



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 03:34 PM UTC

PDB ID : 9N6X / pdb_00009n6x
EMDB ID : EMD-49077
Title : SSU processome maturation and disassembly, State B
Authors : Buzovetsky, O.; Klinge, S.
Deposited on : 2025-02-05
Resolution : 3.71 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

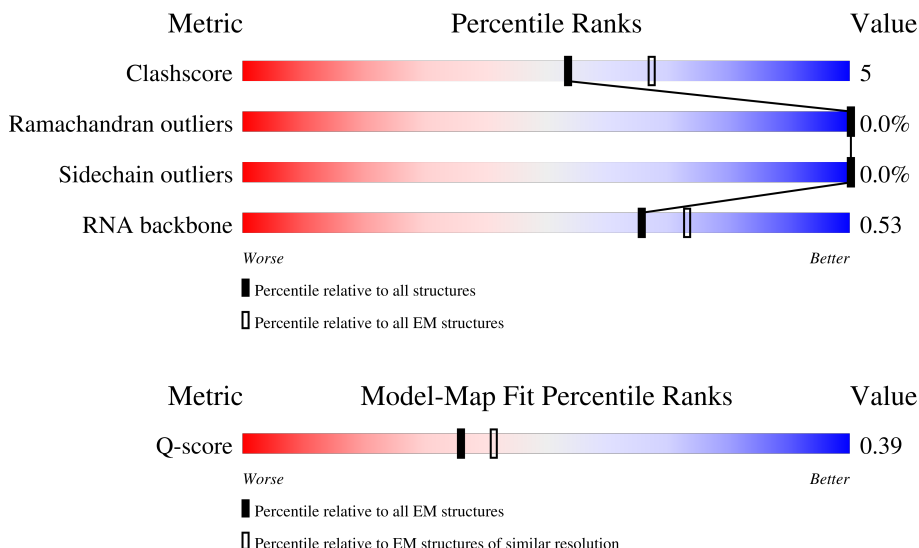
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.71 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	10534 (3.21 - 4.21)

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.

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1	L0	700	
2	L1	1808	
3	L2	333	

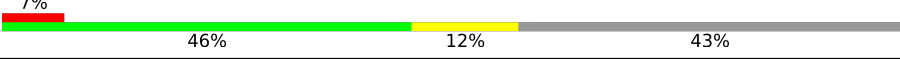
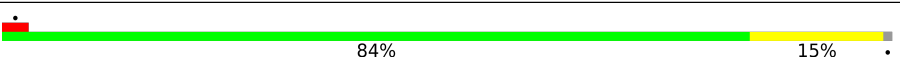
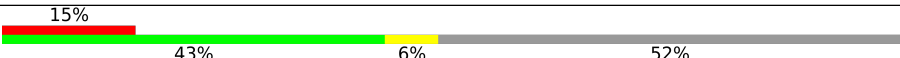
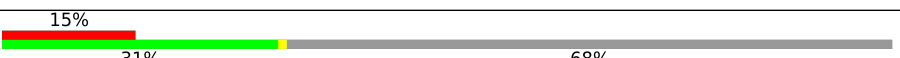
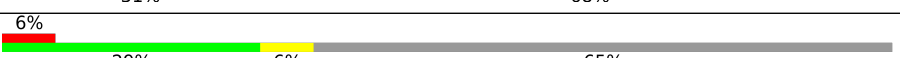
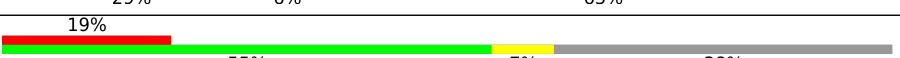
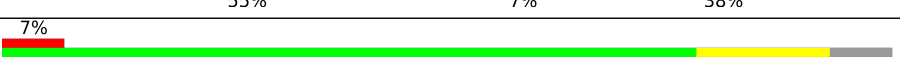
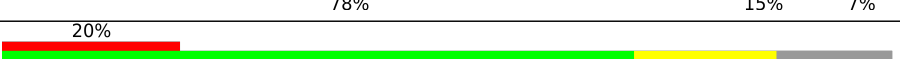
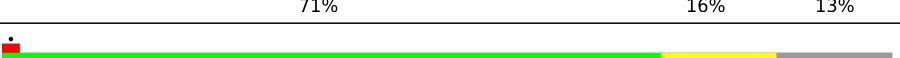
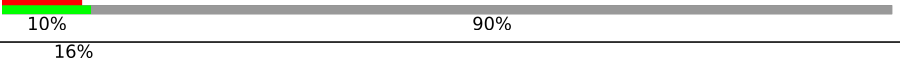
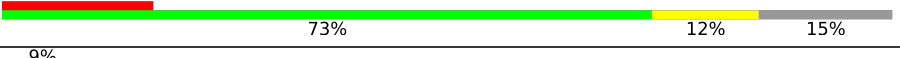
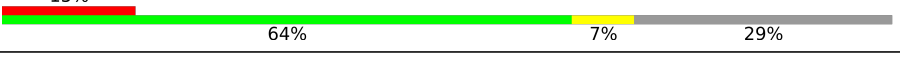
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Mol	Chain	Length	Quality of chain
4	L3	146	
5	L4	261	
6	L5	225	
7	L6	236	
8	L7	190	
9	L8	200	
10	L9	197	
11	LC	143	
12	LD	156	
13	LE	130	
14	LF	135	
15	LG	67	
16	LH	896	
17	LI	713	
18	LJ	513	
19	LK	575	
20	LL	643	
21	LM	1769	
22	LN	776	
23	LO	923	
24	LP	440	
25	LQ	943	
26	LR	817	
27	LS	594	
28	LT	939	

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Mol	Chain	Length	Quality of chain
29	LU	489	
30	LV	707	
31	LW	554	
32	LX	1056	
32	LY	1056	
33	LZ	183	
34	NA	593	
35	NB	610	
36	NC	357	
37	ND	214	
38	NE	346	
39	NF	151	
40	NG	137	
41	NH	1237	
42	NI	297	
43	NK	316	
44	NM	255	
45	NN	534	
46	NQ	82	
47	OA	1729	
48	SA	504	
49	SB	511	
50	SC	327	
50	SD	327	
51	SE	126	

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Mol	Chain	Length	Quality of chain
51	SF	126	
52	SG	573	
53	SH	367	
54	SI	1183	
55	SJ	252	
55	SK	252	
56	SL	189	
57	SM	290	
58	SN	274	
59	SP	2493	
60	SQ	217	
61	SR	145	
62	SS	899	
63	ST	810	
64	SU	552	
65	SV	206	
66	SW	274	
67	SY	250	
68	SZ	483	

2 Entry composition

There are 72 unique types of molecules in this entry. The entry contains 244461 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 5'ETS rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L0	445	Total	C	N	O	P	0	0
			9483	4239	1674	3125	445		

- Molecule 2 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L1	1205	Total	C	N	O	P	0	0
			25709	11494	4600	8410	1205		

- Molecule 3 is a RNA chain called TPA: *Saccharomyces cerevisiae* U3a gene for small nucleolar RNA U3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L2	175	Total	C	N	O	P	0	0
			3712	1661	649	1227	175		

- Molecule 4 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L3	97	Total	C	N	O	S	0	0
			786	498	144	142	2		

- Molecule 5 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L4	244	Total	C	N	O	S	0	0
			1936	1239	359	335	3		

- Molecule 6 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L5	206	Total	C	N	O	S	0	0
			1635	1027	300	305	3		

- Molecule 7 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L6	206	Total	C	N	O	S	0	0
			1653	1043	315	293	2		

- Molecule 8 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L7	169	Total	C	N	O	S	0	0
			1347	869	230	248			

- Molecule 9 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L8	170	Total	C	N	O	S	0	0
			1348	836	269	241	2		

- Molecule 10 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L9	171	Total	C	N	O	S	0	0
			1388	879	268	240	1		

- Molecule 11 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LC	125	Total	C	N	O	S	0	0
			973	625	174	174			

- Molecule 12 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LD	137	Total	C	N	O	S	0	0
			1112	714	212	183	3		

- Molecule 13 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LE	129	Total	C	N	O	S	0	0
			1022	650	188	181	3		

- Molecule 14 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	LF	130	Total	C	N	O	0	0
			1046	662	204	180		

- Molecule 15 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LG	62	Total	C	N	O	S	0	0
			490	302	98	89	1		

- Molecule 16 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH	808	Total	C	N	O	S	0	0
			6465	4123	1090	1233	19		

- Molecule 17 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LI	600	Total	C	N	O	S	0	0
			3792	2375	679	733	5		

- Molecule 18 is a protein called U3 small nucleolar RNA-associated protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LJ	493	Total	C	N	O	S	0	0
			3911	2462	702	735	12		

- Molecule 19 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LK	132	Total	C	N	O	S	0	0
			1068	681	185	199	3		

- Molecule 20 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LL	504	Total	C	N	O	S	0	0
			3982	2522	679	768	13		

- Molecule 21 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LM	1613	Total	C	N	O	S	0	0
			9380	5798	1748	1822	12		

- Molecule 22 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LN	663	Total	C	N	O	S	0	0
			5263	3333	913	995	22		

- Molecule 23 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	LO	834	Total	C	N	O	P	S	0	0
			6639	4223	1140	1256	1	19		

- Molecule 24 is a protein called U3 small nucleolar RNA-associated protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LP	380	Total	C	N	O	S	0	0
			3220	2081	545	578	16		

- Molecule 25 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LQ	841	Total	C	N	O	S	0	0
			6707	4284	1125	1271	27		

- Molecule 26 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LR	793	Total	C	N	O	S	0	0
			6207	3931	1044	1203	29		

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	LS	480	Total	C	N	O	P	S	0	0
			3793	2402	666	715	1	9		

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LT	873	Total	C	N	O	S	0	0
			6876	4363	1188	1303	22		

- Molecule 29 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LU	460	Total	C	N	O	S	0	0
			3756	2349	685	706	16		

- Molecule 30 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LV	405	Total	C	N	O	S	0	0
			3286	2083	567	626	10		

- Molecule 31 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LW	535	Total	C	N	O	S	0	0
			4237	2656	762	807	12		

- Molecule 32 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LX	842	Total	C	N	O	S	0	0
			6720	4301	1155	1238	26		
32	LY	846	Total	C	N	O	S	0	0
			6179	3918	1079	1165	17		

- Molecule 33 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LZ	181	Total	C	N	O	S	0	0
			1524	964	286	267	7		

- Molecule 34 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	NA	286	Total	C	N	O	S	0	0
			2075	1279	378	414	4		

- Molecule 35 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	NB	267	Total	C	N	O	S	0	0
			1873	1156	360	356	1		

- Molecule 36 is a protein called U3 small nucleolar ribonucleoprotein protein LCP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	NC	115	Total	C	N	O		0	0
			575	345	115	115			

- Molecule 37 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	ND	74	Total	C	N	O		0	0
			609	380	119	110			

- Molecule 38 is a protein called Protein FAF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	NE	215	Total	C	N	O	S	0	0
			1649	1021	327	298	3		

- Molecule 39 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	NF	141	Total	C	N	O	S	0	0
			1135	725	214	194	2		

- Molecule 40 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	NG	119	Total	C	N	O	S	0	0
			875	541	166	165	3		

- Molecule 41 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	NH	1077	Total	C	N	O	S	0	0
			8693	5650	1434	1585	24		

- Molecule 42 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	NI	240	Total	C	N	O	S	0	0
			1953	1248	331	366	8		

- Molecule 43 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	NK	257	Total	C	N	O	S	0	0
			2107	1344	369	381	13		

- Molecule 44 is a protein called Small ribosomal subunit protein eS1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	NM	230	Total	C	N	O	S	0	0
			1838	1163	337	334	4		

- Molecule 45 is a protein called Protein BFR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	NN	267	Total	C	N	O	S	0	0
			1481	909	280	292			

- Molecule 46 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	NQ	79	Total	C	N	O	S	0	0
			595	371	108	111	5		

- Molecule 47 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	OA	171	Total	C	N	O	S	0	0
			888	539	172	177			

- Molecule 48 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SA	385	Total	C	N	O	S	0	0
			3035	1926	521	579	9		

- Molecule 49 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SB	436	Total	C	N	O	S	0	0
			3357	2116	574	657	10		

- Molecule 50 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SC	241	Total	C	N	O	S	0	0
			1871	1185	337	339	10		
50	SD	232	Total	C	N	O	S	0	0
			1817	1153	324	330	10		

- Molecule 51 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SE	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
51	SF	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 52 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SG	459	Total	C	N	O	S	0	0
			3672	2331	645	686	10		

- Molecule 53 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SH	360	Total	C	N	O	S	0	0
			2781	1781	473	516	11		

- Molecule 54 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SI	811	Total	C	N	O	S	0	0
			6577	4219	1156	1173	29		

- Molecule 55 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SJ	213	Total	C	N	O	S	0	0
			1678	1069	292	306	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
55	SK	229	Total	C	N	O	S	0	0
			1793	1141	312	329	11		

- Molecule 56 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SL	173	Total	C	N	O	S	0	0
			1384	881	254	239	10		

- Molecule 57 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SM	282	Total	C	N	O	S	0	0
			2296	1441	430	418	7		

- Molecule 58 is a protein called Ribosome biogenesis protein UTP30.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SN	253	Total	C	N	O	S	0	0
			2053	1313	364	368	8		

- Molecule 59 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SP	2356	Total	C	N	O	S	0	0
			18367	11791	3084	3434	58		

- Molecule 60 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SQ	151	Total	C	N	O	S	0	0
			1280	807	240	228	5		

- Molecule 61 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SR	104	Total	C	N	O	S	0	0
			792	506	145	139	2		

- Molecule 62 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SS	272	Total	C	N	O	S	0	0
			2267	1415	427	415	10		

- Molecule 63 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	ST	582	Total	C	N	O	S	0	0
			4448	2823	802	811	12		

- Molecule 64 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SU	534	Total	C	N	O	S	0	0
			4370	2845	709	802	14		

- Molecule 65 is a protein called Regulator of rDNA transcription protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SV	147	Total	C	N	O		0	0
			869	529	160	180			

- Molecule 66 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SW	199	Total	C	N	O	S	0	0
			1565	998	284	279	4		

- Molecule 67 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SY	233	Total	C	N	O	S	0	0
			1953	1218	379	349	7		

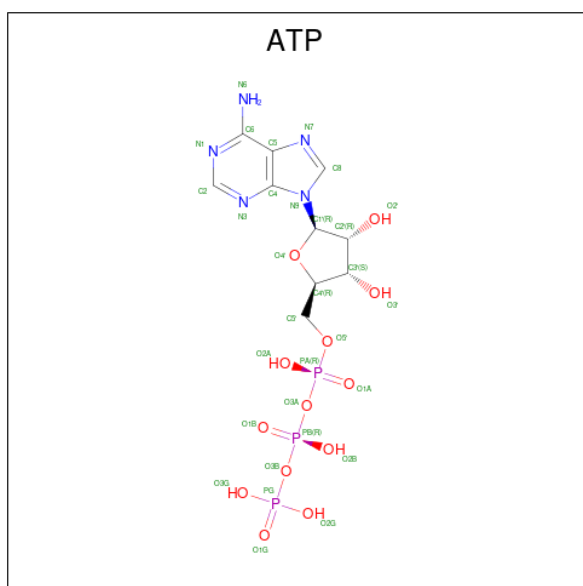
- Molecule 68 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SZ	259	Total	C	N	O		0	0
			1314	796	259	259			

- Molecule 69 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
69	L0	3	Total 3 Mg 3	0
69	L1	27	Total 27 Mg 27	0
69	L2	2	Total 2 Mg 2	0
69	NH	1	Total 1 Mg 1	0
69	SI	1	Total 1 Mg 1	0

- Molecule 70 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).

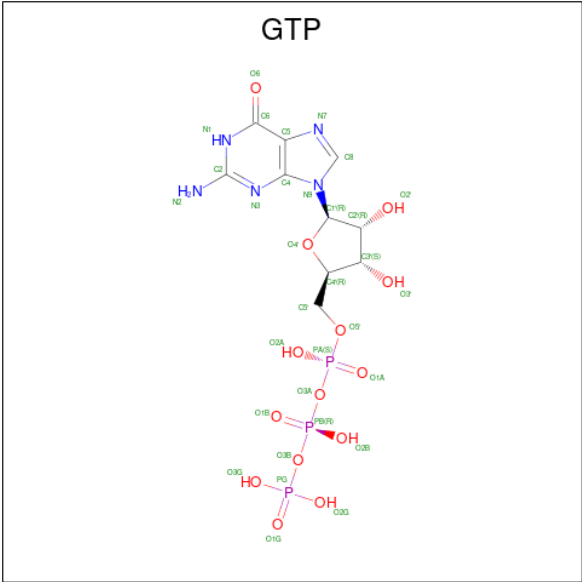


Mol	Chain	Residues	Atoms					AltConf
70	NH	1	Total 31	C 10	N 5	O 13	P 3	0

- Molecule 71 is ZINC ION (CCD ID: ZN) (formula: Zn).

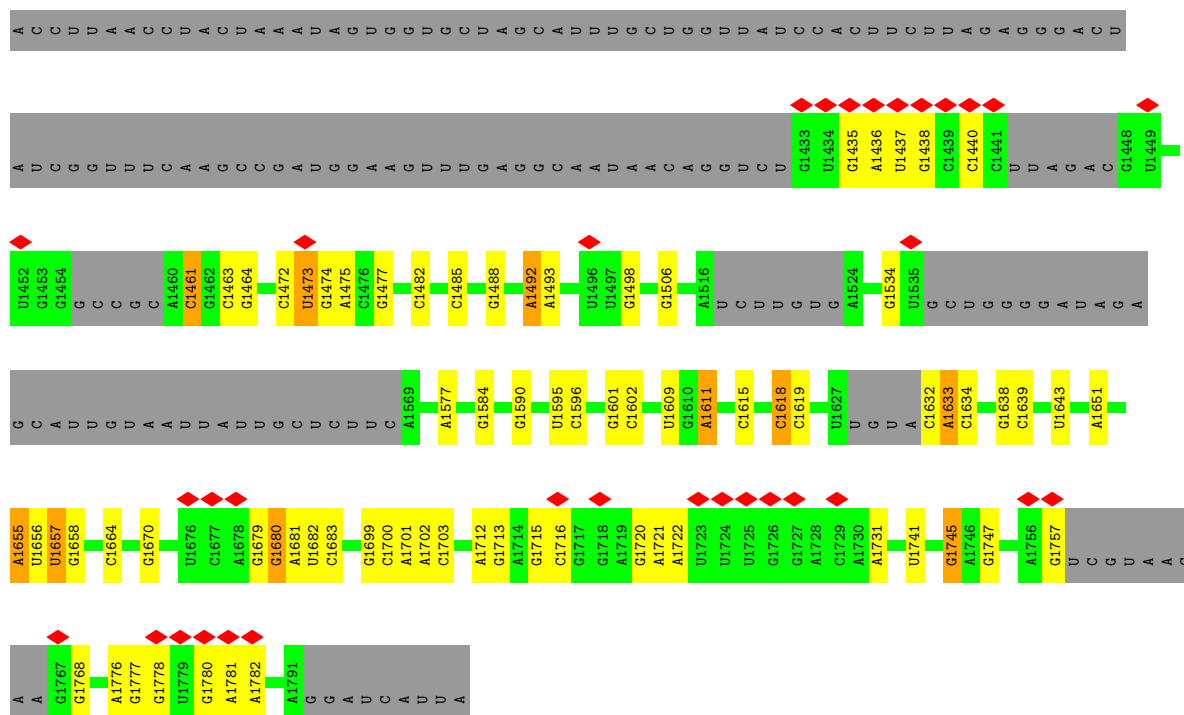
Mol	Chain	Residues	Atoms	AltConf
71	NQ	1	Total Zn 1 1	0
71	SL	1	Total Zn 1 1	0

- Molecule 72 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

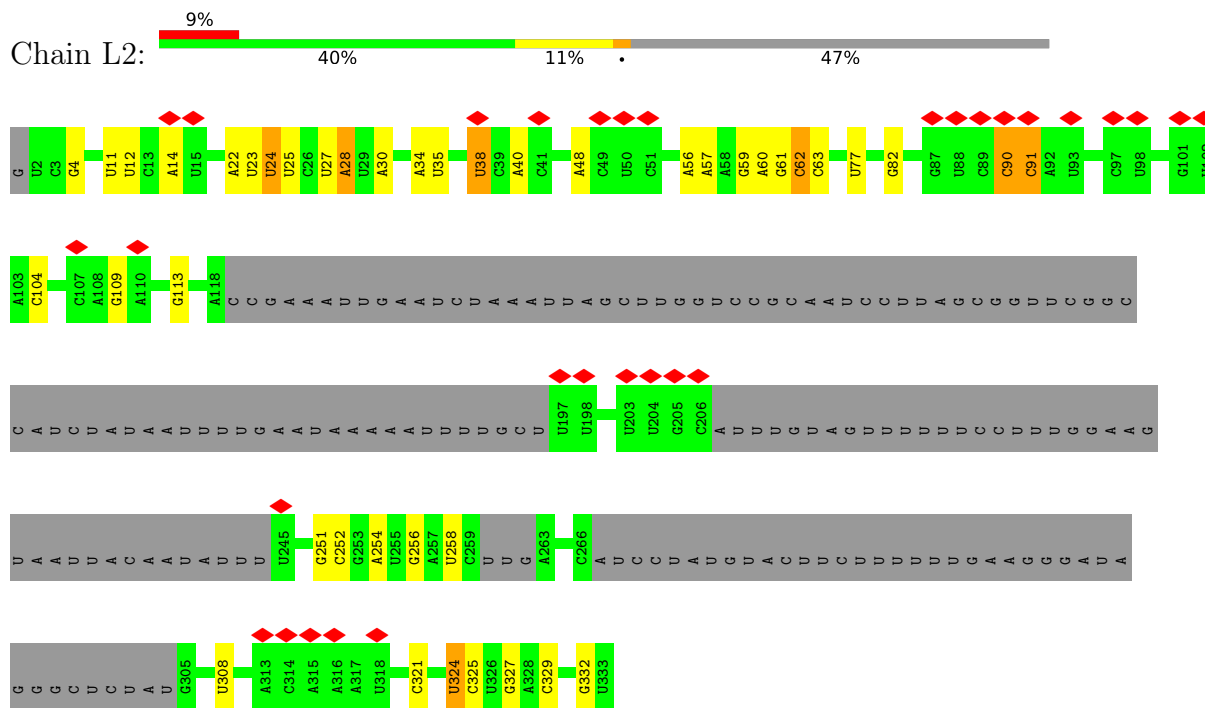


Mol	Chain	Residues	Atoms					AltConf
72	SI	1	Total	C	N	O	P	0
			32	10	5	14	3	



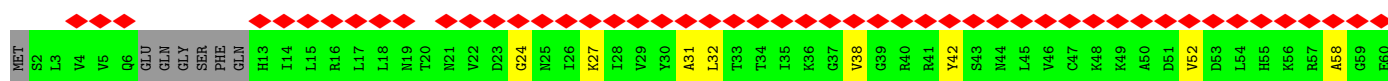


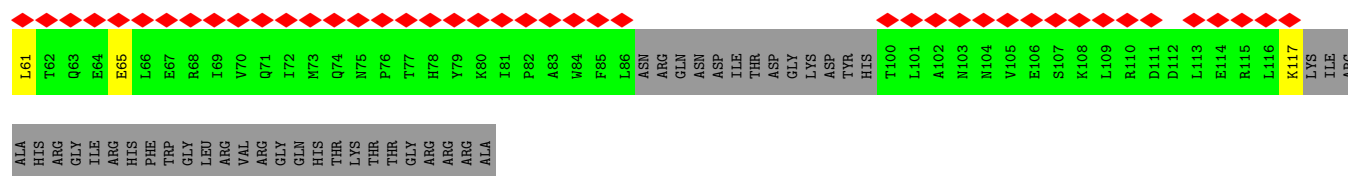
Chain L2: 9% 40% 11% 47%



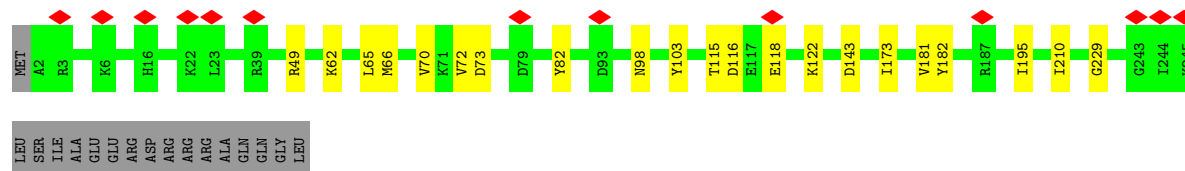
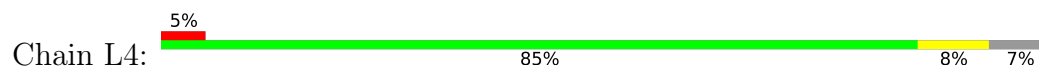
• Molecule 4: 40S ribosomal protein S18-A

Chain L3: 64% 59% 8% 34%

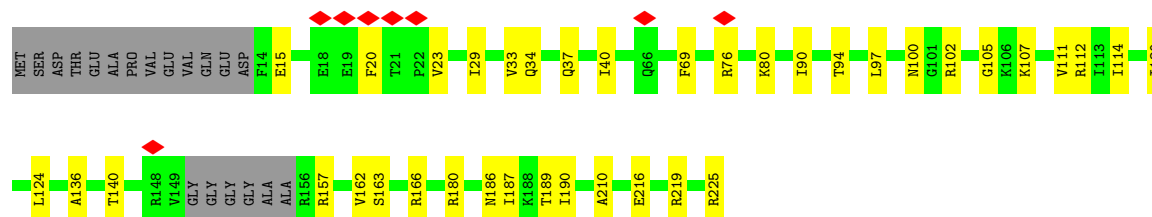
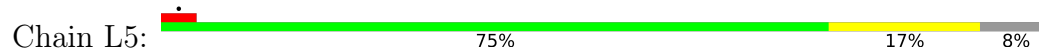




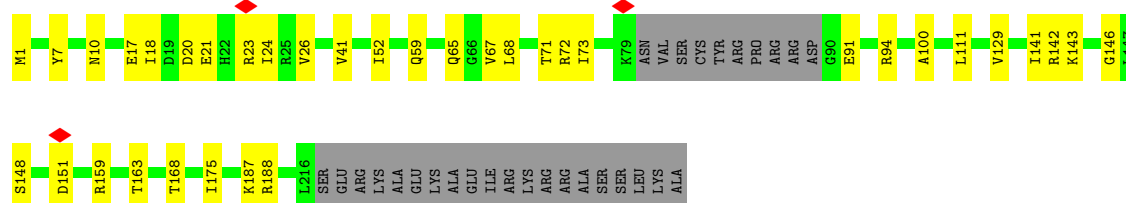
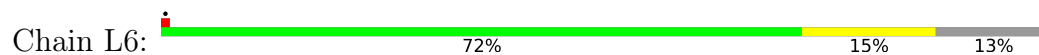
• Molecule 5: 40S ribosomal protein S4-A



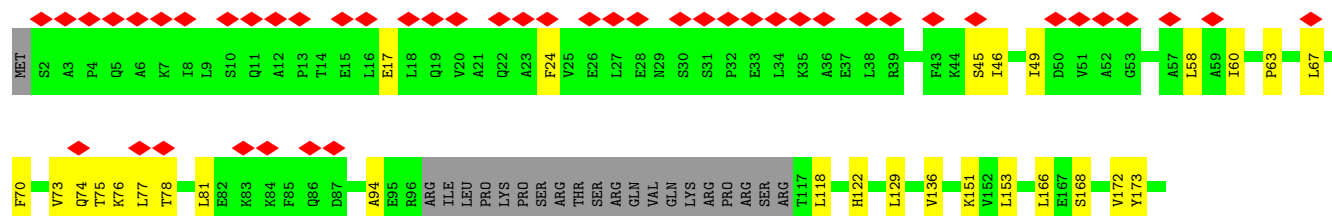
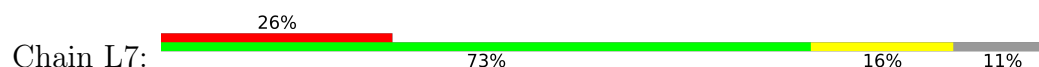
• Molecule 6: 40S ribosomal protein S5

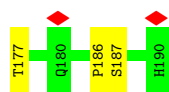


• Molecule 7: 40S ribosomal protein S6-A

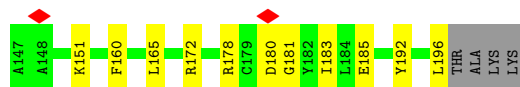
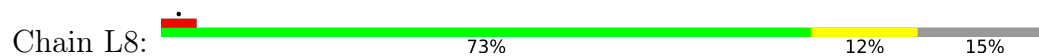


• Molecule 8: 40S ribosomal protein S7-A

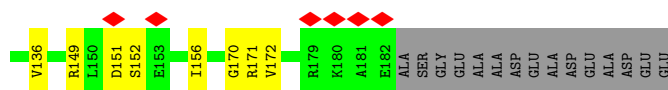
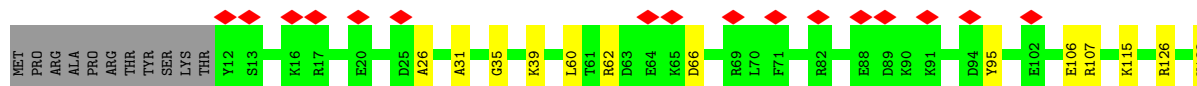
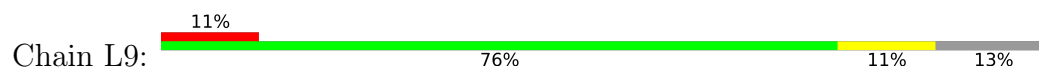




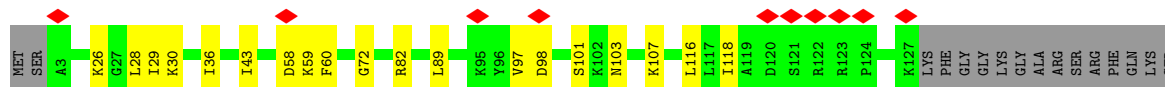
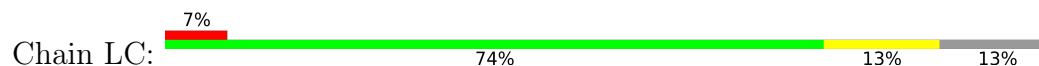
- Molecule 9: 40S ribosomal protein S8-A



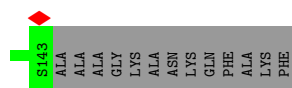
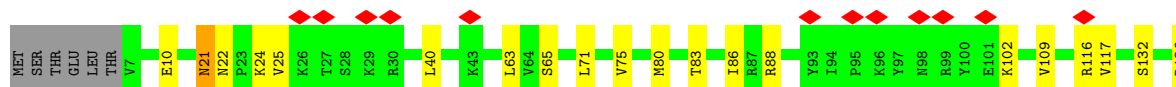
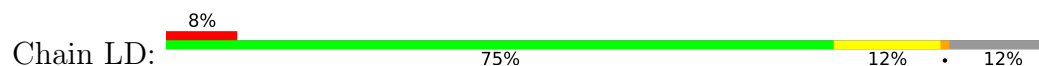
- Molecule 10: 40S ribosomal protein S9-A



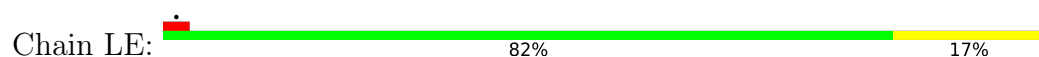
- Molecule 11: 40S ribosomal protein S16-A



- Molecule 12: 40S ribosomal protein S11-A

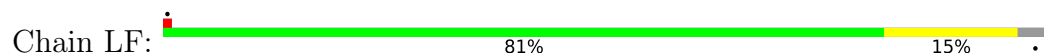


- Molecule 13: 40S ribosomal protein S22-A

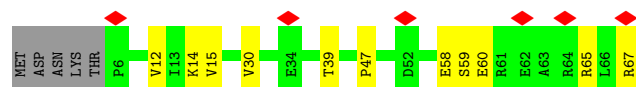
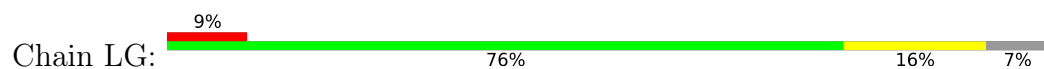




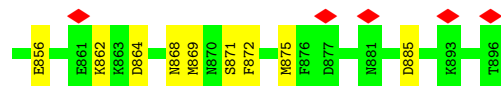
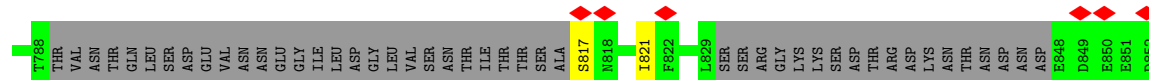
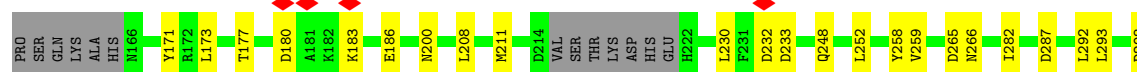
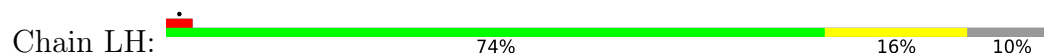
- Molecule 14: 40S ribosomal protein S24-A



- Molecule 15: 40S ribosomal protein S28-A

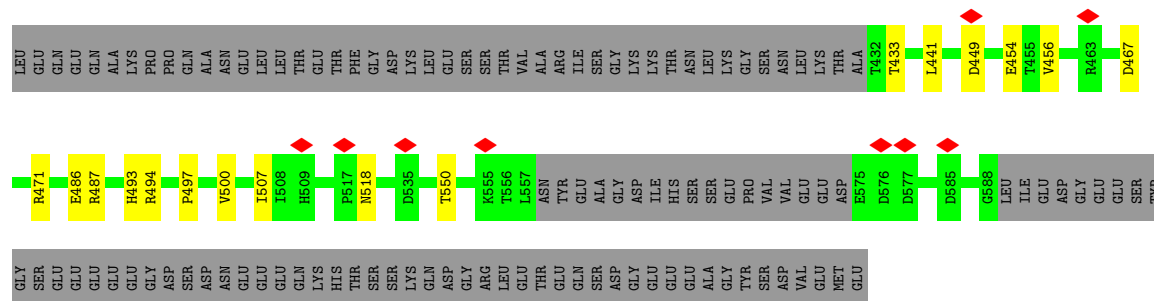


- Molecule 16: NET1-associated nuclear protein 1

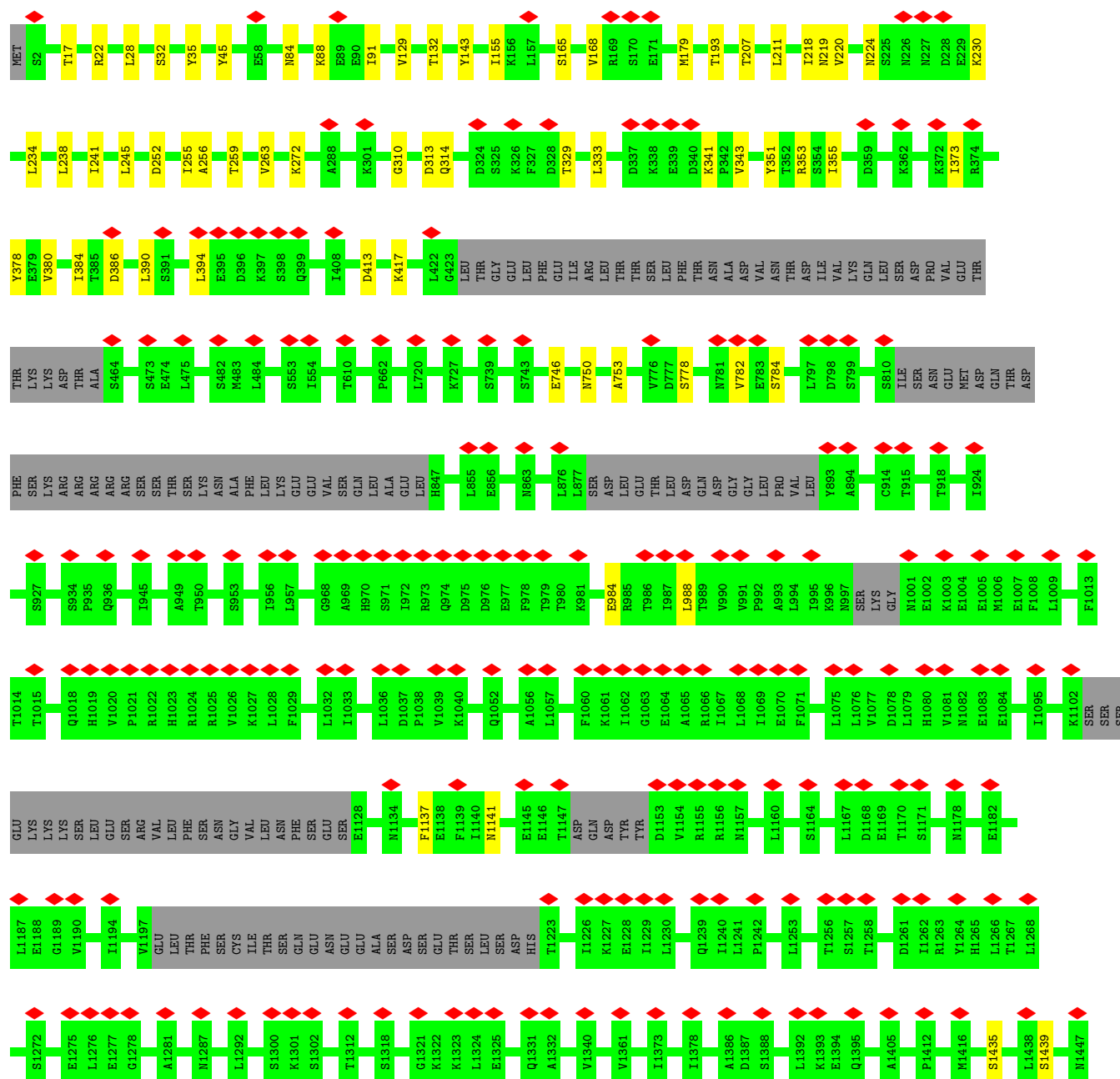


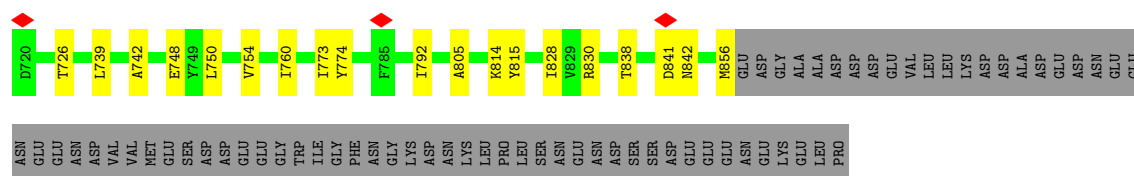
- Molecule 17: U3 small nucleolar RNA-associated protein 8



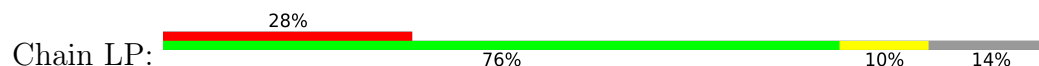


• Molecule 21: U3 small nucleolar RNA-associated protein 10

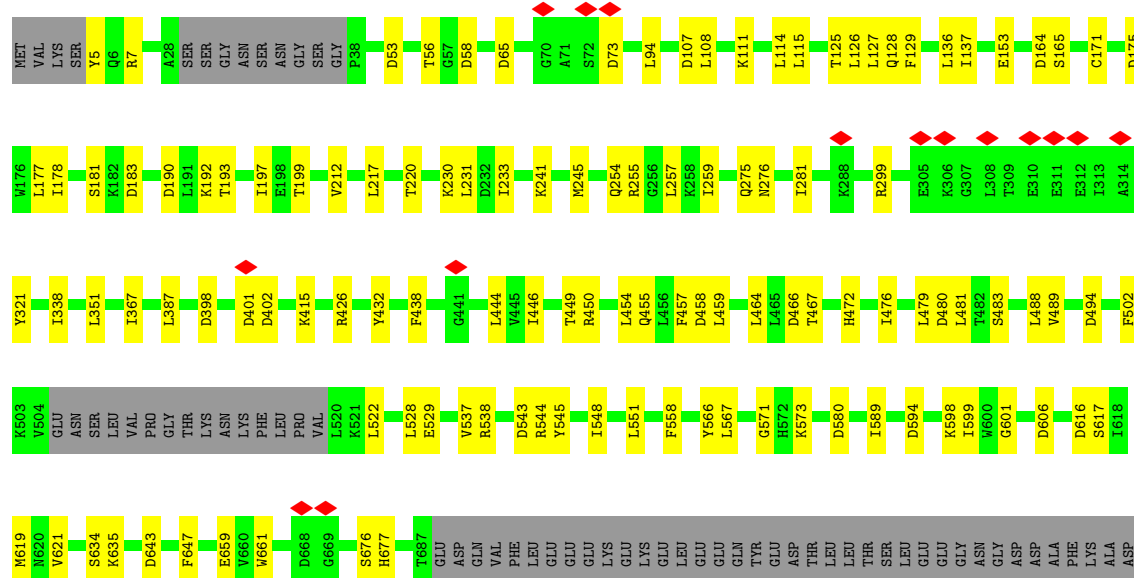
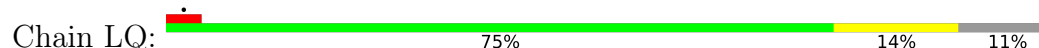


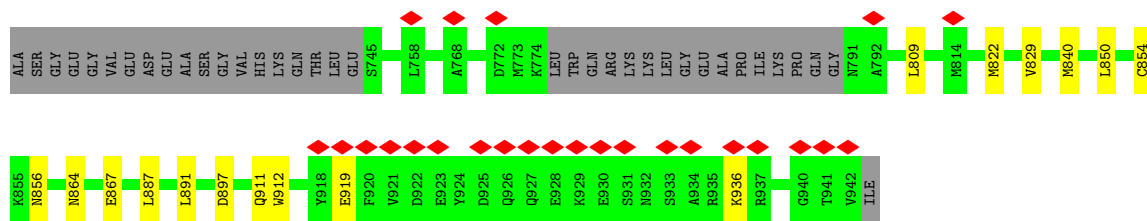


• Molecule 24: U3 small nucleolar RNA-associated protein 6



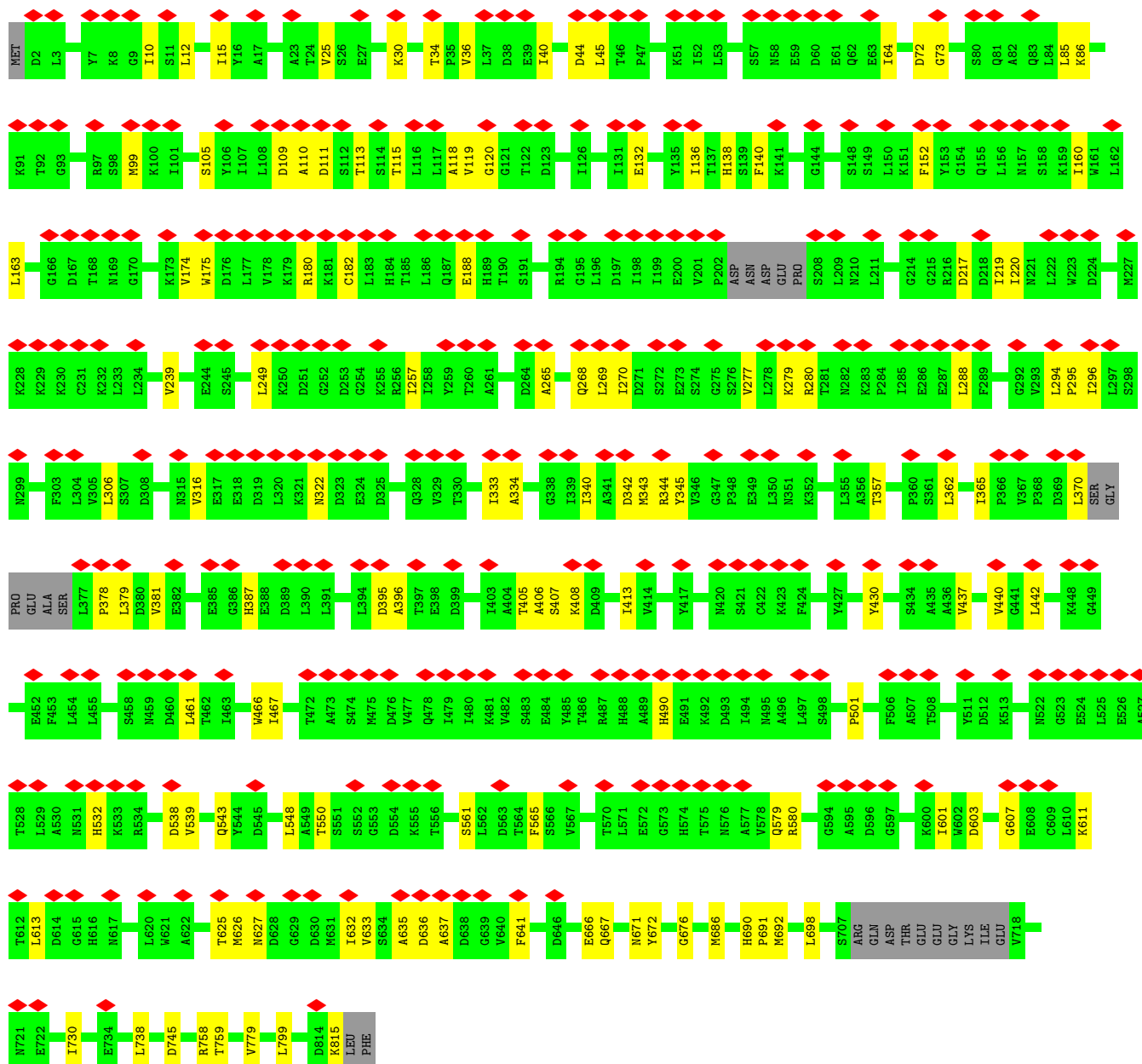
• Molecule 25: U3 small nucleolar RNA-associated protein 12





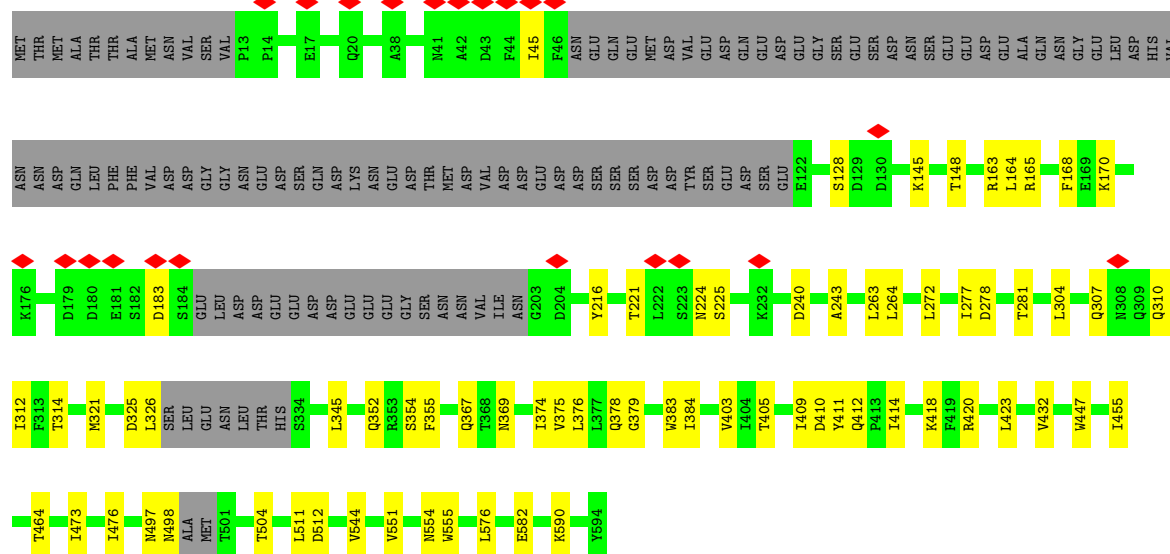
• Molecule 26: U3 small nucleolar RNA-associated protein 13

