



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 04:06 AM UTC

PDB ID : 7PUB / pdb_00007pub
EMDB ID : EMD-13661
Title : Late assembly intermediate of the Trypanosoma brucei mitoribosomal small subunit
Authors : Lenarcic, T.; Leibundgut, M.; Saurer, M.; Ramrath, D.J.F.; Fluegel, T.; Boehringer, D.; Ban, N.
Deposited on : 2021-09-29
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

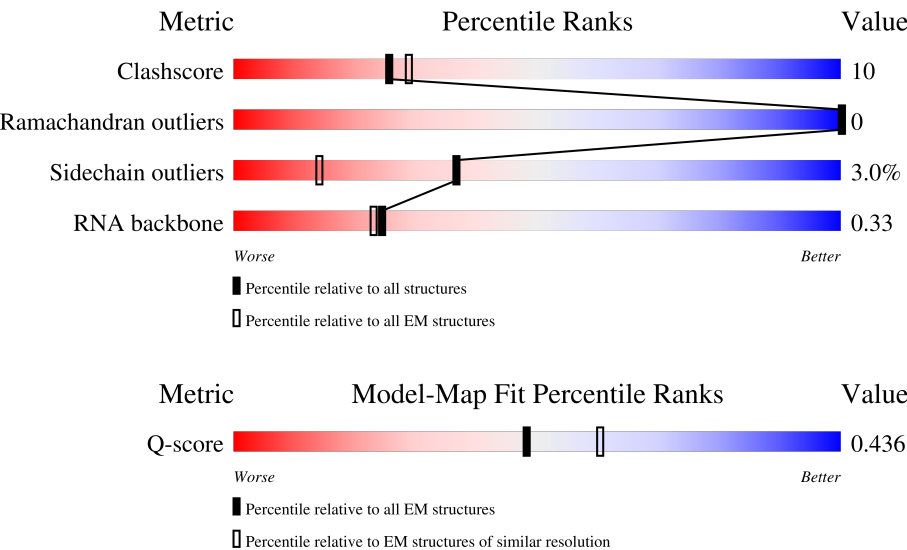
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.70 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.



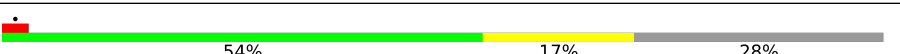
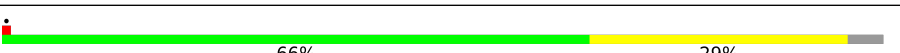
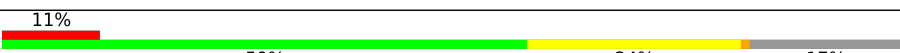
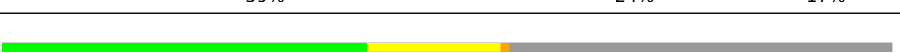
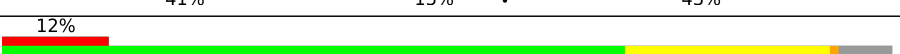
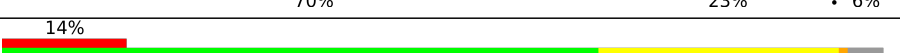
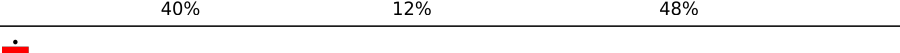
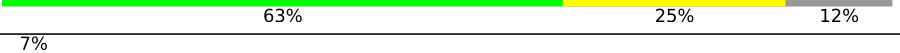
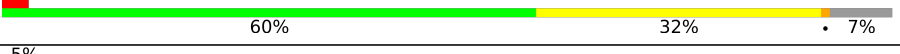
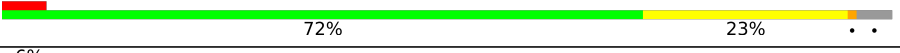
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	CA	621	13% 37% 48% 15%
2	CC	74	11% 62% 34% .
3	CE	435	9% 68% 29% ..

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Mol	Chain	Length	Quality of chain
4	CF	160	
5	CH	282	
6	CI	443	
7	CJ	817	
8	CK	326	
9	CL	87	
10	CN	166	
11	CO	429	
12	CP	188	
13	CQ	307	
14	CR	320	
15	CS	244	
16	CU	193	
17	Ca	602	
18	Cb	325	
19	Cd	440	
20	Cg	498	
21	Ci	181	
22	Cj	257	
23	Ck	874	
24	Cm	215	
25	Cn	250	
26	Cp	187	
27	Cq	263	
28	Cr	439	

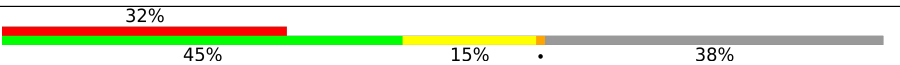
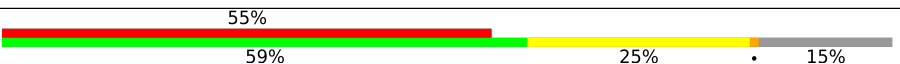
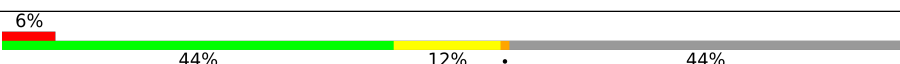
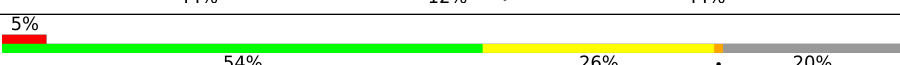
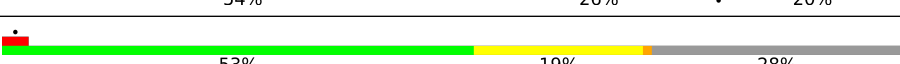
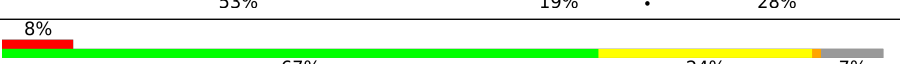
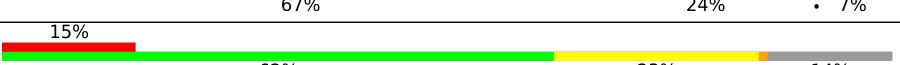
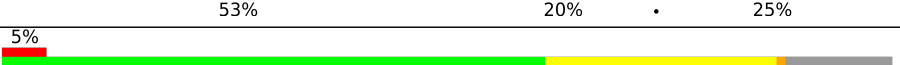
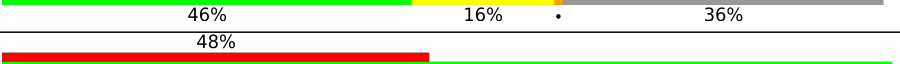
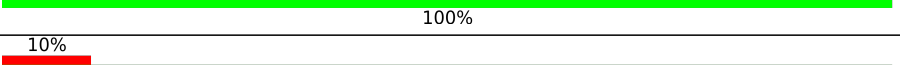
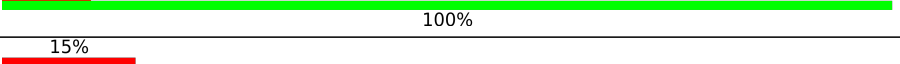
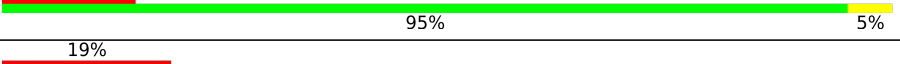
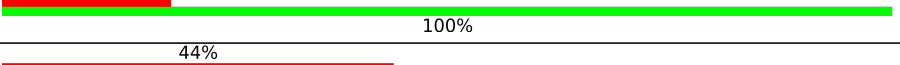
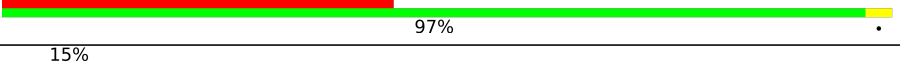
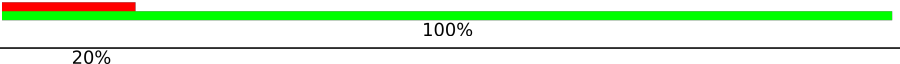
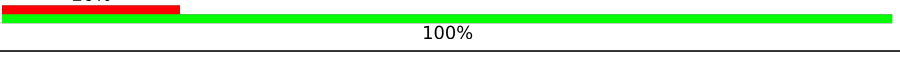
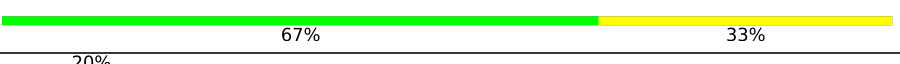
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Mol	Chain	Length	Quality of chain
29	Cv	1211	
30	DA	1788	
31	DB	1181	
32	DC	1165	
33	DD	812	
34	DE	747	
35	DF	666	
36	DG	631	
37	DH	581	
38	DI	407	
39	DJ	396	
40	DK	324	
41	DL	307	
42	DM	294	
43	DN	293	
44	DO	282	
45	DP	274	
46	DQ	268	
47	DR	270	
48	DS	261	
49	DT	247	
50	DU	228	
51	DV	183	
52	DW	179	
53	DX	169	

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Mol	Chain	Length	Quality of chain
54	DY	163	
55	DZ	94	
56	Da	64	
57	F3	966	
58	F6	676	
59	F7	679	
60	F9	608	
61	FO	334	
62	Ff	848	
63	Fg	550	
64	Fh	318	
65	Fi	629	
66	IA	787	
67	IB	803	
68	U6	21	
68	UJ	21	
69	U7	40	
70	UE	53	
71	UF	39	
72	UG	13	
73	UI	10	
74	UK	3	
75	UL	20	

2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 212864 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 RNA chain called 9S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CA	621	Total	C	N	O	P	0	0
			12330	5513	1927	4269	621		

- Molecule 2 is a protein called uS3m.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CC	74	Total	C	N	O	S	0	0
			646	451	96	98	1		

- Molecule 3 is a protein called Ribosomal_S5_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CE	426	Total	C	N	O	S	0	0
			3459	2188	642	613	16		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CE	341	ARG	LYS	variant	UNP Q38AX6

- Molecule 4 is a protein called bS6m.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CF	149	Total	C	N	O	S	0	0
			1240	791	217	226	6		

- Molecule 5 is a protein called 30S ribosomal protein S8, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	CH	273	Total	C	N	O	S	0	0
			2228	1387	432	398	11		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CH	74	ASN	SER	variant	UNP Q388R7

- Molecule 6 is a protein called uS9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CI	427	Total	C	N	O	S	0	0
			3410	2148	615	630	17		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CI	370	ALA	VAL	variant	UNP Q57W62

- Molecule 7 is a protein called LysM domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CJ	803	Total	C	N	O	S	0	0
			6535	4133	1152	1221	29		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CJ	311	LEU	TYR	variant	UNP Q57Z45
CJ	484	HIS	ARG	variant	UNP Q57Z45
CJ	488	SER	ASN	variant	UNP Q57Z45
CJ	629	ARG	LYS	variant	UNP Q57Z45

- Molecule 8 is a protein called uS11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CK	298	Total	C	N	O	S	0	0
			2447	1520	465	445	17		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CK	3	ARG	GLN	variant	UNP Q389T7
CK	138	UNK	ILE	conflict	UNP Q389T7

- Molecule 9 is a protein called uS12m.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CL	87	Total	C	N	O	S	0	0
			733	503	113	107	10		

- Molecule 10 is a protein called uS14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CN	157	Total	C	N	O	S	0	0
			1322	843	251	220	8		

- Molecule 11 is a protein called uS15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	CO	308	Total	C	N	O	S	0	0
			2552	1615	476	448	13		

- Molecule 12 is a protein called bS16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CP	180	Total	C	N	O	S	0	0
			1489	956	274	250	9		

- Molecule 13 is a protein called 30S Ribosomal protein S17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	CQ	226	Total	C	N	O	S	0	0
			1866	1186	355	317	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CQ	138	ALA	VAL	variant	UNP Q38DP8

- Molecule 14 is a protein called bS18m.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	CR	267	Total	C	N	O	S	0	0
			2210	1398	405	402	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CR	8	ILE	VAL	variant	UNP Q38AS2

- Molecule 15 is a protein called uS19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	CS	139	Total	C	N	O	S	0	0
			1149	743	205	195	6		

- Molecule 16 is a protein called bS21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	CU	181	Total	C	N	O	S	0	0
			1522	957	303	250	12		

- Molecule 17 is a protein called mS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Ca	575	Total	C	N	O	S	0	0
			4911	3146	875	867	23		

- Molecule 18 is a protein called mS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Cb	252	Total	C	N	O	S	0	0
			2056	1300	368	380	8		

- Molecule 19 is a protein called mS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Cd	230	Total	C	N	O	S	0	0
			1961	1242	358	350	11		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cd	299	UNK	GLY	conflict	UNP Q38DK6
Cd	364	UNK	GLY	conflict	UNP Q38DK6

- Molecule 20 is a protein called mS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Cg	480	Total	C	N	O	S	0	0
			3895	2494	682	699	20		

- Molecule 21 is a protein called mS33.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Ci	164	Total	C	N	O	S	0	0
			1343	845	246	243	9		

- Molecule 22 is a protein called mS34.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Cj	227	Total	C	N	O	S	0	0
			1799	1142	311	342	4		

- Molecule 23 is a protein called mS35.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Ck	682	Total	C	N	O	S	0	0
			5442	3411	990	1016	25		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ck	107	SER	LEU	variant	UNP Q387C7
Ck	144	PHE	LEU	variant	UNP Q387C7
Ck	253	TYR	PHE	variant	UNP Q387C7
Ck	339	GLU	VAL	variant	UNP Q387C7
Ck	815	GLY	ARG	variant	UNP Q387C7
Ck	871	GLY	GLU	variant	UNP Q387C7

- Molecule 24 is a protein called mS37.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Cm	145	Total	C	N	O	S	0	0
			1184	735	230	210	9		

- Molecule 25 is a protein called mS38.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Cn	62	Total	C	N	O	S	0	0
			528	345	105	75	3		

- Molecule 26 is a protein called Protein FYV4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Cp	173	Total	C	N	O	S	0	0
			1466	928	265	268	5		

- Molecule 27 is a protein called Superoxide dismutase, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Cq	252	Total	C	N	O	S	0	0
			2005	1285	342	369	9		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cq	48	THR	ALA	variant	UNP Q586A1
Cq	167	MET	VAL	variant	UNP Q586A1

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Cr	267	Total	C	N	O	S	0	0
			2083	1317	382	369	15		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cr	351	LYS	GLU	variant	UNP Q585I1

- Molecule 29 is a protein called ECH_2 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Cv	1040	Total	C	N	O	S	0	0
			8404	5291	1508	1568	37		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cv	1179	GLU	GLY	variant	UNP Q383R4

- Molecule 30 is a protein called mS48.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	DA	1552	Total	C	N	O	S	0	0
			12448	7861	2220	2329	38		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DA	1181	THR	ILE	variant	UNP Q57UJ2
DA	1333	ALA	VAL	variant	UNP Q57UJ2
DA	1700	ARG	HIS	variant	UNP Q57UJ2
DA	1761	LYS	ARG	variant	UNP Q57UJ2

- Molecule 31 is a protein called mS49.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	DB	1111	Total	C	N	O	S	0	0
			9148	5691	1717	1711	29		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DB	23	VAL	ALA	variant	UNP Q586P5
DB	359	ILE	THR	variant	UNP Q586P5
DB	384	GLN	HIS	variant	UNP Q586P5
DB	402	THR	ILE	variant	UNP Q586P5
DB	423	THR	ALA	variant	UNP Q586P5
DB	586	ARG	HIS	variant	UNP Q586P5
DB	593	ARG	LYS	variant	UNP Q586P5
DB	647	SER	GLY	variant	UNP Q586P5

- Molecule 32 is a protein called mS50.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	DC	1089	Total	C	N	O	S	0	0
			8709	5498	1538	1642	31		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DC	53	ALA	THR	variant	UNP Q57YB5
DC	365	LYS	GLU	variant	UNP Q57YB5
DC	385	THR	ALA	variant	UNP Q57YB5
DC	405	ILE	VAL	variant	UNP Q57YB5
DC	641	SER	PRO	variant	UNP Q57YB5
DC	651	LYS	GLU	variant	UNP Q57YB5
DC	731	GLU	ASP	variant	UNP Q57YB5
DC	814	GLN	HIS	variant	UNP Q57YB5
DC	1097	ALA	VAL	variant	UNP Q57YB5
DC	1113	THR	ILE	variant	UNP Q57YB5

- Molecule 33 is a protein called mS51.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	DD	790	Total	C	N	O	S	0	0
			6513	4121	1181	1170	41		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DD	371	PRO	SER	variant	UNP Q385L8
DD	599	ALA	VAL	variant	UNP Q385L8

- Molecule 34 is a protein called mS52.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	DE	588	Total	C	N	O	S	0	0
			4798	3052	868	859	19		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DE	378	UNK	LYS	variant	UNP Q386Q7
DE	384	UNK	THR	variant	UNP Q386Q7

- Molecule 35 is a protein called mS53.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	DF	589	Total	C	N	O	S	0	0
			4738	2974	895	844	25		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DF	18	THR	ALA	variant	UNP Q38ET1
DF	258	ASP	ASN	variant	UNP Q38ET1
DF	372	ASN	ASP	variant	UNP Q38ET1
DF	406	ASN	SER	variant	UNP Q38ET1
DF	510	ASP	GLY	variant	UNP Q38ET1
DF	577	ALA	VAL	variant	UNP Q38ET1
DF	636	UNK	GLY	conflict	UNP Q38ET1
DF	638	LYS	ARG	variant	UNP Q38ET1

- Molecule 36 is a protein called mS54.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	DG	552	Total	C	N	O	S	0	0
			4482	2820	818	813	31		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DG	428	ASN	SER	variant	UNP Q57ZP8
DG	429	GLY	SER	variant	UNP Q57ZP8

- Molecule 37 is a protein called mS55.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	DH	559	Total	C	N	O	S	0	0
			4541	2849	843	828	21		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DH	191	HIS	GLN	variant	UNP Q580V1
DH	194	PRO	ARG	variant	UNP Q580V1
DH	488	GLY	SER	variant	UNP Q580V1

- Molecule 38 is a protein called mS56.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	DI	390	Total	C	N	O	S	0	0
			3182	2020	554	594	14		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DI	92	GLU	GLY	variant	UNP Q587C2
DI	116	ASP	GLU	variant	UNP Q587C2

- Molecule 39 is a protein called mS57.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	DJ	357	Total	C	N	O	S	0	0
			2914	1858	512	530	14		

- Molecule 40 is a protein called mS58.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	DK	263	Total	C	N	O	S	0	0
			2083	1312	374	392	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DK	61	SER	PRO	variant	UNP Q38BP1
DK	257	GLY	SER	variant	UNP Q38BP1

- Molecule 41 is a protein called mS59.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	DL	291	Total	C	N	O	S	0	0
			2360	1495	441	412	12		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DL	274	THR	ALA	variant	UNP Q38BS2

- Molecule 42 is a protein called mS60.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	DM	294	Total	C	N	O	S	0	0
			2430	1533	459	426	12		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DM	69	PHE	TYR	variant	UNP Q57XL2
DM	97	ASN	SER	variant	UNP Q57XL2
DM	138	SER	PRO	variant	UNP Q57XL2
DM	173	ALA	THR	variant	UNP Q57XL2
DM	206	ALA	THR	variant	UNP Q57XL2

- Molecule 43 is a protein called mS61.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	DN	253	Total	C	N	O	S	0	0
			2062	1313	374	365	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DN	51	GLY	SER	variant	UNP Q38D60

- Molecule 44 is a protein called mS62.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	DO	221	Total	C	N	O	S	0	0
			1796	1123	325	338	10		

- Molecule 45 is a protein called mS63.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	DP	207	Total	C	N	O	S	0	0
			1760	1132	312	307	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DP	3	HIS	ARG	variant	UNP Q38F25

- Molecule 46 is a protein called AKAP7_NLS domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	DQ	255	Total	C	N	O	S	0	0
			2055	1290	388	368	9		

- Molecule 47 is a protein called mS65.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	DR	250	Total	C	N	O	S	0	0
			2019	1301	368	340	10		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DR	65	GLY	SER	variant	UNP Q57UA2
DR	94	GLY	GLU	variant	UNP Q57UA2
DR	128	PRO	SER	variant	UNP Q57UA2
DR	229	ARG	GLN	variant	UNP Q57UA2

- Molecule 48 is a protein called mS66.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	DS	243	Total	C	N	O	S	0	0
			1950	1216	364	356	14		

- Molecule 49 is a protein called Rhodanese domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	DT	239	Total	C	N	O	S	0	0
			2058	1321	364	362	11		

- Molecule 50 is a protein called Ubiquitin-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	DU	213	Total	C	N	O	S	0	0
			1754	1103	310	335	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DU	119	ILE	LEU	variant	UNP Q582T9
DU	152	ILE	VAL	variant	UNP Q582T9

- Molecule 51 is a protein called mS69.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	DV	160	Total	C	N	O	S	0	0
			1346	855	252	235	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DV	163	ALA	THR	variant	UNP Q57UZ6

- Molecule 52 is a protein called mS70.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	DW	161	Total	C	N	O	S	0	0
			1359	866	260	228	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DW	74	THR	MET	variant	UNP Q383N9

- Molecule 53 is a protein called mS71.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	DX	139	Total	C	N	O	S	0	0
			1174	747	223	197	7		

- Molecule 54 is a protein called mS72.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	DY	154	Total	C	N	O	S	0	0
			1295	829	247	214	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DY	34	HIS	ASP	variant	UNP Q57YD4

- Molecule 55 is a protein called mS73.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	DZ	82	Total	C	N	O	S	0	0
			697	457	113	123	4		

- Molecule 56 is a protein called mS74.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Da	34	Total	C	N	O	S	0	0
			305	193	67	43	2		

- Molecule 57 is a protein called mt-SAF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	F3	252	Total	C	N	O	S	0	0
			2003	1259	354	378	12		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F3	44	THR	ALA	variant	UNP Q38E61
F3	190	VAL	ILE	variant	UNP Q38E61
F3	303	ALA	SER	variant	UNP Q38E61
F3	418	ASP	ASN	variant	UNP Q38E61

- Molecule 58 is a protein called mt-SAF6.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	F6	416	Total	C	N	O	S	0	0
			3358	2124	580	636	18		

- Molecule 59 is a protein called mt-SAF7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	F7	576	Total	C	N	O	S	0	0
			4584	2922	792	837	33		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F7	36	ILE	THR	variant	UNP Q57UW6
F7	470	GLU	LYS	variant	UNP Q57UW6
F7	474	VAL	ALA	variant	UNP Q57UW6

- Molecule 60 is a protein called mt-SAF9.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	F9	342	Total	C	N	O	S	0	0
			2815	1736	530	539	10		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F9	117	ALA	SER	variant	UNP Q57YC0
F9	145	TYR	HIS	variant	UNP Q57YC0
F9	316	LYS	GLU	variant	UNP Q57YC0
F9	412	GLY	VAL	variant	UNP Q57YC0
F9	449	VAL	ALA	variant	UNP Q57YC0
F9	537	GLY	SER	variant	UNP Q57YC0

- Molecule 61 is a protein called mt-SAF22.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	FO	267	Total	C	N	O	S	0	0
			2236	1407	432	385	12		

- Molecule 62 is a protein called DNA photolyase, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Ff	614	Total	C	N	O	S	0	0
			4941	3135	885	898	23		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ff	109	ALA	VAL	variant	UNP Q382U6
Ff	127	UNK	TYR	conflict	UNP Q382U6
Ff	138	GLN	ARG	variant	UNP Q382U6
Ff	200	CYS	SER	variant	UNP Q382U6
Ff	319	ALA	THR	variant	UNP Q382U6
Ff	334	ASN	THR	variant	UNP Q382U6
Ff	350	ILE	THR	variant	UNP Q382U6
Ff	362	ALA	VAL	variant	UNP Q382U6
Ff	844	THR	SER	variant	UNP Q382U6

- Molecule 63 is a protein called Acyl transferase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Fg	513	Total	C	N	O	S	0	0
			3994	2512	698	754	30		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Fg	90	LYS	ARG	variant	UNP Q38DK4
Fg	152	VAL	LEU	variant	UNP Q38DK4
Fg	159	ILE	VAL	variant	UNP Q38DK4
Fg	363	MET	ARG	variant	UNP Q38DK4
Fg	399	UNK	GLU	conflict	UNP Q38DK4
Fg	525	LYS	ARG	variant	UNP Q38DK4

- Molecule 64 is a protein called mt-SAF37.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Fh	274	Total	C	N	O	S	0	0
			2230	1384	420	411	15		

- Molecule 65 is a protein called mt-SAF38.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Fi	469	Total	C	N	O	S	0	0
			3734	2363	683	665	23		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Fi	35	THR	SER	variant	UNP Q57ZP1
Fi	69	GLY	SER	variant	UNP Q57ZP1
Fi	185	PRO	HIS	variant	UNP Q57ZP1

- Molecule 66 is a protein called Translation initiation factor IF-2, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	IA	693	Total	C	N	O	S	0	0
			5414	3397	972	1018	27		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
IA	373	LYS	GLU	variant	UNP Q57WE3
IA	451	ILE	VAL	variant	UNP Q57WE3
IA	584	ASN	SER	variant	UNP Q57WE3
IA	679	ASP	VAL	variant	UNP Q57WE3

- Molecule 67 is a protein called mt-SAF39.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	IB	511	Total	C	N	O	S	0	0
			4103	2561	764	760	18		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
IB	136	LYS	GLU	variant	UNP Q387Q6
IB	226	ASP	ASN	variant	UNP Q387Q6
IB	237	CYS	SER	variant	UNP Q387Q6
IB	259	THR	ARG	variant	UNP Q387Q6
IB	268	GLU	LYS	variant	UNP Q387Q6
IB	275	CYS	TYR	variant	UNP Q387Q6
IB	312	THR	SER	variant	UNP Q387Q6
IB	459	ASP	ALA	variant	UNP Q387Q6
IB	572	HIS	ARG	variant	UNP Q387Q6

- Molecule 68 is a protein called Unk.

Mol	Chain	Residues	Atoms				AltConf	Trace
68	U6	21	Total	C	N	O	0	0
			105	63	21	21		
68	UJ	21	Total	C	N	O	0	0
			105	63	21	21		

- Molecule 69 is a protein called Unk7.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	U7	40	Total	C	N	O	0	0
			200	120	40	40		

- Molecule 70 is a protein called UnkE.

Mol	Chain	Residues	Atoms				AltConf	Trace
70	UE	53	Total	C	N	O	0	0
			265	159	53	53		

- Molecule 71 is a protein called UnkF.

Mol	Chain	Residues	Atoms				AltConf	Trace
71	UF	39	Total	C	N	O	0	0
			195	117	39	39		

- Molecule 72 is a protein called UnkG.

Mol	Chain	Residues	Atoms				AltConf	Trace
72	UG	13	Total	C	N	O	0	0
			65	39	13	13		

- Molecule 73 is a protein called UnkI.

Mol	Chain	Residues	Atoms				AltConf	Trace
73	UI	10	Total	C	N	O	0	0
			50	30	10	10		

- Molecule 74 is a protein called UnkK.

Mol	Chain	Residues	Atoms				AltConf	Trace
74	UK	3	Total	C	N	O	0	0
			15	9	3	3		

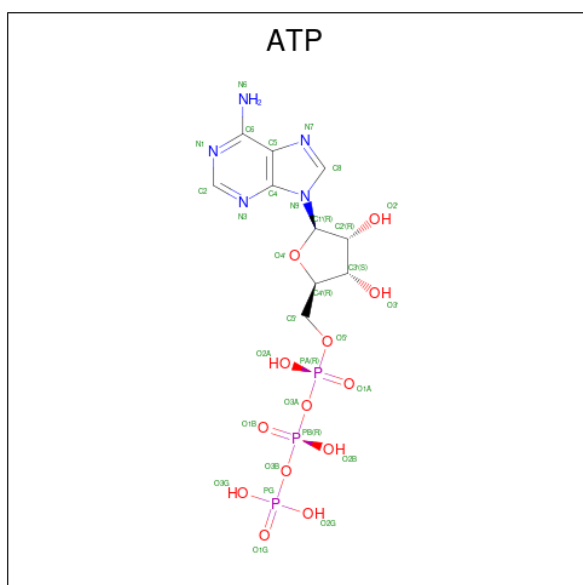
- Molecule 75 is a protein called UnkL.

Mol	Chain	Residues	Atoms				AltConf	Trace
75	UL	20	Total	C	N	O	0	0
			100	60	20	20		

- Molecule 76 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
76	CA	3	Total	Mg	0
			3	3	
76	CQ	1	Total	Mg	0
			1	1	
76	Cg	1	Total	Mg	0
			1	1	
76	IA	1	Total	Mg	0
			1	1	

- Molecule 77 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).

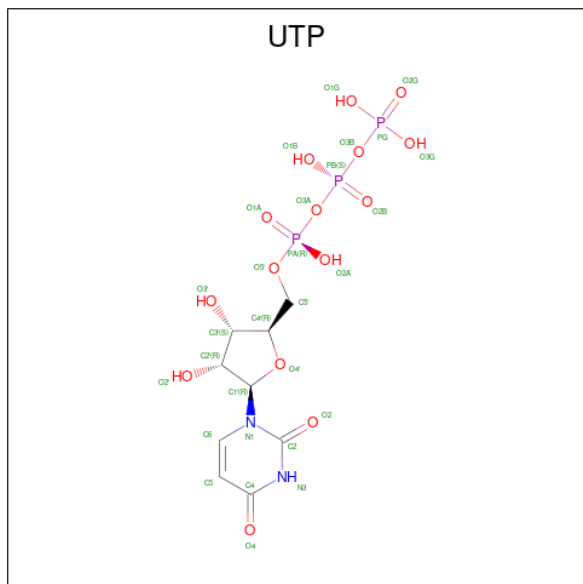


Mol	Chain	Residues	Atoms					AltConf
77	Cg	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 78 is ZINC ION (CCD ID: ZN) (formula: Zn).

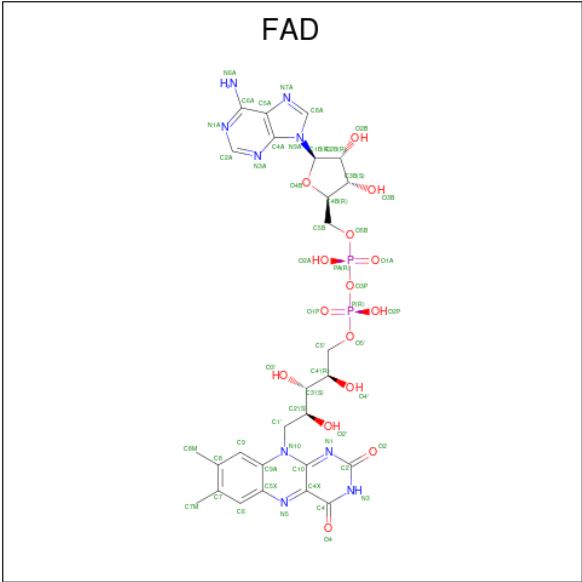
Mol	Chain	Residues	Atoms		AltConf
78	Cr	1	Total	Zn	0
			1	1	
78	DA	1	Total	Zn	0
			1	1	
78	DS	2	Total	Zn	0
			2	2	

- Molecule 79 is URIDINE 5'-TRIPHOSPHATE (CCD ID: UTP) (formula: $C_9H_{15}N_2O_{15}P_3$).



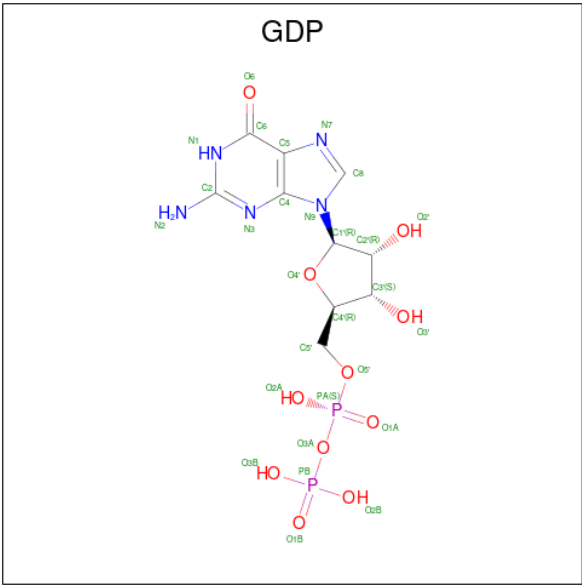
Mol	Chain	Residues	Atoms					AltConf
79	DJ	1	Total	C	N	O	P	0
			29	9	2	15	3	

- Molecule 80 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



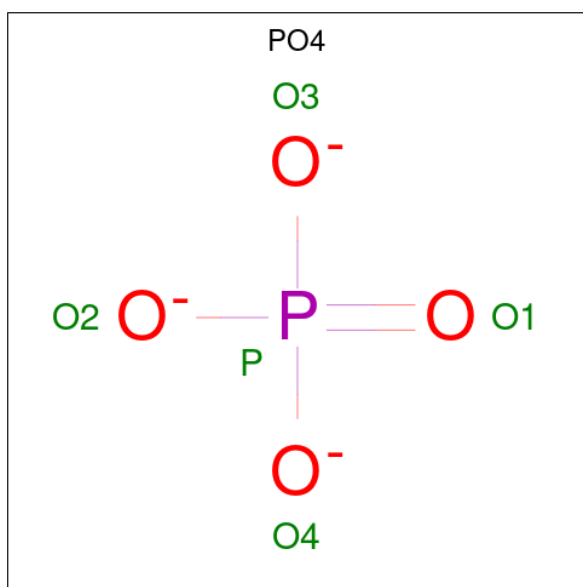
Mol	Chain	Residues	Atoms					AltConf
80	Ff	1	Total	C	N	O	P	0
			53	27	9	15	2	

- Molecule 81 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf
81	IA	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 82 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			AltConf
82	IA	1	Total	O	P	0
			5	4	1	

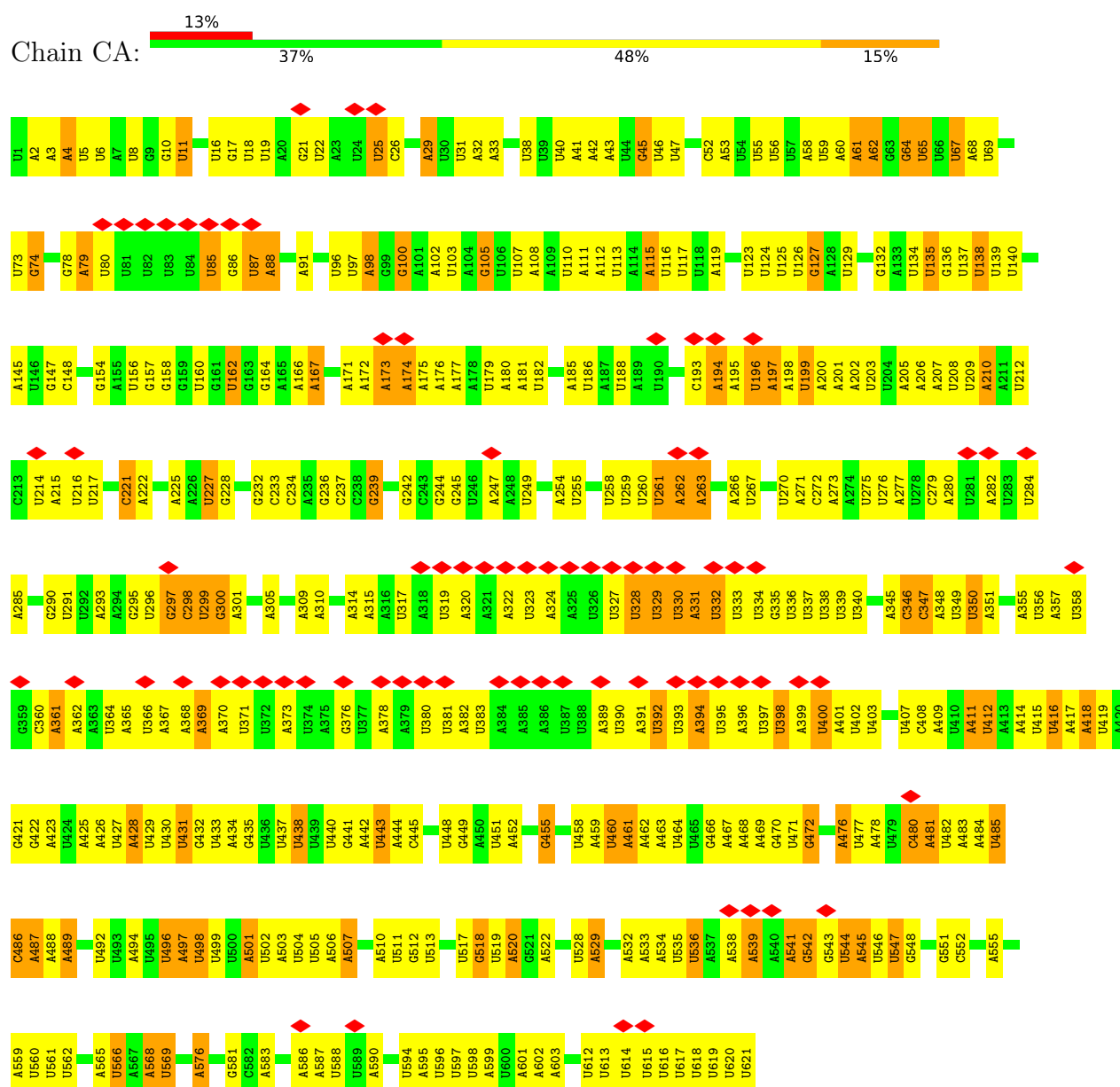
- Molecule 83 is water.

Mol	Chain	Residues	Atoms		AltConf
83	Cg	3	Total	O	0
			3	3	
83	IA	2	Total	O	0
			2	2	

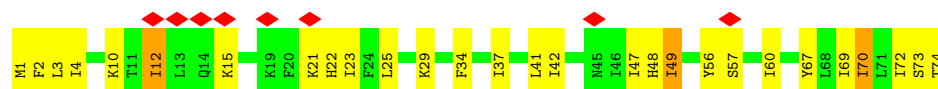
3 Residue-property plots

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

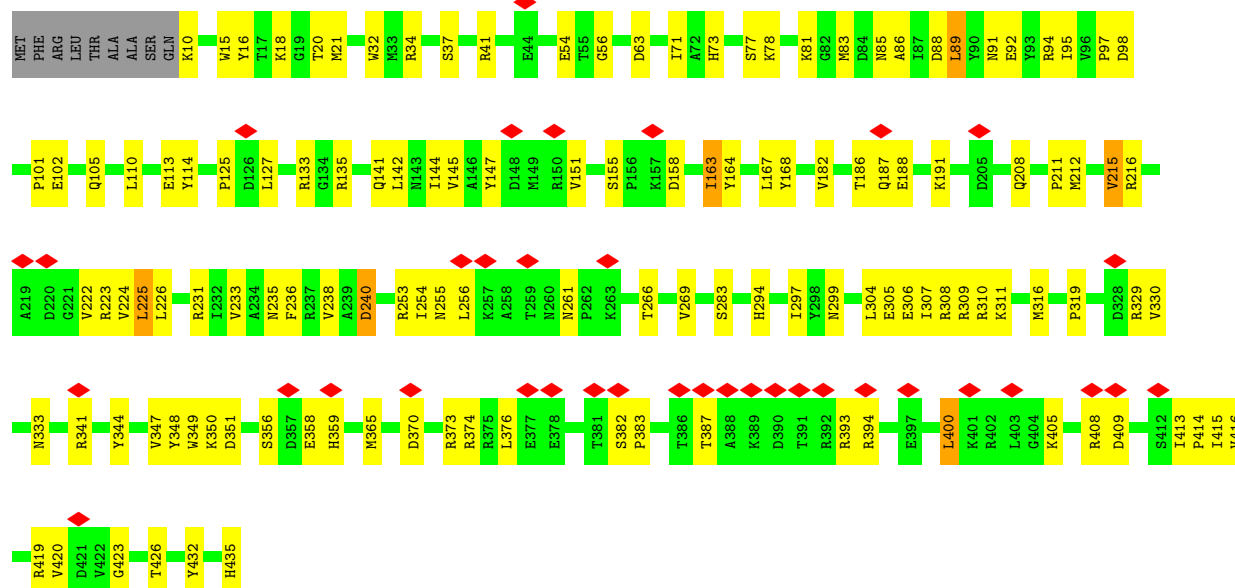
• Molecule 1: 9S rRNA



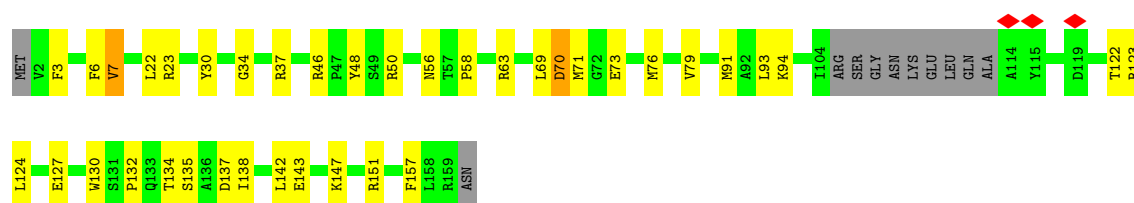
• Molecule 2: uS3m



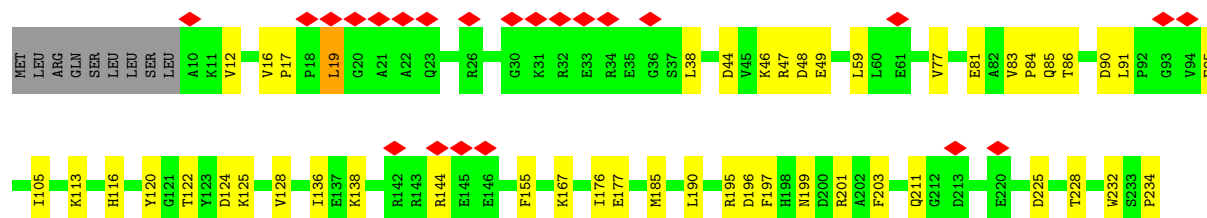
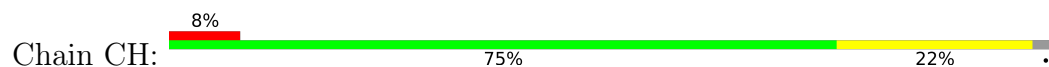
• Molecule 3: Ribosomal_S5_C domain-containing protein

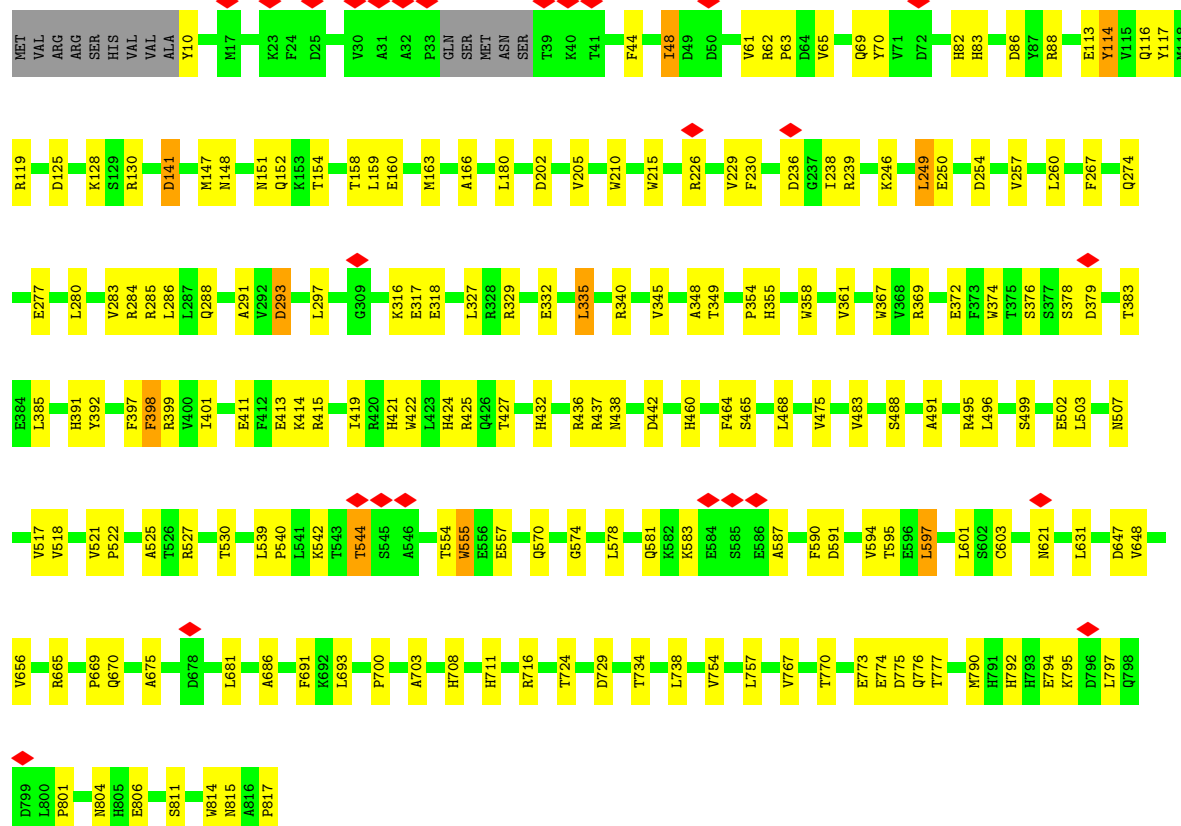


• Molecule 4: bS6m



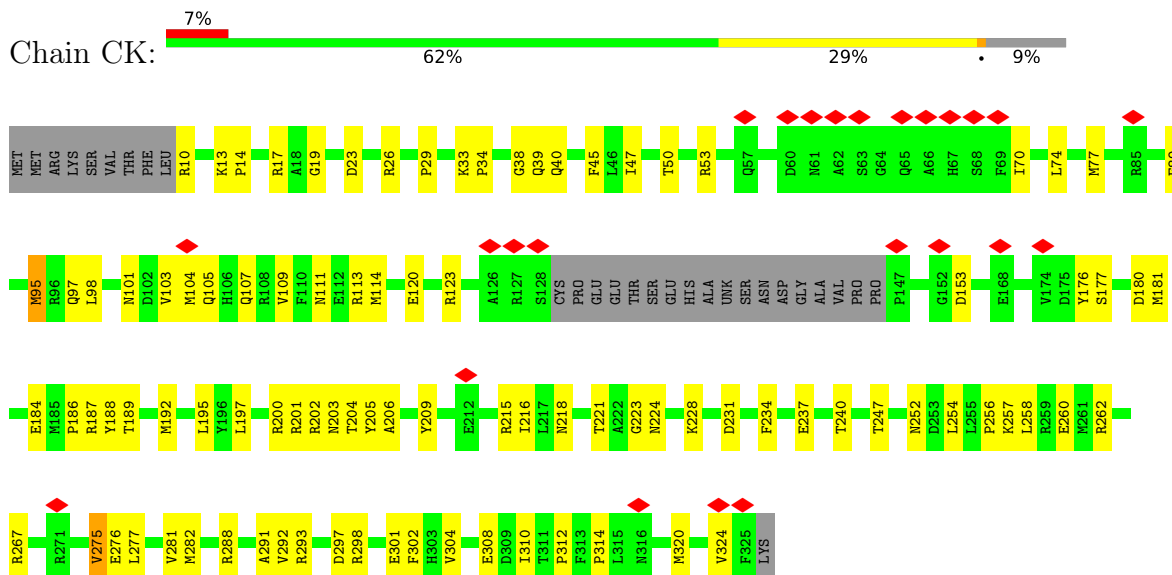
• Molecule 5: 30S ribosomal protein S8, putative





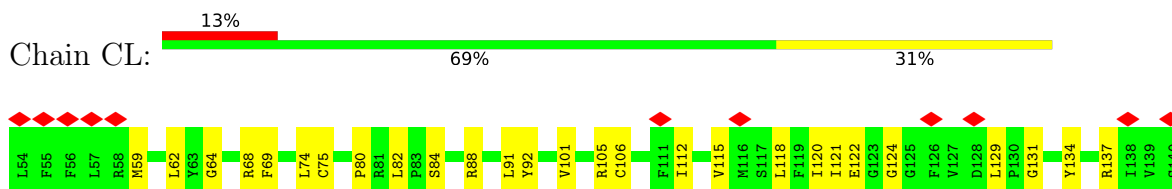
- Molecule 8: uS11m

Chain CK:



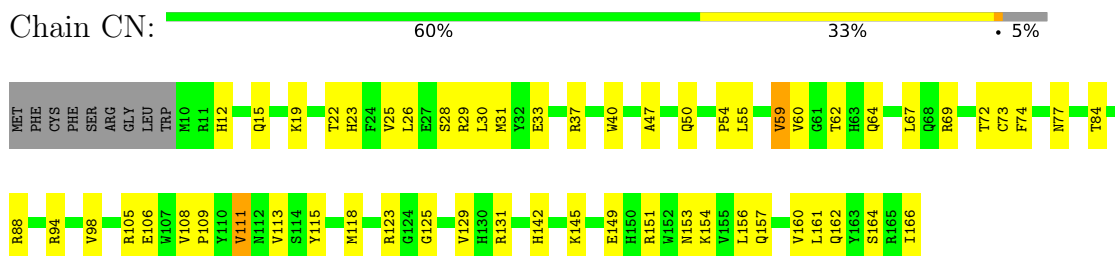
- Molecule 9: uS12m

Chain CL:



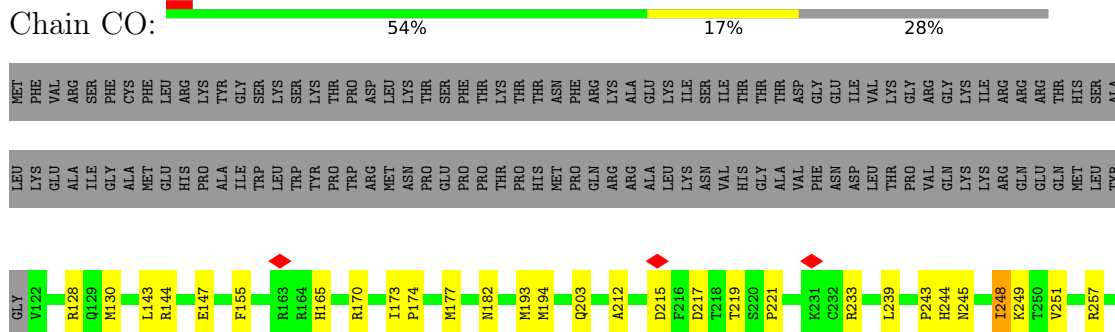
- Molecule 10: uS14m

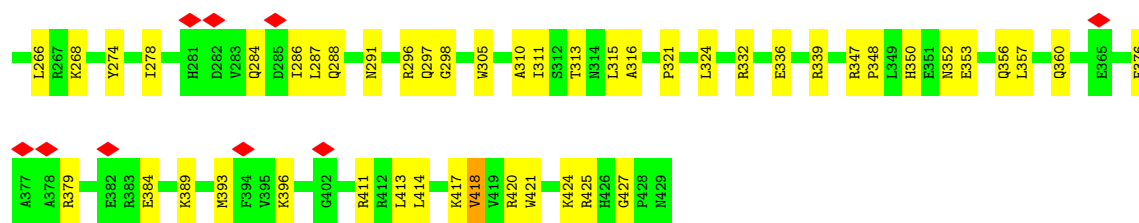
Chain CN:



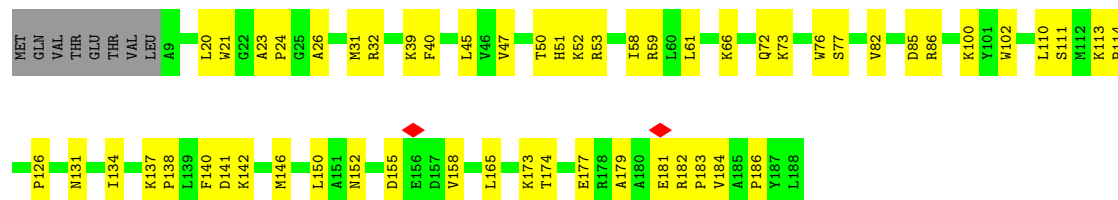
- Molecule 11: uS15m

Chain CO:

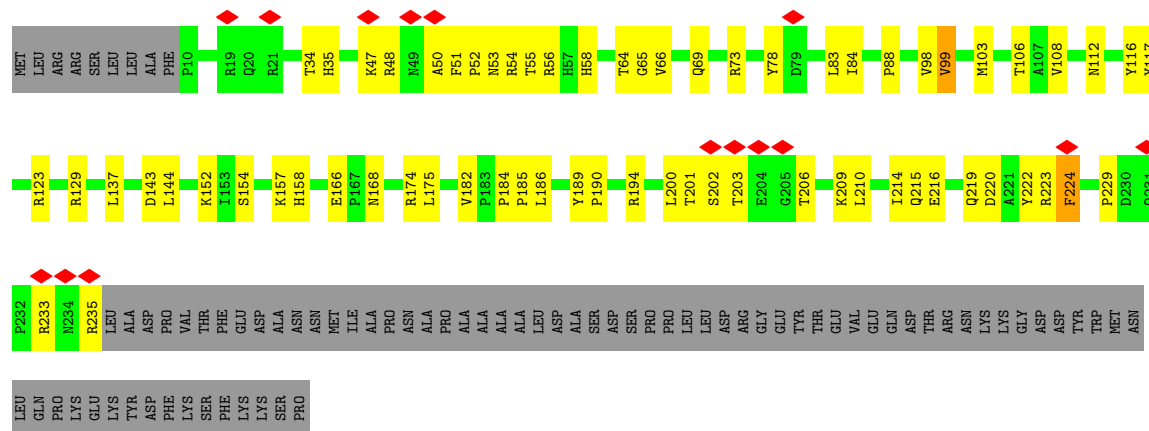




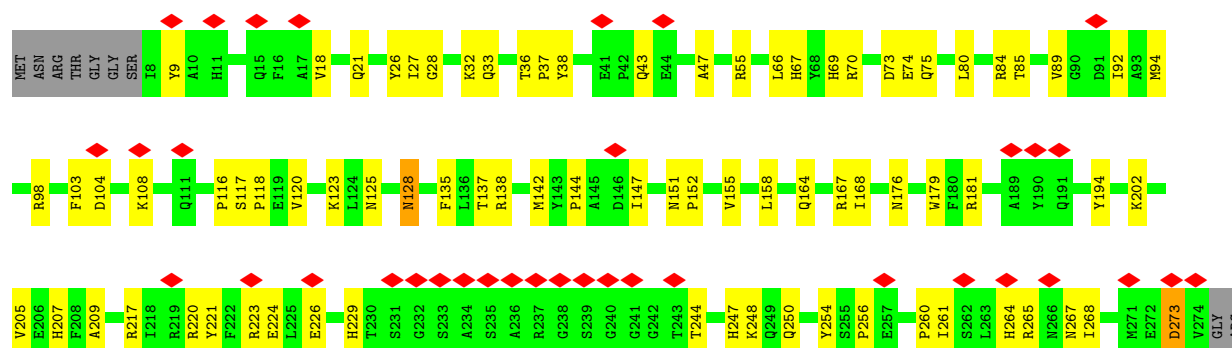
• Molecule 12: bS16m



• Molecule 13: 30S Ribosomal protein S17, putative

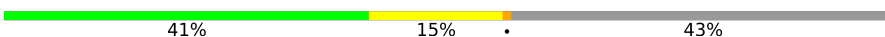


• Molecule 14: bS18m



SER VAL
LYS LYS
ASN ASN
PRO PRO
THR THR
VAL VAL
PRO PRO
GLY GLY
MET MET
SER SER
THR THR
LYS LYS
GLY GLY
MET MET
VAL VAL
LYS LYS
LYS LYS
PHE PHE
HIS HIS
ASN ASN
LEU LEU
TYR TYR
SER SER
SER SER
THR THR
SER SER
THR THR
VAL VAL
ARG ARG
MET MET
GLY GLY
PHE PHE
ALA ALA
SER SER
ASN ASN
PRO PRO
THR THR
VAL VAL
LEU LEU
PRO PRO

• Molecule 15: uS19m

Chain CS: 

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

ILE VAL
THR THR
PHE PHE
HIS HIS
CYS CYS
CYS CYS
THR THR
ARG ARG
THR THR
LYS LYS
GLY GLY
SER SER
MET MET
LEU LEU
ARG ARG
VAL VAL
CYS CYS
PRO PRO
CYS CYS
VAL VAL
TRP TRP
ASP ASP
GLY GLY
PRO PRO
THR THR
LYS LYS
SER SER
SER SER
VAL VAL
VAL VAL
PHE PHE
LEU LEU
ARG ARG
ALA ALA
GLY GLY
PHE PHE
THR THR
LEU LEU
GLN GLN
LYS LYS
SER SER
PHE PHE
VAL VAL
MET MET
LEU LEU
PRO PRO
VAL VAL
SER SER
K106
K107
F124
L125
I130
A140
F143
T148
S151

Q152
F156
L156
E159
N160
Y161
I162
W166
K169
F170
F171
K174
R175
Q176
V177
H182
R190
I197
S204
R205
W206
G209
N213
K217
M220
D221
L222
I223
D224
L228
T229
Q232
R233
L234
R238
P243
LYS

• Molecule 16: bS21m

Chain CU: 

MET LEU
HIS HIS
THR THR
THR THR
ARG ARG
LEU LEU
TRP TRP
GLY GLY
Y12
M13
M14
Y15
H16
R17
K18
A19
K27
H32
S36
Y39
P43
N44
V45
V48
N51
T54
T55
V57
D58
R59
R60
M62
V65
F76
Y79
Q80
E81
K82
E92
M112
T116

M117
K118
E121
D122
R125
L126
M128
T129
Q132
V135
W143
T146
D147
M148
V149
A150
R151
E152
R153
A157
V158
R159
R160
Q161
V162
R163
A164
L165
P166
M167
V168
M169
V175
Q180
I181
H182
M183
D184
R185
Y188
R189
W190
R191
V192
ASN

• Molecule 17: mS22

Chain Ca: 

MET LEU
ARG ARG
ALA ALA
TYR TYR
ILE ILE
GLN GLN
ARG ARG
TYR TYR
PRO PRO
PHE PHE
ASN ASN
LYS LYS
ARG ARG
GLY GLY
PRO PRO
ARG ARG
GLU GLU
H21
W24
K25
H26
H27
V28
L29
T30
E31
P32
P33
LYS LYS
PRO PRO
LEU LEU
GLN GLN
TRP TRP
ARG ARG
D40
P41
K42
V43
W44
T45
R46
D47
L48
S49
V50
M51
K52
S53
F54
D55
A56
R65
P66
R67

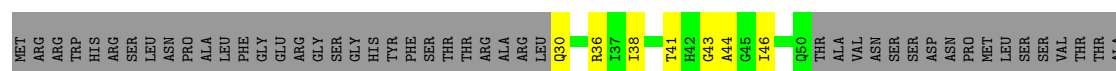
D70
M71
D72
E73
A74
L75
F78
M79
D80
M81
P82
L85
K86
R89
Y90
D91
M106
S109
L110
E111
L112
K116
M120
A121
I124
Y127
R132
A135
S136
G137
K138
D139
N140
T141
D145
D146
N150
E154
R155
M165
A166
G167
L179
N180

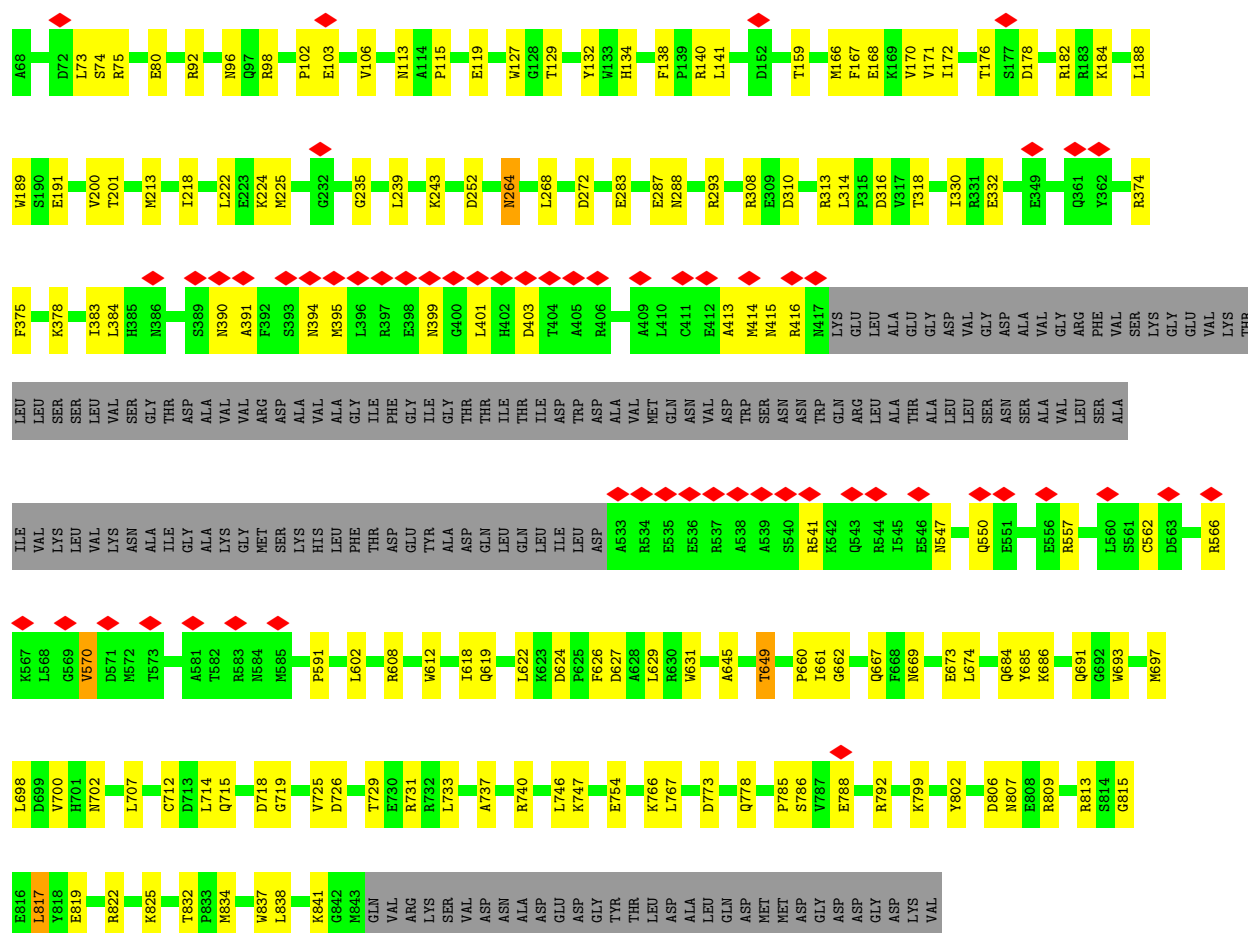
E181
K184
D187
R193
E196
H197
R200
R201
I202
L205
D213
D216
W217
L217
E218
A219
L220
T221
Q222
N223
S224
P225
H226
N227
C228
E229
Q230
L231
Q232
R233
K234
I235
A236
F237
Q238
T239
S240
L241
G242
T243
P244
E245
F246
F247
D248
M249
R252
L253
E256
D260

L267
G268
P269
E270
L271
F272
A273
L274
W275
S276
D277
A278
P283
P284
E285
R286
L297
V298
L302
V303
V304
H305
H306
F307
K308
Y311
D312
A313
C314
V315
E316
F317
W319
S320
F326
A327
L328
E329
W330
V334
R335
A336
R337
K338
H339
G340
L341
F342
Y343
G344
K345
M346

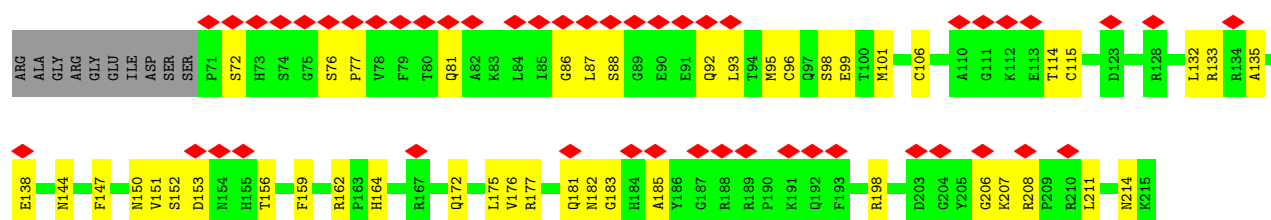
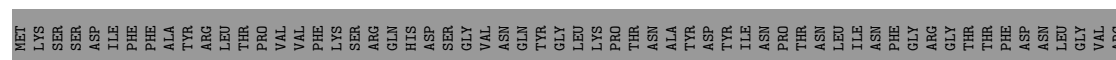
R347
T354
F355
D358
L361
F362
R363
D364
L365
V366
R367
R368
R384
D391
D398
G412
R413
T414
G415
Q419
Q420
Y421
P430
H431
R432
Q433
K437
W442
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E460
R474
L480
E487
M488
R489
A490
W491
Y492



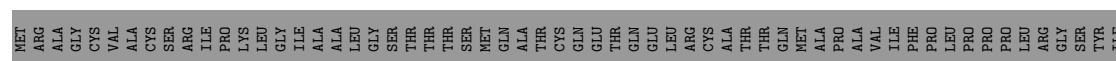


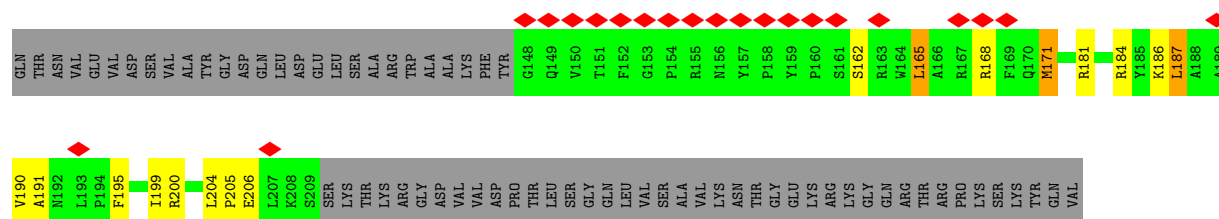


• Molecule 24: mS37

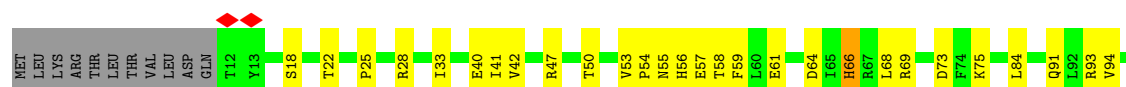


• Molecule 25: mS38

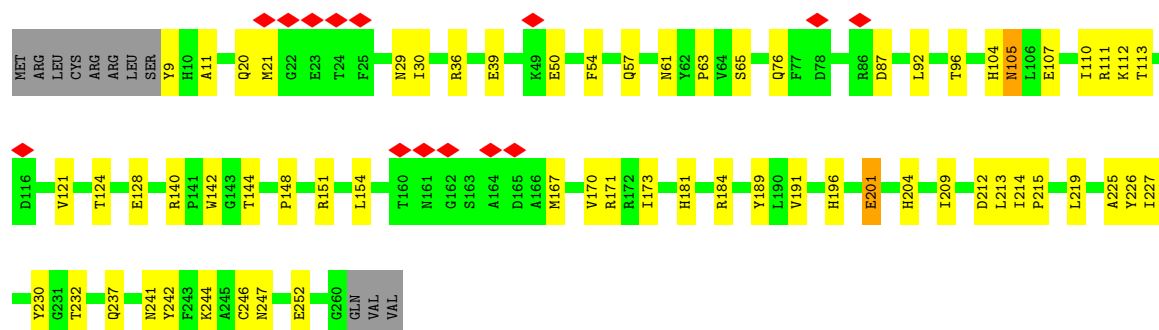
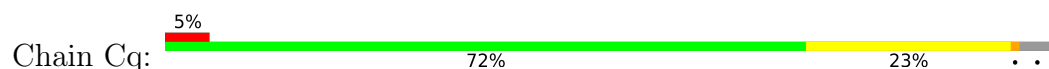




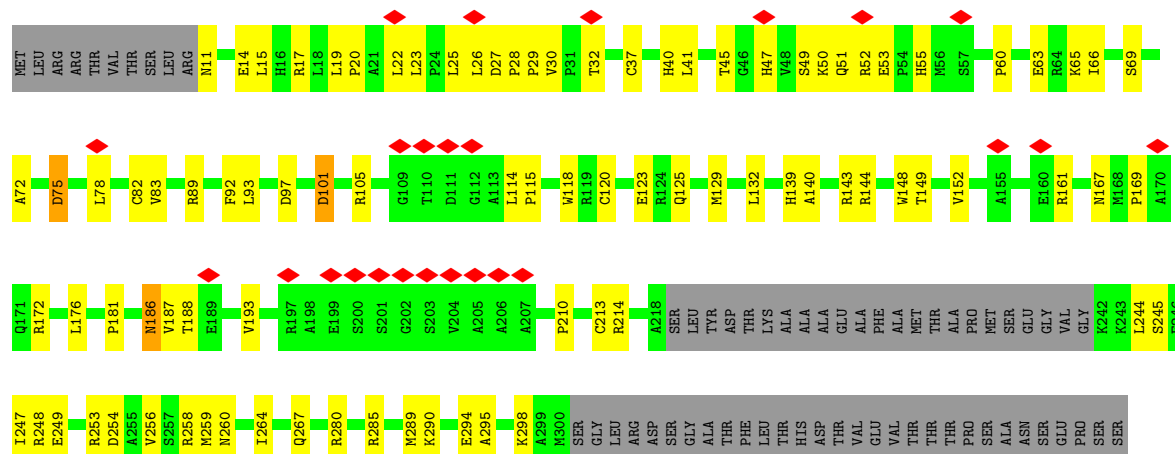
- Molecule 26: Protein FYV4, mitochondrial

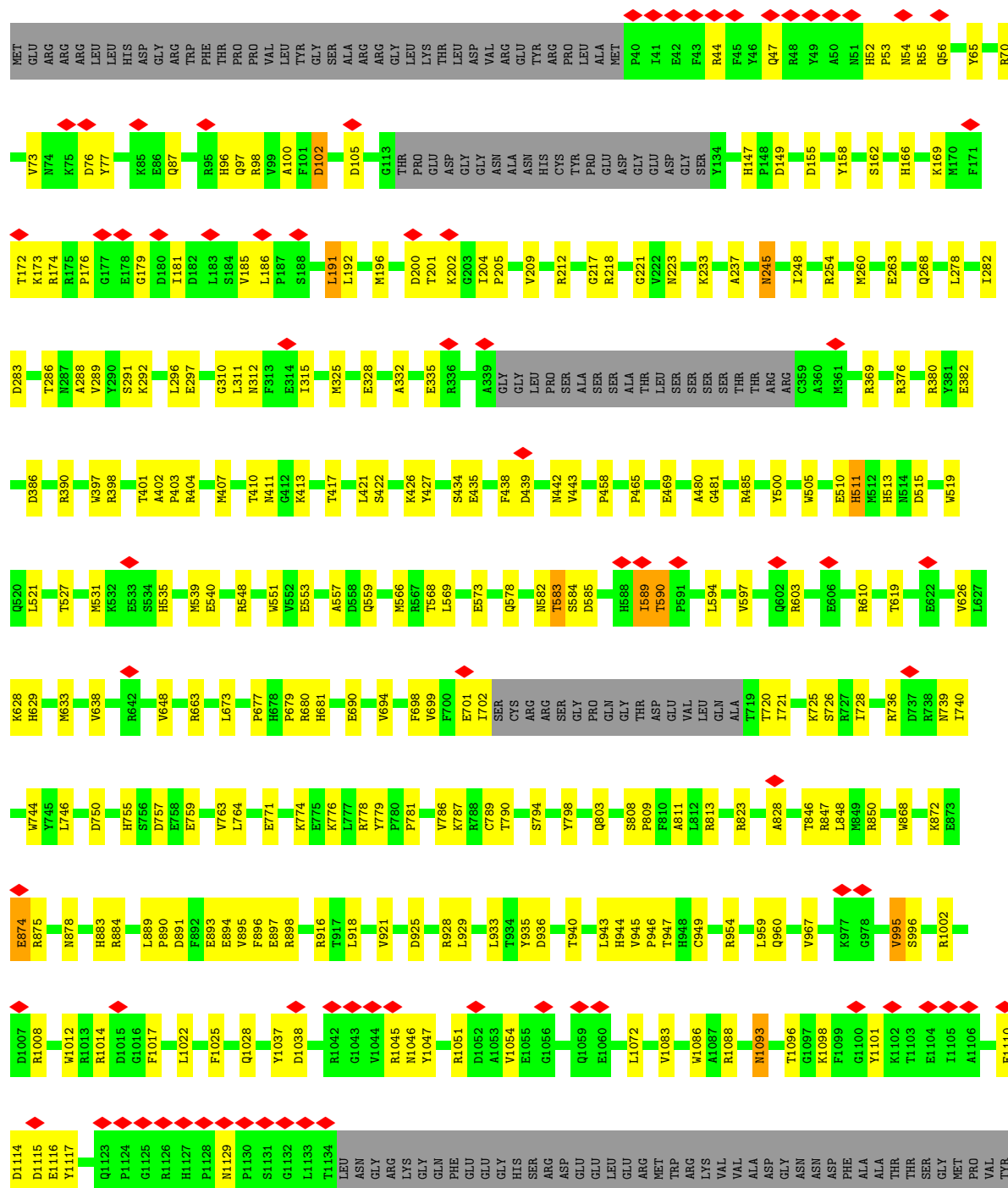


- Molecule 27: Superoxide dismutase, putative



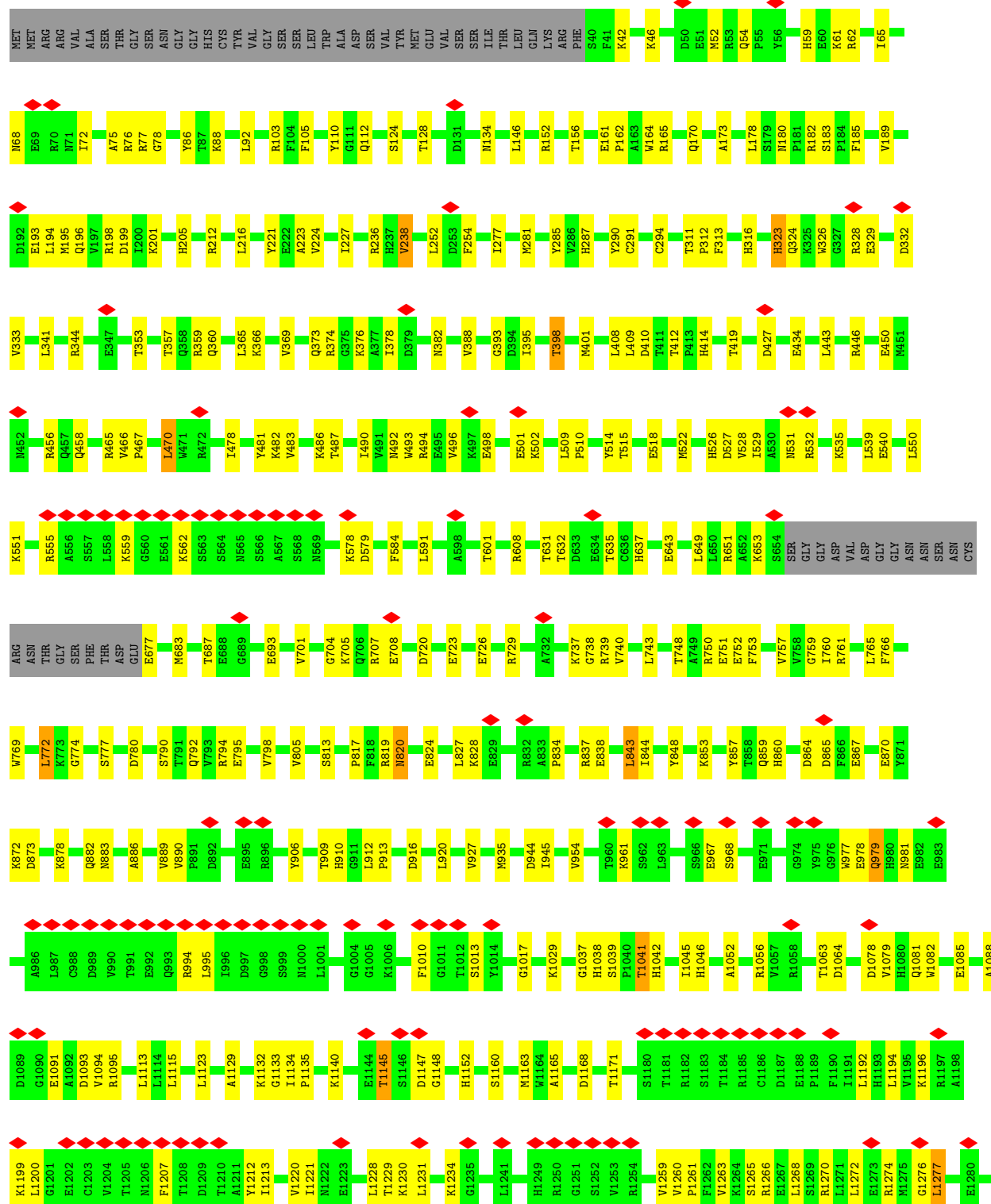
- Molecule 28: Sod_Fe_C domain-containing protein

