



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 08:40 AM UTC

PDB ID : 8BRM / pdb_00008brm
EMDB ID : EMD-16222
Title : Giardia ribosome in POST-T state, no E-site tRNA (A6)
Authors : Majumdar, S.; Emmerich, A.G.; Sanyal, S.
Deposited on : 2022-11-23
Resolution : 3.33 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
MolProbity : 4-5-2 with Phenix2.0
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

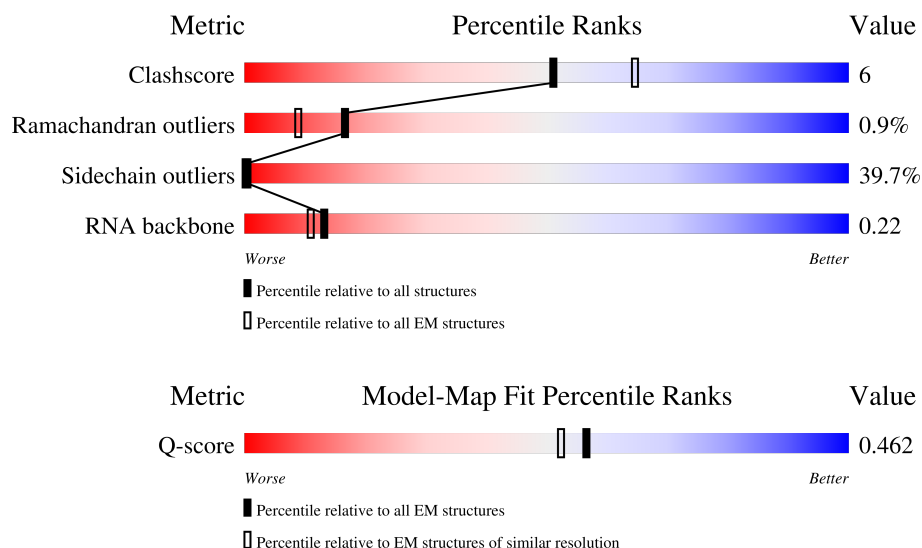
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.33 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.



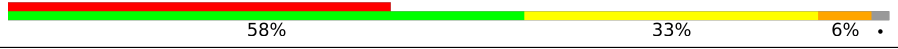
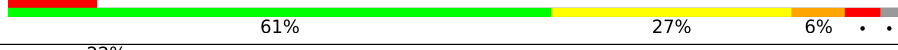
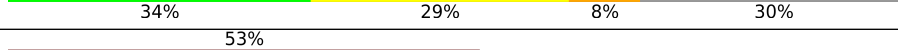
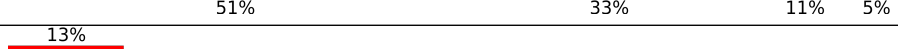
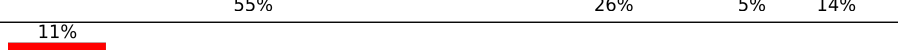
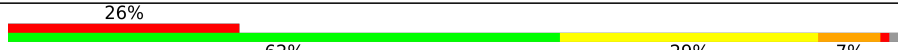
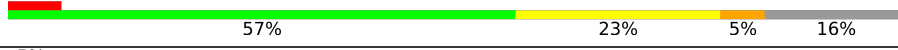
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14484 (2.83 - 3.83)

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

Mol	Chain	Length	Quality of chain
1	LA	251	10% 71% 25% .
2	LB	379	10% 58% 35% 6%
3	LC	316	8% 64% 27% 7% .

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Mol	Chain	Length	Quality of chain
4	LD	143	
5	LE	121	
6	LF	297	
7	LG	51	
8	LH	235	
9	LI	225	
10	LJ	185	
11	LK	210	
12	LL	173	
13	LM	234	
14	LN	131	
15	LO	204	
16	LP	197	
17	LQ	164	
18	LR	179	
19	LS	196	
20	LT	173	
21	LU	159	
22	LV	124	
23	LW	142	
24	LX	189	
25	LY	141	
26	LZ	135	
27	La	135	
28	Lb	149	

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Mol	Chain	Length	Quality of chain
29	Lc	62	
30	Ld	109	
31	Le	106	
32	Lf	136	
33	Lg	123	
34	Lh	120	
35	Li	124	
36	Lj	90	
37	Lk	89	
38	Ll	77	
39	Ln	217	
40	Lo	25	
41	Lp	106	
42	Lq	94	
43	Ls	127	
44	Lt	2697	
45	SA	245	
46	SB	242	
47	SC	217	
48	SD	248	
49	SE	268	
50	SF	190	
51	SG	248	
52	SH	190	
53	SI	174	

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Mol	Chain	Length	Quality of chain
54	SJ	130	
55	SK	189	
56	SL	134	
57	SM	154	
58	SO	143	
59	SP	154	
60	SQ	145	
61	SR	145	
62	ST	158	
63	SU	137	
64	SV	154	
65	SW	139	
66	SX	126	
67	SY	89	
68	Sb	132	
69	Sc	88	
70	Sd	109	
71	Se	81	
72	Sg	64	
73	Sh	51	
74	Sj	69	
75	St	1454	

2 Entry composition

There are 75 unique types of molecules in this entry. The entry contains 173978 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	LA	250	Total	C	N	O	S	0	0
			1886	1163	389	322	12		

- Molecule 2 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	LB	378	Total	C	N	O	S	0	0
			2987	1886	566	514	21		

- Molecule 3 is a protein called Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LC	309	Total	C	N	O	S	0	0
			2408	1514	468	418	8		

- Molecule 4 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LD	142	Total	C	N	O	P	0	0
			3038	1350	563	983	142		

- Molecule 5 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LE	117	Total	C	N	O	P	0	0
			2502	1116	457	812	117		

- Molecule 6 is a protein called Ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LF	291	Total	C	N	O	S	0	0
			2337	1479	435	415	8		

- Molecule 7 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	LG	50	Total	C	N	O	0	0
			439	281	94	64		

- Molecule 8 is a protein called Ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LH	213	Total	C	N	O	S	0	0
			1726	1097	314	310	5		

- Molecule 9 is a protein called Ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LI	187	Total	C	N	O	S	0	0
			1494	952	274	263	5		

- Molecule 10 is a protein called Ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LJ	184	Total	C	N	O	S	0	0
			1452	917	264	261	10		

- Molecule 11 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LK	147	Total	C	N	O	S	0	0
			1207	762	231	210	4		

- Molecule 12 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LL	165	Total	C	N	O	S	0	0
			1322	833	247	237	5		

- Molecule 13 is a protein called Ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LM	201	Total	C	N	O	S	0	0
			1605	999	325	274	7		

- Molecule 14 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LN	130	Total	C	N	O	S	0	0
			1024	649	186	183	6		

- Molecule 15 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LO	203	Total	C	N	O	S	0	0
			1708	1080	357	265	6		

- Molecule 16 is a protein called Ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LP	194	Total	C	N	O	S	0	0
			1578	994	306	266	12		

- Molecule 17 is a protein called Ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LQ	153	Total	C	N	O	S	0	0
			1231	778	239	210	4		

- Molecule 18 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LR	178	Total	C	N	O	S	0	0
			1402	871	279	243	9		

- Molecule 19 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LS	192	Total	C	N	O	S	0	0
			1592	983	334	270	5		

- Molecule 20 is a protein called Ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LT	170	Total	C	N	O	S	0	0
			1423	899	272	243	9		

- Molecule 21 is a protein called Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LU	156	Total	C	N	O	S	0	0
			1257	784	259	207	7		

- Molecule 22 is a protein called Ribosomal protein L22e.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LV	103	Total	C	N	O	S	0	0
			845	540	145	158	2		

- Molecule 23 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LW	132	Total	C	N	O	S	0	0
			1015	641	193	176	5		

- Molecule 24 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LX	63	Total	C	N	O	S	0	0
			538	340	109	82	7		

- Molecule 25 is a protein called Ribosomal protein L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LY	119	Total	C	N	O	S	0	0
			962	619	174	166	3		

- Molecule 26 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LZ	133	Total	C	N	O	S	0	0
			1076	665	219	184	8		

- Molecule 27 is a protein called Ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	La	127	Total	C	N	O	S	0	0
			1013	638	190	179	6		

- Molecule 28 is a protein called Ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Lb	148	Total	C	N	O	S	0	0
			1201	759	240	199	3		

- Molecule 29 is a protein called Ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Lc	51	Total	C	N	O	S	0	0
			425	254	97	72	2		

- Molecule 30 is a protein called Ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ld	102	Total	C	N	O	S	0	0
			770	485	135	146	4		

- Molecule 31 is a protein called Ribosomal protein L31B.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Le	100	Total	C	N	O		0	0
			818	518	158	142			

- Molecule 32 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lf	130	Total	C	N	O	S	0	0
			1077	683	215	173	6		

- Molecule 33 is a protein called Ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lg	98	Total	C	N	O	S	0	0
			778	498	147	130	3		

- Molecule 34 is a protein called Ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lh	96	Total	C	N	O	S	0	0
			774	478	161	131	4		

- Molecule 35 is a protein called Ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Li	120	Total	C	N	O	S	0	0
			969	613	190	161	5		

- Molecule 36 is a protein called Ribosomal protein L36-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lj	89	Total	C	N	O	S	0	0
			731	462	146	119	4		

- Molecule 37 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lk	88	Total	C	N	O	S	0	0
			711	435	152	117	7		

- Molecule 38 is a protein called Ribosomal protein L38e.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ll	72	Total	C	N	O	S	0	0
			558	353	99	102	4		

- Molecule 39 is a protein called Ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Ln	211	Total	C	N	O	S	0	0
			1678	1082	294	297	5		

- Molecule 40 is a protein called Ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lo	25	Total	C	N	O	S	0	0
			227	140	57	27	3		

- Molecule 41 is a protein called Ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lp	93	Total	C	N	O	S	0	0
			767	478	159	125	5		

- Molecule 42 is a protein called Ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lq	91	Total	C	N	O	S	0	0
			708	437	144	120	7		

- Molecule 43 is a protein called Ubiquitin/Ribosomal protein L40e.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Ls	47	Total	C	N	O	S	0	0
			388	234	83	64	7		

- Molecule 44 is a RNA chain called Large Subunit rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lt	2594	Total	C	N	O	P	0	0
			55663	24736	10313	18020	2594		

- Molecule 45 is a protein called Ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SA	196	Total	C	N	O	S	0	0
			1569	1013	274	274	8		

- Molecule 46 is a protein called Ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SB	216	Total	C	N	O	S	0	0
			1667	1059	302	301	5		

- Molecule 47 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SC	209	Total	C	N	O	S	0	0
			1658	1045	305	292	16		

- Molecule 48 is a protein called Ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SD	229	Total	C	N	O	S	0	0
			1855	1172	346	324	13		

- Molecule 49 is a protein called Ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SE	260	Total	C	N	O	S	0	0
			2085	1333	384	356	12		

- Molecule 50 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SF	186	Total	C	N	O	S	0	0
			1442	896	275	262	9		

- Molecule 51 is a protein called Ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SG	209	Total	C	N	O	S	0	0
			1646	1033	312	291	10		

- Molecule 52 is a protein called Ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SH	184	Total	C	N	O	S	0	0
			1481	948	258	268	7		

- Molecule 53 is a protein called Ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SI	173	Total	C	N	O	S	0	0
			1357	850	260	244	3		

- Molecule 54 is a protein called Ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SJ	129	Total	C	N	O	S	0	0
			1031	659	192	177	3		

- Molecule 55 is a protein called Ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SK	176	Total	C	N	O	S	0	0
			1423	889	281	247	6		

- Molecule 56 is a protein called Ribosomal protein S10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SL	100	Total	C	N	O	S	0	0
			819	530	138	148	3		

- Molecule 57 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SM	151	Total	C	N	O	S	0	0
			1251	794	246	205	6		

- Molecule 58 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SO	139	Total	C	N	O	S	0	0
			1080	683	213	181	3		

- Molecule 59 is a protein called Ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SP	150	Total	C	N	O	S	0	0
			1192	758	228	201	5		

- Molecule 60 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SQ	125	Total	C	N	O	S	0	0
			916	564	189	160	3		

- Molecule 61 is a protein called Ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SR	116	Total	C	N	O	S	0	0
			943	601	184	150	8		

- Molecule 62 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	ST	151	Total	C	N	O	S	0	0
			1180	736	229	212	3		

- Molecule 63 is a protein called Ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SU	108	Total	C	N	O	S	0	0
			872	542	167	158	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SU	104	THR	ALA	conflict	UNP A8BRG5

- Molecule 64 is a protein called Ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SV	141	Total	C	N	O	S	0	0
			1117	687	227	197	6		

- Molecule 65 is a protein called Ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SW	137	Total	C	N	O	S	0	0
			1071	680	202	186	3		

- Molecule 66 is a protein called Ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SX	100	Total	C	N	O	S	0	0
			794	507	145	137	5		

- Molecule 67 is a protein called Ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SY	86	Total	C	N	O	S	0	0
			651	403	120	122	6		

- Molecule 68 is a protein called Ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Sb	118	Total	C	N	O	S	0	0
			941	598	177	160	6		

- Molecule 69 is a protein called Ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sc	73	Total	C	N	O	S	0	0
			578	366	104	102	6		

- Molecule 70 is a protein called Ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Sd	101	Total	C	N	O	S	0	0
			821	504	171	139	7		

- Molecule 71 is a protein called Ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Se	79	Total	C	N	O	S	0	0
			621	392	109	115	5		

- Molecule 72 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Sg	63	Total	C	N	O	S	0	0
			505	311	100	92	2		

- Molecule 73 is a protein called Ribosomal protein S29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Sh	50	Total	C	N	O	S	0	0
			417	264	80	67	6		

- Molecule 74 is a protein called Ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sj	62	Total	C	N	O	S	0	0
			509	322	104	82	1		

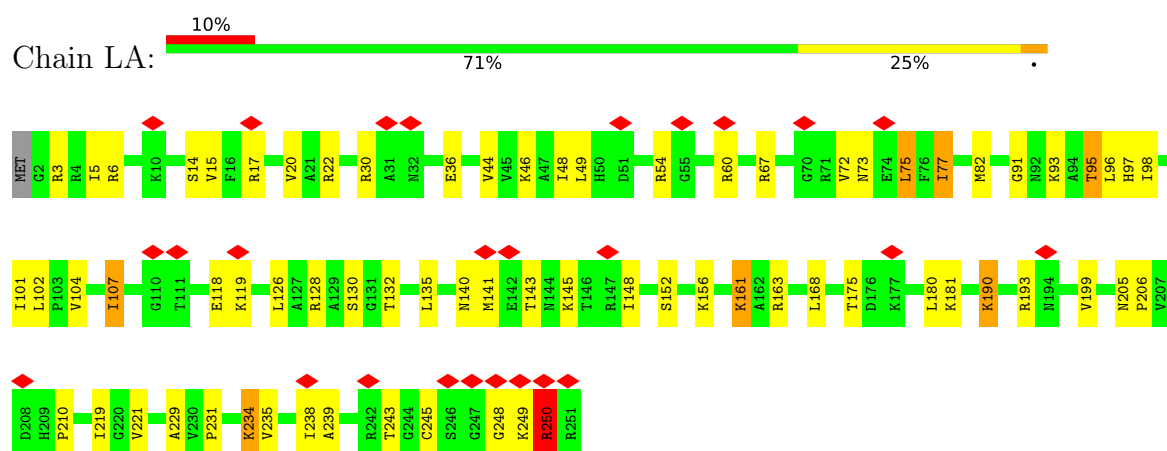
- Molecule 75 is a RNA chain called Small Subunit rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	St	1454	Total	C	N	O	P	0	0
			31176	13861	5772	10090	1453		

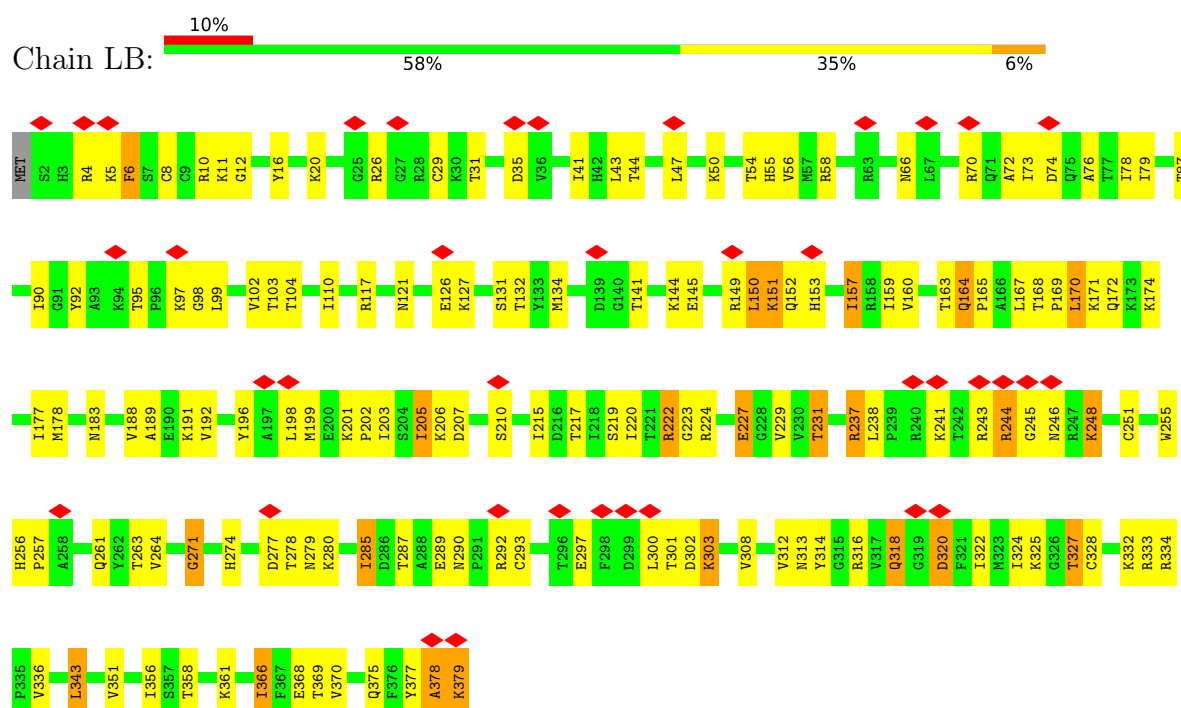
3 Residue-property plots

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

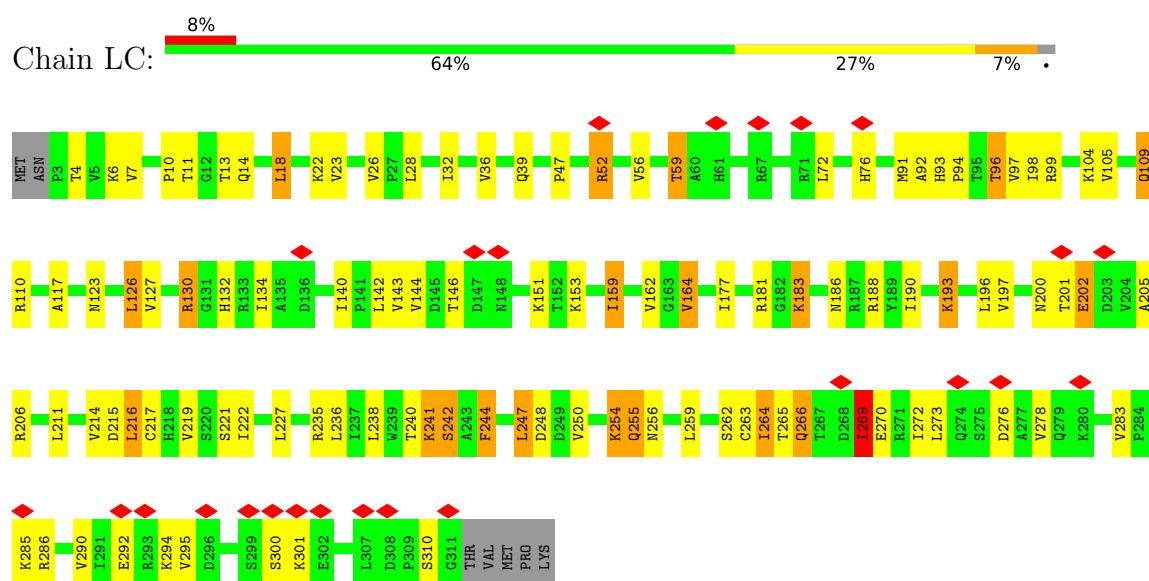
- Molecule 1: Ribosomal protein L2



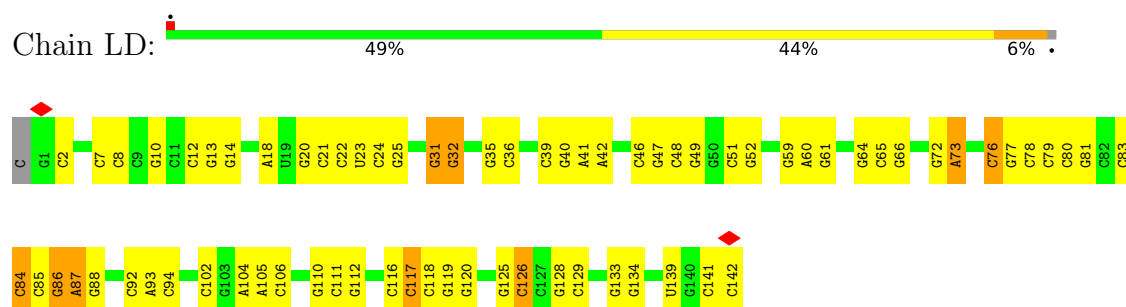
- Molecule 2: Ribosomal protein L3



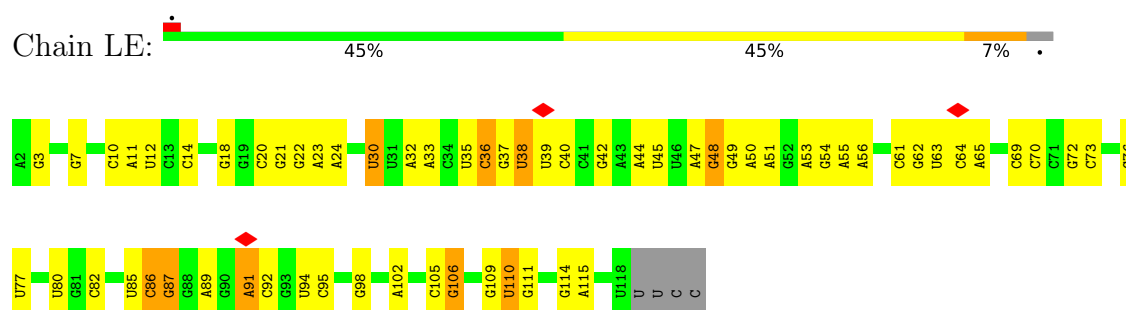
- Molecule 3: Ribosomal protein L4



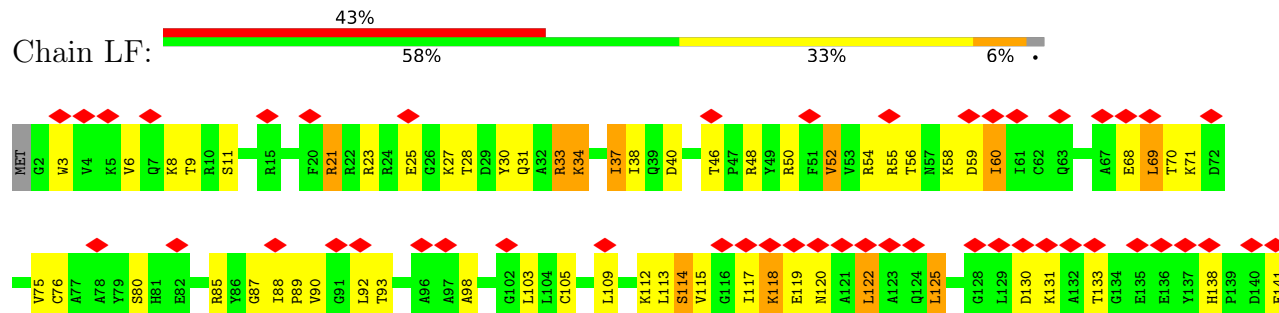
• Molecule 4: 5.8S rRNA

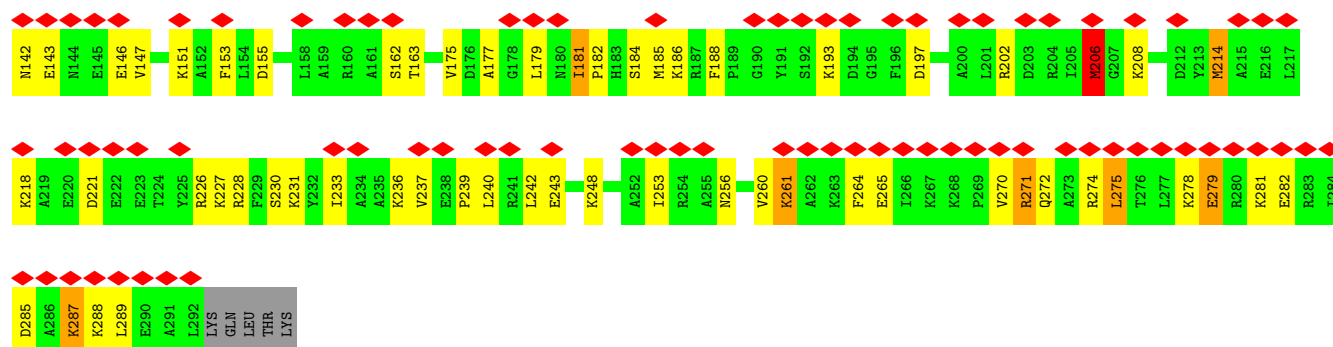


• Molecule 5: 5S rRNA

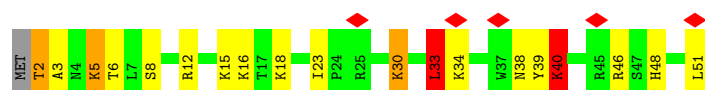


• Molecule 6: Ribosomal protein L5

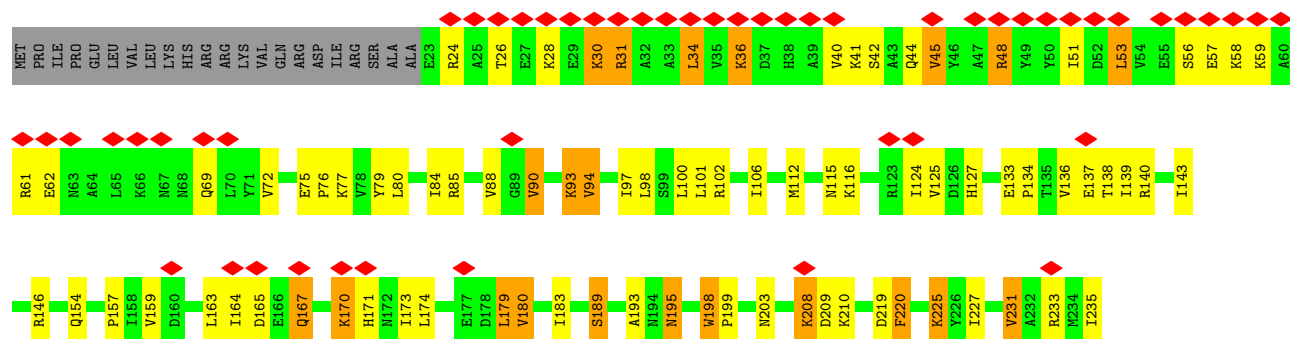




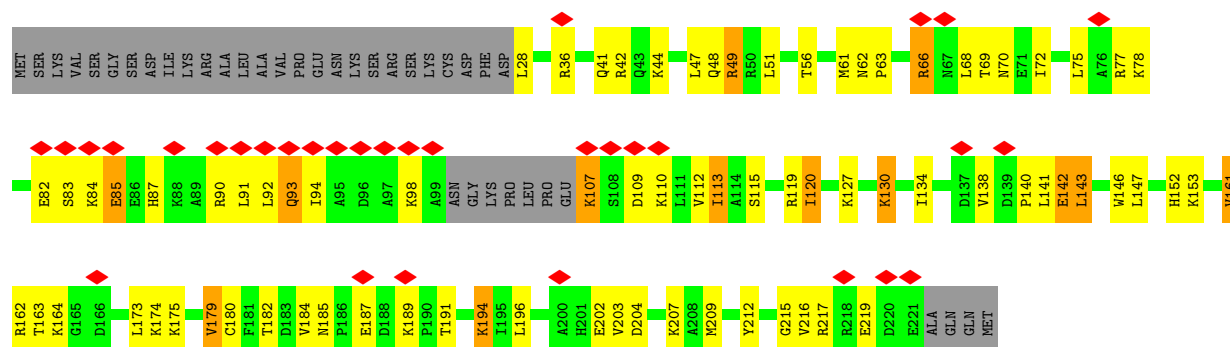
• Molecule 7: Ribosomal protein L39



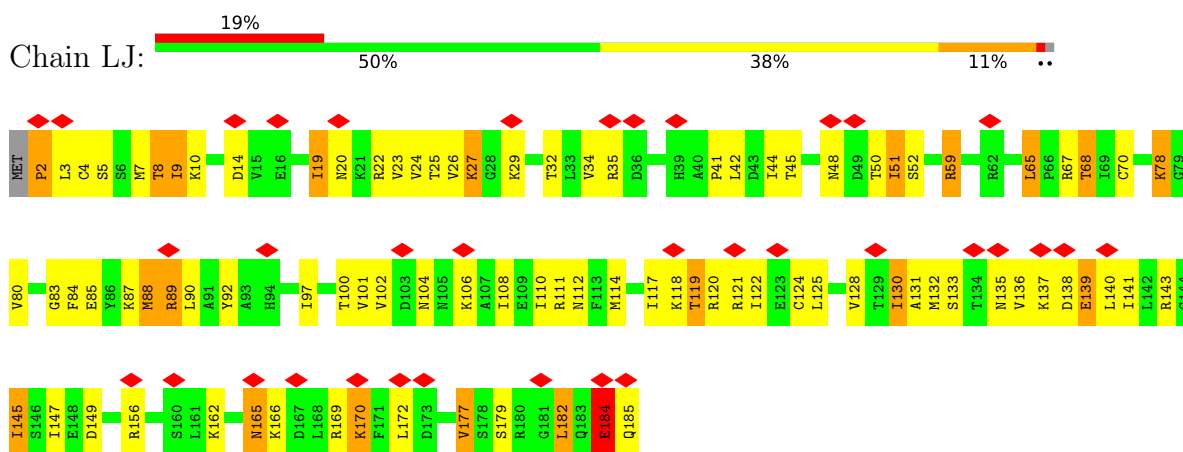
• Molecule 8: Ribosomal protein L7



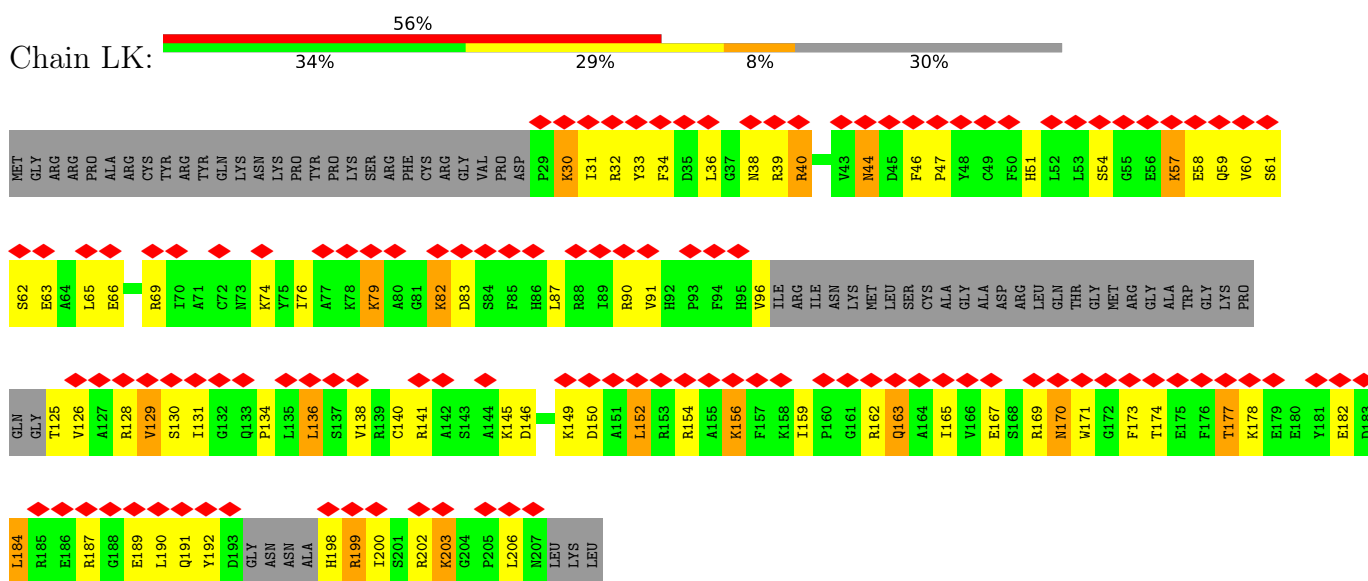
• Molecule 9: Ribosomal protein L7a



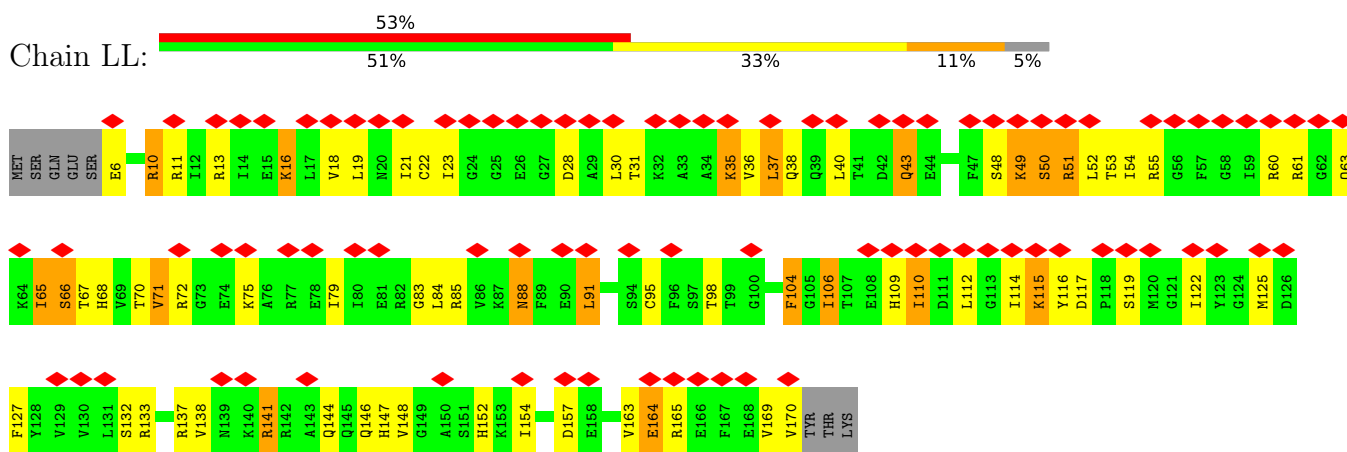
• Molecule 10: Ribosomal protein L6



• Molecule 11: Ribosomal protein L10

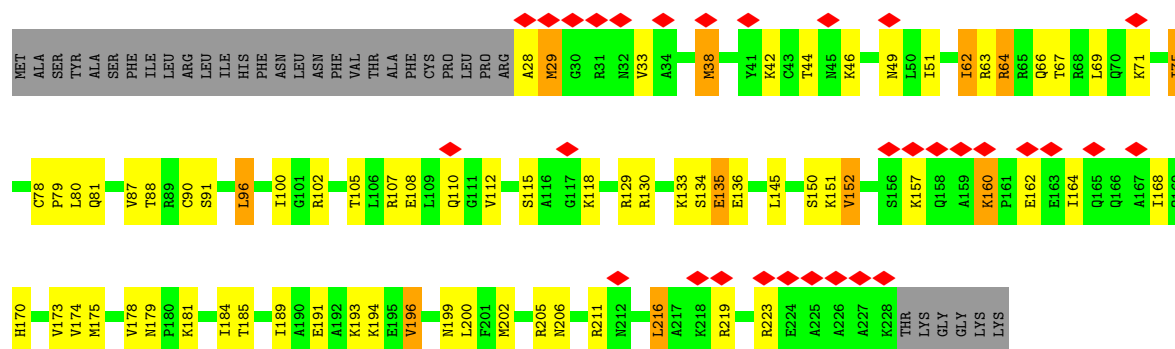


• Molecule 12: Ribosomal protein L11

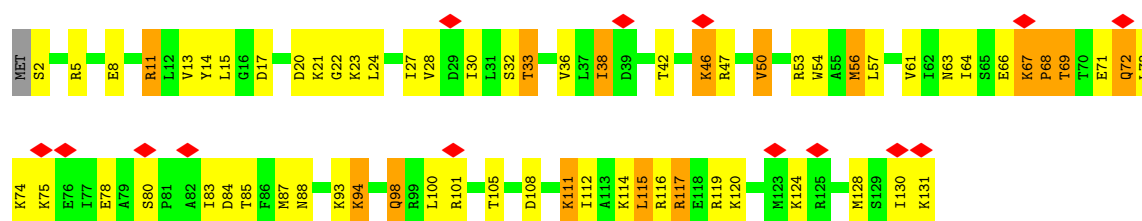


• Molecule 13: Ribosomal protein L13

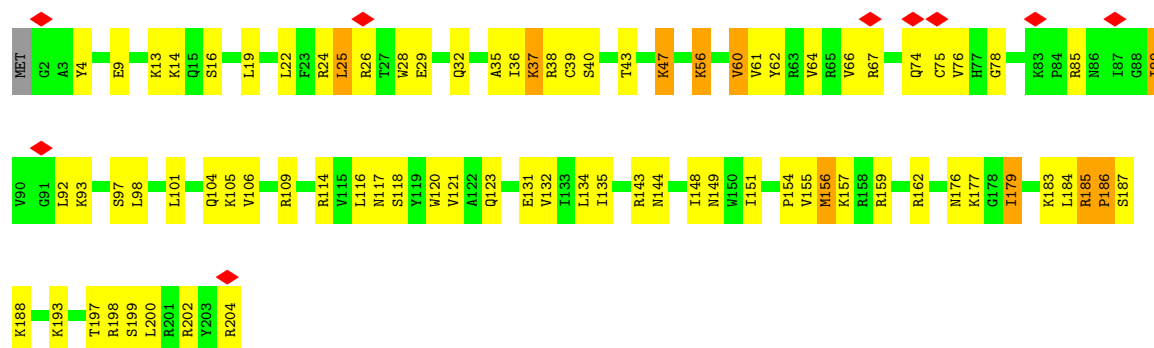




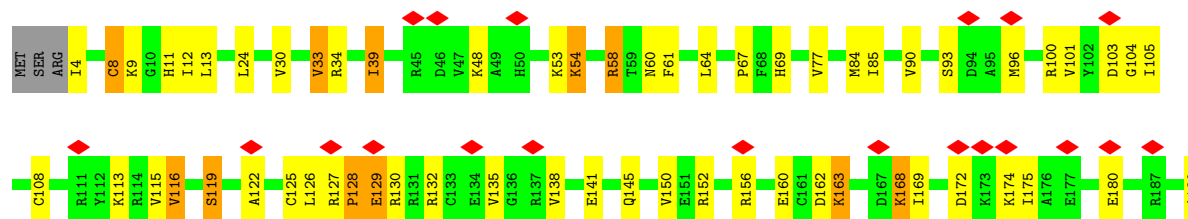
• Molecule 14: Ribosomal protein L14

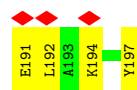


• Molecule 15: Ribosomal protein L15

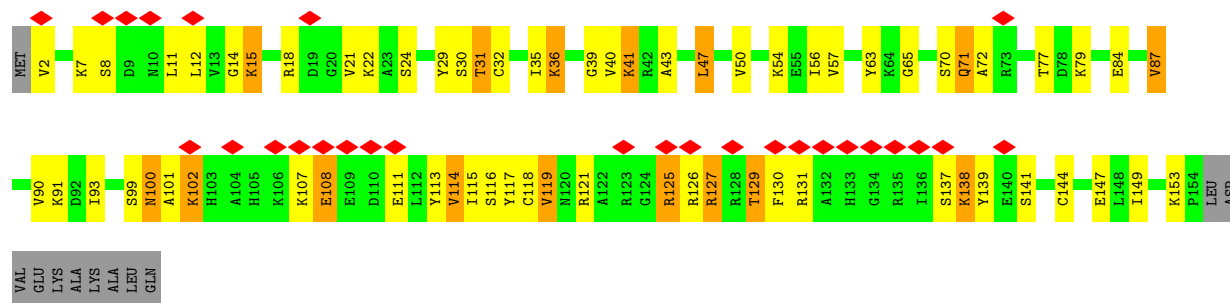


• Molecule 16: Ribosomal protein L13a

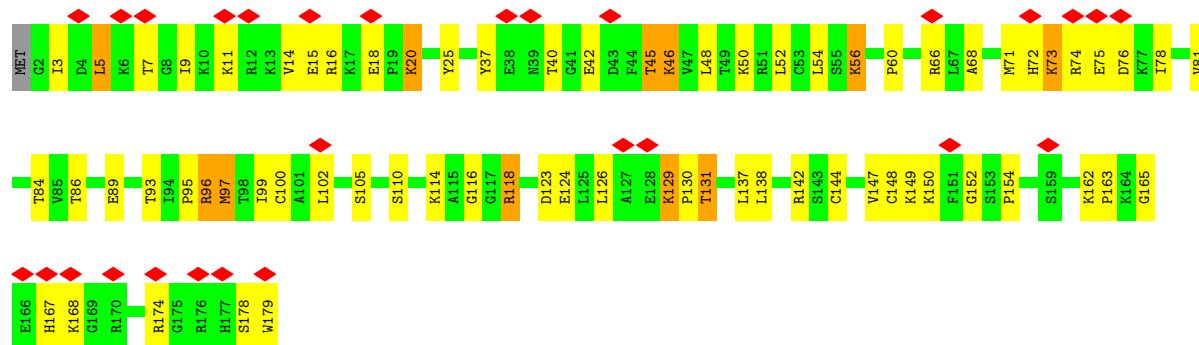




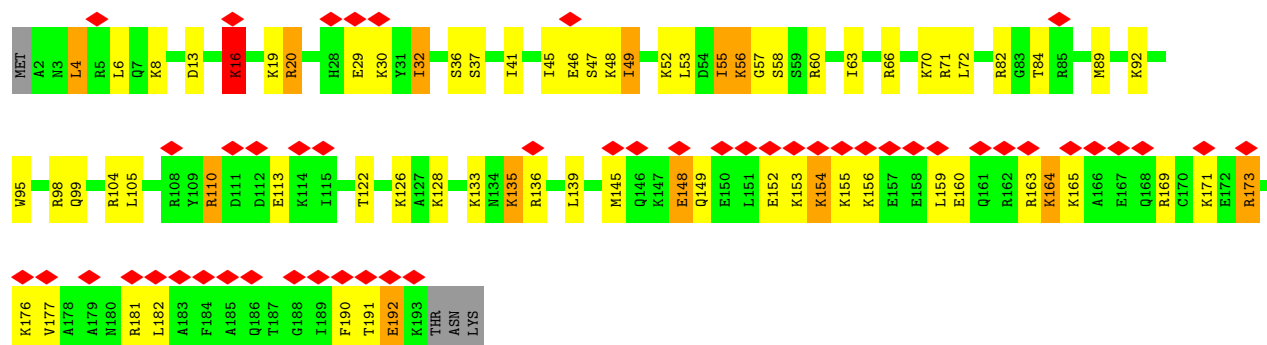
• Molecule 17: Ribosomal protein L17



• Molecule 18: Ribosomal protein L18

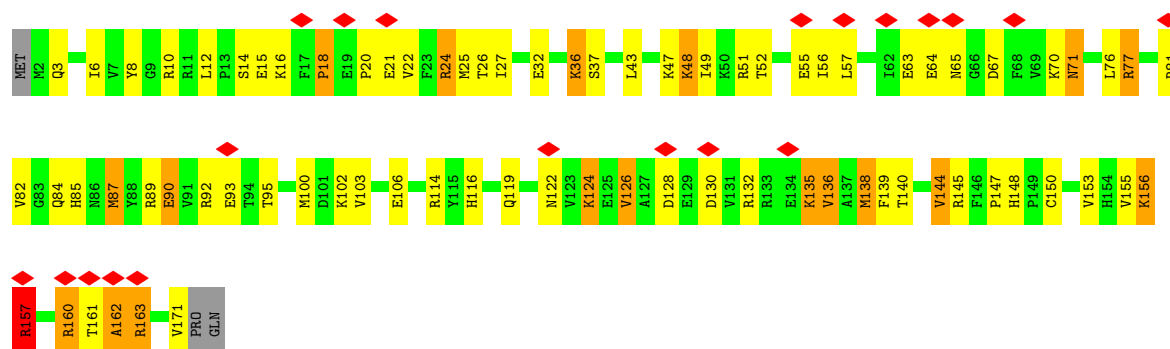


• Molecule 19: Ribosomal protein L19

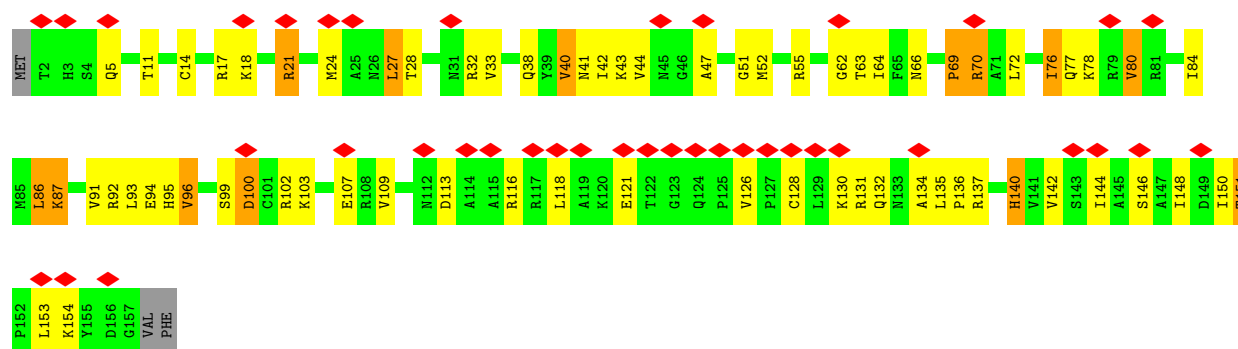


• Molecule 20: Ribosomal protein L18a

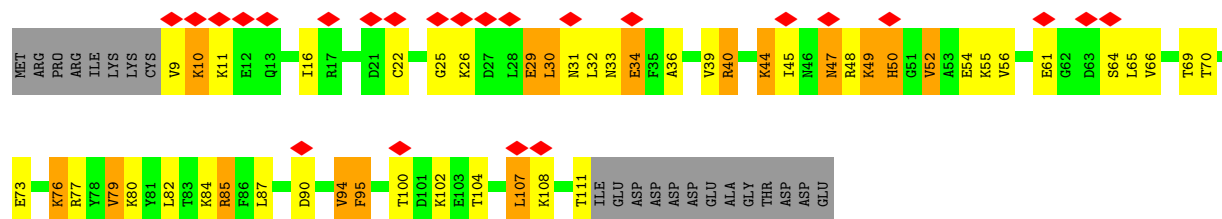
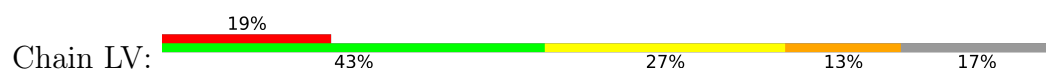




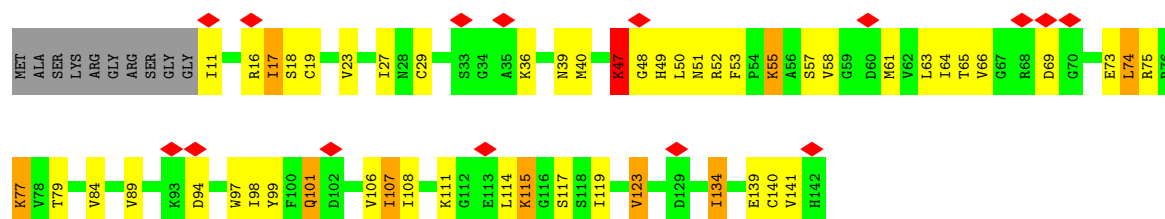
• Molecule 21: Ribosomal protein L21



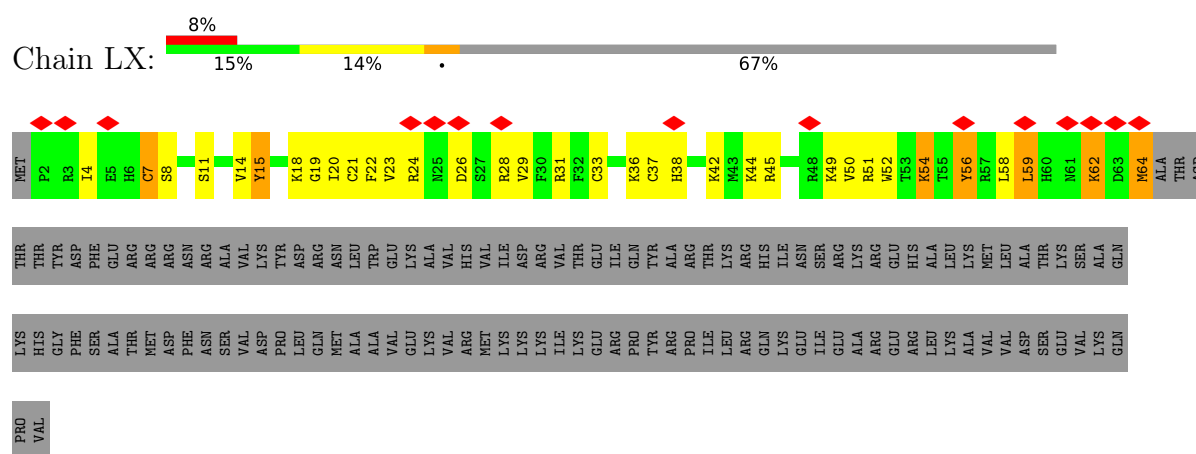
• Molecule 22: Ribosomal protein L22e



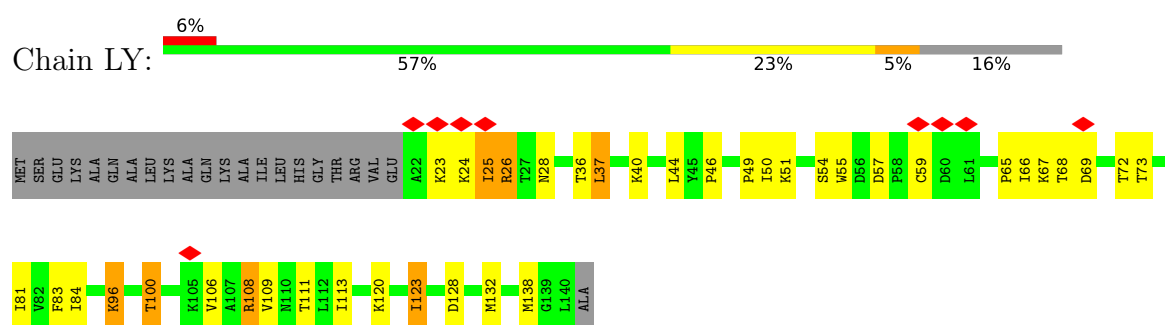
• Molecule 23: Ribosomal protein L23



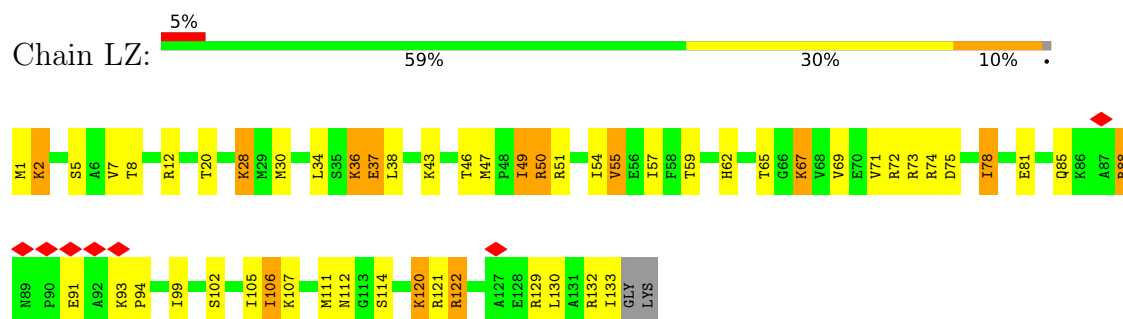
• Molecule 24: Ribosomal protein L24



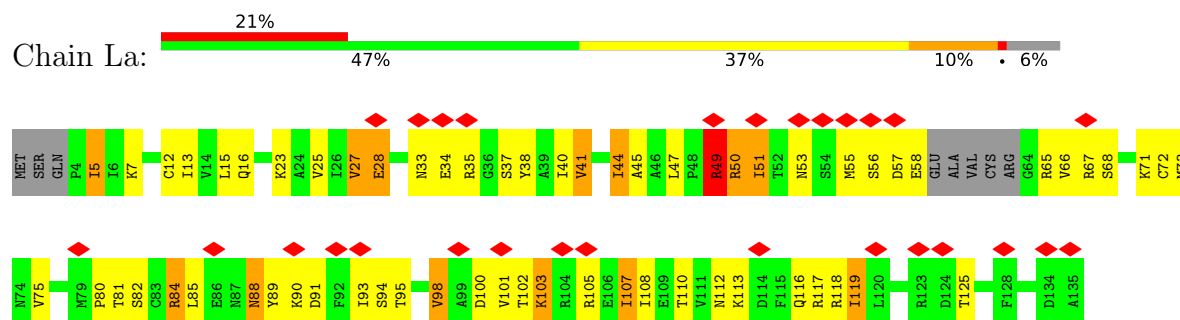
- Molecule 25: Ribosomal protein L23A



- Molecule 26: Ribosomal protein L26

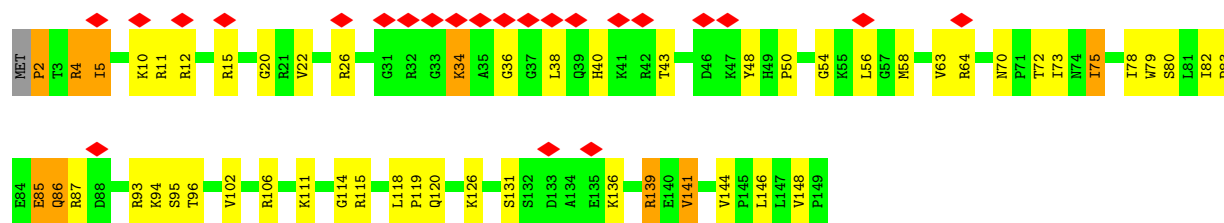


- Molecule 27: Ribosomal protein L27

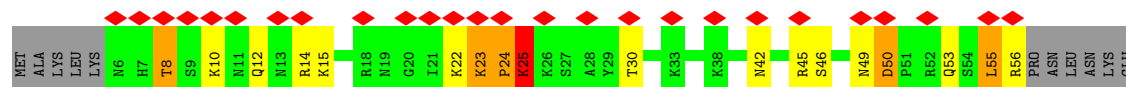
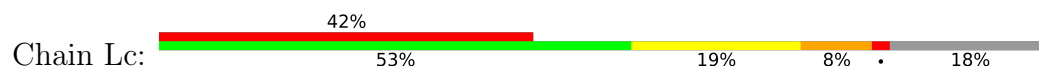


- Molecule 28: Ribosomal protein L27a

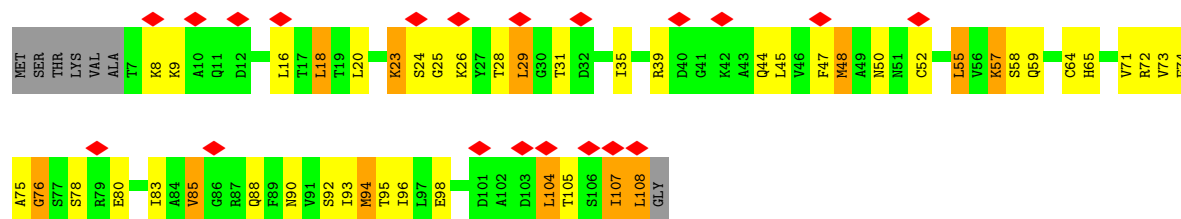




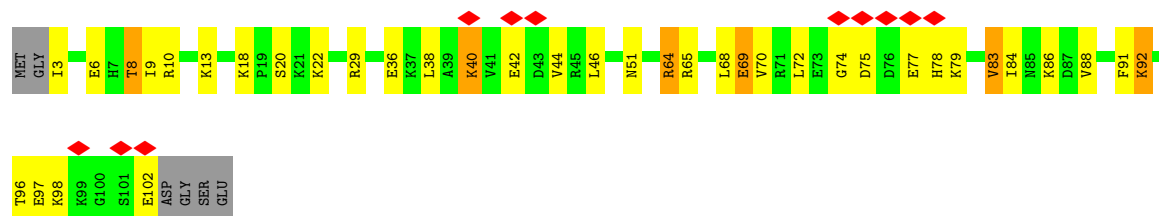
• Molecule 29: Ribosomal protein L29



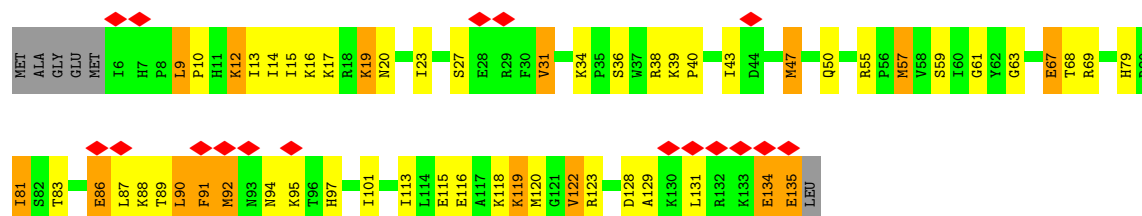
• Molecule 30: Ribosomal protein L30



• Molecule 31: Ribosomal protein L31B

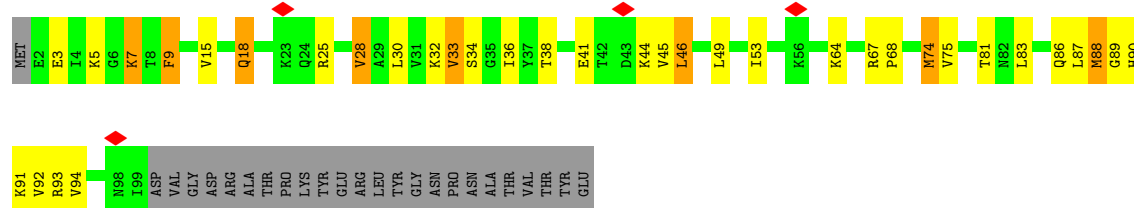


• Molecule 32: Ribosomal protein L32



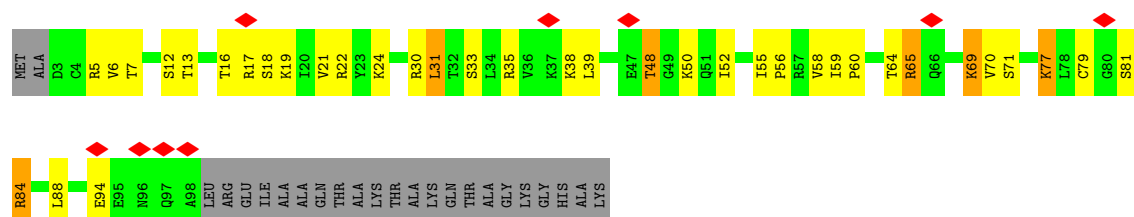
• Molecule 33: Ribosomal protein L35a

Chain Lg: 



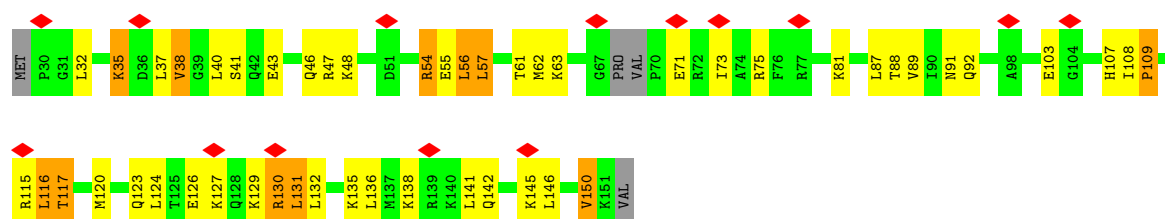
• Molecule 34: Ribosomal protein L34

Chain Lh: 



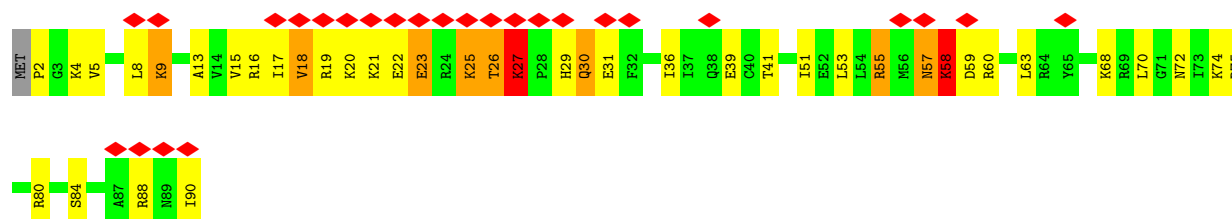
• Molecule 35: Ribosomal protein L29

Chain Li: 



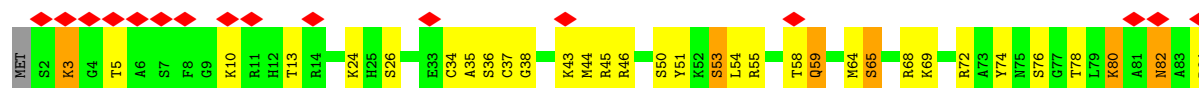
• Molecule 36: Ribosomal protein L36-1

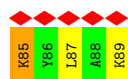
Chain Lj: 



• Molecule 37: Ribosomal protein L37

Chain Lk: 