Chain LR: 37% 81% 16%



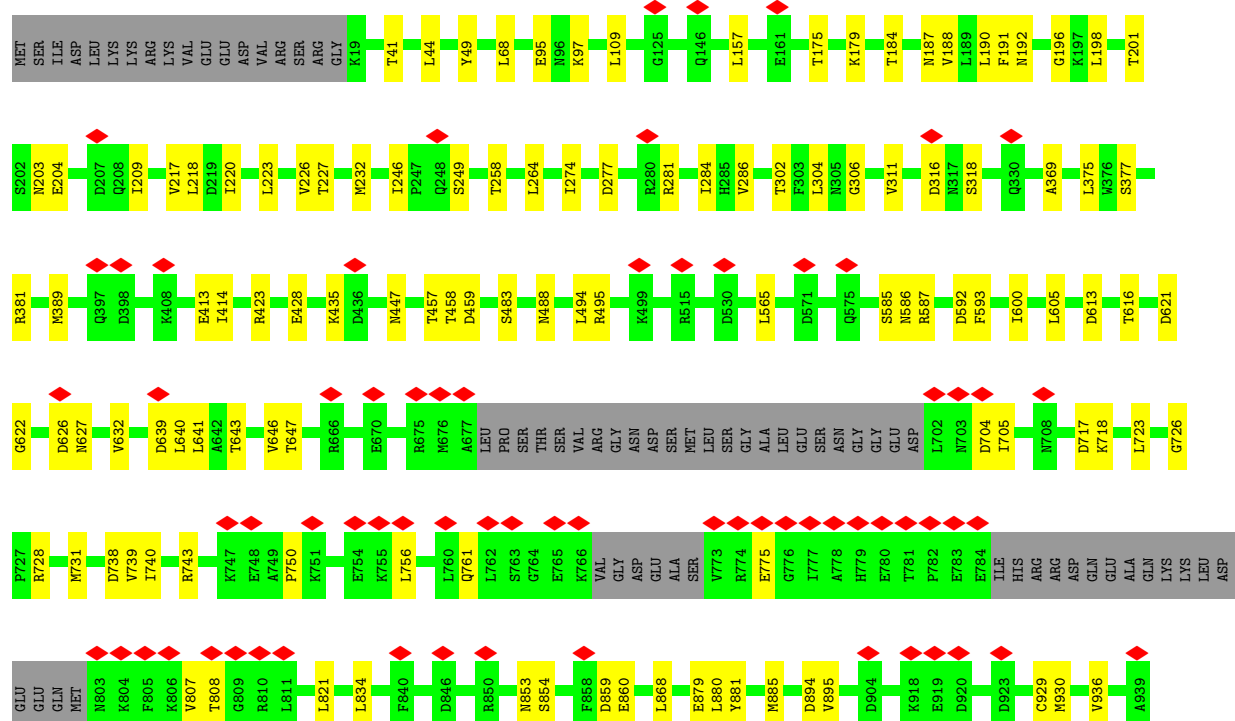
• Molecule 27: U3 small nucleolar RNA-associated protein 18

Chain LS: 



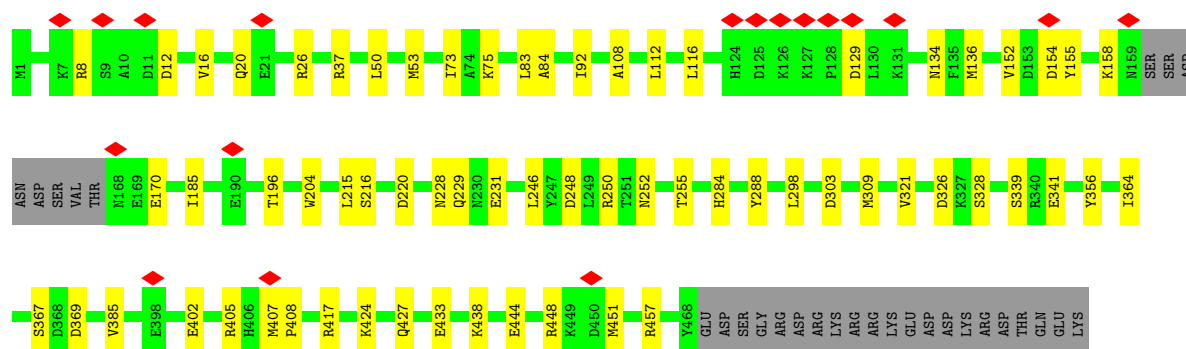
- Molecule 28: U3 small nucleolar RNA-associated protein 21

Chain LT: 

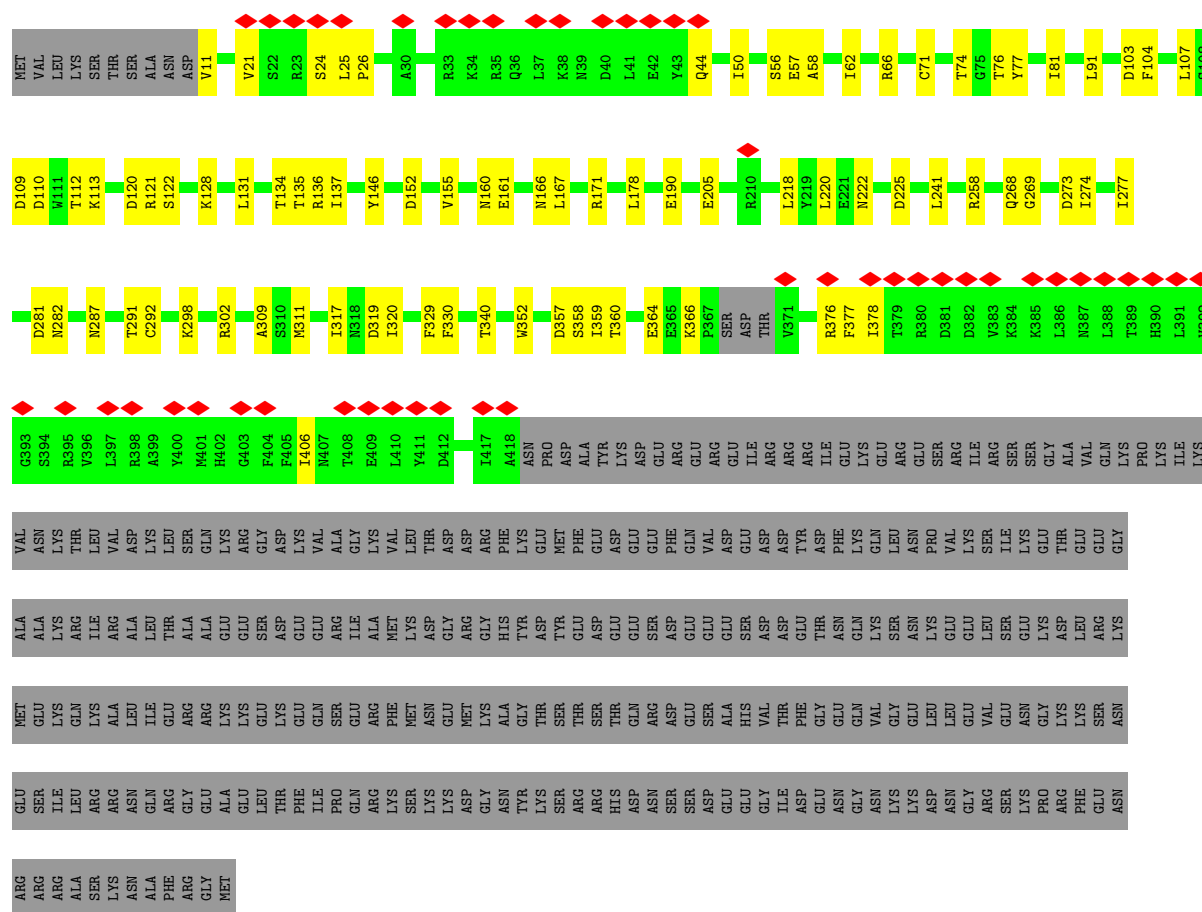


- Molecule 29: Protein SOF1

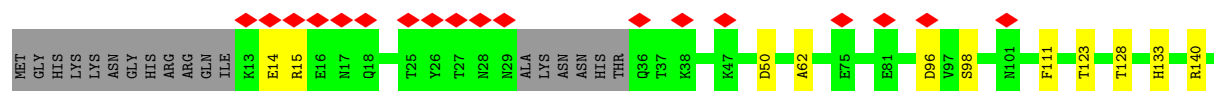
Chain LU: 

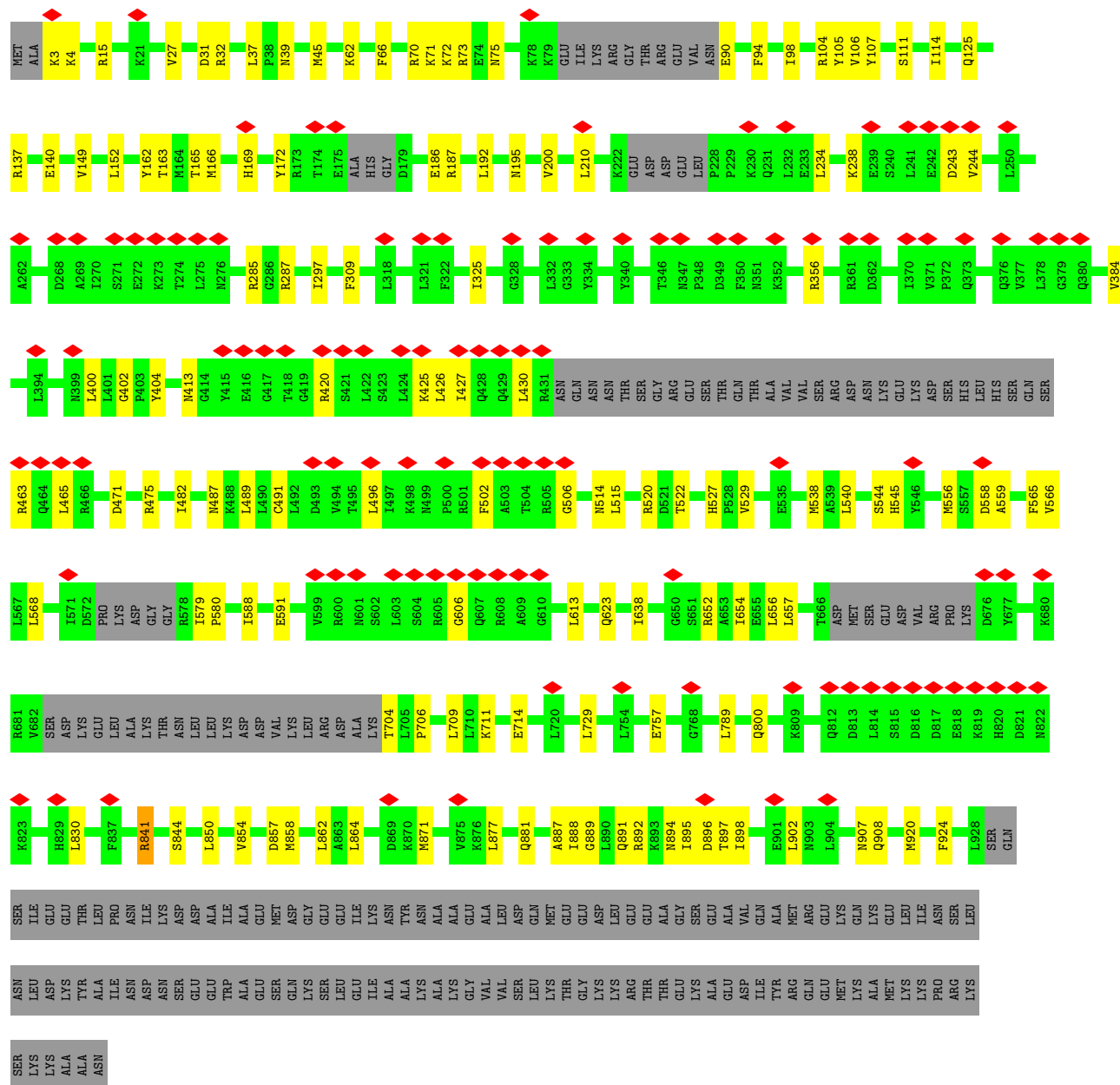


• Molecule 30: Ribosome biogenesis protein ENP2

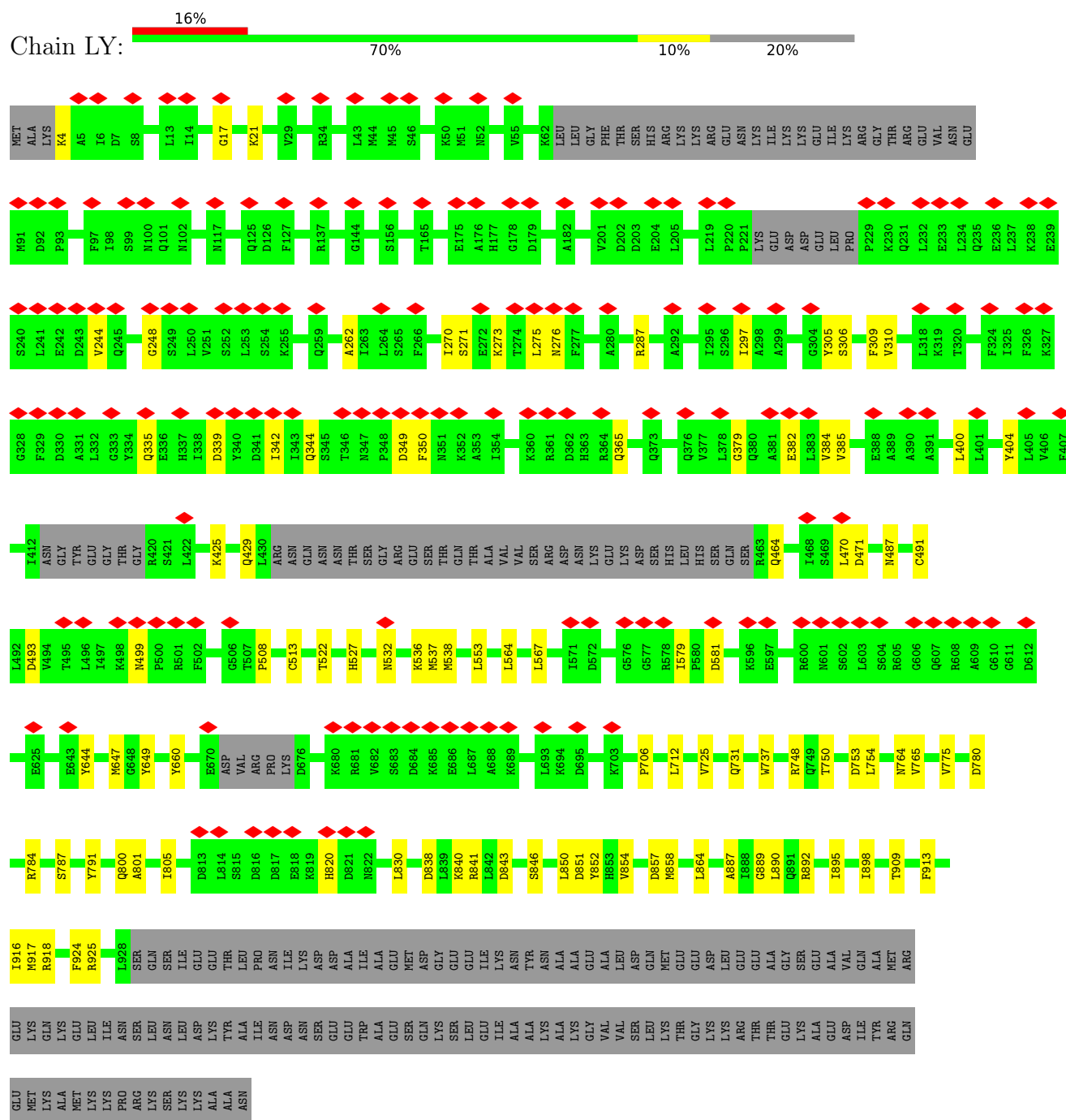


• Molecule 31: U3 small nucleolar RNA-associated protein 7

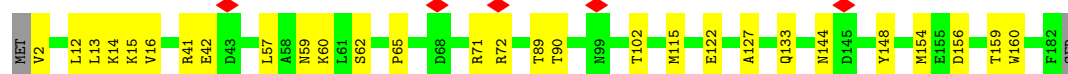
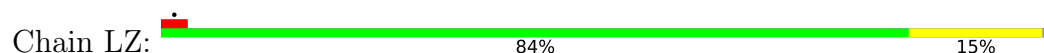




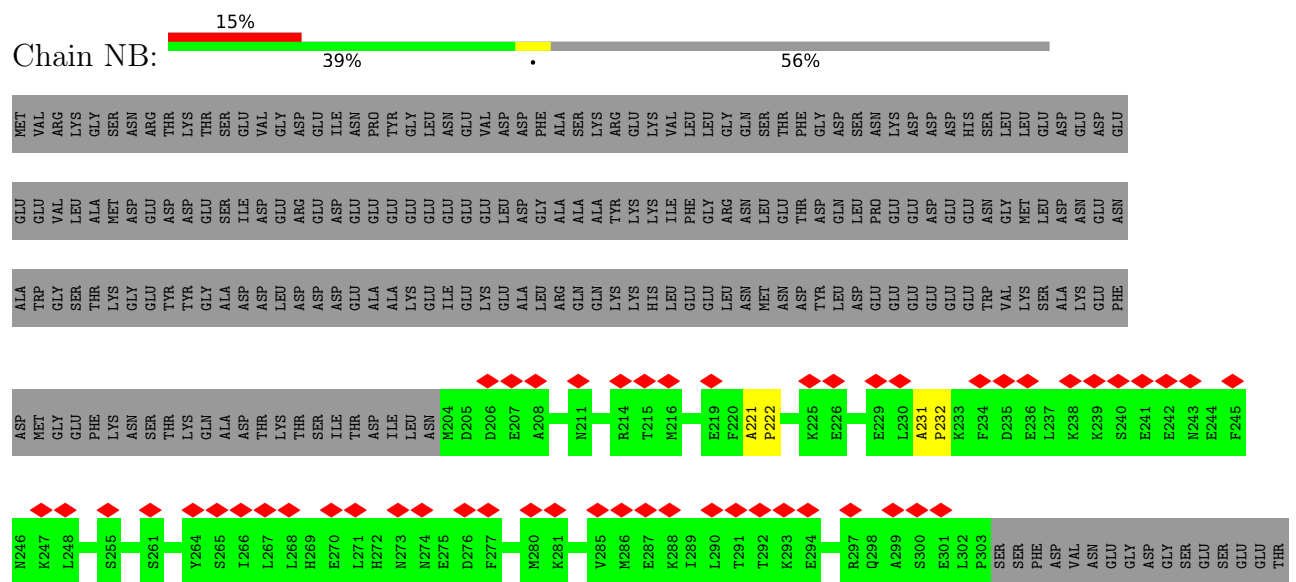
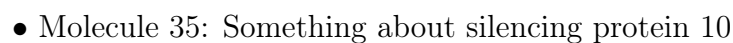
- Molecule 32: RNA cytidine acetyltransferase

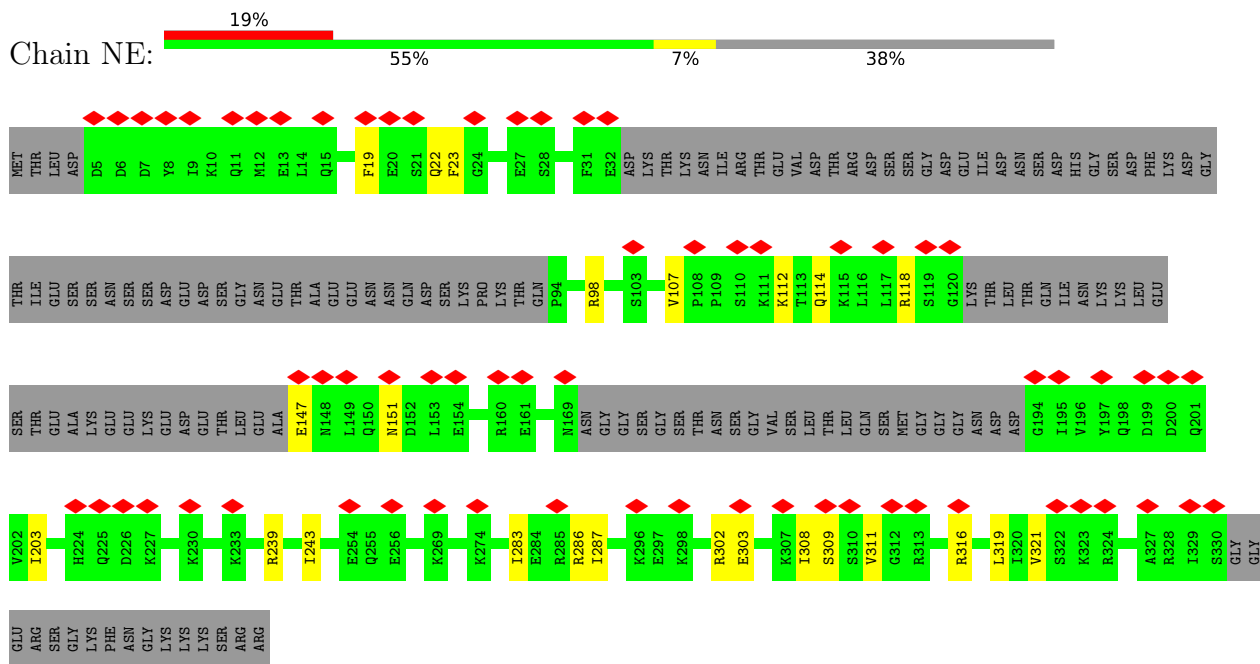


- Molecule 33: U3 small nucleolar ribonucleoprotein protein IMP3

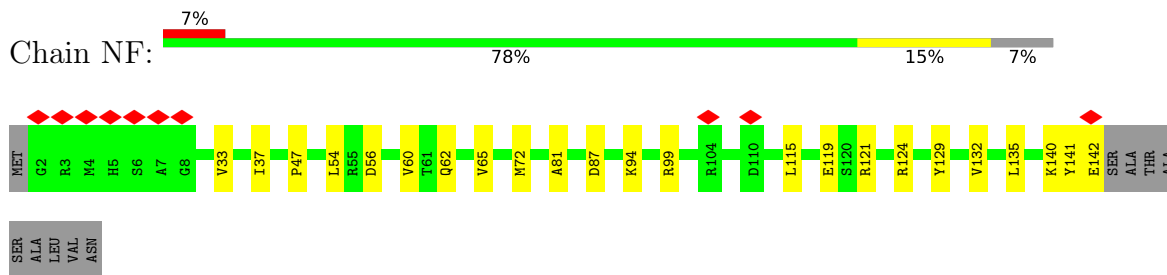


- Molecule 34: U3 small nucleolar RNA-associated protein MPP10

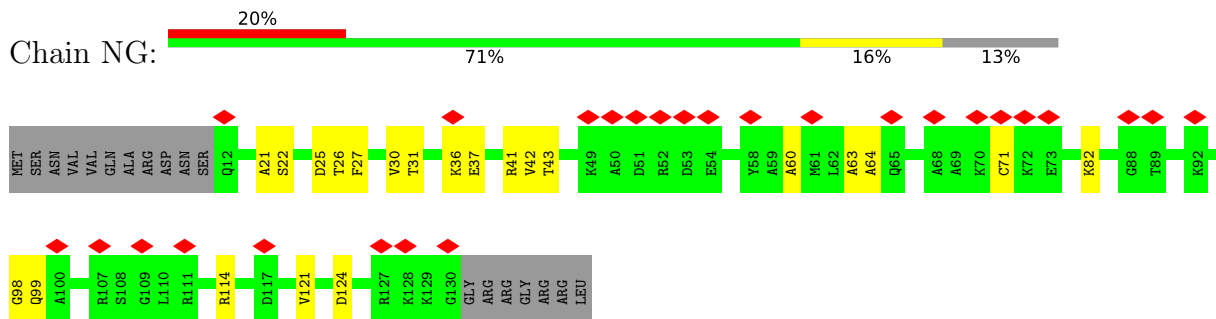




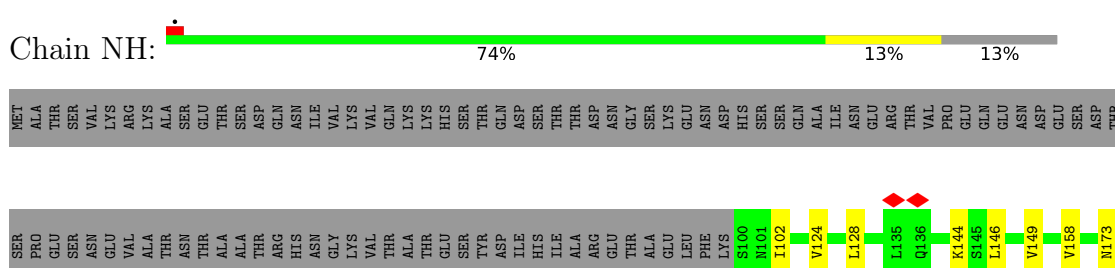
- Molecule 39: 40S ribosomal protein S13

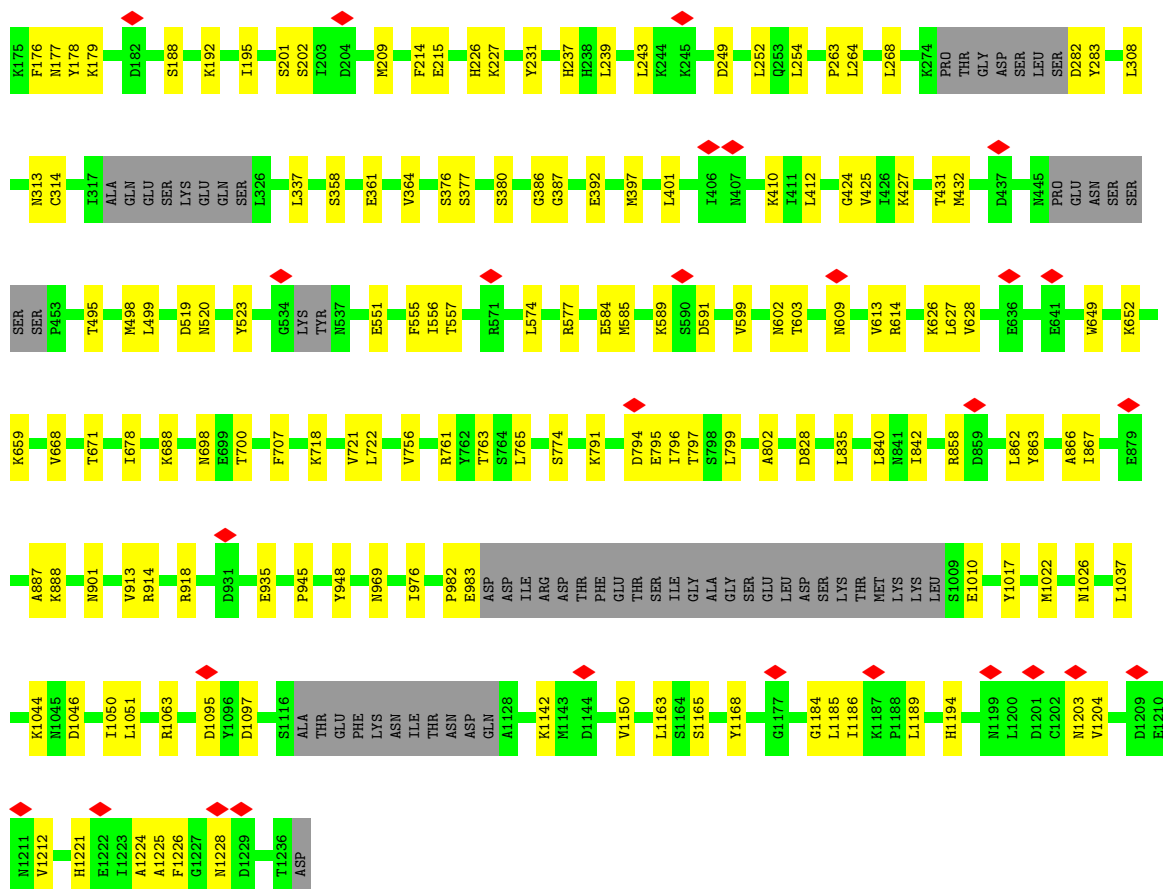


- Molecule 40: 40S ribosomal protein S14-A

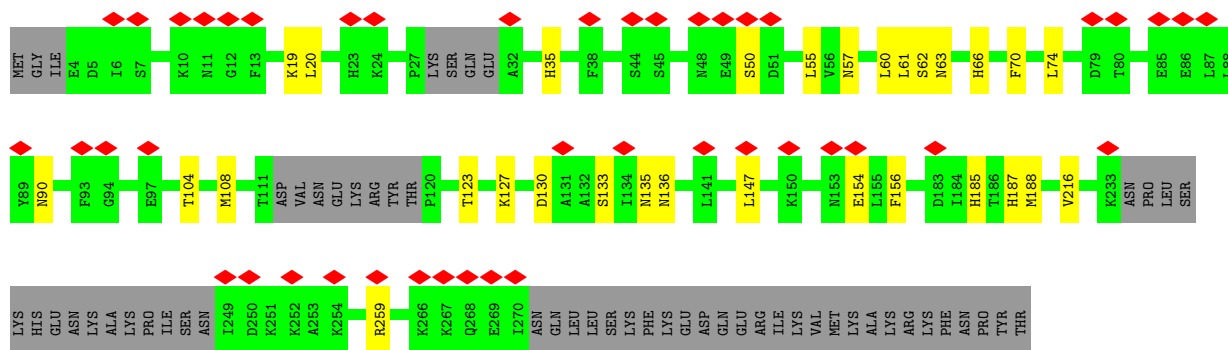


- Molecule 41: U3 small nucleolar RNA-associated protein 22

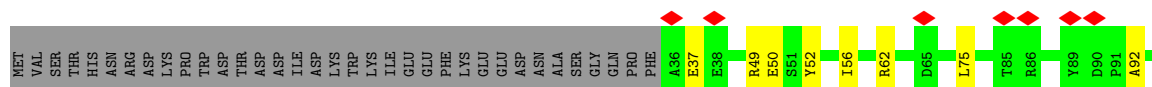
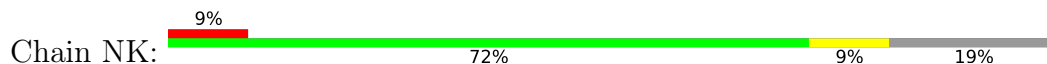




• Molecule 42: Ribosomal RNA-processing protein 7

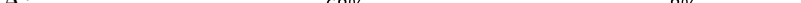


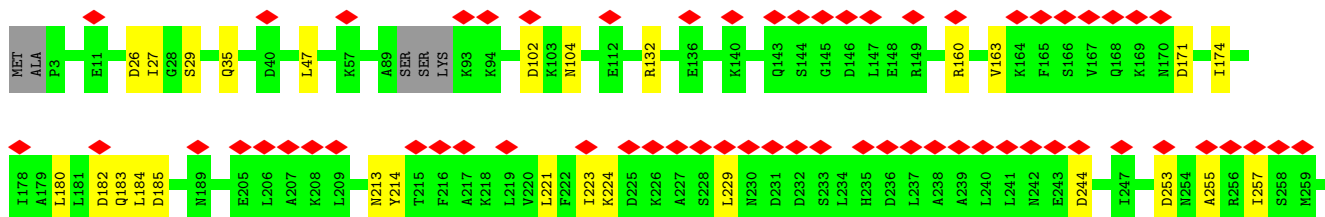
• Molecule 43: KRR1 small subunit processome component

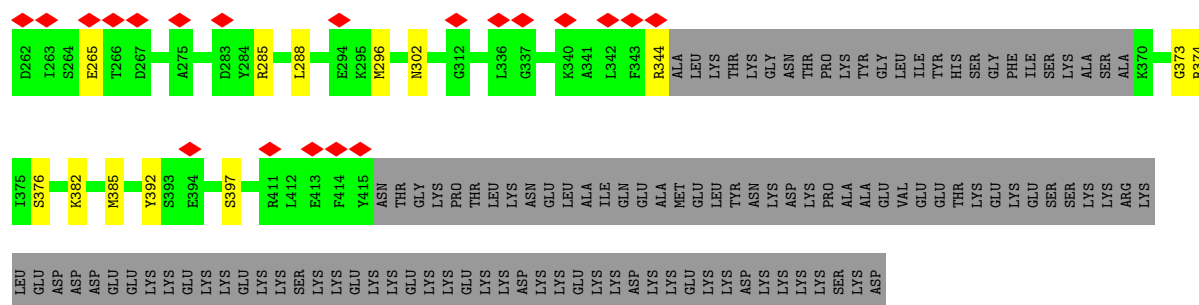


[illegible]

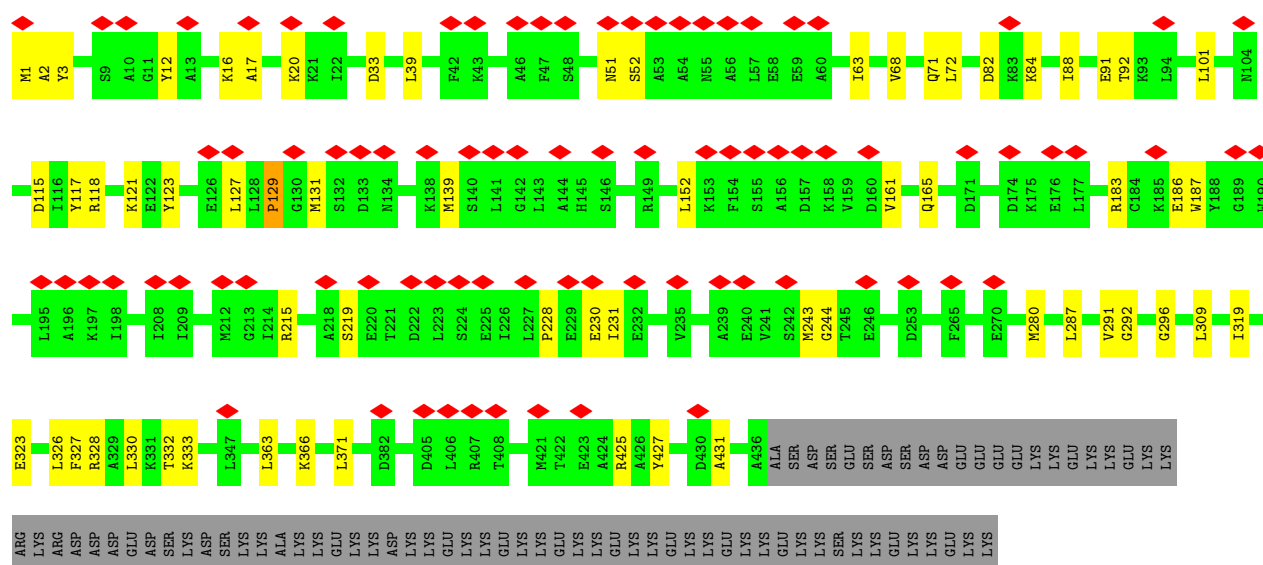
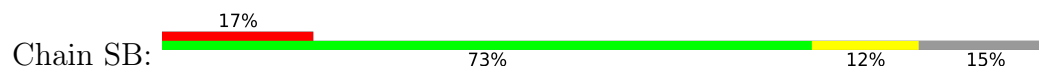


Chain SA: 

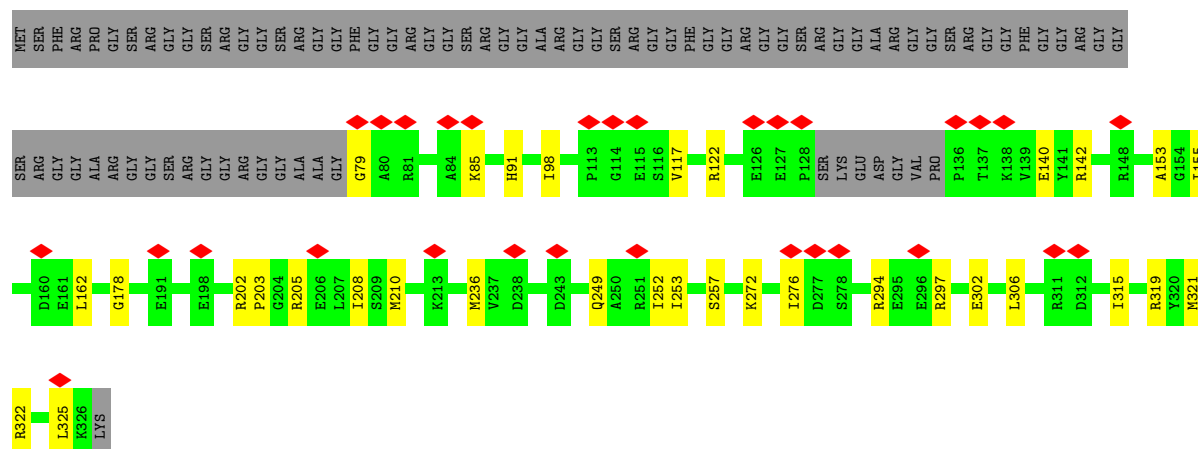




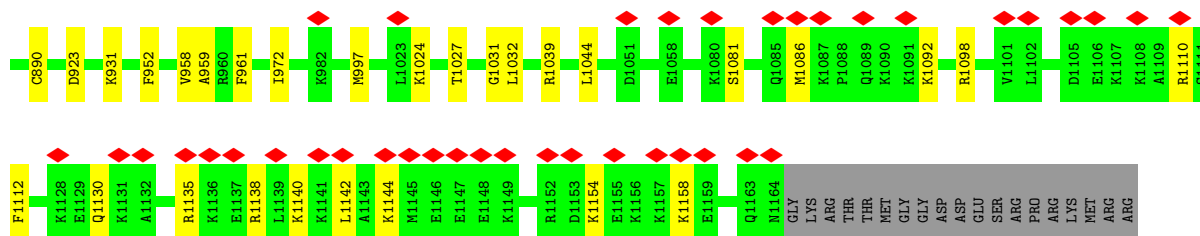
• Molecule 49: Nucleolar protein 58



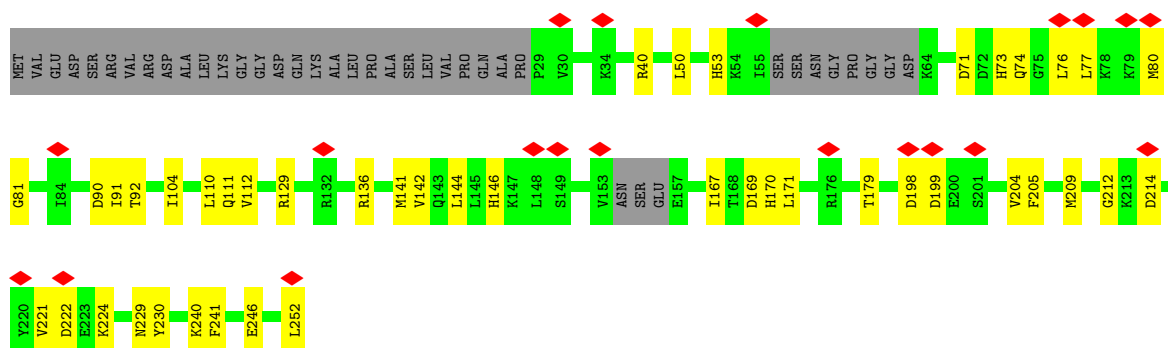
• Molecule 50: rRNA 2'-O-methyltransferase fibrillar



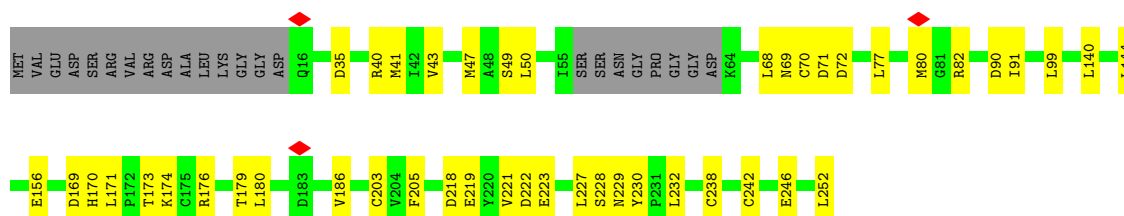
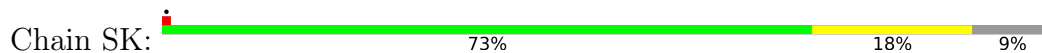
• Molecule 50: rRNA 2'-O-methyltransferase fibrillar



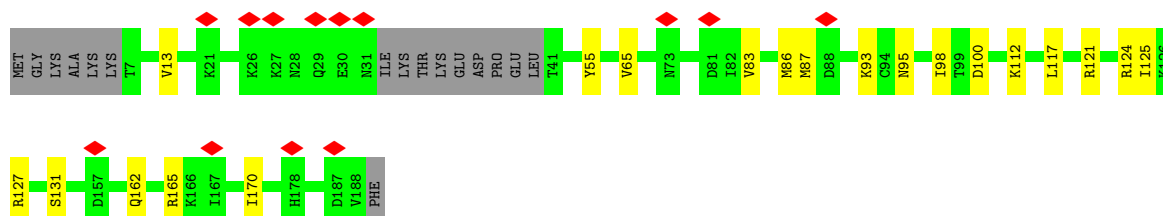
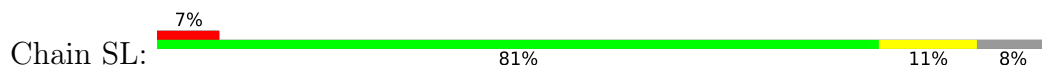
• Molecule 55: Ribosomal RNA small subunit methyltransferase NEP1



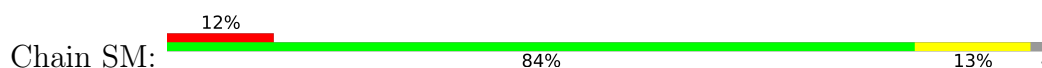
• Molecule 55: Ribosomal RNA small subunit methyltransferase NEP1

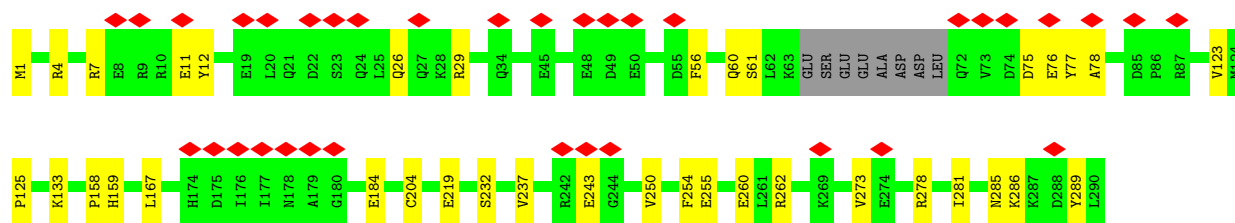


• Molecule 56: rRNA-processing protein FCF1

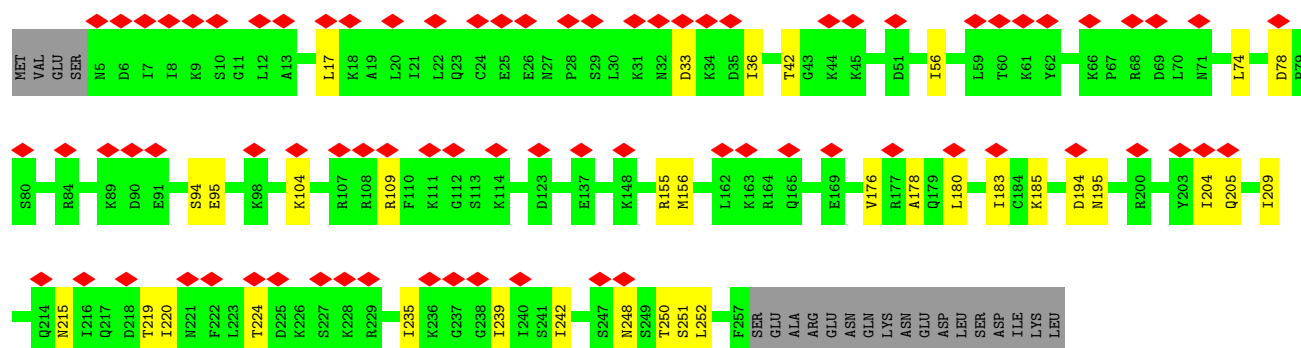
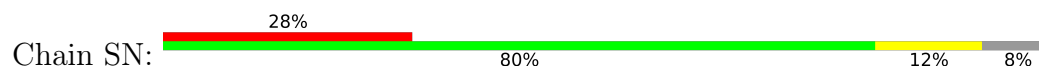


• Molecule 57: U3 small nucleolar ribonucleoprotein protein IMP4

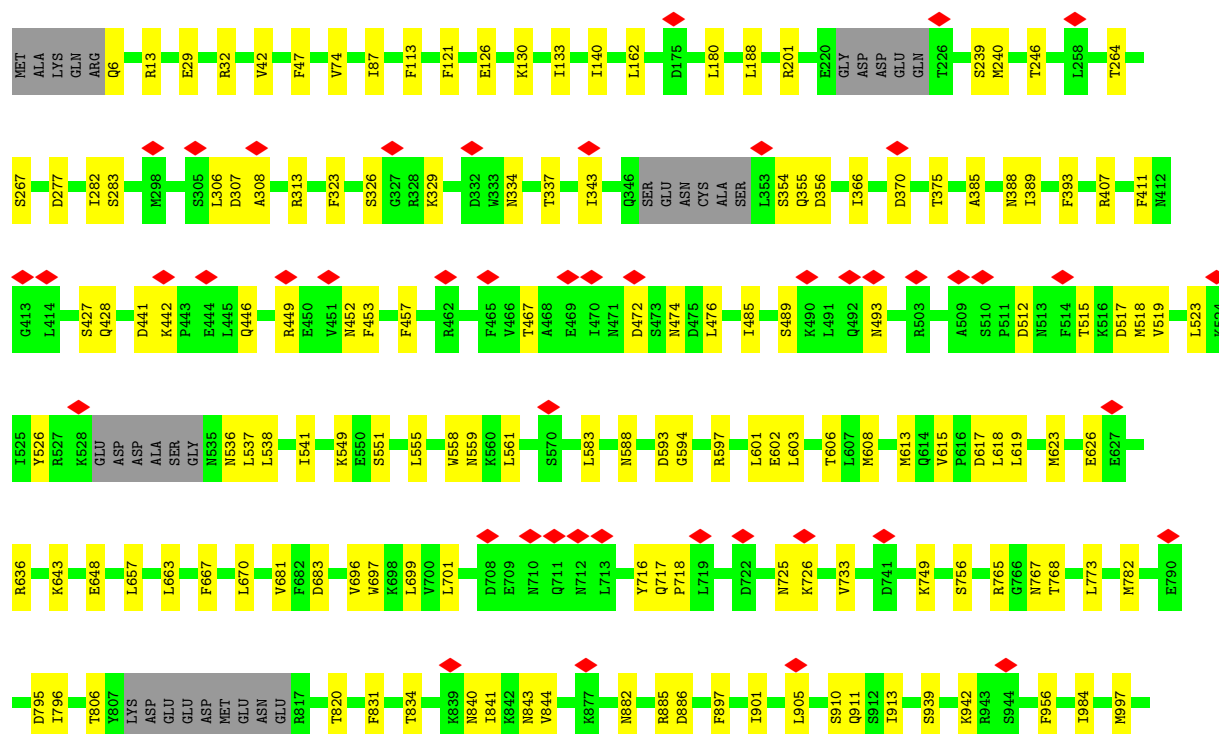
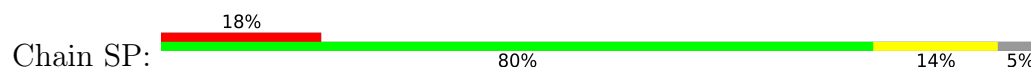




• Molecule 58: Ribosome biogenesis protein UTP30



• Molecule 59: U3 small nucleolar RNA-associated protein 20

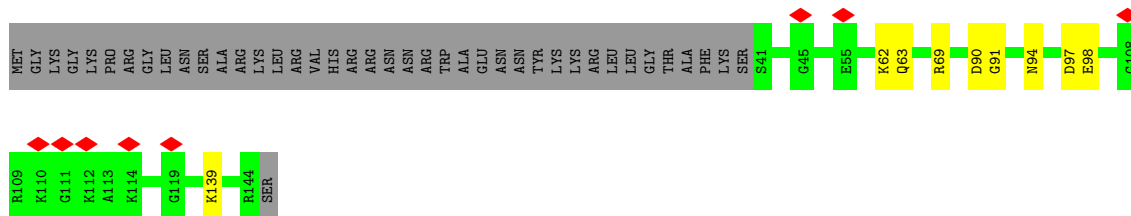




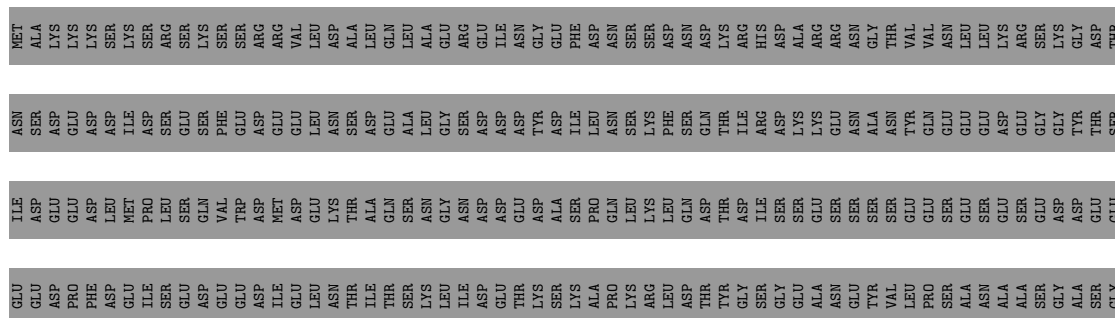
- Molecule 60: rRNA-processing protein FCF2