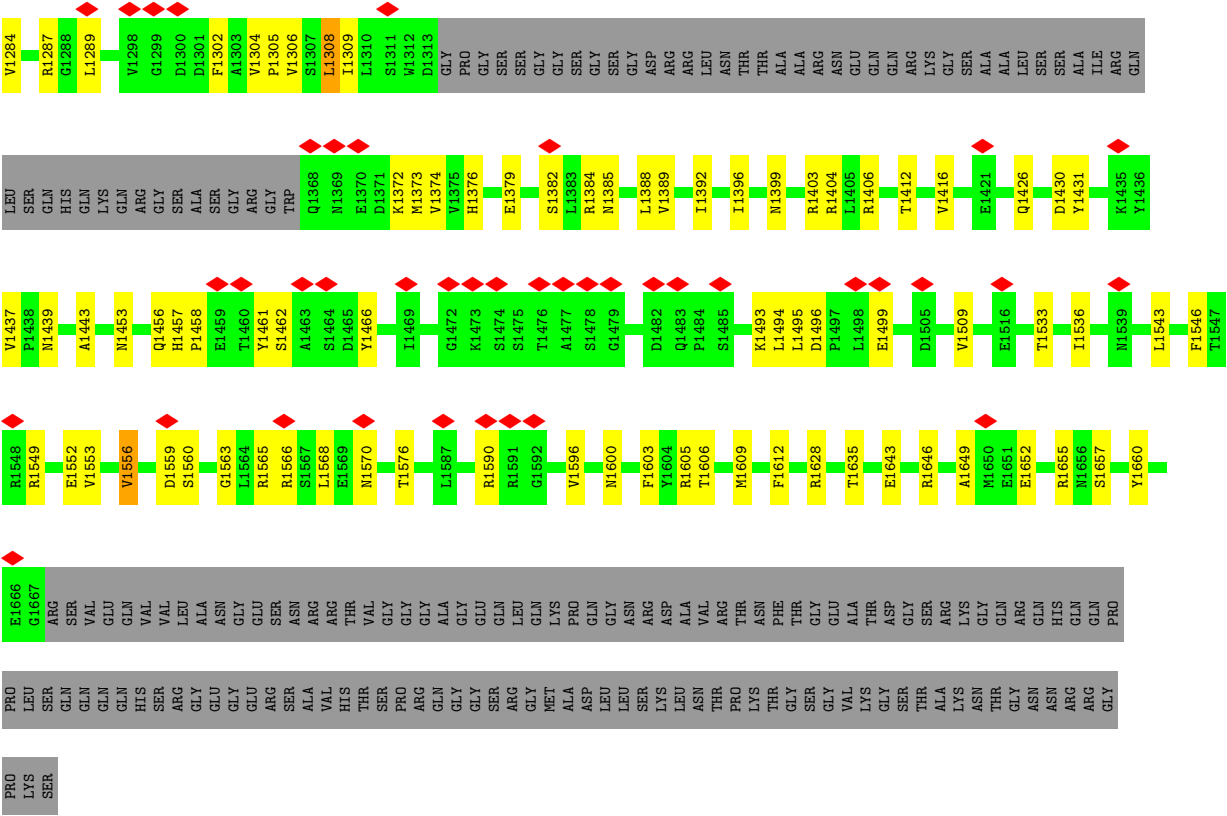




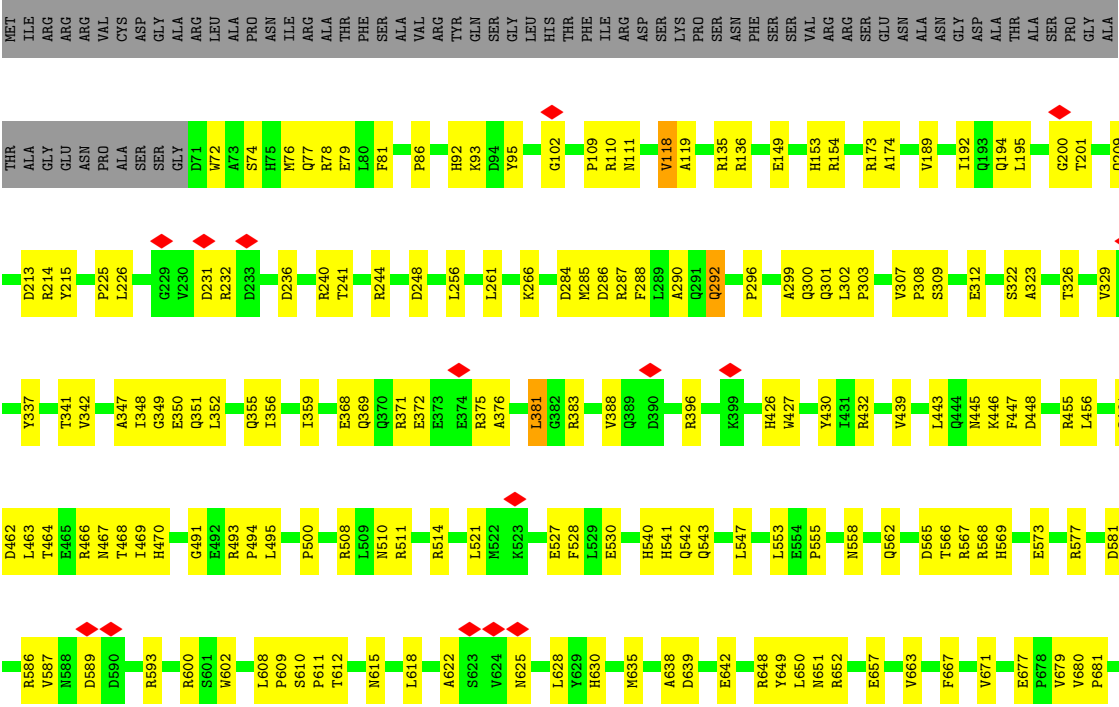
ASP GLU MET
ASP ARG
ALA LYS
VAL ASN
ALA ALA
GLU ASP
SER SER
TYR THR
ALA ALA
GLY GLY
ASP ASP
ASP VAL
VAL ASP
VAL VAL
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ALA ASP
ASN VAL
VAL VAL
PRO VAL
MET VAL
ASP GLY
GLY ASP
ASP ASP
SER SER

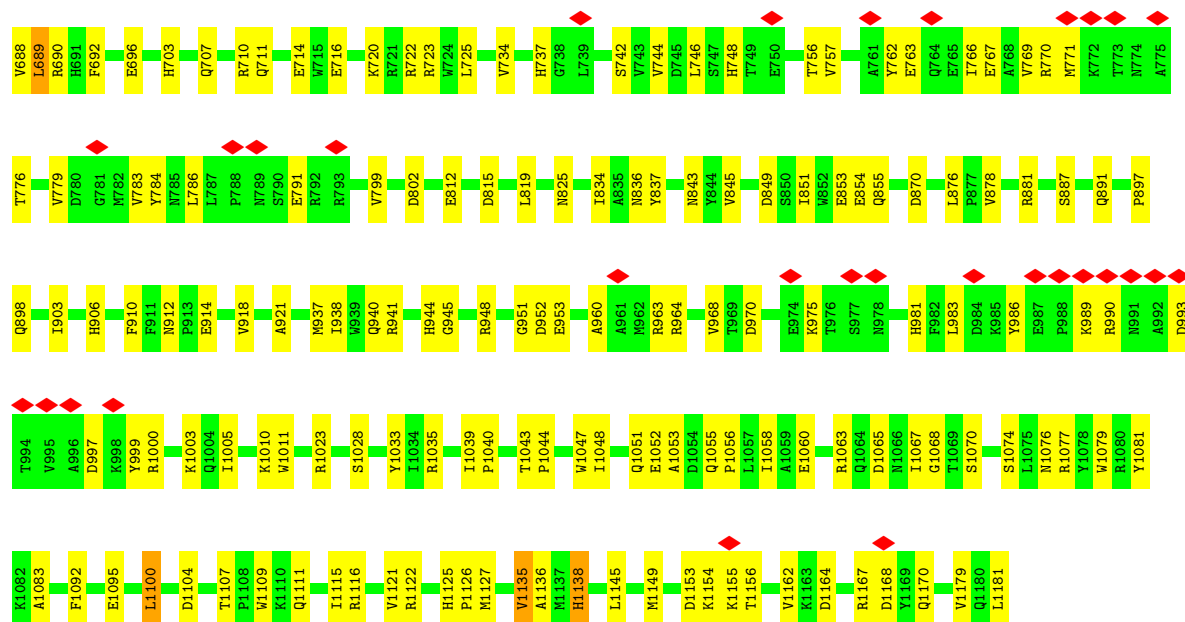
• Molecule 30: mS48



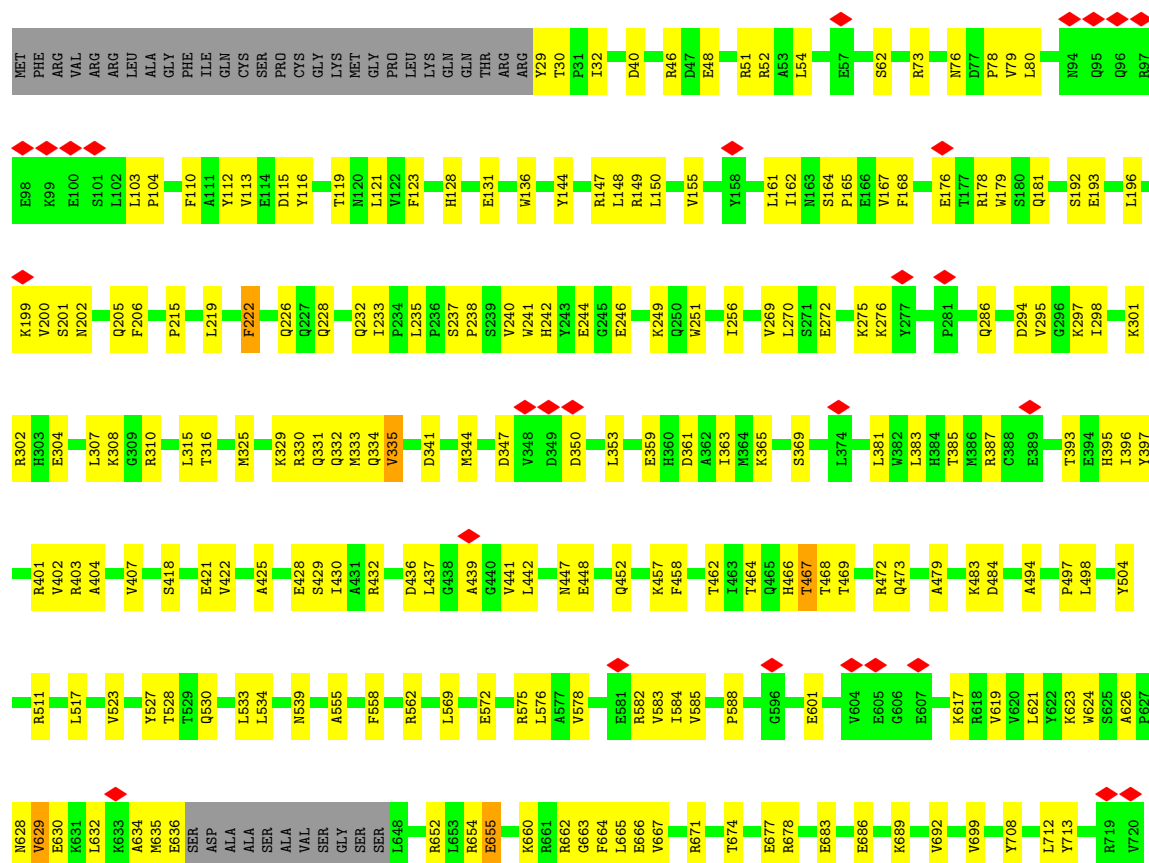


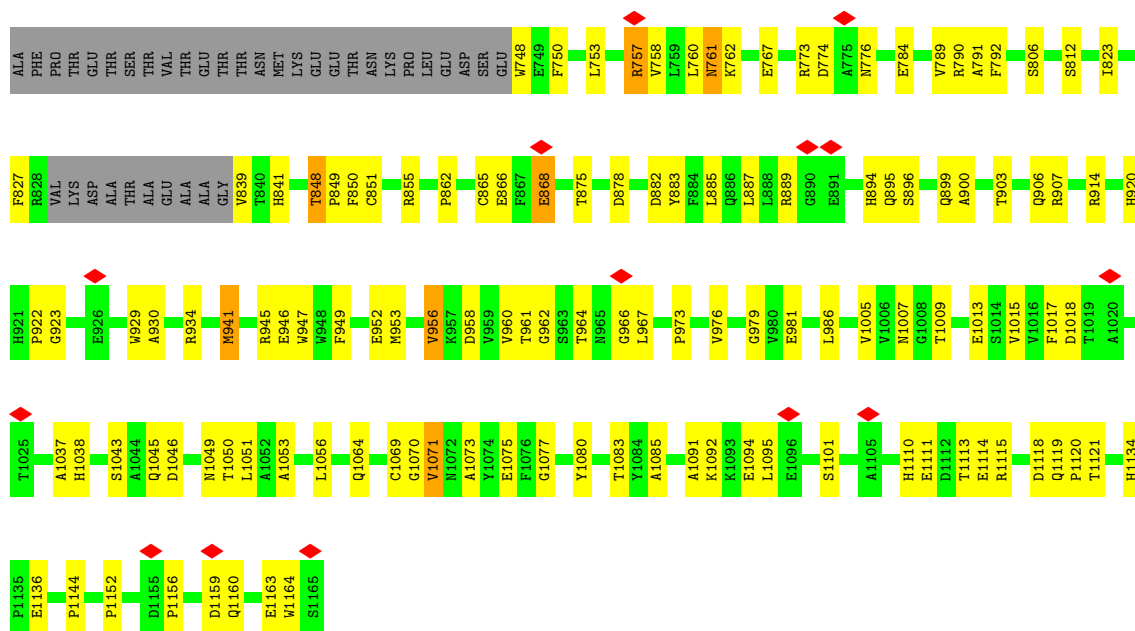
• Molecule 31: mS49





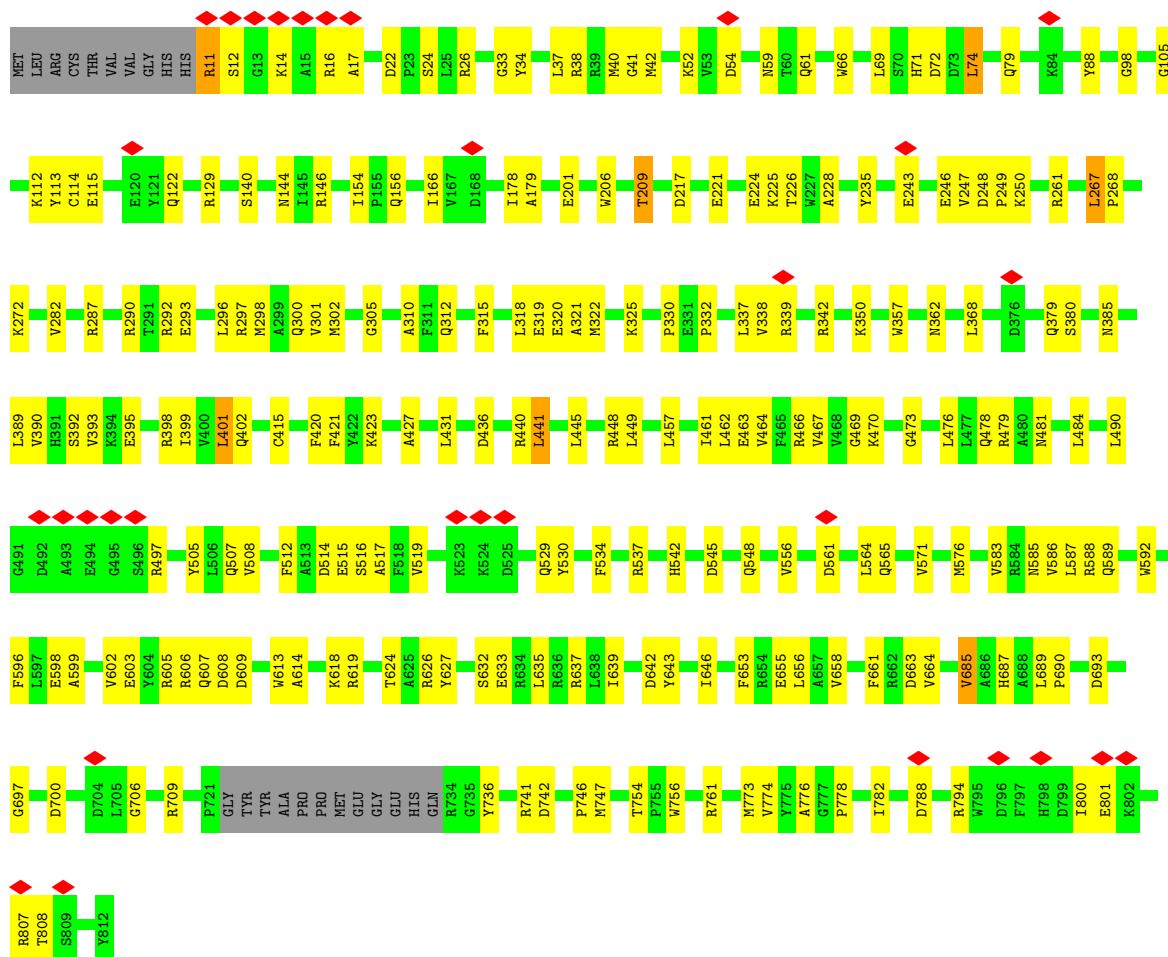
• Molecule 32: mS50





• Molecule 33: mS51

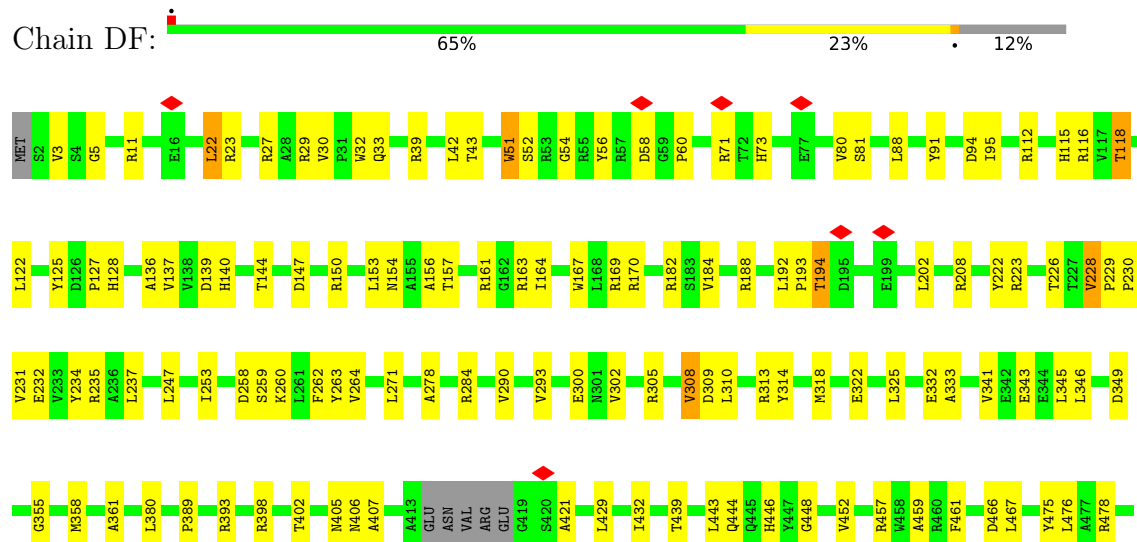
Chain DD:

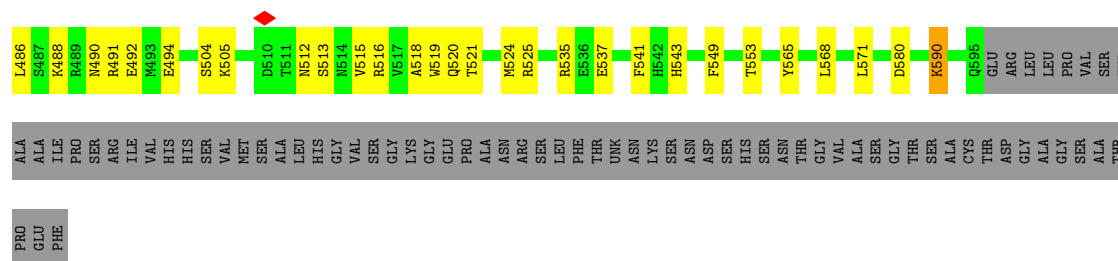


Chain DE:

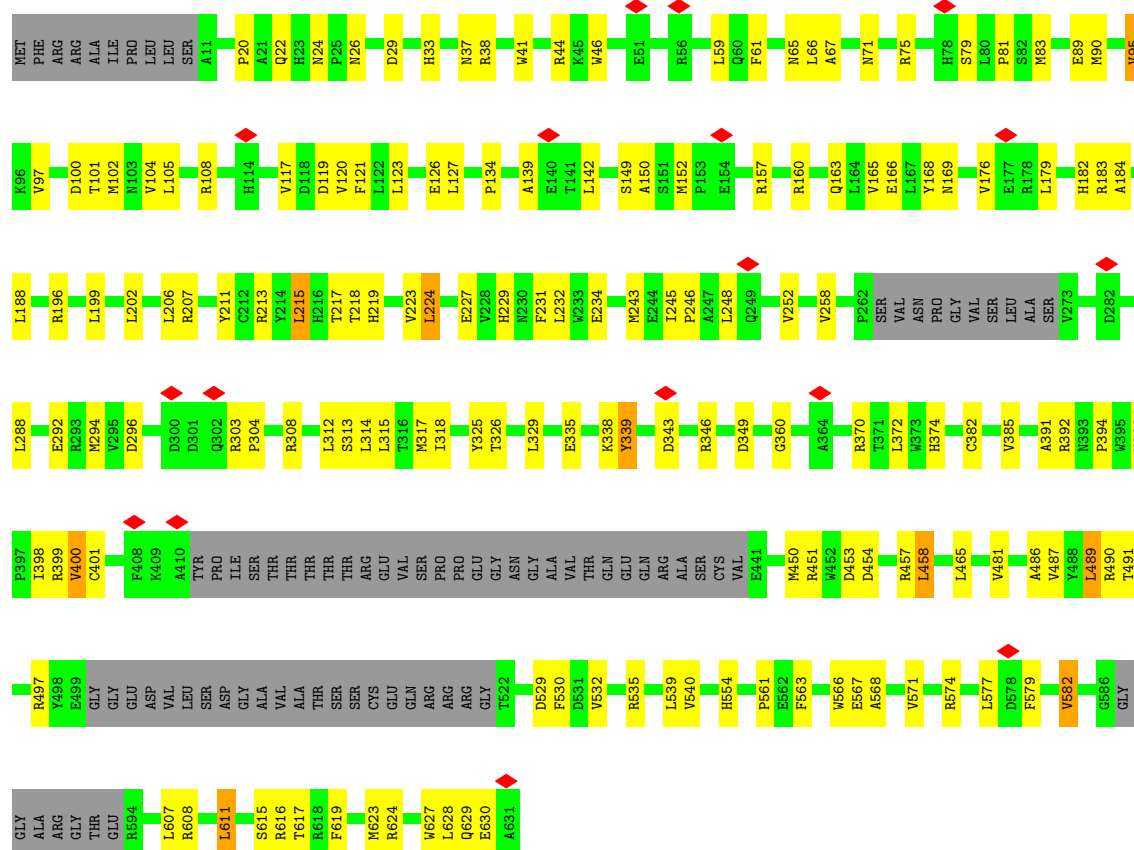


Chain DF:

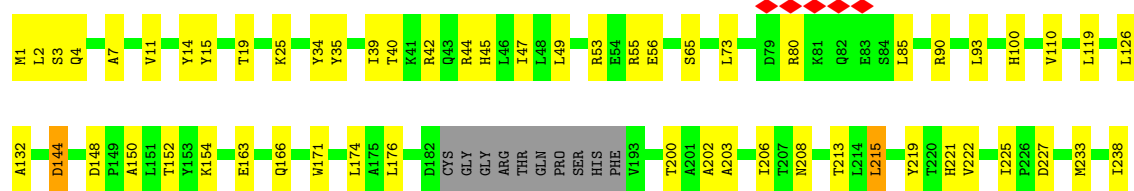


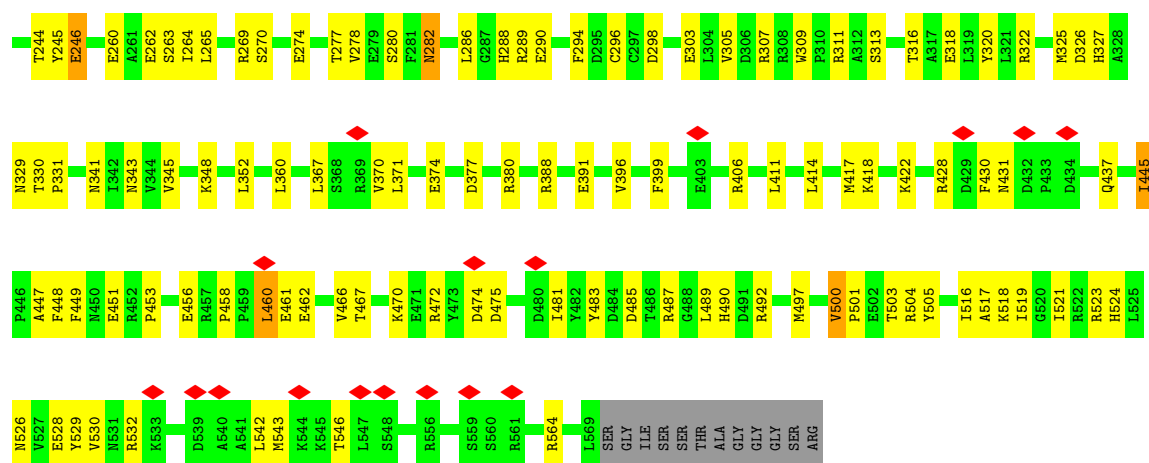


• Molecule 36: mS54

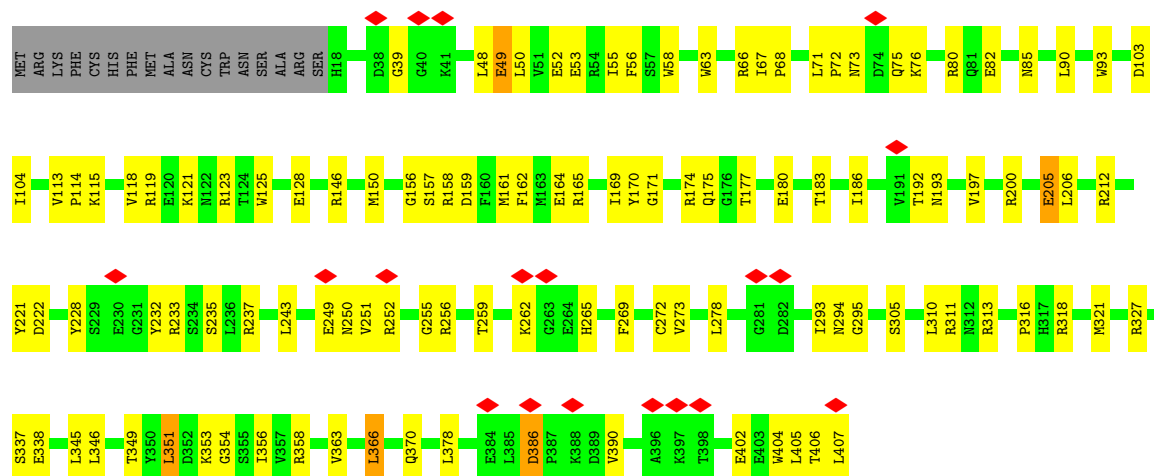


• Molecule 37: mS55

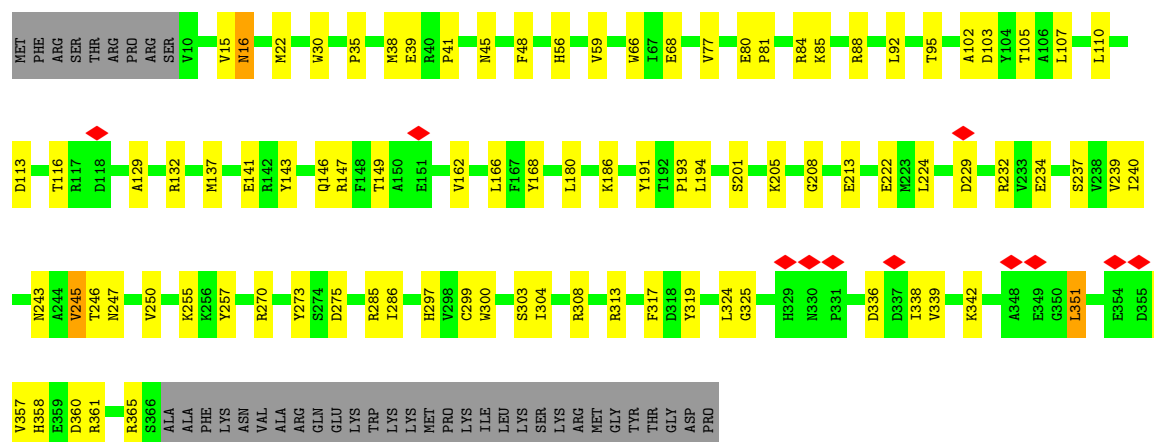




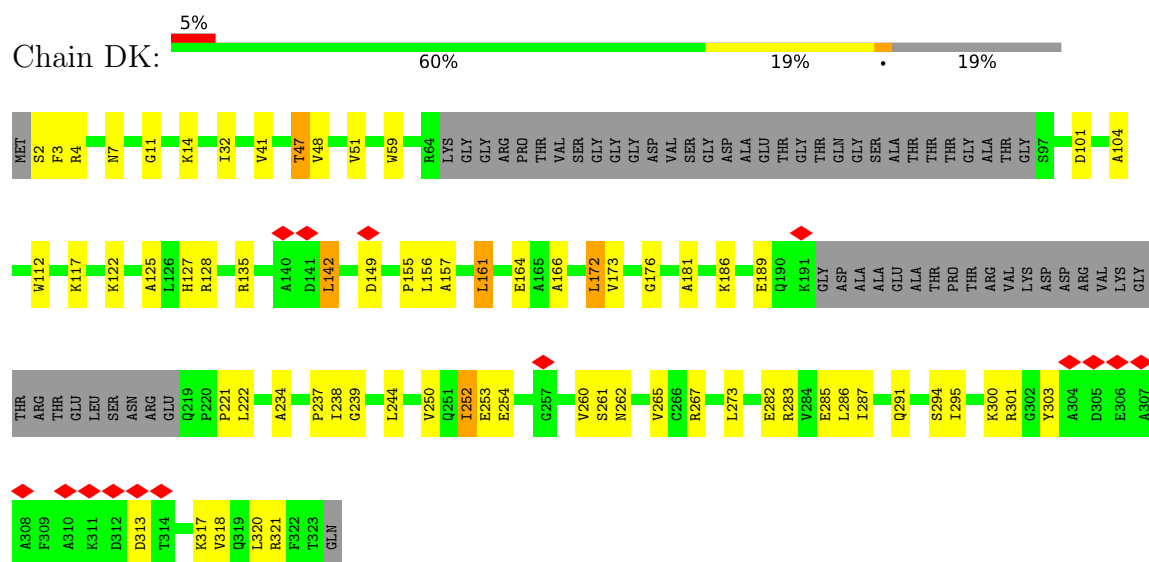
• Molecule 38: mS56



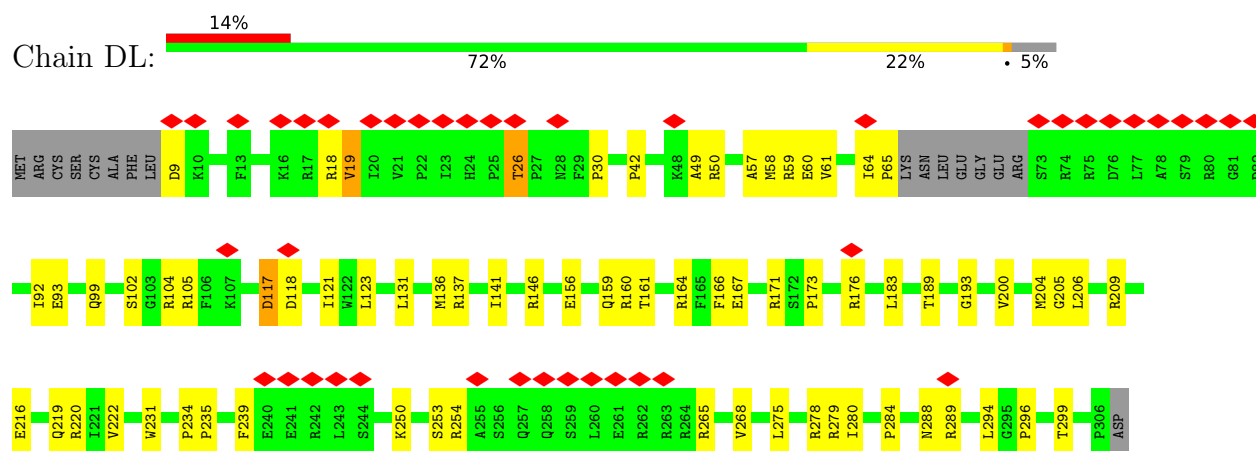
• Molecule 39: mS57



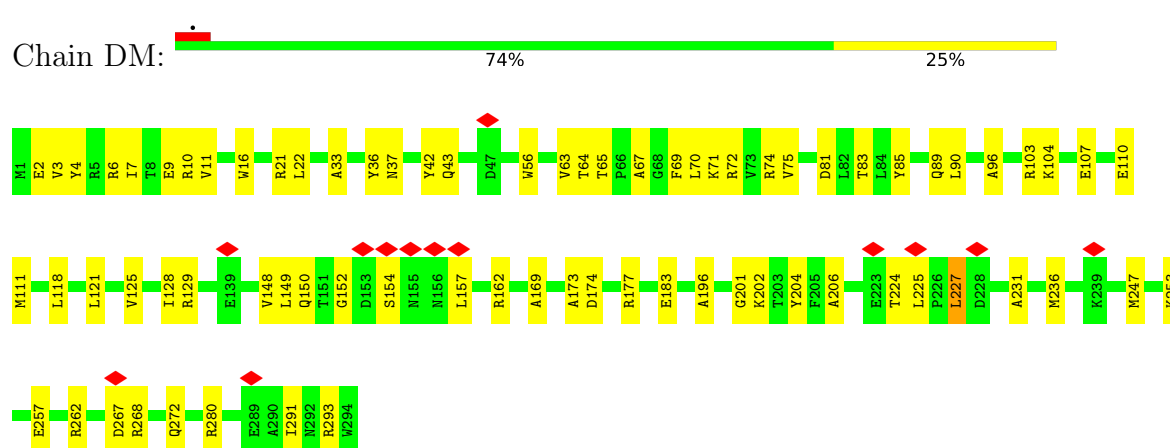
• Molecule 40: mS58



- Molecule 41: mS59

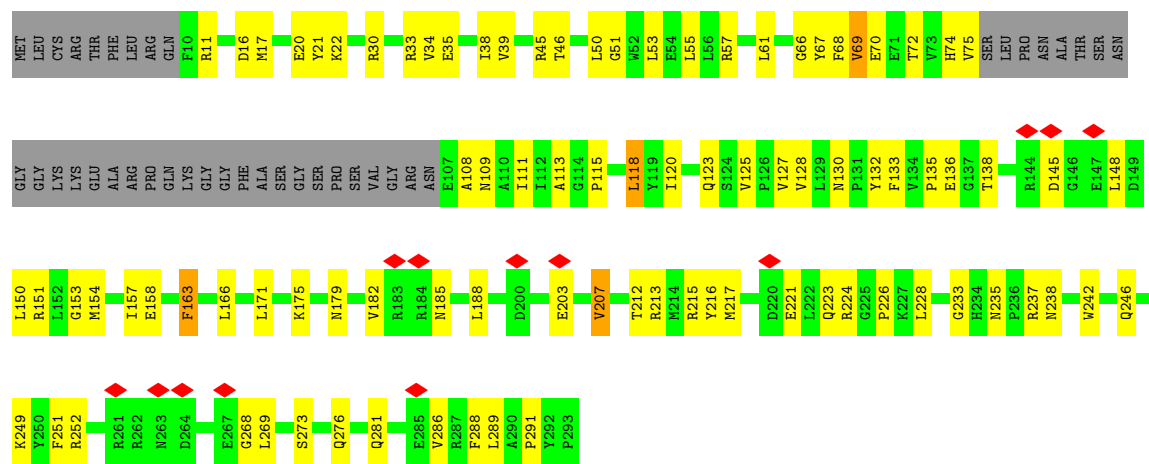


- Molecule 42: mS60

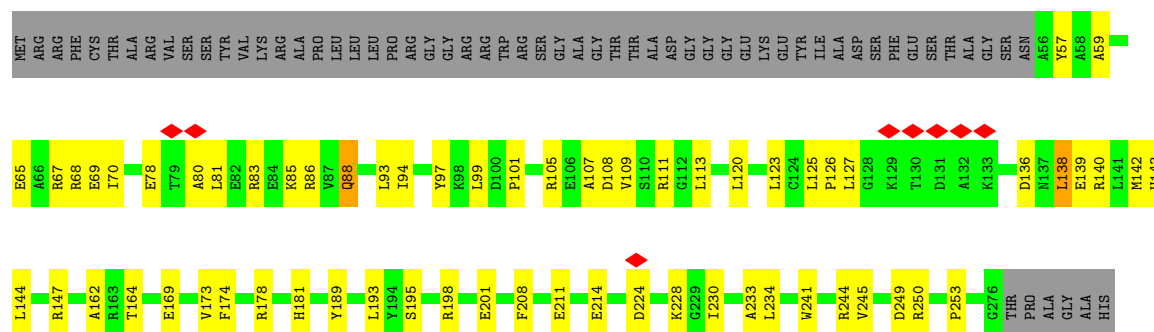


- Molecule 43: mS61

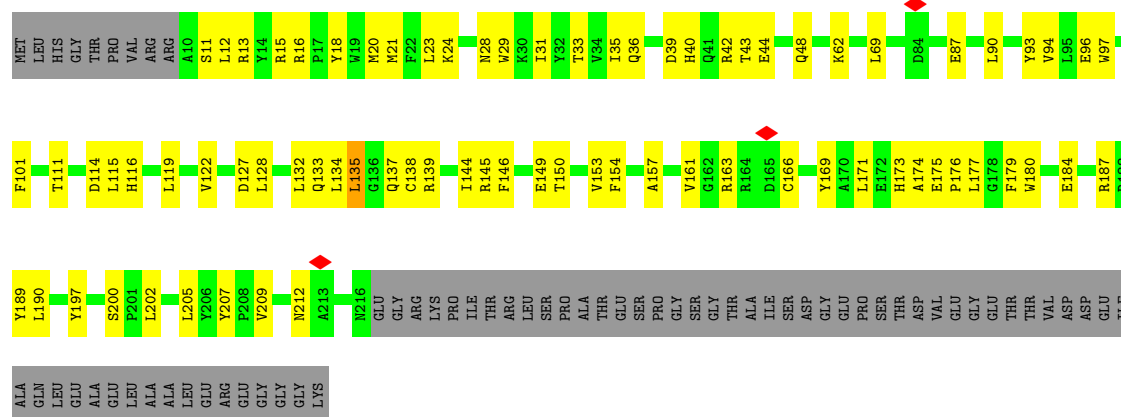




• Molecule 44: mS62

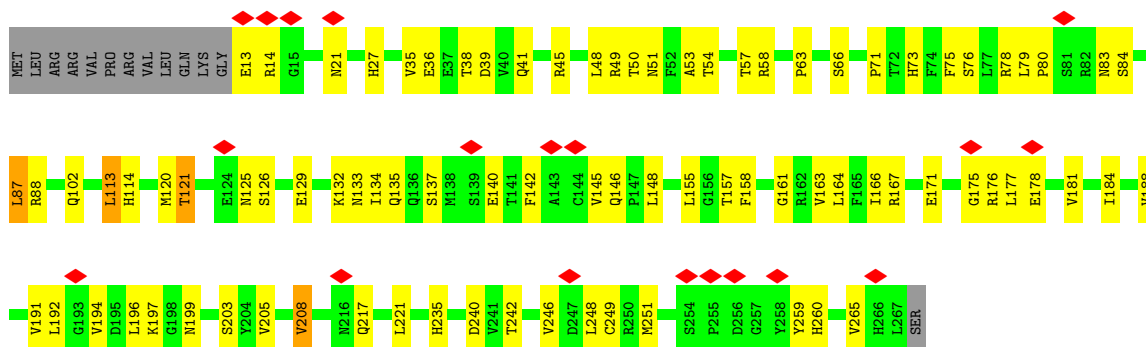


• Molecule 45: mS63



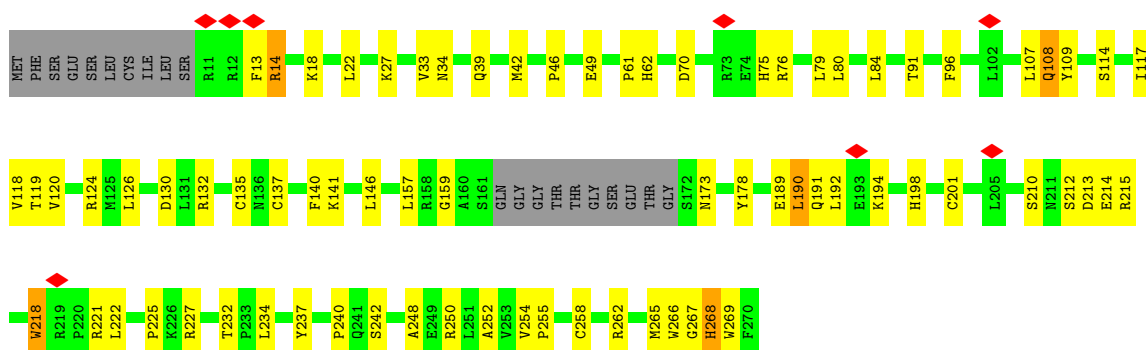
• Molecule 46: AKAP7_NLS domain-containing protein





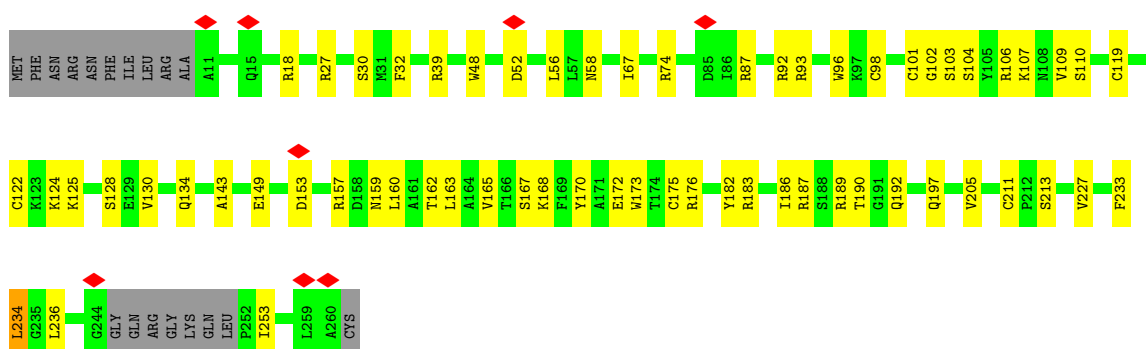
• Molecule 47: mS65

Chain DR: 64% 26% 7%



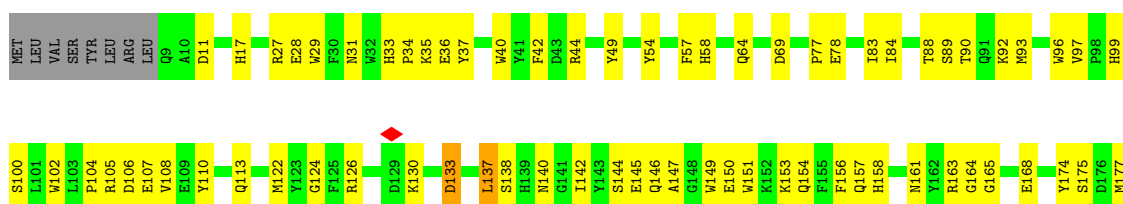
• Molecule 48: mS66

Chain DS: 69% 24% 7%



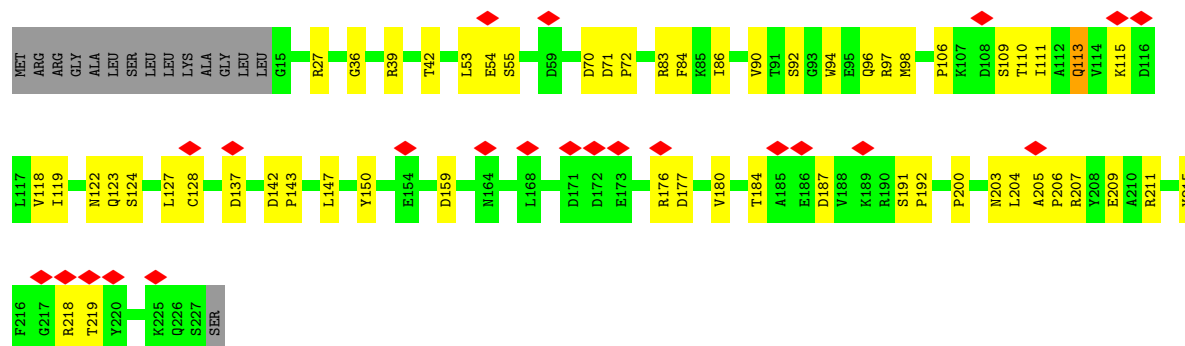
• Molecule 49: Rhodanese domain-containing protein

Chain DT: 61% 34% 5%

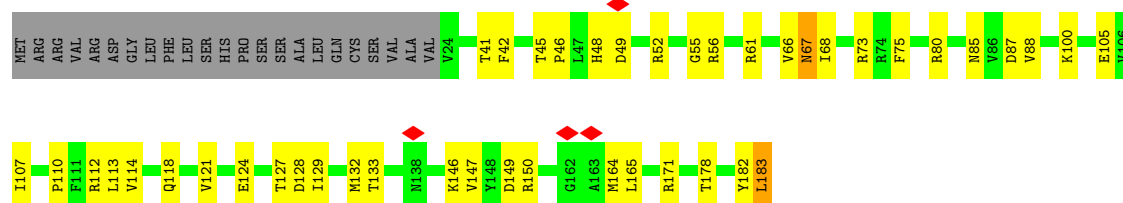




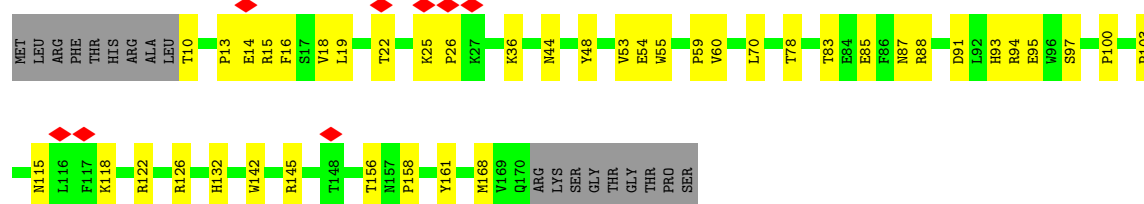
- Molecule 50: Ubiquitin-like domain-containing protein



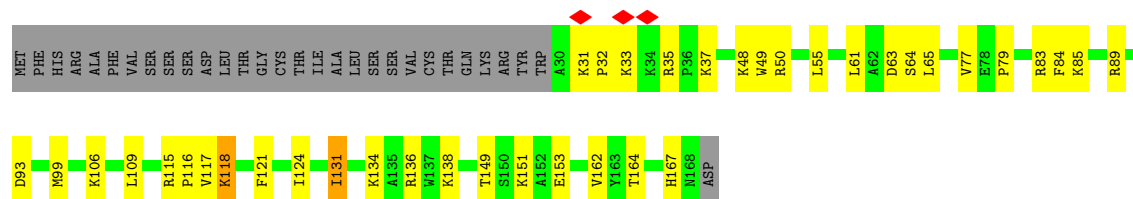
- Molecule 51: mS69



- Molecule 52: mS70

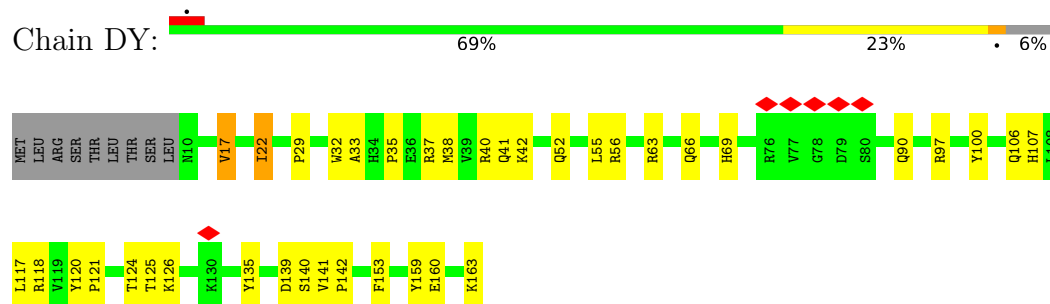


- Molecule 53: mS71



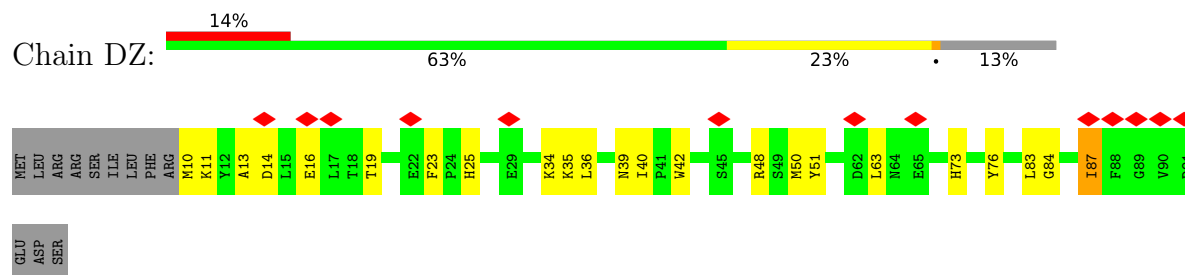
- Molecule 54: mS72

Chain DY:



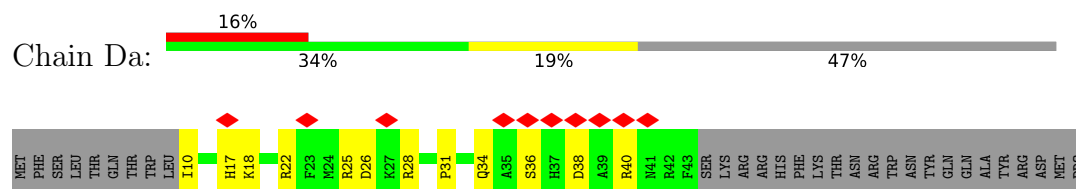
- Molecule 55: mS73

Chain DZ:



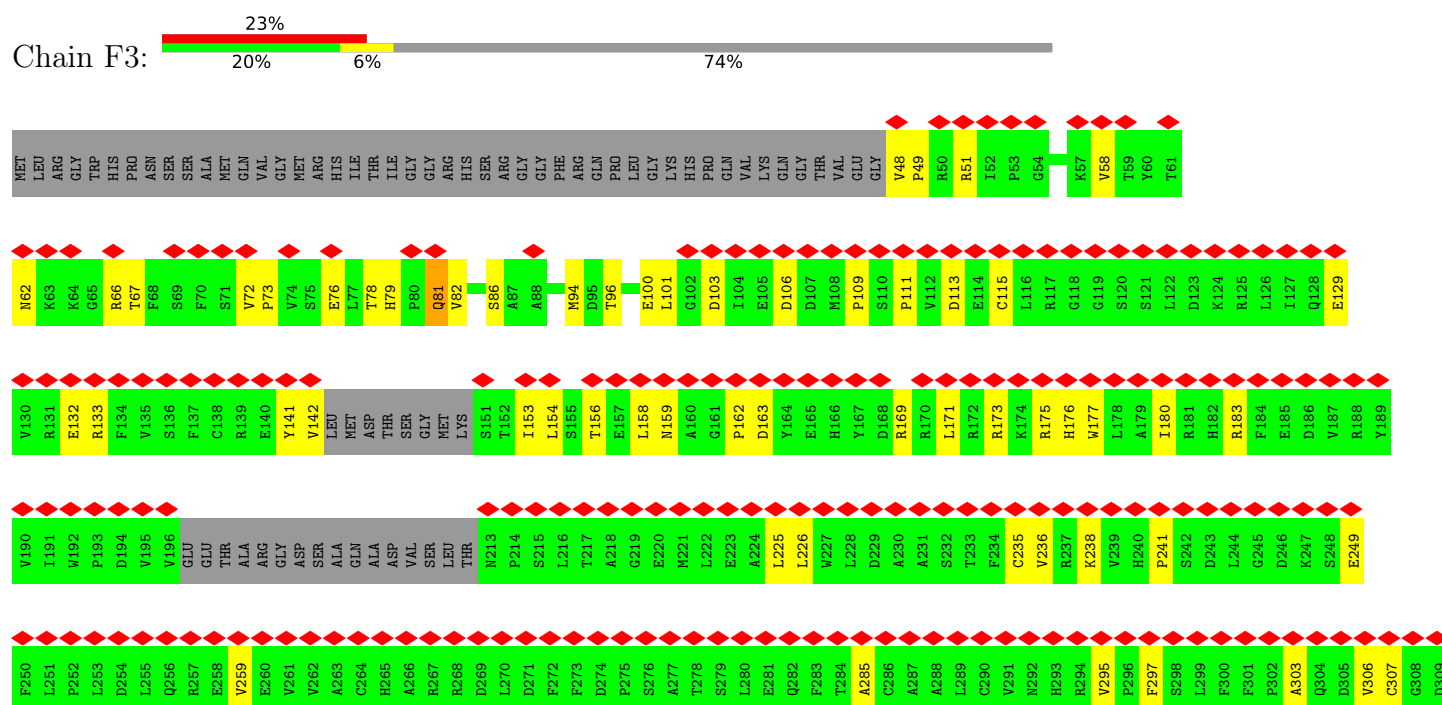
- Molecule 56: mS74

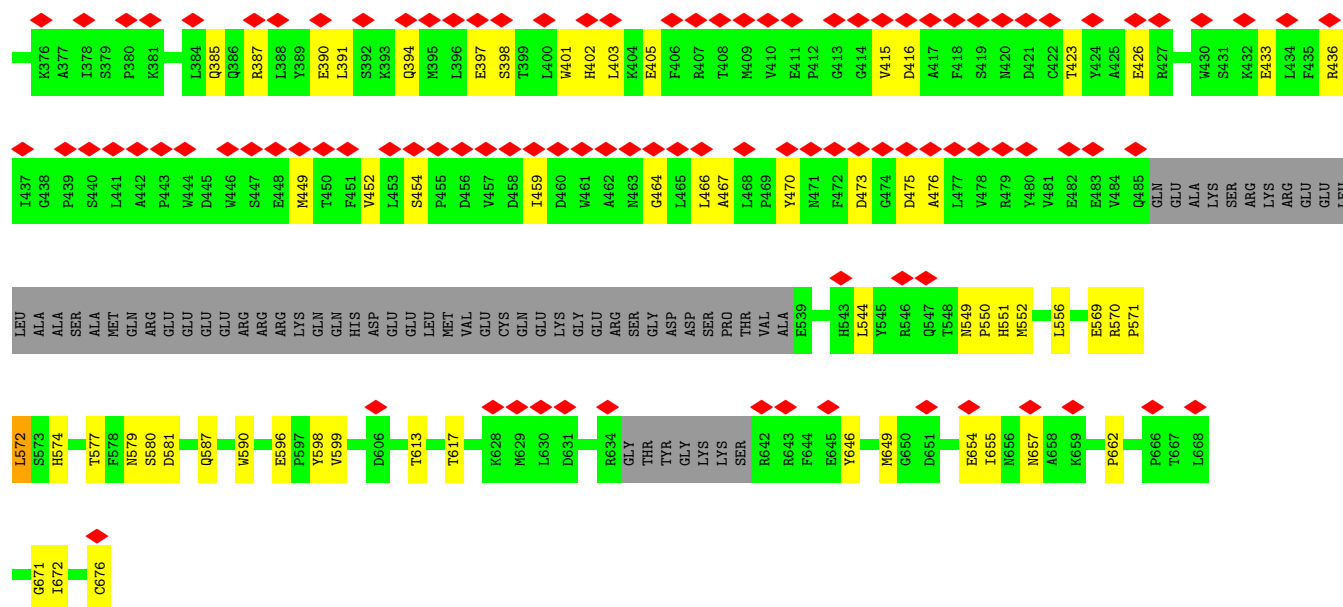
Chain Da:



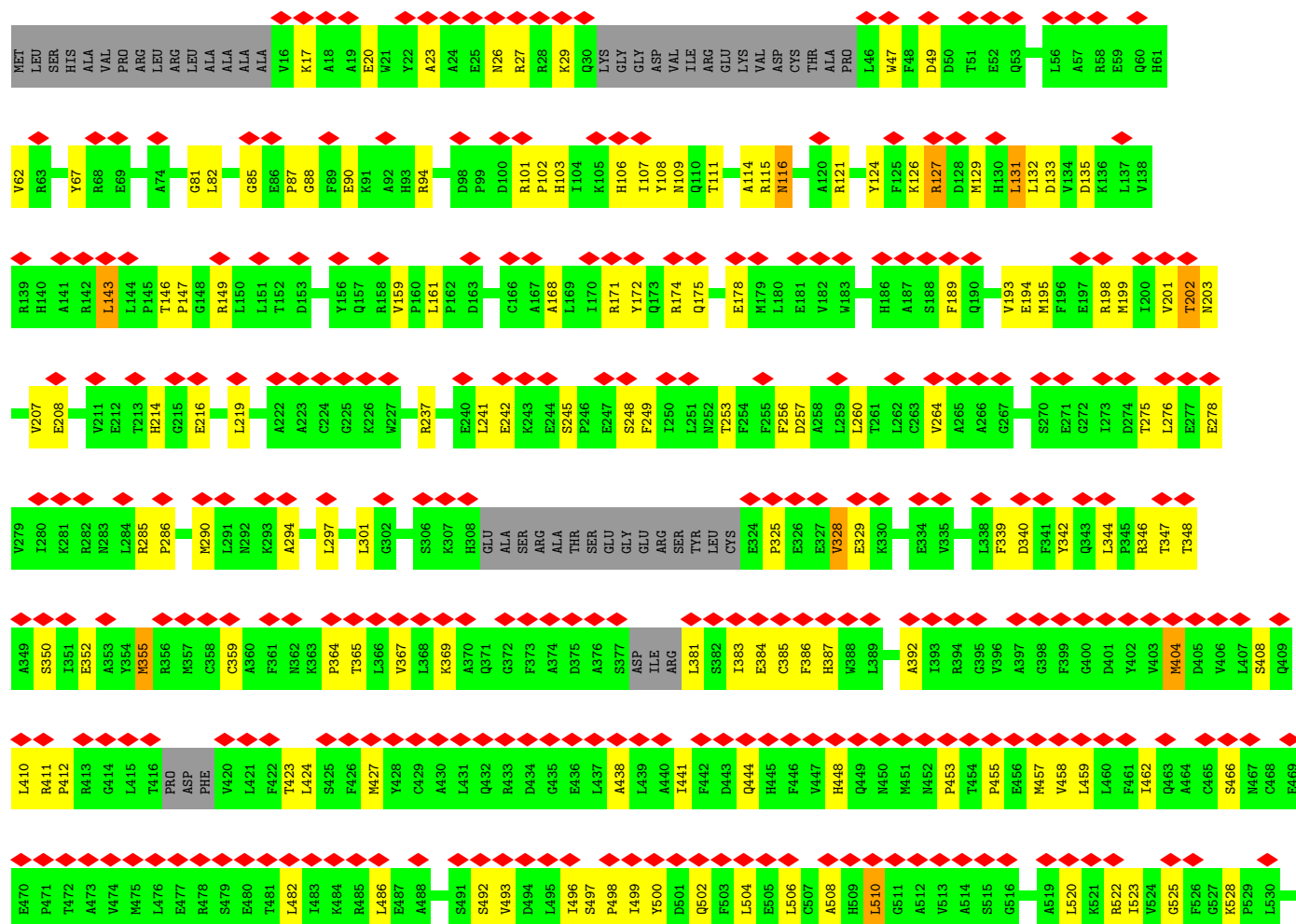
- Molecule 57: mt-SAF3

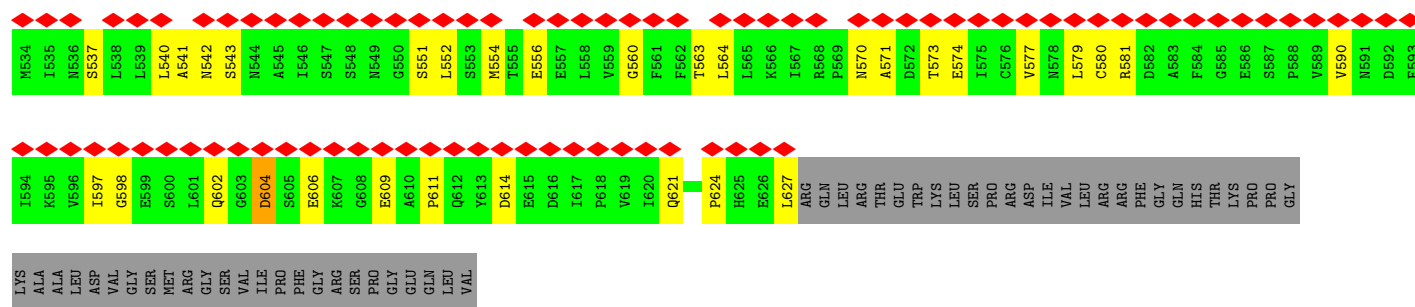
Chain F3:



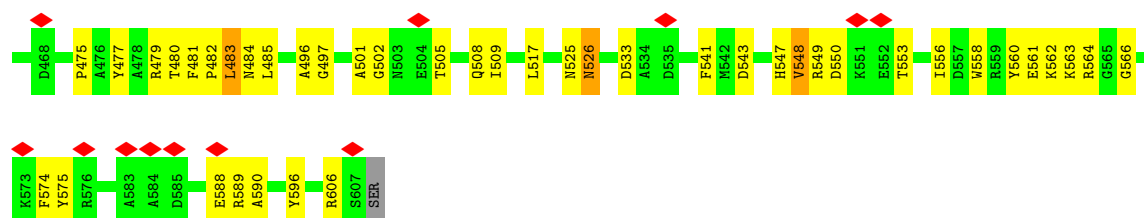
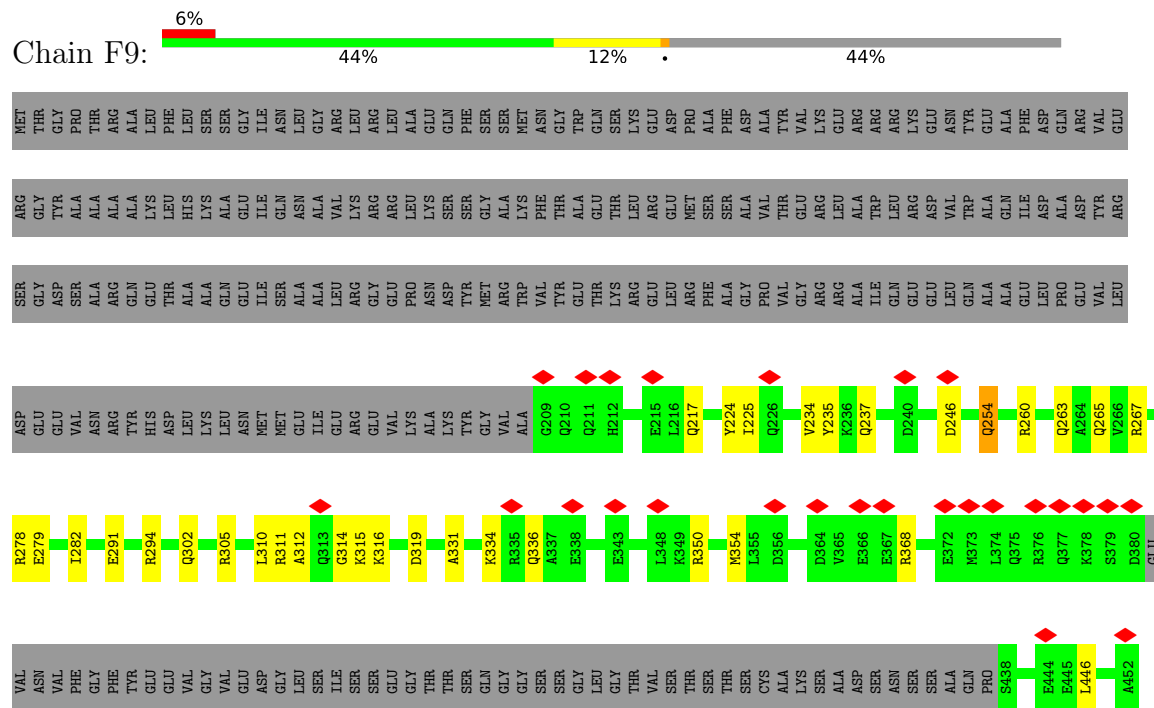


• Molecule 59: mt-SAF7

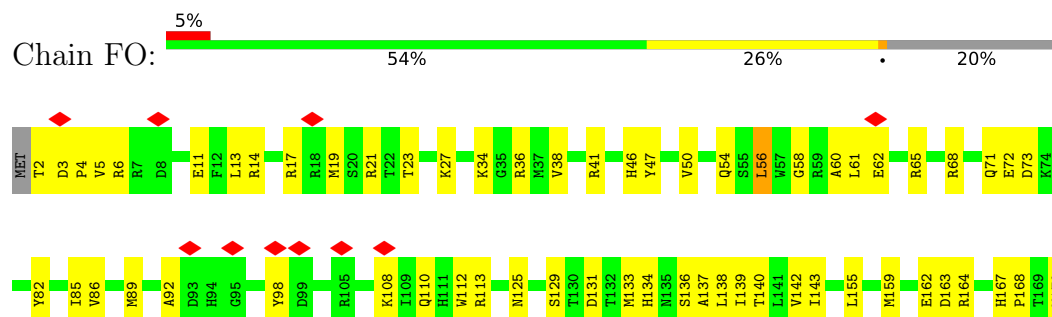


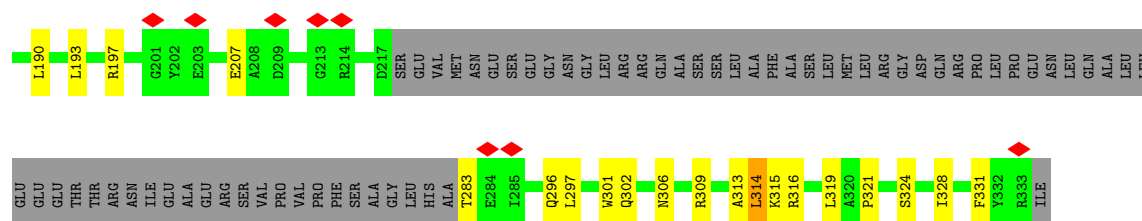


• Molecule 60: mt-SAF9

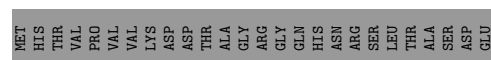
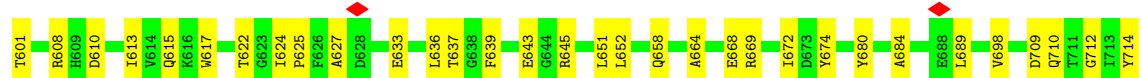
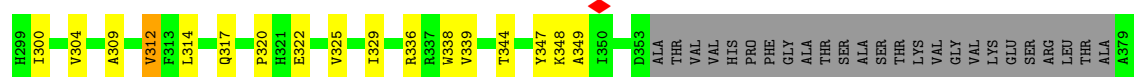
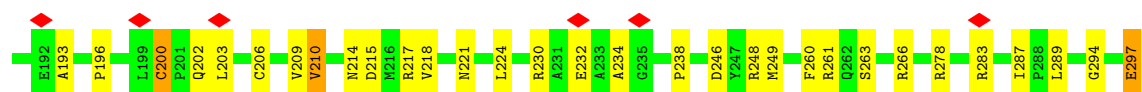
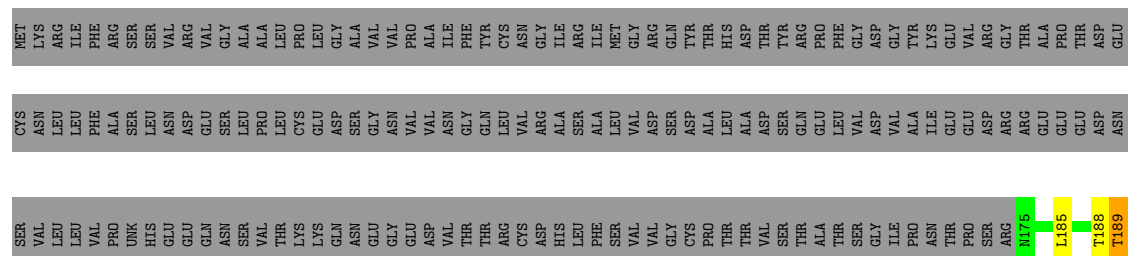


• Molecule 61: mt-SAF22

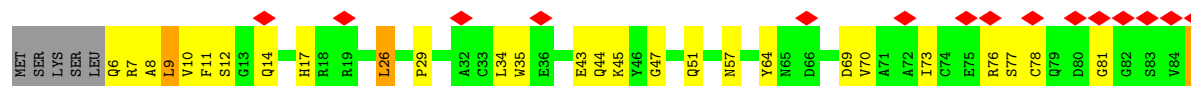


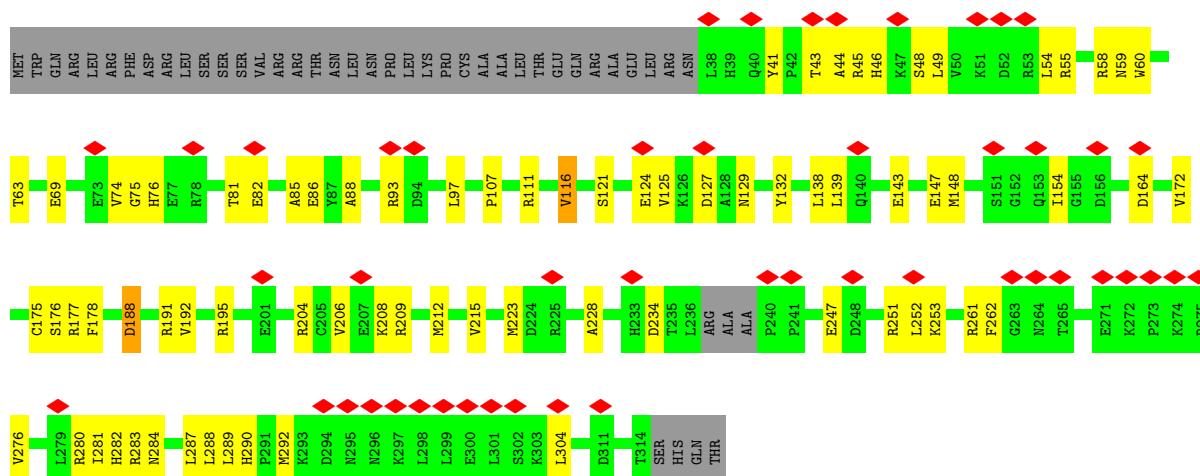
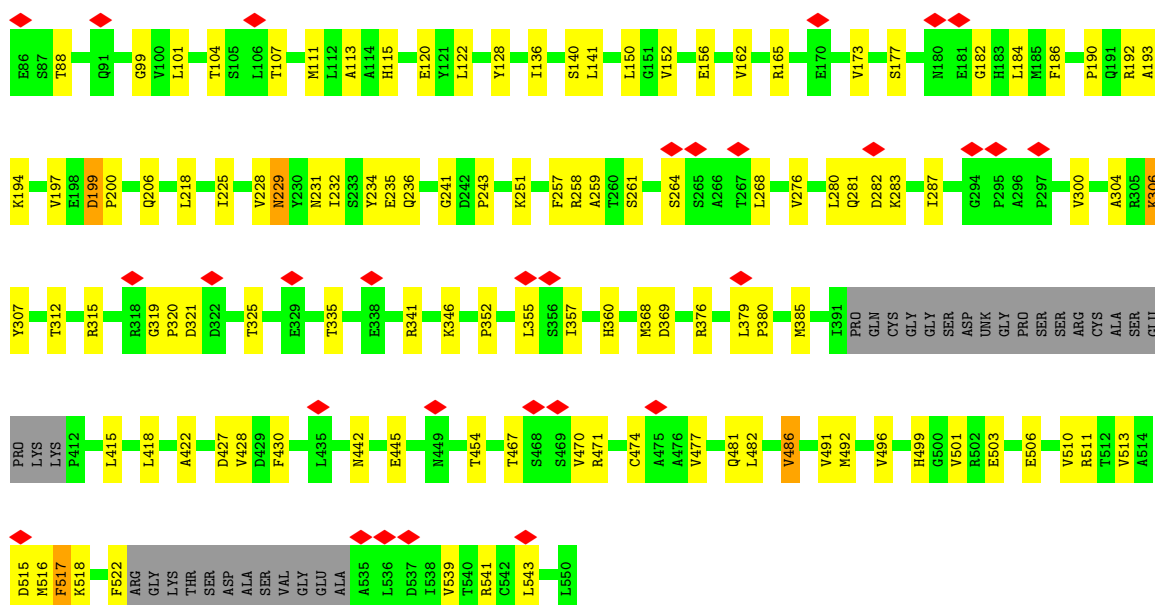


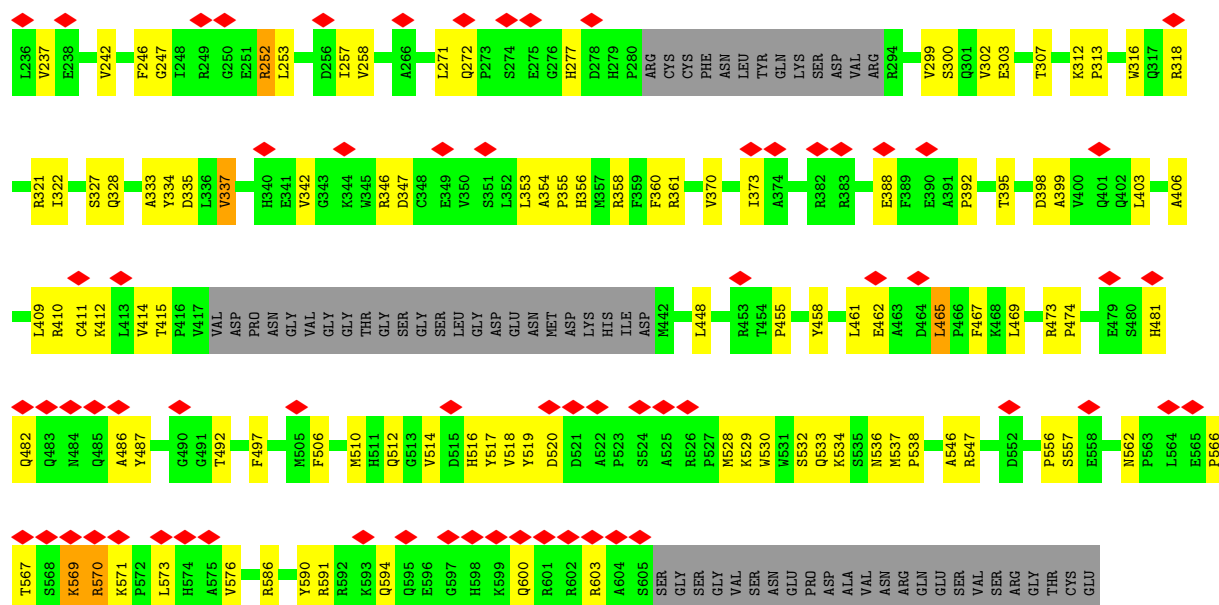
• Molecule 62: DNA photolyase, putative



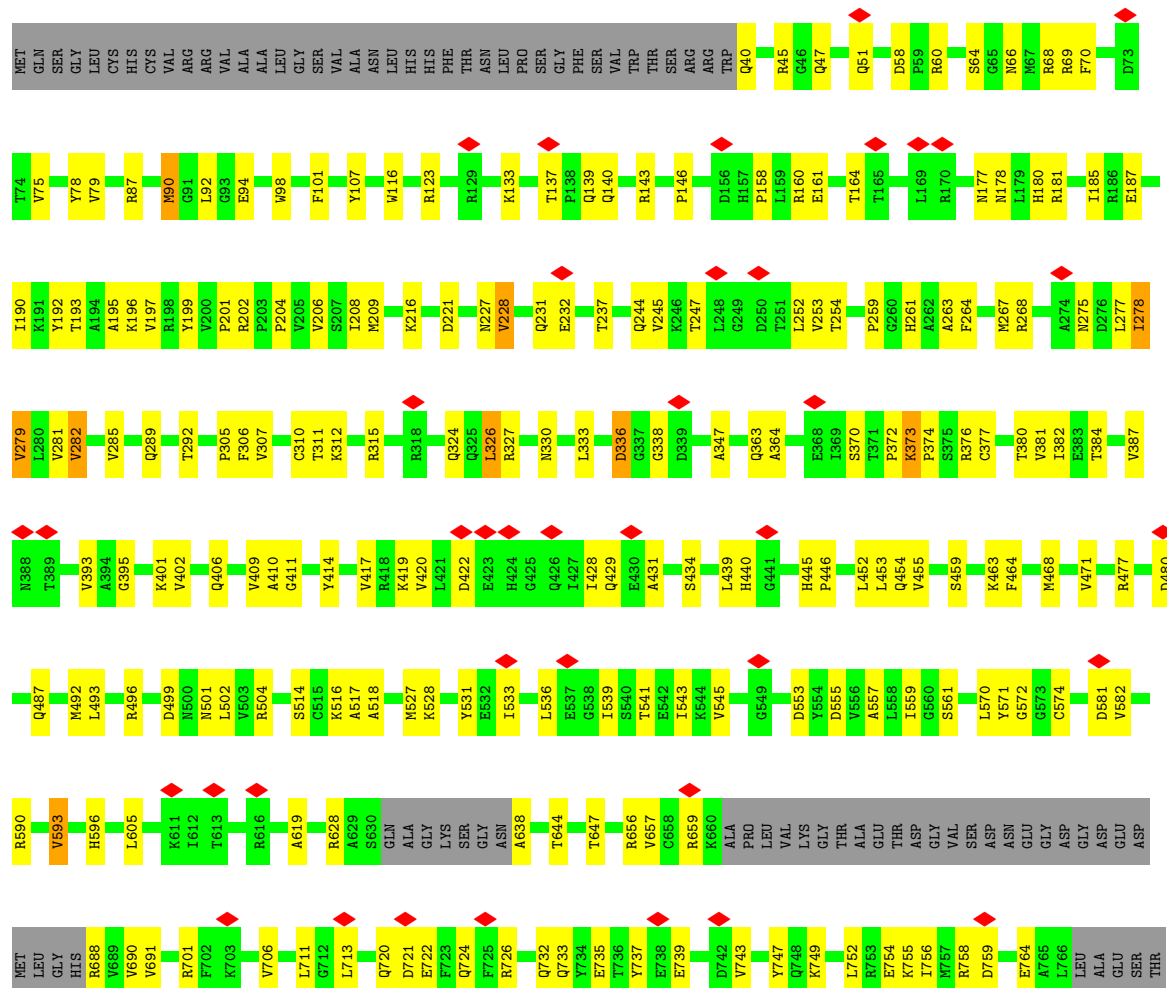
• Molecule 63: Acyl transferase-like protein

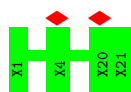




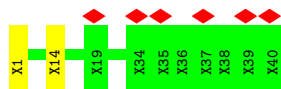


• Molecule 66: Translation initiation factor IF-2, putative

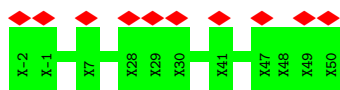




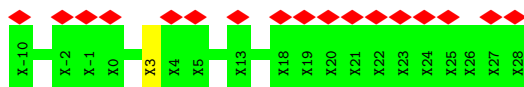
- Molecule 69: Unk7



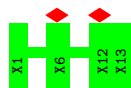
- Molecule 70: UnkE



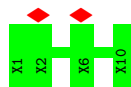
- Molecule 71: UnkF



- Molecule 72: UnkG



- Molecule 73: UnkI



- Molecule 74: UnkK



- Molecule 75: UnkL





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	17391	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.222	Depositor
Minimum map value	-0.107	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	500.4, 500.4, 500.4	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.39, 1.39, 1.39	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FAD, PO4, ZN, MG, ATP, UTP, GDP

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	CA	0.09	0/13759	0.18	0/21382
2	CC	0.11	0/666	0.29	0/900
3	CE	0.11	0/3547	0.25	0/4798
4	CF	0.10	0/1266	0.24	0/1708
5	CH	0.10	0/2276	0.24	0/3071
6	CI	0.10	0/3479	0.25	0/4693
7	CJ	0.10	0/6725	0.25	0/9152
8	CK	0.09	0/2502	0.24	0/3357
9	CL	0.11	0/759	0.27	0/1026
10	CN	0.11	0/1361	0.25	0/1840
11	CO	0.10	0/2614	0.24	0/3520
12	CP	0.10	0/1533	0.26	0/2074
13	CQ	0.10	0/1919	0.23	0/2595
14	CR	0.10	0/2276	0.24	0/3087
15	CS	0.10	0/1183	0.24	0/1593
16	CU	0.09	0/1560	0.23	0/2094
17	Ca	0.10	0/5066	0.23	0/6852
18	Cb	0.10	0/2105	0.24	0/2842
19	Cd	0.10	0/2016	0.21	0/2715
20	Cg	0.08	0/4016	0.21	0/5455
21	Ci	0.10	0/1383	0.23	0/1871
22	Cj	0.09	0/1849	0.23	0/2521
23	Ck	0.09	0/5540	0.23	0/7490
24	Cm	0.09	0/1215	0.25	0/1630
25	Cn	0.08	0/543	0.22	0/725
26	Cp	0.09	0/1511	0.23	0/2049
27	Cq	0.09	0/2066	0.23	0/2815
28	Cr	0.11	0/2131	0.26	0/2895
29	Cv	0.09	0/8625	0.24	0/11690
30	DA	0.09	0/12744	0.23	0/17248
31	DB	0.10	0/9369	0.24	0/12692
32	DC	0.11	0/8913	0.27	0/12092

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	DD	0.09	0/6699	0.24	0/9072
34	DE	0.10	0/4920	0.26	0/6666
35	DF	0.10	0/4847	0.26	0/6569
36	DG	0.11	0/4578	0.26	0/6202
37	DH	0.11	0/4645	0.28	0/6295
38	DI	0.10	0/3248	0.25	0/4401
39	DJ	0.10	0/2999	0.24	0/4071
40	DK	0.10	0/2123	0.24	0/2865
41	DL	0.10	0/2420	0.24	0/3262
42	DM	0.10	0/2488	0.24	0/3362
43	DN	0.09	0/2118	0.25	0/2874
44	DO	0.11	0/1832	0.27	0/2471
45	DP	0.10	0/1813	0.25	0/2457
46	DQ	0.09	0/2105	0.24	0/2855
47	DR	0.09	0/2084	0.27	0/2841
48	DS	0.08	0/1997	0.22	0/2694
49	DT	0.10	0/2133	0.25	0/2889
50	DU	0.09	0/1799	0.25	0/2438
51	DV	0.11	0/1382	0.28	0/1871
52	DW	0.10	0/1407	0.25	0/1916
53	DX	0.11	0/1207	0.27	0/1620
54	DY	0.11	0/1337	0.27	0/1814
55	DZ	0.10	0/725	0.25	0/984
56	Da	0.08	0/317	0.22	0/422
57	F3	0.08	0/2049	0.22	0/2782
58	F6	0.09	0/3434	0.24	0/4661
59	F7	0.09	0/4684	0.26	0/6341
60	F9	0.10	0/2863	0.25	0/3835
61	FO	0.10	0/2292	0.25	0/3096
62	Ff	0.10	0/5082	0.24	0/6918
63	Fg	0.10	0/4074	0.26	0/5522
64	Fh	0.10	0/2278	0.26	0/3073
65	Fi	0.10	0/3833	0.28	0/5202
66	IA	0.12	0/5512	0.27	0/7462
67	IB	0.10	0/4193	0.26	0/5672
All	All	0.10	0/218034	0.24	0/297947

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CA	12330	0	6168	233	0
2	CC	646	0	682	23	0
3	CE	3459	0	3440	97	0
4	CF	1240	0	1232	28	0
5	CH	2228	0	2204	48	0
6	CI	3410	0	3384	85	0
7	CJ	6535	0	6274	148	0
8	CK	2447	0	2379	83	0
9	CL	733	0	738	22	0
10	CN	1322	0	1304	55	0
11	CO	2552	0	2554	61	0
12	CP	1489	0	1510	49	0
13	CQ	1866	0	1869	63	0
14	CR	2210	0	2122	74	0
15	CS	1149	0	1154	33	0
16	CU	1522	0	1527	39	0
17	Ca	4911	0	4735	142	0
18	Cb	2056	0	2031	48	0
19	Cd	1961	0	1892	53	0
20	Cg	3895	0	3777	88	0
21	Ci	1343	0	1301	53	0
22	Cj	1799	0	1751	56	0
23	Ck	5442	0	5455	119	0
24	Cm	1184	0	1141	32	0
25	Cn	528	0	563	14	0
26	Cp	1466	0	1426	44	0
27	Cq	2005	0	1916	49	0
28	Cr	2083	0	2107	61	0
29	Cv	8404	0	8091	191	0
30	DA	12448	0	12128	266	0
31	DB	9148	0	8834	240	0
32	DC	8709	0	8502	235	0
33	DD	6513	0	6300	169	0
34	DE	4798	0	4756	119	0
35	DF	4738	0	4717	114	0
36	DG	4482	0	4404	99	0
37	DH	4541	0	4491	128	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	DI	3182	0	3153	72	0
39	DJ	2914	0	2820	65	0
40	DK	2083	0	2071	61	0
41	DL	2360	0	2352	61	0
42	DM	2430	0	2427	56	0
43	DN	2062	0	2047	63	0
44	DO	1796	0	1746	55	0
45	DP	1760	0	1723	56	0
46	DQ	2055	0	2036	57	0
47	DR	2019	0	2024	61	0
48	DS	1950	0	1904	46	0
49	DT	2058	0	1928	68	0
50	DU	1754	0	1687	38	0
51	DV	1346	0	1335	36	0
52	DW	1359	0	1342	32	0
53	DX	1174	0	1175	32	0
54	DY	1295	0	1290	37	0
55	DZ	697	0	644	23	0
56	Da	305	0	286	11	0
57	F3	2003	0	1945	43	0
58	F6	3358	0	3280	77	0
59	F7	4584	0	4547	115	0
60	F9	2815	0	2745	63	0
61	FO	2236	0	2210	72	0
62	Ff	4941	0	4789	104	0
63	Fg	3994	0	3953	95	0
64	Fh	2230	0	2186	67	0
65	Fi	3734	0	3703	93	0
66	IA	5414	0	5443	144	0
67	IB	4103	0	4045	101	0
68	U6	105	0	23	0	0
68	UJ	105	0	23	0	0
69	U7	200	0	43	3	0
70	UE	265	0	56	0	0
71	UF	195	0	44	1	0
72	UG	65	0	15	0	0
73	UI	50	0	12	0	0
74	UK	15	0	6	1	0
75	UL	100	0	22	1	0
76	CA	3	0	0	0	0
76	CQ	1	0	0	0	0
76	Cg	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
76	IA	1	0	0	0	0
77	Cg	31	0	12	0	0
78	Cr	1	0	0	0	0
78	DA	1	0	0	0	0
78	DS	2	0	0	0	0
79	DJ	29	0	11	3	0
80	Ff	53	0	31	0	0
81	IA	28	0	12	1	0
82	IA	5	0	0	1	0
83	Cg	3	0	0	0	0
83	IA	2	0	0	0	0
All	All	212864	0	202005	4246	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 10.