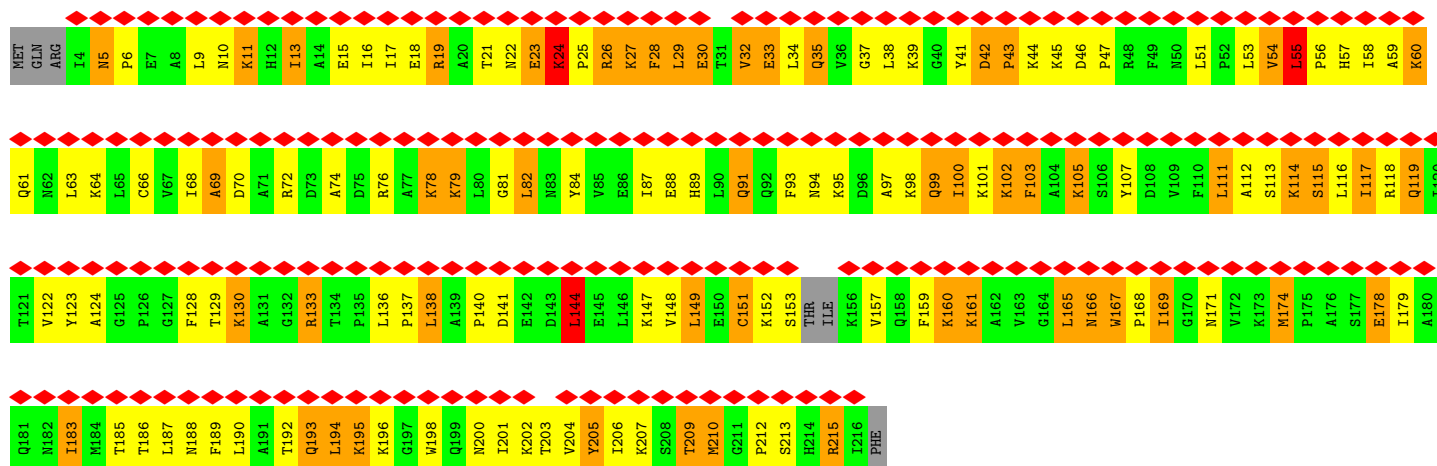




• Molecule 38: Ribosomal protein L38e



• Molecule 39: Ribosomal protein L10a

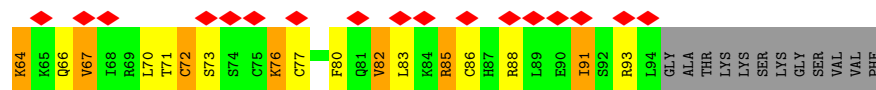


• Molecule 40: Ribosomal protein L41

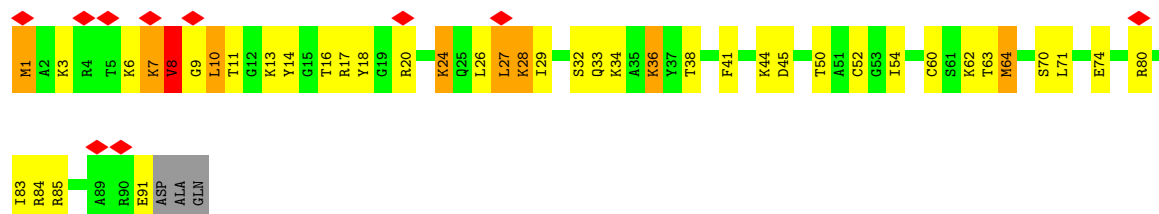


• Molecule 41: Ribosomal protein L44

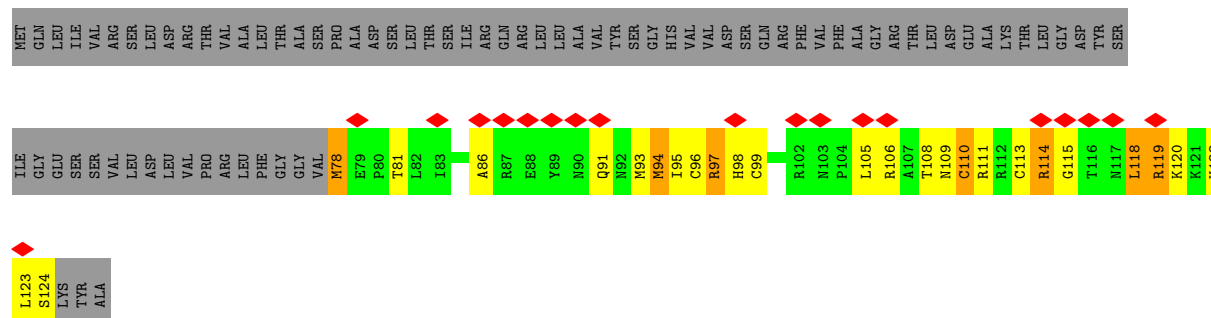




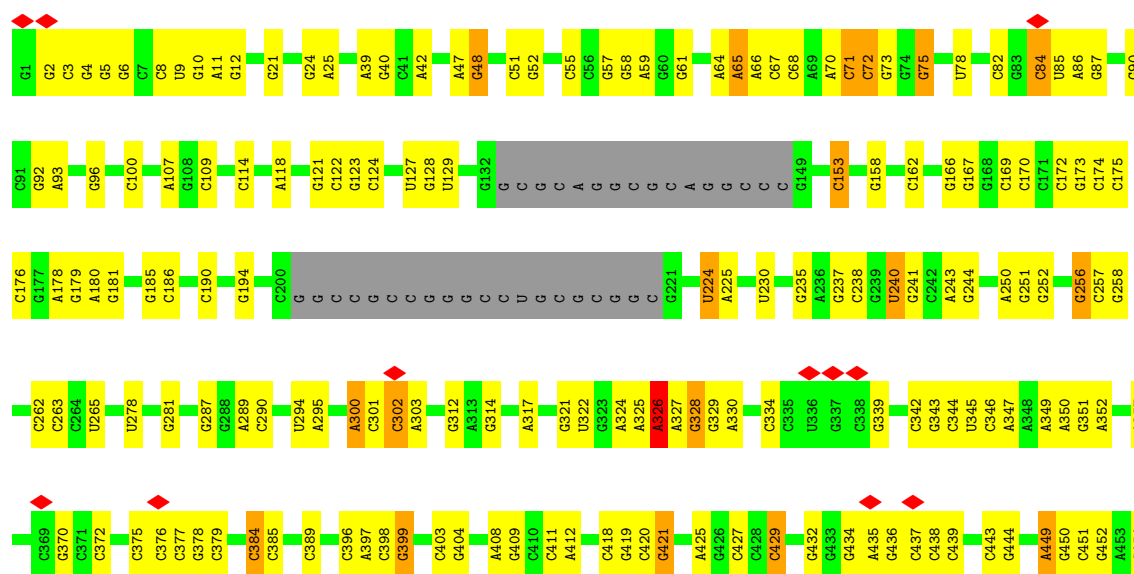
• Molecule 42: Ribosomal protein L37a



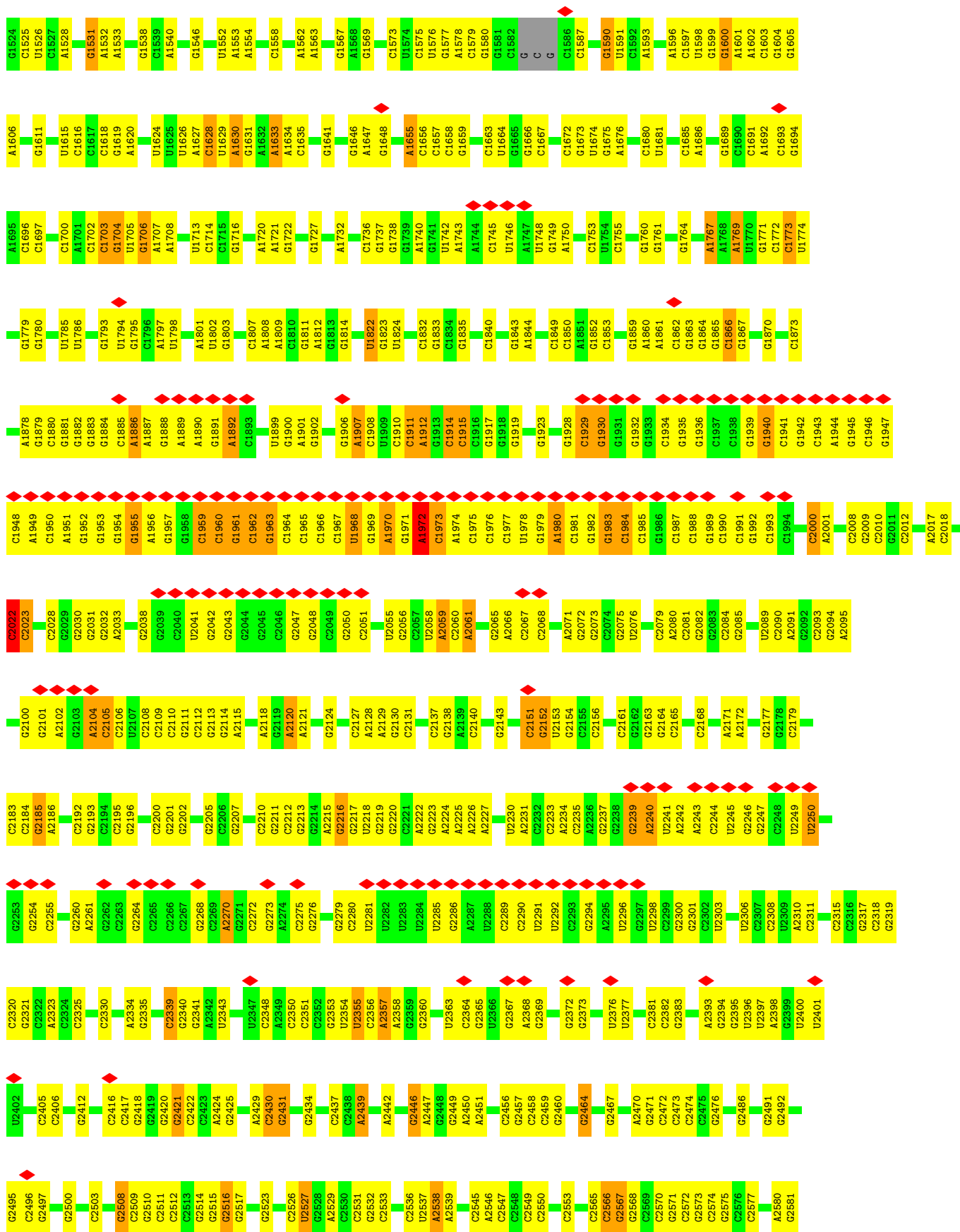
• Molecule 43: Ubiquitin/Ribosomal protein L40e

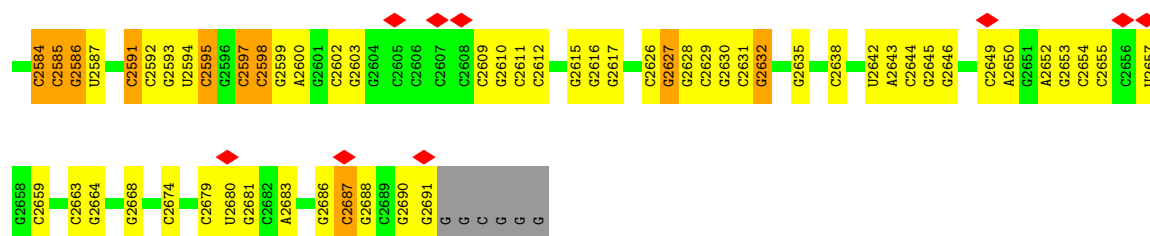


• Molecule 44: Large Subunit rRNA

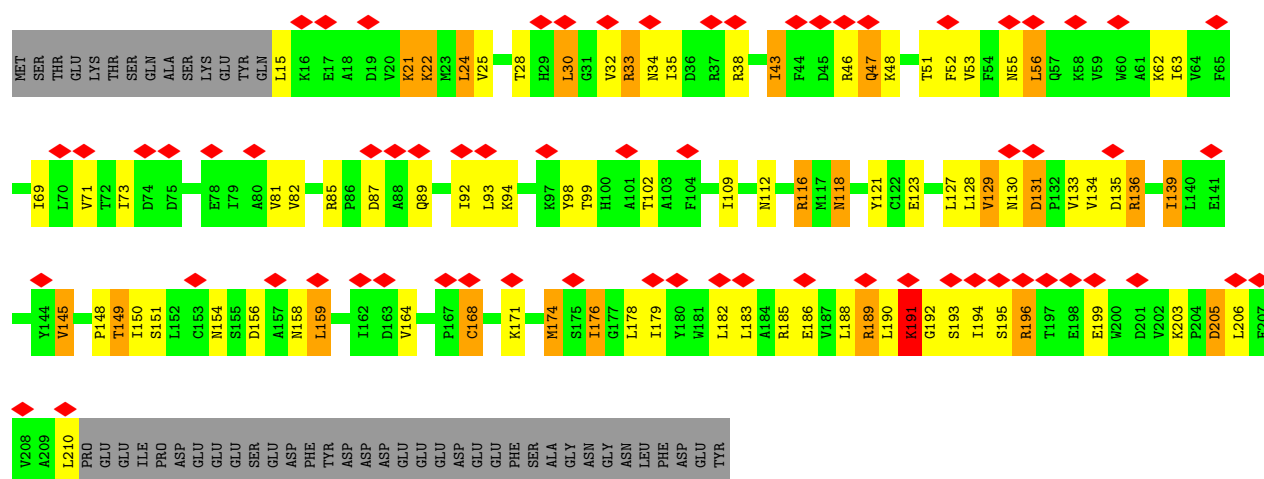




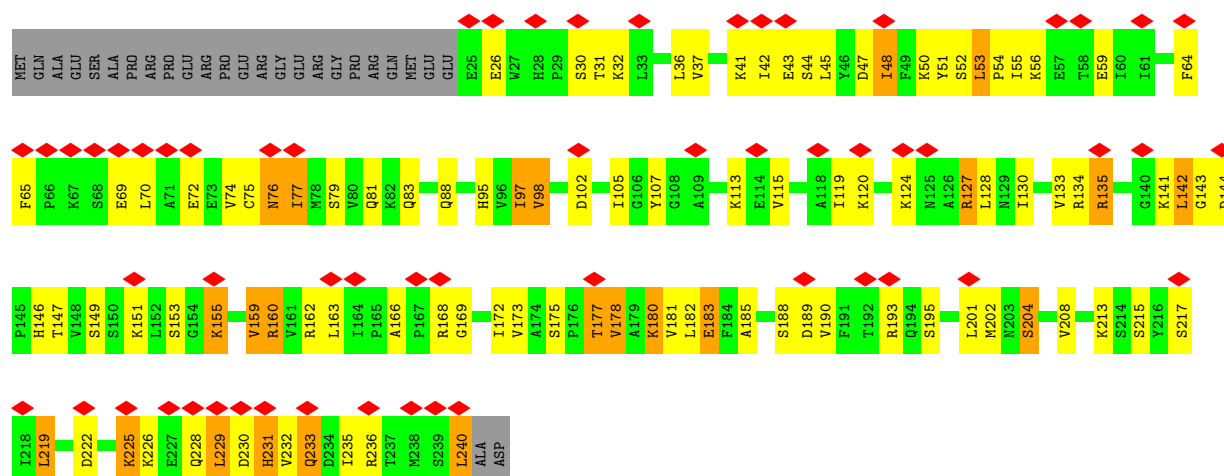




• Molecule 45: Ribosomal protein SA

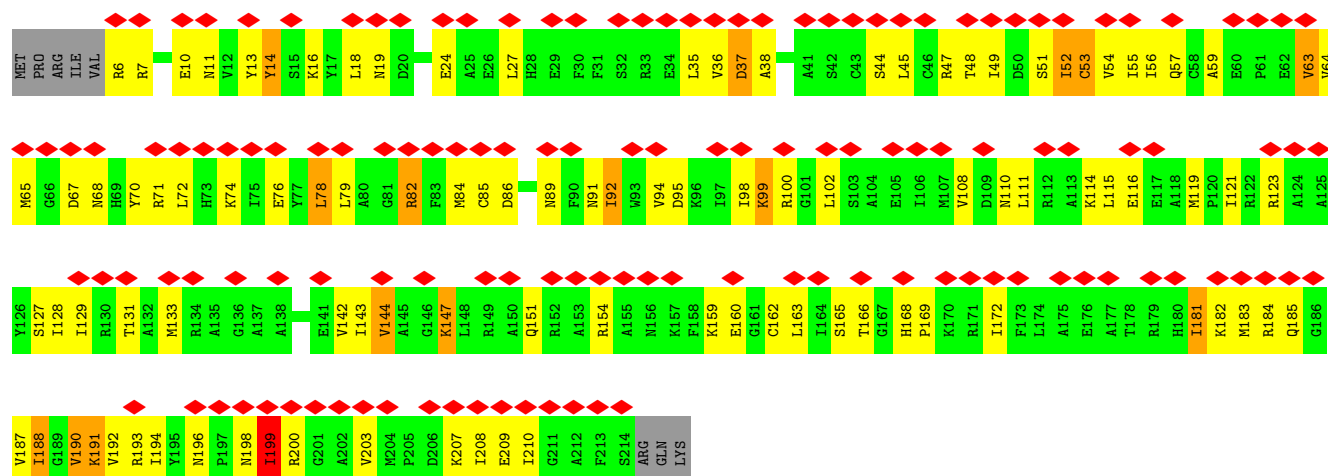


• Molecule 46: Ribosomal protein S2

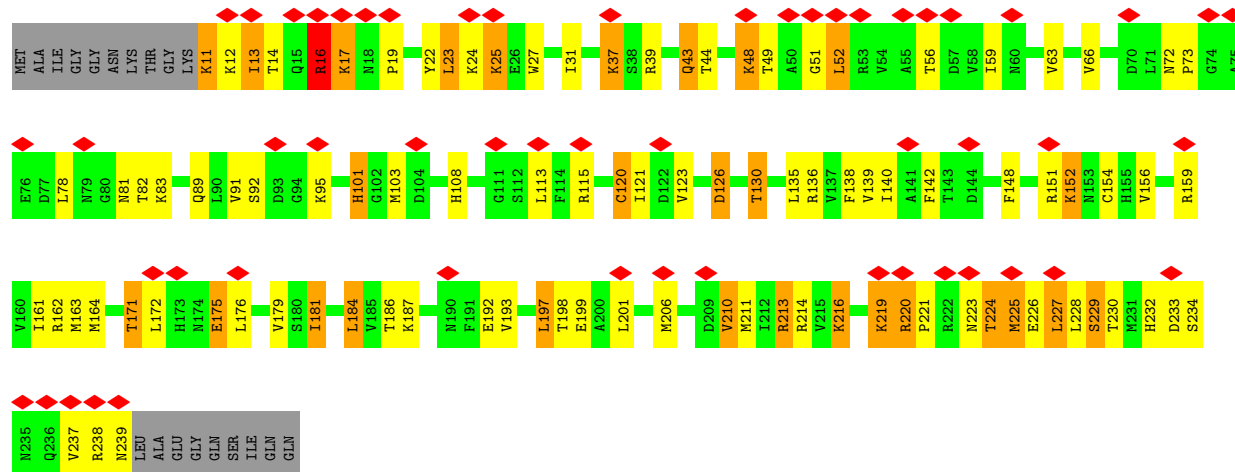


• Molecule 47: Ribosomal protein S3

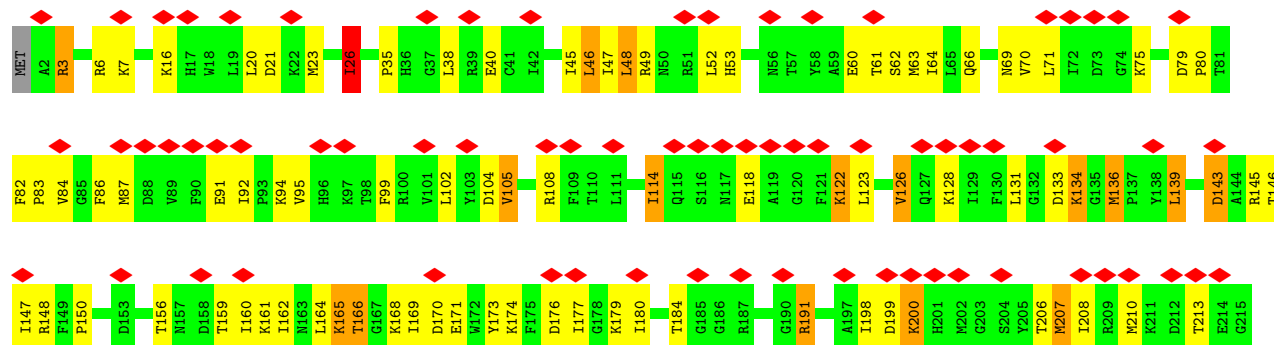


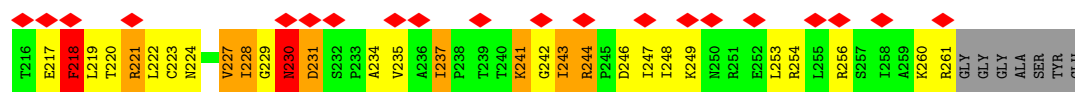


• Molecule 48: Ribosomal protein S3a

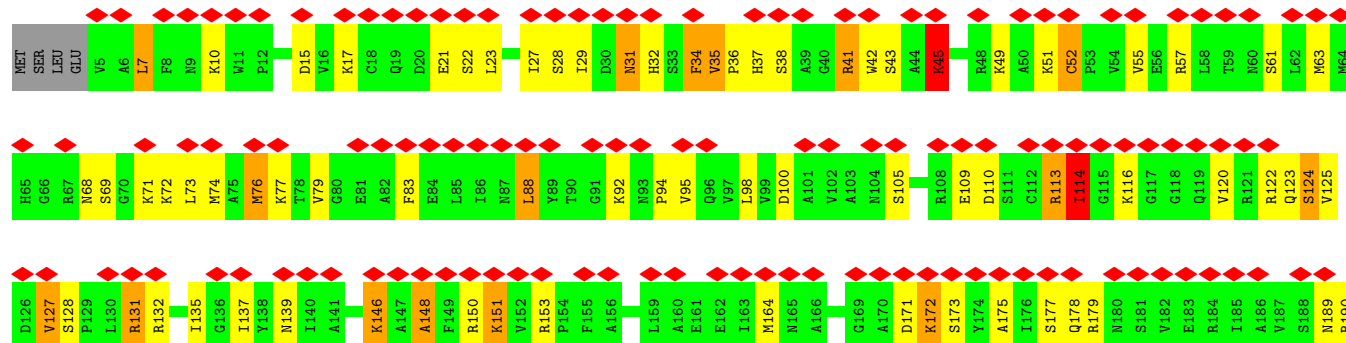


• Molecule 49: Ribosomal protein S4





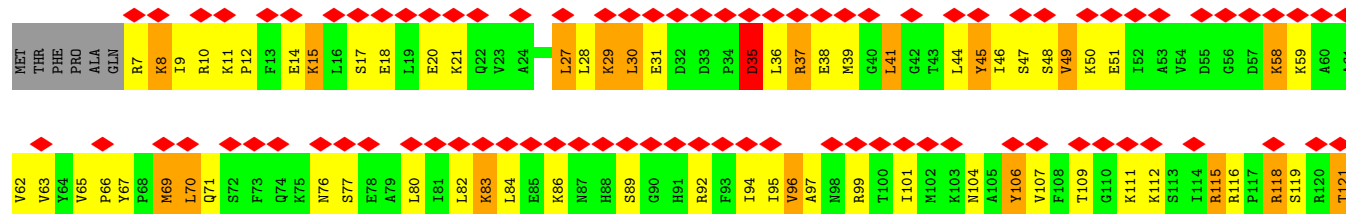
• Molecule 50: Ribosomal protein S5

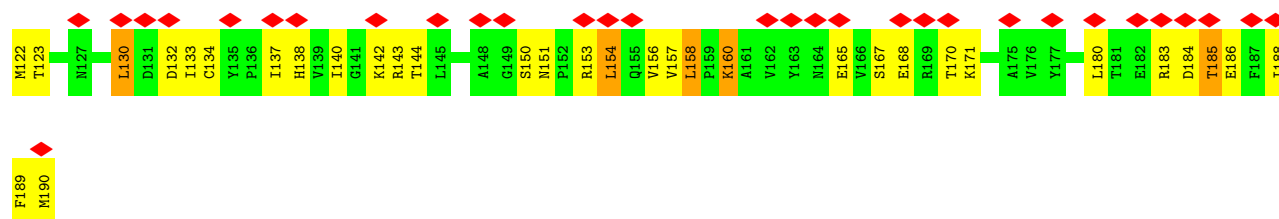


• Molecule 51: Ribosomal protein S6

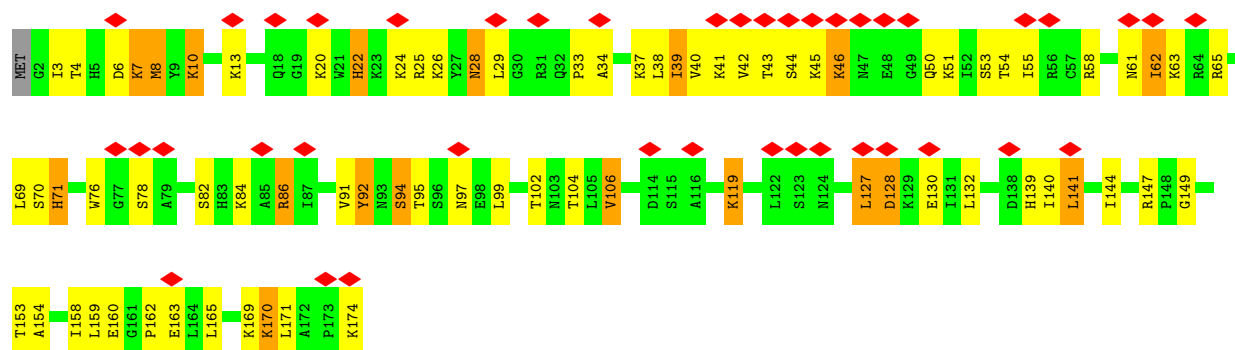


• Molecule 52: Ribosomal protein S7

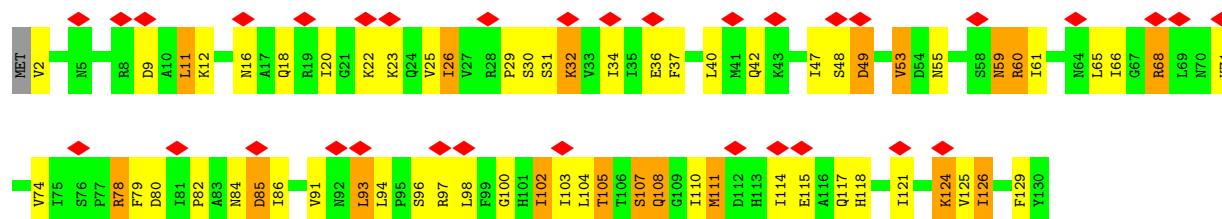




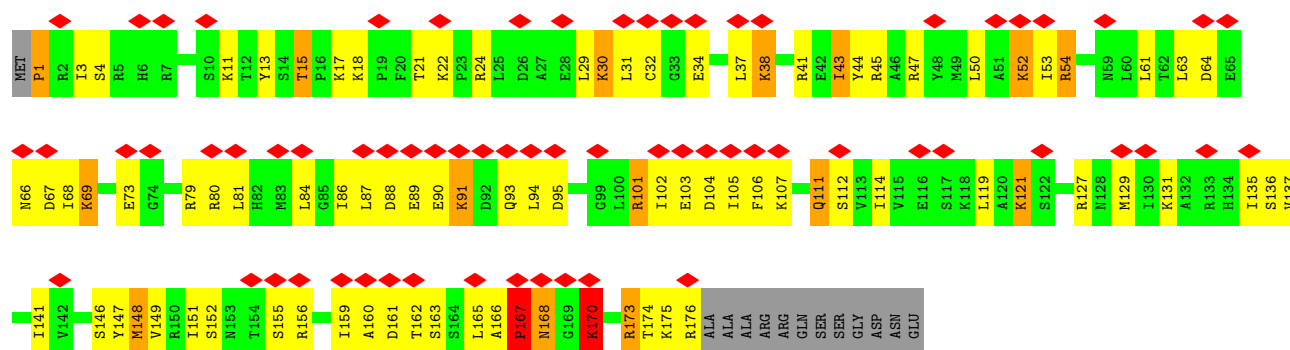
• Molecule 53: Ribosomal protein S8



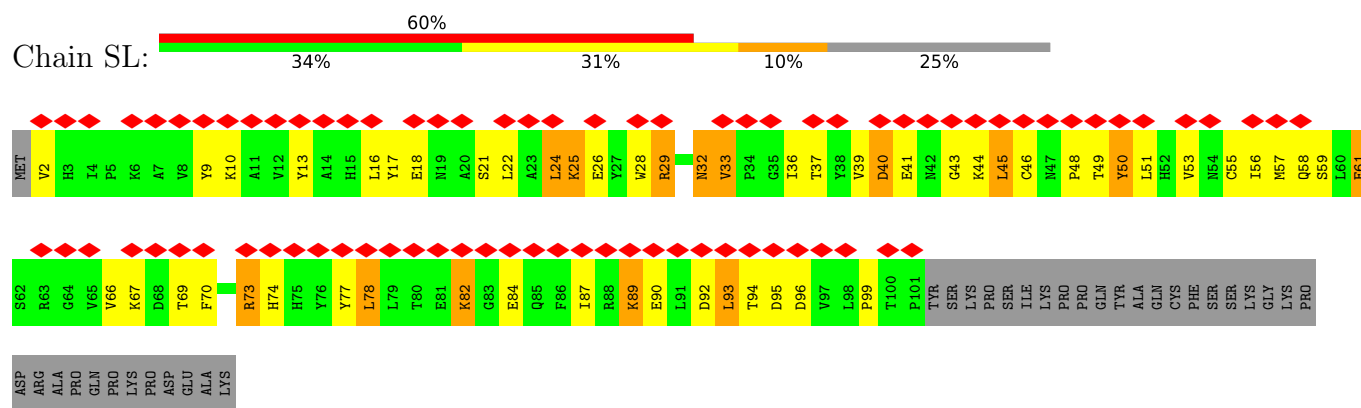
• Molecule 54: Ribosomal protein S15A



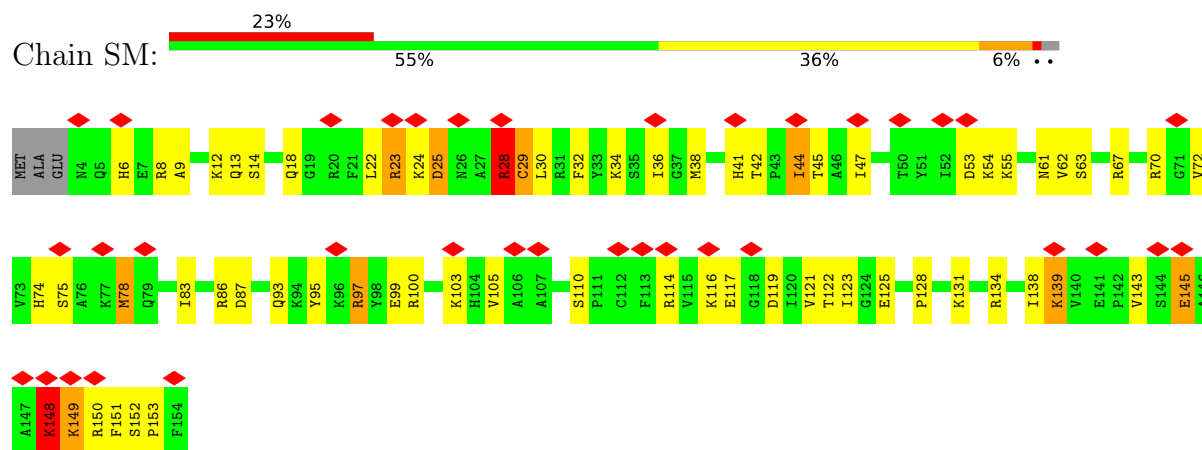
• Molecule 55: Ribosomal protein S9



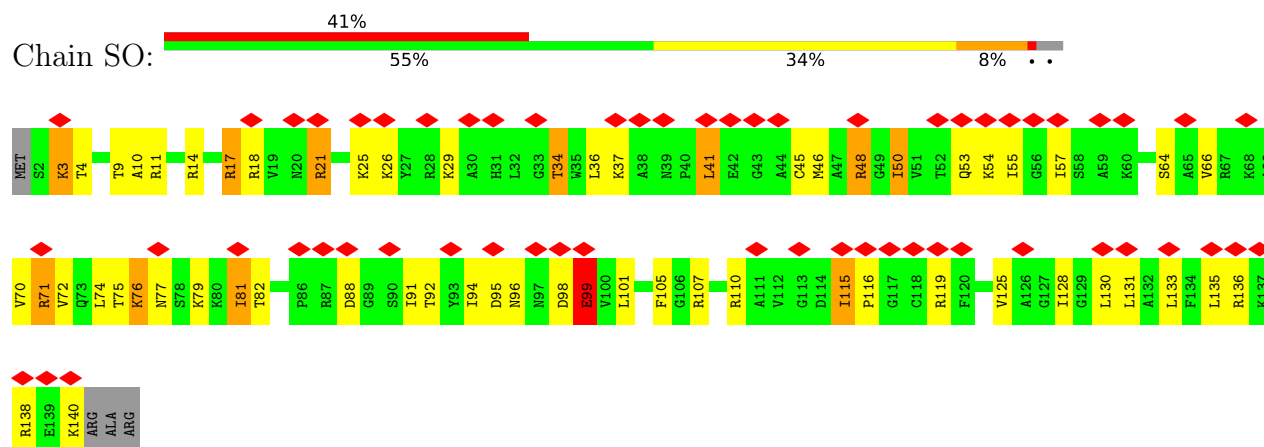
• Molecule 56: Ribosomal protein S10B



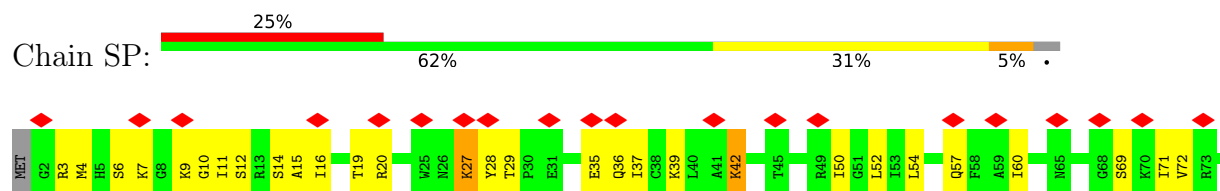
• Molecule 57: Ribosomal protein S11

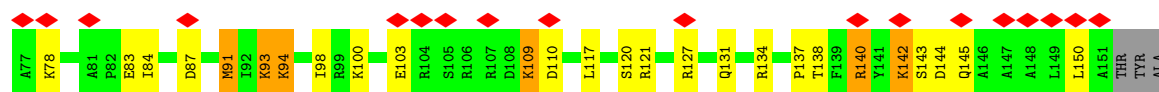


• Molecule 58: Ribosomal protein S23

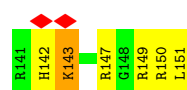
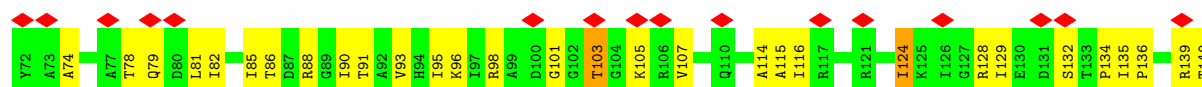
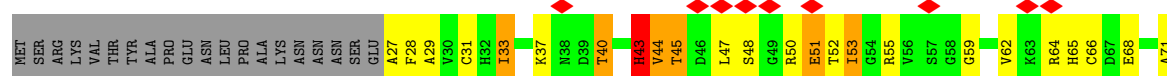


• Molecule 59: Ribosomal protein S13

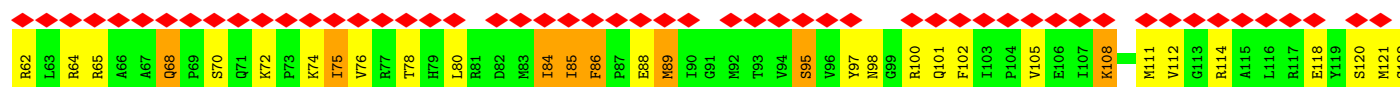




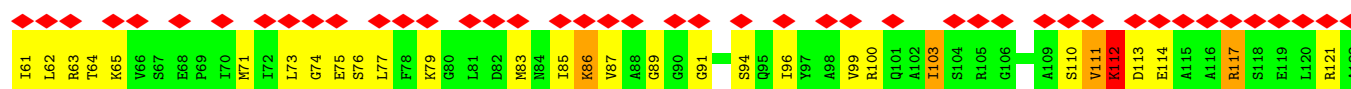
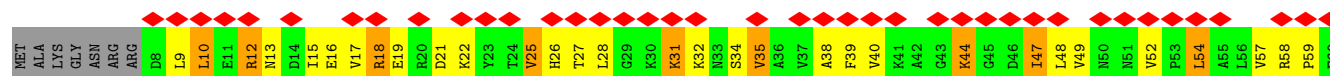
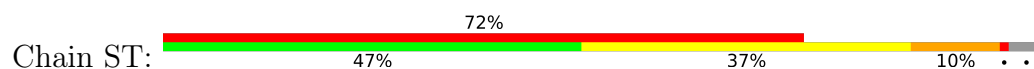
• Molecule 60: Ribosomal protein S14



• Molecule 61: Ribosomal protein S15



• Molecule 62: Ribosomal protein S16

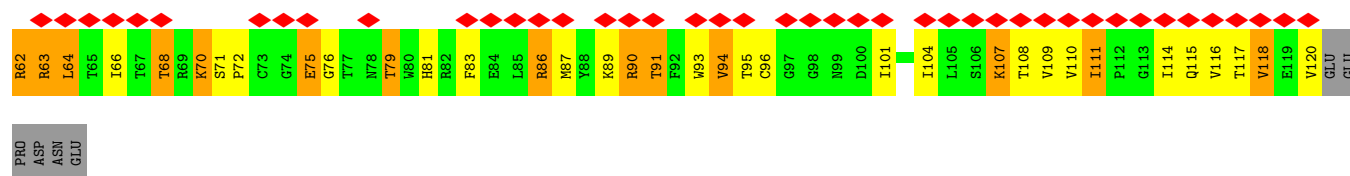


• Molecule 63: Ribosomal protein S17

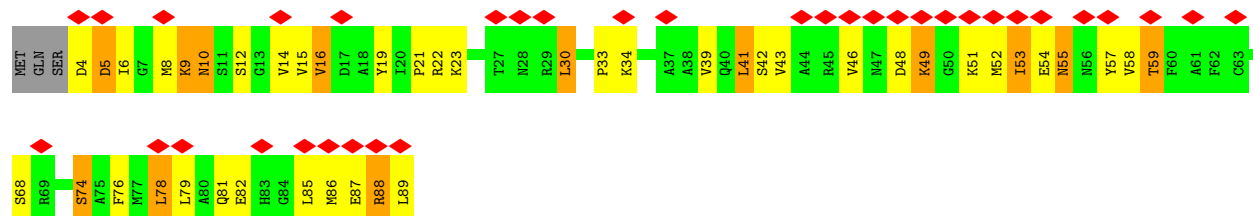
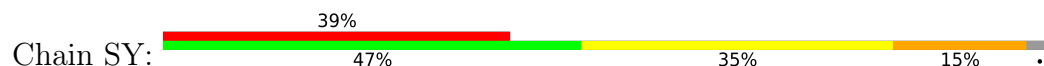
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T61	A62	A63	E64	E65	D66	A67	L68	M69	V71	L72	E73	D74	P75	L76	S77	H78	G79	I80	P81	A82	H83	M84	L85	N86	R87	N88	N89	D90	F91	E92	S93	G94	K95	D96	N97	H98	I99	L100	V101	N102	T103	I104	A105	S106	T107	H108	R109	A110	D111	L112	E113	R114	L115	R116	K117	T118	R119	G120
THR	ILE	VAL	GLN	PRO	N8	D9	R11	D12	L13	L14	R15	M16	F17	M18	T19	N20	I21	Q22	G23	K24	M25	V26	L27	E28	C29	A30	L31	V32	G33	I34	K35	G36	I37	G38	R39	R40	F41	A42	N43	V44	A45	L46	K47	K48	A49	N50	I51	D52	V53	H54	K55	R56	A57	G58	E59	I60		

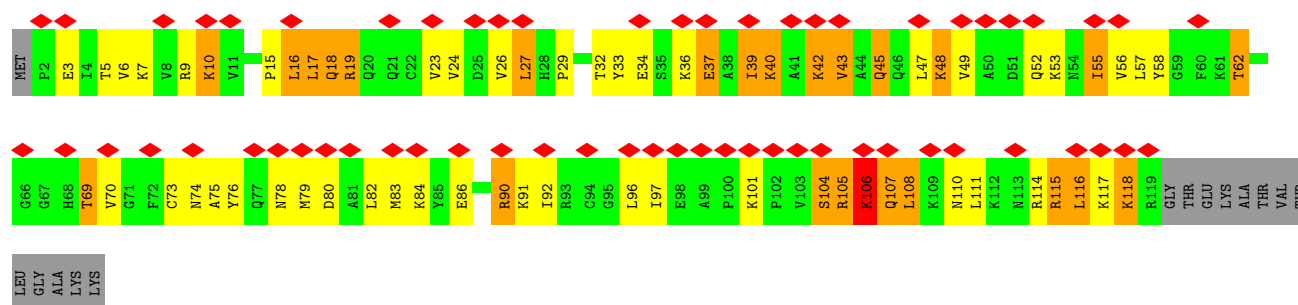
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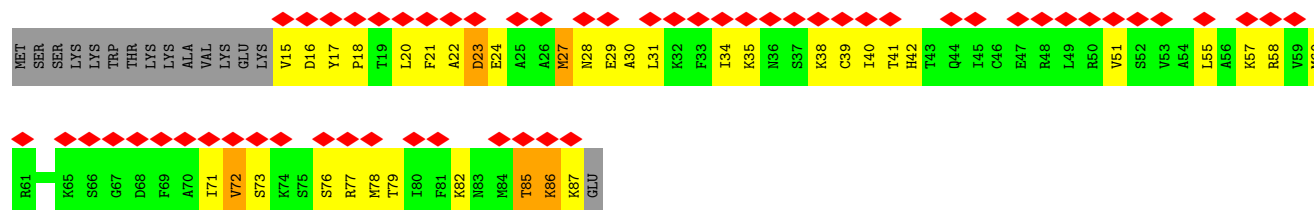
- Molecule 67: Ribosomal protein S21



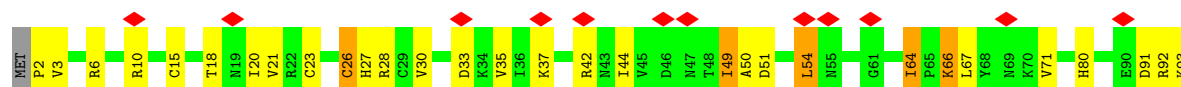
- Molecule 68: Ribosomal protein S24

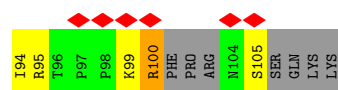


- Molecule 69: Ribosomal protein S25

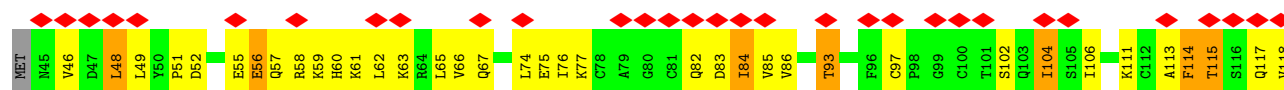
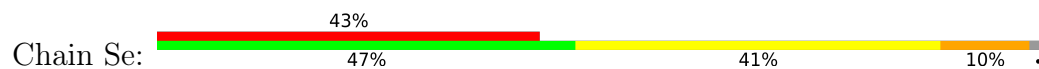


- Molecule 70: Ribosomal protein S26

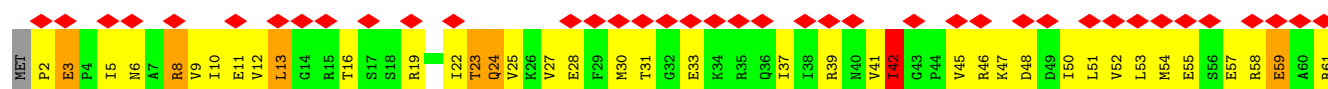




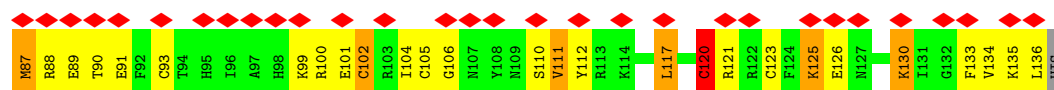
• Molecule 71: Ribosomal protein S27



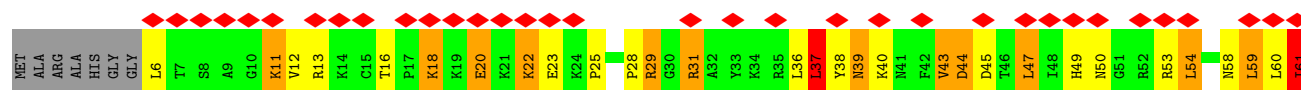
• Molecule 72: Ribosomal protein S28



• Molecule 73: Ribosomal protein S29A

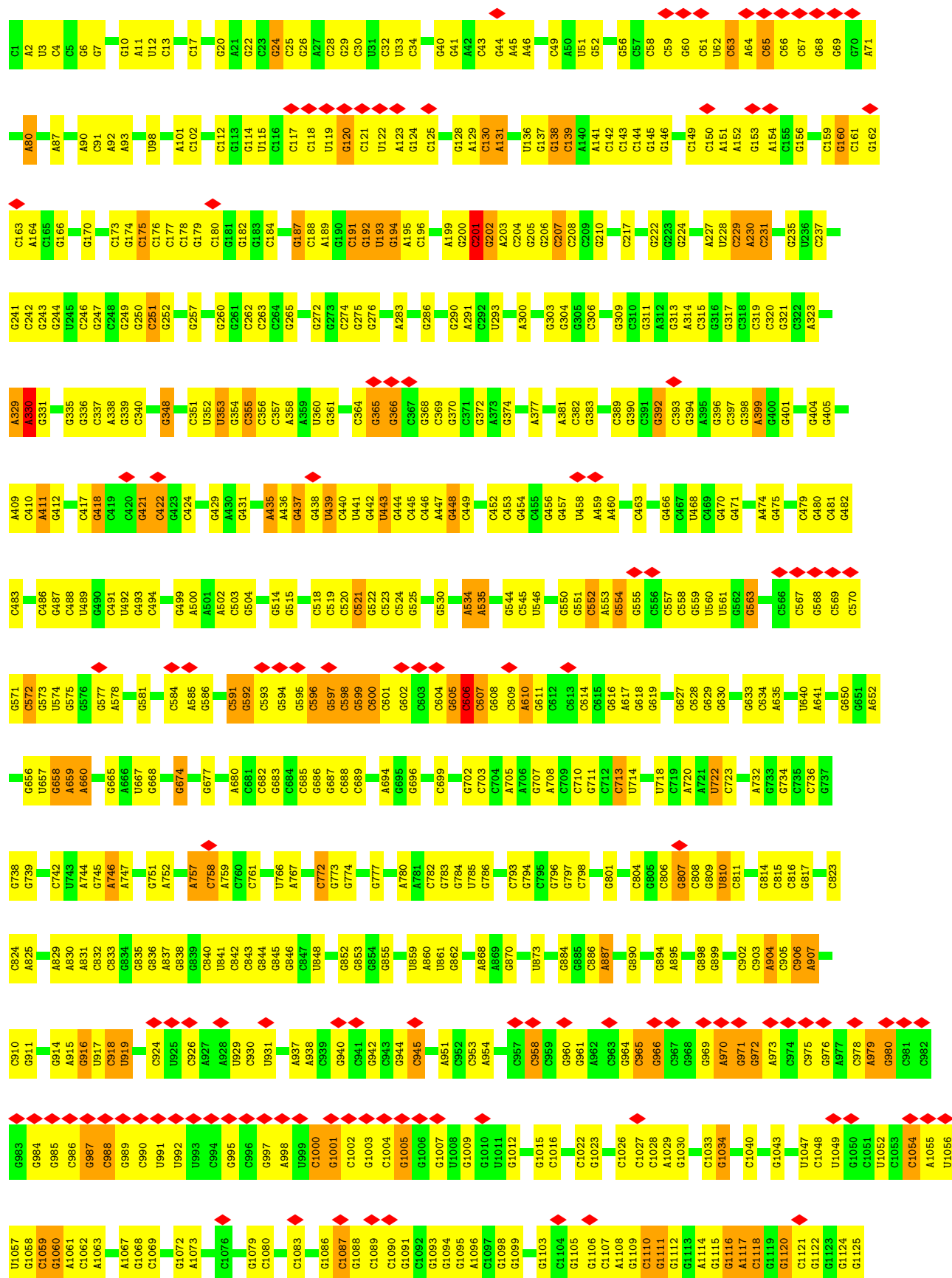


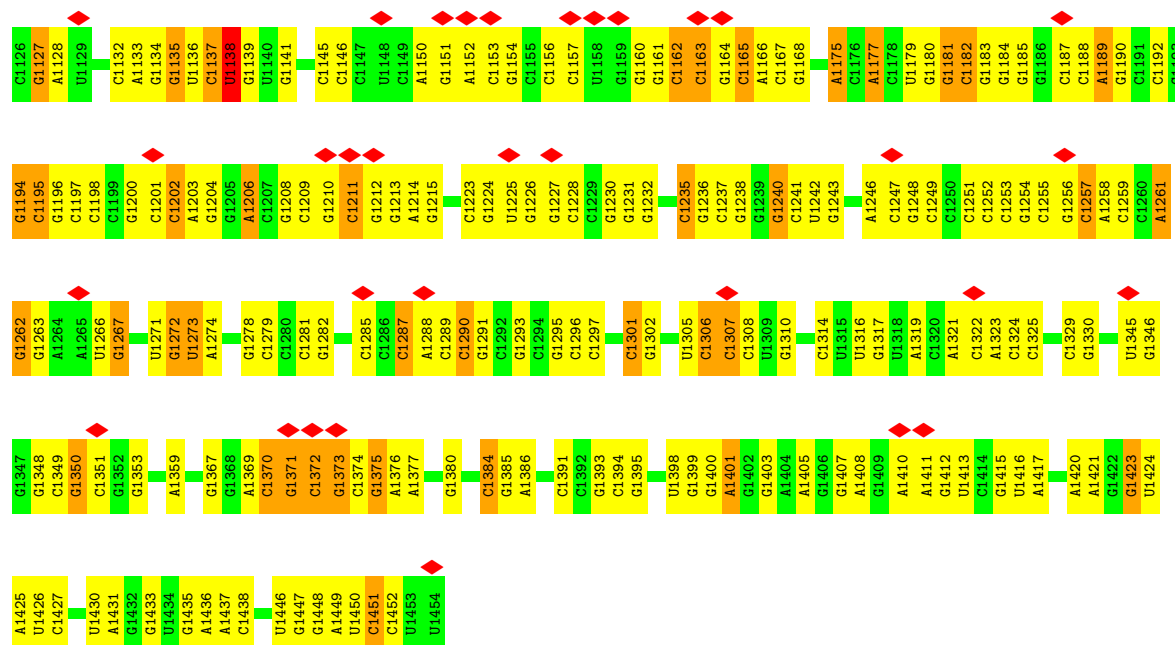
• Molecule 74: Ribosomal protein S30



• Molecule 75: Small Subunit rRNA







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	17963	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30.0	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1900	Depositor
Magnification	Not provided	
Image detector	GATAN K2 BASE (4k x 4k)	Depositor
Maximum map value	15.203	Depositor
Minimum map value	-7.156	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.84	Depositor
Map size (Å)	410.0, 410.0, 410.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	LA	0.91	0/1919	1.35	6/2577 (0.2%)
2	LB	0.90	0/3058	1.38	18/4129 (0.4%)
3	LC	0.89	0/2459	1.37	8/3335 (0.2%)
4	LD	0.56	0/3393	0.79	1/5292 (0.0%)
5	LE	0.57	0/2798	0.78	2/4361 (0.0%)
6	LF	0.89	0/2380	1.31	4/3193 (0.1%)
7	LG	0.79	0/450	1.34	3/601 (0.5%)
8	LH	0.85	0/1756	1.36	6/2367 (0.3%)
9	LI	0.88	0/1520	1.31	3/2052 (0.1%)
10	LJ	0.88	0/1479	1.38	2/1997 (0.1%)
11	LK	0.89	0/1231	1.33	2/1646 (0.1%)
12	LL	0.90	0/1346	1.35	5/1807 (0.3%)
13	LM	0.90	0/1628	1.37	4/2180 (0.2%)
14	LN	0.86	1/1037 (0.1%)	1.35	4/1390 (0.3%)
15	LO	0.86	0/1751	1.33	7/2346 (0.3%)
16	LP	0.84	0/1610	1.34	10/2160 (0.5%)
17	LQ	0.88	0/1257	1.34	1/1681 (0.1%)
18	LR	0.90	0/1425	1.43	11/1907 (0.6%)
19	LS	0.83	0/1609	1.35	4/2129 (0.2%)
20	LT	0.87	0/1457	1.34	4/1957 (0.2%)
21	LU	0.87	0/1283	1.32	3/1725 (0.2%)
22	LV	0.84	0/861	1.41	7/1158 (0.6%)
23	LW	0.90	0/1035	1.40	3/1396 (0.2%)
24	LX	0.82	0/553	1.48	4/736 (0.5%)
25	LY	0.88	0/982	1.40	4/1326 (0.3%)
26	LZ	0.89	0/1091	1.33	3/1454 (0.2%)
27	La	0.90	0/1030	1.35	1/1388 (0.1%)
28	Lb	0.91	0/1231	1.33	4/1647 (0.2%)
29	Lc	0.90	0/432	1.38	2/572 (0.3%)
30	Ld	0.90	0/778	1.42	7/1051 (0.7%)
31	Le	0.86	0/832	1.38	5/1118 (0.4%)
32	Lf	0.88	0/1101	1.30	1/1467 (0.1%)
33	Lg	0.90	0/793	1.36	4/1062 (0.4%)
34	Lh	0.90	0/789	1.36	2/1060 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Li	0.84	0/980	1.32	3/1302 (0.2%)
36	Lj	0.87	0/741	1.39	3/982 (0.3%)
37	Lk	0.87	0/727	1.37	1/963 (0.1%)
38	Ll	0.87	0/562	1.36	1/749 (0.1%)
39	Ln	0.98	0/1710	1.48	15/2305 (0.7%)
40	Lo	0.76	0/229	1.23	0/291
41	Lp	0.91	0/778	1.30	3/1029 (0.3%)
42	Lq	0.86	0/717	1.37	1/955 (0.1%)
43	Ls	0.89	0/392	1.47	1/522 (0.2%)
44	Lt	0.58	0/62235	0.80	47/97128 (0.0%)
45	SA	0.91	0/1603	1.40	2/2178 (0.1%)
46	SB	0.91	0/1700	1.43	8/2293 (0.3%)
47	SC	0.90	0/1685	1.38	6/2262 (0.3%)
48	SD	0.90	0/1890	1.42	9/2546 (0.4%)
49	SE	0.91	0/2131	1.32	8/2874 (0.3%)
50	SF	0.89	0/1465	1.41	4/1970 (0.2%)
51	SG	0.89	0/1665	1.41	5/2219 (0.2%)
52	SH	0.89	0/1508	1.41	4/2032 (0.2%)
53	SI	0.89	0/1378	1.33	1/1848 (0.1%)
54	SJ	0.91	0/1048	1.38	4/1412 (0.3%)
55	SK	0.88	0/1443	1.39	3/1930 (0.2%)
56	SL	0.91	0/842	1.36	3/1147 (0.3%)
57	SM	0.90	0/1280	1.35	6/1712 (0.4%)
58	SO	0.87	0/1095	1.37	3/1467 (0.2%)
59	SP	0.86	0/1215	1.34	1/1632 (0.1%)
60	SQ	0.93	0/928	1.48	3/1246 (0.2%)
61	SR	0.96	0/961	1.39	3/1284 (0.2%)
62	ST	0.94	0/1192	1.39	3/1594 (0.2%)
63	SU	0.88	0/879	1.43	4/1170 (0.3%)
64	SV	0.90	0/1133	1.47	8/1519 (0.5%)
65	SW	0.95	0/1095	1.36	6/1473 (0.4%)
66	SX	0.91	0/809	1.33	3/1092 (0.3%)
67	SY	0.93	0/659	1.41	3/883 (0.3%)
68	Sb	0.87	0/956	1.38	3/1279 (0.2%)
69	Sc	0.94	0/584	1.43	4/779 (0.5%)
70	Sd	0.86	0/833	1.31	2/1118 (0.2%)
71	Se	0.94	0/635	1.36	4/861 (0.5%)
72	Sg	0.96	0/508	1.37	3/677 (0.4%)
73	Sh	0.86	0/425	1.46	2/563 (0.4%)
74	Sj	0.91	0/518	1.51	8/690 (1.2%)
75	St	0.58	0/34858	0.81	24/54401 (0.0%)
All	All	0.73	1/186346 (0.0%)	1.07	380/272644 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	LN	67	LYS	N-CA	5.08	1.50	1.46