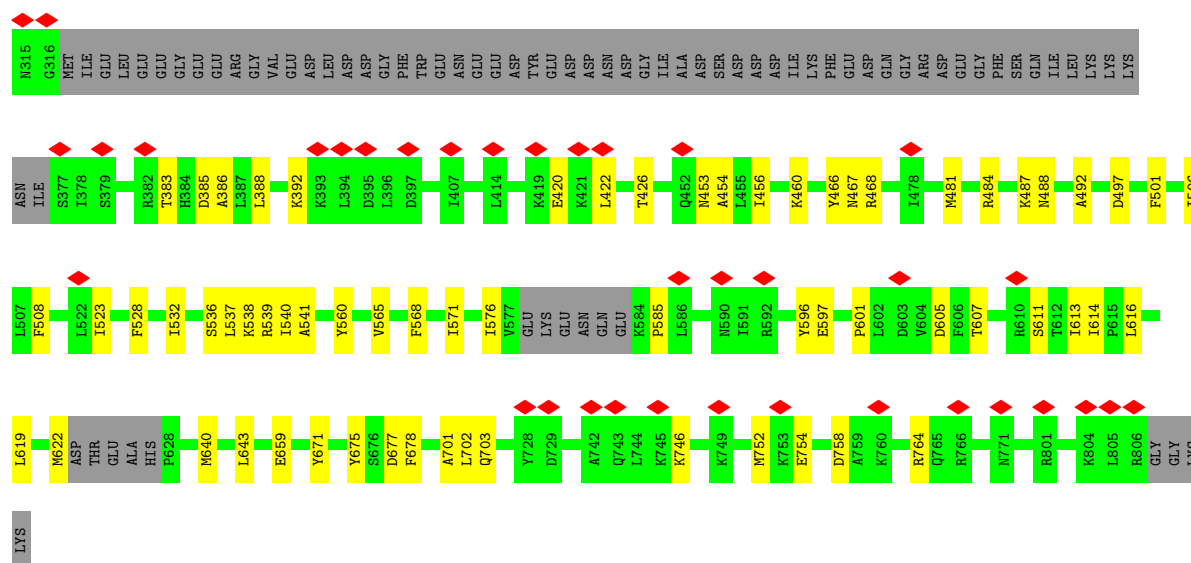


- Molecule 61: 40S ribosomal protein S23-A

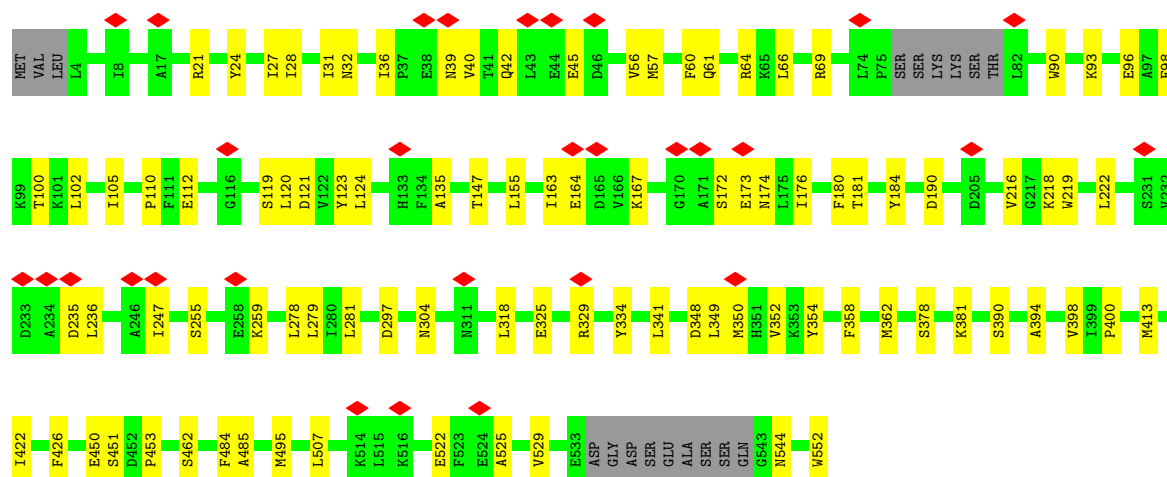
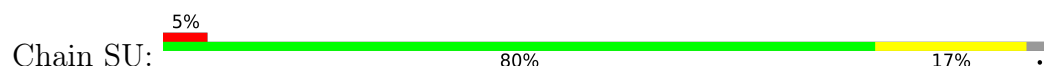


- Molecule 62: U3 small nucleolar RNA-associated protein 14

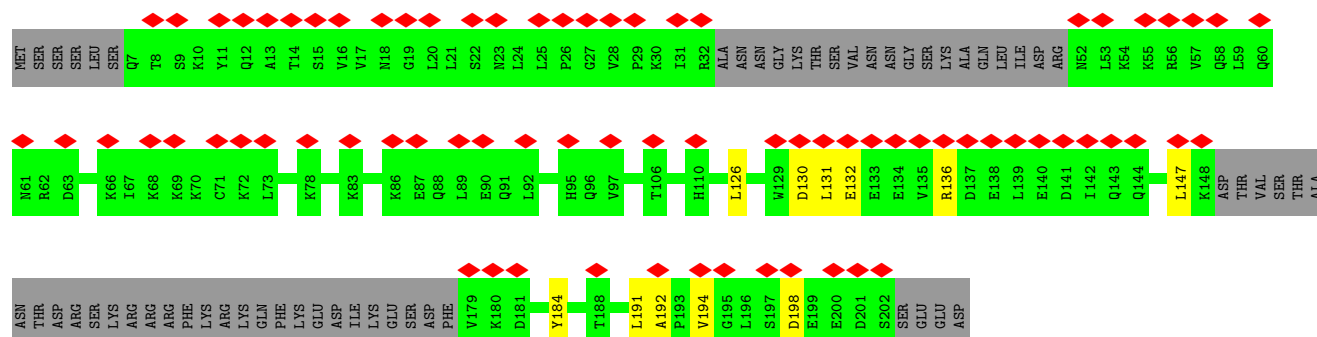
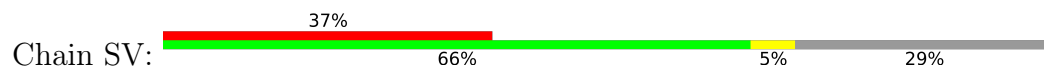




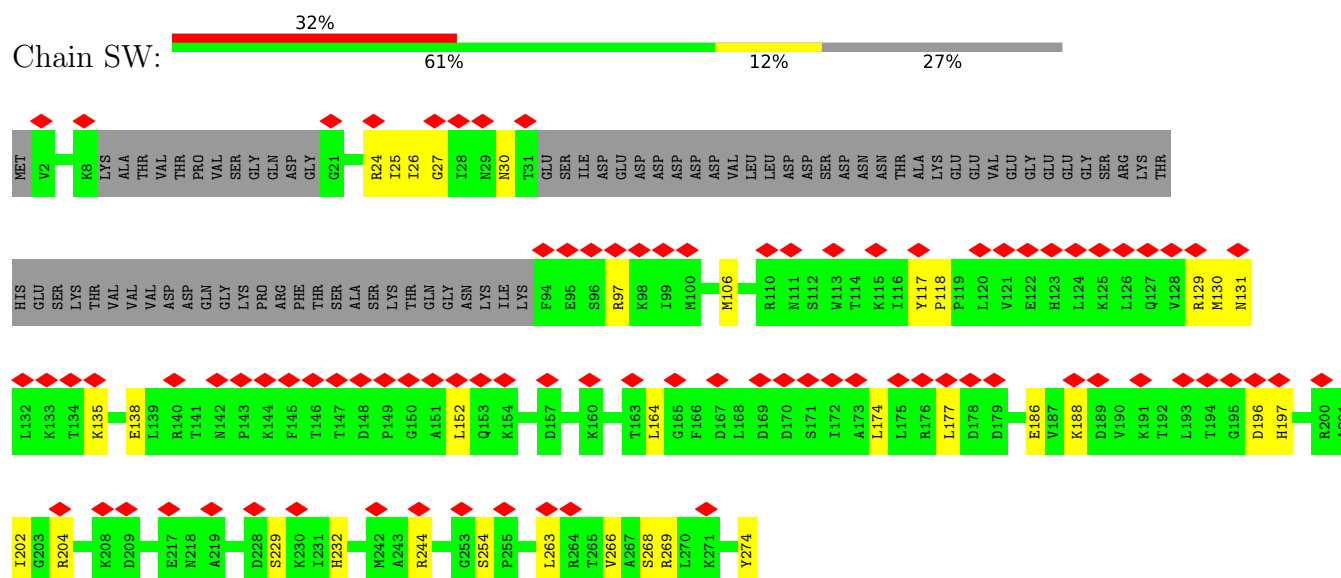
- Molecule 64: Nucleolar complex protein 4



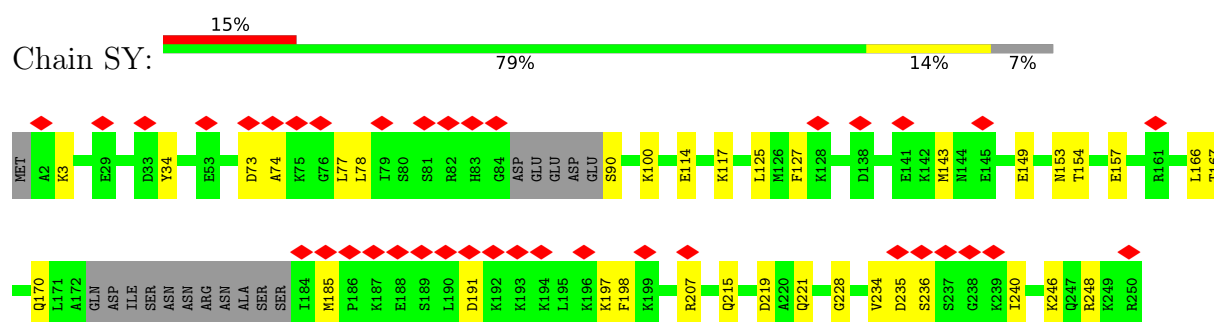
- Molecule 65: Regulator of rDNA transcription protein 14



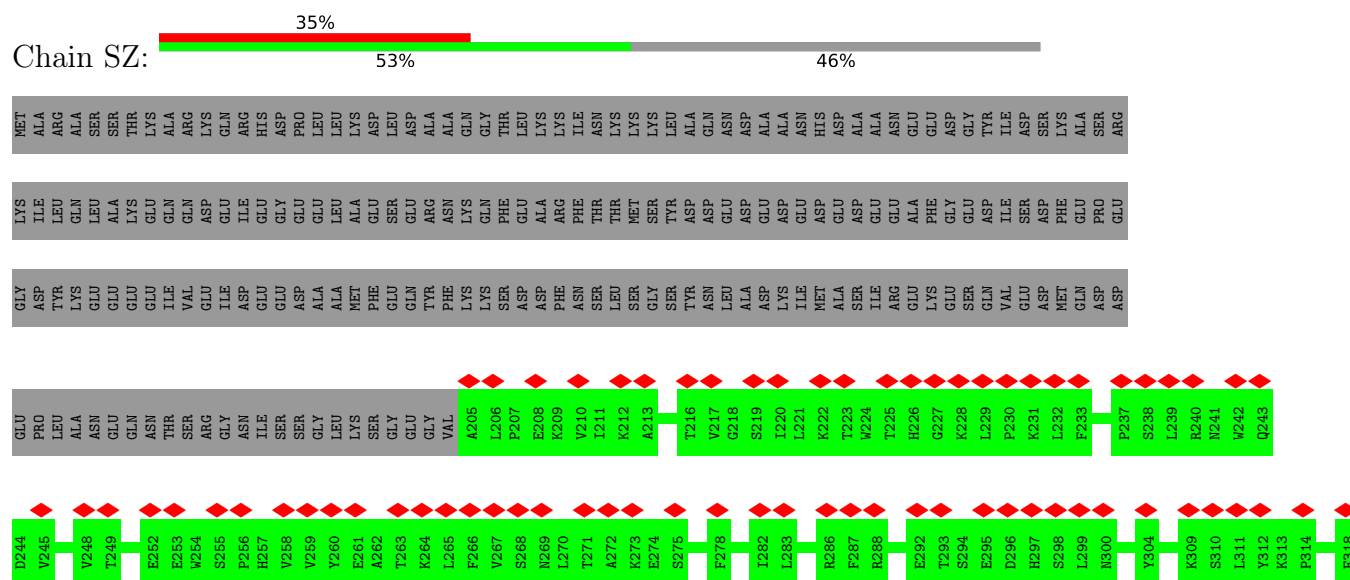
- Molecule 66: Pre-rRNA-processing protein PNO1

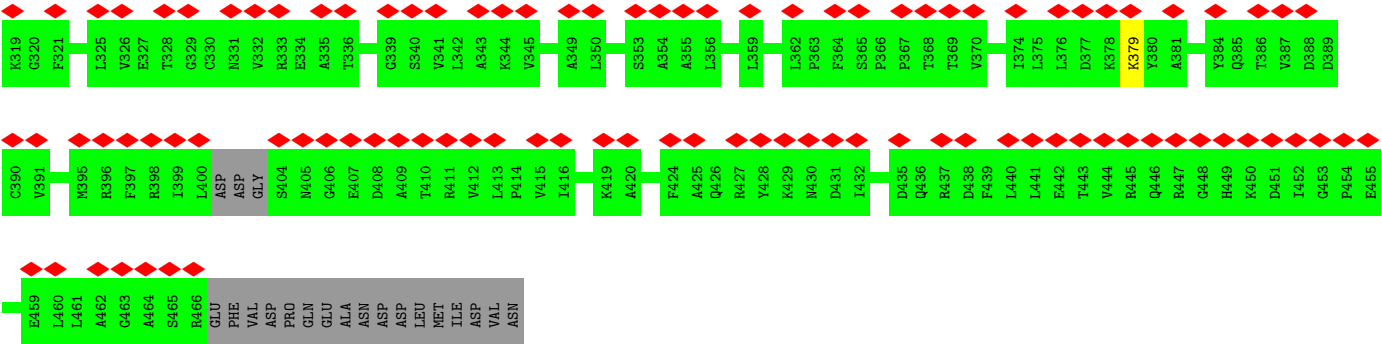


- Molecule 67: U3 small nucleolar RNA-associated protein 11



- Molecule 68: Essential nuclear protein 1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	28151	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	25000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.891	Depositor
Minimum map value	0.000	Depositor
Average map value	0.115	Depositor
Map value standard deviation	0.183	Depositor
Recommended contour level	0.77	Depositor
Map size (Å)	535.75195, 535.75195, 535.75195	wwPDB
Map dimensions	504, 504, 504	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.063, 1.063, 1.063	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	L0	0.19	0/10603	0.28	0/16514
2	L1	0.22	0/28743	0.30	0/44737
3	L2	0.20	0/4143	0.27	0/6440
4	L3	0.13	0/794	0.29	0/1069
5	L4	0.23	0/1977	0.40	0/2664
6	L5	0.21	0/1655	0.38	0/2237
7	L6	0.23	0/1674	0.36	0/2236
8	L7	0.19	0/1369	0.44	0/1846
9	L8	0.25	0/1371	0.38	0/1833
10	L9	0.21	0/1410	0.38	0/1888
11	LC	0.24	0/990	0.40	0/1335
12	LD	0.21	0/1138	0.40	0/1533
13	LE	0.24	0/1039	0.44	0/1395
14	LF	0.26	0/1060	0.41	0/1412
15	LG	0.18	0/492	0.34	0/659
16	LH	0.25	0/6592	0.41	0/8924
17	LI	0.14	0/3835	0.34	0/5263
18	LJ	0.24	0/3993	0.36	0/5413
19	LK	0.18	0/1085	0.34	0/1463
20	LL	0.22	0/4052	0.37	0/5501
21	LM	0.17	0/9462	0.35	0/13078
22	LN	0.25	0/5359	0.34	0/7255
23	LO	0.24	0/6773	0.38	0/9164
24	LP	0.18	0/3288	0.32	0/4419
25	LQ	0.20	0/6837	0.36	0/9227
26	LR	0.17	0/6313	0.36	0/8551
27	LS	0.28	0/3866	0.35	0/5239
28	LT	0.22	0/7015	0.34	0/9479
29	LU	0.26	0/3835	0.39	0/5162
30	LV	0.27	0/3360	0.39	0/4549
31	LW	0.23	0/4321	0.34	0/5832
32	LX	0.21	0/6852	0.36	0/9258

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LY	0.19	0/6292	0.35	0/8556
33	LZ	0.24	0/1553	0.40	0/2089
34	NA	0.25	1/2090 (0.0%)	0.44	3/2817 (0.1%)
35	NB	0.19	0/1891	0.38	0/2541
36	NC	0.14	0/576	0.29	0/801
37	ND	0.20	0/613	0.38	0/811
38	NE	0.18	0/1662	0.36	0/2212
39	NF	0.19	0/1158	0.37	0/1559
40	NG	0.18	0/886	0.34	0/1194
41	NH	0.22	0/8899	0.37	0/12035
42	NI	0.18	0/1994	0.35	0/2684
43	NK	0.19	0/2144	0.38	0/2880
44	NM	0.21	0/1862	0.39	0/2494
45	NN	0.17	0/1491	0.34	0/2063
46	NQ	0.21	0/605	0.37	0/817
47	OA	0.14	0/892	0.30	0/1241
48	SA	0.18	0/3082	0.34	0/4151
49	SB	0.24	1/3396 (0.0%)	0.41	3/4576 (0.1%)
50	SC	0.21	0/1906	0.36	0/2570
50	SD	0.18	0/1852	0.34	0/2500
51	SE	0.26	0/928	0.37	0/1262
51	SF	0.20	0/928	0.35	0/1262
52	SG	0.22	1/3744 (0.0%)	0.39	2/5040 (0.0%)
53	SH	0.19	0/2832	0.36	0/3825
54	SI	0.21	0/6719	0.35	0/9043
55	SJ	0.19	0/1703	0.36	0/2295
55	SK	0.21	0/1822	0.37	0/2462
56	SL	0.21	0/1406	0.36	0/1890
57	SM	0.21	0/2337	0.35	0/3148
58	SN	0.17	0/2088	0.36	0/2808
59	SP	0.17	0/18707	0.35	1/25354 (0.0%)
60	SQ	0.18	0/1302	0.38	0/1728
61	SR	0.21	0/804	0.38	0/1074
62	SS	0.18	0/2307	0.41	2/3091 (0.1%)
63	ST	0.26	1/4513 (0.0%)	0.45	4/6075 (0.1%)
64	SU	0.19	0/4480	0.34	0/6073
65	SV	0.16	0/875	0.37	0/1206
66	SW	0.18	0/1591	0.37	0/2143
67	SY	0.20	0/1978	0.35	0/2616
68	SZ	0.22	0/1326	0.35	0/1859
All	All	0.21	4/252530 (0.0%)	0.35	15/350420 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

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

Mol	Chain	#Chirality outliers	#Planarity outliers
21	LM	0	1
32	LX	0	1
All	All	0	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
63	ST	585	PRO	CG-CD	-11.48	1.11	1.50
34	NA	458	PRO	CG-CD	-7.19	1.26	1.50
49	SB	129	PRO	CG-CD	-7.00	1.26	1.50
52	SG	365	PRO	CG-CD	-5.49	1.32	1.50

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
63	ST	585	PRO	N-CD-CG	-15.73	79.60	103.20
49	SB	129	PRO	CA-N-CD	-11.01	96.59	112.00
34	NA	458	PRO	N-CD-CG	-10.18	87.92	103.20
52	SG	365	PRO	CA-N-CD	-10.05	97.92	112.00
63	ST	585	PRO	CA-CB-CG	-9.30	86.82	104.50
49	SB	129	PRO	N-CD-CG	-8.52	90.43	103.20
63	ST	285	PRO	CA-N-CD	-7.55	101.44	112.00
63	ST	585	PRO	CA-N-CD	-7.21	101.90	112.00
52	SG	365	PRO	N-CD-CG	-6.88	92.87	103.20
34	NA	458	PRO	CA-CB-CG	-6.12	92.87	104.50
59	SP	1248	LYS	CB-CG-CD	5.82	124.69	111.30
34	NA	458	PRO	CA-N-CD	-5.73	103.98	112.00
49	SB	129	PRO	CA-CB-CG	-5.39	94.27	104.50
62	SS	313	PHE	CA-C-N	-5.15	113.40	119.84
62	SS	313	PHE	C-N-CA	-5.15	113.40	119.84

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	LM	1586	LEU	Peptide
32	LX	841	ARG	Sidechain

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	L0	9483	0	4770	42	0
2	L1	25709	0	12967	148	0
3	L2	3712	0	1882	29	0
4	L3	786	0	823	8	0
5	L4	1936	0	2019	14	0
6	L5	1635	0	1697	28	0
7	L6	1653	0	1750	27	0
8	L7	1347	0	1406	22	0
9	L8	1348	0	1366	18	0
10	L9	1388	0	1467	14	0
11	LC	973	0	1029	19	0
12	LD	1112	0	1179	16	0
13	LE	1022	0	1060	21	0
14	LF	1046	0	1114	16	0
15	LG	490	0	529	10	0
16	LH	6465	0	6415	102	0
17	LI	3792	0	2859	29	0
18	LJ	3911	0	3906	48	0
19	LK	1068	0	1120	17	0
20	LL	3982	0	3983	70	0
21	LM	9380	0	6279	45	0
22	LN	5263	0	5270	53	0
23	LO	6639	0	6524	86	0
24	LP	3220	0	3272	36	0
25	LQ	6707	0	6738	95	0
26	LR	6207	0	6247	94	0
27	LS	3793	0	3770	53	0
28	LT	6876	0	6853	84	0
29	LU	3756	0	3708	54	0
30	LV	3286	0	3208	57	0
31	LW	4237	0	4239	50	0
32	LX	6720	0	6840	94	0
32	LY	6179	0	5745	62	0
33	LZ	1524	0	1567	25	0
34	NA	2075	0	1915	32	0
35	NB	1873	0	1638	25	0
36	NC	575	0	274	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	ND	609	0	671	11	0
38	NE	1649	0	1669	20	0
39	NF	1135	0	1197	21	0
40	NG	875	0	905	19	0
41	NH	8693	0	8806	119	0
42	NI	1953	0	1933	21	0
43	NK	2107	0	2184	25	0
44	NM	1838	0	1933	38	0
45	NN	1481	0	866	14	0
46	NQ	595	0	609	6	0
47	OA	888	0	484	5	0
48	SA	3035	0	3059	34	0
49	SB	3357	0	3471	48	0
50	SC	1871	0	1916	27	0
50	SD	1817	0	1857	19	0
51	SE	916	0	964	12	0
51	SF	916	0	964	13	0
52	SG	3672	0	3690	35	0
53	SH	2781	0	2878	18	0
54	SI	6577	0	6743	81	0
55	SJ	1678	0	1756	28	0
55	SK	1793	0	1874	31	0
56	SL	1384	0	1464	15	0
57	SM	2296	0	2325	29	0
58	SN	2053	0	2168	24	0
59	SP	18367	0	17934	238	0
60	SQ	1280	0	1331	15	0
61	SR	792	0	847	6	0
62	SS	2267	0	2300	34	0
63	ST	4448	0	4337	57	0
64	SU	4370	0	4365	74	0
65	SV	869	0	554	12	0
66	SW	1565	0	1647	20	0
67	SY	1953	0	2050	28	0
68	SZ	1314	0	649	1	0
69	L0	3	0	0	0	0
69	L1	27	0	0	0	0
69	L2	2	0	0	0	0
69	NH	1	0	0	0	0
69	SI	1	0	0	0	0
70	NH	31	0	12	1	0
71	NQ	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
71	SL	1	0	0	0	0
72	SI	32	0	12	0	0
All	All	244461	0	219852	2386	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 5.