All (4246) 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)
34:DE:33:ILE:N	34:DE:547:THR:HG1	1.66	0.93
7:CJ:716:ARG:HE	21:CI:77:ARG:HE	1.20	0.85
57:F3:103:ASP:HB2	61:FO:65:ARG:HH22	1.42	0.85
11:CO:263:LEU:O	11:CO:274:TYR:OH	1.96	0.83
36:DG:292:GLU:O	36:DG:296:ASP:HB2	1.79	0.83
36:DG:215:LEU:HD12	36:DG:224:LEU:HD12	1.63	0.81
39:DJ:351:LEU:HD21	64:Fh:107:PRO:HB3	1.65	0.79
30:DA:369:VAL:HG23	30:DA:408:LEU:HB2	1.64	0.78
63:Fg:225:ILE:HG22	63:Fg:241:GLY:HA3	1.64	0.78
49:DT:83:ILE:HG22	49:DT:137:LEU:HD11	1.65	0.78
38:DI:72:PRO:HD2	38:DI:75:GLN:HE21	1.49	0.78
34:DE:72:ARG:HH22	34:DE:197:ARG:HD3	1.46	0.78
59:F7:508:ALA:HA	59:F7:541:ALA:HB2	1.67	0.77
35:DF:54:GLY:HA2	35:DF:156:ALA:HB3	1.65	0.76
6:CI:9:THR:HG1	6:CI:12:HIS:HD1	1.31	0.76
43:DN:46:THR:HG22	43:DN:153:GLY:H	1.50	0.76
22:Cj:115:ARG:HE	22:Cj:179:ARG:HH12	1.33	0.76
1:CA:520:A:OP2	52:DW:126:ARG:NH2	2.19	0.76
51:DV:41:THR:HA	52:DW:59:PRO:HG3	1.68	0.76
57:F3:100:GLU:HB2	61:FO:108:LYS:HB3	1.68	0.76
36:DG:308:ARG:NH1	36:DG:349:ASP:OD2	2.18	0.76
45:DP:146:PHE:HB3	45:DP:150:THR:HG21	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:Cg:220:THR:HA	20:Cg:242:ASN:HD21	1.52	0.76
1:CA:417:A:H4'	35:DF:161:ARG:HH21	1.51	0.75
21:Ci:27:CYS:HB3	51:DV:110:PRO:HB3	1.69	0.75
59:F7:543:SER:OG	59:F7:580:CYS:SG	2.45	0.75
61:FO:21:ARG:HH12	63:Fg:319:GLY:HA2	1.50	0.75
64:Fh:127:ASP:HB3	66:IA:161:GLU:HG3	1.69	0.74
58:F6:228:THR:HG1	58:F6:232:HIS:HE2	1.34	0.74
66:IA:419:LYS:HB3	66:IA:440:HIS:HB2	1.68	0.74
17:Ca:269:PRO:HB2	17:Ca:272:PHE:HB2	1.68	0.74
9:CL:74:LEU:HB3	9:CL:92:TYR:HB3	1.68	0.73
57:F3:158:LEU:HD21	59:F7:101:ARG:HG2	1.70	0.73
5:CH:234:PRO:HB2	5:CH:238:ARG:HH21	1.52	0.73
24:Cm:87:LEU:HD21	24:Cm:133:ARG:HD2	1.68	0.73
36:DG:169:ASN:HD22	36:DG:207:ARG:HE	1.35	0.73
62:Ff:210:VAL:HG13	62:Ff:314:LEU:HB3	1.70	0.73
8:CK:123:ARG:HD3	58:F6:338:GLN:HG2	1.71	0.73
64:Fh:282:HIS:HD2	64:Fh:283:ARG:HG3	1.54	0.73
37:DH:318:GLU:HG2	37:DH:371:LEU:HD22	1.71	0.73
7:CJ:801:PRO:HG2	51:DV:80:ARG:HH12	1.53	0.72
34:DE:172:ASP:OD2	34:DE:176:ARG:NH1	2.22	0.72
14:CR:89:VAL:HG21	27:Cq:112:LYS:HG3	1.70	0.72
36:DG:394:PRO:O	36:DG:451:ARG:NH1	2.22	0.72
12:CP:184:VAL:HG13	12:CP:186:PRO:HD2	1.71	0.72
1:CA:217:U:H3	1:CA:259:U:H3	1.38	0.72
35:DF:144:THR:HG23	35:DF:147:ASP:H	1.54	0.72
62:Ff:716:LYS:HD2	62:Ff:723:SER:HA	1.70	0.72
49:DT:28:GLU:HB2	49:DT:31:ASN:HB2	1.71	0.71
19:Cd:13:ARG:HH12	19:Cd:26:ARG:HD3	1.55	0.71
60:F9:562:LYS:HA	60:F9:590:ALA:HA	1.72	0.71
17:Ca:283:PRO:HD2	17:Ca:286:ARG:HD2	1.71	0.71
24:Cm:211:LEU:HB2	24:Cm:214:ASN:HD22	1.55	0.71
36:DG:67:ALA:O	36:DG:71:ASN:ND2	2.23	0.71
38:DI:192:THR:O	38:DI:193:ASN:ND2	2.24	0.71
30:DA:777:SER:HB3	30:DA:780:ASP:HB2	1.72	0.71
32:DC:562:ARG:NH2	32:DC:923:GLY:O	2.23	0.71
59:F7:424:LEU:HD21	59:F7:624:PRO:HB3	1.72	0.71
33:DD:664:VAL:HG11	48:DS:236:LEU:HD22	1.72	0.71
1:CA:499:U:HO2'	51:DV:48:HIS:HD1	1.32	0.71
31:DB:288:PHE:O	31:DB:292:GLN:NE2	2.24	0.70
60:F9:315:LYS:HB3	60:F9:319:ASP:HB2	1.72	0.70
1:CA:507:A:N6	7:CJ:711:HIS:O	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:DK:2:SER:N	49:DT:78:GLU:OE2	2.24	0.70
23:Ck:662:GLY:H	23:Ck:669:ASN:HD21	1.38	0.70
30:DA:961:LYS:HD3	30:DA:979:GLN:HB3	1.72	0.70
20:Cg:294:GLU:HA	20:Cg:329:PRO:HA	1.74	0.70
23:Ck:272:ASP:OD2	31:DB:898:GLN:NE2	2.24	0.70
35:DF:407:ALA:HB1	35:DF:421:ALA:HB3	1.74	0.70
32:DC:1152:PRO:HG2	32:DC:1160:GLN:HE22	1.57	0.70
47:DR:225:PRO:HG2	47:DR:227:ARG:HH12	1.57	0.70
61:FO:134:HIS:HB3	61:FO:159:MET:HE2	1.73	0.70
32:DC:161:LEU:HD11	40:DK:294:SER:HB2	1.74	0.70
32:DC:242:HIS:HE2	32:DC:464:THR:HG1	1.40	0.70
12:CP:31:MET:HG3	12:CP:114:PRO:HG3	1.73	0.70
29:Cv:147:HIS:HD2	29:Cv:149:ASP:H	1.39	0.69
35:DF:23:ARG:HH11	49:DT:238:PRO:HD3	1.57	0.69
46:DQ:71:PRO:HA	46:DQ:121:THR:HG22	1.73	0.69
37:DH:150:ALA:HB2	37:DH:286:LEU:HD11	1.74	0.69
31:DB:110:ARG:NH2	31:DB:309:SER:O	2.24	0.69
43:DN:118:LEU:HB3	43:DN:127:VAL:HG23	1.75	0.69
52:DW:25:LYS:HD3	52:DW:26:PRO:HD2	1.74	0.69
58:F6:549:ASN:HB2	58:F6:552:MET:HE2	1.74	0.69
34:DE:148:PHE:HE2	37:DH:528:GLU:HB3	1.57	0.69
59:F7:551:SER:H	59:F7:554:MET:HB3	1.57	0.69
3:CE:125:PRO:O	3:CE:133:ARG:NH1	2.26	0.69
11:CO:212:ALA:HB1	11:CO:217:ASP:HB3	1.74	0.69
3:CE:86:ALA:HB1	3:CE:89:LEU:HD11	1.74	0.69
6:CI:196:THR:HG21	27:Cq:107:GLU:HB2	1.75	0.69
10:CN:106:GLU:HA	10:CN:115:TYR:HB3	1.73	0.69
13:CQ:152:LYS:NZ	13:CQ:154:SER:O	2.23	0.69
15:CS:156:LEU:HD21	31:DB:1121:VAL:HG21	1.74	0.69
45:DP:139:ARG:NH1	45:DP:176:PRO:O	2.25	0.69
52:DW:103:PRO:HB3	54:DY:97:ARG:HH12	1.56	0.69
65:Fi:258:VAL:HG12	65:Fi:299:VAL:HG12	1.75	0.69
17:Ca:335:ARG:NH2	17:Ca:391:ASP:OD1	2.26	0.69
32:DC:1080:TYR:HE2	34:DE:579:ARG:HG3	1.58	0.69
58:F6:205:LEU:HD11	58:F6:242:GLU:HG3	1.75	0.69
63:Fg:280:LEU:HD13	63:Fg:283:LYS:HD3	1.75	0.69
8:CK:19:GLY:O	41:DL:265:ARG:NH2	2.26	0.68
30:DA:1566:ARG:O	30:DA:1570:ASN:ND2	2.26	0.68
29:Cv:702:ILE:HG13	29:Cv:720:THR:HG21	1.76	0.68
30:DA:584:PHE:HB3	30:DA:759:GLY:HA3	1.74	0.68
26:Cp:69:ARG:HD2	26:Cp:104:ALA:HB2	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:DD:603:GLU:HA	33:DD:606:ARG:HD2	1.75	0.68
36:DG:152:MET:O	36:DG:157:ARG:NH1	2.26	0.68
63:Fg:368:MET:HG2	63:Fg:482:LEU:HB2	1.76	0.68
3:CE:350:LYS:HE2	29:Cv:1045:ARG:HG2	1.76	0.68
7:CJ:621:ASN:ND2	21:Ci:24:PRO:O	2.26	0.68
17:Ca:597:LYS:HZ1	48:DS:48:TRP:H	1.41	0.68
22:Cj:205:ARG:HH12	47:DR:234:LEU:HA	1.59	0.68
35:DF:192:LEU:HD13	35:DF:264:VAL:HG12	1.75	0.68
52:DW:44:ASN:HD21	54:DY:17:VAL:HA	1.59	0.68
8:CK:200:ARG:NH2	16:CU:17:ARG:O	2.26	0.68
31:DB:586:ARG:HH21	31:DB:953:GLU:HG3	1.58	0.68
33:DD:415:CYS:HB3	33:DD:517:ALA:HB1	1.74	0.68
66:IA:619:ALA:HB3	66:IA:733:GLN:HB3	1.76	0.68
26:Cp:181:ARG:HH21	26:Cp:182:GLN:HB2	1.59	0.68
30:DA:651:ARG:HH21	30:DA:677:GLU:HB3	1.59	0.68
30:DA:790:SER:OG	30:DA:794:ARG:NH1	2.27	0.68
59:F7:257:ASP:HB2	59:F7:290:MET:HE2	1.75	0.68
66:IA:216:LYS:NZ	82:IA:1001:PO4:O4	2.27	0.68
4:CF:37:ARG:HA	19:Cd:150:TYR:HD1	1.57	0.68
42:DM:65:THR:HG22	42:DM:69:PHE:H	1.59	0.67
62:Ff:734:HIS:HA	62:Ff:748:LEU:HD21	1.76	0.67
19:Cd:17:ASN:ND2	19:Cd:31:PHE:O	2.26	0.67
28:Cr:26:LEU:HB3	28:Cr:29:PRO:HD2	1.76	0.67
48:DS:149:GLU:HA	48:DS:157:ARG:HH22	1.60	0.67
64:Fh:59:ASN:O	67:IB:686:ARG:NH2	2.26	0.67
23:Ck:188:LEU:HD13	23:Ck:224:LYS:HZ3	1.59	0.67
43:DN:38:ILE:HB	43:DN:151:ARG:HG2	1.76	0.67
50:DU:111:ILE:HB	50:DU:143:PRO:HA	1.74	0.67
18:Cb:216:LYS:HG3	18:Cb:217:LEU:HD22	1.75	0.67
30:DA:212:ARG:NH2	48:DS:130:VAL:O	2.27	0.67
31:DB:455:ARG:NH1	31:DB:461:GLN:O	2.26	0.67
1:CA:437:U:OP1	35:DF:29:ARG:NH2	2.26	0.67
47:DR:210:SER:O	47:DR:215:ARG:NH2	2.27	0.67
62:Ff:214:ASN:HD21	62:Ff:317:GLN:HG3	1.59	0.67
7:CJ:794:GLU:HG3	10:CN:160:VAL:HG21	1.76	0.67
28:Cr:60:PRO:HB2	28:Cr:66:ILE:HG22	1.77	0.67
35:DF:112:ARG:HH12	35:DF:118:THR:HG23	1.59	0.67
41:DL:136:MET:HG3	41:DL:193:GLY:HA2	1.76	0.67
1:CA:503:A:N3	53:DX:118:LYS:NZ	2.43	0.67
20:Cg:118:LEU:HD12	20:Cg:158:LEU:HD12	1.77	0.67
30:DA:103:ARG:NH2	33:DD:40:MET:SD	2.67	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:Ff:507:MET:O	62:Ff:565:GLN:NE2	2.28	0.67
6:CI:250:ASN:ND2	6:CI:272:THR:O	2.26	0.67
8:CK:186:PRO:HD3	16:CU:45:VAL:HG11	1.76	0.67
17:Ca:267:LEU:HD12	17:Ca:308:LYS:HE3	1.76	0.67
47:DR:240:PRO:HG3	47:DR:269:TRP:HB3	1.75	0.67
46:DQ:41:GLN:HE22	50:DU:124:SER:HB2	1.60	0.66
8:CK:74:LEU:O	18:Cb:178:ARG:NH2	2.28	0.66
12:CP:138:PRO:HG2	19:Cd:46:TRP:HE1	1.60	0.66
23:Ck:44:ALA:O	31:DB:511:ARG:NH2	2.28	0.66
27:Cq:181:HIS:ND1	27:Cq:201:GLU:OE2	2.23	0.66
29:Cv:410:THR:HG1	29:Cv:422:SER:HG	1.42	0.66
35:DF:553:THR:O	35:DF:571:LEU:HB3	1.95	0.66
1:CA:123:U:O2'	11:CO:425:ARG:NH1	2.28	0.66
66:IA:160:ARG:NH1	66:IA:161:GLU:OE2	2.29	0.66
6:CI:293:ARG:HA	36:DG:65:ASN:HD21	1.59	0.66
6:CI:424:ARG:NH1	6:CI:434:LYS:O	2.28	0.66
37:DH:518:LYS:O	37:DH:523:ARG:NH1	2.29	0.66
59:F7:174:ARG:NH2	59:F7:216:GLU:OE1	2.27	0.66
59:F7:571:ALA:HB2	59:F7:611:PRO:HB2	1.77	0.66
1:CA:428:A:N7	39:DJ:232:ARG:NH1	2.44	0.66
20:Cg:374:GLU:HG2	54:DY:40:ARG:HH12	1.61	0.66
39:DJ:85:LYS:HB3	39:DJ:95:THR:HG21	1.76	0.66
46:DQ:41:GLN:HE21	50:DU:123:GLN:HG3	1.59	0.66
66:IA:593:VAL:HG13	66:IA:596:HIS:HB2	1.77	0.66
7:CJ:116:GLN:HG2	31:DB:910:PHE:HA	1.77	0.66
15:CS:174:LYS:HB3	15:CS:213:ASN:HB3	1.77	0.66
16:CU:127:VAL:HA	16:CU:135:VAL:HG21	1.78	0.66
20:Cg:88:PHE:O	20:Cg:167:ARG:NH1	2.29	0.66
1:CA:196:U:H5'	1:CA:197:A:H5''	1.76	0.66
3:CE:224:VAL:HG22	3:CE:254:ILE:HG22	1.77	0.66
34:DE:223:GLU:HB3	34:DE:312:LEU:HD11	1.78	0.66
64:Fh:111:ARG:NH2	64:Fh:147:GLU:OE1	2.28	0.66
4:CF:48:TYR:OH	8:CK:181:MET:O	2.14	0.66
30:DA:608:ARG:HH21	30:DA:798:VAL:HG12	1.61	0.65
57:F3:73:PRO:HB2	57:F3:76:GLU:HB2	1.77	0.65
31:DB:1076:ASN:HB3	35:DF:223:ARG:HB3	1.78	0.65
35:DF:343:GLU:HG3	35:DF:345:LEU:HD23	1.78	0.65
38:DI:186:ILE:HG12	38:DI:197:VAL:HG22	1.78	0.65
51:DV:164:MET:N	51:DV:164:MET:SD	2.70	0.65
1:CA:305:A:OP2	8:CK:201:ARG:NH2	2.29	0.65
19:Cd:45:LEU:O	19:Cd:48:ASN:ND2	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Cv:398:ARG:HH21	29:Cv:949:CYS:HB3	1.61	0.65
44:DO:245:VAL:HB	44:DO:250:ARG:HE	1.60	0.65
47:DR:33:VAL:HA	47:DR:39:GLN:HE22	1.61	0.65
13:CQ:229:PRO:HG3	13:CQ:233:ARG:HE	1.62	0.65
36:DG:566:TRP:HE1	36:DG:615:SER:HB3	1.60	0.65
59:F7:26:ASN:OD1	59:F7:29:LYS:NZ	2.29	0.65
59:F7:574:GLU:HG3	59:F7:597:ILE:HD13	1.78	0.65
62:Ff:263:SER:HB3	62:Ff:669:ARG:HG2	1.79	0.65
63:Fg:228:VAL:HG13	63:Fg:360:HIS:HB2	1.78	0.65
65:Fi:202:MET:HE1	65:Fi:237:VAL:HG21	1.77	0.65
67:IB:207:TYR:HB3	67:IB:343:ARG:HE	1.62	0.65
12:CP:137:LYS:O	22:Cj:228:ARG:NH1	2.29	0.65
17:Ca:66:PRO:HG3	17:Ca:530:ALA:HB2	1.78	0.65
30:DA:529:ILE:HA	30:DA:532:ARG:HG2	1.79	0.65
34:DE:429:ILE:HG22	37:DH:564:ARG:HH21	1.62	0.65
35:DF:518:ALA:HB2	35:DF:549:PHE:HB3	1.78	0.65
30:DA:201:LYS:O	30:DA:205:HIS:ND1	2.28	0.65
1:CA:227:U:OP1	67:IB:777:ARG:NH2	2.30	0.65
7:CJ:601:LEU:HD12	7:CJ:675:ALA:HB3	1.79	0.65
23:Ck:384:LEU:O	23:Ck:415:ASN:ND2	2.30	0.65
26:Cp:141:ARG:HH11	45:DP:15:ARG:HE	1.44	0.65
31:DB:1164:ASP:OD2	31:DB:1167:ARG:NH1	2.30	0.65
32:DC:334:GLN:O	32:DC:387:ARG:NH1	2.30	0.65
52:DW:103:PRO:O	54:DY:90:GLN:NE2	2.30	0.65
59:F7:147:PRO:HB2	59:F7:195:MET:HE1	1.77	0.65
1:CA:442:A:H4'	1:CA:443:U:H5'	1.77	0.65
11:CO:420:ARG:NH2	46:DQ:13:GLU:O	2.26	0.65
48:DS:52:ASP:O	48:DS:58:ASN:ND2	2.30	0.65
8:CK:23:ASP:HB2	8:CK:26:ARG:HB3	1.79	0.65
35:DF:147:ASP:O	35:DF:150:ARG:NH2	2.30	0.65
39:DJ:162:VAL:HG23	39:DJ:180:LEU:HD21	1.79	0.65
42:DM:72:ARG:HH21	42:DM:74:ARG:HD3	1.62	0.65
43:DN:57:ARG:HG3	43:DN:66:GLY:HA3	1.79	0.65
65:Fi:86:SER:HB3	65:Fi:87:PRO:HD3	1.79	0.65
28:Cr:105:ARG:O	28:Cr:260:ASN:ND2	2.29	0.64
31:DB:92:HIS:HB3	31:DB:95:TYR:HB2	1.79	0.64
60:F9:217:GLN:HE22	67:IB:731:THR:HA	1.62	0.64
42:DM:64:THR:HG22	42:DM:70:LEU:HA	1.79	0.64
45:DP:69:LEU:HB2	50:DU:180:VAL:HA	1.77	0.64
62:Ff:266:ARG:NH1	62:Ff:668:GLU:O	2.27	0.64
3:CE:127:LEU:HD21	3:CE:191:LYS:HD2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CL:69:PHE:HE1	9:CL:118:LEU:HD12	1.62	0.64
21:CI:25:VAL:HG21	51:DV:112:ARG:HH12	1.62	0.64
26:Cp:56:HIS:HB2	26:Cp:84:LEU:HD13	1.79	0.64
26:Cp:128:LEU:HD12	64:Fh:261:ARG:HG2	1.79	0.64
62:Ff:200:CYS:SG	62:Ff:202:GLN:NE2	2.71	0.64
1:CA:124:U:OP2	11:CO:296:ARG:NH2	2.31	0.64
42:DM:128:ILE:HG22	42:DM:231:ALA:HB2	1.79	0.64
62:Ff:550:ARG:NH1	67:IB:377:MET:O	2.30	0.64
1:CA:97:U:H2'	13:CQ:56:ARG:HH21	1.62	0.64
23:Ck:113:ASN:HB3	31:DB:558:ASN:HD21	1.62	0.64
23:Ck:288:ASN:HD22	23:Ck:626:PHE:HD2	1.44	0.64
29:Cv:925:ASP:OD1	29:Cv:928:ARG:NH2	2.31	0.64
60:F9:533:ASP:O	66:IA:496:ARG:NH1	2.31	0.64
26:Cp:73:ASP:OD2	64:Fh:253:LYS:NZ	2.24	0.64
28:Cr:101:ASP:OD2	28:Cr:105:ARG:NH1	2.31	0.64
30:DA:152:ARG:NH2	30:DA:156:THR:OG1	2.30	0.64
37:DH:521:ILE:HG13	40:DK:287:ILE:HD13	1.80	0.64
46:DQ:242:THR:HB	59:F7:444:GLN:HG2	1.79	0.64
7:CJ:254:ASP:OD1	7:CJ:399:ARG:NH2	2.30	0.64
34:DE:612:HIS:HD1	40:DK:112:TRP:CD1	2.15	0.64
44:DO:139:GLU:O	44:DO:143:HIS:ND1	2.30	0.64
62:Ff:338:TRP:HB2	62:Ff:347:TYR:HB2	1.79	0.64
63:Fg:173:VAL:HG21	63:Fg:357:ILE:HD12	1.79	0.64
66:IA:244:GLN:HG2	66:IA:254:THR:HG22	1.79	0.64
67:IB:356:GLU:OE1	67:IB:359:ARG:NH2	2.30	0.64
1:CA:45:G:N2	26:Cp:140:TYR:OH	2.31	0.64
32:DC:582:ARG:HH21	32:DC:623:LYS:HG3	1.63	0.64
32:DC:1121:THR:OG1	49:DT:69:ASP:OD1	2.16	0.64
37:DH:492:ARG:NH2	49:DT:150:GLU:OE1	2.30	0.64
46:DQ:78:ARG:NH2	46:DQ:249:CYS:SG	2.71	0.64
1:CA:480:C:O2'	21:CI:153:ARG:NH1	2.31	0.64
5:CH:12:VAL:HG12	43:DN:34:VAL:HG12	1.79	0.64
24:Cm:153:ASP:HB2	24:Cm:156:THR:HB	1.80	0.64
29:Cv:369:ARG:NH1	38:DI:157:SER:OG	2.31	0.64
33:DD:700:ASP:HB2	33:DD:709:ARG:HD2	1.79	0.64
37:DH:305:VAL:HG23	37:DH:360:LEU:HD11	1.79	0.64
59:F7:570:ASN:ND2	59:F7:614:ASP:OD1	2.30	0.64
62:Ff:595:GLY:O	65:Fi:590:TYR:OH	2.16	0.64
1:CA:221:C:H5'	1:CA:249:U:H2'	1.80	0.64
1:CA:440:U:H3	21:CI:152:ASN:HB2	1.61	0.64
8:CK:205:TYR:HB3	8:CK:221:THR:HA	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DB:93:LYS:HD2	34:DE:505:ILE:HG12	1.80	0.64
32:DC:1163:GLU:OE2	37:DH:44:ARG:NH2	2.31	0.64
33:DD:585:ASN:ND2	47:DR:201:CYS:SG	2.71	0.64
8:CK:282:MET:HB3	8:CK:310:ILE:HG13	1.81	0.63
12:CP:174:THR:OG1	12:CP:177:GLU:OE1	2.14	0.63
31:DB:746:LEU:HB3	31:DB:784:TYR:HB3	1.79	0.63
31:DB:960:ALA:HB1	31:DB:963:ARG:HB2	1.81	0.63
33:DD:217:ASP:OD1	33:DD:297:ARG:NH1	2.30	0.63
37:DH:34:TYR:HA	39:DJ:45:ASN:HD21	1.61	0.63
1:CA:98:A:N7	13:CQ:48:ARG:NH2	2.46	0.63
29:Cv:286:THR:HG21	29:Cv:402:ALA:HB1	1.80	0.63
32:DC:663:GLY:HA3	32:DC:760:LEU:HD22	1.78	0.63
45:DP:111:THR:HG23	45:DP:114:ASP:H	1.62	0.63
62:Ff:501:TRP:CE2	62:Ff:529:SER:HB2	2.32	0.63
21:Ci:30:ARG:HH21	23:Ck:788:GLU:HG2	1.63	0.63
27:Cq:140:ARG:HH22	30:DA:1063:THR:H	1.46	0.63
31:DB:464:THR:O	31:DB:467:ASN:ND2	2.32	0.63
37:DH:500:VAL:O	40:DK:301:ARG:NH1	2.31	0.63
46:DQ:45:ARG:HE	46:DQ:48:LEU:HD11	1.62	0.63
66:IA:275:ASN:ND2	66:IA:277:LEU:O	2.31	0.63
10:CN:33:GLU:OE1	35:DF:167:TRP:NE1	2.31	0.63
20:Cg:183:THR:HG23	20:Cg:295:THR:HG22	1.81	0.63
30:DA:601:THR:HG22	30:DA:805:VAL:HG22	1.77	0.63
32:DC:148:LEU:HD22	32:DC:511:ARG:HE	1.63	0.63
61:FO:60:ALA:HA	61:FO:89:MET:HE1	1.79	0.63
1:CA:298:C:H5'	8:CK:215:ARG:HH21	1.63	0.63
18:Cb:40:LEU:O	18:Cb:43:THR:OG1	2.17	0.63
23:Ck:726:ASP:OD1	23:Ck:778:GLN:NE2	2.30	0.63
24:Cm:181:GLN:NE2	24:Cm:185:ALA:O	2.31	0.63
30:DA:1029:LYS:NZ	42:DM:257:GLU:OE1	2.31	0.63
31:DB:677:GLU:OE2	34:DE:471:ARG:NH2	2.31	0.63
51:DV:105:GLU:OE2	51:DV:150:ARG:NH1	2.30	0.63
65:Fi:335:ASP:HB2	65:Fi:355:PRO:HD3	1.78	0.63
59:F7:340:ASP:OD1	59:F7:346:ARG:NH2	2.26	0.63
64:Fh:172:VAL:HG22	64:Fh:212:MET:HE3	1.80	0.63
19:Cd:186:LEU:HB2	19:Cd:195:GLU:HB2	1.80	0.63
30:DA:1643:GLU:HA	30:DA:1646:ARG:HH21	1.63	0.63
31:DB:543:GLN:HE22	31:DB:581:ASP:H	1.45	0.63
35:DF:237:LEU:HB3	35:DF:253:ILE:HD13	1.80	0.63
30:DA:632:THR:HG1	30:DA:635:THR:HG1	1.46	0.63
33:DD:423:LYS:HE3	33:DD:469:GLY:HA2	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:IA:278:ILE:O	66:IA:306:PHE:HA	1.97	0.63
13:CQ:144:LEU:HB3	13:CQ:166:GLU:HB3	1.80	0.63
17:Ca:516:SER:OG	17:Ca:522:GLU:O	2.15	0.63
31:DB:567:ARG:NH2	31:DB:853:GLU:OE2	2.31	0.63
44:DO:230:ILE:HB	44:DO:233:ALA:HB2	1.80	0.63
1:CA:100:G:O2'	1:CA:127:G:N2	2.32	0.62
1:CA:222:A:N6	1:CA:239:G:O6	2.32	0.62
7:CJ:495:ARG:O	7:CJ:527:ARG:NH1	2.31	0.62
36:DG:196:ARG:NH2	36:DG:211:TYR:OH	2.31	0.62
40:DK:291:GLN:NE2	49:DT:107:GLU:OE2	2.30	0.62
46:DQ:129:GLU:O	46:DQ:133:ASN:ND2	2.32	0.62
2:CC:42:ILE:HG12	2:CC:69:ILE:HG22	1.81	0.62
7:CJ:236:ASP:OD2	23:Ck:313:ARG:NH1	2.28	0.62
10:CN:149:GLU:O	10:CN:153:ASN:ND2	2.32	0.62
17:Ca:449:VAL:O	17:Ca:453:HIS:NE2	2.32	0.62
49:DT:113:GLN:OE1	49:DT:154:GLN:NE2	2.29	0.62
64:Fh:280:ARG:HH21	64:Fh:284:ASN:HB3	1.65	0.62
2:CC:1:MET:HE2	32:DC:530:GLN:HA	1.82	0.62
14:CR:125:ASN:H	14:CR:128:ASN:HD21	1.46	0.62
20:Cg:421:GLU:HG2	20:Cg:426:GLY:HA3	1.81	0.62
20:Cg:463:LEU:HD21	54:DY:42:LYS:HG3	1.80	0.62
29:Cv:809:PRO:HB3	29:Cv:918:LEU:HG	1.81	0.62
38:DI:250:ASN:HD21	38:DI:262:LYS:HB2	1.64	0.62
45:DP:20:MET:HB2	45:DP:23:LEU:HD22	1.81	0.62
62:Ff:778:GLY:O	62:Ff:783:ARG:NH1	2.31	0.62
67:IB:362:LEU:HD21	67:IB:621:GLU:HA	1.80	0.62
7:CJ:438:ASN:HD21	23:Ck:669:ASN:HD22	1.45	0.62
7:CJ:488:SER:H	7:CJ:491:ALA:HB3	1.63	0.62
18:Cb:24:TRP:HH2	41:DL:235:PRO:HB2	1.65	0.62
32:DC:630:GLU:OE2	32:DC:662:ARG:NH2	2.33	0.62
49:DT:144:SER:OG	49:DT:161:ASN:ND2	2.32	0.62
58:F6:205:LEU:HD21	58:F6:242:GLU:HA	1.80	0.62
64:Fh:125:VAL:HA	66:IA:158:PRO:HA	1.80	0.62
7:CJ:125:ASP:OD2	7:CJ:128:LYS:NZ	2.33	0.62
20:Cg:91:GLU:OE2	20:Cg:167:ARG:NH2	2.33	0.62
30:DA:1453:ASN:OD1	30:DA:1457:HIS:NE2	2.32	0.62
35:DF:459:ALA:O	35:DF:478:ARG:NH1	2.32	0.62
45:DP:36:GLN:HG2	50:DU:204:LEU:HD11	1.79	0.62
52:DW:83:THR:O	52:DW:87:ASN:ND2	2.32	0.62
2:CC:41:LEU:HB3	2:CC:70:ILE:HG23	1.82	0.62
3:CE:20:THR:HG23	3:CE:231:ARG:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CN:73:CYS:O	10:CN:77:ASN:ND2	2.28	0.62
32:DC:418:SER:OG	32:DC:421:GLU:OE1	2.16	0.62
32:DC:882:ASP:OD1	34:DE:47:TYR:OH	2.17	0.62
8:CK:187:ARG:NH1	19:Cb:199:SER:O	2.33	0.62
14:CR:89:VAL:O	18:Cb:112:TYR:OH	2.17	0.62
66:IA:387:VAL:HG23	66:IA:574:CYS:HA	1.81	0.62
4:CF:132:PRO:HB3	14:CR:128:ASN:HB3	1.82	0.62
63:Fg:379:LEU:HD13	63:Fg:380:PRO:HD2	1.82	0.62
1:CA:270:U:OP1	56:Da:10:ILE:N	2.33	0.62
1:CA:329:U:H4'	1:CA:330:U:OP2	1.98	0.62
1:CA:392:U:H5'	1:CA:539:A:H5''	1.82	0.62
5:CH:85:GLN:OE1	29:Cv:376:ARG:NH1	2.33	0.62
7:CJ:250:GLU:HB3	7:CJ:398:PHE:HD2	1.64	0.62
7:CJ:345:VAL:HG13	7:CJ:348:ALA:H	1.63	0.62
22:Cj:46:TYR:HA	22:Cj:165:PHE:HE2	1.65	0.62
23:Ck:308:ARG:NH1	23:Ck:715:GLN:OE1	2.33	0.62
27:Cq:124:THR:HG21	28:Cr:144:ARG:HE	1.65	0.62
32:DC:116:TYR:O	34:DE:150:ARG:NH1	2.33	0.62
39:DJ:141:GLU:O	39:DJ:146:GLN:NE2	2.32	0.62
46:DQ:50:THR:HG23	46:DQ:53:ALA:H	1.65	0.62
11:CO:296:ARG:NH1	13:CQ:189:TYR:OH	2.33	0.61
19:Cd:195:GLU:HB3	19:Cd:216:HIS:HB2	1.81	0.61
23:Ck:624:ASP:N	23:Ck:627:ASP:OD2	2.31	0.61
27:Cq:111:ARG:NH1	27:Cq:212:ASP:OD1	2.33	0.61
32:DC:436:ASP:HB3	32:DC:441:VAL:HB	1.81	0.61
65:Fi:247:GLY:HA3	65:Fi:252:ARG:HB2	1.82	0.61
29:Cv:597:VAL:HG21	29:Cv:759:GLU:HB3	1.80	0.61
31:DB:763:GLU:HA	31:DB:766:ILE:HG12	1.81	0.61
51:DV:46:PRO:O	51:DV:52:ARG:NH1	2.33	0.61
66:IA:570:LEU:HD12	66:IA:590:ARG:HG2	1.82	0.61
67:IB:626:VAL:HG21	67:IB:653:TRP:HA	1.80	0.61
1:CA:100:G:H1	1:CA:127:G:HO2'	1.48	0.61
1:CA:260:U:O2'	17:Ca:579:VAL:O	2.17	0.61
30:DA:1289:LEU:HD13	30:DA:1304:VAL:HG11	1.80	0.61
32:DC:232:GLN:OE1	32:DC:472:ARG:NH2	2.34	0.61
44:DO:138:LEU:HD22	44:DO:142:MET:HE2	1.82	0.61
10:CN:113:VAL:HG23	10:CN:118:MET:HG2	1.82	0.61
31:DB:514:ARG:NH1	31:DB:854:GLU:OE2	2.33	0.61
37:DH:530:VAL:O	37:DH:532:ARG:NH2	2.34	0.61
42:DM:174:ASP:OD1	42:DM:177:ARG:NH1	2.33	0.61
59:F7:127:ARG:HH12	65:Fi:534:LYS:HG2	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:F7:453:PRO:HG2	59:F7:486:LEU:HD22	1.82	0.61
2:CC:56:TYR:HA	2:CC:73:SER:HB2	1.82	0.61
17:Ca:213:ASP:OD2	17:Ca:252:ARG:NH2	2.33	0.61
24:Cm:198:ARG:HA	24:Cm:207:LYS:HB3	1.82	0.61
64:Fh:88:ALA:O	64:Fh:93:ARG:NH1	2.34	0.61
67:IB:409:ASN:HB3	67:IB:460:LEU:HG	1.81	0.61
6:CI:300:ASP:OD1	7:CJ:119:ARG:NH1	2.33	0.61
30:DA:945:ILE:HD13	42:DM:125:VAL:HG13	1.82	0.61
33:DD:571:VAL:HG23	33:DD:603:GLU:HB2	1.82	0.61
40:DK:254:GLU:HB3	40:DK:261:SER:HB3	1.82	0.61
61:FO:47:TYR:OH	61:FO:73:ASP:OD2	2.18	0.61
63:Fg:51:GLN:NE2	66:IA:232:GLU:O	2.29	0.61
66:IA:628:ARG:NH2	66:IA:722:GLU:OE2	2.34	0.61
15:CS:152:GLN:OE1	31:DB:1122:ARG:NH1	2.34	0.61
17:Ca:146:ASP:O	17:Ca:150:ASN:ND2	2.33	0.61
23:Ck:602:LEU:HD13	23:Ck:622:LEU:HD11	1.81	0.61
27:Cq:237:GLN:NE2	27:Cq:241:ASN:OD1	2.33	0.61
32:DC:150:LEU:HD11	37:DH:524:HIS:HB3	1.81	0.61
44:DO:86:ARG:HH12	44:DO:126:PRO:HD2	1.66	0.61
57:F3:153:ILE:HG13	57:F3:238:LYS:HE2	1.82	0.61
66:IA:324:GLN:OE1	66:IA:327:ARG:NH2	2.33	0.61
1:CA:351:A:OP2	67:IB:397:LYS:NZ	2.28	0.61
2:CC:49:ILE:HD11	67:IB:765:LEU:HD21	1.83	0.61
4:CF:123:ARG:HD2	29:Cv:196:MET:HE1	1.82	0.61
16:CU:51:ASN:O	58:F6:579:ASN:ND2	2.33	0.61
30:DA:1284:VAL:HG22	30:DA:1287:ARG:HH21	1.66	0.61
31:DB:149:GLU:O	31:DB:153:HIS:ND1	2.31	0.61
61:FO:138:LEU:HD22	61:FO:170:MET:HE2	1.82	0.61
19:Cd:99:GLU:HB2	30:DA:146:LEU:HD11	1.83	0.61
57:F3:115:CYS:SG	57:F3:133:ARG:NH1	2.73	0.61
1:CA:546:U:O2'	64:Fh:58:ARG:NE	2.34	0.61
23:Ck:698:LEU:O	23:Ck:702:ASN:ND2	2.34	0.61
30:DA:1010:PHE:N	41:DL:205:GLY:O	2.34	0.61
30:DA:1373:MET:HE3	30:DA:1374:VAL:HG12	1.83	0.61
58:F6:238:TYR:HB2	58:F6:287:ARG:HH22	1.65	0.61
59:F7:339:PHE:HA	59:F7:344:LEU:HD23	1.82	0.61
1:CA:194:A:N7	1:CA:197:A:N6	2.48	0.60
1:CA:328:U:O2'	11:CO:257:ARG:NH1	2.34	0.60
1:CA:438:U:H5'	21:CI:156:VAL:HG21	1.82	0.60
6:CI:156:VAL:HG22	18:Cb:204:ALA:HB2	1.82	0.60
6:CI:247:MET:HE2	41:DL:92:ILE:HD11	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:CR:43:GLN:HG2	14:CR:66:LEU:HB2	1.81	0.60
19:CD:118:LYS:NZ	38:DI:406:THR:O	2.35	0.60
21:CI:84:LEU:HD23	21:CI:84:LEU:H	1.66	0.60
23:CK:415:ASN:OD1	23:CK:541:ARG:NH2	2.35	0.60
27:CQ:191:VAL:HG12	27:CQ:215:PRO:HA	1.82	0.60
29:CV:626:VAL:O	29:CV:628:LYS:NZ	2.33	0.60
30:DA:458:GLN:HG3	30:DA:843:LEU:HB2	1.82	0.60
32:DC:899:GLN:HB3	32:DC:907:ARG:HH12	1.65	0.60
8:CK:189:THR:H	8:CK:192:MET:HE2	1.66	0.60
17:CA:89:ARG:HA	55:DZ:13:ALA:HB2	1.82	0.60
21:CI:134:ARG:NH2	35:DF:33:GLN:OE1	2.34	0.60
22:CJ:20:MET:HG2	22:CJ:21:THR:HG23	1.84	0.60
30:DA:977:TRP:O	30:DA:981:ASN:ND2	2.34	0.60
35:DF:541:PHE:HB2	37:DH:260:GLU:HB3	1.82	0.60
36:DG:465:LEU:HD21	36:DG:481:VAL:HG21	1.81	0.60
52:DW:158:PRO:HA	52:DW:161:TYR:HD2	1.65	0.60
59:F7:423:THR:HG22	59:F7:457:MET:HB2	1.83	0.60
66:IA:376:ARG:NH1	66:IA:454:GLN:O	2.34	0.60
8:CK:231:ASP:HB2	62:FF:710:GLN:HB3	1.84	0.60
14:CR:261:ILE:HG12	20:Cg:473:ARG:HH12	1.65	0.60
20:Cg:339:LEU:HD12	20:Cg:353:PHE:HE1	1.66	0.60
31:DB:348:ILE:HG23	31:DB:350:GLU:H	1.65	0.60
33:DD:466:ARG:HB2	33:DD:476:LEU:HD21	1.83	0.60
34:DE:246:ILE:HD11	34:DE:420:VAL:HA	1.82	0.60
41:DL:59:ARG:HG2	41:DL:60:GLU:HG3	1.83	0.60
46:DQ:203:SER:O	50:DU:39:ARG:NH2	2.34	0.60
57:F3:106:ASP:O	57:F3:175:ARG:NH1	2.34	0.60
60:F9:563:LYS:NZ	66:IA:531:TYR:O	2.31	0.60
64:Fh:55:ARG:HH21	67:IB:696:ARG:HG3	1.67	0.60
1:CA:129:U:OP1	11:CO:424:LYS:NZ	2.26	0.60
5:CH:81:GLU:HG2	5:CH:85:GLN:HE21	1.66	0.60
32:DC:671:ARG:NH1	32:DC:677:GLU:OE1	2.33	0.60
33:DD:519:VAL:HB	33:DD:529:GLN:HB3	1.82	0.60
58:F6:236:LEU:H	58:F6:236:LEU:HD13	1.67	0.60
61:FO:72:GLU:HG2	65:Fi:20:LEU:HB3	1.84	0.60
7:CJ:583:LYS:HB2	7:CJ:587:ALA:HB3	1.84	0.60
8:CK:97:GLN:O	8:CK:101:ASN:ND2	2.34	0.60
29:CV:746:LEU:HD12	29:CV:750:ASP:HB2	1.84	0.60
31:DB:587:VAL:HG21	31:DB:593:ARG:HG2	1.83	0.60
33:DD:481:ASN:HA	33:DD:497:ARG:HH21	1.66	0.60
35:DF:258:ASP:HA	35:DF:263:TYR:HA	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:DI:161:MET:HB3	38:DI:164:GLU:HB2	1.84	0.60
38:DI:200:ARG:NH1	38:DI:205:GLU:OE2	2.34	0.60
54:DY:66:GLN:O	54:DY:69:HIS:ND1	2.27	0.60
59:F7:208:GLU:HG2	65:Fi:360:PHE:HB3	1.83	0.60
62:Ff:608:ARG:NH1	62:Ff:610:ASP:OD2	2.34	0.60
1:CA:566:U:N3	63:Fg:306:LYS:O	2.34	0.60
29:Cv:1008:ARG:HE	42:DM:227:LEU:HD12	1.66	0.60
61:FO:315:LYS:HD2	64:Fh:287:LEU:HD21	1.84	0.60
63:Fg:43:GLU:HA	63:Fg:47:GLY:HA2	1.84	0.60
67:IB:773:GLY:O	67:IB:774:ASN:ND2	2.34	0.60
5:CH:136:ILE:O	5:CH:201:ARG:NH1	2.34	0.60
6:CI:105:THR:O	16:CU:132:GLN:NE2	2.34	0.60
6:CI:179:CYS:SG	27:Cq:112:LYS:NZ	2.74	0.60
13:CQ:201:THR:HA	59:F7:132:LEU:HA	1.82	0.60
21:CI:123:THR:HG21	37:DH:399:PHE:HB3	1.84	0.60
21:CI:140:ASN:OD1	37:DH:14:TYR:OH	2.19	0.60
23:Ck:73:LEU:HD11	34:DE:655:ARG:HH12	1.66	0.60
23:Ck:660:PRO:HG3	31:DB:1068:GLY:HA2	1.84	0.60
29:Cv:551:TRP:HE1	29:Cv:583:THR:HG23	1.66	0.60
30:DA:378:ILE:HD11	30:DA:409:LEU:HD11	1.83	0.60
31:DB:323:ALA:O	31:DB:326:THR:OG1	2.19	0.60
32:DC:29:TYR:HD2	32:DC:32:ILE:HD11	1.67	0.60
38:DI:67:ILE:HG12	38:DI:80:ARG:HG2	1.83	0.60
66:IA:202:ARG:HD2	66:IA:434:SER:HB3	1.84	0.60
1:CA:64:G:N2	1:CA:65:U:O4	2.35	0.60
5:CH:19:LEU:HD21	43:DN:136:GLU:HB2	1.82	0.60
8:CK:180:ASP:O	14:CR:181:ARG:NH1	2.33	0.60
9:CL:64:GLY:HA3	60:F9:502:GLY:HA2	1.84	0.60
9:CL:88:ARG:HG3	9:CL:129:LEU:HD11	1.83	0.60
14:CR:144:PRO:HA	29:Cv:176:PRO:HB3	1.84	0.60
23:Ck:413:ALA:HA	23:Ck:416:ARG:HG2	1.84	0.60
30:DA:374:ARG:NH1	30:DA:412:THR:O	2.35	0.60
33:DD:250:LYS:O	33:DD:287:ARG:NH1	2.35	0.60
35:DF:521:THR:HG23	35:DF:524:MET:H	1.66	0.60
1:CA:518:G:OP1	1:CA:518:G:N2	2.33	0.60
14:CR:55:ARG:NH1	18:Cb:67:GLN:OE1	2.35	0.60
45:DP:44:GLU:OE2	45:DP:48:GLN:NE2	2.34	0.60
54:DY:118:ARG:NH2	54:DY:160:GLU:O	2.35	0.60
62:Ff:249:MET:HA	62:Ff:261:ARG:HD3	1.83	0.60
66:IA:143:ARG:NH2	66:IA:492:MET:O	2.35	0.60
1:CA:394:A:H3'	24:Cm:88:SER:HB2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CN:29:ARG:HD3	21:CI:103:ALA:HA	1.83	0.60
18:Cb:217:LEU:HB3	18:Cb:276:LYS:HB3	1.84	0.60
25:Cn:191:ALA:HB2	61:FO:4:PRO:HG3	1.84	0.60
59:F7:81:GLY:HA2	61:FO:27:LYS:HE3	1.84	0.60
65:Fi:346:ARG:NH1	65:Fi:347:ASP:OD1	2.35	0.60
66:IA:40:GLN:NE2	66:IA:123:ARG:O	2.35	0.60
1:CA:67:U:OP1	11:CO:411:ARG:NH1	2.34	0.59
2:CC:10:LYS:HD2	2:CC:12:ILE:HG12	1.83	0.59
6:CI:356:MET:HE2	6:CI:392:ARG:HD2	1.84	0.59
12:CP:53:ARG:NH2	30:DA:75:ALA:O	2.35	0.59
34:DE:618:ARG:O	34:DE:625:SER:OG	2.19	0.59
35:DF:188:ARG:NH1	79:DJ:401:UTP:O1G	2.34	0.59
42:DM:33:ALA:O	42:DM:37:ASN:ND2	2.35	0.59
59:F7:438:ALA:HA	59:F7:441:ILE:HG12	1.83	0.59
60:F9:278:ARG:NH1	60:F9:575:TYR:OH	2.35	0.59
67:IB:758:PRO:HG2	67:IB:761:GLU:HB2	1.83	0.59
1:CA:478:A:O5'	21:CI:144:ARG:NH2	2.34	0.59
6:CI:136:GLN:HG2	6:CI:182:ARG:HE	1.67	0.59
17:Ca:200:ARG:HH11	43:DN:216:TYR:HB2	1.68	0.59
30:DA:751:GLU:OE2	42:DM:202:LYS:NZ	2.32	0.59
30:DA:1590:ARG:H	30:DA:1590:ARG:HD3	1.67	0.59
47:DR:75:HIS:HB3	47:DR:79:LEU:HD23	1.84	0.59
62:Ff:435:LEU:HD12	62:Ff:436:PRO:HD2	1.84	0.59
17:Ca:243:THR:HB	17:Ca:246:PHE:HB2	1.82	0.59
30:DA:212:ARG:NE	48:DS:134:GLN:OE1	2.33	0.59
32:DC:104:PRO:HG2	32:DC:112:TYR:HE1	1.67	0.59
33:DD:420:PHE:O	33:DD:470:LYS:NZ	2.31	0.59
36:DG:90:MET:HG3	36:DG:95:VAL:HG22	1.84	0.59
45:DP:42:ARG:NH1	61:FO:207:GLU:OE1	2.36	0.59
7:CJ:10:TYR:HH	49:DT:33:HIS:HE2	1.50	0.59
7:CJ:367:TRP:NE1	7:CJ:806:GLU:OE1	2.29	0.59
59:F7:500:TYR:OH	59:F7:522:ARG:NH1	2.34	0.59
1:CA:596:U:OP1	65:Fi:529:LYS:NZ	2.26	0.59
3:CE:135:ARG:NH2	41:DL:156:GLU:OE2	2.35	0.59
4:CF:157:PHE:HB2	19:Cd:143:GLN:HE22	1.68	0.59
7:CJ:267:PHE:HB2	31:DB:1023:ARG:HH22	1.68	0.59
11:CO:305:TRP:HA	11:CO:310:ALA:HB2	1.83	0.59
12:CP:152:ASN:ND2	33:DD:663:ASP:OD2	2.34	0.59
15:CS:220:MET:HE3	15:CS:222:LEU:HB3	1.85	0.59
29:Cv:874:GLU:HG2	29:Cv:878:ASN:HD22	1.66	0.59
32:DC:428:GLU:OE1	32:DC:432:ARG:NH1	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DE:85:ARG:HA	34:DE:88:LYS:HE2	1.84	0.59
34:DE:659:ARG:HG3	34:DE:737:MET:HG3	1.83	0.59
40:DK:32:ILE:HG12	40:DK:41:VAL:HG22	1.84	0.59
51:DV:73:ARG:HE	51:DV:75:PHE:HE1	1.50	0.59
64:Fh:280:ARG:NH2	64:Fh:284:ASN:O	2.35	0.59
65:Fi:208:PHE:O	65:Fi:211:ARG:NH1	2.33	0.59
67:IB:208:ARG:HG3	67:IB:209:THR:HG23	1.84	0.59
1:CA:259:U:O2'	1:CA:261:U:OP1	2.20	0.59
3:CE:216:ARG:HG2	3:CE:225:LEU:HD12	1.84	0.59
23:Ck:200:VAL:HG13	23:Ck:201:THR:HG23	1.85	0.59
37:DH:148:ASP:OD1	37:DH:289:ARG:NH2	2.36	0.59
47:DR:190:LEU:HD13	47:DR:190:LEU:H	1.67	0.59
63:Fg:369:ASP:OD2	63:Fg:454:THR:OG1	2.21	0.59
64:Fh:281:ILE:HG22	64:Fh:282:HIS:H	1.66	0.59
65:Fi:481:HIS:NE2	65:Fi:486:ALA:O	2.35	0.59
32:DC:634:ALA:O	32:DC:652:ARG:NH2	2.34	0.59
33:DD:564:LEU:HB2	33:DD:596:PHE:HE1	1.68	0.59
37:DH:163:GLU:HG2	40:DK:117:LYS:HE3	1.85	0.59
39:DJ:245:VAL:HG23	39:DJ:250:VAL:HG13	1.84	0.59
45:DP:128:LEU:HD22	45:DP:161:VAL:HG11	1.85	0.59
29:Cv:382:GLU:OE1	29:Cv:850:ARG:NH1	2.31	0.59
29:Cv:679:PRO:HB3	29:Cv:699:VAL:HG22	1.83	0.59
37:DH:208:ASN:OD1	37:DH:244:THR:OG1	2.20	0.59
47:DR:13:PHE:H	47:DR:14:ARG:HE	1.49	0.59
62:Ff:439:GLY:HA2	62:Ff:442:LEU:HD23	1.84	0.59
66:IA:228:VAL:HG22	66:IA:231:GLN:HE21	1.66	0.59
17:Ca:569:ARG:NH2	17:Ca:571:GLU:OE2	2.36	0.59
27:Cq:142:TRP:HD1	30:DA:1163:MET:HE3	1.67	0.59
29:Cv:1083:VAL:O	29:Cv:1088:ARG:NH1	2.36	0.59
47:DR:96:PHE:HB3	47:DR:126:LEU:HB3	1.84	0.59
61:FO:17:ARG:O	61:FO:21:ARG:HG2	2.03	0.59
1:CA:290:G:H1	24:Cm:208:ARG:HD2	1.67	0.59
1:CA:569:U:OP2	57:F3:62:ASN:ND2	2.35	0.59
17:Ca:511:ILE:O	17:Ca:519:GLN:NE2	2.36	0.59
32:DC:958:ASP:OD2	34:DE:163:LYS:NZ	2.28	0.59
37:DH:470:LYS:NZ	37:DH:483:TYR:OH	2.35	0.59
44:DO:164:THR:O	44:DO:198:ARG:NH2	2.36	0.59
53:DX:85:LYS:HG2	53:DX:134:LYS:HD3	1.85	0.59
31:DB:997:ASP:HA	31:DB:1000:ARG:HD3	1.84	0.58
34:DE:236:LYS:NZ	34:DE:238:SER:O	2.32	0.58
64:Fh:143:GLU:OE2	64:Fh:195:ARG:NE	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:IA:133:LYS:HG2	66:IA:140:GLN:HE22	1.67	0.58
1:CA:185:A:H5''	1:CA:186:U:H3'	1.86	0.58
1:CA:293:A:H1'	1:CA:315:A:H5'	1.85	0.58
3:CE:373:ARG:NH1	3:CE:415:ILE:O	2.37	0.58
20:Cg:404:PHE:O	20:Cg:450:ARG:NH1	2.35	0.58
30:DA:540:GLU:OE1	43:DN:185:ASN:ND2	2.34	0.58
32:DC:350:ASP:HA	32:DC:353:LEU:HD23	1.85	0.58
37:DH:472:ARG:HH12	60:F9:235:TYR:HE2	1.51	0.58
44:DO:162:ALA:O	44:DO:198:ARG:NH2	2.36	0.58
52:DW:95:GLU:OE2	52:DW:145:ARG:NH1	2.36	0.58
60:F9:475:PRO:O	60:F9:564:ARG:NH1	2.36	0.58
1:CA:167:A:OP1	30:DA:76:ARG:NH2	2.35	0.58
4:CF:7:VAL:HG13	4:CF:93:LEU:HB3	1.84	0.58
29:Cv:155:ASP:HB3	29:Cv:158:TYR:HB2	1.85	0.58
45:DP:94:VAL:HG22	45:DP:134:LEU:HD11	1.85	0.58
48:DS:128:SER:OG	48:DS:197:GLN:OE1	2.22	0.58
52:DW:48:TYR:HD1	54:DY:126:LYS:HB2	1.69	0.58
59:F7:109:ASN:OD1	59:F7:116:ASN:ND2	2.37	0.58
63:Fg:199:ASP:N	63:Fg:199:ASP:OD1	2.37	0.58
3:CE:147:TYR:HB2	67:IB:697:ALA:HB3	1.85	0.58
8:CK:103:VAL:O	18:Cb:103:ARG:NH1	2.36	0.58
17:Ca:415:GLY:O	30:DA:182:ARG:NH2	2.36	0.58
19:Cd:122:LEU:HD23	38:DI:404:TRP:CE2	2.39	0.58
20:Cg:310:SER:OG	20:Cg:312:ASN:OD1	2.22	0.58
22:Cj:205:ARG:NH2	47:DR:232:THR:O	2.36	0.58
27:Cq:191:VAL:HG21	27:Cq:213:LEU:HD13	1.85	0.58
49:DT:89:SER:OG	49:DT:92:LYS:NZ	2.29	0.58
63:Fg:45:LYS:HZ1	63:Fg:76:ARG:HD2	1.67	0.58
27:Cq:65:SER:HB2	42:DM:152:GLY:H	1.68	0.58
29:Cv:893:GLU:OE2	29:Cv:898:ARG:NH2	2.36	0.58
29:Cv:1072:LEU:HD21	30:DA:467:PRO:HD2	1.85	0.58
30:DA:332:ASP:OD1	30:DA:373:GLN:NE2	2.34	0.58
30:DA:1259:VAL:HG22	31:DB:628:LEU:HD23	1.84	0.58
30:DA:1437:VAL:N	30:DA:1543:LEU:O	2.36	0.58
32:DC:430:ILE:HD11	32:DC:442:LEU:HD21	1.85	0.58
37:DH:543:MET:O	37:DH:546:THR:OG1	2.19	0.58
39:DJ:143:TYR:O	39:DJ:147:ARG:NH1	2.36	0.58
43:DN:75:VAL:O	43:DN:109:ASN:ND2	2.36	0.58
65:Fi:213:ILE:HG13	65:Fi:214:VAL:HG23	1.85	0.58
7:CJ:442:ASP:HB3	23:Ck:667:GLN:HG2	1.85	0.58
8:CK:70:ILE:HD13	18:Cb:186:VAL:HG22	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CO:414:LEU:HA	11:CO:418:VAL:HG22	1.85	0.58
17:Ca:24:TRP:CD1	17:Ca:25:LYS:HG2	2.38	0.58
28:Cr:11:ASN:HD21	28:Cr:97:ASP:HB2	1.68	0.58
30:DA:216:LEU:HB3	30:DA:238:VAL:HG12	1.86	0.58
30:DA:486:LYS:HG3	30:DA:487:THR:HG23	1.85	0.58
31:DB:368:GLU:HG2	31:DB:371:ARG:HH21	1.68	0.58
33:DD:140:SER:O	33:DD:144:ASN:ND2	2.34	0.58
33:DD:607:GLN:O	47:DR:227:ARG:NH2	2.35	0.58
35:DF:467:LEU:HB3	35:DF:475:TYR:HB2	1.84	0.58
37:DH:489:LEU:O	49:DT:153:LYS:NZ	2.37	0.58
40:DK:4:ARG:NH2	49:DT:133:ASP:OD1	2.37	0.58
41:DL:278:ARG:NH1	41:DL:296:PRO:O	2.33	0.58
57:F3:51:ARG:NH2	63:Fg:282:ASP:OD1	2.36	0.58
66:IA:514:SER:HB2	66:IA:559:ILE:HD11	1.86	0.58
1:CA:47:U:H4'	19:Cd:10:ARG:HD3	1.84	0.58
4:CF:63:ARG:NH2	19:Cd:187:GLU:OE1	2.36	0.58
7:CJ:738:LEU:HD23	20:Cg:196:GLY:HA2	1.86	0.58
23:Ck:310:ASP:HA	31:DB:891:GLN:HG3	1.85	0.58
41:DL:117:ASP:O	41:DL:121:ILE:HG12	2.03	0.58
58:F6:599:VAL:HG11	62:Ff:723:SER:HB3	1.86	0.58
14:CR:70:ARG:HH21	41:DL:131:LEU:HD13	1.69	0.58
17:Ca:43:VAL:HG21	29:Cv:1129:ASN:HB3	1.86	0.58
23:Ck:172:ILE:HG22	23:Ck:182:ARG:HD2	1.86	0.58
23:Ck:218:ILE:HG13	23:Ck:243:LYS:HD3	1.86	0.58
48:DS:211:CYS:SG	48:DS:213:SER:OG	2.58	0.58
61:FO:113:ARG:HH21	74:UK:1:UNK:HA	1.68	0.58
62:Ff:593:GLU:O	65:Fi:590:TYR:OH	2.19	0.58
63:Fg:229:ASN:HB3	63:Fg:486:VAL:HG13	1.86	0.58
1:CA:21:G:O6	1:CA:382:A:N6	2.36	0.58
3:CE:376:LEU:HD12	3:CE:416:VAL:HG22	1.84	0.58
5:CH:84:PRO:HG3	33:DD:736:TYR:HB3	1.85	0.58
6:CI:236:ARG:NE	41:DL:254:ARG:O	2.37	0.58
17:Ca:308:LYS:NZ	17:Ca:312:ASP:OD2	2.30	0.58
23:Ck:113:ASN:O	23:Ck:140:ARG:NH2	2.37	0.58
37:DH:282:ASN:OD1	37:DH:282:ASN:N	2.34	0.58
67:IB:195:GLN:O	67:IB:199:LYS:HG2	2.03	0.58
1:CA:158:G:H1'	11:CO:393:MET:HE1	1.86	0.58
7:CJ:503:LEU:O	7:CJ:507:ASN:ND2	2.36	0.58
7:CJ:774:GLU:OE1	20:Cg:298:ARG:NH1	2.37	0.58
22:Cj:213:ASP:N	22:Cj:213:ASP:OD1	2.37	0.58
23:Ck:395:MET:O	23:Ck:399:ASN:ND2	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:DA:483:VAL:HG12	30:DA:490:ILE:HG12	1.85	0.58
31:DB:611:PRO:O	31:DB:615:ASN:ND2	2.37	0.58
34:DE:656:ARG:HH21	34:DE:738:ALA:HB3	1.68	0.58
41:DL:160:ARG:HE	41:DL:239:PHE:HB2	1.69	0.58
43:DN:45:ARG:NH1	43:DN:130:ASN:O	2.37	0.58
43:DN:276:GLN:N	43:DN:281:GLN:OE1	2.31	0.58
63:Fg:70:VAL:HA	63:Fg:73:ILE:HG12	1.84	0.58
4:CF:124:LEU:N	4:CF:127:GLU:OE2	2.37	0.57
23:Ck:707:LEU:HD21	23:Ck:767:LEU:HD22	1.85	0.57
23:Ck:815:GLY:O	23:Ck:819:GLU:HG2	2.04	0.57
28:Cr:115:PRO:HG2	28:Cr:118:TRP:HB2	1.86	0.57
29:Cv:386:ASP:O	29:Cv:390:ARG:HG2	2.04	0.57
32:DC:635:MET:HE3	32:DC:762:LYS:HE3	1.85	0.57
37:DH:490:HIS:NE2	49:DT:153:LYS:O	2.37	0.57
44:DO:67:ARG:NH1	44:DO:113:LEU:O	2.36	0.57
62:Ff:248:ARG:NH1	62:Ff:297:GLU:OE2	2.37	0.57
64:Fh:206:VAL:HG13	64:Fh:209:ARG:HH21	1.69	0.57
65:Fi:482:GLN:OE1	65:Fi:487:TYR:OH	2.20	0.57
10:CN:37:ARG:HD3	35:DF:115:HIS:HD2	1.67	0.57
14:CR:33:GLN:O	18:Cb:114:ASN:ND2	2.37	0.57
17:Ca:567:GLN:OE1	55:DZ:48:ARG:NH1	2.31	0.57
28:Cr:152:VAL:HG12	28:Cr:181:PRO:HA	1.85	0.57
32:DC:575:ARG:HG3	32:DC:576:LEU:HD12	1.85	0.57
34:DE:35:SER:H	34:DE:38:GLN:HE21	1.52	0.57
35:DF:11:ARG:NH1	35:DF:42:LEU:O	2.37	0.57
39:DJ:319:TYR:O	49:DT:27:ARG:NH2	2.37	0.57
41:DL:166:PHE:O	41:DL:171:ARG:NH2	2.37	0.57
44:DO:144:LEU:HD22	44:DO:147:ARG:HH21	1.68	0.57
65:Fi:403:LEU:HD13	65:Fi:469:LEU:HD22	1.86	0.57
11:CO:182:ASN:ND2	19:Cd:146:ASN:OD1	2.36	0.57
17:Ca:216:TRP:HH2	55:DZ:87:ILE:HD13	1.69	0.57
17:Ca:528:THR:OG1	17:Ca:539:GLN:O	2.22	0.57
28:Cr:37:CYS:HB2	28:Cr:40:HIS:ND1	2.19	0.57
29:Cv:469:GLU:OE2	29:Cv:823:ARG:NH1	2.37	0.57
30:DA:748:THR:O	30:DA:750:ARG:NH1	2.37	0.57
30:DA:1064:ASP:OD2	30:DA:1160:SER:OG	2.20	0.57
32:DC:62:SER:O	32:DC:539:ASN:ND2	2.37	0.57
32:DC:242:HIS:CD2	32:DC:464:THR:HG1	2.22	0.57
35:DF:402:THR:O	35:DF:406:ASN:ND2	2.37	0.57
36:DG:335:GLU:OE2	36:DG:339:TYR:OH	2.21	0.57
59:F7:602:GLN:NE2	59:F7:606:GLU:OE2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:Ff:386:TRP:HB3	62:Ff:392:HIS:CD2	2.39	0.57
15:CS:182:HIS:HD2	35:DF:91:TYR:HB2	1.69	0.57
17:Ca:326:PHE:HB3	17:Ca:329:GLU:HB2	1.87	0.57
28:Cr:210:PRO:HG2	28:Cr:213:CYS:HB2	1.86	0.57
37:DH:245:TYR:HD1	37:DH:264:ILE:HD11	1.68	0.57
38:DI:318:ARG:NH2	44:DO:249:ASP:OD2	2.38	0.57
44:DO:105:ARG:O	44:DO:111:ARG:NH2	2.36	0.57
53:DX:99:MET:HE2	53:DX:121:PHE:HZ	1.69	0.57
62:Ff:224:LEU:HD23	62:Ff:429:ILE:HG12	1.86	0.57
67:IB:466:LEU:HB3	67:IB:476:VAL:HG13	1.86	0.57
7:CJ:631:LEU:HD13	7:CJ:656:VAL:HG13	1.87	0.57
20:Cg:348:ASP:OD1	20:Cg:351:LYS:NZ	2.37	0.57
33:DD:312:GLN:OE1	33:DD:440:ARG:NH1	2.37	0.57
36:DG:176:VAL:HG23	36:DG:188:LEU:HD21	1.86	0.57
48:DS:173:TRP:HZ2	48:DS:186:ILE:HG22	1.69	0.57
66:IA:221:ASP:OD2	66:IA:228:VAL:N	2.32	0.57
3:CE:144:ILE:HA	3:CE:167:LEU:HB3	1.87	0.57
17:Ca:367:ASN:OD1	29:Cv:954:ARG:NH2	2.35	0.57
31:DB:241:THR:HG22	31:DB:244:ARG:HH21	1.70	0.57
32:DC:1015:VAL:HG23	40:DK:104:ALA:HB1	1.86	0.57
53:DX:83:ARG:NH1	54:DY:135:TYR:OH	2.36	0.57
63:Fg:6:GLN:NE2	63:Fg:499:HIS:O	2.37	0.57
66:IA:539:ILE:HG21	66:IA:605:LEU:HG	1.86	0.57
20:Cg:406:GLU:OE1	20:Cg:406:GLU:N	2.34	0.57
30:DA:470:LEU:HD13	30:DA:510:PRO:HD2	1.86	0.57
31:DB:248:ASP:OD1	31:DB:375:ARG:NH1	2.36	0.57
31:DB:716:GLU:O	31:DB:720:LYS:NZ	2.37	0.57
31:DB:1070:SER:HB3	31:DB:1074:SER:HB2	1.87	0.57
32:DC:128:HIS:ND1	32:DC:131:GLU:OE2	2.38	0.57
34:DE:576:HIS:O	34:DE:579:ARG:NH1	2.34	0.57
41:DL:49:ALA:HB1	67:IB:728:LEU:HD23	1.86	0.57
67:IB:334:ALA:O	67:IB:337:GLN:NE2	2.37	0.57
12:CP:76:TRP:HE1	17:Ca:487:GLU:HG2	1.70	0.57
13:CQ:65:GLY:O	13:CQ:69:GLN:NE2	2.38	0.57
14:CR:123:LYS:O	14:CR:128:ASN:ND2	2.37	0.57
17:Ca:315:VAL:HA	30:DA:882:GLN:HG3	1.86	0.57
23:Ck:129:THR:HG23	23:Ck:132:TYR:H	1.68	0.57
29:Cv:944:HIS:HB3	29:Cv:947:THR:HG22	1.86	0.57
44:DO:108:ASP:OD2	44:DO:147:ARG:NH2	2.37	0.57
49:DT:233:HIS:ND1	49:DT:238:PRO:O	2.37	0.57
53:DX:164:THR:HG23	53:DX:167:HIS:H	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:Fg:418:LEU:HD11	63:Fg:481:GLN:HB3	1.87	0.57
65:Fi:342:VAL:HG12	65:Fi:406:ALA:HB2	1.85	0.57
1:CA:177:A:OP1	19:Cd:10:ARG:N	2.37	0.57
7:CJ:369:ARG:NH2	7:CJ:804:ASN:O	2.36	0.57
7:CJ:773:GLU:HG3	51:DV:100:LYS:HG2	1.86	0.57
10:CN:28:SER:HA	10:CN:31:MET:HE3	1.87	0.57
32:DC:791:ALA:HB3	32:DC:806:SER:HB2	1.87	0.57
32:DC:1069:CYS:SG	32:DC:1070:GLY:N	2.77	0.57
35:DF:310:LEU:HD11	35:DF:345:LEU:HD21	1.87	0.57
47:DR:212:SER:O	47:DR:215:ARG:NH2	2.37	0.57
47:DR:237:TYR:OH	47:DR:269:TRP:O	2.22	0.57
60:F9:311:ARG:HG3	60:F9:314:GLY:H	1.68	0.57
64:Fh:247:GLU:OE2	64:Fh:251:ARG:NH1	2.37	0.57
65:Fi:333:ALA:H	65:Fi:356:HIS:HE1	1.53	0.57
66:IA:656:ARG:NH2	66:IA:732:GLN:OE1	2.36	0.57
66:IA:659:ARG:O	66:IA:688:ARG:N	2.37	0.57
3:CE:145:VAL:HG21	3:CE:269:VAL:HG21	1.87	0.57
7:CJ:437:ARG:NH2	31:DB:1065:ASP:OD2	2.35	0.57
7:CJ:581:GLN:NE2	7:CJ:591:ASP:OD1	2.37	0.57
22:Cj:217:PRO:HG2	22:Cj:220:PHE:HB2	1.86	0.57
26:Cp:165:TYR:HA	26:Cp:168:ILE:HG12	1.87	0.57
27:Cq:21:MET:N	27:Cq:21:MET:SD	2.78	0.57
30:DA:916:ASP:HB2	43:DN:11:ARG:HA	1.86	0.57
34:DE:327:ASN:HB2	34:DE:437:LYS:HA	1.87	0.57
36:DG:160:ARG:NH2	36:DG:163:GLN:OE1	2.38	0.57
37:DH:80:ARG:HG3	37:DH:85:LEU:HD13	1.87	0.57
37:DH:458:PRO:HG2	37:DH:461:GLU:HG3	1.87	0.57
44:DO:67:ARG:HA	44:DO:70:ILE:HG22	1.87	0.57
67:IB:343:ARG:O	67:IB:551:ARG:NH2	2.37	0.57
1:CA:399:A:OP2	8:CK:17:ARG:NH1	2.38	0.56
3:CE:54:GLU:HB2	30:DA:1039:SER:HB3	1.87	0.56
19:Cd:36:ARG:NH1	26:Cp:119:GLU:OE2	2.37	0.56
31:DB:573:GLU:HB3	31:DB:577:ARG:HH21	1.69	0.56
38:DI:249:GLU:OE2	38:DI:250:ASN:ND2	2.38	0.56
58:F6:226:LEU:HA	58:F6:229:LEU:HD23	1.86	0.56
58:F6:247:ILE:HB	58:F6:262:THR:HG22	1.87	0.56
60:F9:368:ARG:HD2	64:Fh:204:ARG:HH12	1.70	0.56
63:Fg:232:ILE:HG21	63:Fg:235:GLU:HB2	1.88	0.56
67:IB:727:ARG:NH2	67:IB:744:ASN:O	2.34	0.56
1:CA:98:A:H62	13:CQ:48:ARG:HH21	1.54	0.56
1:CA:371:U:HO2'	1:CA:381:U:HO2'	1.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CP:58:ILE:O	30:DA:77:ARG:NH1	2.38	0.56
15:CS:170:PHE:O	15:CS:190:ARG:NH2	2.38	0.56
28:Cr:22:LEU:HD12	28:Cr:25:LEU:HD12	1.87	0.56
30:DA:1652:GLU:HG2	30:DA:1655:ARG:HE	1.70	0.56
32:DC:1156:PRO:HA	32:DC:1160:GLN:HE21	1.69	0.56
34:DE:233:SER:OG	34:DE:234:GLU:OE1	2.23	0.56
64:Fh:139:LEU:HD12	64:Fh:192:VAL:HG13	1.86	0.56
1:CA:295:G:N2	1:CA:295:G:OP2	2.37	0.56
1:CA:455:G:OP2	8:CK:10:ARG:NH2	2.39	0.56
3:CE:341:ARG:NH2	29:Cv:1047:TYR:OH	2.37	0.56
3:CE:387:THR:OG1	3:CE:419:ARG:NH2	2.39	0.56
8:CK:216:ILE:HD13	8:CK:258:LEU:HD13	1.86	0.56
13:CQ:215:GLN:NE2	65:Fi:327:SER:OG	2.38	0.56
16:CU:48:VAL:HG21	16:CU:54:ILE:HG22	1.87	0.56
17:Ca:311:TYR:O	43:DN:213:ARG:NH2	2.37	0.56
20:Cg:337:ARG:NH2	23:Ck:807:ASN:OD1	2.35	0.56
22:Cj:155:GLU:OE1	33:DD:626:ARG:NH1	2.38	0.56
22:Cj:226:LYS:NZ	22:Cj:232:PRO:O	2.38	0.56
24:Cm:106:CYS:HB3	24:Cm:115:CYS:SG	2.45	0.56
26:Cp:177:CYS:SG	26:Cp:180:ARG:NH2	2.78	0.56
29:Cv:162:SER:H	29:Cv:166:HIS:HD2	1.51	0.56
29:Cv:726:SER:HB2	29:Cv:736:ARG:HH21	1.70	0.56
31:DB:349:GLY:HA2	31:DB:352:LEU:HB2	1.87	0.56
31:DB:383:ARG:HA	31:DB:396:ARG:HH12	1.69	0.56
31:DB:494:PRO:HB3	31:DB:510:ASN:HD21	1.70	0.56
31:DB:722:ARG:NH2	31:DB:802:ASP:OD1	2.38	0.56
31:DB:769:VAL:HG21	31:DB:786:LEU:HD21	1.86	0.56
34:DE:591:LEU:HD13	34:DE:592:PRO:HD2	1.86	0.56
38:DI:85:ASN:ND2	38:DI:228:TYR:OH	2.38	0.56
38:DI:293:ILE:HG22	38:DI:295:GLY:H	1.69	0.56
43:DN:17:MET:HE3	43:DN:171:LEU:HB2	1.86	0.56
49:DT:145:GLU:OE2	49:DT:149:TRP:NE1	2.38	0.56
59:F7:62:VAL:HA	59:F7:67:TYR:HD2	1.70	0.56
59:F7:203:ASN:HA	65:Fi:473:ARG:HG3	1.87	0.56
60:F9:564:ARG:NE	66:IA:531:TYR:OH	2.39	0.56
64:Fh:276:VAL:HG22	64:Fh:288:LEU:HD12	1.87	0.56
67:IB:380:GLU:OE2	67:IB:598:SER:OG	2.23	0.56
12:CP:179:ALA:HA	12:CP:182:ARG:HE	1.71	0.56
23:Ck:813:ARG:HG3	23:Ck:817:LEU:HD23	1.86	0.56
33:DD:463:GLU:OE2	33:DD:466:ARG:NH2	2.37	0.56
34:DE:40:ASN:ND2	34:DE:182:ASP:OD2	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DF:512:ASN:HB3	35:DF:515:VAL:HG12	1.88	0.56
36:DG:608:ARG:NH2	36:DG:630:GLU:OE1	2.38	0.56
40:DK:283:ARG:HD3	49:DT:124:GLY:HA3	1.87	0.56
43:DN:249:LYS:HB2	55:DZ:36:LEU:HD11	1.86	0.56
1:CA:416:U:O2	10:CN:15:GLN:NE2	2.33	0.56
1:CA:547:U:O3'	67:IB:666:ARG:NH2	2.39	0.56
8:CK:281:VAL:HG21	8:CK:288:ARG:HG3	1.88	0.56
29:Cv:292:LYS:NZ	29:Cv:511:HIS:O	2.37	0.56
34:DE:60:ALA:HA	34:DE:63:LYS:HE3	1.87	0.56
34:DE:581:THR:H	34:DE:585:ARG:HB2	1.71	0.56
48:DS:125:LYS:O	48:DS:167:SER:OG	2.16	0.56
57:F3:51:ARG:NH1	63:Fg:281:GLN:OE1	2.39	0.56
57:F3:163:ASP:OD1	57:F3:163:ASP:N	2.39	0.56
60:F9:596:TYR:HB3	66:IA:764:GLU:HG3	1.85	0.56
62:Ff:304:VAL:HG13	62:Ff:309:ALA:HB3	1.87	0.56
1:CA:262:A:N6	26:Cp:18:SER:OG	2.38	0.56
7:CJ:413:GLU:OE2	31:DB:1063:ARG:NH2	2.38	0.56
7:CJ:436:ARG:HD2	23:Ck:673:GLU:HB3	1.87	0.56
15:CS:190:ARG:NH2	35:DF:81:SER:O	2.34	0.56
17:Ca:508:GLU:HG3	17:Ca:558:ALA:HB2	1.88	0.56
23:Ck:645:ALA:O	23:Ck:649:THR:OG1	2.22	0.56
31:DB:696:GLU:OE2	34:DE:640:ARG:NH2	2.38	0.56
36:DG:252:VAL:HG11	36:DG:317:MET:HG3	1.87	0.56
37:DH:303:GLU:OE2	37:DH:307:ARG:NH1	2.39	0.56
41:DL:250:LYS:HB2	41:DL:253:SER:HB2	1.87	0.56
44:DO:201:GLU:HB2	44:DO:230:ILE:HD11	1.86	0.56
6:CI:94:TYR:HE2	16:CU:117:MET:HB2	1.71	0.56
7:CJ:291:ALA:HB2	37:DH:274:GLU:HA	1.87	0.56
31:DB:970:ASP:HB2	31:DB:975:LYS:HE2	1.87	0.56
32:DC:115:ASP:OD1	32:DC:116:TYR:N	2.39	0.56
35:DF:39:ARG:NH2	35:DF:157:THR:OG1	2.38	0.56
45:DP:171:LEU:HD22	45:DP:190:LEU:HB3	1.87	0.56
46:DQ:166:ILE:HB	46:DQ:208:VAL:HG13	1.87	0.56
49:DT:192:GLN:NE2	60:F9:246:ASP:OD2	2.38	0.56
50:DU:70:ASP:OD1	50:DU:71:ASP:N	2.39	0.56
63:Fg:141:LEU:HD23	63:Fg:141:LEU:H	1.71	0.56
66:IA:261:HIS:O	66:IA:268:ARG:NH2	2.39	0.56
7:CJ:425:ARG:NH2	39:DJ:39:GLU:OE2	2.38	0.56
7:CJ:670:GLN:OE1	21:CI:39:ARG:NH1	2.39	0.56
14:CR:55:ARG:NH2	18:Cb:68:GLU:OE2	2.37	0.56
23:Ck:41:THR:HG22	23:Ck:43:GLY:H	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Cv:65:TYR:HB3	29:Cv:73:VAL:HG21	1.88	0.56
30:DA:637:HIS:NE2	30:DA:643:GLU:OE1	2.39	0.56
32:DC:385:THR:HG23	32:DC:442:LEU:HD22	1.88	0.56
35:DF:318:MET:O	35:DF:322:GLU:HG2	2.06	0.56
37:DH:288:HIS:NE2	37:DH:296:CYS:SG	2.76	0.56
38:DI:353:LYS:HE3	38:DI:378:LEU:HG	1.87	0.56
60:F9:497:GLY:HA3	60:F9:509:ILE:HD13	1.88	0.56
66:IA:557:ALA:O	66:IA:561:SER:OG	2.23	0.56
8:CK:77:MET:HB2	18:Cb:178:ARG:HH22	1.71	0.56
11:CO:425:ARG:NH2	11:CO:427:GLY:O	2.39	0.56
19:Cd:118:LYS:HZ1	38:DI:407:LEU:HA	1.71	0.56
26:Cp:40:GLU:OE1	48:DS:187:ARG:NH1	2.39	0.56
31:DB:1092:PHE:HB3	31:DB:1095:GLU:HB2	1.87	0.56
32:DC:294:ASP:HA	32:DC:297:LYS:HG2	1.88	0.56
32:DC:941:MET:O	32:DC:945:ARG:NE	2.28	0.56
39:DJ:81:PRO:HA	39:DJ:84:ARG:HE	1.70	0.56
42:DM:154:SER:HB3	42:DM:157:LEU:HD23	1.88	0.56
46:DQ:217:GLN:HB3	46:DQ:221:LEU:HD12	1.86	0.56
58:F6:276:MET:HE1	58:F6:283:VAL:HG11	1.86	0.56
1:CA:103:U:HO2'	1:CA:129:U:HO2'	1.54	0.56
6:CI:335:VAL:HB	6:CI:343:VAL:HG21	1.88	0.56
7:CJ:438:ASN:ND2	23:Ck:660:PRO:O	2.39	0.56
17:Ca:442:TRP:HB2	17:Ca:474:ARG:HB3	1.88	0.56
21:CI:74:ARG:NH2	51:DV:87:ASP:OD2	2.29	0.56
27:Cq:110:ILE:HD12	27:Cq:209:ILE:HD11	1.87	0.56
29:Cv:397:TRP:CD1	29:Cv:949:CYS:HG	2.24	0.56
30:DA:578:LYS:HA	30:DA:817:PRO:HG2	1.87	0.56
35:DF:349:ASP:CG	35:DF:457:ARG:HH12	2.13	0.56
38:DI:278:LEU:HG	38:DI:310:LEU:HD13	1.86	0.56
45:DP:39:ASP:OD1	45:DP:40:HIS:ND1	2.39	0.56
62:Ff:624:ILE:HG22	62:Ff:627:ALA:H	1.71	0.56
64:Fh:81:THR:OG1	64:Fh:82:GLU:OE1	2.23	0.56
1:CA:285:A:H1'	24:Cm:182:ASN:HD22	1.71	0.55
1:CA:301:A:OP2	8:CK:224:ASN:ND2	2.39	0.55
7:CJ:83:HIS:O	7:CJ:83:HIS:ND1	2.37	0.55
10:CN:40:TRP:HD1	21:CI:93:LEU:HD11	1.72	0.55
17:Ca:574:VAL:HG23	17:Ca:580:ILE:HG21	1.87	0.55
21:CI:139:ILE:O	21:CI:143:GLN:NE2	2.37	0.55
23:Ck:729:THR:OG1	23:Ck:778:GLN:NE2	2.39	0.55
26:Cp:64:ASP:OD1	26:Cp:124:LYS:NZ	2.39	0.55
29:Cv:740:ILE:HG23	29:Cv:786:VAL:HG13	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:DC:1007:ASN:ND2	32:DC:1013:GLU:OE2	2.38	0.55
32:DC:1164:TRP:NE1	37:DH:326:ASP:OD1	2.30	0.55
33:DD:225:LYS:HD3	33:DD:305:GLY:HA3	1.88	0.55
59:F7:253:THR:HB	59:F7:290:MET:HE1	1.87	0.55
61:FO:306:ASN:HB2	61:FO:309:ARG:HG3	1.87	0.55
63:Fg:287:ILE:HD11	63:Fg:341:ARG:HH21	1.71	0.55
64:Fh:208:LYS:HE3	64:Fh:212:MET:HE2	1.88	0.55
1:CA:237:C:OP2	9:CL:88:ARG:NH2	2.38	0.55
3:CE:83:MET:N	3:CE:83:MET:SD	2.79	0.55
5:CH:124:ASP:OD1	5:CH:138:LYS:NZ	2.38	0.55
10:CN:50:GLN:NE2	21:CI:83:ASN:O	2.38	0.55
10:CN:125:GLY:HA3	39:DJ:22:MET:HB2	1.87	0.55
11:CO:128:ARG:HH22	11:CO:165:HIS:CG	2.25	0.55
17:Ca:75:LEU:HB2	17:Ca:78:PHE:HD2	1.71	0.55
30:DA:374:ARG:HH12	30:DA:419:THR:HG21	1.71	0.55
32:DC:667:VAL:HG22	32:DC:789:VAL:HG12	1.88	0.55
33:DD:22:ASP:OD2	33:DD:24:SER:OG	2.20	0.55
62:Ff:200:CYS:HB3	62:Ff:203:LEU:HB2	1.88	0.55
65:Fi:373:ILE:HG12	65:Fi:467:PHE:HE2	1.71	0.55
7:CJ:376:SER:HB3	7:CJ:385:LEU:HD23	1.88	0.55
12:CP:23:ALA:HB2	12:CP:51:HIS:CG	2.41	0.55
16:CU:59:ARG:HH21	16:CU:169:ASN:HA	1.72	0.55
20:Cg:102:PRO:O	20:Cg:107:ARG:NH1	2.36	0.55
20:Cg:436:ASP:OD2	20:Cg:470:GLN:NE2	2.39	0.55
26:Cp:55:ASN:OD1	26:Cp:56:HIS:N	2.40	0.55
33:DD:11:ARG:HH21	33:DD:12:SER:HA	1.71	0.55
35:DF:139:ASP:OD1	35:DF:140:HIS:N	2.39	0.55
39:DJ:85:LYS:NZ	39:DJ:103:ASP:OD2	2.28	0.55
65:Fi:566:PRO:HG2	65:Fi:569:LYS:HE2	1.88	0.55
66:IA:187:GLU:HA	66:IA:190:ILE:HG13	1.88	0.55
5:CH:225:ASP:HB2	5:CH:228:THR:HG22	1.87	0.55
7:CJ:230:PHE:O	7:CJ:239:ARG:NH2	2.39	0.55
14:CR:9:TYR:OH	29:Cv:803:GLN:NE2	2.40	0.55
22:Cj:29:LEU:O	47:DR:262:ARG:NH1	2.39	0.55
26:Cp:148:GLU:HG2	26:Cp:149:LYS:HG2	1.88	0.55
30:DA:1165:ALA:HB3	42:DM:148:VAL:HG23	1.88	0.55
32:DC:903:THR:OG1	32:DC:906:GLN:OE1	2.24	0.55
37:DH:330:THR:O	37:DH:343:ASN:ND2	2.39	0.55
38:DI:49:GLU:OE1	38:DI:158:ARG:NH2	2.39	0.55
62:Ff:610:ASP:HB2	62:Ff:658:GLN:HE21	1.71	0.55
67:IB:338:ARG:NH1	67:IB:562:ASP:OD2	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:441:G:O6	21:Ci:140:ASN:ND2	2.38	0.55
20:Cg:60:HIS:HE1	20:Cg:422:LEU:HD22	1.71	0.55
20:Cg:317:ASP:HA	20:Cg:320:LEU:HD23	1.89	0.55
22:Cj:125:THR:OG1	47:DR:268:HIS:O	2.17	0.55
29:Cv:1017:PHE:HD2	29:Cv:1022:LEU:HD21	1.72	0.55
30:DA:446:ARG:HH12	30:DA:450:GLU:HB2	1.72	0.55
30:DA:522:MET:O	30:DA:526:HIS:ND1	2.39	0.55
30:DA:1382:SER:HA	30:DA:1389:VAL:HG11	1.86	0.55
32:DC:479:ALA:HB1	32:DC:484:ASP:HB3	1.88	0.55
34:DE:578:GLN:NE2	49:DT:126:ARG:HD3	2.21	0.55
66:IA:527:MET:HE1	66:IA:543:ILE:HD13	1.89	0.55
1:CA:22:U:H4'	29:Cv:44:ARG:HE	1.71	0.55
3:CE:81:LYS:HE3	29:Cv:404:ARG:HH12	1.69	0.55
62:Ff:501:TRP:NE1	62:Ff:506:GLY:HA3	2.21	0.55
67:IB:424:PRO:HD2	67:IB:429:PRO:HD2	1.87	0.55
1:CA:382:A:H5'	25:Cn:168:ARG:HH22	1.71	0.55
10:CN:37:ARG:HD3	35:DF:115:HIS:CD2	2.42	0.55
17:Ca:196:GLU:OE2	43:DN:215:ARG:N	2.34	0.55
30:DA:1399:ASN:ND2	30:DA:1609:MET:SD	2.80	0.55
32:DC:54:LEU:O	40:DK:267:ARG:NH1	2.35	0.55
33:DD:655:GLU:HA	33:DD:658:VAL:HG12	1.88	0.55
37:DH:524:HIS:HB2	40:DK:286:LEU:HD21	1.88	0.55
6:CI:250:ASN:HD21	6:CI:273:VAL:HA	1.70	0.55
9:CL:74:LEU:HD11	66:IA:51:GLN:HG2	1.89	0.55
13:CQ:235:ARG:HH22	57:F3:72:VAL:HG21	1.72	0.55
20:Cg:260:ASP:OD1	23:Ck:825:LYS:NZ	2.38	0.55
23:Ck:401:LEU:HD21	23:Ck:557:ARG:HD3	1.88	0.55
30:DA:514:TYR:HE1	30:DA:834:PRO:HG3	1.72	0.55
31:DB:469:ILE:HD12	37:DH:343:ASN:HD21	1.72	0.55
39:DJ:342:LYS:NZ	40:DK:318:VAL:O	2.37	0.55
48:DS:227:VAL:HB	48:DS:233:PHE:HB2	1.89	0.55
3:CE:34:ARG:NH2	3:CE:98:ASP:O	2.40	0.55
7:CJ:797:LEU:HD13	21:Ci:97:THR:HG21	1.88	0.55
11:CO:284:GLN:O	13:CQ:174:ARG:NH1	2.40	0.55
12:CP:39:LYS:O	33:DD:71:HIS:NE2	2.37	0.55
30:DA:193:GLU:HG2	30:DA:194:LEU:HD22	1.89	0.55
31:DB:540:HIS:NE2	31:DB:642:GLU:OE2	2.40	0.55
31:DB:945:GLY:HA2	36:DG:26:ASN:HD21	1.72	0.55
36:DG:97:VAL:HG11	36:DG:127:LEU:HD22	1.88	0.55
57:F3:66:ARG:NH1	57:F3:67:THR:O	2.40	0.55
5:CH:81:GLU:HG3	5:CH:83:VAL:H	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CN:156:LEU:HD23	21:CI:73:MET:HE3	1.88	0.55
14:CR:202:LYS:HA	14:CR:205:VAL:HG12	1.88	0.55
32:DC:365:LYS:O	32:DC:369:SER:OG	2.20	0.55
64:Fh:86:GLU:N	67:IB:786:ALA:O	2.40	0.55
1:CA:166:A:OP2	11:CO:396:LYS:NZ	2.39	0.54
7:CJ:260:LEU:HD13	7:CJ:427:THR:HG21	1.88	0.54
9:CL:121:ILE:HG23	9:CL:134:TYR:HB3	1.88	0.54
17:Ca:519:GLN:HG2	55:DZ:50:MET:HG3	1.88	0.54
23:Ck:264:ASN:OD1	23:Ck:264:ASN:N	2.36	0.54
31:DB:622:ALA:HB3	31:DB:625:ASN:HB2	1.89	0.54
33:DD:589:GLN:O	47:DR:198:HIS:ND1	2.39	0.54
35:DF:505:LYS:HA	35:DF:516:ARG:HH21	1.72	0.54
42:DM:11:VAL:HG21	42:DM:121:LEU:HD21	1.89	0.54
43:DN:226:PRO:HD2	43:DN:289:LEU:HB2	1.89	0.54
1:CA:206:A:O2'	48:DS:32:PHE:O	2.24	0.54
1:CA:492:U:OP1	15:CS:105:ILE:N	2.40	0.54
28:Cr:125:GLN:OE1	28:Cr:161:ARG:NH2	2.36	0.54
28:Cr:143:ARG:HD2	28:Cr:149:THR:HG22	1.88	0.54
30:DA:1207:PHE:HB2	30:DA:1213:ILE:HD11	1.89	0.54
36:DG:338:LYS:HA	36:DG:391:ALA:HB2	1.89	0.54
49:DT:147:ALA:O	49:DT:151:TRP:HD1	1.90	0.54
55:DZ:23:PHE:HB3	55:DZ:25:HIS:HD2	1.72	0.54
60:F9:479:ARG:NH2	60:F9:564:ARG:O	2.40	0.54
10:CN:69:ARG:NH1	31:DB:1115:ILE:O	2.41	0.54
17:Ca:181:GLU:HG2	55:DZ:10:MET:HG3	1.90	0.54
30:DA:1453:ASN:ND2	30:DA:1461:TYR:OH	2.40	0.54
31:DB:849:ASP:O	31:DB:853:GLU:HG2	2.07	0.54
32:DC:1007:ASN:HB2	32:DC:1013:GLU:HG3	1.89	0.54
34:DE:316:ARG:HH12	34:DE:399:PRO:HD2	1.72	0.54
54:DY:38:MET:HG3	54:DY:55:LEU:HD11	1.90	0.54
3:CE:188:GLU:OE1	3:CE:188:GLU:N	2.39	0.54
5:CH:59:LEU:HD22	43:DN:61:LEU:HB2	1.90	0.54
11:CO:221:PRO:HB2	11:CO:266:LEU:HB2	1.88	0.54
14:CR:33:GLN:HE21	41:DL:189:THR:HG23	1.73	0.54
17:Ca:597:LYS:HE2	17:Ca:599:ILE:HB	1.90	0.54
29:Cv:778:ARG:NH2	29:Cv:779:TYR:OH	2.41	0.54
29:Cv:1002:ARG:NH1	30:DA:865:ASP:OD1	2.39	0.54
32:DC:862:PRO:HG2	32:DC:865:CYS:HB2	1.90	0.54
35:DF:349:ASP:OD1	35:DF:349:ASP:N	2.36	0.54
43:DN:228:LEU:HB3	43:DN:286:VAL:HG13	1.89	0.54
61:FO:297:LEU:HD13	61:FO:328:ILE:HD12	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:Fh:176:SER:HB3	64:Fh:212:MET:HE1	1.88	0.54
1:CA:535:U:O2'	1:CA:536:U:H5'	2.06	0.54
17:Ca:27:HIS:NE2	17:Ca:593:ALA:O	2.40	0.54
18:Cb:104:LEU:O	18:Cb:108:GLU:HB2	2.06	0.54
18:Cb:175:ILE:HG23	18:Cb:179:GLU:HB2	1.90	0.54
62:Ff:425:PHE:HE1	67:IB:182:LEU:HD22	1.72	0.54
6:CI:175:ARG:NH2	27:Cq:112:LYS:O	2.40	0.54
11:CO:144:ARG:NH2	59:F7:525:GLY:O	2.41	0.54
12:CP:66:LYS:HD2	33:DD:61:GLN:HB2	1.90	0.54
17:Ca:193:ARG:NH1	43:DN:212:THR:OG1	2.39	0.54
17:Ca:201:ARG:HB2	17:Ca:202:ILE:HD12	1.89	0.54
20:Cg:128:TRP:CD1	20:Cg:280:PRO:HB3	2.41	0.54
22:Cj:210:PRO:HA	47:DR:266:TRP:CG	2.43	0.54
29:Cv:481:GLY:O	29:Cv:485:ARG:HG2	2.08	0.54
30:DA:378:ILE:O	30:DA:382:ASN:ND2	2.35	0.54
30:DA:1037:GLY:O	42:DM:268:ARG:NH1	2.41	0.54
31:DB:986:TYR:OH	36:DG:119:ASP:OD2	2.18	0.54
32:DC:885:LEU:HB3	32:DC:889:ARG:HH12	1.73	0.54
33:DD:564:LEU:HB2	33:DD:596:PHE:CE1	2.43	0.54
37:DH:500:VAL:HG22	37:DH:501:PRO:HD2	1.89	0.54
45:DP:184:GLU:HA	45:DP:187:ARG:HG2	1.89	0.54
58:F6:202:LEU:HD13	58:F6:234:GLY:HA3	1.89	0.54
58:F6:308:LEU:HB3	58:F6:310:LEU:HG	1.90	0.54
59:F7:171:ARG:NH2	59:F7:216:GLU:OE2	2.40	0.54
1:CA:282:A:O2'	24:Cm:183:GLY:O	2.25	0.54
7:CJ:530:THR:OG1	7:CJ:665:ARG:NH1	2.41	0.54
7:CJ:734:THR:HG22	7:CJ:738:LEU:HD22	1.88	0.54
7:CJ:792:HIS:HB3	7:CJ:795:LYS:HB2	1.89	0.54
12:CP:77:SER:O	26:Cp:28:ARG:NH2	2.40	0.54
39:DJ:80:GLU:OE1	39:DJ:88:ARG:NH2	2.40	0.54
49:DT:105:ARG:HE	49:DT:146:GLN:HE21	1.55	0.54
62:Ff:260:PHE:N	62:Ff:796:GLU:OE2	2.35	0.54
66:IA:305:PRO:HB3	66:IA:363:GLN:HE21	1.73	0.54
67:IB:499:LEU:O	67:IB:502:GLN:NE2	2.40	0.54
3:CE:142:LEU:HD11	3:CE:167:LEU:HD22	1.90	0.54
6:CI:203:ASP:OD2	6:CI:210:THR:OG1	2.25	0.54
19:Cd:13:ARG:HH21	19:Cd:28:MET:HB3	1.73	0.54
20:Cg:91:GLU:HG3	20:Cg:210:TYR:HB3	1.90	0.54
23:Ck:383:ILE:HD11	23:Ck:570:VAL:HG11	1.90	0.54
28:Cr:41:LEU:O	28:Cr:45:THR:HG22	2.08	0.54
33:DD:466:ARG:NH1	33:DD:514:ASP:OD2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DF:402:THR:HG22	35:DF:406:ASN:HD21	1.73	0.54
36:DG:75:ARG:NH1	36:DG:100:ASP:OD1	2.40	0.54
38:DI:338:GLU:OE1	38:DI:338:GLU:N	2.41	0.54
46:DQ:76:SER:HB2	46:DQ:114:HIS:HB2	1.90	0.54
48:DS:87:ARG:HH12	48:DS:92:ARG:HH12	1.56	0.54
53:DX:64:SER:HA	53:DX:162:VAL:HG13	1.89	0.54
61:FO:41:ARG:HD2	65:Fi:30:ALA:HB2	1.89	0.54
67:IB:418:ARG:NH1	67:IB:440:THR:O	2.40	0.54
1:CA:110:U:O4	1:CA:111:A:N6	2.41	0.54
4:CF:30:TYR:OH	19:Cd:151:VAL:O	2.26	0.54
5:CH:122:THR:HG23	5:CH:125:LYS:H	1.73	0.54
6:CI:313:ASP:HB3	6:CI:316:LYS:HB3	1.89	0.54
14:CR:74:GLU:OE1	41:DL:231:TRP:NE1	2.33	0.54
17:Ca:328:LEU:HB3	33:DD:776:ALA:HB2	1.90	0.54
33:DD:614:ALA:O	33:DD:618:LYS:HG2	2.07	0.54
38:DI:222:ASP:OD2	38:DI:235:SER:OG	2.26	0.54
42:DM:63:VAL:HB	42:DM:72:ARG:HB2	1.89	0.54
49:DT:133:ASP:HA	49:DT:158:HIS:HB2	1.90	0.54
52:DW:91:ASP:OD1	52:DW:94:ARG:NH2	2.41	0.54
63:Fg:304:ALA:HB2	63:Fg:312:THR:HG21	1.89	0.54
65:Fi:409:LEU:HD23	65:Fi:414:VAL:HG13	1.89	0.54
14:CR:104:ASP:OD2	14:CR:108:LYS:NZ	2.34	0.54
17:Ca:45:THR:OG1	17:Ca:50:VAL:O	2.25	0.54
24:Cm:175:LEU:HD21	29:Cv:54:ASN:HD21	1.72	0.54
27:Cq:246:CYS:SG	27:Cq:247:ASN:N	2.80	0.54
31:DB:456:LEU:HD21	31:DB:462:ASP:HB2	1.90	0.54
31:DB:1111:GLN:NE2	35:DF:94:ASP:O	2.41	0.54
34:DE:612:HIS:HD1	40:DK:112:TRP:HD1	1.56	0.54
42:DM:9:GLU:OE1	42:DM:262:ARG:NH1	2.41	0.54
58:F6:403:LEU:HD22	58:F6:415:VAL:HG11	1.90	0.54
62:Ff:590:LEU:HD21	62:Ff:680:TYR:HB3	1.89	0.54
63:Fg:10:VAL:HG21	63:Fg:517:PHE:HE2	1.73	0.54
1:CA:242:G:OP1	64:Fh:48:SER:OG	2.26	0.53
1:CA:273:A:H5''	33:DD:17:ALA:HB2	1.88	0.53
3:CE:105:GLN:N	3:CE:105:GLN:OE1	2.40	0.53
17:Ca:256:GLU:HB2	43:DN:223:GLN:HA	1.89	0.53
30:DA:224:VAL:HG11	30:DA:287:HIS:HB3	1.91	0.53
30:DA:443:LEU:HD23	30:DA:443:LEU:H	1.73	0.53
30:DA:482:LYS:HE3	30:DA:492:ASN:HD22	1.73	0.53
32:DC:1136:GLU:OE2	37:DH:3:SER:OG	2.24	0.53
36:DG:489:LEU:HD23	36:DG:540:VAL:HG12	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:DU:106:PRO:HG2	50:DU:109:SER:HB3	1.91	0.53
58:F6:252:PHE:HB3	58:F6:264:PRO:HD3	1.90	0.53
1:CA:234:C:N4	1:CA:244:G:O2'	2.40	0.53
3:CE:423:GLY:O	3:CE:426:THR:OG1	2.23	0.53
20:Cg:285:VAL:HB	20:Cg:355:THR:HG22	1.89	0.53
24:Cm:92:GLN:HG3	24:Cm:93:LEU:H	1.73	0.53
30:DA:1305:PRO:HG2	30:DA:1308:LEU:HB2	1.89	0.53
32:DC:179:TRP:NE1	32:DC:201:SER:O	2.29	0.53
65:Fi:337:VAL:HG13	65:Fi:354:ALA:HA	1.89	0.53
7:CJ:202:ASP:HB3	7:CJ:205:VAL:HG12	1.89	0.53
17:Ca:241:LEU:HD22	67:IB:739:GLN:HG3	1.91	0.53
35:DF:461:PHE:H	35:DF:466:ASP:HA	1.74	0.53
37:DH:325:MET:HE3	37:DH:374:GLU:HG2	1.89	0.53
45:DP:119:LEU:HD23	45:DP:153:VAL:HG23	1.90	0.53
49:DT:93:MET:HE1	49:DT:102:TRP:HE1	1.73	0.53
67:IB:333:ASP:OD2	67:IB:524:ARG:NH2	2.42	0.53
8:CK:195:LEU:HB2	8:CK:277:LEU:HD11	1.91	0.53
11:CO:414:LEU:HD11	11:CO:421:TRP:HB2	1.90	0.53
15:CS:107:LYS:HD2	53:DX:37:LYS:HD3	1.91	0.53
15:CS:182:HIS:CD2	35:DF:91:TYR:HB2	2.44	0.53
29:Cv:673:LEU:HD21	44:DO:111:ARG:HE	1.73	0.53
31:DB:514:ARG:HD3	31:DB:851:ILE:HD12	1.90	0.53
33:DD:588:ARG:NE	33:DD:627:TYR:OH	2.41	0.53
34:DE:704:LEU:HD23	40:DK:112:TRP:HZ3	1.73	0.53
59:F7:135:ASP:OD1	59:F7:135:ASP:N	2.41	0.53
61:FO:13:LEU:HB2	61:FO:46:HIS:HE2	1.72	0.53
63:Fg:162:VAL:HA	63:Fg:165:ARG:HG2	1.90	0.53
11:CO:245:ASN:HB2	11:CO:248:ILE:HB	1.89	0.53
22:Cj:226:LYS:HD2	22:Cj:233:ASP:HB2	1.90	0.53
23:Ck:168:GLU:OE2	23:Ck:189:TRP:NE1	2.36	0.53
23:Ck:268:LEU:HD21	23:Ck:330:ILE:HD11	1.91	0.53
23:Ck:686:LYS:HA	23:Ck:691:GLN:HB2	1.91	0.53
31:DB:553:LEU:O	31:DB:567:ARG:NH1	2.41	0.53
31:DB:981:HIS:HD2	31:DB:983:LEU:HB2	1.74	0.53
33:DD:248:ASP:HB3	33:DD:249:PRO:HD3	1.89	0.53
34:DE:707:ARG:NH1	37:DH:166:GLN:OE1	2.42	0.53
49:DT:83:ILE:HD12	49:DT:99:HIS:HB2	1.91	0.53
50:DU:84:PHE:HD2	50:DU:127:LEU:HD13	1.74	0.53
50:DU:92:SER:OG	50:DU:211:ARG:O	2.26	0.53
50:DU:209:GLU:OE2	50:DU:211:ARG:NH2	2.41	0.53
65:Fi:312:LYS:HB3	65:Fi:313:PRO:HD3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:IA:261:HIS:HB3	66:IA:264:PHE:HD2	1.73	0.53
1:CA:455:G:H2'	41:DL:268:VAL:HG22	1.90	0.53
7:CJ:554:THR:HG23	7:CJ:557:GLU:H	1.73	0.53
21:CI:96:ASN:HD21	23:CK:697:MET:HA	1.74	0.53
28:CR:114:LEU:HD12	28:CR:115:PRO:HD2	1.90	0.53
31:DB:231:ASP:OD1	31:DB:232:ARG:N	2.41	0.53
31:DB:1126:PRO:HB3	31:DB:1149:MET:HE2	1.91	0.53
32:DC:464:THR:HG22	32:DC:473:GLN:HG3	1.91	0.53
48:DS:74:ARG:NH2	48:DS:104:SER:OG	2.42	0.53
55:DZ:73:HIS:HA	55:DZ:76:TYR:CE2	2.44	0.53
58:F6:398:SER:O	58:F6:402:HIS:ND1	2.41	0.53
66:IA:701:ARG:HH12	66:IA:713:LEU:HD22	1.74	0.53
1:CA:160:U:H5'	50:DU:207:ARG:HD3	1.89	0.53
10:CN:23:HIS:HA	10:CN:26:LEU:HD13	1.91	0.53
12:CP:182:ARG:NH1	33:DD:224:GLU:OE1	2.40	0.53
13:CQ:235:ARG:HD3	57:F3:58:VAL:HG21	1.90	0.53
23:CK:684:GLN:HG3	23:CK:685:TYR:H	1.74	0.53
29:CV:434:SER:HB2	29:CV:480:ALA:HB2	1.89	0.53
31:DB:1168:ASP:O	31:DB:1170:GLN:NE2	2.41	0.53
47:DR:157:LEU:HG	47:DR:159:GLY:H	1.74	0.53
58:F6:416:ASP:HB3	58:F6:452:VAL:HG23	1.91	0.53
60:F9:481:PHE:HB3	60:F9:484:ASN:HD22	1.74	0.53
60:F9:533:ASP:HB3	66:IA:496:ARG:HH12	1.73	0.53
61:FO:129:SER:O	61:FO:164:ARG:NH1	2.41	0.53
62:Ff:668:GLU:HG2	62:Ff:674:TYR:CE1	2.44	0.53
63:Fg:415:LEU:HD23	63:Fg:491:VAL:HG13	1.91	0.53
66:IA:164:THR:H	66:IA:464:PHE:HE2	1.57	0.53
67:IB:667:ASP:O	67:IB:671:MET:HG2	2.09	0.53
6:CI:134:TYR:N	14:CR:226:GLU:OE2	2.41	0.53
8:CK:201:ARG:NH1	16:CU:79:TYR:OH	2.42	0.53
18:Cb:135:ARG:O	29:CV:755:HIS:ND1	2.42	0.53
20:Cg:435:SER:O	20:Cg:440:LYS:NZ	2.39	0.53
23:CK:374:ARG:HH12	31:DB:635:MET:HG3	1.73	0.53
29:CV:439:ASP:HB2	29:CV:442:ASN:HD21	1.74	0.53
30:DA:1192:LEU:HD22	30:DA:1221:ILE:HD12	1.91	0.53
48:DS:96:TRP:NE1	48:DS:107:LYS:O	2.37	0.53
61:FO:21:ARG:HH12	63:Fg:320:PRO:HD3	1.73	0.53
62:Ff:617:TRP:CD2	62:Ff:652:LEU:HD12	2.44	0.53
66:IA:75:VAL:HB	66:IA:79:VAL:HG21	1.90	0.53
66:IA:78:TYR:HB2	67:IB:517:GLY:HA2	1.89	0.53
66:IA:468:MET:HA	66:IA:471:VAL:HG12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:17:G:H1'	1:CA:29:A:H1'	1.89	0.53
1:CA:115:A:O2'	46:DQ:14:ARG:NH2	2.40	0.53
3:CE:350:LYS:NZ	3:CE:351:ASP:OD2	2.41	0.53
7:CJ:130:ARG:NH1	23:Ck:712:CYS:SG	2.81	0.53
9:CL:59:MET:HB3	9:CL:62:LEU:HD12	1.91	0.53
29:Cv:390:ARG:HD2	29:Cv:943:LEU:HD13	1.91	0.53
30:DA:737:LYS:NZ	30:DA:738:GLY:O	2.34	0.53
31:DB:72:TRP:O	31:DB:76:MET:HG2	2.09	0.53
31:DB:562:GLN:HE21	35:DF:571:LEU:HG	1.74	0.53
31:DB:569:HIS:CE1	31:DB:648:ARG:HH22	2.27	0.53
32:DC:76:ASN:OD1	32:DC:1064:GLN:NE2	2.34	0.53
33:DD:154:ILE:HG22	33:DD:156:GLN:H	1.73	0.53
38:DI:63:TRP:HH2	38:DI:90:LEU:HD12	1.74	0.53
57:F3:100:GLU:HG3	57:F3:109:PRO:HD2	1.90	0.53
62:Ff:463:THR:N	62:Ff:466:GLU:OE1	2.37	0.53
4:CF:3:PHE:HB3	4:CF:70:ASP:HA	1.89	0.53
7:CJ:274:GLN:O	7:CJ:277:GLU:HG3	2.09	0.53
7:CJ:355:HIS:NE2	31:DB:914:GLU:OE2	2.42	0.53
7:CJ:603:CYS:SG	35:DF:208:ARG:NH2	2.82	0.53
8:CK:101:ASN:O	8:CK:105:GLN:NE2	2.42	0.53
15:CS:171:PHE:HB3	15:CS:197:ILE:HD11	1.91	0.53
25:Cn:204:LEU:HD12	25:Cn:205:PRO:HD2	1.91	0.53
26:Cp:171:MET:N	26:Cp:171:MET:SD	2.82	0.53
28:Cr:63:GLU:HG3	28:Cr:65:LYS:HG2	1.91	0.53
29:Cv:1012:TRP:HH2	42:DM:236:MET:HE3	1.74	0.53
32:DC:1110:HIS:CE1	32:DC:1120:PRO:HD2	2.44	0.53
34:DE:568:SER:HB3	34:DE:571:ASP:HB2	1.91	0.53
35:DF:314:TYR:HB2	35:DF:345:LEU:HD12	1.91	0.53
37:DH:526:ASN:HD21	37:DH:529:TYR:HA	1.74	0.53
50:DU:184:THR:OG1	50:DU:187:ASP:OD1	2.23	0.53
52:DW:54:GLU:OE2	54:DY:111:ARG:NH2	2.37	0.53
58:F6:571:PRO:HA	62:Ff:735:VAL:HG23	1.91	0.53
59:F7:260:LEU:HD22	59:F7:290:MET:HB2	1.91	0.53
67:IB:335:TYR:HE2	67:IB:524:ARG:HE	1.56	0.53
67:IB:580:VAL:HG12	67:IB:589:CYS:HB2	1.91	0.53
1:CA:460:U:H4'	1:CA:461:A:H5'	1.90	0.52
1:CA:576:A:H5'	64:Fh:43:THR:HG21	1.90	0.52
4:CF:37:ARG:H	4:CF:69:LEU:HA	1.73	0.52
13:CQ:143:ASP:OD1	13:CQ:168:ASN:N	2.42	0.52
20:Cg:110:LEU:HD21	20:Cg:408:GLU:HB3	1.90	0.52
26:Cp:55:ASN:OD1	26:Cp:56:HIS:ND1	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:DO:94:ILE:HA	44:DO:99:LEU:HD23	1.90	0.52
51:DV:46:PRO:HB2	51:DV:49:ASP:HB3	1.91	0.52
52:DW:94:ARG:NH1	52:DW:156:THR:O	2.42	0.52
59:F7:348:THR:O	59:F7:352:GLU:HG2	2.09	0.52
63:Fg:229:ASN:N	63:Fg:229:ASN:OD1	2.42	0.52
63:Fg:232:ILE:HD11	63:Fg:516:MET:HA	1.91	0.52
63:Fg:280:LEU:HA	63:Fg:283:LYS:HG2	1.91	0.52
65:Fi:333:ALA:H	65:Fi:356:HIS:CE1	2.27	0.52
67:IB:187:ARG:HA	67:IB:190:ILE:HG22	1.91	0.52
7:CJ:148:ASN:ND2	7:CJ:151:ASN:OD1	2.42	0.52
7:CJ:460:HIS:O	7:CJ:465:SER:OG	2.26	0.52
17:Ca:334:VAL:HG13	17:Ca:501:ARG:HB3	1.91	0.52
29:Cv:260:MET:HG2	29:Cv:297:GLU:HG3	1.91	0.52
31:DB:521:LEU:HD22	31:DB:663:VAL:HG23	1.91	0.52
32:DC:761:ASN:OD1	32:DC:761:ASN:N	2.41	0.52
40:DK:300:LYS:NZ	49:DT:106:ASP:OD2	2.28	0.52
60:F9:483:LEU:HD11	60:F9:496:ALA:HB2	1.90	0.52
65:Fi:97:CYS:SG	65:Fi:205:HIS:ND1	2.81	0.52
1:CA:331:A:H5'	1:CA:332:U:C6	2.44	0.52
1:CA:358:U:H5'	24:Cm:206:GLY:H	1.75	0.52
4:CF:34:GLY:HA2	11:CO:193:MET:HE1	1.92	0.52
7:CJ:437:ARG:HB3	23:Ck:674:LEU:HD23	1.90	0.52
15:CS:169:LYS:H	35:DF:88:LEU:HD11	1.74	0.52
17:Ca:109:SER:HB3	17:Ca:112:LEU:HD21	1.91	0.52
17:Ca:421:TYR:HB2	17:Ca:480:LEU:HD13	1.90	0.52
22:Cj:160:PRO:HB2	47:DR:108:GLN:HE21	1.74	0.52
29:Cv:376:ARG:HH12	29:Cv:380:ARG:HH11	1.56	0.52
31:DB:1079:TRP:NE1	35:DF:226:THR:O	2.38	0.52
35:DF:284:ARG:NH1	35:DF:332:GLU:OE2	2.42	0.52
35:DF:535:ARG:HG3	37:DH:227:ASP:HB2	1.92	0.52
44:DO:99:LEU:HD11	44:DO:109:VAL:HB	1.91	0.52
45:DP:202:LEU:HD23	45:DP:202:LEU:H	1.74	0.52
46:DQ:79:LEU:HB2	46:DQ:83:ASN:ND2	2.24	0.52
47:DR:91:THR:O	47:DR:178:TYR:OH	2.17	0.52
48:DS:93:ARG:NH2	48:DS:106:ARG:O	2.42	0.52
52:DW:70:LEU:HA	54:DY:117:LEU:HD21	1.91	0.52
60:F9:350:ARG:O	60:F9:354:MET:HG2	2.10	0.52
1:CA:107:U:O2'	13:CQ:103:MET:SD	2.68	0.52
7:CJ:44:PHE:HZ	41:DL:289:ARG:HG2	1.73	0.52
14:CR:205:VAL:HG23	16:CU:112:MET:HE2	1.91	0.52
29:Cv:569:LEU:O	29:Cv:573:GLU:HG2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:DA:238:VAL:HG21	30:DA:281:MET:HE1	1.91	0.52
30:DA:373:GLN:HB3	30:DA:376:LYS:HB3	1.91	0.52
32:DC:332:GLN:HG3	32:DC:397:TYR:HB3	1.90	0.52
33:DD:393:VAL:HG21	33:DD:441:LEU:HG	1.91	0.52
48:DS:182:TYR:OH	48:DS:189:ARG:NH2	2.37	0.52
59:F7:493:VAL:O	59:F7:528:LYS:NZ	2.35	0.52
61:FO:19:MET:O	61:FO:23:THR:OG1	2.16	0.52
1:CA:499:U:O2'	51:DV:48:HIS:ND1	2.24	0.52
2:CC:21:LYS:HB3	2:CC:25:LEU:HD12	1.92	0.52
3:CE:215:VAL:HG13	3:CE:226:LEU:HB3	1.91	0.52
5:CH:144:ARG:NH1	56:Da:38:ASP:OD2	2.42	0.52
8:CK:256:PRO:HD3	58:F6:570:ARG:HH22	1.74	0.52
10:CN:88:ARG:HH12	15:CS:130:ILE:HD13	1.74	0.52
13:CQ:233:ARG:HH12	61:FO:14:ARG:HH11	1.56	0.52
15:CS:217:LYS:O	53:DX:50:ARG:NH1	2.42	0.52
17:Ca:511:ILE:HD13	55:DZ:50:MET:HB2	1.92	0.52
23:Ck:391:ALA:HA	23:Ck:394:ASN:HD21	1.75	0.52
31:DB:81:PHE:O	31:DB:154:ARG:NH1	2.42	0.52
46:DQ:73:HIS:HB3	46:DQ:248:LEU:HD11	1.91	0.52
54:DY:32:TRP:O	54:DY:37:ARG:NH2	2.28	0.52
66:IA:143:ARG:HH12	66:IA:487:GLN:HG2	1.75	0.52
1:CA:547:U:OP1	64:Fh:45:ARG:NH1	2.42	0.52
7:CJ:542:LYS:HD3	7:CJ:544:THR:H	1.75	0.52
9:CL:120:ILE:HB	9:CL:137:ARG:HB2	1.92	0.52
21:Ci:28:ALA:HB3	23:Ck:785:PRO:HA	1.91	0.52
25:Cn:200:ARG:NH1	65:Fi:462:GLU:OE2	2.43	0.52
32:DC:1018:ASP:OD1	32:DC:1018:ASP:N	2.43	0.52
33:DD:296:LEU:HD13	33:DD:392:SER:HB2	1.92	0.52
41:DL:219:GLN:HA	41:DL:222:VAL:HG22	1.91	0.52
45:DP:35:ILE:HD11	45:DP:44:GLU:HB2	1.92	0.52
60:F9:501:ALA:O	60:F9:505:THR:OG1	2.27	0.52
61:FO:79:GLY:HA2	61:FO:82:TYR:HD2	1.75	0.52
66:IA:277:LEU:HD22	66:IA:364:ALA:HB2	1.90	0.52
14:CR:28:GLY:O	18:Cb:91:ARG:NH2	2.43	0.52
17:Ca:197:HIS:CE1	17:Ca:201:ARG:HG3	2.45	0.52
17:Ca:347:ARG:HE	43:DN:237:ARG:HH21	1.58	0.52
21:Ci:109:ASN:HB3	21:Ci:112:ASN:HB2	1.92	0.52
22:Cj:233:ASP:OD2	26:Cp:50:THR:OG1	2.27	0.52
31:DB:445:ASN:ND2	31:DB:448:ASP:OD2	2.38	0.52
32:DC:425:ALA:O	32:DC:428:GLU:HG3	2.10	0.52
35:DF:358:MET:HA	35:DF:361:ALA:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:DL:102:SER:HB3	41:DL:105:ARG:HG2	1.90	0.52
62:Ff:232:GLU:HG2	62:Ff:431:ARG:HH21	1.74	0.52
63:Fg:14:GLN:NE2	63:Fg:14:GLN:O	2.42	0.52
65:Fi:328:GLN:OE1	65:Fi:516:HIS:NE2	2.41	0.52
65:Fi:455:PRO:HG2	65:Fi:537:MET:HG3	1.91	0.52
65:Fi:562:ASN:HB3	65:Fi:566:PRO:HD3	1.91	0.52
65:Fi:571:LYS:HE2	65:Fi:576:VAL:HA	1.90	0.52
1:CA:138:U:O4	33:DD:52:LYS:NZ	2.43	0.52
7:CJ:464:PHE:HB3	7:CJ:468:LEU:HD23	1.92	0.52
10:CN:30:LEU:HD12	35:DF:122:LEU:HD13	1.91	0.52
14:CR:117:SER:HB2	14:CR:120:VAL:HG23	1.92	0.52
14:CR:256:PRO:HA	14:CR:260:PRO:HB3	1.92	0.52
17:Ca:518:GLU:OE1	17:Ca:518:GLU:N	2.43	0.52
24:Cm:81:GLN:HE22	24:Cm:144:ASN:HD22	1.58	0.52
29:Cv:728:ILE:HG21	29:Cv:786:VAL:HG21	1.91	0.52
30:DA:1046:HIS:NE2	41:DL:137:ARG:O	2.36	0.52
30:DA:1163:MET:SD	30:DA:1163:MET:N	2.74	0.52
36:DG:616:ARG:HH21	36:DG:627:TRP:HE1	1.57	0.52
61:FO:72:GLU:HB2	65:Fi:20:LEU:HD23	1.92	0.52
62:Ff:639:PHE:HB2	62:Ff:645:ARG:HH22	1.74	0.52
63:Fg:306:LYS:HZ3	63:Fg:307:TYR:HE2	1.58	0.52
65:Fi:528:MET:HA	65:Fi:532:SER:HB3	1.91	0.52
66:IA:259:PRO:HD2	66:IA:267:MET:HB3	1.91	0.52
1:CA:466:G:H1	8:CK:10:ARG:HH22	1.58	0.52
2:CC:23:ILE:HD11	32:DC:1144:PRO:HB2	1.90	0.52
5:CH:19:LEU:HA	43:DN:51:GLY:HA3	1.91	0.52
5:CH:176:ILE:HG13	5:CH:177:GLU:N	2.24	0.52
7:CJ:246:LYS:HB2	7:CJ:432:HIS:HB2	1.90	0.52
8:CK:45:PHE:HE2	20:Cg:473:ARG:HB3	1.74	0.52
8:CK:275:VAL:HG13	8:CK:302:PHE:HA	1.91	0.52
8:CK:304:VAL:HG22	16:CU:48:VAL:HG11	1.92	0.52
10:CN:164:SER:OG	23:Ck:747:LYS:NZ	2.32	0.52
11:CO:298:GLY:HA2	13:CQ:99:VAL:HG11	1.90	0.52
20:Cg:365:ASP:N	20:Cg:365:ASP:OD1	2.42	0.52
21:Ci:76:MET:HB3	51:DV:88:VAL:HG23	1.92	0.52
23:Ck:287:GLU:O	23:Ck:293:ARG:NH2	2.43	0.52
29:Cv:254:ARG:NH2	29:Cv:510:GLU:OE2	2.43	0.52
32:DC:270:LEU:HD13	32:DC:437:LEU:HG	1.92	0.52
37:DH:2:LEU:HG	37:DH:4:GLN:H	1.75	0.52
37:DH:431:ASN:HD22	41:DL:65:PRO:HD3	1.75	0.52
37:DH:474:ASP:OD1	37:DH:475:ASP:N	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:DS:234:LEU:HD23	48:DS:236:LEU:HD11	1.92	0.52
58:F6:550:PRO:HG2	62:Ff:773:THR:HG21	1.91	0.52
59:F7:624:PRO:HA	59:F7:627:LEU:HD12	1.91	0.52
3:CE:208:GLN:HB3	3:CE:212:MET:HE2	1.91	0.52
3:CE:305:GLU:CD	3:CE:308:ARG:HH12	2.18	0.52
7:CJ:539:LEU:HD12	7:CJ:540:PRO:HD2	1.92	0.52
9:CL:80:PRO:HD3	9:CL:88:ARG:HG2	1.91	0.52
10:CN:142:HIS:CD2	10:CN:154:LYS:HG3	2.45	0.52
14:CR:116:PRO:HB2	14:CR:120:VAL:HB	1.91	0.52
17:Ca:459:LEU:HD11	33:DD:114:CYS:HA	1.91	0.52
20:Cg:409:TYR:OH	20:Cg:441:LEU:O	2.27	0.52
22:Cj:206:LEU:HD21	33:DD:619:ARG:HD3	1.92	0.52
28:Cr:114:LEU:HD21	28:Cr:129:MET:HG2	1.92	0.52
30:DA:333:VAL:HG22	55:DZ:63:LEU:HB3	1.91	0.52
37:DH:233:MET:HE1	37:DH:244:THR:HG21	1.91	0.52
39:DJ:132:ARG:NH1	79:DJ:401:UTP:O2B	2.43	0.52
44:DO:85:LYS:HD2	44:DO:88:GLN:HE21	1.74	0.52
53:DX:35:ARG:NH1	67:IB:350:THR:OG1	2.39	0.52
65:Fi:17:THR:OG1	65:Fi:21:ARG:NH1	2.43	0.52
1:CA:100:G:O6	56:Da:28:ARG:NH2	2.43	0.51
1:CA:471:U:O2'	7:CJ:378:SER:OG	2.27	0.51
7:CJ:114:TYR:HA	7:CJ:117:TYR:HD2	1.75	0.51
7:CJ:293:ASP:OD1	7:CJ:293:ASP:N	2.21	0.51
7:CJ:770:THR:HG1	21:Ci:11:GLY:N	2.07	0.51
8:CK:70:ILE:HD11	18:Cb:189:LYS:HD2	1.92	0.51
20:Cg:84:GLU:OE1	20:Cg:87:GLN:NE2	2.43	0.51
26:Cp:66:HIS:HB2	26:Cp:69:ARG:CZ	2.40	0.51
30:DA:820:ASN:O	30:DA:820:ASN:ND2	2.35	0.51
30:DA:864:ASP:N	30:DA:864:ASP:OD1	2.43	0.51
32:DC:896:SER:OG	32:DC:899:GLN:OE1	2.27	0.51
32:DC:1080:TYR:CE2	34:DE:579:ARG:HG3	2.41	0.51
33:DD:788:ASP:O	43:DN:242:TRP:NE1	2.31	0.51
37:DH:42:ARG:NE	39:DJ:229:ASP:OD2	2.43	0.51
39:DJ:213:GLU:OE2	39:DJ:246:THR:OG1	2.28	0.51
48:DS:119:CYS:HB3	48:DS:122:CYS:HB2	1.91	0.51
49:DT:138:SER:O	49:DT:165:GLY:HA3	2.10	0.51
58:F6:613:THR:O	58:F6:617:THR:OG1	2.24	0.51
59:F7:496:ILE:HG13	59:F7:499:ILE:HD12	1.92	0.51
3:CE:155:SER:HB3	3:CE:158:ASP:HB3	1.91	0.51
6:CI:5:LEU:N	36:DG:567:GLU:OE2	2.38	0.51
7:CJ:238:ILE:HD13	7:CJ:354:PRO:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CQ:224:PHE:HA	59:F7:87:PRO:HG2	1.91	0.51
17:Ca:514:THR:O	17:Ca:519:GLN:NE2	2.42	0.51
27:Cq:61:ASN:O	30:DA:1056:ARG:NH1	2.43	0.51
27:Cq:154:LEU:HD23	27:Cq:170:VAL:HG21	1.92	0.51
29:Cv:679:PRO:HA	29:Cv:698:PHE:O	2.11	0.51
31:DB:680:VAL:HG12	31:DB:707:GLN:HB3	1.91	0.51
32:DC:1115:ARG:NH2	39:DJ:222:GLU:OE2	2.43	0.51
33:DD:478:GLN:OE1	33:DD:479:ARG:NH2	2.43	0.51
39:DJ:30:TRP:NE1	39:DJ:35:PRO:O	2.41	0.51
58:F6:473:ASP:HB3	58:F6:476:ALA:HB3	1.91	0.51
64:Fh:234:ASP:O	66:IA:192:TYR:OH	2.28	0.51
67:IB:334:ALA:HB2	67:IB:563:GLU:HG3	1.93	0.51
6:CI:22:LEU:HD11	7:CJ:166:ALA:HB2	1.93	0.51
7:CJ:361:VAL:HG22	7:CJ:401:ILE:HG12	1.92	0.51
8:CK:177:SER:O	14:CR:181:ARG:NH1	2.43	0.51
11:CO:170:ARG:HH11	11:CO:194:MET:HA	1.75	0.51
12:CP:86:ARG:HD3	48:DS:130:VAL:HG21	1.93	0.51
29:Cv:590:THR:O	29:Cv:787:LYS:NZ	2.36	0.51
31:DB:426:HIS:HB3	31:DB:432:ARG:HG2	1.91	0.51
31:DB:1179:VAL:HG12	31:DB:1181:LEU:H	1.75	0.51
47:DR:46:PRO:O	47:DR:49:GLU:HG3	2.11	0.51
47:DR:191:GLN:NE2	50:DU:137:ASP:O	2.44	0.51
52:DW:60:VAL:HG11	54:DY:111:ARG:HE	1.74	0.51
58:F6:654:GLU:OE1	58:F6:657:ASN:ND2	2.43	0.51
59:F7:386:PHE:CD2	59:F7:410:LEU:HB3	2.45	0.51
63:Fg:515:ASP:HA	63:Fg:518:LYS:HG2	1.92	0.51
11:CO:291:ASN:HD21	56:Da:40:ARG:HH12	1.59	0.51
12:CP:155:ASP:HB3	12:CP:158:VAL:HG22	1.91	0.51
13:CQ:47:LYS:HB2	13:CQ:50:ALA:HB3	1.92	0.51
17:Ca:337:ARG:HD3	17:Ca:344:GLY:H	1.76	0.51
27:Cq:184:ARG:NH2	27:Cq:232:THR:O	2.43	0.51
31:DB:612:THR:HA	31:DB:615:ASN:HD21	1.76	0.51
47:DR:130:ASP:HB2	47:DR:132:ARG:HD3	1.91	0.51
56:Da:22:ARG:NH1	56:Da:26:ASP:OD1	2.43	0.51
65:Fi:567:THR:O	65:Fi:570:ARG:NH2	2.43	0.51
67:IB:178:LEU:HD23	67:IB:178:LEU:H	1.76	0.51
6:CI:293:ARG:NE	36:DG:59:LEU:O	2.37	0.51
13:CQ:35:HIS:CD2	64:Fh:283:ARG:HH22	2.29	0.51
18:Cb:300:TYR:OH	28:Cr:267:GLN:NE2	2.44	0.51
27:Cq:9:TYR:HB3	42:DM:272:GLN:HB2	1.93	0.51
29:Cv:584:SER:OG	29:Cv:790:THR:OG1	2.28	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Cv:895:VAL:HG23	29:Cv:896:PHE:HD2	1.75	0.51
29:Cv:959:LEU:HD13	33:DD:747:MET:HG3	1.92	0.51
