Z:584:TRP:HE3	2.29	0.41
1:A:842:ALA:HB1	1:A:920:ALA:HB1	2.03	0.41
1:A:1312:PRO:CD	1:A:1541:THR:CG2	2.99	0.41
1:A:1425:LYS:CB	37:R:417:ASN:OD1	2.69	0.41
1:A:1755:SER:HB2	21:1:938:TRP:CH2	2.54	0.41
1:A:2117:ILE:HG21	1:A:2301:PRO:HB2	2.02	0.41
3:C:149:LEU:HD11	3:C:427:PHE:CB	2.51	0.41
3:C:354:ARG:CG	3:C:354:ARG:HH11	2.34	0.41
3:C:513:ASN:ND2	3:C:513:ASN:C	2.78	0.41
13:F:42:C:C2	13:F:43:A:C8	3.09	0.41
15:H:24:A:O2'	15:H:26:A:OP2	2.38	0.41
21:1:1286:ARG:N	23:3:1006:GLN:HE22	2.19	0.41
23:3:274:ARG:HD2	23:3:389:PRO:HD3	2.02	0.41
25:5:14:PRO:O	25:5:17:VAL:HG22	2.21	0.41
28:J:423:GLU:OE1	28:J:423:GLU:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:L:49:ARG:NH1	29:L:53:TRP:HB3	2.36	0.41
34:N:40:LYS:O	34:N:44:GLU:HB3	2.21	0.41
34:N:113:PHE:HD1	37:R:200:VAL:HG21	1.86	0.41
38:S:11:PRO:O	38:S:29:TRP:NE1	2.41	0.41
38:S:20:MET:CE	38:S:141:ARG:HD2	2.51	0.41
39:T:399:LYS:HB2	39:T:404:SER:HB3	2.03	0.41
39:T:434:GLY:HA2	39:T:464:GLY:N	2.36	0.41
41:V:585:ILE:O	41:V:588:GLN:N	2.54	0.41
1:A:76:MET:HE2	1:A:88:TYR:CE2	2.55	0.40
1:A:329:LEU:HD12	3:C:177:ARG:HG2	2.03	0.40
1:A:593:ARG:CD	14:G:-4:A:H4'	2.43	0.40
1:A:1119:ASP:CG	1:A:1123:GLU:H	2.29	0.40
3:C:221:ILE:HG13	3:C:479:THR:OG1	2.21	0.40
3:C:235:VAL:HG13	3:C:239:THR:OG1	2.22	0.40
3:C:392:LEU:N	3:C:393:PRO:CD	2.84	0.40
5:E:178:LEU:CD2	5:E:208:ILE:HD11	2.51	0.40
5:E:257:ASN:ND2	42:W:149:SER:O	2.53	0.40
14:G:146:C:C4	14:G:147:C:N4	2.89	0.40
15:H:112:G:O5'	15:H:112:G:H8	2.04	0.40
21:1:765:TYR:O	21:1:769:VAL:HG23	2.20	0.40
21:1:806:ILE:HG12	21:1:810:ILE:HD12	2.03	0.40
21:1:997:LEU:O	21:1:1001:VAL:HG23	2.21	0.40
21:1:1126:PHE:HA	21:1:1165:TYR:CZ	2.56	0.40
23:3:6:LEU:HD12	23:3:1128:ILE:HD11	2.03	0.40
23:3:194:ASN:O	23:3:196:PRO:HD3	2.21	0.40
25:5:27:PRO:HG3	25:5:85:ARG:NH1	2.36	0.40
32:I:361:HIS:C	32:I:372:ARG:CB	2.95	0.40
34:N:70:ILE:HG23	34:N:74:LEU:HD23	2.01	0.40
35:O:155:PRO:HD3	37:R:188:PHE:CE1	2.56	0.40
35:O:220:MET:HE3	35:O:220:MET:HB3	1.72	0.40
36:P:63:LEU:C	36:P:63:LEU:CD2	2.93	0.40
41:V:530:LYS:O	41:V:531:GLU:C	2.64	0.40
43:X:263:PRO:CG	43:X:265:LYS:H	2.34	0.40
45:Z:563:ARG:HH21	45:Z:563:ARG:HG3	1.83	0.40
1:A:1251:SER:O	1:A:1298:ARG:NH2	2.55	0.40
1:A:1263:TRP:CZ2	1:A:1292:GLU:HG2	2.56	0.40
1:A:1451:ASN:HB2	37:R:428:GLY:O	2.21	0.40
3:C:64:LYS:NZ	36:P:209:ARG:NH1	2.70	0.40
3:C:85:ASP:HA	39:T:238:LEU:HB3	2.03	0.40
3:C:534:VAL:HG12	3:C:535:ALA:N	2.31	0.40
3:C:856:HIS:ND1	3:C:856:HIS:C	2.79	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:642:THR:C	4:D:644:GLU:H	2.29	0.40
13:F:42:C:H2'	13:F:43:A:O4'	2.21	0.40
15:H:2:U:H2'	15:H:3:C:C6	2.55	0.40
15:H:149:A:N3	15:H:150:U:C6	2.89	0.40
17:p:172:ASN:O	17:p:173:GLN:C	2.64	0.40
21:1:658:TRP:CZ3	21:1:700:LYS:HD2	2.55	0.40
21:1:935:THR:O	21:1:939:ARG:HG2	2.21	0.40
21:1:1126:PHE:HA	21:1:1165:TYR:CE2	2.56	0.40
22:2:614:ARG:O	22:2:618:GLY:N	2.51	0.40
22:2:648:LEU:O	22:2:649:LYS:HD3	2.21	0.40
23:3:614:VAL:HB	23:3:633:LEU:HD11	2.03	0.40
23:3:983:ASN:HB2	23:3:1021:LEU:HB2	2.03	0.40
24:4:17:VAL:HG13	24:4:84:ILE:CG2	2.48	0.40
28:J:338:GLU:O	37:R:116:TYR:CD2	2.75	0.40
28:J:376:VAL:HG13	28:J:377:LYS:N	2.36	0.40
36:P:44:ARG:HG3	39:T:258:SER:CA	2.51	0.40
38:S:12:PRO:CD	38:S:166:GLY:HA2	2.51	0.40
38:S:25:LEU:HD12	38:S:25:LEU:N	2.36	0.40
38:S:55:ARG:HH12	42:W:96:GLU:HA	1.86	0.40
42:W:528:GLY:O	42:W:552:VAL:HA	2.21	0.40
43:X:238:THR:O	43:X:393:VAL:HG23	2.21	0.40
46:x:558:ALA:O	46:x:561:SER:N	2.54	0.40
1:A:212:PRO:HD2	1:A:225:TYR:OH	2.21	0.40
1:A:652:LEU:HD23	1:A:652:LEU:HA	1.84	0.40
1:A:1057:ARG:O	1:A:1060:GLU:HB2	2.22	0.40
1:A:1273:TYR:HD2	1:A:1274:PHE:CD2	2.39	0.40
1:A:1342:TRP:CD2	3:C:921:LEU:HD21	2.50	0.40
3:C:375:GLU:N	3:C:376:PRO:HD2	2.37	0.40
4:D:455:PHE:CB	23:3:573:GLN:CG	2.99	0.40
5:E:255:MET:O	5:E:257:ASN:N	2.54	0.40
17:p:156:ASN:N	17:p:219:LYS:O	2.54	0.40
21:1:922:GLY:O	21:1:925:VAL:HG12	2.22	0.40
21:1:933:CYS:HA	21:1:936:VAL:HB	2.02	0.40
21:1:1130:PRO:HB3	22:2:528:ILE:HG23	2.04	0.40
23:3:63:ARG:HD2	23:3:83:ASP:HA	2.03	0.40
23:3:379:LEU:HB2	23:3:383:ASP:HB3	2.04	0.40
23:3:388:GLN:NE2	23:3:389:PRO:HD2	2.36	0.40
23:3:690:ARG:HE	23:3:695:GLY:N	2.20	0.40
28:J:275:ASN:OD1	28:J:275:ASN:C	2.65	0.40
31:K:92:PRO:O	31:K:93:SER:C	2.64	0.40
37:R:424:SER:O	37:R:425:GLY:C	2.65	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:S:15:TYR:CE2	38:S:22:ILE:HG21	2.57	0.40
38:S:65:GLY:O	38:S:110:SER:OG	2.40	0.40
39:T:339:GLN:CG	39:T:340:ALA:N	2.84	0.40
40:U:1:MET:O	40:U:2:TYR:C	2.64	0.40
44:Y:37:TRP:HH2	45:Z:498:GLY:HA3	1.59	0.40
45:Z:491:ASP:O	45:Z:495:ALA:HB3	2.21	0.40
1:A:282:LEU:C	1:A:282:LEU:CD2	2.93	0.40
1:A:372:PRO:CG	3:C:342:ARG:HG2	2.51	0.40
1:A:460:LYS:HA	1:A:460:LYS:HD2	1.94	0.40
1:A:938:PRO:O	1:A:941:LYS:HD3	2.22	0.40
1:A:2259:VAL:HG22	1:A:2260:GLN:H	1.86	0.40
3:C:71:GLU:C	3:C:71:GLU:CD	2.88	0.40
3:C:229:ILE:HG12	3:C:239:THR:HG21	2.04	0.40
3:C:567:GLU:O	3:C:567:GLU:HG3	2.20	0.40
13:F:96:U:H2'	13:F:97:U:C6	2.56	0.40
21:1:1052:ALA:HA	21:1:1055:TRP:CD1	2.51	0.40
21:1:1248:GLN:NE2	23:3:1030:PRO:HD3	2.36	0.40
23:3:179:ASN:HB3	23:3:213:LEU:O	2.22	0.40
23:3:192:ALA:HA	23:3:200:ALA:HB3	2.02	0.40
25:5:42:TYR:CZ	25:5:73:ALA:HA	2.56	0.40
28:J:322:MET:HA	28:J:322:MET:HE2	2.03	0.40
36:P:210:PHE:CD2	39:T:455:GLN:CD	2.90	0.40
37:R:89:GLN:HG2	38:S:155:ASP:OD2	2.21	0.40
39:T:220:VAL:HG12	39:T:221:THR:N	2.37	0.40
1:A:109:PRO:HD3	1:A:630:TRP:HZ2	1.83	0.40
1:A:120:TYR:CE1	1:A:485:THR:CG2	3.04	0.40
1:A:460:LYS:O	1:A:462:ARG:HD2	2.22	0.40
1:A:692:ASP:HA	39:T:376:ARG:HH21	1.72	0.40
1:A:718:ARG:NH2	37:R:259:LYS:HG3	2.36	0.40
1:A:787:GLU:OE1	1:A:790:ARG:NH2	2.53	0.40
1:A:923:ASP:OD2	1:A:1439:ARG:HD3	2.22	0.40
1:A:1161:LEU:HD23	1:A:1161:LEU:HA	1.85	0.40
1:A:1637:TRP:O	1:A:1656:THR:HA	2.22	0.40
2:B:20:G:C1'	2:B:21:A:OP1	2.69	0.40
2:B:57:G:C2'	2:B:58:U:H5'	2.51	0.40
3:C:144:CYS:SG	3:C:148:CYS:SG	3.15	0.40
3:C:259:LYS:HG3	50:C:1500:GTP:C5	2.57	0.40
3:C:592:VAL:HG12	3:C:603:MET:SD	2.62	0.40
3:C:673:LYS:HD3	3:C:673:LYS:H	1.86	0.40
3:C:926:ALA:N	3:C:927:PRO:CD	2.84	0.40
10:f:5:LEU:O	11:e:49:GLY:HA3	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:w:420:LYS:O	18:w:424:ARG:HG3	2.20	0.40
21:1:570:TYR:O	21:1:574:ILE:HG12	2.22	0.40
21:1:839:GLU:O	21:1:842:ASN:HB2	2.22	0.40
21:1:1023:ILE:O	21:1:1026:ASN:HB2	2.21	0.40
23:3:443:GLU:HA	23:3:735:SER:OG	2.20	0.40
23:3:717:SER:O	23:3:738:THR:HG22	2.22	0.40
23:3:999:ARG:NE	23:3:1041:TYR:OH	2.54	0.40
28:J:216:ASP:O	28:J:217:GLU:C	2.64	0.40
32:I:365:ALA:CA	32:I:369:GLY:N	2.85	0.40
37:R:422:MET:C	37:R:424:SER:N	2.73	0.40
38:S:12:PRO:HB2	38:S:13:ASN:H	1.75	0.40
39:T:218:TRP:HZ3	39:T:220:VAL:CG2	2.35	0.40
40:U:25:LEU:C	40:U:25:LEU:CD1	2.94	0.40
42:W:101:THR:C	42:W:103:GLN:N	2.79	0.40
43:X:231:ALA:O	43:X:236:THR:OG1	2.39	0.40
44:Y:32:TYR:C	44:Y:34:ASP:N	2.80	0.40
45:Z:612:TYR:C	45:Z:614:TRP:H	2.29	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1970/2335 (84%)	1835 (93%)	108 (6%)	27 (1%)	9	40
3	C	854/972 (88%)	777 (91%)	57 (7%)	20 (2%)	5	28
4	D	1720/2136 (80%)	1632 (95%)	85 (5%)	3 (0%)	43	78
5	E	297/357 (83%)	272 (92%)	16 (5%)	9 (3%)	3	22
6	a	77/126 (61%)	76 (99%)	1 (1%)	0	100	100
6	h	76/126 (60%)	75 (99%)	1 (1%)	0	100	100
7	b	80/231 (35%)	78 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	i	84/231 (36%)	82 (98%)	2 (2%)	0	100	100
8	c	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
8	j	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
9	d	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
9	k	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
10	f	72/86 (84%)	69 (96%)	3 (4%)	0	100	100
10	m	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
11	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
11	l	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
12	g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
12	n	64/76 (84%)	62 (97%)	2 (3%)	0	100	100
16	o	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	9	42
17	p	159/225 (71%)	138 (87%)	9 (6%)	12 (8%)	1	10
18	w	420/501 (84%)	380 (90%)	37 (9%)	3 (1%)	18	56
19	u	92/793 (12%)	86 (94%)	4 (4%)	2 (2%)	5	29
20	v	153/464 (33%)	124 (81%)	22 (14%)	7 (5%)	2	16
21	1	1022/1304 (78%)	897 (88%)	119 (12%)	6 (1%)	21	59
22	2	171/895 (19%)	154 (90%)	17 (10%)	0	100	100
23	3	1165/1217 (96%)	1081 (93%)	80 (7%)	4 (0%)	36	72
24	4	76/424 (18%)	69 (91%)	6 (8%)	1 (1%)	9	42
25	5	106/125 (85%)	90 (85%)	16 (15%)	0	100	100
26	6	87/110 (79%)	80 (92%)	7 (8%)	0	100	100
27	7	64/86 (74%)	55 (86%)	9 (14%)	0	100	100
28	J	483/848 (57%)	452 (94%)	24 (5%)	7 (1%)	9	40
29	L	324/802 (40%)	304 (94%)	18 (6%)	2 (1%)	21	59
30	q	130/504 (26%)	119 (92%)	7 (5%)	4 (3%)	3	22
30	r	129/504 (26%)	118 (92%)	9 (7%)	2 (2%)	7	38
30	s	65/504 (13%)	62 (95%)	2 (3%)	1 (2%)	8	40
30	t	65/504 (13%)	64 (98%)	0	1 (2%)	8	40
31	K	144/225 (64%)	134 (93%)	6 (4%)	4 (3%)	4	24
32	I	498/855 (58%)	479 (96%)	11 (2%)	8 (2%)	7	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	Q	1297/1485 (87%)	1271 (98%)	26 (2%)	0	100	100
34	N	141/144 (98%)	126 (89%)	12 (8%)	3 (2%)	5	30
35	O	283/420 (67%)	247 (87%)	26 (9%)	10 (4%)	3	20
36	P	92/229 (40%)	82 (89%)	8 (9%)	2 (2%)	5	29
37	R	274/540 (51%)	234 (85%)	25 (9%)	15 (6%)	1	14
38	S	157/166 (95%)	144 (92%)	10 (6%)	3 (2%)	6	32
39	T	311/514 (60%)	282 (91%)	17 (6%)	12 (4%)	2	18
40	U	24/2752 (1%)	20 (83%)	3 (12%)	1 (4%)	2	17
41	V	444/908 (49%)	412 (93%)	27 (6%)	5 (1%)	11	46
42	W	477/579 (82%)	421 (88%)	32 (7%)	24 (5%)	1	16
43	X	144/396 (36%)	134 (93%)	10 (7%)	0	100	100
44	Y	103/322 (32%)	92 (89%)	11 (11%)	0	100	100
45	Z	109/619 (18%)	93 (85%)	10 (9%)	6 (6%)	1	14
46	x	561/1041 (54%)	536 (96%)	20 (4%)	5 (1%)	14	51
47	y	224/301 (74%)	217 (97%)	7 (3%)	0	100	100
All	All	16082/29057 (55%)	14914 (93%)	957 (6%)	211 (1%)	12	42