All (2386) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:NM:240:LYS:O	44:NM:242:LYS:NZ	2.01	0.93
67:SY:114:GLU:OE1	67:SY:207:ARG:NH2	2.01	0.93
35:NB:393:ALA:O	64:SU:167:LYS:NZ	2.03	0.91
23:LO:828:ILE:HG21	28:LT:930:MET:HE3	1.52	0.91
31:LW:433:LEU:HD21	33:LZ:16:VAL:HG21	1.51	0.91
56:SL:65:VAL:HG11	56:SL:86:MET:HE1	1.51	0.89
41:NH:671:THR:OG1	41:NH:718:LYS:O	1.92	0.88
48:SA:160:ARG:NH2	49:SB:243:MET:O	2.07	0.87
20:LL:185:PRO:O	20:LL:215:TYR:OH	1.94	0.86
22:LN:140:ASN:OD1	50:SD:292:LYS:NZ	2.09	0.86
2:L1:885:G:N2	40:NG:124:ASP:OD2	2.09	0.85
32:LX:623:GLN:OE1	32:LY:840:LYS:NZ	2.09	0.85
2:L1:549:G:OP1	67:SY:3:LYS:NZ	2.10	0.85
25:LQ:538:ARG:NH1	25:LQ:580:ASP:OD1	2.10	0.85
2:L1:894:U:O2'	40:NG:36:LYS:NZ	2.10	0.85
49:SB:121:LYS:NZ	50:SD:236:MET:SD	2.49	0.85
59:SP:1324:ILE:HD12	59:SP:1363:LEU:HD21	1.59	0.84
55:SK:176:ARG:NH2	55:SK:222:ASP:OD2	2.11	0.83
22:LN:748:SER:OG	22:LN:751:GLU:OE1	1.94	0.83
32:LY:644:TYR:OH	45:NN:492:GLU:OE2	1.95	0.83
2:L1:629:U:O2'	43:NK:259:LYS:NZ	2.12	0.83
26:LR:10:ILE:HD12	26:LR:370:LEU:HD22	1.59	0.82
32:LX:889:GLY:O	32:LX:892:ARG:NH1	2.12	0.82
41:NH:828:ASP:OD2	41:NH:888:LYS:NZ	2.11	0.82
41:NH:627:LEU:HD11	41:NH:671:THR:HG23	1.60	0.82
26:LR:111:ASP:OD2	26:LR:113:THR:OG1	1.96	0.82
2:L1:330:G:OP2	9:L8:172:ARG:NH1	2.13	0.82
63:ST:538:LYS:NZ	63:ST:619:LEU:O	2.11	0.82
11:LC:98:ASP:OD2	28:LT:488:ASN:ND2	2.13	0.81
2:L1:1700:C:OP1	41:NH:173:ASN:ND2	2.12	0.81
55:SJ:40:ARG:NH1	55:SJ:111:GLN:OE1	2.13	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L1:1482:C:O2'	11:LC:72:GLY:O	1.98	0.81
43:NK:50:GLU:OE2	43:NK:75:LEU:HD22	1.81	0.81
2:L1:341:A:OP1	30:LV:121:ARG:NH1	2.14	0.81
32:LY:425:LYS:O	32:LY:429:GLN:NE2	2.13	0.81
66:SW:24:ARG:NH1	66:SW:174:LEU:O	2.13	0.81
3:L2:258:U:OP1	48:SA:374:ARG:NH2	2.14	0.81
27:LS:278:ASP:OD2	27:LS:281:THR:OG1	1.99	0.81
2:L1:1611:A:OP1	6:L5:107:LYS:NZ	2.13	0.81
3:L2:12:U:O4	54:SI:1158:LYS:NZ	2.14	0.80
30:LV:376:ARG:NH1	30:LV:377:PHE:O	2.14	0.80
59:SP:354:SER:OG	59:SP:356:ASP:OD2	1.99	0.80
8:L7:67:LEU:HD22	8:L7:94:ALA:HB2	1.63	0.80
14:LF:38:ASP:OD2	14:LF:39:GLU:N	2.15	0.80
2:L1:1655:A:N1	2:L1:1745:G:O6	2.15	0.80
25:LQ:275:GLN:NE2	25:LQ:276:ASN:O	2.15	0.80
55:SK:169:ASP:OD1	55:SK:170:HIS:ND1	2.14	0.80
32:LY:400:LEU:O	32:LY:404:TYR:OH	2.00	0.79
59:SP:355:GLN:NE2	59:SP:388:ASN:O	2.15	0.79
1:L0:233:G:OP1	67:SY:246:LYS:NZ	2.15	0.79
32:LX:400:LEU:O	32:LX:404:TYR:OH	1.99	0.79
52:SG:522:THR:OG1	52:SG:542:SER:OG	2.00	0.79
10:L9:106:GLU:OE1	10:L9:115:LYS:NZ	2.11	0.79
2:L1:443:C:O2	2:L1:445:A:N6	2.16	0.79
2:L1:207:U:O2	9:L8:178:ARG:NH2	2.15	0.79
59:SP:489:SER:OG	59:SP:493:ASN:OD1	2.00	0.79
64:SU:61:GLN:OE1	64:SU:64:ARG:NH2	2.16	0.79
9:L8:151:LYS:O	12:LD:24:LYS:NZ	2.15	0.79
2:L1:1040:G:O2'	29:LU:433:GLU:OE1	1.99	0.78
2:L1:1473:U:O4	6:L5:180:ARG:NE	2.17	0.78
32:LX:591:GLU:OE2	32:LX:613:LEU:N	2.16	0.78
29:LU:402:GLU:OE1	29:LU:405:ARG:NH1	2.17	0.78
22:LN:141:SER:HG	22:LN:160:CYS:HG	1.14	0.78
38:NE:147:GLU:O	38:NE:151:ASN:ND2	2.16	0.78
59:SP:831:PHE:O	59:SP:834:THR:OG1	2.01	0.78
2:L1:904:G:N2	43:NK:216:ALA:O	2.17	0.77
17:LI:632:THR:HG22	19:LK:492:ILE:HD11	1.66	0.77
21:LM:353:ARG:NH1	21:LM:386:ASP:OD2	2.17	0.77
1:L0:297:U:OP1	23:LO:96:LYS:NZ	2.16	0.77
25:LQ:220:THR:HG23	25:LQ:259:ILE:HD11	1.66	0.77
2:L1:592:A:O3'	10:L9:39:LYS:NZ	2.18	0.77
2:L1:1638:G:N2	2:L1:1638:G:OP2	2.14	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:LJ:227:VAL:HG12	18:LJ:236:VAL:HG12	1.66	0.77
26:LR:343:MET:HE3	26:LR:635:ALA:HB2	1.66	0.77
41:NH:707:PHE:O	41:NH:918:ARG:NH1	2.18	0.77
2:L1:932:U:OP2	44:NM:155:TYR:OH	2.03	0.77
2:L1:1618:C:OP2	23:LO:505:ARG:NH2	2.18	0.77
30:LV:269:GLY:O	30:LV:376:ARG:NH1	2.18	0.76
54:SI:118:LEU:HD12	54:SI:245:LEU:HD21	1.66	0.76
3:L2:256:G:N7	51:SF:38:ASN:ND2	2.33	0.76
22:LN:314:SER:O	22:LN:318:ASN:N	2.18	0.76
28:LT:743:ARG:NH2	34:NA:480:GLN:O	2.19	0.76
2:L1:913:G:OP1	26:LR:408:LYS:NZ	2.19	0.76
25:LQ:199:THR:OG1	26:LR:667:GLN:OE1	2.04	0.76
30:LV:171:ARG:HH21	45:NN:468:VAL:HG23	1.51	0.76
59:SP:984:ILE:HG23	59:SP:1032:MET:HE1	1.67	0.76
48:SA:180:LEU:HD22	49:SB:183:ARG:HH22	1.50	0.75
5:L4:115:THR:OG1	5:L4:118:GLU:OE1	2.03	0.75
32:LX:413:ASN:OD1	32:LX:420:ARG:NH2	2.20	0.75
2:L1:1584:G:N2	2:L1:1611:A:OP2	2.15	0.75
28:LT:246:ILE:O	28:LT:249:SER:OG	2.05	0.75
41:NH:243:LEU:HD11	41:NH:252:LEU:HD12	1.69	0.75
20:LL:441:LEU:HD13	20:LL:456:VAL:HG11	1.69	0.75
3:L2:256:G:OP1	48:SA:382:LYS:NZ	2.19	0.75
59:SP:1352:LEU:O	59:SP:1356:ASN:ND2	2.19	0.74
25:LQ:233:ILE:O	25:LQ:241:LYS:NZ	2.19	0.74
42:NI:55:LEU:O	42:NI:123:THR:OG1	2.03	0.74
32:LY:532:ASN:OD1	32:LY:536:LYS:NZ	2.20	0.74
3:L2:23:U:O4	3:L2:28:A:N6	2.21	0.74
27:LS:412:GLN:OE1	27:LS:420:ARG:NH2	2.21	0.74
26:LR:636:ASP:OD2	26:LR:637:ALA:N	2.20	0.74
32:LY:843:ASP:OD1	32:LY:925:ARG:NH2	2.21	0.74
59:SP:1523:TYR:OH	59:SP:1551:LEU:O	2.05	0.74
64:SU:164:GLU:O	64:SU:172:SER:OG	2.03	0.73
4:L3:38:VAL:HG13	4:L3:42:TYR:HD2	1.54	0.73
23:LO:105:SER:OG	23:LO:107:ASP:OD1	2.06	0.73
30:LV:58:ALA:HB3	30:LV:76:THR:HG21	1.69	0.73
20:LL:271:LYS:NZ	28:LT:585:SER:OG	2.21	0.73
59:SP:1902:SER:O	59:SP:1905:SER:OG	2.01	0.73
58:SN:185:LYS:NZ	65:SV:198:ASP:OD1	2.20	0.73
2:L1:1776:A:O3'	26:LR:180:ARG:NH2	2.21	0.73
47:OA:1408:ASP:OD2	47:OA:1413:ILE:N	2.22	0.73
59:SP:1189:LEU:HD11	59:SP:1198:PHE:CE2	2.23	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L1:1609:U:O2'	6:L5:105:GLY:O	2.03	0.73
24:LP:38:ASP:OD1	24:LP:42:ARG:NH2	2.21	0.73
64:SU:341:LEU:HD11	64:SU:362:MET:HE1	1.70	0.73
40:NG:114:ARG:NH2	43:NK:37:GLU:OE2	2.22	0.73
16:LH:724:ILE:HG21	16:LH:762:TYR:CD2	2.24	0.73
17:LI:591:THR:OG1	17:LI:593:ASP:OD1	2.05	0.73
26:LR:175:TRP:NE1	26:LR:182:CYS:SG	2.62	0.73
53:SH:60:THR:O	63:ST:108:LYS:NZ	2.22	0.73
2:L1:494:U:OP1	54:SI:1138:ARG:NH2	2.21	0.72
59:SP:1502:ASN:OD1	59:SP:1503:ILE:HD12	1.89	0.72
17:LI:570:LEU:HD21	17:LI:637:LEU:HD21	1.69	0.72
35:NB:390:MET:HE1	63:ST:487:LYS:C	2.14	0.72
2:L1:-1:G:N7	29:LU:457:ARG:NH1	2.38	0.72
22:LN:389:ARG:NH2	22:LN:405:GLY:O	2.23	0.72
37:ND:171:VAL:HG23	67:SY:143:MET:HE2	1.72	0.72
56:SL:93:LYS:NZ	56:SL:95:ASN:OD1	2.22	0.72
2:L1:495:C:OP1	54:SI:1135:ARG:NH2	2.23	0.72
2:L1:1028:C:N4	43:NK:193:ASN:OD1	2.22	0.72
32:LX:857:ASP:OD2	32:LY:787:SER:OG	2.08	0.72
2:L1:113:U:O2'	2:L1:115:G:O2'	2.08	0.71
2:L1:151:G:N7	14:LF:124:ARG:NH1	2.37	0.71
31:LW:50:ASP:OD2	62:SS:859:ARG:NH2	2.24	0.71
56:SL:117:LEU:HD21	56:SL:121:ARG:HE	1.55	0.71
1:L0:296:C:O2'	28:LT:68:LEU:O	2.03	0.71
26:LR:692:MET:HE2	34:NA:519:GLU:OE2	1.91	0.71
32:LX:165:THR:O	54:SI:410:LYS:NZ	2.20	0.71
39:NF:99:ARG:NH2	39:NF:141:TYR:OH	2.23	0.71
52:SG:288:PHE:CE1	52:SG:295:LEU:HD13	2.26	0.71
59:SP:334:ASN:O	59:SP:337:THR:OG1	2.07	0.71
29:LU:250:ARG:O	62:SS:447:ASN:ND2	2.23	0.71
35:NB:371:ASP:OD1	35:NB:372:PHE:N	2.24	0.71
50:SC:294:ARG:NH1	56:SL:131:SER:OG	2.23	0.71
39:NF:119:GLU:OE2	39:NF:141:TYR:OH	2.06	0.71
41:NH:652:LYS:NZ	41:NH:668:VAL:O	2.23	0.71
49:SB:161:VAL:O	49:SB:165:GLN:NE2	2.24	0.71
54:SI:972:ILE:HD11	67:SY:34:TYR:CZ	2.25	0.71
35:NB:521:ARG:NH2	54:SI:1044:LEU:O	2.24	0.71
33:LZ:59:ASN:O	33:LZ:62:SER:OG	2.06	0.70
3:L2:321:C:OP1	67:SY:117:LYS:NZ	2.20	0.70
31:LW:96:ASP:OD2	31:LW:98:SER:OG	2.08	0.70
56:SL:100:ASP:OD1	56:SL:127:ARG:NH2	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:LZ:89:THR:HG23	33:LZ:90:THR:HG23	1.73	0.70
9:L8:180:ASP:OD1	9:L8:181:GLY:N	2.24	0.70
59:SP:717:GLN:NE2	59:SP:718:PRO:O	2.23	0.70
2:L1:340:U:OP2	45:NN:460:LYS:NZ	2.21	0.70
2:L1:551:G:OP1	54:SI:1144:LYS:NZ	2.25	0.70
27:LS:369:ASN:OD1	27:LS:418:LYS:NZ	2.25	0.70
52:SG:241:THR:HG21	52:SG:285:SER:HA	1.71	0.70
62:SS:432:ASP:OD1	62:SS:433:ILE:HD12	1.91	0.70
23:LO:450:LEU:HD13	23:LO:475:PRO:HB2	1.72	0.70
13:LE:51:GLU:OE2	13:LE:52:TYR:N	2.25	0.69
31:LW:189:GLN:OE1	31:LW:224:LEU:HD22	1.92	0.69
52:SG:184:ARG:NH2	52:SG:200:ASP:OD2	2.24	0.69
50:SD:225:ARG:NH2	50:SD:246:GLN:OE1	2.25	0.69
51:SE:94:SER:OG	67:SY:248:ARG:NH1	2.25	0.69
18:LJ:297:LYS:NZ	20:LL:449:ASP:OD2	2.23	0.69
29:LU:407:MET:HE1	62:SS:842:TYR:HA	1.73	0.69
59:SP:1356:ASN:OD1	59:SP:1417:TYR:OH	2.11	0.69
25:LQ:387:LEU:O	25:LQ:415:LYS:NZ	2.25	0.69
2:L1:1084:A:N6	38:NE:309:SER:O	2.26	0.69
2:L1:1220:C:O2'	68:SZ:379:LYS:O	2.09	0.69
11:LC:29:ILE:HG21	11:LC:36:ILE:HD11	1.74	0.69
42:NI:130:ASP:O	42:NI:133:SER:OG	2.10	0.69
57:SM:260:GLU:OE2	57:SM:262:ARG:NH1	2.25	0.69
16:LH:714:ASP:OD1	16:LH:715:GLU:N	2.26	0.69
35:NB:396:PHE:CE1	64:SU:352:VAL:HG22	2.27	0.69
29:LU:367:SER:OG	29:LU:369:ASP:OD1	2.04	0.69
55:SK:35:ASP:O	55:SK:40:ARG:NH2	2.25	0.69
59:SP:749:LYS:O	59:SP:756:SER:OG	2.11	0.69
20:LL:25:ASP:OD1	27:LS:576:LEU:HD11	1.93	0.69
21:LM:32:SER:OG	21:LM:35:TYR:O	2.11	0.69
22:LN:205:CYS:SG	22:LN:211:ARG:NH1	2.65	0.69
26:LR:344:ARG:NH2	26:LR:395:ASP:OD1	2.26	0.69
35:NB:529:ALA:O	35:NB:532:VAL:HG12	1.91	0.69
14:LF:8:ARG:NH1	52:SG:351:ILE:O	2.26	0.69
44:NM:97:LEU:HD22	44:NM:232:HIS:ND1	2.07	0.69
16:LH:29:THR:O	16:LH:200:ASN:ND2	2.26	0.68
1:L0:329:A:OP1	31:LW:229:ARG:NH1	2.25	0.68
41:NH:308:LEU:HD12	41:NH:337:LEU:HD13	1.73	0.68
41:NH:1022:MET:SD	41:NH:1026:ASN:ND2	2.67	0.68
61:SR:69:ARG:NE	61:SR:90:ASP:OD2	2.16	0.68
1:L0:254:C:OP2	65:SV:184:TYR:OH	2.10	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:SF:106:ASP:O	51:SF:111:LYS:NZ	2.16	0.68
23:LO:311:ASN:OD1	23:LO:312:GLN:N	2.26	0.68
32:LY:846:SER:O	32:LY:918:ARG:NH2	2.27	0.68
41:NH:763:THR:OG1	41:NH:935:GLU:OE2	2.11	0.68
59:SP:1133:LEU:O	59:SP:1136:THR:OG1	2.12	0.68
64:SU:378:SER:OG	64:SU:453:PRO:O	2.10	0.68
2:L1:1670:G:O2'	2:L1:1731:A:N6	2.22	0.68
22:LN:257:ASP:OD1	22:LN:259:THR:OG1	2.10	0.68
24:LP:203:MET:SD	62:SS:359:LYS:NZ	2.64	0.68
59:SP:1966:PHE:O	59:SP:1970:THR:OG1	2.10	0.68
1:L0:295:A:N7	28:LT:381:ARG:NH1	2.41	0.68
3:L2:82:G:OP1	49:SB:366:LYS:NZ	2.23	0.68
41:NH:765:LEU:O	41:NH:914:ARG:NE	2.27	0.68
2:L1:467:G:O2'	2:L1:469:C:OP2	2.11	0.67
18:LJ:258:LEU:HD21	18:LJ:272:LEU:HD11	1.75	0.67
22:LN:532:ASN:OD1	22:LN:546:GLY:N	2.26	0.67
32:LY:780:ASP:OD2	32:LY:784:ARG:NH2	2.27	0.67
35:NB:592:GLU:OE1	50:SC:79:GLY:N	2.26	0.67
59:SP:264:THR:O	59:SP:313:ARG:NH1	2.27	0.67
18:LJ:472:ASN:OD1	18:LJ:473:THR:N	2.27	0.67
50:SC:253:ILE:O	50:SC:257:SER:OG	2.07	0.67
58:SN:33:ASP:OD2	58:SN:248:ASN:N	2.27	0.67
29:LU:341:GLU:OE1	29:LU:417:ARG:NH2	2.28	0.67
59:SP:551:SER:O	59:SP:555:LEU:HD23	1.95	0.67
2:L1:31:C:O3'	61:SR:139:LYS:NZ	2.26	0.67
2:L1:1192:C:N3	55:SJ:136:ARG:NH1	2.41	0.67
21:LM:413:ASP:OD2	21:LM:417:LYS:NZ	2.27	0.67
59:SP:643:LYS:NZ	59:SP:683:ASP:OD2	2.27	0.67
64:SU:123:TYR:OH	64:SU:147:THR:O	2.12	0.67
3:L2:38:U:O3'	31:LW:423:LYS:NZ	2.28	0.67
27:LS:414:ILE:HD11	27:LS:420:ARG:HE	1.60	0.67
50:SD:309:TYR:OH	67:SY:127:PHE:O	2.08	0.67
3:L2:254:A:OP2	51:SF:95:ARG:NE	2.28	0.67
59:SP:512:ASP:OD1	59:SP:515:THR:HG23	1.95	0.67
26:LR:188:GLU:OE1	26:LR:188:GLU:N	2.27	0.67
43:NK:258:ARG:N	43:NK:261:ASP:OD1	2.28	0.67
23:LO:358:SER:OG	23:LO:830:ARG:NH2	2.28	0.66
32:LX:27:VAL:HG21	32:LX:192:LEU:HD21	1.75	0.66
22:LN:385:ASN:ND2	22:LN:387:GLU:O	2.28	0.66
29:LU:116:LEU:HD11	29:LU:136:MET:HE3	1.77	0.66
59:SP:1946:LYS:NZ	62:SS:455:ILE:HG23	2.11	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:LX:15:ARG:NH1	54:SI:369:ASP:OD1	2.29	0.66
64:SU:325:GLU:OE2	64:SU:329:ARG:NE	2.28	0.66
32:LY:310:VAL:HG23	32:LY:385:VAL:HG23	1.78	0.66
3:L2:324:U:N3	49:SB:323:GLU:OE2	2.28	0.66
59:SP:2047:LEU:HD13	59:SP:2060:GLN:OE1	1.96	0.66
28:LT:807:VAL:O	66:SW:244:ARG:NH1	2.29	0.66
37:ND:182:SER:O	50:SD:294:ARG:NH2	2.28	0.66
59:SP:1515:ALA:HA	59:SP:1518:MET:HE2	1.78	0.66
20:LL:146:VAL:HG13	20:LL:147:GLN:OE1	1.96	0.66
21:LM:784:SER:O	49:SB:84:LYS:NZ	2.24	0.66
25:LQ:529:GLU:OE1	38:NE:98:ARG:NH2	2.29	0.66
28:LT:930:MET:N	28:LT:930:MET:HE2	2.11	0.66
29:LU:75:LYS:HZ2	29:LU:364:ILE:HD13	1.60	0.66
30:LV:137:ILE:HD13	30:LV:155:VAL:HG11	1.78	0.66
41:NH:1010:GLU:O	41:NH:1044:LYS:NZ	2.25	0.66
3:L2:90:C:O2'	3:L2:91:C:OP1	2.14	0.65
6:L5:94:THR:HG22	6:L5:114:ILE:HG13	1.76	0.65
20:LL:224:CYS:SG	20:LL:273:LYS:NZ	2.63	0.65
2:L1:512:A:O2'	10:L9:133:HIS:NE2	2.23	0.65
32:LY:775:VAL:HG11	32:LY:820:HIS:NE2	2.11	0.65
57:SM:243:GLU:OE1	57:SM:243:GLU:N	2.29	0.65
2:L1:967:A:OP2	39:NF:124:ARG:NH2	2.29	0.65
28:LT:592:ASP:OD1	28:LT:593:PHE:N	2.29	0.65
31:LW:453:ASP:O	31:LW:456:SER:OG	2.13	0.65
2:L1:561:G:OP2	57:SM:286:LYS:NZ	2.29	0.65
31:LW:462:ASN:OD1	31:LW:464:LYS:N	2.30	0.65
35:NB:381:LEU:HD13	64:SU:112:GLU:OE1	1.95	0.65
44:NM:127:VAL:HG11	44:NM:176:VAL:HG21	1.79	0.65
59:SP:1182:LEU:CD2	59:SP:1202:LEU:HD21	2.26	0.65
65:SV:131:LEU:HD11	67:SY:191:ASP:OD2	1.97	0.65
25:LQ:190:ASP:OD2	25:LQ:193:THR:OG1	2.10	0.65
32:LY:297:ILE:HD11	32:LY:385:VAL:HG21	1.79	0.65
1:L0:240:C:OP1	11:LC:26:LYS:NZ	2.23	0.65
26:LR:343:MET:CE	26:LR:635:ALA:HB2	2.26	0.65
31:LW:510:ASP:HB3	43:NK:75:LEU:HD12	1.77	0.65
48:SA:102:ASP:OD2	48:SA:104:ASN:N	2.28	0.65
1:L0:67:G:N7	16:LH:422:LYS:NZ	2.43	0.65
19:LK:428:ASP:OD2	19:LK:429:HIS:N	2.29	0.65
24:LP:371:ILE:O	24:LP:418:TYR:OH	2.14	0.65
32:LY:487:ASN:ND2	32:LY:493:ASP:OD2	2.29	0.65
59:SP:2025:GLU:OE2	62:SS:435:ARG:NH2	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L1:188:A:N6	2:L1:197:A:O2'	2.30	0.65
8:L7:151:LYS:NZ	29:LU:220:ASP:OD1	2.30	0.65
16:LH:211:MET:HE1	16:LH:259:VAL:HG21	1.78	0.65
59:SP:1678:MET:SD	59:SP:1720:ILE:HD11	2.37	0.65
2:L1:563:U:OP2	57:SM:289:TYR:OH	2.14	0.65
16:LH:73:LEU:HD12	16:LH:129:PRO:HD2	1.78	0.65
22:LN:681:ILE:HG22	22:LN:683:ASP:H	1.62	0.65
48:SA:182:ASP:OD1	48:SA:183:GLN:N	2.30	0.65
63:ST:659:GLU:OE1	63:ST:659:GLU:N	2.29	0.64
67:SY:235:ASP:OD1	67:SY:236:SER:N	2.30	0.64
3:L2:327:G:O2'	51:SE:39:GLU:OE2	2.10	0.64
23:LO:484:GLU:OE2	23:LO:815:TYR:OH	2.15	0.64
58:SN:204:ILE:HG22	58:SN:205:GLN:OE1	1.97	0.64
20:LL:151:LEU:HD11	20:LL:163:LEU:HD23	1.79	0.64
29:LU:424:LYS:O	29:LU:427:GLN:N	2.31	0.64
25:LQ:544:ARG:NH2	25:LQ:545:TYR:OH	2.30	0.64
40:NG:82:LYS:NZ	44:NM:67:GLU:OE1	2.29	0.64
2:L1:436:A:OP2	54:SI:52:ARG:NH2	2.30	0.64
33:LZ:115:MET:HE3	33:LZ:127:ALA:HB1	1.79	0.64
53:SH:60:THR:HG22	53:SH:81:ILE:HD13	1.80	0.64
6:L5:76:ARG:NH2	23:LO:510:GLU:OE2	2.30	0.64
32:LX:309:PHE:HB2	32:LX:384:VAL:HG22	1.80	0.64
2:L1:474:A:O2'	2:L1:475:A:O5'	2.15	0.64
33:LZ:57:LEU:HD12	34:NA:437:ILE:HD12	1.80	0.64
28:LT:457:THR:O	28:LT:458:THR:OG1	2.16	0.64
30:LV:152:ASP:OD1	30:LV:166:ASN:ND2	2.31	0.64
40:NG:99:GLN:OE1	43:NK:92:ALA:HB1	1.98	0.64
62:SS:260:ALA:HB1	62:SS:263:LEU:HD22	1.78	0.64
66:SW:164:LEU:HD22	66:SW:232:HIS:CE1	2.33	0.63
41:NH:188:SER:N	70:NH:1300:ATP:O2B	2.31	0.63
38:NE:239:ARG:NH1	38:NE:286:ARG:O	2.31	0.63
59:SP:476:LEU:HD13	59:SP:515:THR:HG22	1.80	0.63
13:LE:75:ILE:HD13	38:NE:319:LEU:HD23	1.80	0.63
49:SB:1:MET:HE2	49:SB:16:LYS:HB3	1.80	0.63
14:LF:76:TYR:OH	14:LF:86:GLU:OE1	2.12	0.63
19:LK:449:GLU:N	19:LK:449:GLU:OE2	2.31	0.63
27:LS:165:ARG:HD3	28:LT:175:THR:HG21	1.81	0.63
41:NH:1226:PHE:CE2	42:NI:60:LEU:HD21	2.33	0.63
67:SY:100:LYS:NZ	67:SY:221:GLN:OE1	2.19	0.63
2:L1:559:C:O2	61:SR:63:GLN:NE2	2.31	0.63
32:LY:335:GLN:N	32:LY:339:ASP:OD2	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:SP:1156:SER:O	59:SP:1160:ASN:ND2	2.32	0.63
63:ST:540:ILE:HD11	63:ST:571:ILE:HG23	1.81	0.63
52:SG:546:GLU:OE1	52:SG:551:ARG:NH1	2.31	0.63
16:LH:616:SER:OG	16:LH:618:ASP:OD1	2.11	0.63
24:LP:16:ASP:OD2	31:LW:15:ARG:NH1	2.30	0.63
30:LV:258:ARG:O	45:NN:499:GLY:N	2.32	0.63
48:SA:385:MET:SD	51:SF:63:ILE:HD11	2.38	0.63
2:L1:467:G:OP2	54:SI:188:LYS:NZ	2.31	0.63
28:LT:929:CYS:C	28:LT:930:MET:HE2	2.24	0.63
21:LM:17:THR:HA	21:LM:28:LEU:HD21	1.80	0.62
25:LQ:125:THR:C	25:LQ:126:LEU:HD12	2.23	0.62
28:LT:413:GLU:OE2	28:LT:435:LYS:NZ	2.29	0.62
30:LV:378:ILE:HD12	30:LV:406:ILE:HD12	1.79	0.62
41:NH:649:TRP:O	41:NH:688:LYS:NZ	2.32	0.62
49:SB:3:TYR:OH	49:SB:82:ASP:OD2	2.17	0.62
26:LR:538:ASP:OD1	26:LR:539:VAL:N	2.33	0.62
54:SI:610:LYS:NZ	54:SI:612:VAL:O	2.27	0.62
55:SJ:229:ASN:OD1	55:SJ:230:TYR:N	2.31	0.62
8:L7:17:GLU:HG3	8:L7:46:ILE:HG22	1.80	0.62
21:LM:234:LEU:HD12	21:LM:238:LEU:HD11	1.81	0.62
25:LQ:56:THR:OG1	25:LQ:58:ASP:OD1	2.13	0.62
55:SK:228:SER:HB3	55:SK:232:LEU:HD11	1.81	0.62
2:L1:351:C:N3	12:LD:102:LYS:NZ	2.40	0.62
2:L1:1682:U:O2	2:L1:1720:G:N2	2.33	0.62
48:SA:29:SER:O	48:SA:35:GLN:NE2	2.33	0.62
2:L1:931:C:O2'	44:NM:118:GLN:O	2.16	0.62
41:NH:602:ASN:OD1	41:NH:603:THR:N	2.32	0.62
19:LK:428:ASP:OD2	19:LK:429:HIS:ND1	2.33	0.62
34:NA:352:LYS:NZ	63:ST:764:ARG:O	2.33	0.62
49:SB:319:ILE:HD12	49:SB:326:LEU:HD22	1.82	0.62
59:SP:782:MET:HE1	59:SP:796:ILE:HD12	1.79	0.62
59:SP:1189:LEU:HD11	59:SP:1198:PHE:CD2	2.34	0.62
2:L1:763:G:N2	2:L1:774:A:N7	2.48	0.62
22:LN:141:SER:OG	22:LN:160:CYS:SG	2.36	0.62
23:LO:841:ASP:OD1	23:LO:842:ASN:N	2.33	0.62
57:SM:56:PHE:O	57:SM:60:GLN:N	2.32	0.62
2:L1:1657:U:O4'	25:LQ:450:ARG:NH1	2.33	0.62
23:LO:497:ILE:CD1	23:LO:532:VAL:HG11	2.30	0.62
59:SP:427:SER:OG	59:SP:428:GLN:NE2	2.33	0.62
22:LN:581:SER:N	22:LN:596:MET:HE3	2.15	0.62
32:LX:73:ARG:NH1	32:LX:98:ILE:HG22	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:NH:976:ILE:HD11	41:NH:1017:TYR:CZ	2.35	0.62
41:NH:1163:LEU:HD23	41:NH:1184:GLY:HA2	1.80	0.62
18:LJ:168:THR:OG1	18:LJ:190:ASP:OD1	2.11	0.61
64:SU:174:ASN:OD1	64:SU:176:ILE:HG22	1.99	0.61
64:SU:348:ASP:OD1	64:SU:349:LEU:N	2.32	0.61
7:L6:68:LEU:HD21	30:LV:359:ILE:HD13	1.79	0.61
16:LH:657:SER:HG	16:LH:674:THR:HG1	1.45	0.61
26:LR:163:LEU:O	26:LR:175:TRP:N	2.32	0.61
29:LU:116:LEU:HD11	29:LU:136:MET:CE	2.30	0.61
35:NB:390:MET:HE1	63:ST:487:LYS:O	2.00	0.61
20:LL:153:ILE:HG22	20:LL:163:LEU:HG	1.81	0.61
31:LW:186:ARG:NH1	33:LZ:42:GLU:OE2	2.33	0.61
59:SP:2034:GLU:OE2	59:SP:2034:GLU:N	2.34	0.61
2:L1:575:C:OP1	54:SI:931:LYS:NZ	2.33	0.61
6:L5:97:LEU:O	6:L5:180:ARG:NH2	2.34	0.61
6:L5:157:ARG:NH1	55:SK:219:GLU:O	2.32	0.61
8:L7:186:PRO:O	8:L7:187:SER:OG	2.15	0.61
16:LH:27:SER:OG	16:LH:171:TYR:OH	2.18	0.61
16:LH:474:THR:HG22	16:LH:511:GLU:OE1	2.00	0.61
16:LH:156:THR:HG22	16:LH:171:TYR:CE2	2.34	0.61
24:LP:56:TYR:OH	24:LP:91:ARG:NH2	2.34	0.61
1:L0:350:A:OP1	31:LW:512:ARG:NH2	2.33	0.61
5:L4:98:ASN:ND2	5:L4:116:ASP:OD1	2.32	0.61
22:LN:682:THR:OG1	22:LN:684:GLU:OE1	2.16	0.61
23:LO:828:ILE:CG2	28:LT:930:MET:HE3	2.27	0.61
42:NI:70:PHE:CZ	42:NI:74:LEU:HD11	2.35	0.61
63:ST:467:ASN:OD1	63:ST:468:ARG:N	2.33	0.61
32:LX:402:GLY:O	32:LX:463:ARG:NH1	2.33	0.61
42:NI:135:ASN:OD1	42:NI:136:ASN:N	2.33	0.61
48:SA:265:GLU:N	48:SA:265:GLU:OE1	2.32	0.61
54:SI:952:PHE:HD2	54:SI:958:VAL:HG22	1.65	0.61
2:L1:578:U:OP1	54:SI:1039:ARG:NH2	2.33	0.61
16:LH:682:ASN:CG	16:LH:689:ILE:HD11	2.25	0.61
22:LN:95:LYS:O	22:LN:97:ARG:NH1	2.33	0.61
31:LW:333:SER:HB3	31:LW:381:LEU:HD11	1.83	0.61
55:SJ:104:ILE:N	55:SJ:246:GLU:OE1	2.34	0.61
60:SQ:167:LYS:O	60:SQ:170:LYS:NZ	2.33	0.61
63:ST:422:LEU:O	63:ST:426:THR:HG23	2.00	0.61
9:L8:82:VAL:HG12	9:L8:196:LEU:HD11	1.81	0.61
9:L8:87:ASN:OD1	9:L8:88:ASN:N	2.34	0.61
16:LH:769:ASN:OD1	16:LH:770:TYR:N	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LI:632:THR:HG22	19:LK:492:ILE:CD1	2.30	0.61
40:NG:22:SER:OG	40:NG:25:ASP:O	2.10	0.61
59:SP:583:LEU:HD22	59:SP:657:LEU:HD13	1.81	0.61
2:L1:192:U:H3	2:L1:193:U:HO2'	1.49	0.60
2:L1:192:U:N3	2:L1:193:U:O2'	2.33	0.60
52:SG:61:ASP:OD1	52:SG:64:ARG:NH2	2.34	0.60
59:SP:1670:LEU:HD11	59:SP:1701:MET:HE1	1.81	0.60
4:L3:52:VAL:HG21	4:L3:61:LEU:HD11	1.82	0.60
32:LX:871:MET:HE1	32:LX:920:MET:SD	2.41	0.60
64:SU:163:ILE:HG23	64:SU:173:GLU:OE2	2.00	0.60
24:LP:192:PHE:HE2	62:SS:351:LEU:HD21	1.66	0.60
28:LT:175:THR:O	28:LT:175:THR:HG22	2.00	0.60
53:SH:179:THR:HG21	53:SH:307:ASP:OD2	2.01	0.60
6:L5:111:VAL:HG12	11:LC:43:ILE:HD11	1.83	0.60
7:L6:129:VAL:O	59:SP:636:ARG:NH1	2.34	0.60
25:LQ:472:HIS:ND1	25:LQ:494:ASP:OD2	2.31	0.60
25:LQ:480:ASP:OD2	25:LQ:481:LEU:N	2.35	0.60
59:SP:2104:LEU:HA	59:SP:2107:VAL:HG22	1.84	0.60
25:LQ:619:MET:HE2	25:LQ:661:TRP:HE3	1.65	0.60
27:LS:183:ASP:OD1	28:LT:281:ARG:NH1	2.34	0.60
31:LW:380:ASN:OD1	31:LW:381:LEU:N	2.34	0.60
54:SI:748:ASP:OD1	54:SI:749:THR:N	2.33	0.60
59:SP:897:PHE:CZ	59:SP:901:ILE:HD11	2.35	0.60
2:L1:867:G:H21	39:NF:87:ASP:CG	2.08	0.60
35:NB:502:LYS:NZ	58:SN:251:SER:OG	2.18	0.60
16:LH:381:SER:OG	20:LL:349:ASP:OD2	2.19	0.60
24:LP:144:VAL:HG11	24:LP:178:VAL:HG11	1.82	0.60
28:LT:226:VAL:HG13	28:LT:227:THR:HG23	1.83	0.60
30:LV:218:LEU:HD12	45:NN:498:LEU:HD11	1.82	0.60
32:LY:660:TYR:CD1	32:LY:712:LEU:HD12	2.36	0.60
63:ST:460:LYS:NZ	63:ST:506:ILE:O	2.34	0.60
65:SV:126:LEU:O	65:SV:130:ASP:N	2.33	0.60
26:LR:430:TYR:OH	26:LR:467:ILE:O	2.19	0.60
21:LM:143:TYR:HB3	21:LM:179:MET:HE2	1.84	0.60
41:NH:158:VAL:HG11	41:NH:237:HIS:HB2	1.83	0.60
52:SG:470:LEU:O	52:SG:471:GLN:NE2	2.35	0.60
55:SJ:73:HIS:HD2	55:SJ:76:LEU:HD22	1.67	0.60
59:SP:472:ASP:OD2	59:SP:474:ASN:ND2	2.35	0.60
59:SP:1742:VAL:HB	59:SP:1745:ILE:HD12	1.83	0.60
1:L0:372:A:O2'	1:L0:373:U:O4'	2.15	0.60
17:LI:593:ASP:OD1	17:LI:594:SER:N	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LL:21:THR:HG21	20:LL:310:THR:HG21	1.83	0.60
53:SH:219:LEU:HD21	54:SI:628:VAL:HG11	1.82	0.60
63:ST:508:PHE:N	64:SU:522:GLU:OE2	2.35	0.60
16:LH:743:ILE:HD11	16:LH:763:ILE:HD13	1.83	0.59
23:LO:328:LEU:HD13	23:LO:340:LYS:HD3	1.84	0.59
26:LR:217:ASP:OD1	26:LR:219:ILE:HG22	2.02	0.59
23:LO:346:ASP:OD1	23:LO:666:ARG:NH1	2.35	0.59
25:LQ:94:LEU:HB2	25:LQ:108:LEU:HD21	1.83	0.59
31:LW:178:ASP:OD2	31:LW:179:HIS:ND1	2.35	0.59
49:SB:88:ILE:HG22	49:SB:117:TYR:OH	2.02	0.59
21:LM:220:VAL:O	21:LM:224:ASN:ND2	2.35	0.59
50:SD:103:GLU:N	50:SD:103:GLU:OE2	2.35	0.59
26:LR:295:PRO:O	26:LR:296:ILE:HD13	2.01	0.59
66:SW:25:ILE:HD11	66:SW:30:ASN:HB2	1.83	0.59
67:SY:125:LEU:HD22	67:SY:198:PHE:CE1	2.37	0.59
1:L0:467:A:N1	1:L0:468:A:N6	2.49	0.59
41:NH:519:ASP:OD2	41:NH:614:ARG:NH1	2.36	0.59
57:SM:75:ASP:OD1	57:SM:76:GLU:N	2.36	0.59
64:SU:255:SER:OG	64:SU:259:LYS:NZ	2.36	0.59
66:SW:24:ARG:NH1	66:SW:177:LEU:O	2.35	0.59
16:LH:366:ASN:HA	16:LH:399:ILE:HD13	1.85	0.59
29:LU:134:ASN:OD1	29:LU:152:VAL:HG11	2.02	0.59
32:LX:841:ARG:HD2	32:LX:854:VAL:HG12	1.84	0.59
41:NH:254:LEU:CD1	41:NH:268:LEU:HD21	2.32	0.59
41:NH:551:GLU:N	41:NH:551:GLU:OE1	2.35	0.59
51:SE:54:MET:O	51:SE:81:VAL:HG22	2.02	0.59
59:SP:2144:TYR:CZ	62:SS:251:ILE:HD13	2.37	0.59
41:NH:628:VAL:HG13	44:NM:240:LYS:NZ	2.18	0.59
41:NH:1063:ARG:NH1	47:OA:1405:ALA:O	2.34	0.59
49:SB:183:ARG:O	49:SB:186:GLU:N	2.36	0.59
8:L7:70:PHE:O	8:L7:74:GLN:N	2.36	0.59
21:LM:313:ASP:OD2	21:LM:314:GLN:N	2.36	0.59
28:LT:587:ARG:HE	28:LT:605:LEU:HD11	1.66	0.59
32:LY:287:ARG:NH1	32:LY:471:ASP:O	2.36	0.59
1:L0:151:U:O2'	1:L0:152:U:OP2	2.19	0.59
1:L0:411:A:O2'	54:SI:1110:ARG:NH1	2.36	0.59
2:L1:454:U:O4'	5:L4:66:MET:HE1	2.03	0.59
31:LW:451:SER:O	62:SS:843:GLN:NE2	2.36	0.59
31:LW:497:LEU:O	31:LW:501:LEU:HD12	2.02	0.59
41:NH:177:ASN:OD1	41:NH:178:TYR:N	2.36	0.59
59:SP:1486:ILE:HD12	59:SP:1511:ILE:HG13	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LT:375:LEU:HD22	28:LT:389:MET:HG3	1.84	0.58
30:LV:24:SER:OG	59:SP:886:ASP:OD2	2.20	0.58
41:NH:401:LEU:O	41:NH:410:LYS:NZ	2.30	0.58
58:SN:215:ASN:O	58:SN:219:THR:HG23	2.03	0.58
17:LI:534:LEU:O	17:LI:537:THR:HG22	2.03	0.58
22:LN:289:ASP:OD1	22:LN:290:THR:N	2.35	0.58
25:LQ:245:MET:HE2	25:LQ:321:TYR:OH	2.02	0.58
27:LS:240:ASP:OD1	27:LS:243:ALA:HB2	2.03	0.58
32:LX:427:ILE:HG23	32:LX:465:LEU:CD2	2.33	0.58
32:LX:896:ASP:OD1	32:LX:897:THR:N	2.36	0.58
21:LM:22:ARG:NH2	29:LU:20:GLN:O	2.35	0.58
30:LV:378:ILE:CD1	30:LV:406:ILE:HD12	2.32	0.58
59:SP:1620:VAL:HG21	59:SP:1635:ILE:HD11	1.84	0.58
13:LE:69:LEU:HD21	13:LE:72:CYS:SG	2.43	0.58
28:LT:626:ASP:OD1	28:LT:627:ASN:N	2.36	0.58
30:LV:66:ARG:NH2	30:LV:107:LEU:O	2.37	0.58
34:NA:311:ILE:HD11	54:SI:1032:LEU:N	2.18	0.58
41:NH:427:LYS:O	41:NH:431:THR:HG22	2.02	0.58
41:NH:585:MET:SD	41:NH:613:VAL:HG12	2.43	0.58
41:NH:983:GLU:O	44:NM:222:LYS:NZ	2.35	0.58
57:SM:123:VAL:HG12	57:SM:125:PRO:HD2	1.84	0.58
23:LO:792:ILE:HD13	28:LT:723:LEU:HG	1.84	0.58
34:NA:311:ILE:HD11	54:SI:1031:GLY:C	2.29	0.58
57:SM:12:TYR:OH	57:SM:75:ASP:OD2	2.04	0.58
1:L0:121:G:H21	1:L0:124:A:H62	1.51	0.58
20:LL:111:ASP:OD1	20:LL:112:LEU:N	2.36	0.58
30:LV:25:LEU:HD23	30:LV:26:PRO:O	2.03	0.58
32:LY:270:ILE:O	32:LY:305:TYR:OH	2.18	0.58
35:NB:415:THR:HG23	35:NB:418:PHE:H	1.69	0.58
49:SB:230:GLU:HG2	49:SB:231:ILE:HD12	1.86	0.58
59:SP:549:LYS:O	59:SP:555:LEU:HD21	2.04	0.58
2:L1:340:U:OP1	30:LV:136:ARG:NH2	2.36	0.58
7:L6:148:SER:OG	7:L6:151:ASP:OD2	2.21	0.58
14:LF:10:ARG:NE	14:LF:26:ASP:OD2	2.37	0.58
16:LH:520:LEU:HD11	18:LJ:464:ALA:HB2	1.85	0.58
18:LJ:416:THR:O	18:LJ:419:GLN:N	2.37	0.58
25:LQ:5:TYR:OH	25:LQ:643:ASP:OD2	2.10	0.58
64:SU:522:GLU:N	64:SU:522:GLU:OE1	2.36	0.58
2:L1:475:A:OP2	10:L9:126:ARG:NE	2.33	0.58
3:L2:59:G:H5'	23:LO:570:THR:HG23	1.85	0.58
4:L3:32:LEU:HD23	4:L3:38:VAL:HG11	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SI:849:LEU:HD21	54:SI:890:CYS:HB2	1.85	0.58
56:SL:65:VAL:HG11	56:SL:86:MET:CE	2.31	0.58
59:SP:441:ASP:OD1	59:SP:442:LYS:N	2.37	0.58
59:SP:1610:MET:HE1	59:SP:1639:ILE:HG23	1.83	0.58
23:LO:586:SER:OG	23:LO:588:ASP:OD1	2.17	0.58
41:NH:174:TYR:OH	41:NH:226:HIS:ND1	2.37	0.58
2:L1:186:C:O3'	59:SP:1143:LYS:NZ	2.37	0.57
3:L2:104:C:O3'	48:SA:344:ARG:NH2	2.37	0.57
6:L5:225:ARG:NE	15:LG:58:GLU:OE2	2.37	0.57
25:LQ:398:ASP:OD2	25:LQ:438:PHE:N	2.35	0.57
25:LQ:455:GLN:OE1	25:LQ:467:THR:HG23	2.04	0.57
25:LQ:659:GLU:O	25:LQ:676:SER:OG	2.18	0.57
54:SI:952:PHE:CD2	54:SI:958:VAL:HG22	2.39	0.57
55:SJ:240:LYS:NZ	55:SK:246:GLU:OE1	2.28	0.57
59:SP:601:LEU:HD22	59:SP:623:MET:HG3	1.86	0.57
16:LH:180:ASP:O	16:LH:183:LYS:NZ	2.24	0.57
22:LN:579:ARG:NH1	22:LN:660:ASP:OD1	2.37	0.57
55:SK:90:ASP:OD1	55:SK:91:ILE:N	2.37	0.57
60:SQ:112:ASN:OD1	60:SQ:113:MET:N	2.36	0.57
61:SR:91:GLY:O	61:SR:94:ASN:ND2	2.37	0.57
20:LL:22:VAL:HG12	20:LL:27:GLN:HG2	1.85	0.57
25:LQ:919:GLU:OE1	25:LQ:919:GLU:N	2.38	0.57
41:NH:1095:ASP:OD2	47:OA:1407:PHE:N	2.37	0.57
59:SP:1667:ALA:HA	59:SP:1670:LEU:HD13	1.86	0.57
64:SU:39:ASN:ND2	64:SU:42:GLN:OE1	2.38	0.57
2:L1:113:U:HO2'	2:L1:115:G:HO2'	1.51	0.57
2:L1:1045:C:OP1	44:NM:153:HIS:NE2	2.32	0.57
18:LJ:90:ARG:NH1	18:LJ:92:ASP:OD2	2.36	0.57
26:LR:406:ALA:HB2	26:LR:440:VAL:HG13	1.85	0.57
43:NK:141:ARG:NH1	43:NK:191:MET:O	2.37	0.57
22:LN:382:VAL:HG11	22:LN:755:ILE:HD13	1.86	0.57
24:LP:182:TRP:CG	24:LP:277:CYS:HG	2.23	0.57
32:LX:186:GLU:N	32:LX:186:GLU:OE2	2.37	0.57
32:LX:425:LYS:NZ	32:LX:544:SER:O	2.26	0.57
32:LY:753:ASP:OD1	32:LY:754:LEU:N	2.37	0.57
40:NG:25:ASP:OD1	40:NG:26:THR:N	2.38	0.57
55:SJ:77:LEU:O	55:SJ:81:GLY:N	2.38	0.57
58:SN:56:ILE:HD12	65:SV:192:ALA:HA	1.87	0.57
59:SP:1202:LEU:HD22	59:SP:1220:LEU:CD1	2.35	0.57
64:SU:358:PHE:CE2	64:SU:362:MET:HE3	2.39	0.57
7:L6:17:GLU:OE1	7:L6:18:ILE:N	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LS:352:GLN:NE2	27:LS:354:SER:O	2.37	0.57
58:SN:17:LEU:HD23	58:SN:209:ILE:HG13	1.86	0.57
59:SP:1946:LYS:HZ2	62:SS:455:ILE:HG23	1.67	0.57
59:SP:1987:LEU:CD2	59:SP:2019:ILE:HD13	2.34	0.57
18:LJ:227:VAL:CG1	18:LJ:236:VAL:HG12	2.35	0.57
28:LT:646:VAL:HG13	28:LT:647:THR:HG23	1.87	0.57
2:L1:1028:C:OP2	43:NK:144:ARG:NH2	2.38	0.57
23:LO:269:HIS:NE2	23:LO:312:GLN:O	2.33	0.57
25:LQ:171:CYS:HB2	25:LQ:177:LEU:HD13	1.87	0.57
32:LX:520:ARG:NH1	32:LX:556:MET:O	2.35	0.57
58:SN:176:VAL:O	58:SN:180:LEU:HD12	2.05	0.57
64:SU:216:VAL:O	64:SU:219:TRP:N	2.38	0.57
9:L8:84:HIS:CD2	9:L8:90:LEU:HD12	2.39	0.57
16:LH:720:ILE:HD12	16:LH:774:PHE:CD2	2.40	0.57
20:LL:51:LEU:HD22	20:LL:88:TYR:CD1	2.40	0.57
21:LM:1747:GLU:O	21:LM:1752:LEU:N	2.38	0.57
32:LX:709:LEU:HD11	54:SI:419:PHE:CD1	2.40	0.57
32:LY:851:ASP:OD1	32:LY:852:TYR:N	2.37	0.57
41:NH:519:ASP:OD1	41:NH:520:ASN:N	2.38	0.57
43:NK:103:LEU:HD13	43:NK:174:MET:HE2	1.86	0.57
64:SU:24:TYR:OH	64:SU:69:ARG:NH1	2.38	0.57
66:SW:129:ARG:O	66:SW:138:GLU:N	2.29	0.57
20:LL:209:ASP:N	20:LL:231:ASP:OD2	2.38	0.57
44:NM:127:VAL:CG1	44:NM:176:VAL:HG21	2.35	0.57
54:SI:89:LEU:HD23	54:SI:220:ILE:HG23	1.87	0.57
59:SP:806:THR:OG1	59:SP:820:THR:OG1	2.13	0.57
67:SY:154:THR:HG22	67:SY:166:LEU:O	2.04	0.57
2:L1:488:G:OP2	54:SI:1130:GLN:NE2	2.38	0.56
29:LU:75:LYS:NZ	29:LU:364:ILE:HD13	2.20	0.56
29:LU:92:ILE:HD12	29:LU:136:MET:HE2	1.86	0.56
32:LX:71:LYS:O	32:LX:75:ASN:ND2	2.38	0.56
49:SB:129:PRO:HD2	49:SB:129:PRO:O	2.05	0.56
55:SK:169:ASP:OD1	55:SK:170:HIS:N	2.38	0.56
64:SU:348:ASP:O	64:SU:352:VAL:HG23	2.05	0.56
16:LH:682:ASN:ND2	16:LH:689:ILE:HD11	2.19	0.56
54:SI:628:VAL:O	54:SI:628:VAL:HG12	2.05	0.56
59:SP:608:MET:N	59:SP:608:MET:HE2	2.20	0.56
6:L5:216:GLU:OE2	6:L5:219:ARG:NH2	2.38	0.56
8:L7:24:PHE:HE1	8:L7:81:LEU:HD11	1.69	0.56
18:LJ:375:HIS:NE2	18:LJ:377:ASP:OD2	2.39	0.56
18:LJ:452:ASP:OD2	18:LJ:454:ARG:NH1	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LS:376:LEU:HD13	27:LS:409:ILE:HD11	1.87	0.56
29:LU:26:ARG:NH1	31:LW:414:LEU:HD12	2.20	0.56
32:LX:200:VAL:HG21	32:LX:210:LEU:HD11	1.87	0.56
32:LY:857:ASP:OD1	32:LY:858:MET:N	2.38	0.56
41:NH:313:ASN:OD1	41:NH:314:CYS:N	2.38	0.56
58:SN:178:ALA:HB1	65:SV:194:VAL:HG23	1.85	0.56
59:SP:457:PHE:CE2	59:SP:485:ILE:HD13	2.41	0.56
59:SP:618:LEU:HD21	59:SP:648:GLU:OE2	2.04	0.56
59:SP:1201:LEU:HD23	59:SP:1201:LEU:O	2.05	0.56
64:SU:352:VAL:HG12	64:SU:354:TYR:H	1.69	0.56
22:LN:279:HIS:ND1	22:LN:301:ASP:OD2	2.31	0.56
25:LQ:571:GLY:O	25:LQ:598:LYS:NZ	2.21	0.56
32:LX:31:ASP:OD1	32:LX:32:ARG:N	2.38	0.56
33:LZ:65:PRO:HD3	38:NE:203:ILE:HG22	1.88	0.56
39:NF:33:VAL:O	39:NF:37:ILE:HD12	2.05	0.56
44:NM:48:VAL:HG11	44:NM:61:LEU:HD21	1.88	0.56
51:SF:23:VAL:HG21	51:SF:117:VAL:HG21	1.87	0.56
53:SH:283:ILE:O	54:SI:634:ARG:NH1	2.36	0.56
8:L7:168:SER:O	8:L7:172:VAL:HG23	2.05	0.56
28:LT:316:ASP:OD1	28:LT:318:SER:OG	2.21	0.56
44:NM:91:VAL:HG23	44:NM:96:LEU:HD23	1.86	0.56
67:SY:234:VAL:HG12	67:SY:240:ILE:HD12	1.86	0.56
8:L7:173:TYR:CE2	8:L7:177:THR:HG21	2.40	0.56
32:LX:898:ILE:HG23	32:LX:902:LEU:HD13	1.86	0.56
37:ND:121:ASP:OD1	64:SU:21:ARG:NH1	2.38	0.56
52:SG:235:HIS:ND1	52:SG:257:ASP:OD2	2.37	0.56
16:LH:656:ASP:OD1	16:LH:657:SER:N	2.38	0.56
26:LR:288:LEU:HD21	26:LR:306:LEU:HB3	1.87	0.56
28:LT:157:LEU:HD21	28:LT:196:GLY:HA2	1.88	0.56
16:LH:366:ASN:OD1	16:LH:367:SER:N	2.38	0.56
16:LH:778:ASP:O	16:LH:781:SER:N	2.36	0.56
21:LM:984:GLU:O	21:LM:988:LEU:N	2.37	0.56
28:LT:761:GLN:N	28:LT:761:GLN:OE1	2.38	0.56
32:LX:104:ARG:NH1	32:LX:105:TYR:O	2.39	0.56
32:LX:106:VAL:HG21	32:LX:114:ILE:CG2	2.36	0.56
35:NB:606:VAL:N	50:SC:302:GLU:OE1	2.39	0.56
42:NI:108:MET:HE1	42:NI:187:HIS:CE1	2.41	0.56
59:SP:307:ASP:OD1	59:SP:308:ALA:N	2.39	0.56
22:LN:39:VAL:HG22	22:LN:402:TRP:CZ3	2.42	0.56
27:LS:263:LEU:HD13	27:LS:277:ILE:HD11	1.88	0.56
30:LV:113:LYS:HE2	45:NN:475:TYR:CZ	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:NM:108:ASP:OD1	44:NM:111:ARG:NH2	2.38	0.56
49:SB:309:LEU:HD23	49:SB:371:LEU:HD21	1.87	0.56
58:SN:239:ILE:HG21	58:SN:242:ILE:HD11	1.88	0.56
59:SP:283:SER:O	59:SP:329:LYS:NZ	2.32	0.56
1:L0:386:A:H4'	31:LW:224:LEU:HD23	1.88	0.55
2:L1:896:U:O2	40:NG:41:ARG:NH1	2.38	0.55
16:LH:302:SER:OG	16:LH:344:CYS:N	2.39	0.55
17:LI:611:ILE:HG23	17:LI:658:LEU:HD21	1.88	0.55
48:SA:302:ASN:ND2	48:SA:397:SER:O	2.38	0.55
51:SF:60:PRO:O	51:SF:63:ILE:HG22	2.06	0.55
9:L8:165:LEU:HD13	9:L8:183:ILE:HD12	1.87	0.55
24:LP:192:PHE:CE2	62:SS:351:LEU:HD21	2.42	0.55
26:LR:691:PRO:HB2	34:NA:514:ALA:HB3	1.88	0.55
41:NH:756:VAL:HG22	41:NH:756:VAL:O	2.06	0.55
55:SJ:141:MET:HA	55:SJ:141:MET:HE3	1.87	0.55
59:SP:446:GLN:OE1	59:SP:449:ARG:NE	2.38	0.55
2:L1:1170:G:OP1	63:ST:66:LYS:NZ	2.39	0.55
13:LE:81:VAL:O	13:LE:122:SER:OG	2.25	0.55
23:LO:497:ILE:HD13	23:LO:532:VAL:HG11	1.88	0.55
26:LR:625:THR:HG22	26:LR:632:ILE:HD12	1.87	0.55
55:SJ:73:HIS:CD2	55:SJ:76:LEU:HD22	2.40	0.55
59:SP:1633:PRO:O	59:SP:1637:THR:HG23	2.06	0.55
61:SR:97:ASP:OD1	61:SR:98:GLU:N	2.39	0.55
7:L6:1:MET:HG2	7:L6:24:ILE:HD12	1.88	0.55
8:L7:136:VAL:N	8:L7:153:LEU:O	2.39	0.55
15:LG:14:LYS:NZ	25:LQ:822:MET:HE3	2.21	0.55
15:LG:39:THR:OG1	25:LQ:867:GLU:OE1	2.22	0.55
25:LQ:128:GLN:NE2	25:LQ:129:PHE:O	2.40	0.55
28:LT:740:ILE:HD13	34:NA:474:ILE:HG21	1.89	0.55
49:SB:328:ARG:O	49:SB:332:THR:HG22	2.07	0.55
51:SF:23:VAL:HG22	51:SF:113:GLN:OE1	2.06	0.55
54:SI:775:GLU:OE1	54:SI:779:ARG:NH2	2.40	0.55
2:L1:1170:G:P	63:ST:66:LYS:HZ1	2.29	0.55
10:L9:31:ALA:O	10:L9:35:GLY:N	2.40	0.55
28:LT:95:GLU:OE2	28:LT:97:LYS:NZ	2.39	0.55
50:SD:106:LEU:HD22	50:SD:156:MET:HE3	1.89	0.55
55:SJ:141:MET:HE1	55:SJ:144:LEU:HD23	1.89	0.55
66:SW:268:SER:OG	66:SW:269:ARG:NH1	2.40	0.55
2:L1:448:C:OP1	5:L4:49:ARG:NH2	2.39	0.55
20:LL:74:VAL:HG23	20:LL:90:VAL:HG12	1.88	0.55
20:LL:433:THR:OG1	20:LL:467:ASP:OD2	2.15	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LL:486:GLU:OE2	20:LL:487:ARG:NH1	2.39	0.55
21:LM:390:LEU:O	21:LM:394:LEU:N	2.38	0.55
29:LU:37:ARG:NH1	31:LW:449:ILE:O	2.39	0.55
29:LU:170:GLU:OE1	29:LU:170:GLU:N	2.37	0.55
32:LX:568:LEU:HD22	32:LX:580:PRO:HB2	1.88	0.55
32:LX:729:LEU:HD11	32:LX:800:GLN:HE22	1.71	0.55
32:LY:17:GLY:O	32:LY:21:LYS:N	2.39	0.55
64:SU:96:GLU:OE2	64:SU:100:THR:OG1	2.24	0.55
22:LN:394:TRP:CG	22:LN:431:CYS:HG	2.25	0.55
28:LT:157:LEU:HD23	28:LT:191:PHE:CD2	2.41	0.55
59:SP:1738:TYR:CE2	59:SP:1745:ILE:HG21	2.42	0.55
12:LD:75:VAL:HG21	12:LD:117:VAL:CG2	2.36	0.55
41:NH:584:GLU:OE2	41:NH:614:ARG:NH1	2.39	0.55
44:NM:244:VAL:HG13	44:NM:244:VAL:O	2.06	0.55
55:SK:77:LEU:HD11	55:SK:82:ARG:HB2	1.89	0.55
1:L0:161:A:OP1	18:LJ:353:LYS:NZ	2.40	0.55
9:L8:69:SER:OG	9:L8:185:GLU:OE2	2.21	0.55
20:LL:112:LEU:HD11	20:LL:131:LEU:HD11	1.88	0.55
59:SP:526:TYR:CD1	59:SP:561:LEU:HD13	2.42	0.55
64:SU:450:GLU:OE2	64:SU:451:SER:N	2.40	0.55
25:LQ:476:ILE:O	25:LQ:476:ILE:HG23	2.07	0.55
32:LY:306:SER:OG	32:LY:382:GLU:OE2	2.24	0.55
41:NH:795:GLU:OE1	41:NH:797:THR:N	2.39	0.55
41:NH:1150:VAL:HG21	41:NH:1165:SER:CB	2.37	0.55
55:SJ:169:ASP:OD1	55:SJ:170:HIS:N	2.38	0.55
1:L0:309:A:N3	27:LS:145:LYS:NZ	2.55	0.54
16:LH:566:SER:OG	16:LH:618:ASP:O	2.25	0.54
20:LL:72:ASP:OD1	20:LL:73:THR:N	2.39	0.54
29:LU:83:LEU:HD11	29:LU:364:ILE:HG21	1.88	0.54
29:LU:129:ASP:OD2	29:LU:158:LYS:NZ	2.40	0.54
41:NH:794:ASP:OD1	41:NH:858:ARG:NH2	2.41	0.54
43:NK:268:GLU:OE2	43:NK:279:LYS:NZ	2.32	0.54
51:SE:23:VAL:HG21	51:SE:117:VAL:HG21	1.90	0.54
2:L1:1085:G:N7	38:NE:302:ARG:NH1	2.55	0.54
16:LH:33:ASN:OD1	16:LH:357:ILE:HD11	2.07	0.54
19:LK:492:ILE:HG22	19:LK:496:LEU:HG	1.89	0.54
23:LO:726:THR:HG21	23:LO:750:LEU:HD11	1.89	0.54
25:LQ:299:ARG:NH2	25:LQ:320:SER:OG	2.41	0.54
32:LY:271:SER:O	32:LY:273:LYS:NZ	2.30	0.54
41:NH:239:LEU:O	41:NH:239:LEU:HD23	2.06	0.54
11:LC:58:ASP:OD1	11:LC:59:LYS:N	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:LX:62:LYS:O	32:LX:125:GLN:NE2	2.39	0.54
55:SJ:71:ASP:O	55:SJ:74:GLN:NE2	2.39	0.54
5:L4:181:VAL:HG11	5:L4:195:ILE:HD11	1.90	0.54
41:NH:589:LYS:O	41:NH:609:ASN:ND2	2.39	0.54
59:SP:1453:ASN:OD1	59:SP:1464:ARG:NH2	2.41	0.54
59:SP:1591:TYR:OH	59:SP:1634:SER:OG	2.25	0.54
59:SP:1971:ASP:OD1	59:SP:1972:SER:N	2.40	0.54
5:L4:72:VAL:HG11	5:L4:82:TYR:HE2	1.72	0.54
11:LC:60:PHE:CZ	11:LC:89:LEU:HD22	2.43	0.54
26:LR:249:LEU:N	26:LR:257:ILE:O	2.36	0.54
28:LT:97:LYS:HD2	28:LT:109:LEU:HD21	1.89	0.54
28:LT:639:ASP:OD1	28:LT:640:LEU:N	2.40	0.54
32:LY:889:GLY:O	32:LY:892:ARG:NH1	2.40	0.54
42:NI:63:ASN:OD1	42:NI:66:HIS:ND1	2.39	0.54
54:SI:298:VAL:HG23	54:SI:791:ILE:HG23	1.90	0.54
59:SP:29:GLU:OE2	59:SP:32:ARG:NH2	2.40	0.54
59:SP:240:MET:HE3	59:SP:282:ILE:HG21	1.89	0.54
2:L1:1757:G:H21	34:NA:510:LYS:HE3	1.72	0.54
14:LF:7:ILE:HD13	14:LF:43:LYS:HD3	1.90	0.54
16:LH:546:LYS:NZ	20:LL:358:GLU:OE2	2.36	0.54
27:LS:312:ILE:HD11	27:LS:326:LEU:HD11	1.90	0.54
30:LV:178:LEU:HD22	30:LV:205:GLU:OE1	2.06	0.54
30:LV:190:GLU:O	45:NN:484:LYS:NZ	2.37	0.54
59:SP:1987:LEU:HD21	59:SP:2019:ILE:HD13	1.90	0.54
16:LH:550:PRO:HG2	16:LH:557:ILE:HD11	1.88	0.54
18:LJ:43:THR:O	18:LJ:304:SER:OG	2.26	0.54
32:LX:3:LYS:HE3	32:LX:3:LYS:HA	1.90	0.54
52:SG:327:ASP:OD1	52:SG:328:ILE:N	2.41	0.54
55:SJ:80:MET:HE2	55:SJ:80:MET:HA	1.89	0.54
10:L9:107:ARG:NH2	10:L9:149:ARG:O	2.41	0.54
25:LQ:466:ASP:OD2	25:LQ:467:THR:N	2.41	0.54
28:LT:854:SER:HB2	28:LT:895:VAL:HG21	1.89	0.54
29:LU:407:MET:HE3	29:LU:408:PRO:HD2	1.88	0.54
31:LW:552:ARG:NH2	41:NH:791:LYS:O	2.38	0.54
32:LX:37:LEU:CD2	32:LX:149:VAL:HG11	2.38	0.54
32:LX:545:HIS:NE2	32:LX:638:ILE:O	2.39	0.54
54:SI:959:ALA:HB2	63:ST:752:MET:HE1	1.89	0.54
58:SN:36:ILE:HD11	58:SN:204:ILE:HG13	1.90	0.54
59:SP:519:VAL:O	59:SP:523:LEU:HD23	2.08	0.54
59:SP:2030:ASN:HD22	59:SP:2035:ILE:HG21	1.73	0.54
20:LL:51:LEU:HD22	20:LL:88:TYR:CE1	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:LQ:599:ILE:HD12	25:LQ:647:PHE:CE2	2.43	0.54
32:LX:287:ARG:NH1	32:LX:471:ASP:O	2.41	0.54
43:NK:279:LYS:NZ	43:NK:283:GLU:OE2	2.19	0.54
54:SI:819:GLU:OE1	54:SI:819:GLU:N	2.41	0.54
59:SP:2104:LEU:HD21	62:SS:263:LEU:CD2	2.38	0.54
63:ST:420:GLU:OE1	63:ST:420:GLU:N	2.40	0.54
2:L1:500:C:OP2	35:NB:596:THR:OG1	2.25	0.54
2:L1:1192:C:OP2	55:SJ:129:ARG:NE	2.37	0.54
10:L9:62:ARG:NE	10:L9:66:ASP:OD2	2.40	0.54
18:LJ:319:VAL:HG22	18:LJ:329:ILE:CD1	2.37	0.54
26:LR:539:VAL:HG22	26:LR:548:LEU:HD11	1.90	0.54
26:LR:672:TYR:O	26:LR:676:GLY:N	2.38	0.54
27:LS:504:THR:HG23	27:LS:504:THR:O	2.08	0.54
30:LV:357:ASP:OD1	30:LV:358:SER:N	2.41	0.54
41:NH:627:LEU:CD1	41:NH:671:THR:HG23	2.34	0.54
62:SS:248:MET:O	62:SS:251:ILE:HG22	2.08	0.54
63:ST:703:GLN:NE2	64:SU:484:PHE:O	2.41	0.54
2:L1:1615:C:N4	6:L5:80:LYS:O	2.41	0.53
16:LH:885:ASP:OD1	21:LM:255:ILE:HD13	2.08	0.53
23:LO:27:LYS:NZ	66:SW:274:TYR:OH	2.38	0.53
23:LO:838:THR:O	23:LO:842:ASN:ND2	2.41	0.53
27:LS:376:LEU:CD1	27:LS:409:ILE:HD11	2.38	0.53
32:LX:789:LEU:HD22	32:LX:891:GLN:HE21	1.73	0.53
52:SG:278:ASP:OD1	52:SG:279:ARG:N	2.41	0.53
53:SH:307:ASP:OD1	54:SI:765:ASN:ND2	2.38	0.53
55:SK:180:LEU:HD13	55:SK:227:LEU:HD23	1.91	0.53
55:SK:229:ASN:OD1	55:SK:230:TYR:N	2.40	0.53
59:SP:588:ASN:ND2	59:SP:588:ASN:O	2.40	0.53
59:SP:841:ILE:O	59:SP:844:VAL:HG22	2.08	0.53
63:ST:95:ARG:NH1	63:ST:758:ASP:OD1	2.41	0.53
3:L2:59:G:OP1	23:LO:573:ASN:ND2	2.35	0.53
9:L8:165:LEU:HD13	9:L8:183:ILE:CD1	2.38	0.53
26:LR:362:LEU:HD12	26:LR:405:THR:HG21	1.90	0.53
26:LR:532:HIS:NE2	26:LR:550:THR:OG1	2.39	0.53
27:LS:352:GLN:NE2	27:LS:378:GLN:O	2.38	0.53
59:SP:1352:LEU:HD13	59:SP:1401:ASN:HD22	1.74	0.53
7:L6:67:VAL:HG21	7:L6:73:ILE:HD11	1.89	0.53
18:LJ:82:ASP:OD2	18:LJ:83:VAL:N	2.39	0.53
22:LN:279:HIS:HD1	22:LN:301:ASP:CG	2.14	0.53
26:LR:561:SER:O	26:LR:565:PHE:N	2.40	0.53
32:LY:508:PRO:O	32:LY:649:TYR:OH	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:SA:180:LEU:HD22	49:SB:183:ARG:NH2	2.20	0.53
51:SE:54:MET:HE1	51:SE:68:PRO:HD3	1.90	0.53
58:SN:220:ILE:O	58:SN:224:THR:HG22	2.07	0.53
59:SP:306:LEU:HD11	59:SP:343:ILE:HD13	1.88	0.53
59:SP:1711:ASP:OD1	59:SP:1712:THR:N	2.41	0.53
1:L0:461:A:C2	56:SL:13:VAL:HG11	2.44	0.53
16:LH:682:ASN:O	16:LH:686:GLY:N	2.38	0.53
27:LS:272:LEU:HD11	27:LS:314:THR:HG21	1.90	0.53
59:SP:1151:ILE:HG23	59:SP:1201:LEU:HD12	1.90	0.53
59:SP:1612:ILE:HG22	59:SP:1616:LEU:CD2	2.38	0.53
59:SP:2102:PHE:O	59:SP:2106:LEU:HD23	2.08	0.53
25:LQ:829:VAL:HG21	25:LQ:864:ASN:HD21	1.73	0.53
27:LS:221:THR:OG1	27:LS:224:ASN:ND2	2.41	0.53
32:LX:285:ARG:NH1	32:LX:413:ASN:O	2.42	0.53
49:SB:333:LYS:NZ	54:SI:1098:ARG:O	2.35	0.53
52:SG:397:PHE:O	52:SG:437:ARG:NH2	2.41	0.53
59:SP:2012:MET:O	59:SP:2013:LEU:HD22	2.08	0.53
64:SU:120:LEU:HD21	64:SU:180:PHE:HB2	1.89	0.53
2:L1:1699:G:N2	2:L1:1702:A:OP2	2.42	0.53
16:LH:743:ILE:HD11	16:LH:763:ILE:CD1	2.38	0.53
20:LL:112:LEU:HD12	20:LL:116:GLN:O	2.08	0.53
22:LN:121:THR:HG1	22:LN:139:CYS:HG	1.55	0.53
22:LN:392:VAL:HG22	22:LN:401:ILE:HD12	1.90	0.53
23:LO:316:TRP:NE1	23:LO:331:GLU:OE2	2.40	0.53
23:LO:707:ASN:OD1	23:LO:708:ASP:N	2.42	0.53
30:LV:241:LEU:HD11	32:LY:647:MET:HG3	1.90	0.53
41:NH:863:TYR:O	41:NH:867:ILE:HD12	2.09	0.53
48:SA:185:ASP:OD2	48:SA:285:ARG:NH2	2.39	0.53
59:SP:467:THR:HG23	59:SP:467:THR:O	2.07	0.53
59:SP:905:LEU:HD12	59:SP:956:PHE:HE1	1.74	0.53
2:L1:1124:A:OP2	38:NE:112:LYS:NZ	2.18	0.53
24:LP:23:LEU:HD21	24:LP:75:LEU:HD23	1.91	0.53
27:LS:164:LEU:HD22	49:SB:427:TYR:OH	2.08	0.53
32:LY:309:PHE:HB2	32:LY:384:VAL:HG22	1.91	0.53
53:SH:117:LEU:HD21	53:SH:165:GLU:HG3	1.90	0.53
16:LH:232:ASP:OD1	16:LH:233:ASP:N	2.42	0.53
21:LM:45:TYR:CE2	29:LU:16:VAL:HG11	2.44	0.53
23:LO:467:ASP:OD1	23:LO:468:ALA:N	2.41	0.53
31:LW:263:MET:HE3	31:LW:264:PRO:HD2	1.91	0.53
50:SD:221:ILE:HG23	50:SD:221:ILE:O	2.08	0.53
64:SU:27:ILE:O	64:SU:31:ILE:HD12	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:NI:50:SER:O	42:NI:127:LYS:NZ	2.42	0.53
59:SP:2376:VAL:O	59:SP:2380:GLY:N	2.41	0.53
8:L7:46:ILE:HD11	8:L7:58:LEU:HB3	1.91	0.53
36:NC:114:GLU:O	36:NC:118:ALA:N	2.42	0.53
41:NH:376:SER:O	41:NH:387:GLY:N	2.41	0.53
50:SC:117:VAL:HG22	50:SC:142:ARG:NH2	2.23	0.53
50:SC:297:ARG:NH2	50:SC:322:ARG:O	2.41	0.53
59:SP:2070:TYR:O	59:SP:2076:ARG:NE	2.42	0.53
1:L0:258:C:OP1	54:SI:1092:LYS:NZ	2.28	0.52
28:LT:179:LYS:HB3	28:LT:190:LEU:HD11	1.91	0.52
4:L3:32:LEU:CD2	4:L3:38:VAL:HG11	2.39	0.52
27:LS:384:ILE:HG21	27:LS:423:LEU:HD21	1.92	0.52
31:LW:238:MET:SD	31:LW:247:MET:HE3	2.49	0.52
32:LX:894:ASN:OD1	32:LX:895:ILE:N	2.41	0.52
41:NH:774:SER:OG	41:NH:1142:LYS:O	2.18	0.52
53:SH:16:ASN:N	54:SI:607:ASP:OD1	2.39	0.52
59:SP:1066:PHE:O	59:SP:1070:GLY:N	2.42	0.52
63:ST:453:ASN:OD1	63:ST:454:ALA:N	2.41	0.52
2:L1:1477:G:OP1	58:SN:109:ARG:NH2	2.41	0.52
25:LQ:212:VAL:HG22	25:LQ:217:LEU:HD12	1.91	0.52
26:LR:334:ALA:HB2	26:LR:381:VAL:HG11	1.91	0.52
32:LX:862:LEU:HD22	32:LX:920:MET:HE2	1.91	0.52
55:SK:43:VAL:HG11	55:SK:99:LEU:HD11	1.90	0.52
59:SP:1738:TYR:HE2	59:SP:1745:ILE:HG21	1.74	0.52
2:L1:953:G:OP1	39:NF:94:LYS:NZ	2.28	0.52
7:L6:7:TYR:CD2	7:L6:10:ASN:ND2	2.78	0.52
8:L7:166:LEU:HD12	62:SS:277:ARG:NH1	2.24	0.52
32:LX:94:PHE:CE2	32:LX:98:ILE:HD11	2.44	0.52
59:SP:366:ILE:O	59:SP:407:ARG:NE	2.41	0.52
60:SQ:120:ASP:CG	60:SQ:173:ILE:HD13	2.33	0.52
2:L1:1656:U:OP1	25:LQ:432:TYR:OH	2.20	0.52
25:LQ:127:LEU:HD11	25:LQ:136:LEU:CG	2.38	0.52
26:LR:249:LEU:HD21	26:LR:316:VAL:HG11	1.90	0.52
28:LT:232:MET:HE1	28:LT:264:LEU:HD22	1.90	0.52
28:LT:775:GLU:OE1	28:LT:775:GLU:N	2.42	0.52
29:LU:231:GLU:OE1	62:SS:298:TRP:NE1	2.38	0.52
41:NH:1150:VAL:HG21	41:NH:1165:SER:HB3	1.91	0.52
44:NM:172:LEU:O	44:NM:176:VAL:HG22	2.10	0.52
57:SM:26:GLN:OE1	57:SM:29:ARG:NH1	2.41	0.52
58:SN:94:SER:OG	58:SN:95:GLU:OE1	2.28	0.52
59:SP:670:LEU:HD12	59:SP:681:VAL:HG11	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LU:215:LEU:O	29:LU:216:SER:OG	2.26	0.52
30:LV:364:GLU:OE1	30:LV:366:LYS:N	2.43	0.52
53:SH:339:LEU:HB3	53:SH:350:MET:HE2	1.91	0.52
63:ST:576:ILE:O	63:ST:576:ILE:HG22	2.09	0.52
16:LH:282:ILE:HD13	16:LH:293:LEU:HD13	1.92	0.52
16:LH:498:LEU:HD11	16:LH:507:MET:HE3	1.92	0.52
18:LJ:319:VAL:HG22	18:LJ:329:ILE:HD12	1.91	0.52
25:LQ:502:PHE:CE1	25:LQ:522:LEU:HD21	2.45	0.52
26:LR:12:LEU:HD11	26:LR:378:PRO:HG2	1.92	0.52
26:LR:601:ILE:HD12	26:LR:611:LYS:HB3	1.91	0.52
32:LY:538:MET:HE2	32:LY:553:LEU:HD13	1.92	0.52
34:NA:340:LEU:HD21	54:SI:961:PHE:CE1	2.45	0.52
59:SP:910:SER:OG	59:SP:911:GLN:OE1	2.27	0.52
2:L1:552:G:OP1	54:SI:1140:LYS:NZ	2.25	0.52
7:L6:142:ARG:O	7:L6:146:GLY:N	2.43	0.52
16:LH:341:ILE:HG21	16:LH:344:CYS:SG	2.50	0.52
24:LP:23:LEU:CD2	24:LP:75:LEU:HD23	2.40	0.52
25:LQ:676:SER:OG	25:LQ:677:HIS:N	2.41	0.52
26:LR:85:LEU:HD23	26:LR:86:LYS:N	2.25	0.52
48:SA:223:ILE:HG23	48:SA:223:ILE:O	2.09	0.52
10:L9:26:ALA:HB2	56:SL:55:TYR:CD1	2.45	0.52
18:LJ:447:LEU:O	18:LJ:490:LYS:NZ	2.36	0.52
25:LQ:850:LEU:HD21	25:LQ:891:LEU:HD22	1.92	0.52
26:LR:174:VAL:HG23	26:LR:174:VAL:O	2.10	0.52
26:LR:666:GLU:CD	26:LR:690:HIS:HE2	2.18	0.52
32:LX:527:HIS:HB3	54:SI:416:LEU:HD11	1.92	0.52
2:L1:629:U:O3'	43:NK:259:LYS:NZ	2.42	0.52
2:L1:867:G:N2	39:NF:87:ASP:OD1	2.42	0.52
6:L5:90:ILE:O	6:L5:94:THR:HG23	2.09	0.52
16:LH:656:ASP:OD2	16:LH:676:THR:OG1	2.27	0.52
25:LQ:449:THR:O	25:LQ:476:ILE:HG22	2.08	0.52
28:LT:738:ASP:OD1	28:LT:739:VAL:N	2.43	0.52
32:LX:187:ARG:NH1	32:LX:489:LEU:O	2.41	0.52
32:LY:244:VAL:O	32:LY:248:GLY:N	2.42	0.52
34:NA:473:THR:OG1	34:NA:487:ALA:O	2.05	0.52
35:NB:390:MET:HE3	35:NB:391:PRO:HD2	1.91	0.52
53:SH:111:LYS:NZ	54:SI:923:ASP:OD2	2.37	0.52
55:SK:180:LEU:CD1	55:SK:227:LEU:HD23	2.39	0.52
59:SP:536:ASN:OD1	59:SP:537:LEU:N	2.42	0.52
1:L0:65:U:OP2	16:LH:418:ASN:ND2	2.43	0.51
2:L1:1461:C:OP2	63:ST:746:LYS:NZ	2.31	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L2:60:A:N7	23:LO:563:ARG:NH2	2.58	0.51
20:LL:116:GLN:OE1	20:LL:128:GLN:NE2	2.43	0.51
22:LN:69:ILE:HD12	22:LN:79:TRP:CD1	2.45	0.51
27:LS:264:LEU:HD11	27:LS:272:LEU:HD22	1.92	0.51
32:LX:529:VAL:HG13	32:LX:579:ILE:HD12	1.91	0.51
54:SI:91:ARG:O	54:SI:95:LYS:N	2.40	0.51
59:SP:939:SER:OG	59:SP:942:LYS:NZ	2.33	0.51
59:SP:1202:LEU:HD22	59:SP:1220:LEU:HD13	1.92	0.51
64:SU:24:TYR:HD1	64:SU:27:ILE:HD11	1.75	0.51
2:L1:802:G:OP1	59:SP:1685:SER:OG	2.17	0.51
20:LL:112:LEU:HD13	20:LL:117:LEU:HD13	1.91	0.51
26:LR:265:ALA:HB2	26:LR:288:LEU:HD22	1.90	0.51
26:LR:626:MET:HE3	26:LR:627:ASN:OD1	2.10	0.51
28:LT:565:LEU:HD22	28:LT:586:ASN:O	2.10	0.51
44:NM:138:PHE:O	44:NM:213:ARG:N	2.43	0.51
62:SS:319:THR:O	62:SS:319:THR:HG23	2.10	0.51
64:SU:381:LYS:NZ	64:SU:462:SER:O	2.43	0.51
18:LJ:277:LEU:HD12	18:LJ:301:PRO:HB2	1.92	0.51
22:LN:285:CYS:O	22:LN:286:LEU:HD22	2.10	0.51
23:LO:814:LYS:NZ	28:LT:936:VAL:O	2.38	0.51
25:LQ:175:ASP:OD1	25:LQ:192:LYS:NZ	2.25	0.51
26:LR:365:ILE:HG22	26:LR:381:VAL:HG12	1.92	0.51
26:LR:579:GLN:O	26:LR:580:ARG:NH1	2.37	0.51
44:NM:51:SER:HG	44:NM:57:ALA:H	1.58	0.51
54:SI:247:ASP:N	54:SI:272:TYR:O	2.35	0.51
1:L0:484:G:O6	62:SS:876:GLN:NE2	2.43	0.51
2:L1:321:C:N4	30:LV:135:THR:OG1	2.43	0.51
20:LL:123:SER:O	20:LL:141:ARG:NH1	2.42	0.51
26:LR:220:ILE:HD12	26:LR:239:VAL:HG11	1.91	0.51
28:LT:44:LEU:HD21	28:LT:49:TYR:HE2	1.75	0.51
31:LW:202:HIS:HB3	31:LW:204:LEU:HD13	1.91	0.51
59:SP:1131:THR:HG23	59:SP:1134:MET:HE2	1.91	0.51
1:L0:268:G:N2	67:SY:90:SER:OG	2.44	0.51
24:LP:271:LEU:HD11	24:LP:334:LEU:HD23	1.93	0.51
26:LR:334:ALA:CB	26:LR:381:VAL:HG11	2.41	0.51
30:LV:319:ASP:OD1	30:LV:320:ILE:N	2.44	0.51
32:LY:349:ASP:OD1	32:LY:350:PHE:N	2.43	0.51
41:NH:209:MET:HE3	41:NH:214:PHE:CZ	2.46	0.51
59:SP:1621:LEU:O	59:SP:1621:LEU:HD23	2.09	0.51
67:SY:73:ASP:OD1	67:SY:74:ALA:N	2.41	0.51
16:LH:875:MET:HE2	16:LH:875:MET:HA	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:LJ:467:LEU:HD21	18:LJ:484:MET:SD	2.50	0.51
20:LL:203:ILE:HG21	20:LL:235:LEU:HD21	1.93	0.51
21:LM:132:THR:OG1	21:LM:155:ILE:HD11	2.11	0.51
27:LS:148:THR:OG1	27:LS:163:ARG:NH2	2.44	0.51
28:LT:717:ASP:OD1	28:LT:718:LYS:N	2.44	0.51
29:LU:196:THR:HG23	29:LU:204:TRP:CD1	2.45	0.51
30:LV:274:ILE:HG21	30:LV:277:ILE:HD11	1.93	0.51
41:NH:901:ASN:ND2	44:NM:131:ASP:OD1	2.44	0.51
49:SB:12:TYR:CE2	49:SB:72:LEU:HD13	2.46	0.51
52:SG:304:ILE:CD1	52:SG:338:THR:HG21	2.39	0.51
55:SJ:252:LEU:HD21	55:SK:186:VAL:HG11	1.91	0.51
66:SW:196:ASP:OD1	66:SW:197:HIS:N	2.44	0.51
5:L4:62:LYS:HG3	5:L4:66:MET:HE3	1.93	0.51
8:L7:17:GLU:CG	8:L7:46:ILE:HG22	2.40	0.51
20:LL:5:VAL:HG23	20:LL:306:LEU:HD11	1.92	0.51
40:NG:37:GLU:OE1	44:NM:64:ARG:NH2	2.44	0.51
59:SP:1597:ILE:O	59:SP:1609:ARG:NH1	2.44	0.51
59:SP:1685:SER:OG	59:SP:1745:ILE:HD11	2.11	0.51
2:L1:320:U:OP2	45:NN:459:SER:N	2.44	0.51
16:LH:21:ALA:C	16:LH:22:LEU:HD12	2.36	0.51
20:LL:163:LEU:CD1	20:LL:175:ILE:HD11	2.41	0.51
21:LM:272:LYS:NZ	21:LM:310:GLY:O	2.34	0.51
29:LU:196:THR:OG1	29:LU:204:TRP:NE1	2.40	0.51
54:SI:311:PRO:O	54:SI:314:GLN:N	2.43	0.51
54:SI:424:GLU:C	54:SI:425:LEU:HD12	2.36	0.51
55:SK:218:ASP:HA	55:SK:221:VAL:HG12	1.92	0.51
56:SL:170:ILE:HG23	56:SL:170:ILE:O	2.10	0.51
16:LH:627:ASP:OD1	16:LH:628:ASP:N	2.43	0.51
16:LH:744:ILE:HD11	17:LI:431:PHE:HZ	1.75	0.51
17:LI:614:ILE:CD1	17:LI:634:LEU:HD21	2.41	0.51
27:LS:511:LEU:CD1	27:LS:544:VAL:HG21	2.40	0.51
32:LX:565:PHE:CE1	32:LX:588:ILE:HD12	2.45	0.51
40:NG:30:VAL:HG11	40:NG:71:CYS:SG	2.51	0.51
41:NH:361:GLU:HA	41:NH:364:VAL:HG12	1.93	0.51
50:SC:122:ARG:NE	50:SC:140:GLU:OE1	2.44	0.51
55:SK:71:ASP:OD2	55:SK:72:ASP:N	2.44	0.51
65:SV:131:LEU:HD12	65:SV:132:GLU:OE1	2.11	0.51
6:L5:140:THR:OG1	6:L5:210:ALA:HB1	2.11	0.51
11:LC:97:VAL:HG12	11:LC:98:ASP:H	1.75	0.51
19:LK:496:LEU:O	19:LK:500:GLN:N	2.38	0.51
23:LO:473:GLU:OE2	57:SM:1:MET:HE3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:NH:1221:HIS:ND1	42:NI:20:LEU:HD13	2.25	0.51
43:NK:52:TYR:CE1	43:NK:56:ILE:HD13	2.46	0.51
48:SA:257:ILE:HG23	48:SA:257:ILE:O	2.12	0.51
49:SB:68:VAL:HG11	49:SB:101:LEU:HD11	1.91	0.51
1:L0:272:A:O2'	67:SY:228:GLY:O	2.26	0.50
2:L1:163:G:OP2	2:L1:163:G:N2	2.31	0.50
2:L1:1492:A:OP1	60:SQ:210:LYS:NZ	2.37	0.50
9:L8:192:TYR:O	9:L8:196:LEU:HD23	2.11	0.50
18:LJ:132:PHE:CE1	18:LJ:140:LEU:HD13	2.47	0.50
26:LR:44:ASP:OD1	26:LR:45:LEU:N	2.44	0.50
27:LS:554:ASN:OD1	27:LS:555:TRP:N	2.44	0.50
29:LU:73:ILE:HG23	29:LU:83:LEU:HD21	1.93	0.50
32:LY:4:LYS:N	38:NE:22:GLN:O	2.45	0.50
41:NH:982:PRO:O	44:NM:222:LYS:NZ	2.39	0.50
52:SG:288:PHE:HE1	52:SG:295:LEU:HD13	1.75	0.50
59:SP:1106:LEU:HD11	59:SP:1150:ILE:HD11	1.92	0.50
59:SP:1910:VAL:O	59:SP:1913:SER:OG	2.23	0.50
62:SS:430:ASP:OD1	62:SS:431:HIS:N	2.44	0.50
16:LH:856:GLU:OE2	21:LM:378:TYR:N	2.44	0.50
18:LJ:85:TYR:O	18:LJ:86:SER:OG	2.19	0.50
25:LQ:164:ASP:OD1	25:LQ:165:SER:N	2.39	0.50
28:LT:304:LEU:HD21	28:LT:311:VAL:HG23	1.93	0.50
28:LT:723:LEU:HD22	28:LT:879:GLU:HB3	1.93	0.50
59:SP:2113:ASP:OD1	59:SP:2115:ALA:N	2.38	0.50
63:ST:481:MET:HE3	63:ST:497:ASP:CG	2.37	0.50
23:LO:479:LEU:O	23:LO:480:SER:OG	2.27	0.50
23:LO:567:ASP:OD1	33:LZ:144:ASN:ND2	2.44	0.50
30:LV:357:ASP:O	30:LV:360:THR:HG23	2.11	0.50
32:LX:862:LEU:HD22	32:LX:920:MET:CE	2.42	0.50
50:SC:155:ILE:HD11	50:SC:162:LEU:HD21	1.94	0.50
52:SG:365:PRO:O	52:SG:369:LEU:HD13	2.12	0.50
59:SP:1603:ASP:O	59:SP:1606:ILE:HG22	2.11	0.50
33:LZ:62:SER:O	33:LZ:71:ARG:NH1	2.44	0.50
41:NH:1226:PHE:O	41:NH:1228:ASN:ND2	2.45	0.50
50:SC:306:LEU:HD11	50:SC:315:ILE:HD12	1.93	0.50
53:SH:314:ASN:OD1	53:SH:315:LYS:N	2.44	0.50
55:SJ:179:THR:HG22	55:SJ:205:PHE:HB2	1.93	0.50
7:L6:18:ILE:HD12	7:L6:23:ARG:HD2	1.92	0.50
14:LF:86:GLU:O	59:SP:13:ARG:NH2	2.42	0.50
18:LJ:140:LEU:O	18:LJ:152:TRP:N	2.43	0.50
23:LO:856:MET:H	23:LO:856:MET:HE2	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:LQ:426:ARG:NE	25:LQ:459:LEU:O	2.45	0.50
29:LU:303:ASP:OD2	29:LU:339:SER:N	2.33	0.50
32:LX:538:MET:HE1	32:LX:556:MET:HE1	1.94	0.50
32:LY:305:TYR:O	32:LY:365:GLN:NE2	2.43	0.50
34:NA:348:ASP:OD1	34:NA:349:ARG:N	2.45	0.50
37:ND:115:GLU:OE2	37:ND:115:GLU:N	2.43	0.50
55:SK:69:ASN:OD1	55:SK:70:CYS:N	2.45	0.50
17:LI:432:ASP:OD1	17:LI:433:ASP:N	2.44	0.50
20:LL:126:PHE:CE2	20:LL:165:VAL:HG11	2.46	0.50
21:LM:1743:GLU:O	21:LM:1746:ARG:N	2.44	0.50
23:LO:33:VAL:HG23	23:LO:33:VAL:O	2.12	0.50
25:LQ:897:ASP:OD2	26:LR:758:ARG:NH1	2.45	0.50
32:LX:234:LEU:HD21	32:LX:238:LYS:HE3	1.94	0.50
41:NH:577:ARG:NH1	41:NH:626:LYS:O	2.38	0.50
13:LE:105:THR:HG23	13:LE:105:THR:O	2.11	0.50
14:LF:92:VAL:HG11	14:LF:99:LYS:HE2	1.92	0.50
23:LO:285:ARG:NE	23:LO:297:GLN:OE1	2.43	0.50
25:LQ:446:ILE:CG1	25:LQ:454:LEU:HD21	2.41	0.50
38:NE:303:GLU:O	56:SL:112:LYS:NZ	2.44	0.50
41:NH:397:MET:HG3	41:NH:425:VAL:HG21	1.93	0.50
52:SG:288:PHE:CD1	52:SG:295:LEU:HD13	2.46	0.50
55:SJ:110:LEU:HD21	55:SJ:112:VAL:HG23	1.94	0.50
2:L1:1777:G:O2'	26:LR:136:ILE:HD11	2.12	0.50
3:L2:332:G:H21	16:LH:869:MET:CE	2.25	0.50
11:LC:29:ILE:CG2	11:LC:36:ILE:HD11	2.41	0.50
25:LQ:181:SER:OG	25:LQ:183:ASP:OD1	2.28	0.50
30:LV:277:ILE:HD12	30:LV:291:THR:HG22	1.92	0.50
49:SB:51:ASN:OD1	49:SB:52:SER:N	2.45	0.50
59:SP:375:THR:HG22	59:SP:411:PHE:HE1	1.77	0.50
2:L1:170:U:OP1	2:L1:267:U:O2'	2.30	0.50
2:L1:913:G:OP2	44:NM:17:LYS:NZ	2.45	0.50
26:LR:115:THR:OG1	26:LR:132:GLU:OE1	2.24	0.50
30:LV:222:ASN:ND2	30:LV:225:ASP:O	2.44	0.50
32:LY:385:VAL:HG23	32:LY:385:VAL:O	2.11	0.50
48:SA:213:ASN:OD1	48:SA:214:TYR:N	2.44	0.50
59:SP:1755:GLU:OE1	59:SP:1799:GLY:N	2.45	0.50
64:SU:121:ASP:O	64:SU:124:LEU:N	2.44	0.50
2:L1:630:A:N6	2:L1:969:C:O2'	2.45	0.49
11:LC:107:LYS:HE2	11:LC:107:LYS:HA	1.94	0.49
23:LO:706:THR:O	23:LO:709:THR:HG23	2.12	0.49
25:LQ:125:THR:O	25:LQ:126:LEU:HD12	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:LR:539:VAL:CG2	26:LR:548:LEU:HD11	2.42	0.49
28:LT:203:ASN:OD1	28:LT:204:GLU:N	2.45	0.49
29:LU:326:ASP:OD1	29:LU:328:SER:OG	2.20	0.49
31:LW:333:SER:CB	31:LW:381:LEU:HD11	2.42	0.49
32:LX:356:ARG:NH1	32:LY:379:GLY:O	2.45	0.49
32:LY:731:GLN:NE2	32:LY:800:GLN:OE1	2.43	0.49
38:NE:308:ILE:HG22	38:NE:308:ILE:O	2.11	0.49
42:NI:62:SER:O	42:NI:90:ASN:ND2	2.46	0.49
63:ST:6:LEU:HD21	63:ST:10:LYS:HE2	1.94	0.49
63:ST:388:LEU:O	63:ST:392:LYS:N	2.45	0.49
24:LP:391:TYR:CZ	24:LP:395:ILE:HD11	2.47	0.49
32:LX:427:ILE:HG23	32:LX:465:LEU:HD22	1.94	0.49
34:NA:515:MET:SD	34:NA:520:LEU:HD21	2.52	0.49
67:SY:215:GLN:NE2	67:SY:219:ASP:OD2	2.45	0.49
2:L1:628:G:N2	2:L1:629:U:O4	2.46	0.49
20:LL:80:MET:HE2	20:LL:86:TRP:CZ3	2.47	0.49
21:LM:165:SER:O	21:LM:168:VAL:HG12	2.11	0.49
24:LP:178:VAL:O	24:LP:178:VAL:HG13	2.12	0.49
24:LP:391:TYR:CE2	24:LP:395:ILE:HD11	2.47	0.49
29:LU:248:ASP:O	29:LU:252:ASN:N	2.44	0.49
39:NF:62:GLN:HB2	39:NF:65:VAL:HG12	1.94	0.49
41:NH:796:ILE:H	42:NI:104:THR:HG21	1.76	0.49
52:SG:156:ASN:ND2	52:SG:546:GLU:OE2	2.43	0.49
53:SH:47:ASP:OD1	53:SH:48:TYR:N	2.46	0.49
57:SM:278:ARG:HB2	57:SM:281:ILE:HD12	1.94	0.49
59:SP:1655:ARG:HE	59:SP:1693:THR:HG22	1.77	0.49
2:L1:493:U:H4'	54:SI:1142:LEU:HD11	1.94	0.49
32:LX:864:LEU:O	32:LX:864:LEU:HD23	2.12	0.49
52:SG:157:LEU:HD11	52:SG:189:THR:HB	1.95	0.49
52:SG:234:GLY:O	52:SG:259:LYS:NZ	2.45	0.49
59:SP:897:PHE:CE2	59:SP:901:ILE:HD11	2.47	0.49
59:SP:1181:ILE:O	59:SP:1181:ILE:HG22	2.12	0.49
59:SP:1265:TYR:HA	59:SP:1268:ILE:HG22	1.94	0.49
59:SP:1675:LYS:HB3	59:SP:1716:MET:HE1	1.94	0.49
59:SP:2104:LEU:HD11	62:SS:263:LEU:HD21	1.94	0.49
63:ST:701:ALA:HB1	64:SU:422:ILE:HD11	1.93	0.49
32:LX:39:ASN:CG	54:SI:373:ILE:HD11	2.38	0.49
63:ST:536:SER:O	63:ST:539:ARG:N	2.46	0.49
2:L1:158:U:OP1	32:LX:72:LYS:NZ	2.41	0.49
5:L4:65:LEU:HD22	5:L4:70:VAL:HG21	1.94	0.49
8:L7:63:PRO:O	8:L7:67:LEU:N	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LH:722:LEU:HD13	16:LH:743:ILE:CD1	2.43	0.49
16:LH:725:ASN:ND2	17:LI:441:VAL:HG21	2.27	0.49
20:LL:248:THR:OG1	20:LL:252:SER:O	2.25	0.49
23:LO:369:ILE:HG21	23:LO:402:MET:CE	2.42	0.49
49:SB:287:LEU:HD22	49:SB:371:LEU:HD13	1.93	0.49
3:L2:23:U:OP2	33:LZ:14:LYS:NZ	2.46	0.49
5:L4:181:VAL:HG21	5:L4:210:ILE:HD12	1.94	0.49
23:LO:709:THR:OG1	23:LO:748:GLU:OE2	2.29	0.49
25:LQ:619:MET:HE2	25:LQ:661:TRP:CE3	2.46	0.49
28:LT:632:VAL:HG22	28:LT:643:THR:HG22	1.95	0.49
48:SA:180:LEU:HD23	48:SA:288:LEU:HD22	1.94	0.49
49:SB:1:MET:HE3	49:SB:17:ALA:O	2.12	0.49
49:SB:131:MET:HE1	49:SB:139:MET:HE3	1.93	0.49
64:SU:120:LEU:HD22	64:SU:176:ILE:HG13	1.94	0.49
1:L0:309:A:H61	49:SB:431:ALA:HB3	1.77	0.49
16:LH:313:LEU:HD23	16:LH:321:MET:CE	2.43	0.49
16:LH:817:SER:O	16:LH:821:ILE:HD12	2.12	0.49
26:LR:625:THR:HG22	26:LR:632:ILE:CD1	2.42	0.49
26:LR:686:MET:HE2	26:LR:738:LEU:HD23	1.95	0.49
32:LX:140:GLU:O	32:LX:475:ARG:NH1	2.46	0.49
32:LX:487:ASN:O	32:LX:491:CYS:N	2.43	0.49
35:NB:395:ASP:OD2	35:NB:395:ASP:N	2.46	0.49
59:SP:474:ASN:OD1	59:SP:716:TYR:OH	2.30	0.49
59:SP:1586:ILE:HG21	59:SP:1623:LEU:HD21	1.93	0.49
3:L2:60:A:C4	23:LO:635:MET:HE1	2.47	0.49
11:LC:118:ILE:HD11	23:LO:515:TYR:CD1	2.48	0.49
15:LG:14:LYS:HZ3	25:LQ:822:MET:HE3	1.77	0.49
22:LN:39:VAL:HG22	22:LN:402:TRP:HZ3	1.77	0.49
30:LV:131:LEU:HD11	30:LV:134:THR:HG23	1.95	0.49
32:LX:789:LEU:HD22	32:LX:891:GLN:NE2	2.28	0.49
32:LY:579:ILE:HG23	32:LY:579:ILE:O	2.13	0.49
32:LY:748:ARG:NH2	32:LY:750:THR:OG1	2.46	0.49
40:NG:31:THR:OG1	40:NG:37:GLU:O	2.17	0.49
41:NH:282:ASP:OD1	41:NH:283:TYR:N	2.46	0.49
41:NH:1189:LEU:HD21	41:NH:1194:HIS:CE1	2.47	0.49
49:SB:215:ARG:NH1	49:SB:244:GLY:O	2.43	0.49
52:SG:296:TYR:HD1	52:SG:306:THR:HG22	1.78	0.49
55:SJ:141:MET:CE	55:SJ:144:LEU:HD23	2.43	0.49
59:SP:140:ILE:HD11	59:SP:188:LEU:HD11	1.95	0.49
59:SP:1158:ILE:HD12	59:SP:1201:LEU:HD21	1.95	0.49
59:SP:1534:LEU:HD11	59:SP:1548:ILE:CD1	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:SP:1563:ARG:NH2	59:SP:1622:GLY:O	2.41	0.49
62:SS:363:LEU:HD11	62:SS:379:GLU:OE2	2.12	0.49
14:LF:86:GLU:O	59:SP:13:ARG:NH1	2.43	0.49
23:LO:295:ILE:HG22	23:LO:296:GLN:HG3	1.94	0.49
25:LQ:281:ILE:HD11	25:LQ:338:ILE:HD12	1.95	0.49
41:NH:254:LEU:HD12	41:NH:268:LEU:HD21	1.95	0.49
50:SC:91:HIS:CD2	50:SC:98:ILE:HD11	2.48	0.49
50:SC:319:ARG:HD2	50:SC:321:MET:HE2	1.95	0.49
59:SP:601:LEU:HD21	59:SP:619:LEU:O	2.13	0.49
17:LI:611:ILE:CG2	17:LI:658:LEU:HD21	2.43	0.48
21:LM:193:THR:OG1	21:LM:241:ILE:HD11	2.13	0.48
26:LR:340:ILE:CD1	26:LR:357:THR:HG22	2.43	0.48
29:LU:228:ASN:OD1	29:LU:229:GLN:N	2.45	0.48
30:LV:190:GLU:C	45:NN:484:LYS:HZ1	2.19	0.48
37:ND:120:ILE:O	37:ND:124:ASP:N	2.44	0.48
57:SM:219:GLU:HG3	63:ST:6:LEU:HD13	1.95	0.48
59:SP:1267:THR:O	59:SP:1271:LEU:HD12	2.13	0.48
59:SP:2030:ASN:OD1	59:SP:2031:HIS:N	2.46	0.48
20:LL:246:VAL:O	20:LL:253:LEU:HD12	2.13	0.48
21:LM:218:ILE:HD12	21:LM:263:VAL:HG21	1.95	0.48
41:NH:802:ALA:HB2	42:NI:188:MET:HE1	1.95	0.48
53:SH:302:VAL:HG21	53:SH:329:ILE:HG12	1.95	0.48
55:SJ:90:ASP:OD1	55:SJ:91:ILE:N	2.46	0.48
55:SK:173:THR:OG1	55:SK:174:LYS:N	2.46	0.48
62:SS:331:GLN:O	62:SS:331:GLN:NE2	2.37	0.48
64:SU:304:ASN:OD1	64:SU:334:TYR:OH	2.15	0.48
3:L2:11:U:OP1	54:SI:1154:LYS:NZ	2.36	0.48
6:L5:136:ALA:O	6:L5:140:THR:HG22	2.13	0.48
23:LO:297:GLN:C	23:LO:298:LEU:HD22	2.38	0.48
25:LQ:444:LEU:HD23	25:LQ:458:ASP:HA	1.94	0.48
27:LS:379:GLY:N	27:LS:383:TRP:O	2.44	0.48
28:LT:593:PHE:CZ	28:LT:600:ILE:HD11	2.49	0.48
30:LV:330:PHE:HD1	30:LV:340:THR:HG22	1.78	0.48
32:LY:487:ASN:O	32:LY:491:CYS:N	2.46	0.48
59:SP:1085:VAL:HG23	59:SP:1086:VAL:HG23	1.95	0.48
59:SP:1606:ILE:HG21	59:SP:1650:LEU:HD11	1.95	0.48
63:ST:385:ASP:OD1	63:ST:386:ALA:N	2.46	0.48
11:LC:103:ASN:ND2	23:LO:554:ASP:OD2	2.46	0.48
20:LL:58:LEU:HD13	20:LL:82:ASN:OD1	2.14	0.48
32:LX:162:TYR:CE1	32:LX:166:MET:HE3	2.49	0.48
32:LX:858:MET:HA	32:LX:858:MET:HE2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:SD:263:ASP:OD1	50:SD:264:GLN:N	2.47	0.48
56:SL:98:ILE:CD1	56:SL:125:ILE:HG21	2.43	0.48
57:SM:237:VAL:HB	63:ST:6:LEU:HD12	1.96	0.48
59:SP:1553:VAL:HB	59:SP:1554:PRO:HD3	1.95	0.48
2:L1:512:A:OP1	10:L9:170:GLY:N	2.41	0.48
7:L6:67:VAL:HG21	7:L6:73:ILE:CD1	2.43	0.48
8:L7:49:ILE:HD11	8:L7:172:VAL:HG22	1.94	0.48
12:LD:21:ASN:O	12:LD:21:ASN:ND2	2.47	0.48
16:LH:414:ILE:H	16:LH:414:ILE:HD12	1.79	0.48
24:LP:278:MET:SD	24:LP:312:LEU:HD22	2.53	0.48
25:LQ:220:THR:CG2	25:LQ:259:ILE:HD11	2.41	0.48
26:LR:85:LEU:HD12	26:LR:119:VAL:HG21	1.96	0.48