32:DC:329:LYS:HG3	32:DC:333:MET:HE3	1.93	0.51
37:DH:466:VAL:HG23	37:DH:487:ARG:HG3	1.92	0.51
38:DI:52:GLU:OE2	38:DI:165:ARG:NE	2.36	0.51
38:DI:337:SER:OG	38:DI:338:GLU:OE1	2.17	0.51
65:Fi:318:ARG:O	65:Fi:322:ILE:HG12	2.11	0.51
1:CA:416:U:O4	10:CN:12:HIS:N	2.39	0.51
3:CE:21:MET:HG3	43:DN:233:GLY:HA2	1.93	0.51
5:CH:232:TRP:CE2	5:CH:277:GLY:HA3	2.45	0.51
14:CR:265:ARG:NH1	54:DY:69:HIS:O	2.43	0.51
27:Cq:20:GLN:H	42:DM:280:ARG:HH22	1.58	0.51
29:Cv:505:TRP:HB2	41:DL:173:PRO:HB3	1.92	0.51
30:DA:1495:LEU:HG	30:DA:1605:ARG:HG3	1.92	0.51
32:DC:823:ILE:HG22	32:DC:850:PHE:HZ	1.74	0.51
33:DD:221:GLU:HA	33:DD:402:GLN:HE22	1.76	0.51
35:DF:380:LEU:HD23	35:DF:380:LEU:H	1.75	0.51
38:DI:180:GLU:O	38:DI:183:THR:OG1	2.29	0.51
39:DJ:208:GLY:HA3	39:DJ:240:ILE:HG22	1.93	0.51
57:F3:66:ARG:HB2	63:Fg:306:LYS:HG3	1.92	0.51
61:FO:131:ASP:HA	61:FO:164:ARG:HD3	1.93	0.51
63:Fg:8:ALA:HB2	63:Fg:501:VAL:HG11	1.92	0.51
8:CK:288:ARG:NH1	16:CU:62:MET:SD	2.84	0.51
17:Ca:219:ALA:HA	17:Ca:222:GLN:HB2	1.92	0.51
17:Ca:276:SER:HB3	30:DA:912:LEU:HD12	1.93	0.51
23:Ck:167:PHE:HD1	23:Ck:171:VAL:HB	1.76	0.51
24:Cm:86:GLY:O	24:Cm:92:GLN:NE2	2.44	0.51
29:Cv:619:THR:HG21	44:DO:105:ARG:HH12	1.74	0.51
31:DB:565:ASP:OD1	31:DB:566:THR:N	2.43	0.51
32:DC:123:PHE:HE2	32:DC:534:LEU:HB3	1.75	0.51
32:DC:635:MET:HG3	32:DC:636:GLU:HG2	1.93	0.51
33:DD:401:LEU:HD11	33:DD:464:VAL:HA	1.92	0.51
33:DD:576:MET:SD	47:DR:221:ARG:NH2	2.81	0.51
33:DD:606:ARG:HH12	47:DR:222:LEU:HA	1.76	0.51
35:DF:488:LYS:HA	35:DF:491:ARG:HD3	1.93	0.51
35:DF:490:ASN:O	35:DF:494:GLU:HG2	2.10	0.51
37:DH:25:LYS:NZ	37:DH:418:LYS:O	2.41	0.51
44:DO:162:ALA:HB2	44:DO:253:PRO:HA	1.93	0.51
46:DQ:27:HIS:CD2	50:DU:55:SER:HB2	2.45	0.51
59:F7:253:THR:HA	59:F7:256:PHE:HD2	1.76	0.51
60:F9:267:ARG:NH1	66:IA:146:PRO:O	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:F9:548:VAL:HG11	60:F9:560:TYR:HB2	1.92	0.51
62:Ff:300:ILE:HD12	62:Ff:329:ILE:HD13	1.93	0.51
63:Fg:257:PHE:O	63:Fg:261:SER:OG	2.25	0.51
1:CA:598:U:O4	1:CA:599:A:N6	2.43	0.51
3:CE:15:TRP:HA	3:CE:18:LYS:HE3	1.93	0.51
18:Cb:282:SER:HB3	18:Cb:285:GLN:HG3	1.93	0.51
22:Cj:155:GLU:OE2	33:DD:619:ARG:NH2	2.44	0.51
29:Cv:263:GLU:HB3	29:Cv:268:GLN:HA	1.93	0.51
30:DA:1265:SER:OG	30:DA:1302:PHE:O	2.25	0.51
31:DB:618:LEU:HD23	31:DB:652:ARG:HE	1.76	0.51
32:DC:30:THR:OG1	49:DT:44:ARG:NH1	2.43	0.51
32:DC:73:ARG:NH2	40:DK:253:GLU:OE2	2.43	0.51
32:DC:467:THR:OG1	32:DC:472:ARG:NH2	2.43	0.51
35:DF:247:LEU:HD22	35:DF:278:ALA:HA	1.92	0.51
59:F7:577:VAL:HG22	59:F7:590:VAL:HG13	1.92	0.51
60:F9:482:PRO:HA	60:F9:485:LEU:HG	1.93	0.51
17:Ca:65:ARG:NH2	17:Ca:70:ASP:OD1	2.44	0.51
20:Cg:159:MET:HE3	20:Cg:356:CYS:HB2	1.92	0.51
25:Cn:206:GLU:HG3	65:Fi:28:ALA:HA	1.92	0.51
30:DA:1212:TYR:OH	31:DB:999:TYR:O	2.26	0.51
31:DB:650:LEU:HD12	31:DB:845:VAL:HG12	1.93	0.51
37:DH:148:ASP:O	37:DH:152:THR:HG23	2.11	0.51
38:DI:237:ARG:NH2	38:DI:255:GLY:O	2.44	0.51
44:DO:78:GLU:HG2	44:DO:80:ALA:H	1.75	0.51
46:DQ:120:MET:N	46:DQ:120:MET:SD	2.84	0.51
55:DZ:40:ILE:HG23	55:DZ:42:TRP:HE3	1.76	0.51
59:F7:108:TYR:HA	59:F7:116:ASN:HD21	1.76	0.51
59:F7:325:PRO:O	59:F7:329:GLU:HG2	2.10	0.51
62:Ff:488:PRO:HG2	62:Ff:493:ALA:HB1	1.92	0.51
63:Fg:12:SER:HG	63:Fg:115:HIS:HE2	1.58	0.51
7:CJ:141:ASP:N	7:CJ:141:ASP:OD1	2.43	0.51
11:CO:413:LEU:HB2	11:CO:417:LYS:HB2	1.92	0.51
17:Ca:91:ASP:HA	55:DZ:11:LYS:HA	1.91	0.51
20:Cg:289:ASN:ND2	20:Cg:358:THR:O	2.42	0.51
21:Ci:39:ARG:NH2	23:Ck:773:ASP:OD1	2.39	0.51
21:Ci:120:TYR:O	21:Ci:124:VAL:HG12	2.11	0.51
31:DB:618:LEU:HD23	31:DB:652:ARG:NE	2.26	0.51
34:DE:206:LEU:HD21	34:DE:426:PHE:HE2	1.76	0.51
34:DE:228:TYR:HD2	34:DE:424:GLY:HA3	1.76	0.51
38:DI:316:PRO:HG2	38:DI:321:MET:HE1	1.91	0.51
44:DO:234:LEU:HD23	44:DO:234:LEU:H	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DP:29:TRP:O	45:DP:33:THR:HG23	2.11	0.51
52:DW:115:ASN:ND2	52:DW:118:LYS:O	2.40	0.51
58:F6:228:THR:HG1	58:F6:232:HIS:CD2	2.27	0.51
58:F6:228:THR:OG1	58:F6:232:HIS:NE2	2.32	0.51
58:F6:235:GLU:N	58:F6:235:GLU:OE1	2.43	0.51
59:F7:199:MET:HG3	59:F7:207:VAL:HG11	1.92	0.51
60:F9:260:ARG:HH11	66:IA:493:LEU:HD22	1.76	0.51
1:CA:259:U:OP2	17:Ca:589:ARG:NH1	2.43	0.50
30:DA:518:GLU:O	30:DA:522:MET:HG2	2.11	0.50
30:DA:1041:THR:O	30:DA:1041:THR:OG1	2.29	0.50
30:DA:1556:VAL:HG22	30:DA:1596:VAL:HG13	1.92	0.50
33:DD:300:GLN:HB2	33:DD:399:ILE:HG13	1.92	0.50
33:DD:431:LEU:HD11	33:DD:469:GLY:HA3	1.94	0.50
33:DD:481:ASN:OD1	33:DD:497:ARG:NH2	2.44	0.50
34:DE:603:LYS:NZ	40:DK:149:ASP:OD2	2.41	0.50
44:DO:101:PRO:HD3	44:DO:140:ARG:HG3	1.93	0.50
65:Fi:321:ARG:NH2	65:Fi:536:ASN:OD1	2.43	0.50
65:Fi:474:PRO:HB3	65:Fi:506:PHE:CE1	2.46	0.50
8:CK:298:ARG:NH2	8:CK:301:GLU:OE2	2.43	0.50
13:CQ:53:ASN:ND2	13:CQ:56:ARG:O	2.44	0.50
23:Ck:119:GLU:OE2	23:Ck:132:TYR:OH	2.28	0.50
30:DA:1168:ASP:OD1	30:DA:1171:THR:OG1	2.28	0.50
32:DC:1134:HIS:NE2	37:DH:1:MET:O	2.44	0.50
34:DE:595:PRO:HA	34:DE:598:VAL:HG12	1.92	0.50
48:DS:153:ASP:HA	48:DS:157:ARG:HD2	1.93	0.50
57:F3:111:PRO:HB2	57:F3:133:ARG:HD3	1.92	0.50
67:IB:380:GLU:OE2	67:IB:600:LYS:NZ	2.44	0.50
1:CA:105:G:O4'	57:F3:169:ARG:NH1	2.44	0.50
2:CC:29:LYS:HE3	37:DH:422:LYS:HB3	1.93	0.50
7:CJ:716:ARG:NH1	21:CI:50:PRO:HD2	2.26	0.50
13:CQ:78:TYR:HE1	33:DD:42:MET:HE1	1.76	0.50
17:Ca:496:GLU:OE2	33:DD:88:TYR:OH	2.29	0.50
18:Cb:169:LYS:HZ3	18:Cb:176:THR:HB	1.77	0.50
20:Cg:383:ASP:OD1	51:DV:100:LYS:NZ	2.44	0.50
23:Ck:737:ALA:HB1	23:Ck:740:ARG:HB2	1.93	0.50
26:Cp:54:PRO:HD2	26:Cp:58:THR:HG21	1.93	0.50
29:Cv:245:ASN:O	29:Cv:245:ASN:ND2	2.38	0.50
29:Cv:1093:ASN:HA	29:Cv:1096:THR:HG22	1.94	0.50
31:DB:493:ARG:NH2	36:DG:29:ASP:OD1	2.43	0.50
32:DC:46:ARG:HH12	32:DC:401:ARG:HH11	1.60	0.50
34:DE:33:ILE:HG23	34:DE:547:THR:HG23	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:F7:543:SER:HB3	59:F7:579:LEU:HG	1.93	0.50
60:F9:508:GLN:OE1	60:F9:508:GLN:N	2.43	0.50
62:Ff:512:ARG:NH1	62:Ff:519:THR:OG1	2.45	0.50
64:Fh:69:GLU:HB2	67:IB:753:TYR:CE1	2.47	0.50
1:CA:472:G:C8	7:CJ:379:ASP:HB3	2.47	0.50
14:CR:194:TYR:HB2	14:CR:207:HIS:CE1	2.47	0.50
22:Cj:149:TYR:CZ	22:Cj:160:PRO:HG3	2.46	0.50
27:Cq:140:ARG:HH11	27:Cq:144:THR:HG22	1.77	0.50
29:Cv:936:ASP:OD1	42:DM:56:TRP:NE1	2.34	0.50
30:DA:1168:ASP:OD1	30:DA:1168:ASP:N	2.43	0.50
32:DC:686:GLU:HA	32:DC:689:LYS:HG2	1.92	0.50
33:DD:545:ASP:O	33:DD:548:GLN:HG3	2.12	0.50
37:DH:85:LEU:HD11	37:DH:90:ARG:HG3	1.94	0.50
39:DJ:360:ASP:OD1	39:DJ:360:ASP:N	2.44	0.50
44:DO:83:ARG:HB2	44:DO:86:ARG:NH2	2.26	0.50
59:F7:82:LEU:HD23	59:F7:82:LEU:H	1.77	0.50
63:Fg:104:THR:HA	63:Fg:107:THR:HG22	1.92	0.50
14:CR:37:PRO:HD3	18:Cb:110:MET:HG3	1.93	0.50
22:Cj:66:LEU:HD23	45:DP:133:GLN:HG3	1.93	0.50
24:Cm:101:MET:HB2	58:F6:581:ASP:HB3	1.94	0.50
29:Cv:413:LYS:HA	29:Cv:435:GLU:HB2	1.94	0.50
29:Cv:1014:ARG:HD2	42:DM:227:LEU:HD11	1.92	0.50
30:DA:1134:ILE:HG12	30:DA:1140:LYS:HG2	1.94	0.50
31:DB:906:HIS:O	31:DB:912:ASN:ND2	2.35	0.50
33:DD:505:TYR:HE2	33:DD:556:VAL:HG21	1.75	0.50
35:DF:543:HIS:H	37:DH:263:SER:HB2	1.75	0.50
43:DN:74:HIS:HB2	43:DN:108:ALA:H	1.76	0.50
50:DU:83:ARG:HD2	50:DU:98:MET:SD	2.51	0.50
58:F6:662:PRO:HG3	67:IB:672:LEU:HD13	1.94	0.50
60:F9:477:TYR:OH	66:IA:445:HIS:O	2.26	0.50
1:CA:8:U:O2'	17:Ca:339:HIS:ND1	2.40	0.50
10:CN:28:SER:O	10:CN:31:MET:HG2	2.12	0.50
21:Ci:172:ILE:N	49:DT:11:ASP:OD1	2.40	0.50
26:Cp:53:VAL:HG11	26:Cp:59:PHE:HD1	1.77	0.50
26:Cp:164:ASP:OD1	26:Cp:164:ASP:N	2.42	0.50
29:Cv:465:PRO:HG2	29:Cv:553:GLU:HB2	1.93	0.50
30:DA:886:ALA:HA	43:DN:207:VAL:HG21	1.92	0.50
30:DA:1388:LEU:O	30:DA:1392:ILE:HG12	2.10	0.50
30:DA:1563:GLY:HA2	30:DA:1566:ARG:HD3	1.92	0.50
31:DB:308:PRO:HG3	34:DE:496:LEU:HD21	1.94	0.50
31:DB:341:THR:HG21	34:DE:38:GLN:HA	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DB:707:GLN:OE1	31:DB:710:ARG:NH2	2.44	0.50
33:DD:206:TRP:HD1	33:DD:282:VAL:HG21	1.77	0.50
34:DE:204:VAL:HG23	34:DE:409:TRP:HB2	1.92	0.50
34:DE:424:GLY:HA2	34:DE:428:LEU:HD13	1.93	0.50
43:DN:57:ARG:NH2	43:DN:70:GLU:OE1	2.45	0.50
51:DV:67:ASN:N	51:DV:67:ASN:OD1	2.44	0.50
57:F3:154:LEU:HG	57:F3:156:THR:HG22	1.92	0.50
66:IA:409:VAL:HG23	66:IA:414:TYR:HB3	1.94	0.50
2:CC:60:ILE:HD13	41:DL:284:PRO:HG3	1.94	0.50
6:CI:317:TYR:HE2	6:CI:386:ILE:HB	1.76	0.50
7:CJ:283:VAL:HG23	7:CJ:327:LEU:HD22	1.93	0.50
8:CK:107:GLN:NE2	8:CK:109:VAL:O	2.45	0.50
22:Cj:102:GLN:O	22:Cj:106:GLN:NE2	2.43	0.50
23:Ck:80:GLU:O	23:Ck:92:ARG:NE	2.44	0.50
31:DB:767:GLU:HA	31:DB:770:ARG:HG2	1.94	0.50
39:DJ:243:ASN:ND2	39:DJ:273:TYR:OH	2.42	0.50
45:DP:145:ARG:HE	45:DP:180:TRP:CD1	2.30	0.50
48:DS:125:LYS:HG3	48:DS:163:LEU:HD11	1.94	0.50
59:F7:241:LEU:HB3	65:Fi:361:ARG:HH21	1.76	0.50
62:Ff:392:HIS:ND1	62:Ff:393:ILE:O	2.45	0.50
62:Ff:546:TYR:OH	67:IB:597:ARG:NH2	2.40	0.50
62:Ff:566:TYR:CE2	67:IB:383:MET:HB3	2.46	0.50
64:Fh:46:HIS:HB2	64:Fh:49:LEU:HD23	1.93	0.50
67:IB:507:LYS:HB3	67:IB:538:HIS:CD2	2.46	0.50
1:CA:487:A:C2	10:CN:88:ARG:HG3	2.46	0.50
6:CI:329:HIS:ND1	6:CI:367:ASP:OD1	2.45	0.50
8:CK:234:PHE:N	8:CK:237:GLU:OE1	2.45	0.50
22:Cj:34:HIS:CD2	22:Cj:35:ARG:HG3	2.46	0.50
26:Cp:91:GLN:HA	26:Cp:94:VAL:HG22	1.94	0.50
31:DB:1052:GLU:O	37:DH:348:LYS:NZ	2.34	0.50
32:DC:136:TRP:HB3	32:DC:523:VAL:HG12	1.94	0.50
32:DC:147:ARG:HH11	32:DC:232:GLN:HB2	1.77	0.50
33:DD:350:LYS:O	33:DD:362:ASN:ND2	2.45	0.50
36:DG:248:LEU:HD11	36:DG:313:SER:HB2	1.93	0.50
41:DL:93:GLU:O	41:DL:99:GLN:NE2	2.38	0.50
43:DN:238:ASN:HD21	55:DZ:51:TYR:HB3	1.76	0.50
47:DR:126:LEU:HB2	47:DR:135:CYS:HB3	1.94	0.50
58:F6:206:ILE:HD13	58:F6:211:ILE:HG21	1.94	0.50
58:F6:596:GLU:HB3	58:F6:598:TYR:HD1	1.75	0.50
61:FO:296:GLN:HG2	63:Fg:321:ASP:HA	1.93	0.50
63:Fg:177:SER:OG	66:IA:647:THR:O	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:Fg:427:ASP:HB3	63:Fg:430:PHE:HB3	1.93	0.50
1:CA:544:U:H5''	1:CA:545:A:OP2	2.11	0.50
3:CE:235:ASN:HB3	3:CE:238:VAL:HG22	1.93	0.50
4:CF:91:MET:SD	14:CR:167:ARG:NH1	2.84	0.50
6:CI:12:HIS:CE1	6:CI:45:VAL:HG21	2.47	0.50
7:CJ:69:GLN:HA	7:CJ:82:HIS:HE1	1.76	0.50
7:CJ:288:GLN:NE2	37:DH:270:SER:OG	2.27	0.50
8:CK:111:ASN:HD22	8:CK:114:MET:HG2	1.76	0.50
28:Cr:75:ASP:OD1	28:Cr:75:ASP:N	2.45	0.50
32:DC:895:GLN:HB3	32:DC:900:ALA:HB2	1.93	0.50
33:DD:201:GLU:OE1	33:DD:235:TYR:OH	2.22	0.50
33:DD:243:GLU:HB2	33:DD:246:GLU:HG3	1.93	0.50
36:DG:454:ASP:OD1	36:DG:457:ARG:NH2	2.44	0.50
37:DH:73:LEU:HB2	37:DH:93:LEU:HD11	1.93	0.50
38:DI:305:SER:O	38:DI:311:ARG:NH1	2.42	0.50
40:DK:282:GLU:O	40:DK:285:GLU:HG3	2.12	0.50
66:IA:311:THR:HG23	66:IA:312:LYS:HG2	1.94	0.50
66:IA:755:LYS:HA	66:IA:758:ARG:HG2	1.93	0.50
2:CC:1:MET:HE1	32:DC:533:LEU:HB2	1.94	0.49
8:CK:47:ILE:HD12	36:DG:182:HIS:ND1	2.27	0.49
12:CP:53:ARG:HD2	12:CP:58:ILE:HG21	1.93	0.49
13:CQ:84:ILE:O	33:DD:272:LYS:NZ	2.30	0.49
17:Ca:443:MET:HE2	17:Ca:491:TRP:HE1	1.77	0.49
33:DD:421:PHE:HE2	33:DD:519:VAL:HG23	1.77	0.49
35:DF:125:TYR:O	35:DF:182:ARG:NH1	2.45	0.49
36:DG:325:TYR:N	36:DG:360:GLY:O	2.36	0.49
44:DO:224:ASP:O	44:DO:228:LYS:HG2	2.12	0.49
1:CA:64:G:N7	61:FO:316:ARG:HG3	2.26	0.49
6:CI:40:TRP:CE2	7:CJ:163:MET:HE2	2.47	0.49
7:CJ:284:ARG:NH1	23:Ck:103:GLU:OE2	2.44	0.49
8:CK:153:ASP:N	8:CK:153:ASP:OD1	2.44	0.49
8:CK:197:LEU:HD13	8:CK:291:ALA:HB1	1.93	0.49
13:CQ:203:THR:O	13:CQ:206:THR:OG1	2.31	0.49
23:Ck:102:PRO:HA	36:DG:22:GLN:HE21	1.77	0.49
23:Ck:700:VAL:HG22	23:Ck:754:GLU:HB3	1.94	0.49
27:Cq:11:ALA:HB2	42:DM:291:ILE:HG13	1.95	0.49
29:Cv:513:HIS:ND1	29:Cv:515:ASP:OD1	2.43	0.49
30:DA:446:ARG:NH1	30:DA:450:GLU:HB2	2.27	0.49
30:DA:1392:ILE:O	30:DA:1396:ILE:HG12	2.12	0.49
33:DD:530:TYR:OH	33:DD:606:ARG:NH2	2.41	0.49
34:DE:57:ASP:OD1	34:DE:57:ASP:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:DG:33:HIS:O	36:DG:37:ASN:ND2	2.45	0.49
36:DG:370:ARG:O	36:DG:374:HIS:ND1	2.43	0.49
38:DI:55:ILE:HG21	38:DI:90:LEU:HD13	1.94	0.49
42:DM:43:GLN:HE22	42:DM:67:ALA:HB2	1.77	0.49
46:DQ:45:ARG:O	46:DQ:49:ARG:HG2	2.12	0.49
65:Fi:195:LYS:HB3	65:Fi:199:LEU:HD13	1.93	0.49
66:IA:384:THR:HG21	66:IA:446:PRO:HD2	1.94	0.49
1:CA:445:C:O2	67:IB:645:ARG:NE	2.45	0.49
2:CC:37:ILE:HA	2:CC:74:THR:HA	1.93	0.49
2:CC:56:TYR:HB3	2:CC:72:ILE:HG23	1.94	0.49
5:CH:185:MET:HE3	5:CH:281:VAL:HG21	1.94	0.49
6:CI:292:VAL:H	14:CR:250:GLN:NE2	2.10	0.49
7:CJ:691:PHE:CD2	31:DB:1109:TRP:HD1	2.30	0.49
17:Ca:495:GLU:HB3	33:DD:105:GLY:HA3	1.93	0.49
19:Cd:121:ASP:OD2	44:DO:241:TRP:NE1	2.39	0.49
24:Cm:177:ARG:O	24:Cm:181:GLN:HG2	2.12	0.49
30:DA:967:GLU:OE1	30:DA:968:SER:N	2.46	0.49
30:DA:1134:ILE:HD12	30:DA:1135:PRO:HD2	1.93	0.49
33:DD:332:PRO:HG3	50:DU:72:PRO:HD3	1.95	0.49
46:DQ:21:ASN:HD22	46:DQ:45:ARG:HH12	1.60	0.49
61:FO:313:ALA:HB2	64:Fh:292:MET:HG2	1.94	0.49
65:Fi:271:LEU:HG	65:Fi:272:GLN:HG3	1.94	0.49
5:CH:167:LYS:HG3	29:Cv:100:ALA:HB1	1.94	0.49
6:CI:15:LEU:HB2	6:CI:41:VAL:HG23	1.94	0.49
17:Ca:205:LEU:HD22	17:Ca:249:MET:HG3	1.95	0.49
17:Ca:313:ALA:HB1	30:DA:912:LEU:HD21	1.95	0.49
20:Cg:308:LEU:HD13	20:Cg:316:THR:HG21	1.94	0.49
25:Cn:184:ARG:HH11	65:Fi:530:TRP:HZ3	1.61	0.49
27:Cq:227:ILE:HG21	28:Cr:193:VAL:HG21	1.94	0.49
30:DA:290:TYR:O	30:DA:326:TRP:NE1	2.46	0.49
31:DB:1127:MET:HE1	31:DB:1145:LEU:HD23	1.94	0.49
32:DC:664:PHE:HB3	32:DC:792:PHE:HB2	1.93	0.49
37:DH:53:ARG:O	37:DH:56:GLU:HG2	2.12	0.49
37:DH:542:LEU:O	37:DH:546:THR:HG23	2.12	0.49
41:DL:141:ILE:HD12	41:DL:171:ARG:HH11	1.76	0.49
54:DY:22:ILE:HG13	54:DY:100:TYR:OH	2.12	0.49
62:Ff:312:VAL:HG13	62:Ff:382:ALA:HA	1.94	0.49
62:Ff:684:ALA:HB1	62:Ff:689:LEU:HB2	1.93	0.49
66:IA:336:ASP:OD1	66:IA:336:ASP:N	2.37	0.49
66:IA:417:VAL:HG13	66:IA:439:LEU:HD23	1.93	0.49
67:IB:418:ARG:HH12	67:IB:441:ASP:HA	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:157:G:H1'	61:FO:98:TYR:HE1	1.77	0.49
3:CE:329:ARG:NH2	30:DA:944:ASP:OD2	2.46	0.49
12:CP:141:ASP:OD1	12:CP:141:ASP:N	2.45	0.49
29:Cv:53:PRO:HA	29:Cv:56:GLN:HE22	1.76	0.49
29:Cv:312:ASN:HB3	29:Cv:315:ILE:HG22	1.95	0.49
30:DA:1494:LEU:HD12	30:DA:1605:ARG:HB2	1.95	0.49
32:DC:226:GLN:HB3	32:DC:468:THR:HA	1.94	0.49
44:DO:97:TYR:HB3	44:DO:109:VAL:HG21	1.94	0.49
1:CA:116:U:N3	57:F3:142:VAL:O	2.45	0.49
1:CA:371:U:OP1	33:DD:12:SER:OG	2.24	0.49
1:CA:468:A:N7	41:DL:289:ARG:NE	2.57	0.49
1:CA:504:U:OP1	53:DX:115:ARG:NH1	2.45	0.49
8:CK:203:ASN:OD1	8:CK:204:THR:N	2.45	0.49
17:Ca:90:TYR:CE2	30:DA:427:ASP:HB2	2.48	0.49
20:Cg:173:THR:H	20:Cg:215:ASN:HD21	1.61	0.49
20:Cg:439:ARG:HH12	20:Cg:443:LYS:HE2	1.78	0.49
22:Cj:12:ASP:HB3	47:DR:262:ARG:HB3	1.94	0.49
23:Ck:283:GLU:OE2	31:DB:887:SER:N	2.27	0.49
28:Cr:14:GLU:HA	28:Cr:17:ARG:HG2	1.93	0.49
30:DA:170:GLN:HB2	30:DA:173:ALA:HB2	1.94	0.49
31:DB:111:ASN:HA	31:DB:200:GLY:HA3	1.95	0.49
31:DB:1111:GLN:HG3	35:DF:95:ILE:HA	1.94	0.49
34:DE:712:MET:O	34:DE:717:ARG:NH2	2.45	0.49
35:DF:512:ASN:OD1	35:DF:513:SER:N	2.45	0.49
37:DH:144:ASP:N	37:DH:144:ASP:OD1	2.45	0.49
37:DH:411:LEU:HA	37:DH:414:LEU:HD23	1.95	0.49
44:DO:59:ALA:HB2	44:DO:107:ALA:HA	1.94	0.49
65:Fi:90:LEU:HD11	65:Fi:388:GLU:HA	1.93	0.49
66:IA:90:MET:HG2	67:IB:660:LEU:HD21	1.94	0.49
1:CA:59:U:O4	30:DA:76:ARG:NH1	2.46	0.49
1:CA:96:U:H3	1:CA:132:G:H1	1.61	0.49
3:CE:144:ILE:HB	67:IB:703:VAL:HG11	1.95	0.49
4:CF:143:GLU:O	4:CF:147:LYS:HG2	2.11	0.49
7:CJ:44:PHE:CZ	41:DL:289:ARG:HG2	2.48	0.49
8:CK:304:VAL:HG11	16:CU:54:ILE:HG21	1.95	0.49
8:CK:312:PRO:HG2	16:CU:15:TYR:HB3	1.94	0.49
12:CP:53:ARG:HH21	12:CP:59:ARG:NH2	2.10	0.49
17:Ca:297:LEU:HD21	43:DN:221:GLU:HB2	1.93	0.49
23:Ck:318:THR:OG1	23:Ck:608:ARG:NH1	2.46	0.49
30:DA:393:GLY:HA3	43:DN:179:ASN:ND2	2.27	0.49
30:DA:559:LYS:O	30:DA:562:LYS:HG3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:DA:1013:SER:HB3	30:DA:1017:GLY:H	1.77	0.49
30:DA:1113:LEU:HB3	30:DA:1145:THR:HG21	1.93	0.49
32:DC:683:GLU:O	32:DC:686:GLU:HG3	2.12	0.49
35:DF:127:PRO:HA	35:DF:136:ALA:HB3	1.94	0.49
35:DF:193:PRO:HG2	35:DF:228:VAL:HG11	1.94	0.49
62:Ff:709:ASP:O	62:Ff:731:HIS:NE2	2.40	0.49
67:IB:383:MET:N	67:IB:383:MET:SD	2.86	0.49
3:CE:304:LEU:HD11	17:Ca:361:LEU:HD12	1.95	0.49
7:CJ:729:ASP:N	7:CJ:729:ASP:OD1	2.46	0.49
11:CO:173:ILE:HG23	11:CO:177:MET:HE2	1.95	0.49
15:CS:224:ASP:OD1	15:CS:224:ASP:N	2.44	0.49
23:Ck:562:CYS:SG	23:Ck:566:ARG:NH1	2.85	0.49
31:DB:903:ILE:HD11	31:DB:921:ALA:HB2	1.94	0.49
45:DP:116:HIS:HE1	45:DP:150:THR:HB	1.78	0.49
48:DS:143:ALA:HB3	48:DS:165:VAL:HG21	1.93	0.49
60:F9:354:MET:SD	64:Fh:191:ARG:HD3	2.52	0.49
61:FO:34:LYS:O	61:FO:38:VAL:HG12	2.13	0.49
62:Ff:444:THR:HG23	62:Ff:447:GLU:H	1.78	0.49
62:Ff:622:THR:HG21	62:Ff:651:LEU:HD21	1.94	0.49
66:IA:92:LEU:O	67:IB:653:TRP:NE1	2.27	0.49
67:IB:459:ASP:N	67:IB:459:ASP:OD1	2.44	0.49
4:CF:22:LEU:HD13	19:Cd:160:ILE:HD12	1.94	0.49
8:CK:53:ARG:HG3	20:Cg:488:ARG:HH22	1.77	0.49
13:CQ:215:GLN:OE1	61:FO:2:THR:OG1	2.28	0.49
17:Ca:72:ASP:O	30:DA:328:ARG:NH1	2.44	0.49
30:DA:1546:PHE:HB2	30:DA:1549:ARG:HB2	1.94	0.49
31:DB:284:ASP:HB3	31:DB:287:ARG:HB3	1.95	0.49
31:DB:1033:TYR:HE1	31:DB:1040:PRO:HD3	1.76	0.49
32:DC:865:CYS:HA	32:DC:868:GLU:OE2	2.13	0.49
32:DC:946:GLU:HG2	32:DC:986:LEU:HD11	1.94	0.49
37:DH:318:GLU:OE2	37:DH:322:ARG:NH2	2.46	0.49
40:DK:303:TYR:HB2	49:DT:177:MET:HE1	1.95	0.49
41:DL:164:ARG:NE	41:DL:167:GLU:OE2	2.46	0.49
43:DN:17:MET:HB2	43:DN:39:VAL:HB	1.94	0.49
45:DP:93:TYR:HA	45:DP:96:GLU:HG2	1.95	0.49
46:DQ:57:THR:OG1	46:DQ:167:ARG:NH1	2.45	0.49
46:DQ:158:PHE:HB2	46:DQ:163:VAL:HB	1.94	0.49
51:DV:133:THR:HG21	51:DV:146:LYS:HE2	1.95	0.49
51:DV:171:ARG:HH11	51:DV:171:ARG:HA	1.77	0.49
58:F6:475:ASP:N	58:F6:475:ASP:OD1	2.46	0.49
60:F9:525:ASN:ND2	66:IA:480:ASP:OD2	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:Fg:44:GLN:NE2	63:Fg:81:GLY:O	2.45	0.49
1:CA:157:G:H1'	61:FO:98:TYR:CE1	2.48	0.49
1:CA:369:A:O2'	33:DD:14:LYS:HD2	2.12	0.49
10:CN:69:ARG:HB2	31:DB:1109:TRP:HZ3	1.77	0.49
23:Ck:817:LEU:HD11	23:Ck:837:TRP:HB3	1.95	0.49
24:Cm:98:SER:OG	24:Cm:99:GLU:OE1	2.30	0.49
28:Cr:72:ALA:HA	28:Cr:78:LEU:HD21	1.94	0.49
29:Cv:679:PRO:HG3	44:DO:57:TYR:HE1	1.78	0.49
29:Cv:874:GLU:O	29:Cv:878:ASN:HB2	2.12	0.49
30:DA:277:ILE:HG12	30:DA:359:ARG:HH22	1.77	0.49
31:DB:776:THR:HG23	31:DB:783:VAL:HG13	1.94	0.49
34:DE:152:ALA:HA	34:DE:157:ARG:HH21	1.78	0.49
35:DF:116:ARG:HB2	35:DF:125:TYR:OH	2.12	0.49
44:DO:125:LEU:HD11	44:DO:173:VAL:HG21	1.95	0.49
46:DQ:39:ASP:HB2	47:DR:27:LYS:HE2	1.94	0.49
59:F7:411:ARG:HB2	59:F7:412:PRO:HD3	1.94	0.49
62:Ff:633:GLU:OE1	62:Ff:714:TYR:OH	2.18	0.49
63:Fg:315:ARG:N	66:IA:581:ASP:OD2	2.46	0.49
65:Fi:96:LEU:HD11	65:Fi:208:PHE:HB3	1.95	0.49
1:CA:267:U:H5''	9:CL:59:MET:HG3	1.95	0.48
3:CE:309:ARG:NH1	42:DM:36:TYR:OH	2.44	0.48
5:CH:249:ARG:HD2	17:Ca:354:THR:HG23	1.94	0.48
6:CI:372:ILE:HG21	6:CI:391:LEU:HD22	1.95	0.48
10:CN:47:ALA:HB2	21:CI:88:ILE:HG21	1.94	0.48
10:CN:74:PHE:HB2	31:DB:1107:THR:HG21	1.95	0.48
15:CS:156:LEU:HD11	31:DB:1116:ARG:HB2	1.94	0.48
21:CI:104:ARG:NH2	35:DF:170:ARG:O	2.45	0.48
22:Cj:216:ASN:OD1	22:Cj:216:ASN:N	2.46	0.48
28:Cr:27:ASP:HB2	28:Cr:28:PRO:HD3	1.93	0.48
31:DB:990:ARG:H	31:DB:993:ASP:HB3	1.78	0.48
31:DB:1127:MET:HE1	31:DB:1145:LEU:HA	1.93	0.48
32:DC:381:LEU:O	32:DC:385:THR:HG22	2.13	0.48
32:DC:497:PRO:O	32:DC:504:TYR:OH	2.22	0.48
36:DG:616:ARG:HG2	36:DG:617:THR:HG23	1.95	0.48
39:DJ:113:ASP:OD2	39:DJ:116:THR:OG1	2.29	0.48
40:DK:122:LYS:NZ	40:DK:155:PRO:O	2.41	0.48
44:DO:208:PHE:O	44:DO:211:GLU:HG2	2.12	0.48
47:DR:84:LEU:HD13	47:DR:192:LEU:HD21	1.94	0.48
66:IA:185:ILE:HG21	66:IA:193:THR:HG21	1.94	0.48
66:IA:206:VAL:HG12	66:IA:279:VAL:HG12	1.95	0.48
8:CK:176:TYR:HE1	19:Cd:182:GLN:HA	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Cd:77:ILE:O	19:Cd:81:ASN:ND2	2.38	0.48
26:Cp:150:TYR:CD1	26:Cp:151:ARG:HG2	2.48	0.48
32:DC:219:LEU:HD11	32:DC:249:LYS:HA	1.95	0.48
35:DF:519:TRP:NE1	35:DF:537:GLU:OE2	2.46	0.48
36:DG:150:ALA:O	36:DG:157:ARG:NH1	2.46	0.48
38:DI:68:PRO:HB2	38:DI:71:LEU:HD13	1.95	0.48
60:F9:482:PRO:HG3	60:F9:517:LEU:HD22	1.95	0.48
3:CE:211:PRO:HG2	3:CE:226:LEU:HG	1.94	0.48
6:CI:231:LEU:HD12	41:DL:209:ARG:NH1	2.27	0.48
13:CQ:186:LEU:HD23	13:CQ:186:LEU:H	1.77	0.48
19:Cd:35:TYR:CZ	22:Cj:223:ARG:HG2	2.49	0.48
32:DC:1071:VAL:O	32:DC:1077:GLY:HA3	2.12	0.48
34:DE:310:VAL:HA	34:DE:445:LEU:HD21	1.95	0.48
35:DF:389:PRO:O	35:DF:393:ARG:HD3	2.13	0.48
36:DG:101:THR:HA	36:DG:104:VAL:HG12	1.95	0.48
44:DO:85:LYS:HA	44:DO:88:GLN:HE21	1.78	0.48
46:DQ:51:ASN:HA	46:DQ:54:THR:HG22	1.94	0.48
51:DV:128:ASP:OD1	51:DV:129:ILE:N	2.38	0.48
62:Ff:479:GLU:HB2	62:Ff:636:LEU:HD11	1.94	0.48
1:CA:79:A:OP2	22:Cj:10:ARG:N	2.46	0.48
1:CA:227:U:H2'	1:CA:228:G:H8	1.78	0.48
1:CA:317:U:O2	14:CR:164:GLN:NE2	2.46	0.48
2:CC:67:TYR:OH	41:DL:30:PRO:O	2.18	0.48
29:Cv:411:ASN:O	29:Cv:411:ASN:ND2	2.46	0.48
30:DA:649:LEU:HD12	30:DA:729:ARG:HH21	1.78	0.48
31:DB:256:LEU:HG	31:DB:261:LEU:HD12	1.95	0.48
31:DB:312:GLU:HA	34:DE:511:LEU:HD11	1.95	0.48
31:DB:508:ARG:HD3	36:DG:26:ASN:HA	1.94	0.48
31:DB:734:VAL:HG12	31:DB:799:VAL:HG12	1.95	0.48
32:DC:325:MET:HE1	32:DC:403:ARG:HE	1.77	0.48
32:DC:1113:THR:HG21	32:DC:1119:GLN:HB3	1.95	0.48
33:DD:395:GLU:O	33:DD:399:ILE:HG12	2.13	0.48
33:DD:756:TRP:HB2	33:DD:761:ARG:HH21	1.77	0.48
36:DG:574:ARG:NH2	36:DG:630:GLU:OE1	2.47	0.48
49:DT:140:ASN:ND2	49:DT:174:TYR:O	2.41	0.48
56:Da:36:SER:OG	56:Da:38:ASP:OD1	2.27	0.48
60:F9:549:ARG:HE	66:IA:502:LEU:HD23	1.79	0.48
61:FO:301:TRP:HE1	61:FO:328:ILE:HD11	1.78	0.48
65:Fi:247:GLY:N	65:Fi:252:ARG:O	2.39	0.48
66:IA:720:GLN:OE1	66:IA:721:ASP:N	2.46	0.48
1:CA:108:A:H4'	13:CQ:106:THR:HG21	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:568:A:C8	13:CQ:233:ARG:HD2	2.48	0.48
1:CA:618:U:C2	14:CR:147:ILE:HD11	2.49	0.48
5:CH:190:LEU:HD13	5:CH:281:VAL:HG22	1.95	0.48
8:CK:252:ASN:HD22	58:F6:569:GLU:HA	1.78	0.48
11:CO:268:LYS:NZ	13:CQ:166:GLU:OE2	2.39	0.48
12:CP:150:LEU:HD11	33:DD:643:TYR:HD2	1.78	0.48
19:Cd:201:LEU:HD22	19:Cd:215:PRO:HB3	1.95	0.48
20:Cg:172:VAL:HB	20:Cg:218:THR:HG21	1.95	0.48
23:Ck:74:SER:H	34:DE:736:TRP:HE1	1.60	0.48
27:Cq:29:ASN:OD1	27:Cq:30:ILE:N	2.47	0.48
27:Cq:76:GLN:NE2	27:Cq:225:ALA:O	2.46	0.48
28:Cr:260:ASN:O	28:Cr:264:ILE:HG13	2.14	0.48
29:Cv:875:ARG:HE	29:Cv:889:LEU:HD23	1.78	0.48
31:DB:430:TYR:HB3	37:DH:331:PRO:HB3	1.94	0.48
31:DB:1081:TYR:CD2	35:DF:260:LYS:HD3	2.48	0.48
33:DD:315:PHE:HZ	33:DD:393:VAL:HG22	1.78	0.48
43:DN:145:ASP:OD1	43:DN:145:ASP:N	2.46	0.48
45:DP:189:TYR:CD2	45:DP:197:TYR:HB3	2.48	0.48
47:DR:191:GLN:O	47:DR:194:LYS:NZ	2.45	0.48
58:F6:202:LEU:HD23	58:F6:202:LEU:H	1.78	0.48
62:Ff:523:MET:N	62:Ff:523:MET:SD	2.86	0.48
6:CI:217:GLY:HA3	14:CR:84:ARG:HD2	1.96	0.48
12:CP:142:LYS:NZ	22:Cj:213:ASP:OD1	2.36	0.48
12:CP:173:LYS:NZ	12:CP:181:GLU:OE1	2.40	0.48
22:Cj:112:ARG:HH21	22:Cj:187:VAL:HG23	1.78	0.48
28:Cr:120:CYS:O	28:Cr:123:GLU:HG3	2.12	0.48
28:Cr:129:MET:N	28:Cr:129:MET:SD	2.87	0.48
28:Cr:140:ALA:HA	28:Cr:149:THR:HG21	1.95	0.48
30:DA:398:THR:HG22	30:DA:401:MET:HE2	1.96	0.48
30:DA:532:ARG:HA	30:DA:535:LYS:HB3	1.95	0.48
32:DC:301:LYS:O	32:DC:304:GLU:HG3	2.14	0.48
33:DD:330:PRO:HD2	50:DU:27:ARG:HD2	1.94	0.48
33:DD:449:LEU:HD22	33:DD:490:LEU:HD21	1.95	0.48
34:DE:580:VAL:HG23	34:DE:585:ARG:HB3	1.95	0.48
34:DE:656:ARG:O	34:DE:660:GLN:HG2	2.13	0.48
36:DG:123:LEU:O	36:DG:126:GLU:HG3	2.13	0.48
49:DT:49:TYR:HE2	49:DT:142:ILE:HG23	1.79	0.48
58:F6:352:HIS:CD2	58:F6:363:ASN:H	2.31	0.48
65:Fi:600:GLN:OE1	65:Fi:603:ARG:NH1	2.46	0.48
66:IA:64:SER:O	66:IA:69:ARG:NH2	2.47	0.48
66:IA:199:TYR:HE1	66:IA:372:PRO:HG3	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:IB:535:LEU:HD22	67:IB:573:ALA:HB2	1.96	0.48
1:CA:373:A:H61	56:Da:18:LYS:NZ	2.11	0.48
3:CE:223:ARG:N	3:CE:255:ASN:OD1	2.47	0.48
6:CI:84:ASN:HB2	14:CR:217:ARG:HH11	1.78	0.48
6:CI:98:TYR:HB3	14:CR:38:TYR:CE2	2.49	0.48
7:CJ:345:VAL:O	7:CJ:349:THR:OG1	2.25	0.48
29:Cv:204:ILE:HG23	29:Cv:209:VAL:HG22	1.95	0.48
29:Cv:282:ILE:HD11	29:Cv:296:LEU:HD13	1.95	0.48
29:Cv:578:GLN:OE1	29:Cv:578:GLN:N	2.45	0.48
29:Cv:739:ASN:HB2	29:Cv:789:CYS:HB2	1.95	0.48
29:Cv:813:ARG:HD2	29:Cv:921:VAL:HG21	1.96	0.48
29:Cv:884:ARG:O	38:DI:358:ARG:NH2	2.45	0.48
32:DC:674:THR:HG23	32:DC:677:GLU:H	1.77	0.48
34:DE:186:ARG:HD3	34:DE:193:ILE:HG12	1.96	0.48
43:DN:148:LEU:HD23	43:DN:150:LEU:HD11	1.95	0.48
46:DQ:251:MET:N	46:DQ:251:MET:SD	2.87	0.48
58:F6:556:LEU:HA	75:UL:107:UNK:HA	1.96	0.48
59:F7:121:ARG:HD2	59:F7:143:LEU:HD21	1.96	0.48
61:FO:86:VAL:O	61:FO:136:SER:OG	2.31	0.48
63:Fg:427:ASP:HB3	63:Fg:430:PHE:CB	2.44	0.48
1:CA:427:U:H3'	39:DJ:232:ARG:HD2	1.95	0.48
1:CA:437:U:H2'	21:Ci:161:GLY:HA3	1.94	0.48
1:CA:511:U:OP1	51:DV:73:ARG:NH1	2.46	0.48
6:CI:428:PRO:HB2	10:CN:105:ARG:HH12	1.77	0.48
17:Ca:443:MET:HE2	17:Ca:491:TRP:NE1	2.29	0.48
28:Cr:49:SER:OG	28:Cr:50:LYS:N	2.45	0.48
29:Cv:233:LYS:HG3	29:Cv:500:TYR:CD2	2.49	0.48
29:Cv:1115:ASP:N	29:Cv:1115:ASP:OD1	2.46	0.48
30:DA:105:PHE:O	30:DA:112:GLN:NE2	2.45	0.48
30:DA:1094:VAL:HG13	30:DA:1635:THR:HG22	1.96	0.48
30:DA:1276:GLY:HA3	31:DB:989:LYS:HG2	1.96	0.48
32:DC:558:PHE:HB2	32:DC:922:PRO:HB2	1.96	0.48
36:DG:401:CYS:HA	36:DG:458:LEU:HD11	1.96	0.48
43:DN:235:ASN:HB3	43:DN:238:ASN:HB2	1.96	0.48
46:DQ:84:SER:O	46:DQ:88:ARG:HG2	2.12	0.48
48:DS:167:SER:HB3	48:DS:186:ILE:HD11	1.96	0.48
60:F9:302:GLN:OE1	60:F9:305:ARG:NH2	2.44	0.48
61:FO:110:GLN:OE1	61:FO:112:TRP:NE1	2.38	0.48
66:IA:178:ASN:HB3	66:IA:376:ARG:HE	1.79	0.48
67:IB:626:VAL:O	67:IB:643:TYR:OH	2.22	0.48
6:CI:89:ARG:CZ	8:CK:114:MET:HE1	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Cd:118:LYS:HZ1	38:DI:313:ARG:HH21	1.61	0.48
20:Cg:140:ASN:HB2	51:DV:178:THR:HG22	1.95	0.48
24:Cm:101:MET:HE2	58:F6:580:SER:HA	1.96	0.48
29:Cv:1028:GLN:HB3	30:DA:848:TYR:HE1	1.78	0.48
30:DA:223:ALA:HB3	30:DA:285:TYR:HA	1.95	0.48
31:DB:812:GLU:OE1	31:DB:812:GLU:N	2.46	0.48
31:DB:1053:ALA:HB2	37:DH:345:VAL:HB	1.95	0.48
32:DC:652:ARG:O	32:DC:655:GLU:HG2	2.14	0.48
32:DC:1101:SER:OG	37:DH:55:ARG:NH1	2.46	0.48
33:DD:113:TYR:OH	33:DD:709:ARG:NH1	2.46	0.48
33:DD:292:ARG:HH11	33:DD:322:MET:HE1	1.78	0.48
33:DD:512:PHE:O	33:DD:515:GLU:HG2	2.13	0.48
38:DI:170:TYR:HE2	38:DI:174:ARG:HH21	1.62	0.48
54:DY:52:GLN:OE1	54:DY:52:GLN:N	2.46	0.48
59:F7:453:PRO:HG3	59:F7:482:LEU:HD11	1.95	0.48
1:CA:373:A:H2	1:CA:376:G:H5'	1.79	0.48
1:CA:444:A:H2'	1:CA:481:A:N1	2.29	0.48
6:CI:110:ARG:NE	16:CU:143:TRP:O	2.46	0.48
12:CP:100:LYS:HD2	33:DD:685:VAL:HB	1.96	0.48
13:CQ:200:LEU:O	59:F7:133:ASP:N	2.43	0.48
17:Ca:499:ASP:N	17:Ca:499:ASP:OD1	2.47	0.48
22:Cj:103:LEU:HD22	22:Cj:173:MET:HB3	1.96	0.48
29:Cv:808:SER:HB2	29:Cv:811:ALA:HB3	1.96	0.48
29:Cv:996:SER:HB2	30:DA:927:VAL:HB	1.95	0.48
30:DA:1277:LEU:HD13	30:DA:1277:LEU:HA	1.72	0.48
36:DG:232:LEU:HD12	36:DG:317:MET:HE2	1.96	0.48
39:DJ:107:LEU:HA	39:DJ:110:LEU:HD13	1.96	0.48
49:DT:181:ASP:OD1	49:DT:181:ASP:N	2.47	0.48
55:DZ:23:PHE:HB3	55:DZ:25:HIS:CD2	2.49	0.48
55:DZ:34:LYS:HG2	64:Fh:85:ALA:HB2	1.95	0.48
58:F6:229:LEU:HA	58:F6:233:LEU:HB2	1.95	0.48
66:IA:514:SER:OG	66:IA:555:ASP:OD1	2.17	0.48
1:CA:225:A:OP1	55:DZ:39:ASN:ND2	2.41	0.47
3:CE:63:ASP:OD2	3:CE:78:LYS:NZ	2.43	0.47
3:CE:432:TYR:O	30:DA:1095:ARG:NH1	2.47	0.47
4:CF:50:ARG:HB3	4:CF:58:PRO:HB3	1.96	0.47
6:CI:84:ASN:OD1	6:CI:85:LEU:N	2.47	0.47
7:CJ:790:MET:HE2	51:DV:80:ARG:HE	1.79	0.47
8:CK:209:TYR:CD2	16:CU:32:HIS:HB2	2.49	0.47
9:CL:75:CYS:HB3	60:F9:543:ASP:O	2.14	0.47
23:Ck:414:MET:HE2	23:Ck:541:ARG:HB2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DB:195:LEU:HB2	34:DE:486:ILE:HD11	1.96	0.47
32:DC:1085:ALA:HB2	40:DK:252:ILE:HD11	1.96	0.47
33:DD:401:LEU:HD21	33:DD:464:VAL:HB	1.96	0.47
33:DD:423:LYS:HE2	33:DD:427:ALA:HB3	1.95	0.47
35:DF:232:GLU:HA	35:DF:235:ARG:HG2	1.96	0.47
46:DQ:188:VAL:HG12	46:DQ:194:VAL:HG11	1.96	0.47
49:DT:237:GLY:HA3	49:DT:240:GLN:HE21	1.78	0.47
63:Fg:182:GLY:O	63:Fg:243:PRO:HD3	2.14	0.47
66:IA:330:ASN:ND2	66:IA:330:ASN:O	2.46	0.47
66:IA:376:ARG:HH22	66:IA:453:LEU:HD13	1.79	0.47
1:CA:126:U:O2'	11:CO:297:GLN:NE2	2.47	0.47
7:CJ:63:PRO:HD2	7:CJ:70:TYR:OH	2.14	0.47
7:CJ:86:ASP:OD1	7:CJ:88:ARG:NH2	2.47	0.47
11:CO:315:LEU:HD22	11:CO:321:PRO:HB3	1.96	0.47
14:CR:69:HIS:ND1	14:CR:74:GLU:OE2	2.38	0.47
17:Ca:510:GLY:O	17:Ca:514:THR:OG1	2.31	0.47
22:Cj:73:ARG:HH22	45:DP:87:GLU:HG3	1.78	0.47
31:DB:1047:TRP:CG	39:DJ:41:PRO:HG3	2.49	0.47
33:DD:602:VAL:HG22	33:DD:606:ARG:HE	1.79	0.47
35:DF:258:ASP:OD1	35:DF:259:SER:N	2.47	0.47
40:DK:238:ILE:HD11	40:DK:260:VAL:HB	1.95	0.47
43:DN:45:ARG:HB2	43:DN:132:TYR:HE1	1.79	0.47
45:DP:122:VAL:HG21	45:DP:157:ALA:HB1	1.96	0.47
47:DR:252:ALA:HA	47:DR:262:ARG:HD2	1.97	0.47
58:F6:354:THR:OG1	58:F6:385:GLN:NE2	2.47	0.47
59:F7:47:TRP:CD1	59:F7:285:ARG:HD2	2.49	0.47
60:F9:480:THR:HB	60:F9:485:LEU:HD23	1.96	0.47
61:FO:168:PRO:HG2	64:Fh:304:LEU:HD11	1.96	0.47
1:CA:232:G:N2	1:CA:245:G:OP1	2.31	0.47
1:CA:555:A:N3	1:CA:601:A:O2'	2.42	0.47
12:CP:179:ALA:O	12:CP:182:ARG:HG2	2.14	0.47
14:CR:75:GLN:HB3	14:CR:94:MET:HG3	1.95	0.47
20:Cg:130:THR:OG1	20:Cg:131:LYS:NZ	2.46	0.47
27:Cq:170:VAL:HA	27:Cq:173:ILE:HG22	1.96	0.47
28:Cr:47:HIS:CE1	28:Cr:176:LEU:HB3	2.49	0.47
29:Cv:677:PRO:HB3	29:Cv:701:GLU:HG2	1.97	0.47
30:DA:311:THR:HG22	30:DA:313:PHE:H	1.79	0.47
32:DC:823:ILE:HG22	32:DC:850:PHE:CZ	2.49	0.47
33:DD:59:ASN:ND2	33:DD:59:ASN:O	2.48	0.47
34:DE:566:ARG:NH1	34:DE:567:HIS:O	2.48	0.47
38:DI:119:ARG:NH2	38:DI:156:GLY:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:DI:252:ARG:HG3	38:DI:259:THR:HG23	1.96	0.47
54:DY:124:THR:N	54:DY:135:TYR:O	2.45	0.47
3:CE:261:ASN:O	33:DD:16:ARG:NH1	2.47	0.47
6:CI:209:TYR:OH	14:CR:73:ASP:OD2	2.17	0.47
11:CO:286:ILE:HG23	11:CO:287:LEU:HD13	1.96	0.47
13:CQ:123:ARG:HH21	30:DA:110:TYR:HB2	1.80	0.47
17:Ca:249:MET:HA	17:Ca:252:ARG:HD2	1.96	0.47
23:Ck:115:PRO:HD3	23:Ck:140:ARG:HH12	1.80	0.47
29:Cv:172:THR:HG23	29:Cv:174:ARG:H	1.79	0.47
30:DA:61:LYS:HE3	33:DD:122:GLN:HE21	1.80	0.47
30:DA:693:GLU:N	30:DA:693:GLU:OE1	2.47	0.47
30:DA:1496:ASP:OD1	30:DA:1496:ASP:N	2.47	0.47
31:DB:635:MET:N	31:DB:635:MET:SD	2.87	0.47
32:DC:1073:ALA:HB2	34:DE:576:HIS:ND1	2.29	0.47
32:DC:1092:LYS:NZ	40:DK:234:ALA:O	2.45	0.47
36:DG:46:TRP:CD1	36:DG:89:GLU:HG3	2.50	0.47
38:DI:232:TYR:OH	38:DI:346:LEU:HB3	2.15	0.47
38:DI:366:LEU:HD23	38:DI:370:GLN:HG3	1.95	0.47
39:DJ:247:ASN:HB3	39:DJ:250:VAL:HG12	1.96	0.47
44:DO:83:ARG:HA	44:DO:86:ARG:HB3	1.96	0.47
45:DP:174:ALA:HB1	45:DP:179:PHE:HB2	1.96	0.47
46:DQ:66:SER:O	46:DQ:197:LYS:NZ	2.36	0.47
46:DQ:191:VAL:HG23	46:DQ:192:LEU:HD23	1.97	0.47
48:DS:159:ASN:O	48:DS:162:THR:OG1	2.33	0.47
51:DV:45:THR:OG1	51:DV:52:ARG:NH2	2.45	0.47
67:IB:520:PRO:HA	67:IB:523:VAL:HG22	1.96	0.47
1:CA:522:A:H62	52:DW:122:ARG:HD2	1.79	0.47
3:CE:95:ILE:HG12	29:Cv:289:VAL:HG11	1.96	0.47
7:CJ:114:TYR:HA	7:CJ:117:TYR:CD2	2.50	0.47
7:CJ:475:VAL:HG11	7:CJ:669:PRO:HB2	1.97	0.47
11:CO:315:LEU:HB2	33:DD:261:ARG:NH2	2.29	0.47
18:Cb:284:ARG:HB3	28:Cr:52:ARG:HH12	1.79	0.47
20:Cg:216:ARG:NH1	20:Cg:244:TYR:OH	2.48	0.47
22:Cj:78:ASP:OD1	45:DP:163:ARG:NH2	2.46	0.47
27:Cq:241:ASN:HA	27:Cq:244:LYS:HG2	1.96	0.47
31:DB:447:PHE:CD2	37:DH:154:LYS:HG2	2.50	0.47
31:DB:742:SER:OG	31:DB:791:GLU:OE2	2.32	0.47
32:DC:144:TYR:CE1	32:DC:233:ILE:HD11	2.50	0.47
32:DC:200:VAL:HG23	32:DC:205:GLN:HG3	1.95	0.47
32:DC:304:GLU:HA	32:DC:307:LEU:HB2	1.97	0.47
33:DD:542:HIS:HA	33:DD:545:ASP:OD2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:DD:741:ARG:HH22	38:DI:103:ASP:HA	1.79	0.47
50:DU:115:LYS:HA	50:DU:118:VAL:HG22	1.97	0.47
59:F7:404:MET:HE3	59:F7:441:ILE:HG22	1.97	0.47
60:F9:596:TYR:N	66:IA:764:GLU:OE2	2.47	0.47
62:Ff:601:THR:HG22	62:Ff:689:LEU:HA	1.97	0.47
1:CA:119:A:H4'	11:CO:352:ASN:HB2	1.96	0.47
1:CA:498:U:C2	51:DV:68:ILE:HD11	2.50	0.47
1:CA:576:A:O2'	66:IA:45:ARG:NH2	2.48	0.47
6:CI:285:ASP:OD1	6:CI:285:ASP:N	2.46	0.47
6:CI:353:MET:HB2	6:CI:392:ARG:HD3	1.97	0.47
7:CJ:806:GLU:OE2	10:CN:151:ARG:NH1	2.46	0.47
20:Cg:120:LEU:O	20:Cg:124:LYS:HG2	2.14	0.47
20:Cg:273:LEU:HD21	20:Cg:281:VAL:HG11	1.96	0.47
20:Cg:413:LEU:HD22	20:Cg:441:LEU:HD12	1.97	0.47
22:Cj:28:LYS:HD3	22:Cj:43:ALA:HB2	1.96	0.47
33:DD:293:GLU:O	33:DD:297:ARG:HG3	2.14	0.47
33:DD:461:ILE:HA	33:DD:464:VAL:HG12	1.97	0.47
36:DG:561:PRO:HG3	36:DG:619:PHE:CZ	2.49	0.47
37:DH:294:PHE:CG	37:DH:327:HIS:HB2	2.48	0.47
38:DI:159:ASP:HB2	38:DI:162:PHE:HB2	1.96	0.47
40:DK:164:GLU:HG2	40:DK:222:LEU:HD11	1.97	0.47
43:DN:72:THR:HG23	43:DN:111:ILE:HD13	1.97	0.47
48:DS:124:LYS:HB3	48:DS:168:LYS:HG3	1.95	0.47
52:DW:93:HIS:HB2	54:DY:109:PHE:HZ	1.80	0.47
54:DY:37:ARG:HH12	54:DY:106:GLN:NE2	2.12	0.47
59:F7:581:ARG:HG3	59:F7:590:VAL:HG11	1.95	0.47
60:F9:224:TYR:HB2	67:IB:728:LEU:HD13	1.96	0.47
63:Fg:10:VAL:HB	63:Fg:506:GLU:HB3	1.97	0.47
63:Fg:136:ILE:HG21	63:Fg:150:LEU:HD21	1.96	0.47
65:Fi:303:GLU:OE2	69:U7:1:UNK:N	2.28	0.47
1:CA:45:G:H5'	26:Cp:68:LEU:HD11	1.97	0.47
3:CE:405:LYS:HB2	3:CE:409:ASP:HB2	1.96	0.47
5:CH:113:LYS:O	5:CH:120:TYR:OH	2.22	0.47
5:CH:232:TRP:CZ2	5:CH:277:GLY:HA3	2.50	0.47
7:CJ:280:LEU:HA	7:CJ:283:VAL:HG12	1.95	0.47
9:CL:115:VAL:HG13	60:F9:526:ASN:HD21	1.78	0.47
14:CR:137:THR:O	14:CR:176:ASN:ND2	2.48	0.47
14:CR:244:THR:HG23	14:CR:247:HIS:H	1.79	0.47
17:Ca:564:ARG:HH21	17:Ca:586:ILE:HB	1.79	0.47
19:Cd:36:ARG:HA	19:Cd:39:MET:HG2	1.96	0.47
19:Cd:48:ASN:HA	19:Cd:51:GLU:HG2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Cd:174:PRO:HB2	29:Cv:638:VAL:HB	1.95	0.47
19:Cd:215:PRO:HD3	58:F6:401:TRP:CH2	2.50	0.47
20:Cg:45:LEU:HA	20:Cg:50:PRO:HA	1.96	0.47
20:Cg:333:LEU:HB2	20:Cg:336:VAL:HG23	1.95	0.47
21:Ci:39:ARG:NE	23:Ck:773:ASP:OD2	2.47	0.47
27:Cq:148:PRO:HA	27:Cq:151:ARG:HG2	1.96	0.47
28:Cr:11:ASN:HB2	28:Cr:93:LEU:HD12	1.96	0.47
29:Cv:1008:ARG:NH1	42:DM:224:THR:OG1	2.48	0.47
30:DA:162:PRO:HA	30:DA:165:ARG:HD3	1.96	0.47
30:DA:720:ASP:HA	30:DA:723:GLU:HG2	1.97	0.47
31:DB:232:ARG:NE	32:DC:966:GLY:O	2.23	0.47
31:DB:541:HIS:HD2	31:DB:845:VAL:HG23	1.79	0.47
31:DB:1044:PRO:O	31:DB:1048:ILE:HG12	2.14	0.47
32:DC:404:ALA:HA	32:DC:407:VAL:HG12	1.97	0.47
32:DC:582:ARG:HH11	32:DC:584:ILE:HG23	1.80	0.47
32:DC:601:GLU:N	32:DC:601:GLU:OE1	2.47	0.47
33:DD:395:GLU:OE1	33:DD:398:ARG:NH2	2.39	0.47
34:DE:163:LYS:HB2	34:DE:556:LEU:HD21	1.96	0.47
34:DE:341:GLU:OE2	34:DE:345:ASN:ND2	2.45	0.47
35:DF:520:GLN:HB2	35:DF:525:ARG:HE	1.79	0.47
37:DH:200:THR:HG23	37:DH:203:ALA:H	1.79	0.47
37:DH:233:MET:HG3	37:DH:238:ILE:HB	1.95	0.47
37:DH:428:ARG:HH21	67:IB:730:MET:HG2	1.80	0.47
38:DI:146:ARG:HH22	42:DM:81:ASP:HA	1.80	0.47
45:DP:62:LYS:HD2	50:DU:200:PRO:HA	1.96	0.47
61:FO:174:TYR:HD2	61:FO:190:LEU:HD22	1.78	0.47
62:Ff:185:LEU:HD21	62:Ff:298:ASP:HB3	1.97	0.47
62:Ff:266:ARG:HG2	62:Ff:672:ILE:HG22	1.97	0.47
63:Fg:69:ASP:O	63:Fg:73:ILE:HG23	2.15	0.47
64:Fh:212:MET:HA	64:Fh:215:VAL:HG12	1.96	0.47
65:Fi:461:LEU:HD12	65:Fi:512:GLN:HG3	1.96	0.47
67:IB:363:GLN:HA	67:IB:366:THR:HG22	1.97	0.47
1:CA:8:U:HO2'	17:Ca:339:HIS:HD1	1.57	0.47
3:CE:15:TRP:NE1	5:CH:245:GLY:O	2.45	0.47
3:CE:187:GLN:O	3:CE:191:LYS:HG2	2.15	0.47
3:CE:344:TYR:HB3	3:CE:348:TYR:HB2	1.97	0.47
7:CJ:152:GLN:OE1	7:CJ:152:GLN:N	2.46	0.47
17:Ca:275:TRP:HH2	17:Ca:306:HIS:HD2	1.63	0.47
17:Ca:546:PHE:O	30:DA:344:ARG:NH1	2.40	0.47
17:Ca:549:SER:O	17:Ca:552:THR:OG1	2.32	0.47
19:Cd:17:ASN:HB3	19:Cd:28:MET:HE3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Cd:72:ASN:ND2	33:DD:687:HIS:HA	2.29	0.47
19:Cd:81:ASN:HA	19:Cd:84:LYS:HG2	1.96	0.47
22:Cj:115:ARG:HG3	22:Cj:129:TYR:CD2	2.50	0.47
23:Ck:602:LEU:HG	23:Ck:618:ILE:HD11	1.96	0.47
28:Cr:169:PRO:HD2	28:Cr:172:ARG:HB2	1.95	0.47
30:DA:236:ARG:CZ	30:DA:312:PRO:HG3	2.45	0.47
30:DA:591:LEU:HD23	30:DA:760:ILE:HD11	1.96	0.47
30:DA:1042:HIS:HD2	30:DA:1045:ILE:HG12	1.79	0.47
31:DB:102:GLY:H	31:DB:136:ARG:HD3	1.80	0.47
31:DB:232:ARG:NH1	32:DC:953:MET:O	2.40	0.47
31:DB:748:HIS:HA	31:DB:784:TYR:HD1	1.78	0.47
32:DC:272:GLU:OE1	32:DC:276:LYS:NZ	2.42	0.47
32:DC:469:THR:HG21	40:DK:285:GLU:HB2	1.96	0.47
32:DC:757:ARG:NH1	32:DC:934:ARG:HE	2.12	0.47
32:DC:773:ARG:NH1	32:DC:889:ARG:O	2.48	0.47
36:DG:163:GLN:O	36:DG:166:GLU:HG3	2.14	0.47
37:DH:309:TRP:O	37:DH:311:ARG:HG2	2.15	0.47
37:DH:503:THR:OG1	37:DH:504:ARG:N	2.48	0.47
41:DL:136:MET:HE1	41:DL:166:PHE:HZ	1.79	0.47
44:DO:86:ARG:NH1	44:DO:123:LEU:O	2.47	0.47
45:DP:209:VAL:HA	45:DP:212:ASN:HD22	1.78	0.47
51:DV:85:ASN:O	51:DV:88:VAL:HG12	2.15	0.47
61:FO:321:PRO:O	61:FO:324:SER:OG	2.31	0.47
62:Ff:278:ARG:HG3	62:Ff:289:LEU:HB3	1.95	0.47
62:Ff:728:VAL:O	62:Ff:732:ARG:NH1	2.46	0.47
63:Fg:152:VAL:O	63:Fg:380:PRO:HG3	2.15	0.47
63:Fg:511:ARG:HH12	63:Fg:541:ARG:HA	1.80	0.47
64:Fh:49:LEU:O	64:Fh:58:ARG:NH2	2.48	0.47
66:IA:98:TRP:NE1	67:IB:552:GLU:OE2	2.41	0.47
66:IA:518:ALA:HB2	66:IA:572:GLY:HA3	1.96	0.47
5:CH:250:LEU:HA	17:Ca:355:PHE:HE2	1.80	0.47
12:CP:76:TRP:CD1	12:CP:77:SER:HG	2.33	0.47
20:Cg:350:ASN:OD1	20:Cg:351:LYS:NZ	2.41	0.47
20:Cg:464:VAL:HG21	54:DY:35:PRO:HB3	1.97	0.47
23:Ck:390:ASN:O	23:Ck:394:ASN:ND2	2.48	0.47
29:Cv:325:MET:O	29:Cv:328:GLU:HG2	2.14	0.47
29:Cv:891:ASP:HB3	29:Cv:894:GLU:HB3	1.95	0.47
30:DA:195:MET:O	30:DA:198:ARG:HG3	2.15	0.47
30:DA:1372:LYS:HE3	30:DA:1376:HIS:HB3	1.95	0.47
31:DB:1010:LYS:O	36:DG:38:ARG:NH2	2.48	0.47
32:DC:686:GLU:HA	32:DC:689:LYS:HE3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:DC:841:HIS:HB3	32:DC:878:ASP:HB3	1.97	0.47
35:DF:310:LEU:HA	35:DF:313:ARG:HD3	1.95	0.47
53:DX:33:LYS:NZ	58:F6:676:CYS:SG	2.72	0.47
59:F7:168:ALA:HA	59:F7:171:ARG:HG2	1.97	0.47
61:FO:11:GLU:HA	61:FO:14:ARG:HG2	1.96	0.47
63:Fg:11:PHE:HE2	63:Fg:136:ILE:HD11	1.79	0.47
66:IA:178:ASN:HB3	66:IA:376:ARG:NE	2.30	0.47
1:CA:290:G:H22	24:Cm:208:ARG:HB2	1.79	0.47
4:CF:135:SER:OG	4:CF:137:ASP:OD1	2.30	0.47
7:CJ:372:GLU:OE2	7:CJ:391:HIS:NE2	2.47	0.47
18:Cb:57:MET:SD	29:Cv:511:HIS:NE2	2.85	0.47
22:Cj:90:ARG:O	22:Cj:94:ILE:HG12	2.14	0.47
23:Ck:225:MET:HE3	23:Ck:235:GLY:HA3	1.97	0.47
30:DA:88:LYS:NZ	30:DA:92:LEU:O	2.48	0.47
30:DA:291:CYS:SG	30:DA:324:GLN:N	2.76	0.47
30:DA:414:HIS:HB2	30:DA:419:THR:HG23	1.96	0.47
31:DB:290:ALA:HB1	31:DB:296:PRO:HD3	1.96	0.47
32:DC:40:ASP:N	32:DC:40:ASP:OD1	2.44	0.47
32:DC:110:PHE:HA	32:DC:113:VAL:HG13	1.96	0.47
32:DC:947:TRP:CE3	32:DC:1051:LEU:HB3	2.49	0.47
34:DE:195:ILE:HD11	34:DE:423:PHE:HB2	1.96	0.47
36:DG:554:HIS:O	36:DG:554:HIS:ND1	2.45	0.47
37:DH:246:GLU:OE2	37:DH:280:SER:N	2.48	0.47
40:DK:291:GLN:O	40:DK:295:ILE:HG12	2.15	0.47
42:DM:183:GLU:OE1	42:DM:204:TYR:OH	2.32	0.47
59:F7:198:ARG:HA	59:F7:201:VAL:HG12	1.97	0.47
59:F7:458:VAL:O	59:F7:462:ILE:HG12	2.15	0.47
59:F7:504:LEU:O	59:F7:537:SER:OG	2.33	0.47
61:FO:76:GLN:NE2	61:FO:77:PRO:O	2.46	0.47
65:Fi:222:LEU:HD11	65:Fi:458:TYR:HB3	1.96	0.47
66:IA:192:TYR:OH	66:IA:196:LYS:NZ	2.45	0.47
66:IA:533:ILE:HG23	66:IA:747:TYR:HE2	1.80	0.47
66:IA:659:ARG:HH12	66:IA:726:ARG:H	1.62	0.47
66:IA:754:GLU:OE2	66:IA:758:ARG:NH2	2.48	0.47
67:IB:208:ARG:HE	67:IB:209:THR:H	1.63	0.47
1:CA:11:U:C2	3:CE:10:LYS:HG2	2.50	0.46
1:CA:319:U:H2'	1:CA:320:A:H8	1.80	0.46
3:CE:164:TYR:HB2	3:CE:182:VAL:HG12	1.96	0.46
4:CF:130:TRP:O	14:CR:125:ASN:ND2	2.48	0.46
7:CJ:522:PRO:HG2	7:CJ:525:ALA:HB2	1.97	0.46
7:CJ:555:TRP:CH2	7:CJ:570:GLN:HG2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:CR:152:PRO:HB3	29:Cv:181:ILE:HG21	1.97	0.46
20:Cg:143:THR:HG21	20:Cg:343:ILE:HG23	1.97	0.46
30:DA:291:CYS:HB3	30:DA:294:CYS:SG	2.55	0.46
31:DB:173:ARG:HH12	32:DC:654:ARG:CZ	2.27	0.46
31:DB:500:PRO:HA	36:DG:41:TRP:NE1	2.31	0.46
31:DB:610:SER:OG	31:DB:639:ASP:OD2	2.33	0.46
32:DC:588:PRO:HA	32:DC:619:VAL:HG23	1.96	0.46
34:DE:311:VAL:O	34:DE:315:HIS:ND1	2.45	0.46
34:DE:560:ALA:O	34:DE:564:ILE:HD12	2.15	0.46
38:DI:73:ASN:HA	38:DI:76:LYS:HB3	1.96	0.46
40:DK:321:ARG:HH12	64:Fh:97:LEU:HD13	1.80	0.46
54:DY:107:HIS:O	54:DY:111:ARG:HD3	2.15	0.46
60:F9:547:HIS:CE1	60:F9:566:GLY:HA2	2.50	0.46
65:Fi:206:VAL:HG11	65:Fi:257:ILE:HD12	1.96	0.46
66:IA:376:ARG:HB2	66:IA:454:GLN:HB3	1.97	0.46
67:IB:409:ASN:O	67:IB:450:ARG:NH1	2.44	0.46
67:IB:428:GLY:N	67:IB:429:PRO:HD3	2.30	0.46
3:CE:253:ARG:HE	3:CE:256:LEU:HA	1.80	0.46
3:CE:393:ARG:HE	3:CE:394:ARG:H	1.63	0.46
11:CO:357:LEU:HD23	46:DQ:235:HIS:CE1	2.51	0.46
11:CO:379:ARG:NH1	50:DU:128:CYS:O	2.48	0.46
12:CP:61:LEU:HB3	12:CP:102:TRP:CZ2	2.50	0.46
17:Ca:202:ILE:HD11	55:DZ:84:GLY:HA3	1.97	0.46
17:Ca:509:TRP:HA	17:Ca:514:THR:HG23	1.97	0.46
19:Cd:183:MET:HE3	19:Cd:184:PRO:HD2	1.96	0.46
20:Cg:471:ARG:NH1	20:Cg:474:GLN:OE1	2.49	0.46
28:Cr:26:LEU:HD23	28:Cr:29:PRO:HG2	1.95	0.46
30:DA:369:VAL:HA	30:DA:408:LEU:HD22	1.97	0.46
31:DB:981:HIS:CD2	31:DB:983:LEU:HB2	2.50	0.46
32:DC:202:ASN:HB3	32:DC:205:GLN:HG2	1.97	0.46
33:DD:598:GLU:OE2	33:DD:632:SER:OG	2.28	0.46
33:DD:697:GLY:HA2	33:DD:706:GLY:HA3	1.96	0.46
35:DF:444:GLN:HA	35:DF:448:GLY:HA2	1.98	0.46
37:DH:322:ARG:HH21	37:DH:371:LEU:HB2	1.80	0.46
41:DL:146:ARG:HG3	41:DL:200:VAL:HG23	1.96	0.46
43:DN:21:TYR:HB3	43:DN:120:ILE:HD13	1.97	0.46
48:DS:101:CYS:SG	48:DS:103:SER:OG	2.70	0.46
54:DY:118:ARG:HA	54:DY:159:TYR:CZ	2.50	0.46
59:F7:520:LEU:O	59:F7:523:ILE:HG13	2.15	0.46
66:IA:377:CYS:HB2	66:IA:402:VAL:HG22	1.96	0.46
67:IB:530:ILE:HG23	67:IB:540:VAL:HG11	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:297:G:H5''	16:CU:27:LYS:HG2	1.96	0.46
3:CE:32:TRP:CD2	33:DD:778:PRO:HB3	2.50	0.46
3:CE:56:GLY:HA3	29:Cv:519:TRP:HA	1.96	0.46
3:CE:319:PRO:HD2	42:DM:111:MET:HE2	1.98	0.46
7:CJ:297:LEU:HD11	7:CJ:316:LYS:HD3	1.98	0.46
7:CJ:716:ARG:NE	21:Ci:77:ARG:HE	2.01	0.46
8:CK:95:MET:HE2	8:CK:98:LEU:HD22	1.96	0.46
14:CR:118:PRO:HB2	29:Cv:191:LEU:HD12	1.96	0.46
18:Cb:285:GLN:O	18:Cb:288:GLU:HG3	2.15	0.46
21:Ci:112:ASN:O	35:DF:169:ARG:HD3	2.15	0.46
27:Cq:128:GLU:OE2	27:Cq:204:HIS:ND1	2.48	0.46
28:Cr:47:HIS:HE1	28:Cr:176:LEU:HB3	1.80	0.46
29:Cv:397:TRP:O	29:Cv:401:THR:HG22	2.14	0.46
29:Cv:559:GLN:NE2	29:Cv:568:THR:OG1	2.28	0.46
29:Cv:744:TRP:CE3	29:Cv:763:VAL:HG22	2.50	0.46
31:DB:630:HIS:HB3	31:DB:638:ALA:HB1	1.97	0.46
32:DC:310:ARG:HH12	32:DC:315:LEU:HD21	1.79	0.46
36:DG:303:ARG:HD2	36:DG:304:PRO:HD2	1.97	0.46
46:DQ:178:GLU:HA	46:DQ:181:VAL:HG12	1.97	0.46
48:DS:165:VAL:HG12	48:DS:190:THR:HG21	1.97	0.46
62:Ff:348:LYS:HD3	62:Ff:349:ALA:H	1.80	0.46
63:Fg:85:VAL:HG12	63:Fg:88:THR:HG21	1.97	0.46
1:CA:33:A:H4'	13:CQ:35:HIS:ND1	2.30	0.46
1:CA:383:U:OP1	25:Cn:162:SER:OG	2.27	0.46
1:CA:507:A:N1	15:CS:151:SER:HB3	2.29	0.46
3:CE:94:ARG:NH2	3:CE:299:ASN:OD1	2.48	0.46
6:CI:294:ILE:HD11	6:CI:408:ILE:HD11	1.96	0.46
7:CJ:421:HIS:CD2	31:DB:1055:GLN:HG3	2.50	0.46
10:CN:25:VAL:O	10:CN:29:ARG:HG2	2.16	0.46
20:Cg:89:PHE:HZ	20:Cg:164:HIS:HB2	1.81	0.46
29:Cv:527:THR:HG21	41:DL:173:PRO:HD2	1.96	0.46
31:DB:337:TYR:HD2	34:DE:33:ILE:HB	1.81	0.46
31:DB:446:LYS:HE3	40:DK:127:HIS:CE1	2.50	0.46
31:DB:1011:TRP:HD1	41:DL:64:ILE:HG22	1.81	0.46
35:DF:305:ARG:HD2	39:DJ:66:TRP:CD2	2.50	0.46
50:DU:191:SER:HB2	50:DU:192:PRO:HD3	1.97	0.46
52:DW:100:PRO:HB3	52:DW:142:TRP:CE3	2.51	0.46
59:F7:214:HIS:HE1	59:F7:237:ARG:HH11	1.64	0.46
62:Ff:336:ARG:HB2	62:Ff:349:ALA:HB2	1.96	0.46
65:Fi:246:PHE:CD2	67:IB:400:LEU:HB3	2.50	0.46
66:IA:285:VAL:HG11	66:IA:315:ARG:HE	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CE:311:LYS:NZ	17:Ca:368:ARG:O	2.48	0.46
16:CU:185:ARG:NH1	16:CU:189:ARG:O	2.48	0.46
22:Cj:37:ARG:O	50:DU:215:TYR:OH	2.32	0.46
23:Ck:715:GLN:HG2	23:Ck:725:VAL:HG23	1.96	0.46
27:Cq:92:LEU:O	27:Cq:96:THR:OG1	2.30	0.46
28:Cr:139:HIS:O	28:Cr:167:ASN:ND2	2.49	0.46
29:Cv:846:THR:HG21	29:Cv:940:THR:HG21	1.97	0.46
31:DB:711:GLN:O	31:DB:714:GLU:HG3	2.16	0.46
34:DE:466:VAL:O	34:DE:469:GLU:HG3	2.15	0.46
41:DL:50:ARG:HE	60:F9:225:ILE:HD13	1.80	0.46
52:DW:18:VAL:HG22	53:DX:48:LYS:HZ2	1.79	0.46
53:DX:149:THR:HG22	53:DX:151:LYS:H	1.81	0.46
59:F7:355:MET:HE3	59:F7:385:CYS:HA	1.97	0.46
66:IA:261:HIS:HB3	66:IA:264:PHE:CD2	2.51	0.46
66:IA:347:ALA:N	81:IA:1000:GDP:O6	2.41	0.46
67:IB:385:THR:HG22	67:IB:595:THR:HG21	1.97	0.46
1:CA:266:A:H4'	9:CL:124:GLY:H	1.80	0.46
3:CE:97:PRO:HB3	3:CE:283:SER:HB2	1.96	0.46
3:CE:333:ASN:ND2	42:DM:129:ARG:O	2.49	0.46
6:CI:297:ALA:HB2	6:CI:404:PRO:HG3	1.97	0.46
6:CI:346:ASN:OD1	20:Cg:458:HIS:NE2	2.49	0.46
7:CJ:285:ARG:HE	37:DH:269:ARG:NH2	2.14	0.46
16:CU:181:ILE:H	16:CU:181:ILE:HD12	1.79	0.46
25:Cn:205:PRO:HB3	65:Fi:25:TYR:CD2	2.51	0.46
26:Cp:131:LYS:HD3	64:Fh:262:PHE:HE2	1.81	0.46
28:Cr:244:LEU:HD12	28:Cr:247:ILE:HD11	1.98	0.46
29:Cv:200:ASP:OD1	29:Cv:201:THR:N	2.48	0.46
29:Cv:868:TRP:HB3	29:Cv:872:LYS:NZ	2.31	0.46
30:DA:853:LYS:HB2	30:DA:860:HIS:CD2	2.51	0.46
31:DB:600:ARG:NE	31:DB:608:LEU:O	2.33	0.46
33:DD:321:ALA:O	33:DD:325:LYS:HB2	2.16	0.46
33:DD:445:LEU:HD23	33:DD:448:ARG:HH21	1.80	0.46
36:DG:294:MET:HE1	36:DG:314:LEU:HB2	1.98	0.46
37:DH:35:TYR:H	39:DJ:45:ASN:ND2	2.13	0.46
38:DI:278:LEU:HD21	38:DI:310:LEU:HB3	1.97	0.46
39:DJ:325:GLY:O	60:F9:254:GLN:NE2	2.49	0.46
41:DL:57:ALA:O	41:DL:61:VAL:HB	2.15	0.46
42:DM:173:ALA:HB1	42:DM:225:LEU:HD13	1.97	0.46
43:DN:30:ARG:HD3	43:DN:55:LEU:O	2.15	0.46
45:DP:205:LEU:HB2	45:DP:212:ASN:OD1	2.15	0.46
48:DS:56:LEU:HG	48:DS:67:ILE:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:Ff:215:ASP:HA	62:Ff:538:GLY:HA3	1.96	0.46
65:Fi:518:VAL:HG22	65:Fi:532:SER:HB2	1.98	0.46
66:IA:553:ASP:N	66:IA:553:ASP:OD1	2.47	0.46
4:CF:71:MET:HB2	4:CF:76:MET:HE2	1.98	0.46
4:CF:151:ARG:O	44:DO:181:HIS:NE2	2.45	0.46
8:CK:50:THR:HG23	8:CK:53:ARG:HH12	1.81	0.46
13:CQ:222:TYR:HB3	61:FO:6:ARG:HD2	1.98	0.46
17:Ca:600:PRO:HG3	64:Fh:178:PHE:CZ	2.50	0.46
20:Cg:289:ASN:OD1	20:Cg:289:ASN:N	2.48	0.46
20:Cg:293:HIS:HA	23:Ck:799:LYS:HZ3	1.81	0.46
29:Cv:589:ILE:HG13	29:Cv:787:LYS:HE2	1.98	0.46
30:DA:1093:ASP:OD1	30:DA:1094:VAL:N	2.49	0.46
31:DB:940:GLN:HB3	31:DB:948:ARG:HH11	1.80	0.46
39:DJ:193:PRO:HG2	39:DJ:194:LEU:HD22	1.97	0.46
43:DN:69:VAL:O	43:DN:113:ALA:HA	2.15	0.46
43:DN:163:PHE:HA	43:DN:166:LEU:HD23	1.97	0.46
44:DO:195:SER:O	44:DO:198:ARG:HG3	2.16	0.46
48:DS:160:LEU:HA	48:DS:163:LEU:HD23	1.98	0.46
49:DT:83:ILE:O	49:DT:100:SER:HA	2.16	0.46
62:Ff:405:GLU:OE2	62:Ff:597:ARG:NH2	2.41	0.46
63:Fg:474:CYS:HA	63:Fg:477:VAL:HG12	1.97	0.46
64:Fh:228:ALA:HB2	66:IA:192:TYR:HA	1.97	0.46
65:Fi:257:ILE:HG23	65:Fi:300:SER:HB3	1.97	0.46
66:IA:58:ASP:OD2	66:IA:60:ARG:NH2	2.48	0.46
67:IB:459:ASP:OD2	67:IB:484:HIS:ND1	2.48	0.46
1:CA:411:A:H1'	1:CA:412:U:H5	1.81	0.46
1:CA:594:U:H2'	1:CA:595:A:H8	1.80	0.46
3:CE:294:HIS:HB2	17:Ca:354:THR:HB	1.98	0.46
3:CE:358:GLU:HG2	3:CE:359:HIS:CD2	2.50	0.46
6:CI:231:LEU:HD23	6:CI:231:LEU:HA	1.76	0.46
10:CN:72:THR:HG21	15:CS:155:PHE:HD2	1.80	0.46
11:CO:336:GLU:HA	11:CO:339:ARG:HG2	1.98	0.46
13:CQ:210:LEU:O	13:CQ:214:ILE:HG12	2.16	0.46
17:Ca:306:HIS:HE1	17:Ca:318:ASP:H	1.64	0.46
23:Ck:819:GLU:OE1	23:Ck:822:ARG:NH2	2.42	0.46
29:Cv:680:ARG:HG3	29:Cv:764:LEU:HD22	1.98	0.46
29:Cv:1012:TRP:CH2	42:DM:236:MET:HE3	2.51	0.46
30:DA:813:SER:OG	30:DA:819:ARG:NH2	2.49	0.46
30:DA:1231:LEU:HD11	30:DA:1274:ARG:HH22	1.81	0.46
31:DB:493:ARG:HH22	36:DG:29:ASP:CG	2.22	0.46
32:DC:215:PRO:HA	32:DC:256:ILE:HD12	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:DC:295:VAL:HA	32:DC:298:ILE:HG22	1.98	0.46
32:DC:347:ASP:OD1	32:DC:347:ASP:N	2.49	0.46
32:DC:1017:PHE:HZ	32:DC:1037:ALA:HB2	1.81	0.46
33:DD:505:TYR:HA	33:DD:508:VAL:HG22	1.98	0.46
34:DE:50:GLU:OE1	34:DE:50:GLU:N	2.41	0.46
35:DF:51:TRP:HZ3	35:DF:147:ASP:HB3	1.81	0.46
35:DF:271:LEU:HD12	35:DF:308:VAL:HG11	1.98	0.46
46:DQ:58:ARG:NH2	50:DU:42:THR:OG1	2.49	0.46
51:DV:124:GLU:HB2	51:DV:127:THR:HG21	1.98	0.46
52:DW:55:TRP:NE1	52:DW:132:HIS:O	2.29	0.46
63:Fg:385:MET:HE2	63:Fg:470:VAL:HG13	1.98	0.46
64:Fh:76:HIS:NE2	67:IB:743:GLU:O	2.42	0.46
66:IA:197:VAL:HG23	66:IA:374:PRO:HD2	1.98	0.46
1:CA:40:U:H4'	48:DS:18:ARG:HD2	1.97	0.46
1:CA:125:U:OP2	13:CQ:189:TYR:OH	2.26	0.46
1:CA:402:U:H2'	1:CA:403:U:C6	2.51	0.46
1:CA:477:U:OP1	21:Ci:140:ASN:ND2	2.48	0.46
6:CI:438:ARG:HD3	7:CJ:383:THR:HG22	1.97	0.46
8:CK:104:MET:HE1	14:CR:38:TYR:CE2	2.50	0.46
22:Cj:225:LEU:HD22	22:Cj:230:VAL:HG21	1.98	0.46
23:Ck:330:ILE:HG21	23:Ck:591:PRO:HG2	1.98	0.46
28:Cr:23:LEU:HD13	28:Cr:32:THR:HA	1.98	0.46
28:Cr:148:TRP:NE1	28:Cr:186:ASN:OD1	2.49	0.46
29:Cv:52:HIS:HD2	29:Cv:55:ARG:HH11	1.63	0.46
29:Cv:96:HIS:HD1	29:Cv:97:GLN:HG3	1.80	0.46
29:Cv:332:ALA:O	29:Cv:335:GLU:HG3	2.16	0.46
29:Cv:407:MET:HA	29:Cv:427:TYR:O	2.16	0.46
31:DB:79:GLU:OE1	34:DE:447:ARG:NH2	2.49	0.46
31:DB:687:GLU:OE1	31:DB:690:ARG:NH1	2.49	0.46
33:DD:37:LEU:HD13	33:DD:42:MET:HG3	1.98	0.46
36:DG:215:LEU:O	36:DG:218:THR:OG1	2.34	0.46
37:DH:221:HIS:O	37:DH:225:ILE:HG13	2.15	0.46
39:DJ:336:ASP:OD1	39:DJ:361:ARG:NE	2.40	0.46
43:DN:16:ASP:HB3	43:DN:175:LYS:NZ	2.31	0.46
43:DN:228:LEU:HB2	43:DN:288:PHE:CD1	2.51	0.46
49:DT:29:TRP:O	49:DT:37:TYR:OH	2.28	0.46
50:DU:110:THR:O	50:DU:113:GLN:HG2	2.16	0.46
60:F9:354:MET:HE1	64:Fh:191:ARG:HH11	1.81	0.46
60:F9:541:PHE:HZ	60:F9:556:ILE:HG12	1.81	0.46
62:Ff:636:LEU:HD12	62:Ff:718:TRP:HZ3	1.81	0.46
67:IB:535:LEU:HD12	71:UF:3:UNK:HA	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:25:U:OP1	33:DD:14:LYS:NZ	2.49	0.46
4:CF:6:PHE:CE2	4:CF:94:LYS:HG2	2.51	0.46
8:CK:13:LYS:HE3	8:CK:14:PRO:HD2	1.98	0.46
8:CK:310:ILE:HA	16:CU:43:PRO:HD2	1.98	0.46
9:CL:68:ARG:HB3	9:CL:121:ILE:HB	1.97	0.46
11:CO:248:ILE:HA	11:CO:251:VAL:HG12	1.97	0.46
14:CR:273:ASP:N	14:CR:273:ASP:OD1	2.49	0.46
18:Cb:125:MET:SD	18:Cb:146:VAL:HG22	2.56	0.46
31:DB:135:ARG:HG3	31:DB:225:PRO:HG3	1.97	0.46
31:DB:568:ARG:NE	31:DB:849:ASP:OD2	2.49	0.46
32:DC:584:ILE:HD11	32:DC:621:LEU:HD23	1.98	0.46
33:DD:516:SER:HA	33:DD:534:PHE:CE1	2.51	0.46
34:DE:172:ASP:O	34:DE:176:ARG:HD3	2.16	0.46
34:DE:201:PHE:HA	34:DE:204:VAL:HG12	1.98	0.46
34:DE:462:SER:HB3	34:DE:465:ASN:HB3	1.98	0.46
39:DJ:234:GLU:OE2	39:DJ:237:SER:OG	2.34	0.46
44:DO:70:ILE:HG12	44:DO:120:LEU:HB2	1.96	0.46
48:DS:98:CYS:O	48:DS:102:GLY:N	2.48	0.46
57:F3:78:THR:HG23	57:F3:79:HIS:CD2	2.51	0.46
58:F6:672:ILE:HD11	66:IA:87:ARG:NH2	2.31	0.46
59:F7:466:SER:HB3	59:F7:506:LEU:HB2	1.96	0.46
62:Ff:559:ASP:OD1	62:Ff:559:ASP:N	2.46	0.46
62:Ff:601:THR:O	65:Fi:586:ARG:NH1	2.49	0.46
63:Fg:346:LYS:HB3	63:Fg:352:PRO:HD3	1.98	0.46
66:IA:94:GLU:HB3	67:IB:653:TRP:CD2	2.51	0.46
66:IA:373:LYS:HB3	66:IA:374:PRO:HD3	1.98	0.46
66:IA:402:VAL:HB	66:IA:431:ALA:HB3	1.97	0.46
1:CA:299:U:H4'	1:CA:300:G:O5'	2.16	0.45
1:CA:547:U:C4	64:Fh:44:ALA:HB3	2.51	0.45
5:CH:90:ASP:OD1	5:CH:91:LEU:N	2.36	0.45
6:CI:243:ASP:OD2	6:CI:280:LYS:NZ	2.39	0.45
10:CN:30:LEU:HD21	35:DF:164:ILE:HG23	1.98	0.45
10:CN:166:ILE:HD11	23:Ck:766:LYS:HB3	1.98	0.45
11:CO:348:PRO:HB2	13:CQ:175:LEU:HB3	1.98	0.45
12:CP:58:ILE:HD12	30:DA:78:GLY:HA3	1.97	0.45
14:CR:152:PRO:HA	14:CR:155:VAL:HG22	1.98	0.45
29:Cv:192:LEU:O	29:Cv:196:MET:HG2	2.15	0.45
29:Cv:960:GLN:HG2	33:DD:761:ARG:HH11	1.81	0.45
31:DB:748:HIS:HD2	31:DB:783:VAL:O	1.98	0.45
32:DC:674:THR:O	32:DC:678:ARG:HG3	2.15	0.45
32:DC:1075:GLU:OE2	34:DE:582:GLU:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:DD:794:ARG:HH21	33:DD:808:THR:HA	1.81	0.45
35:DF:341:VAL:HG12	35:DF:346:LEU:HD11	1.96	0.45
36:DG:215:LEU:HD13	36:DG:215:LEU:HA	1.86	0.45
37:DH:530:VAL:HG13	37:DH:532:ARG:HH21	1.81	0.45
38:DI:66:ARG:HA	38:DI:177:THR:HG21	1.97	0.45
41:DL:18:ARG:HG2	41:DL:19:VAL:HG22	1.98	0.45
46:DQ:142:PHE:HA	46:DQ:145:VAL:HG12	1.98	0.45
50:DU:94:TRP:CD1	50:DU:177:ASP:HB3	2.51	0.45
50:DU:159:ASP:OD1	50:DU:159:ASP:N	2.48	0.45
53:DX:85:LYS:HD2	54:DY:163:LYS:HE2	1.98	0.45
57:F3:113:ASP:OD1	57:F3:183:ARG:NH1	2.49	0.45
59:F7:102:PRO:HB3	59:F7:107:ILE:HD11	1.98	0.45
65:Fi:334:TYR:HA	65:Fi:353:LEU:HD22	1.98	0.45
67:IB:470:ILE:HG13	67:IB:472:ASP:H	1.80	0.45
1:CA:116:U:H4'	57:F3:173:ARG:HD3	1.98	0.45
1:CA:132:G:H21	13:CQ:58:HIS:CD2	2.35	0.45
1:CA:435:G:N2	35:DF:22:LEU:O	2.49	0.45
1:CA:529:A:H3'	6:CI:423:GLU:HA	1.99	0.45
3:CE:91:ASN:O	3:CE:299:ASN:HB3	2.16	0.45
5:CH:105:ILE:HD11	29:Cv:221:GLY:HA3	1.99	0.45
6:CI:417:SER:HB3	8:CK:29:PRO:HG2	1.99	0.45
8:CK:262:ARG:NH1	8:CK:267:ARG:O	2.50	0.45
12:CP:110:LEU:HD13	19:Cd:54:PHE:HZ	1.81	0.45
17:Ca:90:TYR:CZ	30:DA:427:ASP:HB2	2.52	0.45
19:Cd:157:ARG:HA	19:Cd:157:ARG:HD2	1.67	0.45
20:Cg:222:TRP:NE1	20:Cg:272:GLU:OE2	2.50	0.45
29:Cv:52:HIS:CD2	29:Cv:55:ARG:HH11	2.34	0.45
30:DA:180:ASN:OD1	30:DA:183:SER:N	2.49	0.45
31:DB:109:PRO:HG2	31:DB:119:ALA:HB3	1.98	0.45
31:DB:657:GLU:OE2	35:DF:565:TYR:OH	2.25	0.45
32:DC:46:ARG:HH22	32:DC:401:ARG:NH1	2.14	0.45
32:DC:79:VAL:HG21	32:DC:712:LEU:HD23	1.98	0.45
32:DC:494:ALA:HB1	32:DC:517:LEU:HD13	1.99	0.45
33:DD:606:ARG:NH1	47:DR:221:ARG:O	2.49	0.45
39:DJ:303:SER:OG	39:DJ:308:ARG:NH1	2.50	0.45
46:DQ:38:THR:HB	50:DU:98:MET:HE3	1.97	0.45
47:DR:34:ASN:H	47:DR:39:GLN:NE2	2.14	0.45
48:DS:98:CYS:O	48:DS:102:GLY:CA	2.64	0.45
49:DT:130:LYS:HA	49:DT:156:PHE:CD2	2.51	0.45
49:DT:227:GLU:HG2	49:DT:228:LEU:HD22	1.98	0.45
59:F7:508:ALA:HB1	59:F7:540:LEU:HD23	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:Ff:283:ARG:HA	62:Ff:283:ARG:NH1	2.32	0.45
62:Ff:533:PRO:HB3	62:Ff:672:ILE:HG13	1.97	0.45
2:CC:34:PHE:HB3	37:DH:437:GLN:HB3	1.98	0.45
28:Cr:214:ARG:HH11	29:Cv:557:ALA:HB1	1.82	0.45
30:DA:498:GLU:HG3	30:DA:502:LYS:HZ2	1.81	0.45
30:DA:653:LYS:HB3	30:DA:726:GLU:HB2	1.97	0.45
30:DA:740:VAL:HG12	30:DA:743:LEU:H	1.82	0.45
30:DA:906:TYR:O	30:DA:910:HIS:HB3	2.16	0.45
30:DA:1266:ARG:O	30:DA:1270:ARG:HG2	2.17	0.45
32:DC:429:SER:HB3	32:DC:447:ASN:HD21	1.81	0.45
32:DC:1083:THR:OG1	49:DT:77:PRO:O	2.28	0.45
35:DF:325:LEU:HD22	35:DF:486:LEU:HD11	1.98	0.45
36:DG:529:ASP:OD1	36:DG:530:PHE:N	2.49	0.45
36:DG:568:ALA:HA	36:DG:571:VAL:HG12	1.98	0.45
45:DP:139:ARG:HG3	45:DP:146:PHE:CE2	2.51	0.45
46:DQ:155:LEU:HD12	46:DQ:164:LEU:HG	1.98	0.45
57:F3:225:LEU:HD21	57:F3:259:VAL:HG22	1.98	0.45
59:F7:245:SER:HB2	59:F7:248:SER:HB3	1.97	0.45
64:Fh:74:VAL:HG12	67:IB:747:THR:HA	1.97	0.45
65:Fi:214:VAL:HG21	65:Fi:253:LEU:HD13	1.99	0.45
67:IB:416:PHE:CD1	67:IB:473:ARG:HB3	2.52	0.45
1:CA:64:G:N2	1:CA:135:U:O4'	2.49	0.45
1:CA:85:U:OP1	33:DD:342:ARG:NH2	2.50	0.45
7:CJ:647:ASP:OD1	7:CJ:648:VAL:N	2.49	0.45
8:CK:308:GLU:HG2	16:CU:45:VAL:HG13	1.97	0.45
9:CL:131:GLY:HA3	66:IA:47:GLN:HE21	1.81	0.45
11:CO:143:LEU:HD21	11:CO:155:PHE:HB2	1.99	0.45
17:Ca:600:PRO:HB3	64:Fh:129:ASN:HB2	1.98	0.45
27:Cq:63:PRO:HD3	42:DM:149:LEU:HD23	1.98	0.45
27:Cq:181:HIS:HB2	27:Cq:201:GLU:HG3	1.97	0.45
29:Cv:531:MET:N	29:Cv:531:MET:SD	2.90	0.45
30:DA:1261:PRO:O	30:DA:1305:PRO:HA	2.16	0.45
31:DB:189:VAL:HA	31:DB:194:GLN:HE21	1.82	0.45
31:DB:527:GLU:N	31:DB:530:GLU:OE1	2.50	0.45
31:DB:615:ASN:HA	31:DB:618:LEU:HD12	1.98	0.45
32:DC:961:THR:OG1	34:DE:563:ASP:OD2	2.23	0.45
32:DC:1164:TRP:HZ2	37:DH:322:ARG:HG3	1.81	0.45
33:DD:325:LYS:O	33:DD:385:ASN:ND2	2.49	0.45
34:DE:474:LEU:HD23	34:DE:474:LEU:H	1.80	0.45
36:DG:102:MET:HE1	36:DG:134:PRO:HA	1.97	0.45
36:DG:223:VAL:O	36:DG:227:GLU:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:DI:233:ARG:NH2	38:DI:272:CYS:O	2.46	0.45
44:DO:83:ARG:HD2	44:DO:126:PRO:HB2	1.99	0.45
46:DQ:35:VAL:HG13	46:DQ:36:GLU:HG2	1.98	0.45
58:F6:655:ILE:HA	67:IB:669:LYS:HD2	1.97	0.45
1:CA:400:U:H2'	1:CA:401:A:O4'	2.16	0.45
16:CU:157:ALA:O	16:CU:161:GLN:HG2	2.16	0.45
20:Cg:304:PHE:HA	53:DX:106:LYS:HE2	1.98	0.45
22:Cj:83:LEU:HD23	45:DP:169:TYR:HD2	1.81	0.45
23:Ck:792:ARG:HB3	51:DV:149:ASP:HA	1.99	0.45
29:Cv:169:LYS:HG2	29:Cv:179:GLY:HA3	1.99	0.45
30:DA:1412:THR:HG21	30:DA:1606:THR:HG21	1.98	0.45
32:DC:629:VAL:HA	32:DC:632:LEU:HB2	1.99	0.45
32:DC:750:PHE:HZ	32:DC:753:LEU:HB2	1.81	0.45
36:DG:486:ALA:HB1	36:DG:568:ALA:HB3	1.99	0.45
37:DH:313:SER:HB2	37:DH:316:THR:HG23	1.99	0.45
39:DJ:129:ALA:HB2	39:DJ:168:TYR:HA	1.99	0.45
50:DU:203:ASN:HD21	50:DU:205:ALA:HB2	1.81	0.45
60:F9:336:GLN:NE2	66:IA:195:ALA:O	2.49	0.45
61:FO:167:HIS:ND1	61:FO:168:PRO:HD2	2.30	0.45
64:Fh:63:THR:HA	67:IB:756:GLN:HG3	1.99	0.45
3:CE:88:ASP:OD2	3:CE:92:GLU:N	2.49	0.45
5:CH:77:VAL:HG22	33:DD:746:PRO:HD3	1.99	0.45
17:Ca:89:ARG:NH1	55:DZ:11:LYS:O	2.49	0.45
20:Cg:73:ASP:O	20:Cg:76:SER:OG	2.28	0.45
23:Ck:834:MET:HA	23:Ck:838:LEU:HB3	1.98	0.45
32:DC:228:GLN:NE2	32:DC:237:SER:OG	2.49	0.45
32:DC:310:ARG:NH1	32:DC:315:LEU:HD21	2.32	0.45
32:DC:617:LYS:HB3	32:DC:767:GLU:OE2	2.17	0.45
32:DC:1009:THR:HA	40:DK:157:ALA:HB3	1.98	0.45
33:DD:462:LEU:HD23	33:DD:507:GLN:HB2	1.99	0.45
35:DF:194:THR:HG21	35:DF:230:PRO:HB3	1.97	0.45
35:DF:355:GLY:HA3	39:DJ:77:VAL:HG13	1.98	0.45
37:DH:504:ARG:HD2	40:DK:291:GLN:HG2	1.98	0.45
40:DK:11:GLY:O	40:DK:14:LYS:HG2	2.16	0.45
41:DL:9:ASP:O	41:DL:18:ARG:NH2	2.39	0.45
42:DM:4:TYR:OH	42:DM:110:GLU:OE2	2.24	0.45
44:DO:65:GLU:OE1	44:DO:68:ARG:NH2	2.40	0.45
44:DO:88:GLN:H	44:DO:88:GLN:HG2	1.56	0.45
45:DP:28:ASN:HB3	45:DP:31:ILE:HG13	1.99	0.45
47:DR:189:GLU:O	47:DR:191:GLN:NE2	2.49	0.45
54:DY:37:ARG:HA	54:DY:40:ARG:HE	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:Da:17:HIS:CE1	56:Da:18:LYS:HG3	2.52	0.45
57:F3:259:VAL:HB	57:F3:295:VAL:HG21	1.99	0.45
59:F7:49:ASP:HB3	59:F7:285:ARG:HD3	1.97	0.45
63:Fg:7:ARG:HA	63:Fg:503:GLU:O	2.17	0.45
65:Fi:232:GLN:NE2	65:Fi:556:PRO:HG3	2.32	0.45
1:CA:486:C:OP1	1:CA:489:A:N6	2.50	0.45
1:CA:548:G:O6	58:F6:646:TYR:OH	2.31	0.45
8:CK:176:TYR:CE2	8:CK:180:ASP:HB3	2.51	0.45
10:CN:55:LEU:HB2	10:CN:59:VAL:HG23	1.98	0.45
19:Cd:100:LYS:O	19:Cd:103:ILE:HG12	2.17	0.45
26:Cp:57:GLU:HB3	26:Cp:75:LYS:NZ	2.31	0.45
28:Cr:92:PHE:HD2	28:Cr:93:LEU:HD22	1.82	0.45
29:Cv:96:HIS:ND1	29:Cv:97:GLN:HG3	2.31	0.45
29:Cv:774:LYS:O	29:Cv:776:LYS:NZ	2.48	0.45
29:Cv:944:HIS:CE1	29:Cv:946:PRO:HG2	2.51	0.45
32:DC:103:LEU:HG	34:DE:158:LEU:HD11	1.99	0.45
32:DC:330:ARG:HH12	32:DC:341:ASP:HA	1.82	0.45
33:DD:605:ARG:NH1	33:DD:642:ASP:OD2	2.33	0.45
35:DF:71:ARG:O	35:DF:71:ARG:NE	2.50	0.45
36:DG:179:LEU:HD12	36:DG:184:ALA:HB3	1.99	0.45
36:DG:529:ASP:HB3	36:DG:532:VAL:HG23	1.99	0.45
38:DI:256:ARG:HD3	38:DI:269:PHE:HE1	1.81	0.45
38:DI:327:ARG:NH2	44:DO:201:GLU:OE2	2.50	0.45
48:DS:175:CYS:SG	48:DS:211:CYS:HB3	2.56	0.45
52:DW:93:HIS:O	52:DW:97:SER:HB3	2.17	0.45
59:F7:275:THR:HA	59:F7:278:GLU:HG2	1.98	0.45
62:Ff:320:PRO:HG3	62:Ff:591:PHE:CE1	2.52	0.45
66:IA:373:LYS:HE2	66:IA:374:PRO:HD3	1.99	0.45
3:CE:400:LEU:HG	3:CE:405:LYS:O	2.17	0.45
7:CJ:249:LEU:H	7:CJ:249:LEU:HG	1.66	0.45
17:Ca:267:LEU:HD13	17:Ca:267:LEU:HA	1.86	0.45
17:Ca:326:PHE:HE2	33:DD:782:ILE:HD11	1.82	0.45
21:Ci:77:ARG:HD3	21:Ci:80:TYR:HB2	1.97	0.45
23:Ck:36:ARG:HH22	31:DB:285:MET:HE3	1.81	0.45
23:Ck:75:ARG:HE	34:DE:736:TRP:HH2	1.65	0.45
23:Ck:733:LEU:HD21	23:Ck:746:LEU:HD12	1.97	0.45
30:DA:65:ILE:HG23	33:DD:690:PRO:HG2	1.98	0.45
30:DA:1533:THR:HG22	30:DA:1600:ASN:HD22	1.82	0.45
31:DB:876:LEU:HD21	31:DB:938:ILE:HD11	1.98	0.45
32:DC:396:ILE:HA	32:DC:402:VAL:HG21	1.98	0.45
32:DC:666:GLU:HB3	32:DC:790:ARG:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DE:558:ASP:O	34:DE:561:THR:HG22	2.17	0.45
35:DF:52:SER:HB2	35:DF:60:PRO:HB2	1.99	0.45
43:DN:53:LEU:O	43:DN:67:TYR:OH	2.30	0.45
49:DT:208:ARG:NH2	49:DT:217:GLU:OE1	2.44	0.45
58:F6:387:ARG:HA	58:F6:390:GLU:HG2	1.97	0.45
58:F6:572:LEU:HD11	62:Ff:740:MET:HE1	1.99	0.45
62:Ff:217:ARG:NE	62:Ff:541:SER:HB3	2.32	0.45
65:Fi:398:ASP:OD1	65:Fi:399:ALA:N	2.49	0.45
67:IB:576:THR:HG23	67:IB:600:LYS:HG2	1.98	0.45
1:CA:332:U:H2'	1:CA:333:U:C6	2.52	0.45
6:CI:329:HIS:HD2	6:CI:366:ARG:NH1	2.15	0.45
10:CN:33:GLU:CD	35:DF:170:ARG:HH12	2.24	0.45
15:CS:206:TRP:O	31:DB:1125:HIS:NE2	2.47	0.45
22:Cj:102:GLN:HE21	22:Cj:142:ASN:ND2	2.15	0.45
30:DA:1148:GLY:O	42:DM:162:ARG:NH1	2.46	0.45
31:DB:369:GLN:O	31:DB:372:GLU:HG3	2.17	0.45
33:DD:267:LEU:HG	33:DD:268:PRO:HD2	1.99	0.45
36:DG:165:VAL:HG23	36:DG:199:LEU:HD22	1.98	0.45
37:DH:448:PHE:HA	37:DH:451:GLU:HG2	1.99	0.45
39:DJ:137:MET:HE2	39:DJ:168:TYR:HE2	1.82	0.45
41:DL:275:LEU:HD23	41:DL:275:LEU:H	1.82	0.45
44:DO:136:ASP:HA	44:DO:139:GLU:HG2	1.99	0.45
59:F7:146:THR:HG23	59:F7:149:ARG:H	1.82	0.45
62:Ff:196:PRO:HD2	62:Ff:441:LEU:HD21	1.99	0.45
63:Fg:122:LEU:HG	63:Fg:543:LEU:HD23	1.99	0.45
1:CA:59:U:H5'	1:CA:167:A:H8	1.81	0.45
1:CA:258:U:P	17:Ca:589:ARG:HH12	2.40	0.45
3:CE:382:SER:HB2	3:CE:383:PRO:HD3	1.98	0.45
4:CF:46:ARG:HD3	19:Cd:200:LEU:HD22	1.99	0.45
6:CI:255:SER:HB3	31:DB:1003:LYS:HG2	1.99	0.45
7:CJ:414:LYS:HD3	37:DH:352:LEU:HD11	1.99	0.45
8:CK:201:ARG:HH21	8:CK:202:ARG:HD2	1.82	0.45
10:CN:108:VAL:HG11	10:CN:118:MET:HG3	1.97	0.45
11:CO:347:ARG:HH12	13:CQ:137:LEU:HD12	1.82	0.45
13:CQ:190:PRO:HA	59:F7:109:ASN:HD22	1.82	0.45
14:CR:116:PRO:HB3	14:CR:135:PHE:CZ	2.52	0.45
16:CU:126:LEU:HA	16:CU:129:THR:HG22	1.99	0.45
17:Ca:566:MET:HE2	33:DD:98:GLY:HA2	1.99	0.45
21:CI:141:LYS:HA	21:CI:144:ARG:HD2	1.99	0.45
23:Ck:718:ASP:OD1	23:Ck:719:GLY:N	2.47	0.45
30:DA:124:SER:HB2	30:DA:134:ASN:HD21	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:DA:708:GLU:OE1	30:DA:708:GLU:N	2.50	0.45
30:DA:824:GLU:O	30:DA:828:LYS:HG2	2.16	0.45
31:DB:173:ARG:HD3	31:DB:173:ARG:HA	1.74	0.45
31:DB:322:SER:O	31:DB:326:THR:HG23	2.17	0.45
31:DB:350:GLU:OE1	34:DE:168:GLN:NE2	2.49	0.45
32:DC:914:ARG:HD3	32:DC:929:TRP:CD1	2.52	0.45
33:DD:589:GLN:OE1	33:DD:589:GLN:N	2.50	0.45
36:DG:453:ASP:OD1	36:DG:454:ASP:N	2.50	0.45
36:DG:624:ARG:HB3	51:DV:183:LEU:C	2.40	0.45
46:DQ:102:GLN:N	46:DQ:102:GLN:OE1	2.43	0.45
49:DT:140:ASN:HD21	49:DT:175:SER:HA	1.79	0.45
58:F6:367:THR:OG1	58:F6:368:SER:N	2.50	0.45
58:F6:574:HIS:ND1	58:F6:587:GLN:OE1	2.50	0.45
61:FO:137:ALA:O	61:FO:140:THR:OG1	2.28	0.45
63:Fg:140:SER:OG	63:Fg:165:ARG:NH2	2.37	0.45
65:Fi:448:LEU:HD11	65:Fi:546:ALA:HB2	1.98	0.45
1:CA:476:A:N6	41:DL:26:THR:OG1	2.50	0.44
5:CH:44:ASP:HA	5:CH:47:ARG:HG2	1.99	0.44
7:CJ:154:THR:OG1	7:CJ:202:ASP:OD1	2.32	0.44
9:CL:91:LEU:HB3	9:CL:106:CYS:SG	2.57	0.44
17:Ca:285:GLU:OE1	17:Ca:285:GLU:N	2.40	0.44
29:Cv:70:ARG:NH1	29:Cv:76:ASP:O	2.37	0.44
30:DA:515:THR:HG23	30:DA:837:ARG:HH22	1.82	0.44
31:DB:388:VAL:HG12	49:DT:110:TYR:CE1	2.52	0.44
31:DB:491:GLY:O	31:DB:964:ARG:NH2	2.50	0.44
31:DB:964:ARG:HB2	31:DB:1005:ILE:HD13	1.98	0.44
32:DC:164:SER:N	32:DC:165:PRO:HD3	2.32	0.44
32:DC:448:GLU:O	32:DC:452:GLN:HG2	2.17	0.44
32:DC:626:ALA:HA	32:DC:629:VAL:HG22	1.99	0.44
34:DE:676:GLU:HA	34:DE:679:THR:HG22	1.99	0.44
37:DH:277:THR:OG1	37:DH:278:VAL:N	2.49	0.44
37:DH:517:ALA:O	37:DH:523:ARG:HD2	2.17	0.44
40:DK:3:PHE:HD2	40:DK:4:ARG:HG3	1.82	0.44
47:DR:42:MET:HB2	47:DR:109:TYR:CZ	2.53	0.44
51:DV:114:VAL:HB	51:DV:118:GLN:HB2	1.99	0.44
51:DV:149:ASP:OD1	51:DV:150:ARG:N	2.49	0.44
59:F7:264:VAL:HA	59:F7:297:LEU:HD21	1.98	0.44
60:F9:291:GLU:O	60:F9:294:ARG:HG2	2.17	0.44
1:CA:401:A:O2'	1:CA:402:U:O4'	2.34	0.44
5:CH:38:LEU:HG	30:DA:185:PHE:CE2	2.52	0.44
8:CK:188:TYR:OH	8:CK:308:GLU:OE2	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CP:126:PRO:HG2	17:Ca:432:ARG:HB3	1.99	0.44
15:CS:159:GLU:OE1	15:CS:175:ARG:HB2	2.17	0.44
17:Ca:110:LEU:HD23	30:DA:844:ILE:HD11	1.99	0.44
18:Cb:222:SER:HB2	18:Cb:272:GLN:HB2	1.99	0.44
19:Cd:13:ARG:NH2	19:Cd:28:MET:HB3	2.33	0.44
29:Cv:673:LEU:HD22	44:DO:105:ARG:HB3	1.99	0.44
29:Cv:947:THR:HG21	42:DM:96:ALA:HB2	1.98	0.44
30:DA:1379:GLU:O	30:DA:1382:SER:OG	2.34	0.44
32:DC:269:VAL:O	32:DC:272:GLU:HG3	2.16	0.44
32:DC:361:ASP:O	32:DC:365:LYS:HG2	2.17	0.44
32:DC:439:ALA:HB2	32:DC:498:LEU:HB3	1.98	0.44
38:DI:265:HIS:HB2	38:DI:295:GLY:HA2	1.99	0.44
39:DJ:313:ARG:HG2	49:DT:246:LEU:HD11	1.99	0.44
45:DP:138:CYS:SG	45:DP:144:ILE:HD12	2.58	0.44
45:DP:173:HIS:O	45:DP:176:PRO:HD2	2.17	0.44
47:DR:124:ARG:HB2	47:DR:137:CYS:SG	2.57	0.44
59:F7:111:THR:N	59:F7:115:ARG:HE	2.14	0.44
61:FO:314:LEU:HD11	61:FO:319:LEU:HD23	1.99	0.44
63:Fg:200:PRO:HB2	63:Fg:234:TYR:CG	2.52	0.44
64:Fh:252:LEU:HD22	66:IA:429:GLN:HB3	2.00	0.44
64:Fh:281:ILE:HG13	64:Fh:287:LEU:HB2	1.98	0.44
5:CH:267:HIS:O	5:CH:271:GLU:HG2	2.18	0.44
6:CI:87:TYR:HB3	8:CK:113:ARG:HG2	1.98	0.44
7:CJ:260:LEU:HD12	7:CJ:424:HIS:CG	2.52	0.44
8:CK:184:GLU:HG3	14:CR:181:ARG:HH21	1.82	0.44
10:CN:19:LYS:HB2	10:CN:22:THR:HG23	1.98	0.44
11:CO:239:LEU:HD11	11:CO:249:LYS:HG2	1.99	0.44
12:CP:72:GLN:HE22	33:DD:69:LEU:HD12	1.81	0.44
17:Ca:29:LEU:HD21	64:Fh:116:VAL:HG11	1.99	0.44
23:Ck:46:ILE:HG23	31:DB:511:ARG:NH2	2.32	0.44
24:Cm:162:ARG:HD2	24:Cm:164:HIS:CE1	2.52	0.44
29:Cv:960:GLN:HG2	33:DD:761:ARG:NH1	2.33	0.44
29:Cv:1114:ASP:OD2	29:Cv:1117:TYR:N	2.43	0.44
30:DA:52:MET:HE2	30:DA:52:MET:HB3	1.89	0.44
31:DB:337:TYR:CD2	34:DE:33:ILE:HB	2.52	0.44
31:DB:1047:TRP:CD1	39:DJ:41:PRO:HG3	2.53	0.44
32:DC:80:LEU:HD21	32:DC:1050:THR:HG22	2.00	0.44
32:DC:624:TRP:HB3	32:DC:628:ASN:OD1	2.18	0.44
32:DC:1075:GLU:O	32:DC:1080:TYR:HB2	2.16	0.44
33:DD:228:ALA:HB3	33:DD:301:VAL:HG11	1.98	0.44
33:DD:801:GLU:O	33:DD:807:ARG:NH2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DE:671:ASN:O	34:DE:674:GLU:HG3	2.17	0.44
35:DF:590:LYS:HE2	35:DF:590:LYS:HB3	1.76	0.44
39:DJ:66:TRP:CD1	39:DJ:68:GLU:H	2.35	0.44
43:DN:50:LEU:HA	43:DN:133:PHE:HB3	1.98	0.44
43:DN:109:ASN:HB2	43:DN:138:THR:HG21	1.98	0.44
44:DO:125:LEU:HB3	44:DO:126:PRO:HD3	1.98	0.44
49:DT:49:TYR:OH	49:DT:146:GLN:OE1	2.35	0.44
58:F6:423:THR:HG23	58:F6:426:GLU:H	1.82	0.44
59:F7:242:GLU:HA	59:F7:249:PHE:HB3	1.99	0.44
62:Ff:298:ASP:HB3	62:Ff:339:VAL:HG21	1.99	0.44
63:Fg:193:ALA:O	63:Fg:258:ARG:NH1	2.50	0.44
67:IB:462:ARG:HG3	67:IB:477:ALA:HB1	1.99	0.44
1:CA:398:U:OP2	41:DL:265:ARG:NH1	2.51	0.44
2:CC:4:ILE:HD13	32:DC:964:THR:HB	1.99	0.44
3:CE:41:ARG:HH12	42:DM:247:MET:HE2	1.82	0.44
3:CE:71:ILE:O	3:CE:73:HIS:ND1	2.50	0.44
7:CJ:392:TYR:HD1	10:CN:131:ARG:HA	1.83	0.44
7:CJ:499:SER:HB3	7:CJ:502:GLU:HG2	1.99	0.44
8:CK:293:ARG:HG2	58:F6:590:TRP:CD2	2.51	0.44
17:Ca:437:LYS:HD2	26:Cp:41:ILE:HG23	2.00	0.44
19:Cd:239:VAL:HG11	58:F6:423:THR:OG1	2.17	0.44
25:Cn:195:PHE:O	25:Cn:199:ILE:HG12	2.18	0.44
30:DA:357:THR:HB	30:DA:360:GLN:HG3	1.97	0.44
30:DA:466:VAL:HG23	30:DA:838:GLU:HB3	2.00	0.44
30:DA:1088:ALA:HB3	30:DA:1091:GLU:HB2	1.99	0.44
32:DC:121:LEU:HD11	32:DC:527:TYR:HB2	1.99	0.44
35:DF:325:LEU:HB3	35:DF:333:ALA:HB2	1.98	0.44
50:DU:218:ARG:HG3	50:DU:219:THR:HG23	1.99	0.44
59:F7:598:GLY:O	59:F7:602:GLN:HB3	2.17	0.44
1:CA:547:U:H5"	58:F6:649:MET:HB3	1.98	0.44
2:CC:57:SER:H	2:CC:73:SER:HB2	1.82	0.44
5:CH:116:HIS:CD2	38:DI:405:LEU:HD23	2.53	0.44
11:CO:356:GLN:O	11:CO:360:GLN:HG2	2.17	0.44
11:CO:396:LYS:HE3	47:DR:18:LYS:HD2	2.00	0.44
16:CU:79:TYR:CD2	16:CU:80:GLN:HG3	2.53	0.44
17:Ca:127:TYR:HA	29:Cv:1025:PHE:HZ	1.82	0.44
18:Cb:119:ARG:HH21	27:Cq:50:GLU:HG3	1.82	0.44
26:Cp:57:GLU:O	26:Cp:61:GLU:HG2	2.18	0.44
32:DC:73:ARG:HE	40:DK:250:VAL:HG22	1.83	0.44
32:DC:233:ILE:HG22	32:DC:235:LEU:HG	2.00	0.44
33:DD:390:VAL:HG13	33:DD:457:LEU:HD22	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:DD:613:TRP:CZ3	33:DD:646:ILE:HD11	2.53	0.44
34:DE:698:GLN:HG3	40:DK:59:TRP:HZ2	1.82	0.44
36:DG:382:CYS:HA	36:DG:385:VAL:HG12	1.99	0.44
45:DP:12:LEU:O	45:DP:16:ARG:HG2	2.16	0.44
47:DR:213:ASP:OD1	47:DR:213:ASP:N	2.44	0.44
52:DW:13:PRO:HD2	53:DX:55:LEU:HD23	1.99	0.44
58:F6:449:MET:HG2	58:F6:464:GLY:HA2	1.99	0.44
58:F6:454:SER:HB3	58:F6:467:ALA:HB1	2.00	0.44
62:Ff:217:ARG:HH21	62:Ff:543:ARG:HH22	1.64	0.44
62:Ff:561:PHE:O	62:Ff:565:GLN:HG2	2.17	0.44
65:Fi:497:PHE:O	65:Fi:557:SER:N	2.32	0.44
66:IA:68:ARG:HG2	66:IA:107:TYR:CD2	2.52	0.44
3:CE:349:TRP:HH2	17:Ca:132:ARG:HB2	1.81	0.44
4:CF:71:MET:HE1	4:CF:79:VAL:HG21	1.98	0.44
5:CH:195:ARG:HG3	29:Cv:237:ALA:O	2.18	0.44
6:CI:40:TRP:CE2	7:CJ:159:LEU:HG	2.52	0.44
7:CJ:496:LEU:HD13	7:CJ:521:VAL:HG13	2.00	0.44
7:CJ:716:ARG:HG2	21:Ci:77:ARG:HH21	1.83	0.44
8:CK:320:MET:HB2	16:CU:81:GLU:HB2	2.00	0.44
13:CQ:214:ILE:HG23	61:FO:34:LYS:HD2	2.00	0.44
17:Ca:225:PRO:HD2	17:Ca:228:LYS:HG2	2.00	0.44
20:Cg:356:CYS:SG	20:Cg:357:THR:N	2.91	0.44
22:Cj:126:TYR:HD2	47:DR:268:HIS:HA	1.83	0.44
30:DA:739:ARG:HB2	30:DA:792:GLN:HE22	1.82	0.44
30:DA:1426:GLN:NE2	30:DA:1430:ASP:OD2	2.50	0.44
31:DB:762:TYR:OH	31:DB:779:VAL:HB	2.18	0.44
32:DC:332:GLN:O	32:DC:335:VAL:HG12	2.18	0.44
33:DD:608:ASP:N	33:DD:608:ASP:OD1	2.50	0.44
33:DD:754:THR:OG1	33:DD:756:TRP:NE1	2.50	0.44
34:DE:480:ARG:H	34:DE:480:ARG:HG3	1.57	0.44
39:DJ:102:ALA:HA	39:DJ:105:THR:HG22	1.98	0.44
39:DJ:201:SER:HB2	39:DJ:234:GLU:HG2	2.00	0.44
39:DJ:229:ASP:CG	39:DJ:232:ARG:HG2	2.43	0.44
39:DJ:300:TRP:O	39:DJ:304:ILE:HG12	2.17	0.44
40:DK:221:PRO:HG2	40:DK:222:LEU:HD12	2.00	0.44
46:DQ:145:VAL:HG23	46:DQ:176:ARG:HD2	2.00	0.44
48:DS:98:CYS:O	48:DS:102:GLY:HA2	2.18	0.44
50:DU:86:ILE:HG23	50:DU:97:ARG:HG3	2.00	0.44
58:F6:551:HIS:CD2	58:F6:552:MET:HG3	2.53	0.44
59:F7:359:CYS:SG	59:F7:392:ALA:HB2	2.58	0.44
61:FO:85:ILE:O	61:FO:89:MET:HG2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:Ff:749:GLY:N	62:Ff:752:TYR:O	2.35	0.44
63:Fg:442:ASN:HB2	63:Fg:445:GLU:HB2	2.00	0.44
65:Fi:207:ASN:HD22	65:Fi:302:VAL:HG12	1.83	0.44
1:CA:10:G:O2'	5:CH:238:ARG:NH1	2.50	0.44
1:CA:79:A:OP1	22:Cj:10:ARG:NH2	2.51	0.44
1:CA:497:A:OP1	6:Cl:438:ARG:NH1	2.51	0.44
3:CE:141:GLN:NE2	43:DN:268:GLY:O	2.41	0.44
5:CH:176:ILE:HD13	30:DA:128:THR:HA	2.00	0.44
7:CJ:374:TRP:CE2	10:CN:105:ARG:HB2	2.53	0.44
8:CK:39:GLN:OE1	14:CR:254:TYR:HB2	2.17	0.44
11:CO:143:LEU:O	11:CO:147:GLU:HG3	2.17	0.44
14:CR:98:ARG:HD3	18:Cb:112:TYR:O	2.18	0.44
18:Cb:33:HIS:CE1	41:DL:161:THR:HG21	2.52	0.44
18:Cb:179:GLU:OE1	18:Cb:179:GLU:N	2.50	0.44
19:Cd:57:LEU:HA	19:Cd:60:VAL:HG12	2.00	0.44
20:Cg:306:ARG:HG3	23:Ck:841:LYS:HD2	1.99	0.44
23:Ck:96:ASN:HB2	31:DB:470:HIS:HB3	2.00	0.44
29:Cv:248:ILE:HD12	29:Cv:278:LEU:HD13	2.00	0.44
30:DA:366:LYS:HA	30:DA:369:VAL:HG12	2.00	0.44
30:DA:1392:ILE:HD12	30:DA:1612:PHE:CZ	2.52	0.44
30:DA:1403:ARG:NH2	30:DA:1406:ARG:HD3	2.33	0.44
31:DB:825:ASN:HA	31:DB:836:ASN:HD22	1.83	0.44
32:DC:1095:LEU:HD21	40:DK:14:LYS:HB2	1.99	0.44
33:DD:146:ARG:HD3	33:DD:179:ALA:HB1	1.99	0.44
33:DD:609:ASP:OD1	33:DD:609:ASP:N	2.51	0.44
36:DG:607:LEU:O	36:DG:611:LEU:HB2	2.18	0.44
38:DI:82:GLU:OE2	38:DI:221:TYR:OH	2.32	0.44
58:F6:433:GLU:OE2	58:F6:436:ARG:NH2	2.35	0.44
59:F7:459:LEU:HB2	59:F7:499:ILE:HG12	1.99	0.44