All (380) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	LW	47	LYS	CA-C-N	-12.53	111.31	122.47
23	LW	47	LYS	C-N-CA	-12.53	111.31	122.47
75	St	1416	U	C2'-C3'-O3'	10.21	124.82	109.50
3	LC	269	ILE	N-CA-C	-10.11	102.85	112.96
51	SG	56	PHE	CB-CA-C	-9.79	97.33	111.23
19	LS	190	PHE	N-CA-C	-9.69	101.14	113.16
55	SK	167	PRO	N-CA-CB	-9.09	93.71	103.25
44	Lt	1356	C	C2'-C3'-O3'	9.03	127.24	113.70
44	Lt	1506	A	C2'-C3'-O3'	8.95	127.12	113.70
44	Lt	1349	G	C2'-C3'-O3'	8.90	127.06	113.70
46	SB	228	GLN	CB-CA-C	-8.87	106.34	116.63
64	SV	38	GLY	N-CA-C	-8.85	104.16	114.69
44	Lt	2000	C	C4'-C3'-O3'	8.54	122.21	109.40
13	LM	135	GLU	N-CA-C	-8.49	103.10	113.97
2	LB	366	ILE	N-CA-C	-8.43	105.70	113.71
44	Lt	2022	C	C2'-C3'-O3'	8.37	126.25	113.70
48	SD	19	PRO	N-CA-C	8.32	123.22	111.33
65	SW	31	PHE	N-CA-C	-8.29	102.88	113.16
74	Sj	64	LYS	N-CA-C	-8.24	103.36	113.50
44	Lt	1252	G	C2'-C3'-O3'	8.23	126.04	113.70
54	SJ	126	ILE	N-CA-C	-8.12	103.95	111.67
39	Ln	16	ILE	N-CA-C	-8.12	105.27	113.47
29	Lc	50	ASP	CB-CA-C	8.10	126.13	110.17
75	St	1261	A	C2'-C3'-O3'	8.09	121.64	109.50
25	LY	26	ARG	CB-CA-C	8.03	121.63	110.06
39	Ln	144	LEU	N-CA-C	-7.99	102.23	108.78
48	SD	23	LEU	N-CA-C	-7.96	103.71	113.50
46	SB	215	SER	N-CA-C	-7.93	103.74	113.41
44	Lt	1277	G	C2'-C3'-O3'	7.88	121.33	109.50
25	LY	72	THR	N-CA-C	-7.88	104.19	113.88
73	Sh	120	CYS	CB-CA-C	-7.82	95.63	109.62
64	SV	39	ARG	N-CA-C	-7.77	103.12	114.39
15	LO	186	PRO	N-CA-C	-7.68	102.49	113.47
75	St	175	C	C2'-C3'-O3'	7.65	120.98	109.50
49	SE	237	ILE	N-CA-CB	-7.60	106.59	111.83
44	Lt	2591	C	C2'-C3'-O3'	7.55	120.82	109.50
44	Lt	1150	C	C2'-C3'-O3'	7.48	120.72	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	LN	83	ILE	N-CA-C	-7.47	103.25	110.42
44	Lt	2508	G	C4'-C3'-O3'	7.47	120.60	109.40
44	Lt	1511	G	C2'-C3'-O3'	7.37	124.75	113.70
75	St	435	A	C2'-C3'-O3'	7.31	124.67	113.70
30	Ld	85	VAL	N-CA-C	-7.29	105.62	112.83
44	Lt	2574	C	C2'-C3'-O3'	7.26	124.60	113.70
44	Lt	2355	U	C2'-C3'-O3'	7.24	120.36	109.50
26	LZ	112	ASN	CB-CA-C	-7.24	107.18	115.79
8	LH	220	PHE	CA-CB-CG	7.23	121.03	113.80
30	Ld	55	LEU	N-CA-C	-7.12	104.22	113.12
51	SG	129	GLY	CA-C-O	-7.11	115.00	120.76
11	LK	47	PRO	N-CA-C	7.06	122.86	113.40
18	LR	116	GLY	CA-C-N	-7.03	116.19	122.73
18	LR	116	GLY	C-N-CA	-7.03	116.19	122.73
18	LR	131	THR	CB-CA-C	-7.02	99.14	110.79
20	LT	156	LYS	N-CA-C	-6.96	104.52	112.87
39	Ln	87	ILE	N-CA-C	-6.95	105.76	112.29
11	LK	173	PHE	N-CA-C	-6.92	104.84	113.28
44	Lt	1135	G	C4'-C3'-O3'	6.91	119.76	109.40
20	LT	162	ALA	N-CA-C	-6.90	105.31	113.38
1	LA	152	SER	N-CA-C	-6.88	105.04	113.50
44	Lt	2627	G	C2'-C3'-O3'	6.84	123.96	113.70
31	Le	91	PHE	N-CA-C	-6.84	103.24	112.26
12	LL	104	PHE	CA-C-N	-6.81	117.02	121.65
12	LL	104	PHE	C-N-CA	-6.81	117.02	121.65
69	Sc	18	PRO	CB-CA-C	-6.78	103.10	111.64
7	LG	3	ALA	N-CA-C	-6.76	104.29	112.54
65	SW	49	ASP	N-CA-C	-6.75	103.63	112.41
22	LV	76	LYS	N-CA-C	-6.75	104.91	113.01
44	Lt	1236	G	C2'-C3'-O3'	6.75	123.83	113.70
55	SK	167	PRO	CB-CA-C	-6.74	100.45	111.56
51	SG	123	GLY	CA-C-O	-6.73	117.20	122.52
9	LI	120	ILE	N-CA-C	-6.70	104.48	111.58
74	Sj	39	ASN	N-CA-C	-6.68	104.08	111.36
8	LH	170	LYS	N-CA-C	-6.64	104.20	112.90
44	Lt	1121	A	C1'-C2'-O2'	-6.61	101.89	111.80
2	LB	271	GLY	CA-C-O	-6.58	117.71	122.45
44	Lt	2687	C	C2'-C3'-O3'	6.57	119.36	109.50
44	Lt	2584	C	C4'-C3'-O3'	6.52	119.18	109.40
33	Lg	9	PHE	CA-CB-CG	6.52	120.32	113.80
44	Lt	2508	G	C2'-C3'-O3'	6.51	119.27	109.50
33	Lg	86	GLN	N-CA-C	-6.51	105.30	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	LD	76	C	C4'-C3'-O3'	6.50	119.15	109.40
8	LH	220	PHE	CB-CA-C	6.49	122.99	109.68
24	LX	33	CYS	CB-CA-C	-6.49	100.69	110.88
49	SE	165	LYS	N-CA-C	-6.46	104.09	112.68
74	Sj	37	LEU	N-CA-C	-6.46	104.88	112.89
39	Ln	105	LYS	N-CA-C	-6.46	103.84	112.94
44	Lt	1972	A	C4'-C3'-O3'	-6.45	99.72	109.40
44	Lt	694	C	C1'-C2'-O2'	-6.45	98.73	108.40
75	St	90	A	C2'-C3'-O3'	6.43	119.15	109.50
44	Lt	2537	U	C2'-C3'-O3'	-6.41	99.88	109.50
58	SO	34	THR	N-CA-C	-6.41	104.30	111.28
57	SM	30	LEU	N-CA-C	-6.39	104.74	113.30
44	Lt	1121	A	C4'-C3'-O3'	6.38	118.97	109.40
51	SG	141	PRO	CB-CA-C	-6.36	103.56	111.64
30	Ld	44	GLN	N-CA-C	-6.36	105.54	113.55
6	LF	181	ILE	CA-C-O	-6.35	115.57	119.51
75	St	191	C	C2'-C3'-O3'	6.30	123.15	113.70
63	SU	114	PHE	CA-CB-CG	6.28	120.08	113.80
16	LP	128	PRO	N-CA-C	-6.28	101.35	111.14
75	St	201	C	C1'-C2'-O2'	6.28	121.22	111.80
44	Lt	1914	C	C2'-C3'-O3'	6.27	123.10	113.70
13	LM	179	ASN	CB-CA-C	6.26	116.07	110.44
68	Sb	106	LYS	N-CA-C	-6.24	104.56	111.36
2	LB	245	GLY	CA-C-O	-6.23	118.17	122.22
15	LO	4	TYR	CB-CA-C	6.23	122.16	110.63
1	LA	77	ILE	N-CA-C	-6.23	101.55	109.58
34	Lh	5	ARG	CB-CA-C	6.23	119.62	109.90
63	SU	65	VAL	N-CA-C	-6.23	104.98	111.58
18	LR	89	GLU	N-CA-C	-6.22	105.17	112.89
39	Ln	5	ASN	CB-CA-C	6.20	119.91	109.32
72	Sg	19	ARG	N-CA-C	-6.17	104.53	114.09
74	Sj	59	LEU	N-CA-C	-6.17	105.71	113.18
48	SD	229	SER	N-CA-C	-6.16	104.48	111.14
15	LO	35	ALA	CA-C-N	-6.14	114.93	123.10
15	LO	35	ALA	C-N-CA	-6.14	114.93	123.10
5	LE	91	A	C1'-C2'-O2'	6.13	121.00	111.80
44	Lt	1135	G	C2'-C3'-O3'	6.13	118.70	109.50
47	SC	68	ASN	N-CA-C	-6.13	105.04	113.56
30	Ld	25	GLY	CA-C-O	-6.12	117.90	122.37
19	LS	56	LYS	CB-CA-C	-6.12	102.78	111.95
44	Lt	1248	G	C2'-C3'-O3'	6.11	122.86	113.70
24	LX	19	GLY	CA-C-O	-6.09	117.92	122.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	LI	142	GLU	N-CA-C	-6.09	105.81	113.18
46	SB	228	GLN	N-CA-C	6.09	118.37	108.08
9	LI	109	ASP	N-CA-C	-6.08	106.12	112.93
2	LB	12	GLY	CA-C-O	-6.08	118.27	122.22
74	Sj	28	PRO	CB-CA-C	-6.07	103.46	111.23
47	SC	19	ASN	N-CA-C	-6.07	104.59	112.23
3	LC	10	PRO	N-CA-C	-6.06	105.47	113.65
45	SA	98	TYR	CB-CA-C	6.05	121.14	110.85
56	SL	9	TYR	CB-CA-C	-6.05	101.38	110.88
75	St	599	G	C2'-C3'-O3'	6.05	122.77	113.70
3	LC	240	THR	N-CA-C	-6.02	102.59	110.53
6	LF	177	ALA	N-CA-C	-6.01	106.07	113.41
44	Lt	84	C	C4'-C3'-O3'	6.01	118.42	109.40
48	SD	16	ARG	N-CA-C	6.01	115.40	108.49
39	Ln	140	PRO	N-CA-C	-6.00	105.36	113.40
16	LP	104	GLY	CA-C-O	-5.99	117.03	122.24
46	SB	64	PHE	CB-CA-C	5.98	122.57	110.38
62	ST	111	VAL	CA-C-O	-5.97	114.74	120.95
1	LA	15	VAL	N-CA-C	-5.96	107.48	113.20
63	SU	26	PRO	N-CA-C	5.96	121.81	113.53
44	Lt	1968	U	C4'-C3'-O3'	5.94	121.91	113.00
30	Ld	31	THR	N-CA-C	5.93	117.75	111.28
75	St	202	G	C3'-C2'-C1'	-5.93	95.57	101.50
54	SJ	100	GLY	CA-C-O	-5.93	117.26	121.88
58	SO	9	THR	CB-CA-C	-5.92	101.49	111.02
63	SU	114	PHE	CB-CA-C	5.90	119.74	110.19
44	Lt	71	C	C2'-C3'-O3'	5.89	122.53	113.70
44	Lt	898	C	C4'-C3'-O3'	5.89	118.23	109.40
61	SR	98	ASN	N-CA-C	-5.88	105.68	112.92
24	LX	22	PHE	CB-CA-C	-5.86	99.59	109.72
24	LX	7	CYS	CB-CA-C	-5.85	100.00	109.72
48	SD	101	HIS	CB-CA-C	5.85	118.85	109.02
44	Lt	1079	G	C2'-C3'-O3'	5.84	118.26	109.50
28	Lb	20	GLY	CA-C-O	-5.83	118.21	122.23
68	Sb	90	ARG	N-CA-C	-5.79	104.87	111.07
13	LM	206	ASN	N-CA-C	-5.78	104.35	111.40
39	Ln	81	GLY	N-CA-C	-5.76	107.37	115.32
21	LU	140	HIS	CA-C-N	-5.75	114.69	122.91
21	LU	140	HIS	C-N-CA	-5.75	114.69	122.91
15	LO	25	LEU	N-CA-C	-5.75	104.99	112.23
22	LV	94	VAL	CA-C-O	-5.75	117.14	121.68
46	SB	65	PHE	CB-CA-C	-5.75	102.18	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	LP	61	PHE	CA-CB-CG	5.74	119.54	113.80
2	LB	255	TRP	N-CA-C	-5.73	104.72	110.97
65	SW	8	PRO	N-CA-C	-5.73	102.20	111.03
6	LF	206	MET	N-CA-C	-5.73	106.45	113.50
30	Ld	104	LEU	N-CA-C	-5.73	105.17	111.82
42	Lq	60	CYS	CB-CA-C	-5.72	101.12	110.85
75	St	330	A	C4'-C3'-O3'	5.72	117.99	109.40
39	Ln	30	GLU	N-CA-C	-5.72	106.52	112.93
50	SF	21	GLU	N-CA-C	-5.72	106.46	113.50
8	LH	76	PRO	CB-CA-C	-5.71	104.30	111.56
52	SH	121	THR	CB-CA-C	5.70	120.64	109.35
25	LY	69	ASP	N-CA-C	-5.70	105.82	112.89
61	SR	21	GLU	CA-C-O	-5.68	114.86	120.82
49	SE	166	THR	N-CA-C	-5.67	106.41	113.38
17	LQ	100	ASN	CB-CA-C	5.66	120.46	110.85
75	St	1059	C	C2'-C3'-O3'	5.65	122.17	113.70
39	Ln	205	TYR	CB-CA-C	-5.64	101.25	110.85
1	LA	248	GLY	N-CA-C	-5.64	106.21	114.90
60	SQ	139	ARG	N-CA-C	5.64	117.97	110.53
2	LB	274	HIS	CA-CB-CG	5.63	119.43	113.80
74	Sj	43	VAL	CA-C-O	-5.62	113.76	120.78
55	SK	50	LEU	N-CA-C	-5.60	104.80	111.69
64	SV	41	PHE	CB-CA-C	5.60	120.18	110.94
44	Lt	861	C	C2'-C3'-O3'	-5.59	105.32	113.70
33	Lg	3	GLU	N-CA-C	-5.58	105.20	111.28
67	SY	48	ASP	N-CA-C	-5.58	105.29	111.71
16	LP	96	MET	N-CA-C	-5.58	106.43	113.18
57	SM	23	ARG	CB-CA-C	-5.58	108.53	116.34
39	Ln	33	GLU	N-CA-C	-5.58	105.24	113.61
1	LA	250	ARG	N-CA-C	-5.58	106.32	113.01
57	SM	28	ARG	CA-C-N	-5.58	112.77	121.02
57	SM	28	ARG	C-N-CA	-5.58	112.77	121.02
67	SY	74	SER	N-CA-C	-5.57	106.61	113.41
2	LB	98	GLY	CA-C-O	-5.57	116.48	122.05
46	SB	51	TYR	CB-CA-C	5.57	120.45	110.81
64	SV	43	ASN	CB-CA-C	5.57	118.08	110.06
18	LR	5	LEU	N-CA-C	-5.57	105.80	112.59
36	Lj	29	HIS	N-CA-C	-5.57	105.13	111.14
7	LG	40	LYS	N-CA-C	-5.57	105.70	112.88
23	LW	47	LYS	N-CA-C	-5.56	101.22	110.17
44	Lt	1121	A	C2'-C3'-O3'	5.55	117.83	109.50
60	SQ	43	HIS	CB-CA-C	5.55	118.69	110.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
73	Sh	120	CYS	N-CA-CB	-5.55	101.88	110.04
10	LJ	83	GLY	CA-C-O	-5.54	117.56	121.88
32	Lf	10	PRO	N-CA-C	5.54	121.23	113.53
49	SE	218	PHE	CA-CB-CG	5.54	119.34	113.80
3	LC	248	ASP	N-CA-C	-5.53	105.26	112.23
7	LG	33	LEU	N-CA-C	5.53	117.11	111.14
64	SV	139	SER	N-CA-C	5.52	117.10	111.14
64	SV	128	HIS	N-CA-C	-5.51	106.59	113.15
18	LR	130	PRO	N-CA-C	-5.51	106.22	113.65
47	SC	53	CYS	CA-C-N	-5.49	115.98	123.12
47	SC	53	CYS	C-N-CA	-5.49	115.98	123.12
35	Li	88	THR	CB-CA-C	-5.49	102.27	110.88
41	Lp	23	ALA	N-CA-C	5.47	118.01	108.76
15	LO	43	THR	N-CA-C	-5.47	105.31	111.28
2	LB	313	ASN	CB-CA-C	5.47	120.39	111.26
10	LJ	2	PRO	CA-N-CD	-5.47	104.34	112.00
53	SI	22	HIS	CA-CB-CG	5.47	119.27	113.80
20	LT	18	PRO	N-CA-C	-5.47	106.58	114.18
54	SJ	105	THR	CB-CA-C	-5.47	101.14	109.89
49	SE	231	ASP	N-CA-C	-5.46	105.48	111.82
44	Lt	326	A	C2'-C3'-O3'	-5.45	101.33	109.50
26	LZ	94	PRO	CB-CA-C	-5.44	104.44	111.46
48	SD	210	VAL	CA-C-O	-5.44	117.90	122.63
2	LB	361	LYS	N-CA-C	-5.43	106.50	113.23
12	LL	117	ASP	CB-CA-C	5.43	116.20	108.76
44	Lt	484	U	C4'-C3'-O3'	5.42	121.14	113.00
38	Ll	45	TYR	CB-CA-C	-5.42	98.80	110.45
64	SV	51	ILE	N-CA-C	5.41	116.32	110.21
75	St	1187	C	C4'-C3'-O3'	5.40	121.10	113.00
44	Lt	590	C	C2'-C3'-O3'	-5.40	105.61	113.70
14	LN	33	THR	N-CA-C	-5.39	106.66	113.18
75	St	552	C	C2'-C3'-O3'	-5.38	101.42	109.50
2	LB	237	ARG	N-CA-C	-5.38	101.01	109.25
71	Se	115	THR	N-CA-C	5.38	116.95	111.14
12	LL	37	LEU	N-CA-C	-5.38	104.97	112.45
26	LZ	75	ASP	N-CA-C	-5.38	106.49	113.16
31	Le	44	VAL	CA-C-N	-5.38	115.41	122.99
31	Le	44	VAL	C-N-CA	-5.38	115.41	122.99
20	LT	157	ARG	N-CA-C	-5.37	106.86	113.41
2	LB	95	THR	CA-C-O	-5.36	115.70	121.27
44	Lt	2022	C	C4'-C3'-O3'	5.35	121.03	113.00
69	Sc	18	PRO	N-CA-C	5.35	119.27	111.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	SH	35	ASP	CA-C-O	-5.34	115.96	122.64
71	Se	114	PHE	CB-CA-C	5.34	119.03	110.16
35	Li	38	VAL	N-CA-C	-5.34	104.53	110.62
27	La	49	ARG	CB-CA-C	-5.33	110.41	116.54
29	Lc	24	PRO	CA-C-O	-5.33	112.30	120.03
71	Se	48	LEU	CA-C-O	-5.33	115.43	121.72
61	SR	42	ARG	N-CA-C	-5.33	105.05	112.45
44	Lt	1079	G	C4'-C3'-O3'	5.32	117.38	109.40
75	St	1138	U	C2'-C3'-O3'	5.32	117.47	109.50
30	Ld	76	GLY	CA-C-O	-5.31	115.69	121.48
49	SE	26	ILE	N-CA-C	-5.31	106.69	112.80
14	LN	117	ARG	N-CA-C	-5.31	105.07	112.45
48	SD	162	ARG	N-CA-C	-5.30	105.42	111.14
52	SH	189	PHE	CB-CA-C	5.30	120.15	111.41
69	Sc	30	ALA	N-CA-C	-5.30	105.67	111.82
72	Sg	42	ILE	CA-C-O	-5.30	116.45	121.64
67	SY	33	PRO	CB-CA-C	-5.29	103.89	112.62
48	SD	130	THR	N-CA-C	-5.29	106.89	113.19
13	LM	78	CYS	N-CA-C	5.29	116.49	109.93
8	LH	198	TRP	CA-C-O	-5.29	114.51	119.80
15	LO	188	LYS	N-CA-C	-5.29	105.57	112.23
34	Lh	48	THR	N-CA-CB	5.29	119.42	110.49
44	Lt	1590	G	C3'-C2'-C1'	-5.29	96.21	101.50
75	St	606	C	C2'-C3'-O3'	5.28	121.63	113.70
50	SF	45	LYS	CB-CA-C	-5.28	110.47	116.54
36	Lj	57	ASN	CA-C-O	-5.27	114.94	120.63
16	LP	24	LEU	N-CA-C	-5.26	104.98	111.40
50	SF	34	PHE	CA-CB-CG	5.26	119.06	113.80
66	SX	60	PRO	N-CA-C	-5.26	102.93	111.03
68	Sb	82	LEU	N-CA-C	-5.25	105.56	111.28
16	LP	128	PRO	CA-C-O	-5.25	115.36	121.34
37	Lk	74	TYR	N-CA-C	-5.25	106.14	112.54
44	Lt	1590	G	C2'-C3'-O3'	-5.24	101.65	109.50
28	Lb	139	ARG	N-CA-C	-5.23	105.64	112.23
56	SL	40	ASP	N-CA-C	-5.23	103.49	110.55
75	St	1138	U	C4'-C3'-O3'	5.23	117.25	109.40
45	SA	121	TYR	CB-CA-C	-5.23	102.63	110.16
22	LV	47	ASN	N-CA-C	-5.22	105.76	111.82
5	LE	38	U	C2'-C3'-O3'	5.22	121.53	113.70
49	SE	80	PRO	N-CA-C	-5.22	106.28	113.53
18	LR	165	GLY	CA-C-O	-5.21	117.88	122.16
44	Lt	1257	U	C4'-C3'-O3'	5.21	117.22	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	Le	64	ARG	N-CA-C	-5.21	105.28	111.69
41	Lp	47	GLY	CA-C-O	-5.21	118.63	122.23
72	Sg	16	THR	CA-C-O	-5.21	115.33	120.80
8	LH	137	GLU	N-CA-C	-5.21	105.67	112.23
54	SJ	59	ASN	CB-CA-C	5.21	120.78	110.42
18	LR	178	SER	CA-C-O	-5.21	114.98	120.92
65	SW	4	VAL	N-CA-C	-5.20	105.31	110.62
46	SB	76	ASN	CB-CA-C	-5.20	104.08	112.09
2	LB	358	THR	N-CA-C	-5.20	106.25	112.59
75	St	24	G	C4'-C3'-O3'	5.19	120.79	113.00
3	LC	13	THR	N-CA-C	5.19	117.06	108.49
46	SB	236	ARG	N-CA-C	-5.19	105.24	112.45
33	Lg	89	GLY	N-CA-C	-5.19	108.83	115.42
21	LU	151	THR	CB-CA-C	5.18	116.90	108.87
65	SW	112	LEU	N-CA-C	-5.18	106.98	113.72
44	Lt	1179	U	N1-C1'-C2'	5.18	119.77	112.00
75	St	807	G	C3'-C2'-C1'	-5.18	96.32	101.50
16	LP	61	PHE	CB-CA-C	5.17	119.00	110.88
16	LP	69	HIS	CA-C-N	-5.17	115.81	123.05
16	LP	69	HIS	C-N-CA	-5.17	115.81	123.05
57	SM	95	TYR	CA-C-O	-5.17	115.16	120.54
3	LC	254	LYS	CA-C-O	-5.17	115.08	121.02
1	LA	190	LYS	N-CA-C	-5.17	105.65	111.28
48	SD	227	LEU	N-CA-C	-5.16	105.83	111.82
44	Lt	459	A	C2'-C3'-O3'	-5.16	105.96	113.70
75	St	187	G	C2'-C3'-O3'	5.16	117.24	109.50
2	LB	169	PRO	CB-CA-C	-5.16	104.53	111.85
2	LB	314	TYR	CA-C-O	-5.16	115.92	121.38
64	SV	41	PHE	CA-CB-CG	5.16	118.95	113.80
71	Se	93	THR	CB-CA-C	5.15	116.13	108.87
18	LR	20	LYS	N-CA-C	-5.15	106.59	112.92
22	LV	50	HIS	CB-CA-C	5.15	117.21	110.06
44	Lt	512	G	C2'-C3'-O3'	-5.14	105.98	113.70
22	LV	25	GLY	N-CA-C	-5.14	108.15	115.30
75	St	807	G	C4'-C3'-C2'	-5.14	97.46	102.60
39	Ln	115	SER	N-CA-C	-5.14	105.68	111.28
22	LV	80	LYS	N-CA-C	-5.14	105.37	111.69
66	SX	76	GLY	CA-C-O	-5.13	118.75	122.45
18	LR	152	GLY	CA-C-O	-5.13	117.56	122.13
2	LB	16	TYR	CB-CA-C	5.13	119.24	110.01
62	ST	34	SER	CA-C-N	-5.13	116.45	123.12
62	ST	34	SER	C-N-CA	-5.13	116.45	123.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	Lb	38	LEU	N-CA-C	-5.12	107.06	113.72
60	SQ	45	THR	CB-CA-C	-5.12	99.37	111.65
19	LS	4	LEU	N-CA-C	-5.12	106.63	112.92
35	Li	117	THR	CA-C-O	-5.11	115.97	121.38
50	SF	94	PRO	N-CA-C	-5.10	106.56	113.40
75	St	435	A	C3'-C2'-O2'	5.10	118.35	110.70
51	SG	13	ASN	CB-CA-C	-5.10	104.03	109.85
22	LV	79	VAL	N-CA-C	-5.10	104.90	112.04
19	LS	32	ILE	N-CA-C	-5.10	105.16	112.35
6	LF	98	ALA	N-CA-C	-5.09	105.81	111.36
39	Ln	200	ASN	O-C-N	5.09	124.60	120.83
70	Sd	27	HIS	N-CA-C	-5.09	107.02	113.23
12	LL	88	ASN	N-CA-C	-5.08	106.38	112.58
59	SP	137	PRO	N-CA-C	-5.08	106.79	113.65
41	Lp	22	LYS	CA-C-O	-5.08	115.98	121.87
66	SX	72	PRO	N-CA-C	-5.08	106.47	113.53
44	Lt	1074	C	C2'-C3'-O3'	5.08	117.11	109.50
3	LC	76	HIS	N-CA-C	-5.08	105.66	111.14
16	LP	33	VAL	CA-C-O	-5.08	116.29	121.67
47	SC	110	ASN	N-CA-C	-5.07	105.45	111.69
69	Sc	23	ASP	CA-C-O	-5.07	116.11	120.88
28	Lb	54	GLY	CA-C-O	-5.06	117.62	122.13
75	St	392	G	C2'-C3'-O3'	-5.06	106.11	113.70
18	LR	144	CYS	N-CA-C	-5.06	107.14	113.72
31	Le	40	LYS	N-CA-C	-5.06	106.03	113.72
74	Sj	25	PRO	N-CA-C	-5.06	103.24	111.03
57	SM	95	TYR	N-CA-C	-5.06	99.56	108.20
58	SO	98	ASP	CA-C-O	-5.06	115.06	120.42
3	LC	162	VAL	CB-CA-C	5.05	116.48	110.93
2	LB	202	PRO	N-CA-C	5.05	119.11	111.19
52	SH	106	TYR	CB-CA-C	-5.04	104.57	111.73
65	SW	38	GLY	CA-C-O	-5.04	118.54	122.52
39	Ln	55	LEU	CA-C-O	-5.04	115.03	120.87
47	SC	82	ARG	N-CA-C	-5.03	105.51	111.69
36	Lj	26	THR	CA-C-O	-5.03	115.22	120.55
49	SE	133	ASP	CA-C-O	-5.03	115.91	122.14
74	Sj	61	ILE	N-CA-C	-5.03	105.60	110.42
39	Ln	209	THR	CA-C-O	-5.02	115.28	120.70
70	Sd	27	HIS	CB-CA-C	5.02	119.64	111.26
25	LY	55	TRP	N-CA-C	-5.02	106.85	113.17
75	St	1059	C	C3'-C2'-O2'	5.01	118.22	110.70
2	LB	43	LEU	N-CA-C	-5.01	103.06	110.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	SL	99	PRO	CB-CA-C	-5.01	103.65	111.22
14	LN	68	PRO	N-CA-C	5.01	120.49	113.53
44	Lt	1004	A	C2'-C3'-O3'	-5.01	106.19	113.70
75	St	807	G	C4'-C3'-O3'	-5.01	101.89	109.40
39	Ln	28	PHE	N-CA-C	-5.01	105.82	111.28
2	LB	6	PHE	CB-CA-C	5.00	118.38	109.72
43	Ls	97	ARG	CA-C-O	-5.00	116.36	122.41

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	LA	1886	0	1948	14	0
2	LB	2987	0	3024	44	0
3	LC	2408	0	2491	34	0
4	LD	3038	0	1556	16	0
5	LE	2502	0	1268	9	0
6	LF	2337	0	2395	28	0
7	LG	439	0	479	7	0
8	LH	1726	0	1761	29	0
9	LI	1494	0	1578	24	0
10	LJ	1452	0	1495	26	0
11	LK	1207	0	1217	21	0
12	LL	1322	0	1342	21	0
13	LM	1605	0	1704	20	0
14	LN	1024	0	1091	22	0
15	LO	1708	0	1785	20	0
16	LP	1578	0	1614	18	0
17	LQ	1231	0	1265	25	0
18	LR	1402	0	1478	18	0
19	LS	1592	0	1697	17	0
20	LT	1423	0	1426	27	0
21	LU	1257	0	1294	23	0
22	LV	845	0	840	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	LW	1015	0	1057	30	0
24	LX	538	0	547	10	0
25	LY	962	0	1021	13	0
26	LZ	1076	0	1140	16	0
27	La	1013	0	1044	20	0
28	Lb	1201	0	1233	19	0
29	Lc	425	0	440	8	0
30	Ld	770	0	808	11	0
31	Le	818	0	857	4	0
32	Lf	1077	0	1133	20	0
33	Lg	778	0	816	10	0
34	Lh	774	0	801	12	0
35	Li	969	0	1065	19	0
36	Lj	731	0	794	14	0
37	Lk	711	0	712	9	0
38	Ll	558	0	612	14	0
39	Ln	1678	0	1768	65	0
40	Lo	227	0	272	1	0
41	Lp	767	0	821	18	0
42	Lq	708	0	753	15	0
43	Ls	388	0	401	9	0
44	Lt	55663	0	28291	247	0
45	SA	1569	0	1610	32	0
46	SB	1667	0	1713	32	0
47	SC	1658	0	1694	29	0
48	SD	1855	0	1911	31	0
49	SE	2085	0	2174	35	0
50	SF	1442	0	1469	24	0
51	SG	1646	0	1742	41	0
52	SH	1481	0	1544	29	0
53	SI	1357	0	1421	28	0
54	SJ	1031	0	1082	17	0
55	SK	1423	0	1515	23	0
56	SL	819	0	806	17	0
57	SM	1251	0	1287	17	0
58	SO	1080	0	1165	13	0
59	SP	1192	0	1265	14	0
60	SQ	916	0	927	27	0
61	SR	943	0	1020	16	0
62	ST	1180	0	1250	27	0
63	SU	872	0	922	23	0
64	SV	1117	0	1139	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
65	SW	1071	0	1093	22	0
66	SX	794	0	836	40	0
67	SY	651	0	655	15	0
68	Sb	941	0	1001	28	0
69	Sc	578	0	617	5	0
70	Sd	821	0	848	9	0
71	Se	621	0	614	10	0
72	Sg	505	0	540	11	0
73	Sh	417	0	416	15	0
74	Sj	509	0	553	16	0
75	St	31176	0	15856	192	0
All	All	173978	0	131819	1689	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 6.