27:LS:497:ASN:OD1	27:LS:498:ASN:N	2.47	0.48
29:LU:83:LEU:HD23	29:LU:84:ALA:N	2.29	0.48
31:LW:197:ASP:HB3	31:LW:247:MET:HE1	1.96	0.48
32:LY:895:ILE:HD11	32:LY:909:THR:HG22	1.95	0.48
33:LZ:148:TYR:OH	33:LZ:154:MET:HE1	2.14	0.48
41:NH:264:LEU:HD11	41:NH:556:ILE:HG21	1.95	0.48
41:NH:1037:LEU:HD12	41:NH:1050:ILE:HG13	1.94	0.48
59:SP:47:PHE:CE1	59:SP:74:VAL:HG11	2.49	0.48
59:SP:323:PHE:O	59:SP:326:SER:N	2.37	0.48
59:SP:796:ILE:HD11	59:SP:831:PHE:CE2	2.48	0.48
63:ST:383:THR:OG1	63:ST:385:ASP:OD1	2.25	0.48
2:L1:0:U:OP2	29:LU:438:LYS:NZ	2.46	0.48
6:L5:120:ILE:HD12	18:LJ:117:LEU:HD22	1.95	0.48
11:LC:118:ILE:HD11	23:LO:515:TYR:CE1	2.49	0.48
18:LJ:173:THR:O	18:LJ:174:LEU:HD12	2.14	0.48
23:LO:298:LEU:HD21	28:LT:750:PRO:HB3	1.95	0.48
25:LQ:912:TRP:CG	26:LR:779:VAL:HG21	2.49	0.48
53:SH:199:ARG:NE	53:SH:235:SER:OG	2.47	0.48
55:SK:41:MET:HE1	55:SK:242:CYS:HA	1.94	0.48
57:SM:7:ARG:NH2	57:SM:11:GLU:OE2	2.46	0.48
59:SP:1765:GLU:OE2	59:SP:1768:THR:OG1	2.32	0.48
59:SP:1916:ARG:NH1	59:SP:1958:MET:HE1	2.29	0.48
8:L7:46:ILE:HD13	8:L7:60:ILE:HG12	1.96	0.48
12:LD:22:ASN:ND2	12:LD:25:VAL:HG23	2.29	0.48
16:LH:726:GLN:O	17:LI:441:VAL:HG23	2.13	0.48
25:LQ:114:LEU:C	25:LQ:115:LEU:HD22	2.39	0.48
28:LT:621:ASP:OD1	28:LT:622:GLY:N	2.47	0.48
58:SN:194:ASP:OD1	58:SN:195:ASN:N	2.46	0.48
59:SP:121:PHE:HD2	59:SP:162:LEU:HD11	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L1:143:G:OP1	7:L6:143:LYS:NZ	2.47	0.48
6:L5:112:ARG:HG2	11:LC:43:ILE:HD12	1.95	0.48
11:LC:28:LEU:HD21	11:LC:30:LYS:HE2	1.96	0.48
16:LH:33:ASN:CG	16:LH:357:ILE:HD11	2.38	0.48
16:LH:872:PHE:HB2	21:LM:219:ASN:ND2	2.29	0.48
23:LO:10:LEU:HD13	23:LO:702:LEU:HD23	1.94	0.48
29:LU:448:ARG:HD2	29:LU:451:MET:HE3	1.95	0.48
41:NH:178:TYR:O	41:NH:179:LYS:HE2	2.14	0.48
54:SI:89:LEU:HD21	54:SI:223:LEU:HD23	1.96	0.48
60:SQ:199:THR:HG22	60:SQ:199:THR:O	2.13	0.48
16:LH:112:ASN:OD1	16:LH:113:ASN:N	2.47	0.48
17:LI:505:LYS:O	17:LI:509:LEU:HD23	2.14	0.48
21:LM:778:SER:O	21:LM:782:VAL:N	2.47	0.48
25:LQ:127:LEU:HD11	25:LQ:136:LEU:HG	1.96	0.48
28:LT:192:ASN:O	28:LT:196:GLY:N	2.44	0.48
30:LV:62:ILE:HD11	30:LV:71:CYS:SG	2.54	0.48
49:SB:33:ASP:O	49:SB:123:TYR:OH	2.26	0.48
49:SB:152:LEU:HD22	50:SD:205:ARG:HG3	1.96	0.48
50:SC:117:VAL:HG22	50:SC:142:ARG:HH21	1.79	0.48
64:SU:24:TYR:CE1	64:SU:66:LEU:HD21	2.48	0.48
64:SU:42:GLN:NE2	64:SU:45:GLU:OE2	2.47	0.48
1:L0:156:U:O2'	1:L0:157:U:O4'	2.32	0.48
19:LK:433:ILE:HG22	19:LK:437:ILE:HD12	1.96	0.48
20:LL:80:MET:HE2	20:LL:86:TRP:CE3	2.49	0.48
22:LN:69:ILE:HD12	22:LN:79:TRP:NE1	2.29	0.48
32:LX:111:SER:OG	32:LX:137:ARG:NH1	2.42	0.48
32:LY:342:ILE:HG22	32:LY:344:GLN:OE1	2.14	0.48
41:NH:392:GLU:OE1	41:NH:392:GLU:N	2.44	0.48
59:SP:882:ASN:OD1	59:SP:885:ARG:NH2	2.46	0.48
62:SS:792:GLY:O	66:SW:129:ARG:NH1	2.47	0.48
64:SU:235:ASP:C	64:SU:236:LEU:HD22	2.39	0.48
65:SV:132:GLU:O	65:SV:136:ARG:NH2	2.47	0.48
2:L1:522:U:OP1	14:LF:37:LYS:NZ	2.45	0.47
18:LJ:432:TYR:O	18:LJ:470:TYR:OH	2.32	0.47
23:LO:391:THR:HG21	23:LO:434:ASN:OD1	2.14	0.47
26:LR:160:ILE:O	26:LR:160:ILE:HG22	2.13	0.47
41:NH:195:ILE:HG21	41:NH:364:VAL:HG23	1.96	0.47
41:NH:863:TYR:O	41:NH:866:ALA:N	2.46	0.47
54:SI:98:LEU:HD11	54:SI:354:ILE:HD11	1.95	0.47
59:SP:517:ASP:OD1	59:SP:765:ARG:NH1	2.45	0.47
6:L5:100:ASN:O	6:L5:102:ARG:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LI:603:SER:OG	17:LI:606:ASP:OD2	2.31	0.47
17:LI:668:ILE:HD11	19:LK:448:GLU:OE1	2.15	0.47
24:LP:175:ASN:O	24:LP:178:VAL:HG12	2.13	0.47
30:LV:160:ASN:OD1	30:LV:161:GLU:N	2.46	0.47
59:SP:2104:LEU:HD11	62:SS:263:LEU:CD2	2.44	0.47
11:LC:28:LEU:O	11:LC:28:LEU:HD23	2.14	0.47
25:LQ:616:ASP:OD1	25:LQ:617:SER:N	2.41	0.47
26:LR:395:ASP:OD2	26:LR:442:LEU:N	2.47	0.47
26:LR:603:ASP:O	26:LR:607:GLY:N	2.42	0.47
29:LU:26:ARG:NH1	31:LW:412:ASP:OD1	2.47	0.47
55:SK:49:SER:C	55:SK:50:LEU:HD12	2.39	0.47
63:ST:6:LEU:C	63:ST:6:LEU:HD23	2.39	0.47
2:L1:327:U:O2'	12:LD:10:GLU:OE1	2.30	0.47
6:L5:162:VAL:HG13	6:L5:166:ARG:HD2	1.95	0.47
9:L8:58:LEU:HD11	30:LV:77:TYR:HB3	1.96	0.47
26:LR:163:LEU:N	26:LR:175:TRP:O	2.42	0.47
27:LS:307:GLN:O	27:LS:310:GLN:NE2	2.45	0.47
30:LV:103:ASP:OD1	30:LV:104:PHE:N	2.46	0.47
31:LW:202:HIS:O	31:LW:204:LEU:HD12	2.13	0.47
32:LY:850:LEU:HD22	32:LY:854:VAL:HG11	1.95	0.47
41:NH:380:SER:OG	41:NH:386:GLY:O	2.31	0.47
41:NH:1204:VAL:HG21	41:NH:1212:VAL:HG21	1.96	0.47
51:SE:52:ILE:HD12	51:SE:71:CYS:SG	2.55	0.47
55:SJ:142:VAL:O	55:SJ:146:HIS:ND1	2.36	0.47
59:SP:984:ILE:CG2	59:SP:1032:MET:HE1	2.41	0.47
59:SP:1027:ILE:CG2	59:SP:1085:VAL:HG21	2.43	0.47
59:SP:1578:ASN:OD1	59:SP:1579:LEU:N	2.47	0.47
59:SP:1609:ARG:HB3	59:SP:1612:ILE:HD12	1.96	0.47
63:ST:611:SER:OG	63:ST:613:ILE:HG22	2.15	0.47
14:LF:45:ALA:HB1	14:LF:50:ALA:O	2.15	0.47
15:LG:15:VAL:O	15:LG:15:VAL:HG23	2.14	0.47
16:LH:265:ASP:OD1	16:LH:266:ASN:N	2.47	0.47
41:NH:144:LYS:O	41:NH:176:PHE:N	2.42	0.47
43:NK:103:LEU:HD13	43:NK:174:MET:CE	2.44	0.47
55:SK:77:LEU:HA	55:SK:80:MET:HE2	1.95	0.47
58:SN:204:ILE:HG22	58:SN:205:GLN:CD	2.39	0.47
16:LH:664:LEU:HD12	16:LH:664:LEU:O	2.15	0.47
26:LR:105:SER:OG	26:LR:120:GLY:O	2.32	0.47
31:LW:534:LYS:HE2	31:LW:534:LYS:HA	1.96	0.47
63:ST:540:ILE:CD1	63:ST:571:ILE:HG23	2.43	0.47
64:SU:390:SER:OG	64:SU:394:ALA:HB3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L5:124:LEU:HA	18:LJ:154:ILE:HD12	1.94	0.47
7:L6:59:GLN:OE1	7:L6:59:GLN:N	2.48	0.47
8:L7:118:LEU:O	8:L7:122:HIS:ND1	2.48	0.47
10:L9:171:ARG:HG3	10:L9:172:VAL:N	2.27	0.47
14:LF:72:PHE:CE2	14:LF:74:LEU:HD21	2.50	0.47
19:LK:401:GLU:OE1	19:LK:401:GLU:N	2.48	0.47
20:LL:175:ILE:H	20:LL:175:ILE:HD12	1.80	0.47
22:LN:44:ALA:HB3	22:LN:71:ARG:HB3	1.97	0.47
22:LN:61:THR:HG21	22:LN:681:ILE:HD13	1.95	0.47
23:LO:439:ASP:OD1	23:LO:441:SER:N	2.37	0.47
25:LQ:197:ILE:O	26:LR:671:ASN:ND2	2.43	0.47
25:LQ:573:LYS:N	25:LQ:594:ASP:OD2	2.47	0.47
26:LR:72:ASP:OD1	26:LR:73:GLY:N	2.48	0.47
28:LT:41:THR:HG21	28:LT:302:THR:HG21	1.97	0.47
28:LT:859:ASP:OD1	28:LT:860:GLU:N	2.48	0.47
35:NB:390:MET:HE3	35:NB:391:PRO:CD	2.45	0.47
41:NH:627:LEU:HB2	44:NM:240:LYS:NZ	2.30	0.47
48:SA:26:ASP:OD1	48:SA:27:ILE:N	2.48	0.47
50:SC:153:ALA:HB3	50:SC:306:LEU:HD12	1.97	0.47
55:SK:156:GLU:OE1	55:SK:156:GLU:N	2.48	0.47
55:SK:179:THR:HG22	55:SK:205:PHE:HB2	1.96	0.47
59:SP:1147:ILE:HD11	59:SP:1188:LYS:HE3	1.96	0.47
59:SP:1281:ARG:NH2	59:SP:1309:ASN:OD1	2.48	0.47
59:SP:1502:ASN:OD1	59:SP:1503:ILE:N	2.48	0.47
59:SP:2066:ASP:OD2	62:SS:268:SER:N	2.42	0.47
63:ST:614:ILE:HG23	63:ST:614:ILE:O	2.14	0.47
66:SW:106:MET:HA	66:SW:106:MET:HE3	1.96	0.47
6:L5:163:SER:OG	15:LG:47:PRO:O	2.28	0.47
12:LD:132:SER:O	12:LD:136:ARG:NH1	2.48	0.47
16:LH:724:ILE:HG21	16:LH:762:TYR:HD2	1.79	0.47
18:LJ:227:VAL:HG12	18:LJ:236:VAL:CG1	2.39	0.47
20:LL:93:ASN:O	20:LL:93:ASN:OD1	2.33	0.47
21:LM:88:LYS:O	21:LM:91:ILE:HG22	2.14	0.47
22:LN:563:LEU:HD21	22:LN:582:VAL:HG21	1.97	0.47
25:LQ:115:LEU:HD11	25:LQ:153:GLU:HG2	1.96	0.47
39:NF:140:LYS:NZ	39:NF:142:GLU:O	2.48	0.47
44:NM:97:LEU:CD1	44:NM:229:MET:HE1	2.45	0.47
59:SP:701:LEU:HD21	59:SP:795:ASP:HB3	1.95	0.47
59:SP:1612:ILE:HG22	59:SP:1616:LEU:HD23	1.97	0.47
62:SS:261:ASN:OD1	62:SS:262:LEU:N	2.47	0.47
63:ST:597:GLU:N	63:ST:597:GLU:OE1	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L1:747:C:O3'	13:LE:80:ASN:ND2	2.44	0.47
17:LI:236:LEU:N	17:LI:240:LYS:O	2.41	0.47
21:LM:17:THR:O	21:LM:84:ASN:ND2	2.45	0.47
22:LN:425:ASP:OD1	22:LN:426:GLN:N	2.48	0.47
25:LQ:809:LEU:HD22	25:LQ:856:ASN:ND2	2.30	0.47
30:LV:281:ASP:OD1	30:LV:282:ASN:N	2.48	0.47
48:SA:160:ARG:HD3	50:SC:208:ILE:HG21	1.97	0.47
48:SA:180:LEU:HD12	48:SA:184:LEU:HG	1.97	0.47
56:SL:83:VAL:HG21	56:SL:124:ARG:HE	1.80	0.47
59:SP:1354:PHE:CD1	59:SP:1363:LEU:HD22	2.49	0.47
59:SP:1922:ILE:CD1	59:SP:1965:ALA:HB1	2.45	0.47
2:L1:1498:G:P	58:SN:250:THR:HG22	2.55	0.47
4:L3:27:LYS:O	4:L3:31:ALA:N	2.44	0.47
16:LH:177:THR:OG1	16:LH:186:GLU:OE2	2.13	0.47
21:LM:329:THR:O	21:LM:333:LEU:HD13	2.14	0.47
23:LO:497:ILE:HD11	23:LO:532:VAL:HG11	1.97	0.47
23:LO:678:GLU:OE2	23:LO:678:GLU:N	2.44	0.47
23:LO:739:LEU:HA	23:LO:754:VAL:HG11	1.97	0.47
23:LO:773:ILE:HG23	23:LO:774:TYR:CD1	2.50	0.47
26:LR:666:GLU:OE2	26:LR:690:HIS:NE2	2.35	0.47
32:LX:169:HIS:CE1	54:SI:414:VAL:HG12	2.49	0.47
40:NG:21:ALA:HB2	40:NG:98:GLY:HA3	1.97	0.47
41:NH:173:ASN:OD1	41:NH:174:TYR:N	2.48	0.47
41:NH:1203:ASN:OD1	42:NI:57:ASN:ND2	2.43	0.47
52:SG:195:GLN:NE2	52:SG:197:THR:OG1	2.47	0.47
59:SP:1194:SER:O	59:SP:1197:THR:HG22	2.14	0.47
64:SU:98:PHE:CE2	64:SU:102:LEU:HD11	2.50	0.47
5:L4:103:TYR:O	5:L4:182:TYR:OH	2.33	0.46
16:LH:717:THR:HG23	16:LH:718:GLY:N	2.30	0.46
24:LP:286:ILE:CD1	24:LP:308:THR:HG21	2.45	0.46
25:LQ:107:ASP:O	25:LQ:111:LYS:N	2.49	0.46
25:LQ:454:LEU:HD23	25:LQ:455:GLN:N	2.30	0.46
32:LX:243:ASP:OD1	32:LX:244:VAL:HG23	2.15	0.46
35:NB:598:ILE:HD11	50:SC:98:ILE:HG23	1.96	0.46
49:SB:228:PRO:HD2	49:SB:231:ILE:HD13	1.97	0.46
57:SM:158:PRO:O	57:SM:159:HIS:ND1	2.48	0.46
59:SP:389:ILE:O	59:SP:393:PHE:N	2.48	0.46
62:SS:290:ILE:HD12	62:SS:440:MET:HB3	1.96	0.46
2:L1:40:A:H62	2:L1:467:G:H21	1.62	0.46
13:LE:55:ASP:O	13:LE:55:ASP:OD2	2.33	0.46
24:LP:199:ARG:O	24:LP:203:MET:N	2.42	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LS:345:LEU:HD21	27:LS:355:PHE:CZ	2.51	0.46
30:LV:58:ALA:HB3	30:LV:76:THR:CG2	2.43	0.46
32:LX:90:GLU:OE1	32:LX:90:GLU:N	2.49	0.46
32:LY:527:HIS:HB2	45:NN:530:ILE:HD11	1.98	0.46
41:NH:179:LYS:O	41:NH:231:TYR:OH	2.20	0.46
44:NM:82:ARG:HH21	44:NM:103:MET:HE2	1.80	0.46
49:SB:118:ARG:O	50:SD:236:MET:HE2	2.16	0.46
54:SI:127:ALA:O	54:SI:131:ILE:HD12	2.16	0.46
63:ST:702:LEU:HD13	64:SU:485:ALA:HA	1.97	0.46
2:L1:886:U:O2'	40:NG:121:VAL:O	2.33	0.46
16:LH:308:ASP:OD1	27:LS:367:GLN:NE2	2.49	0.46
19:LK:489:SER:O	19:LK:492:ILE:N	2.42	0.46
20:LL:46:TRP:NE1	20:LL:48:GLU:OE1	2.37	0.46
21:LM:1500:PHE:O	21:LM:1504:LEU:N	2.41	0.46
24:LP:368:THR:OG1	24:LP:372:ARG:NH2	2.46	0.46
25:LQ:617:SER:O	25:LQ:634:SER:OG	2.33	0.46
25:LQ:634:SER:OG	25:LQ:635:LYS:N	2.45	0.46
26:LR:40:ILE:HD11	26:LR:64:ILE:HG12	1.97	0.46
28:LT:868:LEU:HD12	28:LT:885:MET:HE2	1.96	0.46
32:LX:496:LEU:HD21	32:LX:540:LEU:HD22	1.97	0.46
32:LY:537:MET:HE1	32:LY:564:LEU:HD13	1.96	0.46
43:NK:259:LYS:HD3	43:NK:259:LYS:N	2.30	0.46
49:SB:39:LEU:HD23	49:SB:127:LEU:HD12	1.98	0.46
59:SP:663:LEU:HD23	59:SP:696:VAL:CG2	2.46	0.46
63:ST:484:ARG:NH1	63:ST:492:ALA:O	2.48	0.46
67:SY:167:THR:HG1	67:SY:170:GLN:CD	2.23	0.46
2:L1:57:G:OP1	14:LF:112:LYS:NZ	2.35	0.46
2:L1:75:U:O4	59:SP:6:GLN:N	2.49	0.46
4:L3:61:LEU:HD13	4:L3:65:GLU:OE1	2.15	0.46
17:LI:611:ILE:HG21	17:LI:654:LEU:HD21	1.98	0.46
20:LL:123:SER:O	20:LL:123:SER:OG	2.34	0.46
24:LP:64:ASN:HB2	24:LP:88:ILE:HG21	1.98	0.46
26:LR:25:VAL:HG11	26:LR:296:ILE:HD11	1.97	0.46
26:LR:36:VAL:O	26:LR:36:VAL:HG13	2.15	0.46
32:LY:262:ALA:HB2	32:LY:470:LEU:HD21	1.97	0.46
39:NF:115:LEU:HD23	43:NK:252:PRO:CD	2.46	0.46
41:NH:201:SER:OG	41:NH:202:SER:N	2.48	0.46
42:NI:216:VAL:O	42:NI:216:VAL:HG13	2.16	0.46
51:SE:43:THR:OG1	51:SE:49:SER:OG	2.30	0.46
62:SS:837:LYS:HA	62:SS:840:LEU:HD23	1.96	0.46
18:LJ:257:CYS:SG	18:LJ:258:LEU:N	2.88	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:LJ:362:ARG:NH2	27:LS:582:GLU:O	2.48	0.46
25:LQ:455:GLN:NE2	25:LQ:464:LEU:HD11	2.31	0.46
25:LQ:829:VAL:HG21	25:LQ:864:ASN:ND2	2.30	0.46
30:LV:109:ASP:OD1	30:LV:110:ASP:N	2.49	0.46
31:LW:289:MET:HE3	31:LW:303:ILE:CG2	2.46	0.46
32:LX:66:PHE:CD2	32:LX:98:ILE:HD13	2.50	0.46
54:SI:59:VAL:HG11	54:SI:61:ARG:NH1	2.31	0.46
55:SK:47:MET:HA	55:SK:47:MET:HE3	1.97	0.46
65:SV:130:ASP:O	65:SV:131:LEU:HB3	2.15	0.46
10:L9:151:ASP:OD1	10:L9:152:SER:N	2.48	0.46
16:LH:461:ASP:O	16:LH:465:ASN:N	2.49	0.46
23:LO:20:ILE:CG2	23:LO:29:LEU:HD11	2.46	0.46
24:LP:150:CYS:SG	24:LP:167:ILE:HG21	2.56	0.46
27:LS:410:ASP:OD1	27:LS:411:TYR:N	2.49	0.46
32:LX:4:LYS:HE2	32:LX:4:LYS:HA	1.96	0.46
53:SH:103:MET:HE2	53:SH:103:MET:HA	1.97	0.46
55:SK:218:ASP:OD1	55:SK:219:GLU:N	2.49	0.46
57:SM:77:TYR:HD2	57:SM:204:CYS:HG	1.61	0.46
57:SM:167:LEU:HD23	57:SM:254:PHE:CD1	2.51	0.46
59:SP:1032:MET:HA	59:SP:1032:MET:HE2	1.97	0.46
3:L2:24:U:H5'	33:LZ:15:LYS:HZ2	1.80	0.46
7:L6:52:ILE:HA	7:L6:111:LEU:HD23	1.98	0.46
9:L8:160:PHE:CE2	9:L8:165:LEU:HD11	2.50	0.46
17:LI:614:ILE:HD12	17:LI:634:LEU:HD21	1.97	0.46
19:LK:420:ILE:HG22	19:LK:463:LYS:NZ	2.30	0.46
30:LV:273:ASP:OD1	30:LV:273:ASP:N	2.49	0.46
33:LZ:156:ASP:OD2	57:SM:4:ARG:HD2	2.15	0.46
48:SA:392:TYR:HB3	51:SF:65:LEU:HD23	1.96	0.46
55:SJ:167:ILE:O	55:SJ:171:LEU:HD23	2.16	0.46
55:SJ:214:ASP:O	55:SJ:224:LYS:NZ	2.47	0.46
59:SP:1095:SER:HA	59:SP:1136:THR:HG22	1.98	0.46
62:SS:357:ASP:OD1	62:SS:358:SER:N	2.49	0.46
1:L0:6:A:O2'	1:L0:7:A:OP2	2.34	0.46
2:L1:513:U:O2'	2:L1:514:G:O4'	2.26	0.46
4:L3:117:LYS:NZ	63:ST:754:GLU:OE2	2.49	0.46
12:LD:86:ILE:HD11	12:LD:109:VAL:HG11	1.98	0.46
13:LE:75:ILE:CD1	38:NE:319:LEU:HD23	2.46	0.46
25:LQ:480:ASP:O	25:LQ:489:VAL:HG22	2.16	0.46
26:LR:698:LEU:HD13	26:LR:759:THR:HG21	1.98	0.46
41:NH:659:LYS:NZ	44:NM:92:GLN:O	2.48	0.46
59:SP:1081:ASP:O	59:SP:1085:VAL:HG22	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L0:8:A:O2'	19:LK:487:ARG:NH1	2.49	0.46
7:L6:163:THR:HG23	7:L6:168:THR:HG22	1.98	0.46
16:LH:313:LEU:HD23	16:LH:321:MET:HE3	1.97	0.46
22:LN:164:THR:CG2	22:LN:182:ILE:HG23	2.45	0.46
23:LO:369:ILE:HG21	23:LO:402:MET:HE1	1.97	0.46
27:LS:544:VAL:HG22	27:LS:551:VAL:HG22	1.98	0.46
28:LT:369:ALA:HB1	28:LT:414:ILE:HD13	1.97	0.46
38:NE:283:ILE:HG22	38:NE:287:ILE:HG12	1.98	0.46
41:NH:969:ASN:HA	47:OA:1414:LEU:HD11	1.96	0.46
49:SB:291:VAL:HG12	49:SB:363:LEU:HD21	1.98	0.46
52:SG:168:ASN:O	52:SG:172:PHE:N	2.43	0.46
6:L5:40:ILE:HD12	6:L5:69:PHE:CE2	2.51	0.46
16:LH:744:ILE:HD11	17:LI:431:PHE:CZ	2.51	0.46
20:LL:219:SER:OG	20:LL:220:GLY:N	2.47	0.46
22:LN:301:ASP:OD1	22:LN:301:ASP:N	2.48	0.46
26:LR:333:ILE:HG23	26:LR:379:LEU:HB3	1.98	0.46
39:NF:132:VAL:O	39:NF:132:VAL:HG12	2.16	0.46
59:SP:725:ASN:OD1	59:SP:726:LYS:N	2.47	0.46
2:L1:89:G:H21	2:L1:452:A:H5'	1.81	0.45
16:LH:292:LEU:C	16:LH:293:LEU:HD12	2.41	0.45
16:LH:503:ASP:OD2	16:LH:504:GLY:N	2.49	0.45
23:LO:393:VAL:O	23:LO:394:GLN:NE2	2.45	0.45
31:LW:123:THR:HG23	31:LW:140:ARG:NH2	2.31	0.45
40:NG:60:ALA:O	40:NG:64:ALA:N	2.43	0.45
54:SI:129:ILE:O	54:SI:132:ALA:N	2.49	0.45
59:SP:1212:GLN:HA	59:SP:1254:TYR:CZ	2.51	0.45
59:SP:1265:TYR:OH	59:SP:1301:ILE:HG21	2.16	0.45
1:L0:407:A:O2'	54:SI:1086:MET:O	2.31	0.45
3:L2:332:G:H21	16:LH:869:MET:HE1	1.81	0.45
16:LH:49:ASN:OD1	16:LH:50:ASN:N	2.49	0.45
16:LH:404:SER:OG	16:LH:405:ALA:N	2.49	0.45
21:LM:1731:PRO:CB	59:SP:246:THR:HG21	2.46	0.45
32:LX:652:ARG:O	32:LX:656:LEU:HD12	2.16	0.45
32:LY:864:LEU:HD12	32:LY:890:LEU:HD21	1.97	0.45
35:NB:221:ALA:HB3	35:NB:222:PRO:HD3	1.98	0.45
41:NH:1221:HIS:O	41:NH:1224:ALA:N	2.49	0.45
59:SP:1268:ILE:HA	59:SP:1271:LEU:HD13	1.99	0.45
3:L2:62:C:O2'	28:LT:447:ASN:O	2.33	0.45
6:L5:23:VAL:O	6:L5:23:VAL:HG23	2.16	0.45
13:LE:62:VAL:HB	46:NQ:8:LEU:HD21	1.98	0.45
20:LL:160:VAL:HG23	20:LL:160:VAL:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:LN:80:ASN:ND2	22:LN:88:GLU:OE2	2.40	0.45
32:LY:801:ALA:O	32:LY:805:ILE:HD12	2.17	0.45
34:NA:434:HIS:HA	34:NA:437:ILE:HG22	1.98	0.45
48:SA:132:ARG:CG	50:SC:236:MET:HE2	2.46	0.45
50:SC:85:LYS:NZ	60:SQ:170:LYS:O	2.44	0.45
51:SE:35:LYS:N	51:SE:39:GLU:OE1	2.48	0.45
59:SP:597:ARG:NH2	59:SP:626:GLU:OE1	2.49	0.45
59:SP:1706:LYS:O	59:SP:1760:ASN:ND2	2.44	0.45
63:ST:488:ASN:HB2	63:ST:492:ALA:HB2	1.97	0.45
6:L5:186:ASN:OD1	6:L5:187:ILE:N	2.50	0.45
16:LH:363:ASN:OD1	16:LH:391:VAL:HG23	2.16	0.45
21:LM:746:GLU:O	21:LM:750:ASN:N	2.46	0.45
22:LN:591:ILE:HD11	22:LN:626:TRP:CZ3	2.52	0.45
26:LR:345:TYR:OH	26:LR:633:VAL:HG23	2.16	0.45
26:LR:362:LEU:CD1	26:LR:405:THR:HG21	2.46	0.45
26:LR:395:ASP:OD1	26:LR:396:ALA:N	2.49	0.45
33:LZ:60:LYS:HB2	34:NA:437:ILE:HD13	1.98	0.45
34:NA:346:GLU:N	34:NA:346:GLU:OE2	2.50	0.45
41:NH:574:LEU:HD22	41:NH:678:ILE:HG23	1.98	0.45
53:SH:33:ILE:HG22	53:SH:36:ILE:HD11	1.99	0.45
53:SH:278:GLN:HG2	54:SI:615:PHE:CE1	2.52	0.45
54:SI:126:ASN:O	54:SI:853:ARG:NH2	2.49	0.45
54:SI:557:ASN:OD1	54:SI:558:ILE:N	2.49	0.45
54:SI:841:THR:HG23	54:SI:859:ILE:HA	1.98	0.45
59:SP:1982:VAL:O	59:SP:1986:VAL:HG23	2.16	0.45
59:SP:2061:PHE:CE1	59:SP:2098:LEU:HD11	2.51	0.45
20:LL:197:ILE:HD11	20:LL:203:ILE:HB	1.98	0.45
27:LS:170:LYS:O	49:SB:425:ARG:NH2	2.50	0.45
27:LS:464:THR:HG21	27:LS:476:ILE:HA	1.99	0.45
32:LX:830:LEU:HD11	32:LX:924:PHE:CD2	2.51	0.45
39:NF:129:TYR:HB2	39:NF:135:LEU:HD12	1.98	0.45
59:SP:1206:THR:HG22	59:SP:1211:ILE:HG21	1.98	0.45
2:L1:246:G:C8	12:LD:40:LEU:HD12	2.52	0.45
2:L1:468:A:N1	2:L1:594:A:O2'	2.47	0.45
2:L1:562:G:C5	57:SM:281:ILE:HG23	2.52	0.45
2:L1:861:U:O2'	13:LE:56:HIS:O	2.34	0.45
6:L5:34:GLN:O	6:L5:37:GLN:HB3	2.17	0.45
17:LI:580:LEU:O	17:LI:583:SER:OG	2.28	0.45
17:LI:596:LYS:NZ	17:LI:643:ASP:OD1	2.36	0.45
22:LN:340:GLN:OE1	22:LN:361:LEU:HD12	2.17	0.45
29:LU:284:HIS:CD2	46:NQ:4:VAL:HG11	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LU:385:VAL:HG21	48:SA:47:LEU:HD21	1.98	0.45
30:LV:21:VAL:HB	30:LV:25:LEU:HD22	1.99	0.45
32:LX:844:SER:HB2	32:LX:850:LEU:HD12	1.98	0.45
41:NH:519:ASP:O	41:NH:523:TYR:N	2.49	0.45
41:NH:1185:LEU:HD11	47:OA:1407:PHE:CE2	2.52	0.45
59:SP:1617:VAL:CG1	59:SP:1665:LEU:HD21	2.47	0.45
59:SP:2134:GLU:OE1	59:SP:2134:GLU:N	2.50	0.45
63:ST:456:ILE:HD13	64:SU:529:VAL:HG21	1.97	0.45
4:L3:24:GLY:HA2	4:L3:58:ALA:HB3	1.99	0.45
6:L5:189:THR:HG22	6:L5:190:ILE:N	2.32	0.45
18:LJ:281:VAL:HG13	18:LJ:281:VAL:O	2.17	0.45
20:LL:225:VAL:HG23	20:LL:225:VAL:O	2.17	0.45
23:LO:380:LEU:HB3	34:NA:484:MET:HE2	1.99	0.45
31:LW:497:LEU:HD22	31:LW:516:VAL:HG13	1.98	0.45
32:LX:514:ASN:OD1	32:LX:515:LEU:N	2.50	0.45
38:NE:107:VAL:HG23	38:NE:107:VAL:O	2.17	0.45
41:NH:1097:ASP:OD1	41:NH:1186:ILE:HD12	2.17	0.45
51:SE:112:THR:OG1	51:SE:113:GLN:OE1	2.34	0.45
55:SJ:204:VAL:HG21	55:SJ:241:PHE:CE2	2.52	0.45
2:L1:114:C:O2'	12:LD:65:SER:OG	2.31	0.45
13:LE:93:LEU:HD23	38:NE:311:VAL:HG21	1.99	0.45
24:LP:191:ASN:CG	60:SQ:62:LEU:HD21	2.42	0.45
26:LR:85:LEU:N	26:LR:99:MET:O	2.45	0.45
26:LR:342:ASP:OD2	26:LR:343:MET:N	2.50	0.45
41:NH:431:THR:HG23	41:NH:432:MET:H	1.81	0.45
41:NH:835:LEU:H	41:NH:835:LEU:HD23	1.81	0.45
41:NH:1221:HIS:O	41:NH:1225:ALA:N	2.48	0.45
2:L1:1680:G:H21	2:L1:1681:A:N6	2.15	0.45
19:LK:456:LEU:C	19:LK:456:LEU:HD23	2.41	0.45
23:LO:792:ILE:H	23:LO:792:ILE:HD12	1.82	0.45
28:LT:894:ASP:OD1	28:LT:895:VAL:N	2.50	0.45
31:LW:183:GLU:OE1	33:LZ:41:ARG:NH1	2.50	0.45
32:LX:297:ILE:HD13	32:LX:325:ILE:HD11	1.99	0.45
41:NH:209:MET:HE3	41:NH:214:PHE:CE2	2.52	0.45
41:NH:698:ASN:OD1	41:NH:700:THR:OG1	2.34	0.45
49:SB:63:ILE:HB	50:SD:232:MET:HE3	1.98	0.45
54:SI:959:ALA:HB2	63:ST:752:MET:CE	2.47	0.45
15:LG:12:VAL:HG12	15:LG:30:VAL:HG12	1.99	0.45
16:LH:666:ASN:OD1	16:LH:667:ASP:N	2.47	0.45
24:LP:34:LYS:NZ	29:LU:12:ASP:OD2	2.29	0.45
26:LR:745:ASP:OD2	34:NA:508:ARG:NH1	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LU:444:GLU:CB	29:LU:451:MET:HE1	2.47	0.45
32:LX:106:VAL:HG12	32:LX:107:TYR:O	2.17	0.45
32:LX:907:ASN:OD1	32:LX:908:GLN:N	2.50	0.45
32:LY:917:MET:N	32:LY:917:MET:HE2	2.32	0.45
48:SA:253:ASP:O	48:SA:257:ILE:HG22	2.17	0.45
50:SC:153:ALA:CB	50:SC:306:LEU:HD12	2.47	0.45
54:SI:118:LEU:CD1	54:SI:245:LEU:HD21	2.40	0.45
59:SP:1478:ASP:OD1	59:SP:1478:ASP:N	2.50	0.45
64:SU:21:ARG:HB2	64:SU:24:TYR:CD2	2.52	0.45
20:LL:277:LYS:NZ	20:LL:319:TRP:O	2.38	0.44
22:LN:743:PHE:HB3	22:LN:755:ILE:HD12	1.99	0.44
28:LT:879:GLU:HG3	28:LT:880:LEU:HD22	1.99	0.44
32:LY:838:ASP:OD1	32:LY:841:ARG:NH2	2.46	0.44
36:NC:76:LEU:O	36:NC:80:GLY:N	2.41	0.44
41:NH:945:PRO:O	41:NH:948:TYR:N	2.50	0.44
45:NN:532:ILE:HD12	45:NN:532:ILE:H	1.81	0.44
52:SG:257:ASP:OD1	52:SG:257:ASP:N	2.44	0.44
59:SP:267:SER:O	59:SP:313:ARG:NH2	2.49	0.44
59:SP:1062:LEU:HA	59:SP:1065:VAL:HG12	1.99	0.44
59:SP:1348:LEU:HD13	59:SP:1398:LEU:HD21	2.00	0.44
65:SV:131:LEU:HD11	67:SY:191:ASP:CG	2.42	0.44
19:LK:426:THR:HG1	19:LK:429:HIS:HD1	1.63	0.44
22:LN:135:ARG:NH1	22:LN:136:ASN:O	2.48	0.44
23:LO:154:TRP:CH2	23:LO:161:ILE:HD11	2.53	0.44
23:LO:293:THR:HG21	28:LT:756:LEU:HD12	1.98	0.44
25:LQ:127:LEU:HD11	25:LQ:136:LEU:HD11	1.99	0.44
25:LQ:616:ASP:O	25:LQ:634:SER:OG	2.33	0.44
26:LR:340:ILE:HD13	26:LR:357:THR:HG22	1.98	0.44
28:LT:217:VAL:HG23	28:LT:220:ILE:HB	1.99	0.44
29:LU:185:ILE:HG13	29:LU:196:THR:HG22	1.99	0.44
30:LV:218:LEU:CD2	30:LV:220:LEU:HD23	2.48	0.44
30:LV:292:CYS:SG	30:LV:317:ILE:HG21	2.56	0.44
40:NG:27:PHE:CD1	40:NG:43:THR:HG22	2.52	0.44
41:NH:761:ARG:HG3	41:NH:763:THR:HG22	1.98	0.44
55:SJ:53:HIS:NE2	55:SJ:80:MET:SD	2.90	0.44
57:SM:273:VAL:HG23	57:SM:273:VAL:O	2.16	0.44
2:L1:249:U:C2	12:LD:63:LEU:HD11	2.52	0.44
2:L1:408:C:O3'	30:LV:128:LYS:NZ	2.49	0.44
13:LE:62:VAL:HG11	46:NQ:8:LEU:CD2	2.48	0.44
13:LE:106:THR:OG1	13:LE:122:SER:O	2.29	0.44
16:LH:330:SER:OG	16:LH:331:GLN:N	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:LO:558:ASP:OD1	28:LT:423:ARG:NH1	2.46	0.44
25:LQ:401:ASP:OD2	25:LQ:402:ASP:N	2.50	0.44
29:LU:8:ARG:NH2	31:LW:386:PHE:O	2.44	0.44
30:LV:11:VAL:HG11	30:LV:309:ALA:HB2	2.00	0.44
30:LV:311:MET:HE1	30:LV:329:PHE:CD2	2.52	0.44
32:LX:94:PHE:CZ	32:LX:98:ILE:HD11	2.53	0.44
39:NF:54:LEU:HD12	39:NF:60:VAL:HG21	1.98	0.44
41:NH:627:LEU:HB3	44:NM:240:LYS:CE	2.48	0.44
44:NM:43:VAL:CG1	44:NM:73:LEU:HD11	2.47	0.44
48:SA:132:ARG:HD2	50:SC:236:MET:HE2	1.99	0.44
52:SG:164:GLN:NE2	52:SG:165:PRO:O	2.51	0.44
55:SK:171:LEU:HD22	55:SK:203:CYS:SG	2.57	0.44
59:SP:201:ARG:NH2	59:SP:239:SER:O	2.50	0.44
59:SP:452:ASN:OD1	59:SP:453:PHE:N	2.50	0.44
59:SP:2124:VAL:O	59:SP:2127:SER:OG	2.18	0.44
64:SU:24:TYR:CD1	64:SU:27:ILE:HD11	2.53	0.44
64:SU:278:LEU:HD23	64:SU:281:LEU:CD1	2.48	0.44
1:L0:156:U:HO2'	1:L0:157:U:P	2.37	0.44
2:L1:415:C:OP1	32:LX:70:ARG:NH2	2.44	0.44
2:L1:1643:U:OP2	34:NA:530:ARG:NH2	2.51	0.44
16:LH:380:THR:HG21	20:LL:343:ARG:HH22	1.82	0.44
18:LJ:451:GLU:OE1	20:LL:493:HIS:NE2	2.51	0.44
23:LO:80:ILE:O	23:LO:80:ILE:HG23	2.18	0.44
23:LO:107:ASP:OD1	23:LO:108:GLY:N	2.50	0.44
23:LO:760:ILE:HD12	23:LO:760:ILE:H	1.82	0.44
24:LP:74:ILE:HG22	24:LP:75:LEU:HD22	1.99	0.44
24:LP:365:ILE:O	24:LP:372:ARG:NH2	2.50	0.44
25:LQ:483:SER:OG	25:LQ:543:ASP:OD2	2.28	0.44
25:LQ:566:TYR:O	25:LQ:567:LEU:HD23	2.18	0.44
41:NH:431:THR:HG23	41:NH:432:MET:N	2.33	0.44
49:SB:327:PHE:HD2	49:SB:330:LEU:HD12	1.82	0.44
52:SG:237:ASP:OD1	52:SG:238:GLU:N	2.46	0.44
55:SJ:50:LEU:HD21	55:SJ:92:THR:HG21	1.98	0.44
58:SN:42:THR:HG23	58:SN:235:ILE:HG23	2.00	0.44
59:SP:767:ASN:OD1	59:SP:768:THR:N	2.50	0.44
59:SP:1147:ILE:O	59:SP:1151:ILE:HD12	2.18	0.44
15:LG:65:ARG:O	15:LG:67:ARG:NH1	2.50	0.44
22:LN:186:GLN:OE1	22:LN:186:GLN:N	2.51	0.44
22:LN:569:PHE:O	22:LN:587:ALA:N	2.50	0.44
24:LP:363:VAL:HG22	24:LP:394:TYR:CE2	2.52	0.44
25:LQ:528:LEU:HD21	25:LQ:558:PHE:CE2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:LR:461:LEU:HD23	26:LR:490:HIS:O	2.18	0.44
27:LS:165:ARG:CD	28:LT:175:THR:HG21	2.47	0.44
28:LT:258:THR:OG1	28:LT:306:GLY:N	2.45	0.44
32:LX:841:ARG:HG3	32:LX:850:LEU:HD11	1.99	0.44
32:LX:877:LEU:HD22	32:LX:881:GLN:HE21	1.83	0.44
34:NA:518:GLU:OE1	34:NA:518:GLU:N	2.47	0.44
39:NF:47:PRO:HG2	39:NF:72:MET:HE1	1.99	0.44
48:SA:163:VAL:HG11	50:SC:205:ARG:HG2	1.99	0.44
55:SK:99:LEU:HD21	55:SK:238:CYS:HB3	2.00	0.44
59:SP:370:ASP:OD1	59:SP:370:ASP:N	2.48	0.44
59:SP:1530:TYR:CZ	59:SP:1547:LEU:HD21	2.53	0.44
1:L0:165:G:H5'	27:LS:403:VAL:HG12	1.99	0.44
1:L0:410:A:H2'	1:L0:411:A:O4'	2.16	0.44
6:L5:15:GLU:N	6:L5:15:GLU:OE2	2.50	0.44
9:L8:58:LEU:HD13	30:LV:57:GLU:HG3	1.99	0.44
17:LI:650:LEU:CD2	17:LI:655:LEU:HD12	2.47	0.44
20:LL:454:GLU:OE2	20:LL:494:ARG:NH1	2.50	0.44
22:LN:97:ARG:NE	37:ND:191:PRO:O	2.43	0.44
23:LO:351:LEU:HD23	23:LO:696:ALA:HB2	1.98	0.44
23:LO:498:ARG:NH2	23:LO:509:VAL:HG11	2.33	0.44
24:LP:399:ASP:OD1	24:LP:402:SER:OG	2.30	0.44
27:LS:321:MET:HE1	27:LS:375:VAL:HG11	1.98	0.44
30:LV:287:ASN:OD1	30:LV:302:ARG:NE	2.50	0.44
32:LY:513:CYS:HB3	32:LY:567:LEU:HD11	2.00	0.44
35:NB:390:MET:HB3	35:NB:393:ALA:HB2	1.99	0.44
41:NH:840:LEU:HD21	41:NH:842:ILE:HD11	1.99	0.44
55:SJ:209:MET:HE1	55:SJ:212:GLY:C	2.43	0.44
59:SP:667:PHE:CD1	59:SP:699:LEU:HD13	2.52	0.44
63:ST:616:LEU:N	64:SU:552:TRP:OXT	2.51	0.44
67:SY:125:LEU:HD21	67:SY:197:LYS:HG3	1.99	0.44
2:L1:1741:U:OP1	25:LQ:254:GLN:NE2	2.50	0.44
8:L7:73:VAL:HG13	8:L7:77:LEU:HD11	1.98	0.44
16:LH:656:ASP:OD1	16:LH:674:THR:HG21	2.18	0.44
16:LH:661:THR:HG22	16:LH:708:ASP:HA	1.99	0.44
23:LO:476:VAL:HG11	23:LO:479:LEU:HD11	2.00	0.44
25:LQ:551:LEU:HD23	25:LQ:551:LEU:O	2.17	0.44
26:LR:118:ALA:HB2	26:LR:152:PHE:CZ	2.53	0.44
26:LR:406:ALA:HB1	26:LR:437:VAL:HG23	2.00	0.44
28:LT:726:GLY:O	28:LT:728:ARG:NH1	2.50	0.44
29:LU:321:VAL:N	29:LU:356:TYR:OH	2.50	0.44
30:LV:50:ILE:HD11	30:LV:352:TRP:CZ3	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:LX:106:VAL:HG21	32:LX:114:ILE:HG21	1.98	0.44
39:NF:47:PRO:CB	39:NF:72:MET:HE1	2.48	0.44
41:NH:195:ILE:HG21	41:NH:364:VAL:CG2	2.48	0.44
44:NM:16:GLN:OE1	44:NM:16:GLN:HA	2.18	0.44
50:SC:252:ILE:HD12	50:SC:252:ILE:H	1.82	0.44
54:SI:94:THR:HG22	54:SI:94:THR:O	2.17	0.44
56:SL:162:GLN:OE1	56:SL:165:ARG:NH1	2.47	0.44
58:SN:56:ILE:HD11	58:SN:183:ILE:HG12	1.99	0.44
59:SP:538:LEU:O	59:SP:538:LEU:HD23	2.18	0.44
59:SP:1102:PRO:HA	59:SP:1106:LEU:HD23	1.98	0.44
64:SU:190:ASP:OD1	64:SU:190:ASP:N	2.49	0.44
3:L2:57:A:N3	33:LZ:133:GLN:NE2	2.66	0.44
13:LE:122:SER:OG	13:LE:123:GLY:N	2.51	0.44
20:LL:22:VAL:CG2	27:LS:278:ASP:HB2	2.48	0.44
21:LM:341:LYS:CE	21:LM:373:ILE:HD13	2.48	0.44
25:LQ:7:ARG:CZ	25:LQ:7:ARG:HA	2.47	0.44
27:LS:311:ASN:OD1	27:LS:312:ILE:N	2.50	0.44
34:NA:311:ILE:HD11	54:SI:1032:LEU:CA	2.48	0.44
34:NA:590:ASN:OD1	34:NA:591:ILE:N	2.51	0.44
51:SF:10:PRO:HG3	51:SF:125:LEU:HD23	1.99	0.44
7:L6:91:GLU:N	7:L6:91:GLU:OE2	2.51	0.44
17:LI:467:LEU:HD22	17:LI:474:SER:OG	2.17	0.44
25:LQ:255:ARG:CZ	25:LQ:257:LEU:HD21	2.48	0.44
30:LV:218:LEU:HD12	45:NN:498:LEU:CD1	2.47	0.44
31:LW:161:GLN:OE1	31:LW:161:GLN:N	2.46	0.44
32:LY:725:VAL:HG11	32:LY:737:TRP:CZ3	2.53	0.44
33:LZ:159:THR:HG22	33:LZ:160:TRP:N	2.33	0.44
41:NH:1189:LEU:HD21	41:NH:1194:HIS:ND1	2.33	0.44
49:SB:91:GLU:OE1	49:SB:92:THR:N	2.48	0.44
54:SI:124:ASP:HB2	54:SI:1027:THR:HG22	1.99	0.44
55:SJ:221:VAL:HG22	55:SJ:222:ASP:N	2.33	0.44
2:L1:1639:C:H42	34:NA:515:MET:CE	2.31	0.43
12:LD:80:MET:HE3	12:LD:83:THR:OG1	2.18	0.43
21:LM:1484:THR:O	21:LM:1488:ILE:N	2.47	0.43
24:LP:289:HIS:NE2	49:SB:219:SER:OG	2.47	0.43
25:LQ:351:LEU:O	25:LQ:367:ILE:N	2.41	0.43
27:LS:374:ILE:HD12	27:LS:376:LEU:HD21	1.99	0.43
27:LS:405:THR:HG21	27:LS:455:ILE:O	2.18	0.43
35:NB:495:TYR:CD2	58:SN:252:LEU:HD21	2.53	0.43
43:NK:120:ASP:OD1	43:NK:121:MET:N	2.51	0.43
55:SJ:198:ASP:OD1	55:SJ:199:ASP:N	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SM:1:MET:O	57:SM:4:ARG:N	2.51	0.43
57:SM:237:VAL:HG13	57:SM:250:VAL:HG21	1.99	0.43
59:SP:87:ILE:HG21	59:SP:113:PHE:CE1	2.53	0.43
60:SQ:180:ASP:OD1	60:SQ:181:GLU:N	2.51	0.43
2:L1:332:U:OP1	9:L8:31:ARG:NH1	2.41	0.43
5:L4:122:LYS:NZ	5:L4:143:ASP:OD2	2.42	0.43
16:LH:616:SER:HA	16:LH:664:LEU:HD21	1.99	0.43
21:LM:207:THR:O	21:LM:211:LEU:HD23	2.18	0.43
23:LO:667:GLY:HA3	34:NA:454:VAL:HG21	1.98	0.43
24:LP:163:SER:O	24:LP:166:ASN:N	2.51	0.43
27:LS:325:ASP:OD1	27:LS:326:LEU:N	2.52	0.43
31:LW:228:LEU:HD22	31:LW:264:PRO:HA	1.99	0.43
33:LZ:12:LEU:O	33:LZ:13:LEU:HD12	2.17	0.43
37:ND:173:ARG:N	37:ND:176:PHE:O	2.47	0.43
43:NK:49:ARG:NH2	43:NK:108:VAL:O	2.51	0.43
49:SB:115:ASP:OD1	50:SD:322:ARG:NH2	2.47	0.43
63:ST:426:THR:HG21	63:ST:466:TYR:HB2	2.00	0.43
63:ST:506:ILE:HG13	64:SU:529:VAL:HG22	2.00	0.43
2:L1:894:U:H2'	2:L1:895:G:C8	2.53	0.43
7:L6:65:GLN:OE1	30:LV:44:GLN:NE2	2.52	0.43
16:LH:555:VAL:HG13	16:LH:555:VAL:O	2.17	0.43
16:LH:864:ASP:OD1	16:LH:864:ASP:N	2.51	0.43
20:LL:143:ASN:OD1	20:LL:144:ASN:N	2.51	0.43
22:LN:61:THR:HG21	22:LN:681:ILE:CD1	2.49	0.43
28:LT:209:ILE:HD13	28:LT:223:LEU:HD23	2.01	0.43
32:LX:515:LEU:HD12	32:LX:566:VAL:O	2.18	0.43
32:LY:527:HIS:CB	45:NN:530:ILE:HD11	2.48	0.43
40:NG:121:VAL:O	40:NG:121:VAL:HG23	2.17	0.43
55:SK:68:LEU:HD13	55:SK:77:LEU:HD13	2.01	0.43
64:SU:318:LEU:HD21	64:SU:354:TYR:CD2	2.53	0.43
64:SU:350:MET:HE3	64:SU:394:ALA:HB1	1.99	0.43
64:SU:358:PHE:CZ	64:SU:362:MET:HE3	2.54	0.43
2:L1:1159:C:N4	57:SM:184:GLU:OE2	2.48	0.43
6:L5:29:ILE:HG22	6:L5:33:VAL:CG2	2.49	0.43
13:LE:9:ASP:OD1	38:NE:316:ARG:NH1	2.48	0.43
16:LH:318:GLU:OE2	16:LH:318:GLU:N	2.40	0.43
16:LH:821:ILE:HD12	16:LH:821:ILE:H	1.83	0.43
16:LH:868:ASN:O	16:LH:871:SER:OG	2.25	0.43
18:LJ:92:ASP:OD2	18:LJ:137:ASN:ND2	2.52	0.43
23:LO:16:ARG:HB3	23:LO:34:GLY:H	1.82	0.43
23:LO:742:ALA:HA	23:LO:750:LEU:HD22	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LS:345:LEU:HD21	27:LS:355:PHE:HZ	1.81	0.43
28:LT:277:ASP:HB2	28:LT:284:ILE:HD11	2.00	0.43
49:SB:71:GLN:HE21	49:SB:71:GLN:HB3	1.69	0.43
59:SP:603:LEU:O	59:SP:606:THR:OG1	2.34	0.43
60:SQ:123:LEU:HD21	60:SQ:174:LEU:HD13	1.99	0.43
8:L7:129:LEU:HD21	8:L7:172:VAL:HG11	2.01	0.43
16:LH:335:PRO:HG2	16:LH:336:ARG:HE	1.83	0.43
18:LJ:266:SER:OG	18:LJ:267:PRO:HD2	2.19	0.43
20:LL:25:ASP:OD2	27:LS:590:LYS:NZ	2.48	0.43
20:LL:109:ASP:OD1	20:LL:110:ILE:N	2.52	0.43
21:LM:1435:SER:O	21:LM:1439:SER:N	2.49	0.43
23:LO:120:GLN:HG2	23:LO:141:VAL:HG23	2.01	0.43
27:LS:512:ASP:N	27:LS:512:ASP:OD1	2.52	0.43
30:LV:74:THR:HG22	30:LV:81:ILE:CD1	2.48	0.43
31:LW:489:ASP:OD1	31:LW:489:ASP:N	2.50	0.43
32:LY:830:LEU:HD11	32:LY:924:PHE:CD1	2.54	0.43
59:SP:593:ASP:OD1	59:SP:594:GLY:N	2.52	0.43
59:SP:1819:PHE:HZ	59:SP:1873:LEU:HD23	1.83	0.43
63:ST:596:TYR:N	63:ST:597:GLU:OE1	2.51	0.43
64:SU:278:LEU:HD23	64:SU:281:LEU:HD11	2.00	0.43
65:SV:147:LEU:HD21	67:SY:127:PHE:CD2	2.54	0.43
5:L4:173:ILE:HD13	5:L4:229:GLY:HA2	2.01	0.43
7:L6:20:ASP:OD2	7:L6:21:GLU:N	2.52	0.43
18:LJ:446:CYS:SG	18:LJ:459:VAL:HG23	2.59	0.43
20:LL:63:LEU:HD23	20:LL:63:LEU:H	1.83	0.43
26:LR:269:LEU:HD11	26:LR:316:VAL:HG13	2.01	0.43
31:LW:128:THR:HG21	31:LW:157:ALA:HB2	2.01	0.43
49:SB:152:LEU:HD21	50:SD:221:ILE:CD1	2.49	0.43
63:ST:537:LEU:HG	63:ST:622:MET:HE1	2.00	0.43
2:L1:249:U:N3	12:LD:63:LEU:HD11	2.34	0.43
14:LF:86:GLU:OE2	14:LF:90:ARG:NE	2.43	0.43
16:LH:306:SER:OG	16:LH:307:HIS:N	2.51	0.43
22:LN:40:ASP:OD1	22:LN:40:ASP:N	2.45	0.43
25:LQ:230:LYS:HB3	25:LQ:245:MET:SD	2.59	0.43
33:LZ:72:ARG:HH12	57:SM:61:SER:HA	1.84	0.43
35:NB:372:PHE:O	35:NB:376:VAL:HG23	2.18	0.43
43:NK:156:LEU:HD21	43:NK:186:VAL:HG21	1.99	0.43
44:NM:70:LEU:HD21	44:NM:189:ILE:HD12	1.99	0.43
50:SD:169:LYS:O	50:SD:238:ASP:N	2.49	0.43
57:SM:232:SER:OG	57:SM:255:GLU:OE2	2.36	0.43
59:SP:277:ASP:OD1	59:SP:733:VAL:HG22	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:SP:1165:ASP:N	59:SP:1165:ASP:OD1	2.51	0.43
1:L0:168:G:H22	1:L0:227:U:H3	1.67	0.43
7:L6:94:ARG:NH2	30:LV:91:LEU:O	2.51	0.43
8:L7:75:THR:O	8:L7:78:THR:OG1	2.31	0.43
10:L9:60:LEU:HD23	56:SL:87:MET:HE1	2.01	0.43
13:LE:75:ILE:HD11	38:NE:321:VAL:HG23	2.00	0.43
23:LO:585:TYR:HE1	23:LO:592:ILE:HD11	1.84	0.43
25:LQ:854:CYS:HB3	26:LR:799:LEU:HD12	2.01	0.43
25:LQ:854:CYS:SG	25:LQ:891:LEU:HD21	2.59	0.43
31:LW:545:VAL:HG13	42:NI:185:HIS:HB2	2.01	0.43
41:NH:799:LEU:HD22	41:NH:862:LEU:HD12	2.00	0.43
44:NM:21:VAL:O	44:NM:21:VAL:HG13	2.19	0.43
55:SK:140:LEU:O	55:SK:144:LEU:N	2.46	0.43
59:SP:913:ILE:H	59:SP:913:ILE:HD12	1.83	0.43
59:SP:1244:LEU:O	59:SP:1248:LYS:N	2.46	0.43
60:SQ:127:ARG:HA	60:SQ:130:LEU:HD13	2.01	0.43
63:ST:677:ASP:OD1	63:ST:678:PHE:N	2.52	0.43
64:SU:181:THR:HG23	64:SU:222:LEU:HD12	2.00	0.43
66:SW:97:ARG:HB2	66:SW:152:LEU:HD21	2.00	0.43
11:LC:82:ARG:NH2	11:LC:116:LEU:HD11	2.34	0.43
16:LH:598:LYS:NZ	16:LH:635:PHE:O	2.49	0.43
20:LL:518:ASN:OD1	20:LL:518:ASN:N	2.51	0.43
22:LN:441:VAL:HG21	22:LN:486:ILE:HD13	2.01	0.43
23:LO:89:VAL:HG11	23:LO:92:HIS:NE2	2.33	0.43
23:LO:492:SER:OG	23:LO:493:TRP:N	2.52	0.43
23:LO:805:ALA:O	26:LR:815:LYS:NZ	2.51	0.43
27:LS:224:ASN:OD1	27:LS:225:SER:N	2.52	0.43
27:LS:432:VAL:HG11	27:LS:447:TRP:CZ2	2.53	0.43
35:NB:511:GLU:HA	35:NB:514:LYS:HB3	2.00	0.43
41:NH:358:SER:HA	41:NH:361:GLU:OE2	2.19	0.43
41:NH:551:GLU:O	41:NH:555:PHE:N	2.38	0.43
46:NQ:23:THR:HG22	46:NQ:24:LEU:N	2.34	0.43
59:SP:1617:VAL:HG13	59:SP:1665:LEU:HD21	2.01	0.43
63:ST:528:PHE:HB3	63:ST:532:ILE:HD12	2.01	0.43
22:LN:340:GLN:NE2	22:LN:345:ASP:OD2	2.52	0.43
26:LR:30:LYS:O	26:LR:45:LEU:N	2.51	0.43
27:LS:45:ILE:H	27:LS:45:ILE:HD12	1.83	0.43
34:NA:380:ASP:OD2	34:NA:381:LEU:N	2.52	0.43
37:ND:120:ILE:HB	64:SU:21:ARG:NH2	2.34	0.43
44:NM:182:ALA:HB2	44:NM:231:LEU:HD11	2.01	0.43
63:ST:537:LEU:HG	63:ST:622:MET:CE	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SU:36:ILE:HD11	64:SU:105:ILE:HA	2.00	0.43
66:SW:131:ASN:O	66:SW:135:LYS:N	2.51	0.43
66:SW:263:LEU:HA	66:SW:266:VAL:HG12	2.00	0.43
1:L0:121:G:N2	1:L0:124:A:H62	2.15	0.42
12:LD:116:ARG:HA	12:LD:116:ARG:NH1	2.34	0.42
16:LH:258:TYR:OH	16:LH:403:ILE:HD13	2.19	0.42
24:LP:167:ILE:H	24:LP:167:ILE:HD12	1.83	0.42
28:LT:613:ASP:CG	28:LT:616:THR:HG22	2.43	0.42
32:LY:276:ASN:ND2	32:LY:464:GLN:OE1	2.52	0.42
32:LY:805:ILE:HD12	32:LY:805:ILE:H	1.84	0.42
39:NF:115:LEU:HD23	43:NK:252:PRO:CG	2.49	0.42
52:SG:156:ASN:HA	52:SG:544:ALA:HB1	2.00	0.42
54:SI:558:ILE:HG23	54:SI:563:CYS:SG	2.59	0.42
56:SL:98:ILE:HD12	56:SL:125:ILE:HG21	2.00	0.42
59:SP:476:LEU:HB3	59:SP:518:MET:SD	2.59	0.42
59:SP:1245:LYS:O	59:SP:1249:LEU:HD23	2.19	0.42
62:SS:791:TRP:CE3	66:SW:130:MET:HE3	2.54	0.42
66:SW:204:ARG:NH2	66:SW:254:SER:O	2.51	0.42
67:SY:149:GLU:O	67:SY:153:ASN:N	2.52	0.42
1:L0:396:A:N7	33:LZ:89:THR:OG1	2.37	0.42
2:L1:1712:A:H2'	2:L1:1713:G:H8	1.84	0.42
5:L4:73:ASP:O	5:L4:73:ASP:OD2	2.37	0.42
7:L6:17:GLU:N	32:LX:606:GLY:O	2.49	0.42
7:L6:23:ARG:O	7:L6:26:VAL:HG12	2.18	0.42
16:LH:152:ARG:HB3	16:LH:173:LEU:HD11	2.01	0.42
18:LJ:129:VAL:HB	18:LJ:143:ALA:HB3	2.01	0.42
20:LL:113:MET:HB2	20:LL:153:ILE:HD11	2.00	0.42
21:LM:1731:PRO:HB3	59:SP:246:THR:HG21	2.00	0.42
28:LT:274:ILE:HG13	28:LT:286:VAL:HG23	2.00	0.42
31:LW:449:ILE:HD12	62:SS:842:TYR:HB3	2.01	0.42
31:LW:483:ILE:HG23	31:LW:516:VAL:HG22	2.00	0.42
31:LW:510:ASP:OD1	31:LW:513:LYS:N	2.37	0.42
32:LX:558:ASP:OD1	32:LX:559:ALA:N	2.53	0.42
32:LY:275:LEU:O	32:LY:404:TYR:N	2.52	0.42
41:NH:144:LYS:N	41:NH:176:PHE:O	2.49	0.42
41:NH:591:ASP:OD1	41:NH:591:ASP:N	2.47	0.42
48:SA:373:GLY:O	48:SA:376:SER:OG	2.30	0.42
50:SD:198:GLU:O	50:SD:222:GLU:N	2.52	0.42
58:SN:155:ARG:HH21	65:SV:191:LEU:HD21	1.84	0.42
63:ST:540:ILE:HG23	63:ST:541:ALA:N	2.34	0.42
11:LC:97:VAL:HG12	11:LC:98:ASP:N	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LH:674:THR:HG23	16:LH:677:THR:H	1.83	0.42
23:LO:250:ILE:O	23:LO:250:ILE:HG13	2.19	0.42
23:LO:814:LYS:HA	23:LO:814:LYS:HD2	1.92	0.42
24:LP:167:ILE:HD11	62:SS:327:PHE:HD1	1.84	0.42
27:LS:168:PHE:CD1	28:LT:218:LEU:HD21	2.54	0.42
37:ND:169:ASP:C	67:SY:143:MET:HE1	2.45	0.42
41:NH:412:LEU:HD21	41:NH:424:GLY:HA3	2.00	0.42
41:NH:887:ALA:CB	41:NH:1051:LEU:HD21	2.49	0.42
49:SB:280:MET:HE2	49:SB:296:GLY:C	2.45	0.42
51:SF:48:ILE:O	51:SF:104:THR:N	2.48	0.42
54:SI:363:GLY:O	54:SI:373:ILE:HD12	2.18	0.42
66:SW:202:ILE:HD11	66:SW:229:SER:OG	2.19	0.42
67:SY:77:LEU:HD23	67:SY:78:LEU:N	2.34	0.42
13:LE:11:LEU:HD12	13:LE:74:VAL:HG23	2.01	0.42
20:LL:253:LEU:CD2	20:LL:301:LEU:HD21	2.49	0.42
21:LM:380:VAL:HG12	21:LM:384:ILE:HD11	2.02	0.42
23:LO:261:ALA:HB2	23:LO:281:SER:HB3	2.00	0.42
25:LQ:911:GLN:OE1	25:LQ:911:GLN:HA	2.20	0.42
28:LT:808:THR:HG22	28:LT:853:ASN:HB2	2.01	0.42
32:LX:704:THR:O	32:LX:704:THR:HG22	2.19	0.42
34:NA:350:THR:O	57:SM:285:ASN:ND2	2.53	0.42
41:NH:215:GLU:OE1	41:NH:227:LYS:NZ	2.52	0.42
41:NH:1046:ASP:OD2	41:NH:1051:LEU:HD13	2.19	0.42
59:SP:840:ASN:OD1	59:SP:843:ASN:N	2.45	0.42
59:SP:1138:SER:HA	59:SP:1181:ILE:HD13	2.01	0.42
64:SU:155:LEU:O	64:SU:218:LYS:NZ	2.51	0.42
1:L0:122:U:N3	64:SU:135:ALA:O	2.53	0.42
2:L1:284:G:N7	7:L6:188:ARG:NH1	2.67	0.42
16:LH:357:ILE:C	16:LH:358:LEU:HD12	2.43	0.42
16:LH:391:VAL:O	16:LH:391:VAL:HG13	2.19	0.42
16:LH:659:ILE:HG21	16:LH:662:VAL:HG23	2.02	0.42
16:LH:722:LEU:HG	16:LH:724:ILE:HD11	2.00	0.42
18:LJ:141:ALA:HB2	18:LJ:176:PHE:HZ	1.84	0.42
28:LT:459:ASP:OD1	28:LT:483:SER:OG	2.35	0.42
30:LV:120:ASP:OD1	30:LV:122:SER:OG	2.33	0.42
31:LW:204:LEU:HD23	31:LW:216:TYR:HB3	2.02	0.42
33:LZ:13:LEU:O	33:LZ:16:VAL:HG12	2.20	0.42
41:NH:887:ALA:HA	41:NH:1051:LEU:HD21	2.01	0.42
49:SB:183:ARG:O	49:SB:187:TRP:N	2.42	0.42
51:SE:88:GLY:HA2	51:SE:97:VAL:HG22	2.01	0.42
54:SI:166:ARG:NH1	54:SI:231:LYS:O	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SI:303:LYS:C	54:SI:304:LEU:HD12	2.45	0.42
54:SI:392:GLU:N	54:SI:392:GLU:OE2	2.52	0.42
54:SI:831:ARG:NH1	54:SI:835:HIS:O	2.52	0.42
63:ST:601:PRO:O	63:ST:675:TYR:OH	2.37	0.42
2:L1:208:U:H2'	2:L1:209:U:O4'	2.20	0.42
8:L7:45:SER:OG	8:L7:46:ILE:N	2.52	0.42
16:LH:248:GLN:O	16:LH:252:LEU:HD13	2.19	0.42
23:LO:261:ALA:HB1	23:LO:279:PHE:HB3	2.01	0.42
25:LQ:457:PHE:CE2	25:LQ:464:LEU:HD12	2.55	0.42
26:LR:343:MET:HE1	26:LR:641:PHE:HD1	1.85	0.42
27:LS:216:TYR:CE1	28:LT:246:ILE:HG23	2.55	0.42
28:LT:184:THR:OG1	28:LT:187:ASN:O	2.34	0.42
28:LT:834:LEU:HD22	28:LT:881:TYR:CE1	2.55	0.42
45:NN:488:ASP:OD1	45:NN:489:GLN:N	2.53	0.42
46:NQ:25:VAL:HG13	46:NQ:25:VAL:O	2.19	0.42
52:SG:63:ARG:NH1	59:SP:42:VAL:HG11	2.34	0.42
52:SG:365:PRO:HD2	52:SG:366:GLN:N	2.34	0.42
54:SI:555:MET:O	54:SI:558:ILE:HG22	2.20	0.42
59:SP:457:PHE:HE2	59:SP:485:ILE:HD13	1.84	0.42
59:SP:1243:ILE:O	59:SP:1247:LEU:HD23	2.19	0.42
59:SP:1284:LEU:HD12	59:SP:1287:LEU:HD12	2.01	0.42
59:SP:1290:GLU:O	59:SP:1293:ARG:N	2.53	0.42
59:SP:1382:PRO:O	59:SP:1430:TYR:OH	2.34	0.42
59:SP:2058:GLU:O	59:SP:2062:LYS:N	2.49	0.42
64:SU:105:ILE:HG21	64:SU:119:SER:OG	2.19	0.42
67:SY:157:GLU:OE1	67:SY:157:GLU:N	2.47	0.42
67:SY:167:THR:N	67:SY:170:GLN:OE1	2.52	0.42
1:L0:102:A:OP2	1:L0:103:G:N2	2.53	0.42
7:L6:67:VAL:O	7:L6:100:ALA:HB3	2.19	0.42
13:LE:83:ILE:HG23	13:LE:84:GLY:N	2.35	0.42
16:LH:56:SER:HB3	16:LH:59:THR:HG22	2.02	0.42
16:LH:741:SER:HB3	16:LH:763:ILE:HD12	2.01	0.42
21:LM:17:THR:HG23	21:LM:129:VAL:HG11	2.02	0.42
21:LM:256:ALA:O	21:LM:259:THR:OG1	2.34	0.42
22:LN:285:CYS:HB2	22:LN:336:ILE:HG22	2.01	0.42
28:LT:428:GLU:OE1	28:LT:428:GLU:N	2.48	0.42
28:LT:704:ASP:OD1	28:LT:705:ILE:HD12	2.19	0.42
29:LU:50:LEU:HD23	29:LU:53:MET:SD	2.60	0.42
38:NE:114:GLN:HG3	38:NE:118:ARG:HE	1.84	0.42
42:NI:20:LEU:HD21	42:NI:35:HIS:HB2	2.02	0.42
42:NI:60:LEU:HG	42:NI:61:LEU:HD23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:SC:249:GLN:NE2	50:SC:276:ILE:HD11	2.33	0.42
50:SD:107:VAL:CG1	50:SD:141:TYR:HB3	2.50	0.42
55:SK:222:ASP:OD1	55:SK:223:GLU:N	2.53	0.42
59:SP:1276:ASP:OD2	59:SP:1276:ASP:N	2.50	0.42
60:SQ:173:ILE:H	60:SQ:173:ILE:HD12	1.85	0.42
1:L0:9:G:O5'	19:LK:487:ARG:NH1	2.53	0.42
21:LM:351:TYR:CE2	21:LM:355:ILE:HD11	2.55	0.42
22:LN:448:THR:OG1	22:LN:475:THR:OG1	2.20	0.42
23:LO:838:THR:OG1	28:LT:731:MET:HE3	2.19	0.42
25:LQ:936:LYS:HZ2	34:NA:467:ILE:HD12	1.84	0.42
28:LT:246:ILE:HG22	28:LT:249:SER:OG	2.20	0.42
34:NA:332:ALA:HA	34:NA:335:ARG:HE	1.85	0.42
41:NH:146:LEU:HA	41:NH:149:VAL:HG22	2.02	0.42
44:NM:48:VAL:HG22	44:NM:49:ASN:N	2.34	0.42
54:SI:867:THR:HG22	61:SR:62:LYS:NZ	2.34	0.42
59:SP:558:TRP:CE3	59:SP:603:LEU:HD11	2.54	0.42
59:SP:1307:ASP:O	59:SP:1310:SER:OG	2.34	0.42
7:L6:71:THR:HG22	7:L6:72:ARG:N	2.35	0.42
11:LC:98:ASP:OD1	11:LC:101:SER:OG	2.33	0.42
12:LD:71:LEU:HD13	12:LD:88:ARG:NH2	2.35	0.42
20:LL:471:ARG:NH2	64:SU:297:ASP:OD1	2.53	0.42
22:LN:375:VAL:O	22:LN:375:VAL:HG13	2.20	0.42
26:LR:279:LYS:NZ	26:LR:322:ASN:O	2.41	0.42
41:NH:249:ASP:OD1	41:NH:249:ASP:N	2.53	0.42
54:SI:1112:PHE:HD2	60:SQ:174:LEU:HD11	1.84	0.42
59:SP:2153:ASP:OD1	59:SP:2154:ASN:N	2.53	0.42
2:L1:1534:G:N7	18:LJ:79:ARG:NH2	2.68	0.42
16:LH:510:TYR:CD1	16:LH:557:ILE:HD12	2.55	0.42
20:LL:126:PHE:HE2	20:LL:165:VAL:HG11	1.85	0.42
20:LL:255:ILE:HD11	20:LL:301:LEU:HD11	2.00	0.42
25:LQ:887:LEU:O	25:LQ:891:LEU:HD23	2.20	0.42
26:LR:12:LEU:HD11	26:LR:378:PRO:CG	2.49	0.42
29:LU:154:ASP:OD2	29:LU:155:TYR:N	2.53	0.42
32:LX:426:LEU:O	32:LX:430:LEU:HD23	2.19	0.42
32:LX:588:ILE:HD11	32:LX:657:LEU:HD11	2.02	0.42
32:LX:711:LYS:N	32:LX:714:GLU:OE1	2.53	0.42
32:LY:499:ASN:ND2	32:LY:581:ASP:OD2	2.50	0.42
41:NH:913:VAL:HG21	41:NH:935:GLU:HG3	2.02	0.42
44:NM:227:ALA:O	44:NM:231:LEU:HD23	2.19	0.42
48:SA:229:LEU:HD21	48:SA:255:ALA:CB	2.50	0.42
49:SB:2:ALA:HB2	49:SB:20:LYS:HA	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SI:253:THR:HG21	54:SI:258:ILE:HD11	2.02	0.42
59:SP:555:LEU:HD12	59:SP:603:LEU:HD13	2.02	0.42
63:ST:640:MET:HE1	63:ST:671:TYR:CE2	2.55	0.42
64:SU:525:ALA:O	64:SU:544:ASN:ND2	2.53	0.42
1:L0:452:A:O3'	54:SI:1081:SER:OG	2.34	0.41
24:LP:163:SER:O	24:LP:167:ILE:HD12	2.19	0.41
26:LR:343:MET:HE1	26:LR:641:PHE:CD1	2.55	0.41
28:LT:198:LEU:HD21	28:LT:201:THR:OG1	2.20	0.41
30:LV:110:ASP:CG	30:LV:112:THR:HG23	2.45	0.41
32:LX:163:THR:HG21	32:LX:172:TYR:HB2	2.01	0.41
32:LY:887:ALA:HB1	32:LY:898:ILE:HD11	2.01	0.41
41:NH:495:THR:O	41:NH:499:LEU:N	2.41	0.41
52:SG:227:GLU:OE1	52:SG:258:ARG:NE	2.51	0.41
59:SP:697:TRP:CZ2	59:SP:701:LEU:HD13	2.55	0.41
59:SP:1447:GLU:O	59:SP:1453:ASN:ND2	2.53	0.41
59:SP:1450:PHE:CE1	59:SP:1469:LEU:HD22	2.55	0.41
1:L0:153:U:O4	1:L0:154:A:N6	2.53	0.41
2:L1:1492:A:H1'	54:SI:997:MET:HE3	2.03	0.41
9:L8:72:ILE:HG22	9:L8:73:SER:N	2.35	0.41
16:LH:510:TYR:HB2	16:LH:560:ILE:HD11	2.01	0.41
18:LJ:165:THR:O	18:LJ:196:TYR:OH	2.19	0.41
18:LJ:210:ASN:ND2	18:LJ:212:ASP:OD1	2.53	0.41
20:LL:95:VAL:HG13	20:LL:95:VAL:O	2.20	0.41
23:LO:473:GLU:OE1	57:SM:1:MET:HB3	2.21	0.41
25:LQ:537:VAL:HG12	25:LQ:548:ILE:HD12	2.02	0.41
25:LQ:840:MET:HE1	25:LQ:887:LEU:HD13	2.02	0.41
28:LT:377:SER:O	28:LT:377:SER:OG	2.37	0.41
29:LU:83:LEU:CD1	29:LU:364:ILE:HG21	2.49	0.41
31:LW:14:GLU:OE1	31:LW:14:GLU:N	2.53	0.41
35:NB:231:ALA:HB3	35:NB:232:PRO:HD3	2.01	0.41
40:NG:42:VAL:HG21	40:NG:63:ALA:O	2.19	0.41
41:NH:192:LYS:HG3	41:NH:192:LYS:O	2.20	0.41
41:NH:263:PRO:HG2	41:NH:557:THR:HG21	2.01	0.41
43:NK:212:ARG:NE	43:NK:212:ARG:HA	2.36	0.41
54:SI:1112:PHE:CD2	60:SQ:174:LEU:HD11	2.55	0.41
55:SK:252:LEU:HD12	64:SU:426:PHE:HE2	1.84	0.41
58:SN:74:LEU:HD11	58:SN:156:MET:HE1	2.02	0.41
2:L1:259:U:H3'	2:L1:260:U:H5''	2.02	0.41
2:L1:1145:U:O2'	34:NA:536:ARG:NH2	2.53	0.41
3:L2:24:U:O2	3:L2:24:U:O2'	2.28	0.41
16:LH:298:ASP:OD1	16:LH:299:SER:N	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:LJ:238:ASP:O	18:LJ:242:ASN:N	2.50	0.41
20:LL:136:LEU:HD23	20:LL:136:LEU:H	1.85	0.41
21:LM:230:LYS:O	21:LM:234:LEU:HD23	2.20	0.41
22:LN:163:GLY:O	22:LN:186:GLN:NE2	2.54	0.41
23:LO:552:ASN:OD1	23:LO:553:ILE:N	2.52	0.41
26:LR:501:PRO:HG3	26:LR:543:GLN:HA	2.03	0.41
26:LR:730:ILE:O	26:LR:730:ILE:HG22	2.20	0.41
27:LS:304:LEU:HD21	27:LS:473:ILE:HD13	2.02	0.41
32:LY:913:PHE:HA	32:LY:916:ILE:HD12	2.01	0.41
33:LZ:59:ASN:C	33:LZ:59:ASN:HD22	2.27	0.41
41:NH:268:LEU:HD23	41:NH:268:LEU:C	2.46	0.41
48:SA:171:ASP:C	48:SA:171:ASP:OD1	2.63	0.41
49:SB:131:MET:HE1	49:SB:139:MET:CE	2.50	0.41
50:SC:272:LYS:O	50:SC:276:ILE:HD12	2.20	0.41
59:SP:2012:MET:C	59:SP:2013:LEU:HD22	2.45	0.41
66:SW:117:TYR:N	66:SW:118:PRO:CD	2.84	0.41
2:L1:327:U:H1'	12:LD:10:GLU:OE1	2.21	0.41
5:L4:195:ILE:HA	5:L4:210:ILE:HD13	2.02	0.41
7:L6:141:ILE:CD1	7:L6:175:ILE:HD12	2.51	0.41
25:LQ:537:VAL:O	25:LQ:537:VAL:HG23	2.20	0.41
26:LR:15:ILE:O	26:LR:34:THR:OG1	2.37	0.41
26:LR:430:TYR:CE1	26:LR:466:TRP:HB3	2.55	0.41
31:LW:196:LEU:CD2	31:LW:207:THR:HG22	2.51	0.41
41:NH:1051:LEU:HD23	41:NH:1051:LEU:C	2.45	0.41
42:NI:19:LYS:N	42:NI:156:PHE:O	2.44	0.41
42:NI:147:LEU:HD23	42:NI:154:GLU:HG3	2.02	0.41
50:SD:169:LYS:HG2	50:SD:193:VAL:HG22	2.01	0.41
59:SP:773:LEU:O	59:SP:773:LEU:HD23	2.21	0.41
2:L1:248:U:O2'	2:L1:249:U:OP1	2.34	0.41
2:L1:1632:C:O2'	23:LO:422:PHE:O	2.29	0.41
18:LJ:217:ASN:OD1	18:LJ:218:VAL:N	2.53	0.41
41:NH:124:VAL:HG12	41:NH:128:LEU:HD13	2.02	0.41
48:SA:229:LEU:HD21	48:SA:255:ALA:HB1	2.02	0.41
49:SB:3:TYR:O	49:SB:88:ILE:N	2.44	0.41
58:SN:78:ASP:OD1	58:SN:104:LYS:NZ	2.48	0.41
59:SP:385:ALA:HA	59:SP:389:ILE:HD13	2.02	0.41
59:SP:613:MET:N	59:SP:613:MET:SD	2.94	0.41
59:SP:1094:PHE:HD2	59:SP:1132:ALA:HB1	1.85	0.41
59:SP:1922:ILE:HD13	59:SP:1965:ALA:HB1	2.02	0.41
64:SU:28:ILE:HG22	64:SU:32:ASN:OD1	2.19	0.41
64:SU:56:VAL:O	64:SU:60:PHE:N	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SU:279:LEU:HD23	64:SU:318:LEU:HD22	2.02	0.41
64:SU:400:PRO:CB	64:SU:495:MET:HE1	2.50	0.41
2:L1:151:G:OP2	14:LF:127:LYS:NZ	2.53	0.41
15:LG:59:SER:O	15:LG:59:SER:OG	2.39	0.41
15:LG:60:GLU:N	15:LG:60:GLU:OE2	2.54	0.41
23:LO:637:GLU:OE1	23:LO:637:GLU:N	2.48	0.41
26:LR:12:LEU:HB3	26:LR:641:PHE:HB2	2.01	0.41
26:LR:268:GLN:HG3	26:LR:270:ILE:HD11	2.03	0.41
26:LR:387:HIS:CD2	26:LR:413:ILE:HD12	2.56	0.41
27:LS:165:ARG:HG2	28:LT:175:THR:HG21	2.02	0.41
28:LT:632:VAL:HG13	28:LT:641:LEU:HD21	2.02	0.41
29:LU:92:ILE:HG12	29:LU:108:ALA:HB2	2.03	0.41
32:LX:27:VAL:HG13	32:LX:152:LEU:HD13	2.01	0.41
32:LX:841:ARG:NH1	32:LY:784:ARG:HE	2.19	0.41
32:LY:522:THR:HG21	32:LY:706:PRO:O	2.21	0.41
34:NA:454:VAL:O	34:NA:454:VAL:HG12	2.20	0.41
39:NF:115:LEU:HD23	43:NK:252:PRO:HD3	2.03	0.41
41:NH:1150:VAL:HG21	41:NH:1165:SER:HB2	2.02	0.41
54:SI:1024:LYS:HD3	54:SI:1024:LYS:N	2.34	0.41
59:SP:667:PHE:HD1	59:SP:699:LEU:HD13	1.85	0.41
59:SP:1376:ASP:OD1	59:SP:1423:TYR:OH	2.31	0.41
63:ST:481:MET:HE1	63:ST:501:PHE:CE2	2.55	0.41
16:LH:287:ASP:OD1	16:LH:287:ASP:N	2.52	0.41
16:LH:741:SER:OG	16:LH:761:GLU:O	2.21	0.41
17:LI:546:ASP:OD1	17:LI:546:ASP:N	2.54	0.41
18:LJ:42:VAL:O	18:LJ:42:VAL:HG23	2.20	0.41
20:LL:497:PRO:O	20:LL:500:VAL:HG22	2.21	0.41
21:LM:750:ASN:O	21:LM:753:ALA:HB3	2.21	0.41
24:LP:80:THR:HG23	24:LP:80:THR:O	2.20	0.41
26:LR:25:VAL:HG12	26:LR:294:LEU:HD13	2.03	0.41
26:LR:109:ASP:OD2	26:LR:110:ALA:N	2.54	0.41
35:NB:376:VAL:HG22	64:SU:57:MET:CE	2.50	0.41
39:NF:56:ASP:OD2	46:NQ:51:GLN:N	2.51	0.41
44:NM:156:ALA:HB3	44:NM:161:ILE:HD11	2.03	0.41
50:SC:178:GLY:CA	50:SC:210:MET:HE2	2.51	0.41
59:SP:1045:VAL:HG13	59:SP:1046:HIS:N	2.36	0.41
59:SP:1151:ILE:HG21	59:SP:1198:PHE:CD1	2.56	0.41
59:SP:1220:LEU:O	59:SP:1224:LEU:HD23	2.21	0.41
59:SP:1658:LEU:CD2	59:SP:1697:ILE:HD11	2.51	0.41
59:SP:2142:GLU:OE2	59:SP:2168:TYR:OH	2.38	0.41
63:ST:560:TYR:OH	63:ST:565:VAL:HG21	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:ST:605:ASP:OD2	63:ST:607:THR:OG1	2.29	0.41
2:L1:139:C:OP2	7:L6:187:LYS:NZ	2.49	0.41
2:L1:917:U:O2	40:NG:41:ARG:NH1	2.54	0.41
2:L1:1498:G:OP1	58:SN:250:THR:HG22	2.20	0.41
8:L7:73:VAL:O	8:L7:73:VAL:HG22	2.21	0.41
16:LH:208:LEU:HB2	16:LH:230:LEU:HD21	2.02	0.41
17:LI:599:MET:HE1	17:LI:641:VAL:HG22	2.01	0.41
20:LL:27:GLN:HB2	20:LL:53:LEU:HD12	2.03	0.41
21:LM:1137:PHE:O	21:LM:1141:ASN:N	2.46	0.41
22:LN:580:LYS:C	22:LN:596:MET:HE3	2.45	0.41
25:LQ:73:ASP:OD1	25:LQ:73:ASP:N	2.53	0.41
25:LQ:479:LEU:HD21	25:LQ:488:LEU:HD11	2.02	0.41
26:LR:277:VAL:HG21	26:LR:280:ARG:HD3	2.03	0.41
29:LU:288:TYR:O	29:LU:298:LEU:N	2.53	0.41
31:LW:348:SER:OG	31:LW:350:ASP:OD1	2.38	0.41
32:LX:475:ARG:NH1	32:LX:475:ARG:HB2	2.36	0.41
35:NB:599:LYS:NZ	60:SQ:138:LYS:O	2.54	0.41
41:NH:376:SER:OG	41:NH:377:SER:N	2.53	0.41
41:NH:765:LEU:HD23	41:NH:1168:TYR:CD2	2.54	0.41
48:SA:244:ASP:OD1	48:SA:244:ASP:N	2.53	0.41
50:SC:325:LEU:HD23	50:SC:325:LEU:H	1.84	0.41
51:SE:54:MET:HE1	51:SE:67:LEU:HB2	2.01	0.41
53:SH:337:VAL:N	54:SI:554:TYR:OH	2.53	0.41
59:SP:617:ASP:N	59:SP:617:ASP:OD1	2.54	0.41
59:SP:663:LEU:HD23	59:SP:696:VAL:HG23	2.02	0.41
64:SU:350:MET:HE1	64:SU:398:VAL:CG2	2.51	0.41
67:SY:185:MET:SD	67:SY:185:MET:N	2.94	0.41
1:L0:320:A:OP1	23:LO:249:ARG:NH1	2.43	0.41
2:L1:438:A:H1'	2:L1:465:G:H22	1.85	0.41
2:L1:1463:C:H2'	2:L1:1464:G:O4'	2.21	0.41
2:L1:1679:G:H1'	2:L1:1722:A:H61	1.86	0.41
3:L2:113:G:N2	3:L2:256:G:N3	2.69	0.41
6:L5:20:PHE:CE2	28:LT:494:LEU:HD22	2.56	0.41
16:LH:211:MET:CE	16:LH:259:VAL:HG21	2.49	0.41
17:LI:544:LEU:HD22	17:LI:550:LEU:HB3	2.02	0.41
19:LK:509:GLN:NE2	20:LL:507:ILE:O	2.47	0.41
20:LL:46:TRP:CE3	20:LL:311:MET:SD	3.14	0.41
20:LL:296:ILE:HG23	20:LL:296:ILE:O	2.20	0.41
20:LL:357:VAL:HG23	20:LL:357:VAL:O	2.21	0.41
21:LM:252:ASP:N	21:LM:252:ASP:OD1	2.53	0.41
25:LQ:178:ILE:HD11	25:LQ:231:LEU:CD1	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:LR:601:ILE:HD11	26:LR:613:LEU:HD11	2.03	0.41
28:LT:188:VAL:HG21	28:LT:223:LEU:HD21	2.02	0.41
28:LT:494:LEU:HD23	28:LT:495:ARG:N	2.35	0.41
31:LW:289:MET:HE3	31:LW:303:ILE:HG22	2.03	0.41
32:LX:502:PHE:O	32:LX:506:GLY:N	2.53	0.41
32:LX:522:THR:HG21	32:LX:706:PRO:O	2.21	0.41
33:LZ:122:GLU:OE1	33:LZ:122:GLU:N	2.53	0.41
40:NG:114:ARG:NH1	44:NM:72:ASP:OD2	2.54	0.41
41:NH:102:ILE:H	41:NH:102:ILE:HD12	1.86	0.41
44:NM:32:ILE:HD11	44:NM:46:THR:HG22	2.03	0.41
50:SC:155:ILE:CD1	50:SC:162:LEU:HD21	2.50	0.41
51:SE:50:GLU:HG2	51:SE:104:THR:HG22	2.02	0.41
51:SF:13:ASP:O	51:SF:17:THR:HG23	2.20	0.41
52:SG:185:LEU:HD13	52:SG:527:VAL:HG11	2.03	0.41
59:SP:541:ILE:CD1	59:SP:558:TRP:CD1	3.03	0.41
59:SP:1110:LEU:HD21	59:SP:1150:ILE:HD13	2.03	0.41
59:SP:1189:LEU:O	59:SP:1190:SER:HB3	2.21	0.41
59:SP:1562:VAL:HG11	59:SP:1579:LEU:HD11	2.02	0.41
59:SP:2104:LEU:HD12	59:SP:2105:ALA:N	2.36	0.41
66:SW:186:GLU:HG2	66:SW:188:LYS:HG2	2.02	0.41
1:L0:392:U:H5"	33:LZ:102:THR:HG22	2.03	0.41
10:L9:136:VAL:HG22	10:L9:156:ILE:HD13	2.03	0.41
18:LJ:452:ASP:OD1	18:LJ:453:VAL:N	2.54	0.41
18:LJ:467:LEU:HD22	20:LL:550:THR:HG21	2.03	0.41
20:LL:53:LEU:HD11	20:LL:60:VAL:HG23	2.03	0.41
25:LQ:601:GLY:N	25:LQ:606:ASP:O	2.48	0.41
28:LT:821:LEU:HD23	28:LT:860:GLU:OE2	2.21	0.41
29:LU:112:LEU:HD12	29:LU:112:LEU:N	2.36	0.41
30:LV:268:GLN:HE22	30:LV:298:LYS:HG3	1.85	0.41
31:LW:111:PHE:HD2	31:LW:133:HIS:HB2	1.85	0.41
32:LX:45:MET:HE3	32:LX:45:MET:HA	2.02	0.41
32:LX:195:ASN:HD21	32:LX:482:ILE:HD13	1.86	0.41
34:NA:311:ILE:HD11	54:SI:1032:LEU:HA	2.02	0.41
34:NA:384:ARG:NH2	57:SM:78:ALA:O	2.46	0.41
39:NF:37:ILE:HD12	39:NF:37:ILE:H	1.86	0.41
44:NM:136:ARG:HB2	44:NM:218:LEU:HD11	2.03	0.41
44:NM:182:ALA:CB	44:NM:231:LEU:HD11	2.51	0.41
48:SA:221:LEU:HD12	48:SA:224:LYS:HZ1	1.86	0.41
52:SG:273:VAL:O	52:SG:273:VAL:HG13	2.21	0.41
52:SG:287:ALA:O	52:SG:295:LEU:HD12	2.21	0.41
54:SI:84:THR:HG23	54:SI:215:TYR:CE2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SI:235:LEU:HD13	54:SI:238:ARG:NH1	2.36	0.41
59:SP:559:ASN:ND2	59:SP:602:GLU:OE1	2.48	0.41
59:SP:997:MET:SD	59:SP:1029:SER:HA	2.61	0.41
59:SP:2104:LEU:HD12	59:SP:2104:LEU:C	2.46	0.41
60:SQ:121:LEU:CD2	60:SQ:143:VAL:HG23	2.51	0.41
64:SU:247:ILE:H	64:SU:247:ILE:HD12	1.85	0.41
66:SW:26:ILE:HG22	66:SW:27:GLY:N	2.36	0.41
2:L1:868:G:OP1	39:NF:121:ARG:NH2	2.54	0.40
2:L1:1633:A:C5	2:L1:1634:C:C5	3.09	0.40
7:L6:23:ARG:HB2	7:L6:41:VAL:HA	2.03	0.40
16:LH:473:LEU:HD22	16:LH:532:TRP:CZ2	2.56	0.40
20:LL:244:ILE:HD12	20:LL:259:PRO:HG3	2.03	0.40
21:LM:241:ILE:HG22	21:LM:245:LEU:HD23	2.02	0.40
22:LN:426:GLN:OE1	37:ND:190:LEU:HD12	2.20	0.40
25:LQ:65:ASP:OD1	25:LQ:65:ASP:N	2.54	0.40
29:LU:246:LEU:O	29:LU:255:THR:N	2.46	0.40
39:NF:81:ALA:HB3	42:NI:259:ARG:HE	1.86	0.40
42:NI:147:LEU:HD23	42:NI:154:GLU:CG	2.51	0.40
49:SB:2:ALA:HB3	49:SB:17:ALA:HB3	2.03	0.40
49:SB:292:GLY:O	49:SB:296:GLY:N	2.48	0.40
52:SG:304:ILE:HD13	52:SG:338:THR:HG21	2.03	0.40
59:SP:1663:ILE:HD13	59:SP:1701:MET:HG2	2.02	0.40
64:SU:163:ILE:HG23	64:SU:173:GLU:CD	2.46	0.40
64:SU:350:MET:HE1	64:SU:398:VAL:HG21	2.01	0.40
2:L1:6:G:C5	29:LU:424:LYS:HE3	2.56	0.40
3:L2:60:A:C4	23:LO:635:MET:CE	3.04	0.40
3:L2:104:C:O2'	48:SA:344:ARG:NH2	2.48	0.40
3:L2:251:G:N7	52:SG:545:LYS:NZ	2.53	0.40
13:LE:20:THR:O	13:LE:20:THR:HG22	2.20	0.40
14:LF:38:ASP:OD2	14:LF:38:ASP:C	2.65	0.40
17:LI:632:THR:OG1	17:LI:633:GLN:N	2.54	0.40
20:LL:22:VAL:HG12	20:LL:27:GLN:CG	2.51	0.40
26:LR:407:SER:O	26:LR:437:VAL:HG22	2.22	0.40
27:LS:272:LEU:HD21	27:LS:314:THR:HG21	2.03	0.40
30:LV:56:SER:OG	30:LV:57:GLU:OE2	2.33	0.40
32:LX:887:ALA:HB2	32:LX:898:ILE:HD11	2.03	0.40
38:NE:19:PHE:O	38:NE:23:PHE:N	2.47	0.40
41:NH:495:THR:O	41:NH:498:MET:N	2.54	0.40
41:NH:867:ILE:HD12	41:NH:867:ILE:H	1.86	0.40
54:SI:879:THR:HG22	54:SI:880:TYR:N	2.36	0.40
59:SP:126:GLU:OE1	59:SP:130:LYS:NZ	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:SP:615:VAL:HG13	59:SP:615:VAL:O	2.21	0.40
63:ST:568:PHE:CG	63:ST:643:LEU:HD13	2.56	0.40
1:L0:347:U:OP1	43:NK:62:ARG:NH2	2.47	0.40
2:L1:49:C:OP2	2:L1:425:A:N6	2.53	0.40
2:L1:447:U:H2'	2:L1:448:C:O4'	2.20	0.40
2:L1:1192:C:O2'	2:L1:1194:A:N6	2.32	0.40
17:LI:634:LEU:HD23	17:LI:634:LEU:C	2.47	0.40
22:LN:341:SER:OG	22:LN:344:ALA:HB3	2.21	0.40
23:LO:473:GLU:OE2	57:SM:133:LYS:HG2	2.22	0.40
24:LP:12:ILE:HG21	31:LW:62:ALA:HB1	2.03	0.40
29:LU:444:GLU:HB3	29:LU:451:MET:HE1	2.04	0.40
31:LW:429:GLU:OE1	33:LZ:2:VAL:HG23	2.21	0.40
32:LX:654:ILE:HD13	32:LX:657:LEU:HD23	2.03	0.40
32:LX:757:GLU:OE1	32:LX:757:GLU:N	2.54	0.40
32:LX:830:LEU:C	32:LX:830:LEU:HD23	2.46	0.40
38:NE:243:ILE:HG13	38:NE:287:ILE:HG22	2.02	0.40
41:NH:721:VAL:HG23	41:NH:722:LEU:HD12	2.03	0.40
50:SD:230:TYR:OH	50:SD:256:ASN:OD1	2.31	0.40
51:SF:14:ALA:O	51:SF:17:THR:OG1	2.33	0.40
51:SF:81:VAL:HG21	51:SF:87:LEU:HD12	2.04	0.40
62:SS:377:THR:OG1	62:SS:381:ARG:NH2	2.53	0.40
63:ST:703:GLN:HG3	64:SU:413:MET:HE3	2.02	0.40
64:SU:90:TRP:O	64:SU:93:LYS:N	2.55	0.40
9:L8:12:SER:OG	9:L8:13:ALA:N	2.54	0.40
10:L9:95:TYR:OH	59:SP:1843:GLU:OE1	2.39	0.40
16:LH:459:ILE:HG22	16:LH:468:VAL:HG22	2.03	0.40
18:LJ:226:ILE:HD13	18:LJ:239:LEU:HD21	2.03	0.40
18:LJ:447:LEU:HD11	18:LJ:483:LEU:HD13	2.04	0.40
23:LO:259:ASN:OD1	23:LO:260:GLN:NE2	2.54	0.40
24:LP:183:TYR:CZ	24:LP:322:LEU:HD12	2.56	0.40
26:LR:138:HIS:HB3	26:LR:140:PHE:CE1	2.56	0.40
28:LT:627:ASN:OD1	28:LT:647:THR:OG1	2.39	0.40
30:LV:146:TYR:CE1	30:LV:167:LEU:HD12	2.57	0.40
32:LX:888:ILE:O	32:LY:791:TYR:OH	2.22	0.40
32:LY:764:ASN:OD1	32:LY:765:VAL:N	2.54	0.40
52:SG:220:TYR:HA	52:SG:232:THR:HG21	2.03	0.40
59:SP:133:ILE:HG23	59:SP:180:LEU:CD1	2.51	0.40
64:SU:40:VAL:HG11	64:SU:110:PRO:HD2	2.03	0.40
64:SU:121:ASP:OD1	64:SU:184:TYR:OH	2.36	0.40
2:L1:79:C:OP1	7:L6:159:ARG:NH2	2.53	0.40
2:L1:332:U:P	9:L8:56:ARG:HH22	2.45	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:L7:75:THR:HG23	8:L7:76:LYS:N	2.36	0.40
13:LE:23:ARG:CZ	29:LU:309:MET:HE1	2.51	0.40
13:LE:23:ARG:NH1	29:LU:309:MET:HE1	2.36	0.40
16:LH:690:ASN:ND2	16:LH:749:ASP:O	2.52	0.40
16:LH:862:LYS:NZ	21:LM:343:VAL:HG11	2.37	0.40
18:LJ:54:ASP:OD2	18:LJ:111:TYR:OH	2.19	0.40
18:LJ:183:LEU:HD23	18:LJ:196:TYR:O	2.22	0.40
22:LN:155:LYS:NZ	22:LN:180:ASP:OD2	2.50	0.40
25:LQ:53:ASP:OD2	25:LQ:56:THR:OG1	2.39	0.40
25:LQ:127:LEU:HD12	25:LQ:137:ILE:O	2.21	0.40
25:LQ:589:ILE:HG21	25:LQ:621:VAL:HG11	2.04	0.40
37:ND:117:LEU:O	64:SU:21:ARG:NH2	2.54	0.40
41:NH:599:VAL:HG11	41:NH:609:ASN:ND2	2.37	0.40
48:SA:174:ILE:HD12	48:SA:296:MET:HG2	2.03	0.40
50:SC:202:ARG:HB2	50:SC:203:PRO:HD3	2.04	0.40
59:SP:1251:VAL:HG11	59:SP:1290:GLU:OE2	2.20	0.40
59:SP:1925:ASP:OD1	59:SP:1926:PHE:N	2.53	0.40
63:ST:523:ILE:HG23	64:SU:507:LEU:HD21	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	L3	91/146 (62%)	91 (100%)	0	0	100	100
5	L4	242/261 (93%)	237 (98%)	5 (2%)	0	100	100
6	L5	202/225 (90%)	197 (98%)	5 (2%)	0	100	100
7	L6	202/236 (86%)	199 (98%)	3 (2%)	0	100	100
8	L7	165/190 (87%)	164 (99%)	1 (1%)	0	100	100
9	L8	166/200 (83%)	163 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	L9	169/197 (86%)	166 (98%)	3 (2%)	0	100	100
11	LC	123/143 (86%)	122 (99%)	1 (1%)	0	100	100
12	LD	135/156 (86%)	132 (98%)	3 (2%)	0	100	100
13	LE	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
14	LF	128/135 (95%)	126 (98%)	2 (2%)	0	100	100
15	LG	60/67 (90%)	59 (98%)	1 (2%)	0	100	100
16	LH	790/896 (88%)	759 (96%)	31 (4%)	0	100	100
17	LI	582/713 (82%)	570 (98%)	12 (2%)	0	100	100
18	LJ	489/513 (95%)	481 (98%)	8 (2%)	0	100	100
19	LK	130/575 (23%)	130 (100%)	0	0	100	100
20	LL	496/643 (77%)	481 (97%)	15 (3%)	0	100	100
21	LM	1597/1769 (90%)	1565 (98%)	32 (2%)	0	100	100
22	LN	649/776 (84%)	632 (97%)	17 (3%)	0	100	100
23	LO	829/923 (90%)	816 (98%)	13 (2%)	0	100	100
24	LP	376/440 (86%)	374 (100%)	2 (0%)	0	100	100
25	LQ	831/943 (88%)	804 (97%)	27 (3%)	0	100	100
26	LR	785/817 (96%)	766 (98%)	19 (2%)	0	100	100
27	LS	469/594 (79%)	452 (96%)	17 (4%)	0	100	100
28	LT	865/939 (92%)	845 (98%)	20 (2%)	0	100	100
29	LU	456/489 (93%)	443 (97%)	13 (3%)	0	100	100
30	LV	401/707 (57%)	388 (97%)	13 (3%)	0	100	100
31	LW	531/554 (96%)	512 (96%)	19 (4%)	0	100	100
32	LX	826/1056 (78%)	811 (98%)	15 (2%)	0	100	100
32	LY	834/1056 (79%)	817 (98%)	17 (2%)	0	100	100
33	LZ	179/183 (98%)	176 (98%)	3 (2%)	0	100	100
34	NA	274/593 (46%)	270 (98%)	4 (2%)	0	100	100
35	NB	255/610 (42%)	251 (98%)	4 (2%)	0	100	100
36	NC	111/357 (31%)	110 (99%)	1 (1%)	0	100	100
37	ND	70/214 (33%)	70 (100%)	0	0	100	100
38	NE	207/346 (60%)	205 (99%)	2 (1%)	0	100	100
39	NF	139/151 (92%)	138 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	NG	117/137 (85%)	113 (97%)	4 (3%)	0	100	100
41	NH	1063/1237 (86%)	1039 (98%)	24 (2%)	0	100	100
42	NI	232/297 (78%)	224 (97%)	8 (3%)	0	100	100
43	NK	253/316 (80%)	249 (98%)	4 (2%)	0	100	100
44	NM	224/255 (88%)	219 (98%)	5 (2%)	0	100	100
45	NN	257/534 (48%)	255 (99%)	2 (1%)	0	100	100
46	NQ	77/82 (94%)	75 (97%)	2 (3%)	0	100	100
47	OA	167/1729 (10%)	165 (99%)	2 (1%)	0	100	100
48	SA	379/504 (75%)	371 (98%)	8 (2%)	0	100	100
49	SB	434/511 (85%)	426 (98%)	8 (2%)	0	100	100
50	SC	237/327 (72%)	231 (98%)	6 (2%)	0	100	100
50	SD	228/327 (70%)	226 (99%)	2 (1%)	0	100	100
51	SE	119/126 (94%)	118 (99%)	1 (1%)	0	100	100
51	SF	119/126 (94%)	114 (96%)	5 (4%)	0	100	100
52	SG	453/573 (79%)	448 (99%)	5 (1%)	0	100	100
53	SH	358/367 (98%)	349 (98%)	9 (2%)	0	100	100
54	SI	799/1183 (68%)	788 (99%)	11 (1%)	0	100	100
55	SJ	207/252 (82%)	202 (98%)	5 (2%)	0	100	100
55	SK	225/252 (89%)	220 (98%)	5 (2%)	0	100	100
56	SL	169/189 (89%)	162 (96%)	7 (4%)	0	100	100
57	SM	278/290 (96%)	272 (98%)	6 (2%)	0	100	100
58	SN	251/274 (92%)	248 (99%)	3 (1%)	0	100	100
59	SP	2334/2493 (94%)	2287 (98%)	46 (2%)	1 (0%)	100	100
60	SQ	147/217 (68%)	140 (95%)	7 (5%)	0	100	100
61	SR	102/145 (70%)	101 (99%)	1 (1%)	0	100	100
62	SS	262/899 (29%)	257 (98%)	5 (2%)	0	100	100
63	ST	566/810 (70%)	559 (99%)	7 (1%)	0	100	100
64	SU	528/552 (96%)	522 (99%)	6 (1%)	0	100	100
65	SV	141/206 (68%)	139 (99%)	2 (1%)	0	100	100
66	SW	193/274 (70%)	189 (98%)	4 (2%)	0	100	100
67	SY	227/250 (91%)	226 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	SZ	255/483 (53%)	252 (99%)	3 (1%)	0	100	100
All	All	26382/35160 (75%)	25830 (98%)	551 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
59	SP	1190	SER