62:Ff:230:ARG:HH12	62:Ff:234:ALA:HB3	1.82	0.44
62:Ff:615:GLN:OE1	62:Ff:794:TYR:N	2.35	0.44
62:Ff:664:ALA:O	62:Ff:668:GLU:HG3	2.18	0.44
64:Fh:172:VAL:HG13	64:Fh:208:LYS:HE2	1.99	0.44
65:Fi:467:PHE:HB3	65:Fi:512:GLN:HG2	1.98	0.44
1:CA:487:A:C8	10:CN:84:THR:HG22	2.53	0.44
1:CA:618:U:N3	14:CR:147:ILE:HD11	2.33	0.44
4:CF:23:ARG:HD3	19:Cd:157:ARG:HD3	2.00	0.44
5:CH:197:PHE:O	5:CH:199:ASN:N	2.45	0.44
6:Cl:91:TYR:CZ	16:CU:116:THR:HG21	2.53	0.44
7:CJ:483:VAL:HG12	7:CJ:517:VAL:O	2.18	0.44
7:CJ:708:HIS:HB3	31:DB:1135:VAL:HG11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CN:111:VAL:HB	10:CN:113:VAL:HG22	1.99	0.44
11:CO:332:ARG:HB2	11:CO:336:GLU:HB2	2.00	0.44
14:CR:67:HIS:HE1	41:DL:231:TRP:H	1.65	0.44
17:Ca:253:LEU:HD22	43:DN:224:ARG:NH1	2.32	0.44
17:Ca:341:LEU:HD23	17:Ca:557:PHE:CE1	2.53	0.44
20:Cg:44:LYS:HE3	20:Cg:46:LYS:HE2	2.00	0.44
21:Ci:25:VAL:HG11	51:DV:113:LEU:HD11	1.99	0.44
22:Cj:176:VAL:HG21	22:Cj:179:ARG:HD3	2.00	0.44
29:Cv:535:HIS:HE2	29:Cv:540:GLU:HB3	1.83	0.44
30:DA:526:HIS:CE1	30:DA:827:LEU:HD21	2.53	0.44
30:DA:1113:LEU:HD23	30:DA:1113:LEU:H	1.83	0.44
31:DB:337:TYR:HE1	31:DB:352:LEU:HD13	1.83	0.44
32:DC:395:HIS:HD2	32:DC:462:THR:HB	1.83	0.44
32:DC:976:VAL:HG11	40:DK:244:LEU:HD11	1.99	0.44
34:DE:437:LYS:HG3	34:DE:438:PHE:CD2	2.53	0.44
37:DH:445:ILE:HG22	37:DH:447:ALA:H	1.83	0.44
46:DQ:246:VAL:HG12	46:DQ:265:VAL:HB	1.99	0.44
47:DR:13:PHE:H	47:DR:14:ARG:NE	2.16	0.44
56:Da:25:ARG:O	56:Da:28:ARG:HG2	2.17	0.44
59:F7:427:MET:SD	59:F7:621:GLN:HA	2.58	0.44
60:F9:550:ASP:HB3	60:F9:553:THR:OG1	2.18	0.44
62:Ff:506:GLY:HA2	62:Ff:527:ARG:HG3	1.99	0.44
63:Fg:57:ASN:ND2	63:Fg:99:GLY:HA3	2.33	0.44
67:IB:413:GLN:HG2	69:U7:1:UNK:O	2.18	0.44
1:CA:52:C:H3'	45:DP:24:LYS:HG2	2.00	0.44
6:CI:101:ALA:HB1	18:Cb:104:LEU:HD22	2.00	0.44
7:CJ:317:GLU:HB3	23:Ck:127:TRP:NE1	2.32	0.44
12:CP:113:LYS:HB2	12:CP:114:PRO:HD3	2.00	0.44
14:CR:89:VAL:HG22	27:Cq:104:HIS:HD2	1.83	0.44
16:CU:57:VAL:O	16:CU:60:ARG:HG2	2.18	0.44
17:Ca:489:ARG:NH1	30:DA:252:LEU:O	2.37	0.44
17:Ca:572:ARG:NH1	17:Ca:580:ILE:O	2.49	0.44
20:Cg:124:LYS:HB2	20:Cg:135:LEU:HD21	2.00	0.44
23:Ck:134:HIS:HE1	23:Ck:141:LEU:HD22	1.83	0.44
23:Ck:184:LYS:O	23:Ck:188:LEU:HG	2.18	0.44
23:Ck:310:ASP:OD1	23:Ck:310:ASP:N	2.50	0.44
32:DC:941:MET:HE1	32:DC:949:PHE:HB2	2.00	0.44
32:DC:1115:ARG:CZ	39:DJ:186:LYS:HB3	2.48	0.44
32:DC:1164:TRP:CD1	37:DH:329:ASN:HD22	2.36	0.44
33:DD:687:HIS:NE2	33:DD:689:LEU:HB2	2.33	0.44
35:DF:290:VAL:HA	35:DF:293:VAL:HG12	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:DG:231:PHE:O	36:DG:234:GLU:HG2	2.18	0.44
36:DG:579:PHE:O	36:DG:582:VAL:HG12	2.18	0.44
41:DL:42:PRO:HG3	67:IB:721:SER:HB3	2.00	0.44
46:DQ:146:GLN:HE21	46:DQ:176:ARG:NH2	2.15	0.44
46:DQ:157:THR:HB	46:DQ:161:GLY:HA2	2.00	0.44
49:DT:90:THR:HA	49:DT:93:MET:HE3	1.99	0.44
58:F6:401:TRP:CH2	58:F6:405:GLU:HG3	2.52	0.44
59:F7:560:GLY:HA2	59:F7:563:THR:HG22	2.00	0.44
61:FO:139:ILE:HG13	61:FO:170:MET:HB3	2.00	0.44
62:Ff:737:THR:H	62:Ff:740:MET:HE3	1.83	0.44
63:Fg:111:MET:HG2	63:Fg:115:HIS:CE1	2.53	0.44
63:Fg:355:LEU:H	63:Fg:355:LEU:HD12	1.83	0.44
63:Fg:379:LEU:O	63:Fg:471:ARG:NH1	2.51	0.44
63:Fg:496:VAL:HG21	63:Fg:522:PHE:CE2	2.53	0.44
1:CA:476:A:N6	41:DL:26:THR:HG1	2.15	0.43
3:CE:85:ASN:ND2	42:DM:2:GLU:OE2	2.51	0.43
6:CI:193:ARG:HH12	14:CR:85:THR:HG22	1.82	0.43
7:CJ:286:LEU:HD21	37:DH:307:ARG:HG3	1.99	0.43
7:CJ:775:ASP:OD1	51:DV:56:ARG:NH2	2.49	0.43
8:CK:192:MET:HG2	8:CK:276:GLU:HB3	1.99	0.43
10:CN:161:LEU:HD13	21:CI:71:TYR:HB3	1.99	0.43
11:CO:315:LEU:HD11	11:CO:324:LEU:HD23	2.00	0.43
15:CS:140:ALA:HB1	53:DX:65:LEU:HD22	1.99	0.43
17:Ca:273:ALA:O	17:Ca:277:LYS:HG2	2.16	0.43
17:Ca:311:TYR:HD1	43:DN:213:ARG:HE	1.65	0.43
17:Ca:419:GLN:HB2	30:DA:198:ARG:HB2	2.00	0.43
17:Ca:460:GLU:OE1	17:Ca:492:TYR:OH	2.31	0.43
24:Cm:153:ASP:OD1	24:Cm:153:ASP:N	2.51	0.43
30:DA:42:LYS:HE3	30:DA:46:LYS:NZ	2.33	0.43
30:DA:1466:TYR:HB2	30:DA:1493:LYS:HB3	2.00	0.43
31:DB:286:ASP:OD2	31:DB:837:TYR:OH	2.35	0.43
31:DB:555:PRO:HB3	31:DB:853:GLU:OE1	2.17	0.43
32:DC:244:GLU:OE1	32:DC:246:GLU:N	2.42	0.43
32:DC:555:ALA:HB2	32:DC:713:TYR:CE2	2.53	0.43
33:DD:319:GLU:HG3	33:DD:389:LEU:HD11	2.00	0.43
33:DD:583:VAL:HA	33:DD:587:LEU:HB2	2.00	0.43
34:DE:187:GLN:HB2	34:DE:189:HIS:CE1	2.52	0.43
37:DH:219:TYR:HA	37:DH:222:VAL:HG12	2.00	0.43
37:DH:505:TYR:HE1	49:DT:122:MET:HE1	1.83	0.43
38:DI:39:GLY:O	38:DI:212:ARG:NH2	2.51	0.43
38:DI:104:ILE:HG22	38:DI:115:LYS:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:DJ:166:LEU:HD23	39:DJ:166:LEU:HA	1.87	0.43
39:DJ:239:VAL:HG13	39:DJ:273:TYR:CD2	2.52	0.43
43:DN:158:GLU:HA	43:DN:163:PHE:HB2	2.00	0.43
47:DR:114:SER:HB3	47:DR:120:VAL:HG22	1.99	0.43
47:DR:117:ILE:HG22	47:DR:118:VAL:HG12	1.99	0.43
52:DW:85:GLU:O	52:DW:88:ARG:HG2	2.17	0.43
62:Ff:483:THR:HB	62:Ff:530:ARG:HH12	1.83	0.43
65:Fi:591:ARG:O	65:Fi:594:GLN:HG3	2.18	0.43
66:IA:376:ARG:NH1	66:IA:453:LEU:HB3	2.33	0.43
66:IA:536:LEU:HB2	66:IA:539:ILE:HB	2.01	0.43
66:IA:644:THR:HA	66:IA:711:LEU:HD13	2.00	0.43
1:CA:134:U:H1'	13:CQ:64:THR:HG21	2.00	0.43
3:CE:73:HIS:CD2	3:CE:78:LYS:HE3	2.53	0.43
3:CE:110:LEU:HB2	3:CE:113:GLU:HG2	2.00	0.43
13:CQ:219:GLN:OE1	65:Fi:517:TYR:OH	2.34	0.43
17:Ca:121:ALA:HB2	29:Cv:1054:VAL:HG13	2.00	0.43
23:Ck:806:ASP:OD2	23:Ck:809:ARG:NH2	2.52	0.43
26:Cp:149:LYS:HA	26:Cp:154:GLN:HE22	1.83	0.43
26:Cp:180:ARG:O	26:Cp:184:LYS:HG3	2.18	0.43
27:Cq:36:ARG:NH2	29:Cv:553:GLU:OE1	2.44	0.43
30:DA:514:TYR:CE1	30:DA:834:PRO:HG3	2.51	0.43
30:DA:1439:ASN:HA	30:DA:1536:ILE:HB	1.99	0.43
31:DB:688:VAL:HG12	31:DB:692:PHE:HE1	1.83	0.43
33:DD:318:LEU:O	33:DD:322:MET:HG2	2.18	0.43
40:DK:321:ARG:HH21	60:F9:263:GLN:HG3	1.83	0.43
42:DM:2:GLU:OE2	42:DM:6:ARG:NE	2.51	0.43
58:F6:310:LEU:HD22	58:F6:344:LEU:H	1.82	0.43
59:F7:129:MET:HA	59:F7:132:LEU:HD22	2.00	0.43
59:F7:346:ARG:HA	59:F7:346:ARG:HD3	1.88	0.43
61:FO:36:ARG:NE	61:FO:73:ASP:OD2	2.39	0.43
1:CA:11:U:O2	3:CE:10:LYS:NZ	2.45	0.43
4:CF:142:LEU:HD23	29:Cv:633:MET:HE1	2.00	0.43
6:CI:123:LYS:NZ	16:CU:128:ASN:O	2.49	0.43
8:CK:33:LYS:HA	8:CK:34:PRO:HA	1.86	0.43
13:CQ:185:PRO:HG2	59:F7:106:HIS:CE1	2.54	0.43
16:CU:92:GLU:OE2	29:Cv:174:ARG:NE	2.37	0.43
20:Cg:296:HIS:HE1	20:Cg:297:PHE:CZ	2.37	0.43
23:Ck:731:ARG:NH1	23:Ck:785:PRO:HG2	2.34	0.43
27:Cq:226:TYR:HB2	27:Cq:230:TYR:HB2	2.01	0.43
29:Cv:548:ARG:NH1	29:Cv:585:ASP:OD2	2.51	0.43
31:DB:215:TYR:HE2	34:DE:541:GLU:HG3	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DB:495:LEU:HB3	31:DB:589:ASP:HB2	1.99	0.43
31:DB:771:MET:HE2	31:DB:771:MET:HB2	1.91	0.43
31:DB:1023:ARG:HD2	31:DB:1043:THR:O	2.18	0.43
32:DC:753:LEU:HD22	32:DC:930:ALA:HB1	1.99	0.43
32:DC:851:CYS:HB2	32:DC:866:GLU:OE2	2.18	0.43
33:DD:561:ASP:O	33:DD:565:GLN:HG2	2.17	0.43
35:DF:229:PRO:HG2	35:DF:234:TYR:CE2	2.53	0.43
36:DG:392:ARG:HH22	36:DG:398:ILE:C	2.26	0.43
41:DL:118:ASP:HB2	41:DL:159:GLN:NE2	2.32	0.43
42:DM:85:TYR:O	42:DM:89:GLN:HG2	2.19	0.43
45:DP:90:LEU:HD23	45:DP:127:ASP:HB3	1.99	0.43
57:F3:48:VAL:HB	57:F3:49:PRO:HD3	2.00	0.43
59:F7:172:TYR:O	59:F7:175:GLN:HG2	2.18	0.43
59:F7:325:PRO:O	59:F7:328:VAL:HG22	2.18	0.43
62:Ff:625:PRO:HG2	62:Ff:730:ILE:O	2.18	0.43
66:IA:237:THR:HG22	66:IA:259:PRO:HG3	1.99	0.43
66:IA:376:ARG:HH12	66:IA:453:LEU:HB3	1.82	0.43
66:IA:659:ARG:HH21	66:IA:691:VAL:HG21	1.83	0.43
1:CA:177:A:O2'	47:DR:250:ARG:NH2	2.52	0.43
1:CA:541:A:H4'	1:CA:542:G:OP1	2.17	0.43
6:CI:132:GLY:H	14:CR:229:HIS:CE1	2.37	0.43
6:CI:387:ALA:O	6:CI:391:LEU:HG	2.18	0.43
7:CJ:398:PHE:CE1	7:CJ:811:SER:HB2	2.53	0.43
9:CL:118:LEU:HD22	60:F9:482:PRO:HG2	2.00	0.43
11:CO:203:GLN:HE22	11:CO:233:ARG:HH12	1.66	0.43
12:CP:179:ALA:HA	12:CP:182:ARG:NE	2.33	0.43
14:CR:33:GLN:HB3	41:DL:183:LEU:HD13	2.00	0.43
17:Ca:75:LEU:O	17:Ca:79:MET:HG3	2.19	0.43
19:Cd:118:LYS:NZ	38:DI:407:LEU:HA	2.32	0.43
20:Cg:99:GLN:HE22	20:Cg:456:VAL:HG21	1.83	0.43
20:Cg:332:ARG:NH2	23:Ck:802:TYR:O	2.51	0.43
25:Cn:187:LEU:HD12	61:FO:5:VAL:HB	2.00	0.43
29:Cv:663:ARG:HA	29:Cv:663:ARG:HD3	1.82	0.43
30:DA:410:ASP:OD1	30:DA:494:ARG:NH1	2.52	0.43
30:DA:1552:GLU:OE1	30:DA:1552:GLU:N	2.48	0.43
31:DB:192:ILE:H	31:DB:192:ILE:HD12	1.84	0.43
31:DB:443:LEU:HD12	40:DK:142:LEU:HD12	2.00	0.43
31:DB:447:PHE:HE1	37:DH:222:VAL:HG11	1.83	0.43
31:DB:941:ARG:HD3	31:DB:951:GLY:HA2	2.00	0.43
33:DD:209:THR:HB	33:DD:290:ARG:HH11	1.84	0.43
33:DD:633:GLU:OE2	33:DD:637:ARG:NE	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DF:51:TRP:CD1	35:DF:154:ASN:HD21	2.37	0.43
35:DF:309:ASP:OD1	35:DF:310:LEU:N	2.51	0.43
36:DG:83:MET:HE1	36:DG:108:ARG:HG3	2.00	0.43
37:DH:202:ALA:O	37:DH:206:ILE:HG12	2.18	0.43
37:DH:215:LEU:HD22	37:DH:225:ILE:HD13	2.01	0.43
50:DU:204:LEU:O	50:DU:207:ARG:HG3	2.18	0.43
54:DY:52:GLN:HB2	54:DY:56:ARG:NH1	2.33	0.43
55:DZ:35:LYS:HB2	67:IB:781:ARG:HH21	1.83	0.43
57:F3:141:TYR:HD1	57:F3:176:HIS:CG	2.37	0.43
58:F6:549:ASN:HB3	58:F6:551:HIS:CE1	2.54	0.43
62:Ff:266:ARG:HH22	62:Ff:674:TYR:HD2	1.67	0.43
62:Ff:643:GLU:OE1	62:Ff:643:GLU:N	2.51	0.43
6:CI:231:LEU:HD12	41:DL:209:ARG:HH12	1.84	0.43
12:CP:146:MET:SD	33:DD:656:LEU:HD11	2.59	0.43
15:CS:176:GLN:HE21	15:CS:182:HIS:CE1	2.36	0.43
16:CU:76:PHE:CZ	16:CU:82:LYS:HG3	2.54	0.43
26:Cp:25:PRO:HD3	30:DA:316:HIS:HB2	2.01	0.43
26:Cp:47:ARG:HG3	26:Cp:113:GLN:HA	2.00	0.43
29:Cv:757:ASP:OD1	29:Cv:757:ASP:N	2.48	0.43
30:DA:857:TYR:HD2	30:DA:859:GLN:HE22	1.67	0.43
32:DC:73:ARG:NH2	40:DK:239:GLY:HA3	2.33	0.43
34:DE:85:ARG:HG2	34:DE:88:LYS:HE2	2.00	0.43
34:DE:182:ASP:O	34:DE:185:GLU:C	2.62	0.43
34:DE:208:LYS:HA	34:DE:212:LEU:HB3	2.00	0.43
38:DI:48:LEU:HA	38:DI:206:LEU:HD11	2.00	0.43
42:DM:10:ARG:NH2	42:DM:267:ASP:OD1	2.50	0.43
43:DN:246:GLN:H	43:DN:246:GLN:CD	2.26	0.43
44:DO:189:TYR:O	44:DO:193:LEU:HG	2.19	0.43
46:DQ:148:LEU:HD13	46:DQ:177:LEU:HB2	2.01	0.43
47:DR:255:PRO:HB3	47:DR:266:TRP:O	2.18	0.43
59:F7:131:LEU:HD21	65:Fi:516:HIS:CD2	2.53	0.43
63:Fg:206:GLN:HG3	63:Fg:268:LEU:HD22	2.00	0.43
1:CA:437:U:C5	49:DT:244:PHE:HB3	2.54	0.43
3:CE:168:TYR:OH	3:CE:240:ASP:OD1	2.34	0.43
7:CJ:317:GLU:OE1	23:Ck:608:ARG:NH2	2.50	0.43
10:CN:54:PRO:HA	10:CN:64:GLN:OE1	2.19	0.43
12:CP:20:LEU:HD23	22:Cj:22:LEU:HD12	2.01	0.43
14:CR:221:TYR:O	14:CR:224:GLU:HG3	2.17	0.43
17:Ca:599:ILE:HG23	64:Fh:177:ARG:HD3	2.01	0.43
30:DA:1229:THR:HG22	31:DB:602:TRP:CZ3	2.53	0.43
31:DB:209:GLN:NE2	34:DE:448:PRO:O	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DB:692:PHE:CZ	34:DE:661:LYS:HG2	2.53	0.43
31:DB:1155:LYS:HG3	31:DB:1156:THR:HG23	2.00	0.43
32:DC:383:LEU:HA	32:DC:387:ARG:HB3	2.00	0.43
33:DD:33:GLY:O	33:DD:37:LEU:HD23	2.18	0.43
34:DE:71:LEU:HG	34:DE:195:ILE:HG22	2.00	0.43
35:DF:153:LEU:HD11	35:DF:164:ILE:HD13	1.99	0.43
36:DG:491:THR:HG22	36:DG:497:ARG:HG2	2.01	0.43
40:DK:32:ILE:O	40:DK:117:LYS:NZ	2.45	0.43
44:DO:169:GLU:O	44:DO:173:VAL:HG23	2.19	0.43
46:DQ:113:LEU:N	46:DQ:259:TYR:OH	2.51	0.43
49:DT:35:LYS:NZ	49:DT:36:GLU:OE2	2.39	0.43
49:DT:133:ASP:OD1	49:DT:133:ASP:N	2.51	0.43
58:F6:459:ILE:HG12	58:F6:466:LEU:HD13	1.99	0.43
59:F7:198:ARG:O	59:F7:202:THR:HG23	2.18	0.43
60:F9:312:ALA:HA	60:F9:316:LYS:HD3	2.00	0.43
63:Fg:190:PRO:HA	63:Fg:193:ALA:HB3	2.01	0.43
63:Fg:194:LYS:HA	63:Fg:197:VAL:HG13	2.01	0.43
1:CA:361:A:OP1	59:F7:124:TYR:OH	2.21	0.43
3:CE:306:GLU:O	3:CE:310:ARG:HG2	2.19	0.43
7:CJ:399:ARG:HD3	7:CJ:399:ARG:HA	1.90	0.43
9:CL:122:GLU:OE1	9:CL:137:ARG:NH1	2.51	0.43
13:CQ:216:GLU:HG3	65:Fi:519:TYR:HD1	1.83	0.43
18:Cb:189:LYS:O	18:Cb:193:GLU:HG2	2.19	0.43
20:Cg:274:SER:O	20:Cg:277:LYS:NZ	2.40	0.43
21:Ci:156:VAL:O	35:DF:5:GLY:HA2	2.19	0.43
23:Ck:403:ASP:OD1	23:Ck:403:ASP:N	2.51	0.43
24:Cm:72:SER:O	24:Cm:152:SER:HB2	2.18	0.43
24:Cm:176:VAL:HG22	29:Cv:77:TYR:CD2	2.54	0.43
25:Cn:181:ARG:HG3	25:Cn:184:ARG:HH21	1.83	0.43
29:Cv:895:VAL:HG23	29:Cv:896:PHE:CD2	2.54	0.43
29:Cv:1096:THR:HG23	29:Cv:1098:LYS:H	1.84	0.43
30:DA:978:GLU:HA	30:DA:981:ASN:HD21	1.83	0.43
31:DB:337:TYR:C	34:DE:38:GLN:HE22	2.26	0.43
31:DB:937:MET:HE3	31:DB:937:MET:HB2	1.83	0.43
31:DB:944:HIS:HB3	36:DG:24:ASN:ND2	2.34	0.43
32:DC:347:ASP:HB2	32:DC:353:LEU:HD21	1.99	0.43
33:DD:112:LYS:O	33:DD:115:GLU:HG2	2.19	0.43
33:DD:585:ASN:ND2	47:DR:201:CYS:H	2.17	0.43
36:DG:183:ARG:HG3	36:DG:219:HIS:ND1	2.33	0.43
36:DG:399:ARG:HE	36:DG:450:MET:HE1	1.83	0.43
36:DG:563:PHE:HD1	36:DG:623:MET:HG2	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:DH:456:GLU:OE1	37:DH:456:GLU:N	2.52	0.43
40:DK:172:LEU:HD11	40:DK:181:ALA:N	2.34	0.43
43:DN:20:GLU:HB3	43:DN:35:GLU:O	2.18	0.43
43:DN:22:LYS:HA	43:DN:33:ARG:HA	2.01	0.43
44:DO:211:GLU:O	44:DO:214:GLU:HG3	2.18	0.43
46:DQ:132:LYS:O	46:DQ:135:GLN:HG3	2.19	0.43
54:DY:37:ARG:O	54:DY:41:GLN:HG2	2.19	0.43
54:DY:116:LEU:HD13	54:DY:116:LEU:HA	1.88	0.43
59:F7:347:THR:O	59:F7:350:SER:OG	2.25	0.43
61:FO:21:ARG:HA	61:FO:21:ARG:HH11	1.82	0.43
63:Fg:300:VAL:HG22	63:Fg:315:ARG:HA	2.00	0.43
66:IA:373:LYS:HB3	66:IA:373:LYS:HE2	1.62	0.43
3:CE:37:SER:HB3	3:CE:101:PRO:HB3	2.00	0.43
6:CI:160:LEU:HD13	6:CI:160:LEU:HA	1.92	0.43
6:CI:224:ALA:O	6:CI:228:GLU:HG2	2.19	0.43
6:CI:408:ILE:HB	6:CI:409:PRO:HD3	2.01	0.43
9:CL:80:PRO:HG2	9:CL:84:SER:O	2.19	0.43
13:CQ:229:PRO:HG3	13:CQ:233:ARG:NE	2.32	0.43
15:CS:124:PHE:CZ	15:CS:125:LEU:HD13	2.54	0.43
24:Cm:135:ALA:O	24:Cm:138:GLU:HG2	2.18	0.43
28:Cr:20:PRO:HA	28:Cr:23:LEU:HD12	2.01	0.43
29:Cv:889:LEU:HD12	29:Cv:890:PRO:HD2	1.99	0.43
30:DA:291:CYS:HB2	30:DA:323:HIS:ND1	2.33	0.43
32:DC:1113:THR:HB	32:DC:1118:ASP:HB3	2.01	0.43
35:DF:302:VAL:HA	35:DF:305:ARG:NH1	2.34	0.43
38:DI:351:LEU:HD22	38:DI:356:ILE:HG13	2.00	0.43
46:DQ:125:ASN:OD1	46:DQ:126:SER:N	2.51	0.43
49:DT:233:HIS:HB3	49:DT:238:PRO:HA	1.99	0.43
55:DZ:34:LYS:N	67:IB:787:THR:OG1	2.37	0.43
59:F7:276:LEU:HD21	59:F7:294:ALA:HB2	2.00	0.43
60:F9:234:VAL:O	60:F9:237:GLN:HG2	2.18	0.43
62:Ff:322:GLU:HA	62:Ff:325:VAL:HG12	2.00	0.43
62:Ff:601:THR:OG1	65:Fi:586:ARG:NH1	2.47	0.43
63:Fg:29:PRO:HA	66:IA:227:ASN:HD22	1.84	0.43
65:Fi:573:LEU:O	65:Fi:576:VAL:HG12	2.19	0.43
66:IA:180:HIS:NE2	66:IA:187:GLU:HB3	2.34	0.43
66:IA:289:GLN:N	66:IA:292:THR:OG1	2.50	0.43
67:IB:382:ALA:HA	67:IB:539:VAL:HG21	2.00	0.43
1:CA:61:A:N6	64:Fh:288:LEU:HG	2.34	0.43
1:CA:452:A:O2'	7:CJ:376:SER:HB2	2.19	0.43
5:CH:46:LYS:O	5:CH:49:GLU:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CH:196:ASP:HA	5:CH:203:PHE:HB2	2.01	0.43
6:CI:45:VAL:O	6:CI:49:LYS:HG2	2.18	0.43
7:CJ:210:TRP:CD1	7:CJ:215:TRP:HB2	2.54	0.43
14:CR:33:GLN:HE21	41:DL:189:THR:H	1.67	0.43
15:CS:204:SER:HB2	52:DW:10:THR:HG23	2.01	0.43
19:Cd:116:LYS:HE3	19:Cd:116:LYS:HB3	1.88	0.43
21:CI:124:VAL:HG13	21:CI:125:HIS:CD2	2.53	0.43
23:Ck:178:ASP:OD1	23:Ck:178:ASP:N	2.50	0.43
26:Cp:50:THR:HG23	26:Cp:53:VAL:H	1.83	0.43
27:Cq:219:LEU:HD13	27:Cq:242:TYR:CG	2.54	0.43
29:Cv:310:GLY:HA2	29:Cv:417:THR:OG1	2.19	0.43
30:DA:761:ARG:HB2	30:DA:766:PHE:HE1	1.84	0.43
32:DC:851:CYS:SG	32:DC:855:ARG:NE	2.91	0.43
33:DD:516:SER:HA	33:DD:534:PHE:HE1	1.84	0.43
35:DF:300:GLU:N	35:DF:300:GLU:OE1	2.52	0.43
37:DH:497:MET:SD	49:DT:110:TYR:OH	2.71	0.43
38:DI:121:LYS:HD3	38:DI:121:LYS:HA	1.83	0.43
43:DN:120:ILE:HB	43:DN:123:GLN:HB2	2.01	0.43
53:DX:138:LYS:HE2	53:DX:138:LYS:HB3	1.84	0.43
57:F3:78:THR:OG1	57:F3:79:HIS:N	2.51	0.43
59:F7:17:LYS:O	59:F7:20:GLU:HG2	2.19	0.43
59:F7:126:LYS:HA	59:F7:129:MET:HG3	2.00	0.43
62:Ff:567:ARG:HG3	67:IB:503:ARG:HB2	2.00	0.43
63:Fg:231:ASN:OD1	63:Fg:236:GLN:NE2	2.51	0.43
66:IA:201:PRO:HA	66:IA:370:SER:HA	2.01	0.43
66:IA:208:ILE:HA	66:IA:279:VAL:HG13	1.99	0.43
3:CE:151:VAL:HG12	64:Fh:54:LEU:O	2.19	0.43
3:CE:307:ILE:HD12	17:Ca:365:LEU:HD11	2.00	0.43
3:CE:347:VAL:HG13	42:DM:169:ALA:HB1	2.00	0.43
6:CI:203:ASP:OD1	6:CI:203:ASP:N	2.51	0.43
6:CI:431:LEU:N	6:CI:436:VAL:O	2.44	0.43
7:CJ:329:ARG:O	7:CJ:332:GLU:HG2	2.18	0.43
15:CS:222:LEU:HD12	53:DX:49:TRP:CD1	2.54	0.43
16:CU:62:MET:HA	16:CU:65:VAL:HG22	2.01	0.43
17:Ca:304:TRP:HB3	43:DN:217:MET:SD	2.59	0.43
24:Cm:72:SER:HA	24:Cm:77:PRO:HA	2.01	0.43
27:Cq:189:TYR:HB3	27:Cq:191:VAL:HG13	2.00	0.43
28:Cr:256:VAL:HA	28:Cr:259:MET:HE3	2.00	0.43
30:DA:501:GLU:HG2	30:DA:889:VAL:HB	2.01	0.43
30:DA:774:GLY:H	42:DM:206:ALA:HA	1.82	0.43
30:DA:1229:THR:HG21	31:DB:528:PHE:HE2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:DC:1038:HIS:HB2	40:DK:51:VAL:HG12	2.00	0.43
33:DD:302:MET:HE2	33:DD:310:ALA:HB3	2.01	0.43
33:DD:537:ARG:NH2	47:DR:218:TRP:O	2.52	0.43
34:DE:463:LEU:HD21	34:DE:467:MET:HE3	2.01	0.43
36:DG:61:PHE:HE1	36:DG:66:LEU:HD11	1.84	0.43
36:DG:79:SER:OG	36:DG:81:PRO:HD2	2.19	0.43
39:DJ:270:ARG:HG3	39:DJ:299:CYS:HA	2.01	0.43
58:F6:347:GLU:HB3	58:F6:361:ILE:HG12	2.01	0.43
60:F9:310:LEU:HD12	60:F9:311:ARG:N	2.33	0.43
60:F9:331:ALA:HA	60:F9:334:LYS:HG2	2.01	0.43
61:FO:23:THR:HB	61:FO:27:LYS:HG3	2.01	0.43
63:Fg:10:VAL:HG21	63:Fg:517:PHE:CE2	2.53	0.43
63:Fg:259:ALA:HA	63:Fg:264:SER:HB3	2.01	0.43
65:Fi:410:ARG:HB2	65:Fi:410:ARG:HH11	1.84	0.43
66:IA:410:ALA:HB2	66:IA:452:LEU:HA	2.00	0.43
66:IA:422:ASP:HB2	66:IA:428:ILE:HB	2.01	0.43
67:IB:448:GLN:O	67:IB:448:GLN:NE2	2.52	0.43
1:CA:173:A:O2'	1:CA:174:A:OP2	2.31	0.42
1:CA:293:A:N3	1:CA:314:A:O2'	2.48	0.42
1:CA:444:A:O2'	67:IB:641:LEU:HG	2.18	0.42
5:CH:95:GLU:OE1	5:CH:95:GLU:N	2.52	0.42
7:CJ:335:LEU:HA	7:CJ:335:LEU:HD13	1.78	0.42
8:CK:223:GLY:HA2	8:CK:228:LYS:HB3	2.01	0.42
10:CN:131:ARG:HG2	41:DL:294:LEU:HD23	2.01	0.42
12:CP:183:PRO:HD2	33:DD:226:THR:OG1	2.19	0.42
20:Cg:225:ARG:NH2	20:Cg:276:GLU:OE1	2.52	0.42
22:Cj:99:ASN:O	22:Cj:103:LEU:HD12	2.19	0.42
23:Ck:38:ILE:HG22	36:DG:20:PRO:HB2	2.01	0.42
24:Cm:150:ASN:HB3	41:DL:234:PRO:HG3	2.01	0.42
26:Cp:148:GLU:H	26:Cp:148:GLU:CD	2.27	0.42
30:DA:193:GLU:O	30:DA:196:GLN:HG3	2.19	0.42
30:DA:1038:HIS:HB2	30:DA:1045:ILE:HD11	2.00	0.42
32:DC:181:GLN:OE1	32:DC:181:GLN:N	2.40	0.42
32:DC:308:LYS:HD2	32:DC:310:ARG:HH21	1.84	0.42
32:DC:569:LEU:O	32:DC:572:GLU:HG3	2.19	0.42
32:DC:883:TYR:HB2	34:DE:47:TYR:CZ	2.54	0.42
38:DI:294:ASN:ND2	38:DI:363:VAL:O	2.52	0.42
39:DJ:224:LEU:HB2	39:DJ:257:TYR:HE1	1.84	0.42
39:DJ:285:ARG:NH1	79:DJ:401:UTP:O2B	2.43	0.42
47:DR:70:ASP:OD1	47:DR:70:ASP:N	2.52	0.42
59:F7:23:ALA:O	59:F7:27:ARG:HG2	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:F7:364:PRO:HA	59:F7:367:VAL:HG12	2.01	0.42
59:F7:455:PRO:HG3	59:F7:492:SER:HB2	2.00	0.42
60:F9:541:PHE:HD2	60:F9:549:ARG:HB2	1.84	0.42
61:FO:56:LEU:HD11	63:Fg:320:PRO:HB2	2.00	0.42
64:Fh:75:GLY:C	67:IB:723:VAL:HG21	2.44	0.42
65:Fi:411:CYS:O	65:Fi:412:LYS:HG2	2.18	0.42
66:IA:66:ASN:HD22	66:IA:69:ARG:HG3	1.84	0.42
66:IA:377:CYS:HB3	66:IA:401:LYS:O	2.19	0.42
1:CA:87:U:H2'	1:CA:88:A:H5'	2.00	0.42
4:CF:134:THR:HB	4:CF:138:ILE:HD13	2.01	0.42
6:CI:56:GLU:HA	6:CI:59:ARG:NH1	2.34	0.42
11:CO:243:PRO:O	11:CO:249:LYS:NZ	2.37	0.42
23:Ck:316:ASP:OD1	23:Ck:316:ASP:N	2.48	0.42
27:Cq:57:GLN:O	42:DM:293:ARG:NH2	2.49	0.42
29:Cv:771:GLU:OE1	44:DO:67:ARG:NH2	2.52	0.42
30:DA:329:GLU:H	30:DA:329:GLU:CD	2.27	0.42
30:DA:539:LEU:HD22	30:DA:579:ASP:HB2	2.00	0.42
30:DA:1228:LEU:HD13	30:DA:1306:VAL:HG13	2.00	0.42
31:DB:376:ALA:HA	31:DB:381:LEU:HB2	2.01	0.42
31:DB:734:VAL:HA	31:DB:799:VAL:HA	2.01	0.42
32:DC:429:SER:HB3	32:DC:447:ASN:ND2	2.34	0.42
32:DC:848:THR:HG23	32:DC:849:PRO:HD3	2.01	0.42
33:DD:602:VAL:O	33:DD:605:ARG:HG2	2.19	0.42
34:DE:182:ASP:O	34:DE:185:GLU:O	2.37	0.42
35:DF:590:LYS:H	35:DF:590:LYS:HG2	1.57	0.42
36:DG:326:THR:HG23	36:DG:329:LEU:H	1.84	0.42
37:DH:311:ARG:HA	37:DH:311:ARG:HD3	1.82	0.42
39:DJ:317:PHE:CD2	49:DT:242:MET:HG2	2.55	0.42
40:DK:3:PHE:CD2	40:DK:4:ARG:HG3	2.54	0.42
41:DL:204:MET:HE3	41:DL:206:LEU:HB2	2.01	0.42
45:DP:97:TRP:CD1	45:DP:101:PHE:HB2	2.54	0.42
49:DT:96:TRP:NE1	49:DT:100:SER:OG	2.52	0.42
49:DT:105:ARG:O	49:DT:108:VAL:HG12	2.19	0.42
50:DU:205:ALA:HB3	50:DU:206:PRO:HD3	2.01	0.42
57:F3:101:LEU:HD22	61:FO:61:LEU:HG	2.01	0.42
58:F6:252:PHE:HD2	58:F6:264:PRO:HG3	1.83	0.42
58:F6:649:MET:HB2	64:Fh:60:TRP:HE1	1.84	0.42
61:FO:62:GLU:OE1	61:FO:62:GLU:N	2.41	0.42
63:Fg:69:ASP:OD1	63:Fg:69:ASP:N	2.49	0.42
65:Fi:97:CYS:H	65:Fi:205:HIS:HD1	1.66	0.42
66:IA:206:VAL:HA	66:IA:277:LEU:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:IA:244:GLN:HB3	66:IA:252:LEU:HD21	2.01	0.42
66:IA:333:LEU:O	66:IA:338:GLY:N	2.46	0.42
67:IB:493:ARG:HG3	67:IB:494:PHE:N	2.32	0.42
1:CA:55:U:OP2	45:DP:11:SER:OG	2.22	0.42
1:CA:206:A:OP2	48:DS:110:SER:OG	2.25	0.42
6:CI:253:LEU:HD21	36:DG:44:ARG:HB2	2.01	0.42
7:CJ:69:GLN:HA	7:CJ:82:HIS:CE1	2.54	0.42
7:CJ:700:PRO:HG2	7:CJ:703:ALA:HB2	2.01	0.42
11:CO:170:ARG:NH1	11:CO:193:MET:O	2.53	0.42
12:CP:140:PHE:HE2	33:DD:661:PHE:HE2	1.66	0.42
13:CQ:201:THR:HG21	13:CQ:209:LYS:HB2	2.00	0.42
14:CR:138:ARG:HD3	14:CR:179:TRP:CD2	2.53	0.42
14:CR:264:HIS:O	14:CR:267:ASN:ND2	2.49	0.42
18:Cb:170:LEU:HD22	28:Cr:169:PRO:HD3	2.01	0.42
23:Ck:391:ALA:HA	23:Ck:394:ASN:ND2	2.35	0.42
28:Cr:245:SER:O	28:Cr:248:ARG:HG2	2.20	0.42
30:DA:1082:TRP:O	30:DA:1085:GLU:HG3	2.19	0.42
31:DB:651:ASN:OD1	31:DB:843:ASN:ND2	2.42	0.42
32:DC:899:GLN:OE1	32:DC:899:GLN:N	2.51	0.42
32:DC:1091:ALA:HA	32:DC:1094:GLU:HG2	2.01	0.42
37:DH:15:TYR:O	37:DH:19:THR:OG1	2.24	0.42
41:DL:216:GLU:OE1	41:DL:220:ARG:NH1	2.46	0.42
45:DP:42:ARG:HD3	61:FO:175:HIS:HE1	1.84	0.42
45:DP:119:LEU:HD21	45:DP:154:PHE:HA	2.00	0.42
45:DP:134:LEU:HA	45:DP:137:GLN:HG2	2.01	0.42
46:DQ:84:SER:O	46:DQ:87:LEU:HG	2.19	0.42
49:DT:196:PHE:O	49:DT:205:VAL:N	2.39	0.42
65:Fi:355:PRO:O	65:Fi:358:ARG:NH1	2.44	0.42
65:Fi:573:LEU:HD21	67:IB:485:ARG:HB3	2.01	0.42
1:CA:145:A:C2	33:DD:26:ARG:HD3	2.54	0.42
1:CA:314:A:P	16:CU:14:MET:HB2	2.60	0.42
3:CE:98:ASP:OD1	3:CE:98:ASP:N	2.50	0.42
6:CI:295:ASP:O	6:CI:404:PRO:HB3	2.20	0.42
11:CO:278:ILE:HD12	11:CO:278:ILE:HA	1.88	0.42
11:CO:311:ILE:HD11	33:DD:261:ARG:CZ	2.50	0.42
13:CQ:152:LYS:HD2	13:CQ:158:HIS:HB3	2.01	0.42
18:Cb:280:ASN:O	18:Cb:285:GLN:NE2	2.48	0.42
20:Cg:194:LEU:HD11	20:Cg:267:LYS:HG3	2.01	0.42
22:Cj:125:THR:HB	22:Cj:208:ALA:HB2	2.02	0.42
23:Ck:374:ARG:NH1	31:DB:635:MET:HG3	2.34	0.42
31:DB:689:LEU:HD13	31:DB:689:LEU:HA	1.90	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:DD:800:ILE:HD12	43:DN:252:ARG:HD2	2.02	0.42
34:DE:206:LEU:HD21	34:DE:426:PHE:CE2	2.55	0.42
34:DE:720:ASP:OD1	34:DE:720:ASP:N	2.53	0.42
34:DE:732:ASP:HA	34:DE:735:ARG:HG2	2.01	0.42
35:DF:222:TYR:CE1	35:DF:229:PRO:HG3	2.55	0.42
37:DH:298:ASP:HA	37:DH:320:TYR:HE1	1.85	0.42
49:DT:54:TYR:HB3	49:DT:57:PHE:HB2	2.01	0.42
49:DT:64:GLN:CD	49:DT:163:ARG:HE	2.27	0.42
53:DX:84:PHE:CD2	53:DX:136:ARG:HB2	2.54	0.42
57:F3:129:GLU:HA	57:F3:132:GLU:HG2	2.01	0.42
57:F3:303:ALA:O	57:F3:307:CYS:N	2.53	0.42
60:F9:541:PHE:CZ	66:IA:504:ARG:HD3	2.55	0.42
62:Ff:287:ILE:HD11	62:Ff:432:LEU:HD22	2.02	0.42
63:Fg:184:LEU:HB3	63:Fg:186:PHE:HE1	1.83	0.42
66:IA:326:LEU:HD13	66:IA:326:LEU:HA	1.88	0.42
66:IA:406:GLN:O	66:IA:417:VAL:HG23	2.20	0.42
2:CC:47:ILE:HG22	67:IB:757:GLY:HA3	2.00	0.42
3:CE:81:LYS:NZ	3:CE:92:GLU:OE1	2.49	0.42
3:CE:163:ILE:HD11	3:CE:186:THR:HA	2.01	0.42
3:CE:358:GLU:CD	3:CE:358:GLU:H	2.28	0.42
7:CJ:113:GLU:HG2	7:CJ:117:TYR:CE2	2.55	0.42
8:CK:215:ARG:NH1	8:CK:218:ASN:HA	2.34	0.42
8:CK:257:LYS:O	8:CK:260:GLU:HG3	2.20	0.42
8:CK:292:VAL:HG23	16:CU:55:THR:HG22	2.02	0.42
11:CO:174:PRO:HG2	11:CO:177:MET:HB2	2.02	0.42
11:CO:288:GLN:NE2	13:CQ:184:PRO:O	2.43	0.42
13:CQ:223:ARG:NH2	59:F7:88:GLY:HA2	2.34	0.42
20:Cg:99:GLN:H	20:Cg:99:GLN:HG3	1.72	0.42
20:Cg:124:LYS:HD2	20:Cg:131:LYS:HD3	2.02	0.42
20:Cg:299:TYR:CE2	20:Cg:328:ILE:HG13	2.55	0.42
22:Cj:83:LEU:HD13	45:DP:132:LEU:HD21	2.01	0.42
30:DA:68:ASN:O	30:DA:72:ILE:HG12	2.20	0.42
30:DA:1230:LYS:O	30:DA:1234:LYS:NZ	2.52	0.42
30:DA:1373:MET:HB3	30:DA:1376:HIS:ND1	2.34	0.42
31:DB:1067:ILE:HD12	31:DB:1067:ILE:HA	1.89	0.42
32:DC:689:LYS:O	32:DC:692:VAL:HG12	2.20	0.42
41:DL:123:LEU:HD23	41:DL:123:LEU:HA	1.82	0.42
43:DN:154:MET:HE3	43:DN:157:ILE:HB	2.02	0.42
49:DT:64:GLN:NE2	49:DT:163:ARG:HE	2.18	0.42
52:DW:70:LEU:HB2	54:DY:117:LEU:HD11	2.01	0.42
54:DY:63:ARG:O	54:DY:66:GLN:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:F3:226:LEU:HD21	57:F3:285:ALA:HB1	2.01	0.42
59:F7:94:ARG:HH22	65:Fi:520:ASP:HB3	1.85	0.42
60:F9:574:PHE:HE1	60:F9:606:ARG:HD2	1.84	0.42
62:Ff:189:THR:OG1	62:Ff:193:ALA:O	2.37	0.42
65:Fi:510:MET:HE3	65:Fi:510:MET:HB2	1.93	0.42
1:CA:31:U:O4	1:CA:32:A:N6	2.52	0.42
1:CA:86:G:OP1	33:DD:339:ARG:NH2	2.53	0.42
1:CA:181:A:O2'	26:Cp:110:GLN:OE1	2.25	0.42
1:CA:301:A:C4	67:IB:498:LYS:HG2	2.55	0.42
5:CH:240:LEU:HD13	5:CH:253:TYR:CD1	2.55	0.42
7:CJ:88:ARG:NH1	36:DG:37:ASN:OD1	2.45	0.42
7:CJ:432:HIS:HB3	7:CJ:817:PRO:HG2	2.00	0.42
10:CN:25:VAL:HG21	10:CN:94:ARG:HA	2.01	0.42
10:CN:123:ARG:HD3	10:CN:123:ARG:HA	1.83	0.42
13:CQ:108:VAL:HG11	13:CQ:129:ARG:NH2	2.35	0.42
15:CS:156:LEU:H	15:CS:156:LEU:HD12	1.85	0.42
17:Ca:275:TRP:CH2	17:Ca:306:HIS:HD2	2.37	0.42
20:Cg:28:ALA:O	20:Cg:33:TRP:NE1	2.37	0.42
21:Ci:116:GLY:HA2	35:DF:169:ARG:HH12	1.85	0.42
24:Cm:76:SER:HB2	24:Cm:159:PHE:HD1	1.85	0.42
29:Cv:594:LEU:HD11	29:Cv:603:ARG:HD2	2.02	0.42
30:DA:493:TRP:HA	30:DA:496:VAL:HG12	2.01	0.42
30:DA:1376:HIS:HA	30:DA:1379:GLU:HG3	2.00	0.42
31:DB:703:HIS:HA	34:DE:668:LEU:HD21	2.00	0.42
32:DC:1043:SER:HA	32:DC:1046:ASP:OD2	2.20	0.42
33:DD:585:ASN:HD22	47:DR:201:CYS:H	1.66	0.42
33:DD:656:LEU:HD23	33:DD:656:LEU:HA	1.86	0.42
36:DG:105:LEU:HD23	36:DG:123:LEU:HD21	2.01	0.42
36:DG:400:VAL:HG22	36:DG:458:LEU:HD12	2.01	0.42
39:DJ:365:ARG:HH11	60:F9:265:GLN:NE2	2.17	0.42
45:DP:42:ARG:HG3	45:DP:43:THR:N	2.34	0.42
46:DQ:63:PRO:HG2	46:DQ:66:SER:HB3	2.02	0.42
47:DR:76:ARG:HA	47:DR:80:LEU:HD23	2.02	0.42
53:DX:77:VAL:HG11	54:DY:153:PHE:CZ	2.54	0.42
56:Da:31:PRO:HA	56:Da:34:GLN:HG2	2.02	0.42
57:F3:94:MET:HE1	61:FO:82:TYR:CE1	2.55	0.42
58:F6:394:GLN:O	58:F6:397:GLU:HG3	2.19	0.42
59:F7:384:GLU:HA	59:F7:387:HIS:HB2	2.02	0.42
60:F9:279:GLU:HA	60:F9:282:ILE:HG22	2.00	0.42
63:Fg:251:LYS:NZ	63:Fg:341:ARG:O	2.39	0.42
64:Fh:148:MET:HE3	64:Fh:154:ILE:HG21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:Fi:195:LYS:O	65:Fi:199:LEU:HB2	2.20	0.42
65:Fi:510:MET:O	65:Fi:538:PRO:HD2	2.19	0.42
66:IA:278:ILE:HG23	66:IA:306:PHE:HB3	2.02	0.42
66:IA:459:SER:O	66:IA:463:LYS:HG2	2.19	0.42
67:IB:469:PRO:HG3	69:U7:14:UNK:HA	2.01	0.42
67:IB:488:MET:O	67:IB:492:ILE:HG12	2.20	0.42
1:CA:426:A:N6	37:DH:47:ILE:HG12	2.35	0.42
3:CE:16:TYR:HD2	17:Ca:342:PHE:HA	1.85	0.42
3:CE:102:GLU:HG3	18:Cb:56:ARG:HH12	1.85	0.42
6:CI:85:LEU:HD23	24:Cm:95:MET:HB2	2.02	0.42
7:CJ:288:GLN:HE21	37:DH:270:SER:HG	1.55	0.42
8:CK:40:GLN:OE1	8:CK:40:GLN:N	2.44	0.42
8:CK:298:ARG:NH1	58:F6:571:PRO:O	2.53	0.42
10:CN:154:LYS:HD3	10:CN:154:LYS:HA	1.87	0.42
11:CO:350:HIS:N	11:CO:353:GLU:OE2	2.38	0.42
13:CQ:103:MET:HB2	13:CQ:106:THR:OG1	2.20	0.42
17:Ca:67:ARG:NH2	29:Cv:1116:GLU:OE1	2.53	0.42
17:Ca:106:ASN:O	17:Ca:155:ARG:NH1	2.49	0.42
17:Ca:442:TRP:HB3	17:Ca:444:PHE:CE1	2.55	0.42
19:Cd:214:LYS:HE3	19:Cd:214:LYS:HB3	1.94	0.42
20:Cg:301:HIS:HB3	20:Cg:304:PHE:HD2	1.85	0.42
21:Ci:130:PRO:HD3	35:DF:32:TRP:CD1	2.53	0.42
22:Cj:168:VAL:HA	22:Cj:169:PRO:HD3	1.87	0.42
29:Cv:162:SER:H	29:Cv:166:HIS:CD2	2.34	0.42
29:Cv:202:LYS:HG3	29:Cv:610:ARG:HH12	1.85	0.42
29:Cv:721:ILE:O	29:Cv:725:LYS:HG3	2.19	0.42
30:DA:705:LYS:HE3	30:DA:705:LYS:HB3	1.91	0.42
30:DA:1385:ASN:ND2	30:DA:1388:LEU:HD23	2.35	0.42
30:DA:1565:ARG:HA	30:DA:1568:LEU:HG	2.02	0.42
31:DB:769:VAL:HG21	31:DB:786:LEU:HD11	2.02	0.42
31:DB:1135:VAL:HG13	31:DB:1136:ALA:H	1.84	0.42
32:DC:162:ILE:H	32:DC:162:ILE:HD12	1.84	0.42
32:DC:176:GLU:CD	32:DC:176:GLU:H	2.27	0.42
32:DC:1152:PRO:HG3	39:DJ:48:PHE:CD1	2.55	0.42
36:DG:628:LEU:HD23	36:DG:628:LEU:HA	1.91	0.42
40:DK:176:GLY:HA3	40:DK:237:PRO:HG3	2.02	0.42
49:DT:198:ASP:OD2	49:DT:201:SER:OG	2.30	0.42
51:DV:41:THR:OG1	51:DV:42:PHE:N	2.51	0.42
53:DX:89:ARG:NH2	53:DX:93:ASP:OD2	2.52	0.42
57:F3:81:GLN:HE21	57:F3:81:GLN:HB3	1.58	0.42
61:FO:21:ARG:NH1	63:Fg:320:PRO:HD3	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:FO:136:SER:O	61:FO:140:THR:HG23	2.20	0.42
61:FO:193:LEU:O	61:FO:197:ARG:HG2	2.19	0.42
63:Fg:492:MET:HE3	63:Fg:517:PHE:CD1	2.55	0.42
66:IA:411:GLY:O	66:IA:468:MET:HG2	2.20	0.42
66:IA:477:ARG:HA	66:IA:477:ARG:HD3	1.86	0.42
67:IB:792:LYS:HG3	67:IB:793:VAL:HG12	2.01	0.42
1:CA:501:A:H5"	51:DV:61:ARG:HD3	2.01	0.42
3:CE:316:MET:HE1	42:DM:103:ARG:HE	1.85	0.42
3:CE:356:SER:OG	3:CE:359:HIS:HB2	2.20	0.42
7:CJ:591:ASP:HB3	7:CJ:594:VAL:HG23	2.02	0.42
11:CO:170:ARG:HG2	11:CO:194:MET:HG2	2.01	0.42
13:CQ:235:ARG:NH2	57:F3:72:VAL:HG21	2.34	0.42
14:CR:26:TYR:CD2	29:Cv:539:MET:HG2	2.55	0.42
17:Ca:179:LEU:HD11	55:DZ:83:LEU:HD11	2.01	0.42
17:Ca:314:CYS:SG	30:DA:883:ASN:ND2	2.92	0.42
18:Cb:197:PRO:HA	18:Cb:200:VAL:HG12	2.02	0.42
20:Cg:446:PHE:HD2	20:Cg:447:LEU:HD12	1.84	0.42
22:Cj:94:ILE:HG23	22:Cj:98:LYS:HE3	2.02	0.42
23:Ck:314:LEU:HD13	23:Ck:314:LEU:HA	1.94	0.42
27:Cq:140:ARG:HH12	30:DA:1063:THR:HB	1.84	0.42
28:Cr:55:HIS:CD2	28:Cr:82:CYS:SG	3.13	0.42
29:Cv:47:GLN:NE2	33:DD:16:ARG:O	2.44	0.42
30:DA:1129:ALA:HA	30:DA:1132:LYS:NZ	2.35	0.42
30:DA:1304:VAL:HG13	30:DA:1309:ILE:HD11	2.01	0.42
30:DA:1443:ALA:HB1	30:DA:1603:PHE:CE2	2.55	0.42
31:DB:356:ILE:HA	31:DB:359:ILE:HG12	2.01	0.42
31:DB:1058:ILE:HG22	31:DB:1060:GLU:H	1.84	0.42
32:DC:628:ASN:HB3	32:DC:760:LEU:HD12	2.02	0.42
32:DC:885:LEU:HB3	32:DC:889:ARG:NH1	2.34	0.42
32:DC:979:GLY:HA3	32:DC:1056:LEU:HD11	2.02	0.42
36:DG:245:ILE:HD12	36:DG:246:PRO:HD2	2.01	0.42
37:DH:428:ARG:NH2	67:IB:730:MET:HG2	2.35	0.42
38:DI:123:ARG:HH12	38:DI:150:MET:HE1	1.84	0.42
40:DK:313:ASP:O	40:DK:317:LYS:HG2	2.20	0.42
42:DM:196:ALA:HA	42:DM:201:GLY:HA3	2.02	0.42
45:DP:97:TRP:CE3	45:DP:134:LEU:HD13	2.55	0.42
52:DW:15:ARG:NH1	52:DW:16:PHE:O	2.53	0.42
52:DW:55:TRP:HA	52:DW:55:TRP:CE3	2.53	0.42
61:FO:155:LEU:HG	61:FO:159:MET:HE3	2.00	0.42
66:IA:499:ASP:OD1	66:IA:501:ASN:ND2	2.47	0.42
67:IB:512:VAL:HG21	67:IB:530:ILE:HG12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:346:C:H5'	1:CA:347:C:C6	2.55	0.42
1:CA:485:U:H5'	35:DF:56:TYR:CE1	2.54	0.42
1:CA:562:U:H5''	9:CL:105:ARG:CZ	2.50	0.42
2:CC:3:LEU:HD13	32:DC:1069:CYS:HB2	2.00	0.42
6:CI:138:VAL:HG12	6:CI:177:LEU:HB3	2.01	0.42
7:CJ:147:MET:HG2	51:DV:132:MET:HE2	2.01	0.42
10:CN:157:GLN:HA	10:CN:161:LEU:HB2	2.02	0.42
12:CP:32:ARG:HB3	33:DD:54:ASP:HB2	2.02	0.42
15:CS:162:ILE:HG22	15:CS:166:TRP:CZ3	2.54	0.42
17:Ca:120:ASN:O	17:Ca:124:ILE:HG12	2.19	0.42
26:Cp:127:TRP:CZ3	26:Cp:131:LYS:HD2	2.55	0.42
28:Cr:93:LEU:HD13	28:Cr:93:LEU:HA	1.93	0.42
29:Cv:1038:ASP:OD1	29:Cv:1038:ASP:N	2.51	0.42
30:DA:86:TYR:HE1	30:DA:88:LYS:HE3	1.85	0.42
30:DA:1384:ARG:NH1	30:DA:1628:ARG:HG2	2.34	0.42
30:DA:1649:ALA:HB1	30:DA:1660:TYR:HE1	1.85	0.42
31:DB:1033:TYR:O	31:DB:1035:ARG:N	2.49	0.42
35:DF:51:TRP:CD1	35:DF:157:THR:HG21	2.55	0.42
35:DF:476:LEU:HD13	35:DF:476:LEU:HA	1.93	0.42
36:DG:343:ASP:HB2	36:DG:346:ARG:HH21	1.84	0.42
38:DI:321:MET:HE2	38:DI:321:MET:HB2	1.95	0.42
39:DJ:205:LYS:HG3	39:DJ:240:ILE:HD12	2.01	0.42
49:DT:104:PRO:HB2	49:DT:106:ASP:OD1	2.20	0.42
58:F6:551:HIS:CD2	62:Ff:771:LEU:HD13	2.55	0.42
61:FO:162:GLU:HB3	63:Fg:192:ARG:HH21	1.85	0.42
61:FO:302:GLN:HA	61:FO:314:LEU:HD13	2.01	0.42
62:Ff:553:THR:HG23	62:Ff:562:VAL:HG22	2.01	0.42
62:Ff:712:GLY:O	62:Ff:716:LYS:HG2	2.19	0.42
1:CA:418:A:O2'	1:CA:419:U:H5''	2.20	0.42
3:CE:235:ASN:OD1	3:CE:236:PHE:N	2.52	0.42
6:CI:96:GLY:HA2	14:CR:38:TYR:HB2	2.02	0.42
7:CJ:574:GLY:O	7:CJ:578:LEU:HG	2.20	0.42
10:CN:67:LEU:HD11	31:DB:1100:LEU:HD12	2.01	0.42
17:Ca:25:LYS:HA	17:Ca:25:LYS:HD3	1.87	0.42
17:Ca:443:MET:HE3	17:Ca:487:GLU:HB3	2.01	0.42
20:Cg:362:LYS:NZ	20:Cg:383:ASP:OD2	2.44	0.42
22:Cj:186:ILE:HG13	47:DR:107:LEU:HD13	2.02	0.42
26:Cp:93:ARG:HH11	26:Cp:102:ARG:HH12	1.67	0.42
28:Cr:295:ALA:O	28:Cr:298:LYS:HG2	2.20	0.42
29:Cv:897:GLU:OE1	29:Cv:916:ARG:NH1	2.52	0.42
30:DA:161:GLU:OE1	30:DA:164:TRP:NE1	2.46	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:DA:193:GLU:H	30:DA:193:GLU:CD	2.28	0.42
30:DA:761:ARG:HB2	30:DA:766:PHE:CE1	2.54	0.42
30:DA:1147:ASP:OD1	30:DA:1148:GLY:N	2.53	0.42
30:DA:1196:LYS:O	30:DA:1200:LEU:HB3	2.20	0.42
31:DB:881:ARG:HG2	31:DB:897:PRO:HB3	2.00	0.42
31:DB:1125:HIS:CG	31:DB:1126:PRO:HD2	2.55	0.42
32:DC:1111:GLU:O	37:DH:45:HIS:ND1	2.42	0.42
33:DD:473:GLY:N	33:DD:515:GLU:OE1	2.52	0.42
34:DE:153:HIS:O	34:DE:153:HIS:ND1	2.53	0.42
34:DE:326:SER:HA	34:DE:437:LYS:O	2.20	0.42
38:DI:171:GLY:O	38:DI:175:GLN:HG2	2.19	0.42
42:DM:174:ASP:HA	42:DM:177:ARG:HG2	2.02	0.42
43:DN:251:PHE:CD2	43:DN:273:SER:HB3	2.55	0.42
59:F7:161:LEU:HB2	59:F7:207:VAL:HG13	2.02	0.42
60:F9:311:ARG:NH1	60:F9:311:ARG:O	2.53	0.42
66:IA:638:ALA:HB3	66:IA:724:GLN:HE22	1.84	0.42
1:CA:481:A:N3	53:DX:32:PRO:HD3	2.35	0.41
1:CA:545:A:O2'	1:CA:551:G:N3	2.52	0.41
1:CA:597:U:H2'	1:CA:598:U:C6	2.55	0.41
7:CJ:226:ARG:HD2	7:CJ:815:ASN:HD21	1.85	0.41
11:CO:128:ARG:HH12	11:CO:165:HIS:HB3	1.85	0.41
12:CP:26:ALA:O	12:CP:50:THR:HG23	2.20	0.41
12:CP:52:LYS:NZ	12:CP:53:ARG:O	2.42	0.41
13:CQ:157:LYS:HE2	13:CQ:157:LYS:HB3	1.87	0.41
17:Ca:316:GLU:HG2	30:DA:882:GLN:NE2	2.34	0.41
21:Ci:174:ASP:N	21:Ci:174:ASP:OD1	2.53	0.41
23:Ck:30:GLN:HB3	31:DB:855:GLN:HE22	1.84	0.41
29:Cv:217:GLY:HA3	38:DI:402:GLU:HG2	2.01	0.41
30:DA:59:HIS:HD2	30:DA:86:TYR:H	1.66	0.41
30:DA:1199:LYS:HD3	30:DA:1220:VAL:HG23	2.02	0.41
31:DB:1051:GLN:NE2	39:DJ:38:MET:SD	2.93	0.41
31:DB:1138:HIS:CE1	53:DX:116:PRO:HB3	2.54	0.41
32:DC:297:LYS:HE2	32:DC:297:LYS:HB3	1.82	0.41
32:DC:302:ARG:NH1	32:DC:359:GLU:OE2	2.53	0.41
32:DC:483:LYS:HB2	32:DC:528:THR:HG22	2.00	0.41
32:DC:774:ASP:OD2	32:DC:776:ASN:ND2	2.51	0.41
33:DD:34:TYR:CE2	33:DD:38:ARG:HD2	2.55	0.41
35:DF:73:HIS:O	35:DF:80:VAL:HG12	2.20	0.41
35:DF:231:VAL:HG13	35:DF:235:ARG:HH12	1.85	0.41
37:DH:7:ALA:HB1	49:DT:34:PRO:HB2	2.02	0.41
37:DH:417:MET:HE2	37:DH:417:MET:HB3	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:DM:104:LYS:O	42:DM:107:GLU:HG2	2.20	0.41
46:DQ:121:THR:O	46:DQ:121:THR:OG1	2.33	0.41
50:DU:142:ASP:N	50:DU:150:TYR:OH	2.44	0.41
52:DW:53:VAL:HG13	54:DY:111:ARG:HH12	1.85	0.41
54:DY:139:ASP:OD1	54:DY:140:SER:N	2.53	0.41
59:F7:510:LEU:HD13	59:F7:510:LEU:HA	1.86	0.41
60:F9:446:LEU:HD11	64:Fh:191:ARG:HB3	2.01	0.41
62:Ff:246:ASP:HA	62:Ff:294:GLY:O	2.20	0.41
62:Ff:317:GLN:CD	62:Ff:322:GLU:HB3	2.45	0.41
63:Fg:17:HIS:ND1	63:Fg:17:HIS:O	2.53	0.41
66:IA:177:ASN:OD1	66:IA:181:ARG:NH2	2.35	0.41
66:IA:737:TYR:CE2	66:IA:739:GLU:HB3	2.54	0.41
67:IB:589:CYS:SG	67:IB:590:TYR:N	2.93	0.41
1:CA:199:U:O2'	48:DS:39:ARG:NE	2.52	0.41
1:CA:227:U:H2'	1:CA:228:G:C8	2.55	0.41
1:CA:472:G:N7	7:CJ:379:ASP:HB3	2.35	0.41
5:CH:155:PHE:HE2	5:CH:279:MET:HE1	1.85	0.41
6:CI:191:LEU:HD23	27:Cq:214:ILE:HG12	2.01	0.41
6:CI:202:LEU:HD21	30:DA:1052:ALA:HB1	2.01	0.41
6:CI:224:ALA:HB2	6:CI:267:TYR:CE1	2.55	0.41
7:CJ:88:ARG:HH22	36:DG:38:ARG:HD3	1.84	0.41
7:CJ:369:ARG:HH21	10:CN:109:PRO:HB2	1.84	0.41
8:CK:77:MET:HE1	18:Cb:286:LEU:HB2	2.02	0.41
8:CK:293:ARG:HA	8:CK:293:ARG:HD2	1.90	0.41
13:CQ:116:TYR:HD1	13:CQ:123:ARG:HG2	1.85	0.41
14:CR:209:ALA:HB1	24:Cm:132:LEU:HD21	2.01	0.41
17:Ca:82:PRO:HG3	29:Cv:1110:GLU:HB2	2.02	0.41
18:Cb:82:ASP:OD2	41:DL:176:ARG:NE	2.44	0.41
23:Ck:375:PHE:HA	23:Ck:378:LYS:NZ	2.34	0.41
25:Cn:186:LYS:O	25:Cn:190:VAL:HG23	2.21	0.41
26:Cp:99:ARG:O	26:Cp:102:ARG:HG2	2.20	0.41
30:DA:870:GLU:HA	30:DA:873:ASP:OD2	2.20	0.41
31:DB:110:ARG:HA	31:DB:118:VAL:HA	2.01	0.41
31:DB:667:PHE:O	31:DB:671:VAL:HG22	2.20	0.41
31:DB:681:PRO:HD2	31:DB:707:GLN:HG2	2.02	0.41
31:DB:723:ARG:HH12	31:DB:815:ASP:HA	1.84	0.41
32:DC:149:ARG:NH1	32:DC:168:PHE:HB3	2.36	0.41
34:DE:67:ASN:ND2	34:DE:72:ARG:O	2.48	0.41
34:DE:81:ASP:OD1	34:DE:82:TRP:N	2.52	0.41
34:DE:228:TYR:HA	34:DE:231:ILE:HG22	2.01	0.41
35:DF:488:LYS:O	35:DF:492:GLU:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:DG:312:LEU:HD13	36:DG:312:LEU:HA	1.93	0.41
37:DH:322:ARG:HE	37:DH:371:LEU:HD13	1.85	0.41
37:DH:341:ASN:OD1	37:DH:341:ASN:N	2.52	0.41
44:DO:241:TRP:HA	44:DO:244:ARG:HE	1.85	0.41
46:DQ:199:ASN:ND2	50:DU:36:GLY:O	2.53	0.41
58:F6:299:GLN:HG3	58:F6:577:THR:HG23	2.03	0.41
63:Fg:35:TRP:HZ3	63:Fg:113:ALA:HB1	1.85	0.41
66:IA:70:PHE:HB2	66:IA:116:TRP:CE3	2.55	0.41
2:CC:22:HIS:CE1	2:CC:25:LEU:HG	2.54	0.41
6:CI:400:VAL:HG23	6:CI:410:LEU:HD12	2.02	0.41
7:CJ:734:THR:HA	7:CJ:738:LEU:HB2	2.02	0.41
11:CO:130:MET:SD	59:F7:493:VAL:HG12	2.61	0.41
11:CO:389:LYS:HE3	47:DR:22:LEU:HB2	2.01	0.41
12:CP:39:LYS:HE3	12:CP:40:PHE:HE2	1.86	0.41
12:CP:82:VAL:HB	12:CP:85:ASP:HB2	2.02	0.41
13:CQ:202:SER:O	13:CQ:206:THR:HG23	2.20	0.41
14:CR:38:TYR:CE1	18:Cb:99:ALA:HB1	2.55	0.41
15:CS:156:LEU:HD22	15:CS:160:ASN:ND2	2.35	0.41
18:Cb:212:GLN:HB3	28:Cr:49:SER:OG	2.20	0.41
19:Cd:201:LEU:HD11	58:F6:401:TRP:CZ2	2.55	0.41
21:Ci:104:ARG:HH21	23:Ck:693:TRP:CD1	2.38	0.41
23:Ck:73:LEU:HD21	34:DE:649:TYR:CE2	2.56	0.41
26:Cp:99:ARG:HA	26:Cp:102:ARG:NE	2.34	0.41
28:Cr:15:LEU:O	28:Cr:19:LEU:HG	2.20	0.41
29:Cv:1086:TRP:HB3	30:DA:434:GLU:HG2	2.01	0.41
30:DA:456:ARG:NH2	43:DN:203:GLU:O	2.47	0.41
31:DB:79:GLU:HB3	31:DB:86:PRO:HG3	2.02	0.41
31:DB:725:LEU:HD13	31:DB:725:LEU:HA	1.95	0.41
31:DB:744:VAL:HG23	31:DB:757:VAL:HG23	2.01	0.41
32:DC:275:LYS:HE3	32:DC:275:LYS:HB3	1.90	0.41
32:DC:457:LYS:HG3	32:DC:458:PHE:CD2	2.55	0.41
33:DD:505:TYR:CE2	33:DD:556:VAL:HG21	2.54	0.41
34:DE:156:ARG:HB3	34:DE:563:ASP:OD1	2.21	0.41
35:DF:429:LEU:HD12	35:DF:446:HIS:CD2	2.54	0.41
35:DF:504:SER:HB3	35:DF:549:PHE:CE2	2.55	0.41
36:DG:243:MET:N	36:DG:243:MET:SD	2.94	0.41
36:DG:315:LEU:HD12	36:DG:318:ILE:HD11	2.03	0.41
38:DI:56:PHE:HZ	38:DI:93:TRP:CD1	2.37	0.41
57:F3:96:THR:O	61:FO:68:ARG:NH2	2.53	0.41
64:Fh:138:LEU:HB3	64:Fh:175:CYS:HB2	2.01	0.41
65:Fi:84:MET:HE1	65:Fi:90:LEU:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:Fi:465:LEU:HD13	65:Fi:465:LEU:HA	1.94	0.41
67:IB:528:ILE:HG22	67:IB:532:LYS:NZ	2.35	0.41
1:CA:4:A:N3	17:Ca:363:ARG:NH2	2.68	0.41
1:CA:62:A:O4'	64:Fh:290:HIS:ND1	2.53	0.41
1:CA:350:U:H1'	1:CA:351:A:C8	2.55	0.41
1:CA:503:A:N7	51:DV:55:GLY:HA3	2.35	0.41
5:CH:244:HIS:ND1	5:CH:244:HIS:O	2.54	0.41
7:CJ:69:GLN:HB3	7:CJ:83:HIS:CE1	2.56	0.41
7:CJ:415:ARG:NH1	31:DB:1052:GLU:OE1	2.54	0.41
14:CR:27:ILE:O	14:CR:32:LYS:NZ	2.50	0.41
16:CU:127:VAL:HG22	16:CU:135:VAL:HG11	2.02	0.41
17:Ca:81:MET:HG3	17:Ca:85:LEU:HD23	2.01	0.41
18:Cb:115:ILE:HD13	27:Cq:54:PHE:HD1	1.86	0.41
27:Cq:39:GLU:OE2	29:Cv:485:ARG:NH1	2.53	0.41
27:Cq:87:ASP:HB2	28:Cr:244:LEU:HB3	2.02	0.41
27:Cq:237:GLN:NE2	30:DA:1133:GLY:HA3	2.34	0.41
29:Cv:288:ALA:HB3	29:Cv:291:SER:HB2	2.02	0.41
30:DA:683:MET:HG2	30:DA:743:LEU:HD13	2.02	0.41
30:DA:704:GLY:HA2	30:DA:707:ARG:NH1	2.35	0.41
31:DB:74:SER:O	31:DB:78:ARG:HG3	2.21	0.41
31:DB:609:PRO:HG3	31:DB:649:TYR:CE2	2.55	0.41
32:DC:200:VAL:HG21	32:DC:206:PHE:CA	2.50	0.41
32:DC:241:TRP:HB3	32:DC:466:HIS:CE1	2.56	0.41
34:DE:594:LEU:HD21	34:DE:636:TYR:HE1	1.85	0.41
39:DJ:339:VAL:HG13	40:DK:320:LEU:HD21	2.03	0.41
42:DM:65:THR:HB	42:DM:71:LYS:HE3	2.02	0.41
44:DO:174:PHE:HE1	44:DO:178:ARG:HE	1.68	0.41
49:DT:40:TRP:CH2	49:DT:214:ARG:HB3	2.55	0.41
54:DY:29:PRO:HA	54:DY:33:ALA:HB3	2.02	0.41
54:DY:121:PRO:HB2	54:DY:125:THR:HG21	2.02	0.41
57:F3:159:ASN:ND2	59:F7:103:HIS:HB3	2.36	0.41
59:F7:604:ASP:OD2	59:F7:609:GLU:HB2	2.21	0.41
61:FO:139:ILE:O	61:FO:143:ILE:HG23	2.20	0.41
62:Ff:589:LEU:HD12	62:Ff:592:TYR:CD2	2.55	0.41
63:Fg:12:SER:OG	63:Fg:115:HIS:NE2	2.45	0.41
66:IA:139:GLN:HA	66:IA:496:ARG:HA	2.02	0.41
66:IA:209:MET:HE3	66:IA:268:ARG:HG2	2.02	0.41
66:IA:263:ALA:HA	66:IA:528:LYS:HD2	2.03	0.41
67:IB:359:ARG:HD2	67:IB:624:ARG:HE	1.85	0.41
1:CA:441:G:H1	1:CA:477:U:P	2.43	0.41
1:CA:496:U:OP2	7:CJ:383:THR:HG23	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CH:177:GLU:OE2	5:CH:256:ARG:NH1	2.53	0.41
6:CI:100:PRO:HG2	14:CR:92:ILE:HD12	2.02	0.41
6:CI:360:GLU:CD	8:CK:38:GLY:H	2.28	0.41
7:CJ:340:ARG:HH21	7:CJ:358:TRP:HD1	1.67	0.41
13:CQ:88:PRO:HB3	33:DD:129:ARG:HA	2.02	0.41
13:CQ:194:ARG:NH1	13:CQ:220:ASP:OD2	2.46	0.41
14:CR:220:ARG:HA	14:CR:223:ARG:HG2	2.02	0.41
15:CS:229:THR:HB	67:IB:629:ASP:OD1	2.21	0.41
20:Cg:311:PHE:HB2	53:DX:109:LEU:HD23	2.02	0.41
29:Cv:681:HIS:O	29:Cv:781:PRO:HA	2.20	0.41
29:Cv:935:TYR:CD1	42:DM:90:LEU:HD21	2.56	0.41
29:Cv:960:GLN:HB2	33:DD:746:PRO:HB2	2.02	0.41
29:Cv:1101:TYR:HB3	55:DZ:14:ASP:OD2	2.21	0.41
30:DA:772:LEU:HA	30:DA:772:LEU:HD23	1.81	0.41
30:DA:864:ASP:HB2	30:DA:867:GLU:HB2	2.02	0.41
30:DA:878:LYS:HD2	30:DA:913:PRO:HD3	2.02	0.41
31:DB:1077:ARG:HH21	31:DB:1083:ALA:HB2	1.84	0.41
32:DC:240:VAL:HG13	32:DC:251:TRP:CZ3	2.55	0.41
32:DC:956:VAL:HG23	32:DC:962:GLY:HA3	2.01	0.41
37:DH:406:ARG:NH2	37:DH:417:MET:SD	2.93	0.41
38:DI:345:LEU:HD23	38:DI:345:LEU:HA	1.91	0.41
43:DN:68:PHE:HB3	43:DN:115:PRO:HD3	2.02	0.41
45:DP:115:LEU:HD11	45:DP:135:LEU:HB2	2.03	0.41
48:DS:27:ARG:O	48:DS:30:SER:OG	2.34	0.41
49:DT:140:ASN:ND2	49:DT:175:SER:HA	2.35	0.41
50:DU:90:VAL:HG11	50:DU:211:ARG:HG2	2.01	0.41
58:F6:313:ILE:HG21	58:F6:326:MET:HE1	2.02	0.41
62:Ff:218:VAL:O	62:Ff:429:ILE:HD13	2.21	0.41
62:Ff:726:PRO:O	62:Ff:730:ILE:HG23	2.20	0.41
63:Fg:101:LEU:O	63:Fg:107:THR:HB	2.19	0.41
65:Fi:110:ILE:HD13	67:IB:396:ARG:HB2	2.03	0.41
65:Fi:198:MET:O	65:Fi:202:MET:HG2	2.20	0.41
1:CA:4:A:H2'	1:CA:5:U:H2'	2.02	0.41
2:CC:29:LYS:HG2	37:DH:422:LYS:HB2	2.02	0.41
7:CJ:257:VAL:HG11	7:CJ:397:PHE:O	2.19	0.41
7:CJ:285:ARG:NH1	37:DH:262:GLU:OE2	2.52	0.41
7:CJ:419:ILE:HA	7:CJ:422:TRP:NE1	2.36	0.41
7:CJ:815:ASN:HA	10:CN:162:GLN:NE2	2.36	0.41
8:CK:89:GLU:H	8:CK:89:GLU:CD	2.28	0.41
10:CN:30:LEU:HD13	10:CN:30:LEU:HA	1.85	0.41
17:Ca:521:GLN:HG3	17:Ca:564:ARG:HH12	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Ca:597:LYS:NZ	17:Ca:601:GLU:OE2	2.46	0.41
19:Cd:136:GLU:OE1	44:DO:189:TYR:OH	2.38	0.41
23:Ck:817:LEU:HD13	23:Ck:817:LEU:HA	1.91	0.41
28:Cr:254:ASP:O	28:Cr:258:ARG:HG2	2.21	0.41
30:DA:178:LEU:HD21	30:DA:189:VAL:HG11	2.03	0.41
30:DA:388:VAL:HB	43:DN:163:PHE:CE1	2.55	0.41
30:DA:551:LYS:O	30:DA:555:ARG:HG2	2.20	0.41
30:DA:1404:ARG:HG3	30:DA:1499:GLU:HG3	2.03	0.41
31:DB:296:PRO:HG2	31:DB:299:ALA:HB3	2.02	0.41
31:DB:347:ALA:HB1	31:DB:351:GLN:HB2	2.01	0.41
32:DC:178:ARG:H	32:DC:181:GLN:NE2	2.18	0.41
32:DC:331:GLN:O	32:DC:334:GLN:HG2	2.20	0.41
34:DE:166:ARG:O	34:DE:170:ILE:HG12	2.20	0.41
34:DE:588:PRO:HA	34:DE:589:PRO:HD3	1.95	0.41
35:DF:402:THR:HG22	35:DF:406:ASN:ND2	2.35	0.41
37:DH:367:LEU:HD23	37:DH:371:LEU:HD23	2.02	0.41
37:DH:430:PHE:HE2	41:DL:58:MET:HA	1.86	0.41
38:DI:55:ILE:O	38:DI:58:TRP:HB2	2.21	0.41
40:DK:7:ASN:HB3	40:DK:135:ARG:CZ	2.50	0.41
41:DL:275:LEU:HA	41:DL:279:ARG:HG3	2.03	0.41
45:DP:21:MET:HE2	45:DP:21:MET:HB3	1.96	0.41
45:DP:175:GLU:HB2	45:DP:176:PRO:HD3	2.02	0.41
46:DQ:137:SER:HA	46:DQ:140:GLU:HG2	2.02	0.41
49:DT:164:GLY:HA3	49:DT:168:GLU:HG2	2.03	0.41
53:DX:83:ARG:HB2	54:DY:120:TYR:CE1	2.56	0.41
59:F7:365:THR:O	59:F7:369:LYS:HG2	2.21	0.41
62:Ff:300:ILE:O	62:Ff:304:VAL:HG23	2.21	0.41
62:Ff:613:ILE:HG23	62:Ff:756:LEU:HD23	2.03	0.41
63:Fg:128:TYR:CZ	63:Fg:543:LEU:HD21	2.55	0.41
63:Fg:376:ARG:HH12	63:Fg:471:ARG:HE	1.67	0.41
66:IA:749:LYS:O	66:IA:752:LEU:HG	2.21	0.41
66:IA:756:ILE:HA	66:IA:759:ASP:OD2	2.21	0.41
1:CA:164:G:H22	12:CP:24:PRO:HD2	1.84	0.41
1:CA:422:G:OP1	37:DH:391:GLU:HG2	2.20	0.41
2:CC:4:ILE:O	34:DE:576:HIS:NE2	2.43	0.41
3:CE:305:GLU:OE2	17:Ca:384:ARG:NH2	2.53	0.41
4:CF:56:ASN:ND2	4:CF:56:ASN:O	2.54	0.41
4:CF:122:THR:HG21	19:Cd:141:ARG:HB3	2.02	0.41
5:CH:86:THR:O	29:Cv:380:ARG:NH1	2.49	0.41
6:CI:2:GLN:HE21	20:Cg:70:SER:HB2	1.86	0.41
7:CJ:160:GLU:OE1	20:Cg:406:GLU:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CJ:318:GLU:OE2	23:Ck:612:TRP:NE1	2.31	0.41
7:CJ:411:GLU:O	7:CJ:415:ARG:HG2	2.20	0.41
7:CJ:539:LEU:N	7:CJ:597:LEU:O	2.51	0.41
8:CK:200:ARG:NH1	16:CU:19:ALA:O	2.44	0.41
17:Ca:318:ASP:OD1	17:Ca:320:SER:OG	2.31	0.41
17:Ca:474:ARG:HH21	17:Ca:480:LEU:HD23	1.86	0.41
18:Cb:138:ASP:OD1	18:Cb:138:ASP:N	2.41	0.41
19:Cd:234:MET:HE2	19:Cd:238:MET:HE2	2.02	0.41
20:Cg:61:PRO:HG2	20:Cg:79:CYS:SG	2.60	0.41
21:Ci:97:THR:HG22	21:Ci:98:HIS:H	1.85	0.41
22:Cj:15:ASN:O	22:Cj:15:ASN:ND2	2.54	0.41
27:Cq:167:MET:HB3	27:Cq:171:ARG:NH1	2.36	0.41
30:DA:1559:ASP:OD1	30:DA:1560:SER:N	2.53	0.41
31:DB:542:GLN:HE22	31:DB:941:ARG:HH12	1.68	0.41
32:DC:80:LEU:HD22	32:DC:1053:ALA:HB3	2.02	0.41
32:DC:1045:GLN:OE1	40:DK:47:THR:HA	2.21	0.41
32:DC:1049:ASN:CG	40:DK:161:LEU:HB2	2.46	0.41
32:DC:1114:GLU:HG3	32:DC:1115:ARG:HG3	2.03	0.41
32:DC:1159:ASP:HB3	37:DH:39:ILE:H	1.84	0.41
34:DE:719:LEU:HD23	34:DE:723:GLY:HA2	2.01	0.41
37:DH:171:TRP:HA	37:DH:174:LEU:HG	2.03	0.41
39:DJ:162:VAL:HG11	39:DJ:191:TYR:CD2	2.56	0.41
40:DK:262:ASN:HA	40:DK:265:VAL:HG22	2.03	0.41
46:DQ:80:PRO:HD2	46:DQ:83:ASN:HD21	1.86	0.41
46:DQ:134:ILE:HG21	46:DQ:248:LEU:HD22	2.03	0.41
53:DX:79:PRO:HG2	53:DX:117:VAL:HG21	2.03	0.41
57:F3:162:PRO:HG2	57:F3:171:LEU:HB2	2.01	0.41
59:F7:194:GLU:OE2	59:F7:198:ARG:NH2	2.54	0.41
60:F9:354:MET:HG3	64:Fh:223:MET:HE1	2.02	0.41
61:FO:174:TYR:CD2	61:FO:190:LEU:HD22	2.56	0.41
65:Fi:128:LEU:HD22	65:Fi:277:HIS:CD2	2.55	0.41
66:IA:180:HIS:CE1	66:IA:187:GLU:HB3	2.56	0.41
66:IA:517:ALA:HA	66:IA:571:TYR:HB3	2.02	0.41
1:CA:55:U:OP1	45:DP:13:ARG:NH1	2.54	0.41
5:CH:211:GLN:HG2	18:Cb:31:TRP:CZ3	2.56	0.41
6:CI:432:ASP:H	6:CI:436:VAL:HG13	1.85	0.41
7:CJ:776:GLN:OE1	53:DX:131:ILE:HG12	2.21	0.41
8:CK:314:PRO:HB3	16:CU:15:TYR:CZ	2.55	0.41
11:CO:316:ALA:HA	11:CO:321:PRO:HD3	2.03	0.41
13:CQ:233:ARG:HH12	61:FO:14:ARG:NH1	2.18	0.41
14:CR:21:GLN:CD	14:CR:21:GLN:H	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CS:234:LEU:HG	15:CS:238:ARG:HH12	1.86	0.41
17:Ca:414:THR:HG22	30:DA:182:ARG:HH12	1.85	0.41
20:Cg:219:LEU:HD22	20:Cg:243:LEU:HD23	2.03	0.41
23:Ck:547:ASN:HA	23:Ck:550:GLN:NE2	2.35	0.41
26:Cp:174:TRP:O	26:Cp:178:GLU:HG3	2.20	0.41
28:Cr:69:SER:HA	28:Cr:89:ARG:CZ	2.50	0.41
28:Cr:249:GLU:O	28:Cr:253:ARG:HG3	2.21	0.41
28:Cr:290:LYS:O	28:Cr:294:GLU:HG2	2.21	0.41
29:Cv:102:ASP:OD1	29:Cv:102:ASP:N	2.54	0.41
29:Cv:673:LEU:HD11	44:DO:111:ARG:CZ	2.51	0.41
30:DA:792:GLN:O	30:DA:795:GLU:HG3	2.21	0.41
30:DA:935:MET:HG3	42:DM:118:LEU:HD12	2.02	0.41
31:DB:355:GLN:O	31:DB:359:ILE:HG23	2.21	0.41
31:DB:589:ASP:OD1	31:DB:589:ASP:N	2.53	0.41
31:DB:723:ARG:HD3	31:DB:819:LEU:HG	2.03	0.41
31:DB:870:ASP:OD2	31:DB:948:ARG:NH2	2.54	0.41
33:DD:635:LEU:O	33:DD:639:ILE:HG12	2.20	0.41
35:DF:39:ARG:HD2	35:DF:163:ARG:NH1	2.36	0.41
36:DG:213:ARG:NH1	36:DG:217:THR:OG1	2.54	0.41
37:DH:501:PRO:HA	40:DK:301:ARG:HB3	2.02	0.41
40:DK:125:ALA:HA	40:DK:128:ARG:HE	1.85	0.41
43:DN:135:PRO:HG2	43:DN:138:THR:HG23	2.03	0.41
44:DO:69:GLU:HG3	44:DO:93:LEU:HD11	2.03	0.41
44:DO:86:ARG:NH1	44:DO:126:PRO:HD2	2.34	0.41
46:DQ:75:PHE:CE1	46:DQ:248:LEU:HD13	2.56	0.41
47:DR:13:PHE:H	47:DR:14:ARG:HH21	1.68	0.41
47:DR:61:PRO:HB2	47:DR:62:HIS:ND1	2.36	0.41
48:DS:163:LEU:HD13	48:DS:163:LEU:HA	1.91	0.41
59:F7:189:PHE:O	59:F7:193:VAL:HG13	2.21	0.41
60:F9:446:LEU:HD23	64:Fh:195:ARG:HD3	2.01	0.41
63:Fg:9:LEU:HD22	63:Fg:9:LEU:HA	1.94	0.41
64:Fh:132:TYR:OH	64:Fh:188:ASP:HB3	2.21	0.41
66:IA:382:ILE:HG12	66:IA:395:GLY:HA2	2.01	0.41
66:IA:411:GLY:C	66:IA:468:MET:HG2	2.45	0.41
66:IA:417:VAL:HG12	66:IA:420:VAL:HG22	2.01	0.41
1:CA:173:A:H4'	1:CA:174:A:O5'	2.21	0.41
1:CA:207:A:OP1	1:CA:210:A:N6	2.53	0.41
1:CA:217:U:O2'	1:CA:263:A:O2'	2.38	0.41
1:CA:425:A:N6	37:DH:388:ARG:HD2	2.36	0.41
1:CA:520:A:N6	52:DW:36:LYS:HE3	2.36	0.41
1:CA:559:A:H2'	1:CA:560:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CE:223:ARG:HH11	33:DD:16:ARG:HE	1.68	0.41
3:CE:394:ARG:O	30:DA:1657:SER:OG	2.30	0.41
3:CE:408:ARG:HB3	29:Cv:1051:ARG:HD2	2.02	0.41
5:CH:243:THR:HG22	5:CH:244:HIS:CD2	2.56	0.41
6:CI:54:SER:O	6:CI:57:GLU:HG3	2.21	0.41
6:CI:377:HIS:CE1	10:CN:145:LYS:HA	2.56	0.41
7:CJ:61:VAL:HG23	7:CJ:62:ARG:HG3	2.02	0.41
7:CJ:125:ASP:HB3	7:CJ:128:LYS:HG2	2.03	0.41
7:CJ:442:ASP:OD1	7:CJ:442:ASP:N	2.53	0.41
10:CN:26:LEU:H	10:CN:26:LEU:HD12	1.85	0.41
12:CP:20:LEU:HG	12:CP:21:TRP:CD1	2.55	0.41
12:CP:45:LEU:HD12	12:CP:45:LEU:H	1.86	0.41
12:CP:165:LEU:O	19:Cd:63:ARG:NH1	2.46	0.41
13:CQ:51:PHE:CD1	13:CQ:52:PRO:HD2	2.55	0.41
14:CR:47:ALA:HA	18:Cb:67:GLN:HE22	1.86	0.41
14:CR:142:MET:HE3	14:CR:158:LEU:HD22	2.03	0.41
15:CS:143:PHE:CE1	53:DX:61:LEU:HD11	2.56	0.41
15:CS:228:LEU:HD13	15:CS:232:GLN:HB3	2.03	0.41
17:Ca:450:ASN:ND2	33:DD:693:ASP:H	2.19	0.41
21:CI:157:LEU:HD23	21:CI:157:LEU:HA	1.94	0.41
23:Ck:166:MET:HB3	23:Ck:170:VAL:HG22	2.02	0.41
23:Ck:308:ARG:HE	23:Ck:308:ARG:HB3	1.73	0.41
23:Ck:332:GLU:HG3	23:Ck:629:LEU:HD12	2.02	0.41
24:Cm:147:PHE:HA	24:Cm:151:VAL:HG23	2.02	0.41
24:Cm:172:GLN:O	24:Cm:176:VAL:HG23	2.20	0.41
29:Cv:98:ARG:NH1	29:Cv:105:ASP:OD2	2.54	0.41
29:Cv:218:ARG:HA	29:Cv:223:ASN:HD22	1.85	0.41
29:Cv:690:GLU:HB3	29:Cv:798:TYR:CE1	2.56	0.41
29:Cv:847:ARG:NH1	29:Cv:928:ARG:O	2.54	0.41
29:Cv:1028:GLN:HB3	30:DA:848:TYR:CE1	2.56	0.41
29:Cv:1037:TYR:HB3	29:Cv:1045:ARG:HG3	2.03	0.41
30:DA:465:ARG:NH1	30:DA:838:GLU:O	2.48	0.41
30:DA:995:LEU:HD13	30:DA:995:LEU:HA	1.95	0.41
31:DB:543:GLN:NE2	31:DB:581:ASP:H	2.16	0.41
31:DB:1028:SER:HA	37:DH:449:PHE:CE1	2.56	0.41
31:DB:1056:PRO:HD3	37:DH:35:TYR:CE1	2.55	0.41
31:DB:1153:ASP:OD1	31:DB:1154:LYS:N	2.54	0.41
32:DC:104:PRO:O	32:DC:112:TYR:OH	2.35	0.41
32:DC:192:SER:O	32:DC:196:LEU:HB3	2.21	0.41
32:DC:193:GLU:OE2	32:DC:199:LYS:HA	2.20	0.41
32:DC:941:MET:HE2	32:DC:945:ARG:HD3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:DD:72:ASP:O	33:DD:74:LEU:HD22	2.21	0.41
33:DD:571:VAL:HG21	33:DD:599:ALA:O	2.21	0.41
34:DE:44:ASN:OD1	34:DE:176:ARG:NH2	2.54	0.41
34:DE:480:ARG:HD2	34:DE:481:ASN:H	1.85	0.41
35:DF:231:VAL:HG13	35:DF:235:ARG:NH1	2.36	0.41
36:DG:121:PHE:CE2	36:DG:142:LEU:HD12	2.56	0.41
36:DG:139:ALA:HB1	36:DG:168:TYR:CZ	2.55	0.41
37:DH:65:SER:HB2	37:DH:100:HIS:HE1	1.85	0.41
37:DH:80:ARG:HD3	37:DH:80:ARG:HA	1.74	0.41
37:DH:445:ILE:HG13	37:DH:449:PHE:HD2	1.86	0.41
38:DI:169:ILE:HG21	38:DI:206:LEU:HD22	2.03	0.41
39:DJ:255:LYS:HG2	39:DJ:297:HIS:NE2	2.36	0.41
44:DO:125:LEU:O	44:DO:127:LEU:N	2.54	0.41
45:DP:200:SER:HB2	45:DP:207:TYR:CE2	2.55	0.41
46:DQ:88:ARG:NH2	59:F7:408:SER:O	2.49	0.41
46:DQ:175:GLY:O	46:DQ:178:GLU:HG3	2.21	0.41
47:DR:141:LYS:NZ	47:DR:173:ASN:HB3	2.35	0.41
48:DS:190:THR:HG23	48:DS:192:GLN:H	1.86	0.41
50:DU:119:ILE:O	50:DU:122:ASN:ND2	2.54	0.41
50:DU:176:ARG:NH2	50:DU:187:ASP:OD2	2.54	0.41
53:DX:79:PRO:HA	53:DX:138:LYS:HD2	2.03	0.41
58:F6:305:CYS:SG	58:F6:306:THR:N	2.94	0.41
63:Fg:26:LEU:HD13	63:Fg:26:LEU:HA	1.93	0.41
63:Fg:506:GLU:HG2	63:Fg:513:VAL:HG23	2.02	0.41
64:Fh:121:SER:O	64:Fh:124:GLU:HG2	2.20	0.41
65:Fi:97:CYS:N	65:Fi:205:HIS:HD1	2.19	0.41
65:Fi:392:PRO:O	65:Fi:395:THR:OG1	2.38	0.41
66:IA:204:PRO:HG2	66:IA:253:VAL:HG13	2.01	0.41
66:IA:282:VAL:O	66:IA:310:CYS:HA	2.20	0.41
1:CA:208:U:H5'	48:DS:30:SER:HA	2.03	0.41
1:CA:561:U:H4'	66:IA:47:GLN:O	2.21	0.41
3:CE:223:ARG:NH1	33:DD:16:ARG:HE	2.19	0.41
5:CH:16:VAL:HB	5:CH:17:PRO:HD3	2.02	0.41
5:CH:48:ASP:OD1	5:CH:49:GLU:N	2.54	0.41
6:CI:335:VAL:HA	6:CI:372:ILE:HB	2.03	0.41
7:CJ:814:TRP:O	10:CN:162:GLN:NE2	2.39	0.41
9:CL:69:PHE:HB2	60:F9:509:ILE:HG23	2.02	0.41
14:CR:151:ASN:OD1	14:CR:152:PRO:HD2	2.21	0.41
15:CS:209:GLY:HA3	31:DB:1122:ARG:HG2	2.02	0.41
17:Ca:361:LEU:HD22	29:Cv:289:VAL:HG23	2.01	0.41
18:Cb:292:ASP:OD2	28:Cr:280:ARG:NH1	2.32	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Cd:148:ILE:HB	29:Cv:629:HIS:CD2	2.55	0.41
20:Cg:304:PHE:CG	53:DX:124:ILE:HD13	2.56	0.41
22:Cj:156:THR:HG21	22:Cj:190:PRO:O	2.21	0.41
23:Ck:619:GLN:HB3	23:Ck:631:TRP:CZ2	2.56	0.41
29:Cv:172:THR:OG1	29:Cv:173:LYS:N	2.53	0.41
30:DA:54:GLN:HG3	33:DD:41:GLY:HA3	2.02	0.41
30:DA:1456:GLN:HE22	30:DA:1576:THR:HB	1.86	0.41
31:DB:241:THR:HG22	31:DB:244:ARG:NH2	2.36	0.41
31:DB:878:VAL:HG12	31:DB:938:ILE:HG13	2.02	0.41
32:DC:664:PHE:HZ	32:DC:757:ARG:HH21	1.69	0.41
32:DC:973:PRO:HA	32:DC:976:VAL:HG12	2.02	0.41
33:DD:592:TRP:CD1	33:DD:592:TRP:H	2.39	0.41
36:DG:487:VAL:HG23	36:DG:490:ARG:CZ	2.51	0.41
37:DH:110:VAL:HG21	37:DH:171:TRP:CH2	2.57	0.41
38:DI:386:ASP:O	38:DI:390:VAL:HG23	2.21	0.41
39:DJ:338:ILE:HG21	40:DK:318:VAL:HG21	2.02	0.41
39:DJ:358:HIS:ND1	39:DJ:358:HIS:O	2.53	0.41
40:DK:186:LYS:O	40:DK:189:GLU:HG3	2.21	0.41
42:DM:16:TRP:CZ2	42:DM:253:LYS:HG3	2.56	0.41
45:DP:146:PHE:O	45:DP:180:TRP:NE1	2.46	0.41
47:DR:214:GLU:N	47:DR:214:GLU:OE1	2.54	0.41
47:DR:248:ALA:HB3	47:DR:265:MET:SD	2.61	0.41
57:F3:86:SER:HB2	61:FO:125:ASN:HA	2.02	0.41
57:F3:141:TYR:OH	57:F3:235:CYS:HA	2.21	0.41
57:F3:241:PRO:O	59:F7:101:ARG:NH2	2.53	0.41
60:F9:588:GLU:HG3	60:F9:589:ARG:N	2.35	0.41
62:Ff:217:ARG:O	62:Ff:221:ASN:ND2	2.54	0.41
63:Fg:47:GLY:HA3	63:Fg:64:TYR:CE1	2.56	0.41
63:Fg:218:LEU:HD11	63:Fg:276:VAL:HG21	2.03	0.41
1:CA:74:G:O5'	47:DR:14:ARG:NH2	2.54	0.40
1:CA:162:U:H4'	45:DP:18:TYR:CD1	2.55	0.40
1:CA:435:G:C6	35:DF:27:ARG:HB2	2.56	0.40
3:CE:413:ILE:HA	3:CE:414:PRO:HD3	1.88	0.40
11:CO:352:ASN:O	11:CO:356:GLN:HG3	2.21	0.40
14:CR:125:ASN:H	14:CR:128:ASN:ND2	2.14	0.40
17:Ca:298:VAL:O	17:Ca:302:LEU:HG	2.20	0.40
17:Ca:330:TRP:NE1	17:Ca:398:ASP:OD2	2.54	0.40
18:Cb:59:PRO:HG3	29:Cv:510:GLU:HB3	2.03	0.40
20:Cg:440:LYS:O	20:Cg:444:ILE:HG12	2.21	0.40
23:Ck:176:THR:O	23:Ck:182:ARG:HD3	2.20	0.40
23:Ck:661:ILE:HG13	23:Ck:669:ASN:ND2	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:Cr:143:ARG:HD3	28:Cr:187:VAL:HG11	2.02	0.40
28:Cr:295:ALA:HA	28:Cr:298:LYS:HE2	2.03	0.40
29:Cv:204:ILE:N	29:Cv:205:PRO:HD2	2.36	0.40
29:Cv:212:ARG:HA	38:DI:404:TRP:NE1	2.37	0.40
29:Cv:458:PRO:HG3	29:Cv:828:ALA:HA	2.04	0.40
29:Cv:925:ASP:O	29:Cv:929:LEU:HG	2.20	0.40
29:Cv:995:VAL:HG21	42:DM:42:TYR:CZ	2.56	0.40
30:DA:152:ARG:HH21	30:DA:156:THR:HG1	1.69	0.40
30:DA:194:LEU:HD13	30:DA:194:LEU:HA	1.96	0.40
30:DA:752:GLU:OE1	30:DA:752:GLU:N	2.54	0.40
30:DA:753:PHE:HB3	30:DA:769:TRP:CZ3	2.56	0.40
30:DA:978:GLU:H	30:DA:978:GLU:CD	2.29	0.40
30:DA:1078:ASP:HB3	30:DA:1081:GLN:HB3	2.02	0.40
31:DB:266:LYS:HE3	31:DB:266:LYS:HB2	1.84	0.40
31:DB:302:LEU:HD12	31:DB:303:PRO:HD2	2.02	0.40
32:DC:78:PRO:HG2	32:DC:708:TYR:CE2	2.56	0.40
32:DC:298:ILE:HG21	32:DC:363:ILE:HG22	2.02	0.40
32:DC:784:GLU:HB3	32:DC:812:SER:HB2	2.03	0.40
34:DE:229:ARG:NE	34:DE:253:THR:OG1	2.54	0.40
36:DG:117:VAL:HG21	36:DG:149:SER:HB2	2.03	0.40
36:DG:211:TYR:CE2	36:DG:231:PHE:HB2	2.57	0.40
36:DG:392:ARG:CZ	36:DG:396:ASN:HD21	2.34	0.40
37:DH:49:LEU:O	37:DH:53:ARG:HG2	2.21	0.40
37:DH:132:ALA:HB2	37:DH:213:THR:HA	2.02	0.40
41:DL:121:ILE:HD11	41:DL:220:ARG:HH21	1.86	0.40
42:DM:22:LEU:HD12	42:DM:22:LEU:HA	1.87	0.40
48:DS:187:ARG:HA	48:DS:190:THR:HG22	2.03	0.40
49:DT:33:HIS:HB3	49:DT:36:GLU:OE1	2.22	0.40
52:DW:14:GLU:OE1	52:DW:14:GLU:N	2.42	0.40
58:F6:363:ASN:ND2	58:F6:365:SER:OG	2.53	0.40
58:F6:570:ARG:NH2	62:Ff:760:ASP:OD2	2.54	0.40
59:F7:85:GLY:N	59:F7:90:GLU:OE2	2.54	0.40
59:F7:111:THR:HB	59:F7:114:ALA:HB3	2.03	0.40
59:F7:552:LEU:HD12	59:F7:556:GLU:HG2	2.03	0.40
62:Ff:494:ALA:O	62:Ff:498:VAL:HG23	2.21	0.40
65:Fi:474:PRO:HB3	65:Fi:506:PHE:HE1	1.84	0.40
1:CA:179:U:H3	12:CP:131:ASN:HD22	1.69	0.40
1:CA:480:C:C5	53:DX:31:LYS:HA	2.56	0.40
3:CE:77:SER:HB2	29:Cv:403:PRO:HA	2.03	0.40
3:CE:297:ILE:HD11	33:DD:774:VAL:HG21	2.04	0.40
3:CE:365:MET:HE3	3:CE:365:MET:HB3	1.98	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CE:370:ASP:O	3:CE:374:ARG:HG2	2.21	0.40
6:CI:400:VAL:HG21	6:CI:416:LEU:HD11	2.03	0.40
8:CK:297:ASP:HB3	58:F6:572:LEU:HB2	2.02	0.40
11:CO:411:ARG:HD3	11:CO:424:LYS:HD2	2.03	0.40
12:CP:73:LYS:HE2	26:Cp:33:ILE:HG12	2.03	0.40
13:CQ:53:ASN:OD1	13:CQ:54:ARG:N	2.54	0.40
13:CQ:56:ARG:NH2	56:Da:28:ARG:HH12	2.19	0.40
14:CR:254:TYR:CZ	20:Cg:473:ARG:HD2	2.55	0.40
16:CU:36:SER:H	16:CU:39:TYR:HB2	1.86	0.40
16:CU:158:VAL:O	16:CU:162:VAL:HG23	2.21	0.40
17:Ca:73:GLU:HA	17:Ca:184:LYS:HD3	2.03	0.40
17:Ca:442:TRP:HB3	17:Ca:444:PHE:HE1	1.86	0.40
18:Cb:173:ARG:NH2	27:Cq:204:HIS:O	2.53	0.40
19:Cd:31:PHE:CZ	22:Cj:48:PRO:HD3	2.56	0.40
21:Ci:30:ARG:NH2	23:Ck:786:SER:O	2.54	0.40
22:Cj:119:LYS:NZ	47:DR:242:SER:HB3	2.36	0.40
29:Cv:166:HIS:CE1	29:Cv:185:VAL:HB	2.56	0.40
29:Cv:883:HIS:HD2	38:DI:358:ARG:HA	1.85	0.40
30:DA:88:LYS:HD2	33:DD:42:MET:SD	2.61	0.40
30:DA:443:LEU:HB3	30:DA:478:ILE:HG21	2.03	0.40
30:DA:1165:ALA:HB2	42:DM:150:GLN:HB3	2.02	0.40
31:DB:226:LEU:HB3	32:DC:946:GLU:OE2	2.21	0.40
31:DB:427:TRP:CZ2	32:DC:1156:PRO:HB3	2.57	0.40
32:DC:947:TRP:CD1	32:DC:1051:LEU:HD23	2.56	0.40
32:DC:1091:ALA:HB1	40:DK:14:LYS:HB3	2.04	0.40
33:DD:178:ILE:HG21	33:DD:337:LEU:HD21	2.03	0.40
33:DD:357:TRP:NE1	47:DR:258:CYS:HB3	2.36	0.40
34:DE:74:ALA:HB3	34:DE:192:ALA:O	2.20	0.40
34:DE:144:PRO:HD2	34:DE:147:MET:HB3	2.02	0.40
34:DE:328:PRO:HA	34:DE:329:PRO:HD3	2.00	0.40
35:DF:122:LEU:H	35:DF:122:LEU:HD12	1.85	0.40
37:DH:460:LEU:O	37:DH:462:GLU:N	2.55	0.40
37:DH:467:THR:HA	37:DH:485:ASP:O	2.20	0.40
38:DI:114:PRO:O	38:DI:118:VAL:HG23	2.22	0.40
38:DI:243:LEU:HD12	38:DI:243:LEU:HA	1.83	0.40
46:DQ:240:ASP:OD2	59:F7:448:HIS:ND1	2.51	0.40
48:DS:165:VAL:HG12	48:DS:192:GLN:HE21	1.86	0.40
57:F3:177:TRP:NE1	57:F3:249:GLU:O	2.48	0.40
58:F6:217:LEU:HD23	58:F6:222:SER:HB3	2.03	0.40
59:F7:497:SER:HB3	59:F7:498:PRO:HD3	2.04	0.40
61:FO:129:SER:HA	61:FO:133:MET:HE2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:Fg:34:LEU:HD13	63:Fg:120:GLU:HG3	2.02	0.40
63:Fg:415:LEU:HD12	63:Fg:422:ALA:HA	2.04	0.40
67:IB:514:PHE:O	67:IB:545:THR:HG22	2.20	0.40
1:CA:59:U:H2'	12:CP:53:ARG:NH1	2.36	0.40
1:CA:148:C:O2'	1:CA:270:U:OP1	2.38	0.40
1:CA:545:A:H4'	1:CA:552:C:H1'	2.02	0.40
2:CC:42:ILE:O	2:CC:48:HIS:HA	2.21	0.40
3:CE:114:TYR:OH	43:DN:291:PRO:O	2.21	0.40
7:CJ:48:ILE:HD11	41:DL:104:ARG:CZ	2.51	0.40
20:Cg:107:ARG:HH21	52:DW:78:THR:HG21	1.85	0.40
22:Cj:153:HIS:HE1	47:DR:267:GLY:HA2	1.86	0.40
23:Ck:98:ARG:HB3	31:DB:466:ARG:HH22	1.87	0.40
23:Ck:222:LEU:HD23	23:Ck:239:LEU:HD12	2.04	0.40
26:Cp:152:PRO:HA	26:Cp:155:SER:HB2	2.02	0.40
27:Cq:105:ASN:OD1	27:Cq:105:ASN:N	2.46	0.40
29:Cv:70:ARG:O	29:Cv:73:VAL:HG12	2.21	0.40
30:DA:291:CYS:HB2	30:DA:323:HIS:CE1	2.57	0.40
30:DA:1194:LEU:HG	30:DA:1277:LEU:HD11	2.03	0.40
31:DB:968:VAL:HG12	36:DG:41:TRP:HZ3	1.87	0.40
32:DC:78:PRO:HG2	32:DC:708:TYR:HE2	1.86	0.40
32:DC:404:ALA:O	32:DC:407:VAL:HG12	2.21	0.40
32:DC:626:ALA:HA	32:DC:629:VAL:HG13	2.03	0.40
32:DC:952:GLU:CD	32:DC:952:GLU:H	2.29	0.40
34:DE:304:ASN:ND2	34:DE:430:VAL:HG21	2.37	0.40
35:DF:127:PRO:O	35:DF:128:HIS:ND1	2.48	0.40
35:DF:443:LEU:HD13	35:DF:452:VAL:HG11	2.03	0.40
38:DI:113:VAL:HG21	38:DI:125:TRP:CZ2	2.56	0.40
38:DI:354:GLY:O	38:DI:358:ARG:NE	2.54	0.40
49:DT:84:ILE:O	49:DT:137:LEU:HD12	2.21	0.40
49:DT:105:ARG:NE	49:DT:146:GLN:HE21	2.19	0.40
57:F3:156:THR:HA	59:F7:103:HIS:O	2.22	0.40
61:FO:138:LEU:O	61:FO:142:VAL:HG22	2.22	0.40
62:Ff:214:ASN:ND2	62:Ff:317:GLN:HG3	2.32	0.40
63:Fg:77:SER:OG	63:Fg:78:CYS:N	2.53	0.40
66:IA:735:GLU:N	66:IA:735:GLU:OE1	2.54	0.40
1:CA:254:A:H2'	1:CA:255:U:O4'	2.21	0.40
3:CE:54:GLU:HB3	30:DA:1042:HIS:ND1	2.36	0.40
5:CH:195:ARG:HD2	5:CH:195:ARG:HA	1.94	0.40
7:CJ:578:LEU:HD21	7:CJ:686:ALA:HB1	2.04	0.40
8:CK:206:ALA:HB2	8:CK:247:THR:HG22	2.04	0.40
13:CQ:73:ARG:HG2	13:CQ:117:TYR:CE2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:CU:180:GLN:NE2	16:CU:183:ASN:HA	2.37	0.40
17:Ca:278:ALA:HB2	30:DA:920:LEU:HD13	2.02	0.40
20:Cg:310:SER:O	20:Cg:314:SER:HB2	2.21	0.40
21:Ci:30:ARG:NE	23:Ck:788:GLU:OE2	2.51	0.40
23:Ck:30:GLN:HE21	31:DB:952:ASP:HB3	1.85	0.40
23:Ck:213:MET:HE3	23:Ck:213:MET:HB3	1.88	0.40
25:Cn:162:SER:HB3	25:Cn:165:LEU:HB2	2.02	0.40
28:Cr:19:LEU:N	28:Cr:20:PRO:HD2	2.36	0.40
29:Cv:426:LYS:HE2	29:Cv:426:LYS:HB3	1.94	0.40
31:DB:77:GLN:HE21	31:DB:174:ALA:HA	1.87	0.40
31:DB:213:ASP:OD1	31:DB:214:ARG:N	2.51	0.40
31:DB:300:GLN:NE2	31:DB:301:GLN:O	2.53	0.40
32:DC:222:PHE:HD1	32:DC:222:PHE:HA	1.74	0.40
32:DC:660:LYS:HE2	32:DC:660:LYS:HB3	1.95	0.40
32:DC:827:PHE:HD2	32:DC:839:VAL:HG21	1.87	0.40
33:DD:379:GLN:OE1	33:DD:380:SER:N	2.55	0.40
33:DD:463:GLU:O	33:DD:467:VAL:HG12	2.21	0.40
35:DF:432:ILE:HD11	35:DF:439:THR:HA	2.03	0.40
38:DI:50:LEU:O	38:DI:53:GLU:HG2	2.22	0.40
39:DJ:16:ASN:OD1	39:DJ:16:ASN:N	2.46	0.40
39:DJ:308:ARG:HG3	49:DT:42:PHE:CE1	2.56	0.40
42:DM:3:VAL:O	42:DM:7:ILE:HG12	2.21	0.40
46:DQ:120:MET:HB3	46:DQ:196:LEU:HD23	2.04	0.40
48:DS:172:GLU:HG3	48:DS:183:ARG:NE	2.36	0.40
54:DY:141:VAL:HA	54:DY:142:PRO:HD3	1.95	0.40
58:F6:426:GLU:HG2	58:F6:470:TYR:CD2	2.56	0.40
58:F6:671:GLY:HA3	66:IA:101:PHE:HB2	2.04	0.40
59:F7:111:THR:H	59:F7:115:ARG:HE	1.68	0.40
59:F7:199:MET:O	59:F7:202:THR:OG1	2.25	0.40
59:F7:462:ILE:HG22	59:F7:502:GLN:HG3	2.03	0.40
61:FO:50:VAL:O	61:FO:54:GLN:HG2	2.20	0.40
61:FO:58:GLY:O	61:FO:92:ALA:HA	2.22	0.40
61:FO:174:TYR:CE2	61:FO:178:LEU:HD11	2.56	0.40
62:Ff:390:LEU:HB3	62:Ff:577:ASP:OD2	2.22	0.40
65:Fi:312:LYS:HE3	65:Fi:316:TRP:HZ3	1.87	0.40
65:Fi:415:THR:HG23	65:Fi:547:ARG:HH21	1.86	0.40
1:CA:431:U:OP2	39:DJ:56:HIS:HA	2.21	0.40
1:CA:602:A:H5''	25:Cn:171:MET:HE1	2.03	0.40
8:CK:120:GLU:O	8:CK:123:ARG:HG2	2.21	0.40
13:CQ:112:ASN:OD1	13:CQ:112:ASN:N	2.50	0.40
14:CR:21:GLN:NE2	29:Cv:539:MET:O	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Ca:216:TRP:CH2	55:DZ:87:ILE:HD13	2.54	0.40
17:Ca:430:PRO:HA	17:Ca:433:GLN:HB2	2.04	0.40
20:Cg:32:MET:HG3	20:Cg:429:PRO:HD3	2.03	0.40
20:Cg:71:PHE:HB2	36:DG:629:GLN:HE22	1.85	0.40
22:Cj:38:MET:H	22:Cj:38:MET:HG2	1.74	0.40
22:Cj:64:GLN:HE21	22:Cj:77:LEU:HD22	1.86	0.40
22:Cj:79:PRO:HB2	45:DP:166:CYS:SG	2.61	0.40
28:Cr:28:PRO:HB2	28:Cr:29:PRO:HD3	2.03	0.40
28:Cr:186:ASN:ND2	28:Cr:188:THR:H	2.20	0.40
28:Cr:285:ARG:O	28:Cr:289:MET:HG2	2.22	0.40
29:Cv:582:ASN:HD21	29:Cv:794:SER:H	1.69	0.40
29:Cv:847:ARG:HH21	29:Cv:933:LEU:HA	1.86	0.40
29:Cv:1012:TRP:HD1	29:Cv:1014:ARG:HG2	1.87	0.40
30:DA:62:ARG:HG2	30:DA:86:TYR:CD2	2.57	0.40
30:DA:867:GLU:HB3	30:DA:872:LYS:HE2	2.04	0.40
30:DA:1134:ILE:HG13	30:DA:1135:PRO:O	2.21	0.40
30:DA:1268:LEU:O	30:DA:1272:LEU:HD23	2.22	0.40
30:DA:1458:PRO:O	30:DA:1462:SER:N	2.33	0.40
31:DB:236:ASP:OD2	31:DB:240:ARG:NH1	2.50	0.40
31:DB:426:HIS:ND1	31:DB:432:ARG:HA	2.36	0.40
32:DC:48:GLU:HA	32:DC:51:ARG:HG2	2.04	0.40
32:DC:52:ARG:HH12	40:DK:262:ASN:ND2	2.19	0.40
32:DC:238:PRO:HA	32:DC:393:THR:HG22	2.03	0.40
32:DC:708:TYR:CE1	40:DK:166:ALA:HA	2.57	0.40
33:DD:11:ARG:HE	33:DD:11:ARG:C	2.28	0.40
34:DE:80:LEU:HD13	34:DE:80:LEU:HA	1.86	0.40
34:DE:210:MET:HG3	34:DE:426:PHE:HZ	1.87	0.40
35:DF:262:PHE:HE1	39:DJ:59:VAL:HG22	1.87	0.40
36:DG:535:ARG:O	36:DG:539:LEU:HG	2.21	0.40
37:DH:377:ASP:OD1	37:DH:380:ARG:NH1	2.55	0.40
37:DH:453:PRO:HB2	37:DH:456:GLU:OE1	2.22	0.40
38:DI:256:ARG:HD3	38:DI:269:PHE:CE1	2.56	0.40
45:DP:97:TRP:CZ3	45:DP:134:LEU:HB3	2.57	0.40
45:DP:189:TYR:CG	45:DP:197:TYR:HB3	2.56	0.40
48:DS:189:ARG:O	48:DS:205:VAL:HG12	2.21	0.40
58:F6:220:LEU:HD12	58:F6:220:LEU:H	1.86	0.40
59:F7:286:PRO:HD2	59:F7:342:TYR:CE2	2.56	0.40
59:F7:556:GLU:N	59:F7:556:GLU:OE1	2.54	0.40
60:F9:558:TRP:HA	60:F9:561:GLU:HB3	2.03	0.40
62:Ff:206:CYS:HB3	62:Ff:238:PRO:HB2	2.02	0.40
64:Fh:54:LEU:H	64:Fh:54:LEU:HD23	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:Fi:312:LYS:HE3	65:Fi:316:TRP:CZ3	2.57	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	
2	CC	72/74 (97%)	66 (92%)	6 (8%)	0	100	100
3	CE	424/435 (98%)	406 (96%)	18 (4%)	0	100	100
4	CF	145/160 (91%)	139 (96%)	6 (4%)	0	100	100
5	CH	271/282 (96%)	263 (97%)	8 (3%)	0	100	100
6	CI	423/443 (96%)	411 (97%)	12 (3%)	0	100	100
7	CJ	799/817 (98%)	771 (96%)	28 (4%)	0	100	100
8	CK	294/326 (90%)	284 (97%)	10 (3%)	0	100	100
9	CL	85/87 (98%)	81 (95%)	4 (5%)	0	100	100
10	CN	155/166 (93%)	149 (96%)	6 (4%)	0	100	100
11	CO	306/429 (71%)	292 (95%)	14 (5%)	0	100	100
12	CP	178/188 (95%)	171 (96%)	7 (4%)	0	100	100
13	CQ	224/307 (73%)	219 (98%)	5 (2%)	0	100	100
14	CR	265/320 (83%)	258 (97%)	7 (3%)	0	100	100
15	CS	137/244 (56%)	132 (96%)	5 (4%)	0	100	100
16	CU	179/193 (93%)	175 (98%)	4 (2%)	0	100	100
17	Ca	571/602 (95%)	549 (96%)	22 (4%)	0	100	100
18	Cb	248/325 (76%)	236 (95%)	12 (5%)	0	100	100
19	Cd	228/440 (52%)	223 (98%)	5 (2%)	0	100	100
20	Cg	478/498 (96%)	473 (99%)	5 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	Ci	162/181 (90%)	156 (96%)	6 (4%)	0	100	100
22	Cj	225/257 (88%)	220 (98%)	5 (2%)	0	100	100
23	Ck	676/874 (77%)	666 (98%)	10 (2%)	0	100	100
24	Cm	143/215 (66%)	138 (96%)	5 (4%)	0	100	100
25	Cn	60/250 (24%)	59 (98%)	1 (2%)	0	100	100
26	Cp	171/187 (91%)	167 (98%)	4 (2%)	0	100	100
27	Cq	250/263 (95%)	241 (96%)	9 (4%)	0	100	100
28	Cr	263/439 (60%)	258 (98%)	5 (2%)	0	100	100
29	Cv	1032/1211 (85%)	994 (96%)	38 (4%)	0	100	100
30	DA	1546/1788 (86%)	1513 (98%)	33 (2%)	0	100	100
31	DB	1109/1181 (94%)	1076 (97%)	33 (3%)	0	100	100
32	DC	1081/1165 (93%)	1023 (95%)	58 (5%)	0	100	100
33	DD	786/812 (97%)	758 (96%)	28 (4%)	0	100	100
34	DE	576/747 (77%)	549 (95%)	27 (5%)	0	100	100
35	DF	585/666 (88%)	559 (96%)	26 (4%)	0	100	100
36	DG	542/631 (86%)	529 (98%)	13 (2%)	0	100	100
37	DH	555/581 (96%)	530 (96%)	25 (4%)	0	100	100
38	DI	388/407 (95%)	372 (96%)	16 (4%)	0	100	100
39	DJ	355/396 (90%)	351 (99%)	4 (1%)	0	100	100
40	DK	257/324 (79%)	249 (97%)	8 (3%)	0	100	100
41	DL	287/307 (94%)	283 (99%)	4 (1%)	0	100	100
42	DM	292/294 (99%)	277 (95%)	15 (5%)	0	100	100
43	DN	249/293 (85%)	243 (98%)	6 (2%)	0	100	100
44	DO	219/282 (78%)	207 (94%)	12 (6%)	0	100	100
45	DP	205/274 (75%)	198 (97%)	7 (3%)	0	100	100
46	DQ	253/268 (94%)	249 (98%)	4 (2%)	0	100	100
47	DR	246/270 (91%)	240 (98%)	6 (2%)	0	100	100
48	DS	239/261 (92%)	238 (100%)	1 (0%)	0	100	100
49	DT	237/247 (96%)	223 (94%)	14 (6%)	0	100	100
50	DU	211/228 (92%)	204 (97%)	7 (3%)	0	100	100
51	DV	158/183 (86%)	144 (91%)	14 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	DW	159/179 (89%)	152 (96%)	7 (4%)	0	100	100
53	DX	137/169 (81%)	129 (94%)	8 (6%)	0	100	100
54	DY	152/163 (93%)	145 (95%)	7 (5%)	0	100	100
55	DZ	80/94 (85%)	78 (98%)	2 (2%)	0	100	100
56	Da	32/64 (50%)	31 (97%)	1 (3%)	0	100	100
57	F3	246/966 (26%)	243 (99%)	3 (1%)	0	100	100
58	F6	410/676 (61%)	402 (98%)	8 (2%)	0	100	100
59	F7	566/679 (83%)	544 (96%)	22 (4%)	0	100	100
60	F9	338/608 (56%)	329 (97%)	9 (3%)	0	100	100
61	FO	263/334 (79%)	255 (97%)	8 (3%)	0	100	100
62	Ff	610/848 (72%)	593 (97%)	17 (3%)	0	100	100
63	Fg	507/550 (92%)	487 (96%)	20 (4%)	0	100	100
64	Fh	270/318 (85%)	259 (96%)	11 (4%)	0	100	100
65	Fi	459/629 (73%)	438 (95%)	21 (5%)	0	100	100
66	IA	687/787 (87%)	668 (97%)	19 (3%)	0	100	100
67	IB	507/803 (63%)	491 (97%)	16 (3%)	0	100	100
All	All	24263/29685 (82%)	23456 (97%)	807 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	
2	CC	73/73 (100%)	68 (93%)	5 (7%)	14	42
3	CE	365/372 (98%)	353 (97%)	12 (3%)	33	55
4	CF	135/144 (94%)	132 (98%)	3 (2%)	45	63
5	CH	237/246 (96%)	235 (99%)	2 (1%)	73	76
6	CI	360/371 (97%)	352 (98%)	8 (2%)	45	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	CJ	710/723 (98%)	686 (97%)	24 (3%)	32	55
8	CK	259/283 (92%)	254 (98%)	5 (2%)	50	65
9	CL	79/79 (100%)	76 (96%)	3 (4%)	29	53
10	CN	142/150 (95%)	136 (96%)	6 (4%)	26	51
11	CO	270/377 (72%)	262 (97%)	8 (3%)	36	57
12	CP	160/168 (95%)	157 (98%)	3 (2%)	50	65
13	CQ	201/270 (74%)	193 (96%)	8 (4%)	28	52
14	CR	233/279 (84%)	224 (96%)	9 (4%)	28	53
15	CS	123/220 (56%)	119 (97%)	4 (3%)	33	55
16	CU	159/169 (94%)	157 (99%)	2 (1%)	61	71
17	Ca	518/543 (95%)	508 (98%)	10 (2%)	50	65
18	Cb	219/277 (79%)	213 (97%)	6 (3%)	39	59
19	Cd	207/381 (54%)	205 (99%)	2 (1%)	68	74
20	Cg	424/437 (97%)	416 (98%)	8 (2%)	50	65
21	Ci	144/160 (90%)	139 (96%)	5 (4%)	32	54
22	Cj	194/219 (89%)	192 (99%)	2 (1%)	68	74
23	Ck	589/746 (79%)	578 (98%)	11 (2%)	50	65
24	Cm	124/184 (67%)	122 (98%)	2 (2%)	55	68
25	Cn	54/210 (26%)	51 (94%)	3 (6%)	19	46
26	Cp	161/175 (92%)	156 (97%)	5 (3%)	35	57
27	Cq	210/221 (95%)	204 (97%)	6 (3%)	37	57
28	Cr	223/369 (60%)	215 (96%)	8 (4%)	31	54
29	Cv	894/1033 (86%)	869 (97%)	25 (3%)	38	58
30	DA	1319/1514 (87%)	1273 (96%)	46 (4%)	32	54
31	DB	976/1030 (95%)	953 (98%)	23 (2%)	43	61
32	DC	923/985 (94%)	889 (96%)	34 (4%)	30	54
33	DD	693/711 (98%)	671 (97%)	22 (3%)	34	56
34	DE	514/642 (80%)	501 (98%)	13 (2%)	42	61
35	DF	499/560 (89%)	481 (96%)	18 (4%)	31	54
36	DG	481/543 (89%)	464 (96%)	17 (4%)	32	54
37	DH	489/504 (97%)	470 (96%)	19 (4%)	28	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	DI	350/365 (96%)	341 (97%)	9 (3%)	40	60
39	DJ	313/347 (90%)	302 (96%)	11 (4%)	32	54
40	DK	218/261 (84%)	208 (95%)	10 (5%)	24	49
41	DL	249/263 (95%)	243 (98%)	6 (2%)	43	61
42	DM	252/252 (100%)	248 (98%)	4 (2%)	55	68
43	DN	225/256 (88%)	216 (96%)	9 (4%)	28	52
44	DO	185/229 (81%)	182 (98%)	3 (2%)	55	68
45	DP	187/239 (78%)	184 (98%)	3 (2%)	55	68
46	DQ	227/239 (95%)	219 (96%)	8 (4%)	32	54
47	DR	219/235 (93%)	210 (96%)	9 (4%)	27	52
48	DS	213/228 (93%)	208 (98%)	5 (2%)	44	62
49	DT	220/228 (96%)	212 (96%)	8 (4%)	31	54
50	DU	190/201 (94%)	185 (97%)	5 (3%)	40	60
51	DV	145/165 (88%)	137 (94%)	8 (6%)	19	46
52	DW	148/163 (91%)	145 (98%)	3 (2%)	48	64
53	DX	122/149 (82%)	118 (97%)	4 (3%)	33	55
54	DY	137/146 (94%)	134 (98%)	3 (2%)	45	63
55	DZ	72/84 (86%)	69 (96%)	3 (4%)	26	51
56	Da	30/59 (51%)	30 (100%)	0	100	100
57	F3	223/809 (28%)	217 (97%)	6 (3%)	39	59
58	F6	368/590 (62%)	350 (95%)	18 (5%)	22	48
59	F7	493/577 (85%)	474 (96%)	19 (4%)	28	53
60	F9	288/504 (57%)	284 (99%)	4 (1%)	59	70
61	FO	234/290 (81%)	226 (97%)	8 (3%)	32	55
62	Ff	519/715 (73%)	499 (96%)	20 (4%)	28	53
63	Fg	441/469 (94%)	426 (97%)	15 (3%)	32	55
64	Fh	242/281 (86%)	237 (98%)	5 (2%)	47	64
65	Fi	404/536 (75%)	389 (96%)	15 (4%)	30	54
66	IA	586/661 (89%)	560 (96%)	26 (4%)	25	50
67	IB	435/675 (64%)	420 (97%)	15 (3%)	32	55
All	All	21296/25584 (83%)	20647 (97%)	649 (3%)	37	57