All (211) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	ARG
1	A	92	LEU
1	A	167	PRO
1	A	188	LEU
1	A	331	TRP
1	A	346	ASP
1	A	383	PHE
1	A	570	ASP
1	A	629	PHE
1	A	701	ILE
3	C	388	VAL
3	C	427	PHE
3	C	444	GLY
3	C	457	VAL
3	C	458	ASP
3	C	516	LEU
3	C	824	THR

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Mol	Chain	Res	Type
4	D	957	VAL
4	D	1584	ILE
5	E	193	THR
17	p	157	ASN
17	p	183	VAL
17	p	195	GLU
18	w	284	ARG
20	v	139	PRO
20	v	165	ARG
20	v	218	PRO
28	J	413	GLU
30	q	59	HIS
30	q	60	PRO
30	s	71	ILE
30	t	69	THR
31	K	78	PRO
31	K	90	PRO
32	I	463	PRO
32	I	721	LYS
32	I	797	PHE
34	N	36	PRO
35	O	20	PHE
35	O	107	MET
35	O	225	PRO
35	O	226	PRO
36	P	49	ASP
37	R	71	GLN
37	R	135	PRO
37	R	136	ASP
37	R	186	VAL
37	R	412	ASP
37	R	416	PHE
37	R	420	LYS
37	R	425	GLY
38	S	164	PRO
39	T	186	PRO
39	T	268	LYS
39	T	341	ALA
39	T	343	PRO
39	T	495	ALA
41	V	596	LEU
41	V	597	PRO

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Mol	Chain	Res	Type
42	W	156	VAL
42	W	199	TYR
42	W	213	GLN
42	W	243	VAL
42	W	258	PRO
42	W	259	GLN
42	W	263	VAL
42	W	267	SER
42	W	279	LYS
42	W	299	LEU
42	W	325	LEU
42	W	372	ASN
42	W	492	ASN
45	Z	499	LYS
45	Z	531	LEU
45	Z	536	ARG
45	Z	569	PRO
46	x	937	ILE
1	A	122	ILE
1	A	308	ILE
1	A	349	ALA
1	A	370	PRO
1	A	374	ASP
1	A	631	ALA
3	C	90	THR
3	C	364	SER
3	C	572	GLU
3	C	711	ARG
16	o	160	LYS
17	p	159	PRO
17	p	160	GLU
17	p	177	PHE
17	p	186	ARG
19	u	280	VAL
20	v	115	PRO
21	1	112	ILE
23	3	775	ASN
28	J	217	GLU
28	J	341	PRO
28	J	376	VAL
28	J	709	VAL
30	q	9	ASN

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Mol	Chain	Res	Type
32	I	618	ARG
32	I	634	ILE
34	N	39	GLY
35	O	132	ARG
35	O	206	ASN
36	P	190	ASP
37	R	191	GLY
37	R	422	MET
38	S	12	PRO
39	T	301	ASP
40	U	2	TYR
41	V	485	GLN
42	W	191	GLY
42	W	318	VAL
42	W	482	ASP
45	Z	613	LYS
1	A	51	PHE
1	A	212	PRO
1	A	378	PHE
1	A	699	GLU
5	E	60	MET
5	E	88	ARG
5	E	256	ASP
17	p	222	TYR
18	w	177	ARG
30	q	19	PRO
30	r	9	ASN
32	I	601	GLN
32	I	752	ALA
35	O	222	ARG
37	R	104	GLN
37	R	173	PRO
39	T	406	ILE
41	V	578	SER
42	W	102	GLN
46	x	1005	SER
1	A	363	HIS
1	A	480	LYS
1	A	698	PRO
1	A	1092	ILE
3	C	63	LYS
3	C	754	VAL