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	
4	L3	88/129 (68%)	88 (100%)	0	100	100
5	L4	208/222 (94%)	208 (100%)	0	100	100
6	L5	179/191 (94%)	179 (100%)	0	100	100
7	L6	175/201 (87%)	175 (100%)	0	100	100
8	L7	149/170 (88%)	149 (100%)	0	100	100
9	L8	137/161 (85%)	137 (100%)	0	100	100
10	L9	147/166 (89%)	147 (100%)	0	100	100
11	LC	105/119 (88%)	105 (100%)	0	100	100
12	LD	124/137 (90%)	123 (99%)	1 (1%)	73	76
13	LE	110/111 (99%)	110 (100%)	0	100	100
14	LF	109/113 (96%)	109 (100%)	0	100	100
15	LG	55/60 (92%)	55 (100%)	0	100	100
16	LH	745/826 (90%)	745 (100%)	0	100	100
17	LI	244/657 (37%)	244 (100%)	0	100	100
18	LJ	437/454 (96%)	437 (100%)	0	100	100
19	LK	124/533 (23%)	124 (100%)	0	100	100
20	LL	452/574 (79%)	452 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	LM	421/1633 (26%)	421 (100%)	0	100	100
22	LN	603/713 (85%)	603 (100%)	0	100	100
23	LO	729/811 (90%)	729 (100%)	0	100	100
24	LP	360/414 (87%)	360 (100%)	0	100	100
25	LQ	746/832 (90%)	746 (100%)	0	100	100
26	LR	698/719 (97%)	698 (100%)	0	100	100
27	LS	423/528 (80%)	423 (100%)	0	100	100
28	LT	763/819 (93%)	763 (100%)	0	100	100
29	LU	415/443 (94%)	415 (100%)	0	100	100
30	LV	366/636 (58%)	366 (100%)	0	100	100
31	LW	465/480 (97%)	465 (100%)	0	100	100
32	LX	751/934 (80%)	751 (100%)	0	100	100
32	LY	592/934 (63%)	592 (100%)	0	100	100
33	LZ	170/172 (99%)	170 (100%)	0	100	100
34	NA	194/535 (36%)	194 (100%)	0	100	100
35	NB	149/538 (28%)	149 (100%)	0	100	100
36	NC	3/315 (1%)	3 (100%)	0	100	100
37	ND	70/196 (36%)	70 (100%)	0	100	100
38	NE	166/304 (55%)	166 (100%)	0	100	100
39	NF	121/128 (94%)	121 (100%)	0	100	100
40	NG	90/105 (86%)	90 (100%)	0	100	100
41	NH	982/1125 (87%)	982 (100%)	0	100	100
42	NI	220/274 (80%)	220 (100%)	0	100	100
43	NK	233/289 (81%)	232 (100%)	1 (0%)	84	81
44	NM	205/224 (92%)	205 (100%)	0	100	100
45	NN	44/482 (9%)	44 (100%)	0	100	100
46	NQ	68/71 (96%)	68 (100%)	0	100	100
47	OA	14/1544 (1%)	14 (100%)	0	100	100
48	SA	328/435 (75%)	328 (100%)	0	100	100
49	SB	360/433 (83%)	360 (100%)	0	100	100
50	SC	200/240 (83%)	200 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	SD	197/240 (82%)	197 (100%)	0	100	100
51	SE	100/104 (96%)	100 (100%)	0	100	100
51	SF	100/104 (96%)	100 (100%)	0	100	100
52	SG	399/503 (79%)	399 (100%)	0	100	100
53	SH	307/312 (98%)	307 (100%)	0	100	100
54	SI	718/1039 (69%)	718 (100%)	0	100	100
55	SJ	192/222 (86%)	192 (100%)	0	100	100
55	SK	205/222 (92%)	205 (100%)	0	100	100
56	SL	155/169 (92%)	155 (100%)	0	100	100
57	SM	251/258 (97%)	251 (100%)	0	100	100
58	SN	236/256 (92%)	236 (100%)	0	100	100
59	SP	1956/2307 (85%)	1956 (100%)	0	100	100
60	SQ	140/200 (70%)	139 (99%)	1 (1%)	76	77
61	SR	86/120 (72%)	86 (100%)	0	100	100
62	SS	251/808 (31%)	251 (100%)	0	100	100
63	ST	441/732 (60%)	441 (100%)	0	100	100
64	SU	490/506 (97%)	490 (100%)	0	100	100
65	SV	42/192 (22%)	42 (100%)	0	100	100
66	SW	172/238 (72%)	172 (100%)	0	100	100
67	SY	218/234 (93%)	218 (100%)	0	100	100
68	SZ	14/424 (3%)	14 (100%)	0	100	100
All	All	21207/31320 (68%)	21204 (100%)	3 (0%)	100	100