All (649) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	CC	2	PHE
2	CC	12	ILE
2	CC	15	LYS
2	CC	49	ILE
2	CC	70	ILE
3	CE	89	LEU
3	CE	163	ILE
3	CE	215	VAL
3	CE	222	VAL
3	CE	225	LEU
3	CE	233	VAL
3	CE	240	ASP
3	CE	266	THR
3	CE	330	VAL
3	CE	400	LEU
3	CE	420	VAL
3	CE	435	HIS
4	CF	7	VAL
4	CF	70	ASP
4	CF	73	GLU
5	CH	19	LEU
5	CH	128	VAL
6	CI	55	GLN
6	CI	133	VAL
6	CI	145	VAL
6	CI	160	LEU
6	CI	250	ASN
6	CI	336	MET
6	CI	342	LEU
6	CI	402	LEU
7	CJ	48	ILE
7	CJ	65	VAL
7	CJ	114	TYR
7	CJ	141	ASP
7	CJ	158	THR
7	CJ	180	LEU
7	CJ	229	VAL
7	CJ	249	LEU
7	CJ	293	ASP
7	CJ	335	LEU
7	CJ	398	PHE
7	CJ	518	VAL

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Mol	Chain	Res	Type
7	CJ	544	THR
7	CJ	555	TRP
7	CJ	590	PHE
7	CJ	595	THR
7	CJ	597	LEU
7	CJ	681	LEU
7	CJ	693	LEU
7	CJ	724	THR
7	CJ	754	VAL
7	CJ	757	LEU
7	CJ	767	VAL
7	CJ	777	THR
8	CK	95	MET
8	CK	240	THR
8	CK	254	LEU
8	CK	275	VAL
8	CK	324	VAL
9	CL	82	LEU
9	CL	101	VAL
9	CL	112	ILE
10	CN	59	VAL
10	CN	60	VAL
10	CN	62	THR
10	CN	98	VAL
10	CN	111	VAL
10	CN	129	VAL
11	CO	215	ASP
11	CO	219	THR
11	CO	244	HIS
11	CO	248	ILE
11	CO	313	THR
11	CO	376	GLU
11	CO	384	GLU
11	CO	418	VAL
12	CP	47	VAL
12	CP	111	SER
12	CP	134	ILE
13	CQ	34	THR
13	CQ	55	THR
13	CQ	66	VAL
13	CQ	83	LEU
13	CQ	98	VAL