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Mol	Chain	Res	Type
3	C	856	HIS
5	E	162	ARG
16	o	32	PRO
17	p	208	GLN
17	p	209	GLY
21	l	417	PRO
21	l	456	VAL
28	J	604	PRO
29	L	585	TYR
31	K	65	ILE
32	I	617	GLU
35	O	134	VAL
35	O	230	THR
37	R	124	VAL
38	S	10	GLN
39	T	401	PRO
42	W	272	GLU
42	W	554	ILE
46	x	935	ASP
1	A	359	ILE
3	C	361	PRO
3	C	615	PRO
5	E	159	PRO
20	v	217	PRO
23	3	442	LEU
35	O	239	LEU
37	R	126	ASN
37	R	423	ASP
39	T	185	MET
39	T	189	GLN
39	T	226	ARG
42	W	301	GLY
42	W	330	GLY
46	x	980	GLN
46	x	981	PRO
3	C	94	ILE
3	C	360	ALA
3	C	623	GLU
5	E	270	LYS
17	p	173	GLN
20	v	141	ILE
20	v	220	PRO

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Mol	Chain	Res	Type
21	1	944	SER
29	L	215	PRO
41	V	609	GLN
42	W	376	PRO
42	W	549	HIS
3	C	66	TYR
5	E	149	GLY
45	Z	571	PRO
1	A	186	GLU
19	u	221	PRO
31	K	17	PRO
1	A	384	VAL
18	w	229	TRP
21	1	418	PRO
24	4	27	PRO
28	J	241	VAL
39	T	411	GLY
42	W	270	PRO
4	D	585	ILE
5	E	324	PRO
17	p	184	PRO
23	3	773	VAL
30	r	60	PRO
34	N	4	VAL
21	1	932	ILE
23	3	491	VAL

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	1773/2108 (84%)	1661 (94%)	112 (6%)	16	37
3	C	745/866 (86%)	676 (91%)	69 (9%)	8	26
5	E	256/300 (85%)	244 (95%)	12 (5%)	23	45
18	w	49/446 (11%)	47 (96%)	2 (4%)	27	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	v	30/382 (8%)	28 (93%)	2 (7%)	15	36
21	1	735/1104 (67%)	735 (100%)	0	100	100
22	2	94/776 (12%)	90 (96%)	4 (4%)	26	47
23	3	1012/1051 (96%)	1011 (100%)	1 (0%)	88	89
24	4	39/336 (12%)	37 (95%)	2 (5%)	21	42
25	5	74/109 (68%)	74 (100%)	0	100	100
26	6	76/95 (80%)	76 (100%)	0	100	100
27	7	57/77 (74%)	57 (100%)	0	100	100
28	J	205/751 (27%)	193 (94%)	12 (6%)	18	39
29	L	131/709 (18%)	123 (94%)	8 (6%)	17	38
31	K	54/196 (28%)	46 (85%)	8 (15%)	3	13
34	N	130/130 (100%)	124 (95%)	6 (5%)	24	45
35	O	250/361 (69%)	240 (96%)	10 (4%)	28	49
36	P	90/203 (44%)	78 (87%)	12 (13%)	4	14
37	R	215/463 (46%)	162 (75%)	53 (25%)	1	4
38	S	129/134 (96%)	121 (94%)	8 (6%)	16	38
39	T	268/441 (61%)	251 (94%)	17 (6%)	16	37
40	U	21/2432 (1%)	16 (76%)	5 (24%)	1	4
43	X	51/349 (15%)	44 (86%)	7 (14%)	3	14
44	Y	57/291 (20%)	56 (98%)	1 (2%)	51	68
45	Z	47/545 (9%)	38 (81%)	9 (19%)	1	8
46	x	1/897 (0%)	1 (100%)	0	100	100
All	All	6589/15552 (42%)	6229 (94%)	360 (6%)	21	41

All (360) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	ARG
1	A	48	LYS
1	A	49	ARG
1	A	50	LYS
1	A	55	ASP
1	A	58	LYS
1	A	59	GLU

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Mol	Chain	Res	Type
1	A	60	ASP
1	A	75	ASP
1	A	77	THR
1	A	78	ASN
1	A	82	ARG
1	A	86	ARG
1	A	88	TYR
1	A	89	LEU
1	A	119	LEU
1	A	152	ARG
1	A	163	ARG
1	A	181	ASN
1	A	185	VAL
1	A	200	ASP
1	A	204	LEU
1	A	212	PRO
1	A	232	LEU
1	A	233	PRO
1	A	250	VAL
1	A	258	PHE
1	A	284	ARG
1	A	294	ASN
1	A	295	GLU
1	A	304	ILE
1	A	310	THR
1	A	325	HIS
1	A	329	LEU
1	A	330	THR
1	A	331	TRP
1	A	336	ASN
1	A	338	VAL
1	A	344	ASP
1	A	359	ILE
1	A	361	HIS
1	A	362	ARG
1	A	363	HIS
1	A	364	SER
1	A	366	LYS
1	A	371	LEU
1	A	377	GLU
1	A	379	GLU
1	A	380	LEU

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Mol	Chain	Res	Type
1	A	382	GLU
1	A	388	LEU
1	A	389	LYS
1	A	391	THR
1	A	394	TYR
1	A	409	ARG
1	A	413	LEU
1	A	433	GLU
1	A	439	GLN
1	A	459	LEU
1	A	462	ARG
1	A	467	GLN
1	A	468	LYS
1	A	535	ARG
1	A	546	LEU
1	A	548	ARG
1	A	579	GLN
1	A	601	GLN
1	A	606	LYS
1	A	621	VAL
1	A	630	TRP
1	A	671	THR
1	A	673	THR
1	A	674	LYS
1	A	675	GLN
1	A	679	SER
1	A	1163	ARG
1	A	1549	VAL
1	A	2073	TRP
1	A	2074	ARG
1	A	2078	ILE
1	A	2085	LEU
1	A	2087	THR
1	A	2090	ILE
1	A	2103	THR
1	A	2108	LYS
1	A	2117	ILE
1	A	2139	VAL
1	A	2143	ARG
1	A	2156	THR
1	A	2157	VAL
1	A	2159	LEU

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Mol	Chain	Res	Type
1	A	2171	GLU
1	A	2193	VAL
1	A	2194	THR
1	A	2219	THR
1	A	2223	CYS
1	A	2226	THR
1	A	2233	SER
1	A	2242	THR
1	A	2254	SER
1	A	2258	ARG
1	A	2259	VAL
1	A	2261	MET
1	A	2268	LEU
1	A	2273	VAL
1	A	2284	MET
1	A	2293	LYS
1	A	2298	LEU
1	A	2303	GLU
1	A	2310	ARG
1	A	2312	SER
1	A	2319	LEU
3	C	61	GLU
3	C	62	ASP
3	C	63	LYS
3	C	64	LYS
3	C	68	THR
3	C	71	GLU
3	C	79	THR
3	C	80	ILE
3	C	81	VAL
3	C	92	PRO
3	C	97	VAL
3	C	131	ASN
3	C	132	VAL
3	C	227	LEU
3	C	259	LYS
3	C	295	ASP
3	C	297	ASN
3	C	298	LEU
3	C	300	LEU
3	C	333	ASP
3	C	336	TYR

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Mol	Chain	Res	Type
3	C	354	ARG
3	C	357	THR
3	C	359	LYS
3	C	362	THR
3	C	366	GLN
3	C	389	ASP
3	C	427	PHE
3	C	428	THR
3	C	438	ILE
3	C	450	GLU
3	C	452	THR
3	C	454	THR
3	C	457	VAL
3	C	458	ASP
3	C	463	GLU
3	C	468	CYS
3	C	474	LEU
3	C	475	MET
3	C	489	GLN
3	C	490	PHE
3	C	495	ARG
3	C	512	GLU
3	C	517	GLU
3	C	519	GLU
3	C	540	GLU
3	C	571	ASN
3	C	572	GLU
3	C	573	GLU
3	C	596	ASN
3	C	673	LYS
3	C	675	PHE
3	C	677	GLU
3	C	704	VAL
3	C	706	GLN
3	C	709	TRP
3	C	724	TRP
3	C	725	ASP
3	C	726	LEU
3	C	730	ARG
3	C	738	ASP
3	C	749	THR
3	C	750	LEU

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Mol	Chain	Res	Type
3	C	813	ARG
3	C	826	ARG
3	C	856	HIS
3	C	885	THR
3	C	941	LYS
3	C	943	LEU
5	E	153	PHE
5	E	161	ARG
5	E	178	LEU
5	E	215	ASN
5	E	229	TYR
5	E	243	LEU
5	E	248	SER
5	E	250	LEU
5	E	265	ARG
5	E	270	LYS
5	E	271	GLU
5	E	289	LEU
18	w	419	PRO
18	w	441	PRO
20	v	18	SER
20	v	56	CYS
22	2	498	VAL
22	2	520	PRO
22	2	614	ARG
22	2	616	SER
23	3	442	LEU
24	4	27	PRO
24	4	83	PRO
28	J	217	GLU
28	J	218	GLU
28	J	219	GLU
28	J	220	LEU
28	J	221	ASN
28	J	229	LYS
28	J	239	ARG
28	J	281	LYS
28	J	308	ARG
28	J	363	ARG
28	J	410	HIS
28	J	411	MET
29	L	219	LYS

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Mol	Chain	Res	Type
29	L	222	LEU
29	L	227	THR
29	L	228	SER
29	L	235	LEU
29	L	731	LEU
29	L	761	SER
29	L	781	GLU
31	K	38	GLU
31	K	90	PRO
31	K	117	GLN
31	K	126	LEU
31	K	147	GLU
31	K	168	LYS
31	K	171	GLN
31	K	173	THR
34	N	24	GLU
34	N	41	ARG
34	N	42	LYS
34	N	102	CYS
34	N	116	ASN
34	N	125	LYS
35	O	45	CYS
35	O	69	GLU
35	O	74	CYS
35	O	115	GLU
35	O	150	LEU
35	O	220	MET
35	O	223	LEU
35	O	225	PRO
35	O	226	PRO
35	O	229	LYS
36	P	29	GLN
36	P	33	ARG
36	P	66	ARG
36	P	67	GLU
36	P	74	LYS
36	P	76	ARG
36	P	78	ARG
36	P	188	TRP
36	P	190	ASP
36	P	191	ASP
36	P	212	ASN