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	LD	21	ASN
43	NK	277	GLN
60	SQ	83	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (180) such sidechains are listed below:

Mol	Chain	Res	Type
6	L5	104	ASN

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Mol	Chain	Res	Type
7	L6	140	ASN
9	L8	84	HIS
14	LF	29	HIS
15	LG	27	GLN
16	LH	31	ASN
16	LH	115	HIS
16	LH	146	HIS
16	LH	150	ASN
16	LH	200	ASN
16	LH	236	ASN
16	LH	350	GLN
16	LH	393	ASN
16	LH	398	HIS
16	LH	738	ASN
16	LH	827	HIS
18	LJ	44	HIS
18	LJ	210	ASN
19	LK	394	HIS
20	LL	128	GLN
20	LL	195	GLN
20	LL	335	ASN
21	LM	10	GLN
21	LM	202	HIS
21	LM	258	HIS
22	LN	385	ASN
22	LN	731	HIS
23	LO	66	GLN
23	LO	147	GLN
23	LO	156	GLN
23	LO	565	ASN
23	LO	791	HIS
23	LO	825	GLN
23	LO	842	ASN
24	LP	51	ASN
24	LP	62	ASN
24	LP	134	ASN
24	LP	415	GLN
25	LQ	195	GLN
25	LQ	254	GLN
25	LQ	383	HIS
25	LQ	403	ASN
25	LQ	847	HIS

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Mol	Chain	Res	Type
25	LQ	871	GLN
25	LQ	910	GLN
26	LR	13	ASN
26	LR	54	HIS
26	LR	301	GLN
26	LR	433	HIS
27	LS	34	GLN
27	LS	224	ASN
27	LS	309	GLN
27	LS	357	ASN
27	LS	372	HIS
27	LS	388	HIS
27	LS	442	HIS
27	LS	520	ASN
28	LT	108	HIS
28	LT	916	HIS
29	LU	133	GLN
29	LU	276	ASN
29	LU	466	HIS
30	LV	96	HIS
30	LV	402	HIS
31	LW	115	HIS
31	LW	185	HIS
31	LW	190	HIS
31	LW	202	HIS
31	LW	248	HIS
31	LW	278	ASN
31	LW	417	ASN
32	LX	35	ASN
32	LX	133	ASN
32	LX	215	ASN
32	LX	261	HIS
32	LX	551	ASN
32	LX	721	HIS
32	LX	829	HIS
32	LX	891	GLN
32	LY	373	GLN
32	LY	429	GLN
32	LY	551	ASN
32	LY	587	GLN
33	LZ	27	HIS
33	LZ	45	HIS

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Mol	Chain	Res	Type
33	LZ	116	HIS
33	LZ	144	ASN
34	NA	480	GLN
35	NB	499	GLN
35	NB	513	HIS
35	NB	573	GLN
37	ND	212	ASN
38	NE	237	HIS
39	NF	5	HIS
39	NF	58	HIS
39	NF	123	HIS
40	NG	29	HIS
41	NH	582	GLN
41	NH	647	ASN
41	NH	705	HIS
41	NH	834	ASN
41	NH	1211	ASN
42	NI	23	HIS
42	NI	73	GLN
42	NI	146	ASN
42	NI	148	HIS
42	NI	151	HIS
43	NK	167	GLN
43	NK	199	HIS
46	NQ	9	HIS
46	NQ	19	HIS
48	SA	170	ASN
48	SA	176	GLN
48	SA	183	GLN
48	SA	235	HIS
48	SA	270	ASN
48	SA	334	GLN
48	SA	391	ASN
49	SB	165	GLN
49	SB	191	HIS
50	SC	93	HIS
50	SC	183	HIS
51	SF	5	ASN
52	SG	69	GLN
52	SG	177	ASN
52	SG	195	GLN
52	SG	226	HIS

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Mol	Chain	Res	Type
52	SG	449	ASN
53	SH	126	ASN
53	SH	176	GLN
53	SH	334	ASN
54	SI	55	HIS
54	SI	112	HIS
54	SI	162	HIS
54	SI	222	ASN
54	SI	426	HIS
54	SI	776	GLN
54	SI	986	HIS
54	SI	1151	GLN
55	SJ	73	HIS
56	SL	64	GLN
58	SN	165	GLN
58	SN	214	GLN
58	SN	217	GLN
59	SP	46	HIS
59	SP	53	GLN
59	SP	58	ASN
59	SP	83	HIS
59	SP	207	ASN
59	SP	346	GLN
59	SP	428	GLN
59	SP	577	HIS
59	SP	611	GLN
59	SP	802	ASN
59	SP	866	GLN
59	SP	941	GLN
59	SP	982	HIS
59	SP	1114	HIS
59	SP	1401	ASN
59	SP	1427	ASN
59	SP	1463	GLN
59	SP	1479	ASN
59	SP	1707	HIS
59	SP	1785	ASN
59	SP	1786	GLN
59	SP	1801	ASN
59	SP	1816	HIS
59	SP	1817	GLN
59	SP	1869	GLN