All (1689) 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)
51:SG:227:LEU:HA	51:SG:230:ARG:HD3	1.30	1.09
25:LY:96:LYS:O	25:LY:100:THR:HG23	1.53	1.08
23:LW:48:GLY:HA3	44:Lt:2339:C:O2'	1.58	1.04
66:SX:111:ILE:HD13	66:SX:111:ILE:N	1.79	0.97
50:SF:124:SER:HB3	50:SF:190:ARG:HA	1.55	0.89
27:La:53:ASN:HB3	27:La:57:ASP:HB2	1.57	0.87
52:SH:70:LEU:HG	52:SH:97:ALA:HB2	1.58	0.86
2:LB:6:PHE:HB3	23:LW:50:LEU:HD13	1.57	0.86
2:LB:6:PHE:CB	23:LW:50:LEU:HD13	2.06	0.85
23:LW:52:ARG:NH1	44:Lt:2460:G:H5''	1.92	0.85
66:SX:24:LYS:NZ	66:SX:93:TRP:HB3	1.92	0.84
57:SM:25:ASP:HA	57:SM:28:ARG:HB3	1.61	0.82
45:SA:55:ASN:HA	63:SU:108:MET:HE1	1.62	0.82
17:LQ:14:GLY:HA3	17:LQ:101:ALA:HB2	1.63	0.80
73:Sh:102:CYS:HB3	73:Sh:120:CYS:N	1.97	0.80
23:LW:47:LYS:HE2	23:LW:47:LYS:H	1.45	0.79
46:SB:178:VAL:HB	46:SB:208:VAL:HG21	1.64	0.78
18:LR:60:PRO:HG2	18:LR:142:ARG:HA	1.66	0.78
51:SG:170:ILE:HG13	51:SG:187:LYS:HD3	1.65	0.78
2:LB:102:VAL:HG21	2:LB:153:HIS:HB3	1.65	0.78
6:LF:59:ASP:HB2	6:LF:80:SER:HB2	1.65	0.77
25:LY:96:LYS:O	25:LY:100:THR:CG2	2.32	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:ST:25:VAL:HB	62:ST:40:VAL:HB	1.66	0.77
73:Sh:102:CYS:HB3	73:Sh:120:CYS:H	1.49	0.76
65:SW:96:SER:HB2	75:St:1202:C:H5'	1.66	0.76
67:SY:81:GLN:HG2	67:SY:88:ARG:HA	1.66	0.76
49:SE:79:ASP:HB3	49:SE:82:PHE:HB2	1.68	0.76
66:SX:24:LYS:HZ2	66:SX:93:TRP:HB3	1.50	0.76
39:Ln:94:ASN:HB2	39:Ln:119:GLN:HA	1.68	0.75
47:SC:208:ILE:HG12	63:SU:44:ILE:HG23	1.68	0.75
13:LM:28:ALA:HB3	44:Lt:821:G:H5'	1.67	0.74
49:SE:35:PRO:HD2	49:SE:83:PRO:HG2	1.70	0.73
61:SR:95:SER:HB3	61:SR:102:PHE:HB3	1.70	0.73
37:Lk:3:LYS:HE2	44:Lt:638:A:H4'	1.71	0.73
53:Sl:71:HIS:HB3	53:Sl:86:ARG:HA	1.72	0.72
44:Lt:2058:U:H3'	44:Lt:2059:A:H5''	1.72	0.72
23:LW:48:GLY:CA	44:Lt:2339:C:O2'	2.35	0.72
14:LN:108:ASP:HA	14:LN:111:LYS:HD2	1.70	0.72
43:Ls:109:ASN:HB3	43:Ls:115:GLY:HA2	1.69	0.71
46:SB:95:HIS:HB3	46:SB:107:TYR:HE1	1.54	0.71
75:St:191:C:H2'	75:St:192:G:H8	1.55	0.71
75:St:970:A:H1'	75:St:971:G:H21	1.55	0.71
32:Lf:39:LYS:HD2	32:Lf:40:PRO:HD2	1.73	0.70
20:LT:90:GLU:HB3	20:LT:136:VAL:HG21	1.73	0.70
46:SB:50:LYS:HA	67:SY:19:TYR:CE1	2.27	0.70
75:St:1420:A:H2	75:St:1423:G:H1	1.40	0.70
4:LD:133:G:H1	44:Lt:9:U:H3	1.38	0.69
9:LI:163:THR:HG21	44:Lt:6:G:H21	1.56	0.69
66:SX:111:ILE:HD13	66:SX:111:ILE:H	1.52	0.68
14:LN:98:GLN:HA	14:LN:101:ARG:HD2	1.76	0.68
15:LO:186:PRO:HB3	44:Lt:61:G:H21	1.59	0.68
32:Lf:14:ILE:HG23	32:Lf:68:THR:HB	1.76	0.68
3:LC:164:VAL:HG21	3:LC:238:LEU:HD11	1.76	0.68
39:Ln:114:LYS:HA	39:Ln:117:ILE:HB	1.75	0.68
39:Ln:69:ALA:HB2	39:Ln:111:LEU:HB3	1.76	0.68
3:LC:200:ASN:HB3	3:LC:242:SER:HB3	1.76	0.67
51:SG:14:PRO:HD3	51:SG:118:VAL:HG22	1.76	0.67
10:LJ:92:TYR:HB3	10:LJ:97:ILE:HG13	1.75	0.67
38:LI:7:GLU:HA	38:LI:49:LEU:HD13	1.76	0.67
15:LO:154:PRO:HB2	44:Lt:57:G:H5''	1.77	0.67
39:Ln:37:GLY:H	39:Ln:205:TYR:HB2	1.60	0.67
46:SB:231:HIS:HB3	67:SY:59:THR:HG21	1.75	0.67
73:Sh:101:GLU:HB3	73:Sh:106:GLY:HA2	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LS:63:ILE:HG12	44:Lt:1493:G:H4'	1.77	0.66
22:LV:45:ILE:HG13	22:LV:52:VAL:HG22	1.77	0.66
4:LD:134:G:H21	9:LI:41:GLN:HE22	1.41	0.66
75:St:915:A:H2'	75:St:916:G:C8	2.31	0.66
27:La:27:VAL:HG22	27:La:28:GLU:HG2	1.76	0.66
65:SW:108:LEU:HG	65:SW:113:LEU:HB3	1.77	0.66
28:Lb:72:THR:HG22	28:Lb:111:LYS:HB3	1.77	0.66
32:Lf:81:ILE:HD12	32:Lf:86:GLU:HB3	1.76	0.66
68:Sb:55:ILE:HA	68:Sb:75:ALA:HA	1.76	0.66
5:LE:30:U:H3	5:LE:48:G:H1	1.44	0.66
15:LO:93:LYS:HG2	44:Lt:244:G:H1'	1.76	0.66
44:Lt:533:A:H5''	44:Lt:637:C:H41	1.61	0.66
2:LB:223:GLY:HA2	2:LB:271:GLY:HA3	1.78	0.65
44:Lt:590:C:H3'	44:Lt:591:U:H4'	1.77	0.65
44:Lt:1767:A:H2	44:Lt:1774:U:H3	1.41	0.65
45:SA:148:PRO:HG3	67:SY:39:VAL:HB	1.77	0.65
47:SC:181:ILE:HG12	47:SC:190:VAL:HG22	1.77	0.65
44:Lt:1960:C:H2'	44:Lt:1961:G:H2'	1.78	0.65
52:SH:65:VAL:HG12	52:SH:69:MET:HB3	1.78	0.65
49:SE:64:ILE:HG23	49:SE:69:ASN:HB2	1.79	0.65
25:LY:109:VAL:HG22	25:LY:123:ILE:HG23	1.79	0.65
39:Ln:26:ARG:HB2	39:Ln:27:LYS:HE3	1.79	0.65
71:Se:62:LEU:HA	71:Se:67:GLN:HG3	1.79	0.65
39:Ln:42:ASP:HB2	39:Ln:46:ASP:HB2	1.78	0.65
46:SB:81:GLN:HB3	46:SB:88:GLN:HB2	1.79	0.65
66:SX:33:ASP:HB3	66:SX:36:LEU:HB2	1.78	0.65
39:Ln:215:ARG:HG2	44:Lt:1951:A:H61	1.62	0.65
42:Lq:10:LEU:HD21	42:Lq:34:LYS:HD3	1.79	0.64
2:LB:6:PHE:HB2	23:LW:50:LEU:HD13	1.80	0.64
43:Ls:94:MET:HB3	43:Ls:119:ARG:HG2	1.80	0.64
39:Ln:100:ILE:HD11	39:Ln:124:ALA:HB2	1.80	0.64
38:Ll:5:ILE:HB	38:Ll:47:TYR:HB3	1.78	0.64
65:SW:41:ARG:HH21	65:SW:81:SER:HB3	1.63	0.64
1:LA:180:LEU:HD11	42:Lq:18:TYR:HB3	1.79	0.64
10:LJ:67:ARG:HG2	44:Lt:2529:A:H4'	1.80	0.64
73:Sh:120:CYS:HB3	73:Sh:123:CYS:H	1.63	0.64
39:Ln:167:TRP:HD1	39:Ln:168:PRO:HD2	1.62	0.64
12:LL:138:VAL:HA	12:LL:141:ARG:HD3	1.80	0.63
31:Le:74:GLY:HA3	31:Le:79:LYS:HA	1.80	0.63
15:LO:179:ILE:HG23	44:Lt:68:C:H5''	1.78	0.63
16:LP:119:SER:HB2	20:LT:163:ARG:HG2	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:St:58:C:H4'	75:St:365:G:H5''	1.79	0.63
11:LK:170:ASN:HB3	11:LK:177:THR:HA	1.81	0.63
44:Lt:903:A:H2'	44:Lt:904:A:C8	2.34	0.63
47:SC:37:ASP:HB2	47:SC:63:VAL:HG21	1.80	0.63
50:SF:105:SER:HB2	50:SF:175:ALA:HB1	1.81	0.63
21:LU:51:GLY:HA3	21:LU:92:ARG:HG2	1.80	0.63
23:LW:107:ILE:HB	23:LW:115:LYS:HG2	1.80	0.63
48:SD:89:GLN:HB2	48:SD:228:LEU:HD22	1.80	0.63
3:LC:7:VAL:HG11	3:LC:241:LYS:HG3	1.80	0.63
3:LC:92:ALA:HB1	44:Lt:520:C:H5''	1.81	0.63
6:LF:48:ARG:HD2	6:LF:153:PHE:HE2	1.64	0.62
21:LU:100:ASP:HB2	44:Lt:705:G:H4'	1.81	0.62
47:SC:14:TYR:HE2	66:SX:62:ARG:HE	1.47	0.62
49:SE:94:LYS:HG2	68:Sb:15:PRO:HB2	1.80	0.62
50:SF:125:VAL:HG21	72:Sg:22:ILE:HD12	1.81	0.62
68:Sb:10:LYS:HG3	75:St:555:G:H22	1.63	0.62
6:LF:182:PRO:HB2	44:Lt:2171:A:H4'	1.81	0.62
71:Se:51:PRO:HB2	71:Se:56:GLU:HG3	1.81	0.62
46:SB:97:ILE:HG21	46:SB:181:VAL:HG22	1.82	0.62
39:Ln:22:ASN:HB3	44:Lt:1959:C:H5'	1.82	0.61
48:SD:22:TYR:HA	48:SD:25:LYS:HG3	1.82	0.61
66:SX:111:ILE:N	66:SX:111:ILE:CD1	2.53	0.61
75:St:1033:C:H2'	75:St:1034:G:C8	2.35	0.61
58:SO:53:GLN:HB3	58:SO:71:ARG:HB3	1.81	0.61
75:St:1000:C:H2'	75:St:1001:G:H8	1.66	0.61
16:LP:13:LEU:HD11	16:LP:77:VAL:HG22	1.82	0.61
27:La:100:ASP:HB3	27:La:103:LYS:HB2	1.81	0.61
32:Lf:69:ARG:HG2	44:Lt:1092:G:H5''	1.81	0.61
75:St:971:G:H1'	75:St:972:G:C8	2.36	0.61
2:LB:290:ASN:HB3	2:LB:293:CYS:HB3	1.82	0.61
44:Lt:2156:C:H5'	44:Lt:2185:G:H5''	1.82	0.61
64:SV:37:ILE:HA	64:SV:40:ARG:HB3	1.81	0.60
19:LS:20:ARG:HD3	44:Lt:1506:A:H3'	1.83	0.60
2:LB:6:PHE:CB	23:LW:50:LEU:CD1	2.79	0.60
42:Lq:38:THR:HA	42:Lq:45:ASP:HA	1.83	0.60
44:Lt:61:G:H22	44:Lt:78:U:H4'	1.67	0.60
75:St:1022:C:H2'	75:St:1023:G:H8	1.66	0.60
48:SD:148:PHE:HB2	75:St:810:U:H5'	1.82	0.60
30:Ld:29:LEU:HD11	30:Ld:85:VAL:HG11	1.83	0.60
58:SO:88:ASP:HA	75:St:448:G:H4'	1.83	0.60
17:LQ:18:ARG:HB2	17:LQ:93:ILE:HD11	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:SA:127:LEU:HB3	45:SA:149:THR:HB	1.84	0.60
58:SO:107:ARG:HB3	58:SO:110:ARG:HB2	1.82	0.60
2:LB:368:GLU:HB3	24:LX:15:TYR:HE2	1.66	0.60
19:LS:55:ILE:HG12	44:Lt:1357:C:H5''	1.83	0.60
60:SQ:101:GLY:HA3	60:SQ:134:PRO:HD2	1.84	0.59
33:Lg:36:ILE:HG23	33:Lg:41:GLU:HB2	1.83	0.59
28:Lb:75:ILE:HB	28:Lb:114:GLY:HA2	1.84	0.59
52:SH:130:LEU:HD21	52:SH:156:VAL:HG21	1.85	0.59
62:ST:47:ILE:HG12	62:ST:54:LEU:HB2	1.84	0.59
32:Lf:90:LEU:HD21	32:Lf:122:VAL:HG21	1.84	0.59
52:SH:20:GLU:HG3	52:SH:49:VAL:HB	1.84	0.59
1:LA:36:GLU:HG3	1:LA:91:GLY:HA2	1.83	0.59
12:LL:83:GLY:HA2	12:LL:106:ILE:HD11	1.83	0.59
30:Ld:78:SER:HB2	30:Ld:90:ASN:HB3	1.85	0.59
24:LX:45:ARG:HB3	44:Lt:1600:G:H2'	1.84	0.59
47:SC:51:SER:HA	47:SC:89:ASN:HB3	1.85	0.59
51:SG:26:ASP:HB2	51:SG:29:LYS:HB2	1.84	0.59
75:St:1195:C:H2'	75:St:1196:G:H8	1.67	0.59
49:SE:148:ARG:HD3	75:St:112:C:H5''	1.84	0.59
10:LJ:26:VAL:HG12	10:LJ:80:VAL:HG21	1.85	0.59
42:Lq:7:LYS:C	42:Lq:9:GLY:H	2.11	0.59
23:LW:101:GLN:HG3	24:LX:24:ARG:HA	1.83	0.59
12:LL:50:SER:HB3	12:LL:65:ILE:HG13	1.85	0.58
44:Lt:1884:G:H3'	44:Lt:1886:A:H5''	1.85	0.58
17:LQ:65:GLY:HA3	44:Lt:1136:U:H5'	1.85	0.58
39:Ln:19:ARG:HE	39:Ln:212:PRO:HG2	1.68	0.58
8:LH:98:LEU:HG	8:LH:125:VAL:HG21	1.85	0.58
55:SK:88:ASP:HB2	55:SK:91:LYS:HD3	1.85	0.58
12:LL:10:ARG:HG2	12:LL:133:ARG:HD3	1.86	0.58
51:SG:18:ALA:HB2	51:SG:133:VAL:HB	1.85	0.58
60:SQ:59:GLY:HA2	60:SQ:68:GLU:HG2	1.85	0.58
64:SV:142:ARG:HD3	75:St:1167:C:H5''	1.84	0.58
6:LF:120:ASN:HA	6:LF:125:LEU:HD13	1.86	0.58
49:SE:3:ARG:HB3	75:St:80:A:H1'	1.86	0.58
2:LB:35:ASP:HA	2:LB:183:ASN:HD22	1.69	0.58
39:Ln:32:VAL:HB	39:Ln:171:ASN:HA	1.84	0.58
12:LL:16:LYS:HD3	12:LL:70:THR:HG23	1.86	0.58
20:LT:135:LYS:HA	20:LT:138:MET:HE2	1.85	0.58
46:SB:183:GLU:C	46:SB:185:ALA:H	2.10	0.58
13:LM:184:ILE:HG13	28:Lb:82:ILE:HG23	1.85	0.58
25:LY:46:PRO:HD2	35:Li:109:PRO:HG3	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:Lt:595:G:H1'	44:Lt:597:G:H21	1.68	0.58
45:SA:189:ARG:HG2	45:SA:196:ARG:HA	1.85	0.58
47:SC:35:LEU:HB3	47:SC:38:ALA:HB3	1.86	0.58
63:SU:63:ARG:HB3	63:SU:69:VAL:HG21	1.85	0.58
64:SV:88:ASN:HA	64:SV:96:ASP:HA	1.85	0.58
6:LF:114:SER:HA	6:LF:117:ILE:HG13	1.86	0.57
51:SG:168:GLU:HB2	51:SG:187:LYS:HE3	1.86	0.57
54:SJ:79:PHE:HZ	57:SM:97:ARG:HH21	1.51	0.57
44:Lt:403:C:H2'	44:Lt:404:G:C8	2.38	0.57
49:SE:122:LYS:HB3	49:SE:164:LEU:HD22	1.87	0.57
75:St:139:C:H1'	75:St:142:C:H41	1.69	0.57
6:LF:3:TRP:HB3	44:Lt:751:C:H1'	1.86	0.57
44:Lt:47:A:H4'	44:Lt:48:G:H5'	1.85	0.57
28:Lb:83:PRO:HB2	28:Lb:86:GLN:HG3	1.86	0.57
44:Lt:1150:C:H2'	44:Lt:1151:G:C8	2.40	0.57
75:St:1004:C:H2'	75:St:1005:G:C8	2.38	0.57
22:LV:31:ASN:HB3	22:LV:34:GLU:HB3	1.86	0.57
23:LW:114:LEU:HD21	23:LW:134:ILE:HG12	1.86	0.57
44:Lt:2599:G:H2'	44:Lt:2600:A:C8	2.40	0.57
75:St:191:C:H2'	75:St:192:G:C8	2.37	0.57
2:LB:277:ASP:HB3	2:LB:280:LYS:HE3	1.87	0.57
8:LH:69:GLN:HA	21:LU:144:ILE:HG22	1.87	0.57
38:Ll:26:SER:HA	38:Ll:73:VAL:HB	1.87	0.57
44:Lt:1176:G:H1'	44:Lt:1475:C:H5''	1.86	0.57
13:LM:28:ALA:HB1	44:Lt:512:G:O2'	2.04	0.56
16:LP:11:HIS:HE1	16:LP:116:VAL:HG12	1.70	0.56
17:LQ:129:THR:HG22	44:Lt:1191:G:H21	1.70	0.56
27:La:38:TYR:HE2	44:Lt:1303:A:H1'	1.70	0.56
66:SX:63:ARG:HA	66:SX:86:ARG:HA	1.86	0.56
6:LF:214:MET:HB2	6:LF:239:PRO:HG3	1.87	0.56
14:LN:38:ILE:HG12	14:LN:50:VAL:HB	1.86	0.56
39:Ln:32:VAL:HG12	39:Ln:168:PRO:HA	1.87	0.56
6:LF:52:VAL:HA	6:LF:155:ASP:HB3	1.87	0.56
11:LK:90:ARG:HG3	11:LK:134:PRO:HB2	1.86	0.56
21:LU:11:THR:HG22	21:LU:55:ARG:HD3	1.88	0.56
33:Lg:30:LEU:HB3	33:Lg:74:MET:HE1	1.87	0.56
47:SC:86:ASP:HB3	47:SC:89:ASN:HB2	1.87	0.56
60:SQ:71:ALA:HB1	60:SQ:114:ALA:HB2	1.87	0.56
75:St:1058:G:H21	75:St:1108:A:H1'	1.70	0.56
26:LZ:130:LEU:C	26:LZ:132:ARG:H	2.14	0.56
45:SA:34:ASN:HB2	45:SA:156:ASP:HB3	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:SC:78:LEU:HG	56:SL:21:SER:HB2	1.86	0.56
48:SD:140:ILE:HB	48:SD:213:ARG:HD3	1.88	0.56
62:ST:137:ARG:HB3	75:St:1272:G:H5''	1.88	0.56
72:Sg:8:ARG:HG2	72:Sg:50:ILE:HG23	1.88	0.56
12:LL:110:ILE:HD13	12:LL:116:TYR:HB2	1.86	0.56
32:Lf:31:VAL:HB	44:Lt:403:C:H5''	1.88	0.56
44:Lt:1914:C:H2'	44:Lt:1915:C:C6	2.41	0.56
52:SH:31:GLU:HG2	52:SH:41:LEU:HD22	1.88	0.56
75:St:1175:A:H4'	75:St:1231:G:H4'	1.86	0.56
57:SM:99:GLU:HG2	58:SO:10:ALA:HB3	1.88	0.56
68:Sb:104:SER:C	68:Sb:106:LYS:H	2.14	0.56
48:SD:37:LYS:HB3	48:SD:73:PRO:HD2	1.87	0.56
49:SE:114:ILE:HB	49:SE:118:GLU:HB3	1.88	0.56
44:Lt:2645:G:H2'	44:Lt:2646:G:C8	2.41	0.56
68:Sb:40:LYS:HD3	68:Sb:57:LEU:HG	1.87	0.56
30:Ld:50:ASN:HB2	30:Ld:76:GLY:HA2	1.86	0.56
64:SV:14:LEU:HB2	64:SV:21:ILE:HB	1.87	0.56
2:LB:8:CYS:SG	23:LW:49:HIS:CE1	2.99	0.55
23:LW:52:ARG:HH12	44:Lt:2460:G:H5''	1.66	0.55
44:Lt:593:A:H5''	44:Lt:1522:C:H5''	1.89	0.55
63:SU:3:LYS:HD2	75:St:1120:G:H1'	1.88	0.55
44:Lt:2061:A:H8	44:Lt:2061:A:H5''	1.70	0.55
49:SE:139:LEU:HD23	49:SE:150:PRO:HB3	1.88	0.55
66:SX:24:LYS:HZ3	66:SX:93:TRP:HB3	1.69	0.55
52:SH:106:TYR:HA	52:SH:115:ARG:H	1.72	0.55
52:SH:157:VAL:HG13	52:SH:190:MET:HA	1.89	0.55
53:SI:94:SER:HB3	57:SM:9:ALA:HB2	1.88	0.55
60:SQ:53:ILE:HG21	60:SQ:90:ILE:HG13	1.87	0.55
1:LA:132:THR:HG21	44:Lt:1666:G:H5''	1.89	0.55
3:LC:59:THR:HG21	44:Lt:646:G:H5''	1.88	0.55
10:LJ:19:ILE:HG22	10:LJ:24:VAL:HG22	1.89	0.55
44:Lt:328:G:H1'	44:Lt:351:G:H21	1.72	0.55
45:SA:168:CYS:HB3	45:SA:179:ILE:HG13	1.88	0.55
68:Sb:62:THR:HA	68:Sb:69:THR:HB	1.88	0.55
14:LN:14:TYR:CE1	14:LN:22:GLY:HA2	2.42	0.55
44:Lt:1311:G:H1	44:Lt:1453:C:H5	1.53	0.55
53:SI:76:TRP:HZ2	53:SI:128:ASP:HB2	1.71	0.55
63:SU:74:LEU:HB3	63:SU:77:GLN:HB2	1.89	0.55
66:SX:70:LYS:HD2	66:SX:79:THR:HB	1.89	0.55
75:St:734:G:H4'	75:St:1431:A:H4'	1.89	0.55
41:Lp:21:HIS:HB3	41:Lp:70:LEU:HB3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:Lt:684:A:H1'	44:Lt:2151:C:H4'	1.88	0.55
60:SQ:31:CYS:HA	60:SQ:44:VAL:HA	1.89	0.55
75:St:1301:C:H2'	75:St:1302:G:C8	2.42	0.55
6:LF:30:TYR:HA	6:LF:33:ARG:HG2	1.88	0.55
49:SE:191:ARG:HD3	49:SE:244:ARG:HB2	1.89	0.55
61:SR:123:TYR:HD2	61:SR:125:ILE:H	1.53	0.55
22:LV:39:VAL:HG13	22:LV:82:LEU:HD13	1.89	0.55
46:SB:97:ILE:HG22	46:SB:105:ILE:HD11	1.88	0.55
46:SB:177:THR:HG21	46:SB:201:LEU:HD22	1.89	0.55
64:SV:41:PHE:HB2	64:SV:45:ALA:HB3	1.88	0.55
17:LQ:35:ILE:HG22	17:LQ:114:VAL:HG21	1.90	0.54
44:Lt:2084:C:H2'	44:Lt:2085:G:C8	2.42	0.54
53:SI:39:ILE:HB	53:SI:86:ARG:HH22	1.72	0.54
66:SX:91:THR:HB	66:SX:93:TRP:CZ2	2.42	0.54
8:LH:42:SER:HA	8:LH:45:VAL:HB	1.88	0.54
75:St:1022:C:H2'	75:St:1023:G:C8	2.43	0.54
75:St:1033:C:H2'	75:St:1034:G:H8	1.72	0.54
37:Lk:26:SER:HB3	37:Lk:35:ALA:HB3	1.89	0.54
8:LH:90:VAL:HG12	8:LH:94:VAL:HB	1.88	0.54
34:Lh:52:ILE:HD11	34:Lh:55:ILE:HG13	1.88	0.54
54:SJ:31:SER:HB3	54:SJ:34:ILE:HG13	1.88	0.54
20:LT:10:ARG:HE	20:LT:20:PRO:HD2	1.73	0.54
50:SF:127:VAL:HA	72:Sg:42:ILE:HG22	1.90	0.54
66:SX:41:VAL:HG21	66:SX:90:ARG:HE	1.72	0.54
2:LB:316:ARG:HB3	2:LB:318:GLN:HG2	1.88	0.54
11:LK:152:LEU:HD12	11:LK:165:ILE:HG23	1.89	0.54
33:Lg:46:LEU:HD11	33:Lg:68:PRO:HD3	1.90	0.54
3:LC:99:ARG:HA	44:Lt:412:A:H5'	1.90	0.54
50:SF:36:PRO:HB3	50:SF:55:VAL:HG13	1.90	0.54
56:SL:33:VAL:HG22	56:SL:50:TYR:HA	1.90	0.54
38:Ll:2:PRO:HG2	44:Lt:1413:G:H4'	1.90	0.54
45:SA:205:ASP:HB3	63:SU:89:PRO:HD2	1.90	0.54
48:SD:126:ASP:HA	48:SD:136:ARG:HA	1.90	0.54
54:SJ:30:SER:HA	54:SJ:61:ILE:HD11	1.89	0.54
51:SG:141:PRO:HB3	51:SG:146:LYS:HB3	1.89	0.54
66:SX:44:ILE:HG12	66:SX:108:THR:HG21	1.90	0.54
15:LO:56:LYS:HG3	44:Lt:129:U:H4'	1.90	0.54
25:LY:36:THR:HG21	44:Lt:12:G:H1'	1.90	0.54
44:Lt:842:C:H2'	44:Lt:843:A:C8	2.43	0.53
48:SD:27:TRP:HE3	48:SD:43:GLN:HB3	1.73	0.53
4:LD:65:C:H2'	4:LD:66:G:H8	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SL:25:LYS:HG2	56:SL:74:HIS:CD2	2.42	0.53
5:LE:105:C:H2'	5:LE:106:G:C8	2.44	0.53
6:LF:185:MET:HA	6:LF:188:PHE:HD2	1.72	0.53
8:LH:171:HIS:HB3	8:LH:189:SER:HB3	1.89	0.53
17:LQ:32:CYS:HB3	17:LQ:117:TYR:HB2	1.91	0.53
62:ST:111:VAL:O	62:ST:112:LYS:HB2	2.09	0.53
75:St:1203:A:H2	75:St:1240:G:H4'	1.73	0.53
21:LU:17:ARG:HE	21:LU:47:ALA:HB2	1.74	0.53
53:SI:22:HIS:HB2	53:SI:25:ARG:HH21	1.73	0.53
68:Sb:6:VAL:HG21	68:Sb:39:ILE:HB	1.91	0.53
73:Sh:87:MET:N	73:Sh:90:THR:HG1	2.06	0.53
5:LE:36:C:H5'	6:LF:163:THR:HB	1.90	0.53
26:LZ:30:MET:HE1	26:LZ:71:VAL:HG13	1.91	0.53
39:Ln:43:PRO:HA	39:Ln:160:LYS:HG3	1.91	0.53
22:LV:95:PHE:HB3	22:LV:107:LEU:HG	1.90	0.53
39:Ln:169:ILE:HG23	39:Ln:186:THR:HG21	1.91	0.53
44:Lt:452:G:H21	44:Lt:455:C:H5	1.56	0.53
44:Lt:2192:C:H2'	44:Lt:2193:G:C8	2.43	0.53
68:Sb:105:ARG:HA	68:Sb:108:LEU:HB2	1.91	0.53
23:LW:19:CYS:HA	23:LW:57:SER:HB3	1.89	0.53
44:Lt:910:U:H5	44:Lt:995:G:H1	1.56	0.53
44:Lt:2663:C:H2'	44:Lt:2664:G:C8	2.44	0.53
68:Sb:104:SER:HB3	68:Sb:107:GLN:H	1.74	0.53
75:St:859:U:H2'	75:St:860:A:H8	1.73	0.53
75:St:1177:A:H2	75:St:1181:G:H1'	1.72	0.53
7:LG:33:LEU:HA	44:Lt:302:C:N4	2.23	0.53
17:LQ:63:TYR:HB2	17:LQ:79:LYS:HD2	1.90	0.53
25:LY:49:PRO:HG3	35:Li:109:PRO:HB3	1.89	0.53
53:SI:92:TYR:HB2	53:SI:171:LEU:HD21	1.91	0.53
75:St:945:C:H2'	75:St:1163:C:N4	2.24	0.53
13:LM:152:VAL:HG23	35:Li:150:VAL:HG12	1.89	0.53
38:Ll:20:LYS:HE3	38:Ll:40:LEU:HD22	1.89	0.53
45:SA:112:ASN:HD22	45:SA:118:ASN:HD22	1.56	0.53
64:SV:25:VAL:HB	64:SV:30:ALA:HB2	1.89	0.53
22:LV:44:LYS:HB3	22:LV:49:LYS:HG2	1.91	0.53
2:LB:287:THR:HA	2:LB:320:ASP:HA	1.90	0.52
4:LD:73:A:H5''	26:LZ:50:ARG:HG2	1.90	0.52
54:SJ:53:VAL:HG13	54:SJ:60:ARG:HB3	1.91	0.52
62:ST:57:VAL:HG22	62:ST:63:ARG:HG3	1.90	0.52
66:SX:75:GLU:HG2	75:St:1135:G:H1'	1.91	0.52
2:LB:292:ARG:HA	2:LB:302:ASP:O	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:SF:41:ARG:HE	62:ST:137:ARG:HH11	1.57	0.52
53:SI:34:ALA:HB2	53:SI:65:ARG:HD3	1.90	0.52
75:St:320:C:H2'	75:St:321:G:C8	2.44	0.52
75:St:365:G:H1'	75:St:366:G:H4'	1.90	0.52
75:St:1374:C:H2'	75:St:1375:G:O4'	2.09	0.52
38:Ll:58:LYS:O	38:Ll:62:LYS:HG2	2.09	0.52
39:Ln:91:GLN:HA	39:Ln:119:GLN:HE22	1.75	0.52
44:Lt:403:C:H2'	44:Lt:404:G:H8	1.73	0.52
6:LF:206:MET:HB3	6:LF:243:GLU:HG3	1.92	0.52
17:LQ:56:ILE:HG21	17:LQ:72:ALA:HB2	1.91	0.52
20:LT:77:ARG:HG3	20:LT:119:GLN:HB2	1.91	0.52
44:Lt:1362:A:H2'	44:Lt:1363:A:C8	2.44	0.52
75:St:757:A:H4'	75:St:758:C:H2'	1.91	0.52
21:LU:78:LYS:HD3	21:LU:87:LYS:HE3	1.91	0.52
44:Lt:2439:A:H61	44:Lt:2450:A:H5''	1.74	0.52
31:Le:68:LEU:HB3	31:Le:83:VAL:HG12	1.91	0.52
3:LC:294:LYS:HB2	8:LH:157:PRO:HB3	1.92	0.52
12:LL:53:THR:HG23	12:LL:60:ARG:HA	1.92	0.52
29:Lc:24:PRO:O	29:Lc:25:LYS:HB2	2.09	0.52
48:SD:171:THR:O	48:SD:175:GLU:HB2	2.09	0.52
5:LE:89:A:C5	44:Lt:903:A:H5''	2.45	0.52
17:LQ:56:ILE:HB	17:LQ:71:GLN:HB2	1.90	0.52
32:Lf:47:MET:HE1	32:Lf:55:ARG:HG3	1.92	0.52
38:Ll:22:LEU:HD13	38:Ll:24:VAL:HG23	1.91	0.52
75:St:1135:G:H2'	75:St:1136:U:C6	2.45	0.52
2:LB:263:THR:HG21	44:Lt:2306:U:H5'	1.91	0.52
39:Ln:47:PRO:HB2	39:Ln:159:PHE:HB2	1.92	0.52
41:Lp:12:CYS:SG	41:Lp:15:GLU:HB2	2.50	0.52
64:SV:34:ILE:HB	64:SV:37:ILE:HG12	1.92	0.52
11:LK:159:ILE:HB	11:LK:163:GLN:HE21	1.75	0.51
44:Lt:742:C:H5''	44:Lt:743:C:H5	1.74	0.51
60:SQ:50:ARG:HH21	75:St:674:G:H1'	1.75	0.51
16:LP:58:ARG:HA	16:LP:67:PRO:HD2	1.91	0.51
39:Ln:37:GLY:N	39:Ln:205:TYR:HB2	2.23	0.51
65:SW:16:PHE:HB3	65:SW:56:ALA:HB1	1.93	0.51
15:LO:120:TRP:HZ2	15:LO:123:GLN:HG2	1.75	0.51
18:LR:163:PRO:HB3	28:Lb:50:PRO:HD2	1.92	0.51
44:Lt:598:C:H1'	44:Lt:1482:A:H5''	1.92	0.51
45:SA:131:ASP:HB3	45:SA:134:VAL:HB	1.92	0.51
48:SD:176:LEU:HD22	48:SD:184:LEU:HG	1.92	0.51
56:SL:40:ASP:HB3	56:SL:43:GLY:HA3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:St:931:U:H3	75:St:942:G:H1	1.58	0.51
67:SY:21:PRO:HB2	67:SY:30:LEU:HD12	1.91	0.51
60:SQ:33:ILE:HG21	60:SQ:115:ALA:HB1	1.92	0.51
66:SX:51:PHE:HD2	66:SX:104:ILE:HG12	1.76	0.51
75:St:1195:C:H2'	75:St:1196:G:C8	2.46	0.51
27:La:15:LEU:HB3	34:Lh:84:ARG:HD3	1.93	0.51
44:Lt:224:U:H2'	44:Lt:225:A:H8	1.76	0.51
72:Sg:8:ARG:HA	72:Sg:50:ILE:HA	1.92	0.51
75:St:1000:C:H2'	75:St:1001:G:C8	2.46	0.51
22:LV:29:GLU:O	22:LV:30:LEU:HB2	2.10	0.51
47:SC:54:VAL:HB	47:SC:92:ILE:HG13	1.93	0.51
10:LJ:9:ILE:HG22	10:LJ:51:ILE:HB	1.91	0.51
18:LR:71:MET:HB2	18:LR:97:MET:HE2	1.93	0.51
44:Lt:598:C:H2'	44:Lt:599:A:H8	1.76	0.51
46:SB:183:GLU:C	46:SB:185:ALA:N	2.69	0.51
50:SF:128:SER:HB3	50:SF:131:ARG:HB3	1.92	0.51
63:SU:75:ARG:HA	63:SU:78:GLU:HB2	1.91	0.51
75:St:1110:C:H2'	75:St:1111:G:C8	2.46	0.51
8:LH:116:LYS:HB2	21:LU:134:ALA:HB3	1.91	0.51
42:Lq:14:TYR:HB3	42:Lq:18:TYR:HD2	1.75	0.51
46:SB:155:LYS:HB3	46:SB:160:ARG:HG3	1.93	0.51
53:SI:141:LEU:HB3	53:SI:159:LEU:HD12	1.92	0.51
44:Lt:2570:C:H2'	44:Lt:2571:G:C8	2.46	0.51
57:SM:87:ASP:HB3	57:SM:151:PHE:CE1	2.46	0.51
63:SU:2:GLY:HA3	75:St:1054:C:H5	1.74	0.51
35:Li:120:MET:HG2	37:Lk:82:ASN:HD22	1.76	0.50
60:SQ:43:HIS:HB2	60:SQ:55:ARG:HG3	1.92	0.50
75:St:746:A:H2	75:St:766:U:H3	1.58	0.50
29:Lc:45:ARG:HH12	44:Lt:788:C:H5'	1.75	0.50
46:SB:169:GLY:HA3	55:SK:54:ARG:HD3	1.93	0.50
50:SF:139:ASN:HB3	50:SF:175:ALA:HA	1.93	0.50
56:SL:13:TYR:HB3	56:SL:87:ILE:HG23	1.92	0.50
56:SL:17:TYR:HB2	56:SL:87:ILE:HG21	1.93	0.50
62:ST:38:ALA:HA	62:ST:85:ILE:HA	1.92	0.50
2:LB:368:GLU:HB3	24:LX:15:TYR:CE2	2.46	0.50
51:SG:22:LEU:HD11	51:SG:47:LEU:HD13	1.92	0.50
64:SV:95:LYS:HB3	64:SV:97:MET:HG3	1.93	0.50
75:St:92:A:H2'	75:St:93:A:C8	2.46	0.50
75:St:979:A:H2'	75:St:980:G:C8	2.46	0.50
46:SB:36:LEU:HD12	46:SB:240:LEU:HB3	1.94	0.50
41:Lp:11:PHE:HA	41:Lp:18:HIS:HA	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:LC:183:LYS:HA	3:LC:188:ARG:HA	1.92	0.50
23:LW:66:VAL:HG21	23:LW:74:LEU:HB3	1.93	0.50
27:La:93:ILE:HG12	27:La:107:ILE:HG23	1.93	0.50
44:Lt:398:C:H2'	44:Lt:399:G:C8	2.47	0.50
44:Lt:2631:C:H2'	44:Lt:2632:G:H5'	1.93	0.50
75:St:1116:G:H22	75:St:1118:C:H3'	1.77	0.50
75:St:1249:C:H4'	75:St:1287:C:H4'	1.94	0.50
11:LK:184:LEU:HD21	11:LK:199:ARG:HH22	1.76	0.50
13:LM:79:PRO:HB3	13:LM:170:HIS:HB3	1.94	0.50
16:LP:180:GLU:CD	16:LP:180:GLU:H	2.19	0.50
44:Lt:224:U:H2'	44:Lt:225:A:C8	2.47	0.50
44:Lt:1972:A:H1'	44:Lt:1973:C:H5''	1.93	0.50
14:LN:117:ARG:HH21	44:Lt:2595:C:H4'	1.77	0.50
30:Ld:48:MET:HE1	30:Ld:57:LYS:HG3	1.94	0.50
3:LC:123:ASN:HB3	3:LC:126:LEU:HB2	1.94	0.50
8:LH:85:ARG:HG3	8:LH:210:LYS:HD3	1.92	0.50
10:LJ:184:GLU:O	10:LJ:185:GLN:C	2.54	0.50
13:LM:29:MET:HA	44:Lt:513:C:H4'	1.94	0.50
39:Ln:93:PHE:HB3	39:Ln:100:ILE:HD12	1.94	0.50
49:SE:87:MET:HG3	49:SE:123:LEU:HB2	1.93	0.50
65:SW:120:ARG:H	65:SW:120:ARG:HD2	1.77	0.50
4:LD:116:C:H2'	4:LD:117:C:C2	2.47	0.49
20:LT:155:VAL:C	20:LT:157:ARG:H	2.19	0.49
37:Lk:34:CYS:HB3	37:Lk:38:GLY:H	1.77	0.49
39:Ln:33:GLU:HB3	39:Ln:166:ASN:HB2	1.94	0.49
44:Lt:602:U:H4'	44:Lt:1483:G:H4'	1.94	0.49
74:Sj:62:ARG:HH22	75:St:437:G:H8	1.59	0.49
2:LB:205:ILE:HD12	2:LB:285:ILE:HG23	1.94	0.49
3:LC:159:ILE:HG12	3:LC:164:VAL:HB	1.93	0.49
11:LK:59:GLN:HB3	11:LK:126:VAL:HG22	1.93	0.49
14:LN:50:VAL:HG22	14:LN:54:TRP:HE3	1.76	0.49
18:LR:37:TYR:HB2	18:LR:45:THR:HB	1.94	0.49
49:SE:66:GLN:HE22	75:St:365:G:H21	1.60	0.49
60:SQ:65:HIS:HB3	75:St:656:G:H1	1.76	0.49
64:SV:45:ALA:HB2	64:SV:84:MET:HE2	1.94	0.49
69:Sc:22:ALA:H	69:Sc:55:LEU:HD11	1.77	0.49
75:St:1306:C:H1'	75:St:1307:C:H5	1.76	0.49
2:LB:54:THR:HG22	2:LB:76:ALA:HB3	1.94	0.49
16:LP:39:ILE:HG12	16:LP:122:ALA:HB2	1.94	0.49
41:Lp:64:LYS:HB3	44:Lt:2216:G:H5''	1.94	0.49
8:LH:173:ILE:HD11	8:LH:189:SER:HB2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LT:8:TYR:CE1	20:LT:24:ARG:HB2	2.46	0.49
44:Lt:326:A:H1'	44:Lt:327:A:H5''	1.94	0.49
75:St:399:A:H61	75:St:421:G:H2'	1.78	0.49
75:St:640:U:H2'	75:St:641:A:C8	2.47	0.49
2:LB:227:GLU:HG3	2:LB:231:THR:HB	1.95	0.49
27:La:89:TYR:HB3	27:La:93:ILE:HD12	1.95	0.49
56:SL:32:ASN:HB3	56:SL:48:PRO:O	2.13	0.49
41:Lp:72:CYS:HB3	41:Lp:77:CYS:HB2	1.95	0.49
52:SH:67:TYR:HB3	75:St:610:A:H1'	1.92	0.49
10:LJ:68:THR:HG21	44:Lt:2538:A:N1	2.28	0.49
20:LT:10:ARG:HG2	20:LT:20:PRO:HB2	1.94	0.49
44:Lt:384:C:H5'	44:Lt:1866:C:H5''	1.93	0.49
75:St:987:G:H1	75:St:992:U:H3	1.61	0.49
10:LJ:84:PHE:HA	10:LJ:182:LEU:HA	1.95	0.49
12:LL:115:LYS:HB2	12:LL:115:LYS:HE2	1.58	0.49
19:LS:105:LEU:HD22	19:LS:135:LYS:HG2	1.93	0.49
75:St:1072:G:H3'	75:St:1073:A:H8	1.76	0.49
75:St:1273:U:H2'	75:St:1274:A:H8	1.78	0.49
14:LN:57:LEU:HG	20:LT:148:HIS:HD2	1.78	0.49
29:Lc:49:ASN:HB3	44:Lt:785:C:H4'	1.95	0.49
44:Lt:2210:C:H2'	44:Lt:2211:G:C8	2.46	0.49
47:SC:147:LYS:HE2	47:SC:185:GLN:HB3	1.94	0.49
49:SE:26:ILE:HD11	55:SK:1:PRO:HB2	1.95	0.49
64:SV:13:LEU:HD13	64:SV:20:ASN:HB3	1.94	0.49
73:Sh:88:ARG:HH12	75:St:1156:C:H1'	1.77	0.49
75:St:707:G:H2'	75:St:708:A:C8	2.48	0.49
3:LC:254:LYS:O	3:LC:255:GLN:C	2.56	0.49
15:LO:118:SER:HB3	15:LO:132:VAL:HG12	1.94	0.49
16:LP:128:PRO:O	16:LP:129:GLU:HB2	2.12	0.49
27:La:25:VAL:HB	27:La:85:LEU:HD23	1.93	0.49
41:Lp:67:VAL:HG13	41:Lp:82:VAL:HG22	1.95	0.49
44:Lt:51:C:H2'	44:Lt:52:G:H8	1.77	0.49
46:SB:98:VAL:HG11	46:SB:127:ARG:HG3	1.93	0.49
71:Se:114:PHE:HB3	71:Se:118:VAL:HG11	1.95	0.49
3:LC:18:LEU:HD23	3:LC:244:PHE:HB3	1.95	0.48
11:LK:199:ARG:HA	11:LK:199:ARG:HD3	1.57	0.48
21:LU:70:ARG:HD3	21:LU:70:ARG:HA	1.60	0.48
26:LZ:55:VAL:HG12	26:LZ:106:ILE:HA	1.95	0.48
47:SC:181:ILE:HG13	47:SC:188:ILE:HB	1.95	0.48
51:SG:42:PHE:HE1	51:SG:117:VAL:HG11	1.76	0.48
53:SI:144:ILE:HD12	53:SI:154:ALA:HB1	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:ST:100:ARG:HH21	62:ST:131:LEU:HD21	1.78	0.48
75:St:1257:C:H2'	75:St:1258:A:C8	2.48	0.48
2:LB:157:ILE:HG12	2:LB:192:VAL:HG22	1.94	0.48
38:Ll:14:ILE:HG23	38:Ll:18:ARG:HB3	1.94	0.48
51:SG:75:LYS:O	51:SG:105:GLY:HA3	2.12	0.48
51:SG:173:LEU:HD12	75:St:64:A:H2	1.78	0.48
54:SJ:107:SER:HA	75:St:578:A:C8	2.48	0.48
75:St:658:G:H2'	75:St:659:A:C8	2.49	0.48
10:LJ:88:MET:HB3	10:LJ:177:VAL:HA	1.93	0.48
30:Ld:108:LEU:H	30:Ld:108:LEU:HG	1.49	0.48
44:Lt:328:G:H1'	44:Lt:351:G:N2	2.27	0.48
44:Lt:2105:C:H2'	44:Lt:2106:C:C6	2.48	0.48
55:SK:114:ILE:HD12	55:SK:119:LEU:HD12	1.94	0.48
68:Sb:43:VAL:HG13	68:Sb:47:LEU:HD12	1.95	0.48
74:Sj:62:ARG:C	74:Sj:64:LYS:H	2.20	0.48
75:St:369:C:H2'	75:St:370:G:C8	2.48	0.48
75:St:520:C:H3'	75:St:521:C:H5'	1.95	0.48
8:LH:143:ILE:HD12	8:LH:180:VAL:HG12	1.96	0.48
8:LH:154:GLN:HE22	44:Lt:1043:G:H21	1.61	0.48
8:LH:195:ASN:HD22	8:LH:195:ASN:HA	1.47	0.48
23:LW:48:GLY:C	44:Lt:2339:C:O2'	2.57	0.48
30:Ld:18:LEU:HD12	30:Ld:18:LEU:HA	1.71	0.48
39:Ln:102:LYS:HE2	39:Ln:102:LYS:HB3	1.67	0.48
43:Ls:110:CYS:SG	43:Ls:113:CYS:N	2.82	0.48
44:Lt:1348:C:H4'	44:Lt:1350:C:H41	1.79	0.48
49:SE:247:ILE:HB	75:St:563:G:H21	1.79	0.48
52:SH:140:ILE:HG13	52:SH:157:VAL:HG12	1.93	0.48
65:SW:3:SER:HA	65:SW:6:ARG:HB2	1.95	0.48
65:SW:26:ILE:HD13	65:SW:106:GLN:HG3	1.96	0.48
75:St:990:C:H2'	75:St:991:U:C6	2.47	0.48
39:Ln:97:ALA:HB1	39:Ln:100:ILE:HB	1.96	0.48
44:Lt:449:A:H61	44:Lt:459:A:H5''	1.79	0.48
49:SE:207:MET:HA	49:SE:221:ARG:HA	1.94	0.48
32:Lf:40:PRO:HB3	32:Lf:47:MET:HG2	1.94	0.48
39:Ln:55:LEU:O	39:Ln:56:PRO:C	2.57	0.48
44:Lt:1779:G:H1'	75:St:1401:A:H1'	1.95	0.48
51:SG:90:TYR:CE2	51:SG:99:LYS:HB3	2.49	0.48
66:SX:57:CYS:HB2	66:SX:93:TRP:CH2	2.49	0.48
72:Sg:62:ARG:HE	72:Sg:62:ARG:HB3	1.50	0.48
3:LC:196:LEU:HB2	3:LC:235:ARG:HD3	1.95	0.48
14:LN:11:ARG:HA	14:LN:11:ARG:HD3	1.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:LX:11:SER:HB3	24:LX:54:LYS:HB2	1.94	0.48
28:Lb:79:TRP:CD1	28:Lb:119:PRO:HD2	2.48	0.48
59:SP:91:MET:HE1	59:SP:121:ARG:HD2	1.95	0.48
66:SX:57:CYS:HB2	66:SX:93:TRP:HH2	1.79	0.48
67:SY:46:VAL:HB	67:SY:51:LYS:HA	1.95	0.48
75:St:230:A:H4'	75:St:231:C:H4'	1.94	0.48
8:LH:198:TRP:O	8:LH:199:PRO:C	2.56	0.48
9:LI:36:ARG:HD3	44:Lt:1239:A:H5''	1.95	0.48
39:Ln:19:ARG:HD3	39:Ln:206:ILE:HG21	1.94	0.48
44:Lt:1270:C:H5'	44:Lt:1362:A:H1'	1.96	0.48
55:SK:44:TYR:HA	55:SK:47:ARG:HD2	1.95	0.48
61:SR:30:ILE:HB	61:SR:86:PHE:HB3	1.96	0.48
75:St:574:U:H2'	75:St:575:G:C8	2.49	0.48
12:LL:21:ILE:HG13	12:LL:37:LEU:HD11	1.95	0.48
16:LP:8:CYS:HB2	16:LP:33:VAL:O	2.14	0.48
22:LV:85:ARG:HA	22:LV:85:ARG:HD3	1.53	0.48
36:Lj:16:ARG:HB3	36:Lj:18:VAL:HG22	1.95	0.48
39:Ln:112:ALA:HB2	39:Ln:128:PHE:CD2	2.49	0.48
44:Lt:92:G:H2'	44:Lt:93:A:C8	2.49	0.48
44:Lt:1248:G:H2'	44:Lt:1249:C:O4'	2.13	0.48
49:SE:253:LEU:HA	49:SE:256:ARG:HD3	1.95	0.48
62:ST:131:LEU:HD23	62:ST:131:LEU:HA	1.76	0.48
66:SX:68:THR:HG22	73:Sh:121:ARG:HG2	1.96	0.48
1:LA:180:LEU:HD13	42:Lq:26:LEU:HD11	1.96	0.48
2:LB:6:PHE:HB2	23:LW:50:LEU:CD1	2.41	0.48
10:LJ:25:THR:HG23	10:LJ:34:VAL:HG22	1.94	0.48
10:LJ:111:ARG:HG3	10:LJ:119:THR:HB	1.96	0.48
39:Ln:35:GLN:HB3	39:Ln:167:TRP:HB3	1.96	0.48
39:Ln:161:LYS:HD2	39:Ln:165:LEU:HD13	1.96	0.48
50:SF:88:LEU:HD21	69:Sc:72:VAL:HG21	1.96	0.48
60:SQ:55:ARG:HH22	75:St:650:G:H1'	1.79	0.48
75:St:1116:G:N2	75:St:1118:C:H3'	2.29	0.48
1:LA:250:ARG:HD3	1:LA:250:ARG:HA	1.78	0.47
9:LI:48:GLN:HG2	15:LO:25:LEU:HD11	1.94	0.47
20:LT:155:VAL:C	20:LT:157:ARG:N	2.70	0.47
30:Ld:94:MET:HE3	30:Ld:94:MET:HB3	1.67	0.47
44:Lt:1282:C:H2'	44:Lt:1283:G:C8	2.49	0.47
44:Lt:1705:U:H2'	44:Lt:1706:G:H8	1.78	0.47
44:Lt:1970:A:H2'	44:Lt:1971:G:C8	2.49	0.47
45:SA:69:ILE:HG13	67:SY:43:VAL:HG13	1.96	0.47
36:Lj:25:LYS:HE3	36:Lj:25:LYS:HB3	1.60	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Ln:69:ALA:HB1	39:Ln:113:SER:HB2	1.95	0.47
44:Lt:1225:G:H21	44:Lt:1239:A:H5'	1.79	0.47
64:SV:47:LYS:HB3	64:SV:47:LYS:HE2	1.47	0.47
6:LF:34:LYS:HA	21:LU:27:LEU:HD11	1.95	0.47
12:LL:109:HIS:HE1	12:LL:116:TYR:HA	1.77	0.47
38:Ll:20:LYS:HD2	38:Ll:40:LEU:HB3	1.95	0.47
44:Lt:243:A:H2'	44:Lt:244:G:C8	2.49	0.47
44:Lt:1136:U:H2'	44:Lt:1137:A:H8	1.80	0.47
44:Lt:1553:A:H2'	44:Lt:1554:A:C8	2.49	0.47
44:Lt:2239:G:H4'	44:Lt:2240:A:H5'	1.96	0.47
46:SB:77:ILE:H	46:SB:77:ILE:HG13	1.41	0.47
1:LA:205:ASN:HB3	1:LA:206:PRO:HD2	1.96	0.47
11:LK:79:LYS:HA	11:LK:79:LYS:HD2	1.51	0.47
18:LR:154:PRO:HD2	28:Lb:48:TYR:HA	1.96	0.47
23:LW:106:VAL:HG21	23:LW:119:ILE:HD13	1.95	0.47
39:Ln:130:LYS:HD2	39:Ln:130:LYS:HA	1.63	0.47
44:Lt:790:G:N2	44:Lt:792:C:H3'	2.29	0.47
53:SI:10:LYS:HB2	53:SI:10:LYS:HE2	1.36	0.47
59:SP:94:LYS:HB2	59:SP:94:LYS:HE2	1.46	0.47
67:SY:53:ILE:HG12	67:SY:55:ASN:H	1.80	0.47
75:St:599:G:C2	75:St:600:C:H1'	2.49	0.47
11:LK:46:PHE:HB3	11:LK:140:CYS:C	2.39	0.47
13:LM:196:VAL:HG22	13:LM:200:LEU:HD13	1.97	0.47
16:LP:54:LYS:HD3	16:LP:54:LYS:HA	1.57	0.47
36:Lj:58:LYS:HA	36:Lj:58:LYS:HD3	1.48	0.47
48:SD:138:PHE:HE1	48:SD:216:LYS:HG2	1.80	0.47
63:SU:13:ALA:HB3	63:SU:56:TYR:HD2	1.80	0.47
71:Se:104:ILE:HD12	71:Se:104:ILE:HA	1.82	0.47
71:Se:106:ILE:HB	71:Se:113:ALA:HB3	1.96	0.47
75:St:470:G:H2'	75:St:471:G:H8	1.79	0.47
22:LV:10:LYS:HD2	22:LV:10:LYS:HA	1.73	0.47
31:Le:6:GLU:HG3	31:Le:69:GLU:HG2	1.95	0.47
54:SJ:32:LYS:HA	54:SJ:32:LYS:HD2	1.42	0.47
54:SJ:37:PHE:HE1	54:SJ:129:PHE:HB3	1.80	0.47
61:SR:25:LEU:HD22	61:SR:25:LEU:HA	1.74	0.47
64:SV:50:ASN:HD22	64:SV:51:ILE:HG12	1.79	0.47
68:Sb:104:SER:C	68:Sb:106:LYS:N	2.73	0.47
8:LH:94:VAL:HG12	8:LH:125:VAL:HG23	1.97	0.47
10:LJ:8:THR:HG23	10:LJ:52:SER:HB2	1.97	0.47
13:LM:64:ARG:HH12	44:Lt:432:G:H5'	1.79	0.47
14:LN:46:LYS:HA	14:LN:46:LYS:HD2	1.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:LZ:2:LYS:HB3	26:LZ:2:LYS:HE3	1.46	0.47
32:Lf:61:GLY:C	32:Lf:63:GLY:H	2.22	0.47
41:Lp:12:CYS:HB3	41:Lp:19:THR:HG23	1.96	0.47
42:Lq:64:MET:HB2	42:Lq:64:MET:HE2	1.60	0.47
44:Lt:554:G:H3'	44:Lt:555:G:H8	1.80	0.47
44:Lt:1448:G:H2'	44:Lt:1449:G:C8	2.50	0.47
48:SD:120:CYS:HB2	48:SD:142:PHE:CE2	2.50	0.47
56:SL:24:LEU:HD11	56:SL:53:VAL:HG12	1.95	0.47
58:SO:76:LYS:HB3	58:SO:76:LYS:HE2	1.52	0.47
64:SV:38:GLY:HA2	64:SV:41:PHE:CZ	2.49	0.47
66:SX:27:ILE:HG23	66:SX:118:VAL:HG22	1.97	0.47
68:Sb:16:LEU:H	68:Sb:16:LEU:HG	1.25	0.47
75:St:1110:C:H2'	75:St:1111:G:H8	1.79	0.47
75:St:1235:C:H2'	75:St:1236:G:C8	2.49	0.47
2:LB:170:LEU:H	2:LB:170:LEU:HG	1.46	0.47
28:Lb:34:LYS:O	44:Lt:93:A:H5''	2.15	0.47
53:SI:127:LEU:HD13	53:SI:127:LEU:HA	1.65	0.47
65:SW:7:VAL:HG23	65:SW:138:GLN:HB3	1.96	0.47
66:SX:107:LYS:HB2	66:SX:107:LYS:HE3	1.67	0.47
15:LO:37:LYS:HB2	15:LO:37:LYS:HE2	1.38	0.47
27:La:5:ILE:HD11	27:La:80:PRO:HG2	1.96	0.47
35:Li:35:LYS:HA	35:Li:35:LYS:HD3	1.50	0.47
41:Lp:82:VAL:HG11	44:Lt:2215:A:H5'	1.97	0.47
47:SC:14:TYR:HE2	66:SX:62:ARG:NE	2.12	0.47
51:SG:57:ARG:HB3	51:SG:118:VAL:HG12	1.96	0.47
54:SJ:42:GLN:HE21	54:SJ:49:ASP:HA	1.80	0.47
55:SK:38:LYS:HE2	55:SK:38:LYS:HB3	1.62	0.47
71:Se:63:LYS:HE3	75:St:816:C:H5''	1.96	0.47
27:La:45:ALA:H	27:La:68:SER:HA	1.80	0.47
28:Lb:4:ARG:H	28:Lb:4:ARG:HG3	1.41	0.47
32:Lf:47:MET:HE3	32:Lf:47:MET:HB2	1.82	0.47
39:Ln:149:LEU:H	39:Ln:149:LEU:HG	1.35	0.47
44:Lt:1914:C:H2'	44:Lt:1915:C:H6	1.79	0.47
44:Lt:1983:G:H3'	44:Lt:1984:C:C6	2.50	0.47
45:SA:81:VAL:HG23	45:SA:92:ILE:HD12	1.97	0.47
51:SG:210:LYS:HA	51:SG:210:LYS:HD3	1.59	0.47
62:ST:10:LEU:H	62:ST:35:VAL:HG21	1.79	0.47
64:SV:89:ASN:HB2	75:St:1238:G:H5''	1.96	0.47
66:SX:110:VAL:C	66:SX:111:ILE:HD13	2.37	0.47
1:LA:229:ALA:HB3	1:LA:234:LYS:HG3	1.96	0.46
2:LB:379:LYS:H	2:LB:379:LYS:HG3	1.53	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:LC:269:ILE:HD13	3:LC:269:ILE:HA	1.69	0.46
6:LF:125:LEU:HD22	6:LF:147:VAL:HB	1.96	0.46
9:LI:140:PRO:C	9:LI:142:GLU:H	2.23	0.46
30:Ld:74:PHE:O	30:Ld:75:ALA:C	2.58	0.46
44:Lt:1962:C:H2'	44:Lt:1963:G:H8	1.80	0.46
53:SI:33:PRO:HA	75:St:244:G:H5'	1.97	0.46
53:SI:46:LYS:HE2	53:SI:46:LYS:HB2	1.72	0.46
55:SK:121:LYS:HE3	55:SK:121:LYS:HB3	1.64	0.46
56:SL:61:GLU:HG3	56:SL:77:TYR:HE1	1.79	0.46
73:Sh:100:ARG:HB3	73:Sh:111:VAL:HG21	1.95	0.46
14:LN:94:LYS:HA	14:LN:94:LYS:HD3	1.76	0.46
23:LW:84:VAL:HB	23:LW:123:VAL:HG22	1.98	0.46
34:Lh:7:THR:HA	44:Lt:1170:G:H21	1.79	0.46
38:Ll:15:ALA:HA	38:Ll:20:LYS:HG3	1.97	0.46
42:Lq:7:LYS:C	42:Lq:9:GLY:N	2.74	0.46
44:Lt:1969:G:N2	44:Lt:1972:A:H8	2.14	0.46
60:SQ:149:ARG:HE	60:SQ:149:ARG:HB3	1.51	0.46
62:ST:40:VAL:HG13	62:ST:83:MET:HG3	1.96	0.46
6:LF:55:ARG:HG3	6:LF:60:ILE:HG23	1.97	0.46
6:LF:114:SER:HB3	6:LF:122:LEU:H	1.80	0.46
13:LM:160:LYS:HD2	13:LM:160:LYS:HA	1.47	0.46
14:LN:14:TYR:HE1	14:LN:22:GLY:HA2	1.81	0.46
15:LO:74:GLN:HA	44:Lt:1655:A:H1'	1.98	0.46
28:Lb:2:PRO:HB2	28:Lb:5:ILE:HD11	1.97	0.46
44:Lt:2120:A:H2'	44:Lt:2121:A:C8	2.50	0.46
52:SH:58:LYS:HE3	52:SH:58:LYS:HB3	1.53	0.46
52:SH:96:VAL:HG13	52:SH:132:ASP:HB3	1.95	0.46
55:SK:69:LYS:HA	55:SK:69:LYS:HD2	1.65	0.46
2:LB:244:ARG:HA	2:LB:244:ARG:HD3	1.32	0.46
21:LU:18:LYS:HB2	21:LU:21:ARG:HB2	1.96	0.46
39:Ln:190:LEU:HD11	39:Ln:193:GLN:HA	1.97	0.46
6:LF:69:LEU:HA	6:LF:69:LEU:HD23	1.76	0.46
9:LI:93:GLN:HG2	9:LI:94:ILE:N	2.30	0.46
26:LZ:120:LYS:HA	26:LZ:120:LYS:HD3	1.43	0.46
33:Lg:7:LYS:H	33:Lg:7:LYS:HG2	1.43	0.46
44:Lt:1911:C:H2'	44:Lt:1912:A:C8	2.50	0.46
47:SC:142:VAL:HG22	47:SC:192:VAL:HG12	1.97	0.46
52:SH:27:LEU:HD12	52:SH:41:LEU:HD11	1.98	0.46
53:SI:8:MET:HB2	53:SI:8:MET:HE3	1.52	0.46
65:SW:71:GLY:HA3	75:St:1196:G:H5''	1.97	0.46
66:SX:51:PHE:CD2	66:SX:104:ILE:HG12	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66: SX:83:PHE:HB3	73: Sh:133:PHE:HB3	1.97	0.46
72: Sg:8:ARG:HE	72: Sg:50:ILE:HG12	1.79	0.46
75: St:660:A:H2	75: St:752:A:H1'	1.79	0.46
75: St:1290:C:H2'	75: St:1291:G:C8	2.50	0.46
9: LI:28:LEU:HB2	25: LY:25:ILE:O	2.16	0.46
11: LK:30:LYS:HG3	11: LK:63:GLU:HG3	1.98	0.46
13: LM:107:ARG:HD3	36: Lj:16:ARG:HE	1.79	0.46
13: LM:196:VAL:HG23	28: Lb:146:LEU:HD23	1.98	0.46
39: Ln:59:ALA:HA	39: Ln:153:SER:H	1.81	0.46
44: Lt:790:G:H22	44: Lt:792:C:H3'	1.80	0.46
53: SI:119:LYS:HD2	53: SI:119:LYS:HA	1.80	0.46
54: SJ:111:MET:HE2	54: SJ:111:MET:HB3	1.64	0.46
61: SR:108:LYS:H	61: SR:111:MET:HB2	1.81	0.46
62: ST:44:LYS:HB3	62: ST:44:LYS:HE2	1.49	0.46
72: Sg:39:ARG:HD3	72: Sg:59:GLU:HA	1.97	0.46
26: LZ:37:GLU:H	26: LZ:37:GLU:HG3	1.45	0.46
51: SG:202:ARG:HD2	51: SG:205:ARG:HD2	1.97	0.46
55: SK:148:MET:HE3	55: SK:148:MET:HB3	1.63	0.46
56: SL:89:LYS:HB2	56: SL:89:LYS:HE3	1.46	0.46
58: SO:74:LEU:HD21	58: SO:81:ILE:HD12	1.97	0.46
68: Sb:108:LEU:HD22	68: Sb:108:LEU:HA	1.73	0.46
75: St:136:U:H3	75: St:145:G:H1	1.64	0.46
75: St:470:G:H2'	75: St:471:G:C8	2.51	0.46
9: LI:140:PRO:HG2	9: LI:143:LEU:HB2	1.98	0.46
10: LJ:59:ARG:HD2	10: LJ:59:ARG:HA	1.67	0.46
21: LU:86:LEU:HD12	21: LU:86:LEU:HA	1.77	0.46
44: Lt:2382:C:H2'	44: Lt:2383:G:C8	2.51	0.46
48: SD:121:ILE:HD11	48: SD:161:ILE:HG23	1.98	0.46
59: SP:93:LYS:HB3	59: SP:93:LYS:HE3	1.47	0.46
63: SU:109:ILE:HA	63: SU:112:ILE:HD12	1.96	0.46
75: St:417:C:H2'	75: St:418:G:C8	2.51	0.46
75: St:1194:G:H1'	75: St:1211:C:C6	2.51	0.46
1: LA:95:THR:HB	1: LA:97:HIS:HD2	1.79	0.46
9: LI:49:ARG:O	9: LI:215:GLY:HA2	2.16	0.46
11: LK:156:LYS:HB2	11: LK:156:LYS:HE3	1.65	0.46
16: LP:163:LYS:HE3	16: LP:163:LYS:HB3	1.46	0.46
32: Lf:129:ALA:HB2	44: Lt:1100:C:H5''	1.98	0.46
38: Ll:20:LYS:HD3	38: Ll:42:THR:HG22	1.97	0.46
44: Lt:1939:G:H2'	44: Lt:1940:G:C5	2.50	0.46
45: SA:136:ARG:HE	45: SA:136:ARG:HB3	1.59	0.46
45: SA:191:LYS:HB3	45: SA:192:GLY:H	1.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:SG:75:LYS:H	51:SG:75:LYS:HG3	1.48	0.46
68:Sb:58:TYR:CE1	68:Sb:74:ASN:HB2	2.51	0.46
70:Sd:100:ARG:HA	70:Sd:100:ARG:HD3	1.68	0.46
75:St:119:U:H3'	75:St:120:G:H8	1.81	0.46
75:St:1059:C:H2'	75:St:1060:G:C8	2.51	0.46
20:LT:161:THR:C	20:LT:163:ARG:N	2.73	0.46
34:Lh:69:LYS:HB2	34:Lh:69:LYS:HE2	1.75	0.46
45:SA:30:LEU:HD23	45:SA:30:LEU:HA	1.73	0.46
52:SH:29:LYS:HB3	52:SH:29:LYS:HE3	1.73	0.46
52:SH:37:ARG:HE	52:SH:37:ARG:HB2	1.21	0.46
53:SI:163:GLU:HB2	57:SM:18:GLN:HG2	1.96	0.46
60:SQ:53:ILE:HG23	60:SQ:88:ARG:HD3	1.97	0.46
61:SR:68:GLN:HE21	61:SR:68:GLN:HB3	1.54	0.46
62:ST:86:LYS:HE3	62:ST:86:LYS:HB3	1.57	0.46
68:Sb:115:ARG:HA	68:Sb:118:LYS:HG2	1.97	0.46
74:Sj:47:LEU:H	74:Sj:47:LEU:HG	1.45	0.46
17:LQ:125:ARG:HE	17:LQ:127:ARG:HH11	1.64	0.45
20:LT:100:MET:HB3	20:LT:100:MET:HE3	1.64	0.45
39:Ln:215:ARG:HA	39:Ln:215:ARG:HD3	1.48	0.45
47:SC:99:LYS:HA	47:SC:99:LYS:HD3	1.39	0.45
62:ST:47:ILE:HB	62:ST:83:MET:HB2	1.98	0.45
63:SU:117:MET:HE2	63:SU:117:MET:HB2	1.59	0.45
1:LA:210:PRO:HB2	1:LA:235:VAL:HG21	1.97	0.45
6:LF:37:ILE:HD12	6:LF:37:ILE:HA	1.71	0.45
8:LH:80:LEU:HD21	8:LH:231:VAL:HG21	1.97	0.45
17:LQ:41:LYS:HE2	17:LQ:41:LYS:HB3	1.57	0.45
17:LQ:108:GLU:H	17:LQ:108:GLU:HG3	1.33	0.45
20:LT:36:LYS:HB3	20:LT:36:LYS:HE2	1.64	0.45
24:LX:52:TRP:CD1	24:LX:52:TRP:H	2.33	0.45
35:Li:130:ARG:HD3	35:Li:130:ARG:HA	1.69	0.45
36:Lj:30:GLN:HE21	36:Lj:30:GLN:HB3	1.53	0.45
39:Ln:19:ARG:HD2	39:Ln:19:ARG:HA	1.78	0.45
39:Ln:74:ALA:HB1	39:Ln:78:LYS:HG2	1.96	0.45
39:Ln:99:GLN:HE21	39:Ln:99:GLN:HB2	1.53	0.45
39:Ln:183:ILE:HD13	39:Ln:183:ILE:HA	1.78	0.45
43:Ls:99:CYS:HB3	43:Ls:113:CYS:HB3	1.43	0.45
44:Lt:240:U:H2'	44:Lt:241:G:C8	2.51	0.45
44:Lt:842:C:H2'	44:Lt:843:A:H8	1.81	0.45
48:SD:25:LYS:HE3	48:SD:25:LYS:HB3	1.67	0.45
49:SE:200:LYS:HA	49:SE:200:LYS:HD2	1.34	0.45
64:SV:85:LEU:HA	64:SV:98:HIS:CD2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:Sb:49:VAL:HG21	68:Sb:75:ALA:HB1	1.98	0.45
6:LF:287:LYS:HD2	6:LF:287:LYS:HA	1.57	0.45
10:LJ:145:ILE:H	10:LJ:145:ILE:HG12	1.49	0.45
19:LS:57:GLY:HA2	44:Lt:1504:C:H4'	1.99	0.45
19:LS:126:LYS:HA	44:Lt:558:G:H4'	1.98	0.45
20:LT:160:ARG:C	20:LT:162:ALA:H	2.25	0.45
30:Ld:107:ILE:H	30:Ld:107:ILE:HG12	1.67	0.45
41:Lp:22:LYS:HB2	41:Lp:22:LYS:HE2	1.56	0.45
42:Lq:7:LYS:HB2	42:Lq:27:LEU:HD13	1.98	0.45
46:SB:53:LEU:HD13	46:SB:53:LEU:HA	1.79	0.45
46:SB:172:ILE:HG23	46:SB:190:VAL:HG12	1.97	0.45
51:SG:27:PHE:HD2	51:SG:27:PHE:HA	1.61	0.45
54:SJ:94:LEU:HG	54:SJ:102:ILE:HG13	1.98	0.45
66:SX:53:ILE:HA	66:SX:94:VAL:HG13	1.97	0.45
68:Sb:55:ILE:HG23	68:Sb:75:ALA:HB2	1.96	0.45
75:St:591:C:H3'	75:St:592:G:H2'	1.98	0.45
14:LN:124:LYS:HE2	14:LN:124:LYS:HB3	1.40	0.45
23:LW:51:ASN:ND2	44:Lt:2303:U:OP1	2.49	0.45
26:LZ:122:ARG:HE	26:LZ:122:ARG:HB2	1.54	0.45
35:Li:54:ARG:HH11	35:Li:57:LEU:HB3	1.82	0.45
39:Ln:82:LEU:HD23	39:Ln:82:LEU:HA	1.76	0.45
39:Ln:194:LEU:HB3	39:Ln:195:LYS:H	1.60	0.45
44:Lt:903:A:H61	44:Lt:1000:G:H2'	1.82	0.45
44:Lt:2585:C:H2'	44:Lt:2586:G:C5	2.52	0.45
48:SD:176:LEU:HG	48:SD:193:VAL:HG11	1.99	0.45
51:SG:33:ILE:H	51:SG:33:ILE:HG12	1.52	0.45
56:SL:93:LEU:HD12	56:SL:93:LEU:HA	1.81	0.45
59:SP:15:ALA:O	75:St:713:C:H5'	2.16	0.45
75:St:657:U:H1'	75:St:660:A:N7	2.32	0.45
8:LH:133:GLU:HA	8:LH:134:PRO:HD3	1.85	0.45
23:LW:47:LYS:HA	44:Lt:2357:A:H61	1.82	0.45
34:Lh:56:PRO:HA	44:Lt:1404:C:H5''	1.99	0.45
45:SA:116:ARG:H	45:SA:116:ARG:HG3	1.38	0.45
61:SR:43:ARG:HA	61:SR:47:LYS:HB2	1.97	0.45
66:SX:42:LYS:HB2	66:SX:42:LYS:HE2	1.65	0.45
75:St:988:C:H2'	75:St:989:G:C8	2.51	0.45
2:LB:205:ILE:H	2:LB:205:ILE:HG13	1.42	0.45
2:LB:343:LEU:HD21	44:Lt:2516:G:H5'	1.99	0.45
3:LC:104:LYS:HA	44:Lt:429:C:H5	1.81	0.45
9:LI:69:THR:HG23	9:LI:161:VAL:HG22	1.98	0.45
12:LL:112:LEU:HD21	12:LL:127:PHE:HZ	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LP:168:LYS:HE2	16:LP:168:LYS:HB3	1.61	0.45
20:LT:77:ARG:HE	20:LT:77:ARG:HB2	1.40	0.45
20:LT:87:MET:HB2	20:LT:87:MET:HE2	1.74	0.45
37:Lk:3:LYS:HB3	44:Lt:1628:C:C4	2.52	0.45
39:Ln:27:LYS:HB3	39:Ln:28:PHE:H	1.47	0.45
44:Lt:65:A:N6	44:Lt:75:G:H1'	2.32	0.45
50:SF:172:LYS:HB3	50:SF:172:LYS:HE2	1.75	0.45
61:SR:89:MET:HE3	61:SR:89:MET:HB3	1.92	0.45
62:ST:138:ARG:HD3	62:ST:138:ARG:HA	1.54	0.45
75:St:1182:C:H2'	75:St:1183:G:H8	1.81	0.45
75:St:1316:U:H2'	75:St:1317:G:C8	2.51	0.45
12:LL:35:LYS:HB3	12:LL:35:LYS:HE3	1.58	0.45
39:Ln:215:ARG:HG2	44:Lt:1951:A:N6	2.30	0.45
42:Lq:36:LYS:HE3	42:Lq:36:LYS:HB3	1.44	0.45
46:SB:225:LYS:HA	46:SB:225:LYS:HD3	1.67	0.45
51:SG:66:GLY:HA3	75:St:138:G:H21	1.82	0.45
51:SG:138:ARG:H	51:SG:138:ARG:HG2	1.66	0.45
51:SG:202:ARG:HD2	51:SG:202:ARG:HA	1.84	0.45
55:SK:30:LYS:HA	74:Sj:38:TYR:HE1	1.82	0.45
55:SK:173:ARG:HD2	55:SK:173:ARG:HA	1.61	0.45
63:SU:7:LYS:HB2	63:SU:7:LYS:HE2	1.47	0.45
63:SU:60:LEU:HD22	63:SU:60:LEU:HA	1.80	0.45
64:SV:75:PRO:HB3	64:SV:85:LEU:HD21	1.97	0.45
2:LB:205:ILE:HD11	2:LB:320:ASP:HB2	1.98	0.45
3:LC:36:VAL:HG11	3:LC:110:ARG:HA	1.98	0.45
4:LD:92:C:H2'	4:LD:93:A:C8	2.51	0.45
8:LH:179:LEU:HD21	8:LH:193:ALA:HB1	1.99	0.45
12:LL:52:LEU:HD23	44:Lt:2104:A:H5''	1.98	0.45
18:LR:54:LEU:HD22	44:Lt:692:C:H5''	1.99	0.45
28:Lb:136:LYS:HB3	28:Lb:136:LYS:HE2	1.75	0.45
39:Ln:24:LYS:HB3	39:Ln:25:PRO:HD3	1.99	0.45
41:Lp:9:ARG:HA	41:Lp:20:VAL:HA	1.98	0.45
45:SA:43:ILE:H	45:SA:43:ILE:HG12	1.37	0.45
46:SB:229:LEU:HD12	46:SB:229:LEU:HA	1.70	0.45
59:SP:10:GLY:HA2	75:St:817:G:H4'	1.97	0.45
63:SU:75:ARG:H	63:SU:75:ARG:HG3	1.41	0.45
68:Sb:42:LYS:HD2	68:Sb:42:LYS:HA	1.52	0.45
75:St:945:C:H5	75:St:1162:C:H2'	1.81	0.45
75:St:1307:C:H2'	75:St:1308:C:H6	1.82	0.45
3:LC:109:GLN:HE22	44:Lt:421:G:H21	1.64	0.45
5:LE:86:C:H2'	5:LE:87:G:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LL:49:LYS:H	12:LL:49:LYS:HG2	1.58	0.45
19:LS:148:GLU:O	19:LS:152:GLU:HG2	2.17	0.45
23:LW:47:LYS:H	23:LW:47:LYS:CE	2.24	0.45
26:LZ:28:LYS:HD2	26:LZ:28:LYS:HA	1.61	0.45
29:Lc:8:THR:O	44:Lt:671:U:H4'	2.17	0.45
34:Lh:31:LEU:HD23	34:Lh:31:LEU:HA	1.80	0.45
36:Lj:9:LYS:HB3	36:Lj:9:LYS:HE3	1.41	0.45
44:Lt:1516:C:H3'	44:Lt:1517:G:C8	2.52	0.45
48:SD:230:THR:O	48:SD:234:SER:HB2	2.16	0.45
49:SE:180:ILE:HG23	49:SE:228:ILE:HD12	1.99	0.45
52:SH:118:ARG:HE	52:SH:118:ARG:HB3	1.44	0.45
57:SM:100:ARG:HB3	57:SM:151:PHE:CE1	2.52	0.45
62:ST:12:ARG:HG2	75:St:1086:G:H21	1.82	0.45
63:SU:20:ASN:HB2	63:SU:23:SER:HB2	1.99	0.45
64:SV:51:ILE:HD12	64:SV:60:LEU:HD11	1.99	0.45
75:St:1273:U:H2'	75:St:1274:A:C8	2.51	0.45
5:LE:95:C:H4'	20:LT:116:HIS:HB3	1.99	0.45
20:LT:139:PHE:HA	20:LT:144:VAL:HG11	1.99	0.45
20:LT:161:THR:C	20:LT:163:ARG:H	2.23	0.45
27:La:84:ARG:HE	27:La:84:ARG:HB3	1.64	0.45
32:Lf:119:LYS:HE2	32:Lf:119:LYS:HB2	1.61	0.45
34:Lh:38:LYS:HE3	34:Lh:38:LYS:HB2	1.77	0.45
39:Ln:114:LYS:HB3	39:Ln:114:LYS:HE3	1.56	0.45
44:Lt:538:U:H2'	44:Lt:539:G:C8	2.52	0.45
51:SG:205:ARG:HE	51:SG:205:ARG:HB3	1.33	0.45
53:SI:106:VAL:HG22	75:St:243:G:H5'	1.99	0.45
60:SQ:134:PRO:HB2	75:St:641:A:H5''	1.99	0.45
61:SR:45:ILE:HD11	61:SR:84:ILE:HG12	1.97	0.45
64:SV:31:LEU:HA	64:SV:31:LEU:HD22	1.80	0.45
69:Sc:42:HIS:CE1	69:Sc:57:LYS:HA	2.51	0.45
73:Sh:120:CYS:HB2	73:Sh:123:CYS:HB2	1.36	0.45
74:Sj:54:LEU:HB3	74:Sj:61:ILE:HG12	1.99	0.45
29:Lc:55:LEU:H	29:Lc:55:LEU:HG	1.54	0.44
32:Lf:91:PHE:O	32:Lf:92:MET:C	2.60	0.44
44:Lt:2458:C:H2'	44:Lt:2459:C:C6	2.53	0.44
51:SG:135:VAL:HA	51:SG:136:PRO:HD3	1.85	0.44
54:SJ:68:ARG:HE	54:SJ:68:ARG:HB3	1.44	0.44
64:SV:115:LEU:HD12	64:SV:115:LEU:HA	1.79	0.44
65:SW:38:GLY:HA2	65:SW:96:SER:H	1.82	0.44
66:SX:63:ARG:H	66:SX:63:ARG:HG2	1.64	0.44
67:SY:41:LEU:HD23	67:SY:41:LEU:HA	1.63	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Sd:2:PRO:HB3	75:St:886:C:H5''	1.99	0.44
70:Sd:66:LYS:HB3	70:Sd:66:LYS:HE2	1.64	0.44
75:St:628:C:H2'	75:St:629:G:C8	2.52	0.44
75:St:1371:G:H1'	75:St:1373:G:H22	1.82	0.44
2:LB:72:ALA:HA	23:LW:94:ASP:HA	2.00	0.44
4:LD:42:A:H4'	37:Lk:59:GLN:HG3	1.99	0.44
7:LG:33:LEU:HA	44:Lt:302:C:H42	1.81	0.44
21:LU:40:VAL:HB	21:LU:96:VAL:HG22	2.00	0.44
23:LW:40:MET:HE3	23:LW:40:MET:HB3	1.71	0.44
47:SC:11:ASN:C	47:SC:13:TYR:H	2.24	0.44
65:SW:106:GLN:H	65:SW:106:GLN:HG2	1.47	0.44
65:SW:111:LYS:HD3	65:SW:111:LYS:HA	1.36	0.44
75:St:1197:C:H42	75:St:1206:A:H61	1.65	0.44
3:LC:127:VAL:HG12	3:LC:132:HIS:HB2	1.99	0.44
3:LC:247:LEU:HD23	3:LC:247:LEU:HA	1.72	0.44
15:LO:47:LYS:HA	15:LO:47:LYS:HD2	1.82	0.44
17:LQ:102:LYS:HE3	17:LQ:102:LYS:HB3	1.81	0.44
25:LY:108:ARG:HE	25:LY:108:ARG:HB2	1.35	0.44
35:Li:146:LEU:HD23	35:Li:146:LEU:HA	1.86	0.44
42:Lq:6:LYS:C	42:Lq:8:VAL:H	2.24	0.44
44:Lt:1429:G:H2'	44:Lt:1430:G:C8	2.52	0.44
46:SB:48:ILE:HG23	46:SB:53:LEU:HB2	2.00	0.44
47:SC:76:GLU:HA	47:SC:92:ILE:HD13	1.99	0.44
48:SD:152:LYS:H	48:SD:152:LYS:HG2	1.56	0.44
48:SD:171:THR:HB	48:SD:197:LEU:HD23	1.99	0.44
49:SE:134:LYS:HD2	49:SE:134:LYS:HA	1.63	0.44
54:SJ:108:GLN:H	54:SJ:108:GLN:HG2	1.39	0.44
55:SK:52:LYS:HE2	55:SK:52:LYS:HB2	1.81	0.44
55:SK:111:GLN:H	55:SK:111:GLN:HG3	1.53	0.44
56:SL:82:LYS:H	56:SL:82:LYS:HG3	1.39	0.44
59:SP:36:GLN:HA	59:SP:39:LYS:HD2	2.00	0.44
63:SU:108:MET:HG3	63:SU:109:ILE:N	2.32	0.44
65:SW:41:ARG:NH2	65:SW:81:SER:HB3	2.32	0.44
68:Sb:48:LYS:HE3	68:Sb:48:LYS:HB3	1.39	0.44
75:St:7:G:H4'	75:St:453:C:H4'	2.00	0.44
75:St:722:U:H2'	75:St:723:C:O4'	2.16	0.44
2:LB:256:HIS:HA	2:LB:257:PRO:C	2.41	0.44
9:LI:113:ILE:HG23	9:LI:179:VAL:HG13	2.00	0.44
27:La:68:SER:HB3	27:La:112:ASN:ND2	2.32	0.44
29:Lc:15:LYS:HD2	44:Lt:669:A:H5''	1.99	0.44
44:Lt:1939:G:H21	44:Lt:1980:A:H62	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:SB:219:LEU:HB2	67:SY:30:LEU:HD23	1.98	0.44
47:SC:196:ASN:HB3	47:SC:199:ILE:HG23	1.99	0.44
48:SD:219:LYS:HE3	48:SD:219:LYS:HB3	1.68	0.44
56:SL:33:VAL:CG2	56:SL:50:TYR:HA	2.47	0.44
56:SL:78:LEU:HD23	56:SL:78:LEU:HA	1.78	0.44
61:SR:85:ILE:HG13	61:SR:112:VAL:HA	2.00	0.44
69:Sc:27:MET:HE2	69:Sc:27:MET:HB3	1.81	0.44
73:Sh:88:ARG:HG3	75:St:958:C:H1'	2.00	0.44
73:Sh:130:LYS:HD2	73:Sh:130:LYS:HA	1.42	0.44
8:LH:100:LEU:HD23	44:Lt:812:G:H1'	2.00	0.44
19:LS:16:LYS:HE2	19:LS:16:LYS:HB2	1.37	0.44
24:LX:62:LYS:HA	24:LX:62:LYS:HD3	1.73	0.44
39:Ln:11:LYS:HB2	39:Ln:11:LYS:HE3	1.41	0.44
42:Lq:28:LYS:HB2	42:Lq:28:LYS:HE3	1.31	0.44
44:Lt:2645:G:H2'	44:Lt:2646:G:H8	1.81	0.44
49:SE:131:LEU:HD11	75:St:182:G:H1'	2.00	0.44
51:SG:129:GLY:O	51:SG:130:LEU:HB2	2.17	0.44
67:SY:58:VAL:HB	67:SY:85:LEU:HD11	1.99	0.44
75:St:1072:G:H3'	75:St:1073:A:C8	2.51	0.44
18:LR:46:LYS:HB3	18:LR:46:LYS:HE3	1.66	0.44
32:Lf:134:GLU:O	32:Lf:135:GLU:C	2.60	0.44
41:Lp:64:LYS:HB2	41:Lp:64:LYS:HE3	1.43	0.44
44:Lt:2446:G:H2'	44:Lt:2447:A:C8	2.53	0.44
47:SC:191:LYS:HB3	47:SC:191:LYS:HE2	1.58	0.44
48:SD:13:ILE:HG21	48:SD:25:LYS:HB2	1.99	0.44
51:SG:78:ARG:H	51:SG:78:ARG:HG3	1.34	0.44
52:SH:115:ARG:HD2	52:SH:115:ARG:HA	1.55	0.44
64:SV:82:ALA:HA	64:SV:85:LEU:HB2	1.98	0.44
66:SX:66:ILE:HG22	66:SX:68:THR:HG23	2.00	0.44
5:LE:21:G:H2'	5:LE:22:G:C8	2.51	0.44
13:LM:62:ILE:H	13:LM:62:ILE:HG12	1.48	0.44
16:LP:141:GLU:H	16:LP:141:GLU:HG2	1.65	0.44
38:Ll:62:LYS:HG2	38:Ll:62:LYS:H	1.40	0.44
39:Ln:27:LYS:HA	39:Ln:210:MET:HB3	1.99	0.44
39:Ln:144:LEU:H	39:Ln:144:LEU:HG	1.46	0.44
41:Lp:76:LYS:HD2	41:Lp:76:LYS:HA	1.62	0.44
44:Lt:1907:A:H2'	44:Lt:1908:C:C6	2.53	0.44
44:Lt:2644:C:H2'	44:Lt:2645:G:O4'	2.17	0.44
50:SF:127:VAL:HG22	50:SF:131:ARG:HG2	1.99	0.44
66:SX:24:LYS:HZ3	66:SX:93:TRP:CB	2.29	0.44
70:Sd:50:ALA:HB1	70:Sd:64:ILE:HD12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:St:179:G:H1	75:St:596:C:H3'	1.82	0.44
2:LB:92:TYR:HB3	2:LB:99:LEU:HG	2.00	0.44
2:LB:151:LYS:HG2	2:LB:189:ALA:HA	1.99	0.44
2:LB:377:TYR:O	2:LB:378:ALA:C	2.60	0.44
3:LC:142:LEU:HD12	3:LC:142:LEU:HA	1.83	0.44
17:LQ:36:LYS:HB3	17:LQ:36:LYS:HE2	1.34	0.44
18:LR:48:LEU:HD12	18:LR:48:LEU:HA	1.80	0.44
18:LR:118:ARG:HE	18:LR:118:ARG:HB2	1.43	0.44
21:LU:24:MET:HE3	21:LU:24:MET:HB2	1.91	0.44
23:LW:55:LYS:HE2	23:LW:55:LYS:HB2	1.58	0.44
27:La:44:ILE:H	27:La:44:ILE:HG13	1.34	0.44
32:Lf:12:LYS:HB2	32:Lf:12:LYS:HE3	1.45	0.44
44:Lt:1425:C:H2'	44:Lt:1426:C:C6	2.52	0.44
44:Lt:2325:C:H4'	44:Lt:2449:G:H4'	2.00	0.44
49:SE:136:MET:H	49:SE:136:MET:HG2	1.51	0.44
50:SF:7:LEU:HD22	50:SF:7:LEU:HA	1.72	0.44
51:SG:93:ARG:HE	51:SG:93:ARG:HB2	1.34	0.44
64:SV:81:PRO:HB2	64:SV:83:TRP:CD1	2.53	0.44
68:Sb:45:GLN:HE21	68:Sb:45:GLN:HB3	1.56	0.44
74:Sj:59:LEU:HD21	75:St:439:U:H4'	2.00	0.44
3:LC:47:PRO:HB2	3:LC:97:VAL:HG12	2.00	0.44
6:LF:40:ASP:HB3	21:LU:69:PRO:HA	2.00	0.44
17:LQ:7:LYS:HD3	17:LQ:7:LYS:HA	1.75	0.44
21:LU:135:LEU:HD23	21:LU:135:LEU:HA	1.84	0.44
28:Lb:75:ILE:HG23	28:Lb:118:LEU:HG	1.99	0.44
35:Li:116:LEU:HD21	37:Lk:85:LYS:HG3	1.99	0.44
44:Lt:1721:A:H3'	44:Lt:1722:G:H8	1.82	0.44
48:SD:13:ILE:HG12	48:SD:25:LYS:H	1.82	0.44
48:SD:225:MET:HE2	48:SD:225:MET:HB2	1.88	0.44
50:SF:42:TRP:CG	50:SF:52:CYS:HG	2.36	0.44
51:SG:174:GLY:HA3	75:St:65:C:O5'	2.18	0.44
51:SG:202:ARG:O	51:SG:206:VAL:HG13	2.17	0.44
68:Sb:33:TYR:CE1	68:Sb:69:THR:HG21	2.52	0.44
70:Sd:54:LEU:HD23	70:Sd:64:ILE:HG23	2.00	0.44
70:Sd:92:ARG:HB3	75:St:1451:C:O2	2.18	0.44
75:St:329:A:H3'	75:St:330:A:H8	1.82	0.44
10:LJ:9:ILE:HD13	10:LJ:70:CYS:HB3	2.00	0.43
10:LJ:65:LEU:HD13	10:LJ:65:LEU:HA	1.79	0.43
13:LM:219:ARG:HE	13:LM:219:ARG:HB3	1.64	0.43
18:LR:129:LYS:HE2	18:LR:129:LYS:HB2	1.31	0.43
19:LS:164:LYS:HA	19:LS:164:LYS:HD3	1.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:LV:36:ALA:O	22:LV:40:ARG:HB2	2.16	0.43
35:Li:116:LEU:HB3	35:Li:117:THR:H	1.66	0.43
44:Lt:1911:C:H2'	44:Lt:1912:A:H8	1.83	0.43
44:Lt:1962:C:H2'	44:Lt:1963:G:C8	2.51	0.43
45:SA:22:LYS:HG3	63:SU:95:ASP:HA	2.00	0.43
45:SA:130:ASN:HD21	45:SA:176:ILE:HD11	1.82	0.43
46:SB:142:LEU:HD12	46:SB:142:LEU:HA	1.84	0.43
50:SF:76:MET:HB2	50:SF:76:MET:HE2	1.66	0.43
53:SI:170:LYS:HE2	53:SI:170:LYS:HB3	1.52	0.43
59:SP:109:LYS:HE3	59:SP:109:LYS:HB2	1.66	0.43
7:LG:38:ASN:C	7:LG:40:LYS:H	2.26	0.43
8:LH:61:ARG:HA	8:LH:61:ARG:HD3	1.81	0.43
11:LK:34:PHE:HD2	44:Lt:722:C:H4'	1.81	0.43
13:LM:75:ILE:H	13:LM:75:ILE:HG13	1.65	0.43
18:LR:68:ALA:HA	18:LR:97:MET:HE1	1.98	0.43
26:LZ:36:LYS:HD2	26:LZ:36:LYS:HA	1.40	0.43
28:Lb:120:GLN:HA	28:Lb:141:VAL:HG22	1.99	0.43
39:Ln:138:LEU:HD23	39:Ln:144:LEU:HA	2.00	0.43
45:SA:145:VAL:HA	46:SB:54:PRO:HG2	2.00	0.43
55:SK:30:LYS:HE2	55:SK:30:LYS:HB2	1.45	0.43
55:SK:146:SER:O	55:SK:147:TYR:C	2.61	0.43
59:SP:140:ARG:HE	59:SP:140:ARG:HB2	1.75	0.43
61:SR:61:LEU:HD22	61:SR:61:LEU:HA	1.76	0.43
62:ST:10:LEU:HD12	62:ST:10:LEU:HA	1.76	0.43
64:SV:48:LYS:HB2	64:SV:48:LYS:HE3	1.55	0.43
74:Sj:37:LEU:HD22	74:Sj:37:LEU:HA	1.73	0.43
75:St:1182:C:H2'	75:St:1183:G:C8	2.54	0.43
9:LI:51:LEU:HD23	9:LI:51:LEU:HA	1.82	0.43
11:LK:40:ARG:HE	11:LK:40:ARG:HB3	1.35	0.43
11:LK:57:LYS:HG2	11:LK:130:SER:HA	2.00	0.43
26:LZ:122:ARG:HG3	44:Lt:153:C:H5'	2.00	0.43
32:Lf:57:MET:HE2	32:Lf:57:MET:HB3	1.68	0.43
32:Lf:67:GLU:H	32:Lf:67:GLU:HG2	1.48	0.43
35:Li:116:LEU:HD12	35:Li:116:LEU:HA	1.79	0.43
44:Lt:2663:C:H2'	44:Lt:2664:G:H8	1.81	0.43
45:SA:21:LYS:H	45:SA:21:LYS:HG3	1.68	0.43
51:SG:184:LYS:HA	51:SG:184:LYS:HD3	1.70	0.43
60:SQ:40:THR:HG21	60:SQ:74:ALA:HB2	2.00	0.43
60:SQ:124:ILE:HD12	60:SQ:124:ILE:HA	1.85	0.43
63:SU:33:LYS:HB3	63:SU:33:LYS:HE3	1.59	0.43
75:St:481:C:H2'	75:St:482:G:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:LF:118:LYS:HB3	6:LF:118:LYS:HE3	1.68	0.43
15:LO:62:TYR:HB2	15:LO:134:LEU:HD11	2.00	0.43
20:LT:10:ARG:HB2	20:LT:57:LEU:HD11	2.00	0.43
20:LT:71:ASN:HB2	20:LT:126:VAL:HG12	1.99	0.43
48:SD:221:PRO:HG2	48:SD:224:THR:HG23	2.00	0.43
49:SE:210:MET:HG3	49:SE:218:PHE:CE2	2.53	0.43
51:SG:190:LYS:HB2	51:SG:190:LYS:HE2	1.73	0.43
51:SG:213:ILE:HA	51:SG:213:ILE:HD13	1.69	0.43
53:SI:162:PRO:HD2	57:SM:18:GLN:HG3	2.00	0.43
57:SM:148:LYS:HE2	57:SM:148:LYS:HB2	1.66	0.43
62:ST:18:ARG:HD2	62:ST:18:ARG:HA	1.70	0.43
65:SW:16:PHE:HD2	65:SW:16:PHE:HA	1.65	0.43
74:Sj:44:ASP:O	74:Sj:45:ASP:HB2	2.17	0.43
75:St:51:U:H2'	75:St:52:G:C8	2.53	0.43
75:St:358:A:H1'	75:St:409:A:H5'	2.01	0.43
2:LB:222:ARG:HE	2:LB:222:ARG:HB2	1.76	0.43
3:LC:126:LEU:HD22	3:LC:126:LEU:HA	1.82	0.43
13:LM:38:MET:HE2	13:LM:38:MET:HB3	1.75	0.43
41:Lp:22:LYS:H	41:Lp:22:LYS:HG3	1.59	0.43
42:Lq:20:ARG:HH21	42:Lq:24:LYS:HD3	1.82	0.43
44:Lt:1929:C:H2'	44:Lt:1930:G:C8	2.53	0.43
45:SA:159:LEU:HD12	45:SA:159:LEU:HA	1.69	0.43
46:SB:133:VAL:HG12	46:SB:135:ARG:H	1.84	0.43
48:SD:27:TRP:CE3	48:SD:43:GLN:HB3	2.53	0.43
51:SG:41:GLU:HG2	51:SG:55:THR:HG22	2.00	0.43
61:SR:52:MET:HE3	61:SR:52:MET:HB2	1.89	0.43
68:Sb:17:LEU:O	68:Sb:18:GLN:C	2.61	0.43
14:LN:47:ARG:HH22	14:LN:69:THR:H	1.66	0.43
19:LS:192:GLU:H	19:LS:192:GLU:HG3	1.39	0.43
25:LY:96:LYS:HD2	25:LY:96:LYS:HA	1.46	0.43
36:Lj:13:ALA:HB3	44:Lt:72:C:H4'	2.01	0.43
44:Lt:1277:G:H4'	44:Lt:1470:A:H4'	1.99	0.43
49:SE:126:VAL:HB	49:SE:139:LEU:HD13	2.01	0.43
51:SG:228:LEU:HD13	51:SG:228:LEU:HA	1.74	0.43
57:SM:149:LYS:H	57:SM:149:LYS:HG3	1.44	0.43
65:SW:21:LYS:HB3	65:SW:21:LYS:HE3	1.56	0.43
66:SX:36:LEU:HB3	66:SX:114:ILE:HD11	1.99	0.43
2:LB:327:THR:HG21	44:Lt:2464:G:H21	1.83	0.43
8:LH:93:LYS:HE3	8:LH:93:LYS:HB2	1.61	0.43
9:LI:85:GLU:H	9:LI:85:GLU:HG3	1.46	0.43
10:LJ:44:ILE:HA	10:LJ:52:SER:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:LJ:170:LYS:HB2	10:LJ:170:LYS:HE2	1.83	0.43
12:LL:43:GLN:HE21	12:LL:71:VAL:HA	1.83	0.43
28:Lb:36:GLY:HA3	28:Lb:40:HIS:CE1	2.54	0.43
28:Lb:85:GLU:H	28:Lb:85:GLU:HG2	1.63	0.43
30:Ld:23:LYS:HB3	30:Ld:23:LYS:HE2	1.61	0.43
44:Lt:1192:C:C2	44:Lt:1512:G:H1'	2.52	0.43
68:Sb:27:LEU:HD12	68:Sb:29:PRO:HG3	2.01	0.43
75:St:59:C:H6	75:St:59:C:H2'	1.70	0.43
2:LB:327:THR:HG23	44:Lt:2512:C:H1'	2.01	0.43
8:LH:53:LEU:HD12	8:LH:53:LEU:HA	1.86	0.43
15:LO:78:GLY:HA2	15:LO:89:ILE:HD13	2.01	0.43
27:La:5:ILE:HD13	30:Ld:39:ARG:HA	2.01	0.43
32:Lf:129:ALA:CB	44:Lt:1100:C:H5''	2.49	0.43
39:Ln:46:ASP:HA	39:Ln:194:LEU:HB2	2.01	0.43
39:Ln:178:GLU:O	39:Ln:183:ILE:HB	2.19	0.43
44:Lt:1446:C:H2'	44:Lt:1447:G:H8	1.84	0.43
44:Lt:2459:C:H2'	44:Lt:2460:G:C8	2.54	0.43
45:SA:33:ARG:H	45:SA:33:ARG:HG2	1.38	0.43
46:SB:146:HIS:CD2	46:SB:147:THR:HG23	2.54	0.43
52:SH:8:LYS:HD2	52:SH:8:LYS:HA	1.68	0.43
55:SK:167:PRO:HB2	55:SK:168:ASN:H	1.57	0.43
60:SQ:27:ALA:HB3	60:SQ:91:THR:H	1.83	0.43
62:ST:47:ILE:HD13	62:ST:103:ILE:HD11	1.99	0.43
62:ST:91:GLY:H	62:ST:94:SER:HB2	1.84	0.43
64:SV:24:LYS:H	64:SV:24:LYS:HG2	1.52	0.43
66:SX:24:LYS:NZ	66:SX:93:TRP:CB	2.72	0.43
66:SX:86:ARG:H	66:SX:86:ARG:HG3	1.49	0.43
68:Sb:19:ARG:HA	68:Sb:76:TYR:HA	2.01	0.43
75:St:1329:C:H2'	75:St:1330:G:C8	2.52	0.43
2:LB:6:PHE:HB3	23:LW:50:LEU:CD1	2.38	0.43
2:LB:99:LEU:HD12	2:LB:99:LEU:HA	1.91	0.43
3:LC:96:THR:HB	3:LC:98:ILE:HG13	2.00	0.43
10:LJ:78:LYS:HE2	10:LJ:78:LYS:HB2	1.75	0.43
13:LM:96:LEU:H	13:LM:96:LEU:HG	1.30	0.43
18:LR:102:LEU:HD12	18:LR:102:LEU:HA	1.75	0.43
20:LT:47:LYS:HD3	20:LT:47:LYS:HA	1.81	0.43
32:Lf:19:LYS:HB3	32:Lf:19:LYS:HE3	1.67	0.43
33:Lg:74:MET:HB3	33:Lg:74:MET:HE3	1.49	0.43
35:Li:54:ARG:HD2	35:Li:54:ARG:HA	1.70	0.43
43:Ls:97:ARG:HD2	43:Ls:118:LEU:HB3	2.01	0.43
44:Lt:1146:U:H2'	44:Lt:1147:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:SB:76:ASN:HD21	46:SB:201:LEU:HB2	1.84	0.43
53:SI:65:ARG:HA	53:SI:149:GLY:HA2	2.00	0.43
66:SX:24:LYS:HA	66:SX:95:THR:HA	2.00	0.43
66:SX:26:THR:HG21	75:St:1087:C:N4	2.34	0.43
75:St:906:C:H3'	75:St:907:A:H8	1.84	0.43
75:St:965:C:H2'	75:St:966:G:C8	2.54	0.43
75:St:1235:C:H2'	75:St:1236:G:H8	1.83	0.43
75:St:1301:C:H2'	75:St:1302:G:H8	1.82	0.43
3:LC:193:LYS:HD2	3:LC:193:LYS:HA	1.75	0.43
4:LD:139:U:H5''	9:LI:66:ARG:CD	2.49	0.43
11:LK:203:LYS:HE2	11:LK:203:LYS:HB2	1.53	0.43
12:LL:137:ARG:HE	12:LL:137:ARG:HB2	1.62	0.43
15:LO:149:ASN:HD22	15:LO:149:ASN:HA	1.59	0.43
17:LQ:15:LYS:HB3	17:LQ:149:ILE:HG12	2.01	0.43
19:LS:110:ARG:HE	19:LS:110:ARG:HB3	1.54	0.43
19:LS:154:LYS:HA	19:LS:154:LYS:HD3	1.69	0.43
21:LU:69:PRO:HB2	21:LU:70:ARG:H	1.46	0.43
27:La:102:THR:HA	27:La:105:ARG:HE	1.81	0.43
36:Lj:57:ASN:O	36:Lj:58:LYS:HB2	2.19	0.43
41:Lp:67:VAL:HG12	41:Lp:80:PHE:HB3	2.01	0.43
44:Lt:51:C:H2'	44:Lt:52:G:C8	2.54	0.43
44:Lt:1362:A:N6	44:Lt:1413:G:H2'	2.34	0.43
44:Lt:1633:A:H1'	44:Lt:1769:A:N6	2.33	0.43
44:Lt:2549:C:H2'	44:Lt:2550:C:C6	2.54	0.43
59:SP:42:LYS:HA	59:SP:42:LYS:HD2	1.57	0.43
65:SW:112:LEU:HA	65:SW:126:GLY:HA3	2.01	0.43
71:Se:77:LYS:HG2	71:Se:84:ILE:HG23	2.00	0.43
75:St:1201:C:H2'	75:St:1202:C:O4'	2.18	0.43
75:St:1251:C:H2'	75:St:1252:C:C6	2.54	0.43
75:St:1394:C:H2'	75:St:1395:G:C8	2.54	0.43
4:LD:31:G:H3'	4:LD:32:G:H8	1.84	0.42
23:LW:23:VAL:HG22	23:LW:53:PHE:HB3	2.01	0.42
27:La:119:ILE:H	27:La:119:ILE:HG13	1.70	0.42
44:Lt:467:C:H2'	44:Lt:468:G:C8	2.53	0.42
44:Lt:575:A:H2'	44:Lt:576:G:C8	2.54	0.42
44:Lt:1446:C:H2'	44:Lt:1447:G:C8	2.54	0.42
49:SE:243:ILE:HD12	49:SE:243:ILE:HA	1.78	0.42
51:SG:227:LEU:CA	51:SG:230:ARG:HD3	2.22	0.42
56:SL:45:LEU:HD13	56:SL:45:LEU:HA	1.84	0.42
60:SQ:147:ARG:HB2	60:SQ:150:ARG:HH11	1.83	0.42
67:SY:49:LYS:HE3	67:SY:49:LYS:HB3	1.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Sd:49:ILE:HD12	70:Sd:49:ILE:HA	1.79	0.42
3:LC:263:CYS:HB3	3:LC:264:ILE:H	1.67	0.42
3:LC:272:ILE:HG22	18:LR:126:LEU:HD23	2.00	0.42
13:LM:174:VAL:O	13:LM:175:MET:C	2.62	0.42
16:LP:174:LYS:HD3	16:LP:174:LYS:HA	1.86	0.42
26:LZ:67:LYS:HB2	26:LZ:67:LYS:HE3	1.60	0.42
29:Lc:23:LYS:HA	29:Lc:23:LYS:HD3	1.75	0.42
34:Lh:39:LEU:HD12	34:Lh:39:LEU:HA	1.78	0.42
35:Li:56:LEU:HD23	35:Li:56:LEU:HA	1.74	0.42
39:Ln:23:GLU:H	44:Lt:1959:C:H5'	1.84	0.42
43:Ls:95:ILE:HG21	44:Lt:2319:G:H4'	2.02	0.42
44:Lt:1441:A:H2'	44:Lt:1442:A:C8	2.54	0.42
44:Lt:1892:A:H2'	44:Lt:1892:A:N3	2.35	0.42
44:Lt:2110:C:H2'	44:Lt:2111:G:O4'	2.19	0.42
48:SD:13:ILE:HG22	48:SD:27:TRP:HE1	1.84	0.42
48:SD:25:LYS:NZ	60:SQ:51:GLU:HG2	2.35	0.42
51:SG:222:GLU:H	51:SG:222:GLU:HG2	1.52	0.42
52:SH:30:LEU:HD21	52:SH:83:LYS:HB3	2.01	0.42
55:SK:13:TYR:HE2	55:SK:15:THR:HG23	1.84	0.42
57:SM:8:ARG:HE	57:SM:8:ARG:HB2	1.42	0.42
59:SP:91:MET:HE2	59:SP:91:MET:HB3	1.61	0.42
60:SQ:143:LYS:HB2	60:SQ:143:LYS:HE2	1.41	0.42
61:SR:20:VAL:HB	61:SR:24:LYS:HB3	2.01	0.42
74:Sj:11:LYS:HZ1	75:St:443:U:H4'	1.84	0.42
75:St:159:C:H3'	75:St:160:G:H5'	2.02	0.42
75:St:831:A:C5	75:St:832:C:H1'	2.54	0.42
75:St:1281:C:H2'	75:St:1282:G:C8	2.54	0.42
2:LB:157:ILE:HD11	2:LB:188:VAL:HG13	2.02	0.42
6:LF:3:TRP:CD1	44:Lt:727:G:H21	2.37	0.42
6:LF:261:LYS:HA	6:LF:261:LYS:HD3	1.53	0.42
9:LI:90:ARG:HH21	9:LI:107:LYS:HA	1.84	0.42
13:LM:216:LEU:HD12	13:LM:216:LEU:HA	1.77	0.42
14:LN:2:SER:HA	20:LT:147:PRO:HB3	2.02	0.42
15:LO:56:LYS:HB2	15:LO:56:LYS:HE2	1.61	0.42
15:LO:156:MET:HE2	15:LO:156:MET:HB2	1.84	0.42
44:Lt:1403:C:H2'	44:Lt:1404:C:C6	2.54	0.42
48:SD:181:ILE:HA	48:SD:181:ILE:HD13	1.68	0.42
49:SE:164:LEU:HD12	49:SE:164:LEU:HA	1.78	0.42
49:SE:229:GLY:HA3	49:SE:234:ALA:HB2	2.01	0.42
52:SH:67:TYR:HE2	52:SH:99:ARG:HE	1.68	0.42
54:SJ:78:ARG:HB3	54:SJ:124:LYS:HB2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:SK:136:SER:HB2	55:SK:160:ALA:HB2	2.00	0.42
60:SQ:33:ILE:HG21	60:SQ:115:ALA:CB	2.49	0.42
64:SV:112:LEU:HD22	64:SV:112:LEU:HA	1.86	0.42
73:Sh:100:ARG:HE	73:Sh:100:ARG:HB2	1.58	0.42
74:Sj:62:ARG:HB2	74:Sj:67:PHE:HD1	1.84	0.42
75:St:353:U:H6	75:St:353:U:H2'	1.70	0.42
75:St:534:A:H2'	75:St:535:A:C8	2.55	0.42
75:St:744:A:H2'	75:St:745:G:O4'	2.20	0.42
8:LH:208:LYS:HE2	8:LH:208:LYS:HB2	1.69	0.42
9:LI:194:LYS:HE2	9:LI:194:LYS:HB3	1.43	0.42
10:LJ:2:PRO:HB2	10:LJ:3:LEU:H	1.35	0.42
11:LK:60:VAL:HG23	11:LK:129:VAL:HG21	2.01	0.42
13:LM:105:THR:HB	13:LM:108:GLU:HG3	2.00	0.42
19:LS:92:LYS:HB3	19:LS:92:LYS:HE3	1.84	0.42
39:Ln:6:PRO:O	39:Ln:198:TRP:HB2	2.18	0.42
39:Ln:57:HIS:CG	39:Ln:58:ILE:H	2.37	0.42
39:Ln:111:LEU:HG	39:Ln:137:PRO:HG3	2.01	0.42
44:Lt:783:C:H2'	44:Lt:784:G:H8	1.83	0.42
44:Lt:2055:U:H2'	44:Lt:2056:G:C8	2.55	0.42
44:Lt:2526:C:H2'	44:Lt:2527:U:C6	2.54	0.42
45:SA:56:LEU:HB2	63:SU:112:ILE:HD11	2.01	0.42
46:SB:143:GLY:HA2	67:SY:10:ASN:HB2	2.01	0.42
48:SD:48:LYS:HE3	48:SD:48:LYS:HB3	1.40	0.42
61:SR:37:LEU:HD23	61:SR:37:LEU:HA	1.85	0.42
62:ST:113:ASP:HA	62:ST:117:ARG:HD3	2.00	0.42
63:SU:74:LEU:HD12	63:SU:74:LEU:HA	1.91	0.42
1:LA:239:ALA:HA	44:Lt:1691:C:H5'	2.01	0.42
2:LB:248:LYS:HE2	2:LB:248:LYS:HB3	1.75	0.42
3:LC:117:ALA:HB1	3:LC:227:LEU:HB3	2.01	0.42
6:LF:275:LEU:HD12	6:LF:279:GLU:HG3	2.00	0.42
25:LY:28:ASN:HD21	44:Lt:1252:G:H3'	1.85	0.42
36:Lj:27:LYS:HB2	36:Lj:27:LYS:HE2	1.58	0.42
39:Ln:133:ARG:HB3	39:Ln:161:LYS:HD3	2.01	0.42
39:Ln:174:MET:HE2	39:Ln:174:MET:HB3	1.64	0.42
41:Lp:17:LYS:HE2	41:Lp:17:LYS:HB2	1.37	0.42
44:Lt:420:C:H2'	44:Lt:421:G:C8	2.54	0.42
44:Lt:1229:G:N2	44:Lt:1231:A:H3'	2.35	0.42
44:Lt:2566:C:O3'	44:Lt:2567:G:H8	2.03	0.42
49:SE:48:LEU:HA	49:SE:52:LEU:HB2	2.01	0.42
55:SK:37:LEU:HD13	55:SK:43:ILE:HG12	2.02	0.42
58:SO:3:LYS:HA	58:SO:3:LYS:HD3	1.57	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SQ:143:LYS:H	60:SQ:143:LYS:HG3	1.52	0.42
70:Sd:23:CYS:HB3	70:Sd:26:CYS:HB2	1.93	0.42
74:Sj:39:ASN:O	74:Sj:44:ASP:HB3	2.19	0.42
75:St:159:C:H5'	75:St:160:G:OP2	2.19	0.42
75:St:364:C:H2'	75:St:365:G:H5'	2.00	0.42
75:St:918:C:H2'	75:St:919:U:C6	2.54	0.42
75:St:1370:C:H42	75:St:1374:C:H42	1.66	0.42
2:LB:150:LEU:HD12	2:LB:150:LEU:HA	1.80	0.42
10:LJ:172:LEU:HB2	43:Ls:78:MET:HE1	2.00	0.42
18:LR:150:LYS:HA	18:LR:150:LYS:HD3	1.84	0.42
20:LT:16:LYS:O	20:LT:18:PRO:HD3	2.19	0.42
41:Lp:91:ILE:H	41:Lp:91:ILE:HG13	1.44	0.42
44:Lt:755:C:H2'	44:Lt:756:C:C6	2.53	0.42
45:SA:129:VAL:HG13	45:SA:135:ASP:HB2	2.01	0.42
47:SC:111:LEU:HD22	47:SC:128:ILE:HG13	2.01	0.42
55:SK:170:LYS:HB2	55:SK:170:LYS:HE3	1.56	0.42
57:SM:78:MET:HE3	57:SM:78:MET:HB2	1.68	0.42
58:SO:41:LEU:HD12	58:SO:41:LEU:HA	1.81	0.42
58:SO:115:ILE:HA	58:SO:116:PRO:HD3	1.90	0.42
62:ST:123:LYS:HB3	62:ST:123:LYS:HE3	1.51	0.42
64:SV:60:LEU:HD12	64:SV:60:LEU:HA	1.82	0.42
74:Sj:20:GLU:H	74:Sj:20:GLU:HG2	1.53	0.42
75:St:399:A:N6	75:St:421:G:H2'	2.34	0.42
75:St:481:C:H2'	75:St:482:G:C8	2.55	0.42
3:LC:94:PRO:HD2	44:Lt:517:G:H1	1.84	0.42
3:LC:130:ARG:HE	3:LC:130:ARG:HB3	1.75	0.42
10:LJ:89:ARG:HA	10:LJ:139:GLU:HA	2.02	0.42
17:LQ:39:GLY:HA2	17:LQ:113:TYR:HD2	1.85	0.42
19:LS:32:ILE:HG12	19:LS:49:ILE:HD11	2.00	0.42
19:LS:173:ARG:HA	75:St:607:C:H42	1.84	0.42
21:LU:62:GLY:HA3	21:LU:76:ILE:HG22	2.00	0.42
21:LU:80:VAL:HG21	44:Lt:2152:G:N7	2.35	0.42
21:LU:92:ARG:HB2	21:LU:95:HIS:HD2	1.84	0.42
21:LU:131:ARG:HH12	44:Lt:702:G:H22	1.68	0.42
34:Lh:50:LYS:HB2	34:Lh:50:LYS:HE2	1.75	0.42
34:Lh:65:ARG:HE	34:Lh:65:ARG:HB2	1.29	0.42
39:Ln:159:PHE:HA	39:Ln:167:TRP:HH2	1.84	0.42
44:Lt:590:C:H4'	44:Lt:1540:A:H5'	2.01	0.42
46:SB:147:THR:HG21	46:SB:166:ALA:H	1.85	0.42
49:SE:241:LYS:HB2	49:SE:241:LYS:HE2	1.38	0.42
60:SQ:44:VAL:HG11	60:SQ:85:ILE:HD13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SQ:147:ARG:HE	60:SQ:147:ARG:HB3	1.50	0.42
75:St:572:C:H2'	75:St:573:G:H8	1.84	0.42
3:LC:200:ASN:C	3:LC:202:GLU:H	2.27	0.42
14:LN:53:ARG:HA	20:LT:153:VAL:HG11	2.00	0.42
14:LN:115:LEU:HD13	16:LP:190:ALA:HB2	2.01	0.42
19:LS:139:LEU:HA	19:LS:139:LEU:HD23	1.74	0.42
22:LV:26:LYS:HA	22:LV:29:GLU:O	2.20	0.42
25:LY:65:PRO:HG3	35:Li:61:THR:HG23	2.02	0.42
26:LZ:88:ARG:H	26:LZ:88:ARG:HG3	1.44	0.42
28:Lb:2:PRO:HD2	44:Lt:509:G:H5''	2.02	0.42
34:Lh:77:LYS:HB2	34:Lh:77:LYS:HE2	1.76	0.42
39:Ln:58:ILE:C	39:Ln:60:LYS:H	2.27	0.42
44:Lt:2597:C:H3'	44:Lt:2598:C:H5'	2.02	0.42
47:SC:168:HIS:O	47:SC:169:PRO:C	2.63	0.42
61:SR:24:LYS:HD2	61:SR:24:LYS:HA	1.34	0.42
64:SV:112:LEU:HD11	64:SV:126:HIS:HB3	2.01	0.42
66:SX:93:TRP:CZ2	75:St:1087:C:H2'	2.54	0.42
74:Sj:31:ARG:HE	74:Sj:31:ARG:HB3	1.74	0.42
75:St:410:C:H2'	75:St:411:A:O4'	2.18	0.42
1:LA:75:LEU:HA	1:LA:75:LEU:HD23	1.78	0.42
4:LD:18:A:H1'	44:Lt:357:A:C2	2.55	0.42
5:LE:12:U:H1'	5:LE:110:U:H4'	2.02	0.42
9:LI:92:LEU:HD23	9:LI:92:LEU:HA	1.85	0.42
47:SC:144:VAL:HG13	47:SC:190:VAL:HG13	2.02	0.42
50:SF:31:ASN:HD22	50:SF:31:ASN:H	1.67	0.42
51:SG:91:LEU:HD13	51:SG:91:LEU:HA	1.71	0.42
53:SI:28:ASN:HD22	53:SI:28:ASN:HA	1.73	0.42
59:SP:142:LYS:HB2	59:SP:142:LYS:HE3	1.45	0.42
64:SV:97:MET:HG3	64:SV:97:MET:H	1.58	0.42
68:Sb:116:LEU:HD13	68:Sb:116:LEU:HA	1.80	0.42
75:St:251:C:H2'	75:St:252:G:C8	2.54	0.42
75:St:422:C:H6	75:St:422:C:H2'	1.66	0.42
75:St:906:C:H3'	75:St:907:A:C8	2.55	0.42
4:LD:25:G:H1'	44:Lt:300:A:C4	2.55	0.42
12:LL:91:LEU:HD11	12:LL:104:PHE:HB3	2.01	0.42
17:LQ:35:ILE:HD13	17:LQ:35:ILE:HA	1.87	0.42
33:Lg:33:VAL:HG21	33:Lg:45:VAL:HG11	2.01	0.42
36:Lj:63:LEU:HD12	36:Lj:63:LEU:HA	1.77	0.42
36:Lj:72:ASN:HB3	36:Lj:75:ARG:HB2	2.01	0.42
39:Ln:13:ILE:HD13	39:Ln:169:ILE:HG21	2.02	0.42
39:Ln:159:PHE:HA	39:Ln:167:TRP:CH2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:Lo:8:LYS:HE3	40:Lo:8:LYS:HB3	1.82	0.42
44:Lt:1703:C:H3'	44:Lt:1704:G:H8	1.85	0.42
45:SA:24:LEU:HD22	45:SA:24:LEU:HA	1.74	0.42
47:SC:79:LEU:HD12	47:SC:92:ILE:HD11	2.01	0.42
60:SQ:103:THR:HB	60:SQ:142:HIS:CD2	2.55	0.42
62:ST:31:LYS:HD2	62:ST:31:LYS:HA	1.80	0.42
62:ST:59:PRO:HB2	62:ST:62:LEU:HB2	2.01	0.42
65:SW:27:LYS:HE3	65:SW:27:LYS:HB3	1.45	0.42
75:St:479:C:H2'	75:St:480:G:C8	2.54	0.42
75:St:861:U:H2'	75:St:862:G:C8	2.54	0.42
75:St:914:G:H1'	75:St:1262:G:H1'	2.01	0.42
3:LC:52:ARG:HE	3:LC:52:ARG:HB2	1.50	0.41
8:LH:167:GLN:H	8:LH:167:GLN:HG2	1.64	0.41
9:LI:146:TRP:CD1	9:LI:146:TRP:H	2.38	0.41
11:LK:90:ARG:HA	11:LK:90:ARG:HD2	1.70	0.41
14:LN:128:MET:HE1	44:Lt:2598:C:H42	1.85	0.41
21:LU:21:ARG:HD2	21:LU:21:ARG:HA	1.78	0.41
25:LY:37:LEU:HD22	25:LY:37:LEU:HA	1.77	0.41
26:LZ:38:LEU:HD23	26:LZ:38:LEU:HA	1.85	0.41
32:Lf:9:LEU:H	32:Lf:9:LEU:HG	1.55	0.41
33:Lg:87:LEU:O	33:Lg:90:HIS:HB2	2.19	0.41
44:Lt:411:C:H2'	44:Lt:412:A:C8	2.54	0.41
44:Lt:1083:A:H4'	44:Lt:1108:C:H4'	2.02	0.41
44:Lt:1136:U:H2'	44:Lt:1137:A:C8	2.55	0.41
44:Lt:1685:C:H4'	44:Lt:1686:A:H5''	2.02	0.41
44:Lt:2631:C:C2'	44:Lt:2632:G:H5'	2.50	0.41
47:SC:18:LEU:HD13	66:SX:64:LEU:HD13	2.01	0.41
49:SE:105:VAL:HG13	49:SE:242:GLY:HA2	2.01	0.41
56:SL:70:PHE:CE1	56:SL:73:ARG:HA	2.55	0.41
1:LA:210:PRO:HD2	1:LA:235:VAL:HG11	2.02	0.41
6:LF:25:GLU:HB3	6:LF:27:LYS:HG3	2.02	0.41
7:LG:5:LYS:HB2	7:LG:5:LYS:HE2	1.59	0.41
8:LH:36:LYS:HE3	8:LH:36:LYS:HB3	1.79	0.41
44:Lt:1630:A:H8	44:Lt:2398:A:H2	1.68	0.41
44:Lt:2421:G:H2'	44:Lt:2422:C:C6	2.55	0.41
46:SB:233:GLN:HE21	46:SB:233:GLN:HB3	1.45	0.41
48:SD:220:ARG:HH21	48:SD:223:ASN:H	1.69	0.41
51:SG:187:LYS:HD2	75:St:63:C:H4'	2.02	0.41
52:SH:45:TYR:CZ	52:SH:66:PRO:HG2	2.55	0.41
53:SI:95:THR:HG23	75:St:241:G:H21	1.86	0.41
57:SM:119:ASP:HA	57:SM:143:VAL:HG13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SW:98:LYS:HZ1	75:St:1200:G:H3'	1.85	0.41
3:LC:164:VAL:HG13	3:LC:236:LEU:HD23	2.02	0.41
4:LD:83:C:H5''	4:LD:84:C:C5	2.55	0.41
11:LK:44:ASN:HA	11:LK:171:TRP:NE1	2.35	0.41
11:LK:82:LYS:H	11:LK:82:LYS:HG3	1.66	0.41
12:LL:51:ARG:HE	12:LL:51:ARG:HB3	1.68	0.41
12:LL:66:SER:HB3	44:Lt:2105:C:H4'	2.01	0.41
14:LN:130:ILE:HD11	16:LP:175:ILE:HG12	2.02	0.41
35:Li:37:LEU:HB2	35:Li:89:VAL:HG21	2.01	0.41
44:Lt:2022:C:H2'	44:Lt:2023:C:C6	2.55	0.41
45:SA:43:ILE:HG21	45:SA:52:PHE:HB3	2.02	0.41
49:SE:143:ASP:HB2	49:SE:145:ARG:HG3	2.02	0.41
51:SG:112:LEU:HD22	51:SG:112:LEU:HA	1.83	0.41
51:SG:187:LYS:NZ	51:SG:189:PRO:HD3	2.35	0.41
54:SJ:11:LEU:HD12	54:SJ:11:LEU:HA	1.86	0.41
56:SL:29:ARG:HA	56:SL:50:TYR:HD2	1.85	0.41
59:SP:150:LEU:HD23	59:SP:150:LEU:HA	1.91	0.41
60:SQ:151:LEU:HD12	60:SQ:151:LEU:HA	1.92	0.41
4:LD:65:C:H2'	4:LD:66:G:C8	2.54	0.41
5:LE:76:G:C8	20:LT:48:LYS:HG2	2.56	0.41
14:LN:46:LYS:O	14:LN:47:ARG:C	2.63	0.41
18:LR:73:LYS:H	18:LR:73:LYS:HG2	1.52	0.41
27:La:49:ARG:HB3	27:La:50:ARG:H	1.53	0.41
35:Li:131:LEU:HD12	35:Li:131:LEU:HA	1.71	0.41
44:Lt:787:G:N3	44:Lt:787:G:H2'	2.34	0.41
45:SA:188:LEU:HB3	45:SA:193:SER:HB3	2.02	0.41
46:SB:128:LEU:HD23	46:SB:128:LEU:HA	1.73	0.41
47:SC:14:TYR:CE2	66:SX:62:ARG:NE	2.87	0.41
48:SD:16:ARG:HE	48:SD:17:LYS:H	1.68	0.41
49:SE:20:LEU:HD21	49:SE:46:LEU:HD11	2.02	0.41
49:SE:159:THR:HB	49:SE:227:VAL:HB	2.03	0.41
50:SF:148:ALA:O	50:SF:151:LYS:HB2	2.21	0.41
72:Sg:23:THR:O	72:Sg:41:VAL:HG22	2.21	0.41
73:Sh:117:LEU:H	73:Sh:117:LEU:HG	1.36	0.41
74:Sj:22:LYS:HE2	74:Sj:22:LYS:HB3	1.64	0.41
74:Sj:29:ARG:HG3	75:St:389:C:H2'	2.01	0.41
75:St:355:C:H2'	75:St:356:C:C6	2.55	0.41
75:St:831:A:H4'	75:St:887:A:H5'	2.02	0.41
75:St:1145:C:H2'	75:St:1146:C:C6	2.55	0.41
2:LB:164:GLN:HA	2:LB:165:PRO:HD3	1.92	0.41
14:LN:68:PRO:O	14:LN:72:GLN:HB3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:LU:131:ARG:HH12	44:Lt:702:G:N2	2.18	0.41
26:LZ:49:ILE:HG21	26:LZ:78:ILE:HG21	2.01	0.41
36:Lj:53:LEU:HD22	36:Lj:57:ASN:HB2	2.02	0.41
37:Lk:50:SER:HB2	37:Lk:53:SER:HB3	2.02	0.41
39:Ln:78:LYS:HA	39:Ln:78:LYS:HD3	1.53	0.41
39:Ln:202:LYS:HD3	39:Ln:202:LYS:HA	1.79	0.41
45:SA:22:LYS:HB3	45:SA:22:LYS:HE2	1.62	0.41
45:SA:183:LEU:HD12	45:SA:183:LEU:HA	1.86	0.41
47:SC:47:ARG:HG2	47:SC:52:ILE:HG23	2.01	0.41
52:SH:15:LYS:H	52:SH:15:LYS:HG3	1.70	0.41
54:SJ:82:PRO:HD2	54:SJ:85:ASP:HB2	2.01	0.41
55:SK:81:LEU:HB3	55:SK:87:LEU:HB2	2.02	0.41
66:SX:44:ILE:HA	66:SX:108:THR:HG21	2.02	0.41
72:Sg:13:LEU:HB3	72:Sg:24:GLN:HB2	2.02	0.41
75:St:177:C:H2'	75:St:178:C:C6	2.56	0.41
75:St:904:A:H2'	75:St:905:C:C6	2.55	0.41
1:LA:161:LYS:HA	1:LA:161:LYS:HD2	1.70	0.41
7:LG:12:ARG:HE	7:LG:12:ARG:HB3	1.71	0.41
8:LH:31:ARG:HD2	8:LH:34:LEU:HD22	2.03	0.41
12:LL:50:SER:HB2	44:Lt:2105:C:OP1	2.20	0.41
14:LN:56:MET:HE3	14:LN:56:MET:HB2	1.62	0.41
15:LO:28:TRP:O	15:LO:32:GLN:HG2	2.20	0.41
18:LR:60:PRO:CG	18:LR:142:ARG:HA	2.42	0.41
18:LR:96:ARG:HE	18:LR:96:ARG:HB3	1.44	0.41
28:Lb:34:LYS:H	28:Lb:34:LYS:HG3	1.55	0.41
37:Lk:80:LYS:HZ3	37:Lk:80:LYS:HG3	1.82	0.41
38:Ll:51:VAL:HB	38:Ll:56:ASP:HB3	2.03	0.41
44:Lt:903:A:N6	44:Lt:1000:G:H2'	2.34	0.41
44:Lt:1309:C:H6	44:Lt:1309:C:H2'	1.69	0.41
50:SF:113:ARG:HH11	50:SF:120:VAL:HB	1.86	0.41
50:SF:114:ILE:HG13	50:SF:123:GLN:HB3	2.03	0.41
52:SH:41:LEU:HG	52:SH:44:LEU:HD12	2.01	0.41
60:SQ:50:ARG:HD3	60:SQ:50:ARG:HA	1.66	0.41
64:SV:69:MET:HA	64:SV:72:LEU:HD12	2.03	0.41
68:Sb:37:GLU:H	68:Sb:37:GLU:HG3	1.32	0.41
75:St:710:C:H2'	75:St:711:G:C8	2.55	0.41
7:LG:2:THR:HG21	44:Lt:1176:G:O6	2.21	0.41
10:LJ:172:LEU:HB3	43:Ls:86:ALA:HB1	2.02	0.41
11:LK:136:LEU:HD12	11:LK:136:LEU:HA	1.85	0.41
19:LS:95:TRP:CE2	44:Lt:572:U:H4'	2.55	0.41
33:Lg:88:MET:C	33:Lg:90:HIS:H	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Ln:61:GLN:HE21	44:Lt:1955:G:H5'	1.86	0.41
42:Lq:1:MET:HE3	42:Lq:1:MET:HB3	1.79	0.41
44:Lt:1482:A:H3'	44:Lt:1483:G:C5'	2.51	0.41
45:SA:174:MET:H	45:SA:174:MET:HG2	1.33	0.41
46:SB:159:VAL:HG21	46:SB:204:SER:HA	2.02	0.41
50:SF:131:ARG:O	50:SF:135:ILE:HG13	2.21	0.41
52:SH:142:LYS:HG2	52:SH:156:VAL:HG22	2.02	0.41
53:SI:76:TRP:CH2	53:SI:127:LEU:HB3	2.56	0.41
53:SI:82:SER:O	75:St:195:A:H4'	2.21	0.41
53:SI:169:LYS:HB2	53:SI:169:LYS:HE3	1.83	0.41
54:SJ:93:LEU:HA	54:SJ:93:LEU:HD13	1.75	0.41
57:SM:145:GLU:H	57:SM:145:GLU:HG2	1.60	0.41
64:SV:80:ILE:H	64:SV:80:ILE:HG12	1.38	0.41
65:SW:5:THR:H	65:SW:5:THR:HG23	1.63	0.41
75:St:1095:G:H21	75:St:1117:A:N6	2.18	0.41
4:LD:86:G:H4'	4:LD:87:A:H5'	2.03	0.41
6:LF:271:ARG:H	6:LF:271:ARG:HG2	1.43	0.41
8:LH:48:ARG:HD3	8:LH:48:ARG:HA	1.57	0.41
9:LI:68:LEU:O	9:LI:72:ILE:HG13	2.21	0.41
9:LI:130:LYS:HE3	9:LI:130:LYS:HB3	1.84	0.41
11:LK:62:SER:HA	11:LK:65:LEU:HD12	2.02	0.41
17:LQ:47:LEU:HD22	17:LQ:87:VAL:HG22	2.01	0.41
18:LR:56:LYS:H	18:LR:56:LYS:HG2	1.55	0.41
24:LX:56:TYR:HD1	24:LX:59:LEU:HB2	1.86	0.41
26:LZ:57:ILE:HG12	26:LZ:99:ILE:HG12	2.03	0.41
34:Lh:60:PRO:HB2	44:Lt:1446:C:H4'	2.03	0.41
43:Ls:114:ARG:HD3	43:Ls:114:ARG:HA	1.55	0.41
44:Lt:235:G:H22	44:Lt:256:G:H21	1.68	0.41
48:SD:11:LYS:HA	48:SD:27:TRP:CG	2.56	0.41
57:SM:28:ARG:O	57:SM:29:CYS:C	2.57	0.41
58:SO:48:ARG:HE	58:SO:48:ARG:HB3	1.35	0.41
62:ST:12:ARG:HH21	75:St:1086:G:H2'	1.85	0.41
1:LA:104:VAL:HA	1:LA:107:ILE:HG13	2.02	0.41
2:LB:261:GLN:H	2:LB:261:GLN:HG3	1.69	0.41
3:LC:205:ALA:HA	3:LC:216:LEU:HD22	2.03	0.41
3:LC:266:GLN:HE21	3:LC:266:GLN:HB3	1.60	0.41
10:LJ:169:ARG:HE	10:LJ:169:ARG:HB2	1.68	0.41
16:LP:152:ARG:HD2	16:LP:156:ARG:HH21	1.86	0.41
17:LQ:14:GLY:CA	17:LQ:101:ALA:HB2	2.44	0.41
20:LT:124:LYS:HZ3	20:LT:124:LYS:HG2	1.71	0.41
23:LW:89:VAL:HG22	23:LW:97:TRP:HE3	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:LX:56:TYR:HD1	24:LX:56:TYR:HA	1.69	0.41
33:Lg:18:GLN:HB2	33:Lg:28:VAL:HB	2.03	0.41
33:Lg:33:VAL:HG11	33:Lg:45:VAL:HG21	2.03	0.41
35:Li:91:ASN:HD22	35:Li:91:ASN:HA	1.68	0.41
36:Lj:55:ARG:HE	36:Lj:55:ARG:HB2	1.31	0.41
38:Ll:61:VAL:HG12	38:Ll:70:VAL:HG11	2.01	0.41
39:Ln:55:LEU:H	39:Ln:55:LEU:HG	1.50	0.41
41:Lp:64:LYS:HA	41:Lp:85:ARG:HH21	1.86	0.41
44:Lt:418:C:H2'	44:Lt:419:G:C8	2.56	0.41
44:Lt:478:U:H3	44:Lt:491:G:H1	1.69	0.41
44:Lt:2350:C:H2'	44:Lt:2351:C:C6	2.55	0.41
44:Lt:2511:C:H2'	44:Lt:2512:C:C6	2.56	0.41
45:SA:139:ILE:HD13	45:SA:139:ILE:HA	1.88	0.41
46:SB:180:LYS:HE3	46:SB:180:LYS:HB3	1.92	0.41
49:SE:221:ARG:H	49:SE:221:ARG:HG3	1.53	0.41
50:SF:17:LYS:HA	50:SF:17:LYS:HD3	1.93	0.41
51:SG:186:LEU:HD13	51:SG:186:LEU:HA	1.80	0.41
52:SH:35:ASP:HB2	52:SH:37:ARG:HH21	1.85	0.41
53:SI:7:LYS:H	53:SI:7:LYS:HG3	1.63	0.41
53:SI:37:LYS:HA	53:SI:37:LYS:HD3	1.84	0.41
55:SK:101:ARG:CZ	55:SK:103:GLU:HB2	2.51	0.41
58:SO:101:LEU:HD11	75:St:348:G:H4'	2.01	0.41
62:ST:89:GLY:HA2	75:St:1189:A:O3'	2.21	0.41
65:SW:36:LYS:HE3	75:St:1252:C:H5''	2.03	0.41
65:SW:68:HIS:O	65:SW:69:SER:HB2	2.21	0.41
71:Se:60:HIS:CE1	71:Se:62:LEU:HD12	2.56	0.41
75:St:130:C:H2'	75:St:131:A:C8	2.55	0.41
75:St:227:A:C2	75:St:229:C:H2'	2.56	0.41
75:St:554:G:H3'	75:St:555:G:H8	1.86	0.41
75:St:605:G:H1'	75:St:606:C:H3'	2.02	0.41
75:St:766:U:H2'	75:St:767:A:H8	1.85	0.41
75:St:772:C:H2'	75:St:773:G:C8	2.56	0.41
75:St:1349:C:H2'	75:St:1350:G:C8	2.56	0.41
2:LB:303:LYS:HB3	2:LB:303:LYS:HE2	1.69	0.41
6:LF:87:GLY:O	6:LF:89:PRO:HD3	2.21	0.41
7:LG:30:LYS:HE3	7:LG:30:LYS:HB3	1.58	0.41
8:LH:30:LYS:HE3	8:LH:30:LYS:HB2	1.29	0.41
9:LI:147:LEU:HD12	9:LI:147:LEU:HA	1.97	0.41
16:LP:169:ILE:HD13	16:LP:169:ILE:HA	1.85	0.41
17:LQ:29:TYR:HA	17:LQ:119:VAL:HG21	2.03	0.41
17:LQ:31:THR:HB	17:LQ:90:VAL:HG21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LQ:35:ILE:HD12	17:LQ:43:ALA:HB1	2.02	0.41
17:LQ:70:SER:HB2	44:Lt:2612:C:H5''	2.02	0.41
23:LW:17:ILE:H	23:LW:17:ILE:HG12	1.82	0.41
35:Li:81:LYS:HA	35:Li:81:LYS:HD3	1.67	0.41
36:Lj:23:GLU:H	36:Lj:23:GLU:HG3	1.75	0.41
42:Lq:54:ILE:HG23	42:Lq:63:THR:HG23	2.03	0.41
44:Lt:1531:G:H1	44:Lt:1822:U:H3'	1.85	0.41
44:Lt:1627:A:H3'	44:Lt:1628:C:H2'	2.03	0.41
44:Lt:1771:G:H1'	44:Lt:1773:C:N4	2.36	0.41
44:Lt:2270:A:H1'	44:Lt:2320:C:O2'	2.21	0.41
45:SA:47:GLN:H	45:SA:47:GLN:HG2	1.43	0.41
49:SE:230:ASN:HB2	49:SE:231:ASP:H	1.61	0.41
55:SK:166:ALA:N	55:SK:167:PRO:HD3	2.36	0.41
57:SM:44:ILE:HD12	57:SM:44:ILE:HA	1.70	0.41
57:SM:139:LYS:HB3	57:SM:139:LYS:HE2	1.35	0.41
63:SU:79:GLU:H	63:SU:79:GLU:HG3	1.57	0.41
65:SW:83:GLN:HE21	65:SW:83:GLN:HB3	1.55	0.41
67:SY:78:LEU:HD13	67:SY:78:LEU:HA	1.90	0.41
75:St:201:C:H5'	75:St:207:C:H4'	2.02	0.41
75:St:597:G:H2'	75:St:598:C:O4'	2.21	0.41
75:St:1004:C:H2'	75:St:1005:G:H8	1.84	0.41
4:LD:126:C:H5''	15:LO:60:VAL:HG11	2.03	0.40
6:LF:21:ARG:HE	6:LF:21:ARG:HB3	1.41	0.40
8:LH:171:HIS:C	8:LH:173:ILE:H	2.29	0.40
12:LL:164:GLU:H	12:LL:164:GLU:HG2	1.39	0.40
15:LO:22:LEU:HD23	15:LO:22:LEU:HA	1.82	0.40
15:LO:121:VAL:HG21	15:LO:131:GLU:HB2	2.03	0.40
21:LU:150:ILE:HD13	21:LU:150:ILE:HA	1.98	0.40
27:La:25:VAL:O	27:La:41:VAL:HA	2.21	0.40
39:Ln:29:LEU:HD23	39:Ln:29:LEU:HA	1.75	0.40
44:Lt:700:U:H2'	44:Lt:701:U:C6	2.56	0.40
47:SC:59:ALA:HB1	47:SC:100:ARG:HD2	2.03	0.40
47:SC:71:ARG:HA	47:SC:74:LYS:HE2	2.02	0.40
49:SE:23:MET:HG3	75:St:551:G:H5''	2.02	0.40
52:SH:158:LEU:HD23	52:SH:158:LEU:HA	1.86	0.40
62:ST:158:ARG:HD2	75:St:1267:G:H5''	2.03	0.40
67:SY:9:LYS:HE3	67:SY:9:LYS:HB3	1.66	0.40
69:Sc:85:THR:HB	69:Sc:86:LYS:H	1.71	0.40
14:LN:119:ARG:NH2	16:LP:191:GLU:HB2	2.37	0.40
17:LQ:138:LYS:HB3	17:LQ:138:LYS:HE3	1.29	0.40
39:Ln:79:LYS:H	39:Ln:79:LYS:HG2	1.43	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:Lt:839:A:H1'	44:Lt:2250:U:H5''	2.02	0.40
44:Lt:1969:G:H1	44:Lt:1972:A:H5''	1.87	0.40
44:Lt:2430:C:H2'	44:Lt:2431:G:C8	2.55	0.40
48:SD:52:LEU:HD12	48:SD:52:LEU:HA	1.81	0.40
50:SF:146:LYS:HE2	50:SF:146:LYS:HB3	1.72	0.40
52:SH:27:LEU:HD13	52:SH:27:LEU:HA	1.79	0.40
52:SH:65:VAL:CG1	52:SH:69:MET:HB3	2.48	0.40
52:SH:154:LEU:O	52:SH:185:THR:HA	2.22	0.40
60:SQ:29:ALA:HB2	60:SQ:90:ILE:HD12	2.03	0.40
64:SV:138:LYS:HE2	64:SV:138:LYS:HB2	1.81	0.40
72:Sg:2:PRO:HB2	72:Sg:3:GLU:H	1.53	0.40
74:Sj:18:LYS:HD3	74:Sj:18:LYS:HA	1.34	0.40
75:St:915:A:H2'	75:St:916:G:H8	1.81	0.40
13:LM:193:LYS:HG3	28:Lb:144:VAL:HG22	2.02	0.40
22:LV:30:LEU:HD13	22:LV:30:LEU:HA	1.95	0.40
25:LY:65:PRO:HD2	35:Li:61:THR:HA	2.01	0.40
29:Lc:22:LYS:HD2	29:Lc:22:LYS:HA	1.76	0.40
31:Le:8:THR:O	44:Lt:2632:G:H5''	2.21	0.40
41:Lp:67:VAL:HG22	41:Lp:82:VAL:HG13	2.01	0.40
44:Lt:695:C:N3	44:Lt:815:G:H1'	2.37	0.40
47:SC:166:THR:HG22	75:St:1127:G:H4'	2.03	0.40
59:SP:27:LYS:HE2	59:SP:27:LYS:HB2	1.91	0.40
64:SV:47:LYS:HB2	64:SV:53:VAL:HB	2.02	0.40
64:SV:138:LYS:HB3	75:St:1165:C:C4	2.57	0.40
66:SX:36:LEU:HD23	66:SX:39:ARG:HH21	1.87	0.40
68:Sb:106:LYS:HD2	68:Sb:106:LYS:HA	1.87	0.40
70:Sd:64:ILE:H	70:Sd:64:ILE:HG12	1.32	0.40
71:Se:77:LYS:HB2	71:Se:119:GLU:HB2	2.03	0.40
72:Sg:39:ARG:NH2	72:Sg:55:GLU:HB2	2.36	0.40
73:Sh:125:LYS:HE2	73:Sh:125:LYS:HB2	1.47	0.40
10:LJ:130:ILE:HG13	10:LJ:131:ALA:N	2.35	0.40
27:La:51:ILE:H	27:La:51:ILE:HG13	1.32	0.40
44:Lt:1051:C:H2'	44:Lt:1052:G:C8	2.56	0.40
50:SF:35:VAL:HG12	50:SF:37:HIS:HB2	2.03	0.40
50:SF:113:ARG:HD3	50:SF:120:VAL:HG12	2.03	0.40
52:SH:160:LYS:HD2	52:SH:160:LYS:HA	1.81	0.40
61:SR:89:MET:H	61:SR:89:MET:HG2	1.75	0.40
63:SU:47:LYS:HE3	63:SU:47:LYS:HB3	1.47	0.40
63:SU:61:MET:HA	63:SU:64:VAL:HG22	2.04	0.40
66:SX:104:ILE:O	66:SX:108:THR:HG23	2.21	0.40
75:St:28:C:H2'	75:St:29:G:C8	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:St:945:C:H2'	75:St:1163:C:H41	1.85	0.40
2:LB:172:GLN:O	2:LB:174:LYS:N	2.48	0.40
4:LD:139:U:H5''	9:LI:66:ARG:HD2	2.02	0.40
8:LH:225:LYS:HB2	8:LH:225:LYS:HE2	1.77	0.40
9:LI:63:PRO:HG2	9:LI:162:ARG:HG3	2.03	0.40
9:LI:138:VAL:HG12	9:LI:141:LEU:H	1.87	0.40
10:LJ:27:LYS:HB3	10:LJ:27:LYS:HE2	1.47	0.40
23:LW:77:LYS:HE3	23:LW:77:LYS:HB3	2.02	0.40
24:LX:64:MET:HB3	24:LX:64:MET:HE3	1.70	0.40
27:La:88:ASN:HB2	27:La:89:TYR:H	1.62	0.40
44:Lt:324:A:H2'	44:Lt:325:A:C8	2.57	0.40
44:Lt:1232:G:C5	44:Lt:1233:A:H1'	2.57	0.40
44:Lt:1769:A:H4'	44:Lt:2396:U:H4'	2.04	0.40
44:Lt:2171:A:H2'	44:Lt:2172:A:C8	2.56	0.40
47:SC:85:CYS:HB3	47:SC:86:ASP:H	1.53	0.40
50:SF:45:LYS:HE2	50:SF:45:LYS:HB2	1.66	0.40
51:SG:80:ARG:HA	51:SG:102:SER:HA	2.02	0.40
53:SI:62:ILE:H	53:SI:62:ILE:HG13	1.78	0.40
54:SJ:26:ILE:HG13	71:Se:48:LEU:HD13	2.03	0.40
58:SO:17:ARG:O	58:SO:21:ARG:HB3	2.21	0.40
58:SO:50:ILE:HA	58:SO:99:GLU:HA	2.02	0.40
59:SP:3:ARG:H	59:SP:3:ARG:HG2	1.77	0.40
68:Sb:24:VAL:HG23	68:Sb:73:CYS:HB3	2.03	0.40
75:St:193:U:H2'	75:St:194:G:C8	2.57	0.40
75:St:1137:C:H5''	75:St:1138:U:H3'	2.03	0.40
75:St:1372:C:H4'	75:St:1373:G:O4'	2.22	0.40
75:St:1384:C:H2'	75:St:1385:G:O4'	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	LA	248/251 (99%)	237 (96%)	11 (4%)	0	100	100
2	LB	376/379 (99%)	357 (95%)	17 (4%)	2 (0%)	24	55
3	LC	307/316 (97%)	293 (95%)	12 (4%)	2 (1%)	18	49
6	LF	289/297 (97%)	271 (94%)	17 (6%)	1 (0%)	36	65
7	LG	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
8	LH	211/235 (90%)	205 (97%)	6 (3%)	0	100	100
9	LI	183/225 (81%)	177 (97%)	6 (3%)	0	100	100
10	LJ	182/185 (98%)	168 (92%)	11 (6%)	3 (2%)	7	32
11	LK	141/210 (67%)	133 (94%)	8 (6%)	0	100	100
12	LL	163/173 (94%)	159 (98%)	3 (2%)	1 (1%)	21	51
13	LM	199/234 (85%)	190 (96%)	7 (4%)	2 (1%)	12	41
14	LN	128/131 (98%)	120 (94%)	7 (6%)	1 (1%)	16	46
15	LO	201/204 (98%)	194 (96%)	6 (3%)	1 (0%)	24	55
16	LP	192/197 (98%)	187 (97%)	4 (2%)	1 (0%)	24	55
17	LQ	151/164 (92%)	144 (95%)	7 (5%)	0	100	100
18	LR	176/179 (98%)	166 (94%)	8 (4%)	2 (1%)	11	40
19	LS	190/196 (97%)	183 (96%)	5 (3%)	2 (1%)	11	40
20	LT	168/173 (97%)	160 (95%)	8 (5%)	0	100	100
21	LU	154/159 (97%)	142 (92%)	9 (6%)	3 (2%)	6	29
22	LV	101/124 (82%)	87 (86%)	12 (12%)	2 (2%)	6	28
23	LW	130/142 (92%)	128 (98%)	2 (2%)	0	100	100
24	LX	61/189 (32%)	58 (95%)	3 (5%)	0	100	100
25	LY	117/141 (83%)	110 (94%)	6 (5%)	1 (1%)	14	43
26	LZ	131/135 (97%)	124 (95%)	6 (5%)	1 (1%)	16	46
27	La	123/135 (91%)	112 (91%)	10 (8%)	1 (1%)	16	46
28	Lb	146/149 (98%)	140 (96%)	4 (3%)	2 (1%)	9	34
29	Lc	49/62 (79%)	44 (90%)	3 (6%)	2 (4%)	2	15
30	Ld	100/109 (92%)	96 (96%)	4 (4%)	0	100	100
31	Le	98/106 (92%)	94 (96%)	3 (3%)	1 (1%)	12	41
32	Lf	128/136 (94%)	121 (94%)	6 (5%)	1 (1%)	16	46
33	Lg	96/123 (78%)	93 (97%)	3 (3%)	0	100	100
34	Lh	94/120 (78%)	89 (95%)	4 (4%)	1 (1%)	11	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	Li	116/124 (94%)	109 (94%)	6 (5%)	1 (1%)	14	43
36	Lj	87/90 (97%)	79 (91%)	6 (7%)	2 (2%)	5	25
37	Lk	86/89 (97%)	79 (92%)	5 (6%)	2 (2%)	5	25
38	Ll	70/77 (91%)	67 (96%)	3 (4%)	0	100	100
39	Ln	207/217 (95%)	169 (82%)	30 (14%)	8 (4%)	2	16
40	Lo	23/25 (92%)	23 (100%)	0	0	100	100
41	Lp	91/106 (86%)	91 (100%)	0	0	100	100
42	Lq	89/94 (95%)	82 (92%)	6 (7%)	1 (1%)	11	40
43	Ls	45/127 (35%)	42 (93%)	2 (4%)	1 (2%)	5	26
45	SA	194/245 (79%)	183 (94%)	10 (5%)	1 (0%)	24	55
46	SB	214/242 (88%)	199 (93%)	15 (7%)	0	100	100
47	SC	207/217 (95%)	191 (92%)	14 (7%)	2 (1%)	12	41
48	SD	227/248 (92%)	213 (94%)	13 (6%)	1 (0%)	30	59
49	SE	258/268 (96%)	244 (95%)	13 (5%)	1 (0%)	30	59
50	SF	184/190 (97%)	173 (94%)	8 (4%)	3 (2%)	7	32
51	SG	203/248 (82%)	192 (95%)	9 (4%)	2 (1%)	12	41
52	SH	182/190 (96%)	166 (91%)	15 (8%)	1 (0%)	24	55
53	SI	171/174 (98%)	161 (94%)	9 (5%)	1 (1%)	21	51
54	SJ	127/130 (98%)	117 (92%)	8 (6%)	2 (2%)	7	32
55	SK	174/189 (92%)	164 (94%)	7 (4%)	3 (2%)	7	30
56	SL	98/134 (73%)	92 (94%)	5 (5%)	1 (1%)	12	41
57	SM	149/154 (97%)	135 (91%)	9 (6%)	5 (3%)	3	19
58	SO	137/143 (96%)	132 (96%)	4 (3%)	1 (1%)	18	49
59	SP	148/154 (96%)	144 (97%)	4 (3%)	0	100	100
60	SQ	123/145 (85%)	111 (90%)	11 (9%)	1 (1%)	16	46
61	SR	114/145 (79%)	103 (90%)	8 (7%)	3 (3%)	4	23
62	ST	149/158 (94%)	141 (95%)	6 (4%)	2 (1%)	9	35
63	SU	102/137 (74%)	99 (97%)	3 (3%)	0	100	100
64	SV	139/154 (90%)	123 (88%)	12 (9%)	4 (3%)	3	21
65	SW	135/139 (97%)	126 (93%)	7 (5%)	2 (2%)	8	33
66	SX	98/126 (78%)	97 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	SY	84/89 (94%)	79 (94%)	2 (2%)	3 (4%)	2	18
68	Sb	116/132 (88%)	108 (93%)	8 (7%)	0	100	100
69	Sc	71/88 (81%)	67 (94%)	4 (6%)	0	100	100
70	Sd	97/109 (89%)	91 (94%)	6 (6%)	0	100	100
71	Se	77/81 (95%)	74 (96%)	3 (4%)	0	100	100
72	Sg	61/64 (95%)	53 (87%)	7 (12%)	1 (2%)	7	32
73	Sh	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
74	Sj	60/69 (87%)	55 (92%)	4 (7%)	1 (2%)	7	30
All	All	10042/11192 (90%)	9447 (94%)	506 (5%)	89 (1%)	16	43