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Mol	Chain	Res	Type
36	P	224	MET
37	R	56	GLU
37	R	66	GLU
37	R	67	ILE
37	R	71	GLN
37	R	72	TYR
37	R	75	ASP
37	R	80	LYS
37	R	81	LYS
37	R	82	MET
37	R	86	LEU
37	R	89	GLN
37	R	92	SER
37	R	95	LYS
37	R	96	ILE
37	R	103	ARG
37	R	104	GLN
37	R	106	GLN
37	R	110	LYS
37	R	111	VAL
37	R	115	LYS
37	R	122	LYS
37	R	125	MET
37	R	128	ASP
37	R	129	ASP
37	R	133	GLN
37	R	137	GLU
37	R	158	LYS
37	R	170	LYS
37	R	171	LEU
37	R	175	GLN
37	R	181	PRO
37	R	183	GLN
37	R	186	VAL
37	R	189	ASN
37	R	195	ARG
37	R	211	ARG
37	R	212	PHE
37	R	213	LYS
37	R	214	ILE
37	R	215	ASN
37	R	216	LYS

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Mol	Chain	Res	Type
37	R	233	HIS
37	R	245	GLU
37	R	250	LYS
37	R	403	PRO
37	R	409	VAL
37	R	411	TYR
37	R	415	LEU
37	R	418	GLN
37	R	420	LYS
37	R	422	MET
37	R	426	PHE
37	R	435	ASN
38	S	10	GLN
38	S	15	TYR
38	S	91	LYS
38	S	102	ASN
38	S	108	ASN
38	S	125	LYS
38	S	129	PHE
38	S	131	ARG
39	T	257	ARG
39	T	282	ARG
39	T	308	ARG
39	T	318	ARG
39	T	387	PHE
39	T	399	LYS
39	T	400	PHE
39	T	401	PRO
39	T	402	ASP
39	T	412	HIS
39	T	416	ILE
39	T	418	THR
39	T	455	GLN
39	T	460	ASP
39	T	461	SER
39	T	463	SER
39	T	478	LEU
40	U	1	MET
40	U	11	ARG
40	U	20	GLN
40	U	23	LEU
40	U	25	LEU

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Mol	Chain	Res	Type
43	X	209	PRO
43	X	224	PRO
43	X	249	PRO
43	X	250	PRO
43	X	263	PRO
43	X	293	PRO
43	X	297	PRO
44	Y	44	PRO
45	Z	524	ARG
45	Z	526	ILE
45	Z	563	ARG
45	Z	569	PRO
45	Z	597	ARG
45	Z	600	ARG
45	Z	604	LYS
45	Z	607	VAL
45	Z	613	LYS

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

Mol	Chain	Res	Type
1	A	38	GLN
1	A	57	GLN
1	A	73	HIS
1	A	78	ASN
1	A	97	HIS
1	A	210	HIS
1	A	270	ASN
1	A	297	ASN
1	A	325	HIS
1	A	336	ASN
1	A	448	GLN
1	A	573	GLN
1	A	584	HIS
1	A	587	GLN
1	A	601	GLN
1	A	659	GLN
1	A	675	GLN
1	A	775	ASN
1	A	792	HIS
1	A	815	HIS
1	A	873	ASN

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Mol	Chain	Res	Type
1	A	924	GLN
1	A	1024	HIS
1	A	1075	GLN
1	A	1217	GLN
1	A	1293	ASN
1	A	1296	GLN
1	A	1352	HIS
1	A	1359	HIS
1	A	1458	GLN
1	A	1460	HIS
1	A	1580	HIS
1	A	1717	ASN
1	A	2089	HIS
1	A	2123	GLN
1	A	2155	GLN
1	A	2291	ASN
1	A	2300	ASN
1	A	2306	HIS
3	C	87	GLN
3	C	245	HIS
3	C	248	GLN
3	C	297	ASN
3	C	437	HIS
3	C	513	ASN
3	C	548	ASN
3	C	575	GLN
3	C	596	ASN
3	C	706	GLN
3	C	743	ASN
5	E	101	ASN
5	E	165	GLN
18	w	425	HIS
18	w	431	HIS
18	w	485	ASN
20	v	23	ASN
20	v	78	HIS
21	1	473	GLN
21	1	572	HIS
21	1	599	ASN
21	1	817	HIS
21	1	832	GLN
21	1	903	GLN

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Mol	Chain	Res	Type
21	1	941	ASN
21	1	942	ASN
21	1	966	GLN
21	1	1026	ASN
21	1	1186	GLN
21	1	1225	HIS
21	1	1248	GLN
21	1	1277	GLN
22	2	490	HIS
23	3	9	GLN
23	3	21	ASN
23	3	51	HIS
23	3	104	GLN
23	3	231	HIS
23	3	254	ASN
23	3	264	GLN
23	3	293	HIS
23	3	304	GLN
23	3	388	GLN
23	3	518	GLN
23	3	730	HIS
23	3	760	ASN
23	3	775	ASN
23	3	870	ASN
23	3	1087	GLN
28	J	221	ASN
28	J	259	GLN
28	J	294	HIS
28	J	351	ASN
29	L	39	HIS
29	L	73	HIS
29	L	211	ASN
31	K	171	GLN
34	N	27	GLN
34	N	37	HIS
34	N	99	ASN
34	N	107	GLN
34	N	136	HIS
35	O	196	GLN
35	O	254	GLN
35	O	268	GLN
35	O	294	ASN

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Mol	Chain	Res	Type
36	P	212	ASN
36	P	220	HIS
37	R	104	GLN
37	R	106	GLN
37	R	126	ASN
37	R	189	ASN
37	R	194	GLN
37	R	215	ASN
37	R	233	HIS
37	R	418	GLN
37	R	435	ASN
38	S	13	ASN
38	S	31	HIS
38	S	54	HIS
38	S	150	GLN
39	T	217	GLN
39	T	278	ASN
39	T	297	HIS
39	T	384	HIS
39	T	413	ASN
39	T	417	ASN
39	T	446	ASN
39	T	451	HIS
39	T	455	GLN
43	X	193	ASN
43	X	307	GLN
44	Y	87	GLN
45	Z	574	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	F	91/107 (85%)	38 (41%)	12 (13%)
14	G	76/274 (27%)	48 (63%)	9 (11%)
15	H	130/188 (69%)	33 (25%)	4 (3%)
2	B	82/117 (70%)	19 (23%)	10 (12%)
All	All	379/686 (55%)	138 (36%)	35 (9%)

All (138) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	12	U
2	B	13	C
2	B	19	A
2	B	20	G
2	B	21	A
2	B	22	U
2	B	23	C
2	B	24	G
2	B	25	C
2	B	26	A
2	B	28	A
2	B	36	C
2	B	38	C
2	B	40	U
2	B	41	U
2	B	45	C
2	B	57	G
2	B	70	A
2	B	71	C
13	F	5	U
13	F	6	C
13	F	7	G
13	F	8	C
13	F	10	U
13	F	12	G
13	F	25	C
13	F	26	U
13	F	27	A
13	F	28	A
13	F	29	A
13	F	33	G
13	F	34	G
13	F	36	A
13	F	37	C
13	F	38	G
13	F	44	G
13	F	45	A
13	F	46	G
13	F	47	A
13	F	48	A
13	F	49	G
13	F	51	U
13	F	54	G

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Mol	Chain	Res	Type
13	F	55	C
13	F	56	A
13	F	58	G
13	F	59	G
13	F	60	C
13	F	61	C
13	F	62	C
13	F	68	C
13	F	74	U
13	F	78	A
13	F	79	C
13	F	85	U
13	F	86	U
13	F	87	C
14	G	-11	G
14	G	-6	C
14	G	-4	A
14	G	-3	A
14	G	1	G
14	G	2	U
14	G	3	A
14	G	4	A
14	G	5	G
14	G	7	G
14	G	8	C
14	G	10	U
14	G	11	A
14	G	12	G
14	G	13	C
14	G	17	U
14	G	21	A
14	G	22	C
14	G	23	U
14	G	24	G
14	G	25	G
14	G	26	U
14	G	27	U
14	G	28	A
14	G	29	C
14	G	30	C
14	G	31	U
14	G	131	U

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Mol	Chain	Res	Type
14	G	132	G
14	G	135	G
14	G	136	U
14	G	137	C
14	G	143	U
14	G	144	A
14	G	145	U
14	G	146	C
14	G	147	C
14	G	148	U
14	G	149	G
14	G	150	U
14	G	151	C
14	G	152	C
14	G	154	U
14	G	156	U
14	G	159	U
14	G	161	U
14	G	162	C
14	G	163	C
15	H	14	C
15	H	20	G
15	H	23	A
15	H	24	A
15	H	25	G
15	H	29	A
15	H	30	A
15	H	31	G
15	H	44	U
15	H	45	C
15	H	46	U
15	H	47	U
15	H	48	A
15	H	65	U
15	H	112	G
15	H	143	A
15	H	147	G
15	H	149	A
15	H	152	G
15	H	153	A
15	H	154	C
15	H	156	U

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Mol	Chain	Res	Type
15	H	157	G
15	H	160	A
15	H	163	G
15	H	164	C
15	H	166	G
15	H	167	U
15	H	169	C
15	H	177	A
15	H	178	A
15	H	179	C
15	H	183	G

All (35) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	12	U
2	B	18	C
2	B	19	A
2	B	20	G
2	B	23	C
2	B	24	G
2	B	25	C
2	B	27	U
2	B	39	C
2	B	40	U
13	F	5	U
13	F	7	G
13	F	25	C
13	F	33	G
13	F	35	A
13	F	36	A
13	F	37	C
13	F	47	A
13	F	48	A
13	F	50	A
13	F	58	G
13	F	59	G
14	G	-12	G
14	G	16	G
14	G	21	A
14	G	22	C
14	G	136	U