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Mol	Chain	Res	Type
13	CQ	99	VAL
13	CQ	182	VAL
13	CQ	224	PHE
14	CR	18	VAL
14	CR	36	THR
14	CR	80	LEU
14	CR	103	PHE
14	CR	128	ASN
14	CR	168	ILE
14	CR	248	LYS
14	CR	268	ILE
14	CR	273	ASP
15	CS	105	ILE
15	CS	148	THR
15	CS	177	VAL
15	CS	228	LEU
16	CU	54	ILE
16	CU	175	VAL
17	Ca	26	HIS
17	Ca	45	THR
17	Ca	220	LEU
17	Ca	228	LYS
17	Ca	235	ILE
17	Ca	267	LEU
17	Ca	270	GLU
17	Ca	480	LEU
17	Ca	520	TYR
17	Ca	579	VAL
18	Cb	71	LEU
18	Cb	111	ARG
18	Cb	138	ASP
18	Cb	141	GLU
18	Cb	193	GLU
18	Cb	217	LEU
19	Cd	196	VAL
19	Cd	239	VAL
20	Cg	101	MET
20	Cg	172	VAL
20	Cg	173	THR
20	Cg	273	LEU
20	Cg	296	HIS
20	Cg	305	LEU

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Mol	Chain	Res	Type
20	Cg	312	ASN
20	Cg	375	THR
21	Ci	15	VAL
21	Ci	25	VAL
21	Ci	84	LEU
21	Ci	97	THR
21	Ci	143	GLN
22	Cj	50	VAL
22	Cj	213	ASP
23	Ck	106	VAL
23	Ck	138	PHE
23	Ck	159	THR
23	Ck	191	GLU
23	Ck	252	ASP
23	Ck	264	ASN
23	Ck	570	VAL
23	Ck	649	THR
23	Ck	714	LEU
23	Ck	817	LEU
23	Ck	832	THR
24	Cm	96	CYS
24	Cm	114	THR
25	Cn	165	LEU
25	Cn	171	MET
25	Cn	187	LEU
26	Cp	22	THR
26	Cp	42	VAL
26	Cp	66	HIS
26	Cp	101	THR
26	Cp	114	ASN
27	Cq	105	ASN
27	Cq	113	THR
27	Cq	121	VAL
27	Cq	196	HIS
27	Cq	201	GLU
27	Cq	252	GLU
28	Cr	30	VAL
28	Cr	51	GLN
28	Cr	53	GLU
28	Cr	75	ASP
28	Cr	83	VAL
28	Cr	101	ASP