All (89) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	LC	255	GLN
27	La	98	VAL
29	Lc	25	LYS
29	Lc	50	ASP
36	Lj	58	LYS
37	Lk	76	SER
39	Ln	69	ALA
43	Ls	98	HIS
45	SA	191	LYS
49	SE	230	ASN
55	SK	167	PRO
61	SR	22	VAL
74	Sj	44	ASP
16	LP	129	GLU
21	LU	69	PRO
31	Le	92	LYS
37	Lk	65	SER
39	Ln	24	LYS
48	SD	51	GLY
50	SF	114	ILE
55	SK	163	SER
57	SM	150	ARG
61	SR	76	VAL
62	ST	74	GLY
62	ST	112	LYS
64	SV	44	VAL

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Mol	Chain	Res	Type
67	SY	16	VAL
2	LB	378	ALA
6	LF	142	ASN
15	LO	185	ARG
18	LR	167	HIS
21	LU	140	HIS
22	LV	30	LEU
25	LY	54	SER
28	Lb	15	ARG
34	Lh	48	THR
39	Ln	103	PHE
39	Ln	151	CYS
50	SF	148	ALA
51	SG	87	ALA
53	SI	92	TYR
57	SM	53	ASP
57	SM	153	PRO
65	SW	27	LYS
65	SW	69	SER
67	SY	5	ASP
2	LB	103	THR
3	LC	292	GLU
10	LJ	165	ASN
12	LL	144	GLN
19	LS	16	LYS
19	LS	113	GLU
26	LZ	62	HIS
32	Lf	50	GLN
50	SF	35	VAL
54	SJ	59	ASN
56	SL	32	ASN
58	SO	99	GLU
61	SR	75	ILE
64	SV	90	ASP
64	SV	101	VAL
72	Sg	33	GLU
13	LM	168	ILE
14	LN	69	THR
18	LR	95	PRO
21	LU	136	PRO
22	LV	95	PHE
28	Lb	95	SER

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Mol	Chain	Res	Type
35	Li	107	HIS
39	Ln	60	LYS
39	Ln	188	ASN
47	SC	147	LYS
47	SC	199	ILE
52	SH	12	PRO
57	SM	148	LYS
64	SV	56	ARG
10	LJ	41	PRO
10	LJ	184	GLU
13	LM	91	SER
60	SQ	136	PRO
39	Ln	43	PRO
55	SK	170	LYS
36	Lj	27	LYS
39	Ln	54	VAL
42	Lq	8	VAL
51	SG	136	PRO
54	SJ	29	PRO
57	SM	128	PRO
67	SY	14	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	LA	191/192 (100%)	135 (71%)	56 (29%)	0	1
2	LB	312/313 (100%)	204 (65%)	108 (35%)	0	1
3	LC	256/263 (97%)	183 (72%)	73 (28%)	0	1
6	LF	236/242 (98%)	143 (61%)	93 (39%)	0	0
7	LG	47/48 (98%)	31 (66%)	16 (34%)	0	1
8	LH	184/204 (90%)	121 (66%)	63 (34%)	0	1
9	LI	165/198 (83%)	108 (66%)	57 (34%)	0	1
10	LJ	163/164 (99%)	93 (57%)	70 (43%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	LK	127/177 (72%)	68 (54%)	59 (46%)	0	0
12	LL	141/149 (95%)	82 (58%)	59 (42%)	0	0
13	LM	169/197 (86%)	113 (67%)	56 (33%)	0	1
14	LN	110/111 (99%)	61 (56%)	49 (44%)	0	0
15	LO	174/175 (99%)	115 (66%)	59 (34%)	0	1
16	LP	162/165 (98%)	119 (74%)	43 (26%)	0	2
17	LQ	130/139 (94%)	83 (64%)	47 (36%)	0	0
18	LR	154/155 (99%)	104 (68%)	50 (32%)	0	1
19	LS	163/167 (98%)	103 (63%)	60 (37%)	0	0
20	LT	151/154 (98%)	90 (60%)	61 (40%)	0	0
21	LU	130/133 (98%)	80 (62%)	50 (38%)	0	0
22	LV	91/110 (83%)	51 (56%)	40 (44%)	0	0
23	LW	108/114 (95%)	74 (68%)	34 (32%)	0	1
24	LX	61/174 (35%)	34 (56%)	27 (44%)	0	0
25	LY	107/123 (87%)	78 (73%)	29 (27%)	0	2
26	LZ	114/115 (99%)	71 (62%)	43 (38%)	0	0
27	La	112/119 (94%)	63 (56%)	49 (44%)	0	0
28	Lb	126/127 (99%)	93 (74%)	33 (26%)	0	2
29	Lc	47/57 (82%)	35 (74%)	12 (26%)	0	2
30	Ld	87/92 (95%)	50 (58%)	37 (42%)	0	0
31	Le	88/92 (96%)	56 (64%)	32 (36%)	0	0
32	Lf	116/120 (97%)	71 (61%)	45 (39%)	0	0
33	Lg	82/103 (80%)	56 (68%)	26 (32%)	0	1
34	Lh	85/100 (85%)	58 (68%)	27 (32%)	0	1
35	Li	103/107 (96%)	63 (61%)	40 (39%)	0	0
36	Lj	77/78 (99%)	44 (57%)	33 (43%)	0	0
37	Lk	73/74 (99%)	44 (60%)	29 (40%)	0	0
38	Ll	63/68 (93%)	32 (51%)	31 (49%)	0	0
39	Ln	183/189 (97%)	83 (45%)	100 (55%)	0	0
40	Lo	22/22 (100%)	13 (59%)	9 (41%)	0	0
41	Lp	83/93 (89%)	42 (51%)	41 (49%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
42	Lq	71/73 (97%)	41 (58%)	30 (42%)	0	0	
43	Ls	43/110 (39%)	25 (58%)	18 (42%)	0	0	
45	SA	171/217 (79%)	104 (61%)	67 (39%)	0	0	
46	SB	179/201 (89%)	104 (58%)	75 (42%)	0	0	
47	SC	174/182 (96%)	102 (59%)	72 (41%)	0	0	
48	SD	207/220 (94%)	129 (62%)	78 (38%)	0	0	
49	SE	228/232 (98%)	141 (62%)	87 (38%)	0	0	
50	SF	153/157 (98%)	94 (61%)	59 (39%)	0	0	
51	SG	176/213 (83%)	84 (48%)	92 (52%)	0	0	
52	SH	165/170 (97%)	82 (50%)	83 (50%)	0	0	
53	SI	147/148 (99%)	89 (60%)	58 (40%)	0	0	
54	SJ	114/115 (99%)	63 (55%)	51 (45%)	0	0	
55	SK	155/164 (94%)	84 (54%)	71 (46%)	0	0	
56	SL	89/119 (75%)	48 (54%)	41 (46%)	0	0	
57	SM	134/136 (98%)	82 (61%)	52 (39%)	0	0	
58	SO	111/114 (97%)	61 (55%)	50 (45%)	0	0	
59	SP	125/130 (96%)	78 (62%)	47 (38%)	0	0	
60	SQ	86/113 (76%)	51 (59%)	35 (41%)	0	0	
61	SR	104/128 (81%)	55 (53%)	49 (47%)	0	0	
62	ST	125/130 (96%)	67 (54%)	58 (46%)	0	0	
63	SU	98/124 (79%)	58 (59%)	40 (41%)	0	0	
64	SV	118/131 (90%)	58 (49%)	60 (51%)	0	0	
65	SW	113/115 (98%)	62 (55%)	51 (45%)	0	0	
66	SX	89/110 (81%)	50 (56%)	39 (44%)	0	0	
67	SY	69/72 (96%)	37 (54%)	32 (46%)	0	0	
68	Sb	103/113 (91%)	50 (48%)	53 (52%)	0	0	
69	Sc	65/79 (82%)	34 (52%)	31 (48%)	0	0	
70	Sd	95/103 (92%)	65 (68%)	30 (32%)	0	1	
71	Se	71/73 (97%)	41 (58%)	30 (42%)	0	0	
72	Sg	56/57 (98%)	23 (41%)	33 (59%)	0	0	
73	Sh	44/45 (98%)	25 (57%)	19 (43%)	0	0	

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
74	Sj	55/58 (95%)	27 (49%)	28 (51%)	0 0
All	All	8726/9575 (91%)	5261 (60%)	3465 (40%)	0 0

All (3465) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	LA	3	ARG
1	LA	5	ILE
1	LA	6	ARG
1	LA	14	SER
1	LA	17	ARG
1	LA	20	VAL
1	LA	22	ARG
1	LA	30	ARG
1	LA	44	VAL
1	LA	46	LYS
1	LA	48	ILE
1	LA	49	LEU
1	LA	54	ARG
1	LA	60	ARG
1	LA	67	ARG
1	LA	72	VAL
1	LA	73	ASN
1	LA	75	LEU
1	LA	77	ILE
1	LA	82	MET
1	LA	93	LYS
1	LA	95	THR
1	LA	96	LEU
1	LA	98	ILE
1	LA	101	ILE
1	LA	102	LEU
1	LA	107	ILE
1	LA	118	GLU
1	LA	119	LYS
1	LA	126	LEU
1	LA	128	ARG
1	LA	130	SER
1	LA	135	LEU
1	LA	140	ASN
1	LA	141	MET
1	LA	143	THR

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Mol	Chain	Res	Type
1	LA	145	LYS
1	LA	148	ILE
1	LA	156	LYS
1	LA	161	LYS
1	LA	163	ARG
1	LA	168	LEU
1	LA	175	THR
1	LA	181	LYS
1	LA	190	LYS
1	LA	193	ARG
1	LA	199	VAL
1	LA	219	ILE
1	LA	221	VAL
1	LA	231	PRO
1	LA	234	LYS
1	LA	238	ILE
1	LA	243	THR
1	LA	245	CYS
1	LA	249	LYS
1	LA	250	ARG
2	LB	4	ARG
2	LB	5	LYS
2	LB	10	ARG
2	LB	11	LYS
2	LB	20	LYS
2	LB	26	ARG
2	LB	29	CYS
2	LB	31	THR
2	LB	41	ILE
2	LB	44	THR
2	LB	47	LEU
2	LB	50	LYS
2	LB	55	HIS
2	LB	56	VAL
2	LB	58	ARG
2	LB	66	ASN
2	LB	70	ARG
2	LB	73	ILE
2	LB	74	ASP
2	LB	78	ILE
2	LB	79	ILE
2	LB	87	THR