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Mol	Chain	Res	Type
14	G	148	U
14	G	151	C
14	G	153	C
14	G	155	U
15	H	29	A
15	H	46	U
15	H	47	U
15	H	156	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 19 ligands modelled in this entry, 16 are monoatomic - leaving 3 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	$\# Z > 2$
50	GTP	C	1500	51	33,34,34	1.45	5 (15%)	50,54,54	2.04	10 (20%)
48	IHP	A	2401	-	36,36,36	1.04	2 (5%)	60,60,60	1.74	15 (25%)
49	ALA	A	2402	-	3,4,5	0.67	0	2,4,6	0.80	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
50	GTP	C	1500	51	-	8/22/38/38	0/3/3/3
48	IHP	A	2401	-	-	6/30/54/54	0/1/1/1
49	ALA	A	2402	-	-	0/1/2/4	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	C	1500	GTP	C5-N7	-3.76	1.31	1.39
50	C	1500	GTP	C6-N1	-3.32	1.32	1.38
50	C	1500	GTP	PA-O3A	3.16	1.62	1.59
48	A	2401	IHP	P5-O45	-2.95	1.43	1.54
48	A	2401	IHP	P2-O12	2.73	1.64	1.59
50	C	1500	GTP	C8-N9	-2.57	1.31	1.37
50	C	1500	GTP	C4-N9	-2.56	1.31	1.38

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	C	1500	GTP	C5-C4-N3	-7.07	117.14	128.39
50	C	1500	GTP	C2-N3-C4	5.94	122.54	112.30
50	C	1500	GTP	N9-C4-N3	5.74	137.44	125.95
48	A	2401	IHP	O35-P5-O15	-4.53	88.19	105.85
48	A	2401	IHP	O45-P5-O35	4.13	123.30	107.80
48	A	2401	IHP	P3-O13-C3	-3.69	113.57	123.43
48	A	2401	IHP	O16-C6-C1	3.64	116.50	108.76
50	C	1500	GTP	O6-C6-C5	-3.58	117.08	126.53
48	A	2401	IHP	C6-C1-C2	-3.22	103.37	110.43
50	C	1500	GTP	C2-N1-C6	-3.08	119.53	125.11
50	C	1500	GTP	C5-C6-N1	2.90	120.64	113.25
50	C	1500	GTP	O2G-PG-O3B	2.89	114.34	104.64
50	C	1500	GTP	O2A-PA-O3A	2.81	114.87	107.27
48	A	2401	IHP	O44-P4-O34	2.74	118.06	107.80
48	A	2401	IHP	C5-C6-C1	-2.65	104.62	110.43
48	A	2401	IHP	O15-C5-C4	-2.40	103.66	108.76
48	A	2401	IHP	O31-P1-O11	-2.37	96.62	105.85
48	A	2401	IHP	O12-C2-C3	2.34	113.74	108.76
48	A	2401	IHP	P6-O16-C6	-2.34	117.18	123.43
50	C	1500	GTP	O4'-C4'-C3'	2.27	109.66	105.15
48	A	2401	IHP	O45-P5-O15	-2.25	97.08	105.85
48	A	2401	IHP	O35-P5-O25	2.22	119.48	110.83
50	C	1500	GTP	C6-C5-N7	2.12	134.15	130.29
48	A	2401	IHP	O42-P2-O22	2.07	118.91	110.83
48	A	2401	IHP	C4-C3-C2	2.07	114.96	110.43

There are no chirality outliers.

All (14) torsion outliers are listed below:

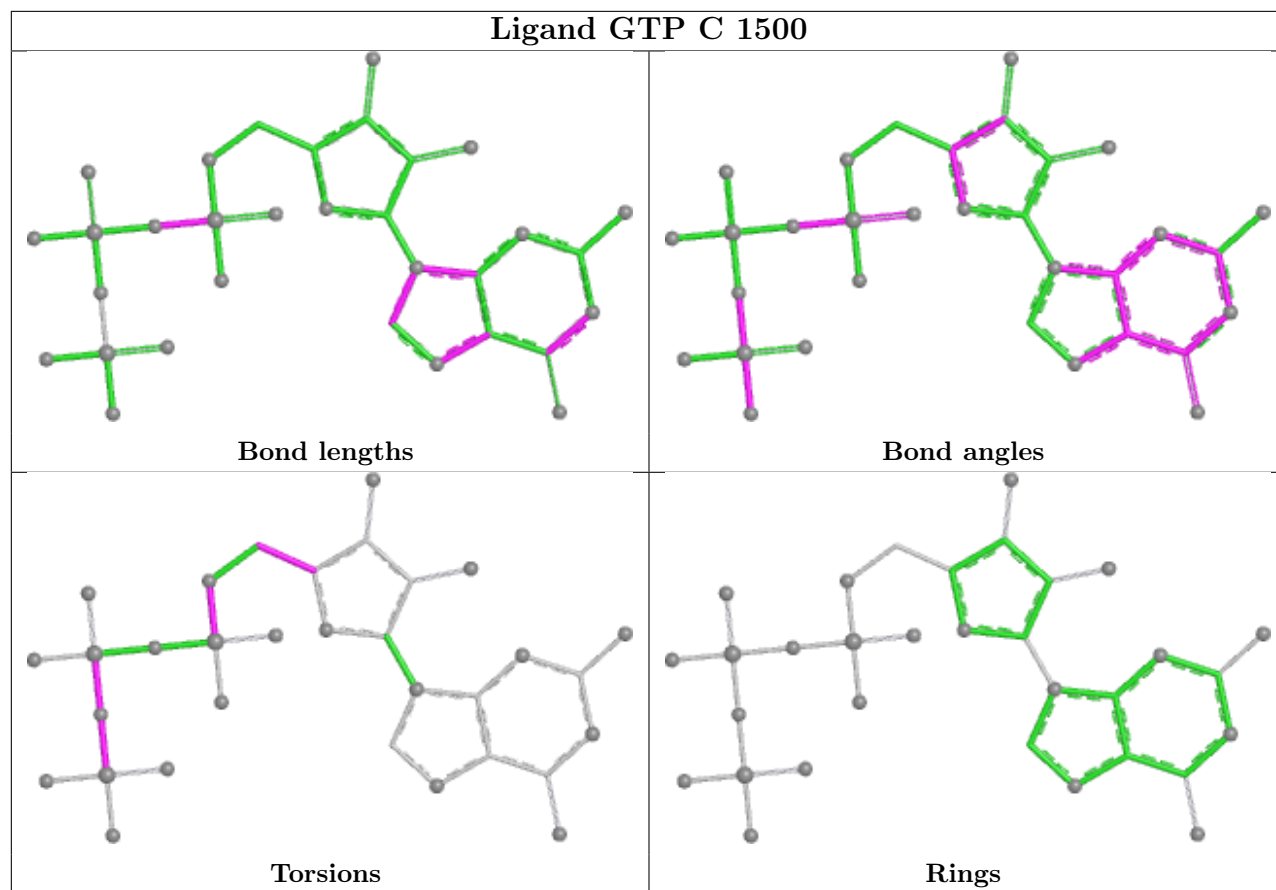
Mol	Chain	Res	Type	Atoms
48	A	2401	IHP	C4-C5-O15-P5
48	A	2401	IHP	C6-C5-O15-P5
50	C	1500	GTP	PB-O3B-PG-O3G
50	C	1500	GTP	C5'-O5'-PA-O1A
50	C	1500	GTP	C5'-O5'-PA-O2A
50	C	1500	GTP	O4'-C4'-C5'-O5'
50	C	1500	GTP	C3'-C4'-C5'-O5'
50	C	1500	GTP	C5'-O5'-PA-O3A
48	A	2401	IHP	C1-O11-P1-O21
48	A	2401	IHP	C2-O12-P2-O22
48	A	2401	IHP	C5-O15-P5-O25
50	C	1500	GTP	PG-O3B-PB-O2B
48	A	2401	IHP	C1-O11-P1-O31
50	C	1500	GTP	PG-O3B-PB-O1B

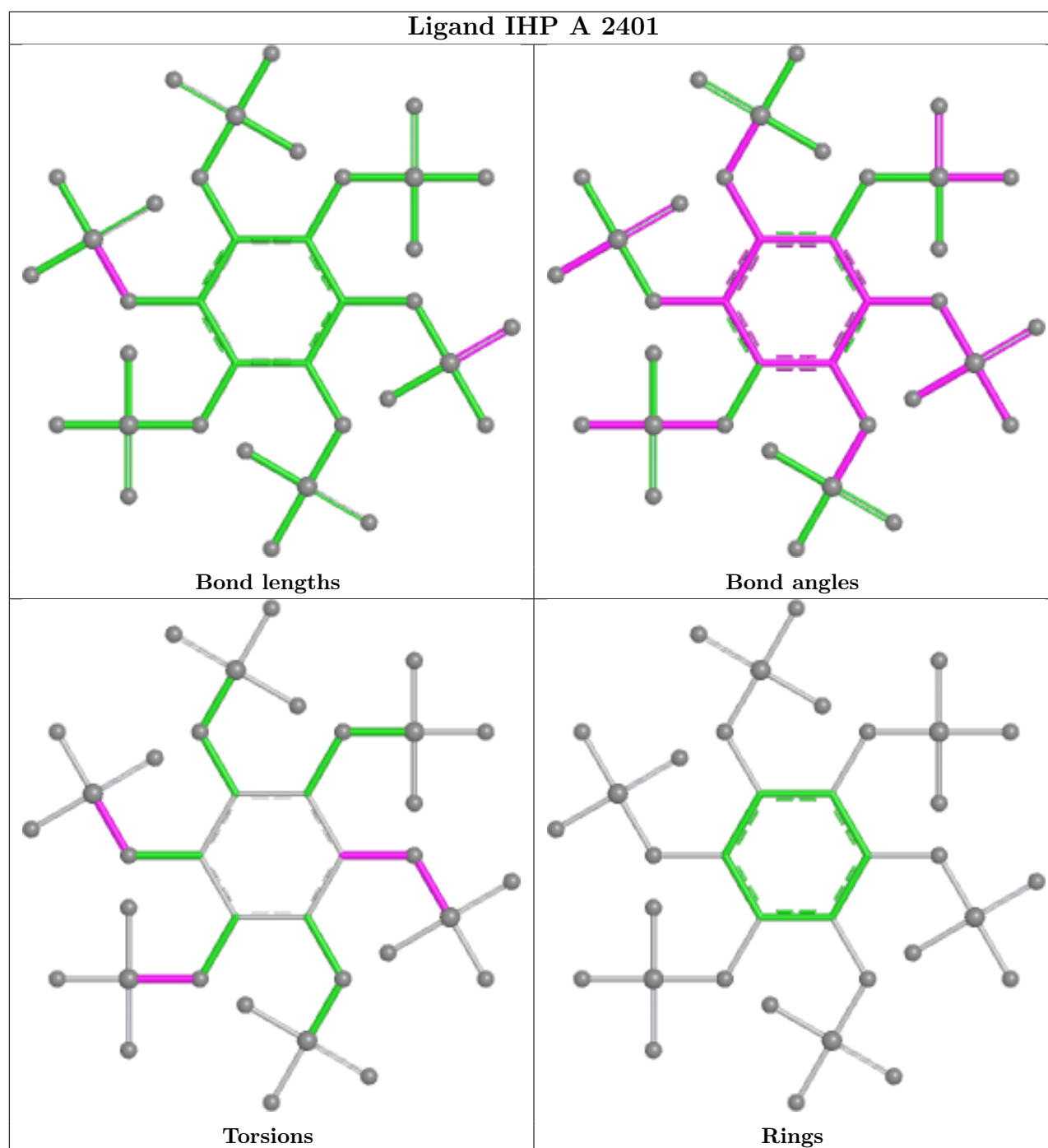
There are no ring outliers.