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Mol	Chain	Res	Type
28	Cr	132	LEU
28	Cr	186	ASN
29	Cv	87	GLN
29	Cv	102	ASP
29	Cv	186	LEU
29	Cv	191	LEU
29	Cv	245	ASN
29	Cv	283	ASP
29	Cv	311	LEU
29	Cv	421	LEU
29	Cv	438	PHE
29	Cv	443	VAL
29	Cv	511	HIS
29	Cv	521	LEU
29	Cv	566	MET
29	Cv	583	THR
29	Cv	589	ILE
29	Cv	590	THR
29	Cv	648	VAL
29	Cv	694	VAL
29	Cv	848	LEU
29	Cv	874	GLU
29	Cv	945	VAL
29	Cv	967	VAL
29	Cv	995	VAL
29	Cv	1046	ASN
29	Cv	1093	ASN
30	DA	199	ASP
30	DA	221	TYR
30	DA	227	ILE
30	DA	238	VAL
30	DA	254	PHE
30	DA	323	HIS
30	DA	341	LEU
30	DA	353	THR
30	DA	365	LEU
30	DA	395	ILE
30	DA	398	THR
30	DA	470	LEU
30	DA	481	TYR
30	DA	509	LEU
30	DA	527	ASP

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Mol	Chain	Res	Type
30	DA	528	VAL
30	DA	531	ASN
30	DA	550	LEU
30	DA	631	THR
30	DA	687	THR
30	DA	701	VAL
30	DA	757	VAL
30	DA	765	LEU
30	DA	772	LEU
30	DA	820	ASN
30	DA	843	LEU
30	DA	890	VAL
30	DA	909	THR
30	DA	954	VAL
30	DA	979	GLN
30	DA	994	ARG
30	DA	1041	THR
30	DA	1079	VAL
30	DA	1115	LEU
30	DA	1123	LEU
30	DA	1145	THR
30	DA	1152	HIS
30	DA	1260	VAL
30	DA	1263	VAL
30	DA	1277	LEU
30	DA	1308	LEU
30	DA	1416	VAL
30	DA	1431	TYR
30	DA	1509	VAL
30	DA	1553	VAL
30	DA	1556	VAL
31	DB	118	VAL
31	DB	201	THR
31	DB	292	GLN
31	DB	307	VAL
31	DB	329	VAL
31	DB	342	VAL
31	DB	381	LEU
31	DB	439	VAL
31	DB	463	LEU
31	DB	468	THR
31	DB	547	LEU

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Mol	Chain	Res	Type
31	DB	679	VAL
31	DB	689	LEU
31	DB	737	HIS
31	DB	756	THR
31	DB	834	ILE
31	DB	918	VAL
31	DB	1039	ILE
31	DB	1100	LEU
31	DB	1104	ASP
31	DB	1135	VAL
31	DB	1138	HIS
31	DB	1162	VAL
32	DC	119	THR
32	DC	155	VAL
32	DC	167	VAL
32	DC	222	PHE
32	DC	286	GLN
32	DC	316	THR
32	DC	335	VAL
32	DC	344	MET
32	DC	422	VAL
32	DC	467	THR
32	DC	578	VAL
32	DC	583	VAL
32	DC	585	VAL
32	DC	629	VAL
32	DC	655	GLU
32	DC	665	LEU
32	DC	699	VAL
32	DC	748	TRP
32	DC	757	ARG
32	DC	758	VAL
32	DC	761	ASN
32	DC	848	THR
32	DC	868	GLU
32	DC	875	THR
32	DC	887	LEU
32	DC	894	HIS
32	DC	920	HIS
32	DC	941	MET
32	DC	956	VAL
32	DC	960	VAL

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Mol	Chain	Res	Type
32	DC	967	LEU
32	DC	981	GLU
32	DC	1005	VAL
32	DC	1071	VAL
33	DD	11	ARG
33	DD	66	TRP
33	DD	74	LEU
33	DD	79	GLN
33	DD	166	ILE
33	DD	209	THR
33	DD	247	VAL
33	DD	267	LEU
33	DD	298	MET
33	DD	320	GLU
33	DD	338	VAL
33	DD	368	LEU
33	DD	401	LEU
33	DD	436	ASP
33	DD	441	LEU
33	DD	484	LEU
33	DD	586	VAL
33	DD	624	THR
33	DD	653	PHE
33	DD	685	VAL
33	DD	742	ASP
33	DD	773	MET
34	DE	80	LEU
34	DE	172	ASP
34	DE	178	GLN
34	DE	203	LEU
34	DE	254	VAL
34	DE	295	TYR
34	DE	397	VAL
34	DE	487	ASP
34	DE	564	ILE
34	DE	584	ASP
34	DE	591	LEU
34	DE	676	GLU
34	DE	737	MET
35	DF	3	VAL
35	DF	22	LEU
35	DF	30	VAL

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Mol	Chain	Res	Type
35	DF	43	THR
35	DF	51	TRP
35	DF	58	ASP
35	DF	118	THR
35	DF	137	VAL
35	DF	184	VAL
35	DF	194	THR
35	DF	202	LEU
35	DF	228	VAL
35	DF	308	VAL
35	DF	398	ARG
35	DF	405	ASN
35	DF	568	LEU
35	DF	580	ASP
35	DF	590	LYS
36	DG	95	VAL
36	DG	120	VAL
36	DG	202	LEU
36	DG	206	LEU
36	DG	215	LEU
36	DG	224	LEU
36	DG	229	HIS
36	DG	258	VAL
36	DG	288	LEU
36	DG	339	TYR
36	DG	372	LEU
36	DG	400	VAL
36	DG	458	LEU
36	DG	489	LEU
36	DG	577	LEU
36	DG	582	VAL
36	DG	611	LEU
37	DH	11	VAL
37	DH	40	THR
37	DH	119	LEU
37	DH	126	LEU
37	DH	144	ASP
37	DH	176	LEU
37	DH	215	LEU
37	DH	246	GLU
37	DH	265	LEU
37	DH	282	ASN

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Mol	Chain	Res	Type
37	DH	290	GLU
37	DH	370	VAL
37	DH	396	VAL
37	DH	445	ILE
37	DH	460	LEU
37	DH	481	ILE
37	DH	500	VAL
37	DH	516	ILE
37	DH	519	ILE
38	DI	49	GLU
38	DI	128	GLU
38	DI	205	GLU
38	DI	251	VAL
38	DI	273	VAL
38	DI	349	THR
38	DI	351	LEU
38	DI	366	LEU
38	DI	386	ASP
39	DJ	15	VAL
39	DJ	16	ASN
39	DJ	92	LEU
39	DJ	149	THR
39	DJ	245	VAL
39	DJ	275	ASP
39	DJ	286	ILE
39	DJ	324	LEU
39	DJ	351	LEU
39	DJ	356	TYR
39	DJ	357	VAL
40	DK	47	THR
40	DK	48	VAL
40	DK	101	ASP
40	DK	142	LEU
40	DK	156	LEU
40	DK	161	LEU
40	DK	172	LEU
40	DK	173	VAL
40	DK	252	ILE
40	DK	273	LEU
41	DL	19	VAL
41	DL	26	THR
41	DL	117	ASP

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Mol	Chain	Res	Type
41	DL	280	ILE
41	DL	288	ASN
41	DL	299	THR
42	DM	21	ARG
42	DM	75	VAL
42	DM	83	THR
42	DM	227	LEU
43	DN	69	VAL
43	DN	118	LEU
43	DN	125	VAL
43	DN	128	VAL
43	DN	163	PHE
43	DN	182	VAL
43	DN	188	LEU
43	DN	207	VAL
43	DN	269	LEU
44	DO	81	LEU
44	DO	88	GLN
44	DO	138	LEU
45	DP	135	LEU
45	DP	149	GLU
45	DP	177	LEU
46	DQ	87	LEU
46	DQ	113	LEU
46	DQ	121	THR
46	DQ	171	GLU
46	DQ	184	ILE
46	DQ	205	VAL
46	DQ	208	VAL
46	DQ	260	HIS
47	DR	14	ARG
47	DR	108	GLN
47	DR	119	THR
47	DR	140	PHE
47	DR	146	LEU
47	DR	190	LEU
47	DR	218	TRP
47	DR	254	VAL
47	DR	268	HIS
48	DS	109	VAL
48	DS	170	TYR
48	DS	176	ARG

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Mol	Chain	Res	Type
48	DS	234	LEU
48	DS	253	ILE
49	DT	17	HIS
49	DT	58	HIS
49	DT	88	THR
49	DT	97	VAL
49	DT	133	ASP
49	DT	137	LEU
49	DT	157	GLN
49	DT	205	VAL
50	DU	53	LEU
50	DU	54	GLU
50	DU	96	GLN
50	DU	113	GLN
50	DU	147	LEU
51	DV	66	VAL
51	DV	67	ASN
51	DV	107	ILE
51	DV	121	VAL
51	DV	147	VAL
51	DV	165	LEU
51	DV	182	TYR
51	DV	183	LEU
52	DW	19	LEU
52	DW	22	THR
52	DW	168	MET
53	DX	63	ASP
53	DX	118	LYS
53	DX	131	ILE
53	DX	153	GLU
54	DY	17	VAL
54	DY	22	ILE
54	DY	116	LEU
55	DZ	16	GLU
55	DZ	19	THR
55	DZ	87	ILE
57	F3	81	GLN
57	F3	82	VAL
57	F3	180	ILE
57	F3	236	VAL
57	F3	297	PHE
57	F3	306	VAL

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Mol	Chain	Res	Type
58	F6	203	GLN
58	F6	207	GLU
58	F6	217	LEU
58	F6	229	LEU
58	F6	233	LEU
58	F6	236	LEU
58	F6	246	VAL
58	F6	285	ARG
58	F6	293	TYR
58	F6	298	GLU
58	F6	303	GLU
58	F6	304	LEU
58	F6	308	LEU
58	F6	326	MET
58	F6	359	VAL
58	F6	391	LEU
58	F6	544	LEU
58	F6	572	LEU
59	F7	116	ASN
59	F7	127	ARG
59	F7	131	LEU
59	F7	143	LEU
59	F7	159	VAL
59	F7	178	GLU
59	F7	202	THR
59	F7	219	LEU
59	F7	301	LEU
59	F7	328	VAL
59	F7	355	MET
59	F7	381	LEU
59	F7	383	ILE
59	F7	404	MET
59	F7	510	LEU
59	F7	542	ASN
59	F7	564	LEU
59	F7	573	THR
59	F7	604	ASP
60	F9	254	GLN
60	F9	483	LEU
60	F9	526	ASN
60	F9	548	VAL
61	FO	3	ASP

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Mol	Chain	Res	Type
61	FO	56	LEU
61	FO	71	GLN
61	FO	75	VAL
61	FO	163	ASP
61	FO	283	THR
61	FO	314	LEU
61	FO	331	PHE
62	Ff	188	THR
62	Ff	189	THR
62	Ff	200	CYS
62	Ff	209	VAL
62	Ff	210	VAL
62	Ff	297	GLU
62	Ff	312	VAL
62	Ff	344	THR
62	Ff	466	GLU
62	Ff	487	HIS
62	Ff	500	ASP
62	Ff	513	TYR
62	Ff	549	LEU
62	Ff	559	ASP
62	Ff	565	GLN
62	Ff	571	LEU
62	Ff	580	HIS
62	Ff	637	THR
62	Ff	698	VAL
62	Ff	732	ARG
63	Fg	9	LEU
63	Fg	26	LEU
63	Fg	85	VAL
63	Fg	156	GLU
63	Fg	199	ASP
63	Fg	229	ASN
63	Fg	306	LYS
63	Fg	325	THR
63	Fg	335	THR
63	Fg	428	VAL
63	Fg	467	THR
63	Fg	486	VAL
63	Fg	510	VAL
63	Fg	517	PHE
63	Fg	539	VAL

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Mol	Chain	Res	Type
64	Fh	41	TYR
64	Fh	116	VAL
64	Fh	164	ASP
64	Fh	188	ASP
64	Fh	289	LEU
65	Fi	128	LEU
65	Fi	197	ILE
65	Fi	199	LEU
65	Fi	231	LEU
65	Fi	242	VAL
65	Fi	252	ARG
65	Fi	307	THR
65	Fi	337	VAL
65	Fi	370	VAL
65	Fi	465	LEU
65	Fi	492	THR
65	Fi	514	VAL
65	Fi	533	GLN
65	Fi	569	LYS
65	Fi	570	ARG
66	IA	90	MET
66	IA	137	THR
66	IA	228	VAL
66	IA	245	VAL
66	IA	247	THR
66	IA	278	ILE
66	IA	279	VAL
66	IA	281	VAL
66	IA	282	VAL
66	IA	307	VAL
66	IA	326	LEU
66	IA	336	ASP
66	IA	373	LYS
66	IA	380	THR
66	IA	381	VAL
66	IA	393	VAL
66	IA	455	VAL
66	IA	516	LYS
66	IA	541	THR
66	IA	545	VAL
66	IA	582	VAL
66	IA	593	VAL

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Mol	Chain	Res	Type
66	IA	657	VAL
66	IA	690	VAL
66	IA	706	VAL
66	IA	743	VAL
67	IB	431	VAL
67	IB	473	ARG
67	IB	476	VAL
67	IB	501	VAL
67	IB	503	ARG
67	IB	525	PHE
67	IB	535	LEU
67	IB	603	VAL
67	IB	636	THR
67	IB	641	LEU
67	IB	672	LEU
67	IB	691	VAL
67	IB	701	THR
67	IB	771	LEU
67	IB	793	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (426) such sidechains are listed below:

Mol	Chain	Res	Type
2	CC	14	GLN
2	CC	22	HIS
3	CE	91	ASN
3	CE	161	GLN
3	CE	208	GLN
3	CE	248	GLN
3	CE	338	HIS
3	CE	433	GLN
3	CE	435	HIS
4	CF	32	ASN
4	CF	141	GLN
5	CH	25	HIS
5	CH	72	GLN
5	CH	80	HIS
6	CI	44	HIS
6	CI	170	GLN
6	CI	174	GLN
6	CI	204	ASN
7	CJ	20	GLN

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Mol	Chain	Res	Type
7	CJ	97	ASN
7	CJ	105	ASN
7	CJ	132	ASN
7	CJ	255	HIS
7	CJ	321	ASN
7	CJ	360	HIS
7	CJ	421	HIS
7	CJ	438	ASN
7	CJ	460	HIS
7	CJ	461	HIS
7	CJ	571	GLN
7	CJ	573	ASN
7	CJ	698	HIS
7	CJ	762	GLN
7	CJ	815	ASN
8	CK	81	ASN
8	CK	101	ASN
8	CK	111	ASN
8	CK	178	GLN
8	CK	252	ASN
10	CN	12	HIS
10	CN	23	HIS
10	CN	68	GLN
10	CN	75	GLN
10	CN	78	GLN
10	CN	142	HIS
10	CN	153	ASN
11	CO	149	GLN
11	CO	203	GLN
11	CO	214	HIS
11	CO	284	GLN
11	CO	297	GLN
11	CO	325	ASN
11	CO	356	GLN
11	CO	360	GLN
11	CO	374	GLN
11	CO	429	ASN
12	CP	72	GLN
12	CP	84	GLN
13	CQ	15	GLN
13	CQ	149	GLN
13	CQ	158	HIS

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Mol	Chain	Res	Type
13	CQ	231	GLN
14	CR	15	GLN
14	CR	33	GLN
14	CR	53	GLN
14	CR	63	GLN
14	CR	214	GLN
14	CR	250	GLN
14	CR	252	GLN
14	CR	259	GLN
15	CS	119	GLN
15	CS	182	HIS
15	CS	207	ASN
16	CU	37	HIS
16	CU	72	HIS
16	CU	105	GLN
16	CU	123	GLN
16	CU	132	GLN
16	CU	148	ASN
16	CU	183	ASN
17	Ca	26	HIS
17	Ca	76	GLN
17	Ca	106	ASN
17	Ca	306	HIS
17	Ca	351	GLN
17	Ca	434	HIS
17	Ca	521	GLN
17	Ca	539	GLN
18	Cb	75	ASN
19	Cd	48	ASN
19	Cd	90	GLN
19	Cd	143	GLN
19	Cd	155	GLN
19	Cd	219	HIS
20	Cg	60	HIS
20	Cg	68	GLN
20	Cg	99	GLN
20	Cg	126	GLN
20	Cg	127	HIS
20	Cg	170	ASN
20	Cg	215	ASN
20	Cg	296	HIS
20	Cg	372	ASN

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Mol	Chain	Res	Type
20	Cg	380	ASN
20	Cg	400	GLN
20	Cg	418	ASN
20	Cg	460	HIS
20	Cg	476	GLN
21	Ci	19	HIS
21	Ci	96	ASN
21	Ci	125	HIS
21	Ci	136	HIS
21	Ci	145	ASN
22	Cj	93	ASN
22	Cj	106	GLN
22	Cj	142	ASN
23	Ck	30	GLN
23	Ck	32	GLN
23	Ck	288	ASN
23	Ck	394	ASN
23	Ck	399	ASN
23	Ck	644	HIS
23	Ck	669	ASN
23	Ck	679	GLN
23	Ck	701	HIS
23	Ck	738	GLN
23	Ck	778	GLN
24	Cm	73	HIS
24	Cm	92	GLN
24	Cm	131	HIS
24	Cm	144	ASN
24	Cm	164	HIS
24	Cm	182	ASN
24	Cm	192	GLN
24	Cm	214	ASN
26	Cp	16	HIS
26	Cp	66	HIS
26	Cp	116	ASN
26	Cp	154	GLN
27	Cq	20	GLN
27	Cq	76	GLN
27	Cq	157	GLN
28	Cr	11	ASN
28	Cr	47	HIS
28	Cr	267	GLN

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Mol	Chain	Res	Type
29	Cv	147	HIS
29	Cv	166	HIS
29	Cv	223	ASN
29	Cv	411	ASN
29	Cv	442	ASN
29	Cv	523	HIS
29	Cv	559	GLN
29	Cv	563	ASN
29	Cv	803	GLN
29	Cv	820	GLN
29	Cv	878	ASN
29	Cv	883	HIS
29	Cv	944	HIS
29	Cv	1059	GLN
29	Cv	1066	GLN
30	DA	59	HIS
30	DA	68	ASN
30	DA	101	ASN
30	DA	145	GLN
30	DA	492	ASN
30	DA	541	GLN
30	DA	542	GLN
30	DA	543	GLN
30	DA	644	HIS
30	DA	883	ASN
30	DA	910	HIS
30	DA	979	GLN
30	DA	1081	GLN
30	DA	1096	GLN
30	DA	1117	ASN
30	DA	1176	GLN
30	DA	1193	HIS
30	DA	1249	HIS
30	DA	1385	ASN
30	DA	1439	ASN
30	DA	1453	ASN
30	DA	1456	GLN
30	DA	1562	GLN
30	DA	1570	ASN
30	DA	1600	ASN
31	DB	106	GLN
31	DB	134	HIS

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Mol	Chain	Res	Type
31	DB	184	HIS
31	DB	254	ASN
31	DB	292	GLN
31	DB	300	GLN
31	DB	340	ASN
31	DB	415	GLN
31	DB	541	HIS
31	DB	543	GLN
31	DB	558	ASN
31	DB	562	GLN
31	DB	615	ASN
31	DB	630	HIS
31	DB	670	HIS
31	DB	684	GLN
31	DB	703	HIS
31	DB	711	GLN
31	DB	764	GLN
31	DB	840	ASN
31	DB	855	GLN
31	DB	868	HIS
31	DB	1064	GLN
31	DB	1066	ASN
31	DB	1086	HIS
31	DB	1170	GLN
32	DC	41	ASN
32	DC	76	ASN
32	DC	96	GLN
32	DC	205	GLN
32	DC	228	GLN
32	DC	263	GLN
32	DC	395	HIS
32	DC	424	GLN
32	DC	473	GLN
32	DC	530	GLN
32	DC	776	ASN
32	DC	801	HIS
32	DC	841	HIS
32	DC	920	HIS
32	DC	1048	HIS
32	DC	1064	GLN
32	DC	1160	GLN
33	DD	59	ASN

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Mol	Chain	Res	Type
33	DD	116	GLN
33	DD	174	HIS
33	DD	176	HIS
33	DD	300	GLN
33	DD	324	ASN
33	DD	348	HIS
33	DD	354	HIS
33	DD	402	GLN
33	DD	529	GLN
33	DD	585	ASN
33	DD	628	ASN
33	DD	707	GLN
34	DE	38	GLN
34	DE	138	ASN
34	DE	178	GLN
34	DE	202	HIS
34	DE	501	HIS
34	DE	534	ASN
34	DE	567	HIS
34	DE	596	HIS
34	DE	619	ASN
34	DE	644	HIS
35	DF	15	HIS
35	DF	110	ASN
35	DF	115	HIS
35	DF	175	GLN
35	DF	273	ASN
35	DF	406	ASN
35	DF	490	ASN
35	DF	520	GLN
35	DF	543	HIS
36	DG	12	ASN
36	DG	22	GLN
36	DG	26	ASN
36	DG	33	HIS
36	DG	65	ASN
36	DG	169	ASN
36	DG	365	GLN
36	DG	396	ASN
37	DH	4	GLN
37	DH	23	HIS
37	DH	27	GLN

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Mol	Chain	Res	Type
37	DH	100	HIS
37	DH	198	GLN
37	DH	255	GLN
37	DH	271	HIS
37	DH	337	GLN
37	DH	343	ASN
37	DH	423	GLN
37	DH	450	ASN
37	DH	513	HIS
38	DI	75	GLN
38	DI	85	ASN
38	DI	216	GLN
38	DI	285	GLN
38	DI	312	ASN
39	DJ	45	ASN
39	DJ	146	GLN
39	DJ	243	ASN
39	DJ	301	HIS
39	DJ	309	GLN
39	DJ	314	GLN
39	DJ	329	HIS
40	DK	7	ASN
40	DK	34	ASN
40	DK	219	GLN
40	DK	251	GLN
41	DL	182	GLN
41	DL	219	GLN
42	DM	89	GLN
42	DM	171	GLN
42	DM	292	ASN
43	DN	223	GLN
43	DN	266	ASN
43	DN	272	HIS
43	DN	280	GLN
44	DO	88	GLN
44	DO	158	GLN
44	DO	210	ASN
44	DO	215	ASN
44	DO	248	GLN
45	DP	194	GLN
45	DP	212	ASN
46	DQ	21	ASN

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Mol	Chain	Res	Type
46	DQ	27	HIS
46	DQ	41	GLN
46	DQ	59	GLN
46	DQ	73	HIS
47	DR	26	ASN
47	DR	39	GLN
47	DR	173	ASN
47	DR	191	GLN
47	DR	217	ASN
47	DR	223	GLN
48	DS	15	GLN
48	DS	91	HIS
48	DS	192	GLN
48	DS	219	ASN
49	DT	16	HIS
49	DT	23	GLN
49	DT	63	HIS
49	DT	146	GLN
49	DT	161	ASN
49	DT	215	GLN
49	DT	240	GLN
50	DU	18	GLN
50	DU	63	HIS
50	DU	164	ASN
50	DU	199	GLN
51	DV	38	GLN
51	DV	51	ASN
52	DW	44	ASN
52	DW	69	GLN
52	DW	119	GLN
53	DX	58	HIS
53	DX	130	GLN
53	DX	167	HIS
54	DY	10	ASN
54	DY	106	GLN
54	DY	112	HIS
55	DZ	59	ASN
56	Da	34	GLN
57	F3	213	ASN
58	F6	203	GLN
58	F6	230	GLN
58	F6	271	GLN

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Mol	Chain	Res	Type
58	F6	292	GLN
58	F6	299	GLN
58	F6	385	GLN
58	F6	547	GLN
58	F6	551	HIS
58	F6	587	GLN
58	F6	601	GLN
59	F7	110	GLN
59	F7	116	ASN
59	F7	157	GLN
59	F7	214	HIS
59	F7	444	GLN
59	F7	542	ASN
60	F9	265	GLN
60	F9	377	GLN
60	F9	451	ASN
60	F9	484	ASN
61	FO	54	GLN
61	FO	97	ASN
61	FO	151	GLN
61	FO	175	HIS
61	FO	306	ASN
61	FO	318	GLN
62	Ff	202	GLN
62	Ff	214	ASN
62	Ff	299	HIS
62	Ff	317	GLN
62	Ff	326	HIS
62	Ff	484	GLN
62	Ff	565	GLN
62	Ff	600	HIS
62	Ff	710	GLN
63	Fg	206	GLN
63	Fg	236	GLN
63	Fg	417	ASN
63	Fg	487	GLN
64	Fh	165	GLN
64	Fh	221	ASN
64	Fh	233	HIS
64	Fh	254	ASN
65	Fi	80	ASN
65	Fi	193	HIS

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Mol	Chain	Res	Type
65	Fi	194	ASN
65	Fi	207	ASN
65	Fi	218	HIS
65	Fi	277	HIS
65	Fi	377	GLN
65	Fi	381	GLN
65	Fi	533	GLN
65	Fi	594	GLN
65	Fi	595	GLN
65	Fi	598	HIS
66	IA	66	ASN
66	IA	77	HIS
66	IA	135	GLN
66	IA	139	GLN
66	IA	157	HIS
66	IA	227	ASN
66	IA	231	GLN
66	IA	289	GLN
66	IA	363	GLN
66	IA	462	GLN
66	IA	724	GLN
67	IB	448	GLN
67	IB	533	HIS
67	IB	538	HIS
67	IB	570	GLN
67	IB	575	HIS
67	IB	608	GLN
67	IB	610	GLN
67	IB	708	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	CA	620/621 (99%)	252 (40%)	2 (0%)

All (252) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	CA	2	A
1	CA	3	A
1	CA	4	A

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Mol	Chain	Res	Type
1	CA	6	U
1	CA	11	U
1	CA	16	U
1	CA	18	U
1	CA	19	U
1	CA	25	U
1	CA	26	C
1	CA	29	A
1	CA	38	U
1	CA	41	A
1	CA	42	A
1	CA	43	A
1	CA	45	G
1	CA	46	U
1	CA	53	A
1	CA	56	U
1	CA	58	A
1	CA	60	A
1	CA	61	A
1	CA	62	A
1	CA	64	G
1	CA	65	U
1	CA	67	U
1	CA	68	A
1	CA	69	U
1	CA	73	U
1	CA	74	G
1	CA	78	G
1	CA	79	A
1	CA	80	U
1	CA	85	U
1	CA	87	U
1	CA	88	A
1	CA	91	A
1	CA	98	A
1	CA	100	G
1	CA	102	A
1	CA	105	G
1	CA	112	A
1	CA	113	U
1	CA	115	A
1	CA	117	U

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Mol	Chain	Res	Type
1	CA	127	G
1	CA	135	U
1	CA	136	G
1	CA	137	U
1	CA	138	U
1	CA	139	U
1	CA	140	U
1	CA	147	G
1	CA	154	G
1	CA	156	U
1	CA	162	U
1	CA	167	A
1	CA	171	A
1	CA	172	A
1	CA	173	A
1	CA	174	A
1	CA	175	A
1	CA	176	A
1	CA	180	A
1	CA	182	U
1	CA	188	U
1	CA	193	C
1	CA	194	A
1	CA	195	A
1	CA	196	U
1	CA	197	A
1	CA	198	A
1	CA	199	U
1	CA	200	A
1	CA	201	A
1	CA	202	A
1	CA	203	U
1	CA	205	A
1	CA	209	U
1	CA	210	A
1	CA	212	U
1	CA	214	U
1	CA	215	A
1	CA	216	U
1	CA	221	C
1	CA	227	U
1	CA	233	C

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Mol	Chain	Res	Type
1	CA	236	G
1	CA	239	G
1	CA	247	A
1	CA	261	U
1	CA	262	A
1	CA	263	A
1	CA	271	A
1	CA	272	C
1	CA	275	U
1	CA	276	U
1	CA	277	A
1	CA	279	C
1	CA	280	A
1	CA	284	U
1	CA	291	U
1	CA	296	U
1	CA	297	G
1	CA	298	C
1	CA	300	G
1	CA	309	A
1	CA	310	A
1	CA	322	A
1	CA	323	U
1	CA	324	A
1	CA	327	U
1	CA	328	U
1	CA	329	U
1	CA	330	U
1	CA	331	A
1	CA	332	U
1	CA	334	U
1	CA	335	G
1	CA	336	U
1	CA	337	U
1	CA	338	U
1	CA	339	U
1	CA	340	U
1	CA	345	A
1	CA	346	C
1	CA	347	C
1	CA	348	A
1	CA	349	U

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Mol	Chain	Res	Type
1	CA	350	U
1	CA	355	A
1	CA	356	U
1	CA	357	A
1	CA	360	C
1	CA	361	A
1	CA	362	A
1	CA	364	U
1	CA	365	A
1	CA	366	U
1	CA	367	A
1	CA	368	A
1	CA	369	A
1	CA	370	A
1	CA	378	A
1	CA	380	U
1	CA	389	A
1	CA	390	U
1	CA	391	A
1	CA	392	U
1	CA	393	U
1	CA	394	A
1	CA	395	U
1	CA	396	A
1	CA	397	U
1	CA	398	U
1	CA	400	U
1	CA	407	U
1	CA	408	C
1	CA	409	A
1	CA	411	A
1	CA	412	U
1	CA	414	A
1	CA	415	U
1	CA	416	U
1	CA	418	A
1	CA	421	G
1	CA	423	A
1	CA	428	A
1	CA	429	U
1	CA	430	U
1	CA	431	U

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Mol	Chain	Res	Type
1	CA	432	G
1	CA	433	U
1	CA	434	A
1	CA	438	U
1	CA	443	U
1	CA	448	U
1	CA	449	G
1	CA	451	U
1	CA	455	G
1	CA	458	U
1	CA	459	A
1	CA	460	U
1	CA	461	A
1	CA	462	A
1	CA	463	A
1	CA	464	U
1	CA	467	A
1	CA	469	A
1	CA	470	G
1	CA	472	G
1	CA	476	A
1	CA	480	C
1	CA	481	A
1	CA	482	U
1	CA	483	A
1	CA	484	A
1	CA	485	U
1	CA	486	C
1	CA	487	A
1	CA	488	A
1	CA	489	A
1	CA	494	A
1	CA	496	U
1	CA	497	A
1	CA	498	U
1	CA	501	A
1	CA	502	U
1	CA	505	U
1	CA	506	A
1	CA	507	A
1	CA	510	A
1	CA	513	U

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Mol	Chain	Res	Type
1	CA	517	U
1	CA	518	G
1	CA	519	U
1	CA	520	A
1	CA	528	U
1	CA	529	A
1	CA	532	A
1	CA	533	A
1	CA	534	A
1	CA	536	U
1	CA	538	A
1	CA	539	A
1	CA	541	A
1	CA	542	G
1	CA	543	G
1	CA	544	U
1	CA	545	A
1	CA	547	U
1	CA	565	A
1	CA	566	U
1	CA	568	A
1	CA	569	U
1	CA	576	A
1	CA	581	G
1	CA	583	A
1	CA	586	A
1	CA	587	A
1	CA	588	U
1	CA	590	A
1	CA	603	A
1	CA	612	U
1	CA	613	U
1	CA	614	U
1	CA	615	U
1	CA	616	U
1	CA	617	U
1	CA	619	U
1	CA	620	U
1	CA	621	U

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	CA	299	U
1	CA	512	G

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 15 ligands modelled in this entry, 10 are monoatomic - leaving 5 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
82	PO4	IA	1001	76	4,4,4	0.96	0	6,6,6	0.47	0
81	GDP	IA	1000	76	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
79	UTP	DJ	401	-	29,30,30	0.57	0	43,47,47	0.70	0
80	FAD	Ff	901	-	58,58,58	0.32	0	85,89,89	0.27	0
77	ATP	Cg	1000	76	32,33,33	0.34	0	48,52,52	0.32	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
81	GDP	IA	1000	76	-	2/16/32/32	0/3/3/3
80	FAD	Ff	901	-	-	11/34/50/50	0/6/6/6
77	ATP	Cg	1000	76	-	3/22/38/38	0/3/3/3
79	UTP	DJ	401	-	-	4/22/38/38	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	IA	1000	GDP	C5-C4	3.12	1.47	1.38
81	IA	1000	GDP	C6-N1	-2.42	1.34	1.38
81	IA	1000	GDP	C5-N7	-2.08	1.34	1.39

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	IA	1000	GDP	C5-C4-N3	-6.03	118.79	128.39
81	IA	1000	GDP	C2-N3-C4	4.98	120.88	112.30
81	IA	1000	GDP	N9-C4-N3	4.52	134.99	125.95
81	IA	1000	GDP	C6-C5-N7	3.20	136.11	130.29
81	IA	1000	GDP	C4-C5-N7	-2.46	106.77	110.67
81	IA	1000	GDP	C3'-C2'-C1'	2.31	105.84	101.46
81	IA	1000	GDP	O6-C6-C5	-2.14	120.88	126.53

There are no chirality outliers.

All (20) torsion outliers are listed below:

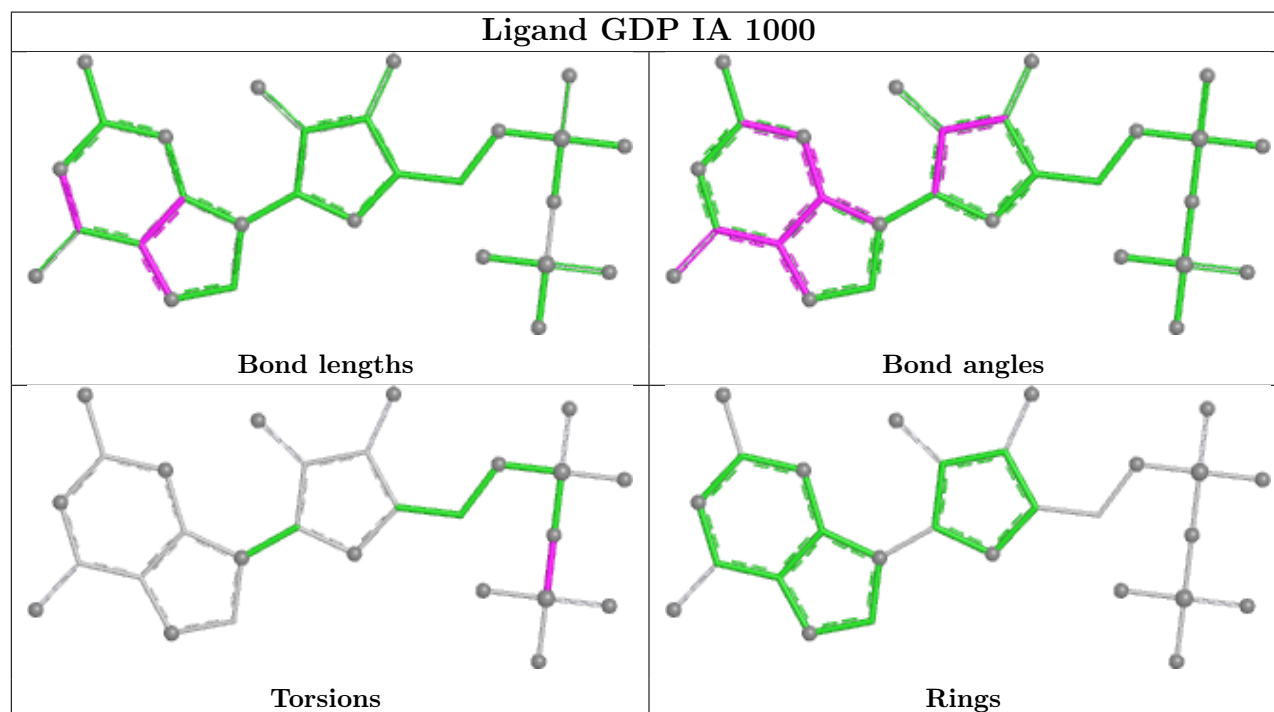
Mol	Chain	Res	Type	Atoms
79	DJ	401	UTP	O4'-C1'-N1-C2
80	Ff	901	FAD	C5B-O5B-PA-O3P
80	Ff	901	FAD	N10-C1'-C2'-O2'
80	Ff	901	FAD	N10-C1'-C2'-C3'
80	Ff	901	FAD	C2'-C3'-C4'-O4'
80	Ff	901	FAD	C2'-C3'-C4'-C5'
80	Ff	901	FAD	O3'-C3'-C4'-O4'
80	Ff	901	FAD	O3'-C3'-C4'-C5'
81	IA	1000	GDP	PA-O3A-PB-O3B
80	Ff	901	FAD	O4B-C4B-C5B-O5B
80	Ff	901	FAD	C3B-C4B-C5B-O5B
79	DJ	401	UTP	O4'-C1'-N1-C6
81	IA	1000	GDP	PA-O3A-PB-O1B
77	Cg	1000	ATP	C5'-O5'-PA-O1A
80	Ff	901	FAD	C5B-O5B-PA-O1A
80	Ff	901	FAD	C4'-C5'-O5'-P
79	DJ	401	UTP	C4'-C5'-O5'-PA
77	Cg	1000	ATP	PA-O3A-PB-O2B
79	DJ	401	UTP	C3'-C4'-C5'-O5'
77	Cg	1000	ATP	PA-O3A-PB-O1B

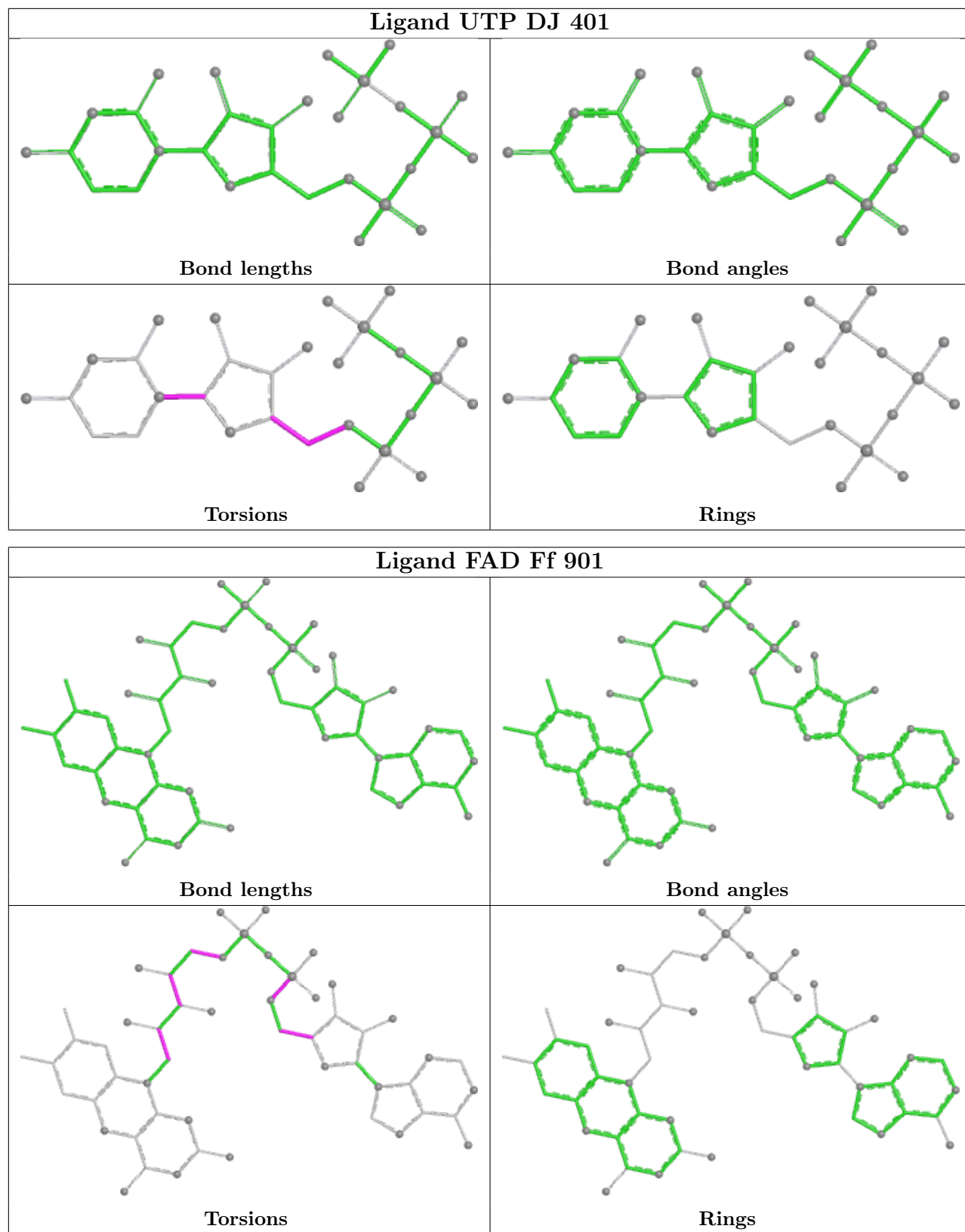
There are no ring outliers.

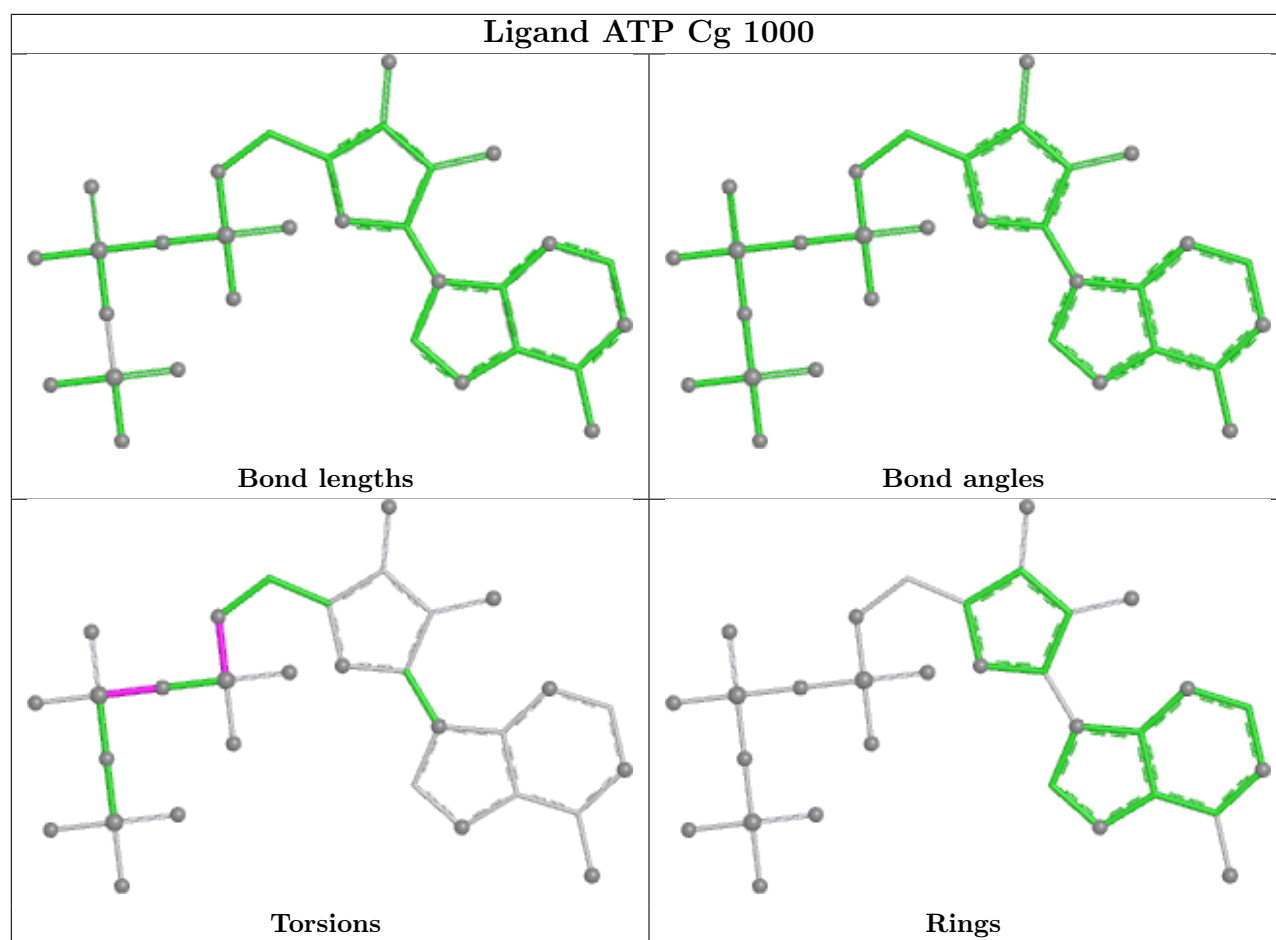
3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
82	IA	1001	PO4	1	0
81	IA	1000	GDP	1	0
79	DJ	401	UTP	3	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.

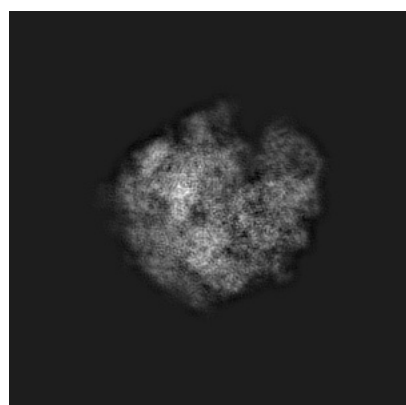
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13661. These allow visual inspection of the internal detail of the map and identification of artifacts.

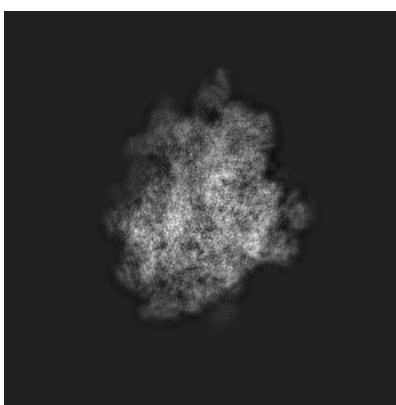
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

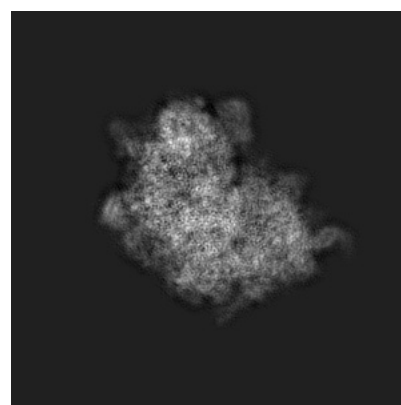
6.1.1 Primary map



X



Y

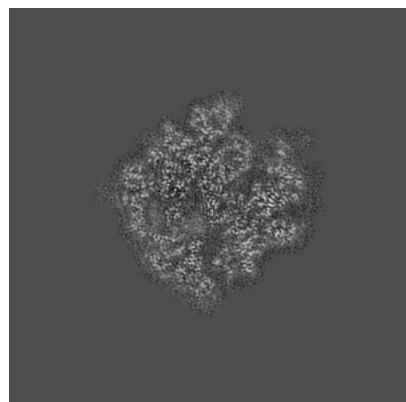


Z

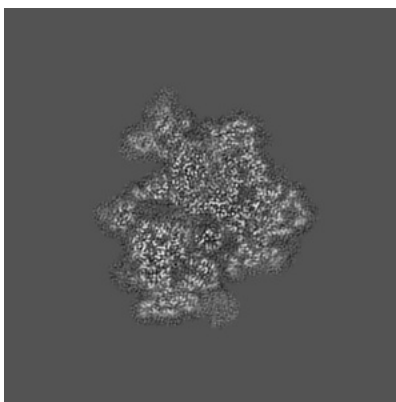
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

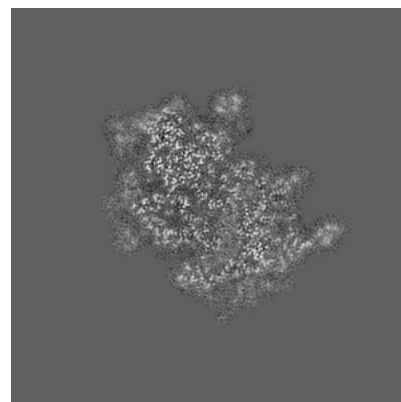
6.2.1 Primary map



X Index: 180



Y Index: 180

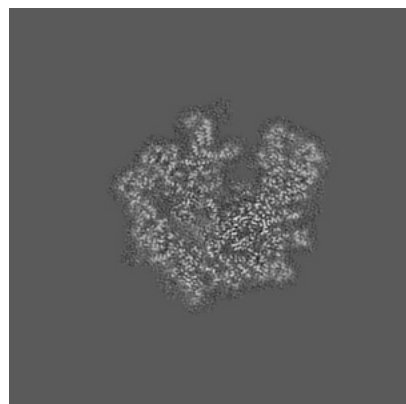


Z Index: 180

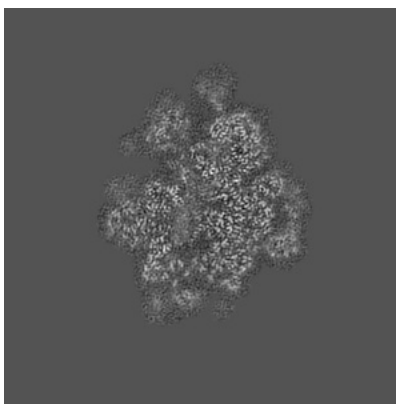
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

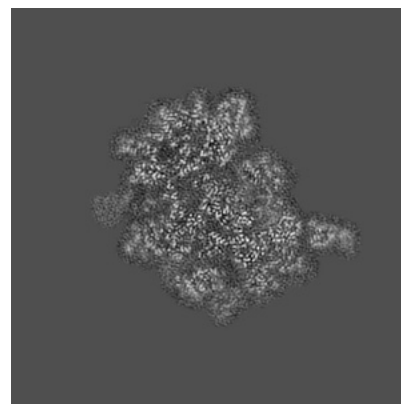
6.3.1 Primary map



X Index: 158



Y Index: 165

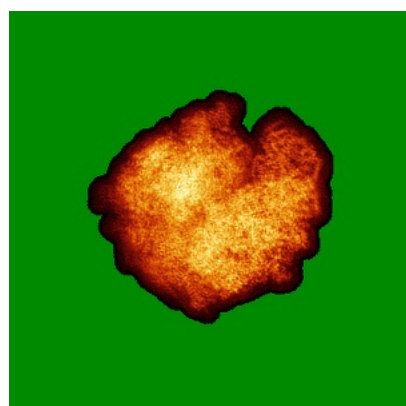


Z Index: 192

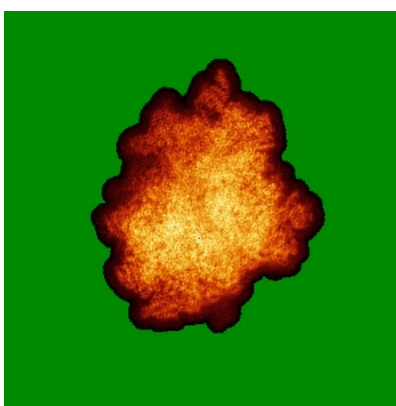
The images above show the largest variance slices of the map in three orthogonal directions.

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

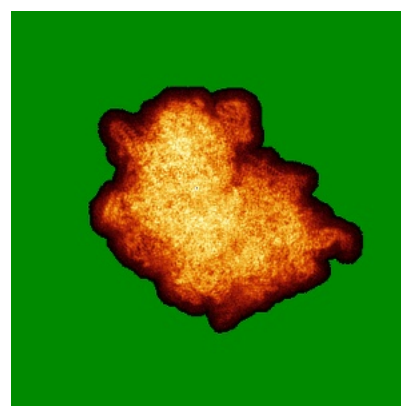
6.4.1 Primary map



X



Y

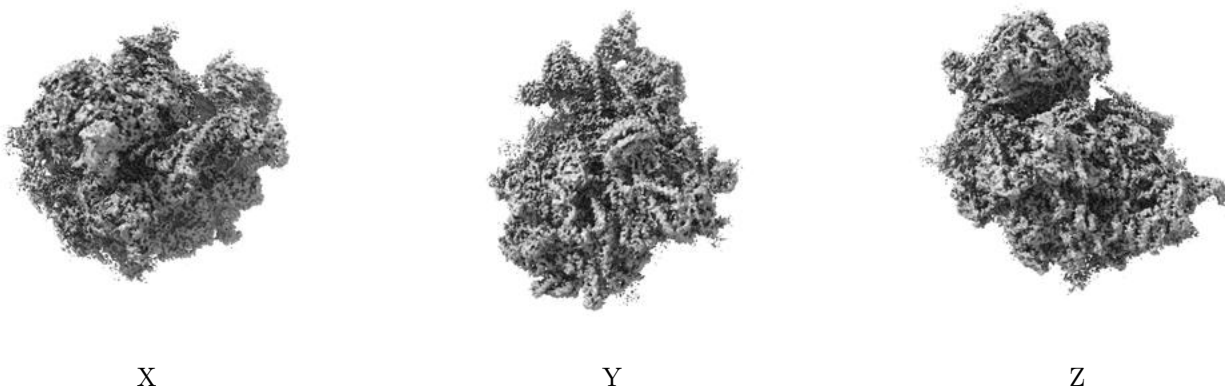


Z

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

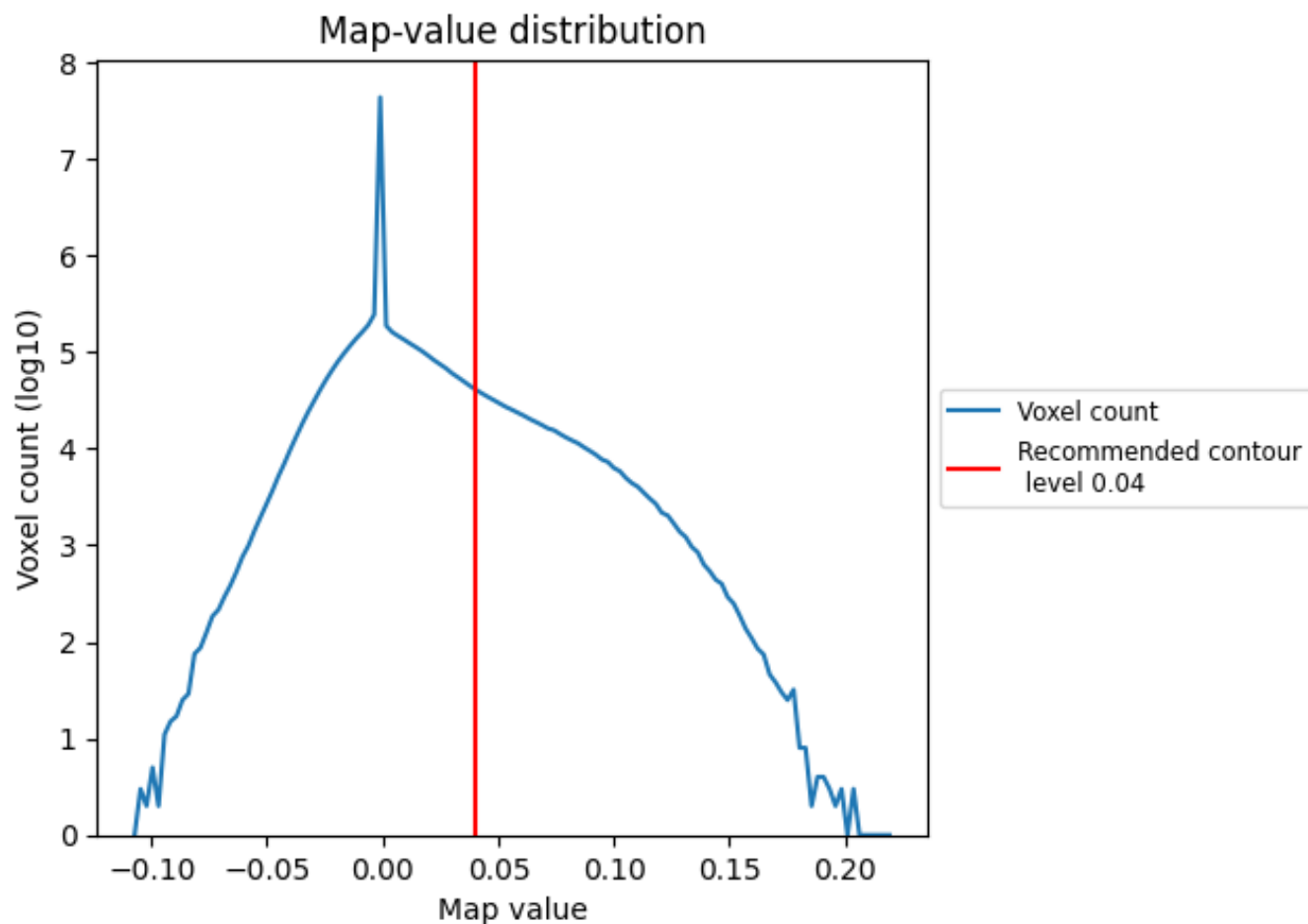
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

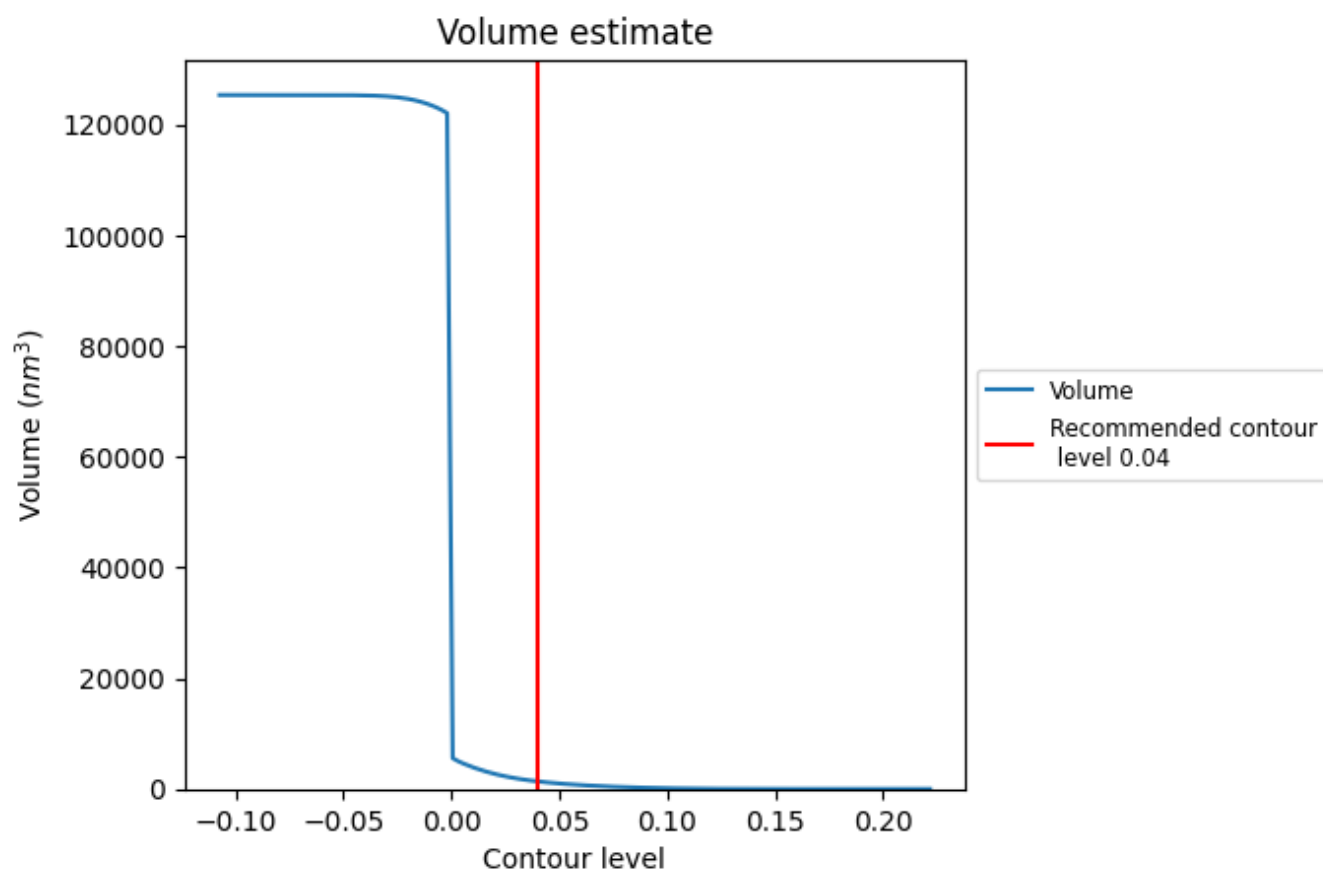
This section contains the results of statistical analysis of the map.

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.

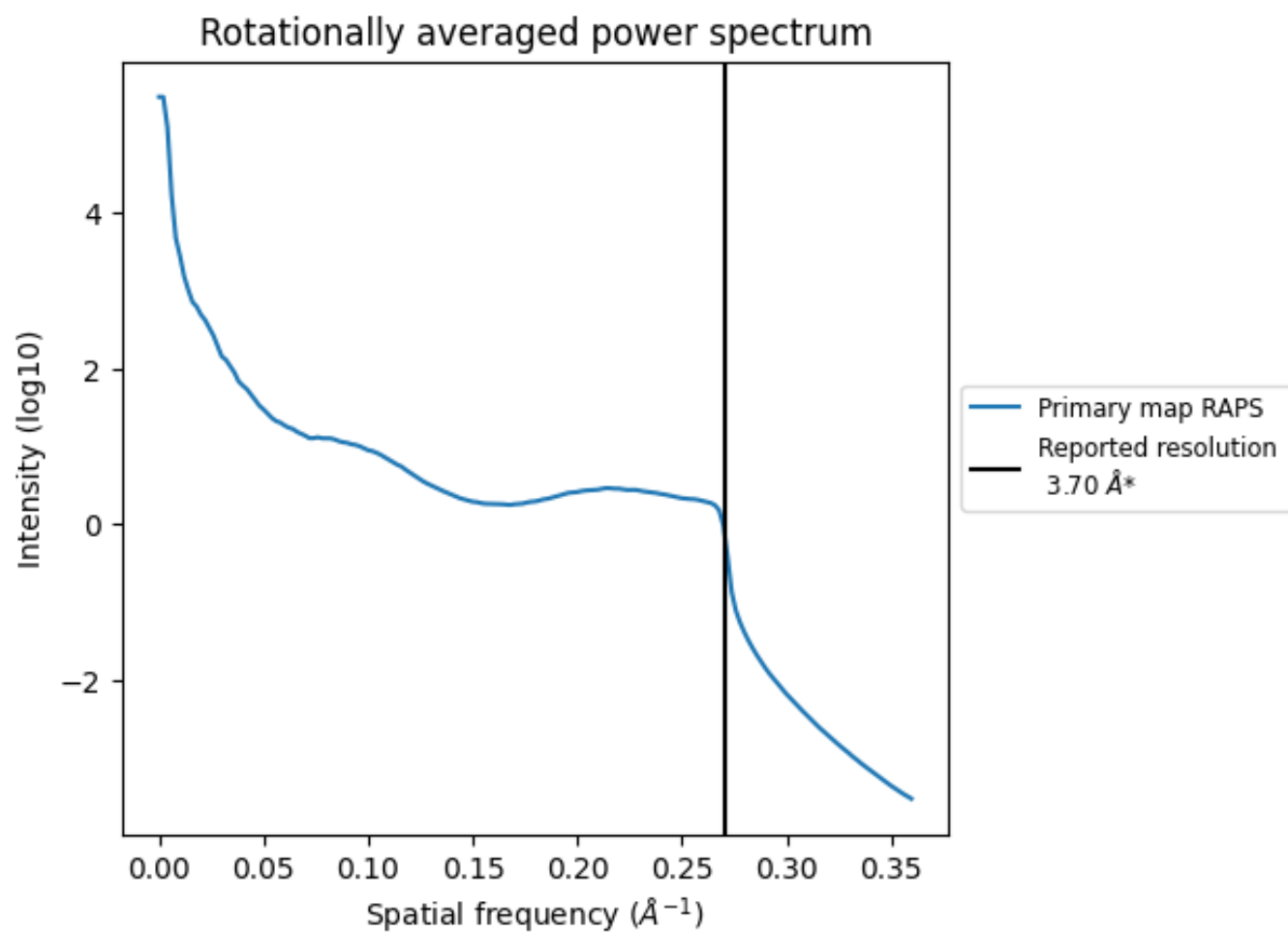
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1367 nm³; this corresponds to an approximate mass of 1235 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 0.270 Å⁻¹

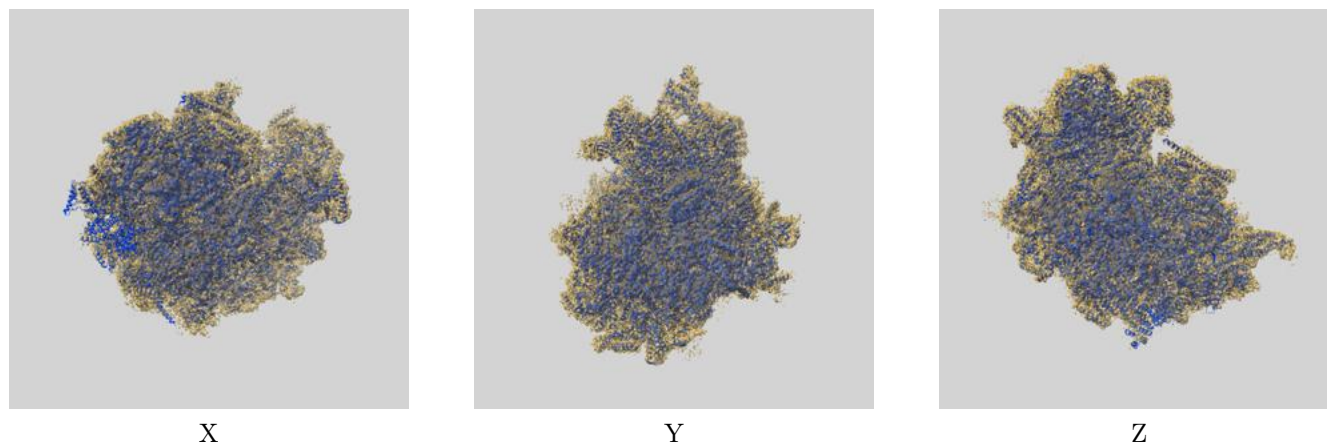
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

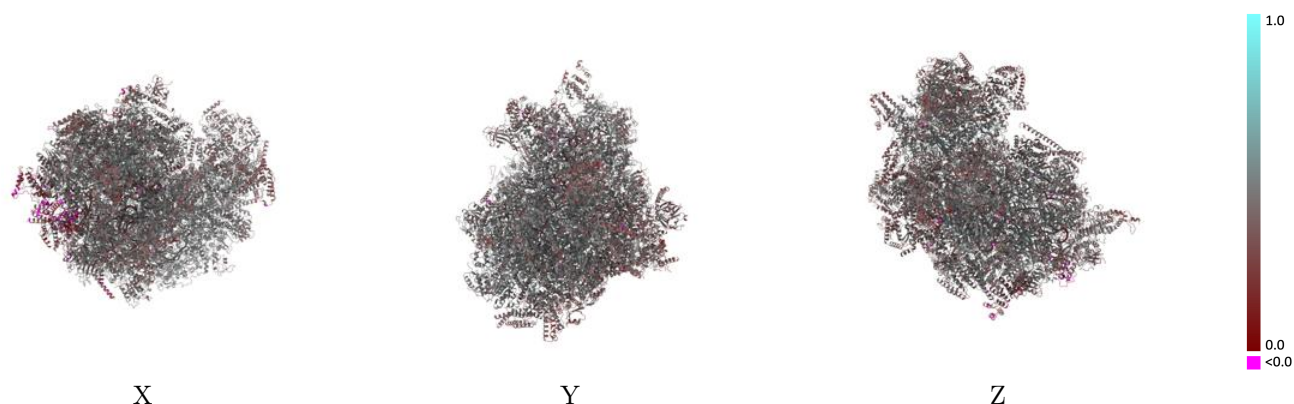
This section contains information regarding the fit between EMDB map EMD-13661 and PDB model 7PUB. Per-residue inclusion information can be found in section [3](#) on page [27](#).

9.1 Map-model overlay [i](#)



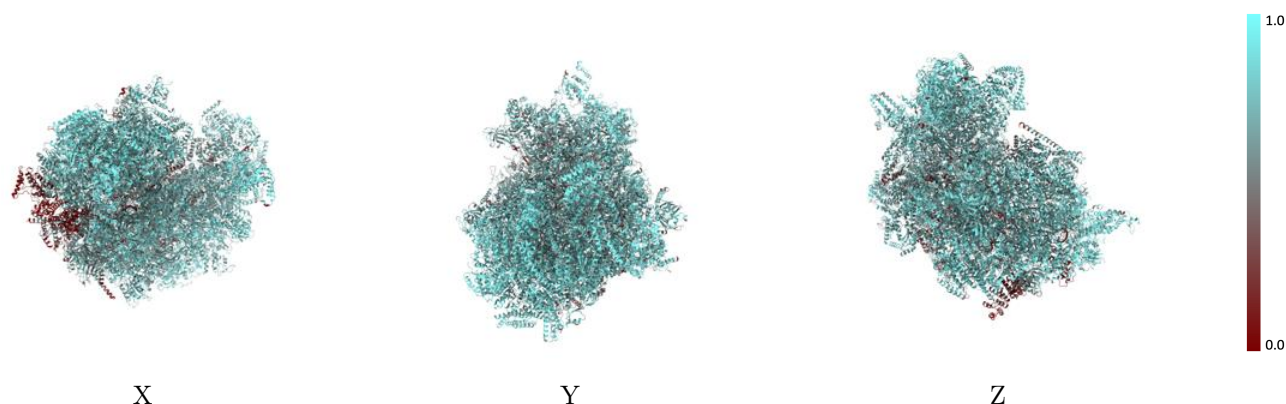
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



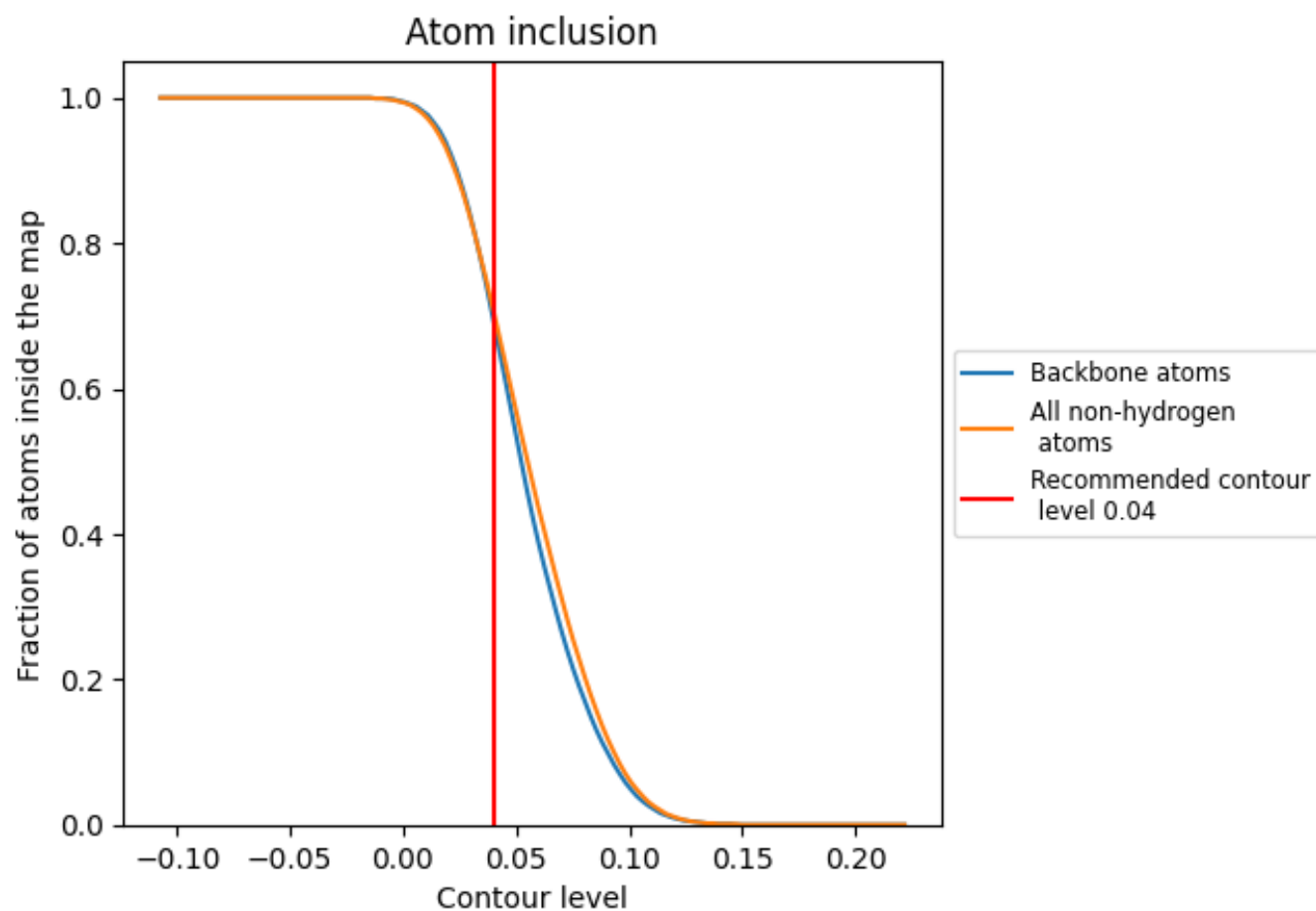
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 71% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7070	 0.4360
CA	 0.7550	 0.4250
CC	 0.6620	 0.4760
CE	 0.6950	 0.4700
CF	 0.7820	 0.4500
CH	 0.6990	 0.4650
CI	 0.7100	 0.4570
CJ	 0.7850	 0.4760
CK	 0.7150	 0.4410
CL	 0.6770	 0.4740
CN	 0.8160	 0.4970
CO	 0.7250	 0.4420
CP	 0.7870	 0.4760
CQ	 0.7380	 0.4790
CR	 0.6760	 0.4530
CS	 0.8250	 0.4850
CU	 0.6630	 0.4440
Ca	 0.6580	 0.4460
Cb	 0.6930	 0.4330
Cd	 0.7700	 0.4470
Cg	 0.8260	 0.4660
Ci	 0.8320	 0.4950
Cj	 0.8230	 0.4410
Ck	 0.7570	 0.4360
Cm	 0.5120	 0.3880
Cn	 0.5280	 0.4310
Cp	 0.7630	 0.4340
Cq	 0.7560	 0.4430
Cr	 0.7010	 0.3850
Cv	 0.7420	 0.4560
DA	 0.7100	 0.4140
DB	 0.7730	 0.4580
DC	 0.7830	 0.4050
DD	 0.7840	 0.4530
DE	 0.7670	 0.4120



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Chain	Atom inclusion	Q-score
DF	 0.8280	 0.4630
DG	 0.7700	 0.4150
DH	 0.7720	 0.4640
DI	 0.7820	 0.4510
DJ	 0.7980	 0.4640
DK	 0.7690	 0.4550
DL	 0.6340	 0.4630
DM	 0.7670	 0.4590
DN	 0.7340	 0.4620
DO	 0.7600	 0.4290
DP	 0.8270	 0.4090
DQ	 0.6800	 0.4240
DR	 0.8150	 0.4230
DS	 0.7940	 0.4500
DT	 0.8160	 0.4840
DU	 0.6730	 0.4450
DV	 0.7860	 0.4790
DW	 0.7890	 0.4610
DX	 0.8370	 0.4650
DY	 0.7970	 0.4690
DZ	 0.6410	 0.4590
Da	 0.6150	 0.4420
F3	 0.1220	 0.1800
F6	 0.4070	 0.3160
F7	 0.3270	 0.3290
F9	 0.6640	 0.4400
FO	 0.7170	 0.4510
Ff	 0.7490	 0.4530
Fg	 0.6900	 0.4100
Fh	 0.6030	 0.4360
Fi	 0.5830	 0.4190
IA	 0.6890	 0.4450
IB	 0.6770	 0.4480
U6	 0.4480	 0.3440
U7	 0.6850	 0.4160
UE	 0.6340	 0.4640
UF	 0.5080	 0.4100
UG	 0.6150	 0.4680
UI	 0.7000	 0.3140
UJ	 0.7240	 0.3360
UK	 0.9330	 0.4980
UL	 0.6500	 0.4290