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Mol	Chain	Res	Type
2	LB	90	ILE
2	LB	97	LYS
2	LB	104	THR
2	LB	110	ILE
2	LB	117	ARG
2	LB	121	ASN
2	LB	126	GLU
2	LB	127	LYS
2	LB	131	SER
2	LB	132	THR
2	LB	134	MET
2	LB	141	THR
2	LB	144	LYS
2	LB	145	GLU
2	LB	149	ARG
2	LB	150	LEU
2	LB	151	LYS
2	LB	152	GLN
2	LB	157	ILE
2	LB	159	ILE
2	LB	160	VAL
2	LB	163	THR
2	LB	164	GLN
2	LB	167	LEU
2	LB	168	THR
2	LB	170	LEU
2	LB	171	LYS
2	LB	177	ILE
2	LB	178	MET
2	LB	191	LYS
2	LB	196	TYR
2	LB	198	LEU
2	LB	199	MET
2	LB	201	LYS
2	LB	203	ILE
2	LB	205	ILE
2	LB	206	LYS
2	LB	207	ASP
2	LB	210	SER
2	LB	215	ILE
2	LB	217	THR
2	LB	219	SER

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Mol	Chain	Res	Type
2	LB	220	ILE
2	LB	222	ARG
2	LB	224	ARG
2	LB	227	GLU
2	LB	229	VAL
2	LB	231	THR
2	LB	237	ARG
2	LB	238	LEU
2	LB	241	LYS
2	LB	243	ARG
2	LB	244	ARG
2	LB	246	ASN
2	LB	248	LYS
2	LB	251	CYS
2	LB	264	VAL
2	LB	278	THR
2	LB	279	ASN
2	LB	285	ILE
2	LB	289	GLU
2	LB	297	GLU
2	LB	300	LEU
2	LB	301	THR
2	LB	303	LYS
2	LB	308	VAL
2	LB	312	VAL
2	LB	318	GLN
2	LB	320	ASP
2	LB	322	ILE
2	LB	324	ILE
2	LB	325	LYS
2	LB	327	THR
2	LB	328	CYS
2	LB	332	LYS
2	LB	333	ARG
2	LB	334	ARG
2	LB	336	VAL
2	LB	343	LEU
2	LB	351	VAL
2	LB	356	ILE
2	LB	366	ILE
2	LB	369	THR
2	LB	370	VAL

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Mol	Chain	Res	Type
2	LB	375	GLN
2	LB	379	LYS
3	LC	4	THR
3	LC	6	LYS
3	LC	11	THR
3	LC	14	GLN
3	LC	18	LEU
3	LC	22	LYS
3	LC	23	VAL
3	LC	26	VAL
3	LC	28	LEU
3	LC	32	ILE
3	LC	39	GLN
3	LC	52	ARG
3	LC	56	VAL
3	LC	59	THR
3	LC	72	LEU
3	LC	91	MET
3	LC	93	HIS
3	LC	96	THR
3	LC	105	VAL
3	LC	109	GLN
3	LC	126	LEU
3	LC	130	ARG
3	LC	134	ILE
3	LC	140	ILE
3	LC	143	VAL
3	LC	144	VAL
3	LC	146	THR
3	LC	151	LYS
3	LC	153	LYS
3	LC	159	ILE
3	LC	164	VAL
3	LC	177	ILE
3	LC	181	ARG
3	LC	183	LYS
3	LC	186	ASN
3	LC	190	ILE
3	LC	193	LYS
3	LC	197	VAL
3	LC	201	THR
3	LC	202	GLU

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Mol	Chain	Res	Type
3	LC	206	ARG
3	LC	211	LEU
3	LC	214	VAL
3	LC	215	ASP
3	LC	216	LEU
3	LC	217	CYS
3	LC	219	VAL
3	LC	221	SER
3	LC	222	ILE
3	LC	241	LYS
3	LC	242	SER
3	LC	244	PHE
3	LC	247	LEU
3	LC	250	VAL
3	LC	256	ASN
3	LC	259	LEU
3	LC	262	SER
3	LC	264	ILE
3	LC	265	THR
3	LC	266	GLN
3	LC	269	ILE
3	LC	270	GLU
3	LC	273	LEU
3	LC	276	ASP
3	LC	278	VAL
3	LC	283	VAL
3	LC	285	LYS
3	LC	286	ARG
3	LC	290	VAL
3	LC	295	VAL
3	LC	300	SER
3	LC	301	LYS
3	LC	310	SER
6	LF	6	VAL
6	LF	8	LYS
6	LF	9	THR
6	LF	11	SER
6	LF	21	ARG
6	LF	23	ARG
6	LF	28	THR
6	LF	31	GLN
6	LF	33	ARG

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Mol	Chain	Res	Type
6	LF	34	LYS
6	LF	37	ILE
6	LF	38	ILE
6	LF	46	THR
6	LF	50	ARG
6	LF	52	VAL
6	LF	54	ARG
6	LF	56	THR
6	LF	58	LYS
6	LF	60	ILE
6	LF	68	GLU
6	LF	69	LEU
6	LF	70	THR
6	LF	71	LYS
6	LF	75	VAL
6	LF	76	CYS
6	LF	85	ARG
6	LF	88	ILE
6	LF	90	VAL
6	LF	92	LEU
6	LF	93	THR
6	LF	103	LEU
6	LF	105	CYS
6	LF	109	LEU
6	LF	112	LYS
6	LF	113	LEU
6	LF	114	SER
6	LF	115	VAL
6	LF	118	LYS
6	LF	119	GLU
6	LF	122	LEU
6	LF	125	LEU
6	LF	130	ASP
6	LF	131	LYS
6	LF	133	THR
6	LF	138	HIS
6	LF	141	GLU
6	LF	143	GLU
6	LF	146	GLU
6	LF	151	LYS
6	LF	162	SER
6	LF	175	VAL

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Mol	Chain	Res	Type
6	LF	179	LEU
6	LF	181	ILE
6	LF	184	SER
6	LF	186	LYS
6	LF	193	LYS
6	LF	197	ASP
6	LF	202	ARG
6	LF	206	MET
6	LF	208	LYS
6	LF	214	MET
6	LF	218	LYS
6	LF	221	ASP
6	LF	226	ARG
6	LF	227	LYS
6	LF	228	ARG
6	LF	230	SER
6	LF	231	LYS
6	LF	233	ILE
6	LF	236	LYS
6	LF	237	VAL
6	LF	240	LEU
6	LF	242	LEU
6	LF	248	LYS
6	LF	253	ILE
6	LF	256	ASN
6	LF	260	VAL
6	LF	261	LYS
6	LF	264	PHE
6	LF	265	GLU
6	LF	270	VAL
6	LF	271	ARG
6	LF	272	GLN
6	LF	274	ARG
6	LF	275	LEU
6	LF	278	LYS
6	LF	279	GLU
6	LF	281	LYS
6	LF	282	GLU
6	LF	285	ASP
6	LF	287	LYS
6	LF	288	LYS
6	LF	289	LEU

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Mol	Chain	Res	Type
7	LG	2	THR
7	LG	5	LYS
7	LG	6	THR
7	LG	8	SER
7	LG	15	LYS
7	LG	16	LYS
7	LG	18	LYS
7	LG	23	ILE
7	LG	30	LYS
7	LG	33	LEU
7	LG	34	LYS
7	LG	39	TYR
7	LG	40	LYS
7	LG	46	ARG
7	LG	48	HIS
7	LG	51	LEU
8	LH	24	ARG
8	LH	26	THR
8	LH	28	LYS
8	LH	30	LYS
8	LH	31	ARG
8	LH	34	LEU
8	LH	36	LYS
8	LH	40	VAL
8	LH	41	LYS
8	LH	44	GLN
8	LH	45	VAL
8	LH	48	ARG
8	LH	51	ILE
8	LH	53	LEU
8	LH	56	SER
8	LH	57	GLU
8	LH	58	LYS
8	LH	59	LYS
8	LH	62	GLU
8	LH	72	VAL
8	LH	75	GLU
8	LH	77	LYS
8	LH	79	TYR
8	LH	84	ILE
8	LH	88	VAL
8	LH	90	VAL

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Mol	Chain	Res	Type
8	LH	93	LYS
8	LH	94	VAL
8	LH	97	ILE
8	LH	101	LEU
8	LH	102	ARG
8	LH	106	ILE
8	LH	112	MET
8	LH	115	ASN
8	LH	124	ILE
8	LH	127	HIS
8	LH	136	VAL
8	LH	138	THR
8	LH	139	ILE
8	LH	140	ARG
8	LH	146	ARG
8	LH	159	VAL
8	LH	163	LEU
8	LH	164	ILE
8	LH	165	ASP
8	LH	167	GLN
8	LH	170	LYS
8	LH	174	LEU
8	LH	179	LEU
8	LH	180	VAL
8	LH	183	ILE
8	LH	189	SER
8	LH	195	ASN
8	LH	203	ASN
8	LH	208	LYS
8	LH	209	ASP
8	LH	219	ASP
8	LH	220	PHE
8	LH	225	LYS
8	LH	227	ILE
8	LH	231	VAL
8	LH	233	ARG
8	LH	235	ILE
9	LI	42	ARG
9	LI	44	LYS
9	LI	47	LEU
9	LI	49	ARG
9	LI	56	THR

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Mol	Chain	Res	Type
9	LI	61	MET
9	LI	62	ASN
9	LI	66	ARG
9	LI	70	ASN
9	LI	75	LEU
9	LI	77	ARG
9	LI	78	LYS
9	LI	82	GLU
9	LI	83	SER
9	LI	84	LYS
9	LI	85	GLU
9	LI	87	HIS
9	LI	91	LEU
9	LI	93	GLN
9	LI	98	LYS
9	LI	107	LYS
9	LI	110	LYS
9	LI	112	VAL
9	LI	113	ILE
9	LI	115	SER
9	LI	119	ARG
9	LI	120	ILE
9	LI	127	LYS
9	LI	130	LYS
9	LI	134	ILE
9	LI	143	LEU
9	LI	152	HIS
9	LI	153	LYS
9	LI	161	VAL
9	LI	164	LYS
9	LI	173	LEU
9	LI	174	LYS
9	LI	175	LYS
9	LI	179	VAL
9	LI	180	CYS
9	LI	182	THR
9	LI	184	VAL
9	LI	185	ASN
9	LI	187	GLU
9	LI	189	LYS
9	LI	191	THR
9	LI	194	LYS

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Mol	Chain	Res	Type
9	LI	196	LEU
9	LI	202	GLU
9	LI	203	VAL
9	LI	204	ASP
9	LI	207	LYS
9	LI	209	MET
9	LI	212	TYR
9	LI	216	VAL
9	LI	217	ARG
9	LI	219	GLU
10	LJ	4	CYS
10	LJ	5	SER
10	LJ	7	MET
10	LJ	8	THR
10	LJ	9	ILE
10	LJ	10	LYS
10	LJ	14	ASP
10	LJ	19	ILE
10	LJ	20	ASN
10	LJ	22	ARG
10	LJ	23	VAL
10	LJ	27	LYS
10	LJ	29	LYS
10	LJ	32	THR
10	LJ	35	ARG
10	LJ	42	LEU
10	LJ	45	THR
10	LJ	48	ASN
10	LJ	50	THR
10	LJ	51	ILE
10	LJ	59	ARG
10	LJ	65	LEU
10	LJ	68	THR
10	LJ	78	LYS
10	LJ	85	GLU
10	LJ	87	LYS
10	LJ	88	MET
10	LJ	89	ARG
10	LJ	90	LEU
10	LJ	100	THR
10	LJ	101	VAL
10	LJ	102	VAL

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Mol	Chain	Res	Type
10	LJ	104	ASN
10	LJ	106	LYS
10	LJ	108	ILE
10	LJ	110	ILE
10	LJ	112	ASN
10	LJ	114	MET
10	LJ	117	ILE
10	LJ	118	LYS
10	LJ	119	THR
10	LJ	120	ARG
10	LJ	121	ARG
10	LJ	122	ILE
10	LJ	124	CYS
10	LJ	125	LEU
10	LJ	128	VAL
10	LJ	130	ILE
10	LJ	132	MET
10	LJ	133	SER
10	LJ	135	ASN
10	LJ	136	VAL
10	LJ	137	LYS
10	LJ	138	ASP
10	LJ	139	GLU
10	LJ	140	LEU
10	LJ	141	ILE
10	LJ	143	ARG
10	LJ	145	ILE
10	LJ	147	ILE
10	LJ	149	ASP
10	LJ	156	ARG
10	LJ	162	LYS
10	LJ	165	ASN
10	LJ	166	LYS
10	LJ	170	LYS
10	LJ	177	VAL
10	LJ	179	SER
10	LJ	182	LEU
10	LJ	184	GLU
11	LK	30	LYS
11	LK	31	ILE
11	LK	32	ARG
11	LK	33	TYR

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Mol	Chain	Res	Type
11	LK	36	LEU
11	LK	38	ASN
11	LK	39	ARG
11	LK	40	ARG
11	LK	44	ASN
11	LK	51	HIS
11	LK	54	SER
11	LK	57	LYS
11	LK	58	GLU
11	LK	61	SER
11	LK	66	GLU
11	LK	69	ARG
11	LK	74	LYS
11	LK	76	ILE
11	LK	79	LYS
11	LK	82	LYS
11	LK	83	ASP
11	LK	87	LEU
11	LK	91	VAL
11	LK	96	VAL
11	LK	125	THR
11	LK	128	ARG
11	LK	129	VAL
11	LK	131	ILE
11	LK	136	LEU
11	LK	138	VAL
11	LK	141	ARG
11	LK	145	LYS
11	LK	146	ASP
11	LK	149	LYS
11	LK	150	ASP
11	LK	152	LEU
11	LK	154	ARG
11	LK	156	LYS
11	LK	162	ARG
11	LK	163	GLN
11	LK	167	GLU
11	LK	169	ARG
11	LK	170	ASN
11	LK	174	THR
11	LK	177	THR
11	LK	178	LYS

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Mol	Chain	Res	Type
11	LK	182	GLU
11	LK	184	LEU
11	LK	187	ARG
11	LK	189	GLU
11	LK	190	LEU
11	LK	191	GLN
11	LK	192	TYR
11	LK	198	HIS
11	LK	199	ARG
11	LK	200	ILE
11	LK	202	ARG
11	LK	203	LYS
11	LK	206	LEU
12	LL	6	GLU
12	LL	10	ARG
12	LL	11	ARG
12	LL	13	ARG
12	LL	16	LYS
12	LL	18	VAL
12	LL	19	LEU
12	LL	22	CYS
12	LL	23	ILE
12	LL	28	ASP
12	LL	30	LEU
12	LL	31	THR
12	LL	35	LYS
12	LL	36	VAL
12	LL	38	GLN
12	LL	40	LEU
12	LL	43	GLN
12	LL	48	SER
12	LL	49	LYS
12	LL	50	SER
12	LL	51	ARG
12	LL	54	ILE
12	LL	55	ARG
12	LL	61	ARG
12	LL	63	GLN
12	LL	65	ILE
12	LL	66	SER
12	LL	67	THR
12	LL	68	HIS

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Mol	Chain	Res	Type
12	LL	71	VAL
12	LL	72	ARG
12	LL	75	LYS
12	LL	79	ILE
12	LL	84	LEU
12	LL	85	ARG
12	LL	88	ASN
12	LL	91	LEU
12	LL	95	CYS
12	LL	98	THR
12	LL	106	ILE
12	LL	110	ILE
12	LL	114	ILE
12	LL	115	LYS
12	LL	119	SER
12	LL	122	ILE
12	LL	125	MET
12	LL	132	SER
12	LL	141	ARG
12	LL	146	GLN
12	LL	147	HIS
12	LL	148	VAL
12	LL	152	HIS
12	LL	154	ILE
12	LL	157	ASP
12	LL	163	VAL
12	LL	164	GLU
12	LL	165	ARG
12	LL	169	VAL
12	LL	170	VAL
13	LM	29	MET
13	LM	33	VAL
13	LM	38	MET
13	LM	42	LYS
13	LM	44	THR
13	LM	46	LYS
13	LM	49	ASN
13	LM	51	ILE
13	LM	62	ILE
13	LM	63	ARG
13	LM	64	ARG
13	LM	66	GLN

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Mol	Chain	Res	Type
13	LM	67	THR
13	LM	69	LEU
13	LM	71	LYS
13	LM	75	ILE
13	LM	80	LEU
13	LM	81	GLN
13	LM	87	VAL
13	LM	88	THR
13	LM	90	CYS
13	LM	96	LEU
13	LM	100	ILE
13	LM	102	ARG
13	LM	110	GLN
13	LM	112	VAL
13	LM	115	SER
13	LM	118	LYS
13	LM	129	ARG
13	LM	130	ARG
13	LM	133	LYS
13	LM	134	SER
13	LM	135	GLU
13	LM	136	GLU
13	LM	145	LEU
13	LM	150	SER
13	LM	151	LYS
13	LM	152	VAL
13	LM	157	LYS
13	LM	160	LYS
13	LM	162	GLU
13	LM	164	ILE
13	LM	173	VAL
13	LM	178	VAL
13	LM	181	LYS
13	LM	185	THR
13	LM	189	ILE
13	LM	191	GLU
13	LM	194	LYS
13	LM	196	VAL
13	LM	199	ASN
13	LM	202	MET
13	LM	205	ARG
13	LM	211	ARG

Continued on next page...

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Mol	Chain	Res	Type
13	LM	216	LEU
13	LM	223	ARG
14	LN	5	ARG
14	LN	8	GLU
14	LN	11	ARG
14	LN	13	VAL
14	LN	15	LEU
14	LN	17	ASP
14	LN	20	ASP
14	LN	21	LYS
14	LN	23	LYS
14	LN	24	LEU
14	LN	27	ILE
14	LN	28	VAL
14	LN	30	ILE
14	LN	32	SER
14	LN	33	THR
14	LN	36	VAL
14	LN	38	ILE
14	LN	42	THR
14	LN	46	LYS
14	LN	50	VAL
14	LN	56	MET
14	LN	61	VAL
14	LN	63	ASN
14	LN	64	ILE
14	LN	66	GLU
14	LN	67	LYS
14	LN	71	GLU
14	LN	72	GLN
14	LN	73	LEU
14	LN	74	LYS
14	LN	75	LYS
14	LN	78	GLU
14	LN	80	SER
14	LN	84	ASP
14	LN	85	THR
14	LN	87	MET
14	LN	88	ASN
14	LN	93	LYS
14	LN	94	LYS
14	LN	98	GLN

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Mol	Chain	Res	Type
14	LN	100	LEU
14	LN	105	THR
14	LN	111	LYS
14	LN	112	ILE
14	LN	114	LYS
14	LN	115	LEU
14	LN	116	ARG
14	LN	120	LYS
14	LN	131	LYS
15	LO	9	GLU
15	LO	13	LYS
15	LO	14	LYS
15	LO	16	SER
15	LO	19	LEU
15	LO	24	ARG
15	LO	26	ARG
15	LO	29	GLU
15	LO	36	ILE
15	LO	37	LYS
15	LO	38	ARG
15	LO	39	CYS
15	LO	40	SER
15	LO	47	LYS
15	LO	56	LYS
15	LO	60	VAL
15	LO	61	VAL
15	LO	64	VAL
15	LO	66	VAL
15	LO	67	ARG
15	LO	75	CYS
15	LO	76	VAL
15	LO	85	ARG
15	LO	89	ILE
15	LO	92	LEU
15	LO	97	SER
15	LO	98	LEU
15	LO	101	LEU
15	LO	104	GLN
15	LO	105	LYS
15	LO	106	VAL
15	LO	109	ARG
15	LO	114	ARG

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Mol	Chain	Res	Type
15	LO	116	LEU
15	LO	117	ASN
15	LO	135	ILE
15	LO	143	ARG
15	LO	144	ASN
15	LO	148	ILE
15	LO	151	ILE
15	LO	155	VAL
15	LO	156	MET
15	LO	157	LYS
15	LO	159	ARG
15	LO	162	ARG
15	LO	176	ASN
15	LO	177	LYS
15	LO	179	ILE
15	LO	183	LYS
15	LO	184	LEU
15	LO	185	ARG
15	LO	187	SER
15	LO	193	LYS
15	LO	197	THR
15	LO	198	ARG
15	LO	199	SER
15	LO	200	LEU
15	LO	202	ARG
15	LO	204	ARG
16	LP	4	ILE
16	LP	8	CYS
16	LP	9	LYS
16	LP	12	ILE
16	LP	30	VAL
16	LP	34	ARG
16	LP	39	ILE
16	LP	48	LYS
16	LP	53	LYS
16	LP	54	LYS
16	LP	58	ARG
16	LP	60	ASN
16	LP	64	LEU
16	LP	84	MET
16	LP	85	ILE
16	LP	90	VAL

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Mol	Chain	Res	Type
16	LP	93	SER
16	LP	100	ARG
16	LP	101	VAL
16	LP	103	ASP
16	LP	105	ILE
16	LP	108	CYS
16	LP	113	LYS
16	LP	115	VAL
16	LP	116	VAL
16	LP	119	SER
16	LP	125	CYS
16	LP	126	LEU
16	LP	127	ARG
16	LP	130	ARG
16	LP	132	ARG
16	LP	135	VAL
16	LP	138	VAL
16	LP	145	GLN
16	LP	150	VAL
16	LP	160	GLU
16	LP	162	ASP
16	LP	163	LYS
16	LP	168	LYS
16	LP	172	ASP
16	LP	192	LEU
16	LP	194	LYS
16	LP	197	TYR
17	LQ	2	VAL
17	LQ	8	SER
17	LQ	11	LEU
17	LQ	12	LEU
17	LQ	15	LYS
17	LQ	21	VAL
17	LQ	22	LYS
17	LQ	24	SER
17	LQ	30	SER
17	LQ	31	THR
17	LQ	36	LYS
17	LQ	40	VAL
17	LQ	41	LYS
17	LQ	47	LEU
17	LQ	50	VAL

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Mol	Chain	Res	Type
17	LQ	54	LYS
17	LQ	57	VAL
17	LQ	71	GLN
17	LQ	77	THR
17	LQ	84	GLU
17	LQ	87	VAL
17	LQ	91	LYS
17	LQ	99	SER
17	LQ	100	ASN
17	LQ	102	LYS
17	LQ	107	LYS
17	LQ	108	GLU
17	LQ	111	GLU
17	LQ	114	VAL
17	LQ	115	ILE
17	LQ	116	SER
17	LQ	118	CYS
17	LQ	119	VAL
17	LQ	121	ARG
17	LQ	125	ARG
17	LQ	126	ARG
17	LQ	127	ARG
17	LQ	129	THR
17	LQ	130	PHE
17	LQ	131	ARG
17	LQ	137	SER
17	LQ	138	LYS
17	LQ	139	TYR
17	LQ	141	SER
17	LQ	144	CYS
17	LQ	147	GLU
17	LQ	153	LYS
18	LR	3	ILE
18	LR	5	LEU
18	LR	7	THR
18	LR	9	ILE
18	LR	11	LYS
18	LR	14	VAL
18	LR	15	GLU
18	LR	16	ARG
18	LR	18	GLU
18	LR	20	LYS

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Mol	Chain	Res	Type
18	LR	25	TYR
18	LR	40	THR
18	LR	42	GLU
18	LR	45	THR
18	LR	46	LYS
18	LR	50	LYS
18	LR	52	LEU
18	LR	56	LYS
18	LR	66	ARG
18	LR	72	HIS
18	LR	73	LYS
18	LR	74	ARG
18	LR	75	GLU
18	LR	76	ASP
18	LR	78	ILE
18	LR	81	VAL
18	LR	84	THR
18	LR	86	THR
18	LR	93	THR
18	LR	96	ARG
18	LR	97	MET
18	LR	99	ILE
18	LR	100	CYS
18	LR	105	SER
18	LR	110	SER
18	LR	114	LYS
18	LR	118	ARG
18	LR	123	ASP
18	LR	124	GLU
18	LR	129	LYS
18	LR	131	THR
18	LR	137	LEU
18	LR	138	LEU
18	LR	147	VAL
18	LR	148	CYS
18	LR	149	LYS
18	LR	162	LYS
18	LR	168	LYS
18	LR	174	ARG
18	LR	179	TRP
19	LS	4	LEU
19	LS	6	LEU

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Mol	Chain	Res	Type
19	LS	8	LYS
19	LS	13	ASP
19	LS	16	LYS
19	LS	19	LYS
19	LS	20	ARG
19	LS	29	GLU
19	LS	30	LYS
19	LS	36	SER
19	LS	37	SER
19	LS	41	ILE
19	LS	45	ILE
19	LS	46	GLU
19	LS	47	SER
19	LS	48	LYS
19	LS	49	ILE
19	LS	52	LYS
19	LS	53	LEU
19	LS	55	ILE
19	LS	56	LYS
19	LS	58	SER
19	LS	60	ARG
19	LS	66	ARG
19	LS	70	LYS
19	LS	71	ARG
19	LS	72	LEU
19	LS	82	ARG
19	LS	84	THR
19	LS	89	MET
19	LS	98	ARG
19	LS	99	GLN
19	LS	104	ARG
19	LS	110	ARG
19	LS	122	THR
19	LS	128	LYS
19	LS	133	LYS
19	LS	135	LYS
19	LS	136	ARG
19	LS	145	MET
19	LS	148	GLU
19	LS	149	GLN
19	LS	153	LYS
19	LS	154	LYS

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Mol	Chain	Res	Type
19	LS	155	LYS
19	LS	156	LYS
19	LS	159	LEU
19	LS	160	GLU
19	LS	163	ARG
19	LS	164	LYS
19	LS	165	LYS
19	LS	169	ARG
19	LS	171	LYS
19	LS	173	ARG
19	LS	176	LYS
19	LS	177	VAL
19	LS	181	ARG
19	LS	182	LEU
19	LS	191	THR
19	LS	192	GLU
20	LT	3	GLN
20	LT	6	ILE
20	LT	12	LEU
20	LT	14	SER
20	LT	15	GLU
20	LT	21	GLU
20	LT	22	VAL
20	LT	24	ARG
20	LT	25	MET
20	LT	26	THR
20	LT	27	ILE
20	LT	32	GLU
20	LT	36	LYS
20	LT	37	SER
20	LT	43	LEU
20	LT	48	LYS
20	LT	49	ILE
20	LT	51	ARG
20	LT	52	THR
20	LT	55	GLU
20	LT	56	ILE
20	LT	63	GLU
20	LT	64	GLU
20	LT	65	ASN
20	LT	67	ASP
20	LT	70	LYS

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Mol	Chain	Res	Type
20	LT	71	ASN
20	LT	76	LEU
20	LT	77	ARG
20	LT	81	ARG
20	LT	82	VAL
20	LT	84	GLN
20	LT	85	HIS
20	LT	87	MET
20	LT	89	ARG
20	LT	90	GLU
20	LT	92	ARG
20	LT	93	GLU
20	LT	95	THR
20	LT	102	LYS
20	LT	103	VAL
20	LT	106	GLU
20	LT	114	ARG
20	LT	122	ASN
20	LT	124	LYS
20	LT	126	VAL
20	LT	128	ASP
20	LT	130	ASP
20	LT	132	ARG
20	LT	135	LYS
20	LT	136	VAL
20	LT	138	MET
20	LT	140	THR
20	LT	144	VAL
20	LT	145	ARG
20	LT	150	CYS
20	LT	156	LYS
20	LT	157	ARG
20	LT	160	ARG
20	LT	163	ARG
20	LT	171	VAL
21	LU	5	GLN
21	LU	14	CYS
21	LU	21	ARG
21	LU	27	LEU
21	LU	28	THR
21	LU	32	ARG
21	LU	33	VAL

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Mol	Chain	Res	Type
21	LU	38	GLN
21	LU	40	VAL
21	LU	41	ASN
21	LU	42	ILE
21	LU	43	LYS
21	LU	44	VAL
21	LU	52	MET
21	LU	63	THR
21	LU	64	ILE
21	LU	66	ASN
21	LU	70	ARG
21	LU	72	LEU
21	LU	76	ILE
21	LU	77	GLN
21	LU	80	VAL
21	LU	84	ILE
21	LU	86	LEU
21	LU	87	LYS
21	LU	91	VAL
21	LU	93	LEU
21	LU	94	GLU
21	LU	96	VAL
21	LU	99	SER
21	LU	100	ASP
21	LU	102	ARG
21	LU	103	LYS
21	LU	107	GLU
21	LU	109	VAL
21	LU	113	ASP
21	LU	116	ARG
21	LU	118	LEU
21	LU	121	GLU
21	LU	126	VAL
21	LU	128	CYS
21	LU	130	LYS
21	LU	132	GLN
21	LU	137	ARG
21	LU	142	VAL
21	LU	146	SER
21	LU	148	ILE
21	LU	151	THR
21	LU	153	LEU

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Mol	Chain	Res	Type
21	LU	154	LYS
22	LV	9	VAL
22	LV	10	LYS
22	LV	11	LYS
22	LV	16	ILE
22	LV	22	CYS
22	LV	29	GLU
22	LV	32	LEU
22	LV	33	ASN
22	LV	34	GLU
22	LV	40	ARG
22	LV	44	LYS
22	LV	47	ASN
22	LV	48	ARG
22	LV	49	LYS
22	LV	50	HIS
22	LV	52	VAL
22	LV	54	GLU
22	LV	55	LYS
22	LV	56	VAL
22	LV	61	GLU
22	LV	64	SER
22	LV	65	LEU
22	LV	66	VAL
22	LV	69	THR
22	LV	70	THR
22	LV	73	GLU
22	LV	76	LYS
22	LV	77	ARG
22	LV	79	VAL
22	LV	84	LYS
22	LV	85	ARG
22	LV	87	LEU
22	LV	90	ASP
22	LV	94	VAL
22	LV	100	THR
22	LV	102	LYS
22	LV	104	THR
22	LV	107	LEU
22	LV	108	LYS
22	LV	111	THR
23	LW	11	ILE

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Mol	Chain	Res	Type
23	LW	16	ARG
23	LW	17	ILE
23	LW	18	SER
23	LW	27	ILE
23	LW	29	CYS
23	LW	36	LYS
23	LW	39	ASN
23	LW	47	LYS
23	LW	55	LYS
23	LW	58	VAL
23	LW	61	MET
23	LW	63	LEU
23	LW	64	ILE
23	LW	65	THR
23	LW	69	ASP
23	LW	73	GLU
23	LW	74	LEU
23	LW	75	ARG
23	LW	77	LYS
23	LW	79	THR
23	LW	98	ILE
23	LW	99	TYR
23	LW	101	GLN
23	LW	107	ILE
23	LW	108	ILE
23	LW	111	LYS
23	LW	115	LYS
23	LW	117	SER
23	LW	123	VAL
23	LW	134	ILE
23	LW	139	GLU
23	LW	140	CYS
23	LW	141	VAL
24	LX	4	ILE
24	LX	7	CYS
24	LX	8	SER
24	LX	14	VAL
24	LX	15	TYR
24	LX	18	LYS
24	LX	20	ILE
24	LX	21	CYS
24	LX	23	VAL

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Mol	Chain	Res	Type
24	LX	26	ASP
24	LX	28	ARG
24	LX	29	VAL
24	LX	31	ARG
24	LX	36	LYS
24	LX	37	CYS
24	LX	38	HIS
24	LX	42	LYS
24	LX	44	LYS
24	LX	49	LYS
24	LX	50	VAL
24	LX	51	ARG
24	LX	54	LYS
24	LX	56	TYR
24	LX	58	LEU
24	LX	59	LEU
24	LX	62	LYS
24	LX	64	MET
25	LY	23	LYS
25	LY	24	LYS
25	LY	25	ILE
25	LY	26	ARG
25	LY	37	LEU
25	LY	40	LYS
25	LY	44	LEU
25	LY	50	ILE
25	LY	51	LYS
25	LY	57	ASP
25	LY	59	CYS
25	LY	66	ILE
25	LY	67	LYS
25	LY	68	THR
25	LY	73	THR
25	LY	81	ILE
25	LY	83	PHE
25	LY	84	ILE
25	LY	96	LYS
25	LY	100	THR
25	LY	106	VAL
25	LY	108	ARG
25	LY	111	THR
25	LY	113	ILE

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Mol	Chain	Res	Type
25	LY	120	LYS
25	LY	123	ILE
25	LY	128	ASP
25	LY	132	MET
25	LY	138	MET
26	LZ	1	MET
26	LZ	2	LYS
26	LZ	5	SER
26	LZ	7	VAL
26	LZ	8	THR
26	LZ	12	ARG
26	LZ	20	THR
26	LZ	28	LYS
26	LZ	34	LEU
26	LZ	36	LYS
26	LZ	37	GLU
26	LZ	43	LYS
26	LZ	46	THR
26	LZ	47	MET
26	LZ	49	ILE
26	LZ	50	ARG
26	LZ	51	ARG
26	LZ	54	ILE
26	LZ	55	VAL
26	LZ	59	THR
26	LZ	65	THR
26	LZ	67	LYS
26	LZ	69	VAL
26	LZ	72	ARG
26	LZ	73	ARG
26	LZ	74	ARG
26	LZ	78	ILE
26	LZ	81	GLU
26	LZ	85	GLN
26	LZ	88	ARG
26	LZ	91	GLU
26	LZ	93	LYS
26	LZ	102	SER
26	LZ	105	ILE
26	LZ	106	ILE
26	LZ	107	LYS
26	LZ	111	MET

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Mol	Chain	Res	Type
26	LZ	114	SER
26	LZ	120	LYS
26	LZ	121	ARG
26	LZ	122	ARG
26	LZ	129	ARG
26	LZ	133	ILE
27	La	5	ILE
27	La	7	LYS
27	La	12	CYS
27	La	13	ILE
27	La	16	GLN
27	La	23	LYS
27	La	27	VAL
27	La	28	GLU
27	La	33	ASN
27	La	34	GLU
27	La	35	ARG
27	La	37	SER
27	La	40	ILE
27	La	41	VAL
27	La	44	ILE
27	La	47	LEU
27	La	49	ARG
27	La	50	ARG
27	La	51	ILE
27	La	55	MET
27	La	56	SER
27	La	58	GLU
27	La	65	ARG
27	La	66	VAL
27	La	67	ARG
27	La	71	LYS
27	La	72	CYS
27	La	73	MET
27	La	75	VAL
27	La	81	THR
27	La	82	SER
27	La	84	ARG
27	La	88	ASN
27	La	90	LYS
27	La	91	ASP
27	La	94	SER

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Mol	Chain	Res	Type
27	La	95	THR
27	La	98	VAL
27	La	101	VAL
27	La	103	LYS
27	La	107	ILE
27	La	108	ILE
27	La	110	THR
27	La	113	LYS
27	La	116	GLN
27	La	117	ARG
27	La	118	ARG
27	La	119	ILE
27	La	125	THR
28	Lb	2	PRO
28	Lb	4	ARG
28	Lb	5	ILE
28	Lb	10	LYS
28	Lb	11	ARG
28	Lb	12	ARG
28	Lb	22	VAL
28	Lb	26	ARG
28	Lb	34	LYS
28	Lb	43	THR
28	Lb	56	LEU
28	Lb	58	MET
28	Lb	63	VAL
28	Lb	64	ARG
28	Lb	70	ASN
28	Lb	73	ILE
28	Lb	75	ILE
28	Lb	78	ILE
28	Lb	80	SER
28	Lb	85	GLU
28	Lb	86	GLN
28	Lb	87	ARG
28	Lb	93	ARG
28	Lb	94	LYS
28	Lb	96	THR
28	Lb	102	VAL
28	Lb	106	ARG
28	Lb	115	ARG
28	Lb	126	LYS

Continued on next page...

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Mol	Chain	Res	Type
28	Lb	131	SER
28	Lb	139	ARG
28	Lb	141	VAL
28	Lb	148	VAL
29	Lc	8	THR
29	Lc	10	LYS
29	Lc	12	GLN
29	Lc	14	ARG
29	Lc	23	LYS
29	Lc	25	LYS
29	Lc	30	THR
29	Lc	42	ASN
29	Lc	46	SER
29	Lc	53	GLN
29	Lc	55	LEU
29	Lc	56	ARG
30	Ld	8	LYS
30	Ld	9	LYS
30	Ld	16	LEU
30	Ld	18	LEU
30	Ld	20	LEU
30	Ld	23	LYS
30	Ld	24	SER
30	Ld	26	LYS
30	Ld	28	THR
30	Ld	29	LEU
30	Ld	35	ILE
30	Ld	45	LEU
30	Ld	47	PHE
30	Ld	48	MET
30	Ld	52	CYS
30	Ld	55	LEU
30	Ld	57	LYS
30	Ld	58	SER
30	Ld	59	GLN
30	Ld	64	CYS
30	Ld	65	HIS
30	Ld	71	VAL
30	Ld	72	ARG
30	Ld	73	VAL
30	Ld	80	GLU
30	Ld	83	ILE

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Mol	Chain	Res	Type
30	Ld	88	GLN
30	Ld	92	SER
30	Ld	93	ILE
30	Ld	94	MET
30	Ld	95	THR
30	Ld	96	ILE
30	Ld	98	GLU
30	Ld	104	LEU
30	Ld	105	THR
30	Ld	107	ILE
30	Ld	108	LEU
31	Le	3	ILE
31	Le	8	THR
31	Le	9	ILE
31	Le	10	ARG
31	Le	13	LYS
31	Le	18	LYS
31	Le	20	SER
31	Le	22	LYS
31	Le	29	ARG
31	Le	36	GLU
31	Le	38	LEU
31	Le	40	LYS
31	Le	42	GLU
31	Le	46	LEU
31	Le	51	ASN
31	Le	64	ARG
31	Le	65	ARG
31	Le	69	GLU
31	Le	70	VAL
31	Le	72	LEU
31	Le	75	ASP
31	Le	77	GLU
31	Le	78	HIS
31	Le	83	VAL
31	Le	84	ILE
31	Le	86	LYS
31	Le	88	VAL
31	Le	92	LYS
31	Le	96	THR
31	Le	97	GLU
31	Le	98	LYS

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Mol	Chain	Res	Type
31	Le	102	GLU
32	Lf	9	LEU
32	Lf	12	LYS
32	Lf	13	ILE
32	Lf	15	ILE
32	Lf	16	LYS
32	Lf	17	LYS
32	Lf	19	LYS
32	Lf	20	ASN
32	Lf	23	ILE
32	Lf	27	SER
32	Lf	31	VAL
32	Lf	34	LYS
32	Lf	36	SER
32	Lf	38	ARG
32	Lf	43	ILE
32	Lf	47	MET
32	Lf	57	MET
32	Lf	59	SER
32	Lf	67	GLU
32	Lf	79	HIS
32	Lf	81	ILE
32	Lf	83	THR
32	Lf	86	GLU
32	Lf	87	LEU
32	Lf	88	LYS
32	Lf	89	THR
32	Lf	90	LEU
32	Lf	91	PHE
32	Lf	92	MET
32	Lf	94	ASN
32	Lf	95	LYS
32	Lf	97	HIS
32	Lf	101	ILE
32	Lf	113	ILE
32	Lf	115	GLU
32	Lf	116	GLU
32	Lf	118	LYS
32	Lf	119	LYS
32	Lf	120	MET
32	Lf	122	VAL
32	Lf	123	ARG

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Mol	Chain	Res	Type
32	Lf	128	ASP
32	Lf	131	LEU
32	Lf	134	GLU
32	Lf	135	GLU
33	Lg	5	LYS
33	Lg	7	LYS
33	Lg	9	PHE
33	Lg	15	VAL
33	Lg	18	GLN
33	Lg	25	ARG
33	Lg	28	VAL
33	Lg	32	LYS
33	Lg	33	VAL
33	Lg	34	SER
33	Lg	38	THR
33	Lg	44	LYS
33	Lg	46	LEU
33	Lg	49	LEU
33	Lg	53	ILE
33	Lg	64	LYS
33	Lg	67	ARG
33	Lg	74	MET
33	Lg	75	VAL
33	Lg	81	THR
33	Lg	83	LEU
33	Lg	88	MET
33	Lg	91	LYS
33	Lg	92	VAL
33	Lg	93	ARG
33	Lg	94	VAL
34	Lh	6	VAL
34	Lh	12	SER
34	Lh	13	THR
34	Lh	16	THR
34	Lh	17	ARG
34	Lh	18	SER
34	Lh	19	LYS
34	Lh	21	VAL
34	Lh	22	ARG
34	Lh	24	LYS
34	Lh	30	ARG
34	Lh	31	LEU

Continued on next page...

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Mol	Chain	Res	Type
34	Lh	33	SER
34	Lh	35	ARG
34	Lh	58	VAL
34	Lh	59	ILE
34	Lh	64	THR
34	Lh	65	ARG
34	Lh	69	LYS
34	Lh	70	VAL
34	Lh	71	SER
34	Lh	77	LYS
34	Lh	79	CYS
34	Lh	81	SER
34	Lh	84	ARG
34	Lh	88	LEU
34	Lh	94	GLU
35	Li	32	LEU
35	Li	35	LYS
35	Li	38	VAL
35	Li	40	LEU
35	Li	41	SER
35	Li	43	GLU
35	Li	46	GLN
35	Li	47	ARG
35	Li	48	LYS
35	Li	54	ARG
35	Li	55	GLU
35	Li	56	LEU
35	Li	57	LEU
35	Li	62	MET
35	Li	63	LYS
35	Li	71	GLU
35	Li	73	ILE
35	Li	75	ARG
35	Li	87	LEU
35	Li	92	GLN
35	Li	103	GLU
35	Li	108	ILE
35	Li	109	PRO
35	Li	115	ARG
35	Li	116	LEU
35	Li	123	GLN
35	Li	124	LEU

Continued on next page...

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Mol	Chain	Res	Type
35	Li	126	GLU
35	Li	127	LYS
35	Li	129	LYS
35	Li	130	ARG
35	Li	131	LEU
35	Li	132	LEU
35	Li	135	LYS
35	Li	136	LEU
35	Li	138	LYS
35	Li	141	LEU
35	Li	142	GLN
35	Li	145	LYS
35	Li	150	VAL
36	Lj	2	PRO
36	Lj	4	LYS
36	Lj	5	VAL
36	Lj	8	LEU
36	Lj	9	LYS
36	Lj	15	VAL
36	Lj	17	ILE
36	Lj	18	VAL
36	Lj	19	ARG
36	Lj	20	LYS
36	Lj	21	LYS
36	Lj	22	GLU
36	Lj	23	GLU
36	Lj	25	LYS
36	Lj	26	THR
36	Lj	27	LYS
36	Lj	30	GLN
36	Lj	31	GLU
36	Lj	36	ILE
36	Lj	39	GLU
36	Lj	41	THR
36	Lj	51	ILE
36	Lj	55	ARG
36	Lj	58	LYS
36	Lj	59	ASP
36	Lj	60	ARG
36	Lj	68	LYS
36	Lj	70	LEU
36	Lj	74	LYS

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Mol	Chain	Res	Type
36	Lj	80	ARG
36	Lj	84	SER
36	Lj	88	ARG
36	Lj	90	ILE
37	Lk	3	LYS
37	Lk	5	THR
37	Lk	10	LYS
37	Lk	13	THR
37	Lk	24	LYS
37	Lk	36	SER
37	Lk	37	CYS
37	Lk	43	LYS
37	Lk	44	MET
37	Lk	45	ARG
37	Lk	46	ARG
37	Lk	51	TYR
37	Lk	53	SER
37	Lk	54	LEU
37	Lk	55	ARG
37	Lk	58	THR
37	Lk	59	GLN
37	Lk	64	MET
37	Lk	65	SER
37	Lk	68	ARG
37	Lk	69	LYS
37	Lk	72	ARG
37	Lk	78	THR
37	Lk	80	LYS
37	Lk	82	ASN
37	Lk	84	ARG
37	Lk	85	LYS
37	Lk	87	LEU
37	Lk	89	LYS
38	Ll	4	THR
38	Ll	9	ASN
38	Ll	10	LEU
38	Ll	11	MET
38	Ll	14	ILE
38	Ll	18	ARG
38	Ll	20	LYS
38	Ll	21	LYS
38	Ll	22	LEU

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Mol	Chain	Res	Type
38	Ll	26	SER
38	Ll	27	CYS
38	Ll	29	LYS
38	Ll	33	GLN
38	Ll	37	LYS
38	Ll	40	LEU
38	Ll	41	ARG
38	Ll	44	LYS
38	Ll	46	LEU
38	Ll	50	THR
38	Ll	51	VAL
38	Ll	53	ASN
38	Ll	55	ASP
38	Ll	56	ASP
38	Ll	58	LYS
38	Ll	59	SER
38	Ll	60	ILE
38	Ll	62	LYS
38	Ll	65	LYS
38	Ll	66	ASP
38	Ll	68	VAL
38	Ll	70	VAL
39	Ln	5	ASN
39	Ln	9	LEU
39	Ln	10	ASN
39	Ln	11	LYS
39	Ln	13	ILE
39	Ln	15	GLU
39	Ln	17	ILE
39	Ln	18	GLU
39	Ln	19	ARG
39	Ln	21	THR
39	Ln	23	GLU
39	Ln	24	LYS
39	Ln	26	ARG
39	Ln	27	LYS
39	Ln	29	LEU
39	Ln	30	GLU
39	Ln	32	VAL
39	Ln	34	LEU
39	Ln	35	GLN
39	Ln	38	LEU

Continued on next page...

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Mol	Chain	Res	Type
39	Ln	39	LYS
39	Ln	41	TYR
39	Ln	42	ASP
39	Ln	44	LYS
39	Ln	45	LYS
39	Ln	51	LEU
39	Ln	53	LEU
39	Ln	54	VAL
39	Ln	55	LEU
39	Ln	63	LEU
39	Ln	64	LYS
39	Ln	66	CYS
39	Ln	68	ILE
39	Ln	70	ASP
39	Ln	72	ARG
39	Ln	76	ARG
39	Ln	78	LYS
39	Ln	79	LYS
39	Ln	82	LEU
39	Ln	84	TYR
39	Ln	88	GLU
39	Ln	89	HIS
39	Ln	91	GLN
39	Ln	95	LYS
39	Ln	98	LYS
39	Ln	99	GLN
39	Ln	100	ILE
39	Ln	101	LYS
39	Ln	102	LYS
39	Ln	103	PHE
39	Ln	105	LYS
39	Ln	107	TYR
39	Ln	111	LEU
39	Ln	114	LYS
39	Ln	115	SER
39	Ln	116	LEU
39	Ln	117	ILE
39	Ln	118	ARG
39	Ln	119	GLN
39	Ln	122	VAL
39	Ln	123	TYR
39	Ln	129	THR

Continued on next page...

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Mol	Chain	Res	Type
39	Ln	130	LYS
39	Ln	133	ARG
39	Ln	136	LEU
39	Ln	138	LEU
39	Ln	141	ASP
39	Ln	144	LEU
39	Ln	147	LYS
39	Ln	148	VAL
39	Ln	149	LEU
39	Ln	151	CYS
39	Ln	152	LYS
39	Ln	157	VAL
39	Ln	160	LYS
39	Ln	161	LYS
39	Ln	165	LEU
39	Ln	166	ASN
39	Ln	167	TRP
39	Ln	169	ILE
39	Ln	174	MET
39	Ln	178	GLU
39	Ln	179	ILE
39	Ln	183	ILE
39	Ln	185	THR
39	Ln	187	LEU
39	Ln	189	PHE
39	Ln	192	THR
39	Ln	193	GLN
39	Ln	194	LEU
39	Ln	195	LYS
39	Ln	196	LYS
39	Ln	201	ILE
39	Ln	203	THR
39	Ln	204	VAL
39	Ln	207	LYS
39	Ln	209	THR
39	Ln	210	MET
39	Ln	213	SER
39	Ln	215	ARG
40	Lo	10	MET
40	Lo	12	LYS
40	Lo	15	ARG
40	Lo	16	LYS

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Mol	Chain	Res	Type
40	Lo	18	ARG
40	Lo	20	MET
40	Lo	21	LYS
40	Lo	24	SER
40	Lo	25	LYS
41	Lp	2	VAL
41	Lp	3	THR
41	Lp	7	GLU
41	Lp	10	THR
41	Lp	12	CYS
41	Lp	14	ARG
41	Lp	15	GLU
41	Lp	17	LYS
41	Lp	18	HIS
41	Lp	19	THR
41	Lp	20	VAL
41	Lp	22	LYS
41	Lp	25	LEU
41	Lp	27	LYS
41	Lp	28	LYS
41	Lp	30	LYS
41	Lp	33	LEU
41	Lp	34	LEU
41	Lp	36	GLN
41	Lp	39	ARG
41	Lp	44	LYS
41	Lp	53	LYS
41	Lp	55	ILE
41	Lp	58	ARG
41	Lp	59	LYS
41	Lp	61	LYS
41	Lp	63	THR
41	Lp	64	LYS
41	Lp	66	GLN
41	Lp	67	VAL
41	Lp	71	THR
41	Lp	72	CYS
41	Lp	73	SER
41	Lp	76	LYS
41	Lp	82	VAL
41	Lp	83	LEU
41	Lp	85	ARG

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Mol	Chain	Res	Type
41	Lp	86	CYS
41	Lp	88	ARG
41	Lp	91	ILE
41	Lp	93	ARG
42	Lq	1	MET
42	Lq	3	LYS
42	Lq	7	LYS
42	Lq	8	VAL
42	Lq	10	LEU
42	Lq	11	THR
42	Lq	13	LYS
42	Lq	16	THR
42	Lq	17	ARG
42	Lq	24	LYS
42	Lq	27	LEU
42	Lq	28	LYS
42	Lq	29	ILE
42	Lq	32	SER
42	Lq	33	GLN
42	Lq	36	LYS
42	Lq	41	PHE
42	Lq	44	LYS
42	Lq	50	THR
42	Lq	52	CYS
42	Lq	62	LYS
42	Lq	64	MET
42	Lq	70	SER
42	Lq	71	LEU
42	Lq	74	GLU
42	Lq	80	ARG
42	Lq	83	ILE
42	Lq	84	ARG
42	Lq	85	ARG
42	Lq	91	GLU
43	Ls	78	MET
43	Ls	81	THR
43	Ls	91	GLN
43	Ls	93	MET
43	Ls	94	MET
43	Ls	96	CYS
43	Ls	105	LEU
43	Ls	106	ARG

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Mol	Chain	Res	Type
43	Ls	108	THR
43	Ls	110	CYS
43	Ls	111	ARG
43	Ls	114	ARG
43	Ls	118	LEU
43	Ls	119	ARG
43	Ls	120	LYS
43	Ls	122	LYS
43	Ls	123	LEU
43	Ls	124	SER
45	SA	15	LEU
45	SA	21	LYS
45	SA	22	LYS
45	SA	24	LEU
45	SA	25	VAL
45	SA	28	THR
45	SA	30	LEU
45	SA	32	VAL
45	SA	33	ARG
45	SA	35	ILE
45	SA	38	ARG
45	SA	43	ILE
45	SA	46	ARG
45	SA	47	GLN
45	SA	48	LYS
45	SA	51	THR
45	SA	53	VAL
45	SA	56	LEU
45	SA	62	LYS
45	SA	63	ILE
45	SA	71	VAL
45	SA	73	ILE
45	SA	82	VAL
45	SA	85	ARG
45	SA	87	ASP
45	SA	89	GLN
45	SA	93	LEU
45	SA	94	LYS
45	SA	99	THR
45	SA	102	THR
45	SA	109	ILE
45	SA	116	ARG

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Mol	Chain	Res	Type
45	SA	118	ASN
45	SA	123	GLU
45	SA	128	LEU
45	SA	129	VAL
45	SA	131	ASP
45	SA	133	VAL
45	SA	136	ARG
45	SA	139	ILE
45	SA	145	VAL
45	SA	149	THR
45	SA	150	ILE
45	SA	151	SER
45	SA	154	ASN
45	SA	158	ASN
45	SA	159	LEU
45	SA	164	VAL
45	SA	168	CYS
45	SA	171	LYS
45	SA	174	MET
45	SA	176	ILE
45	SA	178	LEU
45	SA	182	LEU
45	SA	185	ARG
45	SA	186	GLU
45	SA	189	ARG
45	SA	190	LEU
45	SA	191	LYS
45	SA	194	ILE
45	SA	195	SER
45	SA	196	ARG
45	SA	199	GLU
45	SA	203	LYS
45	SA	205	ASP
45	SA	206	LEU
45	SA	210	LEU
46	SB	26	GLU
46	SB	30	SER
46	SB	31	THR
46	SB	32	LYS
46	SB	37	VAL
46	SB	41	LYS
46	SB	42	ILE

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Mol	Chain	Res	Type
46	SB	43	GLU
46	SB	44	SER
46	SB	45	LEU
46	SB	47	ASP
46	SB	48	ILE
46	SB	52	SER
46	SB	53	LEU
46	SB	55	ILE
46	SB	56	LYS
46	SB	59	GLU
46	SB	69	GLU
46	SB	70	LEU
46	SB	72	GLU
46	SB	74	VAL
46	SB	75	CYS
46	SB	77	ILE
46	SB	79	SER
46	SB	83	GLN
46	SB	97	ILE
46	SB	98	VAL
46	SB	102	ASP
46	SB	113	LYS
46	SB	115	VAL
46	SB	119	ILE
46	SB	120	LYS
46	SB	124	LYS
46	SB	127	ARG
46	SB	130	ILE
46	SB	134	ARG
46	SB	135	ARG
46	SB	141	LYS
46	SB	142	LEU
46	SB	144	ASP
46	SB	149	SER
46	SB	151	LYS
46	SB	153	SER
46	SB	155	LYS
46	SB	159	VAL
46	SB	160	ARG
46	SB	162	ARG
46	SB	163	LEU
46	SB	168	ARG

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Mol	Chain	Res	Type
46	SB	173	VAL
46	SB	175	SER
46	SB	177	THR
46	SB	178	VAL
46	SB	180	LYS
46	SB	182	LEU
46	SB	183	GLU
46	SB	188	SER
46	SB	189	ASP
46	SB	193	ARG
46	SB	195	SER
46	SB	202	MET
46	SB	204	SER
46	SB	213	LYS
46	SB	217	SER
46	SB	219	LEU
46	SB	222	ASP
46	SB	225	LYS
46	SB	226	LYS
46	SB	229	LEU
46	SB	230	ASP
46	SB	231	HIS
46	SB	232	VAL
46	SB	233	GLN
46	SB	235	ILE
46	SB	240	LEU
47	SC	6	ARG
47	SC	7	ARG
47	SC	10	GLU
47	SC	14	TYR
47	SC	16	LYS
47	SC	24	GLU
47	SC	27	LEU
47	SC	36	VAL
47	SC	37	ASP
47	SC	44	SER
47	SC	45	LEU
47	SC	48	THR
47	SC	49	ILE
47	SC	52	ILE
47	SC	53	CYS
47	SC	55	ILE

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Mol	Chain	Res	Type
47	SC	56	ILE
47	SC	57	GLN
47	SC	63	VAL
47	SC	64	VAL
47	SC	65	MET
47	SC	67	ASP
47	SC	70	TYR
47	SC	72	LEU
47	SC	78	LEU
47	SC	82	ARG
47	SC	84	MET
47	SC	91	ASN
47	SC	92	ILE
47	SC	94	VAL
47	SC	95	ASP
47	SC	98	ILE
47	SC	99	LYS
47	SC	102	LEU
47	SC	108	VAL
47	SC	114	LYS
47	SC	115	LEU
47	SC	116	GLU
47	SC	119	MET
47	SC	121	ILE
47	SC	123	ARG
47	SC	127	SER
47	SC	129	ILE
47	SC	131	THR
47	SC	133	MET
47	SC	143	ILE
47	SC	144	VAL
47	SC	151	GLN
47	SC	154	ARG
47	SC	159	LYS
47	SC	160	GLU
47	SC	162	CYS
47	SC	163	LEU
47	SC	165	SER
47	SC	172	ILE
47	SC	181	ILE
47	SC	182	LYS
47	SC	183	MET

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Mol	Chain	Res	Type
47	SC	184	ARG
47	SC	187	VAL
47	SC	188	ILE
47	SC	190	VAL
47	SC	191	LYS
47	SC	193	ARG
47	SC	194	ILE
47	SC	198	ASN
47	SC	199	ILE
47	SC	200	ARG
47	SC	203	VAL
47	SC	207	LYS
47	SC	209	GLU
47	SC	210	ILE
48	SD	11	LYS
48	SD	12	LYS
48	SD	13	ILE
48	SD	14	THR
48	SD	16	ARG
48	SD	17	LYS
48	SD	23	LEU
48	SD	24	LYS
48	SD	25	LYS
48	SD	31	ILE
48	SD	37	LYS
48	SD	39	ARG
48	SD	43	GLN
48	SD	44	THR
48	SD	48	LYS
48	SD	49	THR
48	SD	52	LEU
48	SD	56	THR
48	SD	59	ILE
48	SD	63	VAL
48	SD	66	VAL
48	SD	72	ASN
48	SD	78	LEU
48	SD	81	ASN
48	SD	82	THR
48	SD	83	LYS
48	SD	91	VAL
48	SD	92	SER

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Mol	Chain	Res	Type
48	SD	95	LYS
48	SD	101	HIS
48	SD	103	MET
48	SD	108	HIS
48	SD	113	LEU
48	SD	115	ARG
48	SD	120	CYS
48	SD	123	VAL
48	SD	126	ASP
48	SD	130	THR
48	SD	135	LEU
48	SD	139	VAL
48	SD	151	ARG
48	SD	152	LYS
48	SD	154	CYS
48	SD	156	VAL
48	SD	159	ARG
48	SD	163	MET
48	SD	164	MET
48	SD	171	THR
48	SD	172	LEU
48	SD	175	GLU
48	SD	179	VAL
48	SD	181	ILE
48	SD	184	LEU
48	SD	186	THR
48	SD	187	LYS
48	SD	192	GLU
48	SD	197	LEU
48	SD	198	THR
48	SD	199	GLU
48	SD	201	LEU
48	SD	206	MET
48	SD	210	VAL
48	SD	211	MET
48	SD	213	ARG
48	SD	214	ARG
48	SD	216	LYS
48	SD	219	LYS
48	SD	220	ARG
48	SD	224	THR
48	SD	225	MET

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Mol	Chain	Res	Type
48	SD	226	GLU
48	SD	227	LEU
48	SD	229	SER
48	SD	232	HIS
48	SD	233	ASP
48	SD	237	VAL
48	SD	238	ARG
48	SD	239	ASN
49	SE	3	ARG
49	SE	6	ARG
49	SE	7	LYS
49	SE	16	LYS
49	SE	21	ASP
49	SE	26	ILE
49	SE	38	LEU
49	SE	40	GLU
49	SE	45	ILE
49	SE	46	LEU
49	SE	47	ILE
49	SE	48	LEU
49	SE	49	ARG
49	SE	53	HIS
49	SE	60	GLU
49	SE	61	THR
49	SE	62	SER
49	SE	63	MET
49	SE	70	VAL
49	SE	71	LEU
49	SE	75	LYS
49	SE	84	VAL
49	SE	86	PHE
49	SE	91	GLU
49	SE	92	ILE
49	SE	95	VAL
49	SE	99	PHE
49	SE	102	LEU
49	SE	104	ASP
49	SE	105	VAL
49	SE	108	ARG
49	SE	114	ILE
49	SE	122	LYS
49	SE	126	VAL

Continued on next page...

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Mol	Chain	Res	Type
49	SE	128	LYS
49	SE	134	LYS
49	SE	136	MET
49	SE	139	LEU
49	SE	143	ASP
49	SE	146	THR
49	SE	147	ILE
49	SE	156	THR
49	SE	160	ILE
49	SE	161	LYS
49	SE	162	ILE
49	SE	165	LYS
49	SE	166	THR
49	SE	168	LYS
49	SE	169	ILE
49	SE	170	ASP
49	SE	171	GLU
49	SE	173	TYR
49	SE	174	LYS
49	SE	176	ASP
49	SE	177	ILE
49	SE	179	LYS
49	SE	184	THR
49	SE	191	ARG
49	SE	198	ILE
49	SE	199	ASP
49	SE	200	LYS
49	SE	206	THR
49	SE	207	MET
49	SE	208	ILE
49	SE	213	THR
49	SE	217	GLU
49	SE	218	PHE
49	SE	219	LEU
49	SE	220	THR
49	SE	221	ARG
49	SE	222	LEU
49	SE	223	CYS
49	SE	224	ASN
49	SE	227	VAL
49	SE	228	ILE
49	SE	230	ASN

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Mol	Chain	Res	Type
49	SE	235	VAL
49	SE	237	ILE
49	SE	241	LYS
49	SE	243	ILE
49	SE	244	ARG
49	SE	246	ASP
49	SE	248	ILE
49	SE	249	LYS
49	SE	254	ARG
49	SE	260	LYS
49	SE	261	ARG
50	SF	7	LEU
50	SF	10	LYS
50	SF	15	ASP
50	SF	22	SER
50	SF	23	LEU
50	SF	27	ILE
50	SF	28	SER
50	SF	29	ILE
50	SF	31	ASN
50	SF	32	HIS
50	SF	34	PHE
50	SF	38	SER
50	SF	41	ARG
50	SF	43	SER
50	SF	45	LYS
50	SF	49	LYS
50	SF	51	LYS
50	SF	52	CYS
50	SF	57	ARG
50	SF	61	SER
50	SF	63	MET
50	SF	68	ASN
50	SF	69	SER
50	SF	71	LYS
50	SF	72	LYS
50	SF	73	LEU
50	SF	74	MET
50	SF	76	MET
50	SF	77	LYS
50	SF	79	VAL
50	SF	83	PHE

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Mol	Chain	Res	Type
50	SF	88	LEU
50	SF	92	LYS
50	SF	95	VAL
50	SF	98	LEU
50	SF	100	ASP
50	SF	109	GLU
50	SF	110	ASP
50	SF	113	ARG
50	SF	114	ILE
50	SF	116	LYS
50	SF	122	ARG
50	SF	124	SER
50	SF	127	VAL
50	SF	131	ARG
50	SF	132	ARG
50	SF	137	ILE
50	SF	146	LYS
50	SF	150	ARG
50	SF	151	LYS
50	SF	153	ARG
50	SF	164	MET
50	SF	171	ASP
50	SF	172	LYS
50	SF	173	SER
50	SF	177	SER
50	SF	178	GLN
50	SF	179	ARG
50	SF	189	ASN
51	SG	11	ILE
51	SG	15	VAL
51	SG	16	THR
51	SG	19	ASN
51	SG	22	LEU
51	SG	23	MET
51	SG	24	ILE
51	SG	26	ASP
51	SG	27	PHE
51	SG	29	LYS
51	SG	31	GLN
51	SG	32	THR
51	SG	33	ILE
51	SG	34	HIS

Continued on next page...

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Mol	Chain	Res	Type
51	SG	36	LEU
51	SG	37	ARG
51	SG	38	MET
51	SG	41	GLU
51	SG	47	LEU
51	SG	49	GLU
51	SG	50	GLU
51	SG	55	THR
51	SG	59	THR
51	SG	70	TYR
51	SG	71	GLN
51	SG	73	VAL
51	SG	75	LYS
51	SG	76	SER
51	SG	78	ARG
51	SG	81	LEU
51	SG	82	LEU
51	SG	83	LEU
51	SG	85	GLN
51	SG	88	LYS
51	SG	91	LEU
51	SG	92	HIS
51	SG	93	ARG
51	SG	94	ARG
51	SG	98	ARG
51	SG	101	LYS
51	SG	103	ILE
51	SG	112	LEU
51	SG	117	VAL
51	SG	118	VAL
51	SG	119	LEU
51	SG	120	VAL
51	SG	125	LYS
51	SG	126	THR
51	SG	127	LEU
51	SG	132	ASP
51	SG	134	VAL
51	SG	135	VAL
51	SG	137	LYS
51	SG	140	VAL
51	SG	142	LYS
51	SG	143	ARG

Continued on next page...