3 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
50	C	1500	GTP	11	0
48	A	2401	IHP	10	0
49	A	2402	ALA	2	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

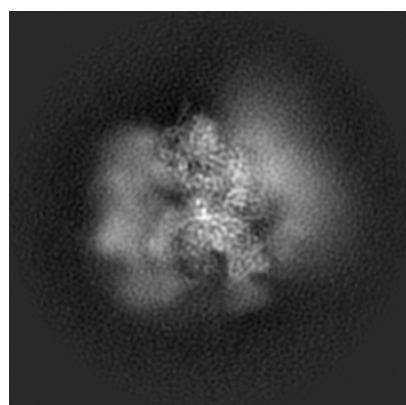
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6890. These allow visual inspection of the internal detail of the map and identification of artifacts.

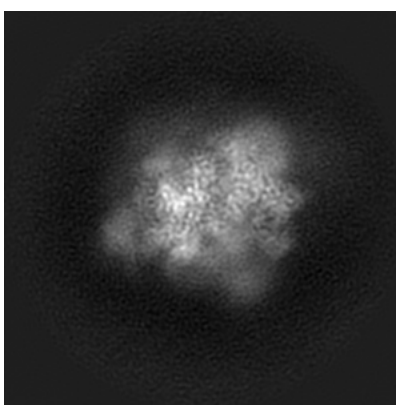
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

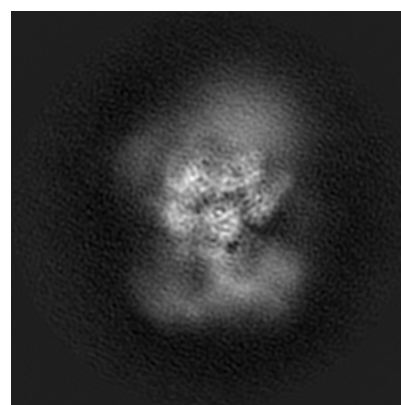
6.1.1 Primary map



X



Y

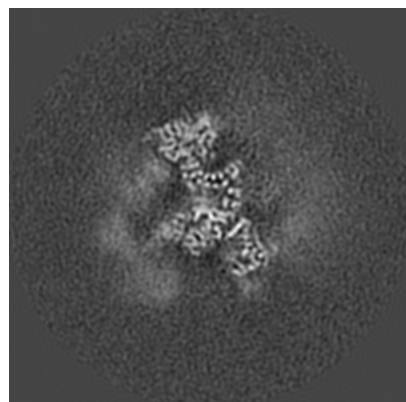


Z

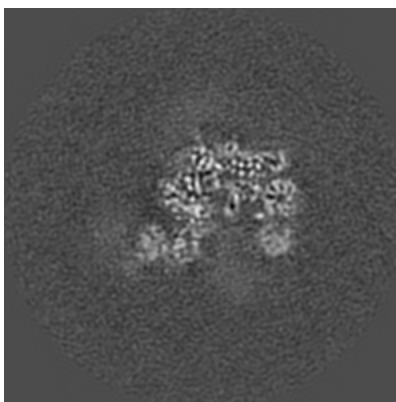
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

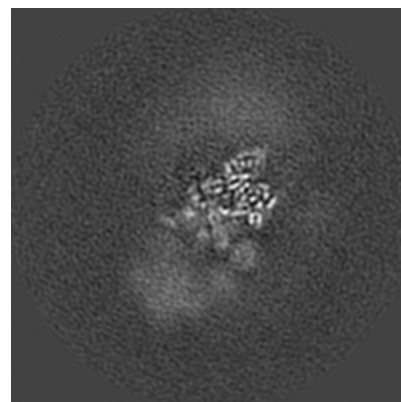
6.2.1 Primary map



X Index: 200



Y Index: 200

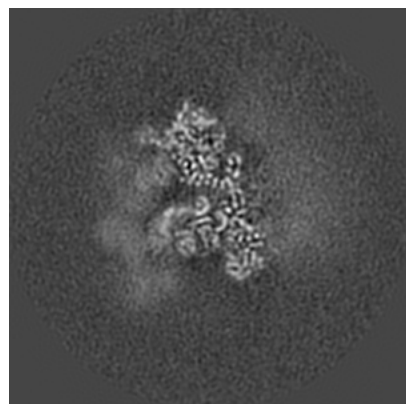


Z Index: 200

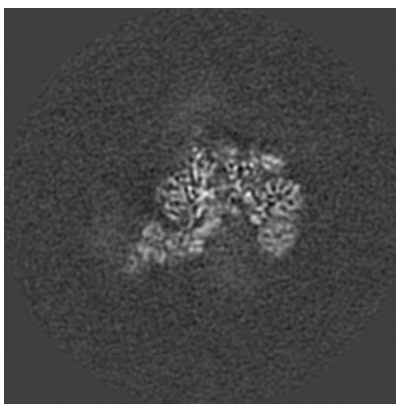
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

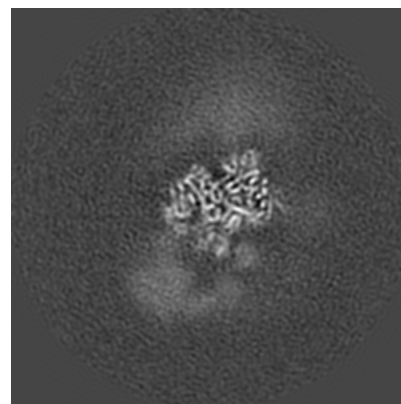
6.3.1 Primary map



X Index: 210



Y Index: 195

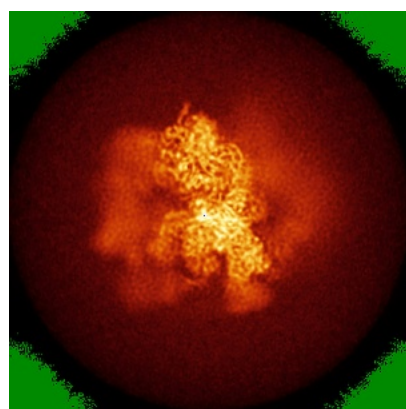


Z Index: 192

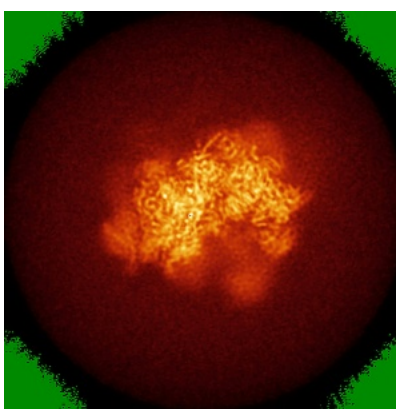
The images above show the largest variance slices of the map in three orthogonal directions.

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

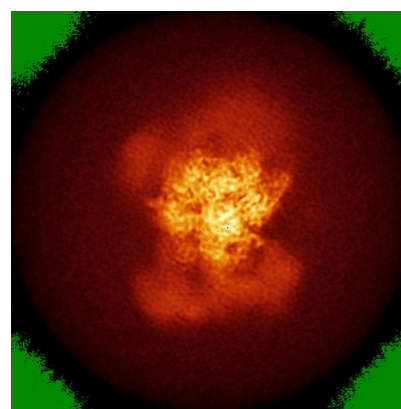
6.4.1 Primary map



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 0.0323. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

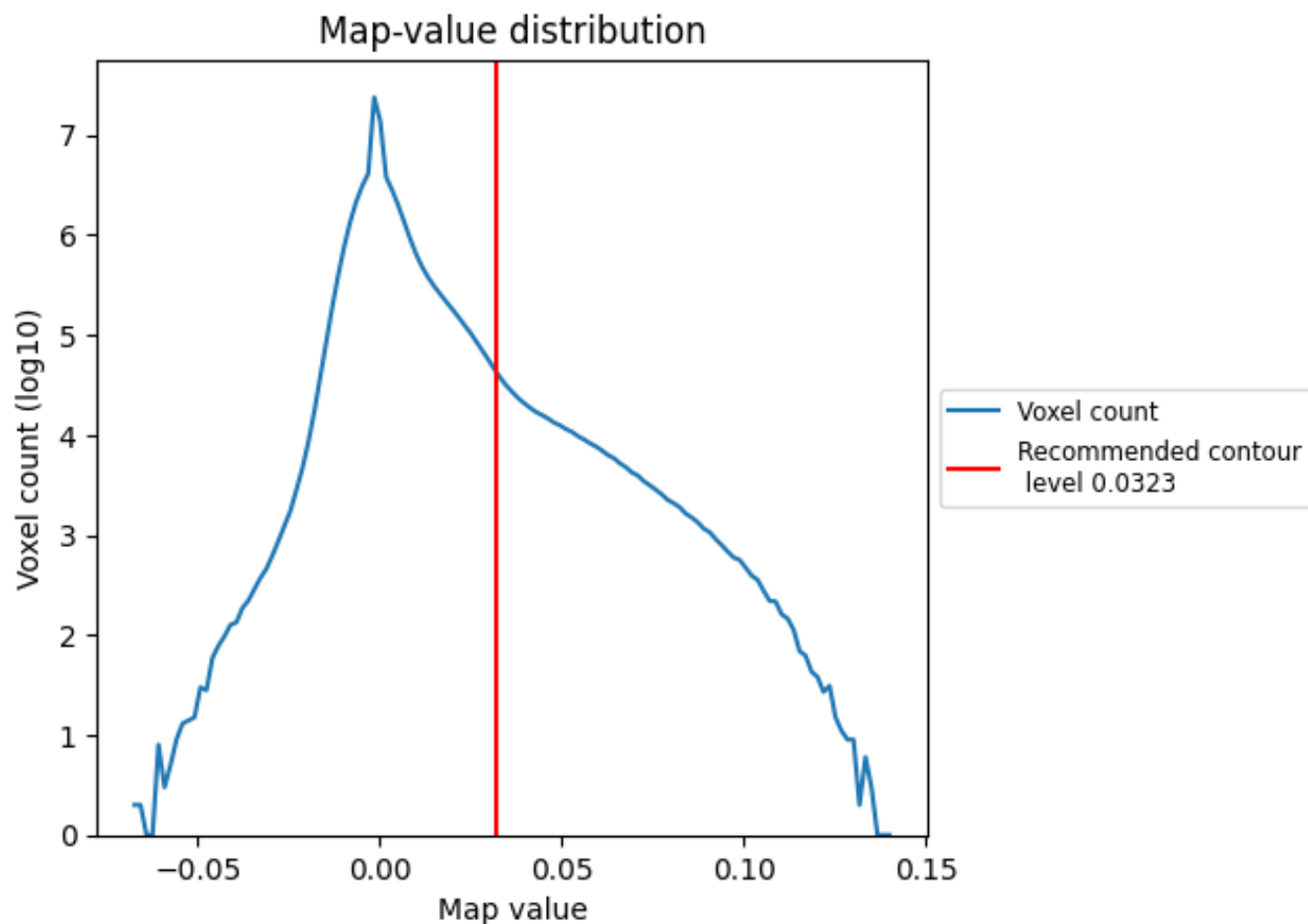
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