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Mol	Chain	Res	Type
60	SQ	126	HIS
62	SS	353	ASN
62	SS	431	HIS
62	SS	444	HIS
63	ST	107	ASN
63	ST	384	HIS
63	ST	705	HIS
63	ST	713	HIS
63	ST	765	GLN
64	SU	228	HIS
67	SY	9	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L0	442/700 (63%)	85 (19%)	0
2	L1	1180/1808 (65%)	200 (16%)	1 (0%)
3	L2	170/333 (51%)	26 (15%)	0
All	All	1792/2841 (63%)	311 (17%)	1 (0%)

All (311) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L0	7	A
1	L0	61	U
1	L0	62	C
1	L0	63	G
1	L0	64	U
1	L0	82	A
1	L0	83	U
1	L0	85	G
1	L0	86	C
1	L0	89	C
1	L0	91	U
1	L0	95	A
1	L0	103	G
1	L0	109	C
1	L0	110	G
1	L0	114	G
1	L0	122	U
1	L0	123	C

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Mol	Chain	Res	Type
1	L0	125	G
1	L0	127	U
1	L0	128	C
1	L0	129	U
1	L0	130	G
1	L0	142	U
1	L0	144	C
1	L0	148	G
1	L0	151	U
1	L0	152	U
1	L0	156	U
1	L0	176	U
1	L0	177	U
1	L0	190	U
1	L0	200	A
1	L0	227	U
1	L0	235	A
1	L0	236	C
1	L0	240	C
1	L0	256	U
1	L0	259	G
1	L0	260	A
1	L0	267	U
1	L0	279	A
1	L0	280	A
1	L0	281	G
1	L0	297	U
1	L0	304	U
1	L0	305	A
1	L0	306	G
1	L0	310	U
1	L0	311	C
1	L0	316	U
1	L0	323	A
1	L0	325	U
1	L0	326	C
1	L0	328	A
1	L0	333	G
1	L0	353	A
1	L0	354	G
1	L0	360	C
1	L0	369	G

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Mol	Chain	Res	Type
1	L0	370	U
1	L0	371	G
1	L0	372	A
1	L0	373	U
1	L0	381	G
1	L0	382	U
1	L0	383	G
1	L0	386	A
1	L0	391	C
1	L0	393	C
1	L0	395	C
1	L0	396	A
1	L0	407	A
1	L0	427	A
1	L0	430	C
1	L0	432	C
1	L0	461	A
1	L0	464	G
1	L0	468	A
1	L0	472	A
1	L0	474	A
1	L0	481	U
1	L0	482	A
1	L0	487	A
1	L0	488	U
2	L1	-6	A
2	L1	5	U
2	L1	18	C
2	L1	23	G
2	L1	25	C
2	L1	34	G
2	L1	35	U
2	L1	39	A
2	L1	57	G
2	L1	60	U
2	L1	61	A
2	L1	67	A
2	L1	71	A
2	L1	73	U
2	L1	74	U
2	L1	76	A
2	L1	77	U

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Mol	Chain	Res	Type
2	L1	88	U
2	L1	100	A
2	L1	103	A
2	L1	104	A
2	L1	114	C
2	L1	116	U
2	L1	127	G
2	L1	128	U
2	L1	138	A
2	L1	140	A
2	L1	145	A
2	L1	160	C
2	L1	164	A
2	L1	168	A
2	L1	187	G
2	L1	188	A
2	L1	189	C
2	L1	190	C
2	L1	192	U
2	L1	193	U
2	L1	195	G
2	L1	196	G
2	L1	201	G
2	L1	202	A
2	L1	204	G
2	L1	249	U
2	L1	260	U
2	L1	261	U
2	L1	265	A
2	L1	275	C
2	L1	276	C
2	L1	277	U
2	L1	278	U
2	L1	279	G
2	L1	280	U
2	L1	299	A
2	L1	309	C
2	L1	311	U
2	L1	316	A
2	L1	320	U
2	L1	321	C
2	L1	322	G

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Mol	Chain	Res	Type
2	L1	333	A
2	L1	334	G
2	L1	337	G
2	L1	340	U
2	L1	387	A
2	L1	388	G
2	L1	389	G
2	L1	393	C
2	L1	400	A
2	L1	402	C
2	L1	423	G
2	L1	424	C
2	L1	425	A
2	L1	426	G
2	L1	428	A
2	L1	430	G
2	L1	435	C
2	L1	437	A
2	L1	438	A
2	L1	439	U
2	L1	444	C
2	L1	447	U
2	L1	453	U
2	L1	456	A
2	L1	467	G
2	L1	468	A
2	L1	475	A
2	L1	477	A
2	L1	495	C
2	L1	496	G
2	L1	501	U
2	L1	505	A
2	L1	516	G
2	L1	520	A
2	L1	538	A
2	L1	539	G
2	L1	542	A
2	L1	545	A
2	L1	551	G
2	L1	552	G
2	L1	564	G
2	L1	565	C

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Mol	Chain	Res	Type
2	L1	575	C
2	L1	579	A
2	L1	583	C
2	L1	586	G
2	L1	594	A
2	L1	630	A
2	L1	635	A
2	L1	765	G
2	L1	766	U
2	L1	774	A
2	L1	803	A
2	L1	863	A
2	L1	865	A
2	L1	876	G
2	L1	893	U
2	L1	901	G
2	L1	906	A
2	L1	933	A
2	L1	935	U
2	L1	951	A
2	L1	960	U
2	L1	965	U
2	L1	966	A
2	L1	970	A
2	L1	1027	A
2	L1	1030	A
2	L1	1033	C
2	L1	1040	G
2	L1	1076	A
2	L1	1079	U
2	L1	1084	A
2	L1	1085	G
2	L1	1114	G
2	L1	1122	G
2	L1	1128	C
2	L1	1132	A
2	L1	1158	C
2	L1	1159	C
2	L1	1167	G
2	L1	1175	U
2	L1	1191	U
2	L1	1192	C

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Mol	Chain	Res	Type
2	L1	1193	A
2	L1	1207	C
2	L1	1208	A
2	L1	1218	G
2	L1	1227	A
2	L1	1228	G
2	L1	1230	A
2	L1	1232	U
2	L1	1256	A
2	L1	1267	G
2	L1	1268	G
2	L1	1269	U
2	L1	1270	G
2	L1	1435	G
2	L1	1436	A
2	L1	1437	U
2	L1	1438	G
2	L1	1440	C
2	L1	1461	C
2	L1	1472	C
2	L1	1473	U
2	L1	1474	G
2	L1	1475	A
2	L1	1485	C
2	L1	1488	G
2	L1	1492	A
2	L1	1493	A
2	L1	1506	G
2	L1	1577	A
2	L1	1590	G
2	L1	1595	U
2	L1	1596	C
2	L1	1601	G
2	L1	1602	C
2	L1	1611	A
2	L1	1618	C
2	L1	1619	C
2	L1	1633	A
2	L1	1651	A
2	L1	1655	A
2	L1	1657	U
2	L1	1658	G

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Mol	Chain	Res	Type
2	L1	1664	C
2	L1	1680	G
2	L1	1683	C
2	L1	1701	A
2	L1	1703	C
2	L1	1715	G
2	L1	1716	C
2	L1	1721	A
2	L1	1745	G
2	L1	1747	G
2	L1	1768	G
2	L1	1778	G
2	L1	1780	G
2	L1	1781	A
2	L1	1782	A
3	L2	4	G
3	L2	14	A
3	L2	22	A
3	L2	24	U
3	L2	25	U
3	L2	27	U
3	L2	28	A
3	L2	30	A
3	L2	34	A
3	L2	35	U
3	L2	38	U
3	L2	40	A
3	L2	48	A
3	L2	56	A
3	L2	61	G
3	L2	62	C
3	L2	63	C
3	L2	77	U
3	L2	90	C
3	L2	91	C
3	L2	109	G
3	L2	252	C
3	L2	308	U
3	L2	324	U
3	L2	325	C
3	L2	329	C

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	L1	248	U

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
27	SEP	LS	128	27	8,9,10	1.61	1 (12%)	7,12,14	1.27	1 (14%)
23	SEP	LO	651	23	8,9,10	1.56	1 (12%)	7,12,14	1.20	1 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
27	SEP	LS	128	27	-	0/6/8/10	-
23	SEP	LO	651	23	-	1/6/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	LS	128	SEP	P-O1P	3.51	1.61	1.50
23	LO	651	SEP	P-O1P	3.44	1.61	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	LS	128	SEP	OG-CB-CA	2.77	110.84	108.14
23	LO	651	SEP	OG-CB-CA	2.42	110.50	108.14

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	LO	651	SEP	CA-CB-OG-P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 38 ligands modelled in this entry, 36 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
70	ATP	NH	1300	69	32,33,33	0.37	0	48,52,52	0.72	1 (2%)
72	GTP	SI	2001	69	33,34,34	1.86	5 (15%)	50,54,54	1.47	6 (12%)

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
70	ATP	NH	1300	69	-	6/22/38/38	0/3/3/3
72	GTP	SI	2001	69	-	0/22/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
72	SI	2001	GTP	C5-N7	6.51	1.52	1.39
72	SI	2001	GTP	C8-N9	-4.39	1.27	1.37
72	SI	2001	GTP	C4-N9	-3.95	1.28	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
72	SI	2001	GTP	C4-N3	2.11	1.39	1.34
72	SI	2001	GTP	PB-O2B	-2.08	1.45	1.55

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
72	SI	2001	GTP	C8-N9-C4	7.26	119.63	106.03
72	SI	2001	GTP	N9-C4-N3	2.69	131.32	125.95
72	SI	2001	GTP	C1'-N9-C8	-2.48	119.70	126.73
72	SI	2001	GTP	C6-C5-N7	2.43	134.71	130.29
72	SI	2001	GTP	C5-C4-N9	-2.17	101.78	105.66
72	SI	2001	GTP	C8-N7-C5	-2.14	100.45	104.26
70	NH	1300	ATP	O2'-C2'-C1'	-2.10	102.87	110.10

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
70	NH	1300	ATP	PB-O3B-PG-O3G
70	NH	1300	ATP	PB-O3B-PG-O2G
70	NH	1300	ATP	O4'-C4'-C5'-O5'
70	NH	1300	ATP	PA-O3A-PB-O3B
70	NH	1300	ATP	PA-O3A-PB-O1B
70	NH	1300	ATP	PA-O3A-PB-O2B

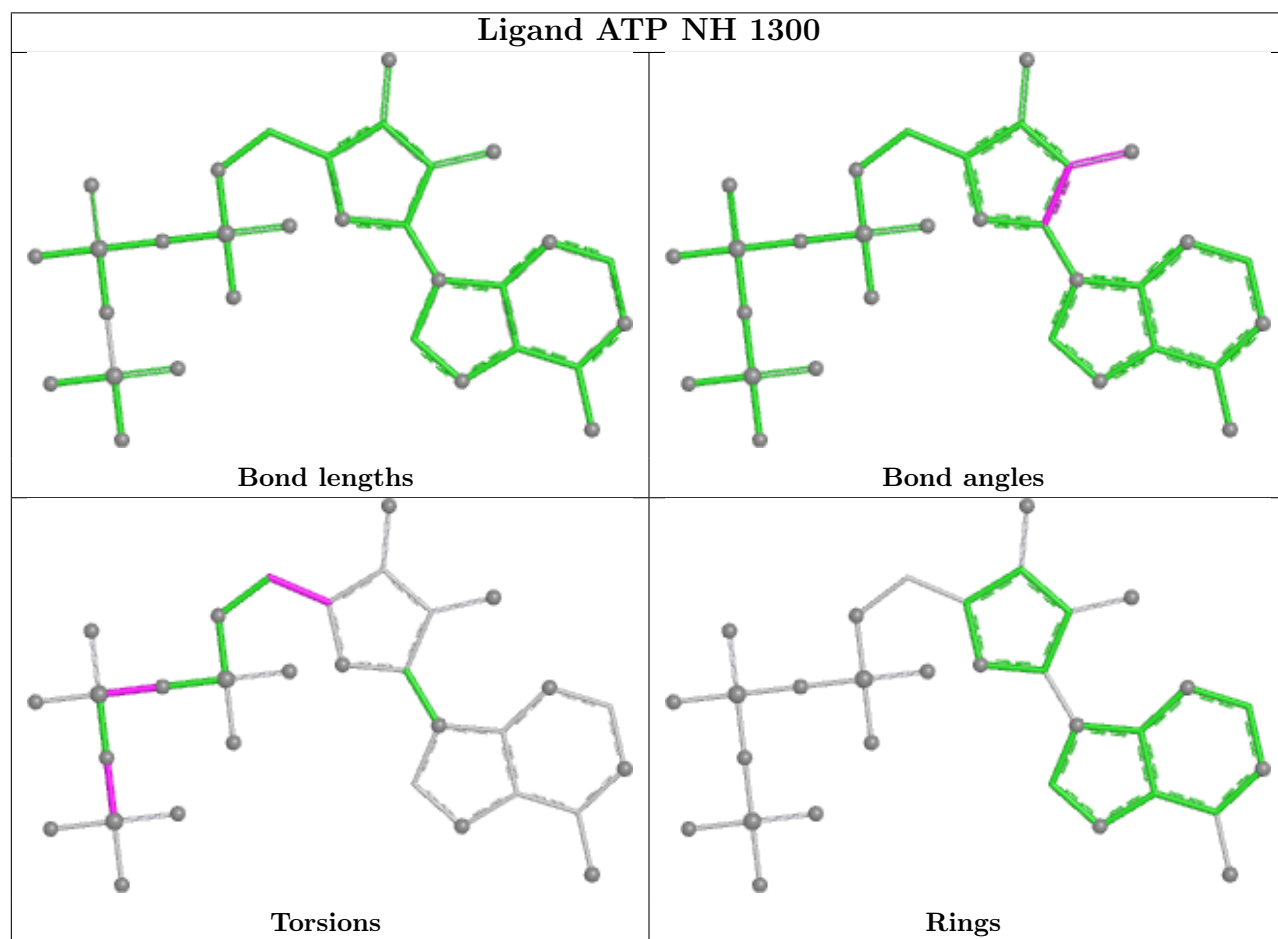
There are no ring outliers.

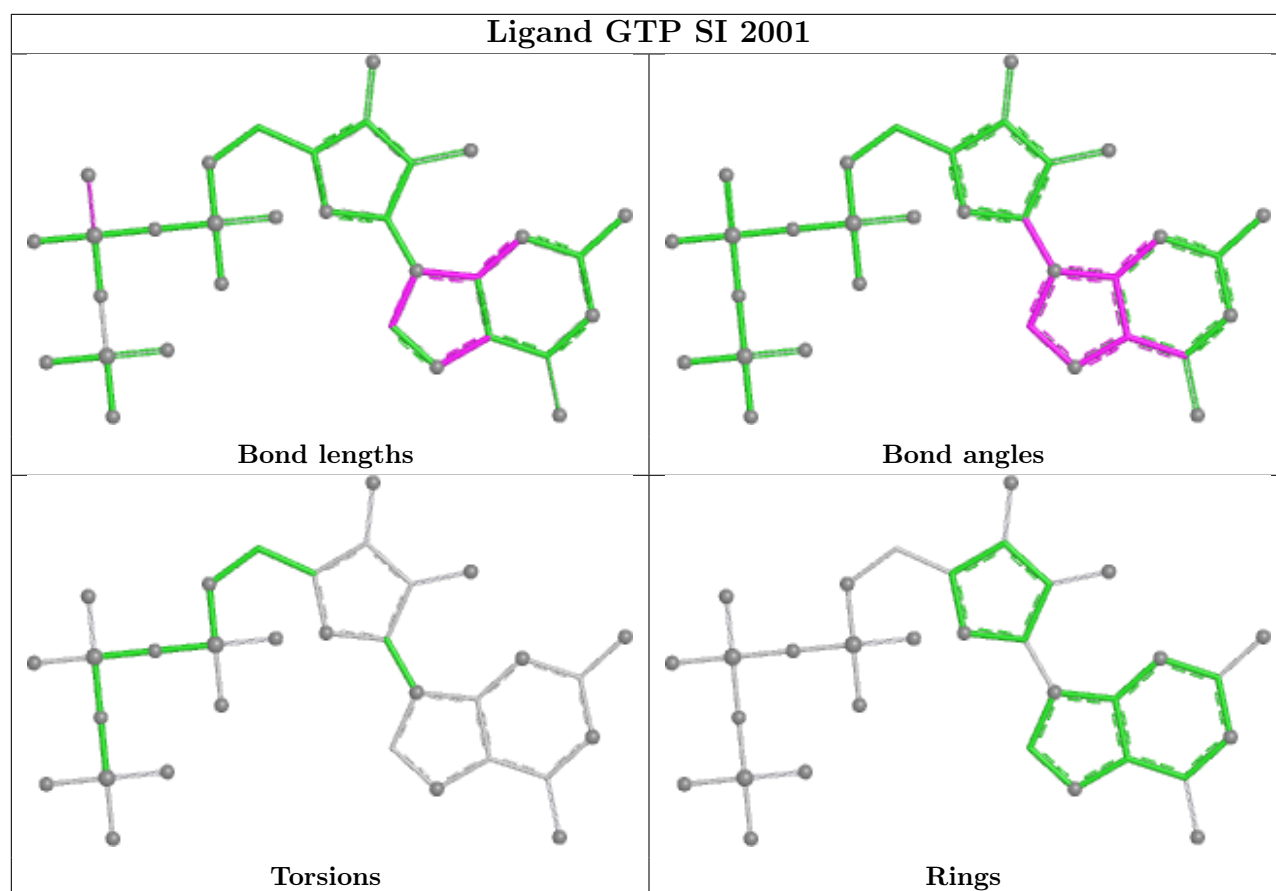
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
70	NH	1300	ATP	1	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.

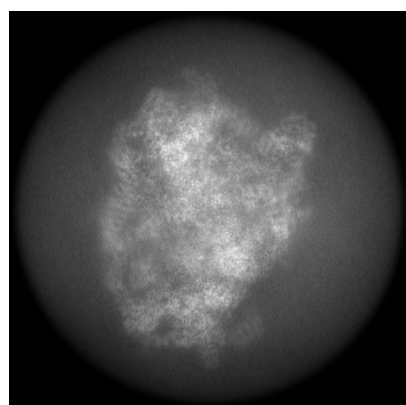
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49077. These allow visual inspection of the internal detail of the map and identification of artifacts.

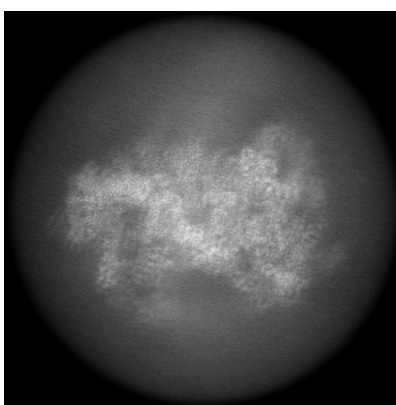
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

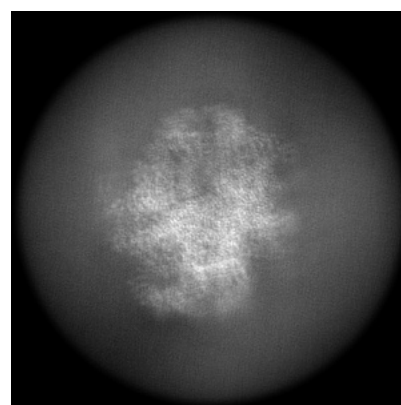
6.1.1 Primary map



X



Y

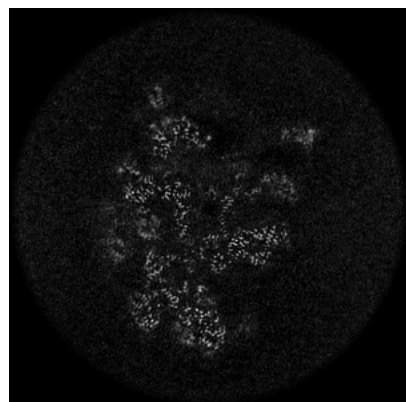


Z

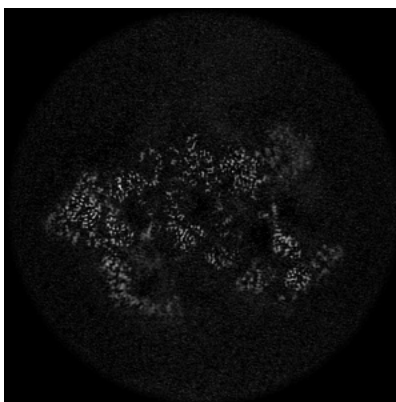
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

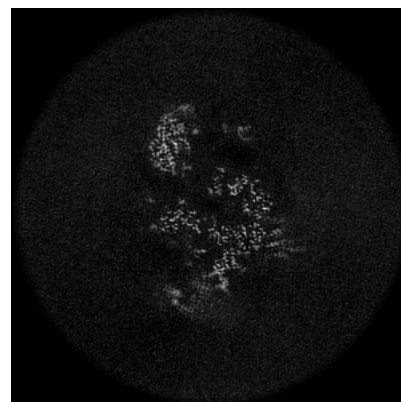
6.2.1 Primary map



X Index: 252



Y Index: 252

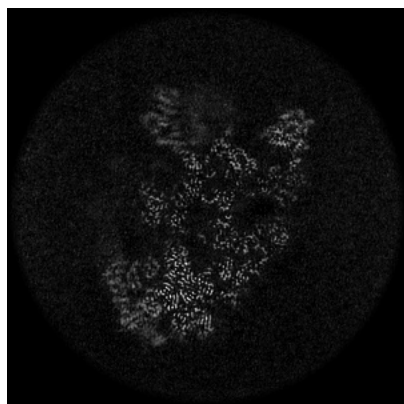


Z Index: 252

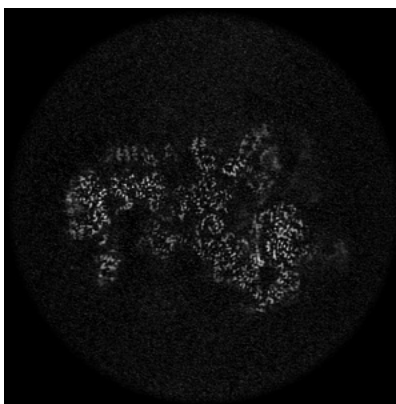
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

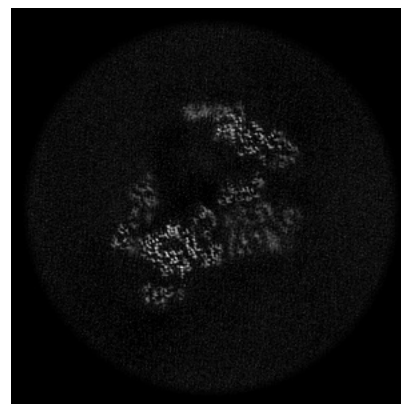
6.3.1 Primary map



X Index: 278



Y Index: 222

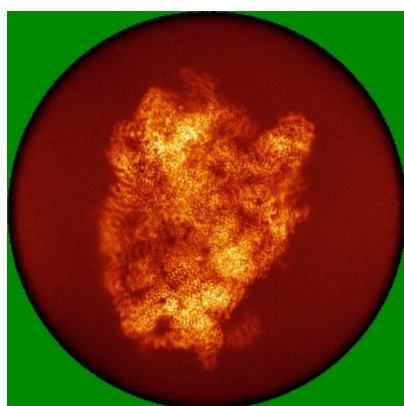


Z Index: 332

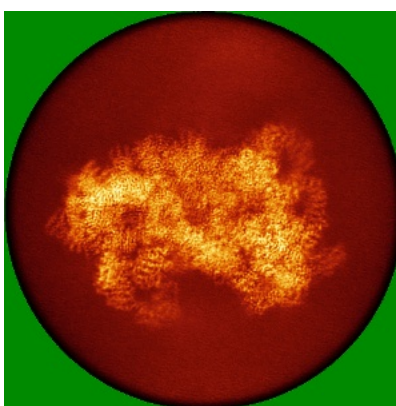
The images above show the largest variance slices of the map in three orthogonal directions.

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

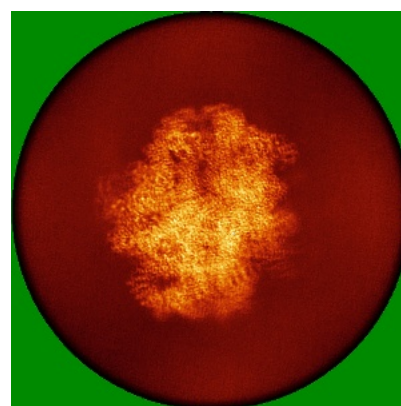
6.4.1 Primary map



X



Y

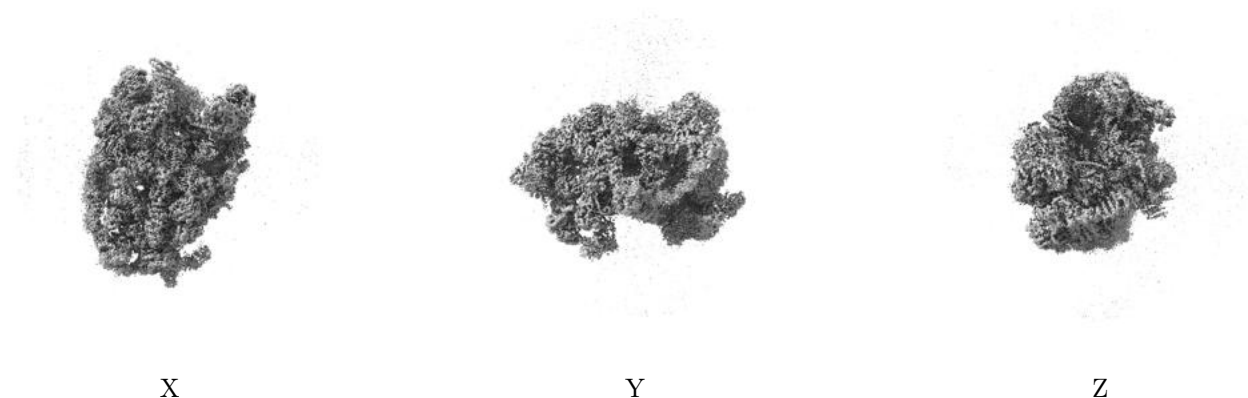


Z

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

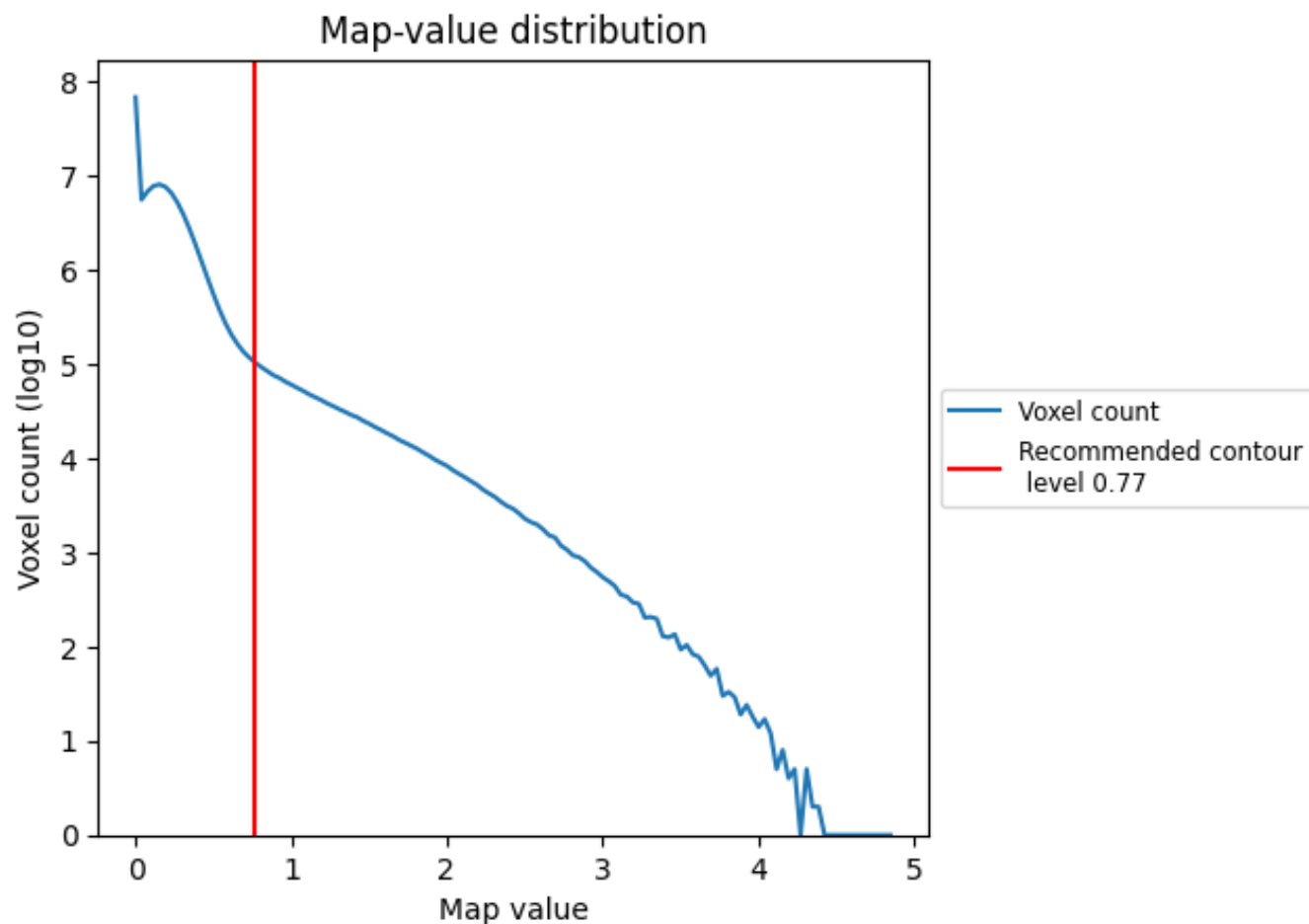
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

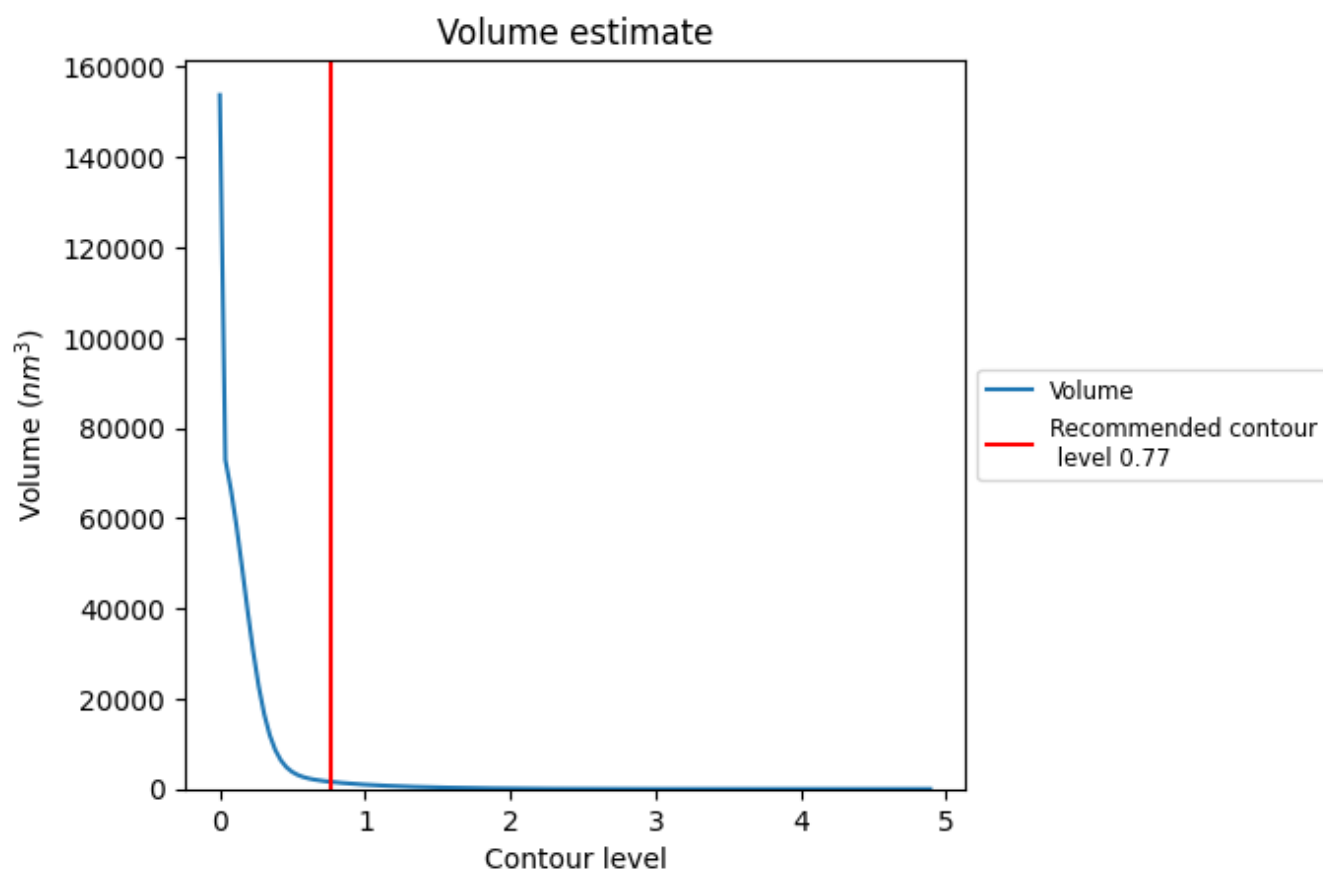
This section contains the results of statistical analysis of the map.

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.

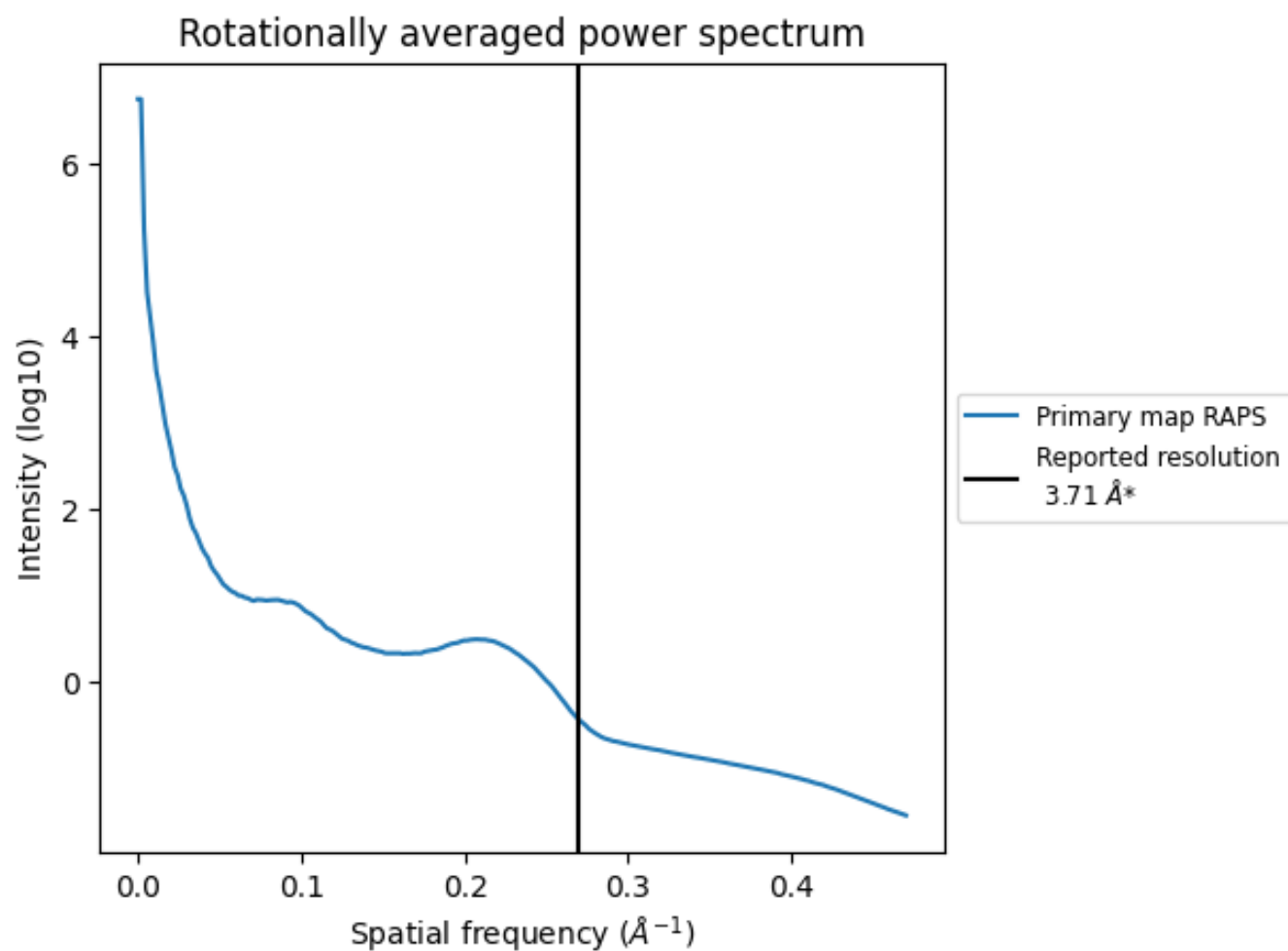
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1552 nm³; this corresponds to an approximate mass of 1402 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

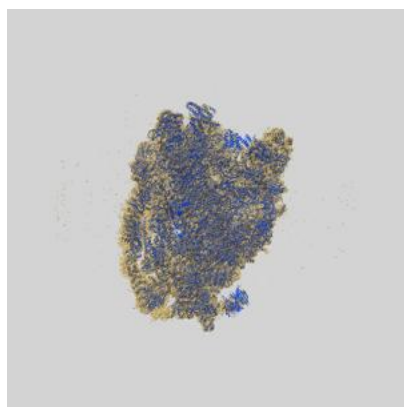
8 Fourier-Shell correlation

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

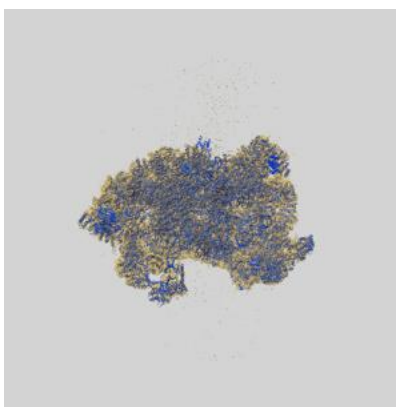
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-49077 and PDB model 9N6X. Per-residue inclusion information can be found in section [3](#) on page [18](#).

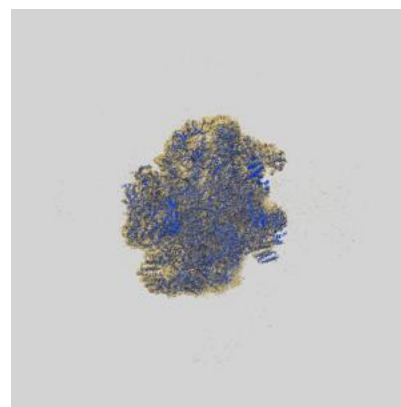
9.1 Map-model overlay [i](#)



X



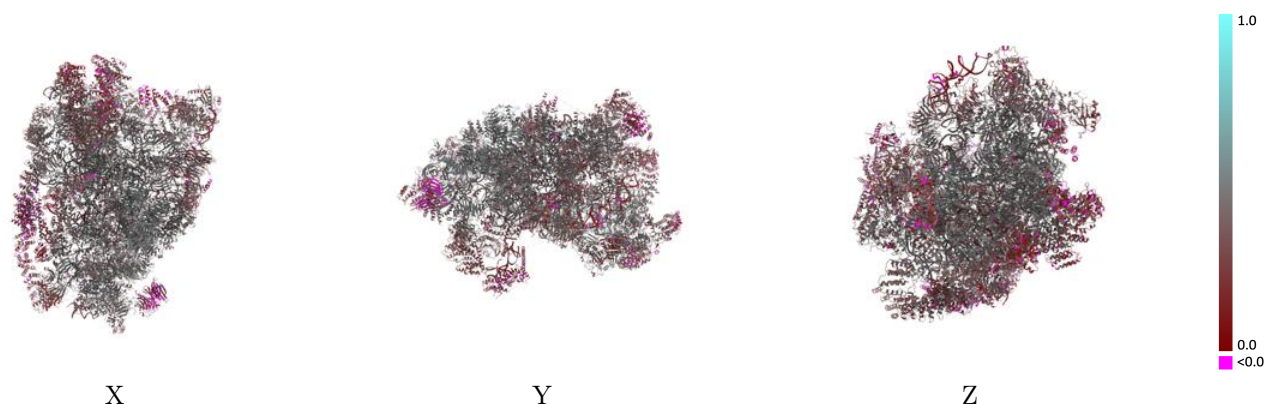
Y



Z

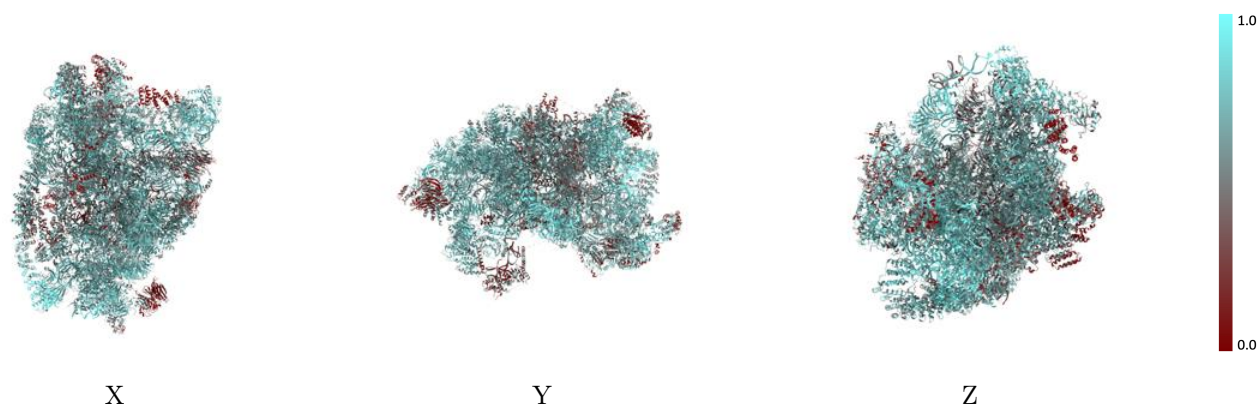
The images above show the 3D surface view of the map at the recommended contour level 0.77 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



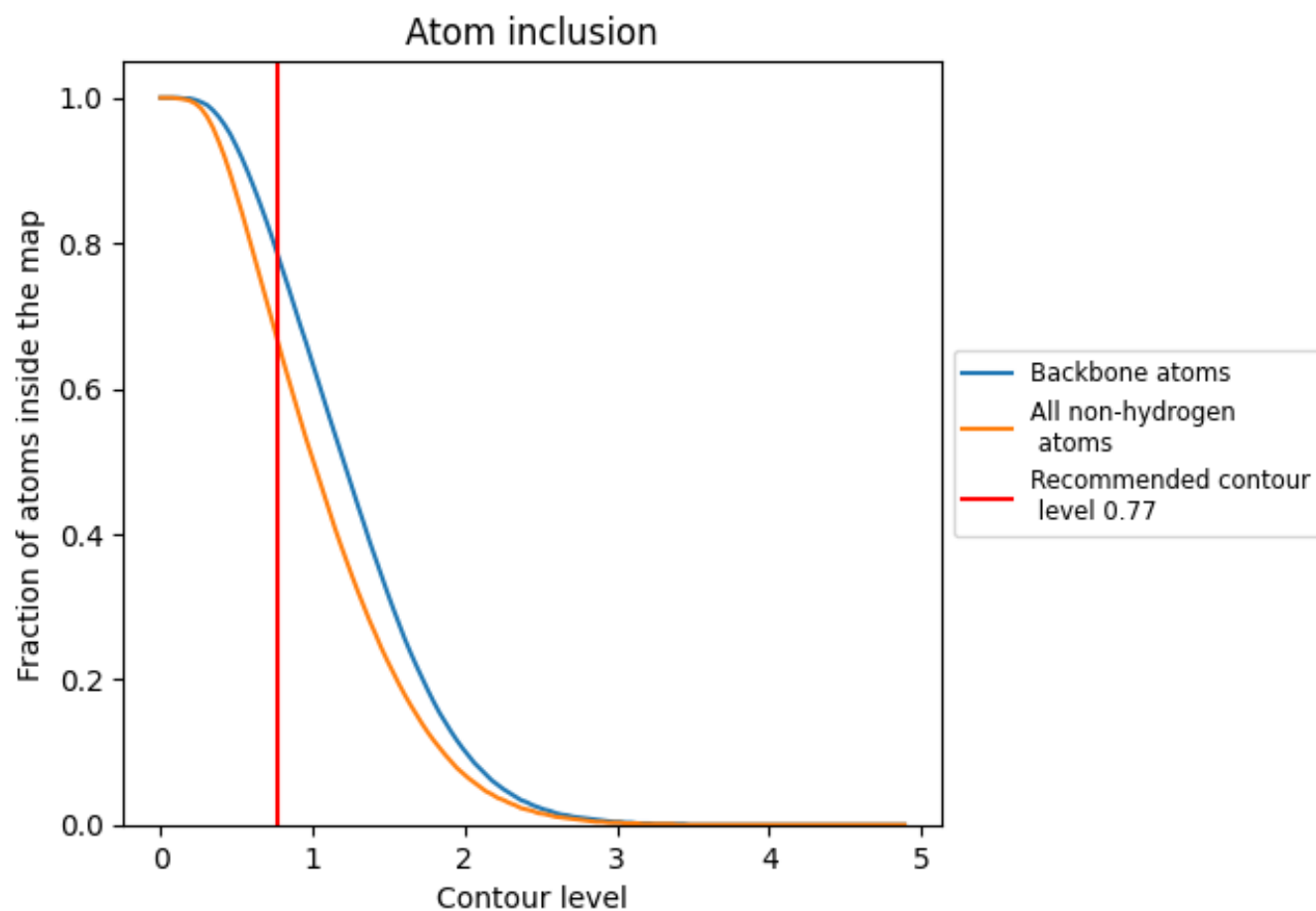
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.77).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 66% 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 (0.77) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6650	 0.3900
L0	 0.6560	 0.3770
L1	 0.7620	 0.3790
L2	 0.6870	 0.3830
L3	 0.0750	 0.2530
L4	 0.7570	 0.4600
L5	 0.7160	 0.4490
L6	 0.8110	 0.4420
L7	 0.5490	 0.3020
L8	 0.8070	 0.4620
L9	 0.6380	 0.4510
LC	 0.6700	 0.4650
LD	 0.7070	 0.4230
LE	 0.7060	 0.4550
LF	 0.8190	 0.4520
LG	 0.6680	 0.4710
LH	 0.7780	 0.4550
LI	 0.3590	 0.2430
LJ	 0.7880	 0.4590
LK	 0.5930	 0.3460
LL	 0.7480	 0.4490
LM	 0.7110	 0.3070
LN	 0.8060	 0.4420
LO	 0.7130	 0.4710
LP	 0.5020	 0.3520
LQ	 0.7720	 0.3880
LR	 0.4890	 0.3500
LS	 0.7540	 0.4700
LT	 0.6900	 0.4660
LU	 0.7480	 0.4650
LV	 0.7540	 0.4310
LW	 0.6530	 0.4700
LX	 0.6590	 0.3810
LY	 0.6460	 0.3540
LZ	 0.7000	 0.4870



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Chain	Atom inclusion	Q-score
NA	 0.5550	 0.3730
NB	 0.5280	 0.3150
NC	 0.5200	 0.3090
ND	 0.6110	 0.3640
NE	 0.5130	 0.4070
NF	 0.7130	 0.4420
NG	 0.5370	 0.4340
NH	 0.7830	 0.3910
NI	 0.5910	 0.3370
NK	 0.5990	 0.4360
NM	 0.6200	 0.4420
NN	 0.5320	 0.2800
NQ	 0.7780	 0.4560
OA	 0.0560	 0.1540
SA	 0.5630	 0.3950
SB	 0.5790	 0.3660
SC	 0.6290	 0.4620
SD	 0.5940	 0.4090
SE	 0.7780	 0.4680
SF	 0.6300	 0.4700
SG	 0.6400	 0.4130
SH	 0.6320	 0.4380
SI	 0.6740	 0.4410
SJ	 0.6640	 0.3330
SK	 0.7960	 0.3800
SL	 0.6470	 0.4670
SM	 0.6210	 0.4610
SN	 0.5080	 0.4080
SP	 0.6300	 0.3270
SQ	 0.4470	 0.4060
SR	 0.6770	 0.4720
SS	 0.4030	 0.3380
ST	 0.5720	 0.3110
SU	 0.7230	 0.3380
SV	 0.4580	 0.2670
SW	 0.4190	 0.3720
SY	 0.6240	 0.4300
SZ	 0.3770	 0.2020