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Mol	Chain	Res	Type
51	SG	147	ILE
51	SG	148	ARG
51	SG	150	LEU
51	SG	160	PRO
51	SG	161	LYS
51	SG	162	ASP
51	SG	163	GLN
51	SG	168	GLU
51	SG	169	LEU
51	SG	170	ILE
51	SG	183	GLU
51	SG	184	LYS
51	SG	185	LYS
51	SG	186	LEU
51	SG	188	TYR
51	SG	190	LYS
51	SG	191	VAL
51	SG	194	VAL
51	SG	195	VAL
51	SG	196	THR
51	SG	198	GLU
51	SG	204	GLN
51	SG	205	ARG
51	SG	206	VAL
51	SG	210	LYS
51	SG	211	LYS
51	SG	213	ILE
51	SG	216	LYS
51	SG	218	LEU
51	SG	221	LEU
51	SG	222	GLU
51	SG	223	GLU
51	SG	227	LEU
51	SG	228	LEU
51	SG	230	ARG
51	SG	231	MET
52	SH	7	ARG
52	SH	8	LYS
52	SH	9	ILE
52	SH	10	ARG
52	SH	11	LYS
52	SH	14	GLU

Continued on next page...

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Mol	Chain	Res	Type
52	SH	15	LYS
52	SH	17	SER
52	SH	18	GLU
52	SH	21	LYS
52	SH	27	LEU
52	SH	28	LEU
52	SH	29	LYS
52	SH	30	LEU
52	SH	35	ASP
52	SH	36	LEU
52	SH	37	ARG
52	SH	38	GLU
52	SH	39	MET
52	SH	41	LEU
52	SH	45	TYR
52	SH	46	ILE
52	SH	47	SER
52	SH	48	SER
52	SH	49	VAL
52	SH	50	LYS
52	SH	51	GLU
52	SH	58	LYS
52	SH	59	LYS
52	SH	62	VAL
52	SH	63	VAL
52	SH	69	MET
52	SH	70	LEU
52	SH	71	GLN
52	SH	76	ASN
52	SH	77	SER
52	SH	80	LEU
52	SH	82	LEU
52	SH	83	LYS
52	SH	84	LEU
52	SH	86	LYS
52	SH	89	SER
52	SH	92	ARG
52	SH	94	ILE
52	SH	95	ILE
52	SH	96	VAL
52	SH	101	ILE
52	SH	104	ASN

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Mol	Chain	Res	Type
52	SH	107	VAL
52	SH	109	THR
52	SH	111	LYS
52	SH	112	LYS
52	SH	115	ARG
52	SH	116	ARG
52	SH	118	ARG
52	SH	119	SER
52	SH	121	THR
52	SH	122	MET
52	SH	123	THR
52	SH	130	LEU
52	SH	133	ILE
52	SH	134	CYS
52	SH	137	ILE
52	SH	138	HIS
52	SH	143	ARG
52	SH	144	THR
52	SH	150	SER
52	SH	151	ASN
52	SH	153	ARG
52	SH	154	LEU
52	SH	158	LEU
52	SH	160	LYS
52	SH	165	GLU
52	SH	167	SER
52	SH	168	GLU
52	SH	170	THR
52	SH	171	LYS
52	SH	180	LEU
52	SH	183	ARG
52	SH	184	ASP
52	SH	185	THR
52	SH	186	GLU
52	SH	188	ILE
53	SI	3	ILE
53	SI	4	THR
53	SI	6	ASP
53	SI	7	LYS
53	SI	8	MET
53	SI	10	LYS
53	SI	13	LYS

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Mol	Chain	Res	Type
53	SI	20	LYS
53	SI	24	LYS
53	SI	26	LYS
53	SI	28	ASN
53	SI	29	LEU
53	SI	38	LEU
53	SI	39	ILE
53	SI	40	VAL
53	SI	41	LYS
53	SI	42	VAL
53	SI	43	THR
53	SI	44	SER
53	SI	45	LYS
53	SI	46	LYS
53	SI	50	GLN
53	SI	51	LYS
53	SI	53	SER
53	SI	54	THR
53	SI	55	ILE
53	SI	58	ARG
53	SI	61	ASN
53	SI	62	ILE
53	SI	63	LYS
53	SI	69	LEU
53	SI	70	SER
53	SI	71	HIS
53	SI	78	SER
53	SI	84	LYS
53	SI	86	ARG
53	SI	91	VAL
53	SI	94	SER
53	SI	97	ASN
53	SI	99	LEU
53	SI	102	THR
53	SI	104	THR
53	SI	106	VAL
53	SI	119	LYS
53	SI	127	LEU
53	SI	128	ASP
53	SI	130	GLU
53	SI	132	LEU
53	SI	139	HIS

Continued on next page...

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Mol	Chain	Res	Type
53	SI	140	ILE
53	SI	141	LEU
53	SI	147	ARG
53	SI	153	THR
53	SI	158	ILE
53	SI	160	GLU
53	SI	165	LEU
53	SI	170	LYS
53	SI	174	LYS
54	SJ	2	VAL
54	SJ	9	ASP
54	SJ	11	LEU
54	SJ	12	LYS
54	SJ	16	ASN
54	SJ	18	GLN
54	SJ	20	ILE
54	SJ	22	LYS
54	SJ	23	LYS
54	SJ	25	VAL
54	SJ	26	ILE
54	SJ	32	LYS
54	SJ	36	GLU
54	SJ	40	LEU
54	SJ	47	ILE
54	SJ	48	SER
54	SJ	49	ASP
54	SJ	53	VAL
54	SJ	55	ASN
54	SJ	60	ARG
54	SJ	65	LEU
54	SJ	66	ILE
54	SJ	68	ARG
54	SJ	71	LYS
54	SJ	74	VAL
54	SJ	78	ARG
54	SJ	80	ASP
54	SJ	84	ASN
54	SJ	85	ASP
54	SJ	86	ILE
54	SJ	91	VAL
54	SJ	93	LEU
54	SJ	96	SER

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Mol	Chain	Res	Type
54	SJ	97	ARG
54	SJ	98	LEU
54	SJ	102	ILE
54	SJ	103	ILE
54	SJ	104	LEU
54	SJ	105	THR
54	SJ	107	SER
54	SJ	108	GLN
54	SJ	110	ILE
54	SJ	111	MET
54	SJ	114	ILE
54	SJ	115	GLU
54	SJ	117	GLN
54	SJ	118	HIS
54	SJ	121	ILE
54	SJ	124	LYS
54	SJ	125	VAL
54	SJ	126	ILE
55	SK	1	PRO
55	SK	3	ILE
55	SK	4	SER
55	SK	11	LYS
55	SK	15	THR
55	SK	17	LYS
55	SK	18	LYS
55	SK	21	THR
55	SK	22	LYS
55	SK	24	ARG
55	SK	29	LEU
55	SK	30	LYS
55	SK	31	LEU
55	SK	32	CYS
55	SK	34	GLU
55	SK	38	LYS
55	SK	41	ARG
55	SK	43	ILE
55	SK	45	ARG
55	SK	52	LYS
55	SK	53	ILE
55	SK	54	ARG
55	SK	61	LEU
55	SK	63	LEU

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Mol	Chain	Res	Type
55	SK	64	ASP
55	SK	66	ASN
55	SK	67	ASP
55	SK	68	ILE
55	SK	69	LYS
55	SK	73	GLU
55	SK	79	ARG
55	SK	80	ARG
55	SK	84	LEU
55	SK	86	ILE
55	SK	89	GLU
55	SK	90	GLU
55	SK	91	LYS
55	SK	93	GLN
55	SK	94	LEU
55	SK	95	ASP
55	SK	101	ARG
55	SK	102	ILE
55	SK	104	ASP
55	SK	105	ILE
55	SK	106	PHE
55	SK	107	LYS
55	SK	111	GLN
55	SK	112	SER
55	SK	121	LYS
55	SK	127	ARG
55	SK	129	MET
55	SK	131	LYS
55	SK	135	ILE
55	SK	137	VAL
55	SK	141	ILE
55	SK	148	MET
55	SK	149	VAL
55	SK	151	ILE
55	SK	152	SER
55	SK	155	SER
55	SK	156	ARG
55	SK	159	ILE
55	SK	161	ASP
55	SK	162	THR
55	SK	165	LEU
55	SK	168	ASN

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Mol	Chain	Res	Type
55	SK	170	LYS
55	SK	173	ARG
55	SK	174	THR
55	SK	175	LYS
55	SK	176	ARG
56	SL	2	VAL
56	SL	10	LYS
56	SL	16	LEU
56	SL	18	GLU
56	SL	22	LEU
56	SL	24	LEU
56	SL	25	LYS
56	SL	26	GLU
56	SL	28	TRP
56	SL	29	ARG
56	SL	33	VAL
56	SL	36	ILE
56	SL	37	THR
56	SL	39	VAL
56	SL	41	GLU
56	SL	44	LYS
56	SL	45	LEU
56	SL	46	CYS
56	SL	49	THR
56	SL	50	TYR
56	SL	51	LEU
56	SL	55	CYS
56	SL	56	ILE
56	SL	57	MET
56	SL	58	GLN
56	SL	59	SER
56	SL	61	GLU
56	SL	66	VAL
56	SL	67	LYS
56	SL	69	THR
56	SL	73	ARG
56	SL	78	LEU
56	SL	82	LYS
56	SL	84	GLU
56	SL	89	LYS
56	SL	90	GLU
56	SL	92	ASP

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Mol	Chain	Res	Type
56	SL	93	LEU
56	SL	94	THR
56	SL	95	ASP
56	SL	96	ASP
57	SM	6	HIS
57	SM	12	LYS
57	SM	13	GLN
57	SM	14	SER
57	SM	22	LEU
57	SM	23	ARG
57	SM	24	LYS
57	SM	25	ASP
57	SM	28	ARG
57	SM	29	CYS
57	SM	32	PHE
57	SM	34	LYS
57	SM	36	ILE
57	SM	38	MET
57	SM	41	HIS
57	SM	42	THR
57	SM	44	ILE
57	SM	45	THR
57	SM	47	ILE
57	SM	54	LYS
57	SM	55	LYS
57	SM	61	ASN
57	SM	62	VAL
57	SM	63	SER
57	SM	67	ARG
57	SM	70	ARG
57	SM	72	VAL
57	SM	74	HIS
57	SM	75	SER
57	SM	78	MET
57	SM	83	ILE
57	SM	86	ARG
57	SM	93	GLN
57	SM	97	ARG
57	SM	103	LYS
57	SM	105	VAL
57	SM	110	SER
57	SM	114	ARG

Continued on next page...

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Mol	Chain	Res	Type
57	SM	116	LYS
57	SM	117	GLU
57	SM	121	VAL
57	SM	122	THR
57	SM	123	ILE
57	SM	125	GLU
57	SM	131	LYS
57	SM	134	ARG
57	SM	138	ILE
57	SM	139	LYS
57	SM	145	GLU
57	SM	148	LYS
57	SM	149	LYS
57	SM	152	SER
58	SO	3	LYS
58	SO	4	THR
58	SO	11	ARG
58	SO	14	ARG
58	SO	17	ARG
58	SO	18	ARG
58	SO	21	ARG
58	SO	25	LYS
58	SO	26	LYS
58	SO	29	LYS
58	SO	34	THR
58	SO	36	LEU
58	SO	37	LYS
58	SO	41	LEU
58	SO	45	CYS
58	SO	46	MET
58	SO	48	ARG
58	SO	50	ILE
58	SO	54	LYS
58	SO	55	ILE
58	SO	57	ILE
58	SO	64	SER
58	SO	66	VAL
58	SO	70	VAL
58	SO	71	ARG
58	SO	72	VAL
58	SO	75	THR
58	SO	76	LYS

Continued on next page...

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Mol	Chain	Res	Type
58	SO	77	ASN
58	SO	79	LYS
58	SO	81	ILE
58	SO	82	THR
58	SO	91	ILE
58	SO	92	THR
58	SO	94	ILE
58	SO	95	ASP
58	SO	96	ASN
58	SO	99	GLU
58	SO	105	PHE
58	SO	115	ILE
58	SO	119	ARG
58	SO	125	VAL
58	SO	128	ILE
58	SO	130	LEU
58	SO	131	LEU
58	SO	133	LEU
58	SO	135	LEU
58	SO	136	ARG
58	SO	138	ARG
58	SO	140	LYS
59	SP	4	MET
59	SP	6	SER
59	SP	7	LYS
59	SP	9	LYS
59	SP	11	ILE
59	SP	12	SER
59	SP	14	SER
59	SP	16	ILE
59	SP	19	THR
59	SP	20	ARG
59	SP	27	LYS
59	SP	28	TYR
59	SP	29	THR
59	SP	35	GLU
59	SP	37	ILE
59	SP	42	LYS
59	SP	50	ILE
59	SP	52	LEU
59	SP	54	LEU
59	SP	57	GLN

Continued on next page...

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Mol	Chain	Res	Type
59	SP	60	ILE
59	SP	69	SER
59	SP	71	ILE
59	SP	72	VAL
59	SP	78	LYS
59	SP	83	GLU
59	SP	84	ILE
59	SP	87	ASP
59	SP	91	MET
59	SP	93	LYS
59	SP	94	LYS
59	SP	98	ILE
59	SP	100	LYS
59	SP	103	GLU
59	SP	109	LYS
59	SP	110	ASP
59	SP	117	LEU
59	SP	120	SER
59	SP	127	ARG
59	SP	131	GLN
59	SP	134	ARG
59	SP	138	THR
59	SP	140	ARG
59	SP	142	LYS
59	SP	143	SER
59	SP	144	ASP
59	SP	145	GLN
60	SQ	28	PHE
60	SQ	33	ILE
60	SQ	37	LYS
60	SQ	40	THR
60	SQ	43	HIS
60	SQ	44	VAL
60	SQ	45	THR
60	SQ	47	LEU
60	SQ	48	SER
60	SQ	51	GLU
60	SQ	52	THR
60	SQ	53	ILE
60	SQ	62	VAL
60	SQ	64	ARG
60	SQ	66	CYS

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Mol	Chain	Res	Type
60	SQ	78	THR
60	SQ	79	GLN
60	SQ	81	LEU
60	SQ	82	ILE
60	SQ	86	THR
60	SQ	93	VAL
60	SQ	95	ILE
60	SQ	96	LYS
60	SQ	98	ARG
60	SQ	103	THR
60	SQ	105	LYS
60	SQ	107	VAL
60	SQ	116	ILE
60	SQ	124	ILE
60	SQ	128	ARG
60	SQ	129	ILE
60	SQ	132	SER
60	SQ	135	ILE
60	SQ	140	THR
60	SQ	143	LYS
61	SR	20	VAL
61	SR	21	GLU
61	SR	23	GLU
61	SR	24	LYS
61	SR	25	LEU
61	SR	29	LYS
61	SR	33	ILE
61	SR	34	LEU
61	SR	36	LYS
61	SR	40	ARG
61	SR	43	ARG
61	SR	44	ARG
61	SR	47	LYS
61	SR	51	SER
61	SR	52	MET
61	SR	54	HIS
61	SR	56	ARG
61	SR	58	VAL
61	SR	61	LEU
61	SR	62	ARG
61	SR	64	ARG
61	SR	65	ARG

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Mol	Chain	Res	Type
61	SR	68	GLN
61	SR	70	SER
61	SR	72	LYS
61	SR	74	LYS
61	SR	75	ILE
61	SR	78	THR
61	SR	80	LEU
61	SR	84	ILE
61	SR	85	ILE
61	SR	86	PHE
61	SR	88	GLU
61	SR	89	MET
61	SR	95	SER
61	SR	97	TYR
61	SR	100	ARG
61	SR	101	GLN
61	SR	105	VAL
61	SR	108	LYS
61	SR	114	ARG
61	SR	118	GLU
61	SR	120	SER
61	SR	121	MET
61	SR	122	SER
61	SR	124	LYS
61	SR	125	ILE
61	SR	126	VAL
61	SR	130	LYS
62	ST	9	LEU
62	ST	10	LEU
62	ST	12	ARG
62	ST	13	ASN
62	ST	15	ILE
62	ST	16	GLU
62	ST	17	VAL
62	ST	18	ARG
62	ST	19	GLU
62	ST	21	ASP
62	ST	22	LYS
62	ST	25	VAL
62	ST	26	HIS
62	ST	27	THR
62	ST	28	LEU

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Mol	Chain	Res	Type
62	ST	31	LYS
62	ST	32	LYS
62	ST	35	VAL
62	ST	39	PHE
62	ST	44	LYS
62	ST	47	ILE
62	ST	48	LEU
62	ST	49	VAL
62	ST	52	VAL
62	ST	54	LEU
62	ST	58	ARG
62	ST	61	ILE
62	ST	64	THR
62	ST	65	LYS
62	ST	71	MET
62	ST	73	LEU
62	ST	75	GLU
62	ST	76	SER
62	ST	77	LEU
62	ST	79	LYS
62	ST	86	LYS
62	ST	87	VAL
62	ST	96	ILE
62	ST	99	VAL
62	ST	103	ILE
62	ST	110	SER
62	ST	112	LYS
62	ST	114	GLU
62	ST	117	ARG
62	ST	121	ARG
62	ST	123	LYS
62	ST	124	LEU
62	ST	125	VAL
62	ST	130	GLN
62	ST	131	LEU
62	ST	132	VAL
62	ST	138	ARG
62	ST	139	CYS
62	ST	140	GLU
62	ST	152	ARG
62	ST	153	ARG
62	ST	154	GLN

Continued on next page...

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Mol	Chain	Res	Type
62	ST	157	TYR
63	SU	5	ARG
63	SU	7	LYS
63	SU	15	LYS
63	SU	16	ILE
63	SU	20	ASN
63	SU	22	GLU
63	SU	23	SER
63	SU	25	LYS
63	SU	30	GLN
63	SU	31	ASN
63	SU	33	LYS
63	SU	38	LYS
63	SU	39	ARG
63	SU	44	ILE
63	SU	47	LYS
63	SU	58	THR
63	SU	59	THR
63	SU	60	LEU
63	SU	61	MET
63	SU	65	VAL
63	SU	66	LYS
63	SU	69	VAL
63	SU	72	ILE
63	SU	75	ARG
63	SU	77	GLN
63	SU	78	GLU
63	SU	79	GLU
63	SU	81	ARG
63	SU	82	GLU
63	SU	84	ARG
63	SU	90	LYS
63	SU	91	LYS
63	SU	105	THR
63	SU	107	GLN
63	SU	108	MET
63	SU	109	ILE
63	SU	111	SER
63	SU	114	PHE
63	SU	117	MET
63	SU	118	SER
64	SV	11	ARG

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Mol	Chain	Res	Type
64	SV	14	LEU
64	SV	16	MET
64	SV	19	THR
64	SV	24	LYS
64	SV	25	VAL
64	SV	26	VAL
64	SV	31	LEU
64	SV	34	ILE
64	SV	37	ILE
64	SV	40	ARG
64	SV	47	LYS
64	SV	48	LYS
64	SV	50	ASN
64	SV	51	ILE
64	SV	53	VAL
64	SV	54	HIS
64	SV	55	LYS
64	SV	56	ARG
64	SV	59	GLU
64	SV	61	THR
64	SV	68	LEU
64	SV	70	LYS
64	SV	73	GLU
64	SV	76	LEU
64	SV	80	ILE
64	SV	84	MET
64	SV	85	LEU
64	SV	86	ASN
64	SV	89	ASN
64	SV	90	ASP
64	SV	91	PHE
64	SV	95	LYS
64	SV	97	MET
64	SV	99	ILE
64	SV	100	LEU
64	SV	101	VAL
64	SV	104	ILE
64	SV	106	SER
64	SV	107	THR
64	SV	112	LEU
64	SV	114	ARG
64	SV	115	LEU

Continued on next page...

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Mol	Chain	Res	Type
64	SV	116	ARG
64	SV	117	LYS
64	SV	119	ARG
64	SV	121	GLU
64	SV	124	VAL
64	SV	125	ARG
64	SV	127	HIS
64	SV	129	ASN
64	SV	132	VAL
64	SV	133	ARG
64	SV	135	GLN
64	SV	136	HIS
64	SV	137	THR
64	SV	138	LYS
64	SV	140	THR
64	SV	143	ARG
64	SV	145	HIS
65	SW	2	SER
65	SW	3	SER
65	SW	4	VAL
65	SW	5	THR
65	SW	6	ARG
65	SW	10	ASP
65	SW	11	VAL
65	SW	15	SER
65	SW	16	PHE
65	SW	20	LEU
65	SW	21	LYS
65	SW	23	ARG
65	SW	25	ILE
65	SW	26	ILE
65	SW	27	LYS
65	SW	28	CYS
65	SW	32	THR
65	SW	34	TYR
65	SW	35	VAL
65	SW	36	LYS
65	SW	39	VAL
65	SW	42	GLN
65	SW	46	ARG
65	SW	54	LYS
65	SW	60	ARG

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Mol	Chain	Res	Type
65	SW	65	SER
65	SW	70	ILE
65	SW	77	ARG
65	SW	78	LYS
65	SW	81	SER
65	SW	83	GLN
65	SW	84	LYS
65	SW	86	LYS
65	SW	88	THR
65	SW	97	CYS
65	SW	98	LYS
65	SW	103	ILE
65	SW	104	VAL
65	SW	106	GLN
65	SW	108	LEU
65	SW	111	LYS
65	SW	113	LEU
65	SW	114	ILE
65	SW	120	ARG
65	SW	122	ILE
65	SW	123	SER
65	SW	127	ARG
65	SW	128	LYS
65	SW	129	MET
65	SW	131	GLU
65	SW	137	LEU
66	SX	24	LYS
66	SX	27	ILE
66	SX	30	VAL
66	SX	32	LYS
66	SX	35	LYS
66	SX	36	LEU
66	SX	37	VAL
66	SX	38	GLU
66	SX	39	ARG
66	SX	44	ILE
66	SX	46	LYS
66	SX	49	ARG
66	SX	53	ILE
66	SX	61	VAL
66	SX	62	ARG
66	SX	63	ARG

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Mol	Chain	Res	Type
66	SX	64	LEU
66	SX	68	THR
66	SX	70	LYS
66	SX	71	SER
66	SX	75	GLU
66	SX	79	THR
66	SX	81	HIS
66	SX	86	ARG
66	SX	87	MET
66	SX	89	LYS
66	SX	90	ARG
66	SX	91	THR
66	SX	94	VAL
66	SX	96	CYS
66	SX	101	ILE
66	SX	107	LYS
66	SX	109	VAL
66	SX	111	ILE
66	SX	115	GLN
66	SX	116	VAL
66	SX	117	THR
66	SX	118	VAL
66	SX	120	VAL
67	SY	4	ASP
67	SY	5	ASP
67	SY	6	ILE
67	SY	8	MET
67	SY	9	LYS
67	SY	10	ASN
67	SY	12	SER
67	SY	15	VAL
67	SY	16	VAL
67	SY	22	ARG
67	SY	23	LYS
67	SY	30	LEU
67	SY	34	LYS
67	SY	41	LEU
67	SY	42	SER
67	SY	49	LYS
67	SY	52	MET
67	SY	53	ILE
67	SY	54	GLU

Continued on next page...

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Mol	Chain	Res	Type
67	SY	55	ASN
67	SY	57	TYR
67	SY	59	THR
67	SY	68	SER
67	SY	74	SER
67	SY	76	PHE
67	SY	78	LEU
67	SY	79	LEU
67	SY	82	GLU
67	SY	86	MET
67	SY	87	GLU
67	SY	88	ARG
67	SY	89	LEU
68	Sb	3	GLU
68	Sb	5	THR
68	Sb	7	LYS
68	Sb	9	ARG
68	Sb	10	LYS
68	Sb	16	LEU
68	Sb	17	LEU
68	Sb	18	GLN
68	Sb	19	ARG
68	Sb	23	VAL
68	Sb	26	VAL
68	Sb	27	LEU
68	Sb	32	THR
68	Sb	34	GLU
68	Sb	36	LYS
68	Sb	37	GLU
68	Sb	39	ILE
68	Sb	40	LYS
68	Sb	42	LYS
68	Sb	43	VAL
68	Sb	45	GLN
68	Sb	48	LYS
68	Sb	52	GLN
68	Sb	53	LYS
68	Sb	55	ILE
68	Sb	56	VAL
68	Sb	62	THR
68	Sb	69	THR
68	Sb	70	VAL

Continued on next page...

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Mol	Chain	Res	Type
68	Sb	78	ASN
68	Sb	79	MET
68	Sb	80	ASP
68	Sb	83	MET
68	Sb	84	LYS
68	Sb	86	GLU
68	Sb	90	ARG
68	Sb	91	LYS
68	Sb	92	ILE
68	Sb	96	LEU
68	Sb	97	ILE
68	Sb	101	LYS
68	Sb	104	SER
68	Sb	105	ARG
68	Sb	106	LYS
68	Sb	107	GLN
68	Sb	108	LEU
68	Sb	110	ASN
68	Sb	111	LEU
68	Sb	114	ARG
68	Sb	115	ARG
68	Sb	116	LEU
68	Sb	117	LYS
68	Sb	118	LYS
69	Sc	15	VAL
69	Sc	16	ASP
69	Sc	17	TYR
69	Sc	20	LEU
69	Sc	21	PHE
69	Sc	23	ASP
69	Sc	24	GLU
69	Sc	27	MET
69	Sc	28	ASN
69	Sc	29	GLU
69	Sc	31	LEU
69	Sc	34	ILE
69	Sc	35	LYS
69	Sc	38	LYS
69	Sc	39	CYS
69	Sc	40	ILE
69	Sc	41	THR
69	Sc	51	VAL

Continued on next page...

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Mol	Chain	Res	Type
69	Sc	58	ARG
69	Sc	60	MET
69	Sc	71	ILE
69	Sc	72	VAL
69	Sc	73	SER
69	Sc	76	SER
69	Sc	77	ARG
69	Sc	78	MET
69	Sc	79	THR
69	Sc	82	LYS
69	Sc	85	THR
69	Sc	86	LYS
69	Sc	87	LYS
70	Sd	3	VAL
70	Sd	6	ARG
70	Sd	10	ARG
70	Sd	15	CYS
70	Sd	18	THR
70	Sd	20	ILE
70	Sd	21	VAL
70	Sd	26	CYS
70	Sd	28	ARG
70	Sd	30	VAL
70	Sd	33	ASP
70	Sd	35	VAL
70	Sd	37	LYS
70	Sd	42	ARG
70	Sd	44	ILE
70	Sd	49	ILE
70	Sd	51	ASP
70	Sd	54	LEU
70	Sd	64	ILE
70	Sd	66	LYS
70	Sd	67	LEU
70	Sd	71	VAL
70	Sd	80	HIS
70	Sd	91	ASP
70	Sd	93	LYS
70	Sd	94	ILE
70	Sd	95	ARG
70	Sd	99	LYS
70	Sd	100	ARG

Continued on next page...

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Mol	Chain	Res	Type
70	Sd	105	SER
71	Se	46	VAL
71	Se	49	LEU
71	Se	52	ASP
71	Se	55	GLU
71	Se	56	GLU
71	Se	57	GLN
71	Se	58	ARG
71	Se	59	LYS
71	Se	61	LYS
71	Se	65	LEU
71	Se	66	VAL
71	Se	74	LEU
71	Se	75	GLU
71	Se	76	ILE
71	Se	82	GLN
71	Se	83	ASP
71	Se	84	ILE
71	Se	85	VAL
71	Se	86	VAL
71	Se	93	THR
71	Se	97	CYS
71	Se	102	SER
71	Se	104	ILE
71	Se	111	LYS
71	Se	115	THR
71	Se	117	GLN
71	Se	119	GLU
71	Se	120	ARG
71	Se	122	ARG
71	Se	123	GLN
72	Sg	3	GLU
72	Sg	5	ILE
72	Sg	6	ASN
72	Sg	8	ARG
72	Sg	9	VAL
72	Sg	10	ILE
72	Sg	11	GLU
72	Sg	12	VAL
72	Sg	13	LEU
72	Sg	23	THR
72	Sg	24	GLN

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Mol	Chain	Res	Type
72	Sg	25	VAL
72	Sg	27	VAL
72	Sg	28	GLU
72	Sg	30	MET
72	Sg	31	THR
72	Sg	37	ILE
72	Sg	42	ILE
72	Sg	45	VAL
72	Sg	46	ARG
72	Sg	47	LYS
72	Sg	48	ASP
72	Sg	51	LEU
72	Sg	52	VAL
72	Sg	53	LEU
72	Sg	54	MET
72	Sg	57	GLU
72	Sg	58	ARG
72	Sg	59	GLU
72	Sg	61	ARG
72	Sg	62	ARG
72	Sg	63	LEU
72	Sg	64	ARG
73	Sh	87	MET
73	Sh	89	GLU
73	Sh	91	GLU
73	Sh	93	CYS
73	Sh	99	LYS
73	Sh	102	CYS
73	Sh	104	ILE
73	Sh	105	CYS
73	Sh	110	SER
73	Sh	111	VAL
73	Sh	112	TYR
73	Sh	117	LEU
73	Sh	120	CYS
73	Sh	125	LYS
73	Sh	126	GLU
73	Sh	130	LYS
73	Sh	134	VAL
73	Sh	135	LYS
73	Sh	136	LEU
74	Sj	6	LEU

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Mol	Chain	Res	Type
74	Sj	11	LYS
74	Sj	12	VAL
74	Sj	13	ARG
74	Sj	16	THR
74	Sj	18	LYS
74	Sj	20	GLU
74	Sj	22	LYS
74	Sj	23	GLU
74	Sj	29	ARG
74	Sj	31	ARG
74	Sj	36	LEU
74	Sj	37	LEU
74	Sj	40	LYS
74	Sj	43	VAL
74	Sj	47	LEU
74	Sj	49	HIS
74	Sj	50	ASN
74	Sj	53	ARG
74	Sj	54	LEU
74	Sj	58	ASN
74	Sj	60	LEU
74	Sj	61	ILE
74	Sj	62	ARG
74	Sj	63	GLN
74	Sj	64	LYS
74	Sj	65	LEU
74	Sj	67	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (237) such sidechains are listed below:

Mol	Chain	Res	Type
1	LA	97	HIS
1	LA	144	ASN
2	LB	3	HIS
2	LB	55	HIS
2	LB	71	GLN
2	LB	146	GLN
2	LB	152	GLN
2	LB	153	HIS
2	LB	164	GLN
2	LB	183	ASN
2	LB	259	ASN

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Mol	Chain	Res	Type
2	LB	261	GLN
2	LB	352	GLN
2	LB	354	GLN
3	LC	61	HIS
3	LC	109	GLN
3	LC	232	HIS
3	LC	266	GLN
3	LC	274	GLN
6	LF	31	GLN
6	LF	142	ASN
6	LF	183	HIS
6	LF	250	HIS
6	LF	256	ASN
7	LG	4	ASN
7	LG	20	ASN
7	LG	38	ASN
7	LG	42	HIS
8	LH	107	ASN
8	LH	115	ASN
8	LH	154	GLN
8	LH	171	HIS
8	LH	194	ASN
8	LH	195	ASN
9	LI	41	GLN
9	LI	58	ASN
9	LI	70	ASN
9	LI	152	HIS
10	LJ	165	ASN
11	LK	191	GLN
12	LL	43	GLN
12	LL	88	ASN
12	LL	109	HIS
13	LM	45	ASN
13	LM	49	ASN
13	LM	66	GLN
14	LN	48	GLN
14	LN	72	GLN
14	LN	88	ASN
14	LN	98	GLN
15	LO	8	GLN
15	LO	123	GLN
15	LO	149	ASN

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Mol	Chain	Res	Type
15	LO	176	ASN
16	LP	11	HIS
16	LP	26	HIS
16	LP	28	HIS
16	LP	60	ASN
17	LQ	71	GLN
17	LQ	100	ASN
18	LR	23	ASN
18	LR	30	HIS
18	LR	39	ASN
18	LR	134	ASN
19	LS	28	HIS
19	LS	67	HIS
19	LS	141	HIS
20	LT	61	HIS
20	LT	110	GLN
21	LU	45	ASN
21	LU	77	GLN
21	LU	97	HIS
21	LU	104	ASN
22	LV	47	ASN
23	LW	13	ASN
23	LW	49	HIS
23	LW	101	GLN
23	LW	142	HIS
24	LX	60	HIS
26	LZ	42	HIS
26	LZ	89	ASN
26	LZ	112	ASN
26	LZ	123	GLN
27	La	16	GLN
27	La	19	HIS
27	La	33	ASN
27	La	76	ASN
27	La	88	ASN
27	La	96	GLN
27	La	116	GLN
28	Lb	14	HIS
28	Lb	25	HIS
28	Lb	39	GLN
28	Lb	40	HIS
28	Lb	66	ASN

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Mol	Chain	Res	Type
28	Lb	86	GLN
30	Ld	37	ASN
30	Ld	59	GLN
31	Le	7	HIS
31	Le	12	ASN
31	Le	51	ASN
31	Le	90	ASN
32	Lf	26	GLN
32	Lf	50	GLN
32	Lf	54	GLN
32	Lf	94	ASN
33	Lg	24	GLN
34	Lh	44	HIS
34	Lh	67	GLN
35	Li	42	GLN
35	Li	91	ASN
36	Lj	30	GLN
36	Lj	38	GLN
37	Lk	32	HIS
37	Lk	82	ASN
38	Ll	33	GLN
39	Ln	5	ASN
39	Ln	99	GLN
39	Ln	119	GLN
39	Ln	193	GLN
41	Lp	36	GLN
41	Lp	51	GLN
41	Lp	81	GLN
41	Lp	87	HIS
43	Ls	90	ASN
43	Ls	91	GLN
45	SA	112	ASN
45	SA	130	ASN
45	SA	154	ASN
45	SA	170	ASN
46	SB	83	GLN
46	SB	129	ASN
46	SB	146	HIS
46	SB	210	ASN
46	SB	231	HIS
46	SB	233	GLN
47	SC	68	ASN

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Mol	Chain	Res	Type
47	SC	69	HIS
48	SD	43	GLN
48	SD	61	HIS
48	SD	79	ASN
48	SD	87	GLN
48	SD	202	GLN
48	SD	223	ASN
49	SE	8	HIS
49	SE	66	GLN
49	SE	69	ASN
49	SE	117	ASN
49	SE	127	GLN
49	SE	188	ASN
49	SE	196	GLN
49	SE	201	HIS
49	SE	224	ASN
50	SF	31	ASN
50	SF	93	ASN
50	SF	180	ASN
50	SF	189	ASN
51	SG	10	ASN
51	SG	19	ASN
51	SG	31	GLN
51	SG	77	GLN
51	SG	85	GLN
51	SG	92	HIS
51	SG	204	GLN
52	SH	71	GLN
52	SH	127	ASN
53	SI	5	HIS
53	SI	18	GLN
53	SI	28	ASN
53	SI	47	ASN
53	SI	61	ASN
53	SI	71	HIS
53	SI	83	HIS
53	SI	112	GLN
53	SI	124	ASN
53	SI	134	GLN
53	SI	150	GLN
53	SI	168	GLN
54	SJ	16	ASN

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Mol	Chain	Res	Type
54	SJ	42	GLN
54	SJ	84	ASN
54	SJ	118	HIS
55	SK	59	ASN
55	SK	153	ASN
56	SL	15	HIS
56	SL	52	HIS
56	SL	85	GLN
57	SM	13	GLN
57	SM	18	GLN
57	SM	61	ASN
58	SO	61	GLN
58	SO	96	ASN
59	SP	5	HIS
60	SQ	38	ASN
60	SQ	43	HIS
60	SQ	65	HIS
60	SQ	94	HIS
60	SQ	110	GLN
60	SQ	142	HIS
61	SR	16	ASN
61	SR	54	HIS
61	SR	68	GLN
62	ST	33	ASN
62	ST	92	HIS
62	ST	95	GLN
63	SU	20	ASN
63	SU	62	ASN
64	SV	8	ASN
64	SV	50	ASN
64	SV	78	HIS
64	SV	89	ASN
64	SV	127	HIS
64	SV	129	ASN
64	SV	135	GLN
65	SW	42	GLN
65	SW	61	HIS
65	SW	68	HIS
65	SW	83	GLN
65	SW	138	GLN
66	SX	22	HIS
66	SX	115	GLN

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Mol	Chain	Res	Type
68	Sb	13	ASN
68	Sb	45	GLN
68	Sb	52	GLN
68	Sb	68	HIS
68	Sb	77	GLN
68	Sb	113	ASN
69	Sc	36	ASN
69	Sc	42	HIS
69	Sc	44	GLN
70	Sd	24	GLN
70	Sd	82	HIS
71	Se	60	HIS
71	Se	123	GLN
72	Sg	40	ASN
73	Sh	107	ASN
73	Sh	109	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	LD	141/143 (98%)	58 (41%)	10 (7%)
44	Lt	2588/2697 (95%)	1106 (42%)	0
5	LE	116/121 (95%)	56 (48%)	4 (3%)
75	St	1453/1454 (99%)	658 (45%)	0
All	All	4298/4415 (97%)	1878 (43%)	14 (0%)

All (1878) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	LD	2	C
4	LD	7	C
4	LD	8	C
4	LD	10	G
4	LD	12	C
4	LD	13	G
4	LD	14	G
4	LD	20	G
4	LD	21	C
4	LD	22	C
4	LD	23	U
4	LD	24	C

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Mol	Chain	Res	Type
4	LD	31	G
4	LD	32	G
4	LD	35	G
4	LD	36	C
4	LD	40	G
4	LD	41	A
4	LD	46	C
4	LD	47	G
4	LD	48	C
4	LD	51	C
4	LD	52	G
4	LD	59	G
4	LD	60	A
4	LD	61	G
4	LD	64	G
4	LD	72	G
4	LD	73	A
4	LD	76	C
4	LD	77	G
4	LD	78	C
4	LD	79	C
4	LD	80	C
4	LD	81	G
4	LD	84	C
4	LD	85	C
4	LD	86	G
4	LD	87	A
4	LD	88	G
4	LD	94	C
4	LD	102	C
4	LD	104	A
4	LD	105	A
4	LD	106	C
4	LD	110	G
4	LD	111	C
4	LD	112	G
4	LD	117	C
4	LD	118	C
4	LD	119	G
4	LD	120	G
4	LD	125	G
4	LD	126	C

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Mol	Chain	Res	Type
4	LD	128	G
4	LD	129	C
4	LD	141	C
4	LD	142	C
5	LE	3	G
5	LE	7	G
5	LE	10	C
5	LE	11	A
5	LE	14	C
5	LE	18	G
5	LE	20	C
5	LE	23	A
5	LE	24	A
5	LE	30	U
5	LE	32	A
5	LE	33	A
5	LE	35	U
5	LE	36	C
5	LE	37	G
5	LE	38	U
5	LE	39	U
5	LE	40	C
5	LE	42	G
5	LE	44	A
5	LE	45	U
5	LE	47	A
5	LE	48	G
5	LE	49	G
5	LE	50	A
5	LE	51	A
5	LE	53	A
5	LE	54	G
5	LE	55	A
5	LE	56	A
5	LE	61	C
5	LE	62	G
5	LE	63	U
5	LE	64	C
5	LE	65	A
5	LE	69	C
5	LE	70	C
5	LE	72	G

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Mol	Chain	Res	Type
5	LE	73	C
5	LE	77	U
5	LE	80	U
5	LE	82	C
5	LE	85	U
5	LE	86	C
5	LE	87	G
5	LE	91	A
5	LE	92	C
5	LE	94	U
5	LE	98	G
5	LE	102	A
5	LE	106	G
5	LE	109	G
5	LE	110	U
5	LE	111	G
5	LE	114	G
5	LE	115	A
44	Lt	2	G
44	Lt	3	C
44	Lt	4	G
44	Lt	5	G
44	Lt	8	C
44	Lt	10	G
44	Lt	11	A
44	Lt	21	G
44	Lt	24	G
44	Lt	25	A
44	Lt	39	A
44	Lt	40	G
44	Lt	42	A
44	Lt	48	G
44	Lt	55	C
44	Lt	58	G
44	Lt	59	A
44	Lt	64	A
44	Lt	65	A
44	Lt	66	A
44	Lt	67	C
44	Lt	70	A
44	Lt	71	C
44	Lt	72	C

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Mol	Chain	Res	Type
44	Lt	73	G
44	Lt	75	G
44	Lt	82	C
44	Lt	84	C
44	Lt	85	U
44	Lt	86	A
44	Lt	87	G
44	Lt	90	G
44	Lt	96	G
44	Lt	100	C
44	Lt	107	A
44	Lt	109	C
44	Lt	114	C
44	Lt	118	A
44	Lt	121	G
44	Lt	122	C
44	Lt	123	G
44	Lt	124	C
44	Lt	127	U
44	Lt	128	G
44	Lt	153	C
44	Lt	158	G
44	Lt	162	C
44	Lt	166	G
44	Lt	167	G
44	Lt	169	C
44	Lt	170	C
44	Lt	172	C
44	Lt	173	G
44	Lt	174	C
44	Lt	175	C
44	Lt	176	C
44	Lt	178	A
44	Lt	179	G
44	Lt	180	A
44	Lt	181	G
44	Lt	185	G
44	Lt	186	C
44	Lt	190	C
44	Lt	194	G
44	Lt	224	U
44	Lt	230	U

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Mol	Chain	Res	Type
44	Lt	237	G
44	Lt	238	C
44	Lt	240	U
44	Lt	250	A
44	Lt	251	G
44	Lt	252	G
44	Lt	256	G
44	Lt	257	C
44	Lt	258	G
44	Lt	262	C
44	Lt	263	C
44	Lt	265	U
44	Lt	278	U
44	Lt	281	G
44	Lt	287	G
44	Lt	289	A
44	Lt	290	C
44	Lt	294	U
44	Lt	295	A
44	Lt	300	A
44	Lt	301	C
44	Lt	302	C
44	Lt	303	A
44	Lt	312	G
44	Lt	314	G
44	Lt	317	A
44	Lt	321	G
44	Lt	322	U
44	Lt	326	A
44	Lt	328	G
44	Lt	329	G
44	Lt	330	A
44	Lt	334	C
44	Lt	339	G
44	Lt	342	C
44	Lt	343	G
44	Lt	344	C
44	Lt	345	U
44	Lt	346	C
44	Lt	347	A
44	Lt	349	A
44	Lt	350	A

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Mol	Chain	Res	Type
44	Lt	352	A
44	Lt	370	G
44	Lt	372	C
44	Lt	375	C
44	Lt	376	C
44	Lt	377	C
44	Lt	378	G
44	Lt	379	C
44	Lt	384	C
44	Lt	385	C
44	Lt	389	C
44	Lt	396	C
44	Lt	397	A
44	Lt	399	G
44	Lt	408	A
44	Lt	409	G
44	Lt	421	G
44	Lt	425	A
44	Lt	427	C
44	Lt	429	C
44	Lt	434	G
44	Lt	435	A
44	Lt	436	G
44	Lt	437	C
44	Lt	438	C
44	Lt	439	C
44	Lt	443	C
44	Lt	444	G
44	Lt	449	A
44	Lt	450	G
44	Lt	451	C
44	Lt	454	G
44	Lt	456	G
44	Lt	459	A
44	Lt	460	G
44	Lt	461	A
44	Lt	463	G
44	Lt	464	C
44	Lt	465	C
44	Lt	468	G
44	Lt	480	C
44	Lt	485	G

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Mol	Chain	Res	Type
44	Lt	486	C
44	Lt	491	G
44	Lt	492	U
44	Lt	493	G
44	Lt	497	G
44	Lt	498	G
44	Lt	501	C
44	Lt	502	G
44	Lt	503	A
44	Lt	507	G
44	Lt	508	C
44	Lt	512	G
44	Lt	513	C
44	Lt	515	U
44	Lt	516	G
44	Lt	517	G
44	Lt	518	G
44	Lt	520	C
44	Lt	523	A
44	Lt	524	A
44	Lt	525	A
44	Lt	534	U
44	Lt	535	C
44	Lt	537	A
44	Lt	539	G
44	Lt	542	C
44	Lt	543	G
44	Lt	546	G
44	Lt	547	A
44	Lt	549	G
44	Lt	550	G
44	Lt	552	G
44	Lt	554	G
44	Lt	561	C
44	Lt	566	G
44	Lt	567	C
44	Lt	575	A
44	Lt	578	C
44	Lt	588	U
44	Lt	589	G
44	Lt	591	U
44	Lt	592	G

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Mol	Chain	Res	Type
44	Lt	596	C
44	Lt	599	A
44	Lt	600	G
44	Lt	601	A
44	Lt	605	C
44	Lt	611	G
44	Lt	612	G
44	Lt	613	A
44	Lt	624	G
44	Lt	625	G
44	Lt	626	G
44	Lt	631	A
44	Lt	632	A
44	Lt	633	G
44	Lt	634	A
44	Lt	637	C
44	Lt	639	U
44	Lt	640	C
44	Lt	641	G
44	Lt	642	A
44	Lt	643	A
44	Lt	650	G
44	Lt	654	G
44	Lt	656	U
44	Lt	661	G
44	Lt	669	A
44	Lt	676	C
44	Lt	677	C
44	Lt	678	C
44	Lt	679	A
44	Lt	680	G
44	Lt	681	G
44	Lt	682	A
44	Lt	691	G
44	Lt	694	C
44	Lt	695	C
44	Lt	696	G
44	Lt	698	A
44	Lt	699	G
44	Lt	705	G
44	Lt	708	C
44	Lt	709	G

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Mol	Chain	Res	Type
44	Lt	717	C
44	Lt	719	G
44	Lt	720	G
44	Lt	722	C
44	Lt	723	G
44	Lt	727	G
44	Lt	729	A
44	Lt	730	G
44	Lt	731	C
44	Lt	732	G
44	Lt	733	G
44	Lt	734	G
44	Lt	735	G
44	Lt	736	G
44	Lt	739	C
44	Lt	740	U
44	Lt	741	G
44	Lt	742	C
44	Lt	743	C
44	Lt	744	C
44	Lt	745	C
44	Lt	747	C
44	Lt	751	C
44	Lt	754	C
44	Lt	755	C
44	Lt	756	C
44	Lt	757	C
44	Lt	760	A
44	Lt	761	A
44	Lt	763	U
44	Lt	764	C
44	Lt	765	C
44	Lt	767	A
44	Lt	769	G
44	Lt	770	G
44	Lt	776	G
44	Lt	777	C
44	Lt	779	G
44	Lt	780	C
44	Lt	783	C
44	Lt	785	C
44	Lt	787	G

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Mol	Chain	Res	Type
44	Lt	788	C
44	Lt	793	C
44	Lt	794	U
44	Lt	795	G
44	Lt	796	G
44	Lt	799	G
44	Lt	802	G
44	Lt	803	C
44	Lt	804	G
44	Lt	805	G
44	Lt	806	G
44	Lt	807	C
44	Lt	808	G
44	Lt	809	A
44	Lt	814	G
44	Lt	818	G
44	Lt	827	G
44	Lt	830	C
44	Lt	834	C
44	Lt	837	G
44	Lt	839	A
44	Lt	840	A
44	Lt	841	G
44	Lt	842	C
44	Lt	844	G
44	Lt	845	G
44	Lt	847	C
44	Lt	848	G
44	Lt	854	G
44	Lt	855	G
44	Lt	861	C
44	Lt	862	G
44	Lt	863	A
44	Lt	865	C
44	Lt	869	A
44	Lt	870	C
44	Lt	873	C
44	Lt	874	G
44	Lt	875	G
44	Lt	876	G
44	Lt	884	G
44	Lt	888	C

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Mol	Chain	Res	Type
44	Lt	889	G
44	Lt	890	C
44	Lt	897	C
44	Lt	899	G
44	Lt	900	C
44	Lt	901	G
44	Lt	903	A
44	Lt	906	G
44	Lt	907	G
44	Lt	908	C
44	Lt	909	G
44	Lt	910	U
44	Lt	912	G
44	Lt	914	C
44	Lt	916	G
44	Lt	917	G
44	Lt	918	U
44	Lt	920	C
44	Lt	921	C
44	Lt	922	G
44	Lt	923	A
44	Lt	982	G
44	Lt	985	G
44	Lt	986	A
44	Lt	987	A
44	Lt	989	C
44	Lt	991	G
44	Lt	992	C
44	Lt	993	C
44	Lt	994	G
44	Lt	995	G
44	Lt	999	G
44	Lt	1001	A
44	Lt	1005	U
44	Lt	1006	G
44	Lt	1007	G
44	Lt	1009	G
44	Lt	1010	C
44	Lt	1012	C
44	Lt	1013	G
44	Lt	1015	C
44	Lt	1016	G

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Mol	Chain	Res	Type
44	Lt	1017	G
44	Lt	1018	A
44	Lt	1019	G
44	Lt	1021	C
44	Lt	1024	G
44	Lt	1025	G
44	Lt	1026	A
44	Lt	1030	G
44	Lt	1031	C
44	Lt	1032	G
44	Lt	1037	G
44	Lt	1038	C
44	Lt	1039	C
44	Lt	1040	G
44	Lt	1045	G
44	Lt	1046	C
44	Lt	1047	G
44	Lt	1053	G
44	Lt	1062	C
44	Lt	1066	A
44	Lt	1070	G
44	Lt	1072	C
44	Lt	1073	C
44	Lt	1074	C
44	Lt	1075	G
44	Lt	1076	G
44	Lt	1079	G
44	Lt	1080	C
44	Lt	1081	G
44	Lt	1087	G
44	Lt	1095	G
44	Lt	1096	G
44	Lt	1109	G
44	Lt	1110	G
44	Lt	1111	C
44	Lt	1116	G
44	Lt	1117	G
44	Lt	1118	U
44	Lt	1120	C
44	Lt	1121	A
44	Lt	1122	G
44	Lt	1125	C

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Mol	Chain	Res	Type
44	Lt	1133	C
44	Lt	1134	A
44	Lt	1135	G
44	Lt	1136	U
44	Lt	1140	C
44	Lt	1141	G
44	Lt	1143	U
44	Lt	1144	A
44	Lt	1150	C
44	Lt	1151	G
44	Lt	1152	C
44	Lt	1153	C
44	Lt	1154	C
44	Lt	1159	G
44	Lt	1160	G
44	Lt	1164	G
44	Lt	1165	A
44	Lt	1166	G
44	Lt	1167	G
44	Lt	1168	G
44	Lt	1169	G
44	Lt	1172	G
44	Lt	1178	U
44	Lt	1179	U
44	Lt	1181	C
44	Lt	1185	G
44	Lt	1186	C
44	Lt	1187	G
44	Lt	1191	G
44	Lt	1192	C
44	Lt	1193	A
44	Lt	1195	C
44	Lt	1198	G
44	Lt	1199	C
44	Lt	1204	G
44	Lt	1207	G
44	Lt	1208	A
44	Lt	1210	U
44	Lt	1211	C
44	Lt	1216	C
44	Lt	1217	U
44	Lt	1220	G

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Mol	Chain	Res	Type
44	Lt	1222	G
44	Lt	1226	G
44	Lt	1231	A
44	Lt	1233	A
44	Lt	1236	G
44	Lt	1237	G
44	Lt	1238	G
44	Lt	1239	A
44	Lt	1240	A
44	Lt	1241	G
44	Lt	1242	G
44	Lt	1247	U
44	Lt	1248	G
44	Lt	1249	C
44	Lt	1250	C
44	Lt	1251	C
44	Lt	1252	G
44	Lt	1253	C
44	Lt	1254	C
44	Lt	1257	U
44	Lt	1258	C
44	Lt	1259	G
44	Lt	1260	A
44	Lt	1261	A
44	Lt	1262	C
44	Lt	1263	G
44	Lt	1273	C
44	Lt	1275	G
44	Lt	1277	G
44	Lt	1278	A
44	Lt	1279	C
44	Lt	1280	U
44	Lt	1281	C
44	Lt	1282	C
44	Lt	1286	A
44	Lt	1290	G
44	Lt	1291	C
44	Lt	1295	C
44	Lt	1298	C
44	Lt	1299	G
44	Lt	1300	C
44	Lt	1308	C

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Mol	Chain	Res	Type
44	Lt	1309	C
44	Lt	1310	C
44	Lt	1311	G
44	Lt	1314	C
44	Lt	1318	G
44	Lt	1324	G
44	Lt	1325	C
44	Lt	1327	C
44	Lt	1328	A
44	Lt	1339	G
44	Lt	1344	G
44	Lt	1345	C
44	Lt	1349	G
44	Lt	1350	C
44	Lt	1353	C
44	Lt	1354	G
44	Lt	1355	G
44	Lt	1356	C
44	Lt	1357	C
44	Lt	1366	C
44	Lt	1367	C
44	Lt	1380	G
44	Lt	1381	A
44	Lt	1382	C
44	Lt	1383	G
44	Lt	1385	C
44	Lt	1387	U
44	Lt	1389	C
44	Lt	1392	G
44	Lt	1394	A
44	Lt	1395	G
44	Lt	1396	A
44	Lt	1401	G
44	Lt	1406	G
44	Lt	1407	G
44	Lt	1408	G
44	Lt	1412	G
44	Lt	1413	G
44	Lt	1423	G
44	Lt	1427	C
44	Lt	1434	C
44	Lt	1435	C

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Mol	Chain	Res	Type
44	Lt	1438	U
44	Lt	1439	G
44	Lt	1440	A
44	Lt	1448	G
44	Lt	1451	G
44	Lt	1454	G
44	Lt	1455	C
44	Lt	1458	G
44	Lt	1461	G
44	Lt	1462	C
44	Lt	1464	C
44	Lt	1466	C
44	Lt	1468	G
44	Lt	1469	U
44	Lt	1470	A
44	Lt	1473	G
44	Lt	1474	A
44	Lt	1478	C
44	Lt	1479	A
44	Lt	1480	G
44	Lt	1481	C
44	Lt	1482	A
44	Lt	1483	G
44	Lt	1485	A
44	Lt	1486	C
44	Lt	1488	C
44	Lt	1490	G
44	Lt	1495	C
44	Lt	1496	A
44	Lt	1498	C
44	Lt	1499	A
44	Lt	1502	C
44	Lt	1503	U
44	Lt	1506	A
44	Lt	1507	G
44	Lt	1509	G
44	Lt	1510	C
44	Lt	1511	G
44	Lt	1512	G
44	Lt	1513	G
44	Lt	1514	A
44	Lt	1515	G

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Mol	Chain	Res	Type
44	Lt	1516	C
44	Lt	1517	G
44	Lt	1518	A
44	Lt	1523	G
44	Lt	1525	C
44	Lt	1526	U
44	Lt	1528	A
44	Lt	1531	G
44	Lt	1532	A
44	Lt	1533	A
44	Lt	1538	G
44	Lt	1546	G
44	Lt	1552	U
44	Lt	1558	C
44	Lt	1562	A
44	Lt	1563	A
44	Lt	1567	G
44	Lt	1569	G
44	Lt	1573	C
44	Lt	1575	C
44	Lt	1576	U
44	Lt	1577	G
44	Lt	1578	A
44	Lt	1579	C
44	Lt	1580	G
44	Lt	1587	C
44	Lt	1590	G
44	Lt	1591	U
44	Lt	1593	A
44	Lt	1596	A
44	Lt	1597	C
44	Lt	1598	U
44	Lt	1599	G
44	Lt	1600	G
44	Lt	1601	A
44	Lt	1602	A
44	Lt	1603	C
44	Lt	1604	G
44	Lt	1605	G
44	Lt	1606	A
44	Lt	1611	G
44	Lt	1615	U

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Mol	Chain	Res	Type
44	Lt	1616	C
44	Lt	1618	C
44	Lt	1619	G
44	Lt	1620	A
44	Lt	1624	U
44	Lt	1626	U
44	Lt	1628	C
44	Lt	1629	U
44	Lt	1630	A
44	Lt	1631	G
44	Lt	1633	A
44	Lt	1634	A
44	Lt	1635	C
44	Lt	1641	G
44	Lt	1646	G
44	Lt	1647	A
44	Lt	1648	G
44	Lt	1655	A
44	Lt	1656	C
44	Lt	1657	C
44	Lt	1658	C
44	Lt	1659	G
44	Lt	1663	C
44	Lt	1664	U
44	Lt	1667	C
44	Lt	1672	C
44	Lt	1673	G
44	Lt	1674	U
44	Lt	1675	G
44	Lt	1676	A
44	Lt	1680	C
44	Lt	1681	U
44	Lt	1689	G
44	Lt	1692	A
44	Lt	1693	C
44	Lt	1694	G
44	Lt	1696	C
44	Lt	1697	C
44	Lt	1700	C
44	Lt	1702	C
44	Lt	1703	C
44	Lt	1704	G

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Mol	Chain	Res	Type
44	Lt	1706	G
44	Lt	1707	A
44	Lt	1708	A
44	Lt	1713	U
44	Lt	1714	C
44	Lt	1716	G
44	Lt	1720	A
44	Lt	1727	G
44	Lt	1732	A
44	Lt	1736	C
44	Lt	1737	G
44	Lt	1738	G
44	Lt	1740	A
44	Lt	1742	U
44	Lt	1743	A
44	Lt	1745	C
44	Lt	1746	U
44	Lt	1748	U
44	Lt	1749	G
44	Lt	1750	A
44	Lt	1753	C
44	Lt	1755	C
44	Lt	1760	G
44	Lt	1761	G
44	Lt	1764	G
44	Lt	1767	A
44	Lt	1769	A
44	Lt	1772	C
44	Lt	1773	C
44	Lt	1780	G
44	Lt	1785	U
44	Lt	1786	U
44	Lt	1793	G
44	Lt	1794	U
44	Lt	1795	G
44	Lt	1797	A
44	Lt	1798	U
44	Lt	1801	A
44	Lt	1802	U
44	Lt	1803	G
44	Lt	1807	C
44	Lt	1808	A

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Mol	Chain	Res	Type
44	Lt	1809	A
44	Lt	1811	G
44	Lt	1812	A
44	Lt	1814	G
44	Lt	1822	U
44	Lt	1823	G
44	Lt	1824	U
44	Lt	1832	C
44	Lt	1833	G
44	Lt	1835	G
44	Lt	1840	C
44	Lt	1843	G
44	Lt	1844	A
44	Lt	1849	C
44	Lt	1850	C
44	Lt	1852	G
44	Lt	1853	C
44	Lt	1859	G
44	Lt	1860	A
44	Lt	1861	A
44	Lt	1862	C
44	Lt	1863	G
44	Lt	1864	G
44	Lt	1865	G
44	Lt	1866	C
44	Lt	1867	G
44	Lt	1870	G
44	Lt	1873	C
44	Lt	1878	A
44	Lt	1879	G
44	Lt	1880	C
44	Lt	1881	G
44	Lt	1882	G
44	Lt	1883	G
44	Lt	1885	C
44	Lt	1886	A
44	Lt	1887	A
44	Lt	1888	G
44	Lt	1889	A
44	Lt	1890	A
44	Lt	1891	G
44	Lt	1892	A

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Mol	Chain	Res	Type
44	Lt	1899	U
44	Lt	1900	G
44	Lt	1901	A
44	Lt	1902	G
44	Lt	1906	G
44	Lt	1907	A
44	Lt	1910	C
44	Lt	1911	C
44	Lt	1912	A
44	Lt	1915	C
44	Lt	1917	G
44	Lt	1919	G
44	Lt	1923	G
44	Lt	1928	G
44	Lt	1929	C
44	Lt	1930	G
44	Lt	1932	G
44	Lt	1934	C
44	Lt	1935	G
44	Lt	1936	G
44	Lt	1940	G
44	Lt	1941	C
44	Lt	1942	G
44	Lt	1943	C
44	Lt	1944	A
44	Lt	1945	G
44	Lt	1946	C
44	Lt	1947	G
44	Lt	1948	C
44	Lt	1949	A
44	Lt	1950	C
44	Lt	1952	G
44	Lt	1953	G
44	Lt	1954	G
44	Lt	1955	G
44	Lt	1956	A
44	Lt	1957	G
44	Lt	1959	C
44	Lt	1960	C
44	Lt	1961	G
44	Lt	1962	C
44	Lt	1963	G

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Mol	Chain	Res	Type
44	Lt	1964	C
44	Lt	1965	C
44	Lt	1966	C
44	Lt	1967	C
44	Lt	1968	U
44	Lt	1970	A
44	Lt	1972	A
44	Lt	1973	C
44	Lt	1974	A
44	Lt	1975	C
44	Lt	1976	C
44	Lt	1977	C
44	Lt	1978	U
44	Lt	1979	G
44	Lt	1980	A
44	Lt	1981	C
44	Lt	1982	G
44	Lt	1983	G
44	Lt	1984	C
44	Lt	1985	C
44	Lt	1987	C
44	Lt	1988	C
44	Lt	1989	G
44	Lt	1990	C
44	Lt	1991	C
44	Lt	1992	G
44	Lt	1993	C
44	Lt	2000	C
44	Lt	2001	A
44	Lt	2008	C
44	Lt	2009	G
44	Lt	2010	C
44	Lt	2012	C
44	Lt	2017	A
44	Lt	2018	C
44	Lt	2022	C
44	Lt	2023	C
44	Lt	2028	C
44	Lt	2030	G
44	Lt	2031	G
44	Lt	2032	G
44	Lt	2033	A

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Mol	Chain	Res	Type
44	Lt	2038	G
44	Lt	2041	U
44	Lt	2042	G
44	Lt	2043	G
44	Lt	2047	G
44	Lt	2048	G
44	Lt	2050	G
44	Lt	2051	C
44	Lt	2059	A
44	Lt	2060	C
44	Lt	2061	A
44	Lt	2065	G
44	Lt	2066	A
44	Lt	2067	C
44	Lt	2068	C
44	Lt	2071	A
44	Lt	2072	G
44	Lt	2073	G
44	Lt	2075	G
44	Lt	2076	U
44	Lt	2079	C
44	Lt	2080	A
44	Lt	2081	C
44	Lt	2082	G
44	Lt	2089	U
44	Lt	2090	C
44	Lt	2091	A
44	Lt	2093	C
44	Lt	2094	G
44	Lt	2095	A
44	Lt	2100	G
44	Lt	2101	G
44	Lt	2102	A
44	Lt	2104	A
44	Lt	2105	C
44	Lt	2108	C
44	Lt	2109	C
44	Lt	2112	C
44	Lt	2113	G
44	Lt	2114	G
44	Lt	2115	A
44	Lt	2118	A

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Mol	Chain	Res	Type
44	Lt	2120	A
44	Lt	2124	G
44	Lt	2127	C
44	Lt	2128	A
44	Lt	2129	A
44	Lt	2130	G
44	Lt	2131	C
44	Lt	2137	C
44	Lt	2138	G
44	Lt	2140	C
44	Lt	2143	G
44	Lt	2151	C
44	Lt	2152	G
44	Lt	2153	U
44	Lt	2154	G
44	Lt	2161	C
44	Lt	2163	G
44	Lt	2164	G
44	Lt	2165	C
44	Lt	2168	C
44	Lt	2177	G
44	Lt	2179	C
44	Lt	2183	C
44	Lt	2184	C
44	Lt	2185	G
44	Lt	2186	A
44	Lt	2195	C
44	Lt	2196	G
44	Lt	2200	C
44	Lt	2201	G
44	Lt	2202	G
44	Lt	2205	G
44	Lt	2207	G
44	Lt	2212	C
44	Lt	2213	G
44	Lt	2216	G
44	Lt	2217	G
44	Lt	2218	U
44	Lt	2219	G
44	Lt	2220	G
44	Lt	2222	A
44	Lt	2223	G