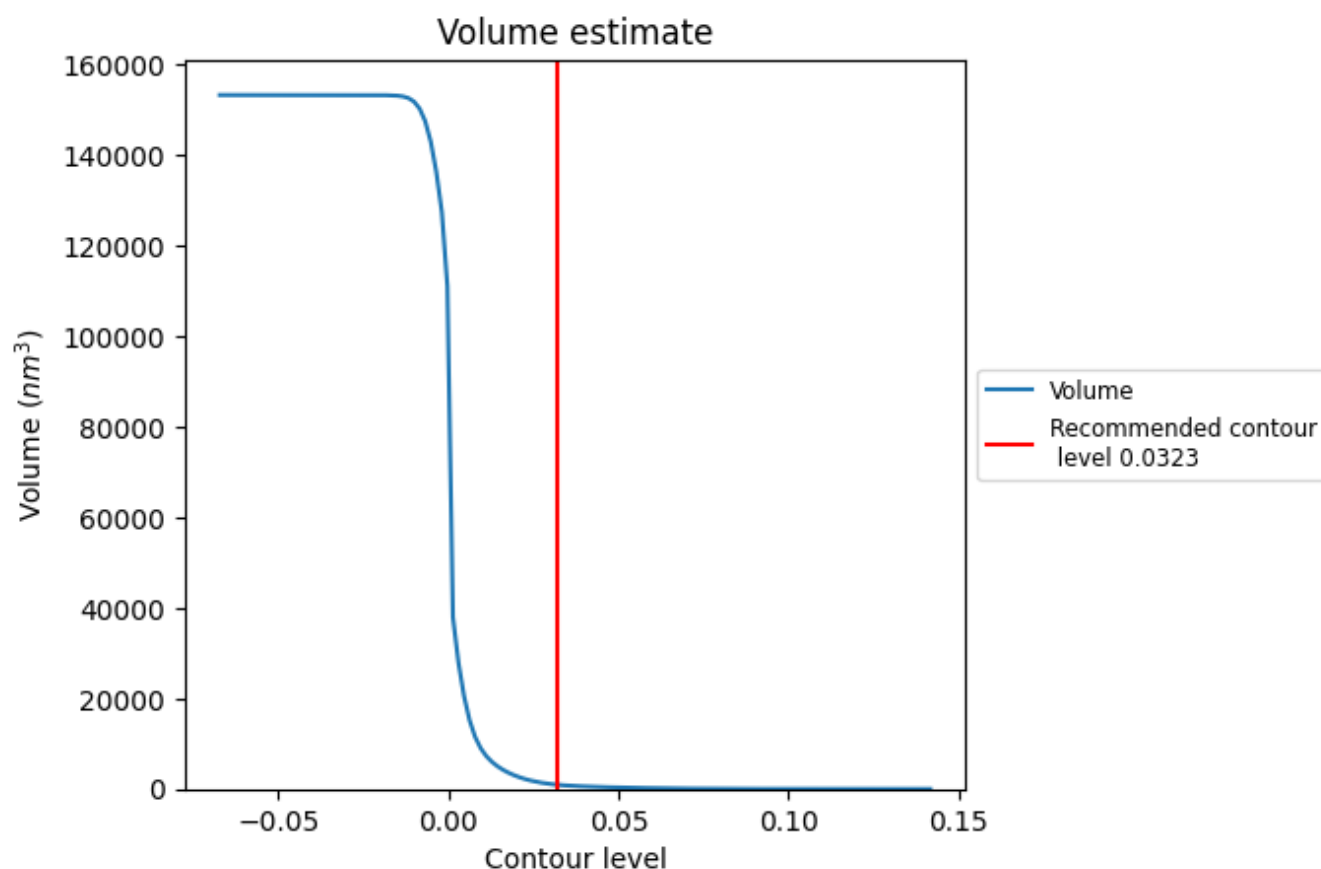
This section contains the results of statistical analysis of the map.

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.

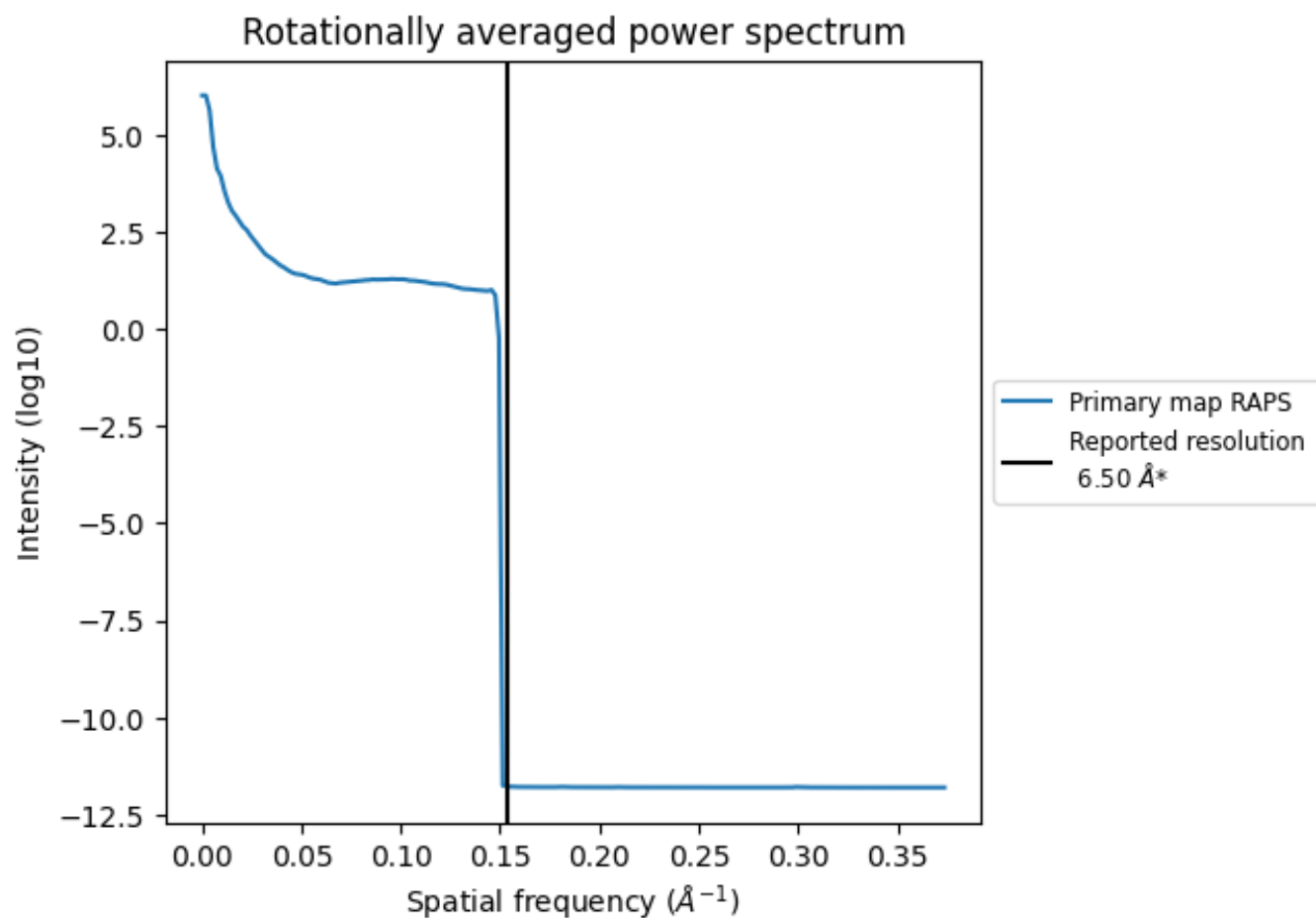
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 909 nm³; this corresponds to an approximate mass of 821 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 0.154 Å⁻¹

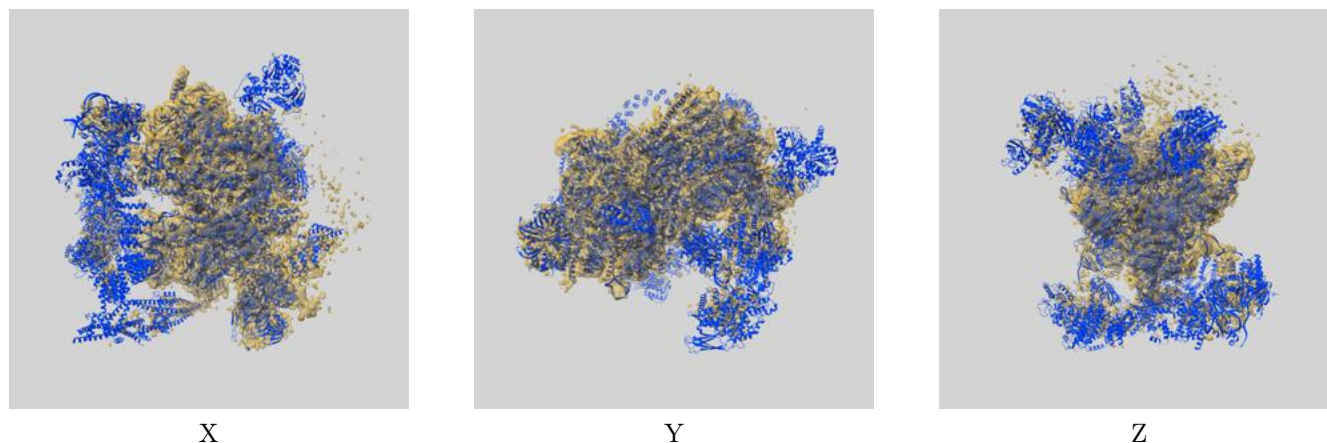
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