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Mol	Chain	Res	Type
44	Lt	2224	A
44	Lt	2225	A
44	Lt	2226	A
44	Lt	2227	A
44	Lt	2230	U
44	Lt	2231	A
44	Lt	2233	C
44	Lt	2234	A
44	Lt	2235	C
44	Lt	2237	G
44	Lt	2239	G
44	Lt	2240	A
44	Lt	2241	U
44	Lt	2242	A
44	Lt	2243	A
44	Lt	2244	C
44	Lt	2245	U
44	Lt	2246	G
44	Lt	2247	G
44	Lt	2249	U
44	Lt	2250	U
44	Lt	2254	G
44	Lt	2255	C
44	Lt	2260	G
44	Lt	2261	A
44	Lt	2264	G
44	Lt	2268	G
44	Lt	2270	A
44	Lt	2272	C
44	Lt	2273	G
44	Lt	2275	C
44	Lt	2276	G
44	Lt	2279	G
44	Lt	2280	C
44	Lt	2281	U
44	Lt	2285	U
44	Lt	2286	G
44	Lt	2289	C
44	Lt	2290	C
44	Lt	2291	U
44	Lt	2292	U
44	Lt	2294	G

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Mol	Chain	Res	Type
44	Lt	2296	U
44	Lt	2298	U
44	Lt	2300	G
44	Lt	2301	G
44	Lt	2308	C
44	Lt	2310	A
44	Lt	2311	C
44	Lt	2315	C
44	Lt	2317	G
44	Lt	2318	C
44	Lt	2321	G
44	Lt	2323	A
44	Lt	2330	C
44	Lt	2334	A
44	Lt	2335	G
44	Lt	2339	C
44	Lt	2340	G
44	Lt	2341	G
44	Lt	2343	U
44	Lt	2348	C
44	Lt	2353	G
44	Lt	2354	U
44	Lt	2355	U
44	Lt	2356	C
44	Lt	2357	A
44	Lt	2358	A
44	Lt	2360	G
44	Lt	2363	U
44	Lt	2364	C
44	Lt	2365	G
44	Lt	2367	G
44	Lt	2368	A
44	Lt	2369	G
44	Lt	2372	G
44	Lt	2373	G
44	Lt	2376	U
44	Lt	2377	U
44	Lt	2381	C
44	Lt	2393	A
44	Lt	2394	G
44	Lt	2395	G
44	Lt	2397	U

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Mol	Chain	Res	Type
44	Lt	2400	U
44	Lt	2401	U
44	Lt	2405	C
44	Lt	2406	C
44	Lt	2412	G
44	Lt	2416	C
44	Lt	2417	C
44	Lt	2418	G
44	Lt	2420	G
44	Lt	2421	G
44	Lt	2424	A
44	Lt	2425	G
44	Lt	2429	A
44	Lt	2430	C
44	Lt	2431	G
44	Lt	2434	G
44	Lt	2437	C
44	Lt	2439	A
44	Lt	2442	A
44	Lt	2446	G
44	Lt	2451	A
44	Lt	2456	C
44	Lt	2457	G
44	Lt	2464	G
44	Lt	2467	G
44	Lt	2470	A
44	Lt	2471	G
44	Lt	2472	C
44	Lt	2473	C
44	Lt	2474	C
44	Lt	2476	G
44	Lt	2486	G
44	Lt	2491	G
44	Lt	2492	G
44	Lt	2495	G
44	Lt	2496	C
44	Lt	2497	G
44	Lt	2500	G
44	Lt	2503	C
44	Lt	2508	G
44	Lt	2509	C
44	Lt	2510	G

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Mol	Chain	Res	Type
44	Lt	2514	G
44	Lt	2515	G
44	Lt	2516	G
44	Lt	2517	G
44	Lt	2523	G
44	Lt	2527	U
44	Lt	2531	C
44	Lt	2532	G
44	Lt	2533	C
44	Lt	2536	C
44	Lt	2538	A
44	Lt	2539	A
44	Lt	2545	C
44	Lt	2546	A
44	Lt	2547	C
44	Lt	2553	C
44	Lt	2565	C
44	Lt	2566	C
44	Lt	2567	G
44	Lt	2568	G
44	Lt	2572	C
44	Lt	2573	G
44	Lt	2575	G
44	Lt	2577	C
44	Lt	2580	A
44	Lt	2581	G
44	Lt	2584	C
44	Lt	2585	C
44	Lt	2586	G
44	Lt	2587	U
44	Lt	2591	C
44	Lt	2592	C
44	Lt	2593	G
44	Lt	2594	U
44	Lt	2595	C
44	Lt	2597	C
44	Lt	2598	C
44	Lt	2602	C
44	Lt	2603	G
44	Lt	2609	C
44	Lt	2610	G
44	Lt	2611	C

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Mol	Chain	Res	Type
44	Lt	2615	G
44	Lt	2616	G
44	Lt	2617	G
44	Lt	2626	C
44	Lt	2627	G
44	Lt	2628	G
44	Lt	2629	C
44	Lt	2630	G
44	Lt	2632	G
44	Lt	2635	G
44	Lt	2638	C
44	Lt	2642	U
44	Lt	2643	A
44	Lt	2649	C
44	Lt	2650	A
44	Lt	2652	A
44	Lt	2653	G
44	Lt	2654	C
44	Lt	2655	C
44	Lt	2657	U
44	Lt	2659	C
44	Lt	2668	G
44	Lt	2674	C
44	Lt	2679	C
44	Lt	2680	U
44	Lt	2681	G
44	Lt	2683	A
44	Lt	2686	G
44	Lt	2687	C
44	Lt	2688	G
44	Lt	2690	G
44	Lt	2691	G
75	St	2	A
75	St	3	U
75	St	4	C
75	St	6	G
75	St	10	G
75	St	11	A
75	St	12	U
75	St	13	C
75	St	17	C
75	St	20	G

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Mol	Chain	Res	Type
75	St	22	G
75	St	24	G
75	St	25	C
75	St	26	G
75	St	30	C
75	St	32	C
75	St	33	U
75	St	34	C
75	St	40	G
75	St	41	G
75	St	43	C
75	St	44	G
75	St	45	A
75	St	46	A
75	St	49	C
75	St	56	G
75	St	60	G
75	St	61	C
75	St	62	U
75	St	63	C
75	St	65	C
75	St	66	C
75	St	67	C
75	St	68	G
75	St	69	G
75	St	71	A
75	St	80	A
75	St	87	A
75	St	91	C
75	St	98	U
75	St	101	A
75	St	102	C
75	St	114	G
75	St	115	U
75	St	117	C
75	St	118	C
75	St	120	G
75	St	121	C
75	St	122	U
75	St	123	A
75	St	124	G
75	St	125	C

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Mol	Chain	Res	Type
75	St	128	G
75	St	129	A
75	St	130	C
75	St	131	A
75	St	137	G
75	St	138	G
75	St	139	C
75	St	141	A
75	St	143	C
75	St	144	C
75	St	146	G
75	St	149	C
75	St	150	C
75	St	151	A
75	St	152	A
75	St	153	G
75	St	154	A
75	St	156	G
75	St	160	G
75	St	161	C
75	St	162	G
75	St	163	C
75	St	164	A
75	St	166	G
75	St	170	G
75	St	173	C
75	St	174	G
75	St	175	C
75	St	176	C
75	St	180	C
75	St	184	C
75	St	187	G
75	St	188	C
75	St	189	A
75	St	192	G
75	St	193	U
75	St	194	G
75	St	196	C
75	St	199	A
75	St	200	G
75	St	201	C
75	St	202	G

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Mol	Chain	Res	Type
75	St	203	A
75	St	204	C
75	St	205	G
75	St	206	G
75	St	207	C
75	St	208	C
75	St	210	G
75	St	217	C
75	St	222	G
75	St	224	G
75	St	228	U
75	St	229	C
75	St	230	A
75	St	231	C
75	St	235	G
75	St	237	C
75	St	242	C
75	St	246	C
75	St	247	G
75	St	249	G
75	St	250	G
75	St	251	C
75	St	257	G
75	St	260	G
75	St	262	C
75	St	263	C
75	St	265	G
75	St	272	G
75	St	274	C
75	St	275	G
75	St	276	G
75	St	283	A
75	St	286	G
75	St	290	G
75	St	291	A
75	St	293	U
75	St	300	A
75	St	303	G
75	St	304	G
75	St	306	C
75	St	309	G
75	St	311	G

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Mol	Chain	Res	Type
75	St	313	G
75	St	314	A
75	St	315	C
75	St	317	G
75	St	319	C
75	St	323	A
75	St	329	A
75	St	330	A
75	St	331	G
75	St	335	G
75	St	336	G
75	St	337	C
75	St	338	A
75	St	339	G
75	St	340	C
75	St	348	G
75	St	351	C
75	St	352	U
75	St	353	U
75	St	354	G
75	St	355	C
75	St	357	C
75	St	360	U
75	St	361	G
75	St	365	G
75	St	366	G
75	St	368	G
75	St	372	G
75	St	374	G
75	St	377	A
75	St	381	A
75	St	382	C
75	St	383	G
75	St	390	G
75	St	392	G
75	St	393	C
75	St	394	G
75	St	396	G
75	St	397	C
75	St	398	G
75	St	399	A
75	St	401	G

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Mol	Chain	Res	Type
75	St	404	G
75	St	405	G
75	St	411	A
75	St	412	G
75	St	418	G
75	St	421	G
75	St	422	C
75	St	424	C
75	St	429	G
75	St	431	G
75	St	435	A
75	St	436	A
75	St	437	G
75	St	438	G
75	St	439	U
75	St	440	C
75	St	441	U
75	St	442	G
75	St	443	U
75	St	444	G
75	St	445	C
75	St	446	C
75	St	447	A
75	St	448	G
75	St	449	C
75	St	452	C
75	St	454	G
75	St	456	G
75	St	457	G
75	St	458	U
75	St	459	A
75	St	460	A
75	St	463	C
75	St	466	G
75	St	468	U
75	St	474	A
75	St	475	G
75	St	483	C
75	St	486	C
75	St	487	G
75	St	488	C
75	St	489	U

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Mol	Chain	Res	Type
75	St	491	C
75	St	492	U
75	St	493	G
75	St	494	C
75	St	499	G
75	St	500	A
75	St	502	A
75	St	503	C
75	St	504	G
75	St	514	G
75	St	515	G
75	St	518	C
75	St	519	C
75	St	521	C
75	St	522	G
75	St	523	C
75	St	524	C
75	St	525	G
75	St	530	G
75	St	534	A
75	St	535	A
75	St	544	G
75	St	545	C
75	St	546	U
75	St	550	G
75	St	552	C
75	St	553	A
75	St	554	G
75	St	557	C
75	St	558	C
75	St	559	G
75	St	560	U
75	St	561	U
75	St	563	G
75	St	567	C
75	St	568	G
75	St	569	C
75	St	570	C
75	St	571	G
75	St	572	C
75	St	577	G
75	St	581	G

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Mol	Chain	Res	Type
75	St	584	C
75	St	585	A
75	St	586	G
75	St	591	C
75	St	592	G
75	St	593	C
75	St	594	G
75	St	595	G
75	St	596	C
75	St	597	G
75	St	598	C
75	St	600	C
75	St	601	C
75	St	602	G
75	St	604	C
75	St	605	G
75	St	606	C
75	St	607	C
75	St	608	G
75	St	609	C
75	St	610	A
75	St	611	G
75	St	614	C
75	St	616	G
75	St	617	A
75	St	618	G
75	St	619	G
75	St	627	G
75	St	630	G
75	St	633	G
75	St	634	C
75	St	635	A
75	St	652	A
75	St	658	G
75	St	659	A
75	St	660	A
75	St	665	G
75	St	667	U
75	St	668	G
75	St	674	G
75	St	677	G
75	St	680	A

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Mol	Chain	Res	Type
75	St	682	C
75	St	683	G
75	St	685	C
75	St	686	G
75	St	687	G
75	St	688	C
75	St	689	C
75	St	694	A
75	St	696	G
75	St	699	C
75	St	702	G
75	St	703	C
75	St	705	A
75	St	713	C
75	St	714	U
75	St	718	U
75	St	720	A
75	St	722	U
75	St	732	A
75	St	736	C
75	St	738	G
75	St	739	G
75	St	742	C
75	St	746	A
75	St	747	A
75	St	751	G
75	St	757	A
75	St	758	C
75	St	759	A
75	St	761	C
75	St	772	C
75	St	774	G
75	St	777	G
75	St	780	A
75	St	782	C
75	St	783	G
75	St	784	G
75	St	785	U
75	St	786	G
75	St	793	C
75	St	794	G
75	St	796	G

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Mol	Chain	Res	Type
75	St	797	G
75	St	798	C
75	St	801	G
75	St	804	C
75	St	806	C
75	St	807	G
75	St	808	C
75	St	809	G
75	St	810	U
75	St	811	C
75	St	814	G
75	St	815	C
75	St	823	C
75	St	824	C
75	St	825	A
75	St	829	A
75	St	830	A
75	St	833	C
75	St	835	G
75	St	836	G
75	St	837	A
75	St	838	G
75	St	840	C
75	St	841	U
75	St	842	C
75	St	843	C
75	St	844	G
75	St	845	G
75	St	846	G
75	St	848	U
75	St	852	G
75	St	853	G
75	St	855	G
75	St	868	A
75	St	870	G
75	St	873	U
75	St	884	G
75	St	887	A
75	St	890	G
75	St	894	G
75	St	895	A
75	St	898	G

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Mol	Chain	Res	Type
75	St	899	G
75	St	902	C
75	St	903	C
75	St	904	A
75	St	906	C
75	St	907	A
75	St	910	C
75	St	911	G
75	St	916	G
75	St	917	U
75	St	918	C
75	St	919	U
75	St	924	C
75	St	926	C
75	St	929	U
75	St	930	C
75	St	937	A
75	St	938	A
75	St	940	G
75	St	944	G
75	St	945	C
75	St	951	A
75	St	953	C
75	St	954	A
75	St	958	C
75	St	960	G
75	St	961	G
75	St	964	G
75	St	965	C
75	St	966	G
75	St	969	G
75	St	970	A
75	St	971	G
75	St	972	G
75	St	973	A
75	St	975	C
75	St	976	G
75	St	978	C
75	St	979	A
75	St	980	G
75	St	984	G
75	St	985	G

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Mol	Chain	Res	Type
75	St	986	C
75	St	987	G
75	St	988	C
75	St	995	G
75	St	997	G
75	St	998	A
75	St	1000	C
75	St	1001	G
75	St	1002	C
75	St	1003	G
75	St	1005	G
75	St	1007	G
75	St	1009	G
75	St	1012	G
75	St	1015	G
75	St	1016	C
75	St	1026	C
75	St	1027	C
75	St	1028	C
75	St	1029	A
75	St	1030	G
75	St	1034	G
75	St	1040	C
75	St	1043	G
75	St	1047	U
75	St	1048	C
75	St	1049	U
75	St	1052	U
75	St	1054	C
75	St	1055	A
75	St	1056	U
75	St	1057	U
75	St	1060	G
75	St	1061	A
75	St	1062	C
75	St	1063	A
75	St	1067	A
75	St	1068	G
75	St	1069	C
75	St	1079	G
75	St	1080	C
75	St	1083	C

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Mol	Chain	Res	Type
75	St	1087	C
75	St	1088	G
75	St	1089	C
75	St	1090	C
75	St	1091	G
75	St	1093	G
75	St	1094	G
75	St	1096	A
75	St	1098	G
75	St	1099	G
75	St	1103	G
75	St	1105	G
75	St	1106	G
75	St	1107	C
75	St	1109	G
75	St	1110	C
75	St	1111	G
75	St	1112	G
75	St	1114	A
75	St	1115	G
75	St	1116	G
75	St	1117	A
75	St	1118	C
75	St	1120	G
75	St	1121	C
75	St	1122	G
75	St	1124	G
75	St	1125	G
75	St	1127	G
75	St	1128	A
75	St	1132	C
75	St	1133	A
75	St	1134	G
75	St	1135	G
75	St	1137	C
75	St	1138	U
75	St	1139	G
75	St	1141	G
75	St	1150	A
75	St	1151	G
75	St	1152	A
75	St	1153	C

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Mol	Chain	Res	Type
75	St	1154	G
75	St	1157	C
75	St	1160	G
75	St	1161	G
75	St	1162	C
75	St	1163	C
75	St	1164	G
75	St	1165	C
75	St	1166	A
75	St	1168	G
75	St	1175	A
75	St	1177	A
75	St	1179	U
75	St	1180	G
75	St	1181	G
75	St	1182	C
75	St	1184	G
75	St	1185	G
75	St	1188	C
75	St	1189	A
75	St	1190	G
75	St	1192	C
75	St	1194	G
75	St	1195	C
75	St	1198	C
75	St	1202	C
75	St	1204	G
75	St	1206	A
75	St	1208	G
75	St	1209	C
75	St	1210	G
75	St	1211	C
75	St	1212	G
75	St	1213	G
75	St	1214	A
75	St	1215	G
75	St	1223	C
75	St	1224	G
75	St	1225	U
75	St	1226	G
75	St	1227	G
75	St	1228	C

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Mol	Chain	Res	Type
75	St	1230	G
75	St	1232	G
75	St	1235	C
75	St	1237	C
75	St	1240	G
75	St	1241	C
75	St	1242	U
75	St	1243	G
75	St	1246	A
75	St	1247	C
75	St	1248	G
75	St	1253	C
75	St	1254	G
75	St	1255	C
75	St	1256	G
75	St	1257	C
75	St	1259	C
75	St	1261	A
75	St	1262	G
75	St	1263	G
75	St	1266	U
75	St	1267	G
75	St	1271	U
75	St	1272	G
75	St	1273	U
75	St	1278	G
75	St	1279	C
75	St	1285	C
75	St	1287	C
75	St	1288	A
75	St	1289	C
75	St	1290	C
75	St	1293	G
75	St	1295	G
75	St	1296	C
75	St	1297	C
75	St	1301	C
75	St	1305	U
75	St	1306	C
75	St	1307	C
75	St	1310	G
75	St	1314	C

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Mol	Chain	Res	Type
75	St	1319	A
75	St	1321	A
75	St	1322	C
75	St	1323	A
75	St	1324	C
75	St	1325	C
75	St	1345	U
75	St	1346	G
75	St	1348	G
75	St	1350	G
75	St	1351	C
75	St	1353	G
75	St	1359	A
75	St	1367	G
75	St	1369	A
75	St	1370	C
75	St	1371	G
75	St	1372	C
75	St	1373	G
75	St	1375	G
75	St	1376	A
75	St	1377	A
75	St	1380	G
75	St	1384	C
75	St	1386	A
75	St	1391	C
75	St	1393	G
75	St	1398	U
75	St	1399	G
75	St	1400	G
75	St	1401	A
75	St	1403	G
75	St	1405	A
75	St	1407	G
75	St	1408	A
75	St	1410	A
75	St	1411	A
75	St	1412	G
75	St	1413	U
75	St	1415	G
75	St	1417	A
75	St	1421	A

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Mol	Chain	Res	Type
75	St	1423	G
75	St	1424	U
75	St	1425	A
75	St	1426	U
75	St	1427	C
75	St	1430	U
75	St	1433	G
75	St	1435	G
75	St	1436	A
75	St	1437	A
75	St	1438	C
75	St	1446	U
75	St	1447	G
75	St	1448	G
75	St	1449	A
75	St	1450	U
75	St	1451	C
75	St	1452	C

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	LD	23	U
4	LD	39	C
4	LD	40	G
4	LD	49	G
4	LD	59	G
4	LD	76	C
4	LD	87	A
4	LD	111	C
4	LD	117	C
4	LD	118	C
5	LE	38	U
5	LE	50	A
5	LE	110	U
5	LE	114	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

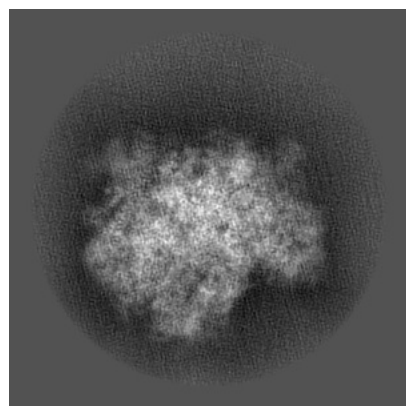
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16222. These allow visual inspection of the internal detail of the map and identification of artifacts.

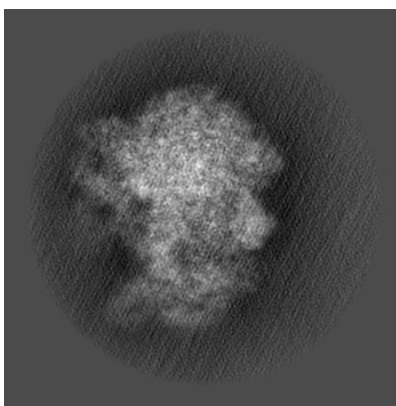
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

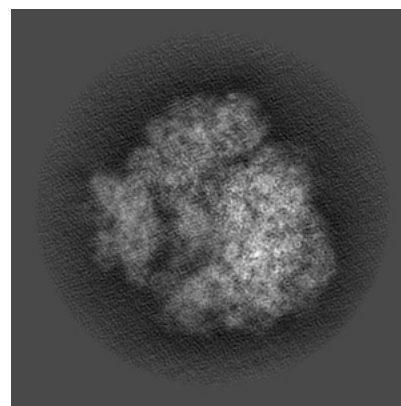
6.1.1 Primary map



X

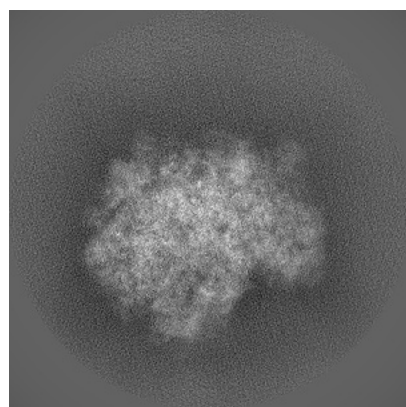


Y

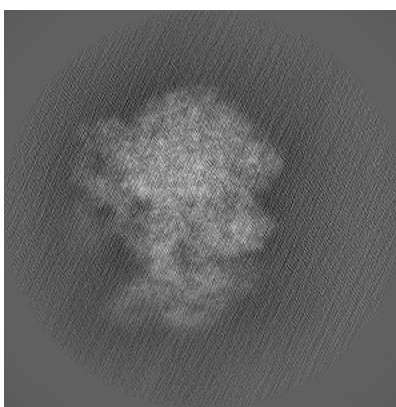


Z

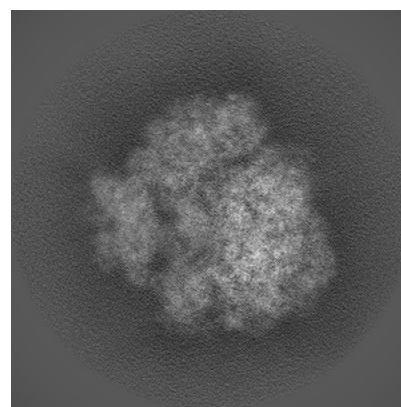
6.1.2 Raw map



X



Y

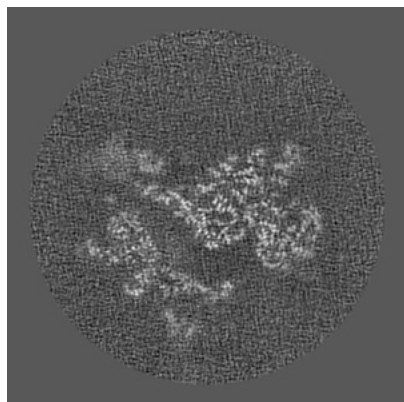


Z

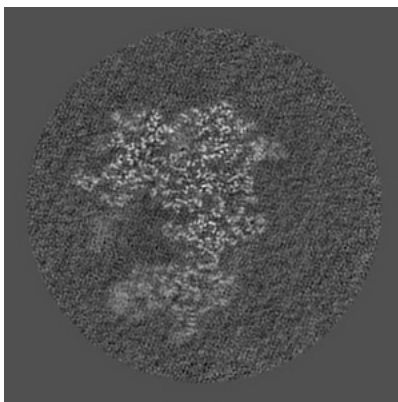
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

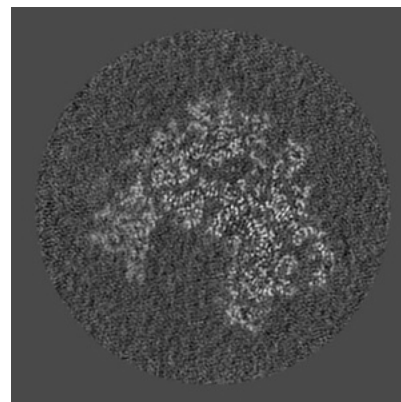
6.2.1 Primary map



X Index: 250

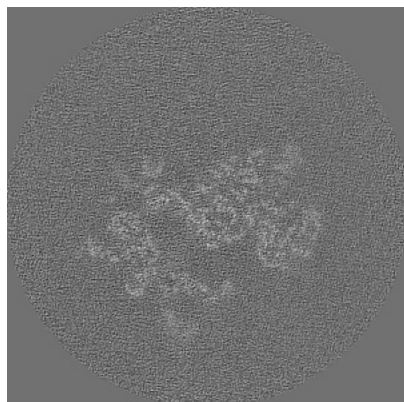


Y Index: 250

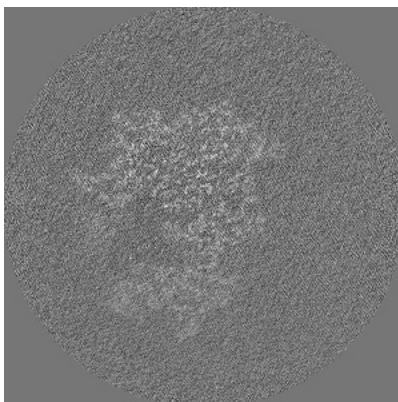


Z Index: 250

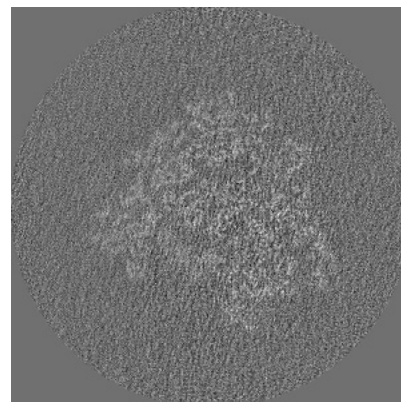
6.2.2 Raw map



X Index: 250



Y Index: 250

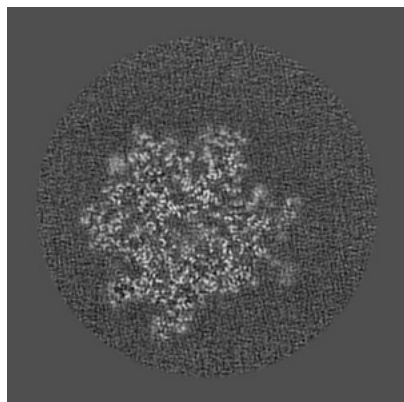


Z Index: 250

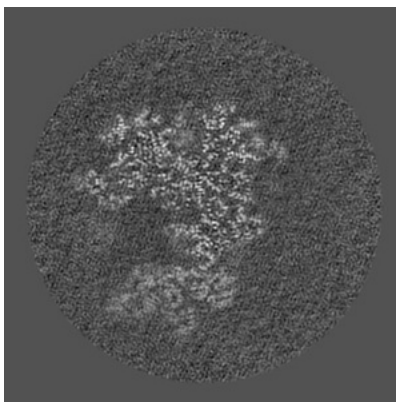
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

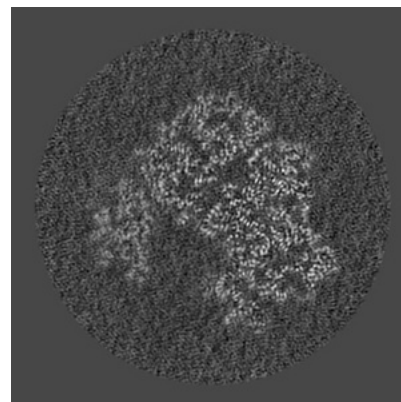
6.3.1 Primary map



X Index: 314

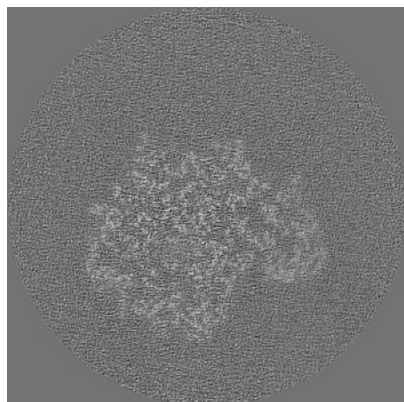


Y Index: 255

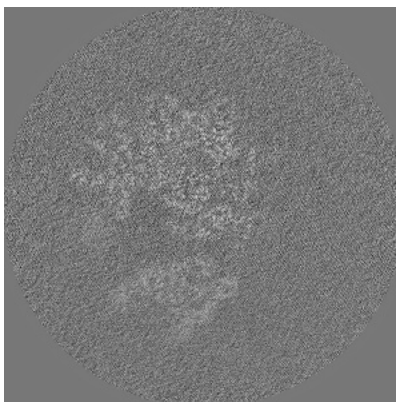


Z Index: 240

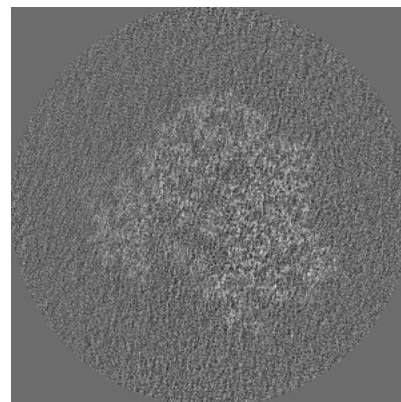
6.3.2 Raw map



X Index: 285



Y Index: 241

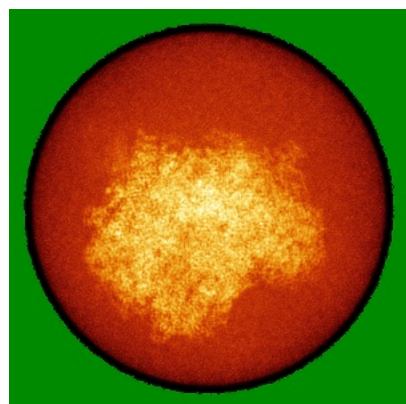


Z Index: 240

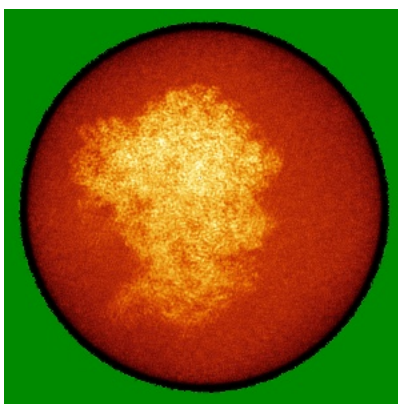
The images above show the largest variance slices of the map in three orthogonal directions.

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

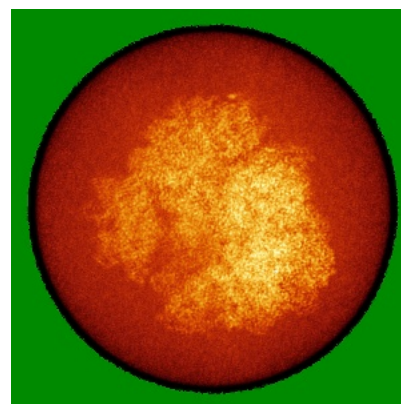
6.4.1 Primary map



X

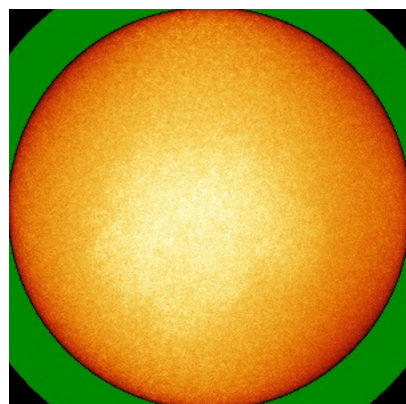


Y

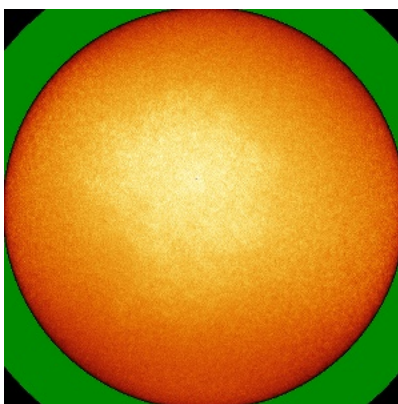


Z

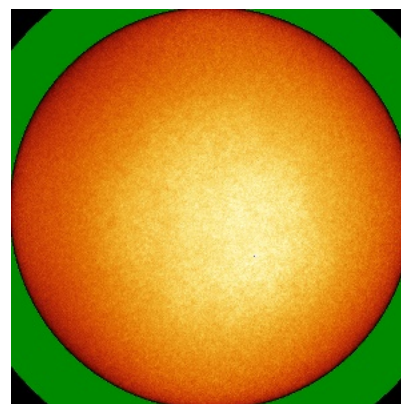
6.4.2 Raw map



X



Y

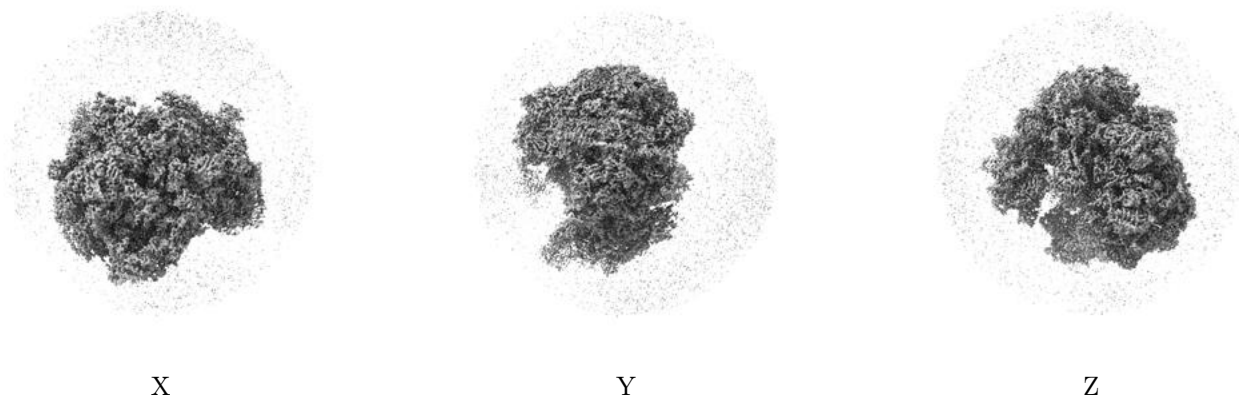


Z

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

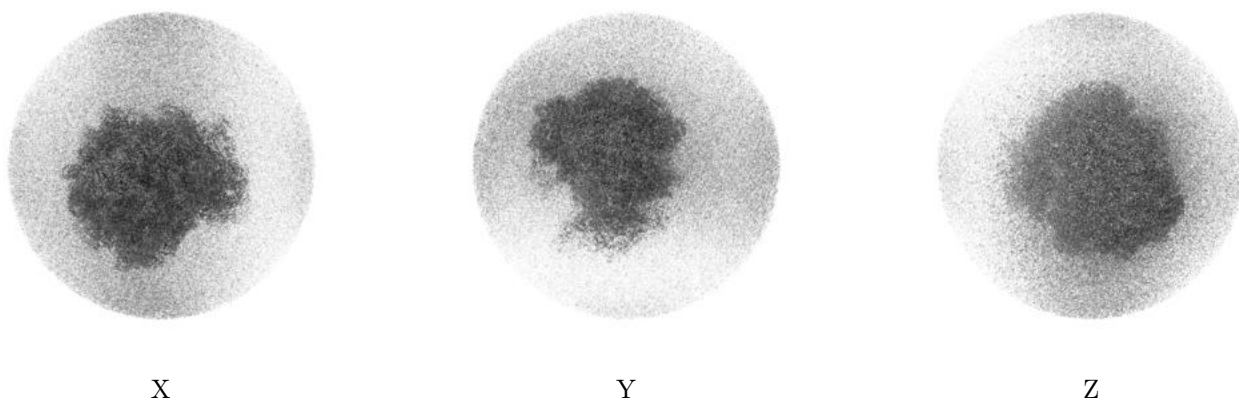
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.84. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

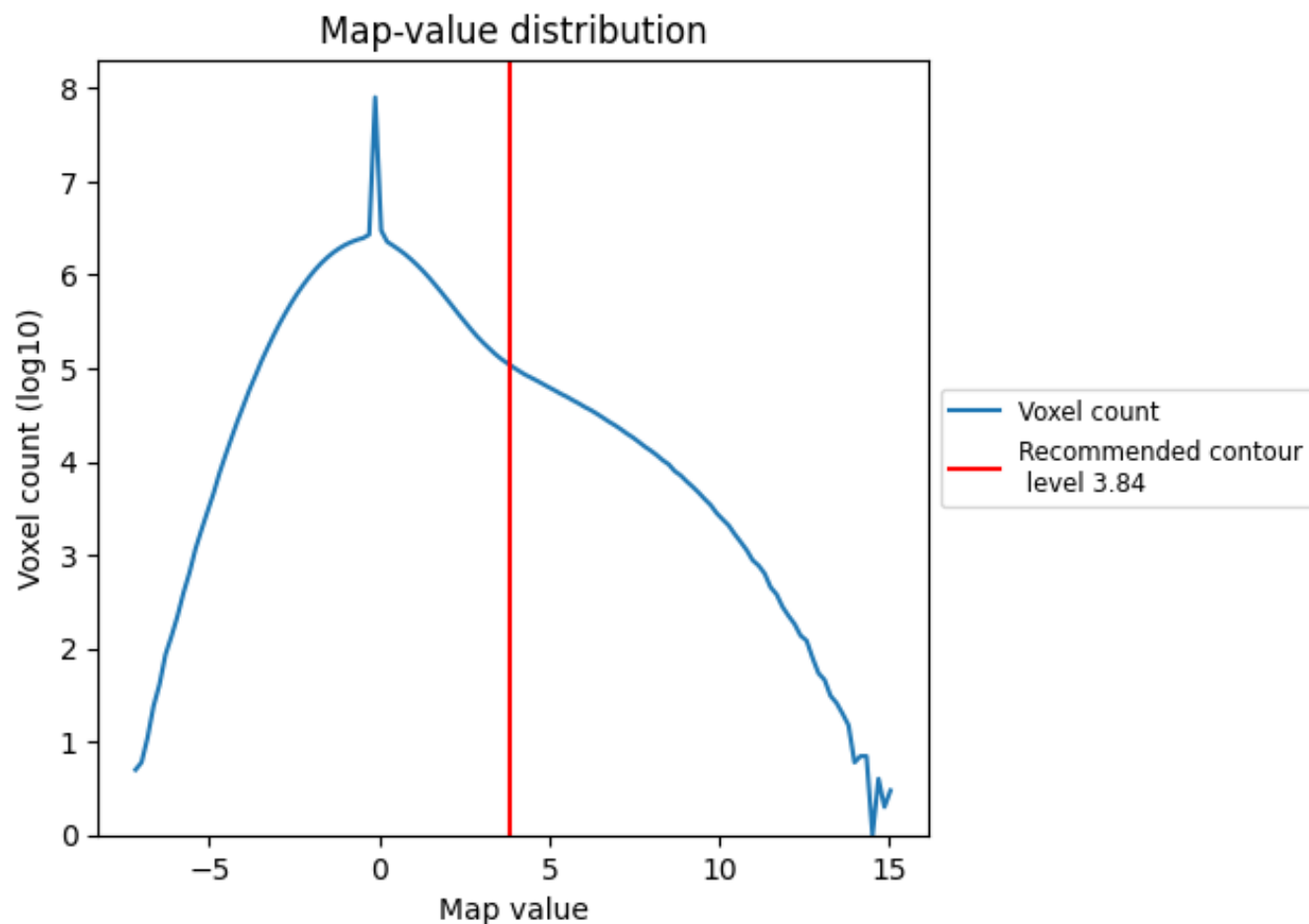
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

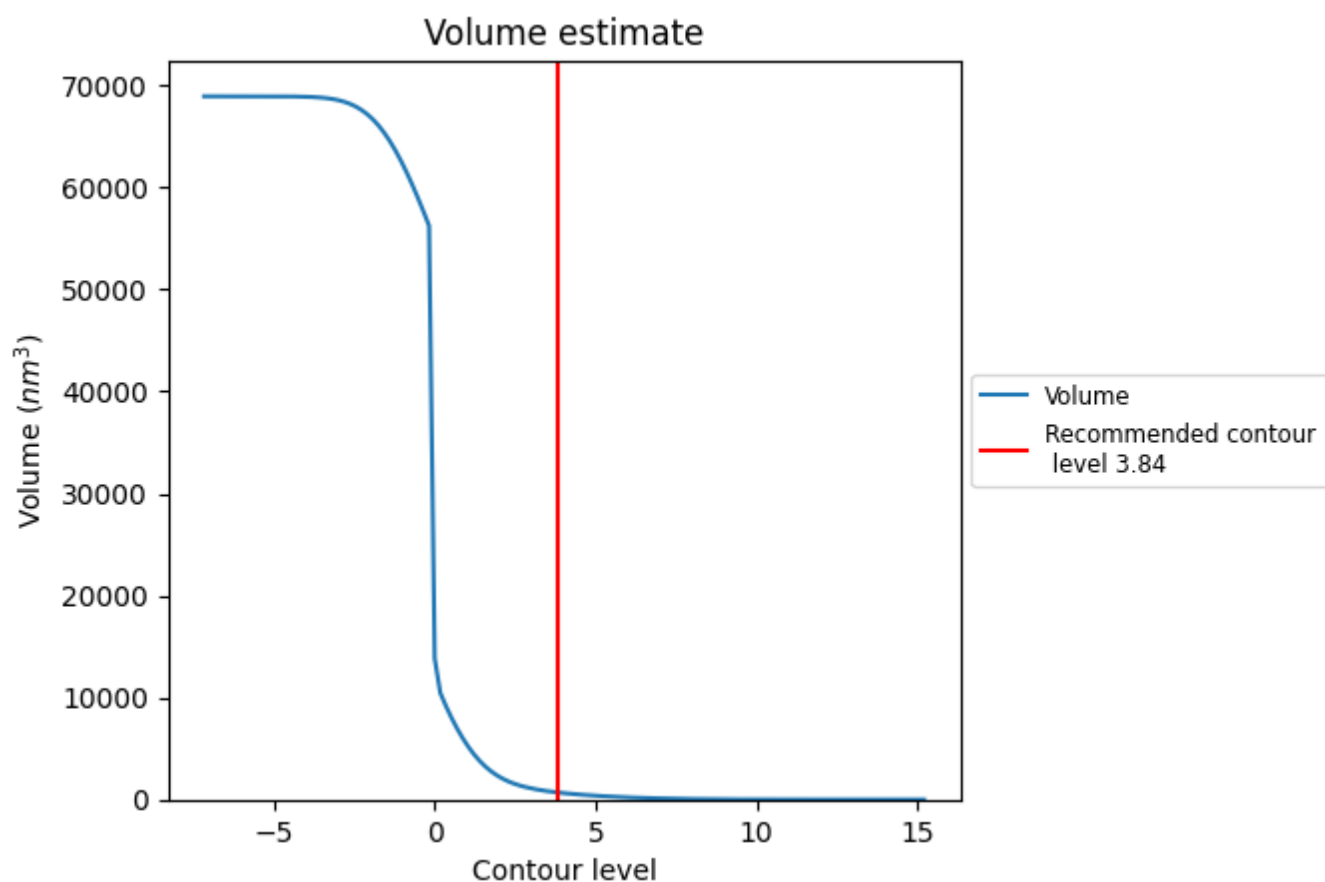
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

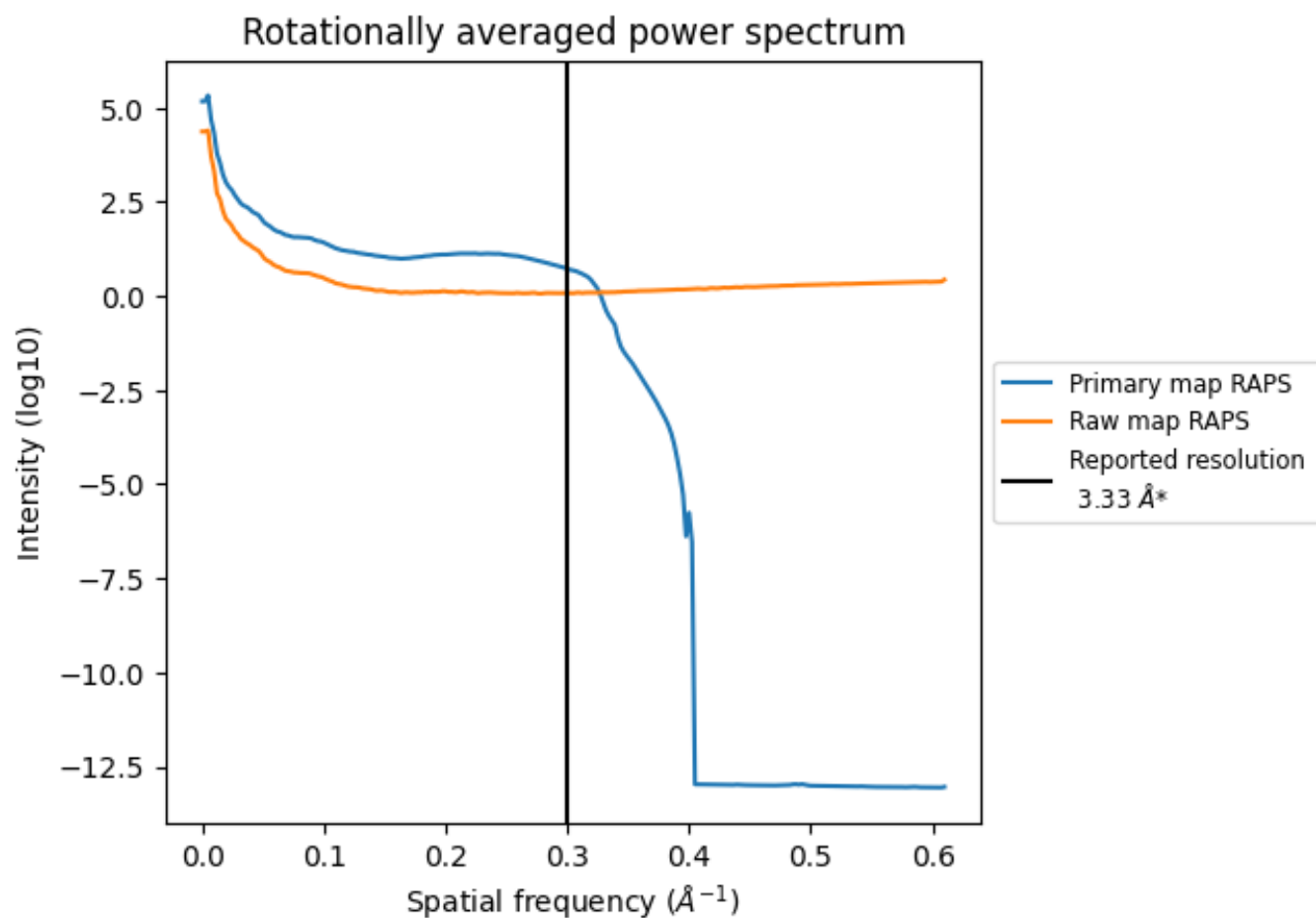
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 690 nm³; this corresponds to an approximate mass of 623 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 [i](#)

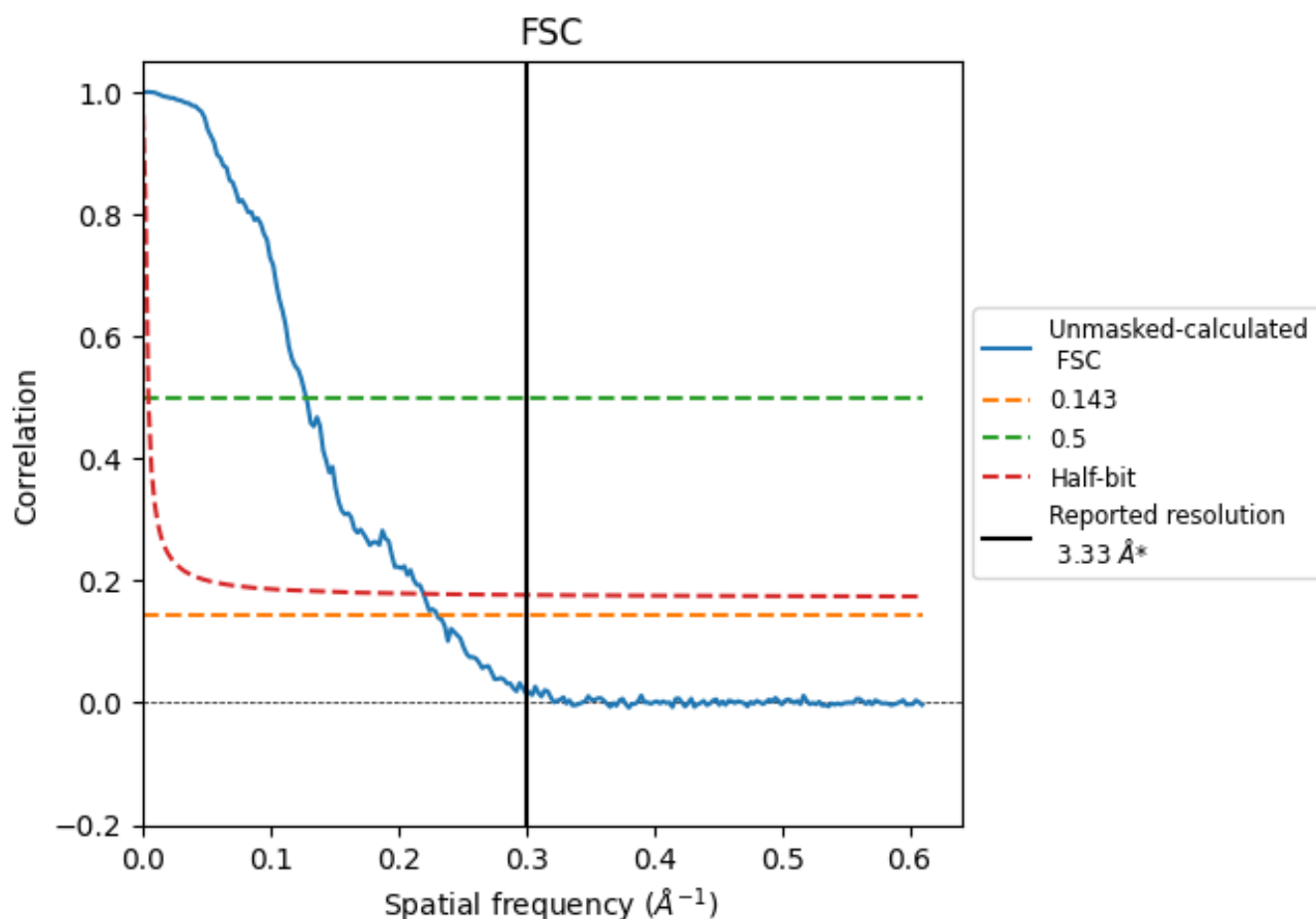


*Reported resolution corresponds to spatial frequency of 0.300 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.300 Å⁻¹

8.2 Resolution estimates [i](#)

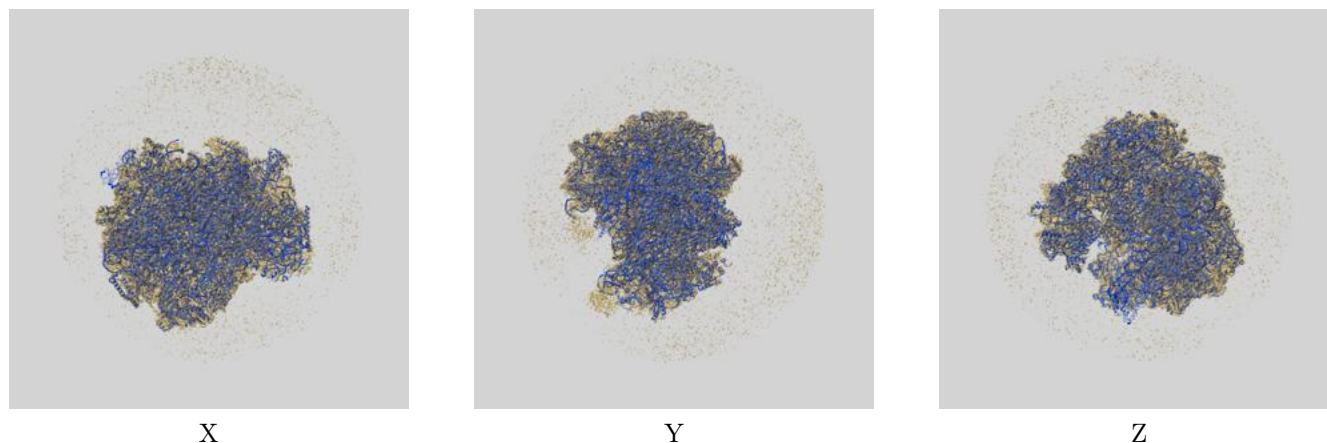
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.33	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.33	7.81	4.55

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.33 differs from the reported value 3.33 by more than 10 %

9 Map-model fit [i](#)

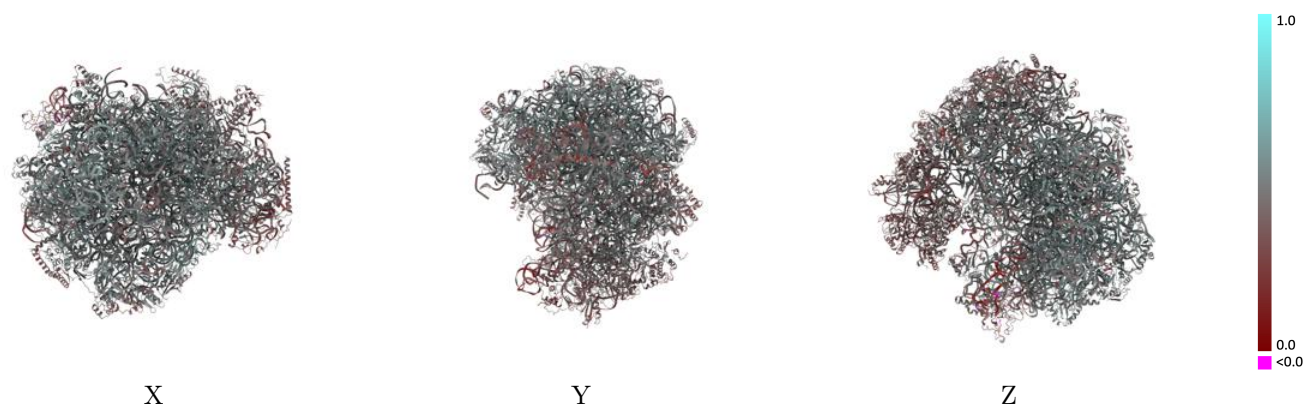
This section contains information regarding the fit between EMDB map EMD-16222 and PDB model 8BRM. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



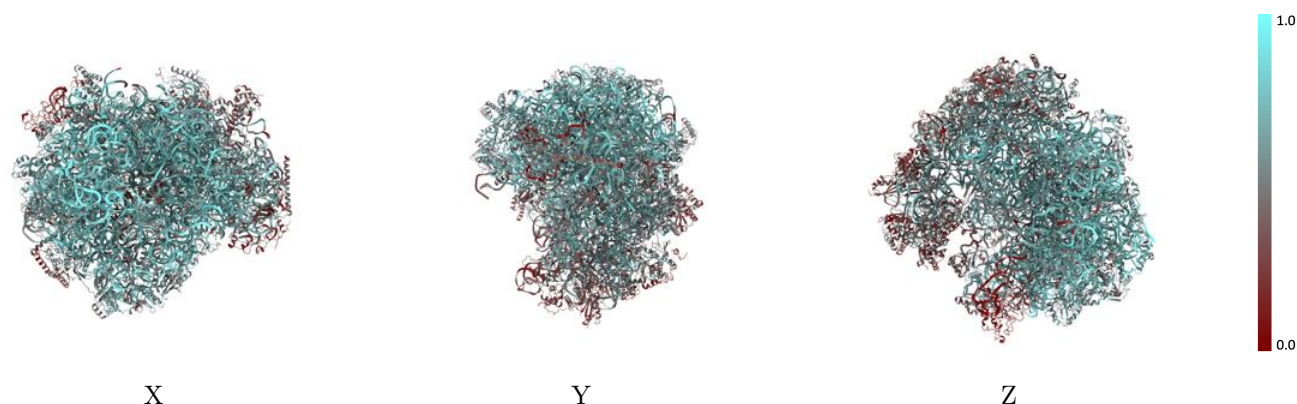
The images above show the 3D surface view of the map at the recommended contour level 3.84 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



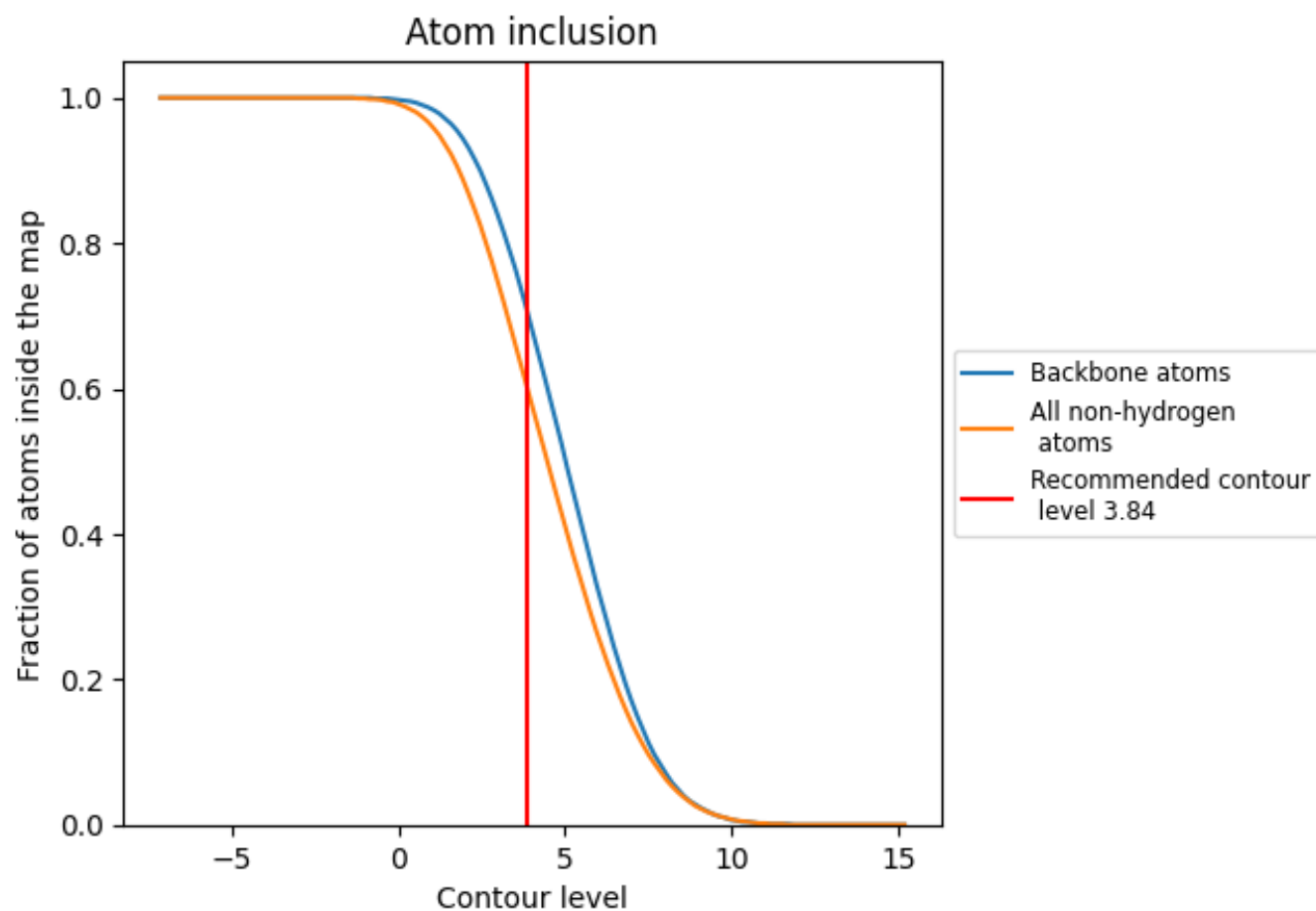
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.84).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 61% 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 (3.84) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6060	 0.4620
LA	 0.6240	 0.5340
LB	 0.6190	 0.5110
LC	 0.6410	 0.5090
LD	 0.8070	 0.5040
LE	 0.7330	 0.4610
LF	 0.4280	 0.4410
LG	 0.6480	 0.5170
LH	 0.5490	 0.4740
LI	 0.5590	 0.4750
LJ	 0.5570	 0.4720
LK	 0.2640	 0.3980
LL	 0.3910	 0.4250
LM	 0.5840	 0.4930
LN	 0.5890	 0.4600
LO	 0.6810	 0.5340
LP	 0.6170	 0.4810
LQ	 0.5950	 0.4910
LR	 0.5800	 0.5070
LS	 0.5650	 0.4830
LT	 0.6180	 0.4970
LU	 0.5400	 0.4850
LV	 0.5320	 0.4370
LW	 0.6000	 0.4970
LX	 0.5760	 0.4630
LY	 0.6300	 0.5090
LZ	 0.6690	 0.5010
La	 0.5180	 0.4570
Lb	 0.5600	 0.5150
Lc	 0.4200	 0.4750
Ld	 0.5420	 0.4720
Le	 0.6190	 0.5120
Lf	 0.5960	 0.5020
Lg	 0.6560	 0.5220
Lh	 0.6420	 0.5160



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Chain	Atom inclusion	Q-score
Li	 0.5970	 0.4830
Lj	 0.5140	 0.4700
Lk	 0.6340	 0.5170
Ll	 0.4920	 0.4250
Ln	 0.0400	 0.2830
Lo	 0.4430	 0.5050
Lp	 0.3860	 0.4610
Lq	 0.6190	 0.5110
Ls	 0.4570	 0.4570
Lt	 0.7260	 0.4880
SA	 0.4740	 0.4160
SB	 0.5130	 0.4580
SC	 0.3390	 0.3970
SD	 0.5300	 0.4600
SE	 0.4700	 0.4490
SF	 0.3170	 0.3810
SG	 0.3300	 0.3950
SH	 0.3470	 0.3910
SI	 0.5330	 0.4730
SJ	 0.5160	 0.4680
SK	 0.4670	 0.4250
SL	 0.2720	 0.3460
SM	 0.5330	 0.4920
SO	 0.4520	 0.4750
SP	 0.5320	 0.4670
SQ	 0.5540	 0.4650
SR	 0.2040	 0.3380
ST	 0.3000	 0.3600
SU	 0.2750	 0.3520
SV	 0.2610	 0.3570
SW	 0.3030	 0.3480
SX	 0.2930	 0.3810
SY	 0.4600	 0.4340
Sb	 0.3870	 0.4080
Sc	 0.2650	 0.3470
Sd	 0.5470	 0.4780
Se	 0.4300	 0.4350
Sg	 0.3340	 0.3990
Sh	 0.3730	 0.3760
Sj	 0.3420	 0.3940
St	 0.6570	 0.4310