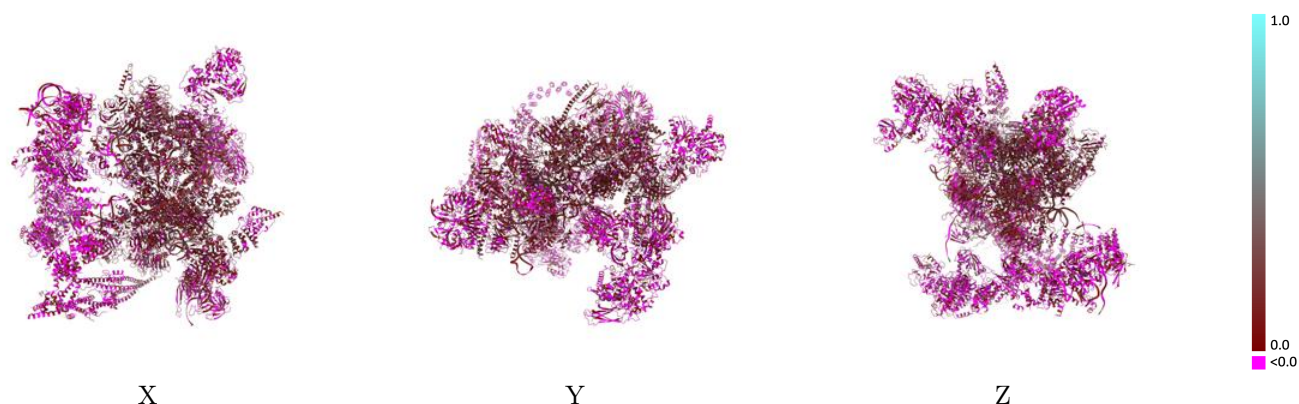
This section contains information regarding the fit between EMDB map EMD-6890 and PDB model 5Z57. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



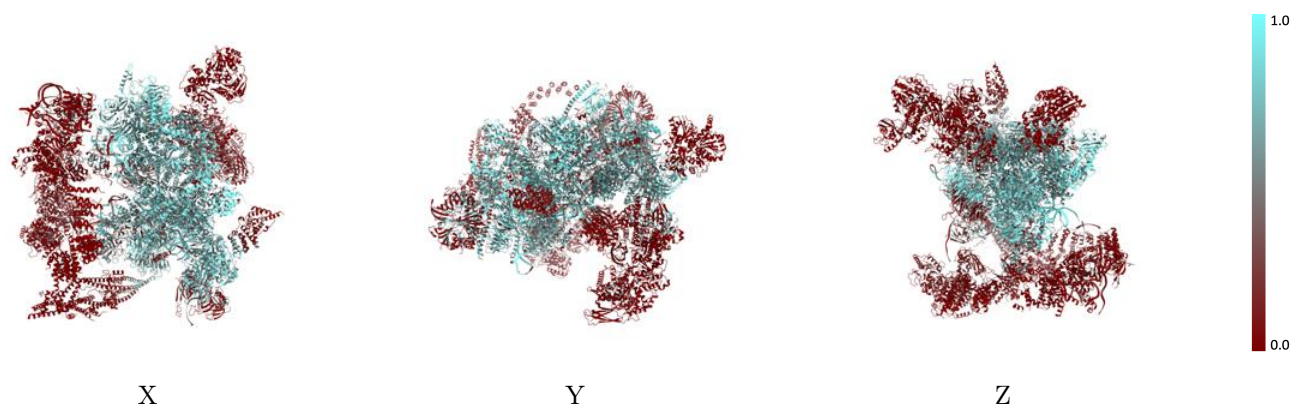
The images above show the 3D surface view of the map at the recommended contour level 0.0323 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



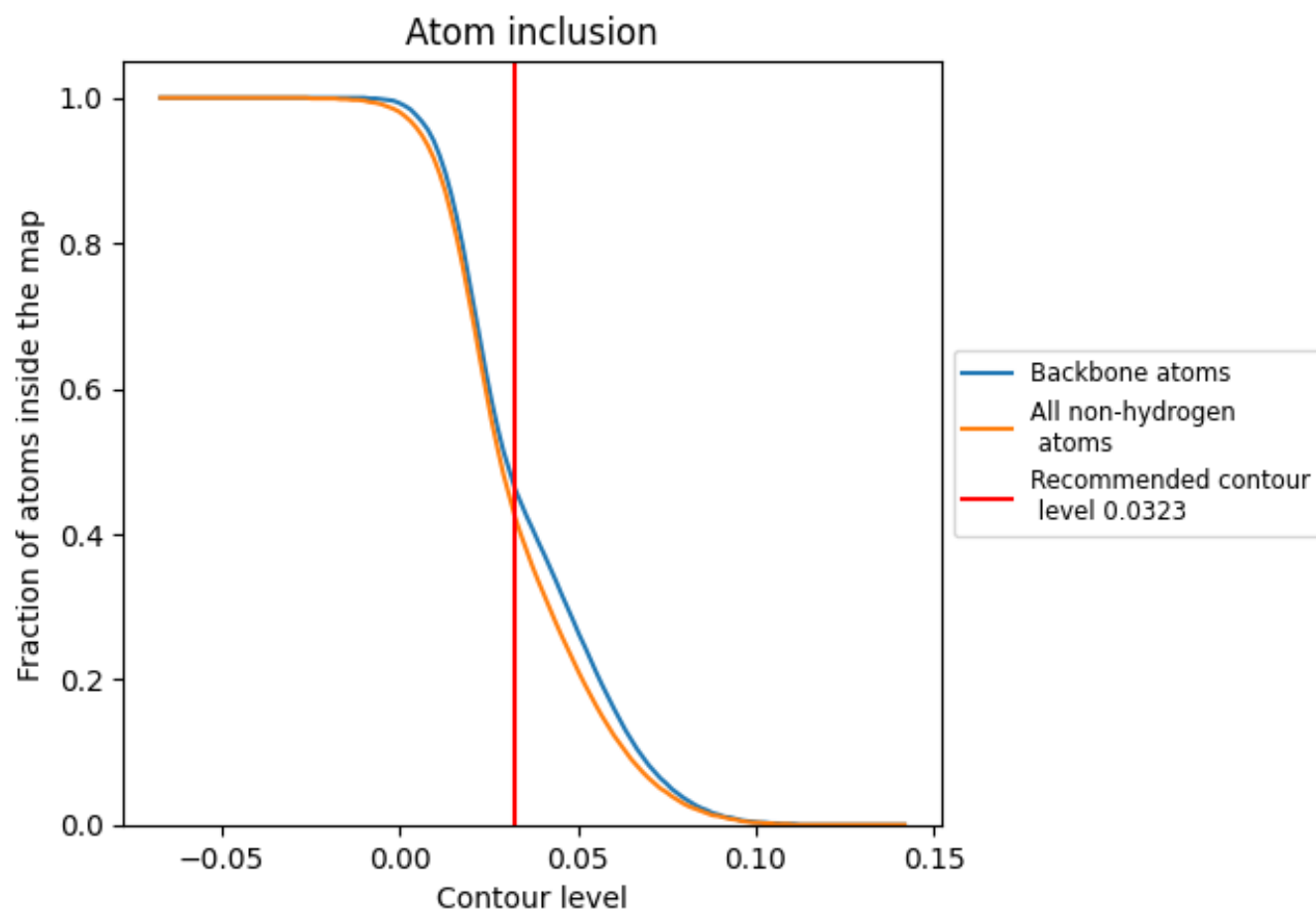
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0323).

9.4 Atom inclusion [i](#)



At the recommended contour level, 46% of all backbone atoms, 42% 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 (0.0323) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4240	 0.0970
1	 0.6630	 0.1660
2	 0.6030	 0.1390
3	 0.6990	 0.1390
4	 0.3290	 0.0210
5	 0.7030	 0.1570
6	 0.6660	 0.1340
7	 0.6700	 0.1450
A	 0.5700	 0.1360
B	 0.7770	 0.1670
C	 0.6930	 0.1510
D	 0.0490	 0.0190
E	 0.6060	 0.1060
F	 0.8090	 0.1690
G	 0.7570	 0.1610
H	 0.4220	 0.0840
I	 0.0380	 0.0050
J	 0.3450	 0.0650
K	 0.1220	 0.0430
L	 0.3250	 0.0880
N	 0.6690	 0.1380
O	 0.4910	 0.1160
P	 0.3290	 0.1440
Q	 0.0240	 0.0100
R	 0.4890	 0.1440
S	 0.4900	 0.1130
T	 0.7380	 0.1470
U	 0.6680	 0.1850
V	 0.4080	 0.1230
W	 0.1940	 0.0690
X	 0.6450	 0.1400
Y	 0.7100	 0.1780
Z	 0.4450	 0.1540
a	 0.1400	 0.0070
b	 0.2860	 0.0520



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Chain	Atom inclusion	Q-score
c	 0.3200	 0.0290
d	 0.3120	 0.0350
e	 0.3480	 0.0300
f	 0.2800	 0.0180
g	 0.2810	 0.0330
h	 0.0590	 -0.0130
i	 0.0690	 0.0440
j	 0.0910	 0.0080
k	 0.0640	 0.0180
l	 0.0790	 -0.0210
m	 0.1190	 -0.0100
n	 0.0870	 0.0230
o	 0.0310	 0.0290
p	 0.1010	 0.0230
q	 0.0210	 -0.0080
r	 0.0460	 0.0430
s	 0.1100	 0.0360
t	 0.0000	 0.0240
u	 0.0130	 0.0250
v	 0.3530	 0.0880
w	 0.2140	 0.0530
x	 0.0000	 0.0020
y	 0.1290	 0.0030